



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 26, 2014 – 07:49 PM GMT

PDB ID : 3OI0  
Title : Structure of the *Thermus thermophilus* 70S ribosome complexed with azithromycin. This file contains the 30S subunit of one 70S ribosome. The entire crystal structure contains two 70S ribosomes.  
Authors : Bulkley, D.P.; Innis, C.A.; Blaha, G.; Steitz, T.A.  
Deposited on : 2010-08-18  
Resolution : 3.00 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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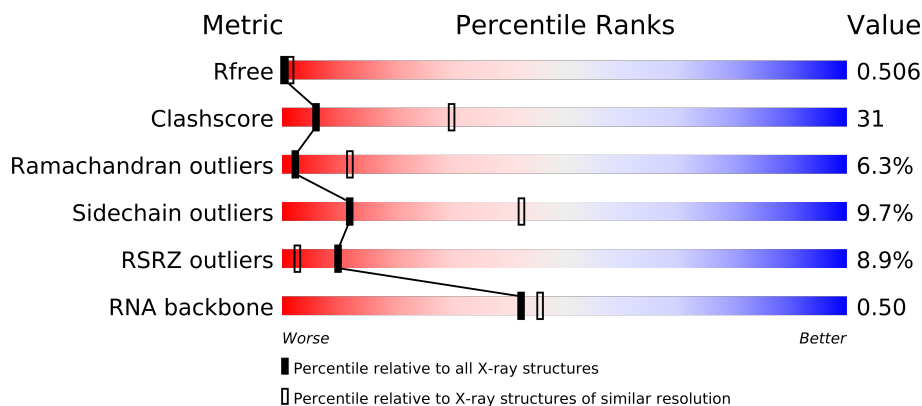
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 3.00 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	66092	1216 (3.00-3.00)
Clashscore	79885	1594 (3.00-3.00)
Ramachandran outliers	78287	1537 (3.00-3.00)
Sidechain outliers	78261	1540 (3.00-3.00)
RSRZ outliers	66119	1217 (3.00-3.00)
RNA backbone	1838	1070 (3.50-2.50)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	1522	
2	B	256	
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	

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Mol	Chain	Length	Quality of chain
12	L	135	<div><div></div></div>
13	M	126	<div><div></div></div>
14	N	61	<div><div></div></div>
15	O	89	<div><div></div></div>
16	P	88	<div><div></div></div>
17	Q	105	<div><div></div></div>
18	R	88	<div><div></div></div>
19	S	93	<div><div></div></div>
20	T	106	<div><div></div></div>
21	U	27	<div><div></div></div>

## 2 Entry composition

There are 23 unique types of molecules in this entry. The entry contains 51469 atoms, of which 0 are hydrogen and 0 are deuterium.

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	1504	Total	C	N	O	P	0	0	0
			32329	14390	5992	10444	1503			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	235	Total	C	N	O	S	0	0	1
			1901	1213	342	341	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
			1011	639	198	174				

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	58	ARG	HIS	CONFLICT	UNP P80374

- 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
			795	499	157	138	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	119	Total	C	N	O	S	0	0	0
			885	549	168	165	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
			971	611	196	163	1			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	2	VAL	-	INSERTION	UNP Q5SHN3
L	3	ALA	-	INSERTION	UNP Q5SHN3
L	4	LEU	-	INSERTION	UNP Q5SHN3

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	115	Total	C	N	O	S	0	0	0
			921	569	190	160	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	1
			824	528	152	142	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	R	70	Total	C	N	O		0	0	0
			574	367	112	95				

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	S	79	Total	C	N	O	S	0	0	1
			630	403	115	110	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 MAGNESIUM ION (three-letter code: MG) (formula: Mg).

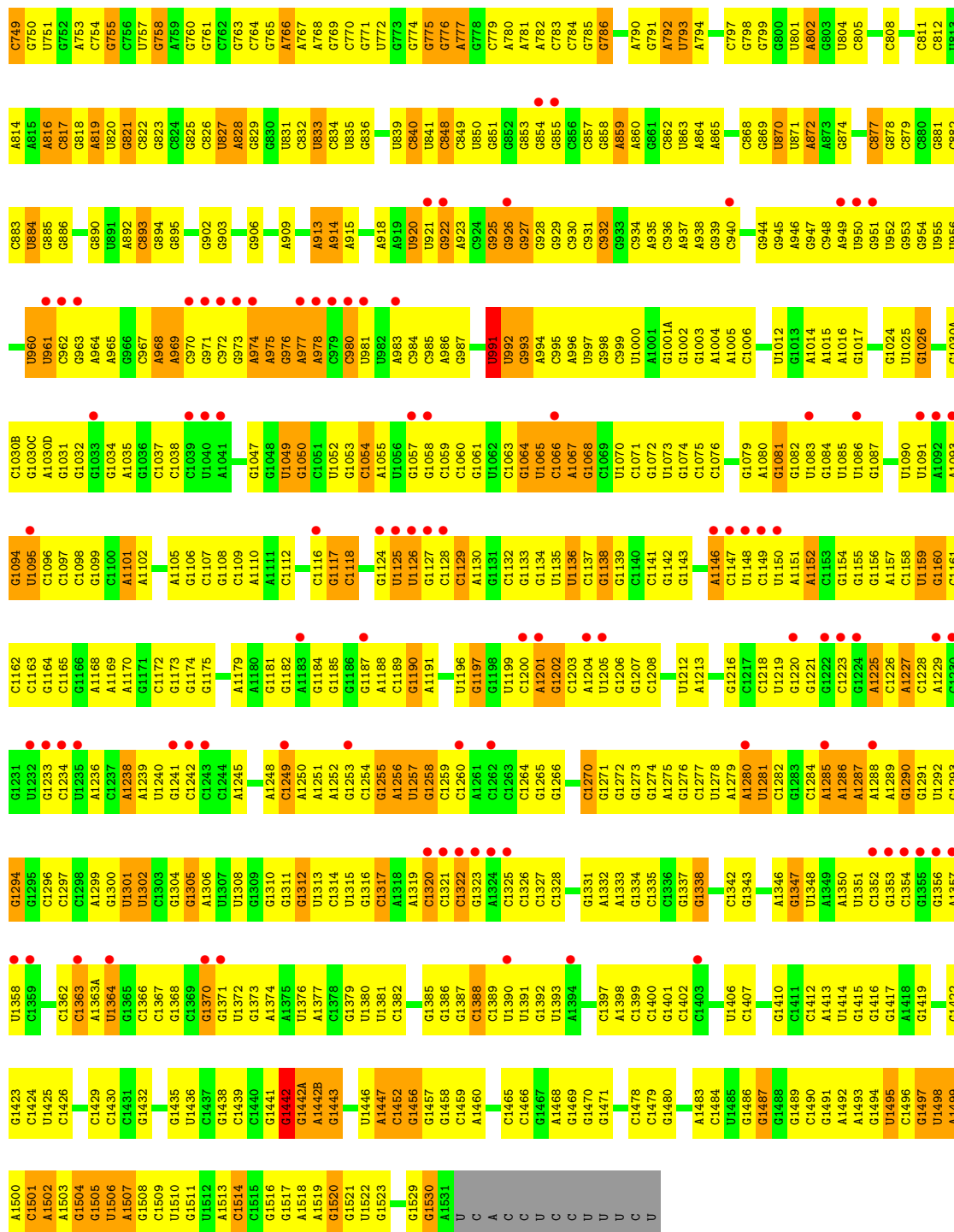
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
22	A	48	Total	Mg	0	0
			48	48		

- Molecule 23 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

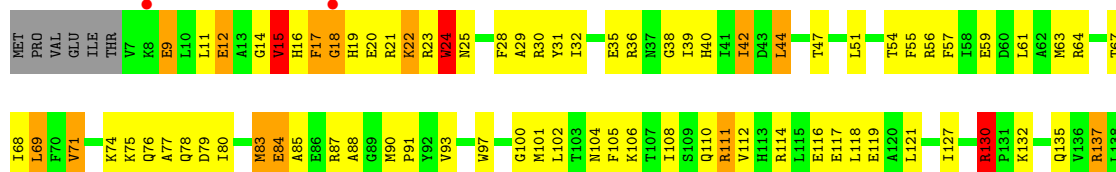


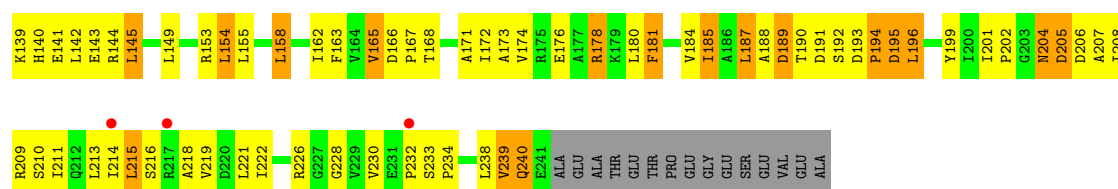




• Molecule 2: 30S ribosomal protein S2

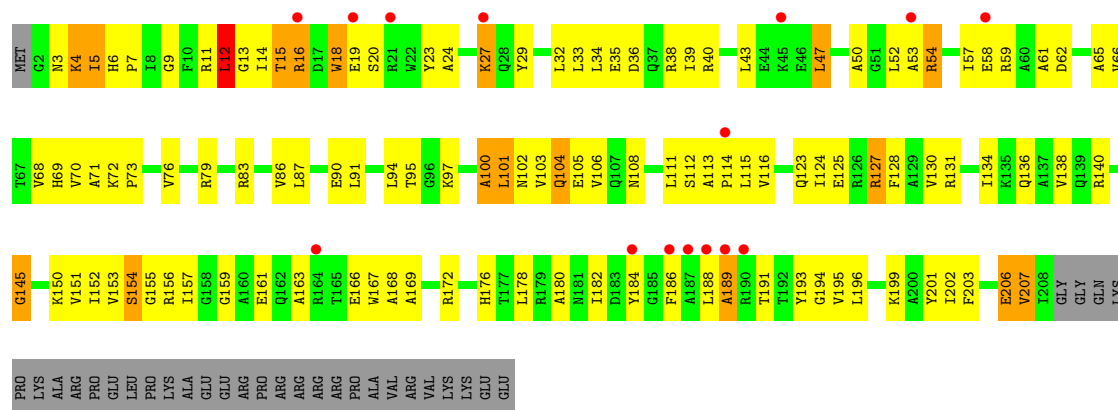
Chain B:

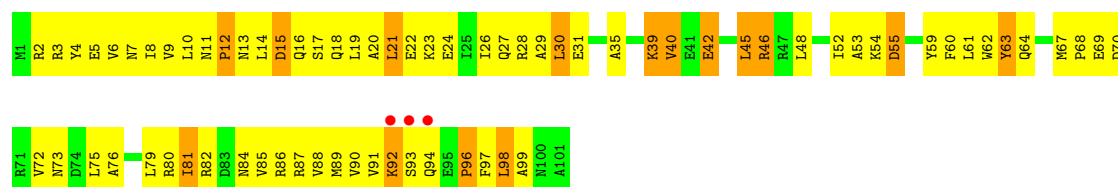




• Molecule 3: 30S ribosomal protein S3

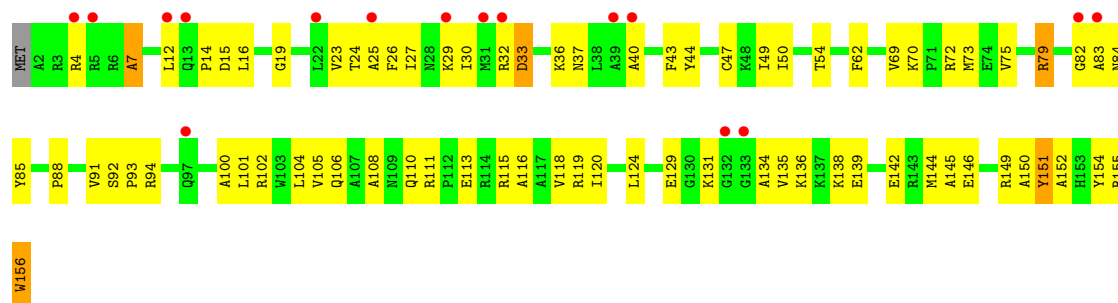
Chain C:





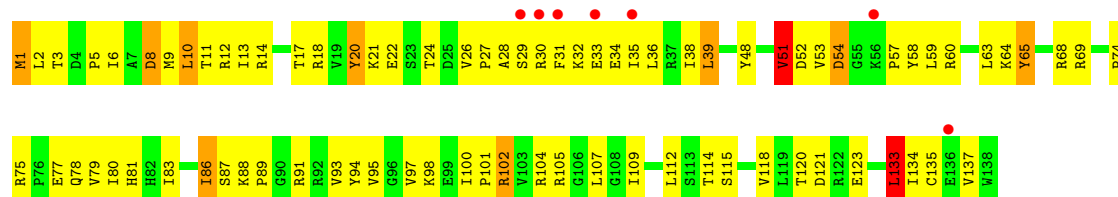
• Molecule 7: 30S ribosomal protein S7

Chain G:



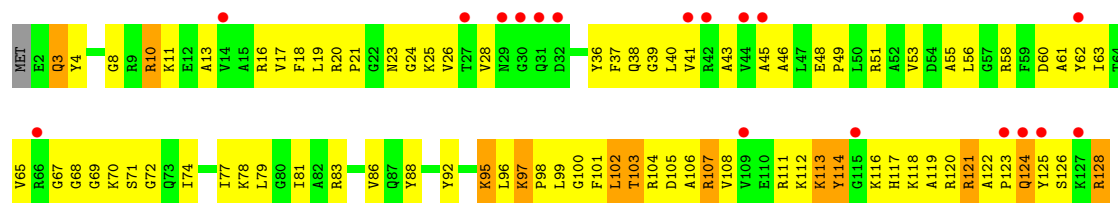
• Molecule 8: 30S ribosomal protein S8

Chain H:



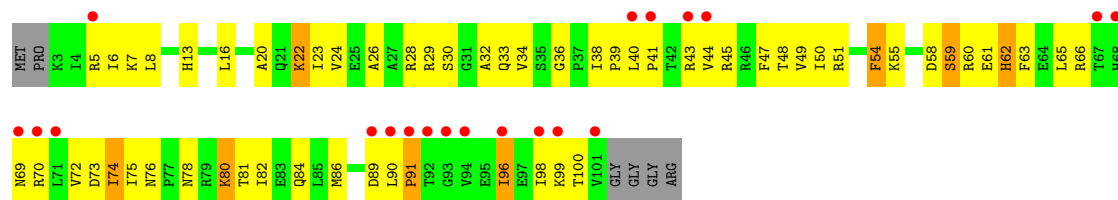
• Molecule 9: 30S ribosomal protein S9

Chain I:



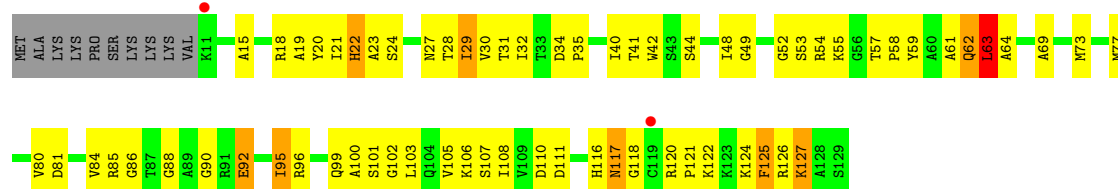
• Molecule 10: 30S ribosomal protein S10

Chain J:



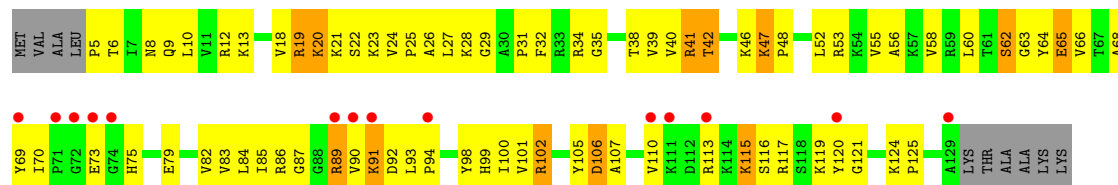
• Molecule 11: 30S ribosomal protein S11

Chain K:



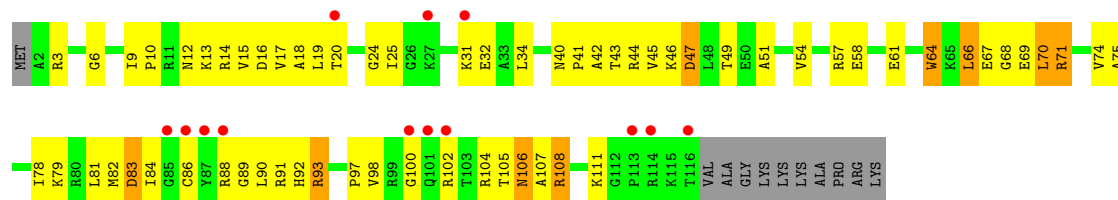
- Molecule 12: 30S ribosomal protein S12

Chain L:



- Molecule 13: 30S ribosomal protein S13

Chain M:



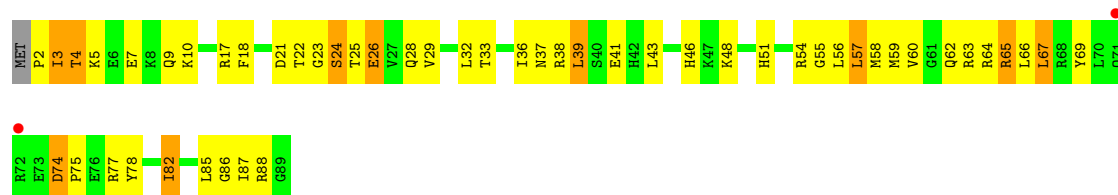
- Molecule 14: 30S ribosomal protein S14

Chain N:



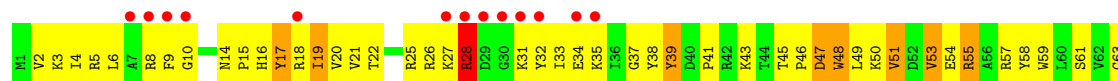
- Molecule 15: 30S ribosomal protein S15

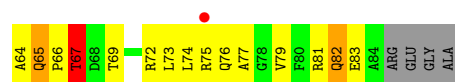
Chain O:



- Molecule 16: 30S ribosomal protein S16

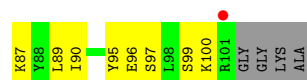
Chain P:





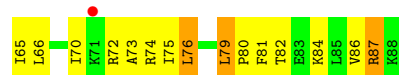
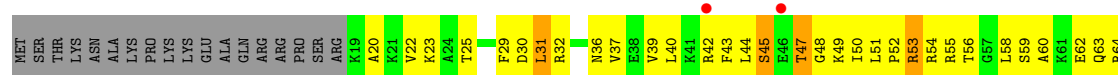
- Molecule 17: 30S ribosomal protein S17

Chain Q:



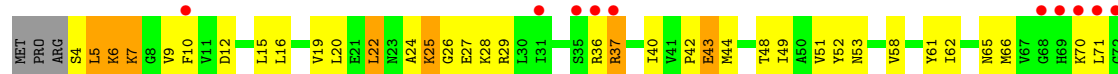
- Molecule 18: 30S ribosomal protein S18

Chain R:



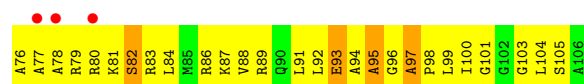
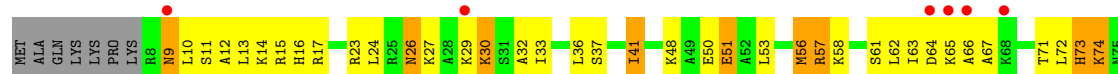
- Molecule 19: 30S ribosomal protein S19

Chain S:



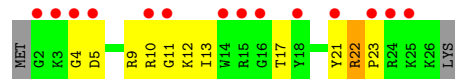
- Molecule 20: 30S ribosomal protein S20

Chain T:



- Molecule 21: 30S ribosomal protein Thx

Chain U:



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	210.22Å 450.25Å 623.81Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.80 – 3.00 49.80 – 3.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) (49.80-3.00) 88.7 (49.80-3.00)	Depositor EDS
$R_{merge}$	0.24	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.09 (at 3.01Å)	Xtriage
Refinement program	Phenix	Depositor
R, $R_{free}$	0.235 , 0.269 0.506 , 0.506	Depositor DCC
$R_{free}$ test set	51892 reflections (5.28%)	DCC
Wilson B-factor (Å <sup>2</sup> )	73.9	Xtriage
Anisotropy	0.352	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.26 , 72.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.43$ , $\langle L^2 \rangle = 0.25$	Xtriage
Outliers	0 of 1035238 reflections	Xtriage
$F_o, F_c$ correlation	0.50	EDS
Total number of atoms	51469	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	136.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.49% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality

### 5.1 Standard geometry

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.50	0/36190	0.88	40/56486 (0.1%)
2	B	0.29	0/1936	0.50	0/2611
3	C	0.27	0/1637	0.45	0/2207
4	D	0.34	0/1733	0.53	0/2318
5	E	0.34	0/1163	0.55	0/1566
6	F	0.36	0/856	0.54	0/1154
7	G	0.26	0/1276	0.44	0/1709
8	H	0.33	0/1136	0.54	0/1527
9	I	0.27	0/1028	0.44	0/1375
10	J	0.29	0/808	0.48	0/1087
11	K	0.32	0/900	0.52	0/1213
12	L	0.39	0/987	0.62	0/1322
13	M	0.27	0/928	0.47	0/1238
14	N	0.28	0/501	0.44	0/664
15	O	0.33	0/745	0.56	0/992
16	P	0.33	0/717	0.55	0/965
17	Q	0.34	0/837	0.56	0/1119
18	R	0.37	0/579	0.57	0/768
19	S	0.28	0/643	0.46	0/867
20	T	0.34	0/765	0.55	0/1007
21	U	0.28	0/213	0.43	0/279
All	All	0.44	0/55578	0.78	40/82474 (0.0%)

There are no bond length outliers.

All (40) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	893	C	C6-N1-C2	8.02	123.51	120.30
1	A	1509	C	C6-N1-C2	7.49	123.30	120.30
1	A	34	C	C6-N1-C2	6.90	123.06	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	895	G	N1-C6-O6	6.57	123.84	119.90
1	A	909	A	C8-N9-C4	6.55	108.42	105.80
1	A	877	C	C6-N1-C2	6.45	122.88	120.30
1	A	1484	C	C6-N1-C2	6.34	122.83	120.30
1	A	1509	C	C5-C6-N1	-6.33	117.83	121.00
1	A	7	G	C8-N9-C1'	6.29	135.18	127.00
1	A	7	G	C4-N9-C1'	-6.18	118.46	126.50
1	A	720	C	N1-C2-O2	6.18	122.61	118.90
1	A	400	C	C6-N1-C2	6.11	122.75	120.30
1	A	894	G	N1-C6-O6	5.95	123.47	119.90
1	A	117	G	N1-C6-O6	5.92	123.45	119.90
1	A	1514	C	N1-C2-O2	-5.88	115.37	118.90
1	A	925	G	C8-N9-C4	5.76	108.70	106.40
1	A	354	G	C4-N9-C1'	5.74	133.97	126.50
1	A	886	G	N3-C2-N2	5.71	123.90	119.90
1	A	34	C	N3-C4-C5	5.60	124.14	121.90
1	A	770	C	C5-C6-N1	-5.53	118.24	121.00
1	A	354	G	N3-C4-N9	5.51	129.31	126.00
1	A	1484	C	C2-N1-C1'	-5.47	112.78	118.80
1	A	398	C	C6-N1-C2	5.45	122.48	120.30
1	A	895	G	C5-C6-O6	-5.44	125.34	128.60
1	A	320	C	C6-N1-C2	5.43	122.47	120.30
1	A	1432	G	C8-N9-C4	-5.41	104.23	106.40
1	A	1442	G	C4-N9-C1'	5.37	133.49	126.50
1	A	117	G	C6-C5-N7	-5.33	127.20	130.40
1	A	354	G	C6-C5-N7	-5.22	127.27	130.40
1	A	689	C	C6-N1-C2	-5.21	118.22	120.30
1	A	322	C	C6-N1-C2	5.20	122.38	120.30
1	A	615	C	C6-N1-C2	-5.16	118.24	120.30
1	A	811	C	C6-N1-C2	5.15	122.36	120.30
1	A	1442	G	C6-C5-N7	-5.14	127.31	130.40
1	A	354	G	N3-C4-C5	-5.13	126.03	128.60
1	A	1501	C	C5-C6-N1	-5.12	118.44	121.00
1	A	720	C	N3-C2-O2	-5.08	118.34	121.90
1	A	1442	G	C8-N9-C1'	-5.03	120.47	127.00
1	A	991	U	C3'-C2'-C1'	5.02	105.51	101.50
1	A	758	G	N3-C4-C5	5.01	131.10	128.60

There are no chirality outliers.

There are no planarity outliers.



## 5.2 Close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32329	0	16318	1374	0
2	B	1901	0	1951	167	0
3	C	1613	0	1677	117	0
4	D	1703	0	1763	160	0
5	E	1147	0	1207	107	0
6	F	843	0	857	86	0
7	G	1257	0	1296	62	0
8	H	1116	0	1177	82	0
9	I	1011	0	1042	85	0
10	J	795	0	840	82	0
11	K	885	0	904	69	0
12	L	971	0	1057	106	0
13	M	921	0	976	61	0
14	N	492	0	529	33	0
15	O	734	0	771	54	0
16	P	701	0	720	91	0
17	Q	824	0	891	49	0
18	R	574	0	644	64	0
19	S	630	0	652	34	0
20	T	763	0	861	75	0
21	U	209	0	221	11	0
22	A	48	0	0	0	0
23	D	1	0	0	0	0
23	N	1	0	0	0	0
All	All	51469	0	36354	2706	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 31.

All (2706) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:111:ARG:HH11	2:B:111:ARG:HG2	1.09	1.14
7:G:113:GLU:HB2	7:G:119:ARG:HG2	1.33	1.11
2:B:185:ILE:HG22	2:B:199:TYR:HB2	1.32	1.09

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:59:A:H5''	1:A:60:A:H5''	1.28	1.09
4:D:128:VAL:HG12	4:D:129:ASN:ND2	1.69	1.06
16:P:28:ARG:HH11	16:P:28:ARG:HG2	1.18	1.05
1:A:1090:U:H2'	1:A:1091:U:H6	1.22	1.02
20:T:50:GLU:HB3	20:T:100:ILE:HG12	1.40	1.02
12:L:47:LYS:HB3	12:L:48:PRO:HD3	1.41	1.02
10:J:34:VAL:HG22	10:J:74:ILE:HG22	1.40	1.01
3:C:47:LEU:HD21	3:C:68:VAL:HG11	1.44	0.99
1:A:1256:A:H61	1:A:1278:U:H1'	1.26	0.98
1:A:664:G:H22	1:A:741:G:H1	1.06	0.97
4:D:128:VAL:HG12	4:D:129:ASN:HD22	1.19	0.97
1:A:15:G:H4'	5:E:24:ARG:HH12	1.29	0.94
16:P:4:ILE:HG13	16:P:21:VAL:HG12	1.48	0.94
3:C:20:SER:HB2	3:C:40:ARG:HH22	1.31	0.94
18:R:79:LEU:HD23	18:R:80:PRO:HD2	1.48	0.94
1:A:737:A:H2'	1:A:738:C:C6	2.03	0.94
2:B:158:LEU:H	2:B:158:LEU:HD12	1.31	0.94
12:L:8:ASN:HD22	17:Q:34:LYS:HE2	1.33	0.93
1:A:475:G:H2'	1:A:476:G:H8	1.33	0.93
1:A:1442(A):G:H3'	1:A:1442(B):A:H5''	1.50	0.93
15:O:56:LEU:O	15:O:60:VAL:HG23	1.68	0.92
1:A:1090:U:H2'	1:A:1091:U:C6	2.04	0.92
16:P:45:THR:HG22	16:P:47:ASP:H	1.34	0.92
11:K:22:HIS:HB3	11:K:29:ILE:HG23	1.49	0.92
1:A:1502:A:H2	1:A:1505:G:H1	0.95	0.92
1:A:376:G:H4'	16:P:5:ARG:HH11	1.33	0.91
1:A:735:C:H2'	1:A:736:C:H6	1.36	0.91
8:H:86:ILE:HG21	8:H:133:LEU:HD13	1.54	0.90
1:A:17:U:H2'	1:A:18:C:C6	2.07	0.89
1:A:250:A:H4'	1:A:251:G:O5'	1.73	0.89
5:E:51:VAL:HB	5:E:52:PRO:HD3	1.56	0.88
4:D:189:PRO:HB2	4:D:194:LEU:HD21	1.55	0.88
1:A:1442(A):G:H3'	1:A:1442(B):A:C5'	2.02	0.88
1:A:954:G:H21	1:A:1227:A:H62	1.17	0.88
1:A:445:G:H2'	1:A:446:G:H8	1.36	0.88
1:A:1065:U:H1'	1:A:1066:C:OP2	1.74	0.88
18:R:50:ILE:HD11	18:R:70:ILE:HG21	1.56	0.87
1:A:685:G:O2'	1:A:686:U:H5'	1.73	0.87
1:A:1502:A:H2	1:A:1505:G:N1	1.70	0.87
17:Q:86:GLU:O	17:Q:90:ILE:HG12	1.76	0.86
1:A:102:G:H2'	1:A:103:C:H6	1.41	0.86
2:B:111:ARG:NH1	2:B:111:ARG:HG2	1.86	0.86

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:101:MET:HA	2:B:108:ILE:HG13	1.55	0.86
1:A:673:G:H2'	1:A:674:G:C8	2.11	0.85
1:A:1169:A:H2'	1:A:1170:A:C8	2.11	0.85
8:H:102:ARG:HE	8:H:102:ARG:H	1.25	0.85
1:A:1070:U:H2'	1:A:1071:C:H6	1.42	0.85
16:P:20:VAL:HG21	16:P:32:TYR:CG	2.12	0.85
10:J:40:LEU:HB2	10:J:41:PRO:HD2	1.57	0.84
1:A:1442:G:O2'	1:A:1442(A):G:H5''	1.77	0.84
2:B:172:ILE:H	2:B:172:ILE:HD12	1.43	0.84
2:B:91:PRO:HG3	2:B:154:LEU:HB2	1.60	0.83
1:A:1505:G:H4'	1:A:1506:U:H5''	1.58	0.83
13:M:66:LEU:HD12	13:M:66:LEU:H	1.44	0.83
1:A:522:C:H41	12:L:53:ARG:HH22	1.24	0.83
12:L:102:ARG:HH11	12:L:102:ARG:CG	1.92	0.83
1:A:1003:G:H2'	1:A:1004:A:H4'	1.61	0.83
4:D:57:ARG:HH22	5:E:107:ARG:HD3	1.39	0.82
1:A:626:U:H2'	1:A:627:G:H8	1.45	0.82
18:R:59:SER:HB3	18:R:62:GLU:HG3	1.59	0.82
5:E:10:MET:HB2	5:E:32:VAL:HG22	1.60	0.82
1:A:627:G:H2'	1:A:628:G:H8	1.41	0.82
2:B:84:GLU:HB3	2:B:219:VAL:HG21	1.60	0.82
4:D:62:GLN:HA	4:D:62:GLN:HE21	1.44	0.82
19:S:40:ILE:HD13	19:S:62:ILE:HD11	1.61	0.82
1:A:353:A:H5'	1:A:353:A:H8	1.44	0.82
8:H:20:TYR:HD1	8:H:65:TYR:CD2	1.97	0.82
12:L:38:THR:HG23	12:L:39:VAL:HG23	1.62	0.82
16:P:22:THR:CG2	16:P:32:TYR:HA	2.10	0.81
1:A:445:G:H2'	1:A:446:G:C8	2.15	0.81
20:T:89:ARG:NH2	20:T:104:LEU:HD21	1.95	0.81
1:A:403:C:O2'	1:A:404:U:H5'	1.81	0.81
13:M:81:LEU:HB3	13:M:89:GLY:HA2	1.62	0.81
1:A:1435:G:H2'	1:A:1436:U:C6	2.16	0.81
1:A:444:C:H2'	1:A:445:G:H8	1.46	0.81
1:A:365:U:H5''	1:A:366:C:OP1	1.81	0.81
16:P:72:ARG:HH21	16:P:73:LEU:HD21	1.46	0.81
1:A:877:C:H5''	8:H:88:LYS:HD3	1.61	0.80
1:A:1238:A:H62	1:A:1299:A:N6	1.78	0.80
9:I:4:TYR:HB2	9:I:19:LEU:HB2	1.63	0.80
19:S:36:ARG:HH12	19:S:75:ALA:HB3	1.46	0.80
3:C:52:LEU:H	3:C:52:LEU:HD23	1.45	0.80
1:A:491:G:H2'	1:A:492:G:H8	1.47	0.80
1:A:532:A:H61	3:C:193:TYR:HB3	1.46	0.80

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:E:72:GLN:O	5:E:73:ASN:HB2	1.82	0.80
19:S:42:PRO:O	19:S:43:GLU:HB3	1.81	0.80
1:A:1281:U:H4'	1:A:1282:C:OP2	1.80	0.80
16:P:22:THR:HG22	16:P:32:TYR:HA	1.63	0.80
1:A:737:A:H2'	1:A:738:C:H6	1.46	0.79
5:E:50:GLU:HG3	5:E:52:PRO:HD2	1.65	0.79
18:R:58:LEU:HB3	18:R:62:GLU:HB2	1.64	0.79
1:A:975:A:H4'	1:A:976:G:H5''	1.64	0.79
1:A:1446:U:H4'	1:A:1447:A:N7	1.98	0.79
4:D:148:VAL:HG12	4:D:149:ALA:H	1.45	0.79
11:K:21:ILE:HB	11:K:84:VAL:HA	1.64	0.79
4:D:119:GLN:HG2	4:D:123:HIS:HD2	1.47	0.79
10:J:78:ASN:HB2	10:J:81:THR:HG23	1.62	0.79
9:I:96:LEU:HG	9:I:102:LEU:HB2	1.62	0.79
5:E:101:ILE:HD11	5:E:119:LEU:HA	1.64	0.79
13:M:68:GLY:O	13:M:69:GLU:HB2	1.83	0.79
2:B:88:ALA:HB2	2:B:219:VAL:HG13	1.64	0.79
1:A:1201:A:H1'	1:A:1202:G:OP2	1.82	0.79
1:A:707:C:O2'	1:A:708:C:H5'	1.83	0.79
1:A:80:G:H1	1:A:89:C:N4	1.81	0.79
1:A:17:U:H2'	1:A:18:C:H6	1.45	0.79
1:A:1226:C:C4	13:M:104:ARG:HB2	2.17	0.79
13:M:91:ARG:HB2	13:M:98:VAL:HG21	1.64	0.79
20:T:56:MET:HG3	20:T:88:VAL:HG21	1.63	0.78
1:A:1321:C:C5'	1:A:1322:C:H5''	2.13	0.78
1:A:1289:A:H3'	1:A:1290:G:H8	1.49	0.78
1:A:1169:A:H2'	1:A:1170:A:H8	1.45	0.78
9:I:40:LEU:HD11	9:I:70:LYS:HG2	1.66	0.78
2:B:154:LEU:HD23	2:B:154:LEU:H	1.49	0.78
8:H:102:ARG:N	8:H:102:ARG:HE	1.80	0.78
1:A:1291:G:H4'	9:I:38:GLN:O	1.83	0.78
2:B:163:PHE:HA	2:B:185:ILE:HG12	1.64	0.78
1:A:1412:C:H2'	1:A:1413:A:H8	1.47	0.78
1:A:200:G:H1	1:A:217:C:H42	1.28	0.78
4:D:119:GLN:HG2	4:D:123:HIS:CD2	2.18	0.78
2:B:97:TRP:CH2	2:B:173:ALA:HA	2.19	0.78
1:A:1199:U:H4'	10:J:54:PHE:CZ	2.18	0.78
1:A:826:C:H2'	1:A:827:U:C6	2.19	0.78
16:P:28:ARG:HH11	16:P:28:ARG:CG	1.97	0.77
1:A:266:G:H5''	1:A:268:C:H41	1.48	0.77
1:A:664:G:N2	1:A:741:G:H1	1.82	0.77
1:A:472:A:H4'	16:P:82:GLN:HE22	1.50	0.77

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:F:62:TRP:CH2	6:F:64:GLN:HB2	2.19	0.77
1:A:878:G:H5'	8:H:89:PRO:HG2	1.67	0.77
1:A:437:U:OP1	4:D:155:LEU:HD22	1.84	0.77
8:H:10:LEU:N	8:H:10:LEU:HD23	1.99	0.77
20:T:50:GLU:CB	20:T:100:ILE:HG12	2.15	0.77
1:A:191:G:C4	20:T:105:SER:HB3	2.19	0.77
16:P:28:ARG:HG2	16:P:28:ARG:NH1	1.95	0.76
1:A:166:G:H2'	1:A:167:G:H8	1.49	0.76
1:A:1152:A:H5''	10:J:13:HIS:CD2	2.20	0.76
6:F:30:LEU:HB2	6:F:35:ALA:HB3	1.67	0.76
1:A:1250:A:H61	1:A:1354:C:H1'	1.50	0.76
1:A:341:C:O2'	1:A:342:C:H5'	1.85	0.76
2:B:87:ARG:HE	2:B:233:SER:HB3	1.48	0.76
4:D:61:LYS:HB2	4:D:203:VAL:HG22	1.68	0.76
5:E:26:PHE:O	5:E:27:ARG:HB2	1.85	0.76
1:A:327:A:H3'	1:A:328:C:H5''	1.68	0.76
6:F:24:GLU:HG3	6:F:28:ARG:NH1	2.00	0.76
13:M:49:THR:HG22	13:M:51:ALA:H	1.50	0.76
1:A:475:G:H2'	1:A:476:G:C8	2.20	0.76
1:A:1070:U:H2'	1:A:1071:C:C6	2.22	0.75
1:A:859:A:H2'	1:A:860:A:O4'	1.86	0.75
1:A:1030(A):G:H1'	1:A:1031:G:H22	1.51	0.75
1:A:1285:A:H1'	1:A:1286:A:OP2	1.86	0.75
3:C:180:ALA:HB1	3:C:182:ILE:HG13	1.66	0.75
12:L:60:LEU:HD21	12:L:66:VAL:HG22	1.68	0.75
1:A:1117:G:H4'	9:I:104:ARG:NH2	2.00	0.75
10:J:26:ALA:HB1	10:J:29:ARG:HH21	1.51	0.75
1:A:114:U:H2'	1:A:115:G:C8	2.21	0.75
2:B:137:ARG:HA	2:B:137:ARG:HH11	1.51	0.75
1:A:735:C:H2'	1:A:736:C:C6	2.20	0.75
16:P:43:LYS:HA	16:P:48:TRP:HB3	1.69	0.75
8:H:10:LEU:HD13	8:H:83:ILE:HD11	1.68	0.75
1:A:59:A:H5''	1:A:60:A:C5'	2.13	0.74
1:A:1279:A:H5''	1:A:1280:A:OP1	1.86	0.74
12:L:25:PRO:O	12:L:27:LEU:HD22	1.87	0.74
1:A:775:G:C2'	1:A:776:G:H5'	2.17	0.74
1:A:38:G:C2	1:A:397:A:C2	2.74	0.74
20:T:50:GLU:HB3	20:T:100:ILE:CG1	2.17	0.74
1:A:1079:G:H2'	1:A:1080:A:C8	2.23	0.74
1:A:247:G:OP2	17:Q:100:LYS:HG2	1.87	0.74
1:A:499:A:H4'	1:A:500:G:OP1	1.87	0.74
1:A:159:G:O2'	1:A:160:A:C8	2.39	0.74

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:162:ILE:HD11	2:B:184:VAL:HG22	1.69	0.74
1:A:192:U:H2'	1:A:193:C:H6	1.52	0.74
10:J:63:PHE:HZ	14:N:45:ARG:HG3	1.52	0.74
2:B:180:LEU:O	2:B:181:PHE:HB2	1.86	0.74
10:J:49:VAL:HG13	14:N:41:ARG:HB2	1.70	0.74
1:A:377:G:OP1	16:P:3:LYS:HD2	1.88	0.74
1:A:1412:C:H2'	1:A:1413:A:C8	2.23	0.74
15:O:33:THR:HG21	15:O:85:LEU:HD22	1.70	0.74
12:L:47:LYS:CB	12:L:48:PRO:HD3	2.18	0.73
1:A:826:C:H2'	1:A:827:U:H6	1.53	0.73
16:P:74:LEU:O	16:P:79:VAL:HG23	1.88	0.73
1:A:627:G:H2'	1:A:628:G:C8	2.23	0.73
7:G:15:ASP:HB3	7:G:19:GLY:H	1.52	0.73
17:Q:18:THR:HG23	17:Q:69:LYS:HE3	1.67	0.73
1:A:1228:C:H2'	1:A:1229:A:H8	1.53	0.73
1:A:224:C:H2'	1:A:225:C:C6	2.24	0.73
6:F:67:MET:HB2	6:F:68:PRO:HD2	1.70	0.73
1:A:922:G:H4'	5:E:20:GLN:HA	1.69	0.73
1:A:1096:C:O2'	1:A:1097:C:H5'	1.88	0.73
3:C:182:ILE:HG12	3:C:203:PHE:HD1	1.52	0.73
18:R:53:ARG:HH21	18:R:60:ALA:N	1.87	0.73
1:A:819:A:H4'	1:A:820:U:OP2	1.88	0.73
1:A:1226:C:H42	13:M:104:ARG:HD2	1.54	0.73
1:A:600:C:H2'	1:A:601:C:C6	2.24	0.73
1:A:243:A:H4'	1:A:244:U:O5'	1.88	0.73
1:A:148:G:O2'	1:A:149:A:H5'	1.88	0.73
18:R:31:LEU:HD23	18:R:31:LEU:H	1.52	0.73
16:P:22:THR:HA	16:P:33:ILE:HG12	1.70	0.73
1:A:333:G:H4'	20:T:16:HIS:CE1	2.24	0.73
2:B:11:LEU:HB3	2:B:213:LEU:HD11	1.71	0.73
11:K:111:ASP:HA	18:R:84:LYS:HE2	1.71	0.73
16:P:4:ILE:HG13	16:P:21:VAL:CG1	2.19	0.72
12:L:47:LYS:HB3	12:L:48:PRO:CD	2.17	0.72
13:M:10:PRO:O	13:M:45:VAL:HG11	1.89	0.72
6:F:89:MET:HG2	6:F:91:VAL:HG23	1.71	0.72
4:D:57:ARG:NH2	5:E:107:ARG:HD3	2.04	0.72
1:A:673:G:H2'	1:A:674:G:H8	1.55	0.72
4:D:23:GLY:HA3	4:D:112:VAL:HG22	1.71	0.72
3:C:70:VAL:HG12	3:C:72:LYS:H	1.54	0.72
7:G:113:GLU:HB2	7:G:119:ARG:CG	2.18	0.72
1:A:522:C:H41	12:L:53:ARG:NH2	1.87	0.72
1:A:390:C:O3'	16:P:28:ARG:NH2	2.23	0.72

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:H:20:TYR:HA	8:H:65:TYR:CE2	2.25	0.72
5:E:100:VAL:HG13	5:E:118:ILE:HG22	1.72	0.72
10:J:34:VAL:CG2	10:J:74:ILE:HG22	2.18	0.72
1:A:976:G:H5'	1:A:1358:U:O2'	1.90	0.72
1:A:1228:C:H2'	1:A:1229:A:C8	2.25	0.72
12:L:124:LYS:HD2	12:L:125:PRO:HD2	1.71	0.72
1:A:1063:C:H3'	1:A:1064:G:H2'	1.70	0.71
15:O:87:ILE:HG22	15:O:88:ARG:N	2.04	0.71
1:A:1203:C:OP1	14:N:3:ARG:HD3	1.90	0.71
10:J:6:ILE:HG13	10:J:72:VAL:O	1.90	0.71
1:A:1446:U:O2'	1:A:1447:A:C8	2.43	0.71
1:A:163:C:H2'	1:A:164:U:C6	2.26	0.71
10:J:75:ILE:HG13	10:J:76:ASN:N	2.06	0.71
1:A:1072:G:H2'	1:A:1073:U:C6	2.25	0.71
13:M:25:ILE:HD11	13:M:66:LEU:HD23	1.71	0.71
1:A:1172:C:H2'	1:A:1173:G:C8	2.26	0.71
3:C:50:ALA:HB1	3:C:70:VAL:HG11	1.73	0.71
1:A:428:G:H4'	1:A:429:U:O5'	1.90	0.71
6:F:46:ARG:HH12	18:R:37:VAL:HG21	1.54	0.71
1:A:1057:G:H5''	3:C:154:SER:HB2	1.71	0.71
17:Q:74:LEU:HD12	17:Q:75:ARG:HG2	1.72	0.71
1:A:1441:G:H5''	1:A:1442:G:O5'	1.90	0.71
1:A:1456:G:H2'	1:A:1457:G:O4'	1.91	0.71
1:A:328:C:O2	1:A:328:C:H2'	1.90	0.70
1:A:741:G:H2'	1:A:742:G:O4'	1.91	0.70
1:A:579:G:H2'	1:A:580:U:H6	1.57	0.70
9:I:114:TYR:H	9:I:114:TYR:HD2	1.36	0.70
3:C:9:GLY:HA2	3:C:12:LEU:HD23	1.74	0.70
1:A:377:G:O2'	1:A:378:G:H5'	1.91	0.70
4:D:141:ARG:HB3	4:D:142:PRO:CD	2.22	0.70
1:A:559:A:H4'	1:A:560:U:C5'	2.22	0.70
1:A:659:U:C2'	1:A:660:G:H5'	2.22	0.70
1:A:735:C:O2'	1:A:736:C:H5'	1.91	0.70
1:A:1274:G:N2	1:A:1275:A:H62	1.88	0.70
5:E:80:ILE:HD11	5:E:138:ALA:HB1	1.73	0.70
8:H:86:ILE:HG22	8:H:87:SER:N	2.06	0.69
1:A:503:C:OP2	12:L:116:SER:HB3	1.91	0.69
1:A:626:U:H2'	1:A:627:G:C8	2.27	0.69
5:E:10:MET:CB	5:E:32:VAL:HG22	2.23	0.69
1:A:775:G:O2'	1:A:776:G:H5'	1.92	0.69
5:E:68:GLU:O	5:E:70:PRO:HD3	1.93	0.69
8:H:58:TYR:O	8:H:59:LEU:HD23	1.92	0.69

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:H:5:PRO:HB2	8:H:32:LYS:HE2	1.73	0.69
1:A:542:G:H2'	1:A:543:C:H6	1.56	0.69
1:A:503:C:H2'	1:A:504:C:H6	1.57	0.69
1:A:930:C:O2'	1:A:931:C:H5'	1.93	0.69
1:A:392:G:H2'	1:A:393:A:H8	1.57	0.69
1:A:1256:A:N6	1:A:1278:U:H1'	2.03	0.69
1:A:601:C:H2'	1:A:602:A:H8	1.58	0.69
1:A:598:U:H4'	8:H:94:TYR:CD2	2.26	0.69
2:B:61:LEU:CD2	2:B:68:ILE:HD11	2.22	0.69
1:A:1442:G:C8	1:A:1442(B):A:C2	2.81	0.69
1:A:1504:G:OP1	1:A:1507:A:H4'	1.92	0.69
16:P:53:VAL:HG12	16:P:79:VAL:HG13	1.74	0.69
15:O:78:TYR:O	15:O:82:ILE:HG22	1.93	0.69
1:A:559:A:H5''	1:A:560:U:H3'	1.74	0.69
11:K:34:ASP:HB3	11:K:40:ILE:HD11	1.75	0.69
11:K:24:SER:HB3	11:K:27:ASN:O	1.92	0.69
1:A:671:G:H2'	1:A:672:U:H6	1.58	0.69
1:A:1226:C:N4	13:M:104:ARG:HD2	2.08	0.69
9:I:17:VAL:HG11	9:I:81:ILE:HD13	1.75	0.69
2:B:204:ASN:ND2	2:B:206:ASP:H	1.91	0.69
3:C:58:GLU:H	3:C:65:ALA:HB3	1.58	0.69
7:G:116:ALA:O	7:G:120:ILE:HG12	1.93	0.69
4:D:31:CYS:C	4:D:33:MET:H	1.93	0.68
1:A:783:C:O2'	1:A:784:C:H5'	1.94	0.68
1:A:658:G:H2'	1:A:659:U:H6	1.57	0.68
1:A:1073:U:H2'	1:A:1074:G:H8	1.57	0.68
6:F:26:ILE:HG22	6:F:30:LEU:HD21	1.75	0.68
1:A:1074:G:C4	1:A:1102:A:C2	2.82	0.68
1:A:192:U:H2'	1:A:193:C:C6	2.28	0.68
7:G:73:MET:HA	7:G:91:VAL:HG23	1.73	0.68
5:E:78:HIS:HE1	5:E:142:LEU:HA	1.57	0.68
1:A:60:A:P	1:A:60:A:H8	2.17	0.68
13:M:10:PRO:HB2	13:M:18:ALA:HB1	1.75	0.68
1:A:828:A:H2'	1:A:829:G:O4'	1.94	0.68
1:A:1513:A:H2'	1:A:1514:C:C6	2.28	0.68
1:A:639:G:O2'	1:A:640:A:H5'	1.93	0.68
1:A:1190:G:H3'	3:C:3:ASN:HD21	1.59	0.68
4:D:12:CYS:HA	4:D:19:LEU:HD12	1.76	0.68
13:M:92:HIS:CE1	13:M:98:VAL:HG23	2.29	0.68
1:A:450:G:OP1	16:P:43:LYS:NZ	2.27	0.68
8:H:97:VAL:O	8:H:100:ILE:HG13	1.94	0.68
1:A:52:G:C2'	1:A:53:A:H5'	2.24	0.68

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:111:ARG:CG	2:B:111:ARG:HH11	1.99	0.68
6:F:21:LEU:O	6:F:24:GLU:HB3	1.94	0.68
1:A:450:G:H5''	16:P:41:PRO:O	1.94	0.68
1:A:15:G:H4'	5:E:24:ARG:NH1	2.08	0.67
4:D:18:LYS:HE3	4:D:31:CYS:SG	2.33	0.67
15:O:82:ILE:HG12	15:O:87:ILE:HB	1.76	0.67
12:L:87:GLY:HA2	12:L:98:TYR:HA	1.75	0.67
1:A:1442(A):G:C3'	1:A:1442(B):A:H5''	2.24	0.67
1:A:102:G:H2'	1:A:103:C:C6	2.27	0.67
1:A:892:A:H2'	1:A:893:C:C6	2.30	0.67
4:D:138:TYR:C	4:D:138:TYR:HD2	1.96	0.67
2:B:187:LEU:HD13	2:B:187:LEU:O	1.95	0.67
16:P:45:THR:HG23	16:P:46:PRO:HD2	1.75	0.67
8:H:77:GLU:HG3	8:H:78:GLN:H	1.60	0.67
7:G:32:ARG:O	7:G:33:ASP:HB2	1.94	0.67
2:B:112:VAL:HG22	2:B:149:LEU:HD13	1.75	0.67
1:A:509:A:H2'	1:A:510:A:C8	2.28	0.67
2:B:114:ARG:HD2	2:B:141:GLU:OE1	1.94	0.67
3:C:100:ALA:O	3:C:101:LEU:HB2	1.95	0.67
1:A:135:C:H2'	1:A:136:C:H5'	1.75	0.67
16:P:82:GLN:HE21	16:P:82:GLN:N	1.91	0.67
6:F:17:SER:O	6:F:21:LEU:HD22	1.95	0.67
10:J:63:PHE:HB3	14:N:57:ARG:O	1.94	0.67
15:O:62:GLN:HA	15:O:65:ARG:NH1	2.09	0.67
2:B:29:ALA:O	2:B:32:ILE:HG22	1.93	0.67
1:A:523:A:H61	12:L:53:ARG:HH12	1.43	0.67
1:A:748:C:H4'	1:A:749:C:O5'	1.94	0.67
4:D:138:TYR:CD2	4:D:138:TYR:C	2.69	0.67
3:C:104:GLN:NE2	3:C:105:GLU:H	1.93	0.67
2:B:44:LEU:H	2:B:44:LEU:HD12	1.59	0.67
15:O:64:ARG:HH11	15:O:64:ARG:HG3	1.59	0.67
3:C:127:ARG:HD2	3:C:127:ARG:N	2.10	0.67
3:C:43:LEU:O	3:C:47:LEU:HB3	1.95	0.66
1:A:102:G:C4	1:A:103:C:C5	2.83	0.66
1:A:1076:C:C2	1:A:1082:G:N2	2.62	0.66
1:A:1342:C:H1'	9:I:124:GLN:HE22	1.59	0.66
18:R:79:LEU:HD23	18:R:80:PRO:CD	2.22	0.66
12:L:83:VAL:HG11	12:L:100:ILE:HG12	1.77	0.66
4:D:91:SER:HA	4:D:94:LEU:HD12	1.77	0.66
2:B:77:ALA:HB2	2:B:211:ILE:HD13	1.76	0.66
10:J:30:SER:OG	10:J:81:THR:HG22	1.95	0.66
2:B:61:LEU:HA	2:B:64:ARG:HG2	1.75	0.66

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:20:GLU:HG3	2:B:191:ASP:HB2	1.77	0.66
2:B:211:ILE:O	2:B:215:LEU:HB2	1.95	0.66
4:D:172:PRO:HB2	4:D:187:ARG:HH22	1.59	0.66
4:D:158:ILE:HG23	4:D:162:LEU:HD12	1.78	0.66
1:A:502:G:C2	1:A:503:C:O2	2.48	0.66
2:B:233:SER:HB2	2:B:234:PRO:HD2	1.76	0.66
1:A:1342:C:H4'	9:I:125:TYR:HB3	1.77	0.66
12:L:41:ARG:CG	12:L:42:THR:H	2.08	0.66
9:I:114:TYR:N	9:I:114:TYR:HD2	1.94	0.66
4:D:108:LEU:HD11	4:D:174:LEU:HD22	1.77	0.66
1:A:155:C:H2'	1:A:156:G:H8	1.60	0.66
1:A:64:G:H4'	1:A:65:U:H5''	1.78	0.66
4:D:128:VAL:O	4:D:130:GLY:N	2.28	0.66
1:A:1342:C:H1'	9:I:124:GLN:NE2	2.09	0.66
1:A:622:A:C8	1:A:623:C:C6	2.84	0.66
1:A:1337:G:H5''	1:A:1338:G:OP1	1.94	0.66
5:E:33:VAL:HG11	5:E:109:ILE:HA	1.78	0.66
11:K:34:ASP:HB2	11:K:35:PRO:HD2	1.78	0.66
5:E:57:LYS:O	5:E:61:TYR:HD2	1.78	0.66
1:A:359:U:H2'	1:A:360:A:H8	1.61	0.66
15:O:3:ILE:HG12	15:O:3:ILE:O	1.96	0.66
2:B:188:ALA:HB1	2:B:192:SER:HB2	1.77	0.66
1:A:983:A:H2	1:A:984:C:C5	2.14	0.65
9:I:55:ALA:HB1	9:I:58:ARG:HD2	1.77	0.65
1:A:353:A:H5'	1:A:353:A:C8	2.31	0.65
11:K:29:ILE:HB	11:K:44:SER:CB	2.25	0.65
1:A:437:U:O2'	1:A:438:G:H5'	1.96	0.65
1:A:559:A:H4'	1:A:560:U:H5''	1.78	0.65
1:A:590:C:H2'	1:A:591:U:C6	2.31	0.65
1:A:66:G:H4'	1:A:173:U:C5	2.31	0.65
11:K:29:ILE:HB	11:K:44:SER:HB3	1.77	0.65
5:E:51:VAL:O	5:E:55:VAL:HG23	1.96	0.65
4:D:148:VAL:HG12	4:D:149:ALA:N	2.12	0.65
10:J:5:ARG:HG3	10:J:73:ASP:OD1	1.96	0.65
4:D:149:ALA:O	4:D:153:ARG:HG3	1.95	0.65
1:A:881:G:P	12:L:12:ARG:HH22	2.19	0.65
1:A:750:G:N3	15:O:23:GLY:HA3	2.11	0.65
1:A:973:G:H3'	1:A:974:A:H5''	1.79	0.65
1:A:184:G:H2'	1:A:185:A:H8	1.61	0.65
4:D:62:GLN:HA	4:D:62:GLN:NE2	2.12	0.65
1:A:254:G:OP1	17:Q:67:LYS:O	2.15	0.65
1:A:963:G:H21	10:J:55:LYS:CE	2.09	0.65

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:409:G:H2'	1:A:410:G:H5'	1.78	0.65
1:A:1106:G:H5''	3:C:172:ARG:HG2	1.79	0.65
4:D:13:ARG:O	4:D:15:GLU:N	2.30	0.65
4:D:126:ILE:HG22	4:D:127:THR:H	1.60	0.65
12:L:55:VAL:HG12	12:L:56:ALA:H	1.62	0.65
2:B:178:ARG:NH2	8:H:74:PRO:HG3	2.11	0.65
12:L:8:ASN:ND2	17:Q:34:LYS:HE2	2.08	0.65
1:A:963:G:H21	10:J:55:LYS:HE2	1.61	0.65
1:A:1117:G:H4'	9:I:104:ARG:CZ	2.27	0.65
8:H:77:GLU:HG3	8:H:78:GLN:N	2.10	0.65
9:I:97:LYS:HB3	9:I:98:PRO:HD3	1.79	0.65
2:B:165:VAL:HG23	2:B:166:ASP:H	1.62	0.65
1:A:775:G:H2'	1:A:776:G:H5'	1.79	0.64
9:I:103:THR:HG22	9:I:105:ASP:H	1.63	0.64
7:G:26:PHE:O	7:G:30:ILE:HG12	1.96	0.64
18:R:62:GLU:HA	18:R:65:ILE:HD11	1.79	0.64
1:A:327:A:C4	1:A:329:A:C8	2.85	0.64
1:A:622:A:C8	1:A:623:C:C5	2.86	0.64
4:D:20:TYR:CD2	4:D:26:CYS:HB3	2.33	0.64
3:C:134:ILE:HG23	3:C:151:VAL:HB	1.79	0.64
20:T:48:LYS:HB3	20:T:51:GLU:HG3	1.79	0.64
1:A:159:G:H2'	1:A:161:A:OP2	1.97	0.64
15:O:87:ILE:HG22	15:O:88:ARG:H	1.60	0.64
1:A:1109:C:H2'	1:A:1110:A:O4'	1.97	0.64
1:A:376:G:OP2	16:P:67:THR:HG21	1.98	0.64
1:A:437:U:H5''	4:D:155:LEU:HD13	1.79	0.64
2:B:22:LYS:NZ	2:B:40:HIS:HE1	1.94	0.64
1:A:688:G:H2'	1:A:689:C:H6	1.62	0.64
2:B:28:PHE:HD1	2:B:190:THR:HG22	1.63	0.64
17:Q:22:LEU:HD12	17:Q:23:VAL:N	2.13	0.64
1:A:250:A:H1'	1:A:251:G:OP2	1.97	0.64
12:L:102:ARG:HH11	12:L:102:ARG:HG2	1.61	0.64
1:A:579:G:C4	1:A:580:U:C5	2.85	0.64
9:I:61:ALA:HB1	9:I:63:ILE:HD11	1.78	0.64
3:C:73:PRO:O	3:C:76:VAL:HG22	1.97	0.64
13:M:46:LYS:HG3	13:M:47:ASP:H	1.62	0.64
1:A:939:G:H5''	7:G:102:ARG:HH12	1.63	0.64
1:A:386:C:O2'	1:A:387:U:H5'	1.97	0.64
6:F:63:TYR:N	6:F:63:TYR:HD2	1.95	0.64
7:G:40:ALA:O	7:G:44:TYR:CD1	2.51	0.64
10:J:39:PRO:HB3	10:J:70:ARG:HH12	1.62	0.64
5:E:101:ILE:HD13	5:E:118:ILE:O	1.97	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:C:104:GLN:CD	3:C:105:GLU:H	2.00	0.64
12:L:55:VAL:HG12	12:L:56:ALA:N	2.12	0.64
4:D:8:VAL:HB	4:D:21:LEU:HD12	1.80	0.64
6:F:82:ARG:HA	6:F:82:ARG:HH11	1.63	0.64
15:O:39:LEU:HD13	15:O:56:LEU:HB2	1.80	0.64
1:A:103:C:OP2	20:T:14:LYS:HD3	1.97	0.64
16:P:6:LEU:HD23	16:P:17:TYR:CG	2.33	0.63
1:A:1096:C:H2'	1:A:1097:C:H6	1.63	0.63
3:C:6:HIS:NE2	3:C:184:TYR:HE2	1.96	0.63
1:A:1316:G:H2'	1:A:1317:C:H5''	1.79	0.63
5:E:76:ILE:HG12	5:E:77:PRO:HD2	1.79	0.63
3:C:20:SER:HB2	3:C:40:ARG:NH2	2.08	0.63
20:T:97:ALA:O	20:T:99:LEU:N	2.31	0.63
16:P:55:ARG:HE	16:P:55:ARG:HA	1.62	0.63
1:A:1160:G:H2'	1:A:1160:G:N3	2.13	0.63
1:A:632:A:C8	1:A:633:G:C8	2.85	0.63
1:A:1162:C:H2'	1:A:1163:C:C6	2.34	0.63
6:F:63:TYR:CD2	6:F:63:TYR:N	2.66	0.63
1:A:779:C:O2'	1:A:780:A:H5'	1.98	0.63
11:K:20:TYR:C	11:K:21:ILE:HD12	2.19	0.63
1:A:579:G:H2'	1:A:580:U:C6	2.33	0.63
2:B:67:THR:HG21	2:B:155:LEU:HG	1.79	0.63
2:B:194:PRO:O	2:B:196:LEU:N	2.31	0.63
1:A:1497:G:H2'	1:A:1498:U:H5'	1.80	0.63
1:A:992:U:H1'	1:A:993:G:OP2	1.98	0.63
17:Q:59:ILE:CG2	17:Q:71:PHE:HB3	2.28	0.63
1:A:1072:G:C5	1:A:1073:U:C4	2.87	0.63
1:A:659:U:H2'	1:A:660:G:H5'	1.80	0.63
1:A:1190:G:OP1	3:C:4:LYS:HA	1.98	0.63
12:L:91:LYS:HG3	12:L:91:LYS:O	1.98	0.63
1:A:108:G:O6	20:T:15:ARG:HD2	1.99	0.63
16:P:20:VAL:HG23	16:P:35:LYS:HA	1.79	0.63
7:G:37:ASN:HD21	9:I:40:LEU:HD22	1.64	0.63
2:B:97:TRP:HZ2	2:B:102:LEU:HD13	1.62	0.63
3:C:36:ASP:OD2	3:C:57:ILE:HG21	1.99	0.62
1:A:877:C:H5''	8:H:88:LYS:CD	2.28	0.62
1:A:1321:C:H5'	1:A:1322:C:H5''	1.80	0.62
2:B:22:LYS:HA	2:B:22:LYS:HZ3	1.63	0.62
13:M:34:LEU:HD13	13:M:41:PRO:HG3	1.81	0.62
16:P:4:ILE:HB	16:P:66:PRO:HB3	1.79	0.62
1:A:437:U:C5	1:A:438:G:N7	2.67	0.62
1:A:322:C:H5	1:A:328:C:H5	1.47	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
18:R:56:THR:OG1	18:R:58:LEU:HD13	1.98	0.62
1:A:952:U:H4'	1:A:964:A:H61	1.65	0.62
1:A:78:G:H1	1:A:91:C:H42	1.47	0.62
1:A:538:G:OP2	12:L:115:LYS:HG3	2.00	0.62
1:A:999:C:H2'	1:A:1000:U:C6	2.34	0.62
1:A:833:U:H2'	1:A:834:C:H6	1.64	0.62
1:A:1392:G:O2'	1:A:1393:U:H5'	1.99	0.62
1:A:1172:C:H2'	1:A:1173:G:H8	1.61	0.62
1:A:503:C:H2'	1:A:504:C:C6	2.34	0.62
1:A:983:A:H2	1:A:984:C:C6	2.17	0.62
11:K:69:ALA:HB1	11:K:103:LEU:HD23	1.79	0.62
6:F:10:LEU:HD12	6:F:10:LEU:N	2.13	0.62
1:A:78:G:H22	1:A:91:C:H42	1.47	0.62
1:A:491:G:H2'	1:A:492:G:C8	2.30	0.62
6:F:18:GLN:HA	6:F:21:LEU:CD2	2.29	0.62
14:N:23:ARG:NH1	14:N:30:ALA:HB2	2.15	0.62
1:A:625:G:H2'	1:A:626:U:H6	1.64	0.62
1:A:1238:A:H62	1:A:1299:A:H62	1.46	0.62
1:A:543:C:C2	1:A:544:G:C8	2.88	0.62
9:I:3:GLN:HB3	9:I:20:ARG:NH1	2.15	0.62
1:A:719:C:H5	1:A:720:C:C4	2.17	0.62
1:A:667:G:H4'	15:O:51:HIS:CE1	2.35	0.62
1:A:355:C:H5'	1:A:389:A:OP2	2.00	0.62
5:E:101:ILE:HG12	5:E:101:ILE:O	1.98	0.62
1:A:224:C:H2'	1:A:225:C:H6	1.61	0.62
1:A:1388:C:H2'	1:A:1389:C:H6	1.65	0.62
1:A:1067:A:H1'	1:A:1068:G:C8	2.35	0.62
1:A:946:A:H2'	1:A:947:G:H8	1.64	0.62
1:A:952:U:H2'	1:A:953:G:H8	1.65	0.61
1:A:748:C:H1'	1:A:749:C:OP2	1.99	0.61
1:A:590:C:H2'	1:A:591:U:H6	1.63	0.61
1:A:946:A:H2'	1:A:947:G:C8	2.35	0.61
6:F:69:GLU:O	6:F:72:VAL:HG12	2.00	0.61
3:C:34:LEU:O	3:C:38:ARG:HG2	2.00	0.61
1:A:1225:A:N3	1:A:1225:A:H2'	2.14	0.61
1:A:344:A:O2'	1:A:346:G:N7	2.24	0.61
1:A:509:A:H4'	1:A:510:A:OP1	2.00	0.61
12:L:87:GLY:H	12:L:99:HIS:H	1.48	0.61
2:B:178:ARG:NH2	8:H:68:ARG:HH22	1.98	0.61
3:C:111:LEU:HD21	3:C:145:GLY:O	2.00	0.61
16:P:9:PHE:CE2	16:P:18:ARG:NE	2.68	0.61
1:A:674:G:H2'	1:A:675:A:H8	1.64	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
16:P:39:TYR:HA	16:P:48:TRP:O	2.00	0.61
2:B:19:HIS:O	2:B:39:ILE:HG23	1.99	0.61
1:A:801:U:H2'	1:A:802:A:H8	1.65	0.61
1:A:9:G:H5'	5:E:122:GLU:OE2	1.99	0.61
1:A:81:U:H2'	1:A:82:U:C5	2.35	0.61
1:A:1128:C:H5'	9:I:16:ARG:NH2	2.15	0.61
18:R:50:ILE:HD12	18:R:70:ILE:HD12	1.82	0.61
1:A:709:G:H2'	1:A:710:G:H8	1.65	0.61
12:L:27:LEU:HD11	12:L:64:TYR:CE1	2.35	0.61
1:A:820:U:H4'	1:A:821:G:OP2	1.99	0.61
10:J:32:ALA:CB	10:J:76:ASN:HB3	2.30	0.61
12:L:6:THR:HG23	12:L:9:GLN:HE21	1.65	0.61
1:A:105:G:H2'	1:A:106:C:C6	2.35	0.61
9:I:114:TYR:HD1	10:J:60:ARG:HG2	1.64	0.61
1:A:1321:C:C3'	1:A:1322:C:H5''	2.30	0.61
1:A:1278:U:O4	10:J:99:LYS:HE3	1.99	0.61
4:D:108:LEU:HD23	4:D:183:GLY:HA3	1.81	0.61
1:A:687:A:N3	1:A:688:G:H1'	2.16	0.61
11:K:31:THR:HA	11:K:42:TRP:HA	1.82	0.61
5:E:147:ASP:HA	5:E:150:ARG:HH11	1.65	0.61
11:K:34:ASP:HB2	11:K:35:PRO:CD	2.31	0.61
1:A:623:C:C4	1:A:624:C:C5	2.89	0.61
1:A:1133:G:N3	1:A:1142:G:N2	2.48	0.61
14:N:40:CYS:SG	14:N:42:ILE:HG12	2.41	0.61
1:A:1097:C:H1'	1:A:1170:A:H1'	1.81	0.61
5:E:43:LEU:HD21	5:E:132:ALA:HB1	1.83	0.61
1:A:827:U:H5''	1:A:828:A:OP2	2.01	0.61
9:I:48:GLU:N	9:I:49:PRO:HD2	2.16	0.61
1:A:336:C:O2'	1:A:337:C:H5'	2.01	0.61
1:A:674:G:H21	11:K:116:HIS:HB2	1.64	0.61
1:A:253:U:H2'	1:A:254:G:H8	1.66	0.61
10:J:6:ILE:HD11	10:J:72:VAL:HB	1.83	0.61
12:L:21:LYS:HD2	12:L:21:LYS:N	2.16	0.61
1:A:192:U:O4'	20:T:103:GLY:HA2	2.01	0.60
1:A:52:G:O2'	1:A:53:A:H5'	2.00	0.60
6:F:19:LEU:HD11	6:F:59:TYR:CZ	2.35	0.60
2:B:71:VAL:HG13	2:B:93:VAL:HB	1.82	0.60
2:B:187:LEU:HD23	2:B:201:ILE:HG22	1.83	0.60
2:B:228:GLY:O	2:B:230:VAL:HG13	2.00	0.60
13:M:82:MET:HB2	13:M:93:ARG:NH1	2.16	0.60
4:D:22:LYS:O	4:D:113:SER:HB3	2.01	0.60
1:A:509:A:O2'	1:A:510:A:P	2.60	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:189(K):U:H2'	1:A:189(L):G:C8	2.37	0.60
20:T:73:HIS:O	20:T:76:ALA:HB3	2.01	0.60
1:A:1392:G:N2	1:A:1502:A:C8	2.68	0.60
1:A:1064:G:H1'	1:A:1065:U:OP2	2.01	0.60
2:B:14:GLY:O	2:B:15:VAL:HG13	2.01	0.60
16:P:76:GLN:HG2	16:P:76:GLN:O	2.02	0.60
5:E:51:VAL:HB	5:E:52:PRO:CD	2.29	0.60
8:H:9:MET:HG2	8:H:10:LEU:HD23	1.83	0.60
1:A:1216:G:H5''	14:N:5:ALA:CB	2.32	0.60
1:A:1279:A:H2	10:J:43:ARG:HH12	1.49	0.60
1:A:1399:C:C2	1:A:1502:A:N6	2.69	0.60
5:E:101:ILE:CD1	5:E:119:LEU:HA	2.32	0.60
1:A:505:G:C6	1:A:535:A:C2	2.89	0.60
1:A:767:A:H2'	1:A:768:A:O4'	2.01	0.60
1:A:1285:A:H4'	1:A:1286:A:O5'	2.02	0.60
2:B:17:PHE:CD1	2:B:44:LEU:HD11	2.37	0.60
1:A:1416:G:H2'	1:A:1417:G:O4'	2.01	0.60
5:E:145:LYS:O	5:E:149:GLU:HG2	2.02	0.60
2:B:116:GLU:HA	2:B:119:GLU:CB	2.30	0.60
2:B:21:ARG:CB	2:B:39:ILE:HA	2.32	0.60
1:A:1311:G:N2	1:A:1327:C:C2	2.70	0.60
1:A:147:G:H2'	1:A:148:G:H5'	1.84	0.60
2:B:21:ARG:HB3	2:B:39:ILE:HA	1.83	0.60
3:C:150:LYS:HB3	3:C:201:TYR:HB2	1.83	0.60
1:A:681:C:N3	1:A:710:G:C2	2.70	0.60
1:A:673:G:O3'	6:F:87:ARG:NH2	2.35	0.60
1:A:562:C:H4'	1:A:563:A:O5'	2.01	0.60
4:D:12:CYS:HA	4:D:19:LEU:CD1	2.31	0.60
1:A:949:A:H1'	1:A:1364:U:H3	1.66	0.60
1:A:359:U:H2'	1:A:360:A:C8	2.36	0.60
1:A:1189:C:O3'	3:C:5:ILE:HD12	2.02	0.60
5:E:18:ARG:HH21	5:E:25:ARG:HG2	1.67	0.60
1:A:1521:G:H2'	1:A:1522:U:C6	2.37	0.60
1:A:1442:G:O2'	1:A:1442(A):G:C5'	2.48	0.59
1:A:1391:U:H2'	1:A:1392:G:C8	2.37	0.59
3:C:6:HIS:HD2	3:C:7:PRO:HD2	1.66	0.59
1:A:524:G:H2'	1:A:525:C:C6	2.37	0.59
1:A:386:C:C2'	1:A:387:U:H5'	2.32	0.59
1:A:1399:C:H4'	1:A:1400:C:H5''	1.85	0.59
6:F:3:ARG:HB3	6:F:93:SER:HB2	1.84	0.59
1:A:1049:U:H4'	1:A:1050:G:O5'	2.02	0.59
8:H:31:PHE:O	8:H:35:ILE:HG13	2.02	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:90:MET:HE2	2:B:90:MET:HA	1.83	0.59
1:A:1372:U:H5''	9:I:71:SER:HB3	1.83	0.59
1:A:1372:U:OP1	9:I:72:GLY:N	2.35	0.59
1:A:341:C:C2'	1:A:342:C:H5'	2.32	0.59
1:A:1159:U:H4'	1:A:1160:G:OP1	2.02	0.59
1:A:1521:G:H2'	1:A:1522:U:H6	1.67	0.59
9:I:111:ARG:O	9:I:113:LYS:HD2	2.02	0.59
8:H:53:VAL:O	8:H:54:ASP:HB2	2.02	0.59
1:A:392:G:H2'	1:A:393:A:C8	2.37	0.59
6:F:4:TYR:HA	6:F:91:VAL:O	2.03	0.59
13:M:97:PRO:C	13:M:98:VAL:HA	2.23	0.59
1:A:774:G:H2'	1:A:775:G:H5'	1.85	0.59
6:F:61:LEU:HB3	6:F:63:TYR:HE2	1.67	0.59
17:Q:59:ILE:HG22	17:Q:71:PHE:HD1	1.68	0.59
9:I:83:ARG:O	9:I:86:VAL:HG12	2.02	0.59
1:A:299:G:C6	1:A:300:A:C6	2.91	0.59
1:A:56:U:H2'	1:A:57:G:C8	2.38	0.59
7:G:75:VAL:HG12	7:G:88:PRO:HB3	1.83	0.59
1:A:1313:U:P	19:S:6:LYS:HG3	2.42	0.59
18:R:50:ILE:CD1	18:R:70:ILE:HG21	2.29	0.59
12:L:90:VAL:O	12:L:92:ASP:N	2.32	0.59
1:A:193:C:H2'	1:A:194:C:H6	1.66	0.59
18:R:43:PHE:C	18:R:44:LEU:HD12	2.23	0.59
1:A:114:U:H2'	1:A:115:G:H8	1.68	0.59
5:E:80:ILE:CD1	5:E:138:ALA:HB1	2.32	0.59
3:C:105:GLU:HG2	3:C:106:VAL:H	1.67	0.59
9:I:26:VAL:HG22	9:I:61:ALA:HB3	1.83	0.59
1:A:375:U:O3'	16:P:6:LEU:HB2	2.02	0.59
1:A:921:U:O2	5:E:19:MET:HB2	2.02	0.59
2:B:219:VAL:HA	2:B:222:ILE:HD12	1.85	0.59
3:C:6:HIS:CD2	3:C:7:PRO:HD2	2.38	0.59
1:A:509:A:O2'	1:A:510:A:O5'	2.21	0.59
6:F:69:GLU:CD	6:F:69:GLU:H	2.06	0.59
1:A:1325:C:H4'	21:U:17:THR:HG21	1.84	0.59
12:L:18:VAL:HG23	12:L:19:ARG:H	1.67	0.59
1:A:1348:U:H4'	9:I:120:ARG:HD2	1.82	0.59
1:A:7:G:N2	5:E:121:LYS:HG2	2.18	0.59
1:A:142:G:C2	1:A:143:A:C8	2.91	0.59
1:A:1442(B):A:OP1	1:A:1442(B):A:H4'	2.02	0.59
20:T:63:ILE:HD13	20:T:80:ARG:HB2	1.84	0.59
15:O:3:ILE:HD13	15:O:3:ILE:H	1.68	0.59
2:B:116:GLU:HA	2:B:119:GLU:HB2	1.84	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:C:155:GLY:O	3:C:156:ARG:HB2	2.02	0.59
20:T:61:SER:O	20:T:65:LYS:HG3	2.02	0.59
1:A:137:C:H42	1:A:226:G:H1	1.50	0.59
20:T:56:MET:HG2	20:T:84:LEU:CD1	2.33	0.59
6:F:62:TRP:O	6:F:62:TRP:HE3	1.85	0.59
1:A:774:G:C2'	1:A:775:G:H5'	2.32	0.59
2:B:168:THR:HG21	2:B:192:SER:HA	1.84	0.59
1:A:853:G:H2'	1:A:854:G:H8	1.68	0.59
21:U:9:ARG:O	21:U:13:ILE:HG13	2.03	0.59
1:A:147:G:C2'	1:A:148:G:H5'	2.32	0.59
5:E:57:LYS:HB3	5:E:61:TYR:HE2	1.67	0.59
1:A:376:G:H2'	1:A:377:G:H8	1.68	0.58
1:A:542:G:P	4:D:10:ARG:HH21	2.24	0.58
10:J:32:ALA:HB2	10:J:76:ASN:HB3	1.85	0.58
1:A:672:U:H2'	1:A:672:U:O2	2.02	0.58
7:G:79:ARG:NE	7:G:84:ASN:HD21	2.01	0.58
3:C:29:TYR:O	3:C:33:LEU:HB2	2.02	0.58
1:A:16:A:O2'	1:A:17:U:H5'	2.03	0.58
1:A:1392:G:C2'	1:A:1393:U:H5'	2.33	0.58
1:A:1366:C:OP1	9:I:117:HIS:CE1	2.56	0.58
1:A:262:A:H2'	1:A:263:A:C8	2.37	0.58
10:J:34:VAL:HG13	10:J:73:ASP:O	2.03	0.58
6:F:53:ALA:O	6:F:54:LYS:HB2	2.02	0.58
1:A:577:G:C8	1:A:816:A:C6	2.91	0.58
1:A:370:C:H2'	1:A:371:G:O4'	2.02	0.58
1:A:1065:U:C1'	1:A:1066:C:OP2	2.50	0.58
18:R:59:SER:H	18:R:62:GLU:CD	2.07	0.58
5:E:12:LEU:O	5:E:13:ILE:HD12	2.02	0.58
1:A:779:C:C2'	1:A:780:A:H5'	2.34	0.58
1:A:724:G:C2	1:A:725:G:C8	2.92	0.58
12:L:6:THR:OG1	12:L:9:GLN:HG3	2.03	0.58
2:B:24:TRP:CG	2:B:25:ASN:N	2.69	0.58
5:E:55:VAL:O	5:E:58:ALA:HB3	2.04	0.58
1:A:502:G:C6	1:A:503:C:N3	2.71	0.58
1:A:233:C:H2'	1:A:234:C:H6	1.69	0.58
1:A:1301:U:H3'	1:A:1302:U:H5''	1.85	0.58
3:C:86:VAL:O	3:C:90:GLU:HG2	2.03	0.58
1:A:1003:G:H2'	1:A:1004:A:C4'	2.32	0.58
1:A:1216:G:OP1	14:N:2:ALA:HA	2.04	0.58
4:D:100:ARG:NH2	4:D:118:ARG:HH22	2.01	0.58
7:G:23:VAL:O	7:G:27:ILE:HD12	2.04	0.58
1:A:661:G:C2	1:A:662:G:C8	2.92	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1227:A:OP2	13:M:111:LYS:HE2	2.04	0.58
1:A:155:C:H2'	1:A:156:G:C8	2.38	0.58
5:E:96:PRO:HA	5:E:117:ASP:OD2	2.02	0.58
2:B:185:ILE:HG22	2:B:199:TYR:CB	2.21	0.58
5:E:10:MET:HG3	5:E:13:ILE:HD13	1.85	0.58
3:C:6:HIS:HE2	3:C:184:TYR:HE2	1.51	0.58
1:A:1346:A:N1	1:A:1374:A:H5''	2.18	0.58
1:A:417:C:O2'	1:A:418:C:H5'	2.02	0.58
1:A:484:G:H4'	1:A:485:G:OP1	2.04	0.58
1:A:22:G:H2'	1:A:23:C:C6	2.38	0.58
1:A:1090:U:C2	1:A:1091:U:C5	2.92	0.58
20:T:97:ALA:O	20:T:99:LEU:HG	2.04	0.58
13:M:25:ILE:CD1	13:M:66:LEU:HD23	2.33	0.58
1:A:1306:A:H1'	1:A:1332:A:C2	2.39	0.58
19:S:24:ALA:O	19:S:25:LYS:HB2	2.02	0.58
20:T:32:ALA:O	20:T:36:LEU:HD23	2.04	0.58
1:A:1016:A:H2'	1:A:1017:G:O4'	2.04	0.58
4:D:30:LYS:HA	4:D:35:ARG:HD2	1.86	0.58
1:A:706:A:N7	1:A:707:C:H5	2.01	0.58
1:A:1162:C:H2'	1:A:1163:C:H6	1.69	0.58
1:A:411:A:C4	1:A:413:G:O4'	2.57	0.58
1:A:539:A:OP2	12:L:115:LYS:HE3	2.04	0.58
2:B:71:VAL:CG1	2:B:93:VAL:HB	2.34	0.58
6:F:7:ASN:O	6:F:88:VAL:HA	2.04	0.58
10:J:90:LEU:N	10:J:91:PRO:HD3	2.19	0.58
14:N:4:LYS:O	14:N:7:ILE:HG12	2.04	0.58
12:L:102:ARG:HH11	12:L:102:ARG:HG3	1.66	0.57
1:A:601:C:H2'	1:A:602:A:C8	2.38	0.57
1:A:611:A:H61	1:A:629:G:H1	1.50	0.57
1:A:640:A:N3	8:H:115:SER:HB2	2.19	0.57
6:F:61:LEU:HD23	6:F:63:TYR:OH	2.04	0.57
6:F:27:GLN:O	6:F:31:GLU:HB2	2.03	0.57
2:B:163:PHE:HA	2:B:185:ILE:O	2.05	0.57
1:A:1256:A:H61	1:A:1278:U:C1'	2.09	0.57
5:E:71:LEU:HD23	5:E:71:LEU:N	2.19	0.57
1:A:1379:G:C6	1:A:1380:U:O4	2.58	0.57
2:B:101:MET:HG2	2:B:108:ILE:HG21	1.87	0.57
1:A:1058:G:H2'	1:A:1059:C:O4'	2.04	0.57
1:A:951:G:H1'	1:A:970:C:O2'	2.03	0.57
1:A:477:A:O2'	1:A:479:C:H5'	2.04	0.57
13:M:86:CYS:HB2	19:S:73:GLU:HB3	1.86	0.57
5:E:71:LEU:O	5:E:72:GLN:HG3	2.04	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:539:A:H2'	1:A:540:G:C8	2.39	0.57
1:A:617:G:C6	1:A:618:C:C5	2.93	0.57
1:A:556:C:O2'	1:A:557:G:H5'	2.04	0.57
1:A:59:A:N3	1:A:59:A:H2'	2.17	0.57
18:R:62:GLU:O	18:R:65:ILE:HD12	2.03	0.57
2:B:204:ASN:HD21	2:B:207:ALA:H	1.51	0.57
10:J:70:ARG:HG3	10:J:70:ARG:HH11	1.68	0.57
1:A:109:A:H2'	1:A:326:G:N2	2.20	0.57
1:A:1218:C:H2'	1:A:1219:U:C6	2.39	0.57
4:D:146:ILE:HD12	4:D:146:ILE:N	2.20	0.57
5:E:88:LYS:HB3	5:E:123:LEU:HB2	1.85	0.57
14:N:25:VAL:HG23	14:N:38:GLY:O	2.05	0.57
4:D:14:ARG:HA	4:D:39:PRO:HB3	1.87	0.57
10:J:6:ILE:HG22	10:J:98:ILE:HG13	1.84	0.57
1:A:1109:C:P	3:C:176:HIS:HD1	2.27	0.57
1:A:977:A:H2'	1:A:978:A:H5'	1.85	0.57
1:A:822:C:O2'	1:A:823:G:H5'	2.04	0.57
1:A:1004:A:H2'	1:A:1038:C:O2	2.04	0.57
9:I:114:TYR:CD2	9:I:114:TYR:N	2.66	0.57
17:Q:40:LYS:HD2	17:Q:42:TYR:CZ	2.39	0.57
1:A:1347:G:N2	1:A:1373:G:H2'	2.20	0.57
1:A:458:C:H2'	1:A:460:G:H8	1.70	0.57
11:K:57:THR:HG22	11:K:59:TYR:H	1.70	0.57
16:P:26:ARG:HD2	16:P:31:LYS:O	2.05	0.57
13:M:15:VAL:O	13:M:19:LEU:HD23	2.05	0.57
12:L:41:ARG:HG2	12:L:42:THR:H	1.70	0.57
17:Q:22:LEU:HD12	17:Q:23:VAL:H	1.69	0.57
1:A:1158:C:N3	1:A:1181:G:N2	2.52	0.57
5:E:18:ARG:NH2	5:E:25:ARG:HG2	2.20	0.57
1:A:577:G:C4	1:A:816:A:C2	2.92	0.57
20:T:58:LYS:HE3	20:T:62:LEU:HD11	1.87	0.57
7:G:115:ARG:HB2	7:G:118:VAL:HG22	1.86	0.57
1:A:131:C:H2'	1:A:132:C:C6	2.40	0.57
1:A:674:G:N2	11:K:116:HIS:HB2	2.19	0.57
2:B:218:ALA:O	2:B:222:ILE:HG13	2.04	0.57
15:O:87:ILE:CG2	15:O:88:ARG:H	2.18	0.57
2:B:178:ARG:HH21	8:H:68:ARG:HH22	1.52	0.57
1:A:457:C:H2'	1:A:458:C:C6	2.40	0.57
1:A:1228:C:P	13:M:108:ARG:HH22	2.28	0.56
12:L:70:ILE:HG12	12:L:100:ILE:HD12	1.85	0.56
3:C:130:VAL:O	3:C:134:ILE:HG12	2.05	0.56
1:A:986:A:H2'	1:A:987:G:O4'	2.05	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:C:32:LEU:HD22	3:C:59:ARG:NH1	2.20	0.56
1:A:707:C:OP1	11:K:85:ARG:NH1	2.38	0.56
1:A:626:U:C2	1:A:627:G:C8	2.94	0.56
6:F:18:GLN:HA	6:F:21:LEU:HD22	1.87	0.56
6:F:42:GLU:OE1	6:F:59:TYR:HE2	1.88	0.56
1:A:22:G:H2'	1:A:23:C:H6	1.71	0.56
1:A:240:C:H2'	1:A:241:C:H6	1.70	0.56
1:A:927:G:OP2	1:A:1503:A:C4	2.58	0.56
3:C:27:LYS:HA	3:C:27:LYS:NZ	2.20	0.56
1:A:60:A:H4'	1:A:61:G:O5'	2.05	0.56
1:A:706:A:C8	1:A:707:C:H5	2.23	0.56
1:A:1452:C:H5'	1:A:1456:G:C4	2.40	0.56
20:T:56:MET:HG2	20:T:84:LEU:HD11	1.87	0.56
16:P:48:TRP:H	16:P:48:TRP:HD1	1.52	0.56
2:B:201:ILE:HG21	2:B:214:ILE:HG21	1.87	0.56
2:B:22:LYS:HA	2:B:22:LYS:NZ	2.20	0.56
7:G:32:ARG:O	7:G:33:ASP:CB	2.54	0.56
1:A:687:A:H1'	1:A:688:G:OP2	2.05	0.56
1:A:457:C:H2'	1:A:458:C:H6	1.69	0.56
1:A:594:G:H1	1:A:645:C:H42	1.53	0.56
2:B:106:LYS:O	2:B:110:GLN:HG3	2.05	0.56
15:O:37:ASN:HD22	15:O:37:ASN:N	2.04	0.56
18:R:72:ARG:O	18:R:76:LEU:HD23	2.05	0.56
5:E:50:GLU:OE2	5:E:51:VAL:HG23	2.05	0.56
1:A:561:U:O2'	1:A:562:C:P	2.63	0.56
3:C:34:LEU:HD23	3:C:34:LEU:O	2.05	0.56
3:C:23:TYR:CG	3:C:24:ALA:N	2.74	0.56
1:A:1012:U:H6	1:A:1012:U:O5'	1.87	0.56
16:P:39:TYR:HB2	16:P:49:LEU:HD12	1.88	0.56
6:F:23:LYS:O	6:F:27:GLN:HG2	2.06	0.56
10:J:51:ARG:HE	10:J:61:GLU:HB2	1.70	0.56
1:A:650:G:O2'	1:A:651:C:H5'	2.05	0.56
3:C:113:ALA:HB3	3:C:114:PRO:HD3	1.88	0.56
9:I:4:TYR:HA	9:I:88:TYR:CE1	2.41	0.56
1:A:1446:U:HO2'	1:A:1447:A:H8	1.44	0.56
6:F:5:GLU:HG2	6:F:62:TRP:CZ2	2.40	0.56
1:A:542:G:H2'	1:A:543:C:C6	2.40	0.56
13:M:66:LEU:HD12	13:M:66:LEU:N	2.18	0.56
2:B:213:LEU:HD23	2:B:213:LEU:O	2.05	0.56
12:L:21:LYS:HD2	12:L:21:LYS:H	1.69	0.56
1:A:521:G:H4'	12:L:73:GLU:HG2	1.88	0.56
1:A:1362:C:O2'	1:A:1363:C:H5''	2.06	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
10:J:40:LEU:HD21	10:J:69:ASN:HB3	1.86	0.56
1:A:963:G:N2	10:J:55:LYS:HE2	2.21	0.56
13:M:46:LYS:HG3	13:M:47:ASP:N	2.21	0.56
4:D:109:GLY:O	4:D:111:ALA:N	2.39	0.56
11:K:99:GLN:O	11:K:101:SER:N	2.38	0.56
4:D:33:MET:CE	4:D:37:PRO:HA	2.36	0.56
5:E:43:LEU:HB2	5:E:136:MET:SD	2.46	0.56
17:Q:67:LYS:HA	17:Q:70:ARG:HH12	1.71	0.56
10:J:48:THR:HG23	10:J:62:HIS:HB3	1.87	0.56
5:E:112:LEU:N	5:E:112:LEU:HD23	2.21	0.56
1:A:495:A:H4'	1:A:496:A:OP1	2.06	0.56
2:B:172:ILE:H	2:B:172:ILE:CD1	2.17	0.56
5:E:100:VAL:HG13	5:E:118:ILE:CG2	2.35	0.56
2:B:55:PHE:HE1	2:B:218:ALA:HA	1.71	0.56
1:A:41:G:H2'	1:A:42:G:C8	2.40	0.56
1:A:1410:G:C4	1:A:1491:G:N2	2.74	0.56
6:F:98:LEU:H	6:F:98:LEU:HD12	1.70	0.56
9:I:11:LYS:HG2	9:I:11:LYS:O	2.05	0.56
1:A:134:A:H61	16:P:25:ARG:HH12	1.54	0.56
1:A:376:G:P	16:P:67:THR:HG21	2.46	0.55
1:A:963:G:N3	10:J:55:LYS:NZ	2.45	0.55
1:A:1116:C:H3'	1:A:1117:G:H5''	1.88	0.55
10:J:63:PHE:CZ	14:N:45:ARG:HG3	2.36	0.55
15:O:54:ARG:O	15:O:57:LEU:HB2	2.05	0.55
1:A:1049:U:H4'	1:A:1050:G:C5'	2.36	0.55
1:A:792:A:H4'	1:A:793:U:O5'	2.06	0.55
1:A:308:C:H2'	1:A:309:G:H8	1.72	0.55
13:M:71:ARG:O	13:M:71:ARG:HG3	2.06	0.55
1:A:60:A:P	1:A:60:A:C8	3.00	0.55
3:C:182:ILE:HG12	3:C:203:PHE:CD1	2.38	0.55
1:A:541:G:H2'	1:A:542:G:H8	1.70	0.55
1:A:658:G:H1'	15:O:22:THR:HB	1.89	0.55
1:A:1157:A:C1'	1:A:1181:G:H21	2.19	0.55
1:A:665:A:H1'	1:A:733:A:O4'	2.07	0.55
4:D:88:VAL:HG13	5:E:97:GLY:HA3	1.88	0.55
1:A:1259:C:H42	1:A:1276:G:H1	1.52	0.55
8:H:104:ARG:O	8:H:105:ARG:HB2	2.06	0.55
6:F:2:ARG:HB2	6:F:4:TYR:CE2	2.41	0.55
8:H:87:SER:HA	8:H:93:VAL:HG23	1.89	0.55
1:A:629:G:C4	1:A:630:G:C8	2.94	0.55
16:P:39:TYR:HB2	16:P:49:LEU:CD1	2.36	0.55
1:A:411:A:C6	1:A:429:U:C4	2.94	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:C:116:VAL:HG21	3:C:202:ILE:HD11	1.88	0.55
7:G:138:LYS:HE2	7:G:142:GLU:OE2	2.07	0.55
1:A:1452:C:O4'	1:A:1456:G:C2	2.59	0.55
13:M:91:ARG:HD3	19:S:81:ARG:HH21	1.71	0.55
6:F:79:LEU:HB2	6:F:88:VAL:HG21	1.88	0.55
10:J:61:GLU:OE1	14:N:58:LYS:HE2	2.06	0.55
11:K:80:VAL:O	11:K:106:LYS:HB3	2.07	0.55
18:R:63:GLN:OE1	18:R:63:GLN:HA	2.07	0.55
1:A:375:U:H5''	16:P:6:LEU:HD22	1.88	0.55
1:A:532:A:H61	3:C:193:TYR:CB	2.17	0.55
4:D:119:GLN:CG	4:D:123:HIS:CD2	2.89	0.55
1:A:1130:A:H1'	1:A:1146:A:C2	2.42	0.55
3:C:150:LYS:HG3	3:C:169:ALA:HB2	1.88	0.55
7:G:27:ILE:HD11	7:G:43:PHE:CD2	2.42	0.55
1:A:791:G:C6	1:A:792:A:N7	2.74	0.55
1:A:629:G:H2'	1:A:630:G:O4'	2.05	0.55
1:A:922:G:N3	1:A:1398:A:H2	2.04	0.55
1:A:96:U:O2'	1:A:97:G:P	2.64	0.55
4:D:133:VAL:HG13	4:D:135:LEU:HD22	1.87	0.55
1:A:1118:C:H1'	1:A:1179:A:C4	2.42	0.55
3:C:53:ALA:O	3:C:54:ARG:HB2	2.05	0.55
3:C:52:LEU:H	3:C:52:LEU:CD2	2.17	0.55
1:A:115:G:H4'	1:A:116:A:O5'	2.06	0.55
2:B:204:ASN:HD22	2:B:205:ASP:N	2.05	0.55
3:C:71:ALA:HA	3:C:106:VAL:HB	1.89	0.55
1:A:949:A:H1'	1:A:1364:U:N3	2.22	0.55
4:D:118:ARG:O	4:D:121:VAL:HG23	2.05	0.55
21:U:5:ASP:O	21:U:11:GLY:HA3	2.07	0.55
4:D:49:ARG:HA	4:D:49:ARG:HE	1.71	0.55
3:C:69:HIS:N	3:C:69:HIS:CD2	2.73	0.55
5:E:101:ILE:HD11	5:E:119:LEU:HD23	1.89	0.55
15:O:87:ILE:CG2	15:O:88:ARG:N	2.69	0.55
1:A:414:A:H2'	1:A:415:A:H8	1.71	0.55
2:B:28:PHE:CD1	2:B:190:THR:HG22	2.42	0.55
11:K:106:LYS:HG3	11:K:106:LYS:O	2.06	0.55
5:E:34:VAL:O	5:E:41:VAL:HA	2.07	0.55
8:H:64:LYS:HG2	8:H:79:VAL:HG21	1.87	0.55
1:A:355:C:C2'	1:A:356:A:H5'	2.37	0.55
18:R:66:LEU:O	18:R:70:ILE:HG13	2.07	0.55
2:B:158:LEU:H	2:B:158:LEU:CD1	2.08	0.55
1:A:955:U:H1'	1:A:1227:A:N6	2.22	0.55
1:A:80:G:H1	1:A:89:C:H41	1.50	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:D:112:VAL:HG12	4:D:116:GLN:OE1	2.07	0.55
1:A:163:C:H2'	1:A:164:U:H6	1.71	0.55
2:B:44:LEU:HA	2:B:47:THR:HB	1.89	0.55
3:C:35:GLU:O	3:C:39:ILE:HG13	2.07	0.55
6:F:72:VAL:HG13	6:F:73:ASN:N	2.22	0.55
9:I:53:VAL:HB	9:I:92:TYR:CE2	2.42	0.55
1:A:995:C:H1'	14:N:8:GLU:OE2	2.07	0.55
1:A:376:G:H4'	16:P:5:ARG:NH1	2.13	0.55
18:R:59:SER:HB3	18:R:62:GLU:CG	2.36	0.55
6:F:62:TRP:CE3	6:F:62:TRP:O	2.60	0.55
1:A:191:G:N3	20:T:103:GLY:O	2.40	0.55
3:C:39:ILE:HG21	3:C:57:ILE:HD11	1.88	0.55
1:A:665:A:H2'	1:A:732:C:O2	2.07	0.55
1:A:1236:A:O2'	1:A:1304:G:H4'	2.07	0.55
19:S:6:LYS:HD3	19:S:7:LYS:HE3	1.88	0.55
1:A:616:G:C2	1:A:617:G:C8	2.94	0.55
1:A:617:G:N1	1:A:618:C:C4	2.75	0.55
3:C:112:SER:O	3:C:116:VAL:HG23	2.06	0.55
14:N:24:CYS:HB3	14:N:27:CYS:O	2.07	0.55
1:A:628:G:O2'	1:A:629:G:H5'	2.06	0.54
9:I:114:TYR:HE1	10:J:60:ARG:O	1.89	0.54
16:P:53:VAL:O	16:P:57:ARG:HG2	2.07	0.54
1:A:658:G:C4	1:A:659:U:C5	2.95	0.54
1:A:1438:G:H2'	1:A:1439:C:C6	2.43	0.54
1:A:836:G:C6	1:A:851:G:C5	2.94	0.54
1:A:892:A:C6	1:A:893:C:C4	2.95	0.54
9:I:46:ALA:HB2	9:I:74:ILE:HG23	1.89	0.54
1:A:299:G:C6	1:A:300:A:N1	2.75	0.54
1:A:1242:C:P	21:U:10:ARG:HH22	2.30	0.54
18:R:74:ARG:HB3	18:R:81:PHE:CE1	2.42	0.54
8:H:10:LEU:N	8:H:10:LEU:CD2	2.70	0.54
10:J:32:ALA:HB1	10:J:75:ILE:HD11	1.90	0.54
3:C:95:THR:HG22	3:C:97:LYS:H	1.71	0.54
1:A:84:U:H5	1:A:88:A:C8	2.24	0.54
16:P:34:GLU:OE2	16:P:55:ARG:HD3	2.07	0.54
18:R:73:ALA:HB1	18:R:79:LEU:HD12	1.89	0.54
1:A:1072:G:C6	1:A:1073:U:C4	2.95	0.54
12:L:60:LEU:HD21	12:L:66:VAL:CG2	2.36	0.54
1:A:722:A:H2'	1:A:724:G:C8	2.42	0.54
1:A:651:C:O2'	1:A:652:U:H5'	2.07	0.54
1:A:836:G:C6	1:A:851:G:C6	2.95	0.54
8:H:48:TYR:HA	8:H:60:ARG:O	2.07	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1126:U:H2'	1:A:1127:G:O4'	2.08	0.54
3:C:113:ALA:C	3:C:115:LEU:H	2.11	0.54
1:A:1168:A:C6	1:A:1169:A:C6	2.95	0.54
1:A:79:G:C4'	1:A:80:G:OP1	2.55	0.54
1:A:826:C:H4'	8:H:12:ARG:HD3	1.89	0.54
6:F:5:GLU:HG3	6:F:93:SER:OG	2.07	0.54
1:A:579:G:C5	1:A:580:U:C5	2.95	0.54
1:A:228:A:H2'	1:A:229:U:O4'	2.08	0.54
7:G:151:TYR:OH	11:K:54:ARG:HD3	2.08	0.54
15:O:4:THR:OG1	15:O:7:GLU:HB2	2.07	0.54
2:B:114:ARG:HD3	2:B:114:ARG:O	2.08	0.54
1:A:356:A:C2'	1:A:357:G:O5'	2.55	0.54
1:A:1071:C:O2'	1:A:1072:G:H5'	2.08	0.54
20:T:89:ARG:HH21	20:T:104:LEU:HD21	1.68	0.54
1:A:266:G:H5''	1:A:268:C:N4	2.19	0.54
1:A:191:G:H1'	20:T:105:SER:HA	1.90	0.54
3:C:182:ILE:HG12	3:C:203:PHE:HA	1.90	0.54
1:A:11:G:C5	1:A:12:U:C5	2.95	0.54
20:T:26:ASN:HB2	20:T:71:THR:HG23	1.89	0.54
13:M:54:VAL:HG22	13:M:57:ARG:HH21	1.73	0.54
1:A:1026:G:N3	1:A:1026:G:H2'	2.23	0.54
1:A:760:G:H2'	1:A:761:G:H5'	1.89	0.54
20:T:13:LEU:H	20:T:13:LEU:HD12	1.73	0.54
8:H:112:LEU:HB2	8:H:133:LEU:HA	1.89	0.54
1:A:343:U:O2'	1:A:346:G:O6	2.26	0.54
8:H:36:LEU:HD23	8:H:39:LEU:HD23	1.89	0.54
2:B:20:GLU:O	2:B:40:HIS:HB2	2.07	0.54
3:C:73:PRO:HA	3:C:76:VAL:HG13	1.89	0.54
1:A:1315:U:H2'	1:A:1316:G:O4'	2.08	0.54
1:A:1132:C:H2'	1:A:1133:G:O4'	2.08	0.54
4:D:80:GLU:O	4:D:84:LYS:HG2	2.08	0.54
1:A:357:G:O2'	1:A:358:U:H5'	2.07	0.54
1:A:738:C:H2'	1:A:739:C:H6	1.72	0.54
1:A:1392:G:N2	1:A:1502:A:H8	2.06	0.54
12:L:102:ARG:HG3	12:L:102:ARG:NH1	2.23	0.54
6:F:55:ASP:HB2	6:F:86:ARG:HH12	1.73	0.54
1:A:1470:G:C2'	1:A:1471:G:H5'	2.38	0.54
1:A:932:C:H4'	7:G:4:ARG:NH2	2.23	0.54
3:C:6:HIS:NE2	3:C:184:TYR:CE2	2.76	0.54
1:A:1334:G:H8	1:A:1334:G:OP2	1.91	0.54
1:A:1216:G:H5''	14:N:5:ALA:HB2	1.89	0.54
1:A:1015:A:N6	1:A:1016:A:C6	2.76	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:84:U:C5	1:A:88:A:C8	2.96	0.54
1:A:804:U:H5''	1:A:805:C:OP2	2.07	0.54
2:B:189:ASP:N	2:B:189:ASP:OD1	2.41	0.54
15:O:78:TYR:OH	15:O:88:ARG:HD2	2.07	0.54
1:A:719:C:C5	1:A:720:C:C4	2.95	0.54
1:A:189(K):U:H2'	1:A:189(L):G:H8	1.71	0.54
7:G:79:ARG:HE	7:G:84:ASN:HD21	1.56	0.54
10:J:96:ILE:N	10:J:96:ILE:HD13	2.23	0.54
1:A:754:C:O2	1:A:754:C:H3'	2.08	0.54
1:A:1281:U:H5'	1:A:1282:C:H5	1.72	0.53
15:O:67:LEU:HD22	15:O:78:TYR:HE1	1.73	0.53
1:A:411:A:H2'	1:A:412:A:H4'	1.90	0.53
12:L:32:PHE:HB3	12:L:84:LEU:HD21	1.90	0.53
10:J:39:PRO:HB3	10:J:70:ARG:NH1	2.22	0.53
1:A:1346:A:H5''	9:I:120:ARG:HH12	1.73	0.53
1:A:227:G:O2'	1:A:228:A:H5'	2.08	0.53
17:Q:77:VAL:O	17:Q:78:GLU:HB3	2.07	0.53
1:A:180:U:H2'	1:A:181:G:H5'	1.90	0.53
1:A:498:U:H2'	1:A:498:U:O2	2.08	0.53
1:A:662:G:H2'	1:A:663:A:C8	2.44	0.53
3:C:53:ALA:HB2	3:C:115:LEU:HD21	1.90	0.53
13:M:24:GLY:C	13:M:25:ILE:HD12	2.28	0.53
1:A:113:G:H2'	1:A:114:U:C6	2.43	0.53
12:L:86:ARG:HB2	12:L:101:VAL:CG2	2.37	0.53
6:F:20:ALA:O	6:F:23:LYS:HB2	2.08	0.53
1:A:619:U:H2'	4:D:135:LEU:HD21	1.90	0.53
11:K:125:PHE:N	11:K:125:PHE:CD1	2.76	0.53
1:A:316:G:OP2	1:A:351:G:O2'	2.25	0.53
1:A:734:G:C2	1:A:735:C:C2	2.96	0.53
6:F:8:ILE:HG22	6:F:10:LEU:CD1	2.38	0.53
12:L:102:ARG:CG	12:L:102:ARG:NH1	2.59	0.53
15:O:65:ARG:HH11	15:O:65:ARG:HB2	1.72	0.53
2:B:121:LEU:O	2:B:121:LEU:HD23	2.07	0.53
1:A:1356:G:H2'	1:A:1357:A:C8	2.44	0.53
1:A:272:C:H2'	1:A:273:A:H8	1.73	0.53
15:O:5:LYS:O	15:O:9:GLN:HG2	2.08	0.53
3:C:189:ALA:HB3	3:C:196:LEU:HB2	1.90	0.53
1:A:1135:U:H4'	1:A:1136:U:H5	1.74	0.53
1:A:356:A:H2'	1:A:357:G:H8	1.72	0.53
1:A:1091:U:O2	1:A:1093:A:C8	2.62	0.53
1:A:1277:C:O2'	1:A:1279:A:H1'	2.08	0.53
1:A:685:G:N2	1:A:686:U:C4	2.76	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1003:G:C2	1:A:1004:A:H1'	2.43	0.53
1:A:625:G:H2'	1:A:626:U:C6	2.43	0.53
1:A:173:U:C2	1:A:197:A:N1	2.76	0.53
4:D:3:ARG:O	4:D:5:ILE:HG13	2.09	0.53
1:A:189(E):U:O2'	1:A:189(F):U:H5'	2.08	0.53
1:A:564:C:C2'	1:A:565:U:H5'	2.38	0.53
1:A:1478:C:O2'	1:A:1479:C:H5'	2.09	0.53
4:D:79:PHE:CD1	4:D:207:TYR:HD1	2.26	0.53
1:A:953:G:H5'	1:A:965:A:H61	1.73	0.53
1:A:501:C:O2'	1:A:502:G:H5'	2.09	0.53
15:O:64:ARG:NH1	15:O:64:ARG:HG3	2.24	0.53
15:O:54:ARG:HG2	15:O:58:MET:CE	2.39	0.53
7:G:75:VAL:HG21	7:G:144:MET:HB3	1.90	0.53
1:A:556:C:C2'	1:A:557:G:H5'	2.39	0.53
4:D:111:ALA:HB2	4:D:120:LEU:HD12	1.91	0.53
1:A:1470:G:O2'	1:A:1471:G:H5'	2.07	0.53
10:J:8:LEU:HG	10:J:96:ILE:HG22	1.89	0.53
11:K:125:PHE:H	11:K:125:PHE:HD1	1.56	0.53
16:P:64:ALA:O	16:P:65:GLN:C	2.47	0.53
1:A:1256:A:O3'	1:A:1257:U:H4'	2.08	0.53
1:A:250:A:C4'	1:A:251:G:O5'	2.52	0.53
1:A:523:A:H61	12:L:53:ARG:NH1	2.06	0.53
1:A:491:G:C4	1:A:492:G:C8	2.97	0.53
1:A:115:G:C2	1:A:289:G:N7	2.76	0.53
13:M:10:PRO:CB	13:M:18:ALA:HB1	2.37	0.53
1:A:1190:G:H3'	3:C:3:ASN:ND2	2.21	0.53
1:A:1317:C:OP1	14:N:17:LYS:HG2	2.07	0.53
7:G:23:VAL:HG13	7:G:43:PHE:CZ	2.44	0.53
1:A:189(C):C:H2'	1:A:189(D):C:O4'	2.08	0.53
1:A:373:A:O2'	1:A:374:A:H5'	2.09	0.53
4:D:31:CYS:C	4:D:33:MET:N	2.61	0.53
13:M:68:GLY:O	13:M:69:GLU:CB	2.54	0.53
12:L:27:LEU:O	12:L:29:GLY:N	2.41	0.53
1:A:963:G:H21	10:J:55:LYS:HD3	1.73	0.53
1:A:165:C:H2'	1:A:166:G:C8	2.43	0.53
1:A:1128:C:O2'	1:A:1130:A:C8	2.54	0.53
1:A:764:C:H2'	1:A:765:G:H8	1.74	0.53
1:A:1255:G:H5'	1:A:1256:A:OP1	2.08	0.53
6:F:89:MET:SD	18:R:76:LEU:HD21	2.49	0.53
1:A:473:G:H5'	16:P:81:ARG:HG3	1.90	0.53
1:A:1157:A:H4'	1:A:1158:C:O5'	2.09	0.53
13:M:16:ASP:HB3	13:M:41:PRO:HB3	1.91	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:175:C:H2'	1:A:176:C:H6	1.73	0.53
11:K:23:ALA:HB3	11:K:86:GLY:O	2.09	0.53
12:L:40:VAL:O	12:L:40:VAL:HG12	2.07	0.53
8:H:109:ILE:HG22	8:H:137:VAL:HB	1.90	0.53
1:A:1150:U:O4	1:A:1151:A:N6	2.42	0.53
3:C:14:ILE:O	3:C:15:THR:HB	2.08	0.53
1:A:560:U:H4'	1:A:561:U:O5'	2.08	0.53
6:F:99:ALA:HB1	18:R:23:LYS:HZ2	1.74	0.53
6:F:3:ARG:HG3	6:F:3:ARG:HH11	1.74	0.53
2:B:21:ARG:HG3	2:B:21:ARG:O	2.09	0.53
1:A:832:C:N4	1:A:855:G:C6	2.77	0.53
1:A:1129:C:H4'	1:A:1130:A:H5'	1.92	0.53
16:P:21:VAL:HG22	16:P:34:GLU:O	2.09	0.52
1:A:1321:C:H5''	1:A:1322:C:H2'	1.89	0.52
10:J:26:ALA:HB1	10:J:29:ARG:NH2	2.22	0.52
4:D:9:CYS:HA	4:D:12:CYS:HB2	1.91	0.52
13:M:83:ASP:CG	13:M:84:ILE:H	2.13	0.52
13:M:81:LEU:HB3	13:M:89:GLY:CA	2.38	0.52
6:F:30:LEU:H	6:F:30:LEU:HD23	1.75	0.52
5:E:68:GLU:HG3	5:E:68:GLU:O	2.09	0.52
2:B:187:LEU:HD11	2:B:204:ASN:O	2.09	0.52
9:I:18:PHE:HB2	9:I:62:TYR:O	2.09	0.52
11:K:105:VAL:O	11:K:105:VAL:HG23	2.08	0.52
8:H:6:ILE:H	8:H:6:ILE:HD12	1.73	0.52
1:A:340:U:O2'	1:A:341:C:H5'	2.09	0.52
2:B:208:ILE:HA	2:B:211:ILE:HD12	1.91	0.52
1:A:170:U:O2'	1:A:171:A:H5'	2.09	0.52
16:P:59:TRP:O	16:P:64:ALA:HB3	2.09	0.52
20:T:67:ALA:HB2	20:T:77:ALA:HB2	1.91	0.52
1:A:1501:C:H5''	1:A:1502:A:OP2	2.09	0.52
20:T:56:MET:CG	20:T:88:VAL:HG21	2.35	0.52
2:B:102:LEU:HD12	2:B:102:LEU:N	2.24	0.52
1:A:159:G:HO2'	1:A:160:A:H8	1.49	0.52
3:C:11:ARG:O	3:C:13:GLY:N	2.43	0.52
1:A:525:C:H2'	1:A:526:C:C6	2.44	0.52
9:I:112:LYS:HE3	9:I:116:LYS:O	2.10	0.52
18:R:45:SER:H	18:R:51:LEU:HD11	1.74	0.52
1:A:996:A:H2'	1:A:997:U:O4'	2.10	0.52
1:A:808:C:P	15:O:48:LYS:HE3	2.50	0.52
1:A:718:G:H5'	11:K:117:ASN:HB2	1.90	0.52
1:A:1287:A:C2	1:A:1353:G:H1'	2.44	0.52
15:O:18:PHE:CE1	15:O:21:ASP:HB2	2.45	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
16:P:4:ILE:N	16:P:4:ILE:HD12	2.25	0.52
8:H:20:TYR:HD1	8:H:65:TYR:HD2	1.50	0.52
1:A:1321:C:H3'	1:A:1322:C:H5''	1.92	0.52
1:A:963:G:H21	10:J:55:LYS:CD	2.23	0.52
5:E:120:THR:O	5:E:121:LYS:CB	2.57	0.52
15:O:37:ASN:ND2	15:O:37:ASN:N	2.58	0.52
3:C:188:LEU:O	3:C:189:ALA:HB2	2.09	0.52
1:A:175:C:C2	1:A:176:C:C5	2.98	0.52
1:A:441:A:H3'	1:A:442:C:C6	2.44	0.52
12:L:119:LYS:HB2	12:L:120:TYR:HD1	1.74	0.52
1:A:402:G:C6	1:A:403:C:C4	2.98	0.52
20:T:80:ARG:O	20:T:84:LEU:HB2	2.09	0.52
1:A:1162:C:C2	1:A:1175:G:N2	2.78	0.52
1:A:130:A:H1'	1:A:263:A:O2'	2.10	0.52
1:A:447:G:C6	1:A:485:G:H1'	2.45	0.52
11:K:81:ASP:OD2	11:K:106:LYS:HG2	2.09	0.52
6:F:12:PRO:O	6:F:14:LEU:N	2.41	0.52
10:J:45:ARG:HB2	10:J:65:LEU:HB3	1.91	0.52
1:A:49:U:C2	1:A:361:G:N2	2.78	0.52
3:C:18:TRP:CD1	14:N:53:LEU:O	2.63	0.52
1:A:1530:G:H4'	1:A:1530:G:OP1	2.10	0.52
1:A:685:G:C2	1:A:686:U:C4	2.98	0.52
5:E:101:ILE:HA	5:E:107:ARG:NH2	2.25	0.52
20:T:89:ARG:HD2	20:T:104:LEU:HD11	1.92	0.52
1:A:366:C:O2'	1:A:367:U:H5''	2.10	0.52
11:K:110:ASP:O	18:R:84:LYS:HD2	2.10	0.52
1:A:1274:G:H22	1:A:1275:A:H62	1.52	0.52
1:A:892:A:C5	1:A:893:C:C4	2.97	0.52
9:I:18:PHE:HB3	9:I:20:ARG:NH1	2.25	0.52
1:A:1347:G:C8	9:I:107:ARG:HB3	2.45	0.52
8:H:109:ILE:CG2	8:H:137:VAL:HB	2.40	0.52
1:A:1084:G:OP1	1:A:1086:U:C4	2.63	0.52
1:A:913:A:H4'	1:A:914:A:O5'	2.10	0.52
3:C:157:ILE:CD1	3:C:166:GLU:HB2	2.39	0.52
1:A:948:C:C5	13:M:106:ASN:ND2	2.77	0.52
20:T:10:LEU:O	20:T:12:ALA:N	2.35	0.52
16:P:8:ARG:O	16:P:9:PHE:CG	2.62	0.52
6:F:8:ILE:HG22	6:F:10:LEU:HD11	1.90	0.52
1:A:1446:U:O2'	1:A:1447:A:H8	1.89	0.52
1:A:1274:G:N2	1:A:1275:A:N6	2.57	0.52
15:O:3:ILE:N	15:O:3:ILE:HD13	2.24	0.52
1:A:814:A:N7	1:A:816:A:C4	2.78	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:323:U:OP1	20:T:26:ASN:ND2	2.43	0.52
1:A:683:G:C2	1:A:708:C:N3	2.78	0.52
11:K:21:ILE:HG13	11:K:30:VAL:HG12	1.90	0.52
1:A:472:A:C4'	16:P:82:GLN:HE22	2.21	0.52
1:A:194:C:H2'	1:A:195:A:H5''	1.91	0.52
15:O:67:LEU:CD2	15:O:78:TYR:HE1	2.23	0.52
8:H:29:SER:HB3	8:H:32:LYS:HD2	1.92	0.52
2:B:80:ILE:HD13	2:B:208:ILE:HG23	1.92	0.52
9:I:55:ALA:CB	9:I:58:ARG:HD2	2.39	0.52
1:A:939:G:H5''	7:G:102:ARG:NH1	2.25	0.52
1:A:1184:G:H2'	1:A:1185:G:H8	1.74	0.52
1:A:32:A:H2'	1:A:33:A:C8	2.45	0.52
20:T:93:GLU:O	20:T:93:GLU:HG2	2.09	0.52
1:A:1125:U:H2'	1:A:1126:U:OP2	2.10	0.52
5:E:107:ARG:O	5:E:108:ALA:C	2.48	0.52
1:A:1201:A:C1'	1:A:1202:G:OP2	2.55	0.52
1:A:166:G:C4	1:A:167:G:C8	2.98	0.52
7:G:15:ASP:O	7:G:19:GLY:HA2	2.10	0.52
3:C:156:ARG:NH2	3:C:161:GLU:HA	2.24	0.52
1:A:987:G:N2	1:A:1219:U:C2	2.78	0.52
1:A:1362:C:C2'	1:A:1363:C:H5''	2.39	0.52
8:H:86:ILE:HB	8:H:133:LEU:HD22	1.90	0.51
10:J:40:LEU:HD23	10:J:40:LEU:H	1.75	0.51
4:D:79:PHE:CD1	4:D:207:TYR:CD1	2.98	0.51
1:A:1522:U:O2	1:A:1523:G:C8	2.64	0.51
8:H:30:ARG:O	8:H:34:GLU:HG2	2.10	0.51
7:G:92:SER:OG	7:G:93:PRO:HD2	2.09	0.51
18:R:50:ILE:HD11	18:R:70:ILE:CG2	2.36	0.51
1:A:1037:C:H2'	1:A:1038:C:O4'	2.10	0.51
1:A:1290:G:N3	1:A:1290:G:H2'	2.25	0.51
8:H:26:VAL:HG22	8:H:27:PRO:O	2.10	0.51
1:A:723:U:H5''	1:A:724:G:OP2	2.10	0.51
7:G:12:LEU:HD13	7:G:24:THR:OG1	2.10	0.51
20:T:53:LEU:HD21	20:T:92:LEU:HD11	1.92	0.51
1:A:858:G:O6	1:A:869:G:H3'	2.10	0.51
20:T:24:LEU:HD13	20:T:24:LEU:C	2.31	0.51
2:B:97:TRP:HH2	2:B:176:GLU:CG	2.23	0.51
1:A:949:A:C2	1:A:1233:G:N3	2.79	0.51
15:O:55:GLY:HA2	15:O:58:MET:HE3	1.91	0.51
20:T:78:ALA:HA	20:T:81:LYS:HD3	1.91	0.51
1:A:1052:U:H2'	1:A:1055:A:OP1	2.10	0.51
1:A:1207:G:H2'	1:A:1208:C:C6	2.45	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:T:99:LEU:C	20:T:100:ILE:HD12	2.30	0.51
1:A:1125:U:O4	10:J:5:ARG:HD2	2.10	0.51
1:A:611:A:N6	1:A:629:G:H1	2.09	0.51
1:A:1321:C:C4	1:A:1322:C:C4	2.99	0.51
2:B:87:ARG:NE	2:B:233:SER:HB3	2.23	0.51
1:A:776:G:HO2'	1:A:777:A:P	2.33	0.51
3:C:7:PRO:O	3:C:11:ARG:HG2	2.11	0.51
1:A:938:A:N6	1:A:939:G:C6	2.78	0.51
1:A:577:G:C2	1:A:578:C:C6	2.98	0.51
1:A:1350:A:OP1	9:I:121:ARG:HG3	2.10	0.51
10:J:48:THR:HA	10:J:62:HIS:HB3	1.93	0.51
1:A:1490:C:O2'	1:A:1491:G:H5'	2.11	0.51
1:A:20:U:H2'	1:A:21:G:O4'	2.10	0.51
1:A:401:C:OP1	4:D:73:ARG:HD2	2.09	0.51
1:A:438:G:H4'	4:D:123:HIS:ND1	2.26	0.51
1:A:827:U:N3	1:A:870:U:C4	2.79	0.51
6:F:30:LEU:O	6:F:35:ALA:N	2.42	0.51
1:A:818:G:HO2'	1:A:820:U:H6	1.55	0.51
7:G:72:ARG:O	7:G:73:MET:HG3	2.09	0.51
2:B:23:ARG:HG2	2:B:23:ARG:O	2.11	0.51
1:A:630:G:N3	1:A:630:G:H2'	2.25	0.51
1:A:1202:G:C2'	1:A:1203:C:H5'	2.41	0.51
2:B:97:TRP:CH2	2:B:176:GLU:OE2	2.64	0.51
10:J:75:ILE:HG13	10:J:76:ASN:H	1.75	0.51
1:A:1240:U:P	7:G:116:ALA:HB2	2.51	0.51
12:L:24:VAL:HG13	12:L:98:TYR:HE2	1.75	0.51
1:A:66:G:C2	1:A:67:C:C6	2.98	0.51
3:C:206:GLU:HG2	3:C:207:VAL:H	1.76	0.51
1:A:1305:G:H5'	21:U:4:GLY:HA3	1.92	0.51
7:G:47:CYS:O	7:G:50:ILE:HB	2.10	0.51
2:B:130:ARG:HE	2:B:130:ARG:HA	1.76	0.51
1:A:355:C:C4	1:A:356:A:N7	2.79	0.51
16:P:16:HIS:O	16:P:17:TYR:O	2.28	0.51
11:K:29:ILE:HB	11:K:44:SER:HB2	1.92	0.51
1:A:1505:G:H4'	1:A:1506:U:C5'	2.38	0.51
4:D:31:CYS:O	4:D:31:CYS:SG	2.69	0.51
1:A:63:C:O2'	1:A:380:G:H4'	2.10	0.51
1:A:1128:C:H5'	9:I:16:ARG:HH22	1.75	0.51
1:A:1154:G:H2'	1:A:1155:G:H8	1.74	0.51
1:A:706:A:H5''	11:K:22:HIS:CD2	2.46	0.51
1:A:658:G:C1'	15:O:22:THR:HB	2.41	0.51
1:A:504:C:O2	1:A:504:C:H2'	2.10	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
15:O:66:LEU:O	15:O:69:TYR:HB3	2.11	0.51
8:H:134:ILE:O	8:H:135:CYS:HB3	2.11	0.51
17:Q:65:ILE:N	17:Q:65:ILE:HD12	2.26	0.51
1:A:17:U:C2	1:A:18:C:C5	2.99	0.51
8:H:13:ILE:O	8:H:17:THR:HG23	2.11	0.51
10:J:82:ILE:O	10:J:82:ILE:HG22	2.09	0.51
1:A:343:U:H2'	1:A:346:G:O6	2.11	0.51
6:F:18:GLN:O	6:F:21:LEU:HB2	2.11	0.51
12:L:83:VAL:CG1	12:L:100:ILE:HG23	2.41	0.51
12:L:86:ARG:HB2	12:L:101:VAL:HG23	1.93	0.51
3:C:199:LYS:HB3	3:C:201:TYR:HE1	1.76	0.51
6:F:99:ALA:HB3	18:R:29:PHE:CE2	2.46	0.51
8:H:6:ILE:N	8:H:6:ILE:HD12	2.26	0.51
1:A:67:C:H2'	1:A:68:G:C8	2.45	0.51
1:A:1105:A:H2'	1:A:1106:G:H8	1.76	0.51
2:B:12:GLU:HA	2:B:16:HIS:HB2	1.93	0.51
5:E:7:GLU:HG2	5:E:112:LEU:HD22	1.91	0.51
1:A:186:C:C2	1:A:187:C:C5	2.98	0.51
1:A:1468:A:H2'	1:A:1469:G:O4'	2.10	0.51
16:P:18:ARG:HD3	16:P:35:LYS:HD2	1.92	0.50
13:M:91:ARG:HB2	13:M:98:VAL:CG2	2.38	0.50
1:A:1321:C:H5'	1:A:1322:C:C5'	2.40	0.50
1:A:193:C:H2'	1:A:194:C:C6	2.46	0.50
1:A:881:G:OP2	12:L:12:ARG:NH2	2.44	0.50
1:A:832:C:H42	1:A:854:G:H1	1.59	0.50
1:A:143:A:N1	1:A:220:G:O6	2.45	0.50
1:A:655:A:C2	1:A:754:C:C4	2.99	0.50
1:A:181:G:N2	1:A:183:G:N2	2.59	0.50
6:F:11:ASN:O	6:F:14:LEU:HG	2.12	0.50
12:L:5:PRO:HB2	12:L:10:LEU:HD21	1.91	0.50
1:A:1252:A:H2'	1:A:1253:G:O4'	2.11	0.50
6:F:76:ALA:O	6:F:80:ARG:HG3	2.09	0.50
1:A:570:G:H2'	1:A:571:U:C6	2.46	0.50
1:A:668:G:O2'	15:O:46:HIS:HD2	1.94	0.50
2:B:219:VAL:O	2:B:222:ILE:HB	2.10	0.50
3:C:182:ILE:CG1	3:C:203:PHE:HD1	2.21	0.50
1:A:1240:U:OP2	7:G:116:ALA:HB2	2.11	0.50
11:K:102:GLY:C	11:K:103:LEU:HD22	2.32	0.50
10:J:89:ASP:C	10:J:91:PRO:HD3	2.31	0.50
1:A:276:G:C2'	1:A:277:C:H5'	2.41	0.50
4:D:131:ARG:HD3	4:D:131:ARG:H	1.76	0.50
1:A:710:G:H5''	6:F:54:LYS:HE3	1.94	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:L:27:LEU:C	12:L:29:GLY:N	2.63	0.50
4:D:203:VAL:HG12	4:D:204:ILE:N	2.26	0.50
11:K:27:ASN:OD1	11:K:28:THR:N	2.44	0.50
1:A:409:G:C2'	1:A:410:G:H5'	2.40	0.50
20:T:26:ASN:O	20:T:30:LYS:HB2	2.11	0.50
1:A:1084:G:C5	1:A:1085:U:C4	2.99	0.50
1:A:914:A:O2'	1:A:915:A:H5'	2.10	0.50
17:Q:87:LYS:HA	17:Q:87:LYS:HE2	1.92	0.50
1:A:1095:U:H2'	1:A:1096:C:C6	2.45	0.50
12:L:119:LYS:O	12:L:120:TYR:HB2	2.12	0.50
6:F:15:ASP:C	6:F:17:SER:H	2.15	0.50
2:B:28:PHE:CD1	2:B:190:THR:HA	2.47	0.50
1:A:10:A:H2'	1:A:11:G:H8	1.76	0.50
20:T:26:ASN:CB	20:T:71:THR:HG23	2.41	0.50
10:J:8:LEU:HD22	10:J:20:ALA:HB2	1.94	0.50
8:H:14:ARG:O	8:H:18:ARG:HD3	2.11	0.50
1:A:840:C:H4'	1:A:848:C:O2	2.12	0.50
1:A:1279:A:H2	10:J:43:ARG:NH1	2.09	0.50
13:M:19:LEU:HB3	13:M:25:ILE:HG21	1.93	0.50
12:L:25:PRO:C	12:L:27:LEU:H	2.14	0.50
1:A:321:A:H62	1:A:328:C:H1'	1.77	0.50
10:J:32:ALA:HB1	10:J:75:ILE:CG1	2.41	0.50
2:B:67:THR:C	2:B:68:ILE:HD12	2.32	0.50
1:A:1157:A:C4	1:A:1181:G:N2	2.79	0.50
1:A:946:A:C2	1:A:1236:A:C2	2.99	0.50
1:A:1242:C:H5''	21:U:10:ARG:HH12	1.76	0.50
3:C:61:ALA:O	3:C:62:ASP:HB2	2.10	0.50
6:F:22:GLU:OE1	6:F:84:ASN:HB2	2.12	0.50
1:A:701:C:O2	1:A:703:G:N1	2.45	0.50
5:E:144:THR:O	5:E:148:VAL:HG23	2.11	0.50
10:J:24:VAL:O	10:J:28:ARG:HG3	2.11	0.50
1:A:685:G:O2'	1:A:686:U:C5'	2.54	0.50
1:A:559:A:C5'	1:A:560:U:H3'	2.41	0.50
12:L:22:SER:O	12:L:24:VAL:N	2.44	0.50
1:A:152:A:N6	1:A:170:U:C2	2.80	0.50
1:A:936:C:H2'	1:A:937:A:O4'	2.11	0.50
1:A:1086:U:H2'	1:A:1087:G:H8	1.76	0.50
5:E:45:PHE:CE2	5:E:47:LYS:HD2	2.46	0.50
6:F:96:PRO:HB3	18:R:30:ASP:OD2	2.11	0.50
8:H:38:ILE:HD11	8:H:118:VAL:O	2.12	0.50
2:B:141:GLU:O	2:B:145:LEU:HB2	2.12	0.50
1:A:354:G:C6	1:A:355:C:N4	2.80	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:923:A:O2'	1:A:1399:C:OP2	2.27	0.50
1:A:102:G:N3	1:A:103:C:C6	2.79	0.50
20:T:104:LEU:HD23	20:T:104:LEU:C	2.32	0.50
18:R:53:ARG:C	18:R:55:ARG:N	2.65	0.50
10:J:33:GLN:O	10:J:75:ILE:HG23	2.12	0.50
3:C:11:ARG:O	3:C:14:ILE:O	2.30	0.50
8:H:5:PRO:O	8:H:8:ASP:HB3	2.12	0.50
1:A:1081:G:N2	1:A:1082:G:H1'	2.26	0.50
1:A:1233:G:H2'	1:A:1234:C:C6	2.47	0.50
1:A:1128:C:H5'	9:I:16:ARG:CZ	2.42	0.50
1:A:1490:C:H2'	1:A:1491:G:O4'	2.11	0.50
11:K:125:PHE:N	11:K:125:PHE:HD1	2.09	0.50
8:H:1:MET:H3	8:H:1:MET:CE	2.24	0.50
1:A:373:A:C2	1:A:482:A:N6	2.80	0.50
1:A:1148:U:H2'	1:A:1149:C:O4'	2.11	0.50
1:A:1385:G:O2'	1:A:1386:G:H5'	2.11	0.50
1:A:367:U:O2	1:A:369:C:C6	2.65	0.50
20:T:74:LYS:C	20:T:76:ALA:H	2.15	0.50
4:D:133:VAL:HG12	4:D:135:LEU:H	1.75	0.50
1:A:1478:C:H2'	1:A:1479:C:C6	2.47	0.50
19:S:79:THR:O	19:S:80:TYR:HB3	2.12	0.50
4:D:52:SER:O	4:D:54:TYR:N	2.45	0.50
1:A:445:G:N3	1:A:446:G:C8	2.80	0.50
13:M:61:GLU:HA	13:M:66:LEU:HD11	1.93	0.50
4:D:58:LEU:HD22	4:D:62:GLN:HG2	1.93	0.50
1:A:1288:A:H2	1:A:1352:C:O2	1.94	0.50
9:I:10:ARG:HG2	9:I:104:ARG:O	2.11	0.50
1:A:112:G:H2'	1:A:112:G:N3	2.27	0.50
8:H:26:VAL:HG13	8:H:59:LEU:HB2	1.93	0.50
15:O:54:ARG:HG2	15:O:58:MET:HE1	1.94	0.50
5:E:131:ILE:O	5:E:134:ALA:HB3	2.12	0.50
9:I:48:GLU:N	9:I:49:PRO:CD	2.75	0.50
9:I:53:VAL:C	9:I:92:TYR:HE2	2.15	0.50
4:D:105:VAL:HG22	4:D:146:ILE:HG21	1.93	0.50
1:A:791:G:C5	1:A:792:A:N7	2.79	0.50
1:A:174:C:C5	1:A:175:C:H5	2.29	0.50
7:G:25:ALA:O	7:G:29:LYS:HG2	2.12	0.50
1:A:1505:G:H5"	1:A:1506:U:OP1	2.12	0.49
18:R:52:PRO:O	18:R:56:THR:HG23	2.12	0.49
12:L:83:VAL:HG13	12:L:100:ILE:HG23	1.92	0.49
20:T:73:HIS:HB3	20:T:74:LYS:HG2	1.94	0.49
7:G:146:GLU:HA	7:G:149:ARG:HB2	1.92	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:607:A:H2'	1:A:608:A:O4'	2.12	0.49
1:A:1272:G:C6	1:A:1273:G:C5	3.00	0.49
1:A:865:A:C2	1:A:918:A:H4'	2.47	0.49
19:S:48:THR:HG22	19:S:61:TYR:HA	1.94	0.49
16:P:14:ASN:N	16:P:15:PRO:HD3	2.27	0.49
2:B:97:TRP:CZ3	2:B:173:ALA:HA	2.46	0.49
1:A:473:G:H2'	1:A:474:G:H8	1.77	0.49
1:A:328:C:O2	1:A:328:C:C2'	2.60	0.49
1:A:833:U:H2'	1:A:834:C:C6	2.47	0.49
3:C:150:LYS:HE3	3:C:167:TRP:HE1	1.77	0.49
4:D:150:GLU:HG2	4:D:151:LYS:H	1.77	0.49
4:D:202:LEU:N	4:D:202:LEU:HD23	2.27	0.49
1:A:445:G:C2	1:A:446:G:C4	3.00	0.49
1:A:674:G:O2'	1:A:675:A:H5'	2.12	0.49
6:F:10:LEU:CD1	6:F:10:LEU:N	2.75	0.49
13:M:66:LEU:O	13:M:70:LEU:HB2	2.12	0.49
1:A:1388:C:H2'	1:A:1389:C:C6	2.46	0.49
1:A:797:C:O2'	1:A:798:G:H5'	2.12	0.49
1:A:585:G:N3	1:A:879:C:H4'	2.27	0.49
1:A:1099:G:N3	1:A:1099:G:H2'	2.27	0.49
2:B:61:LEU:HD21	2:B:68:ILE:HD11	1.94	0.49
2:B:19:HIS:CE1	2:B:206:ASP:HB2	2.46	0.49
8:H:120:THR:H	8:H:123:GLU:HB2	1.77	0.49
10:J:44:VAL:HG22	10:J:66:ARG:HG2	1.94	0.49
1:A:1271:G:H5'	1:A:1314:C:H5'	1.94	0.49
1:A:382:A:C2	1:A:383:A:C4	3.00	0.49
7:G:62:PHE:HA	7:G:124:LEU:HD22	1.93	0.49
3:C:19:GLU:O	3:C:19:GLU:HG2	2.13	0.49
5:E:10:MET:HB2	5:E:32:VAL:CG2	2.38	0.49
1:A:658:G:C6	1:A:749:C:N4	2.79	0.49
1:A:960:U:H2'	1:A:960:U:O2	2.11	0.49
21:U:22:ARG:N	21:U:23:PRO:HD3	2.27	0.49
1:A:1381:U:H2'	1:A:1382:C:H5'	1.94	0.49
20:T:37:SER:O	20:T:41:ILE:HG12	2.13	0.49
11:K:108:ILE:HB	18:R:87:ARG:HA	1.94	0.49
1:A:340:U:H2'	1:A:341:C:O4'	2.12	0.49
11:K:111:ASP:HA	18:R:84:LYS:CE	2.42	0.49
1:A:1498:U:H1'	1:A:1499:A:OP2	2.13	0.49
1:A:615:C:H2'	1:A:616:G:O4'	2.11	0.49
1:A:279:A:OP2	17:Q:95:TYR:OH	2.26	0.49
1:A:706:A:C5	1:A:707:C:C5	3.00	0.49
19:S:36:ARG:HD2	19:S:52:TYR:O	2.13	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:D:119:GLN:O	4:D:123:HIS:HD2	1.96	0.49
1:A:437:U:C5'	4:D:155:LEU:HD13	2.42	0.49
1:A:1151:A:O2'	1:A:1152:A:H8	1.95	0.49
9:I:77:ILE:O	9:I:81:ILE:HG12	2.12	0.49
5:E:147:ASP:OD2	5:E:147:ASP:N	2.45	0.49
1:A:617:G:N1	1:A:618:C:C5	2.81	0.49
11:K:59:TYR:CE2	11:K:63:LEU:HD12	2.48	0.49
1:A:146:G:O6	1:A:176:C:N3	2.45	0.49
1:A:914:A:C2'	1:A:915:A:H5'	2.42	0.49
1:A:139:G:H2'	1:A:140:A:H8	1.77	0.49
1:A:592:G:C2	1:A:648:A:C2	3.01	0.49
7:G:108:ALA:O	7:G:111:ARG:HB2	2.12	0.49
1:A:1255:G:H2'	1:A:1255:G:N3	2.28	0.49
1:A:664:G:P	18:R:64:ARG:HH21	2.36	0.49
1:A:1452:C:H4'	1:A:1456:G:N3	2.28	0.49
1:A:327:A:C3'	1:A:328:C:H5''	2.39	0.49
12:L:60:LEU:N	12:L:60:LEU:HD22	2.28	0.49
1:A:1187:G:C6	1:A:1188:A:C6	3.00	0.49
1:A:1160:G:N2	1:A:1161:C:C6	2.81	0.49
1:A:834:C:H2'	1:A:835:U:C6	2.48	0.49
1:A:1142:G:H3'	1:A:1143:G:H8	1.77	0.49
1:A:299:G:C5	1:A:300:A:C6	3.01	0.49
1:A:93:G:C6	1:A:96:U:C4	3.00	0.49
20:T:79:ARG:HA	20:T:82:SER:OG	2.13	0.49
2:B:83:MET:O	2:B:85:ALA:N	2.46	0.49
13:M:14:ARG:HA	13:M:43:THR:O	2.13	0.49
15:O:25:THR:O	15:O:26:GLU:C	2.51	0.49
16:P:8:ARG:HG2	16:P:9:PHE:H	1.77	0.49
1:A:682:G:H1	1:A:708:C:H42	1.61	0.49
8:H:65:TYR:CD1	8:H:65:TYR:N	2.81	0.49
1:A:1082:G:C6	1:A:1083:U:N3	2.81	0.49
1:A:1206:G:O4'	3:C:194:GLY:HA2	2.13	0.49
17:Q:83:ASP:O	17:Q:87:LYS:HG2	2.13	0.49
1:A:693:G:H1'	7:G:82:GLY:HA3	1.94	0.49
1:A:356:A:H1'	1:A:368:U:O2'	2.12	0.49
1:A:1076:C:N3	1:A:1082:G:C2	2.81	0.49
12:L:55:VAL:HG13	12:L:68:ALA:O	2.13	0.49
13:M:44:ARG:HB2	13:M:47:ASP:OD1	2.13	0.49
1:A:262:A:C6	1:A:263:A:N6	2.81	0.49
1:A:693:G:O2'	1:A:694:A:H5'	2.13	0.49
3:C:66:VAL:HG11	3:C:91:LEU:HD13	1.95	0.49
2:B:185:ILE:HA	2:B:199:TYR:O	2.13	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
16:P:18:ARG:O	16:P:19:ILE:C	2.52	0.48
1:A:1399:C:H4'	1:A:1400:C:C5'	2.43	0.48
8:H:9:MET:O	8:H:12:ARG:HB2	2.13	0.48
1:A:255:G:O6	1:A:266:G:O6	2.31	0.48
1:A:964:A:N3	1:A:969:A:O2'	2.37	0.48
1:A:658:G:C5	1:A:659:U:C5	3.01	0.48
1:A:1067:A:H1'	1:A:1068:G:H8	1.75	0.48
2:B:167:PRO:HG3	2:B:188:ALA:HB2	1.95	0.48
1:A:1496:C:H2'	1:A:1497:G:O4'	2.12	0.48
1:A:1366:C:OP1	9:I:117:HIS:HE1	1.96	0.48
1:A:132:C:O2'	1:A:133:U:H5'	2.13	0.48
1:A:189(F):U:C2	17:Q:72:ARG:NH1	2.81	0.48
1:A:868:C:H2'	1:A:869:G:O4'	2.13	0.48
1:A:1248:A:C2'	1:A:1249:C:H5'	2.43	0.48
16:P:20:VAL:HG22	16:P:21:VAL:H	1.77	0.48
1:A:1371:G:C6	1:A:1372:U:C4	3.01	0.48
1:A:1412:C:C2	1:A:1489:G:N2	2.81	0.48
1:A:247:G:C6	1:A:248:C:C5	3.01	0.48
1:A:579:G:C6	1:A:580:U:C4	3.01	0.48
5:E:137:GLU:O	5:E:141:GLN:HG3	2.13	0.48
5:E:78:HIS:CE1	5:E:142:LEU:HA	2.45	0.48
1:A:1068:G:N3	1:A:1191:A:C2	2.81	0.48
4:D:2:GLY:O	4:D:3:ARG:C	2.51	0.48
1:A:693:G:O2'	7:G:82:GLY:HA3	2.14	0.48
1:A:890:G:O2'	1:A:906:G:O6	2.25	0.48
5:E:105:VAL:HG21	5:E:128:PRO:HA	1.94	0.48
1:A:355:C:C2	1:A:356:A:C8	3.00	0.48
1:A:444:C:C2	1:A:445:G:C8	3.01	0.48
1:A:490:G:OP2	4:D:132:ARG:NH2	2.46	0.48
16:P:19:ILE:HB	16:P:37:GLY:O	2.12	0.48
1:A:1169:A:C2'	1:A:1170:A:H8	2.20	0.48
1:A:828:A:H5''	1:A:859:A:C2	2.48	0.48
6:F:5:GLU:HG2	6:F:62:TRP:HZ2	1.76	0.48
17:Q:59:ILE:HD13	17:Q:73:VAL:HA	1.95	0.48
1:A:78:G:H22	1:A:91:C:N4	2.10	0.48
1:A:1327:C:H2'	1:A:1328:C:C6	2.48	0.48
1:A:264:U:O2'	17:Q:64:PRO:HB2	2.12	0.48
1:A:986:A:C6	1:A:1220:G:C2	3.02	0.48
1:A:620:C:H2'	1:A:621:A:O4'	2.12	0.48
1:A:533:A:C4'	1:A:534:U:OP1	2.61	0.48
2:B:42:ILE:HD11	2:B:202:PRO:HB2	1.95	0.48
1:A:70:G:H2'	1:A:71:C:C6	2.48	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
15:O:39:LEU:HD22	15:O:43:LEU:HG	1.94	0.48
1:A:438:G:O2'	1:A:493:G:C2	2.63	0.48
10:J:54:PHE:CZ	10:J:55:LYS:NZ	2.82	0.48
1:A:1310:G:N2	1:A:1328:C:C2	2.81	0.48
1:A:7:G:H21	5:E:121:LYS:HG2	1.78	0.48
20:T:29:LYS:O	20:T:33:ILE:HG12	2.12	0.48
13:M:54:VAL:O	13:M:58:GLU:HG2	2.13	0.48
3:C:125:GLU:HA	3:C:191:THR:HG22	1.95	0.48
1:A:668:G:O2'	15:O:46:HIS:CD2	2.66	0.48
18:R:25:THR:HG22	18:R:42:ARG:HH11	1.78	0.48
1:A:1075:C:H4'	1:A:1101:A:N6	2.27	0.48
1:A:961:U:OP2	1:A:1223:C:H4'	2.14	0.48
12:L:110:VAL:CG2	12:L:120:TYR:HB3	2.43	0.48
5:E:12:LEU:C	5:E:12:LEU:HD22	2.33	0.48
1:A:1321:C:H5''	1:A:1322:C:H5''	1.93	0.48
2:B:168:THR:CG2	2:B:192:SER:HA	2.43	0.48
1:A:448:A:H2'	1:A:449:C:C6	2.48	0.48
1:A:872:A:C4	1:A:874:G:N7	2.81	0.48
1:A:1256:A:H5'	1:A:1257:U:OP1	2.13	0.48
19:S:42:PRO:O	19:S:43:GLU:CB	2.55	0.48
1:A:825:G:N2	8:H:11:THR:HG21	2.29	0.48
3:C:134:ILE:HG22	3:C:168:ALA:HB3	1.96	0.48
13:M:31:LYS:HA	13:M:34:LEU:HD12	1.94	0.48
1:A:832:C:O2'	1:A:833:U:P	2.71	0.48
1:A:577:G:H1'	1:A:816:A:C4	2.48	0.48
1:A:1015:A:C6	1:A:1016:A:C6	3.01	0.48
1:A:1438:G:H2'	1:A:1439:C:H6	1.78	0.48
1:A:862:C:O2'	1:A:863:U:H5'	2.14	0.48
1:A:967:C:H5''	1:A:968:A:OP2	2.13	0.48
2:B:135:GLN:O	2:B:139:LYS:HB2	2.13	0.48
1:A:716:A:N3	11:K:118:GLY:HA2	2.29	0.48
1:A:586:C:C2'	1:A:587:G:H5'	2.44	0.48
4:D:64:LEU:HD12	4:D:64:LEU:O	2.13	0.48
1:A:108:G:C6	20:T:15:ARG:HD2	2.48	0.48
1:A:1097:C:O2	1:A:1169:A:H2	1.97	0.48
5:E:12:LEU:HD13	5:E:31:LEU:HB2	1.96	0.48
6:F:18:GLN:HA	6:F:21:LEU:HD23	1.94	0.48
1:A:659:U:O2'	1:A:660:G:H5'	2.13	0.48
1:A:414:A:C5	1:A:431:A:C2	3.01	0.48
9:I:45:ALA:O	9:I:48:GLU:HB2	2.14	0.48
1:A:33:A:H2'	1:A:34:C:C6	2.49	0.48
1:A:857:C:H2'	1:A:858:G:O4'	2.13	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:872:A:C2	1:A:874:G:C6	3.02	0.48
1:A:1406:U:H2'	1:A:1407:C:O4'	2.14	0.48
4:D:17:VAL:HG11	4:D:197:PRO:HB2	1.95	0.48
12:L:119:LYS:HB2	12:L:120:TYR:CD1	2.49	0.48
1:A:184:G:O2'	1:A:185:A:H5'	2.13	0.48
1:A:184:G:N2	1:A:194:C:C2	2.82	0.48
12:L:60:LEU:CD2	12:L:66:VAL:HG22	2.41	0.48
1:A:105:G:H2'	1:A:106:C:H6	1.77	0.48
4:D:100:ARG:NH1	4:D:137:SER:HA	2.29	0.48
1:A:1530:G:C4'	1:A:1530:G:OP1	2.61	0.48
7:G:146:GLU:OE2	7:G:149:ARG:HD2	2.14	0.48
1:A:677:U:H3	1:A:714:G:H22	1.61	0.48
1:A:920:U:H1'	1:A:1080:A:C2	2.49	0.48
4:D:104:VAL:O	4:D:108:LEU:HD13	2.13	0.48
1:A:24:U:O2'	1:A:25:C:H5'	2.13	0.48
1:A:349:A:O2'	1:A:350:G:H5'	2.13	0.48
11:K:126:ARG:O	11:K:127:LYS:C	2.52	0.48
1:A:451:A:C5	1:A:481:G:C5	3.02	0.48
1:A:394:G:H2'	1:A:395:C:H6	1.78	0.48
19:S:51:VAL:HG21	19:S:71:LEU:HB3	1.95	0.48
1:A:1507:A:C2	1:A:1508:G:C4	3.02	0.48
1:A:1097:C:O2'	1:A:1098:C:H5'	2.14	0.48
12:L:46:LYS:HB2	12:L:92:ASP:O	2.13	0.48
5:E:31:LEU:HD22	5:E:43:LEU:HD11	1.96	0.48
6:F:46:ARG:NH1	18:R:37:VAL:HG21	2.24	0.48
4:D:11:LEU:C	4:D:13:ARG:N	2.62	0.48
4:D:15:GLU:HG2	4:D:63:LYS:HG3	1.96	0.48
1:A:1142:G:H3'	1:A:1143:G:C8	2.48	0.48
6:F:75:LEU:HD23	6:F:79:LEU:HD21	1.96	0.48
1:A:977:A:C2'	1:A:978:A:H5'	2.43	0.48
1:A:1443:G:N2	1:A:1460:A:H1'	2.28	0.48
19:S:65:ASN:HB2	19:S:66:MET:HE3	1.96	0.48
9:I:51:ARG:HE	9:I:56:LEU:CD1	2.26	0.48
20:T:100:ILE:HD12	20:T:100:ILE:N	2.28	0.47
20:T:96:GLY:O	20:T:97:ALA:HB3	2.13	0.47
1:A:1372:U:OP1	9:I:71:SER:HB3	2.14	0.47
15:O:67:LEU:CD2	15:O:78:TYR:CE1	2.97	0.47
9:I:118:LYS:O	9:I:119:ALA:HB3	2.14	0.47
3:C:83:ARG:O	3:C:86:VAL:HG22	2.14	0.47
13:M:3:ARG:HA	13:M:9:ILE:HG13	1.95	0.47
2:B:185:ILE:HG12	2:B:185:ILE:O	2.13	0.47
1:A:920:U:H2'	1:A:921:U:C6	2.48	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:954:G:C2	1:A:955:U:C2	3.02	0.47
1:A:1202:G:C6	14:N:42:ILE:HG21	2.49	0.47
1:A:235:C:H5'	17:Q:70:ARG:HG2	1.95	0.47
16:P:54:GLU:O	16:P:57:ARG:HB2	2.14	0.47
1:A:671:G:C5	1:A:672:U:C5	3.02	0.47
1:A:66:G:C4'	1:A:173:U:C5	2.96	0.47
1:A:109:A:C6	1:A:326:G:C6	3.02	0.47
6:F:96:PRO:HB3	18:R:30:ASP:CG	2.34	0.47
13:M:14:ARG:CZ	13:M:42:ALA:HA	2.43	0.47
2:B:114:ARG:HA	2:B:117:GLU:HB2	1.96	0.47
3:C:113:ALA:C	3:C:115:LEU:N	2.68	0.47
1:A:1385:G:C2'	1:A:1386:G:H5'	2.44	0.47
1:A:625:G:C4	1:A:626:U:C5	3.02	0.47
1:A:671:G:C4	1:A:672:U:C6	3.02	0.47
1:A:892:A:H2'	1:A:893:C:H6	1.78	0.47
1:A:380:G:C2	1:A:384:G:N1	2.82	0.47
17:Q:45:HIS:O	17:Q:73:VAL:HG23	2.14	0.47
9:I:113:LYS:H	9:I:119:ALA:HA	1.79	0.47
5:E:36:ASP:O	5:E:37:ARG:HB2	2.14	0.47
1:A:582:U:C2	1:A:760:G:C6	3.02	0.47
1:A:382:A:H2'	1:A:383:A:C8	2.50	0.47
5:E:60:TYR:HE1	5:E:64:ARG:HH21	1.56	0.47
4:D:36:ARG:HG2	4:D:38:TYR:CZ	2.50	0.47
1:A:1147:C:C5	1:A:1148:U:C4	3.03	0.47
1:A:1098:C:N3	1:A:1099:G:C8	2.82	0.47
12:L:62:SER:O	12:L:64:TYR:N	2.47	0.47
1:A:344:A:H4'	1:A:345:C:OP2	2.14	0.47
1:A:411:A:C8	1:A:413:G:C8	3.02	0.47
9:I:28:VAL:HG13	9:I:65:VAL:HG12	1.96	0.47
1:A:832:C:N4	1:A:854:G:H1	2.12	0.47
4:D:30:LYS:C	4:D:32:ALA:H	2.17	0.47
11:K:62:GLN:O	11:K:64:ALA:N	2.47	0.47
20:T:58:LYS:HG3	20:T:62:LEU:HD12	1.96	0.47
10:J:58:ASP:O	10:J:59:SER:C	2.52	0.47
18:R:36:ASN:HD22	18:R:39:VAL:HG21	1.80	0.47
1:A:363:A:C5	12:L:31:PRO:HD2	2.48	0.47
12:L:20:LYS:H	12:L:20:LYS:HD3	1.79	0.47
1:A:355:C:O2'	1:A:356:A:H5'	2.14	0.47
1:A:59:A:H3'	1:A:331:G:H22	1.80	0.47
1:A:343:U:C2'	1:A:346:G:O6	2.63	0.47
8:H:29:SER:HB3	8:H:32:LYS:CD	2.45	0.47
1:A:63:C:H42	1:A:104:G:H1	1.62	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1160:G:C2	1:A:1161:C:C6	3.03	0.47
6:F:9:VAL:HA	6:F:59:TYR:O	2.14	0.47
19:S:10:PHE:HZ	19:S:70:LYS:CE	2.27	0.47
7:G:150:ALA:O	11:K:57:THR:HG21	2.14	0.47
2:B:59:GLU:O	2:B:63:MET:HG2	2.14	0.47
1:A:391:G:C6	1:A:392:G:C5	3.03	0.47
1:A:60:A:C4'	1:A:61:G:O5'	2.63	0.47
17:Q:33:GLY:O	17:Q:34:LYS:C	2.53	0.47
5:E:93:PRO:HA	5:E:118:ILE:HD12	1.97	0.47
1:A:626:U:H4'	16:P:38:TYR:CZ	2.49	0.47
1:A:200:G:H1	1:A:217:C:N4	2.05	0.47
1:A:473:G:C2	1:A:474:G:C8	3.02	0.47
16:P:39:TYR:C	16:P:39:TYR:CD1	2.86	0.47
1:A:922:G:O2'	1:A:1398:A:N1	2.31	0.47
1:A:781:A:C3'	1:A:782:A:H5'	2.45	0.47
1:A:538:G:OP2	12:L:115:LYS:CG	2.62	0.47
1:A:946:A:O2'	1:A:1333:A:N3	2.42	0.47
6:F:72:VAL:CG2	6:F:90:VAL:HG11	2.44	0.47
13:M:78:ILE:HG22	13:M:93:ARG:HH22	1.78	0.47
6:F:6:VAL:HG12	6:F:7:ASN:N	2.30	0.47
11:K:48:ILE:HG21	11:K:63:LEU:HD13	1.96	0.47
1:A:564:C:H2'	1:A:565:U:H5'	1.97	0.47
1:A:276:G:H2'	1:A:277:C:H5'	1.96	0.47
1:A:1001(A):G:H2'	1:A:1002:G:O4'	2.15	0.47
10:J:22:LYS:O	10:J:22:LYS:HD2	2.15	0.47
1:A:444:C:H2'	1:A:445:G:C8	2.36	0.47
16:P:20:VAL:HG21	16:P:32:TYR:CB	2.45	0.47
16:P:20:VAL:HG21	16:P:32:TYR:CD2	2.49	0.47
1:A:1504:G:H4'	1:A:1505:G:O4'	2.15	0.47
1:A:1071:C:H5''	5:E:49:PRO:HG3	1.97	0.47
1:A:1074:G:N3	1:A:1102:A:C2	2.83	0.47
18:R:56:THR:CB	18:R:58:LEU:HD13	2.45	0.47
1:A:629:G:C6	1:A:630:G:N7	2.83	0.47
9:I:4:TYR:N	9:I:4:TYR:CD1	2.81	0.47
14:N:41:ARG:HG3	14:N:42:ILE:N	2.28	0.47
1:A:1371:G:O3'	9:I:69:GLY:HA3	2.15	0.47
1:A:114:U:O2'	1:A:115:G:H5'	2.15	0.47
16:P:50:LYS:HD3	16:P:51:VAL:N	2.30	0.47
1:A:247:G:C2	1:A:248:C:C6	3.02	0.47
12:L:24:VAL:HG13	12:L:98:TYR:CE2	2.50	0.47
4:D:159:ARG:HA	4:D:162:LEU:HB2	1.96	0.47
4:D:159:ARG:O	4:D:163:GLU:N	2.48	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:E:57:LYS:O	5:E:61:TYR:CD2	2.62	0.47
1:A:983:A:H5'	1:A:984:C:OP2	2.15	0.47
1:A:67:C:O2'	1:A:171:A:H1'	2.15	0.47
1:A:853:G:O2'	1:A:854:G:H5'	2.14	0.47
9:I:53:VAL:CG1	9:I:95:LYS:HE3	2.45	0.47
9:I:8:GLY:HA2	9:I:79:LEU:HD12	1.96	0.47
1:A:130:A:C8	17:Q:63:ARG:HG3	2.49	0.47
1:A:577:G:H1'	1:A:816:A:N3	2.29	0.47
1:A:985:C:H2'	1:A:986:A:C8	2.50	0.47
1:A:948:C:OP1	13:M:107:ALA:HA	2.14	0.47
1:A:865:A:H2	1:A:918:A:H4'	1.80	0.47
1:A:518:C:H4'	1:A:519:C:H5''	1.95	0.47
12:L:34:ARG:HG2	12:L:35:GLY:N	2.30	0.47
1:A:35:G:H2'	1:A:36:C:C6	2.49	0.47
8:H:69:ARG:HD3	8:H:75:ARG:O	2.12	0.47
3:C:123:GLN:O	3:C:128:PHE:HB2	2.15	0.47
2:B:239:VAL:O	2:B:239:VAL:HG12	2.15	0.47
10:J:40:LEU:HB2	10:J:41:PRO:CD	2.39	0.47
5:E:10:MET:HG3	5:E:13:ILE:CD1	2.45	0.47
1:A:199:G:O2'	1:A:200:G:H5'	2.14	0.47
1:A:192:U:C1'	20:T:103:GLY:HA2	2.44	0.47
4:D:21:LEU:O	4:D:113:SER:HB2	2.14	0.47
1:A:429:U:H4'	1:A:430:A:O5'	2.14	0.47
2:B:21:ARG:HB2	2:B:38:GLY:O	2.15	0.47
1:A:657:G:C2	1:A:750:G:C5	3.03	0.47
1:A:1189:C:O2'	3:C:176:HIS:CD2	2.67	0.47
1:A:721:G:H4'	1:A:722:A:O4'	2.14	0.47
1:A:1259:C:HO2'	1:A:1284:C:C1'	2.27	0.47
1:A:655:A:C2	1:A:754:C:N4	2.83	0.47
1:A:738:C:H2'	1:A:739:C:C6	2.49	0.47
11:K:21:ILE:N	11:K:21:ILE:HD12	2.30	0.47
4:D:75:PHE:CE2	4:D:93:PHE:HZ	2.33	0.47
1:A:149:A:O2'	1:A:150:C:P	2.73	0.47
1:A:983:A:H3'	1:A:983:A:N3	2.30	0.47
5:E:6:PHE:CD2	5:E:36:ASP:HB3	2.50	0.47
10:J:38:ILE:HG13	10:J:38:ILE:O	2.15	0.47
2:B:111:ARG:O	2:B:145:LEU:HD11	2.14	0.47
2:B:144:ARG:HG3	2:B:145:LEU:N	2.30	0.47
1:A:674:G:H2'	1:A:675:A:C8	2.48	0.47
1:A:675:A:C6	1:A:676:A:C5	3.03	0.47
4:D:68:TYR:N	4:D:68:TYR:CD1	2.83	0.47
12:L:117:ARG:NH2	12:L:124:LYS:HB2	2.30	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:L:32:PHE:HE1	12:L:86:ARG:HG3	1.80	0.47
7:G:155:ARG:O	7:G:156:TRP:HD1	1.98	0.47
1:A:373:A:H2'	1:A:374:A:H8	1.80	0.46
10:J:49:VAL:CG1	14:N:41:ARG:HB2	2.44	0.46
1:A:342:C:H2'	1:A:343:U:O4'	2.14	0.46
15:O:63:ARG:O	15:O:67:LEU:HB2	2.14	0.46
4:D:173:TRP:HA	4:D:187:ARG:NH1	2.30	0.46
9:I:21:PRO:HA	9:I:58:ARG:O	2.15	0.46
1:A:262:A:C6	1:A:263:A:C6	3.03	0.46
17:Q:81:ARG:NH2	17:Q:83:ASP:OD2	2.44	0.46
1:A:373:A:C2	1:A:374:A:C8	3.03	0.46
16:P:5:ARG:HB3	16:P:67:THR:OG1	2.16	0.46
1:A:16:A:C2	1:A:17:U:C6	3.04	0.46
1:A:735:C:H1'	18:R:75:ILE:HD11	1.96	0.46
1:A:1203:C:H2'	1:A:1204:A:O4'	2.16	0.46
1:A:974:A:P	14:N:41:ARG:HH12	2.38	0.46
6:F:97:PHE:O	18:R:31:LEU:HD23	2.14	0.46
1:A:414:A:C4	1:A:415:A:C8	3.03	0.46
1:A:1157:A:H5'	1:A:1158:C:C6	2.50	0.46
1:A:719:C:H5	1:A:720:C:N3	2.13	0.46
12:L:18:VAL:O	12:L:19:ARG:HB3	2.15	0.46
1:A:109:A:H2'	1:A:326:G:H21	1.79	0.46
1:A:458:C:H2'	1:A:460:G:C8	2.50	0.46
8:H:64:LYS:CG	8:H:79:VAL:HG21	2.45	0.46
20:T:81:LYS:C	20:T:83:ARG:N	2.69	0.46
12:L:10:LEU:HB3	17:Q:32:TYR:CE1	2.50	0.46
1:A:678:U:H2'	1:A:679:C:C6	2.50	0.46
5:E:102:ALA:HB1	5:E:106:PRO:HG2	1.96	0.46
1:A:1277:C:H2'	1:A:1278:U:H5'	1.97	0.46
8:H:112:LEU:HD12	8:H:112:LEU:O	2.16	0.46
5:E:48:ALA:HB1	5:E:49:PRO:HD2	1.98	0.46
5:E:69:VAL:HG12	5:E:71:LEU:CD2	2.44	0.46
10:J:82:ILE:O	10:J:86:MET:HB3	2.16	0.46
1:A:473:G:N3	1:A:474:G:C8	2.83	0.46
4:D:8:VAL:O	4:D:10:ARG:N	2.48	0.46
2:B:187:LEU:HA	2:B:201:ILE:HB	1.98	0.46
4:D:173:TRP:O	4:D:174:LEU:HD23	2.15	0.46
1:A:66:G:C6	1:A:67:C:C5	3.03	0.46
11:K:69:ALA:HB1	11:K:103:LEU:CD2	2.45	0.46
1:A:679:C:O2'	1:A:680:C:H5'	2.15	0.46
7:G:106:GLN:O	7:G:110:GLN:HG3	2.15	0.46
1:A:923:A:H61	1:A:1393:U:H3	1.62	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:M:68:GLY:O	13:M:70:LEU:N	2.49	0.46
4:D:68:TYR:H	4:D:68:TYR:HD1	1.63	0.46
1:A:397:A:N7	1:A:548:G:C8	2.84	0.46
1:A:544:G:H2'	1:A:545:C:H6	1.80	0.46
5:E:139:LEU:HD23	5:E:142:LEU:HD11	1.98	0.46
3:C:124:ILE:HG13	3:C:130:VAL:HG22	1.98	0.46
1:A:801:U:H2'	1:A:802:A:C8	2.48	0.46
1:A:1522:U:C2	1:A:1523:G:C8	3.03	0.46
1:A:950:U:H2'	1:A:951:G:H8	1.80	0.46
1:A:451:A:C5	1:A:481:G:C6	3.03	0.46
1:A:691:G:H1'	1:A:696:A:N6	2.30	0.46
6:F:91:VAL:HG12	6:F:92:LYS:O	2.15	0.46
1:A:976:G:P	14:N:32:SER:H	2.37	0.46
1:A:1446:U:O2	1:A:1456:G:O6	2.33	0.46
16:P:43:LYS:CG	16:P:48:TRP:CE3	2.98	0.46
2:B:69:LEU:HB3	2:B:162:ILE:HG22	1.98	0.46
1:A:559:A:H4'	1:A:560:U:O5'	2.15	0.46
1:A:501:C:H2'	1:A:502:G:H8	1.81	0.46
2:B:67:THR:HG21	2:B:155:LEU:CD2	2.44	0.46
1:A:782:A:H4'	1:A:1514:C:O2'	2.15	0.46
2:B:9:GLU:CD	2:B:9:GLU:H	2.17	0.46
1:A:1312:G:N2	1:A:1326:C:C2	2.84	0.46
18:R:44:LEU:HD23	18:R:48:GLY:O	2.15	0.46
4:D:92:VAL:O	4:D:96:LEU:CD2	2.63	0.46
7:G:100:ALA:O	7:G:104:LEU:HD23	2.14	0.46
3:C:186:PHE:CE2	3:C:188:LEU:HD21	2.51	0.46
20:T:87:LYS:HE3	20:T:91:LEU:HD11	1.98	0.46
1:A:432:A:N7	1:A:433:C:C2	2.84	0.46
19:S:22:LEU:O	19:S:26:GLY:HA2	2.16	0.46
1:A:731:G:OP1	1:A:766:A:H1'	2.15	0.46
4:D:126:ILE:HG22	4:D:127:THR:N	2.27	0.46
16:P:21:VAL:O	16:P:33:ILE:HB	2.16	0.46
1:A:1064:G:OP2	1:A:1386:G:H4'	2.16	0.46
1:A:1386:G:C2	1:A:1387:G:C8	3.04	0.46
1:A:685:G:N2	1:A:686:U:N3	2.64	0.46
1:A:827:U:C4	1:A:870:U:N3	2.84	0.46
16:P:43:LYS:HG2	16:P:48:TRP:CE3	2.50	0.46
3:C:108:ASN:HB3	3:C:111:LEU:HB2	1.97	0.46
4:D:2:GLY:O	4:D:4:TYR:N	2.48	0.46
1:A:1478:C:H2'	1:A:1479:C:H6	1.80	0.46
1:A:863:U:H2'	1:A:865:A:OP2	2.16	0.46
1:A:586:C:H2'	1:A:587:G:H5'	1.98	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1377:A:H2'	7:G:7:ALA:CB	2.45	0.46
8:H:107:LEU:HD23	8:H:107:LEU:N	2.30	0.46
17:Q:68:ARG:O	17:Q:68:ARG:HG3	2.14	0.46
7:G:49:ILE:HG22	7:G:49:ILE:O	2.15	0.46
1:A:708:C:O2'	1:A:709:G:H5'	2.15	0.46
1:A:926:G:C6	1:A:1505:G:C6	3.04	0.46
8:H:112:LEU:HD12	8:H:114:THR:HG22	1.97	0.46
4:D:194:LEU:HD22	4:D:194:LEU:N	2.30	0.46
10:J:86:MET:O	10:J:86:MET:HG3	2.15	0.46
6:F:40:VAL:HA	6:F:62:TRP:O	2.16	0.46
1:A:159:G:H21	1:A:161:A:H8	1.62	0.46
1:A:817:C:H4'	1:A:818:G:OP1	2.16	0.46
1:A:602:A:C2	1:A:603:U:C2	3.04	0.46
8:H:8:ASP:O	8:H:11:THR:N	2.49	0.46
1:A:724:G:N3	1:A:725:G:C8	2.84	0.46
2:B:9:GLU:HA	2:B:12:GLU:OE1	2.15	0.46
2:B:116:GLU:HA	2:B:119:GLU:HB3	1.97	0.46
1:A:134:A:H61	16:P:25:ARG:NH1	2.14	0.46
1:A:182:U:OP2	1:A:183:G:OP2	2.33	0.46
1:A:716:A:C2'	1:A:717:C:O5'	2.64	0.46
19:S:37:ARG:HG3	19:S:37:ARG:H	1.61	0.46
1:A:258:G:N3	1:A:259:G:C8	2.84	0.46
2:B:118:LEU:HD11	2:B:141:GLU:HG2	1.97	0.46
1:A:734:G:C6	1:A:735:C:C4	3.04	0.46
5:E:101:ILE:CD1	5:E:119:LEU:HD23	2.46	0.46
1:A:1226:C:OP1	13:M:91:ARG:NH1	2.49	0.46
1:A:827:U:H2'	1:A:859:A:H61	1.80	0.46
1:A:1030(D):A:H62	1:A:1031:G:H21	1.62	0.46
10:J:29:ARG:HH22	10:J:84:GLN:HG2	1.81	0.46
2:B:61:LEU:HD23	2:B:68:ILE:HD11	1.94	0.46
2:B:76:GLN:O	2:B:208:ILE:HG12	2.15	0.46
2:B:167:PRO:HG2	2:B:192:SER:HB3	1.98	0.46
12:L:56:ALA:O	12:L:68:ALA:N	2.49	0.46
1:A:854:G:H3'	1:A:871:U:O4	2.15	0.46
1:A:1128:C:O2	1:A:1130:A:N7	2.48	0.46
1:A:1368:G:OP2	9:I:112:LYS:HD2	2.16	0.46
1:A:1242:C:O5'	1:A:1242:C:H6	1.99	0.46
20:T:94:ALA:O	20:T:95:ALA:HB3	2.15	0.46
1:A:265:G:H4'	17:Q:66:SER:HA	1.97	0.46
18:R:22:VAL:O	18:R:22:VAL:HG12	2.16	0.46
1:A:61:G:OP1	20:T:10:LEU:HD11	2.16	0.46
2:B:51:LEU:HD21	2:B:214:ILE:HD12	1.96	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:E:78:HIS:CE1	5:E:142:LEU:HD23	2.51	0.46
5:E:78:HIS:HE1	5:E:142:LEU:HD23	1.81	0.46
12:L:41:ARG:HG2	12:L:42:THR:N	2.30	0.46
1:A:427:U:OP1	4:D:13:ARG:NH2	2.49	0.46
1:A:177:C:OP1	20:T:65:LYS:HD3	2.16	0.46
1:A:1381:U:C2'	1:A:1382:C:H5'	2.46	0.46
3:C:102:ASN:O	3:C:103:VAL:HG23	2.16	0.46
1:A:1296:C:H5'	1:A:1297:C:OP2	2.16	0.46
16:P:20:VAL:CG2	16:P:32:TYR:HB2	2.46	0.46
1:A:681:C:C2	1:A:710:G:N2	2.84	0.46
20:T:89:ARG:HH22	20:T:104:LEU:HD21	1.78	0.46
1:A:327:A:C6	1:A:329:A:C5	3.04	0.46
16:P:50:LYS:HD3	16:P:50:LYS:C	2.37	0.46
11:K:111:ASP:CA	18:R:84:LYS:HE2	2.44	0.46
1:A:502:G:C2	1:A:503:C:C2	3.04	0.46
2:B:204:ASN:ND2	2:B:205:ASP:N	2.64	0.46
4:D:170:VAL:HG22	4:D:171:GLY:N	2.30	0.46
1:A:409:G:H5'	4:D:24:GLU:OE1	2.16	0.46
17:Q:59:ILE:HG22	17:Q:71:PHE:CD1	2.50	0.46
11:K:69:ALA:O	11:K:73:MET:HG2	2.16	0.46
5:E:122:GLU:OE1	5:E:131:ILE:HG13	2.16	0.46
1:A:950:U:H3'	13:M:102:ARG:HH12	1.80	0.46
1:A:20:U:O2'	1:A:21:G:H5'	2.16	0.46
1:A:533:A:H3'	1:A:533:A:OP1	2.15	0.46
1:A:1429:C:H2'	1:A:1430:C:C6	2.51	0.46
2:B:30:ARG:HG3	2:B:31:TYR:CE2	2.51	0.46
1:A:1079:G:O3'	5:E:14:ARG:NH2	2.49	0.45
8:H:20:TYR:CD1	8:H:65:TYR:CD2	2.89	0.45
1:A:320:C:H2'	1:A:321:A:O4'	2.16	0.45
1:A:407:G:H4'	4:D:115:ARG:O	2.16	0.45
13:M:13:LYS:O	13:M:45:VAL:HG23	2.16	0.45
4:D:108:LEU:HD12	4:D:174:LEU:HD13	1.98	0.45
1:A:272:C:H2'	1:A:273:A:C8	2.51	0.45
7:G:152:ALA:O	7:G:155:ARG:HG3	2.15	0.45
1:A:283:C:H2'	1:A:284:G:O4'	2.16	0.45
1:A:375:U:C4	1:A:376:G:N7	2.84	0.45
1:A:883:C:C2'	1:A:884:U:H5'	2.46	0.45
1:A:90:U:H3'	1:A:90:U:H6	1.82	0.45
2:B:15:VAL:C	2:B:16:HIS:CG	2.90	0.45
1:A:505:G:C5	1:A:535:A:C2	3.04	0.45
1:A:951:G:OP2	13:M:102:ARG:NH2	2.50	0.45
1:A:297:G:H4'	1:A:557:G:H4'	1.98	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:594:G:O2'	1:A:595:G:H5'	2.16	0.45
4:D:102:ASP:HB3	4:D:136:PRO:HA	1.98	0.45
2:B:91:PRO:N	2:B:154:LEU:HD12	2.32	0.45
1:A:626:U:C2	1:A:627:G:N7	2.85	0.45
1:A:1413:A:C2	1:A:1414:U:C2	3.05	0.45
1:A:159:G:N3	1:A:161:A:OP2	2.50	0.45
18:R:31:LEU:H	18:R:31:LEU:CD2	2.24	0.45
1:A:747:C:C5	1:A:748:C:C4	3.04	0.45
1:A:930:C:C2'	1:A:931:C:H5'	2.46	0.45
6:F:60:PHE:C	6:F:61:LEU:HD12	2.36	0.45
10:J:39:PRO:CB	10:J:70:ARG:HH12	2.29	0.45
11:K:41:THR:HG22	11:K:42:TRP:N	2.31	0.45
18:R:45:SER:HB3	18:R:51:LEU:HD21	1.98	0.45
6:F:75:LEU:CD2	6:F:79:LEU:HD21	2.47	0.45
1:A:1118:C:H42	1:A:1155:G:H1	1.64	0.45
20:T:82:SER:O	20:T:86:ARG:CB	2.64	0.45
1:A:303:A:C5	1:A:304:U:C5	3.05	0.45
1:A:1034:G:N2	1:A:1035:A:N6	2.64	0.45
1:A:356:A:H2'	1:A:357:G:O5'	2.16	0.45
1:A:357:G:C2	1:A:358:U:C5	3.05	0.45
1:A:1070:U:C2	1:A:1071:C:C5	3.04	0.45
6:F:39:LYS:O	6:F:40:VAL:HB	2.17	0.45
6:F:3:ARG:HD3	6:F:64:GLN:OE1	2.16	0.45
1:A:1163:C:C2	1:A:1174:G:N2	2.84	0.45
4:D:171:GLY:HA2	4:D:172:PRO:HD3	1.86	0.45
6:F:23:LYS:HB3	6:F:23:LYS:HE2	1.76	0.45
1:A:1320:C:H5'	19:S:70:LYS:HG3	1.97	0.45
1:A:945:G:H2'	1:A:945:G:N3	2.31	0.45
1:A:1064:G:H5'	1:A:1066:C:H1'	1.98	0.45
1:A:1452:C:H4'	1:A:1456:G:O5'	2.16	0.45
1:A:1202:G:H2'	1:A:1203:C:O4'	2.16	0.45
1:A:1199:U:H4'	10:J:54:PHE:CE2	2.52	0.45
1:A:327:A:C2	1:A:329:A:C4	3.04	0.45
1:A:769:G:H4'	1:A:1513:A:H4'	1.98	0.45
17:Q:22:LEU:HD11	17:Q:39:SER:HB2	1.97	0.45
1:A:831:U:O2'	1:A:832:C:H5'	2.17	0.45
1:A:1142:G:H2'	1:A:1143:G:O4'	2.16	0.45
1:A:1248:A:H2'	1:A:1249:C:H5'	1.99	0.45
8:H:51:VAL:O	8:H:52:ASP:HB2	2.16	0.45
4:D:127:THR:HB	4:D:132:ARG:HA	1.98	0.45
16:P:9:PHE:CD2	16:P:18:ARG:HB2	2.52	0.45
4:D:189:PRO:HB2	4:D:194:LEU:CD2	2.38	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:H:17:THR:O	8:H:20:TYR:N	2.48	0.45
1:A:159:G:C4	1:A:161:A:OP2	2.69	0.45
1:A:414:A:H2'	1:A:415:A:C8	2.52	0.45
11:K:102:GLY:O	11:K:103:LEU:HD13	2.17	0.45
1:A:25:C:H5''	1:A:524:G:H1'	1.99	0.45
20:T:26:ASN:HA	20:T:29:LYS:HG2	1.98	0.45
12:L:82:VAL:H	12:L:106:ASP:HB2	1.81	0.45
8:H:80:ILE:HG22	8:H:80:ILE:O	2.16	0.45
1:A:59:A:H1'	1:A:354:G:N2	2.32	0.45
4:D:127:THR:OG1	4:D:128:VAL:N	2.50	0.45
15:O:43:LEU:CD1	15:O:56:LEU:HD22	2.47	0.45
11:K:84:VAL:HG11	11:K:95:ILE:HD12	1.98	0.45
12:L:93:LEU:O	12:L:94:PRO:C	2.55	0.45
1:A:1250:A:H4'	9:I:68:GLY:H	1.81	0.45
4:D:79:PHE:CD2	4:D:79:PHE:C	2.90	0.45
1:A:561:U:HO2'	1:A:562:C:P	2.40	0.45
4:D:138:TYR:HD2	4:D:139:ARG:N	2.14	0.45
3:C:124:ILE:HD11	3:C:130:VAL:HG13	1.97	0.45
1:A:1159:U:C5	1:A:1182:G:C4	3.05	0.45
1:A:665:A:N6	1:A:725:G:O6	2.49	0.45
4:D:100:ARG:HH22	4:D:118:ARG:HH22	1.64	0.45
5:E:6:PHE:HB2	5:E:34:VAL:HG13	1.98	0.45
1:A:406:G:H5'	4:D:5:ILE:HD13	1.97	0.45
7:G:145:ALA:O	7:G:146:GLU:HB2	2.17	0.45
2:B:238:LEU:H	2:B:238:LEU:HD23	1.82	0.45
11:K:52:GLY:H	11:K:55:LYS:HG3	1.81	0.45
19:S:16:LEU:O	19:S:20:LEU:HB2	2.16	0.45
18:R:47:THR:HB	18:R:49:LYS:HG3	1.99	0.45
8:H:21:LYS:O	8:H:22:GLU:C	2.55	0.45
1:A:293:G:C6	1:A:294:U:C4	3.04	0.45
16:P:9:PHE:CE2	16:P:18:ARG:HB2	2.52	0.45
12:L:64:TYR:O	12:L:65:GLU:HB2	2.17	0.45
1:A:79:G:H4'	1:A:80:G:OP1	2.17	0.45
1:A:254:G:O2'	1:A:255:G:H5'	2.15	0.45
1:A:1031:G:H2'	1:A:1032:G:C8	2.52	0.45
1:A:600:C:H2'	1:A:601:C:H6	1.78	0.45
2:B:44:LEU:O	2:B:47:THR:HB	2.17	0.45
1:A:938:A:C6	1:A:939:G:C5	3.05	0.45
1:A:632:A:H8	1:A:633:G:C8	2.34	0.45
17:Q:6:LEU:O	17:Q:58:GLU:HA	2.16	0.45
1:A:78:G:N2	1:A:91:C:H42	2.15	0.45
1:A:335:C:O2'	1:A:336:C:H5'	2.16	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
10:J:16:LEU:O	10:J:16:LEU:HD13	2.17	0.45
1:A:764:C:C2	1:A:765:G:C8	3.05	0.45
1:A:1270:C:H2'	1:A:1271:G:O4'	2.16	0.45
1:A:515:G:H2'	1:A:516:U:O4'	2.17	0.45
1:A:514:C:O2'	1:A:515:G:H5'	2.17	0.45
5:E:79:GLU:HB3	5:E:92:LYS:HG2	1.99	0.45
1:A:366:C:H1'	1:A:367:U:OP1	2.16	0.45
10:J:30:SER:HB2	10:J:80:LYS:HG3	1.98	0.45
1:A:1322:C:OP1	1:A:1322:C:H6	2.00	0.45
16:P:81:ARG:C	16:P:82:GLN:HE21	2.20	0.45
1:A:166:G:C5	1:A:167:G:N7	2.85	0.45
1:A:1250:A:H2	1:A:1370:G:H1'	1.82	0.45
1:A:407:G:O2'	4:D:116:GLN:HG3	2.17	0.45
1:A:542:G:H5'	4:D:41:GLY:HA3	1.99	0.45
1:A:502:G:H4'	1:A:550:G:H4'	1.99	0.45
4:D:158:ILE:HG23	4:D:162:LEU:CD1	2.47	0.45
1:A:414:A:H2'	1:A:415:A:O4'	2.17	0.45
1:A:1189:C:H5''	3:C:5:ILE:HG21	1.98	0.45
2:B:28:PHE:O	2:B:28:PHE:CD1	2.69	0.45
1:A:1158:C:O2	1:A:1158:C:C2'	2.65	0.45
1:A:461:A:C5	1:A:471:G:C6	3.05	0.45
6:F:99:ALA:HB1	18:R:23:LYS:NZ	2.32	0.45
1:A:245:C:O2	1:A:283:C:N3	2.49	0.45
1:A:303:A:C4	1:A:304:U:C6	3.05	0.45
6:F:94:GLN:NE2	18:R:32:ARG:HD2	2.31	0.45
1:A:1264:C:H2'	1:A:1265:G:H8	1.82	0.45
2:B:171:ALA:HA	2:B:174:VAL:HG23	1.99	0.45
1:A:849:C:H2'	1:A:850:U:O4'	2.17	0.45
1:A:356:A:H2'	1:A:357:G:C8	2.52	0.45
3:C:113:ALA:O	3:C:115:LEU:N	2.49	0.45
18:R:74:ARG:HG3	18:R:79:LEU:HB3	2.00	0.45
1:A:1168:A:N6	1:A:1169:A:C6	2.85	0.45
2:B:84:GLU:OE1	2:B:219:VAL:HB	2.16	0.45
12:L:38:THR:HG21	12:L:65:GLU:OE2	2.17	0.45
1:A:473:G:C2	1:A:474:G:N7	2.85	0.45
1:A:1285:A:C4'	1:A:1286:A:O5'	2.65	0.45
1:A:543:C:O2'	1:A:544:G:H5'	2.16	0.45
1:A:1128:C:H5'	9:I:16:ARG:NH1	2.32	0.45
1:A:927:G:OP2	1:A:1503:A:C5	2.70	0.45
10:J:51:ARG:HG3	10:J:61:GLU:N	2.31	0.45
7:G:69:VAL:HG13	7:G:134:ALA:O	2.17	0.45
1:A:93:G:H2'	1:A:96:U:H5'	1.98	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:961:U:C4	1:A:962:C:C4	3.05	0.45
1:A:512:U:H2'	1:A:513:C:H6	1.80	0.45
19:S:58:VAL:O	19:S:58:VAL:HG23	2.17	0.45
4:D:128:VAL:HA	4:D:145:GLU:O	2.16	0.44
16:P:21:VAL:O	16:P:21:VAL:HG23	2.16	0.44
1:A:709:G:H2'	1:A:710:G:C8	2.48	0.44
12:L:110:VAL:HG21	12:L:120:TYR:HB3	1.99	0.44
1:A:1308:U:H5''	13:M:98:VAL:N	2.31	0.44
1:A:1289:A:H2'	1:A:1290:G:O4'	2.17	0.44
16:P:43:LYS:HG2	16:P:48:TRP:CD2	2.51	0.44
1:A:559:A:H4'	1:A:560:U:H3'	1.98	0.44
4:D:117:ALA:O	4:D:121:VAL:HG22	2.16	0.44
1:A:617:G:C2	1:A:618:C:C5	3.06	0.44
1:A:1245:A:N1	1:A:1293:G:C6	2.85	0.44
1:A:295:C:H2'	1:A:296:U:C6	2.52	0.44
1:A:1442:G:C5	1:A:1442(B):A:C2	3.05	0.44
1:A:321:A:C2	1:A:333:G:C2	3.05	0.44
12:L:60:LEU:H	12:L:60:LEU:HD22	1.82	0.44
1:A:659:U:C2	1:A:660:G:C8	3.04	0.44
12:L:32:PHE:CE1	12:L:86:ARG:HG3	2.51	0.44
1:A:1326:C:H2'	1:A:1327:C:C6	2.52	0.44
1:A:677:U:H3	1:A:714:G:N2	2.16	0.44
19:S:19:VAL:HG12	19:S:19:VAL:O	2.16	0.44
1:A:354:G:C4	1:A:355:C:C5	3.06	0.44
1:A:251:G:H4'	1:A:252:U:O5'	2.16	0.44
1:A:612:C:O2	1:A:629:G:N2	2.50	0.44
4:D:119:GLN:O	4:D:123:HIS:CD2	2.70	0.44
1:A:165:C:H2'	1:A:166:G:H8	1.82	0.44
1:A:324:G:N2	1:A:327:A:C8	2.86	0.44
1:A:328:C:H4'	1:A:329:A:H5'	1.99	0.44
1:A:499:A:H4'	1:A:500:G:H5'	2.00	0.44
1:A:197:A:N6	1:A:221:C:H5'	2.33	0.44
1:A:1334:G:C8	1:A:1334:G:OP2	2.70	0.44
7:G:70:LYS:O	7:G:138:LYS:HE3	2.16	0.44
1:A:1265:G:C6	1:A:1266:G:C6	3.06	0.44
1:A:443:C:O2	1:A:443:C:H2'	2.17	0.44
1:A:355:C:N3	1:A:356:A:N7	2.66	0.44
1:A:389:A:H2'	1:A:390:C:H5'	1.99	0.44
1:A:736:C:H2'	1:A:737:A:C8	2.53	0.44
4:D:18:LYS:HD2	4:D:33:MET:HG2	2.00	0.44
12:L:58:VAL:O	12:L:65:GLU:HA	2.16	0.44
1:A:255:G:H2'	1:A:256:U:C6	2.52	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:C:11:ARG:O	3:C:12:LEU:C	2.55	0.44
2:B:67:THR:HG21	2:B:155:LEU:CG	2.46	0.44
2:B:194:PRO:HB2	2:B:195:ASP:H	1.61	0.44
1:A:577:G:C8	1:A:816:A:N1	2.86	0.44
1:A:41:G:H2'	1:A:42:G:H8	1.80	0.44
5:E:41:VAL:HG13	5:E:113:ALA:HA	1.99	0.44
21:U:12:LYS:HB3	21:U:22:ARG:HD2	2.00	0.44
3:C:66:VAL:HG11	3:C:91:LEU:CD1	2.47	0.44
1:A:303:A:H2'	1:A:304:U:O4'	2.18	0.44
1:A:726:C:O2'	1:A:727:G:H5'	2.17	0.44
1:A:353:A:C2'	1:A:354:G:OP2	2.65	0.44
1:A:102:G:C5	1:A:103:C:C5	3.06	0.44
1:A:1107:C:C4	1:A:1108:G:C8	3.04	0.44
2:B:219:VAL:HA	2:B:222:ILE:CD1	2.47	0.44
20:T:63:ILE:O	20:T:66:ALA:HB3	2.17	0.44
1:A:859:A:C8	1:A:860:A:C8	3.05	0.44
1:A:500:G:N2	1:A:546:G:H1'	2.32	0.44
1:A:542:G:O2'	1:A:543:C:H5'	2.17	0.44
1:A:544:G:H2'	1:A:545:C:C6	2.53	0.44
15:O:32:LEU:O	15:O:36:ILE:HG13	2.17	0.44
1:A:601:C:O2'	1:A:602:A:H5'	2.17	0.44
1:A:562:C:N4	1:A:884:U:C6	2.85	0.44
1:A:930:C:C4	1:A:931:C:C5	3.06	0.44
1:A:196:A:N3	1:A:222:U:H1'	2.33	0.44
17:Q:5:VAL:O	17:Q:6:LEU:HD23	2.18	0.44
9:I:111:ARG:HG3	14:N:61:TRP:HE1	1.83	0.44
1:A:137:C:N4	1:A:226:G:H1	2.14	0.44
4:D:92:VAL:O	4:D:96:LEU:HD22	2.17	0.44
10:J:7:LYS:O	10:J:96:ILE:HA	2.17	0.44
1:A:189(F):U:C4	17:Q:72:ARG:NH2	2.86	0.44
20:T:82:SER:O	20:T:86:ARG:HB2	2.17	0.44
1:A:677:U:H2'	1:A:678:U:H6	1.81	0.44
1:A:1138:G:N3	1:A:1138:G:H3'	2.33	0.44
1:A:101:A:C2'	1:A:102:G:H5'	2.47	0.44
1:A:522:C:H5''	12:L:120:TYR:OH	2.18	0.44
2:B:55:PHE:C	2:B:57:PHE:N	2.71	0.44
2:B:97:TRP:HH2	2:B:176:GLU:CD	2.21	0.44
18:R:53:ARG:C	18:R:55:ARG:H	2.20	0.44
1:A:748:C:C4'	1:A:749:C:O5'	2.64	0.44
1:A:66:G:O4'	1:A:173:U:C4	2.70	0.44
8:H:31:PHE:O	8:H:34:GLU:HB2	2.18	0.44
1:A:790:A:N6	1:A:791:G:C6	2.86	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1260:C:H4'	1:A:1284:C:H5'	2.00	0.44
1:A:581:G:N2	1:A:582:U:C4	2.86	0.44
13:M:105:THR:O	13:M:106:ASN:O	2.35	0.44
1:A:1184:G:OP1	1:A:1184:G:H8	2.00	0.44
20:T:81:LYS:O	20:T:83:ARG:N	2.51	0.44
1:A:1206:G:C6	1:A:1207:G:C6	3.06	0.44
1:A:1293:G:O2'	1:A:1294:G:P	2.76	0.44
9:I:13:ALA:HA	9:I:67:GLY:O	2.18	0.44
1:A:1112:C:N3	3:C:178:LEU:HD23	2.33	0.44
11:K:122:LYS:HB3	11:K:122:LYS:HE2	1.66	0.44
1:A:445:G:C6	1:A:490:G:C6	3.06	0.44
1:A:955:U:H1'	1:A:1227:A:H61	1.81	0.44
1:A:1096:C:H2'	1:A:1097:C:C6	2.48	0.44
5:E:100:VAL:O	5:E:107:ARG:NH2	2.41	0.44
1:A:366:C:C1'	1:A:367:U:OP1	2.66	0.44
20:T:84:LEU:O	20:T:88:VAL:HG23	2.17	0.44
1:A:1191:A:H5''	3:C:4:LYS:HZ2	1.83	0.44
4:D:108:LEU:CD1	4:D:174:LEU:HD13	2.48	0.44
1:A:173:U:O4'	1:A:197:A:C4	2.71	0.44
6:F:82:ARG:HB2	6:F:85:VAL:HG23	1.99	0.44
1:A:90:U:C6	1:A:90:U:H3'	2.53	0.44
15:O:55:GLY:O	15:O:59:MET:HG3	2.17	0.44
1:A:97:G:O2'	1:A:98:G:O5'	2.34	0.44
14:N:44:LEU:HD12	14:N:44:LEU:C	2.37	0.44
2:B:185:ILE:CG2	2:B:199:TYR:HB2	2.23	0.44
1:A:1442:G:C8	1:A:1442(B):A:H2	2.35	0.44
1:A:1072:G:C6	1:A:1073:U:O4	2.70	0.44
1:A:976:G:OP1	14:N:32:SER:N	2.41	0.44
1:A:67:C:H2'	1:A:68:G:H8	1.82	0.44
15:O:55:GLY:HA2	15:O:58:MET:CE	2.48	0.44
1:A:1522:U:H2'	1:A:1523:G:H8	1.83	0.44
8:H:30:ARG:HB3	8:H:30:ARG:NH1	2.33	0.44
5:E:120:THR:O	5:E:121:LYS:HB2	2.18	0.44
11:K:96:ARG:O	11:K:99:GLN:HG2	2.17	0.44
15:O:9:GLN:O	15:O:10:LYS:C	2.55	0.44
1:A:1510:U:H2'	1:A:1511:G:C8	2.52	0.44
1:A:663:A:O2'	1:A:664:G:H5'	2.17	0.44
6:F:91:VAL:HG11	18:R:72:ARG:NH1	2.33	0.44
4:D:188:LEU:HA	4:D:189:PRO:HD2	1.88	0.44
8:H:10:LEU:H	8:H:10:LEU:HD23	1.78	0.44
1:A:112:G:C2	1:A:113:G:C8	3.05	0.44
1:A:397:A:H5''	1:A:397:A:N3	2.33	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:603:U:O2'	1:A:604:G:H5'	2.18	0.44
1:A:503:C:C6	1:A:504:C:H5	2.36	0.44
12:L:69:TYR:HB3	12:L:99:HIS:CD2	2.52	0.44
1:A:590:C:O2'	1:A:591:U:H5'	2.17	0.44
17:Q:3:LYS:HB2	17:Q:60:ILE:HD11	2.00	0.44
3:C:152:ILE:HB	3:C:199:LYS:HB2	1.99	0.44
4:D:43:HIS:HA	4:D:46:LYS:HE3	1.99	0.44
1:A:1422:G:O2'	1:A:1423:G:H5'	2.17	0.44
1:A:520:A:H2	1:A:536:C:O2	2.01	0.44
1:A:1465:C:C4	1:A:1466:C:C4	3.06	0.44
1:A:6:G:H4'	1:A:298:A:H4'	2.00	0.44
1:A:706:A:C5	1:A:707:C:H5	2.36	0.43
4:D:17:VAL:HG12	4:D:18:LYS:N	2.32	0.43
1:A:101:A:H2'	1:A:102:G:H5'	2.00	0.43
1:A:437:U:H2'	1:A:438:G:O4'	2.18	0.43
1:A:1057:G:C5	1:A:1204:A:C2	3.05	0.43
17:Q:99:SER:O	17:Q:100:LYS:HD3	2.18	0.43
1:A:541:G:H2'	1:A:542:G:C8	2.52	0.43
15:O:74:ASP:OD2	15:O:77:ARG:HG2	2.17	0.43
3:C:58:GLU:H	3:C:65:ALA:CB	2.26	0.43
3:C:138:VAL:CG2	3:C:151:VAL:HG23	2.48	0.43
1:A:937:A:H1'	1:A:1379:G:N2	2.33	0.43
1:A:997:U:H2'	1:A:998:G:C8	2.52	0.43
5:E:47:LYS:N	5:E:47:LYS:HD3	2.33	0.43
13:M:3:ARG:HG2	13:M:9:ILE:HD11	1.99	0.43
1:A:1054:C:H3'	1:A:1054:C:O2	2.18	0.43
14:N:12:ARG:C	14:N:14:PRO:HD2	2.39	0.43
1:A:1483:A:H8	1:A:1483:A:O5'	2.01	0.43
1:A:1125:U:C2'	1:A:1126:U:OP2	2.65	0.43
4:D:148:VAL:CG1	4:D:149:ALA:H	2.22	0.43
10:J:80:LYS:HB2	10:J:80:LYS:NZ	2.33	0.43
1:A:509:A:O2'	1:A:510:A:C5'	2.66	0.43
2:B:21:ARG:HB2	2:B:39:ILE:HA	2.00	0.43
1:A:750:G:C2	1:A:751:U:C6	3.06	0.43
1:A:1316:G:H1	19:S:5:LEU:HD21	1.84	0.43
1:A:986:A:N1	1:A:1220:G:C2	2.86	0.43
11:K:106:LYS:O	11:K:107:SER:HB3	2.17	0.43
1:A:92:C:H2'	1:A:93:G:C8	2.54	0.43
20:T:81:LYS:C	20:T:83:ARG:H	2.22	0.43
1:A:1305:G:C5'	21:U:4:GLY:HA3	2.48	0.43
1:A:692:U:O2'	1:A:694:A:N7	2.36	0.43
1:A:1429:C:H2'	1:A:1430:C:H6	1.82	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
14:N:13:THR:N	14:N:14:PRO:CD	2.80	0.43
1:A:124:G:C5	1:A:125:U:C4	3.06	0.43
1:A:499:A:C4'	1:A:500:G:H5'	2.49	0.43
1:A:545:C:H5''	4:D:72:GLU:HG2	2.00	0.43
5:E:20:GLN:HB3	5:E:20:GLN:HE21	1.61	0.43
7:G:75:VAL:HG23	7:G:75:VAL:O	2.18	0.43
1:A:1025:U:O2'	1:A:1026:G:H8	2.00	0.43
11:K:124:LYS:HB3	11:K:125:PHE:HD1	1.83	0.43
1:A:32:A:C2	1:A:33:A:C4	3.07	0.43
1:A:567:G:C2	1:A:568:G:H1'	2.53	0.43
1:A:451:A:C6	1:A:481:G:C5	3.06	0.43
1:A:1292:U:O2'	1:A:1293:G:H5'	2.19	0.43
1:A:537:G:OP1	12:L:113:ARG:NH2	2.47	0.43
4:D:196:LEU:HB3	4:D:197:PRO:HD2	2.01	0.43
20:T:14:LYS:HB2	20:T:17:ARG:NH2	2.33	0.43
1:A:629:G:C5	1:A:630:G:N7	2.86	0.43
10:J:54:PHE:CE1	10:J:55:LYS:HE3	2.53	0.43
20:T:57:ARG:HD3	20:T:103:GLY:H	1.83	0.43
1:A:658:G:O2'	1:A:659:U:H5'	2.17	0.43
1:A:509:A:H3'	1:A:509:A:OP2	2.19	0.43
1:A:994:A:C2	14:N:5:ALA:HA	2.54	0.43
1:A:525:C:H2'	1:A:526:C:H6	1.83	0.43
9:I:79:LEU:HD21	9:I:83:ARG:HH21	1.83	0.43
3:C:29:TYR:CD2	3:C:29:TYR:O	2.72	0.43
1:A:1332:A:O5'	1:A:1332:A:H8	2.01	0.43
1:A:950:U:H2'	1:A:951:G:C8	2.53	0.43
19:S:10:PHE:HZ	19:S:70:LYS:HE2	1.83	0.43
4:D:88:VAL:O	4:D:92:VAL:HG23	2.19	0.43
1:A:1479:C:O2'	1:A:1480:G:H5'	2.17	0.43
7:G:50:ILE:O	7:G:54:THR:O	2.37	0.43
21:U:21:TYR:O	21:U:22:ARG:HB2	2.18	0.43
7:G:16:LEU:HD12	9:I:41:VAL:O	2.18	0.43
12:L:105:TYR:C	12:L:107:ALA:H	2.21	0.43
1:A:758:G:O5'	1:A:758:G:H8	2.01	0.43
3:C:79:ARG:HG3	3:C:79:ARG:O	2.18	0.43
1:A:1221:G:H4'	19:S:53:ASN:O	2.18	0.43
1:A:1141:C:H3'	1:A:1141:C:H6	1.84	0.43
7:G:37:ASN:HD21	9:I:40:LEU:CD2	2.29	0.43
1:A:472:A:O2'	16:P:81:ARG:HA	2.19	0.43
1:A:604:G:N7	1:A:605:U:C5	2.87	0.43
6:F:45:LEU:HG	6:F:46:ARG:H	1.83	0.43
1:A:1499:A:H1'	1:A:1520:G:H5'	1.99	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1157:A:N3	1:A:1181:G:N3	2.66	0.43
1:A:853:G:H2'	1:A:854:G:C8	2.52	0.43
1:A:946:A:N1	1:A:1236:A:C2	2.87	0.43
1:A:219:C:C5	1:A:220:G:C8	3.07	0.43
1:A:448:A:C2	1:A:449:C:C4	3.06	0.43
1:A:175:C:N3	1:A:176:C:C5	2.86	0.43
1:A:648:A:H2'	1:A:649:G:H8	1.82	0.43
11:K:126:ARG:O	11:K:126:ARG:HG2	2.18	0.43
14:N:12:ARG:C	14:N:14:PRO:CD	2.87	0.43
1:A:1516:G:H2'	1:A:1518:A:OP2	2.18	0.43
1:A:1425:U:H2'	1:A:1426:C:C6	2.54	0.43
2:B:145:LEU:CD1	2:B:149:LEU:HD12	2.49	0.43
1:A:740:U:O2'	1:A:741:G:H5'	2.18	0.43
3:C:19:GLU:HA	3:C:54:ARG:NH2	2.33	0.43
11:K:92:GLU:O	11:K:95:ILE:HG12	2.18	0.43
10:J:40:LEU:CB	10:J:41:PRO:HD2	2.40	0.43
12:L:26:ALA:O	12:L:27:LEU:HB2	2.19	0.43
1:A:1203:C:H2'	1:A:1204:A:C8	2.53	0.43
1:A:413:G:N2	1:A:429:U:OP2	2.47	0.43
8:H:36:LEU:HD12	8:H:59:LEU:HD12	2.00	0.43
1:A:78:G:H1	1:A:91:C:N4	2.13	0.43
1:A:960:U:C5	1:A:1225:A:H1'	2.53	0.43
1:A:738:C:OP1	6:F:2:ARG:NH1	2.51	0.43
1:A:1505:G:C4'	1:A:1506:U:H5''	2.41	0.43
1:A:1097:C:C2'	1:A:1098:C:H5'	2.49	0.43
3:C:159:GLY:HA2	3:C:193:TYR:CD1	2.54	0.43
1:A:438:G:OP1	4:D:125:HIS:HE1	2.02	0.43
1:A:397:A:H5'	1:A:398:C:P	2.58	0.43
1:A:429:U:H1'	1:A:430:A:H5''	2.00	0.43
1:A:747:C:H5	1:A:748:C:N4	2.17	0.43
1:A:9:G:OP1	5:E:122:GLU:HB2	2.18	0.43
11:K:127:LYS:HA	11:K:127:LYS:CE	2.49	0.43
12:L:34:ARG:CG	12:L:35:GLY:N	2.82	0.43
1:A:434:U:C4	1:A:435:C:N4	2.87	0.43
20:T:23:ARG:O	20:T:27:LYS:HB2	2.18	0.43
1:A:44:G:N2	1:A:399:G:C4	2.87	0.43
3:C:16:ARG:NH1	3:C:16:ARG:HB2	2.34	0.43
4:D:132:ARG:H	4:D:132:ARG:HG3	1.51	0.43
1:A:682:G:H1	1:A:708:C:N4	2.17	0.43
2:B:100:GLY:O	2:B:104:ASN:N	2.50	0.43
5:E:31:LEU:HD11	5:E:129:ILE:HA	2.00	0.43
4:D:93:PHE:O	4:D:97:LEU:HB2	2.18	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:328:C:H4'	1:A:329:A:C5'	2.49	0.43
1:A:504:C:H1'	1:A:510:A:C4	2.54	0.43
1:A:510:A:H5''	1:A:511:C:P	2.59	0.43
2:B:75:LYS:HA	2:B:78:GLN:HG3	2.00	0.43
1:A:90:U:O2'	1:A:91:C:C5	2.66	0.43
1:A:524:G:C6	1:A:525:C:N4	2.87	0.43
1:A:271:C:C2	1:A:272:C:C5	3.07	0.43
1:A:1086:U:H2'	1:A:1087:G:O4'	2.19	0.43
1:A:1085:U:C2	1:A:1094:G:O6	2.71	0.43
1:A:715:A:O2'	1:A:716:A:H5'	2.18	0.43
1:A:1293:G:O2'	1:A:1294:G:H8	2.00	0.43
20:T:12:ALA:O	20:T:15:ARG:HB2	2.19	0.43
1:A:1502:A:C2	1:A:1505:G:N1	2.62	0.43
1:A:193:C:O2'	1:A:194:C:H5'	2.17	0.43
1:A:882:C:O2'	1:A:883:C:H5'	2.18	0.43
2:B:22:LYS:HZ3	2:B:40:HIS:HE1	1.63	0.43
1:A:410:G:OP2	4:D:25:ARG:HG3	2.18	0.43
9:I:28:VAL:HA	9:I:63:ILE:O	2.18	0.43
3:C:73:PRO:HA	3:C:76:VAL:CG1	2.49	0.43
1:A:760:G:C2'	1:A:761:G:H5'	2.49	0.43
3:C:125:GLU:OE2	3:C:189:ALA:HA	2.19	0.43
13:M:17:VAL:O	13:M:20:THR:HB	2.18	0.43
12:L:13:LYS:HD2	12:L:13:LYS:N	2.34	0.43
1:A:734:G:C6	1:A:735:C:N3	2.87	0.43
5:E:13:ILE:HA	5:E:29:GLY:O	2.18	0.43
13:M:81:LEU:HD11	13:M:88:ARG:HH12	1.84	0.43
10:J:78:ASN:O	10:J:82:ILE:HG12	2.19	0.43
17:Q:67:LYS:O	17:Q:69:LYS:N	2.52	0.43
20:T:57:ARG:NH1	20:T:57:ARG:HB2	2.34	0.43
15:O:74:ASP:HA	15:O:75:PRO:HD2	1.82	0.43
1:A:510:A:H5''	1:A:511:C:OP1	2.18	0.43
5:E:139:LEU:O	5:E:142:LEU:HG	2.19	0.43
2:B:75:LYS:C	2:B:77:ALA:H	2.22	0.43
19:S:4:SER:O	19:S:5:LEU:HB2	2.17	0.43
1:A:90:U:O3'	1:A:91:C:H6	2.02	0.43
1:A:25:C:C5'	1:A:524:G:H1'	2.49	0.43
19:S:6:LYS:H	19:S:6:LYS:HD2	1.83	0.43
1:A:448:A:OP2	1:A:485:G:N2	2.38	0.43
11:K:59:TYR:O	11:K:62:GLN:HB3	2.19	0.43
4:D:131:ARG:HD3	4:D:131:ARG:N	2.34	0.43
16:P:58:TYR:O	16:P:61:SER:N	2.52	0.43
1:A:39:G:C6	1:A:40:C:C5	3.07	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:663:A:O3'	18:R:64:ARG:NH2	2.48	0.42
1:A:15:G:C4	1:A:16:A:C8	3.06	0.42
1:A:1053:G:C4	1:A:1199:U:C5	3.07	0.42
1:A:191:G:N9	20:T:105:SER:HB3	2.32	0.42
16:P:39:TYR:CE1	16:P:41:PRO:HA	2.54	0.42
1:A:542:G:C4	1:A:543:C:C5	3.06	0.42
2:B:54:THR:HG21	2:B:201:ILE:HD11	2.00	0.42
15:O:2:PRO:HB2	15:O:3:ILE:H	1.58	0.42
2:B:165:VAL:HG23	2:B:166:ASP:N	2.32	0.42
1:A:1188:A:H2'	1:A:1189:C:H5'	2.00	0.42
13:M:40:ASN:HA	13:M:41:PRO:HD3	1.78	0.42
9:I:79:LEU:C	9:I:79:LEU:HD13	2.39	0.42
1:A:1350:A:H2'	1:A:1351:U:C6	2.54	0.42
17:Q:31:LEU:HG	17:Q:32:TYR:CE2	2.54	0.42
1:A:1272:G:C5	1:A:1273:G:C8	3.07	0.42
1:A:72:C:H2'	1:A:73:G:C8	2.54	0.42
1:A:1164:G:N2	1:A:1165:C:C2	2.87	0.42
1:A:390:C:H6	1:A:390:C:H3'	1.84	0.42
18:R:74:ARG:HE	18:R:81:PHE:HA	1.82	0.42
13:M:66:LEU:HB2	13:M:67:GLU:H	1.53	0.42
12:L:92:ASP:O	12:L:93:LEU:HD23	2.19	0.42
1:A:1452:C:H5'	1:A:1456:G:C5	2.54	0.42
1:A:1457:G:C2	1:A:1458:G:C8	3.07	0.42
1:A:1030(A):G:O2'	1:A:1030(C):G:N7	2.46	0.42
1:A:929:G:C6	1:A:930:C:C4	3.06	0.42
1:A:783:C:C2'	1:A:784:C:H5'	2.48	0.42
1:A:552:U:H4'	12:L:86:ARG:HG2	2.01	0.42
5:E:75:THR:OG1	5:E:76:ILE:N	2.51	0.42
17:Q:5:VAL:HG23	17:Q:60:ILE:HG13	2.00	0.42
9:I:45:ALA:O	9:I:78:LYS:HE3	2.19	0.42
1:A:1346:A:C8	1:A:1348:U:O2	2.72	0.42
1:A:371:G:H5''	1:A:372:C:OP2	2.19	0.42
19:S:12:ASP:OD1	19:S:37:ARG:HD2	2.19	0.42
1:A:771:G:C6	1:A:772:U:C4	3.08	0.42
1:A:488:C:H6	1:A:488:C:O5'	2.02	0.42
1:A:376:G:C4'	16:P:5:ARG:HH11	2.18	0.42
1:A:1095:U:H2'	1:A:1096:C:H6	1.84	0.42
10:J:49:VAL:O	10:J:60:ARG:HB2	2.20	0.42
2:B:102:LEU:CD1	2:B:102:LEU:N	2.83	0.42
2:B:97:TRP:HH2	2:B:176:GLU:HG3	1.84	0.42
1:A:1030(D):A:N7	1:A:1031:G:N3	2.66	0.42
16:P:49:LEU:HG	16:P:50:LYS:N	2.34	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:604:G:C5	1:A:605:U:C5	3.07	0.42
1:A:428:G:OP2	4:D:7:PRO:HG2	2.19	0.42
8:H:97:VAL:HG13	8:H:98:LYS:HG3	2.00	0.42
12:L:41:ARG:CG	12:L:42:THR:N	2.77	0.42
1:A:720:C:H6	1:A:720:C:O5'	2.02	0.42
1:A:189(K):U:H6	1:A:189(K):U:O5'	2.02	0.42
12:L:18:VAL:HG23	12:L:19:ARG:N	2.33	0.42
5:E:91:LEU:HD12	5:E:120:THR:HG22	2.01	0.42
1:A:229:U:C2'	1:A:230:G:H5'	2.50	0.42
1:A:764:C:H2'	1:A:765:G:C8	2.52	0.42
11:K:23:ALA:HB1	11:K:88:GLY:HA3	2.01	0.42
1:A:1086:U:C6	1:A:1087:G:C8	3.07	0.42
2:B:140:HIS:O	2:B:143:GLU:HB2	2.19	0.42
2:B:139:LYS:O	2:B:143:GLU:HG2	2.19	0.42
14:N:21:TYR:CD2	14:N:22:THR:O	2.72	0.42
1:A:928:G:C2	1:A:1390:U:O2	2.72	0.42
1:A:391:G:O6	1:A:392:G:C6	2.72	0.42
11:K:21:ILE:HA	11:K:30:VAL:HG12	2.00	0.42
1:A:1500:A:OP2	1:A:1505:G:OP1	2.37	0.42
1:A:1037:C:O5'	1:A:1037:C:H6	2.02	0.42
5:E:72:GLN:O	5:E:73:ASN:CB	2.58	0.42
1:A:976:G:C5'	1:A:1358:U:O2'	2.64	0.42
1:A:37:U:O2'	1:A:500:G:H4'	2.20	0.42
8:H:100:ILE:HA	8:H:101:PRO:HD3	1.83	0.42
3:C:138:VAL:HG23	3:C:151:VAL:HG23	2.00	0.42
13:M:74:VAL:O	13:M:78:ILE:HG13	2.19	0.42
1:A:262:A:N6	1:A:263:A:N6	2.67	0.42
4:D:146:ILE:HD12	4:D:146:ILE:H	1.84	0.42
11:K:81:ASP:CG	11:K:106:LYS:HG2	2.39	0.42
1:A:587:G:C2	1:A:755:G:C5	3.07	0.42
9:I:56:LEU:O	9:I:56:LEU:HD23	2.20	0.42
5:E:48:ALA:HB1	5:E:49:PRO:CD	2.50	0.42
2:B:153:ARG:O	2:B:154:LEU:C	2.57	0.42
1:A:438:G:H4'	4:D:123:HIS:CE1	2.54	0.42
1:A:1030(B):C:N4	1:A:1030(C):G:C2	2.88	0.42
4:D:106:TYR:CE1	4:D:112:VAL:O	2.73	0.42
1:A:1188:A:C2'	1:A:1189:C:H5'	2.50	0.42
1:A:1498:U:C1'	1:A:1499:A:OP2	2.68	0.42
1:A:1158:C:O2	1:A:1158:C:H2'	2.18	0.42
7:G:75:VAL:CG2	7:G:144:MET:HB3	2.50	0.42
19:S:9:VAL:O	19:S:10:PHE:CD1	2.72	0.42
4:D:14:ARG:HA	4:D:39:PRO:CB	2.49	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:K:57:THR:HG23	11:K:58:PRO:HD2	2.01	0.42
1:A:69:G:H2'	1:A:70:G:H8	1.84	0.42
1:A:1006:C:H42	1:A:1024:G:H21	1.66	0.42
1:A:1003:G:C2'	1:A:1004:A:H4'	2.42	0.42
4:D:65:ARG:HG3	4:D:75:PHE:CD1	2.55	0.42
12:L:27:LEU:C	12:L:29:GLY:H	2.22	0.42
4:D:148:VAL:CG1	4:D:149:ALA:N	2.81	0.42
1:A:328:C:H4'	1:A:329:A:O5'	2.19	0.42
2:B:204:ASN:HD22	2:B:206:ASP:H	1.66	0.42
2:B:80:ILE:HD12	2:B:211:ILE:HB	2.00	0.42
1:A:380:G:C2	1:A:384:G:C6	3.08	0.42
3:C:134:ILE:HG13	3:C:153:VAL:CG2	2.49	0.42
1:A:1160:G:H5'	2:B:132:LYS:HE3	2.01	0.42
2:B:193:ASP:O	2:B:194:PRO:O	2.37	0.42
1:A:1128:C:H1'	1:A:1146:A:H61	1.85	0.42
16:P:59:TRP:O	16:P:64:ALA:CB	2.67	0.42
1:A:35:G:O2'	12:L:121:GLY:HA2	2.20	0.42
1:A:44:G:H2'	1:A:45:U:O4'	2.19	0.42
4:D:190:ASP:HB3	4:D:193:ASP:OD2	2.20	0.42
4:D:74:GLN:O	4:D:78:LEU:HG	2.20	0.42
4:D:62:GLN:HE22	4:D:65:ARG:HH21	1.68	0.42
1:A:167:G:C2'	1:A:168:G:H5'	2.50	0.42
1:A:329:A:C2	1:A:332:G:C4	3.08	0.42
8:H:36:LEU:HA	8:H:39:LEU:HD23	2.00	0.42
12:L:55:VAL:CG1	12:L:56:ALA:N	2.82	0.42
1:A:1320:C:H5'	19:S:70:LYS:CG	2.49	0.42
11:K:62:GLN:O	11:K:63:LEU:C	2.58	0.42
5:E:36:ASP:OD1	5:E:37:ARG:N	2.52	0.42
1:A:273:A:N6	1:A:274:A:N6	2.67	0.42
17:Q:31:LEU:HG	17:Q:32:TYR:CD2	2.55	0.42
1:A:1376:U:H2'	1:A:1377:A:C8	2.54	0.42
1:A:295:C:H2'	1:A:296:U:H6	1.85	0.42
4:D:43:HIS:CE1	4:D:46:LYS:HZ2	2.35	0.42
1:A:124:G:C6	1:A:125:U:C4	3.08	0.42
1:A:812:C:OP1	1:A:903:G:H1'	2.19	0.42
11:K:15:ALA:HA	11:K:77:MET:HA	2.01	0.42
15:O:24:SER:O	15:O:28:GLN:HG3	2.19	0.42
1:A:1415:G:C6	1:A:1486:G:C6	3.08	0.42
7:G:111:ARG:HB2	7:G:119:ARG:HD2	2.01	0.42
1:A:920:U:C1'	1:A:1080:A:C2	3.02	0.42
1:A:1073:U:H2'	1:A:1074:G:C8	2.45	0.42
18:R:58:LEU:HB3	18:R:62:GLU:CB	2.43	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:878:G:C5'	8:H:89:PRO:HG2	2.45	0.42
1:A:491:G:C2	1:A:492:G:C4	3.08	0.42
1:A:192:U:C4'	20:T:103:GLY:HA2	2.50	0.42
1:A:600:C:O2'	1:A:601:C:H5'	2.18	0.42
12:L:83:VAL:HG12	12:L:84:LEU:N	2.35	0.42
1:A:1497:G:C2'	1:A:1498:U:H5'	2.47	0.42
18:R:44:LEU:O	18:R:45:SER:O	2.38	0.42
1:A:1242:C:H5''	21:U:10:ARG:NH1	2.34	0.42
1:A:258:G:H2'	1:A:259:G:H8	1.84	0.42
1:A:1134:G:N2	1:A:1141:C:C2	2.88	0.42
1:A:785:G:C2'	1:A:786:G:H5'	2.50	0.42
7:G:85:TYR:CD1	7:G:154:TYR:HE1	2.38	0.42
11:K:120:ARG:HA	11:K:121:PRO:HD3	1.85	0.42
8:H:121:ASP:N	8:H:121:ASP:OD1	2.53	0.42
2:B:158:LEU:N	2:B:158:LEU:HD12	2.15	0.42
1:A:682:G:C2	1:A:709:G:C6	3.08	0.42
5:E:11:ILE:HB	5:E:31:LEU:HB3	2.02	0.42
12:L:25:PRO:C	12:L:27:LEU:N	2.72	0.42
20:T:84:LEU:HD13	20:T:84:LEU:C	2.40	0.42
2:B:97:TRP:CZ2	2:B:102:LEU:HD13	2.49	0.42
1:A:1151:A:O2'	1:A:1152:A:C8	2.65	0.42
15:O:67:LEU:HD22	15:O:78:TYR:CE1	2.54	0.42
15:O:75:PRO:O	15:O:78:TYR:HB3	2.20	0.42
1:A:501:C:H2'	1:A:502:G:C8	2.55	0.42
1:A:929:G:O6	1:A:930:C:N4	2.53	0.42
1:A:1157:A:C2	1:A:1181:G:N3	2.88	0.42
1:A:834:C:H2'	1:A:835:U:H6	1.84	0.42
1:A:93:G:C2'	1:A:96:U:H5'	2.50	0.42
1:A:1241:G:H2'	1:A:1242:C:C6	2.55	0.42
7:G:92:SER:CB	7:G:94:ARG:HH21	2.33	0.42
1:A:757:U:H2'	1:A:758:G:O4'	2.20	0.42
9:I:25:LYS:HG2	9:I:60:ASP:OD1	2.20	0.42
9:I:122:ALA:HB1	9:I:123:PRO:HD2	2.01	0.42
7:G:101:LEU:O	7:G:105:VAL:HG23	2.20	0.42
4:D:128:VAL:O	4:D:129:ASN:C	2.58	0.42
16:P:9:PHE:HB3	16:P:10:GLY:H	1.68	0.42
11:K:84:VAL:O	11:K:85:ARG:HG3	2.19	0.42
5:E:129:ILE:O	5:E:133:TYR:HD1	2.03	0.42
1:A:1053:G:N7	1:A:1200:C:H5'	2.35	0.42
6:F:15:ASP:OD1	6:F:17:SER:HB2	2.19	0.42
2:B:19:HIS:CD2	2:B:20:GLU:HG2	2.55	0.42
1:A:781:A:H5'	1:A:782:A:OP2	2.20	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:L:32:PHE:CB	12:L:84:LEU:HD21	2.49	0.42
1:A:484:G:C4'	1:A:485:G:O5'	2.68	0.42
19:S:10:PHE:HZ	19:S:70:LYS:HZ3	1.67	0.42
17:Q:31:LEU:O	17:Q:31:LEU:HD12	2.20	0.42
1:A:432:A:C8	1:A:433:C:C5	3.08	0.42
9:I:106:ALA:O	9:I:108:VAL:N	2.53	0.42
1:A:390:C:O2'	1:A:391:G:H5'	2.19	0.41
1:A:1400:C:H4'	1:A:1401:G:OP2	2.19	0.41
1:A:1458:G:H2'	1:A:1459:C:C6	2.55	0.41
10:J:50:ILE:HA	10:J:60:ARG:HB2	2.02	0.41
1:A:266:G:C5'	1:A:268:C:H41	2.27	0.41
1:A:115:G:C2	1:A:289:G:C5	3.08	0.41
10:J:70:ARG:HG3	10:J:70:ARG:NH1	2.35	0.41
17:Q:63:ARG:HG2	17:Q:64:PRO:HD2	2.02	0.41
1:A:814:A:N7	1:A:816:A:C5	2.87	0.41
1:A:230:G:H2'	1:A:231:G:O5'	2.20	0.41
5:E:146:ALA:O	5:E:148:VAL:N	2.53	0.41
18:R:86:VAL:O	18:R:87:ARG:HB3	2.20	0.41
3:C:87:LEU:O	3:C:91:LEU:HG	2.20	0.41
13:M:32:GLU:OE2	13:M:64:TRP:CH2	2.73	0.41
1:A:1254:C:H2'	1:A:1255:G:H8	1.84	0.41
1:A:1442:G:C5	1:A:1442(B):A:N1	2.88	0.41
16:P:72:ARG:HH21	16:P:73:LEU:CD2	2.23	0.41
10:J:78:ASN:HB3	10:J:80:LYS:H	1.84	0.41
16:P:81:ARG:HD3	16:P:83:GLU:OE2	2.20	0.41
1:A:342:C:C2'	1:A:343:U:H5'	2.50	0.41
9:I:104:ARG:O	9:I:104:ARG:HG2	2.20	0.41
2:B:178:ARG:HH21	8:H:74:PRO:HG3	1.82	0.41
4:D:3:ARG:HD3	4:D:3:ARG:O	2.20	0.41
1:A:382:A:H2'	1:A:383:A:H8	1.84	0.41
1:A:533:A:H4'	1:A:534:U:OP1	2.20	0.41
1:A:374:A:C2	1:A:375:U:C2	3.08	0.41
16:P:20:VAL:HG22	16:P:21:VAL:N	2.35	0.41
1:A:925:G:H1'	1:A:1502:A:C4	2.54	0.41
1:A:955:U:H2'	1:A:956:U:C6	2.55	0.41
5:E:129:ILE:O	5:E:132:ALA:HB3	2.20	0.41
1:A:1342:C:O2'	1:A:1343:G:H5'	2.21	0.41
1:A:1017:G:H8	1:A:1017:G:O5'	2.03	0.41
6:F:79:LEU:HD12	6:F:88:VAL:HG11	2.03	0.41
1:A:1014:A:H2	1:A:1219:U:O2	2.03	0.41
2:B:121:LEU:O	2:B:127:ILE:HD11	2.20	0.41
1:A:274:A:H4'	1:A:275:G:OP1	2.19	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1060:C:O2'	1:A:1061:G:H5'	2.21	0.41
1:A:452:A:C2	1:A:453:A:C4	3.09	0.41
1:A:1205:U:H4'	3:C:195:VAL:HG21	2.02	0.41
1:A:376:G:C6	1:A:389:A:N6	2.88	0.41
1:A:445:G:C4	1:A:446:G:C8	3.07	0.41
16:P:18:ARG:HD3	16:P:35:LYS:CD	2.51	0.41
4:D:194:LEU:HB3	4:D:196:LEU:HD11	2.02	0.41
19:S:75:ALA:HA	19:S:76:PRO:HD2	1.93	0.41
1:A:1030(C):G:H2'	1:A:1030(D):A:C8	2.55	0.41
1:A:543:C:N3	1:A:544:G:N7	2.69	0.41
3:C:14:ILE:O	3:C:15:THR:CB	2.68	0.41
2:B:204:ASN:HB3	2:B:210:SER:HB3	2.01	0.41
1:A:783:C:C2	1:A:784:C:C5	3.07	0.41
3:C:3:ASN:O	3:C:4:LYS:O	2.38	0.41
1:A:1316:G:O3'	14:N:18:VAL:HG22	2.20	0.41
11:K:73:MET:SD	11:K:103:LEU:HD21	2.61	0.41
6:F:72:VAL:CG1	6:F:73:ASN:N	2.82	0.41
17:Q:77:VAL:O	17:Q:78:GLU:CB	2.69	0.41
1:A:568:G:O6	12:L:5:PRO:HD3	2.19	0.41
1:A:716:A:H2'	1:A:717:C:O5'	2.20	0.41
12:L:92:ASP:C	12:L:93:LEU:HD23	2.41	0.41
15:O:32:LEU:O	15:O:33:THR:C	2.58	0.41
1:A:149:A:HO2'	1:A:150:C:H6	1.60	0.41
12:L:22:SER:C	12:L:24:VAL:N	2.73	0.41
2:B:14:GLY:C	2:B:15:VAL:HG22	2.40	0.41
9:I:112:LYS:HA	9:I:119:ALA:HA	2.01	0.41
1:A:985:C:H6	1:A:985:C:O5'	2.02	0.41
4:D:49:ARG:HA	4:D:49:ARG:NE	2.36	0.41
1:A:10:A:OP2	5:E:126:ARG:HD3	2.21	0.41
1:A:246:A:C5	1:A:279:A:C6	3.09	0.41
9:I:36:TYR:CE2	9:I:37:PHE:CE2	3.08	0.41
1:A:355:C:H2'	1:A:356:A:H5'	2.01	0.41
16:P:14:ASN:OD1	16:P:16:HIS:HE1	2.03	0.41
1:A:523:A:N1	12:L:92:ASP:HB2	2.36	0.41
1:A:327:A:O2'	1:A:329:A:H8	2.03	0.41
5:E:139:LEU:O	5:E:141:GLN:N	2.53	0.41
6:F:82:ARG:NH1	6:F:82:ARG:HB3	2.35	0.41
17:Q:95:TYR:O	17:Q:97:SER:N	2.54	0.41
15:O:17:ARG:HD3	15:O:26:GLU:HG3	2.02	0.41
1:A:1486:G:H2'	1:A:1487:G:O4'	2.19	0.41
8:H:28:ALA:HB3	8:H:57:PRO:HB2	2.02	0.41
18:R:76:LEU:N	18:R:76:LEU:CD2	2.83	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:L:64:TYR:HB3	12:L:65:GLU:H	1.68	0.41
1:A:342:C:O2'	1:A:343:U:H5'	2.20	0.41
1:A:542:G:C2	1:A:543:C:C5	3.09	0.41
18:R:84:LYS:HA	18:R:84:LYS:HD3	1.77	0.41
2:B:17:PHE:O	2:B:18:GLY:O	2.38	0.41
1:A:552:U:O2'	12:L:86:ARG:O	2.33	0.41
1:A:380:G:N1	1:A:384:G:C6	2.88	0.41
6:F:81:ILE:O	6:F:82:ARG:C	2.59	0.41
3:C:156:ARG:H	3:C:163:ALA:HA	1.86	0.41
1:A:1047:G:H5''	14:N:4:LYS:HG2	2.02	0.41
1:A:1350:A:N6	1:A:1373:G:N2	2.69	0.41
17:Q:65:ILE:H	17:Q:65:ILE:HD12	1.84	0.41
1:A:944:G:H5''	1:A:945:G:OP2	2.21	0.41
1:A:1423:G:H2'	1:A:1424:C:O4'	2.20	0.41
7:G:135:VAL:O	7:G:139:GLU:HG3	2.20	0.41
1:A:1400:C:H6	1:A:1400:C:O5'	2.04	0.41
18:R:65:ILE:HG13	18:R:65:ILE:H	1.60	0.41
2:B:84:GLU:OE1	2:B:216:SER:HA	2.20	0.41
20:T:89:ARG:HB2	20:T:104:LEU:CD1	2.51	0.41
1:A:638:G:O2'	1:A:639:G:H5'	2.20	0.41
1:A:152:A:C8	1:A:153:C:C5	3.08	0.41
6:F:48:LEU:HD21	6:F:60:PHE:CZ	2.56	0.41
1:A:814:A:C8	1:A:816:A:C8	3.09	0.41
2:B:25:ASN:OD1	2:B:25:ASN:C	2.58	0.41
1:A:484:G:H4'	1:A:485:G:O5'	2.14	0.41
11:K:58:PRO:HA	11:K:90:GLY:HA2	2.03	0.41
7:G:69:VAL:HA	7:G:138:LYS:HD2	2.03	0.41
20:T:30:LYS:HA	20:T:30:LYS:HD2	1.69	0.41
1:A:189(F):U:N3	17:Q:72:ARG:NH1	2.69	0.41
1:A:690:G:O2'	1:A:691:G:H5'	2.21	0.41
19:S:12:ASP:HB2	19:S:15:LEU:HD23	2.03	0.41
8:H:21:LYS:O	8:H:63:LEU:HD23	2.21	0.41
13:M:75:ALA:O	13:M:79:LYS:HG3	2.21	0.41
1:A:373:A:C4	1:A:482:A:N7	2.89	0.41
4:D:17:VAL:HG11	4:D:197:PRO:CB	2.51	0.41
2:B:101:MET:O	2:B:105:PHE:HA	2.21	0.41
6:F:8:ILE:HA	6:F:87:ARG:O	2.20	0.41
8:H:88:LYS:CB	8:H:89:PRO:HD2	2.50	0.41
1:A:1288:A:O2'	1:A:1289:A:H5'	2.21	0.41
1:A:827:U:C2	1:A:870:U:C4	3.09	0.41
4:D:79:PHE:CZ	4:D:204:ILE:HD13	2.56	0.41
1:A:503:C:C2	1:A:504:C:C5	3.09	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1067:A:C4'	1:A:1068:G:O5'	2.69	0.41
2:B:74:LYS:NZ	2:B:76:GLN:HB2	2.35	0.41
1:A:221:C:H2'	1:A:222:U:H6	1.86	0.41
1:A:939:G:H5''	7:G:102:ARG:HH22	1.86	0.41
1:A:1495:U:H2'	1:A:1496:C:C6	2.56	0.41
1:A:991:U:O2'	1:A:992:U:P	2.78	0.41
1:A:1333:A:H2'	1:A:1334:G:O4'	2.21	0.41
9:I:43:ALA:HA	9:I:74:ILE:HD13	2.02	0.41
9:I:79:LEU:HD11	9:I:83:ARG:CZ	2.51	0.41
18:R:40:LEU:O	18:R:43:PHE:N	2.53	0.41
3:C:155:GLY:O	3:C:156:ARG:CB	2.68	0.41
7:G:79:ARG:HA	7:G:84:ASN:ND2	2.36	0.41
1:A:448:A:H2'	1:A:449:C:H6	1.84	0.41
19:S:9:VAL:O	19:S:9:VAL:HG12	2.21	0.41
10:J:48:THR:HA	10:J:62:HIS:CB	2.50	0.41
1:A:790:A:C6	1:A:791:G:C6	3.08	0.41
7:G:69:VAL:HG12	7:G:100:ALA:HA	2.03	0.41
1:A:10:A:H2'	1:A:11:G:C8	2.55	0.41
1:A:141:A:H4'	1:A:182:U:H1'	2.02	0.41
4:D:4:TYR:O	4:D:5:ILE:HB	2.21	0.41
1:A:174:C:H6	1:A:174:C:O5'	2.03	0.41
20:T:53:LEU:HD21	20:T:92:LEU:CD1	2.51	0.41
4:D:151:LYS:O	4:D:151:LYS:HG2	2.20	0.41
1:A:258:G:C2	1:A:259:G:C8	3.09	0.41
4:D:43:HIS:O	4:D:45:GLN:N	2.54	0.41
11:K:19:ALA:HA	11:K:32:ILE:HA	2.03	0.41
3:C:136:GLN:HG2	3:C:140:ARG:NH2	2.35	0.41
6:F:89:MET:HG2	6:F:89:MET:O	2.21	0.41
5:E:12:LEU:CD1	5:E:31:LEU:HB2	2.51	0.41
4:D:106:TYR:HE1	4:D:113:SER:CA	2.34	0.41
16:P:74:LEU:HD23	16:P:74:LEU:HA	1.79	0.41
2:B:35:GLU:HA	2:B:39:ILE:O	2.21	0.41
4:D:101:LEU:HB2	4:D:138:TYR:O	2.21	0.41
4:D:14:ARG:HA	4:D:39:PRO:HG3	2.03	0.41
4:D:109:GLY:O	4:D:110:PHE:C	2.59	0.41
17:Q:78:GLU:O	17:Q:78:GLU:HG3	2.20	0.41
1:A:175:C:C2	1:A:176:C:C6	3.08	0.41
1:A:451:A:N7	1:A:481:G:C6	2.89	0.41
20:T:87:LYS:HE3	20:T:91:LEU:HD21	2.03	0.41
1:A:709:G:O2'	1:A:710:G:H5'	2.19	0.40
2:B:104:ASN:O	2:B:108:ILE:HG12	2.22	0.40
2:B:154:LEU:N	2:B:154:LEU:HD23	2.20	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:L:62:SER:O	12:L:64:TYR:HD1	2.03	0.40
1:A:364:A:H2'	1:A:365:U:O2	2.20	0.40
1:A:1352:C:O2	1:A:1371:G:C2	2.73	0.40
1:A:1173:G:C5	1:A:1174:G:N7	2.89	0.40
1:A:748:C:C1'	1:A:749:C:OP2	2.66	0.40
1:A:622:A:N7	1:A:623:C:C5	2.89	0.40
17:Q:59:ILE:HG22	17:Q:60:ILE:N	2.35	0.40
9:I:53:VAL:HB	9:I:92:TYR:HE2	1.86	0.40
1:A:1320:C:O2'	19:S:73:GLU:HG2	2.21	0.40
1:A:565:U:C6	1:A:566:G:C8	3.09	0.40
1:A:763:G:C5	1:A:764:C:C5	3.08	0.40
1:A:1061:G:C4	1:A:1197:G:N2	2.88	0.40
7:G:129:GLU:OE1	7:G:131:LYS:HE2	2.20	0.40
1:A:373:A:N3	1:A:374:A:C8	2.90	0.40
1:A:1098:C:C4	1:A:1099:G:C8	3.08	0.40
1:A:47:C:H5''	1:A:365:U:C6	2.55	0.40
1:A:1291:G:O3'	9:I:39:GLY:HA3	2.21	0.40
17:Q:18:THR:CG2	17:Q:69:LYS:HE3	2.42	0.40
10:J:32:ALA:HB1	10:J:75:ILE:CD1	2.50	0.40
1:A:1173:G:H2'	1:A:1174:G:H8	1.86	0.40
1:A:579:G:C5	1:A:580:U:C4	3.10	0.40
1:A:784:C:C4	1:A:799:G:N1	2.89	0.40
4:D:101:LEU:HD13	4:D:140:VAL:HG22	2.03	0.40
1:A:66:G:C2	1:A:67:C:C5	3.09	0.40
1:A:1316:G:N2	1:A:1319:A:OP2	2.54	0.40
1:A:719:C:C5	1:A:720:C:N3	2.90	0.40
15:O:51:HIS:O	15:O:54:ARG:HB3	2.21	0.40
9:I:49:PRO:O	9:I:53:VAL:HG13	2.22	0.40
3:C:29:TYR:OH	14:N:54:PRO:HD2	2.21	0.40
1:A:310:G:H5''	16:P:31:LYS:HB2	2.03	0.40
1:A:310:G:C5'	16:P:31:LYS:HB2	2.50	0.40
3:C:27:LYS:HZ3	3:C:27:LYS:HA	1.86	0.40
1:A:186:C:O2'	1:A:187:C:H5'	2.22	0.40
1:A:1425:U:H2'	1:A:1426:C:H6	1.86	0.40
1:A:980:C:H5'	1:A:981:U:C5	2.56	0.40
9:I:126:SER:C	9:I:128:ARG:H	2.24	0.40
4:D:181:MET:HE2	4:D:181:MET:HB3	1.97	0.40
1:A:1126:U:H6	1:A:1126:U:P	2.45	0.40
18:R:50:ILE:HG12	18:R:74:ARG:HH12	1.86	0.40
8:H:87:SER:HA	8:H:93:VAL:CG2	2.50	0.40
1:A:101:A:C6	1:A:102:G:N7	2.90	0.40
1:A:1095:U:P	1:A:1108:G:H1	2.43	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:H:88:LYS:HB3	8:H:89:PRO:HD2	2.03	0.40
1:A:965:A:C2	1:A:969:A:N1	2.90	0.40
1:A:149:A:O2'	1:A:150:C:C6	2.68	0.40
1:A:428:G:H5''	4:D:7:PRO:HB3	2.03	0.40
5:E:78:HIS:CE1	5:E:143:ARG:H	2.40	0.40
4:D:104:VAL:HG21	4:D:185:PHE:CD1	2.56	0.40
1:A:63:C:H5'	1:A:64:G:OP2	2.21	0.40
1:A:689:C:O2	1:A:689:C:H2'	2.21	0.40
13:M:44:ARG:HB3	13:M:46:LYS:HG2	2.04	0.40
1:A:720:C:H5''	1:A:721:G:O5'	2.21	0.40
9:I:46:ALA:HA	9:I:78:LYS:HE3	2.02	0.40
11:K:61:ALA:CB	11:K:90:GLY:HA3	2.51	0.40
1:A:862:C:C2'	1:A:863:U:H5'	2.51	0.40
2:B:142:LEU:C	2:B:142:LEU:HD23	2.42	0.40
18:R:36:ASN:ND2	18:R:39:VAL:HG21	2.35	0.40
8:H:51:VAL:HB	8:H:52:ASP:H	1.52	0.40
4:D:127:THR:HA	4:D:132:ARG:HA	2.03	0.40
1:A:1255:G:O2'	1:A:1258:G:O2'	2.33	0.40
3:C:19:GLU:O	3:C:40:ARG:NH2	2.54	0.40
4:D:68:TYR:CD2	4:D:97:LEU:HD22	2.57	0.40
5:E:69:VAL:HG12	5:E:71:LEU:HD21	2.03	0.40
1:A:1281:U:C5'	1:A:1282:C:H5	2.34	0.40
1:A:166:G:O2'	1:A:167:G:H5'	2.21	0.40
1:A:1250:A:C6	1:A:1251:A:C6	3.10	0.40
4:D:79:PHE:CG	4:D:207:TYR:HD1	2.39	0.40
1:A:965:A:C2	1:A:969:A:C2	3.10	0.40
1:A:818:G:C2	1:A:820:U:O2'	2.73	0.40
1:A:410:G:N2	1:A:431:A:C8	2.90	0.40
3:C:134:ILE:CG2	3:C:151:VAL:HB	2.48	0.40
8:H:33:GLU:O	8:H:34:GLU:C	2.59	0.40
18:R:44:LEU:O	18:R:45:SER:C	2.60	0.40
1:A:577:G:C1'	1:A:816:A:C4	3.04	0.40
4:D:3:ARG:HD3	4:D:5:ILE:HG13	2.02	0.40
2:B:238:LEU:O	2:B:240:GLN:N	2.54	0.40
16:P:75:ARG:C	16:P:77:ALA:H	2.23	0.40
16:P:20:VAL:HG22	16:P:32:TYR:HB2	2.04	0.40
8:H:20:TYR:HA	8:H:65:TYR:HE2	1.81	0.40
10:J:54:PHE:HZ	10:J:55:LYS:HZ1	1.67	0.40
1:A:1117:G:O6	1:A:1156:G:N2	2.52	0.40
16:P:43:LYS:HG3	16:P:48:TRP:CE3	2.56	0.40
1:A:953:G:C6	1:A:1229:A:C6	3.09	0.40
4:D:101:LEU:O	4:D:103:ASN:N	2.55	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1233:G:P	9:I:124:GLN:HB2	2.62	0.40
1:A:623:C:C2'	1:A:624:C:H5'	2.52	0.40
6:F:82:ARG:CA	6:F:82:ARG:HH11	2.33	0.40
5:E:75:THR:HG23	5:E:76:ILE:N	2.35	0.40
1:A:1366:C:H2'	1:A:1367:C:H6	1.87	0.40
1:A:308:C:H2'	1:A:309:G:C8	2.54	0.40
10:J:8:LEU:O	10:J:16:LEU:HD21	2.21	0.40
20:T:92:LEU:C	20:T:94:ALA:H	2.24	0.40
1:A:1468:A:H8	1:A:1468:A:O5'	2.05	0.40
4:D:150:GLU:H	4:D:150:GLU:CD	2.25	0.40
1:A:246:A:C2	1:A:282:A:C5	3.10	0.40
2:B:139:LYS:O	2:B:142:LEU:HB3	2.22	0.40
1:A:293:G:C5	1:A:294:U:C4	3.10	0.40
1:A:1054:C:OP1	1:A:1197:G:OP2	2.39	0.40
12:L:52:LEU:HA	12:L:52:LEU:HD23	1.96	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	233/256 (91%)	177 (76%)	39 (17%)	17 (7%)	2	8
3	C	205/239 (86%)	155 (76%)	37 (18%)	13 (6%)	2	12
4	D	206/209 (99%)	137 (66%)	55 (27%)	14 (7%)	2	10
5	E	149/162 (92%)	103 (69%)	33 (22%)	13 (9%)	1	5
6	F	99/101 (98%)	76 (77%)	14 (14%)	9 (9%)	1	5
7	G	153/156 (98%)	131 (86%)	18 (12%)	4 (3%)	8	39
8	H	136/138 (99%)	98 (72%)	31 (23%)	7 (5%)	3	18
9	I	123/128 (96%)	94 (76%)	22 (18%)	7 (6%)	3	16
10	J	97/105 (92%)	81 (84%)	11 (11%)	5 (5%)	3	18
11	K	117/129 (91%)	86 (74%)	27 (23%)	4 (3%)	6	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	L	123/135 (91%)	83 (68%)	29 (24%)	11 (9%)	1	5
13	M	107/126 (85%)	84 (78%)	17 (16%)	6 (6%)	3	16
14	N	58/61 (95%)	44 (76%)	12 (21%)	2 (3%)	6	31
15	O	86/89 (97%)	61 (71%)	21 (24%)	4 (5%)	4	21
16	P	82/88 (93%)	47 (57%)	29 (35%)	6 (7%)	2	8
17	Q	98/105 (93%)	73 (74%)	19 (19%)	6 (6%)	2	14
18	R	68/88 (77%)	51 (75%)	13 (19%)	4 (6%)	2	14
19	S	77/93 (83%)	59 (77%)	12 (16%)	6 (8%)	1	7
20	T	97/106 (92%)	65 (67%)	23 (24%)	9 (9%)	1	5
21	U	23/27 (85%)	18 (78%)	4 (17%)	1 (4%)	4	23
All	All	2337/2541 (92%)	1723 (74%)	466 (20%)	148 (6%)	2	12

All (148) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	15	VAL
2	B	24	TRP
2	B	84	GLU
2	B	154	LEU
2	B	165	VAL
2	B	194	PRO
2	B	195	ASP
2	B	226	ARG
3	C	4	LYS
3	C	12	LEU
3	C	101	LEU
3	C	189	ALA
4	D	3	ARG
4	D	14	ARG
4	D	53	ASP
4	D	129	ASN
5	E	73	ASN
5	E	121	LYS
6	F	13	ASN
6	F	40	VAL
6	F	81	ILE
7	G	33	ASP
9	I	23	ASN

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Mol	Chain	Res	Type
9	I	107	ARG
10	J	59	SER
11	K	100	ALA
12	L	47	LYS
12	L	115	LYS
13	M	12	ASN
13	M	83	ASP
13	M	106	ASN
16	P	17	TYR
16	P	19	ILE
20	T	11	SER
20	T	95	ALA
2	B	18	GLY
2	B	56	ARG
2	B	232	PRO
2	B	239	VAL
3	C	15	THR
3	C	18	TRP
3	C	47	LEU
3	C	100	ALA
3	C	145	GLY
4	D	4	TYR
4	D	10	ARG
4	D	13	ARG
4	D	44	GLY
4	D	47	ARG
4	D	110	PHE
5	E	27	ARG
5	E	108	ALA
5	E	132	ALA
5	E	140	ARG
5	E	146	ALA
5	E	153	LYS
6	F	39	LYS
7	G	7	ALA
8	H	51	VAL
8	H	54	ASP
8	H	133	LEU
9	I	100	GLY
10	J	23	ILE
10	J	36	GLY
11	K	63	LEU

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Mol	Chain	Res	Type
12	L	23	LYS
12	L	28	LYS
12	L	91	LYS
12	L	106	ASP
13	M	100	GLY
17	Q	34	LYS
17	Q	78	GLU
18	R	45	SER
18	R	54	ARG
19	S	27	GLU
19	S	28	LYS
20	T	9	ASN
20	T	74	LYS
2	B	181	PHE
3	C	154	SER
5	E	11	ILE
8	H	2	LEU
9	I	124	GLN
10	J	54	PHE
13	M	90	LEU
15	O	4	THR
15	O	29	VAL
16	P	28	ARG
18	R	20	ALA
19	S	25	LYS
20	T	101	GLY
2	B	83	MET
2	B	209	ARG
2	B	240	GLN
3	C	206	GLU
3	C	207	VAL
4	D	171	GLY
5	E	8	GLU
5	E	37	ARG
8	H	20	TYR
9	I	24	GLY
9	I	97	LYS
9	I	103	THR
12	L	19	ARG
12	L	65	GLU
12	L	79	GLU
14	N	16	PHE

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Mol	Chain	Res	Type
17	Q	3	LYS
17	Q	96	GLU
19	S	43	GLU
20	T	97	ALA
20	T	98	PRO
2	B	130	ARG
3	C	54	ARG
4	D	5	ILE
6	F	16	GLN
6	F	29	ALA
6	F	42	GLU
6	F	96	PRO
10	J	91	PRO
11	K	62	GLN
12	L	89	ARG
13	M	6	GLY
15	O	24	SER
15	O	86	GLY
16	P	63	GLY
16	P	67	THR
17	Q	61	GLU
18	R	87	ARG
19	S	5	LEU
20	T	82	SER
4	D	17	VAL
5	E	133	TYR
6	F	12	PRO
7	G	14	PRO
7	G	83	ALA
8	H	8	ASP
8	H	86	ILE
11	K	49	GLY
17	Q	80	GLY
19	S	80	TYR
20	T	73	HIS
21	U	22	ARG
5	E	128	PRO
4	D	141	ARG
12	L	63	GLY
16	P	51	VAL
14	N	13	THR

### 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	202/220 (92%)	176 (87%)	26 (13%)	6	26
3	C	160/188 (85%)	152 (95%)	8 (5%)	34	77
4	D	180/181 (99%)	156 (87%)	24 (13%)	6	25
5	E	115/123 (94%)	100 (87%)	15 (13%)	6	26
6	F	90/90 (100%)	79 (88%)	11 (12%)	7	29
7	G	126/127 (99%)	121 (96%)	5 (4%)	42	84
8	H	119/119 (100%)	107 (90%)	12 (10%)	11	39
9	I	98/99 (99%)	88 (90%)	10 (10%)	11	38
10	J	88/92 (96%)	81 (92%)	7 (8%)	17	53
11	K	90/99 (91%)	80 (89%)	10 (11%)	9	34
12	L	104/111 (94%)	96 (92%)	8 (8%)	18	56
13	M	93/101 (92%)	86 (92%)	7 (8%)	19	57
14	N	49/50 (98%)	47 (96%)	2 (4%)	41	83
15	O	79/80 (99%)	69 (87%)	10 (13%)	6	27
16	P	72/74 (97%)	60 (83%)	12 (17%)	3	16
17	Q	94/97 (97%)	91 (97%)	3 (3%)	51	89
18	R	61/77 (79%)	55 (90%)	6 (10%)	12	41
19	S	69/80 (86%)	62 (90%)	7 (10%)	11	39
20	T	76/82 (93%)	66 (87%)	10 (13%)	6	25
21	U	19/22 (86%)	19 (100%)	0	100	100
All	All	1984/2112 (94%)	1791 (90%)	193 (10%)	12	42

All (193) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	9	GLU
2	B	12	GLU
2	B	15	VAL
2	B	17	PHE

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Mol	Chain	Res	Type
2	B	22	LYS
2	B	24	TRP
2	B	36	ARG
2	B	42	ILE
2	B	44	LEU
2	B	69	LEU
2	B	71	VAL
2	B	79	ASP
2	B	111	ARG
2	B	130	ARG
2	B	137	ARG
2	B	145	LEU
2	B	158	LEU
2	B	178	ARG
2	B	185	ILE
2	B	187	LEU
2	B	189	ASP
2	B	196	LEU
2	B	204	ASN
2	B	205	ASP
2	B	215	LEU
2	B	221	LEU
3	C	5	ILE
3	C	12	LEU
3	C	16	ARG
3	C	27	LYS
3	C	94	LEU
3	C	104	GLN
3	C	127	ARG
3	C	131	ARG
4	D	3	ARG
4	D	8	VAL
4	D	9	CYS
4	D	11	LEU
4	D	12	CYS
4	D	19	LEU
4	D	26	CYS
4	D	36	ARG
4	D	58	LEU
4	D	62	GLN
4	D	68	TYR
4	D	97	LEU

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Mol	Chain	Res	Type
4	D	121	VAL
4	D	122	ARG
4	D	127	THR
4	D	129	ASN
4	D	131	ARG
4	D	132	ARG
4	D	135	LEU
4	D	138	TYR
4	D	158	ILE
4	D	194	LEU
4	D	196	LEU
4	D	202	LEU
5	E	10	MET
5	E	12	LEU
5	E	15	ARG
5	E	20	GLN
5	E	25	ARG
5	E	31	LEU
5	E	41	VAL
5	E	73	ASN
5	E	76	ILE
5	E	78	HIS
5	E	79	GLU
5	E	91	LEU
5	E	101	ILE
5	E	137	GLU
5	E	147	ASP
6	F	15	ASP
6	F	21	LEU
6	F	30	LEU
6	F	45	LEU
6	F	46	ARG
6	F	52	ILE
6	F	55	ASP
6	F	63	TYR
6	F	70	ASP
6	F	92	LYS
6	F	98	LEU
7	G	36	LYS
7	G	79	ARG
7	G	136	LYS
7	G	151	TYR

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Mol	Chain	Res	Type
7	G	156	TRP
8	H	1	MET
8	H	3	THR
8	H	10	LEU
8	H	24	THR
8	H	39	LEU
8	H	51	VAL
8	H	65	TYR
8	H	81	HIS
8	H	91	ARG
8	H	95	VAL
8	H	102	ARG
8	H	133	LEU
9	I	3	GLN
9	I	10	ARG
9	I	95	LYS
9	I	99	LEU
9	I	101	PHE
9	I	102	LEU
9	I	113	LYS
9	I	114	TYR
9	I	121	ARG
9	I	128	ARG
10	J	22	LYS
10	J	47	PHE
10	J	62	HIS
10	J	74	ILE
10	J	80	LYS
10	J	96	ILE
10	J	100	THR
11	K	18	ARG
11	K	22	HIS
11	K	29	ILE
11	K	53	SER
11	K	63	LEU
11	K	92	GLU
11	K	95	ILE
11	K	117	ASN
11	K	125	PHE
11	K	127	LYS
12	L	20	LYS
12	L	41	ARG

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Mol	Chain	Res	Type
12	L	42	THR
12	L	62	SER
12	L	75	HIS
12	L	85	ILE
12	L	89	ARG
12	L	102	ARG
13	M	47	ASP
13	M	64	TRP
13	M	66	LEU
13	M	70	LEU
13	M	71	ARG
13	M	93	ARG
13	M	108	ARG
14	N	42	ILE
14	N	44	LEU
15	O	3	ILE
15	O	26	GLU
15	O	38	ARG
15	O	39	LEU
15	O	41	GLU
15	O	57	LEU
15	O	65	ARG
15	O	67	LEU
15	O	74	ASP
15	O	82	ILE
16	P	2	VAL
16	P	27	LYS
16	P	28	ARG
16	P	39	TYR
16	P	47	ASP
16	P	48	TRP
16	P	53	VAL
16	P	55	ARG
16	P	65	GLN
16	P	67	THR
16	P	69	THR
16	P	82	GLN
17	Q	52	LYS
17	Q	63	ARG
17	Q	89	LEU
18	R	31	LEU
18	R	47	THR

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Mol	Chain	Res	Type
18	R	53	ARG
18	R	76	LEU
18	R	79	LEU
18	R	82	THR
19	S	6	LYS
19	S	7	LYS
19	S	22	LEU
19	S	29	ARG
19	S	37	ARG
19	S	44	MET
19	S	49	ILE
20	T	9	ASN
20	T	26	ASN
20	T	30	LYS
20	T	41	ILE
20	T	51	GLU
20	T	56	MET
20	T	57	ARG
20	T	64	ASP
20	T	72	LEU
20	T	93	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (42) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	19	HIS
2	B	40	HIS
2	B	113	HIS
2	B	146	GLN
2	B	204	ASN
3	C	28	GLN
3	C	69	HIS
3	C	104	GLN
3	C	170	GLN
4	D	62	GLN
4	D	123	HIS
4	D	129	ASN
5	E	20	GLN
5	E	73	ASN
5	E	78	HIS
6	F	18	GLN
6	F	27	GLN

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Mol	Chain	Res	Type
6	F	32	ASN
6	F	94	GLN
7	G	13	GLN
7	G	37	ASN
7	G	84	ASN
7	G	106	GLN
8	H	82	HIS
9	I	73	GLN
9	I	117	HIS
9	I	124	GLN
10	J	13	HIS
10	J	78	ASN
11	K	22	HIS
11	K	26	ASN
11	K	38	ASN
12	L	8	ASN
12	L	9	GLN
12	L	49	ASN
13	M	77	ASN
15	O	37	ASN
15	O	46	HIS
16	P	82	GLN
17	Q	16	GLN
19	S	53	ASN
20	T	16	HIS

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1503/1522 (98%)	288 (19%)	31 (2%)

All (288) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	9	G
1	A	31	G
1	A	32	A
1	A	39	G
1	A	47	C
1	A	48	C
1	A	50	A

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Mol	Chain	Res	Type
1	A	51	A
1	A	59	A
1	A	61	G
1	A	70	G
1	A	80	G
1	A	81	U
1	A	90	U
1	A	91	C
1	A	97	G
1	A	98	G
1	A	101	A
1	A	116	A
1	A	120	A
1	A	121	C
1	A	122	G
1	A	131	C
1	A	147	G
1	A	150	C
1	A	157	G
1	A	158	G
1	A	163	C
1	A	172	A
1	A	173	U
1	A	189(G)	G
1	A	189(H)	G
1	A	195	A
1	A	197	A
1	A	199	G
1	A	216	G
1	A	220	G
1	A	231	G
1	A	243	A
1	A	244	U
1	A	247	G
1	A	251	G
1	A	266	G
1	A	267	C
1	A	270	A
1	A	281	G
1	A	289	G
1	A	301	G
1	A	321	A

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Mol	Chain	Res	Type
1	A	327	A
1	A	328	C
1	A	329	A
1	A	332	G
1	A	342	C
1	A	343	U
1	A	345	C
1	A	352	C
1	A	353	A
1	A	354	G
1	A	357	G
1	A	366	C
1	A	367	U
1	A	371	G
1	A	372	C
1	A	373	A
1	A	384	G
1	A	388	G
1	A	390	C
1	A	397	A
1	A	398	C
1	A	406	G
1	A	412	A
1	A	413	G
1	A	414	A
1	A	415	A
1	A	420	U
1	A	421	U
1	A	422	C
1	A	424	G
1	A	428	G
1	A	429	U
1	A	430	A
1	A	435	C
1	A	437	U
1	A	439	A
1	A	442	C
1	A	448	A
1	A	452	A
1	A	461	A
1	A	470	C
1	A	472	A

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Mol	Chain	Res	Type
1	A	473	G
1	A	482	A
1	A	484	G
1	A	485	G
1	A	487	A
1	A	495	A
1	A	496	A
1	A	498	U
1	A	500	G
1	A	501	C
1	A	505	G
1	A	509	A
1	A	510	A
1	A	511	C
1	A	513	C
1	A	518	C
1	A	520	A
1	A	527	G
1	A	531	U
1	A	532	A
1	A	533	A
1	A	534	U
1	A	545	C
1	A	547	A
1	A	559	A
1	A	560	U
1	A	561	U
1	A	562	C
1	A	572	A
1	A	573	A
1	A	576	G
1	A	577	G
1	A	588	G
1	A	596	C
1	A	607	A
1	A	616	G
1	A	618	C
1	A	623	C
1	A	630	G
1	A	632	A
1	A	653	A
1	A	665	A

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Mol	Chain	Res	Type
1	A	687	A
1	A	688	G
1	A	693	G
1	A	702	A
1	A	703	G
1	A	720	C
1	A	721	G
1	A	731	G
1	A	733	A
1	A	749	C
1	A	753	A
1	A	755	G
1	A	766	A
1	A	775	G
1	A	776	G
1	A	777	A
1	A	786	G
1	A	792	A
1	A	793	U
1	A	794	A
1	A	802	A
1	A	816	A
1	A	817	C
1	A	819	A
1	A	821	G
1	A	827	U
1	A	828	A
1	A	833	U
1	A	839	U
1	A	840	C
1	A	841	U
1	A	848	C
1	A	859	A
1	A	864	A
1	A	870	U
1	A	872	A
1	A	884	U
1	A	885	G
1	A	902	G
1	A	914	A
1	A	920	U
1	A	922	G

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Mol	Chain	Res	Type
1	A	926	G
1	A	927	G
1	A	932	C
1	A	934	C
1	A	935	A
1	A	940	C
1	A	960	U
1	A	961	U
1	A	968	A
1	A	969	A
1	A	971	G
1	A	972	C
1	A	974	A
1	A	975	A
1	A	976	G
1	A	977	A
1	A	978	A
1	A	980	C
1	A	991	U
1	A	992	U
1	A	993	G
1	A	1005	A
1	A	1026	G
1	A	1050	G
1	A	1054	C
1	A	1065	U
1	A	1066	C
1	A	1068	G
1	A	1081	G
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	1117	G
1	A	1118	C
1	A	1124	G
1	A	1125	U
1	A	1126	U
1	A	1129	C
1	A	1136	U
1	A	1137	C
1	A	1138	G
1	A	1139	G

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Mol	Chain	Res	Type
1	A	1146	A
1	A	1152	A
1	A	1159	U
1	A	1160	G
1	A	1190	G
1	A	1196	U
1	A	1197	G
1	A	1202	G
1	A	1212	U
1	A	1213	A
1	A	1225	A
1	A	1227	A
1	A	1238	A
1	A	1239	A
1	A	1249	C
1	A	1255	G
1	A	1256	A
1	A	1257	U
1	A	1258	G
1	A	1270	C
1	A	1280	A
1	A	1281	U
1	A	1286	A
1	A	1287	A
1	A	1290	G
1	A	1294	G
1	A	1300	G
1	A	1301	U
1	A	1302	U
1	A	1305	G
1	A	1312	G
1	A	1317	C
1	A	1320	C
1	A	1322	C
1	A	1323	G
1	A	1331	G
1	A	1335	C
1	A	1338	G
1	A	1347	G
1	A	1363	C
1	A	1363(A)	A
1	A	1364	U

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Mol	Chain	Res	Type
1	A	1370	G
1	A	1388	C
1	A	1397	C
1	A	1402	C
1	A	1419	G
1	A	1442	G
1	A	1442(A)	G
1	A	1442(B)	A
1	A	1443	G
1	A	1447	A
1	A	1452	C
1	A	1456	G
1	A	1487	G
1	A	1492	A
1	A	1493	A
1	A	1494	G
1	A	1495	U
1	A	1497	G
1	A	1499	A
1	A	1502	A
1	A	1504	G
1	A	1505	G
1	A	1506	U
1	A	1507	A
1	A	1517	G
1	A	1519	A
1	A	1520	G
1	A	1529	G
1	A	1530	G

All (31) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	60	A
1	A	79	G
1	A	115	G
1	A	243	A
1	A	250	A
1	A	266	G
1	A	328	C
1	A	353	A
1	A	366	C

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Mol	Chain	Res	Type
1	A	428	G
1	A	429	U
1	A	484	G
1	A	499	A
1	A	509	A
1	A	533	A
1	A	560	U
1	A	687	A
1	A	748	C
1	A	776	G
1	A	913	A
1	A	991	U
1	A	992	U
1	A	1049	U
1	A	1064	G
1	A	1065	U
1	A	1067	A
1	A	1201	A
1	A	1285	A
1	A	1493	A
1	A	1498	U
1	A	1504	G

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 50 ligands modelled in this entry, 50 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	1504/1522 (98%)	0.43	125 (8%) 11 3	61, 125, 191, 194	0
2	B	235/256 (91%)	0.05	5 (2%) 60 12	107, 158, 185, 191	0
3	C	207/239 (86%)	0.22	15 (7%) 15 4	119, 166, 184, 191	0
4	D	208/209 (99%)	0.25	20 (9%) 8 2	82, 131, 168, 182	0
5	E	151/162 (93%)	0.25	14 (9%) 9 2	84, 117, 162, 189	0
6	F	101/101 (100%)	-0.16	3 (2%) 48 9	86, 132, 165, 182	0
7	G	155/156 (99%)	0.40	16 (10%) 7 2	140, 171, 188, 190	0
8	H	138/138 (100%)	-0.01	7 (5%) 27 6	85, 123, 156, 162	0
9	I	127/128 (99%)	0.68	18 (14%) 3 1	143, 183, 190, 191	0
10	J	99/105 (94%)	0.96	20 (20%) 2 1	130, 177, 190, 193	0
11	K	119/129 (92%)	0.16	2 (1%) 67 15	84, 123, 165, 186	0
12	L	125/135 (92%)	0.47	14 (11%) 6 2	82, 109, 164, 189	0
13	M	115/126 (91%)	0.49	13 (11%) 6 2	149, 185, 190, 192	0
14	N	60/61 (98%)	0.62	2 (3%) 44 8	132, 170, 186, 189	0
15	O	88/89 (98%)	-0.11	2 (2%) 57 12	74, 112, 159, 165	0
16	P	84/88 (95%)	0.75	14 (16%) 2 1	89, 116, 160, 180	0
17	Q	100/105 (95%)	0.43	13 (13%) 4 1	85, 110, 153, 159	0
18	R	70/88 (79%)	0.19	3 (4%) 34 7	93, 122, 171, 183	0
19	S	79/93 (84%)	1.24	16 (20%) 1 1	142, 186, 191, 192	0
20	T	99/106 (93%)	0.39	9 (9%) 9 2	84, 119, 157, 179	0
21	U	25/27 (92%)	2.66	14 (56%) 0 0	141, 172, 188, 189	0
All	All	3889/4063 (95%)	0.39	345 (8%) 10 3	61, 141, 190, 194	0

All (345) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1149	C	19.5
1	A	1148	U	17.2
1	A	1126	U	11.1
1	A	1150	U	10.9
1	A	1322	C	10.3
1	A	1224	G	10.2
19	S	75	ALA	9.9
1	A	950	U	8.2
1	A	1127	G	8.2
1	A	1363	C	7.9
19	S	73	GLU	7.9
1	A	963	G	7.9
1	A	1147	C	7.9
19	S	36	ARG	7.5
11	K	11	LYS	7.4
21	U	24	ARG	7.4
1	A	1125	U	7.2
19	S	74	PHE	7.1
1	A	1092	A	7.1
19	S	76	PRO	7.0
9	I	30	GLY	7.0
1	A	980	C	6.8
1	A	962	C	6.8
1	A	977	A	6.8
12	L	72	GLY	6.5
21	U	11	GLY	6.2
10	J	92	THR	6.1
1	A	1260	C	5.9
7	G	5	ARG	5.9
10	J	90	LEU	5.6
1	A	1394	A	5.6
12	L	129	ALA	5.6
9	I	62	TYR	5.5
1	A	46	G	5.4
12	L	73	GLU	5.4
1	A	1223	C	5.3
1	A	1039	C	5.2
1	A	951	G	5.2
13	M	116	THR	5.2
19	S	37	ARG	5.2
3	C	184	TYR	5.1
10	J	91	PRO	5.1
1	A	1235	U	5.1

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Mol	Chain	Res	Type	RSRZ
7	G	83	ALA	5.1
17	Q	68	ARG	5.1
1	A	949	A	5.0
1	A	308	C	4.9
9	I	123	PRO	4.8
7	G	4	ARG	4.8
19	S	69	HIS	4.7
1	A	1201	A	4.7
16	P	35	LYS	4.7
10	J	71	LEU	4.6
1	A	44	G	4.6
19	S	31	ILE	4.6
2	B	217	ARG	4.6
13	M	87	TYR	4.5
16	P	28	ARG	4.5
1	A	970	C	4.5
9	I	31	GLN	4.5
1	A	194	C	4.5
4	D	4	TYR	4.5
1	A	1040	U	4.4
1	A	1321	C	4.4
9	I	124	GLN	4.4
16	P	29	ASP	4.4
9	I	45	ALA	4.4
3	C	188	LEU	4.3
19	S	71	LEU	4.3
4	D	69	GLY	4.2
10	J	68	HIS	4.2
1	A	1233	G	4.2
13	M	114	ARG	4.2
10	J	41	PRO	4.1
1	A	1324	A	4.1
1	A	45	U	4.1
13	M	102	ARG	4.1
1	A	1280	A	4.1
1	A	522	C	4.1
7	G	12	LEU	4.1
4	D	5	ILE	4.1
19	S	72	GLY	4.1
21	U	5	ASP	4.1
1	A	983	A	4.1
1	A	523	A	4.0

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Mol	Chain	Res	Type	RSRZ
16	P	10	GLY	4.0
1	A	961	U	4.0
10	J	93	GLY	4.0
17	Q	101	ARG	4.0
9	I	66	ARG	4.0
1	A	1057	G	3.9
10	J	69	ASN	4.0
21	U	2	GLY	3.9
10	J	101	VAL	3.9
21	U	4	GLY	3.9
1	A	1058	G	3.9
1	A	979	C	3.9
21	U	10	ARG	3.8
8	H	30	ARG	3.8
1	A	607	A	3.8
12	L	120	TYR	3.8
1	A	926	G	3.8
7	G	39	ALA	3.7
1	A	1146	A	3.7
20	T	66	ALA	3.7
5	E	81	GLU	3.7
5	E	86	ALA	3.7
1	A	940	C	3.7
1	A	1091	U	3.7
17	Q	25	ARG	3.7
21	U	3	LYS	3.7
13	M	101	GLN	3.7
17	Q	70	ARG	3.6
4	D	114	ARG	3.6
1	A	973	G	3.6
16	P	75	ARG	3.6
5	E	83	GLU	3.6
16	P	9	PHE	3.6
1	A	96	U	3.5
20	T	78	ALA	3.5
1	A	307	C	3.5
10	J	70	ARG	3.5
16	P	8	ARG	3.5
1	A	981	U	3.5
10	J	99	LYS	3.5
1	A	112	G	3.5
1	A	1222	G	3.5

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Mol	Chain	Res	Type	RSRZ
5	E	124	GLY	3.5
18	R	46	GLU	3.5
21	U	15	ARG	3.5
17	Q	24	GLU	3.5
17	Q	7	THR	3.4
17	Q	67	LYS	3.4
1	A	972	C	3.4
12	L	94	PRO	3.4
3	C	21	ARG	3.4
4	D	6	GLY	3.4
9	I	115	GLY	3.4
13	M	100	GLY	3.4
7	G	97	GLN	3.4
1	A	1232	U	3.4
13	M	31	LYS	3.3
1	A	1320	C	3.3
1	A	1066	C	3.3
21	U	14	TRP	3.3
9	I	41	VAL	3.3
12	L	111	LYS	3.3
4	D	3	ARG	3.3
7	G	32	ARG	3.3
21	U	18	TYR	3.3
1	A	324	G	3.3
6	F	92	LYS	3.3
1	A	1323	G	3.3
1	A	1357	A	3.2
5	E	88	LYS	3.2
21	U	23	PRO	3.2
1	A	389	A	3.2
1	A	1234	C	3.2
1	A	974	A	3.2
1	A	1093	A	3.2
13	M	27	LYS	3.2
21	U	25	LYS	3.2
12	L	71	PRO	3.2
20	T	9	ASN	3.2
10	J	43	ARG	3.1
2	B	18	GLY	3.1
4	D	115	ARG	3.1
3	C	190	ARG	3.1
4	D	68	TYR	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	1353	G	3.1
10	J	5	ARG	3.1
16	P	30	GLY	3.1
13	M	85	GLY	3.1
7	G	13	GLN	3.1
13	M	113	PRO	3.1
1	A	43	C	3.1
20	T	64	ASP	3.1
10	J	67	THR	3.1
1	A	1229	A	3.0
1	A	1242	C	3.0
21	U	16	GLY	3.0
1	A	1285	A	3.0
3	C	187	ALA	3.0
9	I	42	ARG	3.0
19	S	70	LYS	3.0
5	E	85	GLY	3.0
4	D	2	GLY	3.0
19	S	35	SER	2.9
1	A	1220	G	2.9
6	F	94	GLN	2.9
1	A	9	G	2.9
4	D	102	ASP	2.9
1	A	323	U	2.9
1	A	1124	G	2.9
4	D	47	ARG	2.9
12	L	89	ARG	2.9
1	A	978	A	2.9
9	I	29	ASN	2.8
9	I	127	LYS	2.8
3	C	58	GLU	2.8
9	I	44	VAL	2.8
4	D	42	GLN	2.8
9	I	27	THR	2.8
1	A	1183	A	2.8
15	O	72	ARG	2.8
21	U	21	TYR	2.8
1	A	1033	G	2.8
1	A	1355	G	2.8
1	A	1230	C	2.8
2	B	214	ILE	2.8
1	A	854	G	2.8

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Mol	Chain	Res	Type	RSRZ
12	L	74	GLY	2.8
8	H	56	LYS	2.8
17	Q	26	GLN	2.8
4	D	21	LEU	2.7
4	D	118	ARG	2.7
5	E	87	SER	2.7
1	A	922	G	2.7
12	L	113	ARG	2.7
10	J	96	ILE	2.7
1	A	1352	C	2.7
1	A	971	G	2.7
7	G	133	GLY	2.7
3	C	114	PRO	2.6
13	M	86	CYS	2.6
1	A	1325	C	2.6
3	C	189	ALA	2.6
4	D	132	ARG	2.6
3	C	53	ALA	2.6
1	A	8	A	2.6
2	B	8	LYS	2.6
7	G	40	ALA	2.6
4	D	66	ARG	2.6
1	A	1356	G	2.6
1	A	1204	A	2.6
5	E	126	ARG	2.6
20	T	68	LYS	2.6
1	A	1354	C	2.6
9	I	14	VAL	2.6
1	A	921	U	2.6
4	D	46	LYS	2.5
17	Q	37	LYS	2.5
3	C	19	GLU	2.5
1	A	309	G	2.5
1	A	855	G	2.5
8	H	33	GLU	2.5
12	L	91	LYS	2.5
15	O	71	GLN	2.5
20	T	77	ALA	2.5
1	A	1262	C	2.5
1	A	331	G	2.5
1	A	1370	G	2.5
5	E	74	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
10	J	44	VAL	2.5
19	S	78	ARG	2.5
1	A	149	A	2.5
1	A	175	C	2.5
16	P	18	ARG	2.5
10	J	89	ASP	2.4
1	A	1086	U	2.4
2	B	232	PRO	2.4
1	A	1371	G	2.4
4	D	7	PRO	2.4
1	A	1095	U	2.4
12	L	110	VAL	2.4
8	H	136	GLU	2.4
1	A	1116	C	2.4
7	G	82	GLY	2.4
1	A	1288	A	2.4
3	C	45	LYS	2.4
17	Q	38	ARG	2.4
3	C	186	PHE	2.4
1	A	1205	U	2.4
1	A	354	G	2.4
1	A	1128	C	2.4
17	Q	40	LYS	2.3
1	A	575	G	2.3
7	G	31	MET	2.3
13	M	20	THR	2.3
1	A	735	C	2.3
1	A	1390	U	2.3
3	C	164	ARG	2.3
1	A	1041	A	2.3
10	J	98	ILE	2.3
16	P	31	LYS	2.3
19	S	68	GLY	2.3
14	N	52	GLN	2.3
20	T	29	LYS	2.3
1	A	185	A	2.3
20	T	80	ARG	2.3
1	A	1241	G	2.3
7	G	22	LEU	2.3
19	S	77	THR	2.3
5	E	89	ILE	2.3
1	A	576	G	2.2

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
16	P	27	LYS	2.2
1	A	1249	C	2.2
11	K	119	CYS	2.2
4	D	43	HIS	2.2
9	I	109	VAL	2.2
7	G	132	GLY	2.2
18	R	71	LYS	2.2
1	A	1359	C	2.2
4	D	67	ILE	2.2
9	I	125	TYR	2.2
20	T	65	LYS	2.2
8	H	31	PHE	2.2
1	A	1200	C	2.2
5	E	104	ALA	2.2
7	G	29	LYS	2.2
7	G	25	ALA	2.2
9	I	32	ASP	2.2
1	A	1358	U	2.2
5	E	80	ILE	2.2
1	A	732	C	2.2
17	Q	66	SER	2.2
5	E	122	GLU	2.1
16	P	34	GLU	2.1
3	C	27	LYS	2.1
1	A	1403	C	2.1
1	A	1364	U	2.1
14	N	26	ARG	2.1
16	P	7	ALA	2.1
1	A	1253	G	2.1
8	H	29	SER	2.1
1	A	390	C	2.1
10	J	94	VAL	2.1
12	L	90	VAL	2.1
16	P	32	TYR	2.1
3	C	16	ARG	2.1
17	Q	69	LYS	2.1
12	L	69	TYR	2.1
1	A	734	G	2.1
10	J	40	LEU	2.1
6	F	93	SER	2.0
1	A	548	G	2.0
1	A	733	A	2.0

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Mol	Chain	Res	Type	RSRZ
5	E	123	LEU	2.0
1	A	1083	U	2.0
13	M	88	ARG	2.0
18	R	42	ARG	2.0
1	A	1187	G	2.0
19	S	10	PHE	2.0
1	A	1243	C	2.0
8	H	35	ILE	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
22	MG	A	1550	1/1	0.75	-	72,72,72,72	0
22	MG	A	1571	1/1	0.19	-	66,66,66,66	0
22	MG	A	1574	1/1	0.18	-	77,77,77,77	0
22	MG	A	1578	1/1	1.10	-	87,87,87,87	0
22	MG	A	1572	1/1	0.60	-	75,75,75,75	0
22	MG	A	1585	1/1	1.08	-	87,87,87,87	0
23	ZN	D	210	1/1	0.04	-	93,93,93,93	0
22	MG	A	1580	1/1	1.68	-	79,79,79,79	0
22	MG	A	1573	1/1	0.12	-	82,82,82,82	0
22	MG	A	1545	1/1	0.51	-	83,83,83,83	0
22	MG	A	1577	1/1	0.37	-	87,87,87,87	0
22	MG	A	1583	1/1	0.13	-	64,64,64,64	0
22	MG	A	1556	1/1	0.11	-	77,77,77,77	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
22	MG	A	1568	1/1	0.26	-	65,65,65,65	0
22	MG	A	1563	1/1	0.62	-	75,75,75,75	0
22	MG	A	1582	1/1	0.23	-	71,71,71,71	0
23	ZN	N	62	1/1	0.10	-	157,157,157,157	0
22	MG	A	1575	1/1	0.96	-	70,70,70,70	0
22	MG	A	1579	1/1	0.85	-	86,86,86,86	0
22	MG	A	1592	1/1	0.33	-	79,79,79,79	0
22	MG	A	1551	1/1	0.10	-	82,82,82,82	0
22	MG	A	1576	1/1	0.17	-	79,79,79,79	0
22	MG	A	1581	1/1	0.64	-	80,80,80,80	0
22	MG	A	1569	1/1	0.25	-	74,74,74,74	0
22	MG	A	1548	1/1	0.10	-	86,86,86,86	0
22	MG	A	1553	1/1	0.23	-	94,94,94,94	0
22	MG	A	1587	1/1	0.26	-	62,62,62,62	0
22	MG	A	1557	1/1	0.97	-	80,80,80,80	0
22	MG	A	1547	1/1	0.40	-	63,63,63,63	0
22	MG	A	1562	1/1	0.41	-	62,62,62,62	0
22	MG	A	1567	1/1	0.23	-	67,67,67,67	0
22	MG	A	1554	1/1	0.08	-	61,61,61,61	0
22	MG	A	1561	1/1	0.23	-	61,61,61,61	0
22	MG	A	1555	1/1	0.13	-	81,81,81,81	0
22	MG	A	1549	1/1	0.89	-	61,61,61,61	0
22	MG	A	1560	1/1	0.17	-	73,73,73,73	0
22	MG	A	1590	1/1	0.57	-	80,80,80,80	0
22	MG	A	1552	1/1	0.26	-	51,51,51,51	0
22	MG	A	1564	1/1	0.49	-	66,66,66,66	0
22	MG	A	1558	1/1	1.37	-	76,76,76,76	0
22	MG	A	1589	1/1	0.24	-	97,97,97,97	0
22	MG	A	1584	1/1	0.39	-	68,68,68,68	0
22	MG	A	1570	1/1	0.35	-	78,78,78,78	0
22	MG	A	1591	1/1	0.45	-	84,84,84,84	0
22	MG	A	1559	1/1	0.19	-	67,67,67,67	0
22	MG	A	1566	1/1	0.39	-	78,78,78,78	0
22	MG	A	1586	1/1	0.12	-	62,62,62,62	0
22	MG	A	1546	1/1	2.10	-	70,70,70,70	0
22	MG	A	1565	1/1	0.09	-	68,68,68,68	0
22	MG	A	1588	1/1	0.15	-	74,74,74,74	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.