



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 27, 2014 – 11:31 AM GMT

PDB ID : 2AW7  
Title : Crystal structure of the bacterial ribosome from Escherichia coli at 3.5 Å resolution. This file contains the 30S subunit of the second 70S ribosome. The entire crystal structure contains two 70S ribosomes and is described in remark 400.  
Authors : Schuwirth, B.S.; Borovinskaya, M.A.; Hau, C.W.; Zhang, W.; Vila-Sanjurjo, A.; Holton, J.M.; Cate, J.H.D.  
Deposited on : 2005-08-31  
Resolution : 3.46 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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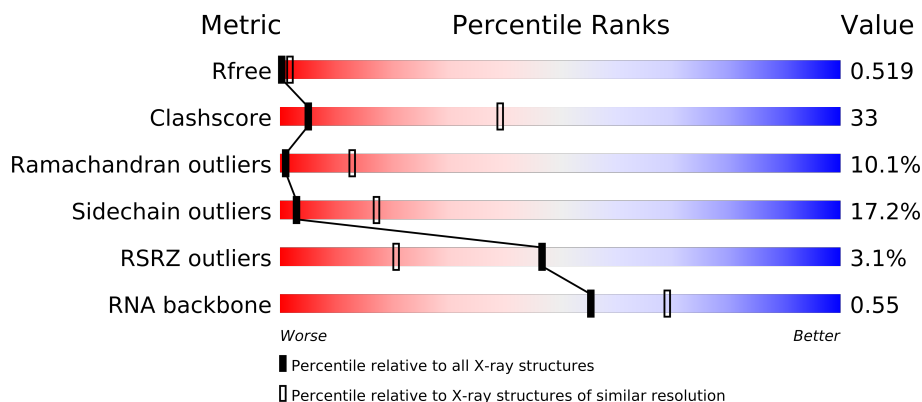
The following versions of software and data (see [references](#)) were used in the production of this report:

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 3.46 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	1149 (3.62-3.30)
Clashscore	79885	1012 (3.60-3.32)
Ramachandran outliers	78287	1401 (3.62-3.30)
Sidechain outliers	78261	1401 (3.62-3.30)
RSRZ outliers	66119	1149 (3.62-3.30)
RNA backbone	1838	1004 (4.10-2.76)

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	1542	
2	C	232	
3	D	205	
4	E	166	
5	F	135	
6	G	178	
7	H	129	
8	I	129	
9	J	103	
10	K	128	
11	L	123	
12	M	117	

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Mol	Chain	Length	Quality of chain
13	N	100	
14	O	89	
15	P	82	
16	Q	83	
17	R	74	
18	S	91	
19	T	86	
20	B	240	
21	U	71	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
22	MG	A	1544	-	X
22	MG	A	1557	-	X
22	MG	A	1565	-	X
22	MG	A	1570	-	X
22	MG	A	1572	-	X
22	MG	A	1574	-	X
22	MG	A	1583	-	X

## 2 Entry composition

There are 23 unique types of molecules in this entry. The entry contains 51759 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 ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1530	Total	C	N	O	P	0	0	0
			32831	14642	6024	10635	1530			

- Molecule 2 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	206	Total	C	N	O	S	0	0	0
			1624	1028	305	288	3			

- Molecule 3 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	205	Total	C	N	O	S	0	0	0
			1643	1026	315	298	4			

- Molecule 4 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	150	Total	C	N	O	S	0	0	0
			1105	687	211	201	6			

- Molecule 5 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	F	100	Total	C	N	O	S	0	0	0
			817	515	148	148	6			

- Molecule 6 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	G	152	Total	C	N	O	S	0	0	0
			1196	745	230	217	4			

- Molecule 7 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	H	129	Total	C	N	O	S	0	0	0
			979	616	173	184	6			

- Molecule 8 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	I	127	Total	C	N	O	S	0	0	0
			1022	634	206	179	3			

- Molecule 9 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	J	98	Total	C	N	O	S	0	0	0
			786	493	150	142	1			

- Molecule 10 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	K	117	Total	C	N	O	S	0	0	0
			877	540	174	160	3			

- Molecule 11 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	L	123	Total	C	N	O	S	0	0	0
			955	590	196	165	4			

- Molecule 12 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	M	113	Total	C	N	O	S	0	0	0
			876	541	177	155	3			

- Molecule 13 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	N	96	Total	C	N	O	S	0	0	0
			774	483	160	128	3			

- Molecule 14 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	O	88	Total	C	N	O	S	0	0	0
			716	440	146	129	1			

- Molecule 15 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	P	80	Total	C	N	O	S	0	0	0
			638	400	126	111	1			

- Molecule 16 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	Q	81	Total	C	N	O	S	0	0	0
			656	417	122	114	3			

- Molecule 17 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
17	R	55	Total	C	N	O	0	0	0
			455	288	86	81			

- Molecule 18 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	S	80	Total	C	N	O	S	0	0	0
			644	413	121	108	2			

- Molecule 19 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	T	85	Total	C	N	O	S	0	0	0
			665	411	137	114	3			

- Molecule 20 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	B	218	Total	C	N	O	S	0	0	0
			1704	1081	305	311	7			

- Molecule 21 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	U	51	Total	C	N	O	S	0	0	0
			425	265	86	73	1			

- Molecule 22 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
22	A	62	Total	Mg	0	0
			62	62		

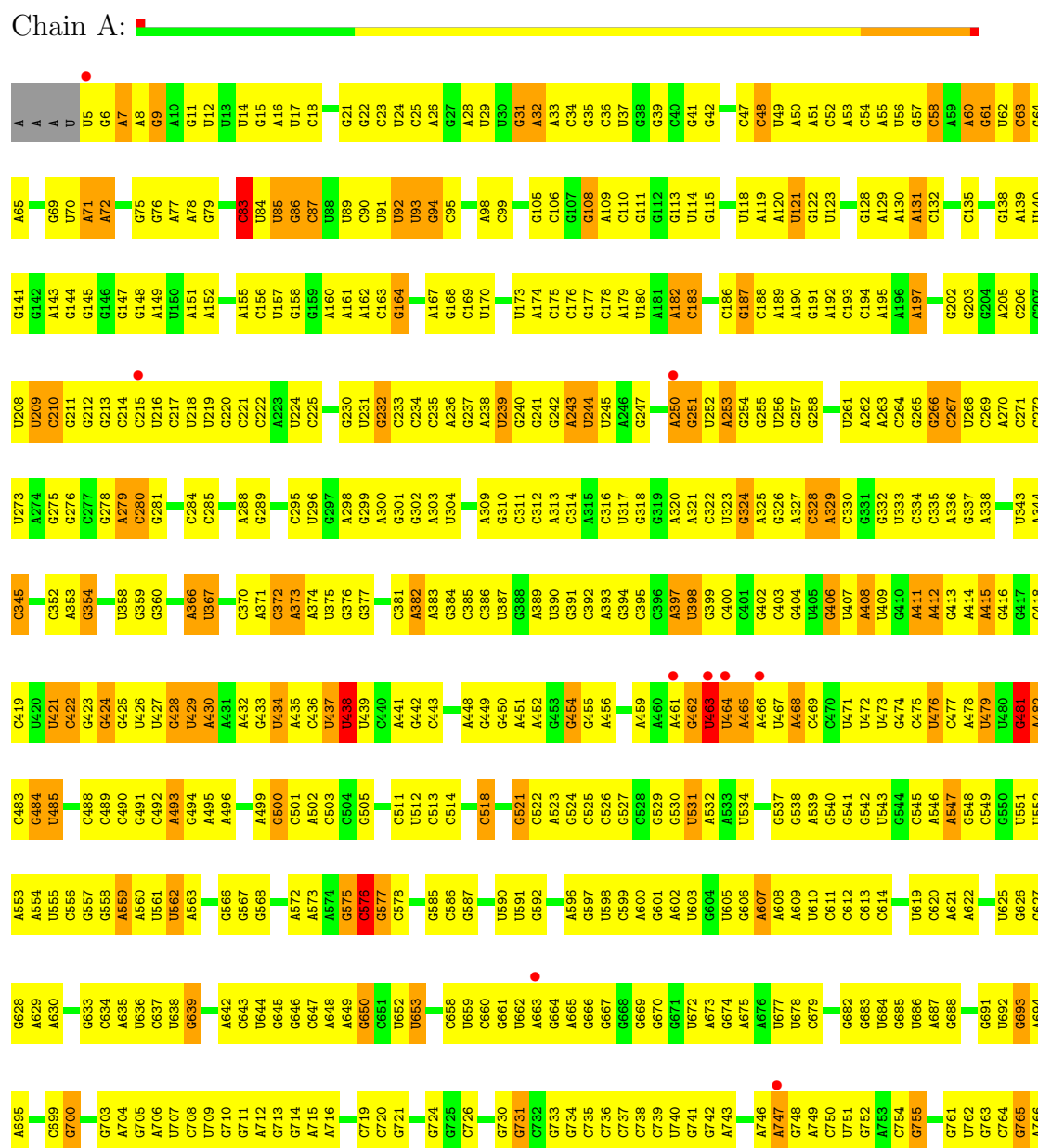
- Molecule 23 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
23	A	304	Total	O	0	0
			304	304		
23	E	1	Total	O	0	0
			1	1		
23	L	1	Total	O	0	0
			1	1		
23	N	2	Total	O	0	0
			2	2		
23	T	1	Total	O	0	0
			1	1		

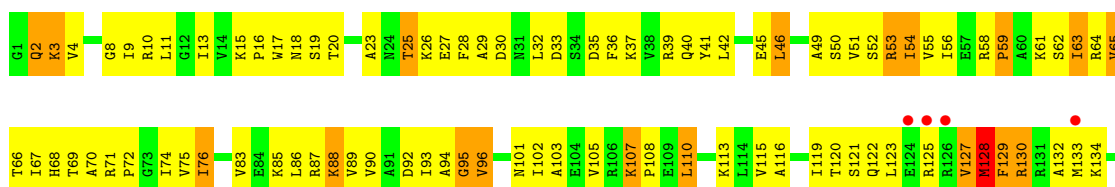
### 3 Residue-property plots

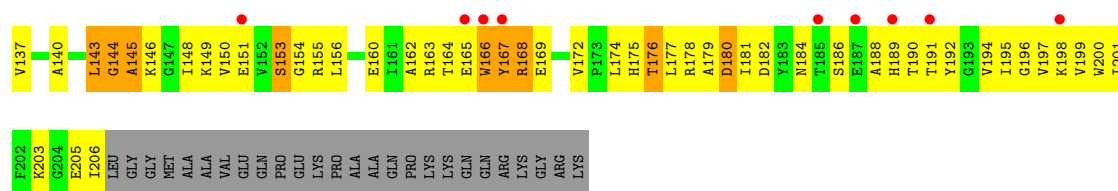
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

#### • Molecule 1: 16S ribosomal RNA



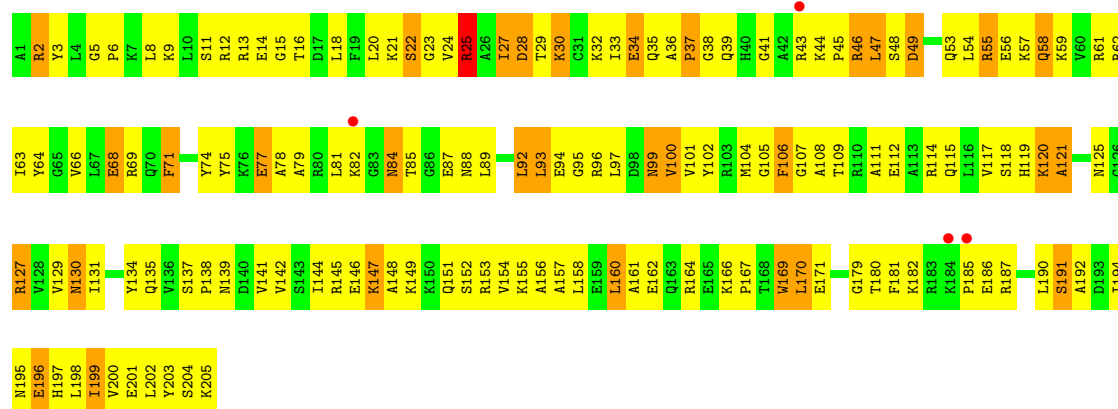






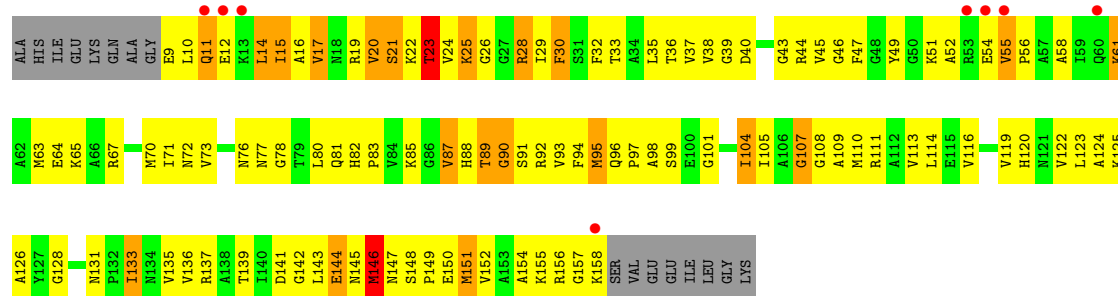
• Molecule 3: 30S ribosomal protein S4

Chain D:



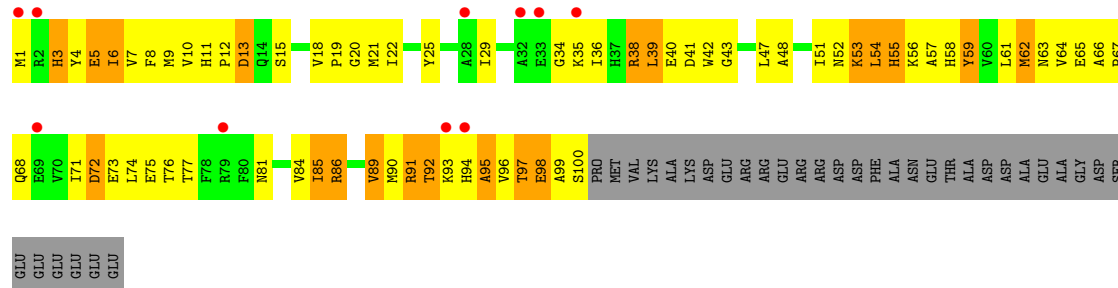
• Molecule 4: 30S ribosomal protein S5

Chain E:



• Molecule 5: 30S ribosomal protein S6

Chain F:



• Molecule 6: 30S ribosomal protein S7

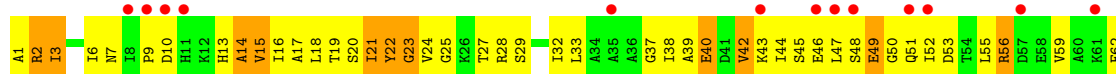
Chain G:

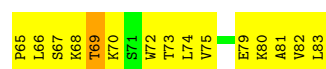




• Molecule 12: 30S ribosomal protein S13

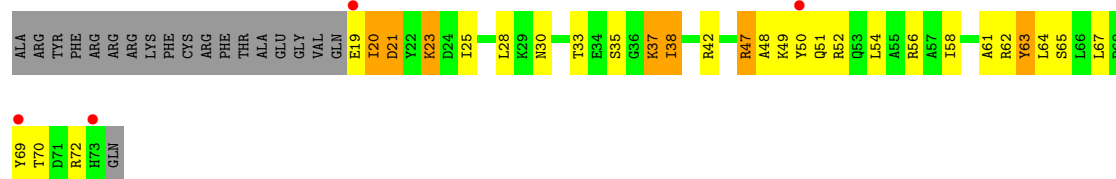
Chain M:





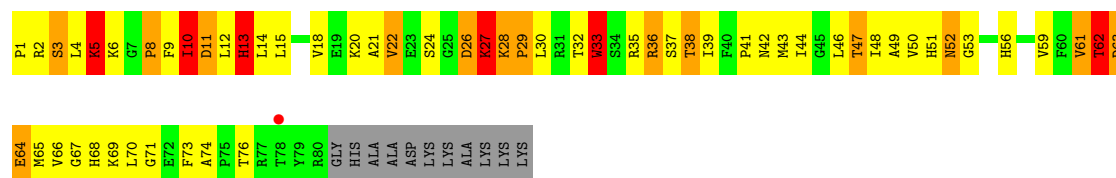
• Molecule 17: 30S ribosomal protein S18

Chain R:



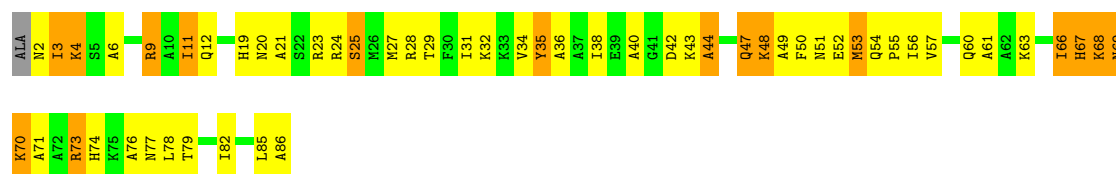
• Molecule 18: 30S ribosomal protein S19

Chain S:



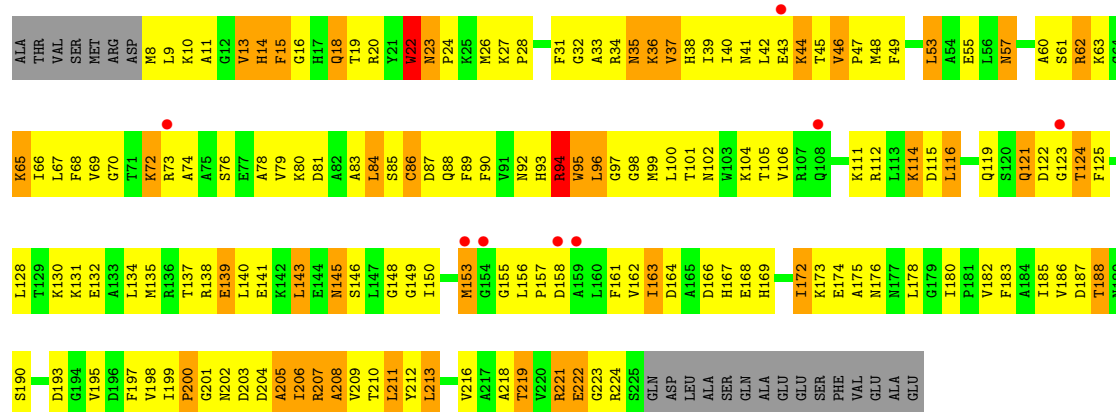
• Molecule 19: 30S ribosomal protein S20

Chain T:



• Molecule 20: 30S ribosomal protein S2

Chain B:



• Molecule 21: 30S ribosomal protein S21

Chain U:



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	208.85Å 379.20Å 739.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	70.00 – 3.46 163.96 – 3.46	Depositor EDS
% Data completeness (in resolution range)	91.6 (70.00-3.46) 91.6 (163.96-3.46)	Depositor EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.19 (at 3.49Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.279 , 0.331 0.512 , 0.519	Depositor DCC
$R_{free}$ test set	26271 reflections (3.79%)	DCC
Wilson B-factor (Å <sup>2</sup> )	77.0	Xtriage
Anisotropy	0.184	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.26 , 44.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 720727 reflections	Xtriage
$F_o, F_c$ correlation	0.48	EDS
Total number of atoms	51759	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.43% 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: 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	0.26	2/36762 (0.0%)	0.75	11/57350 (0.0%)
2	C	0.23	0/1651	0.47	0/2225
3	D	0.23	0/1665	0.45	0/2227
4	E	0.24	0/1118	0.45	0/1504
5	F	0.24	0/835	0.49	0/1128
6	G	0.23	0/1211	0.45	0/1624
7	H	0.23	0/989	0.46	0/1326
8	I	0.24	0/1034	0.46	0/1375
9	J	0.22	0/796	0.49	0/1077
10	K	0.24	0/893	0.47	0/1205
11	L	0.22	0/969	0.48	0/1300
12	M	0.21	0/884	0.46	0/1181
13	N	0.24	0/785	0.45	0/1043
14	O	0.23	0/724	0.44	0/966
15	P	0.25	0/648	0.45	0/870
16	Q	0.24	0/665	0.47	0/892
17	R	0.23	0/462	0.45	0/621
18	S	0.25	0/660	0.47	0/888
19	T	0.24	0/671	0.42	0/888
20	B	0.25	0/1735	0.47	0/2338
21	U	0.98	3/430 (0.7%)	0.82	3/570 (0.5%)
All	All	0.27	5/55587 (0.0%)	0.68	14/82598 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	20



All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
21	U	25	ALA	C-N	15.34	1.60	1.33
21	U	17	ARG	C-N	8.48	1.53	1.34
1	A	463	U	O3'-P	-6.06	1.53	1.61
21	U	8	ASN	C-N	5.74	1.47	1.34
1	A	495	A	N3-C4	-5.08	1.31	1.34

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	765	G	N9-C1'-C2'	-8.20	102.98	112.00
1	A	232	G	C5'-C4'-C3'	-7.36	104.23	116.00
21	U	17	ARG	C-N-CA	-6.85	104.58	121.70
1	A	438	U	N1-C1'-C2'	-6.36	105.01	112.00
1	A	576	C	O5'-P-OP1	-6.31	100.02	105.70
1	A	1250	A	C5'-C4'-C3'	6.09	125.75	116.00
21	U	17	ARG	O-C-N	6.02	132.33	122.70
1	A	1432	G	N9-C1'-C2'	-5.88	105.53	112.00
1	A	814	A	C5'-C4'-C3'	5.69	125.10	116.00
1	A	63	C	C5'-C4'-C3'	-5.43	107.31	116.00
1	A	328	C	C2'-C3'-O3'	5.42	122.36	113.70
1	A	1534	A	C2'-C3'-O3'	-5.34	97.76	109.50
1	A	1461	G	N1-C2-N2	-5.10	111.61	116.20
21	U	25	ALA	O-C-N	-5.08	114.57	123.20

There are no chirality outliers.

All (20) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1009	U	Sidechain
1	A	1048	G	Sidechain
1	A	1133	G	Sidechain
1	A	1319	A	Sidechain
1	A	1362	A	Sidechain
1	A	1432	G	Sidechain
1	A	1441	A	Sidechain
1	A	187	G	Sidechain
1	A	281	G	Sidechain
1	A	437	U	Sidechain
1	A	438	U	Sidechain
1	A	454	G	Sidechain
1	A	481	G	Sidechain

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Mol	Chain	Res	Type	Group
1	A	496	A	Sidechain
1	A	521	G	Sidechain
1	A	575	G	Sidechain
1	A	58	C	Sidechain
1	A	703	G	Sidechain
1	A	83	C	Sidechain
1	A	86	G	Sidechain

## 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	32831	0	16521	1184	0
2	C	1624	0	1699	146	0
3	D	1643	0	1710	166	0
4	E	1105	0	1148	143	0
5	F	817	0	808	92	0
6	G	1196	0	1246	98	0
7	H	979	0	1034	86	0
8	I	1022	0	1070	127	0
9	J	786	0	828	106	0
10	K	877	0	887	108	0
11	L	955	0	1019	101	0
12	M	876	0	937	93	0
13	N	774	0	827	114	0
14	O	716	0	742	46	0
15	P	638	0	656	71	0
16	Q	656	0	702	85	0
17	R	455	0	478	41	0
18	S	644	0	675	85	0
19	T	665	0	714	64	0
20	B	1704	0	1732	152	0
21	U	425	0	449	84	0
22	A	62	0	0	0	0
23	A	304	0	0	1	0
23	E	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
23	L	1	0	0	0	0
23	N	2	0	0	0	0
23	T	1	0	0	0	0
All	All	51759	0	35882	2920	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 33.

All (2920) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:L:43:LYS:HB3	11:L:44:PRO:HD2	1.26	1.08
1:A:974:A:H4'	1:A:975:A:H5'	1.28	1.05
20:B:46:VAL:HG13	20:B:47:PRO:HD3	1.38	1.03
21:U:4:LYS:HB3	21:U:6:ARG:HH12	1.22	1.00
5:F:3:HIS:HB3	5:F:92:THR:HA	1.42	1.00
10:K:113:THR:HG21	21:U:28:LEU:HD11	1.44	0.99
2:C:59:PRO:HG2	2:C:62:SER:HB2	1.46	0.98
20:B:116:LEU:HD22	20:B:140:LEU:HD21	1.47	0.96
1:A:973:G:H3'	1:A:974:A:H5''	1.47	0.95
20:B:10:LYS:HD2	20:B:211:LEU:HD21	1.48	0.95
21:U:24:LYS:HD2	21:U:25:ALA:H	1.29	0.95
5:F:29:ILE:HD13	5:F:64:VAL:HG11	1.49	0.94
12:M:52:ILE:HG13	12:M:56:ARG:HH22	1.33	0.93
1:A:1250:A:H4'	8:I:69:GLY:H	1.35	0.92
2:C:137:VAL:HA	2:C:148:ILE:HD13	1.52	0.92
10:K:20:ALA:HB3	10:K:83:VAL:HA	1.50	0.91
3:D:167:PRO:HG2	3:D:170:LEU:HD11	1.50	0.91
11:L:68:GLY:HA3	11:L:106:VAL:HG21	1.50	0.91
1:A:1306:A:N6	1:A:1331:G:H1'	1.86	0.91
5:F:38:ARG:HH11	5:F:98:GLU:H	1.15	0.91
19:T:61:ALA:HA	19:T:67:HIS:H	1.36	0.91
7:H:105:THR:HA	7:H:122:GLY:HA3	1.53	0.91
10:K:19:VAL:HG22	10:K:34:THR:HG22	1.51	0.90
9:J:51:VAL:HG23	13:N:80:ARG:HB2	1.52	0.89
10:K:88:PRO:HD3	21:U:28:LEU:HD13	1.52	0.89
8:I:27:ILE:HG23	8:I:34:LEU:HB2	1.54	0.89
11:L:43:LYS:HB3	11:L:44:PRO:CD	2.03	0.88
5:F:47:LEU:HD12	5:F:55:HIS:HA	1.56	0.88
1:A:451:A:H5'	15:P:70:ARG:HH22	1.37	0.87
1:A:9:G:H5'	4:E:107:GLY:HA3	1.55	0.87
16:Q:13:SER:HB3	16:Q:21:VAL:HB	1.56	0.87
13:N:26:LEU:HG	13:N:44:VAL:HG22	1.57	0.87

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
21:U:14:ALA:H	21:U:16:ARG:NH2	1.71	0.87
1:A:243:A:H4'	1:A:244:U:H5'	1.57	0.87
14:O:69:LEU:HD11	14:O:76:ARG:HB3	1.56	0.87
8:I:51:LEU:HB3	8:I:56:MET:HG2	1.54	0.87
21:U:3:ILE:HG12	21:U:19:LYS:HB3	1.57	0.86
20:B:163:ILE:HG23	20:B:164:ASP:H	1.39	0.85
3:D:63:ILE:HG23	3:D:64:TYR:HD1	1.41	0.85
20:B:101:THR:HA	20:B:178:LEU:HD21	1.58	0.85
10:K:78:ILE:HD13	10:K:78:ILE:H	1.41	0.85
8:I:118:ARG:HH21	8:I:122:ARG:HE	1.21	0.84
9:J:6:ILE:HD11	9:J:79:PRO:HB3	1.60	0.84
6:G:87:PRO:HG3	6:G:148:LYS:HA	1.57	0.84
21:U:34:ARG:HG2	21:U:35:GLU:H	1.43	0.84
4:E:36:THR:HG21	4:E:63:MET:HG2	1.60	0.84
21:U:14:ALA:H	21:U:16:ARG:HH22	1.26	0.83
15:P:4:ILE:HG12	15:P:21:VAL:HG22	1.60	0.83
1:A:1306:A:H61	1:A:1331:G:H1'	1.41	0.83
10:K:28:ASN:HD21	10:K:47:GLY:H	1.24	0.82
6:G:12:LEU:HD22	6:G:13:PRO:HD2	1.62	0.82
1:A:1320:C:H5''	18:S:2:ARG:HD3	1.61	0.82
9:J:66:GLU:HB2	13:N:98:ALA:HB2	1.60	0.82
13:N:63:CYS:HB3	13:N:68:ARG:H	1.43	0.82
1:A:699:C:H2'	1:A:700:G:H5''	1.59	0.82
20:B:218:ALA:HA	20:B:221:ARG:HD3	1.61	0.82
4:E:89:THR:HG22	4:E:91:SER:H	1.44	0.81
1:A:1367:C:H5''	8:I:115:VAL:HG23	1.60	0.81
1:A:1311:A:H62	18:S:1:PRO:HD3	1.45	0.81
1:A:719:C:H1'	17:R:37:LYS:HB2	1.59	0.81
1:A:664:G:H22	1:A:741:G:H1	1.26	0.81
11:L:84:GLY:H	11:L:94:TYR:HA	1.45	0.81
15:P:4:ILE:HD13	15:P:57:ILE:HG12	1.63	0.81
13:N:40:ARG:HH12	18:S:5:LYS:HB2	1.44	0.81
9:J:83:THR:HG23	9:J:87:LEU:HD23	1.61	0.81
5:F:47:LEU:HD13	5:F:51:ILE:HG22	1.62	0.81
13:N:82:LYS:HE2	13:N:85:GLU:HG3	1.61	0.80
4:E:110:MET:SD	4:E:126:ALA:HB2	2.22	0.80
3:D:58:GLN:HA	3:D:58:GLN:HE21	1.45	0.80
9:J:40:ILE:HD11	9:J:73:LEU:HD12	1.62	0.80
1:A:1399:C:H4'	1:A:1400:C:H5''	1.63	0.80
9:J:9:ARG:HB2	9:J:99:GLN:H	1.47	0.80
1:A:1342:C:H5'	8:I:127:SER:HB3	1.64	0.80
2:C:69:THR:HG22	2:C:71:ARG:H	1.47	0.80

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:N:50:LEU:H	13:N:51:PRO:HD2	1.45	0.79
9:J:52:LEU:HG	9:J:62:ARG:HE	1.48	0.79
8:I:113:LYS:HA	8:I:120:ALA:HB2	1.65	0.79
1:A:1071:C:H2'	1:A:1072:G:H8	1.47	0.79
11:L:98:ARG:HG3	11:L:105:GLY:HA2	1.65	0.79
4:E:109:ALA:HB1	4:E:136:VAL:HG13	1.65	0.79
1:A:1296:C:H4'	1:A:1302:C:N4	1.98	0.79
1:A:430:A:OP1	3:D:8:LEU:HB2	1.83	0.79
1:A:1003:G:H21	1:A:1005:A:H5'	1.46	0.79
1:A:1132:C:H2'	1:A:1133:G:C8	2.18	0.79
4:E:19:ARG:HG2	4:E:20:VAL:H	1.46	0.79
8:I:17:ARG:HB3	8:I:65:THR:HB	1.65	0.79
1:A:1056:U:H5'	2:C:162:ALA:HB2	1.66	0.78
1:A:1078:U:H4'	4:E:137:ARG:NH1	1.98	0.78
6:G:112:ASP:HB2	6:G:118:ARG:HG2	1.65	0.78
15:P:28:ARG:HD3	15:P:29:ASN:H	1.48	0.78
3:D:94:GLU:HG2	3:D:185:PRO:HG3	1.66	0.78
1:A:437:U:H2'	1:A:438:U:O4'	1.84	0.78
4:E:44:ARG:HA	4:E:71:ILE:O	1.82	0.78
18:S:15:LEU:HA	18:S:18:VAL:HG12	1.63	0.78
5:F:11:HIS:ND1	5:F:12:PRO:HD2	1.99	0.78
20:B:15:PHE:HB3	20:B:42:LEU:HD11	1.65	0.77
5:F:4:TYR:HA	5:F:91:ARG:HA	1.66	0.77
17:R:51:GLN:HA	17:R:54:LEU:HD13	1.66	0.77
13:N:12:ARG:HA	13:N:15:LEU:HD12	1.65	0.77
18:S:30:LEU:HD12	18:S:48:ILE:HG12	1.67	0.77
19:T:68:LYS:HB2	19:T:70:LYS:HD3	1.66	0.77
18:S:27:LYS:HZ3	18:S:27:LYS:HB3	1.49	0.77
1:A:1060:U:H4'	9:J:54:SER:HB2	1.67	0.77
1:A:781:A:H2'	1:A:782:A:H5'	1.67	0.77
18:S:51:HIS:HA	18:S:56:HIS:HA	1.67	0.77
4:E:82:HIS:HB2	4:E:83:PRO:HD2	1.67	0.77
1:A:60:A:H2'	19:T:4:LYS:HE3	1.67	0.77
21:U:19:LYS:HG3	21:U:20:ARG:HE	1.47	0.77
8:I:74:GLN:HE21	8:I:74:GLN:HA	1.50	0.77
1:A:264:C:H4'	16:Q:64:ARG:HD2	1.65	0.77
4:E:44:ARG:NH1	4:E:72:ASN:HD21	1.83	0.76
10:K:16:SER:HA	10:K:78:ILE:HA	1.66	0.76
4:E:104:ILE:HD12	4:E:111:ARG:HD3	1.66	0.76
1:A:840:C:H2'	1:A:842:U:H5''	1.67	0.76
12:M:15:VAL:HG22	12:M:40:GLU:HB2	1.68	0.76
1:A:764:C:H3'	1:A:765:G:H21	1.50	0.76

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:M:38:ILE:HG13	12:M:55:LEU:HD21	1.67	0.76
1:A:619:U:H3	3:D:130:ASN:ND2	1.84	0.76
8:I:94:ARG:HD3	8:I:97:LEU:HD12	1.68	0.75
1:A:814:A:H5'	1:A:1511:G:H4'	1.68	0.75
1:A:1097:C:H2'	1:A:1098:C:C6	2.20	0.75
5:F:47:LEU:HD21	5:F:57:ALA:HB2	1.68	0.75
8:I:118:ARG:HH21	8:I:122:ARG:NE	1.83	0.75
1:A:946:A:H2'	1:A:947:G:C8	2.22	0.75
2:C:150:VAL:HG22	2:C:199:VAL:HG12	1.69	0.75
3:D:2:ARG:NH1	3:D:114:ARG:HD3	2.00	0.75
2:C:179:ALA:HA	2:C:205:GLU:HA	1.69	0.75
11:L:49:ARG:HG2	11:L:89:LEU:HD21	1.69	0.75
1:A:974:A:C4'	1:A:975:A:H5'	2.15	0.75
3:D:55:ARG:HG3	3:D:55:ARG:HH11	1.51	0.75
15:P:67:ILE:HG13	15:P:71:VAL:HG13	1.67	0.74
1:A:108:G:O6	19:T:9:ARG:HG2	1.87	0.74
2:C:18:ASN:HA	2:C:55:VAL:HG12	1.67	0.74
1:A:1086:U:H3	1:A:1099:G:H22	1.34	0.74
12:M:89:ARG:NH1	12:M:101:THR:HG21	2.02	0.74
5:F:62:MET:HG3	5:F:64:VAL:HG23	1.67	0.74
20:B:100:LEU:HB3	20:B:178:LEU:HD11	1.68	0.74
20:B:206:ILE:HG22	20:B:207:ARG:HH21	1.52	0.74
12:M:52:ILE:HA	12:M:55:LEU:HD12	1.69	0.74
4:E:33:THR:HG22	4:E:51:LYS:HG2	1.68	0.74
2:C:156:LEU:HB2	2:C:163:ARG:HD3	1.69	0.74
21:U:16:ARG:O	21:U:20:ARG:HD2	1.86	0.74
16:Q:11:VAL:HG22	16:Q:22:VAL:HG22	1.70	0.74
20:B:16:GLY:HA2	20:B:40:ILE:H	1.51	0.74
1:A:262:A:OP2	19:T:70:LYS:HE2	1.88	0.74
15:P:3:THR:HG22	15:P:66:THR:HB	1.68	0.74
8:I:4:GLN:HG2	8:I:21:LYS:HD3	1.70	0.73
16:Q:10:ARG:NH1	16:Q:55:GLY:H	1.87	0.73
10:K:70:ALA:HA	10:K:73:VAL:HG22	1.71	0.73
19:T:69:ASN:H	19:T:69:ASN:ND2	1.85	0.73
10:K:82:GLU:HB3	10:K:108:ASN:HD22	1.53	0.73
16:Q:10:ARG:CZ	16:Q:55:GLY:H	2.01	0.73
3:D:18:LEU:HD12	3:D:63:ILE:HB	1.70	0.73
7:H:75:GLN:NE2	7:H:76:ARG:H	1.86	0.73
2:C:176:THR:OG1	2:C:179:ALA:HB2	1.88	0.73
13:N:96:LYS:HG2	13:N:97:LYS:H	1.53	0.73
6:G:23:ALA:O	6:G:26:VAL:HG22	1.89	0.73
1:A:1132:C:H2'	1:A:1133:G:H8	1.50	0.73

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:E:98:ALA:HB2	4:E:123:LEU:HG	1.69	0.73
1:A:278:G:H21	1:A:279:A:H62	1.36	0.73
3:D:84:ASN:HD21	3:D:87:GLU:H	1.37	0.73
1:A:812:G:N3	1:A:812:G:H2'	2.02	0.73
19:T:66:ILE:HG13	19:T:70:LYS:HG3	1.71	0.72
1:A:1078:U:H4'	4:E:137:ARG:HH12	1.54	0.72
3:D:138:PRO:HA	3:D:181:PHE:HD2	1.54	0.72
13:N:42:ASN:HB3	13:N:46:LYS:HE2	1.71	0.72
2:C:120:THR:HG23	2:C:188:ALA:HB2	1.71	0.72
13:N:30:ILE:HG21	13:N:43:ALA:HB3	1.70	0.72
9:J:25:ILE:HG23	9:J:87:LEU:HD12	1.70	0.72
2:C:182:ASP:HB3	2:C:201:ILE:HB	1.70	0.72
21:U:17:ARG:HD2	21:U:17:ARG:H	1.54	0.72
5:F:6:ILE:HG23	5:F:62:MET:HB3	1.71	0.72
12:M:85:TYR:HA	12:M:88:LEU:HD12	1.70	0.72
12:M:79:LEU:HA	12:M:82:LEU:HG	1.72	0.72
11:L:82:ARG:HG2	11:L:82:ARG:HH11	1.54	0.72
1:A:1412:C:H2'	1:A:1413:A:C8	2.24	0.72
1:A:501:C:H2'	1:A:502:A:H8	1.53	0.72
13:N:60:ARG:O	13:N:61:ASN:HB2	1.90	0.72
3:D:55:ARG:HG3	3:D:55:ARG:NH1	2.05	0.72
1:A:1060:U:H5''	9:J:53:ILE:HG12	1.72	0.72
8:I:98:ARG:HG2	8:I:103:VAL:HG11	1.72	0.72
20:B:139:GLU:O	20:B:143:LEU:HB2	1.90	0.72
1:A:1289:A:H3'	1:A:1290:G:H8	1.53	0.72
21:U:24:LYS:CD	21:U:25:ALA:H	2.03	0.72
1:A:1097:C:H2'	1:A:1098:C:H6	1.53	0.72
5:F:29:ILE:HG21	5:F:64:VAL:HG11	1.72	0.71
2:C:11:LEU:HD22	2:C:17:TRP:HE1	1.55	0.71
11:L:78:VAL:HG12	11:L:101:LEU:HD13	1.70	0.71
1:A:1296:C:H4'	1:A:1302:C:C4	2.24	0.71
6:G:14:ASP:HB3	6:G:18:GLY:N	2.05	0.71
19:T:19:HIS:O	19:T:23:ARG:HG2	1.91	0.71
3:D:63:ILE:HG23	3:D:64:TYR:CD1	2.25	0.71
2:C:149:LYS:HB2	2:C:168:ARG:HG3	1.70	0.71
5:F:29:ILE:HG22	5:F:34:GLY:HA3	1.71	0.71
20:B:16:GLY:HA3	20:B:39:ILE:HA	1.70	0.71
8:I:118:ARG:NH2	8:I:122:ARG:HE	1.87	0.71
1:A:1238:A:H5'	1:A:1336:C:H41	1.56	0.71
1:A:1218:C:H2'	1:A:1219:A:H8	1.55	0.71
8:I:94:ARG:HB3	8:I:98:ARG:NE	2.06	0.71
1:A:922:G:H2'	1:A:923:A:C8	2.26	0.71

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1320:C:H41	18:S:36:ARG:HG3	1.55	0.71
13:N:51:PRO:HG2	13:N:52:ARG:H	1.54	0.71
3:D:21:LYS:O	3:D:21:LYS:HD3	1.91	0.71
8:I:98:ARG:HA	8:I:103:VAL:HG22	1.70	0.71
1:A:1386:G:H2'	1:A:1387:G:H8	1.54	0.71
1:A:239:U:OP1	1:A:239:U:H4'	1.91	0.70
14:O:72:LYS:O	14:O:73:ASP:HB2	1.91	0.70
1:A:412:A:H1'	1:A:413:G:H8	1.55	0.70
1:A:1342:C:H2'	1:A:1343:G:H8	1.57	0.70
1:A:1526:G:P	21:U:38:GLU:HB2	2.31	0.70
21:U:36:PHE:HB2	21:U:39:LYS:HB2	1.73	0.70
18:S:30:LEU:H	18:S:48:ILE:HA	1.57	0.70
3:D:141:VAL:HA	3:D:180:THR:H	1.56	0.70
21:U:37:TYR:O	21:U:40:PRO:HD2	1.90	0.70
4:E:36:THR:HG22	4:E:37:VAL:H	1.56	0.70
12:M:18:LEU:HD22	12:M:29:SER:HA	1.74	0.70
17:R:70:THR:HB	17:R:72:ARG:NH1	2.06	0.70
21:U:34:ARG:HG2	21:U:35:GLU:N	2.06	0.70
10:K:16:SER:CA	10:K:78:ILE:HA	2.22	0.70
13:N:31:SER:HA	13:N:40:ARG:HA	1.74	0.70
1:A:473:U:H2'	1:A:474:G:H8	1.57	0.70
6:G:11:ILE:HG21	6:G:27:ASN:HD21	1.57	0.70
8:I:79:ARG:HA	8:I:82:ILE:HD12	1.74	0.70
2:C:39:ARG:NH2	13:N:91:GLU:HB3	2.07	0.69
1:A:1316:G:H2'	1:A:1318:A:OP2	1.92	0.69
4:E:152:VAL:HG21	7:H:98:LEU:HB3	1.74	0.69
11:L:98:ARG:HB3	11:L:116:TYR:HA	1.73	0.69
11:L:43:LYS:CB	11:L:44:PRO:HD2	2.16	0.69
1:A:1071:C:H2'	1:A:1072:G:C8	2.27	0.69
4:E:35:LEU:HD21	4:E:136:VAL:HG21	1.72	0.69
14:O:38:LEU:HD23	14:O:55:LEU:HD13	1.73	0.69
12:M:10:ASP:HA	12:M:44:ILE:HD11	1.72	0.69
9:J:37:ARG:HB2	9:J:76:ILE:HA	1.72	0.69
1:A:1009:U:H1'	1:A:1021:A:N1	2.07	0.69
7:H:31:LEU:HG	7:H:35:ILE:HD11	1.73	0.69
9:J:57:VAL:HG22	9:J:58:ASN:H	1.56	0.69
1:A:1218:C:H2'	1:A:1219:A:C8	2.28	0.69
1:A:918:A:H2'	1:A:919:A:C8	2.28	0.69
18:S:14:LEU:HD12	18:S:15:LEU:N	2.07	0.69
3:D:87:GLU:HG2	3:D:187:ARG:HD3	1.75	0.69
2:C:95:GLY:O	2:C:96:VAL:HG13	1.91	0.69
4:E:157:GLY:H	7:H:43:GLY:HA3	1.57	0.69

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:390:U:H2'	1:A:391:G:C8	2.27	0.69
1:A:17:U:H2'	1:A:18:C:C6	2.27	0.69
1:A:279:A:H5''	1:A:280:C:H3'	1.75	0.69
19:T:38:ILE:HD11	19:T:82:ILE:HG22	1.74	0.69
3:D:160:LEU:HD13	3:D:161:ALA:N	2.08	0.69
15:P:40:ASN:HD21	15:P:42:ILE:HG12	1.57	0.69
21:U:48:LYS:HA	21:U:51:ALA:HB3	1.73	0.69
4:E:87:VAL:HG13	4:E:88:HIS:N	2.07	0.69
1:A:439:U:H4'	3:D:120:LYS:HD2	1.74	0.69
9:J:32:THR:HG23	9:J:33:GLY:H	1.58	0.69
20:B:65:LYS:HB2	20:B:157:PRO:HA	1.74	0.69
11:L:77:SER:O	11:L:79:ILE:HG23	1.92	0.69
12:M:14:ALA:HB3	12:M:40:GLU:HA	1.75	0.68
1:A:268:U:H2'	1:A:269:C:C6	2.28	0.68
10:K:83:VAL:HG21	10:K:96:ILE:HG23	1.74	0.68
1:A:1030:U:H5''	1:A:1031:C:H5	1.57	0.68
7:H:11:THR:HG22	7:H:14:ARG:HH12	1.56	0.68
1:A:559:A:H4'	1:A:560:A:H3'	1.75	0.68
10:K:69:CYS:O	10:K:73:VAL:HG13	1.92	0.68
21:U:4:LYS:HB3	21:U:6:ARG:NH1	2.04	0.68
1:A:429:U:P	3:D:12:ARG:HH21	2.16	0.68
1:A:1080:A:H4'	4:E:20:VAL:HG21	1.75	0.68
1:A:1031:C:H4'	1:A:1032:G:C5'	2.24	0.68
2:C:116:ALA:HB1	2:C:186:SER:OG	1.94	0.68
16:Q:59:GLU:O	16:Q:75:VAL:HG22	1.93	0.68
20:B:185:ILE:HA	20:B:199:ILE:HG13	1.74	0.68
21:U:15:LEU:HA	21:U:17:ARG:HH11	1.59	0.68
1:A:673:A:H2'	1:A:674:G:C8	2.28	0.68
1:A:1436:U:H2'	1:A:1437:A:H8	1.58	0.68
1:A:1342:C:H2'	1:A:1343:G:C8	2.28	0.68
4:E:87:VAL:HG22	4:E:88:HIS:H	1.58	0.68
2:C:166:TRP:HE1	2:C:168:ARG:HB2	1.58	0.68
19:T:27:MET:HG2	19:T:31:ILE:HD11	1.75	0.68
1:A:518:C:H2'	1:A:530:G:C8	2.29	0.68
5:F:3:HIS:HB3	5:F:92:THR:CA	2.22	0.68
9:J:39:PRO:HA	9:J:74:VAL:HG22	1.76	0.68
1:A:1225:A:H5'	12:M:101:THR:OG1	1.93	0.68
13:N:62:ARG:H	13:N:72:PHE:HZ	1.41	0.68
4:E:95:MET:HA	4:E:124:ALA:HB2	1.74	0.68
6:G:59:GLU:HA	6:G:62:GLU:OE2	1.93	0.68
20:B:94:ARG:HE	20:B:94:ARG:N	1.93	0.67
13:N:26:LEU:HA	13:N:29:ILE:HD12	1.75	0.67

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:I:70:GLY:O	8:I:74:GLN:HG2	1.94	0.67
19:T:47:GLN:HG2	19:T:82:ILE:HD12	1.77	0.67
1:A:89:U:H2'	1:A:90:C:C6	2.30	0.67
20:B:27:LYS:HB3	20:B:28:PRO:HD3	1.76	0.67
1:A:1256:A:N1	1:A:1278:G:H1'	2.10	0.67
1:A:975:A:O2'	1:A:1358:U:H1'	1.95	0.67
4:E:87:VAL:HG13	4:E:88:HIS:H	1.58	0.67
18:S:32:THR:HG22	18:S:33:TRP:H	1.60	0.67
2:C:166:TRP:CG	2:C:167:TYR:N	2.63	0.67
19:T:79:THR:HA	19:T:82:ILE:HG12	1.76	0.67
1:A:131:A:H2'	1:A:132:C:C6	2.30	0.67
13:N:73:LEU:HD12	13:N:83:VAL:HG21	1.76	0.67
16:Q:10:ARG:NH2	16:Q:11:VAL:HB	2.10	0.67
9:J:9:ARG:HH11	9:J:73:LEU:HD23	1.58	0.67
14:O:31:LEU:O	14:O:35:ILE:HG12	1.95	0.67
8:I:114:LYS:HB2	8:I:117:LEU:HD12	1.75	0.67
3:D:187:ARG:HH12	3:D:191:SER:HA	1.60	0.67
12:M:78:ARG:NH1	12:M:79:LEU:HD23	2.10	0.67
1:A:1170:A:H2'	1:A:1171:A:O4'	1.96	0.67
6:G:70:PRO:HA	6:G:141:HIS:HE1	1.58	0.67
3:D:84:ASN:ND2	3:D:87:GLU:H	1.92	0.66
1:A:529:G:O6	11:L:45:ASN:HA	1.95	0.66
20:B:18:GLN:O	20:B:37:VAL:HG23	1.94	0.66
16:Q:10:ARG:NH2	16:Q:55:GLY:N	2.43	0.66
1:A:1124:G:H5'	9:J:37:ARG:NH2	2.10	0.66
1:A:501:C:H2'	1:A:502:A:C8	2.30	0.66
1:A:1034:G:H2'	1:A:1035:A:C8	2.29	0.66
4:E:96:GLN:HG3	4:E:97:PRO:HD2	1.77	0.66
1:A:1241:G:H2'	1:A:1242:G:H8	1.60	0.66
20:B:70:GLY:O	20:B:92:ASN:HA	1.95	0.66
4:E:52:ALA:HB2	4:E:61:LYS:HE2	1.77	0.66
21:U:39:LYS:H	21:U:40:PRO:HD2	1.60	0.66
15:P:61:VAL:HA	15:P:65:ALA:HB3	1.78	0.66
13:N:30:ILE:CG2	13:N:41:TRP:HB3	2.25	0.66
1:A:1244:G:H2'	1:A:1245:C:C6	2.30	0.66
1:A:960:U:O2'	1:A:1223:C:H5'	1.96	0.66
5:F:42:TRP:HB2	5:F:59:TYR:HB2	1.78	0.66
1:A:780:A:O2'	1:A:781:A:H5''	1.94	0.66
1:A:408:A:OP1	3:D:111:ALA:HB3	1.95	0.66
1:A:188:C:H2'	1:A:189:A:O4'	1.95	0.66
5:F:66:ALA:HB1	5:F:67:PRO:HD2	1.77	0.66
20:B:14:HIS:CG	20:B:15:PHE:H	2.13	0.66

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:538:G:OP2	11:L:111:GLN:HB2	1.95	0.66
1:A:909:A:H2'	1:A:910:C:O4'	1.95	0.66
4:E:12:GLU:HG2	4:E:38:VAL:HG22	1.77	0.66
20:B:153:MET:SD	20:B:157:PRO:HD3	2.36	0.66
1:A:505:G:H5'	1:A:534:U:H2'	1.78	0.66
2:C:115:VAL:O	2:C:119:ILE:HG22	1.96	0.66
20:B:26:MET:HE1	20:B:186:VAL:HB	1.78	0.66
12:M:102:LYS:HZ1	12:M:103:THR:HG23	1.60	0.66
19:T:73:ARG:HG3	19:T:74:HIS:N	2.10	0.66
2:C:53:ARG:HA	2:C:113:LYS:NZ	2.11	0.66
1:A:763:G:H2'	1:A:764:C:H6	1.61	0.66
1:A:278:G:N2	1:A:279:A:H62	1.93	0.66
1:A:1323:G:H2'	1:A:1324:A:C8	2.31	0.66
6:G:144:ALA:C	6:G:146:ALA:H	1.99	0.66
9:J:9:ARG:HG3	9:J:99:GLN:HB2	1.77	0.65
9:J:9:ARG:HB3	9:J:99:GLN:HE21	1.61	0.65
12:M:9:PRO:HB2	12:M:17:ALA:HB1	1.78	0.65
1:A:859:G:H2'	1:A:860:A:C8	2.30	0.65
1:A:1191:A:OP1	2:C:3:LYS:HG3	1.96	0.65
7:H:54:THR:HG23	7:H:55:LYS:HE2	1.77	0.65
9:J:56:HIS:O	9:J:57:VAL:HG12	1.97	0.65
1:A:882:C:O2'	1:A:883:C:H5'	1.95	0.65
11:L:14:LYS:HE2	11:L:16:ALA:HB2	1.78	0.65
1:A:1054:C:O2'	1:A:1055:A:H5''	1.95	0.65
19:T:52:GLU:O	19:T:56:ILE:HD13	1.97	0.65
8:I:93:LEU:O	8:I:97:LEU:HG	1.97	0.65
19:T:11:ILE:HG13	19:T:12:GLN:N	2.11	0.65
5:F:38:ARG:HD3	5:F:97:THR:HA	1.78	0.65
5:F:53:LYS:HE2	5:F:54:LEU:HD23	1.79	0.65
9:J:53:ILE:HG13	13:N:84:ARG:CZ	2.26	0.65
1:A:1096:C:H2'	1:A:1097:C:C6	2.32	0.65
3:D:141:VAL:HG12	3:D:180:THR:HA	1.79	0.65
1:A:269:C:H2'	1:A:270:A:C8	2.31	0.65
7:H:11:THR:HA	7:H:14:ARG:NH1	2.12	0.65
1:A:1186:G:H21	13:N:100:TRP:C	1.99	0.65
20:B:212:TYR:O	20:B:216:VAL:HG22	1.97	0.65
4:E:14:LEU:HD22	4:E:15:ILE:N	2.12	0.65
1:A:620:C:C2	3:D:131:ILE:HD13	2.31	0.65
16:Q:16:MET:CB	16:Q:19:SER:HB2	2.26	0.65
1:A:1008:U:H5''	13:N:23:ARG:HH21	1.62	0.65
20:B:95:TRP:HZ3	20:B:98:GLY:H	1.44	0.65
15:P:4:ILE:O	15:P:71:VAL:HG11	1.97	0.65

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:C:8:GLY:HA3	13:N:88:MET:SD	2.37	0.65
13:N:86:ALA:HB1	13:N:91:GLU:HB2	1.79	0.65
1:A:1281:C:H5'	1:A:1282:C:H5	1.61	0.65
1:A:546:A:P	3:D:68:GLU:HB3	2.36	0.65
3:D:78:ALA:HB1	3:D:85:THR:HA	1.78	0.65
16:Q:66:LEU:H	16:Q:66:LEU:HD12	1.62	0.65
13:N:32:ASP:HB2	13:N:34:ASN:ND2	2.12	0.65
1:A:312:C:H2'	1:A:313:A:C8	2.32	0.65
10:K:92:ARG:HH11	10:K:92:ARG:HG2	1.62	0.65
1:A:652:U:H4'	7:H:55:LYS:HE3	1.78	0.65
10:K:85:VAL:HG21	10:K:92:ARG:HH12	1.62	0.65
5:F:86:ARG:NH1	17:R:63:TYR:HB3	2.12	0.65
9:J:37:ARG:HG2	9:J:37:ARG:HH11	1.62	0.65
11:L:80:LEU:O	11:L:97:VAL:HG22	1.97	0.65
1:A:1508:A:H2'	1:A:1509:C:C6	2.33	0.64
1:A:952:U:H2'	1:A:953:G:H8	1.62	0.64
1:A:865:A:H5'	1:A:1078:U:O4	1.97	0.64
1:A:1238:A:H5'	1:A:1336:C:N4	2.13	0.64
1:A:878:A:O4'	7:H:3:GLN:HG3	1.97	0.64
1:A:678:U:H2'	1:A:679:C:C6	2.32	0.64
11:L:34:THR:HB	11:L:53:ARG:HE	1.62	0.64
1:A:205:A:H2'	1:A:206:C:H6	1.62	0.64
20:B:69:VAL:HB	20:B:162:VAL:HB	1.78	0.64
20:B:81:ASP:HA	20:B:84:LEU:HD22	1.78	0.64
12:M:68:LEU:HD22	12:M:69:ARG:NH1	2.13	0.64
1:A:238:A:H2'	1:A:239:U:H5"	1.78	0.64
8:I:27:ILE:HD13	8:I:34:LEU:HD13	1.79	0.64
14:O:24:THR:HG21	14:O:69:LEU:HD23	1.80	0.64
20:B:46:VAL:CG1	20:B:47:PRO:HD3	2.23	0.64
1:A:947:G:H2'	1:A:948:C:C6	2.32	0.64
13:N:50:LEU:H	13:N:51:PRO:CD	2.08	0.64
11:L:65:TYR:HB2	11:L:92:VAL:HG11	1.78	0.64
20:B:130:LYS:HB3	20:B:134:LEU:HB2	1.79	0.64
1:A:1520:C:H2'	1:A:1521:C:C6	2.32	0.64
9:J:53:ILE:HG22	9:J:61:ALA:HB1	1.80	0.64
8:I:45:MET:O	8:I:49:GLN:HG3	1.98	0.64
11:L:64:SER:OG	11:L:96:THR:HG23	1.97	0.64
1:A:441:A:H61	1:A:493:A:H62	1.45	0.64
20:B:195:VAL:HG12	20:B:197:PHE:H	1.62	0.64
21:U:14:ALA:HB3	21:U:16:ARG:NH1	2.13	0.64
1:A:1250:A:H2'	1:A:1251:A:C8	2.33	0.64
18:S:39:ILE:HB	18:S:66:VAL:HA	1.79	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:C:11:LEU:HD22	2:C:17:TRP:NE1	2.11	0.64
1:A:598:U:H4'	7:H:85:TYR:CD2	2.33	0.64
1:A:1422:G:O2'	1:A:1423:G:H5'	1.97	0.64
1:A:524:G:H2'	1:A:525:C:C6	2.33	0.64
1:A:1286:U:O2'	1:A:1287:A:H5''	1.97	0.64
11:L:71:HIS:HD2	11:L:73:LEU:HD12	1.62	0.64
12:M:18:LEU:HG	12:M:21:ILE:HD12	1.79	0.64
1:A:270:A:H2'	1:A:271:C:C6	2.33	0.64
1:A:1031:C:H4'	1:A:1032:G:H5''	1.80	0.64
1:A:1292:G:H2'	1:A:1293:C:C6	2.32	0.64
1:A:1129:C:H1'	1:A:1146:A:H61	1.63	0.64
3:D:97:LEU:HB2	3:D:134:TYR:HB3	1.79	0.64
13:N:30:ILE:HG22	13:N:41:TRP:HB3	1.79	0.64
15:P:54:LEU:HD13	15:P:80:LYS:HZ2	1.63	0.64
1:A:1270:G:H2'	1:A:1271:A:H8	1.63	0.64
13:N:40:ARG:HG3	18:S:6:LYS:O	1.97	0.64
4:E:87:VAL:HG22	4:E:88:HIS:N	2.12	0.64
17:R:72:ARG:HH21	21:U:23:GLU:HG3	1.61	0.64
9:J:36:VAL:HG13	9:J:76:ILE:HD11	1.80	0.64
1:A:1277:C:O2'	1:A:1279:G:H1'	1.98	0.64
20:B:83:ALA:O	20:B:88:GLN:HB2	1.98	0.64
5:F:68:GLN:O	5:F:71:ILE:HG22	1.98	0.64
10:K:110:THR:HG22	21:U:5:VAL:H	1.62	0.63
5:F:47:LEU:HD21	5:F:57:ALA:CB	2.28	0.63
11:L:86:VAL:HG11	11:L:89:LEU:HD23	1.79	0.63
1:A:1436:U:H2'	1:A:1437:A:C8	2.33	0.63
1:A:1354:U:H2'	1:A:1355:G:H8	1.63	0.63
3:D:151:GLN:NE2	3:D:153:ARG:HD2	2.13	0.63
2:C:54:ILE:HB	2:C:67:ILE:HD12	1.81	0.63
20:B:137:THR:HA	20:B:140:LEU:HD12	1.81	0.63
19:T:61:ALA:HA	19:T:67:HIS:N	2.10	0.63
1:A:1213:A:O2'	1:A:1214:C:H5''	1.98	0.63
1:A:476:U:H2'	1:A:477:C:C6	2.34	0.63
1:A:63:C:H5'	1:A:64:G:OP2	1.99	0.63
13:N:44:VAL:HA	13:N:47:LEU:HB3	1.81	0.63
2:C:39:ARG:HH22	13:N:91:GLU:HB3	1.63	0.63
5:F:1:MET:SD	5:F:67:PRO:HD3	2.38	0.63
12:M:92:ARG:CZ	12:M:92:ARG:HA	2.29	0.63
1:A:531:U:H5'	1:A:531:U:H6	1.62	0.63
20:B:202:ASN:ND2	20:B:203:ASP:H	1.95	0.63
8:I:22:PRO:HA	8:I:60:LEU:HA	1.79	0.63
1:A:194:C:O2'	1:A:195:A:H5'	1.98	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
19:T:57:VAL:HG12	19:T:71:ALA:HB1	1.81	0.63
14:O:62:ARG:CZ	14:O:86:LEU:HD21	2.29	0.63
6:G:125:ASP:HB3	6:G:129:ASN:HA	1.81	0.63
20:B:11:ALA:HB1	20:B:42:LEU:HD13	1.81	0.63
20:B:156:LEU:HD11	20:B:178:LEU:HD13	1.80	0.63
1:A:817:C:H1'	1:A:819:A:H5'	1.80	0.63
7:H:76:ARG:HA	7:H:126:CYS:HB3	1.81	0.63
19:T:78:LEU:O	19:T:82:ILE:HG23	1.99	0.63
11:L:6:LEU:HD11	11:L:11:ARG:HE	1.63	0.63
1:A:1320:C:N3	18:S:35:ARG:HD3	2.14	0.63
13:N:82:LYS:O	13:N:85:GLU:HB2	1.99	0.63
6:G:22:LEU:O	6:G:26:VAL:HG13	1.99	0.63
2:C:149:LYS:HE3	2:C:200:TRP:CE3	2.33	0.63
16:Q:74:LEU:HD22	16:Q:75:VAL:N	2.13	0.63
1:A:269:C:H2'	1:A:270:A:H8	1.62	0.62
5:F:38:ARG:NH1	5:F:98:GLU:H	1.95	0.62
1:A:1014:A:C5'	18:S:13:HIS:HB3	2.29	0.62
1:A:1000:A:H2'	1:A:1001:C:C6	2.34	0.62
12:M:53:ASP:HA	12:M:56:ARG:NH2	2.15	0.62
1:A:1287:A:H2'	1:A:1288:A:C8	2.35	0.62
1:A:1386:G:H2'	1:A:1387:G:C8	2.34	0.62
1:A:586:C:O2'	1:A:587:G:H5'	1.99	0.62
13:N:5:MET:HA	13:N:8:ARG:HG3	1.80	0.62
4:E:104:ILE:HG23	4:E:104:ILE:O	2.00	0.62
1:A:1387:G:H2'	1:A:1388:C:C6	2.34	0.62
3:D:71:PHE:HE2	3:D:89:LEU:HD11	1.64	0.62
1:A:105:G:H2'	1:A:106:C:C6	2.34	0.62
1:A:677:U:H3	1:A:713:G:H22	1.48	0.62
1:A:554:A:H5'	11:L:25:ALA:HB1	1.80	0.62
6:G:39:GLU:HG3	6:G:43:TYR:HD2	1.65	0.62
1:A:1072:G:H2'	1:A:1073:U:C6	2.35	0.62
2:C:55:VAL:HG23	2:C:66:THR:HB	1.82	0.62
10:K:121:ARG:HE	21:U:34:ARG:CG	2.13	0.62
21:U:40:PRO:O	21:U:44:ARG:N	2.33	0.62
1:A:1024:G:O2'	1:A:1025:U:H5'	2.00	0.62
14:O:80:LEU:HD23	14:O:84:LEU:HD13	1.81	0.62
4:E:114:LEU:HB3	4:E:119:VAL:HB	1.81	0.62
18:S:48:ILE:O	18:S:59:VAL:HG22	2.00	0.62
1:A:970:C:H42	8:I:128:LYS:HG2	1.65	0.62
1:A:376:G:H5''	15:P:5:ARG:HB2	1.81	0.62
1:A:976:G:OP1	13:N:70:HIS:HA	2.00	0.62
10:K:82:GLU:HB3	10:K:108:ASN:ND2	2.15	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
9:J:37:ARG:N	9:J:76:ILE:HG12	2.14	0.62
1:A:1373:G:H5''	6:G:35:LYS:HB2	1.81	0.62
6:G:2:ARG:NH1	6:G:2:ARG:HB3	2.14	0.62
20:B:163:ILE:HG23	20:B:164:ASP:N	2.13	0.62
1:A:1237:C:H3'	1:A:1336:C:H41	1.65	0.62
6:G:25:PHE:HD1	6:G:100:MET:HB2	1.63	0.62
1:A:7:A:H2	4:E:125:LYS:HE2	1.65	0.62
1:A:1351:U:O2'	1:A:1352:C:H5'	2.00	0.61
5:F:43:GLY:HA2	5:F:58:HIS:CD2	2.35	0.61
6:G:58:LEU:H	6:G:58:LEU:HD23	1.65	0.61
14:O:20:ASP:OD2	14:O:23:SER:HB2	2.00	0.61
1:A:1343:G:H2'	1:A:1344:C:C6	2.34	0.61
19:T:3:ILE:O	19:T:4:LYS:HB2	2.00	0.61
1:A:1134:G:C6	1:A:1135:U:H1'	2.35	0.61
5:F:86:ARG:HD3	17:R:63:TYR:O	1.99	0.61
4:E:35:LEU:HD13	4:E:133:ILE:HA	1.81	0.61
16:Q:64:ARG:HH11	16:Q:64:ARG:HB3	1.65	0.61
1:A:763:G:H2'	1:A:764:C:C6	2.35	0.61
10:K:23:HIS:HB3	10:K:30:ILE:HG13	1.81	0.61
14:O:61:GLN:O	14:O:65:LEU:HG	1.99	0.61
3:D:195:ASN:HB2	3:D:198:LEU:HD12	1.81	0.61
10:K:46:ALA:HB1	10:K:61:ALA:HB1	1.82	0.61
11:L:8:ARG:O	11:L:10:PRO:HD3	1.99	0.61
10:K:22:ILE:HG21	10:K:95:THR:HG21	1.81	0.61
1:A:815:A:H62	1:A:1509:C:H1'	1.66	0.61
2:C:151:GLU:HA	2:C:166:TRP:HA	1.81	0.61
1:A:1171:A:H2'	1:A:1172:C:C6	2.35	0.61
2:C:49:ALA:HB2	2:C:74:ILE:CG2	2.30	0.61
20:B:78:ALA:HB1	20:B:213:LEU:HD22	1.80	0.61
19:T:68:LYS:HB2	19:T:70:LYS:CD	2.30	0.61
9:J:66:GLU:HB2	13:N:98:ALA:CB	2.28	0.61
3:D:151:GLN:HE21	3:D:153:ARG:HD2	1.66	0.61
1:A:590:U:H2'	1:A:591:U:C6	2.36	0.61
12:M:47:LEU:H	12:M:47:LEU:HD23	1.66	0.61
3:D:117:VAL:HG12	3:D:130:ASN:HA	1.81	0.61
1:A:1021:A:H2'	1:A:1022:A:C8	2.35	0.61
1:A:1361:G:H2'	1:A:1362:A:H5''	1.82	0.61
13:N:63:CYS:O	13:N:67:GLY:HA2	2.01	0.61
1:A:451:A:H5'	15:P:70:ARG:NH2	2.14	0.61
13:N:25:GLU:O	13:N:29:ILE:HG13	1.99	0.61
16:Q:12:VAL:HG11	16:Q:42:LYS:NZ	2.16	0.61
13:N:12:ARG:HG3	13:N:53:ASP:O	2.01	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:212:G:H2'	1:A:213:G:H8	1.66	0.61
1:A:939:G:H5''	6:G:101:ARG:NH2	2.15	0.61
1:A:1118:U:H2'	1:A:1119:C:H6	1.66	0.61
1:A:121:U:H3'	1:A:121:U:OP1	2.01	0.61
1:A:451:A:H4'	1:A:452:A:O4'	2.00	0.61
1:A:970:C:N4	8:I:128:LYS:HG2	2.16	0.61
1:A:1151:A:O2'	1:A:1152:A:H5''	2.00	0.61
2:C:37:LYS:HB3	2:C:41:TYR:CE1	2.36	0.61
9:J:38:GLY:O	9:J:74:VAL:HA	2.00	0.61
1:A:1324:A:H5'	1:A:1362:A:O2'	2.01	0.61
7:H:81:GLY:O	7:H:82:LEU:HB2	2.01	0.61
1:A:105:G:H2'	1:A:106:C:H6	1.66	0.61
1:A:501:C:H1'	1:A:549:C:H1'	1.83	0.60
16:Q:60:ILE:HG22	16:Q:74:LEU:HA	1.82	0.60
1:A:89:U:H2'	1:A:90:C:H6	1.64	0.60
14:O:21:THR:HA	14:O:26:VAL:HG11	1.81	0.60
3:D:25:ARG:HH11	3:D:25:ARG:HB2	1.65	0.60
4:E:113:VAL:HG23	4:E:114:LEU:H	1.66	0.60
13:N:53:ASP:HA	13:N:58:ARG:HH11	1.67	0.60
1:A:1508:A:H2'	1:A:1509:C:H6	1.64	0.60
11:L:51:VAL:HG12	11:L:52:CYS:H	1.67	0.60
16:Q:10:ARG:CZ	16:Q:55:GLY:N	2.64	0.60
1:A:1391:U:H2'	1:A:1392:G:C8	2.35	0.60
4:E:91:SER:HA	4:E:128:GLY:O	2.00	0.60
1:A:662:U:H2'	1:A:663:A:C8	2.36	0.60
1:A:1179:A:H2'	1:A:1180:A:O4'	2.01	0.60
10:K:53:GLY:O	10:K:56:LYS:HB3	2.02	0.60
1:A:1105:A:H2'	1:A:1106:G:H8	1.65	0.60
14:O:25:GLU:HA	14:O:80:LEU:HD11	1.82	0.60
1:A:429:U:H1'	1:A:430:A:H5''	1.84	0.60
15:P:44:SER:HB3	15:P:46:LYS:HZ2	1.64	0.60
12:M:2:ARG:HB3	12:M:6:ILE:H	1.65	0.60
20:B:112:ARG:O	20:B:116:LEU:HB2	2.02	0.60
2:C:18:ASN:O	2:C:55:VAL:HA	2.01	0.60
20:B:34:ARG:HG2	20:B:39:ILE:HD11	1.84	0.60
1:A:390:U:H2'	1:A:391:G:H8	1.66	0.60
1:A:858:G:O6	1:A:869:G:H3'	2.01	0.60
1:A:1355:G:H2'	1:A:1356:G:H8	1.67	0.60
15:P:23:ASP:OD1	15:P:25:ARG:HB2	2.02	0.60
18:S:29:PRO:HB3	18:S:47:THR:HB	1.83	0.60
9:J:41:PRO:HA	9:J:72:ARG:HD3	1.83	0.60
15:P:20:VAL:HG23	15:P:34:GLU:O	2.02	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
15:P:20:VAL:HG21	15:P:32:PHE:CD2	2.37	0.60
1:A:1108:G:H5''	2:C:175:HIS:ND1	2.16	0.60
16:Q:60:ILE:HA	16:Q:75:VAL:HG13	1.84	0.60
1:A:203:G:H1'	1:A:465:A:N6	2.17	0.60
8:I:40:ARG:HA	8:I:44:ARG:NH1	2.17	0.60
1:A:539:A:H2'	1:A:540:G:C8	2.37	0.60
1:A:398:U:H2'	1:A:399:G:H8	1.66	0.60
1:A:83:C:O2'	1:A:84:U:H2'	2.02	0.60
1:A:1008:U:H5''	13:N:23:ARG:NH2	2.17	0.59
14:O:29:ALA:HA	14:O:84:LEU:HD21	1.82	0.59
4:E:131:ASN:O	4:E:135:VAL:HG23	2.02	0.59
1:A:33:A:H1'	11:L:27:PRO:HG3	1.84	0.59
1:A:1009:U:H2'	1:A:1010:U:C6	2.37	0.59
2:C:23:ALA:HB1	2:C:27:GLU:HB2	1.83	0.59
8:I:123:ARG:HD3	8:I:124:PRO:HD2	1.84	0.59
1:A:37:U:OP1	11:L:120:ARG:HB3	2.02	0.59
1:A:937:A:H1'	1:A:1379:G:N2	2.17	0.59
1:A:801:U:H2'	1:A:802:A:H8	1.66	0.59
10:K:127:ARG:HG3	10:K:127:ARG:HH11	1.66	0.59
16:Q:68:LYS:HG2	16:Q:69:THR:HG23	1.85	0.59
12:M:78:ARG:HH11	12:M:79:LEU:HD23	1.67	0.59
1:A:1191:A:OP1	2:C:2:GLN:HB2	2.02	0.59
2:C:127:VAL:HG23	2:C:128:MET:H	1.66	0.59
1:A:1041:G:H2'	1:A:1042:A:H8	1.67	0.59
10:K:31:VAL:HG21	10:K:66:ALA:HA	1.84	0.59
7:H:101:ALA:O	7:H:103:VAL:HG23	2.01	0.59
12:M:102:LYS:HB2	12:M:102:LYS:HZ2	1.66	0.59
5:F:18:VAL:HG21	5:F:58:HIS:CE1	2.37	0.59
2:C:41:TYR:O	2:C:45:GLU:HB2	2.03	0.59
2:C:89:VAL:O	2:C:93:ILE:HD12	2.03	0.59
3:D:160:LEU:HD22	3:D:160:LEU:O	2.02	0.59
1:A:678:U:H2'	1:A:679:C:H6	1.66	0.59
20:B:99:MET:HA	20:B:106:VAL:HG21	1.83	0.59
1:A:370:C:H2'	1:A:371:A:H8	1.66	0.59
1:A:783:C:O2'	1:A:784:A:H5'	2.02	0.59
8:I:29:ILE:HB	8:I:64:ILE:HD12	1.84	0.59
1:A:1292:G:H2'	1:A:1293:C:H6	1.67	0.59
1:A:1144:G:N2	1:A:1146:A:H62	2.01	0.59
9:J:84:VAL:HB	9:J:89:ARG:HH21	1.68	0.59
20:B:169:HIS:CE1	20:B:173:LYS:HB2	2.38	0.59
6:G:77:ARG:HD3	6:G:79:VAL:HG23	1.83	0.59
10:K:66:ALA:O	10:K:69:CYS:HB2	2.03	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
10:K:70:ALA:C	10:K:72:ALA:H	2.06	0.59
1:A:977:A:H3'	1:A:1362:A:H62	1.68	0.59
6:G:90:VAL:HG12	6:G:91:ARG:N	2.18	0.59
1:A:77:A:H2'	1:A:78:A:C8	2.37	0.59
8:I:62:LEU:H	8:I:62:LEU:HD22	1.67	0.59
20:B:63:LYS:HG3	20:B:224:ARG:HD3	1.85	0.59
3:D:2:ARG:O	3:D:3:TYR:HB3	2.03	0.59
17:R:47:ARG:CZ	17:R:48:ALA:H	2.14	0.59
16:Q:11:VAL:HG13	16:Q:20:ILE:HG23	1.85	0.59
19:T:2:ASN:O	19:T:4:LYS:N	2.36	0.59
4:E:95:MET:CE	4:E:143:LEU:HD13	2.33	0.59
3:D:61:ARG:HG3	3:D:66:VAL:O	2.02	0.59
1:A:590:U:H2'	1:A:591:U:H6	1.67	0.59
2:C:45:GLU:HB3	2:C:46:LEU:HD23	1.84	0.59
12:M:89:ARG:HB3	12:M:96:VAL:HG22	1.84	0.59
6:G:139:ASP:O	6:G:142:ARG:HB3	2.02	0.59
20:B:57:ASN:HA	20:B:60:ALA:HB3	1.85	0.59
3:D:30:LYS:HB2	3:D:30:LYS:HZ2	1.67	0.59
20:B:67:LEU:HD22	20:B:157:PRO:HG3	1.85	0.58
1:A:1060:U:H2'	1:A:1061:G:H8	1.66	0.58
4:E:110:MET:HG2	4:E:139:THR:OG1	2.03	0.58
3:D:2:ARG:HE	3:D:2:ARG:HA	1.65	0.58
1:A:908:A:H2'	1:A:909:A:H8	1.68	0.58
1:A:599:C:H5''	7:H:86:LYS:O	2.03	0.58
17:R:20:ILE:O	17:R:21:ASP:HB2	2.03	0.58
1:A:118:U:O4	1:A:288:A:H2'	2.03	0.58
15:P:1:MET:HB3	15:P:24:SER:OG	2.03	0.58
1:A:1306:A:O2'	12:M:107:THR:HG21	2.03	0.58
1:A:673:A:H1'	17:R:63:TYR:CE1	2.38	0.58
3:D:58:GLN:O	3:D:62:ARG:HG2	2.02	0.58
16:Q:60:ILE:HG12	16:Q:72:TRP:HE3	1.68	0.58
1:A:1323:G:H2'	1:A:1324:A:H8	1.68	0.58
1:A:545:C:H5''	3:D:68:GLU:HG2	1.84	0.58
20:B:80:LYS:HA	20:B:90:PHE:CE1	2.38	0.58
1:A:1338:G:H2'	1:A:1339:A:C8	2.38	0.58
11:L:75:GLU:H	11:L:75:GLU:CD	2.06	0.58
7:H:75:GLN:HE21	7:H:76:ARG:H	1.50	0.58
1:A:1237:C:H3'	1:A:1238:A:H5'	1.84	0.58
20:B:86:CYS:HB3	20:B:88:GLN:NE2	2.18	0.58
3:D:34:GLU:O	3:D:35:GLN:HG3	2.03	0.58
16:Q:16:MET:HB2	16:Q:19:SER:HB2	1.85	0.58
16:Q:42:LYS:C	16:Q:43:LEU:HD12	2.23	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
16:Q:45:VAL:HG21	16:Q:60:ILE:HG21	1.85	0.58
20:B:96:LEU:HB2	20:B:99:MET:SD	2.43	0.58
1:A:945:G:H21	1:A:1334:G:H4'	1.68	0.58
16:Q:56:ASP:N	16:Q:81:ALA:HB2	2.18	0.58
1:A:1221:G:O3'	18:S:76:THR:HG21	2.03	0.58
9:J:40:ILE:HG13	9:J:73:LEU:HB3	1.85	0.58
4:E:15:ILE:HD12	4:E:35:LEU:HD23	1.85	0.58
8:I:18:VAL:HG12	8:I:64:ILE:HG12	1.86	0.58
10:K:12:ARG:N	10:K:76:TYR:HA	2.19	0.58
1:A:312:C:H2'	1:A:313:A:H8	1.67	0.58
7:H:93:LYS:HG2	7:H:96:ALA:HA	1.83	0.58
3:D:169:TRP:CD1	3:D:170:LEU:HG	2.38	0.58
16:Q:24:ILE:HD13	16:Q:43:LEU:HD13	1.84	0.58
8:I:56:MET:SD	8:I:57:VAL:N	2.77	0.58
1:A:699:C:C2'	1:A:700:G:H5''	2.32	0.58
1:A:1513:A:H2'	1:A:1514:G:H8	1.69	0.58
3:D:75:TYR:HE1	3:D:200:VAL:HG23	1.69	0.58
1:A:1458:G:H5''	19:T:25:SER:HB3	1.84	0.58
6:G:42:VAL:O	6:G:46:LEU:HB2	2.02	0.58
1:A:1254:A:H2'	1:A:1255:G:C8	2.39	0.58
1:A:1355:G:H2'	1:A:1356:G:C8	2.39	0.58
1:A:985:C:H2'	1:A:986:U:C6	2.39	0.58
1:A:832:G:O2'	1:A:833:G:H5'	2.04	0.58
20:B:102:ASN:ND2	20:B:105:THR:HB	2.19	0.58
9:J:65:TYR:HB3	13:N:95:LEU:HD11	1.84	0.58
9:J:64:GLN:HB3	13:N:98:ALA:HB3	1.86	0.58
1:A:1313:U:P	18:S:5:LYS:HA	2.44	0.58
13:N:40:ARG:HH12	18:S:6:LYS:H	1.51	0.58
1:A:1095:U:H2'	1:A:1096:C:C6	2.39	0.58
7:H:78:SER:HB2	7:H:124:ILE:O	2.03	0.58
1:A:98:A:H2'	1:A:99:C:C6	2.39	0.58
1:A:810:C:O2'	1:A:811:C:H5'	2.04	0.58
12:M:39:ALA:O	12:M:42:VAL:HG22	2.04	0.58
1:A:1476:A:H2'	1:A:1477:U:O4'	2.04	0.58
11:L:80:LEU:HD23	11:L:97:VAL:HG21	1.86	0.58
1:A:389:A:H3'	1:A:390:U:H6	1.69	0.58
1:A:406:G:H21	3:D:115:GLN:HE22	1.52	0.58
6:G:15:PRO:HG2	6:G:43:TYR:OH	2.04	0.58
3:D:106:PHE:CD1	3:D:158:LEU:HD21	2.39	0.58
1:A:672:U:H2'	1:A:673:A:C8	2.39	0.58
1:A:190:A:H8	1:A:190:A:O5'	1.86	0.58
2:C:68:HIS:HA	2:C:103:ALA:HB3	1.85	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:G:100:MET:HA	6:G:103:ILE:HD12	1.85	0.58
1:A:1392:G:O2'	1:A:1393:U:H5'	2.04	0.58
3:D:101:VAL:O	3:D:104:MET:HB2	2.04	0.58
21:U:8:ASN:HB2	21:U:9:GLU:CD	2.25	0.58
14:O:10:ILE:HD13	14:O:30:LEU:HA	1.85	0.58
20:B:208:ALA:O	20:B:211:LEU:HB3	2.04	0.57
1:A:254:G:OP1	16:Q:68:LYS:O	2.21	0.57
13:N:23:ARG:O	13:N:26:LEU:HB2	2.04	0.57
9:J:36:VAL:HG13	9:J:76:ILE:CD1	2.34	0.57
13:N:9:GLU:HA	13:N:12:ARG:HB3	1.85	0.57
1:A:626:G:H2'	1:A:627:G:C8	2.39	0.57
20:B:44:LYS:O	20:B:47:PRO:HD2	2.04	0.57
5:F:85:ILE:HG22	5:F:86:ARG:H	1.69	0.57
18:S:30:LEU:HB2	18:S:48:ILE:HG23	1.86	0.57
3:D:130:ASN:H	3:D:130:ASN:HD22	1.49	0.57
12:M:78:ARG:O	12:M:82:LEU:HG	2.04	0.57
1:A:1009:U:H1'	1:A:1021:A:C6	2.39	0.57
1:A:963:G:H2'	1:A:964:A:H8	1.68	0.57
11:L:24:GLU:HB2	11:L:26:CYS:SG	2.44	0.57
1:A:1038:C:H2'	1:A:1039:G:C8	2.39	0.57
1:A:129:A:H1'	1:A:130:A:C8	2.39	0.57
13:N:41:TRP:O	13:N:45:LEU:HG	2.04	0.57
6:G:71:THR:HA	6:G:95:ARG:HE	1.69	0.57
3:D:192:ALA:HB3	3:D:194:ILE:HG22	1.85	0.57
1:A:1461:G:H2'	1:A:1462:C:H6	1.68	0.57
1:A:1298:U:H2'	6:G:113:LYS:NZ	2.19	0.57
2:C:59:PRO:CG	2:C:62:SER:HB2	2.29	0.57
17:R:70:THR:HB	17:R:72:ARG:HH11	1.67	0.57
1:A:239:U:C5'	1:A:239:U:H6	2.18	0.57
1:A:1312:G:H2'	1:A:1313:U:C6	2.39	0.57
7:H:10:LEU:HD22	7:H:74:ILE:HD11	1.85	0.57
11:L:82:ARG:NH1	11:L:82:ARG:HG2	2.16	0.57
3:D:25:ARG:HG3	3:D:25:ARG:O	2.03	0.57
1:A:1063:C:H3'	1:A:1064:G:H2'	1.86	0.57
1:A:1013:G:N2	1:A:1015:G:H3'	2.20	0.57
4:E:142:GLY:HA2	4:E:145:ASN:HD22	1.69	0.57
20:B:209:VAL:O	20:B:213:LEU:HD12	2.05	0.57
1:A:1001:C:H2'	1:A:1002:G:C8	2.40	0.57
3:D:157:ALA:HA	3:D:160:LEU:HD12	1.84	0.57
1:A:1069:C:H4'	1:A:1192:C:O2	2.05	0.57
15:P:44:SER:C	15:P:46:LYS:H	2.08	0.57
3:D:28:ASP:HB3	3:D:33:ILE:HD12	1.85	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:E:21:SER:HA	4:E:29:ILE:O	2.04	0.57
5:F:3:HIS:HA	5:F:65:GLU:HG3	1.87	0.57
8:I:14:SER:HA	8:I:68:GLY:O	2.04	0.57
1:A:1307:U:H2'	1:A:1308:U:H6	1.68	0.57
5:F:9:MET:HE1	17:R:64:LEU:O	2.05	0.57
1:A:1320:C:OP1	18:S:69:LYS:HE3	2.05	0.57
8:I:87:MET:HB2	8:I:94:ARG:NH2	2.20	0.57
2:C:168:ARG:HG2	2:C:169:GLU:N	2.19	0.57
11:L:23:LEU:CD2	11:L:58:ASN:HD22	2.16	0.57
1:A:241:G:O2'	1:A:242:G:H5'	2.05	0.57
1:A:176:C:H2'	1:A:177:G:N3	2.20	0.57
3:D:147:LYS:HD3	3:D:148:ALA:N	2.19	0.57
11:L:23:LEU:HD22	11:L:58:ASN:HD22	1.69	0.57
1:A:922:G:H2'	1:A:923:A:H8	1.70	0.57
3:D:55:ARG:HH11	3:D:55:ARG:CG	2.17	0.57
11:L:72:ASN:ND2	11:L:73:LEU:H	2.03	0.57
1:A:384:G:H2'	1:A:385:C:C6	2.40	0.57
16:Q:10:ARG:NH2	16:Q:55:GLY:H	2.03	0.57
4:E:39:GLY:HA3	4:E:116:VAL:HB	1.85	0.57
15:P:28:ARG:CD	15:P:29:ASN:H	2.18	0.57
7:H:103:VAL:HG22	7:H:124:ILE:HA	1.85	0.57
11:L:23:LEU:C	11:L:25:ALA:H	2.07	0.57
1:A:372:C:H4'	1:A:373:A:H5'	1.86	0.57
20:B:11:ALA:HA	20:B:14:HIS:CE1	2.40	0.57
1:A:1270:G:H2'	1:A:1271:A:C8	2.39	0.57
4:E:33:THR:HB	4:E:49:TYR:CE1	2.39	0.57
1:A:1030:U:H5''	1:A:1031:C:C5	2.38	0.57
1:A:903:G:H2'	1:A:904:U:C6	2.40	0.57
15:P:12:LYS:O	15:P:13:LYS:HB2	2.05	0.57
20:B:46:VAL:HA	20:B:49:PHE:CD2	2.40	0.56
5:F:81:ASN:O	5:F:84:VAL:HG12	2.04	0.56
1:A:1220:G:P	13:N:52:ARG:HH22	2.28	0.56
14:O:48:ASP:CG	14:O:51:SER:HB2	2.25	0.56
1:A:1084:G:H5'	1:A:1102:A:OP2	2.05	0.56
10:K:121:ARG:HH21	21:U:34:ARG:NE	2.03	0.56
13:N:50:LEU:HD12	13:N:51:PRO:HD3	1.87	0.56
1:A:449:G:H2'	1:A:450:G:C8	2.39	0.56
6:G:63:VAL:HG12	6:G:126:ALA:HB1	1.88	0.56
16:Q:10:ARG:CZ	16:Q:11:VAL:H	2.18	0.56
1:A:1217:C:H2'	1:A:1218:C:C6	2.40	0.56
1:A:16:A:O2'	1:A:17:U:H5'	2.05	0.56
4:E:47:PHE:HE1	4:E:137:ARG:HE	1.54	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:F:10:VAL:HG12	5:F:11:HIS:N	2.19	0.56
1:A:1053:G:HO2'	1:A:1199:U:H5	1.52	0.56
20:B:85:SER:O	20:B:86:CYS:HB2	2.05	0.56
2:C:49:ALA:HB2	2:C:74:ILE:HG21	1.87	0.56
1:A:85:U:H4'	1:A:86:G:H5'	1.86	0.56
1:A:415:A:H3'	1:A:416:G:H8	1.71	0.56
12:M:52:ILE:HD12	12:M:55:LEU:HD12	1.88	0.56
5:F:51:ILE:HD13	5:F:86:ARG:HG3	1.87	0.56
18:S:38:THR:HA	18:S:69:LYS:HA	1.88	0.56
4:E:113:VAL:HG23	4:E:114:LEU:N	2.20	0.56
11:L:80:LEU:HB3	11:L:97:VAL:CG2	2.35	0.56
3:D:171:GLU:HG3	3:D:182:LYS:HD2	1.87	0.56
12:M:23:GLY:N	12:M:69:ARG:HH22	2.03	0.56
1:A:160:A:H2'	1:A:161:A:O4'	2.04	0.56
1:A:57:G:H2'	1:A:58:C:C6	2.40	0.56
20:B:15:PHE:HB3	20:B:42:LEU:HD21	1.86	0.56
1:A:1219:A:H2'	1:A:1220:G:C8	2.40	0.56
1:A:1085:U:H3'	1:A:1086:U:C5	2.41	0.56
20:B:16:GLY:CA	20:B:39:ILE:HA	2.33	0.56
10:K:12:ARG:HD3	10:K:13:LYS:NZ	2.21	0.56
1:A:1021:A:H2'	1:A:1022:A:O4'	2.06	0.56
1:A:1141:C:H2'	1:A:1142:G:H8	1.70	0.56
1:A:994:A:C5	1:A:1216:A:H4'	2.40	0.56
4:E:81:GLN:HE22	4:E:148:SER:HA	1.70	0.56
4:E:104:ILE:HG13	4:E:114:LEU:HB2	1.87	0.56
1:A:784:A:H2'	1:A:785:G:H8	1.69	0.56
8:I:50:PRO:O	8:I:54:VAL:HG22	2.05	0.56
1:A:189:A:H2'	1:A:190:A:C8	2.41	0.56
1:A:859:G:H2'	1:A:860:A:H8	1.70	0.56
6:G:39:GLU:HG3	6:G:43:TYR:CD2	2.40	0.56
1:A:275:G:O5'	16:Q:15:LYS:HG2	2.05	0.56
9:J:12:ALA:HB3	9:J:18:ILE:HB	1.88	0.56
9:J:55:PRO:HA	13:N:80:ARG:NH2	2.19	0.56
8:I:54:VAL:HG11	8:I:86:LEU:HD13	1.86	0.56
1:A:270:A:H2'	1:A:271:C:H6	1.70	0.56
1:A:948:C:O2'	1:A:949:A:H5'	2.05	0.56
9:J:51:VAL:O	9:J:62:ARG:HA	2.05	0.56
10:K:124:LYS:CD	21:U:34:ARG:HD3	2.36	0.56
9:J:66:GLU:HG2	9:J:67:ILE:H	1.71	0.56
13:N:27:LYS:O	13:N:31:SER:HB3	2.06	0.56
13:N:17:ASP:C	13:N:19:TYR:H	2.10	0.56
1:A:1348:U:H4'	8:I:121:ARG:HG3	1.87	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:865:A:H2'	1:A:866:C:C6	2.40	0.56
12:M:75:SER:O	12:M:78:ARG:HB3	2.06	0.56
4:E:73:VAL:HG21	4:E:143:LEU:O	2.05	0.56
16:Q:63:CYS:SG	16:Q:66:LEU:HD11	2.46	0.56
9:J:42:LEU:HB3	9:J:43:PRO:HD2	1.88	0.56
6:G:91:ARG:O	6:G:95:ARG:HG3	2.06	0.56
1:A:629:A:H2'	1:A:630:A:O4'	2.05	0.56
1:A:335:C:H2'	1:A:336:A:C8	2.41	0.56
6:G:37:THR:O	6:G:41:ILE:HG13	2.05	0.56
18:S:62:THR:HG21	18:S:64:GLU:OE1	2.06	0.56
20:B:104:LYS:HZ2	20:B:104:LYS:HB2	1.69	0.56
13:N:68:ARG:NH2	13:N:80:ARG:HH12	2.04	0.56
1:A:1006:G:H2'	1:A:1007:U:C6	2.41	0.56
15:P:68:SER:OG	15:P:71:VAL:HG12	2.06	0.56
4:E:136:VAL:HG23	4:E:137:ARG:H	1.70	0.56
4:E:61:LYS:O	4:E:64:GLU:HB3	2.06	0.56
1:A:883:C:O2'	1:A:884:U:H5'	2.06	0.56
20:B:162:VAL:HG11	20:B:172:ILE:HD11	1.88	0.56
2:C:37:LYS:HB3	2:C:41:TYR:CZ	2.41	0.56
4:E:142:GLY:HA2	4:E:145:ASN:ND2	2.21	0.56
1:A:149:A:H1'	1:A:1446:A:C2	2.41	0.56
8:I:49:GLN:N	8:I:50:PRO:HD2	2.21	0.56
1:A:1298:U:H2'	6:G:113:LYS:HZ1	1.69	0.56
11:L:30:ARG:HB3	11:L:57:THR:HG23	1.88	0.56
1:A:16:A:O2'	4:E:20:VAL:HG23	2.06	0.55
1:A:801:U:H2'	1:A:802:A:C8	2.41	0.55
1:A:168:G:O2'	1:A:169:C:H5'	2.06	0.55
7:H:9:MET:HG3	7:H:26:MET:SD	2.46	0.55
1:A:1307:U:H2'	1:A:1308:U:C6	2.41	0.55
9:J:36:VAL:HA	9:J:76:ILE:CG2	2.37	0.55
4:E:10:LEU:HA	4:E:39:GLY:O	2.06	0.55
7:H:82:LEU:HD22	16:Q:35:LYS:HB2	1.86	0.55
10:K:61:ALA:O	10:K:64:VAL:HG22	2.06	0.55
1:A:57:G:H2'	1:A:58:C:H6	1.70	0.55
1:A:1057:G:H4'	2:C:196:GLY:H	1.70	0.55
1:A:272:C:H2'	1:A:273:U:H6	1.71	0.55
9:J:17:LEU:HD22	9:J:17:LEU:O	2.06	0.55
4:E:89:THR:C	4:E:91:SER:H	2.08	0.55
4:E:113:VAL:HG21	4:E:139:THR:HG21	1.88	0.55
1:A:642:A:H2'	1:A:643:C:H6	1.71	0.55
1:A:1355:G:O2'	1:A:1356:G:H5'	2.07	0.55
4:E:22:LYS:HB3	4:E:29:ILE:HB	1.89	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
9:J:15:HIS:HA	9:J:18:ILE:HG22	1.88	0.55
12:M:48:SER:C	12:M:50:GLY:H	2.09	0.55
1:A:973:G:H3'	1:A:974:A:C5'	2.29	0.55
4:E:95:MET:HG3	4:E:124:ALA:HB2	1.88	0.55
1:A:77:A:H2'	1:A:78:A:H8	1.70	0.55
3:D:22:SER:HB3	3:D:109:THR:HG22	1.88	0.55
1:A:1011:C:H2'	1:A:1012:A:C8	2.42	0.55
15:P:60:TRP:HB3	15:P:65:ALA:HB2	1.89	0.55
3:D:115:GLN:NE2	3:D:153:ARG:HH12	2.05	0.55
1:A:556:C:O2'	1:A:557:G:H5'	2.06	0.55
11:L:23:LEU:O	11:L:25:ALA:N	2.39	0.55
3:D:195:ASN:HB3	3:D:197:HIS:NE2	2.22	0.55
9:J:85:ASP:HB2	9:J:89:ARG:CZ	2.36	0.55
1:A:1414:U:H2'	1:A:1415:G:H8	1.72	0.55
12:M:106:ARG:CA	12:M:106:ARG:HH11	2.20	0.55
1:A:1171:A:H2'	1:A:1172:C:H6	1.71	0.55
2:C:110:LEU:HG	2:C:110:LEU:O	2.07	0.55
1:A:844:G:N2	1:A:845:A:H62	2.04	0.55
1:A:845:A:H3'	1:A:846:G:O4'	2.06	0.55
1:A:1250:A:H4'	8:I:69:GLY:N	2.13	0.55
16:Q:16:MET:HB3	16:Q:19:SER:HB2	1.87	0.55
9:J:66:GLU:HG2	9:J:67:ILE:N	2.22	0.55
1:A:436:C:O2'	1:A:437:U:H5'	2.06	0.55
8:I:50:PRO:HD3	8:I:79:ARG:HD3	1.89	0.55
13:N:89:ARG:NH1	13:N:91:GLU:HG3	2.21	0.55
1:A:370:C:H2'	1:A:371:A:C8	2.42	0.55
8:I:24:ASN:OD1	8:I:26:LYS:HG2	2.07	0.55
10:K:126:ARG:HG2	10:K:126:ARG:HH11	1.71	0.55
9:J:83:THR:O	9:J:83:THR:HG22	2.07	0.55
10:K:73:VAL:O	10:K:76:TYR:HB2	2.07	0.55
11:L:54:VAL:HG11	11:L:79:ILE:HD11	1.89	0.55
12:M:10:ASP:HA	12:M:44:ILE:CD1	2.36	0.55
1:A:391:G:HO2'	1:A:482:A:H2	1.55	0.55
20:B:26:MET:HG3	20:B:188:THR:O	2.05	0.55
1:A:1143:G:H2'	1:A:1144:G:H8	1.72	0.55
10:K:22:ILE:HD13	10:K:95:THR:HG23	1.89	0.55
1:A:372:C:H1'	1:A:373:A:OP2	2.07	0.55
5:F:99:ALA:HA	17:R:23:LYS:HE2	1.89	0.55
1:A:1036:A:H2'	1:A:1037:C:C6	2.42	0.55
1:A:575:G:H4'	1:A:576:C:O5'	2.07	0.55
14:O:2:LEU:O	14:O:3:SER:HB3	2.07	0.55
5:F:38:ARG:HH21	5:F:63:ASN:HD21	1.54	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
10:K:28:ASN:HD21	10:K:47:GLY:N	2.00	0.55
1:A:1226:C:H4'	1:A:1227:A:OP1	2.06	0.55
1:A:600:A:H2'	1:A:601:G:H8	1.72	0.55
1:A:476:U:H2'	1:A:477:C:H6	1.72	0.55
1:A:1283:U:O2'	1:A:1284:C:H5'	2.07	0.55
1:A:1026:G:H2'	1:A:1027:C:H6	1.72	0.55
21:U:16:ARG:C	21:U:18:PHE:N	2.60	0.55
5:F:29:ILE:CG2	5:F:34:GLY:HA3	2.37	0.55
19:T:68:LYS:HA	19:T:68:LYS:HE2	1.87	0.55
5:F:86:ARG:HH11	17:R:63:TYR:HB3	1.72	0.55
1:A:411:A:O2'	1:A:412:A:H4'	2.07	0.55
1:A:642:A:H2'	1:A:643:C:C6	2.42	0.55
15:P:40:ASN:ND2	15:P:42:ILE:HG12	2.20	0.55
7:H:54:THR:HG23	7:H:55:LYS:HG2	1.88	0.55
1:A:477:C:H2'	1:A:478:A:C8	2.42	0.55
1:A:1380:U:O4	6:G:2:ARG:HB2	2.06	0.55
1:A:1254:A:H2'	1:A:1255:G:H8	1.70	0.55
4:E:23:THR:HA	4:E:28:ARG:HA	1.88	0.55
1:A:208:U:H2'	1:A:210:C:C5	2.42	0.55
14:O:88:ARG:HG3	14:O:88:ARG:HH11	1.72	0.55
5:F:39:LEU:HD13	5:F:39:LEU:O	2.06	0.55
9:J:37:ARG:HG2	9:J:37:ARG:NH1	2.22	0.54
1:A:1320:C:OP2	18:S:2:ARG:HB3	2.06	0.54
9:J:65:TYR:HE1	13:N:84:ARG:HA	1.71	0.54
7:H:77:VAL:HG23	7:H:126:CYS:HA	1.88	0.54
1:A:1093:A:P	6:G:3:ARG:HH22	2.30	0.54
9:J:22:THR:O	9:J:26:VAL:HG23	2.06	0.54
1:A:1308:U:H2'	1:A:1309:G:C8	2.43	0.54
18:S:28:LYS:HZ3	18:S:28:LYS:H	1.53	0.54
17:R:51:GLN:HE21	17:R:54:LEU:HB2	1.72	0.54
8:I:94:ARG:HG3	8:I:98:ARG:NH2	2.22	0.54
16:Q:45:VAL:HG11	16:Q:60:ILE:HG21	1.89	0.54
1:A:313:A:H2'	1:A:314:C:C6	2.42	0.54
1:A:712:A:O2'	1:A:713:G:H5'	2.07	0.54
3:D:104:MET:SD	3:D:179:GLY:HA2	2.46	0.54
8:I:15:ALA:O	8:I:66:VAL:HA	2.07	0.54
1:A:824:G:O2'	1:A:825:A:H5'	2.07	0.54
20:B:205:ALA:HB3	20:B:208:ALA:HB3	1.89	0.54
17:R:72:ARG:HH21	21:U:23:GLU:CG	2.19	0.54
9:J:64:GLN:CB	13:N:98:ALA:HB3	2.37	0.54
13:N:51:PRO:HB2	13:N:54:SER:HB3	1.88	0.54
2:C:182:ASP:HB2	2:C:203:LYS:HE2	1.88	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1319:A:H2'	1:A:1323:G:N7	2.22	0.54
1:A:981:U:H2'	1:A:982:U:C5	2.42	0.54
1:A:163:C:H2'	1:A:164:G:O4'	2.06	0.54
7:H:45:ILE:HG21	7:H:60:LEU:HD11	1.88	0.54
9:J:11:LYS:HB2	9:J:97:ASP:HB3	1.88	0.54
1:A:1014:A:C2	1:A:1219:A:H1'	2.42	0.54
4:E:19:ARG:O	4:E:20:VAL:HB	2.06	0.54
20:B:45:THR:HG23	20:B:200:PRO:HG2	1.89	0.54
6:G:2:ARG:HH11	6:G:2:ARG:HB3	1.71	0.54
18:S:62:THR:HG23	18:S:63:ASP:H	1.73	0.54
1:A:1057:G:O3'	2:C:196:GLY:HA3	2.07	0.54
1:A:393:A:H5'	1:A:483:C:O2'	2.06	0.54
6:G:16:LYS:HD3	6:G:16:LYS:O	2.06	0.54
1:A:403:C:O2'	1:A:404:G:H5'	2.08	0.54
13:N:63:CYS:HB3	13:N:68:ARG:N	2.17	0.54
1:A:1527:U:H2'	1:A:1528:U:C6	2.42	0.54
1:A:1314:C:OP2	18:S:5:LYS:HG2	2.07	0.54
1:A:1217:C:H2'	1:A:1218:C:H6	1.72	0.54
1:A:764:C:H2'	1:A:765:G:H5'	1.90	0.54
1:A:815:A:H4'	1:A:817:C:C4	2.42	0.54
1:A:279:A:H4'	1:A:280:C:OP2	2.08	0.54
11:L:34:THR:HB	11:L:53:ARG:NE	2.23	0.54
7:H:86:LYS:HB3	7:H:90:GLU:O	2.08	0.54
7:H:107:LYS:HB2	7:H:110:MET:HE1	1.88	0.54
5:F:92:THR:HG22	5:F:93:LYS:N	2.22	0.54
13:N:51:PRO:CB	13:N:54:SER:HB3	2.37	0.54
6:G:55:LYS:HB3	6:G:59:GLU:CD	2.27	0.54
1:A:190:A:H2'	1:A:191:G:O4'	2.07	0.54
1:A:908:A:H2'	1:A:909:A:C8	2.42	0.54
1:A:84:U:O2'	1:A:85:U:H5'	2.07	0.54
1:A:1376:U:H2'	1:A:1377:A:C8	2.43	0.54
5:F:6:ILE:HD12	5:F:7:VAL:N	2.22	0.54
12:M:15:VAL:O	12:M:19:THR:HG23	2.07	0.54
1:A:673:A:H4'	5:F:86:ARG:HD2	1.88	0.54
18:S:27:LYS:HG3	18:S:28:LYS:HD2	1.89	0.54
8:I:20:ILE:HG23	8:I:60:LEU:HD13	1.90	0.54
10:K:70:ALA:HB1	10:K:74:LYS:HD2	1.89	0.54
3:D:138:PRO:O	3:D:139:ASN:HB3	2.07	0.54
4:E:52:ALA:C	4:E:54:GLU:H	2.10	0.54
6:G:2:ARG:HH11	6:G:2:ARG:CB	2.20	0.54
1:A:1216:A:H5''	13:N:4:SER:HB2	1.87	0.54
1:A:93:U:H2'	1:A:94:G:H5'	1.88	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:423:G:H2'	1:A:424:G:O4'	2.08	0.54
21:U:24:LYS:NZ	21:U:24:LYS:HB3	2.23	0.54
3:D:196:GLU:O	3:D:199:ILE:HG23	2.06	0.54
9:J:8:ILE:HD11	9:J:74:VAL:HB	1.90	0.54
1:A:1254:A:H61	1:A:1283:U:H3	1.56	0.54
1:A:638:U:H2'	1:A:639:G:O4'	2.08	0.54
1:A:173:U:H5'	1:A:197:A:O4'	2.08	0.54
1:A:1288:A:N1	1:A:1371:G:H1'	2.23	0.54
1:A:1354:U:H2'	1:A:1355:G:C8	2.42	0.54
11:L:36:VAL:HG12	11:L:52:CYS:HB2	1.89	0.54
1:A:398:U:H2'	1:A:399:G:C8	2.43	0.54
15:P:1:MET:HE3	15:P:1:MET:HA	1.88	0.54
1:A:426:U:OP1	3:D:32:LYS:HE3	2.08	0.54
8:I:34:LEU:HG	8:I:35:GLU:N	2.23	0.54
1:A:1007:U:H2'	1:A:1008:U:C6	2.43	0.54
1:A:16:A:N1	1:A:919:A:H2	2.06	0.54
4:E:136:VAL:HG23	4:E:137:ARG:N	2.22	0.54
1:A:203:G:H1'	1:A:465:A:H62	1.73	0.54
1:A:1141:C:H2'	1:A:1142:G:C8	2.43	0.54
10:K:59:PRO:HA	10:K:91:GLY:H	1.72	0.54
21:U:11:PHE:HD1	21:U:13:VAL:HG12	1.72	0.53
5:F:5:GLU:HA	5:F:63:ASN:HA	1.88	0.53
5:F:55:HIS:ND1	5:F:55:HIS:N	2.56	0.53
1:A:1014:A:H5''	18:S:13:HIS:HB3	1.88	0.53
8:I:29:ILE:HA	8:I:64:ILE:HB	1.91	0.53
1:A:408:A:H3'	1:A:409:U:H6	1.72	0.53
7:H:100:ILE:HG13	7:H:128:VAL:HG23	1.90	0.53
20:B:96:LEU:HB2	20:B:99:MET:CG	2.39	0.53
4:E:55:VAL:N	4:E:56:PRO:HD2	2.22	0.53
10:K:106:ILE:HD11	10:K:109:ILE:HG13	1.89	0.53
6:G:145:GLU:H	6:G:148:LYS:HB2	1.72	0.53
1:A:766:A:H2'	1:A:767:A:O4'	2.08	0.53
9:J:65:TYR:OH	13:N:84:ARG:HG3	2.08	0.53
9:J:40:ILE:CD1	9:J:73:LEU:HB3	2.38	0.53
4:E:109:ALA:HB3	4:E:135:VAL:CG1	2.37	0.53
1:A:131:A:H2'	1:A:132:C:H6	1.74	0.53
1:A:711:G:O2'	1:A:712:A:H5'	2.08	0.53
1:A:1409:C:H2'	1:A:1410:A:C8	2.43	0.53
1:A:997:U:H2'	1:A:998:C:C6	2.43	0.53
1:A:6:G:H4'	1:A:298:A:H4'	1.90	0.53
1:A:218:U:H2'	1:A:219:U:C6	2.43	0.53
4:E:61:LYS:NZ	4:E:61:LYS:HB3	2.24	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1119:C:H2'	1:A:1120:C:H6	1.73	0.53
1:A:797:C:OP1	10:K:125:LYS:HG3	2.08	0.53
8:I:19:PHE:O	8:I:62:LEU:HA	2.08	0.53
1:A:135:C:O2	15:P:1:MET:HB2	2.09	0.53
1:A:128:G:H2'	1:A:129:A:C8	2.43	0.53
15:P:36:VAL:HG23	15:P:56:ARG:HB2	1.89	0.53
2:C:155:ARG:HH21	2:C:160:GLU:HA	1.72	0.53
5:F:38:ARG:HH21	5:F:63:ASN:ND2	2.06	0.53
1:A:1124:G:H5'	9:J:37:ARG:HH21	1.73	0.53
4:E:88:HIS:CE1	4:E:137:ARG:HG2	2.44	0.53
2:C:36:PHE:O	2:C:39:ARG:HB2	2.09	0.53
14:O:42:PHE:CD1	14:O:55:LEU:HD22	2.44	0.53
1:A:1216:A:OP1	13:N:2:LYS:HE2	2.08	0.53
11:L:30:ARG:O	11:L:56:LEU:HA	2.09	0.53
1:A:1234:C:H1'	1:A:1364:U:O2	2.09	0.53
1:A:1181:G:H4'	1:A:1182:G:OP1	2.09	0.53
1:A:53:A:C2	1:A:54:C:H1'	2.43	0.53
20:B:14:HIS:CD2	20:B:15:PHE:H	2.26	0.53
12:M:52:ILE:O	12:M:55:LEU:HB2	2.08	0.53
1:A:1006:G:H2'	1:A:1007:U:H6	1.73	0.53
1:A:922:G:N3	1:A:1398:A:H2	2.07	0.53
12:M:89:ARG:HH12	12:M:101:THR:HG21	1.73	0.53
1:A:1170:A:H5''	20:B:138:ARG:HH22	1.73	0.53
1:A:202:G:H2'	1:A:203:G:C8	2.43	0.53
1:A:370:C:O2'	1:A:371:A:H5'	2.08	0.53
2:C:110:LEU:HD13	2:C:143:LEU:HD23	1.89	0.53
7:H:28:SER:HB2	7:H:58:LEU:HD12	1.91	0.53
1:A:317:U:H2'	1:A:318:G:H8	1.73	0.53
21:U:14:ALA:HB3	21:U:16:ARG:CZ	2.38	0.53
3:D:102:TYR:HE1	3:D:108:ALA:O	1.91	0.53
18:S:29:PRO:HA	18:S:47:THR:O	2.08	0.53
1:A:1190:G:H5'	2:C:175:HIS:HE2	1.74	0.53
1:A:399:G:H2'	1:A:400:C:C6	2.44	0.53
1:A:796:C:OP1	10:K:127:ARG:HB2	2.09	0.53
1:A:994:A:N3	1:A:994:A:H2'	2.23	0.53
16:Q:14:ASP:OD2	16:Q:53:GLY:HA2	2.09	0.53
21:U:15:LEU:HA	21:U:17:ARG:NH1	2.24	0.53
3:D:167:PRO:CG	3:D:170:LEU:HD11	2.30	0.53
20:B:175:ALA:HA	20:B:178:LEU:HD12	1.90	0.53
1:A:764:C:C2'	1:A:765:G:H5'	2.39	0.53
6:G:55:LYS:HB3	6:G:59:GLU:OE2	2.08	0.53
1:A:1143:G:H2'	1:A:1144:G:C8	2.44	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:555:U:H2'	1:A:556:C:C6	2.43	0.53
1:A:120:A:H2'	1:A:121:U:H5''	1.91	0.53
1:A:252:U:H2'	1:A:253:A:H8	1.74	0.53
1:A:1165:U:H2'	1:A:1166:G:O4'	2.09	0.53
1:A:266:G:O2'	1:A:267:C:H3'	2.09	0.53
4:E:36:THR:HG22	4:E:37:VAL:N	2.22	0.53
20:B:40:ILE:HG23	20:B:200:PRO:HB2	1.89	0.53
7:H:102:VAL:HG23	7:H:125:ILE:HB	1.91	0.53
18:S:3:SER:O	18:S:4:LEU:HD12	2.08	0.53
14:O:35:ILE:O	14:O:39:GLN:HG2	2.08	0.53
1:A:586:C:H5''	7:H:81:GLY:HA2	1.89	0.53
3:D:100:VAL:HG12	3:D:101:VAL:N	2.24	0.53
18:S:41:PRO:HA	18:S:44:ILE:HG13	1.90	0.53
1:A:621:A:H2'	1:A:622:A:C8	2.44	0.53
10:K:115:ILE:O	10:K:115:ILE:HD12	2.08	0.53
12:M:106:ARG:NH1	12:M:109:LYS:HD2	2.24	0.53
13:N:15:LEU:O	13:N:19:TYR:HB2	2.08	0.53
4:E:19:ARG:HG2	4:E:20:VAL:N	2.22	0.53
1:A:278:G:H21	1:A:279:A:N6	2.04	0.53
1:A:32:A:H2'	1:A:33:A:C8	2.44	0.53
4:E:156:ARG:HD2	7:H:42:GLU:O	2.08	0.53
15:P:8:ARG:CZ	15:P:15:PRO:HB3	2.39	0.53
1:A:1409:C:H2'	1:A:1410:A:H8	1.73	0.53
14:O:53:ARG:HG2	14:O:53:ARG:HH11	1.72	0.53
1:A:610:U:O2	1:A:610:U:O4'	2.27	0.53
1:A:407:U:O2'	3:D:112:GLU:HG3	2.08	0.53
5:F:3:HIS:CB	5:F:92:THR:HA	2.29	0.53
11:L:49:ARG:CG	11:L:89:LEU:HD21	2.36	0.53
10:K:70:ALA:CA	10:K:73:VAL:HG22	2.36	0.53
1:A:474:G:H2'	1:A:475:C:C6	2.44	0.53
10:K:60:PHE:O	10:K:64:VAL:HG13	2.09	0.53
11:L:35:ARG:NE	11:L:36:VAL:H	2.07	0.53
8:I:19:PHE:HD1	8:I:63:TYR:HB3	1.73	0.53
9:J:93:ALA:HB1	9:J:96:VAL:HG22	1.91	0.53
1:A:846:G:H2'	1:A:846:G:N3	2.24	0.53
1:A:636:U:H2'	1:A:637:C:C6	2.44	0.53
1:A:1068:G:N7	1:A:1094:G:H2'	2.24	0.53
14:O:81:ILE:HD12	14:O:87:ARG:HB2	1.91	0.53
8:I:33:SER:HB2	8:I:36:GLN:HG2	1.91	0.53
1:A:975:A:H1'	1:A:1358:U:O2	2.07	0.52
5:F:92:THR:O	5:F:93:LYS:HB2	2.08	0.52
1:A:954:G:H2'	1:A:955:U:C6	2.44	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:D:64:TYR:CE2	3:D:93:LEU:HB2	2.45	0.52
1:A:860:A:H2'	1:A:861:G:O4'	2.10	0.52
11:L:6:LEU:HB3	16:Q:33:TYR:OH	2.09	0.52
1:A:555:U:H2'	1:A:556:C:H6	1.75	0.52
1:A:1190:G:H5'	2:C:175:HIS:NE2	2.24	0.52
1:A:22:G:H4'	1:A:885:G:C8	2.45	0.52
1:A:1402:C:H2'	1:A:1403:C:O4'	2.08	0.52
4:E:37:VAL:HG12	4:E:116:VAL:HG21	1.92	0.52
13:N:19:TYR:HE2	13:N:50:LEU:HD13	1.73	0.52
18:S:22:VAL:HG22	18:S:42:ASN:OD1	2.09	0.52
2:C:172:VAL:O	2:C:174:LEU:HD12	2.09	0.52
15:P:22:ALA:CB	15:P:32:PHE:HA	2.40	0.52
7:H:13:ILE:HD11	7:H:60:LEU:HD21	1.90	0.52
1:A:320:A:H2'	1:A:321:A:C8	2.44	0.52
8:I:74:GLN:HE21	8:I:74:GLN:CA	2.20	0.52
9:J:56:HIS:H	13:N:80:ARG:NH2	2.06	0.52
9:J:8:ILE:HG12	9:J:75:ASP:HA	1.90	0.52
4:E:15:ILE:HG22	4:E:16:ALA:H	1.74	0.52
14:O:36:ASN:HA	14:O:39:GLN:HG3	1.90	0.52
1:A:1118:U:H2'	1:A:1119:C:C6	2.44	0.52
2:C:63:ILE:HG12	2:C:65:VAL:CG2	2.39	0.52
3:D:101:VAL:HG13	3:D:106:PHE:HD2	1.74	0.52
1:A:1062:U:H2'	1:A:1063:C:C6	2.44	0.52
14:O:48:ASP:OD2	14:O:51:SER:HB2	2.08	0.52
1:A:1026:G:H2'	1:A:1027:C:C6	2.45	0.52
7:H:45:ILE:HD13	7:H:60:LEU:HD11	1.89	0.52
14:O:63:ARG:HH21	14:O:87:ARG:NH1	2.07	0.52
21:U:3:ILE:CG1	21:U:19:LYS:HB3	2.36	0.52
5:F:64:VAL:HG12	5:F:65:GLU:N	2.23	0.52
9:J:37:ARG:H	9:J:76:ILE:HG12	1.74	0.52
8:I:78:ILE:O	8:I:82:ILE:HG13	2.10	0.52
1:A:280:C:O2	16:Q:39:ARG:HG3	2.09	0.52
19:T:79:THR:O	19:T:82:ILE:HG12	2.09	0.52
12:M:102:LYS:HB2	12:M:102:LYS:NZ	2.23	0.52
1:A:545:C:O2'	1:A:546:A:H5'	2.08	0.52
11:L:34:THR:OG1	11:L:53:ARG:HB3	2.10	0.52
1:A:492:C:H2'	1:A:493:A:H5''	1.91	0.52
6:G:134:VAL:O	6:G:138:GLU:HG3	2.09	0.52
13:N:5:MET:HG2	13:N:8:ARG:HD2	1.92	0.52
20:B:23:ASN:HD22	20:B:24:PRO:HD2	1.74	0.52
4:E:65:LYS:HB3	4:E:65:LYS:NZ	2.24	0.52
8:I:8:THR:OG1	8:I:84:ARG:HG3	2.10	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:H:10:LEU:HD11	7:H:126:CYS:SG	2.48	0.52
10:K:30:ILE:HG22	10:K:45:THR:HB	1.91	0.52
21:U:8:ASN:HB2	21:U:9:GLU:OE1	2.09	0.52
3:D:202:LEU:C	3:D:204:SER:H	2.13	0.52
1:A:841:C:H3'	1:A:843:U:OP2	2.10	0.52
20:B:187:ASP:HB3	20:B:201:GLY:O	2.09	0.52
4:E:114:LEU:HD13	4:E:122:VAL:HG21	1.91	0.52
8:I:79:ARG:HD2	8:I:79:ARG:O	2.10	0.52
11:L:88:ASP:C	11:L:89:LEU:HD22	2.29	0.52
2:C:180:ASP:OD1	2:C:203:LYS:HB2	2.09	0.52
2:C:86:LEU:O	2:C:89:VAL:HG22	2.10	0.52
14:O:81:ILE:O	14:O:85:GLY:N	2.41	0.52
2:C:121:SER:O	2:C:125:ARG:HG3	2.09	0.52
1:A:65:A:H2	1:A:381:C:H2'	1.73	0.52
17:R:33:THR:HG22	17:R:37:LYS:HG2	1.92	0.52
3:D:57:LYS:HB2	3:D:199:ILE:HB	1.92	0.52
2:C:174:LEU:HD21	2:C:200:TRP:CD1	2.45	0.52
1:A:1177:G:H3'	1:A:1178:G:H8	1.75	0.52
1:A:900:A:O2'	1:A:901:A:H5'	2.10	0.52
17:R:61:ALA:HB3	17:R:67:LEU:HD12	1.91	0.52
1:A:1363:A:H2'	1:A:1363:A:N3	2.24	0.52
12:M:33:LEU:HD22	12:M:38:ILE:HG21	1.92	0.52
1:A:947:G:H2'	1:A:948:C:H6	1.71	0.52
13:N:30:ILE:O	13:N:44:VAL:HB	2.10	0.52
3:D:118:SER:HA	3:D:130:ASN:HB2	1.91	0.52
8:I:20:ILE:HD12	8:I:85:ALA:HB3	1.92	0.52
3:D:71:PHE:HA	3:D:74:TYR:HD2	1.74	0.52
1:A:56:U:H2'	1:A:57:G:C8	2.45	0.52
1:A:337:G:H2'	1:A:338:A:C8	2.45	0.52
6:G:8:GLN:NE2	6:G:9:ARG:H	2.07	0.52
20:B:216:VAL:C	20:B:218:ALA:H	2.13	0.52
8:I:32:ARG:HD3	8:I:37:TYR:HD1	1.75	0.52
11:L:82:ARG:HB2	11:L:97:VAL:HG13	1.90	0.52
1:A:1461:G:H2'	1:A:1462:C:C6	2.44	0.52
1:A:93:U:C2'	1:A:94:G:H5'	2.40	0.52
6:G:135:LYS:HD3	6:G:136:LYS:HE3	1.91	0.52
12:M:106:ARG:N	12:M:106:ARG:HH11	2.08	0.52
1:A:8:A:C6	3:D:205:LYS:HA	2.45	0.52
13:N:30:ILE:HB	13:N:44:VAL:HB	1.91	0.52
1:A:663:A:O2'	1:A:664:G:H5'	2.10	0.52
1:A:1513:A:H2'	1:A:1514:G:C8	2.45	0.52
7:H:100:ILE:HG13	7:H:128:VAL:CG2	2.39	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:L:85:ARG:NH1	11:L:93:ARG:HB3	2.24	0.52
1:A:1252:A:H2'	1:A:1253:G:O4'	2.11	0.51
2:C:140:ALA:HB2	2:C:148:ILE:HD12	1.91	0.51
8:I:117:LEU:HD21	8:I:123:ARG:HE	1.75	0.51
15:P:54:LEU:HD13	15:P:80:LYS:NZ	2.25	0.51
15:P:75:ILE:HG23	15:P:80:LYS:HD2	1.92	0.51
9:J:48:ARG:HB3	9:J:66:GLU:HG3	1.92	0.51
1:A:1096:C:H2'	1:A:1097:C:H6	1.74	0.51
20:B:40:ILE:HG21	20:B:200:PRO:O	2.11	0.51
1:A:33:A:H2'	1:A:34:C:H6	1.75	0.51
1:A:939:G:H5''	6:G:101:ARG:HH22	1.75	0.51
1:A:1026:G:H2'	1:A:1027:C:O4'	2.10	0.51
1:A:692:U:H2'	1:A:694:A:OP2	2.10	0.51
1:A:157:U:O2'	1:A:158:G:H5'	2.10	0.51
1:A:214:C:H2'	1:A:215:C:C6	2.44	0.51
1:A:926:G:H5'	1:A:927:G:C5'	2.39	0.51
1:A:110:C:H2'	1:A:111:G:O4'	2.11	0.51
20:B:116:LEU:O	20:B:119:GLN:HB2	2.09	0.51
1:A:952:U:H2'	1:A:953:G:C8	2.43	0.51
1:A:499:A:H4'	1:A:500:G:OP1	2.09	0.51
1:A:642:A:C5	7:H:106:SER:HA	2.45	0.51
3:D:148:ALA:O	3:D:151:GLN:HG2	2.11	0.51
6:G:77:ARG:HD3	6:G:79:VAL:CG2	2.39	0.51
3:D:15:GLY:HA2	3:D:34:GLU:HB2	1.92	0.51
12:M:95:PRO:N	12:M:108:ARG:HG2	2.25	0.51
20:B:222:GLU:O	20:B:222:GLU:HG2	2.10	0.51
17:R:62:ARG:HB3	17:R:69:TYR:CE1	2.46	0.51
1:A:255:G:H2'	1:A:256:U:C6	2.45	0.51
4:E:89:THR:C	4:E:91:SER:N	2.64	0.51
1:A:1085:U:H3'	1:A:1086:U:C6	2.45	0.51
3:D:160:LEU:HD13	3:D:160:LEU:C	2.30	0.51
14:O:35:ILE:HD11	14:O:58:MET:HB3	1.92	0.51
1:A:75:G:H3'	1:A:76:G:H8	1.75	0.51
1:A:513:C:H2'	1:A:514:C:H6	1.75	0.51
1:A:932:C:H2'	1:A:933:G:C8	2.46	0.51
13:N:79:SER:O	13:N:83:VAL:HG23	2.09	0.51
18:S:39:ILE:HA	18:S:43:MET:SD	2.50	0.51
11:L:86:VAL:CG1	11:L:89:LEU:HD23	2.40	0.51
2:C:95:GLY:C	2:C:96:VAL:HG22	2.30	0.51
1:A:1299:A:N7	1:A:1301:U:H1'	2.25	0.51
1:A:1176:A:H2'	1:A:1177:G:O4'	2.11	0.51
20:B:53:LEU:HD11	20:B:219:THR:OG1	2.10	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:684:U:O2'	10:K:39:ASN:HB3	2.09	0.51
15:P:52:LEU:HD21	15:P:74:LEU:HB2	1.91	0.51
1:A:716:A:N3	10:K:119:GLY:HA2	2.26	0.51
1:A:1456:A:H2'	1:A:1457:G:H8	1.75	0.51
13:N:71:GLY:O	13:N:79:SER:HA	2.10	0.51
21:U:24:LYS:HD2	21:U:25:ALA:N	2.12	0.51
1:A:923:A:OP1	4:E:25:LYS:HB3	2.10	0.51
1:A:838:G:H2'	1:A:839:C:O4'	2.10	0.51
1:A:33:A:H2'	1:A:34:C:C6	2.46	0.51
6:G:59:GLU:HA	6:G:62:GLU:CD	2.30	0.51
1:A:1053:G:H4'	1:A:1054:C:H5'	1.92	0.51
1:A:587:G:H4'	7:H:3:GLN:HA	1.92	0.51
1:A:600:A:H2'	1:A:601:G:C8	2.46	0.51
2:C:65:VAL:HG21	2:C:90:VAL:HG11	1.93	0.51
2:C:45:GLU:HG2	2:C:85:LYS:NZ	2.25	0.51
9:J:41:PRO:O	9:J:42:LEU:HB2	2.10	0.51
9:J:82:LYS:C	9:J:84:VAL:H	2.14	0.51
5:F:38:ARG:NH2	5:F:63:ASN:HD21	2.08	0.51
1:A:674:G:H2'	1:A:675:A:H8	1.74	0.51
16:Q:68:LYS:O	16:Q:70:LYS:N	2.43	0.51
3:D:58:GLN:HA	3:D:58:GLN:NE2	2.21	0.51
1:A:17:U:H2'	1:A:18:C:H6	1.71	0.51
1:A:36:C:H2'	1:A:37:U:O4'	2.10	0.51
1:A:472:U:H2'	1:A:473:U:C6	2.46	0.51
20:B:172:ILE:CD1	20:B:182:VAL:HG11	2.41	0.51
20:B:96:LEU:HD11	20:B:146:SER:HB2	1.93	0.51
1:A:1337:G:H5''	1:A:1338:G:OP1	2.11	0.51
1:A:708:C:H2'	1:A:709:U:C6	2.45	0.51
1:A:633:G:H2'	1:A:634:C:C6	2.46	0.51
13:N:26:LEU:HD12	13:N:29:ILE:HD12	1.91	0.51
1:A:1072:G:H2'	1:A:1073:U:H6	1.76	0.51
18:S:18:VAL:C	18:S:42:ASN:HD21	2.14	0.51
3:D:13:ARG:HG3	3:D:13:ARG:O	2.10	0.51
2:C:11:LEU:HD22	2:C:17:TRP:CD1	2.46	0.51
1:A:1009:U:H2'	1:A:1010:U:C5	2.46	0.51
1:A:980:C:H2'	1:A:981:U:H5'	1.93	0.51
1:A:219:U:H2'	1:A:220:G:C8	2.46	0.51
1:A:1234:C:H2'	1:A:1235:U:C6	2.45	0.51
1:A:803:G:H2'	1:A:804:U:C6	2.46	0.51
1:A:1082:A:O2'	1:A:1083:U:H5'	2.11	0.51
1:A:1496:C:H2'	1:A:1497:G:O4'	2.11	0.51
4:E:67:ARG:HH11	4:E:67:ARG:HB2	1.75	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
15:P:54:LEU:HD22	15:P:80:LYS:HZ2	1.75	0.51
1:A:865:A:C2	1:A:918:A:H4'	2.46	0.51
8:I:90:ASP:HB3	8:I:93:LEU:HG	1.93	0.51
8:I:98:ARG:HA	8:I:103:VAL:CG2	2.40	0.51
15:P:3:THR:HB	15:P:66:THR:O	2.10	0.51
1:A:195:A:H1'	1:A:222:C:O2'	2.10	0.51
1:A:1226:C:C5	12:M:102:LYS:HB3	2.46	0.51
1:A:1054:C:H1'	1:A:1196:A:C5	2.46	0.51
2:C:122:GLN:HB3	2:C:127:VAL:HG11	1.92	0.51
6:G:90:VAL:HG12	6:G:91:ARG:H	1.76	0.51
1:A:626:G:H2'	1:A:627:G:H8	1.75	0.51
5:F:52:ASN:O	5:F:53:LYS:HB3	2.10	0.51
17:R:62:ARG:C	17:R:64:LEU:H	2.14	0.51
1:A:1060:U:OP1	9:J:53:ILE:HD11	2.11	0.51
1:A:1002:G:H2'	1:A:1003:G:O4'	2.11	0.51
1:A:34:C:H2'	1:A:35:G:H8	1.76	0.51
1:A:34:C:H2'	1:A:35:G:C8	2.46	0.51
1:A:1335:U:H5''	1:A:1337:G:N2	2.26	0.51
1:A:1234:C:O2'	1:A:1235:U:H5'	2.10	0.51
1:A:1326:U:O2'	1:A:1327:C:H5'	2.11	0.51
1:A:1404:C:H2'	1:A:1405:G:C8	2.45	0.51
5:F:62:MET:HG3	5:F:64:VAL:CG2	2.41	0.51
12:M:55:LEU:O	12:M:59:VAL:HG12	2.11	0.51
1:A:1073:U:O2'	1:A:1074:G:H5'	2.10	0.51
10:K:70:ALA:HB1	10:K:74:LYS:HB2	1.93	0.51
16:Q:6:THR:HG23	16:Q:59:GLU:OE1	2.11	0.51
20:B:22:TRP:HA	20:B:188:THR:HB	1.92	0.51
2:C:85:LYS:HG3	2:C:86:LEU:N	2.26	0.51
1:A:1177:G:H3'	1:A:1178:G:C8	2.46	0.51
1:A:693:G:H2'	1:A:694:A:O4'	2.11	0.51
1:A:75:G:H2'	1:A:76:G:O4'	2.11	0.51
1:A:1426:G:H2'	1:A:1427:C:H6	1.75	0.51
2:C:88:LYS:O	2:C:92:ASP:HB2	2.11	0.51
1:A:1370:G:O2'	1:A:1371:G:H5'	2.11	0.50
14:O:84:LEU:HB3	14:O:86:LEU:HD13	1.93	0.50
10:K:122:PRO:HG2	21:U:34:ARG:HA	1.92	0.50
1:A:1060:U:H2'	1:A:1061:G:C8	2.46	0.50
4:E:89:THR:O	4:E:91:SER:N	2.44	0.50
3:D:2:ARG:HH11	3:D:114:ARG:HD3	1.74	0.50
1:A:376:G:H4'	15:P:5:ARG:HD3	1.93	0.50
20:B:132:GLU:HA	20:B:135:MET:HE3	1.93	0.50
1:A:1516:G:H2'	1:A:1518:A:OP2	2.10	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:179:A:H2'	1:A:180:U:C6	2.47	0.50
21:U:41:THR:HA	21:U:45:LYS:HD3	1.92	0.50
5:F:38:ARG:NH2	5:F:96:VAL:HB	2.26	0.50
1:A:1202:U:H1'	13:N:68:ARG:HD2	1.91	0.50
10:K:124:LYS:HD3	21:U:34:ARG:HD3	1.93	0.50
18:S:43:MET:C	18:S:46:LEU:HD23	2.31	0.50
20:B:40:ILE:CG2	20:B:200:PRO:HB2	2.41	0.50
1:A:560:A:H4'	1:A:561:U:H5''	1.92	0.50
1:A:982:U:OP2	13:N:62:ARG:NH2	2.43	0.50
19:T:49:ALA:O	19:T:52:GLU:HB3	2.12	0.50
1:A:1417:G:O2'	1:A:1483:A:N6	2.44	0.50
6:G:29:LEU:HD11	6:G:119:LEU:HD22	1.94	0.50
1:A:366:A:O2'	1:A:394:G:N2	2.45	0.50
6:G:74:VAL:HA	6:G:86:VAL:O	2.11	0.50
3:D:127:ARG:HD2	3:D:127:ARG:H	1.76	0.50
10:K:88:PRO:CD	21:U:28:LEU:HD13	2.33	0.50
10:K:12:ARG:HD3	10:K:13:LYS:HZ1	1.76	0.50
9:J:85:ASP:CG	9:J:89:ARG:HB2	2.31	0.50
1:A:932:C:H2'	1:A:933:G:H8	1.75	0.50
3:D:27:ILE:C	3:D:29:THR:H	2.15	0.50
1:A:607:A:H2'	1:A:608:A:C8	2.45	0.50
1:A:894:G:O2'	1:A:895:G:H5'	2.12	0.50
15:P:57:ILE:HD11	15:P:75:ILE:HD11	1.93	0.50
18:S:24:SER:HB2	18:S:27:LYS:HZ1	1.77	0.50
13:N:40:ARG:NH1	18:S:6:LYS:H	2.10	0.50
1:A:1438:G:O2'	1:A:1439:G:H5'	2.11	0.50
2:C:53:ARG:HG3	2:C:113:LYS:HD3	1.93	0.50
2:C:89:VAL:HG23	2:C:90:VAL:N	2.26	0.50
1:A:1128:C:H4'	1:A:1148:U:O2	2.11	0.50
2:C:190:THR:HG22	2:C:191:THR:H	1.76	0.50
1:A:1251:A:O2'	1:A:1252:A:H5'	2.11	0.50
21:U:36:PHE:O	21:U:38:GLU:N	2.44	0.50
1:A:769:G:O2'	1:A:770:C:H5'	2.12	0.50
8:I:94:ARG:HB3	8:I:98:ARG:HE	1.76	0.50
1:A:205:A:H2'	1:A:206:C:C6	2.44	0.50
1:A:857:C:H2'	1:A:858:G:O4'	2.10	0.50
10:K:17:ASP:OD1	10:K:36:ARG:HG3	2.11	0.50
1:A:1157:A:H5'	1:A:1158:C:C6	2.47	0.50
1:A:746:A:H2'	1:A:747:A:C8	2.46	0.50
1:A:1478:U:H2'	1:A:1479:C:C6	2.46	0.50
12:M:52:ILE:HG13	12:M:56:ARG:NH2	2.15	0.50
8:I:10:ARG:HA	8:I:14:SER:O	2.12	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1250:A:H5''	8:I:69:GLY:N	2.26	0.50
1:A:237:G:O2'	1:A:238:A:H5'	2.12	0.50
1:A:1003:G:N2	1:A:1005:A:H5'	2.23	0.50
3:D:130:ASN:N	3:D:130:ASN:HD22	2.07	0.50
7:H:77:VAL:O	7:H:84:ILE:HD12	2.12	0.50
1:A:1107:C:H4'	2:C:172:VAL:HG23	1.92	0.50
3:D:97:LEU:CB	3:D:134:TYR:HB3	2.40	0.50
8:I:30:ASN:HD21	8:I:66:VAL:N	2.09	0.50
1:A:300:A:H2'	1:A:301:G:O4'	2.11	0.50
1:A:751:U:H2'	1:A:752:G:O4'	2.11	0.50
1:A:940:C:H2'	1:A:941:G:H8	1.77	0.50
3:D:37:PRO:HD2	3:D:41:GLY:CA	2.41	0.50
10:K:92:ARG:HD3	21:U:20:ARG:HH22	1.77	0.50
5:F:92:THR:HG22	5:F:93:LYS:H	1.77	0.50
1:A:664:G:N2	1:A:741:G:H1	2.03	0.50
13:N:65:GLN:HB3	13:N:82:LYS:HG2	1.92	0.50
9:J:8:ILE:HG13	9:J:73:LEU:O	2.11	0.50
8:I:9:GLY:HA2	8:I:80:HIS:HB3	1.93	0.50
16:Q:58:VAL:HB	16:Q:74:LEU:HD23	1.94	0.50
1:A:214:C:H2'	1:A:215:C:H6	1.76	0.50
20:B:132:GLU:HG2	20:B:135:MET:HE2	1.94	0.50
20:B:72:LYS:O	20:B:74:ALA:N	2.44	0.50
3:D:36:ALA:C	3:D:38:GLY:H	2.14	0.50
16:Q:13:SER:HB3	16:Q:21:VAL:CB	2.34	0.50
1:A:1527:U:OP2	21:U:38:GLU:HG3	2.11	0.50
20:B:13:VAL:HG11	20:B:207:ARG:HB3	1.94	0.50
16:Q:74:LEU:HD22	16:Q:75:VAL:H	1.76	0.50
11:L:13:ARG:O	11:L:14:LYS:HB3	2.11	0.50
1:A:15:G:N3	4:E:23:THR:HG21	2.27	0.50
1:A:167:A:O2'	1:A:168:G:H5'	2.12	0.50
1:A:1163:A:H2'	1:A:1164:G:H8	1.76	0.50
3:D:37:PRO:HD2	3:D:41:GLY:HA3	1.94	0.50
1:A:890:G:O2'	1:A:906:A:N6	2.45	0.50
1:A:1471:U:O2'	1:A:1472:U:H5'	2.12	0.50
1:A:975:A:H61	9:J:50:THR:HB	1.77	0.50
21:U:19:LYS:C	21:U:21:SER:H	2.15	0.50
17:R:58:ILE:O	17:R:62:ARG:HG3	2.12	0.50
16:Q:13:SER:O	16:Q:20:ILE:HG13	2.11	0.50
10:K:121:ARG:HE	21:U:34:ARG:HG2	1.77	0.50
16:Q:30:HIS:CE1	16:Q:32:ILE:HG22	2.47	0.50
1:A:1023:U:H2'	1:A:1024:G:C8	2.47	0.50
1:A:1039:G:H2'	1:A:1040:U:H6	1.77	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:C:155:ARG:NH2	2:C:160:GLU:HA	2.27	0.50
1:A:829:G:H4'	20:B:24:PRO:HG3	1.93	0.50
16:Q:25:GLU:HA	16:Q:40:THR:HA	1.94	0.49
15:P:67:ILE:CG1	15:P:71:VAL:HG13	2.40	0.49
1:A:840:C:C2'	1:A:842:U:H5''	2.38	0.49
19:T:54:GLN:N	19:T:55:PRO:HD2	2.27	0.49
15:P:22:ALA:HB2	15:P:32:PHE:HA	1.93	0.49
4:E:149:PRO:HG2	4:E:150:GLU:OE2	2.11	0.49
2:C:108:PRO:C	2:C:110:LEU:H	2.16	0.49
12:M:95:PRO:HB2	12:M:99:GLN:OE1	2.12	0.49
1:A:182:A:H1'	1:A:183:C:C5	2.47	0.49
21:U:7:GLU:OE1	21:U:11:PHE:HZ	1.95	0.49
20:B:137:THR:HA	20:B:140:LEU:CD1	2.42	0.49
14:O:25:GLU:OE2	14:O:76:ARG:HD3	2.11	0.49
1:A:662:U:O2'	1:A:836:G:H5''	2.12	0.49
1:A:1131:G:C2'	1:A:1132:C:H5'	2.42	0.49
20:B:38:HIS:O	20:B:39:ILE:HD13	2.12	0.49
2:C:2:GLN:HE21	2:C:2:GLN:H	1.61	0.49
3:D:30:LYS:HB2	3:D:30:LYS:NZ	2.27	0.49
3:D:106:PHE:HD1	3:D:158:LEU:HD21	1.76	0.49
7:H:72:GLU:H	7:H:129:ALA:HB2	1.76	0.49
21:U:16:ARG:HB3	21:U:20:ARG:HD3	1.95	0.49
3:D:59:LYS:O	3:D:63:ILE:HG22	2.12	0.49
1:A:1060:U:C5'	9:J:53:ILE:HG12	2.41	0.49
1:A:919:A:O2'	1:A:920:U:H5'	2.12	0.49
1:A:1512:U:H2'	1:A:1513:A:H8	1.77	0.49
12:M:84:CYS:O	12:M:88:LEU:HG	2.12	0.49
2:C:85:LYS:HG3	2:C:86:LEU:HD23	1.93	0.49
1:A:83:C:OP1	1:A:83:C:H4'	2.11	0.49
6:G:90:VAL:HG13	6:G:94:ARG:HD3	1.93	0.49
20:B:57:ASN:ND2	20:B:223:GLY:HA2	2.28	0.49
10:K:24:ALA:HB2	10:K:29:THR:HG23	1.93	0.49
1:A:880:C:P	11:L:4:ASN:HD22	2.36	0.49
1:A:930:C:H2'	1:A:931:C:C6	2.47	0.49
1:A:961:U:O4'	1:A:961:U:O2	2.29	0.49
1:A:309:A:H2'	1:A:310:G:H8	1.77	0.49
21:U:3:ILE:HB	21:U:18:PHE:CD2	2.48	0.49
15:P:54:LEU:HA	15:P:57:ILE:CG2	2.42	0.49
15:P:57:ILE:C	15:P:57:ILE:HD13	2.33	0.49
6:G:108:ARG:HA	6:G:118:ARG:HE	1.77	0.49
18:S:15:LEU:HA	18:S:18:VAL:CG1	2.37	0.49
16:Q:18:LYS:HA	16:Q:47:ASP:O	2.13	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1244:G:H2'	1:A:1245:C:H6	1.77	0.49
2:C:2:GLN:N	2:C:2:GLN:HE21	2.10	0.49
3:D:89:LEU:HA	3:D:92:LEU:HB2	1.93	0.49
20:B:55:GLU:HG3	20:B:197:PHE:HZ	1.77	0.49
1:A:272:C:H2'	1:A:273:U:C6	2.47	0.49
13:N:16:ALA:O	13:N:20:PHE:N	2.46	0.49
20:B:111:LYS:O	20:B:114:LYS:HB3	2.11	0.49
1:A:235:C:H2'	1:A:236:A:C8	2.47	0.49
8:I:115:VAL:HG22	8:I:116:GLY:H	1.78	0.49
16:Q:17:GLU:C	16:Q:19:SER:H	2.15	0.49
18:S:27:LYS:HB3	18:S:27:LYS:NZ	2.23	0.49
4:E:15:ILE:HG22	4:E:16:ALA:N	2.27	0.49
1:A:764:C:H3'	1:A:765:G:N2	2.24	0.49
8:I:42:THR:O	8:I:45:MET:HG2	2.12	0.49
10:K:31:VAL:HG21	10:K:66:ALA:CA	2.42	0.49
19:T:34:VAL:HG11	19:T:78:LEU:HD13	1.93	0.49
16:Q:60:ILE:HD13	16:Q:60:ILE:H	1.77	0.49
1:A:1435:G:H2'	1:A:1436:U:C6	2.48	0.49
1:A:89:U:O2'	1:A:90:C:H5'	2.13	0.49
18:S:62:THR:HG22	18:S:65:MET:CE	2.42	0.49
1:A:265:G:H2'	1:A:267:C:H5	1.77	0.49
20:B:150:ILE:O	20:B:150:ILE:HG12	2.13	0.49
12:M:64:VAL:HB	12:M:65:GLU:OE2	2.13	0.49
2:C:56:ILE:N	2:C:56:ILE:HD12	2.28	0.49
1:A:1308:U:P	12:M:97:ARG:HD3	2.53	0.49
1:A:8:A:H1'	4:E:107:GLY:HA2	1.94	0.49
1:A:625:U:H4'	15:P:16:PHE:CE2	2.47	0.49
1:A:537:G:H2'	1:A:538:G:C8	2.48	0.49
5:F:18:VAL:O	5:F:22:ILE:HG13	2.12	0.49
2:C:105:VAL:HG12	2:C:108:PRO:HD3	1.93	0.49
3:D:32:LYS:HG3	3:D:32:LYS:O	2.13	0.49
1:A:21:G:H2'	1:A:22:G:C8	2.48	0.49
1:A:301:G:H2'	1:A:302:G:H8	1.76	0.49
1:A:1137:C:H1'	1:A:1138:G:C2	2.47	0.49
1:A:807:A:H2'	1:A:808:C:C6	2.48	0.49
12:M:37:GLY:O	12:M:38:ILE:HD13	2.12	0.49
16:Q:19:SER:O	16:Q:20:ILE:HD12	2.13	0.49
13:N:42:ASN:HA	13:N:45:LEU:HD12	1.95	0.49
11:L:65:TYR:HB3	11:L:95:HIS:CD2	2.47	0.49
3:D:141:VAL:HG12	3:D:180:THR:CA	2.41	0.49
19:T:38:ILE:HD13	19:T:85:LEU:HD23	1.95	0.49
20:B:86:CYS:HB3	20:B:88:GLN:CD	2.32	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:F:68:GLN:HA	5:F:71:ILE:HG22	1.94	0.49
1:A:1082:A:H2'	1:A:1083:U:O4'	2.12	0.49
1:A:613:C:H2'	1:A:614:C:C6	2.48	0.49
1:A:1451:U:H5''	1:A:1452:C:OP2	2.12	0.49
1:A:49:U:O2'	1:A:50:A:H2'	2.13	0.49
20:B:209:VAL:C	20:B:213:LEU:HD12	2.33	0.49
21:U:16:ARG:O	21:U:18:PHE:N	2.46	0.49
18:S:43:MET:O	18:S:46:LEU:HB2	2.12	0.49
17:R:33:THR:CG2	17:R:37:LYS:HG2	2.43	0.49
1:A:1001:C:H2'	1:A:1002:G:H8	1.76	0.49
1:A:769:G:H4'	1:A:1513:A:H4'	1.95	0.49
1:A:409:U:OP2	3:D:21:LYS:HE2	2.12	0.49
20:B:172:ILE:HD13	20:B:182:VAL:HG11	1.94	0.49
1:A:1373:G:H4'	6:G:30:MET:HE3	1.93	0.49
1:A:708:C:H2'	1:A:709:U:H6	1.78	0.49
1:A:1229:A:H2'	1:A:1230:C:H6	1.78	0.49
1:A:959:A:C6	1:A:1222:G:H4'	2.48	0.49
16:Q:83:LEU:HD22	16:Q:83:LEU:N	2.28	0.49
1:A:577:G:O2'	1:A:578:C:H5'	2.13	0.49
5:F:51:ILE:CD1	5:F:86:ARG:HG3	2.43	0.49
13:N:40:ARG:HG3	13:N:40:ARG:HH11	1.78	0.49
4:E:43:GLY:O	4:E:72:ASN:HA	2.13	0.49
1:A:782:A:H2'	1:A:783:C:O4'	2.12	0.49
2:C:154:GLY:HA2	2:C:163:ARG:HG2	1.94	0.49
12:M:79:LEU:HA	12:M:82:LEU:CG	2.40	0.49
1:A:500:G:H5''	11:L:120:ARG:HH21	1.76	0.49
2:C:8:GLY:O	2:C:11:LEU:HG	2.13	0.49
6:G:61:PHE:O	6:G:62:GLU:C	2.49	0.49
1:A:1142:G:H2'	1:A:1143:G:H8	1.78	0.49
1:A:985:C:H2'	1:A:986:U:H6	1.76	0.49
18:S:62:THR:HG22	18:S:65:MET:HE2	1.95	0.49
1:A:208:U:C2'	1:A:209:U:H5''	2.42	0.49
1:A:1229:A:H2'	1:A:1230:C:C6	2.48	0.49
1:A:1121:U:H2'	1:A:1122:U:C6	2.47	0.49
1:A:1481:U:H2'	1:A:1482:G:C8	2.47	0.49
10:K:110:THR:HB	21:U:3:ILE:O	2.13	0.49
1:A:232:G:H1'	1:A:262:A:N1	2.28	0.49
10:K:34:THR:CG2	10:K:38:GLY:HA2	2.43	0.49
21:U:34:ARG:HH21	21:U:36:PHE:HA	1.77	0.49
15:P:57:ILE:CD1	15:P:75:ILE:HD11	2.43	0.49
18:S:38:THR:HG22	18:S:39:ILE:H	1.78	0.49
4:E:19:ARG:CG	4:E:20:VAL:H	2.20	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1238:A:C2	1:A:1241:G:N3	2.80	0.49
1:A:1318:A:OP2	1:A:1318:A:H8	1.95	0.49
2:C:63:ILE:HG12	2:C:65:VAL:HG23	1.94	0.49
9:J:85:ASP:HB2	9:J:89:ARG:NH2	2.28	0.49
1:A:174:A:O2'	1:A:175:C:H5'	2.12	0.49
14:O:87:ARG:HE	14:O:87:ARG:HA	1.77	0.49
1:A:1426:G:H2'	1:A:1427:C:C6	2.47	0.49
6:G:4:ARG:HB2	6:G:4:ARG:NH1	2.27	0.49
3:D:169:TRP:CE3	3:D:185:PRO:HB3	2.48	0.48
4:E:11:GLN:OE1	4:E:116:VAL:HA	2.12	0.48
1:A:1074:G:H2'	1:A:1075:U:H6	1.78	0.48
1:A:1302:C:H5''	1:A:1303:C:OP2	2.13	0.48
19:T:2:ASN:O	19:T:3:ILE:C	2.51	0.48
1:A:335:C:H2'	1:A:336:A:H8	1.78	0.48
1:A:1480:A:H2'	1:A:1481:U:C6	2.47	0.48
7:H:94:VAL:HG21	7:H:127:TYR:HB2	1.95	0.48
4:E:158:LYS:HB3	7:H:63:LYS:HD3	1.93	0.48
7:H:111:THR:H	7:H:114:ALA:HB3	1.77	0.48
1:A:1492:A:H3'	1:A:1493:A:C5'	2.42	0.48
19:T:66:ILE:HG22	19:T:67:HIS:N	2.28	0.48
3:D:121:ALA:HA	3:D:145:ARG:HG3	1.94	0.48
12:M:21:ILE:HG22	12:M:21:ILE:O	2.13	0.48
16:Q:46:HIS:CG	16:Q:47:ASP:N	2.81	0.48
16:Q:30:HIS:CG	16:Q:33:TYR:HB2	2.47	0.48
2:C:128:MET:O	2:C:130:ARG:N	2.40	0.48
1:A:56:U:H2'	1:A:57:G:H8	1.78	0.48
1:A:844:G:H21	1:A:845:A:H62	1.61	0.48
7:H:107:LYS:HB3	7:H:107:LYS:NZ	2.28	0.48
1:A:301:G:H2'	1:A:302:G:C8	2.49	0.48
1:A:1248:A:H2'	1:A:1249:C:H6	1.79	0.48
1:A:736:C:H2'	1:A:737:C:C6	2.47	0.48
8:I:51:LEU:HD13	8:I:56:MET:SD	2.53	0.48
10:K:78:ILE:H	10:K:78:ILE:CD1	2.18	0.48
15:P:6:LEU:HB3	15:P:17:TYR:HB3	1.94	0.48
8:I:6:TYR:HA	8:I:18:VAL:O	2.13	0.48
6:G:96:ASN:O	6:G:100:MET:HG2	2.14	0.48
1:A:252:U:H2'	1:A:253:A:C8	2.49	0.48
10:K:48:GLY:C	10:K:50:GLY:H	2.15	0.48
8:I:116:GLY:O	8:I:117:LEU:HD23	2.13	0.48
10:K:121:ARG:HE	21:U:34:ARG:CD	2.26	0.48
1:A:1221:G:OP1	18:S:35:ARG:HD2	2.13	0.48
1:A:1060:U:C4'	9:J:54:SER:HB2	2.40	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1311:A:N6	18:S:1:PRO:HD3	2.22	0.48
4:E:82:HIS:CE1	4:E:146:MET:HB2	2.48	0.48
11:L:73:LEU:HD21	11:L:103:CYS:HA	1.95	0.48
1:A:26:A:H61	1:A:558:G:H1'	1.79	0.48
3:D:197:HIS:O	3:D:201:GLU:HG3	2.13	0.48
1:A:218:U:H2'	1:A:219:U:H6	1.78	0.48
1:A:1472:U:O2'	1:A:1473:G:H5'	2.13	0.48
10:K:85:VAL:CG2	10:K:92:ARG:HH12	2.26	0.48
12:M:106:ARG:HA	12:M:106:ARG:HH11	1.78	0.48
1:A:1343:G:H2'	1:A:1344:C:H6	1.76	0.48
13:N:26:LEU:HD21	13:N:47:LEU:HG	1.95	0.48
1:A:1125:U:O2	1:A:1126:U:H6	1.97	0.48
4:E:89:THR:HG23	4:E:90:GLY:N	2.29	0.48
2:C:178:ARG:HG2	2:C:205:GLU:O	2.14	0.48
1:A:1238:A:N3	1:A:1241:G:H1'	2.29	0.48
1:A:1164:G:O2'	1:A:1165:U:H5'	2.12	0.48
1:A:930:C:H2'	1:A:931:C:H6	1.78	0.48
1:A:966:G:H2'	1:A:967:C:C6	2.48	0.48
1:A:432:A:H2'	1:A:433:G:H5'	1.96	0.48
9:J:44:THR:HG21	9:J:70:HIS:ND1	2.29	0.48
6:G:45:ALA:HB2	6:G:116:ALA:HA	1.94	0.48
1:A:685:G:O2'	1:A:686:U:H5'	2.14	0.48
1:A:235:C:H2'	1:A:236:A:H8	1.78	0.48
1:A:238:A:C2'	1:A:239:U:H5''	2.44	0.48
1:A:766:A:H2	1:A:1525:G:N3	2.11	0.48
8:I:32:ARG:HD3	8:I:37:TYR:CD1	2.48	0.48
7:H:77:VAL:CG2	7:H:126:CYS:HA	2.44	0.48
1:A:1278:G:H3'	1:A:1279:G:H5'	1.95	0.48
1:A:546:A:H4'	1:A:548:G:O3'	2.13	0.48
6:G:17:PHE:HD2	6:G:58:LEU:HD22	1.79	0.48
20:B:76:SER:O	20:B:80:LYS:HG2	2.14	0.48
9:J:17:LEU:CD1	9:J:96:VAL:HG13	2.44	0.48
5:F:99:ALA:O	5:F:100:SER:HB2	2.13	0.48
1:A:1174:G:O2'	1:A:1175:G:H5'	2.13	0.48
1:A:1426:G:O2'	1:A:1427:C:H5'	2.13	0.48
1:A:730:G:O6	14:O:50:HIS:NE2	2.46	0.48
1:A:239:U:H5''	1:A:239:U:H6	1.78	0.48
1:A:619:U:N3	3:D:130:ASN:ND2	2.58	0.48
10:K:70:ALA:C	10:K:72:ALA:N	2.67	0.48
2:C:168:ARG:HG2	2:C:169:GLU:H	1.78	0.48
7:H:35:ILE:HG22	7:H:39:LEU:HD23	1.94	0.48
3:D:107:GLY:O	3:D:157:ALA:HB1	2.13	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1041:G:H2'	1:A:1042:A:C8	2.48	0.48
1:A:844:G:N7	1:A:846:G:N3	2.62	0.48
3:D:44:LYS:NZ	3:D:46:ARG:HA	2.28	0.48
1:A:333:U:H2'	1:A:334:C:C6	2.48	0.48
1:A:303:A:H2'	1:A:304:U:O4'	2.13	0.48
19:T:66:ILE:HA	19:T:70:LYS:HZ2	1.79	0.48
3:D:11:SER:HA	3:D:18:LEU:HD23	1.95	0.48
15:P:53:ASP:O	15:P:57:ILE:HG22	2.13	0.48
8:I:120:ALA:O	8:I:121:ARG:HG2	2.13	0.48
18:S:51:HIS:HB2	18:S:56:HIS:CD2	2.49	0.48
4:E:33:THR:HB	4:E:49:TYR:HE1	1.79	0.48
1:A:1238:A:C2	1:A:1241:G:H1'	2.49	0.48
19:T:28:ARG:HA	19:T:31:ILE:HD12	1.94	0.48
1:A:979:C:H2'	1:A:980:C:O4'	2.13	0.48
6:G:55:LYS:HG3	6:G:56:SER:N	2.29	0.48
3:D:78:ALA:HB1	3:D:88:ASN:HB2	1.96	0.48
6:G:91:ARG:HB3	6:G:92:PRO:HD2	1.95	0.48
1:A:254:G:O2'	1:A:255:G:H5'	2.13	0.48
1:A:276:G:H5'	16:Q:16:MET:SD	2.54	0.48
1:A:471:U:H2'	1:A:472:U:H6	1.78	0.48
3:D:115:GLN:NE2	3:D:153:ARG:HH22	2.11	0.48
1:A:1036:A:H2'	1:A:1037:C:H6	1.78	0.48
5:F:39:LEU:HD22	5:F:39:LEU:O	2.14	0.48
1:A:220:G:O2'	1:A:221:C:H5'	2.13	0.48
1:A:1325:C:O2'	1:A:1326:U:H5'	2.13	0.48
14:O:62:ARG:NH1	14:O:86:LEU:HD21	2.28	0.48
9:J:40:ILE:CG1	9:J:73:LEU:HB3	2.43	0.48
9:J:40:ILE:HD11	9:J:73:LEU:HB3	1.96	0.48
1:A:920:U:H2'	1:A:921:U:C6	2.49	0.48
1:A:1000:A:O2'	1:A:1001:C:H5'	2.14	0.48
1:A:840:C:C2	1:A:842:U:H4'	2.48	0.48
1:A:1437:A:H2'	1:A:1438:G:H8	1.78	0.48
1:A:1129:C:H1'	1:A:1146:A:N6	2.28	0.48
6:G:30:MET:HG3	6:G:34:LYS:O	2.14	0.48
2:C:76:ILE:O	2:C:83:VAL:HG23	2.13	0.48
1:A:251:G:H4'	1:A:252:U:H5'	1.94	0.48
1:A:1456:A:H2'	1:A:1457:G:C8	2.49	0.48
1:A:1307:U:H5'	12:M:107:THR:HG21	1.95	0.47
1:A:1014:A:H2	1:A:1219:A:H1'	1.77	0.47
1:A:16:A:N1	1:A:919:A:C2	2.82	0.47
10:K:12:ARG:HB3	10:K:13:LYS:NZ	2.29	0.47
1:A:202:G:H2'	1:A:203:G:H8	1.79	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:L:81:ILE:HD13	11:L:96:THR:HG22	1.95	0.47
15:P:5:ARG:O	15:P:19:VAL:HA	2.14	0.47
1:A:418:C:H2'	1:A:419:C:H6	1.79	0.47
1:A:989:U:O2'	1:A:990:C:H5'	2.14	0.47
1:A:216:U:H2'	1:A:217:C:C6	2.49	0.47
20:B:161:PHE:HA	20:B:183:PHE:O	2.13	0.47
10:K:94:SER:HA	10:K:97:ARG:HG3	1.95	0.47
5:F:51:ILE:HG23	5:F:51:ILE:O	2.14	0.47
1:A:1103:C:O2	20:B:105:THR:HG21	2.14	0.47
1:A:731:G:OP1	1:A:766:A:H1'	2.13	0.47
4:E:89:THR:CG2	4:E:90:GLY:N	2.77	0.47
4:E:85:LYS:HG3	4:E:94:PHE:HD2	1.78	0.47
1:A:837:U:H2'	1:A:838:G:H8	1.78	0.47
1:A:389:A:N3	1:A:389:A:H2'	2.29	0.47
19:T:34:VAL:CG1	19:T:78:LEU:HD22	2.44	0.47
6:G:144:ALA:C	6:G:146:ALA:N	2.67	0.47
3:D:104:MET:HG3	3:D:142:VAL:HG21	1.96	0.47
6:G:106:ALA:HB1	6:G:132:THR:OG1	2.14	0.47
1:A:1157:A:H4'	1:A:1158:C:O5'	2.15	0.47
4:E:154:ALA:HB1	7:H:65:PHE:CZ	2.49	0.47
3:D:152:SER:HA	3:D:155:LYS:HB3	1.95	0.47
10:K:124:LYS:HB3	21:U:33:ARG:NH1	2.29	0.47
18:S:43:MET:CB	18:S:61:VAL:HG11	2.44	0.47
13:N:11:LYS:O	13:N:15:LEU:HG	2.14	0.47
1:A:280:C:N3	16:Q:39:ARG:HA	2.29	0.47
2:C:145:ALA:HA	2:C:203:LYS:HA	1.96	0.47
1:A:1434:A:H2'	1:A:1435:G:C8	2.48	0.47
1:A:193:C:H2'	1:A:194:C:C6	2.49	0.47
1:A:513:C:H2'	1:A:514:C:C6	2.49	0.47
1:A:940:C:H2'	1:A:941:G:C8	2.49	0.47
1:A:695:A:H5'	10:K:52:ARG:HH22	1.79	0.47
3:D:95:GLY:HA3	3:D:135:GLN:NE2	2.29	0.47
1:A:563:A:H2'	1:A:567:G:C8	2.50	0.47
4:E:99:SER:C	4:E:101:GLY:H	2.17	0.47
21:U:6:ARG:C	21:U:7:GLU:HG2	2.34	0.47
1:A:1366:C:H2'	1:A:1367:C:C6	2.50	0.47
16:Q:10:ARG:CZ	16:Q:11:VAL:N	2.77	0.47
14:O:76:ARG:O	14:O:79:ARG:HB2	2.15	0.47
3:D:71:PHE:CE2	3:D:89:LEU:HD11	2.48	0.47
3:D:101:VAL:HG13	3:D:106:PHE:CD2	2.49	0.47
10:K:109:ILE:H	10:K:109:ILE:HD12	1.80	0.47
6:G:147:ASN:C	6:G:149:ALA:H	2.17	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:B:158:ASP:HA	20:B:180:ILE:HD12	1.97	0.47
19:T:42:ASP:OD2	19:T:44:ALA:HB3	2.15	0.47
3:D:43:ARG:HA	3:D:43:ARG:NH1	2.30	0.47
1:A:1252:A:H4'	1:A:1369:C:H4'	1.96	0.47
5:F:48:ALA:H	17:R:65:SER:HB2	1.79	0.47
16:Q:44:HIS:HB2	16:Q:69:THR:O	2.14	0.47
10:K:121:ARG:HE	21:U:34:ARG:HD2	1.78	0.47
15:P:61:VAL:CA	15:P:65:ALA:HB3	2.44	0.47
15:P:67:ILE:HD11	15:P:71:VAL:HG22	1.96	0.47
1:A:1312:G:H2'	1:A:1313:U:H6	1.78	0.47
3:D:118:SER:C	3:D:120:LYS:H	2.18	0.47
11:L:29:LYS:O	11:L:80:LEU:HD12	2.14	0.47
3:D:61:ARG:HE	3:D:68:GLU:N	2.13	0.47
1:A:824:G:H2'	1:A:825:A:H8	1.78	0.47
1:A:109:A:H4'	1:A:110:C:OP2	2.14	0.47
7:H:65:PHE:CD2	7:H:66:GLN:HG2	2.50	0.47
3:D:64:TYR:CD2	3:D:93:LEU:HB2	2.49	0.47
8:I:103:VAL:HG23	8:I:104:THR:N	2.29	0.47
1:A:812:G:N3	1:A:812:G:C2'	2.75	0.47
3:D:171:GLU:HB2	3:D:180:THR:HG21	1.97	0.47
1:A:628:G:H2'	1:A:629:A:C8	2.50	0.47
6:G:132:THR:O	6:G:135:LYS:HB3	2.15	0.47
1:A:806:C:H2'	1:A:807:A:H8	1.80	0.47
1:A:333:U:H2'	1:A:334:C:H6	1.79	0.47
1:A:343:U:O2'	1:A:344:A:H2'	2.15	0.47
1:A:454:G:O2'	1:A:455:G:H5'	2.15	0.47
1:A:647:C:O2'	1:A:648:A:H5'	2.15	0.47
3:D:144:ILE:HG23	3:D:149:LYS:HE2	1.97	0.47
2:C:177:LEU:HD22	2:C:177:LEU:H	1.79	0.47
1:A:1251:A:O2'	1:A:1370:G:H5'	2.15	0.47
19:T:66:ILE:O	19:T:70:LYS:HD3	2.14	0.47
1:A:673:A:H1'	17:R:63:TYR:CD1	2.49	0.47
16:Q:23:ALA:C	16:Q:24:ILE:HD12	2.35	0.47
9:J:36:VAL:HA	9:J:76:ILE:HG23	1.96	0.47
15:P:67:ILE:HG12	15:P:72:ALA:HB2	1.95	0.47
8:I:103:VAL:HG23	8:I:104:THR:H	1.79	0.47
2:C:129:PHE:CE2	2:C:156:LEU:HD13	2.50	0.47
2:C:146:LYS:HD3	2:C:203:LYS:O	2.15	0.47
1:A:1412:C:H2'	1:A:1413:A:H8	1.75	0.47
2:C:94:ALA:O	2:C:96:VAL:N	2.48	0.47
1:A:1438:G:C2'	1:A:1439:G:H5'	2.45	0.47
1:A:1319:A:P	18:S:4:LEU:HD21	2.55	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:G:56:SER:HB3	6:G:59:GLU:HG3	1.96	0.47
1:A:1277:C:H1'	1:A:1282:C:O2	2.15	0.47
1:A:1245:C:H2'	1:A:1246:A:H8	1.79	0.47
1:A:537:G:H2'	1:A:538:G:H8	1.80	0.47
1:A:1054:C:H1'	1:A:1196:A:C6	2.50	0.47
1:A:602:A:O2'	1:A:603:U:H5'	2.14	0.47
3:D:115:GLN:HE22	3:D:153:ARG:HH22	1.62	0.47
15:P:19:VAL:HG13	15:P:37:GLY:C	2.35	0.47
5:F:18:VAL:HG21	5:F:58:HIS:ND1	2.30	0.47
1:A:1390:U:H2'	1:A:1391:U:C6	2.50	0.47
17:R:20:ILE:HG12	17:R:20:ILE:O	2.14	0.47
1:A:1299:A:C5	1:A:1301:U:H1'	2.50	0.47
1:A:841:C:H6	1:A:843:U:OP1	1.98	0.47
1:A:179:A:H2'	1:A:180:U:H6	1.79	0.47
1:A:806:C:H2'	1:A:807:A:C8	2.49	0.47
1:A:1122:U:H2'	1:A:1123:U:C6	2.50	0.47
7:H:71:VAL:O	7:H:71:VAL:HG23	2.14	0.47
19:T:50:PHE:O	19:T:53:MET:HG3	2.13	0.47
1:A:451:A:C5'	15:P:70:ARG:HH22	2.20	0.47
16:Q:43:LEU:HD12	16:Q:43:LEU:N	2.29	0.47
1:A:1313:U:OP2	18:S:5:LYS:HA	2.14	0.47
13:N:82:LYS:HE2	13:N:82:LYS:HA	1.96	0.47
2:C:156:LEU:HD12	2:C:163:ARG:HG3	1.97	0.47
11:L:100:ALA:C	11:L:103:CYS:HG	2.17	0.47
4:E:152:VAL:HA	4:E:155:LYS:HD3	1.96	0.47
1:A:979:C:H41	1:A:1360:A:H62	1.63	0.47
1:A:123:U:H5''	1:A:311:C:O2'	2.15	0.47
11:L:23:LEU:C	11:L:25:ALA:N	2.68	0.47
1:A:1298:U:H4'	1:A:1299:A:C2	2.50	0.47
10:K:126:ARG:HG2	10:K:126:ARG:NH1	2.30	0.47
1:A:317:U:H2'	1:A:318:G:C8	2.49	0.47
1:A:31:G:H2'	1:A:48:C:H5	1.79	0.47
1:A:1019:A:H2'	1:A:1020:G:C8	2.50	0.47
21:U:16:ARG:C	21:U:18:PHE:H	2.18	0.47
1:A:948:C:OP1	12:M:107:THR:HG22	2.15	0.47
1:A:954:G:H2'	1:A:955:U:H6	1.80	0.47
20:B:101:THR:HG22	20:B:174:GLU:OE1	2.14	0.47
4:E:80:LEU:CD2	4:E:122:VAL:HG11	2.45	0.47
19:T:19:HIS:CE1	19:T:23:ARG:HG3	2.50	0.47
2:C:61:LYS:HE2	2:C:96:VAL:HG12	1.96	0.47
1:A:586:C:C2'	1:A:587:G:H5'	2.44	0.47
1:A:1492:A:H2'	1:A:1492:A:N3	2.29	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1268:G:H2'	1:A:1269:A:C8	2.50	0.47
9:J:91:ASP:C	9:J:92:LEU:HD23	2.35	0.47
1:A:1371:G:O3'	8:I:70:GLY:HA3	2.15	0.47
20:B:153:MET:C	20:B:155:GLY:H	2.19	0.47
3:D:57:LYS:HD3	3:D:58:GLN:N	2.30	0.47
13:N:50:LEU:N	13:N:51:PRO:CD	2.75	0.47
1:A:782:A:H4'	1:A:1514:G:O2'	2.15	0.47
1:A:619:U:H3	3:D:130:ASN:HD21	1.57	0.47
12:M:89:ARG:CB	12:M:96:VAL:HG22	2.45	0.47
19:T:74:HIS:O	19:T:78:LEU:HG	2.15	0.47
10:K:117:HIS:O	10:K:118:ASN:HB2	2.14	0.47
20:B:145:ASN:HD22	20:B:145:ASN:HA	1.55	0.47
5:F:3:HIS:NE2	5:F:95:ALA:HB2	2.30	0.46
13:N:63:CYS:CB	13:N:68:ARG:H	2.21	0.46
15:P:67:ILE:HG13	15:P:71:VAL:CG1	2.40	0.46
6:G:11:ILE:HG22	6:G:12:LEU:N	2.30	0.46
9:J:66:GLU:O	13:N:95:LEU:HA	2.15	0.46
1:A:523:A:N1	11:L:88:ASP:HB2	2.30	0.46
20:B:206:ILE:HG22	20:B:207:ARG:NH2	2.26	0.46
10:K:69:CYS:C	10:K:73:VAL:HG22	2.36	0.46
3:D:61:ARG:HE	3:D:68:GLU:CA	2.28	0.46
1:A:1461:G:O2'	1:A:1462:C:H5'	2.15	0.46
5:F:8:PHE:HE1	5:F:21:MET:HE1	1.79	0.46
12:M:56:ARG:HH11	12:M:56:ARG:HG3	1.80	0.46
3:D:94:GLU:HG2	3:D:190:LEU:HD21	1.97	0.46
19:T:67:HIS:CG	19:T:68:LYS:H	2.33	0.46
14:O:32:THR:HG23	14:O:62:ARG:NH1	2.30	0.46
10:K:16:SER:OG	10:K:79:LYS:HB2	2.14	0.46
18:S:56:HIS:CD2	18:S:56:HIS:N	2.83	0.46
4:E:95:MET:HG3	4:E:124:ALA:CB	2.45	0.46
1:A:538:G:P	11:L:111:GLN:HB2	2.55	0.46
1:A:599:C:H4'	7:H:121:GLY:C	2.36	0.46
1:A:182:A:H1'	1:A:183:C:H5	1.80	0.46
1:A:325:A:H2'	1:A:326:G:O4'	2.16	0.46
20:B:89:PHE:HB3	20:B:149:GLY:O	2.15	0.46
1:A:1453:G:H2'	1:A:1454:G:O4'	2.16	0.46
1:A:742:G:O2'	1:A:743:A:H5'	2.16	0.46
1:A:114:U:H2'	1:A:115:G:C8	2.51	0.46
1:A:1028:C:H2'	1:A:1029:U:C6	2.50	0.46
9:J:37:ARG:C	9:J:37:ARG:NE	2.69	0.46
4:E:89:THR:HG22	4:E:91:SER:N	2.22	0.46
18:S:18:VAL:HG22	18:S:42:ASN:ND2	2.31	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
16:Q:64:ARG:CB	16:Q:64:ARG:HH11	2.27	0.46
12:M:79:LEU:HD12	12:M:80:MET:N	2.30	0.46
1:A:1281:C:H5'	1:A:1282:C:C5	2.46	0.46
1:A:1118:U:O2'	1:A:1119:C:H5'	2.15	0.46
2:C:127:VAL:HB	2:C:128:MET:CE	2.46	0.46
3:D:105:GLY:HA3	3:D:158:LEU:HD23	1.98	0.46
1:A:627:G:H2'	1:A:628:G:C8	2.50	0.46
3:D:44:LYS:O	3:D:44:LYS:HD3	2.15	0.46
7:H:17:GLN:HG3	7:H:71:VAL:CG2	2.44	0.46
1:A:138:G:O2'	1:A:139:A:H5'	2.14	0.46
1:A:956:U:H2'	1:A:957:U:C6	2.50	0.46
6:G:49:LEU:C	6:G:51:GLN:H	2.17	0.46
20:B:14:HIS:CG	20:B:15:PHE:N	2.81	0.46
9:J:57:VAL:HG13	9:J:58:ASN:N	2.31	0.46
13:N:31:SER:O	13:N:40:ARG:HD3	2.15	0.46
1:A:719:C:O2'	17:R:37:LYS:HG3	2.16	0.46
8:I:29:ILE:HG23	8:I:29:ILE:O	2.16	0.46
1:A:1021:A:H2'	1:A:1022:A:C1'	2.45	0.46
2:C:85:LYS:O	2:C:89:VAL:HG13	2.15	0.46
1:A:1375:A:H2'	1:A:1376:U:C6	2.50	0.46
1:A:636:U:H2'	1:A:637:C:H6	1.80	0.46
1:A:1483:A:H2'	1:A:1484:C:O4'	2.16	0.46
1:A:608:A:H2'	1:A:609:A:O4'	2.15	0.46
16:Q:57:VAL:HB	16:Q:79:GLU:HB2	1.98	0.46
1:A:434:U:O2	1:A:434:U:H2'	2.15	0.46
12:M:53:ASP:HA	12:M:56:ARG:HH21	1.81	0.46
1:A:1329:A:H5''	12:M:25:GLY:N	2.30	0.46
14:O:83:ARG:C	14:O:84:LEU:HD12	2.35	0.46
15:P:28:ARG:HD3	15:P:29:ASN:OD1	2.16	0.46
4:E:40:ASP:CG	4:E:44:ARG:HB2	2.36	0.46
11:L:110:LYS:O	11:L:113:ARG:HG3	2.15	0.46
11:L:34:THR:CB	11:L:53:ARG:HB3	2.46	0.46
11:L:75:GLU:OE2	11:L:76:HIS:N	2.48	0.46
6:G:63:VAL:CG1	6:G:126:ALA:HB1	2.45	0.46
20:B:148:GLY:C	20:B:150:ILE:H	2.19	0.46
16:Q:82:VAL:O	16:Q:83:LEU:HD13	2.15	0.46
7:H:17:GLN:HE21	7:H:71:VAL:HG22	1.81	0.46
1:A:552:U:H2'	1:A:553:A:C8	2.51	0.46
12:M:3:ILE:O	12:M:56:ARG:HD3	2.15	0.46
8:I:56:MET:O	8:I:58:GLU:HG2	2.15	0.46
3:D:93:LEU:HA	3:D:96:ARG:HG3	1.98	0.46
1:A:1312:G:O6	18:S:1:PRO:HA	2.15	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1271:A:H5'	1:A:1314:C:OP1	2.15	0.46
13:N:9:GLU:OE2	13:N:60:ARG:HB3	2.15	0.46
4:E:109:ALA:HB3	4:E:135:VAL:HG11	1.96	0.46
1:A:1302:C:H4'	1:A:1303:C:OP1	2.14	0.46
1:A:1030:U:H4'	1:A:1031:C:OP2	2.16	0.46
6:G:55:LYS:HG3	6:G:56:SER:H	1.81	0.46
1:A:1275:A:H2'	1:A:1276:G:O4'	2.16	0.46
1:A:538:G:H2'	1:A:539:A:C8	2.51	0.46
5:F:18:VAL:N	5:F:19:PRO:HD2	2.30	0.46
1:A:1039:G:H2'	1:A:1040:U:C6	2.51	0.46
12:M:95:PRO:HD3	12:M:108:ARG:HG2	1.96	0.46
13:N:21:ALA:N	13:N:24:ALA:HB2	2.30	0.46
8:I:48:ARG:HA	8:I:51:LEU:HD12	1.97	0.46
6:G:24:LYS:HA	6:G:27:ASN:HD22	1.81	0.46
11:L:100:ALA:O	11:L:101:LEU:C	2.54	0.46
2:C:61:LYS:O	2:C:96:VAL:HB	2.15	0.46
4:E:67:ARG:NH1	4:E:67:ARG:HB2	2.30	0.46
1:A:659:U:H2'	1:A:660:C:C6	2.51	0.46
13:N:30:ILE:HB	13:N:44:VAL:CG2	2.46	0.46
6:G:24:LYS:O	6:G:28:ILE:HG12	2.16	0.46
1:A:1295:U:H2'	1:A:1296:C:O4'	2.16	0.46
11:L:79:ILE:C	11:L:101:LEU:HD12	2.36	0.46
2:C:166:TRP:HE1	2:C:168:ARG:CB	2.25	0.46
11:L:111:GLN:HB3	11:L:112:ALA:H	1.64	0.46
1:A:212:G:H2'	1:A:213:G:C8	2.46	0.46
6:G:98:LEU:HA	6:G:101:ARG:HB3	1.98	0.46
2:C:58:ARG:HA	2:C:63:ILE:HA	1.97	0.46
1:A:1057:G:H5''	2:C:153:SER:HB2	1.97	0.46
1:A:299:G:H2'	1:A:300:A:C8	2.50	0.46
1:A:649:A:H2'	1:A:650:G:O4'	2.15	0.46
20:B:209:VAL:HG23	20:B:210:THR:H	1.81	0.46
21:U:17:ARG:CD	21:U:17:ARG:H	2.19	0.46
7:H:104:SER:O	7:H:122:GLY:HA3	2.15	0.46
1:A:1367:C:H5''	8:I:115:VAL:CG2	2.39	0.46
8:I:115:VAL:HG21	9:J:62:ARG:HG3	1.98	0.46
3:D:18:LEU:HD11	3:D:59:LYS:HG3	1.97	0.46
3:D:96:ARG:O	3:D:99:ASN:HB3	2.16	0.46
4:E:111:ARG:HG2	4:E:111:ARG:HH11	1.80	0.46
8:I:87:MET:HB2	8:I:94:ARG:HH21	1.80	0.46
1:A:1095:U:H2'	1:A:1096:C:H6	1.81	0.46
2:C:129:PHE:CD2	2:C:129:PHE:C	2.89	0.46
6:G:144:ALA:O	6:G:146:ALA:N	2.46	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:D:75:TYR:HA	3:D:89:LEU:HD13	1.98	0.46
12:M:63:VAL:O	12:M:68:LEU:HD12	2.16	0.46
1:A:1119:C:H2'	1:A:1120:C:C6	2.51	0.46
15:P:44:SER:C	15:P:46:LYS:N	2.68	0.46
21:U:8:ASN:HB2	21:U:9:GLU:OE2	2.15	0.46
1:A:327:A:H1'	1:A:329:A:O4'	2.15	0.46
1:A:1328:C:H5''	12:M:27:THR:HG21	1.97	0.46
18:S:50:VAL:HG21	18:S:70:LEU:HG	1.98	0.46
1:A:975:A:C2'	1:A:976:G:OP2	2.64	0.46
19:T:66:ILE:HG23	19:T:70:LYS:CG	2.46	0.46
8:I:112:ARG:O	8:I:114:LYS:HD2	2.16	0.46
15:P:21:VAL:O	15:P:33:ILE:HB	2.15	0.46
1:A:864:A:H2'	1:A:865:A:C8	2.51	0.46
1:A:1080:A:C4'	4:E:20:VAL:HG21	2.44	0.46
2:C:120:THR:OG1	2:C:197:VAL:HG21	2.16	0.46
18:S:8:PRO:O	18:S:9:PHE:HB2	2.14	0.46
6:G:129:ASN:HB3	6:G:134:VAL:HG21	1.97	0.46
1:A:26:A:N6	1:A:558:G:H1'	2.30	0.46
11:L:85:ARG:HA	11:L:93:ARG:HA	1.98	0.46
1:A:462:G:H3'	1:A:463:U:H5''	1.96	0.46
1:A:230:G:O2'	1:A:231:U:H5'	2.16	0.46
2:C:15:LYS:NZ	2:C:16:PRO:HD2	2.30	0.46
1:A:1200:C:C4'	1:A:1201:A:H5'	2.46	0.46
14:O:49:HIS:O	14:O:52:ARG:HB3	2.16	0.46
5:F:59:TYR:N	5:F:59:TYR:CD1	2.85	0.45
1:A:8:A:C5	3:D:205:LYS:HA	2.51	0.45
20:B:101:THR:HG22	20:B:174:GLU:CD	2.36	0.45
1:A:815:A:N6	1:A:1509:C:H1'	2.29	0.45
6:G:65:LEU:CD2	6:G:69:ARG:HH21	2.29	0.45
7:H:82:LEU:HD21	11:L:3:VAL:HG21	1.97	0.45
6:G:125:ASP:O	6:G:129:ASN:ND2	2.49	0.45
2:C:128:MET:SD	2:C:132:ALA:N	2.89	0.45
1:A:432:A:C2'	1:A:433:G:H5'	2.46	0.45
8:I:56:MET:C	8:I:58:GLU:H	2.19	0.45
9:J:67:ILE:O	9:J:67:ILE:HG23	2.16	0.45
5:F:11:HIS:NE2	5:F:13:ASP:HB3	2.31	0.45
1:A:839:C:O2'	1:A:840:C:H5'	2.17	0.45
1:A:1387:G:H2'	1:A:1388:C:H6	1.81	0.45
2:C:113:LYS:HA	2:C:184:ASN:ND2	2.32	0.45
2:C:72:PRO:HB2	2:C:76:ILE:HG12	1.98	0.45
1:A:397:A:H5'	1:A:398:U:OP1	2.16	0.45
1:A:251:G:H4'	1:A:252:U:C5'	2.47	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:321:A:O2'	1:A:322:C:H5'	2.16	0.45
2:C:189:HIS:CD2	2:C:194:VAL:HG22	2.52	0.45
1:A:734:G:H2'	1:A:735:C:C6	2.51	0.45
7:H:29:SER:O	7:H:30:LYS:C	2.54	0.45
19:T:36:ALA:O	19:T:40:ALA:N	2.50	0.45
11:L:68:GLY:HA3	11:L:106:VAL:CG2	2.33	0.45
1:A:234:C:H2'	1:A:235:C:C6	2.52	0.45
5:F:47:LEU:HD22	17:R:65:SER:OG	2.15	0.45
18:S:26:ASP:OD2	18:S:46:LEU:HA	2.15	0.45
9:J:11:LYS:HE3	9:J:99:GLN:NE2	2.31	0.45
8:I:17:ARG:O	8:I:65:THR:N	2.50	0.45
4:E:17:VAL:O	4:E:17:VAL:HG22	2.17	0.45
20:B:69:VAL:HB	20:B:162:VAL:CB	2.46	0.45
20:B:130:LYS:N	20:B:130:LYS:HE2	2.32	0.45
20:B:86:CYS:SG	20:B:87:ASP:N	2.89	0.45
2:C:51:VAL:HB	2:C:68:HIS:O	2.16	0.45
1:A:1280:A:O4'	9:J:43:PRO:HG3	2.16	0.45
12:M:95:PRO:CD	12:M:108:ARG:HG2	2.46	0.45
15:P:74:LEU:O	15:P:78:VAL:HG12	2.16	0.45
1:A:1427:C:O2'	1:A:1428:A:H5'	2.16	0.45
1:A:1260:G:HO2'	1:A:1261:A:H8	1.59	0.45
10:K:14:GLN:HA	10:K:77:GLY:HA3	1.97	0.45
20:B:209:VAL:HG23	20:B:210:THR:N	2.32	0.45
1:A:674:G:H2'	1:A:675:A:C8	2.52	0.45
10:K:121:ARG:NE	21:U:34:ARG:HD2	2.31	0.45
1:A:1219:A:H2'	1:A:1220:G:H8	1.81	0.45
8:I:6:TYR:OH	8:I:8:THR:HG22	2.17	0.45
1:A:1238:A:H2	1:A:1241:G:N3	2.12	0.45
1:A:1388:C:H2'	1:A:1389:C:H6	1.81	0.45
19:T:73:ARG:HG3	19:T:74:HIS:H	1.79	0.45
1:A:1499:A:O2'	1:A:1500:A:H5'	2.16	0.45
2:C:83:VAL:HA	2:C:86:LEU:CD1	2.46	0.45
20:B:96:LEU:HB2	20:B:99:MET:HG3	1.97	0.45
1:A:1382:C:H2'	1:A:1383:C:H6	1.81	0.45
1:A:1358:U:OP2	13:N:74:ARG:HG3	2.17	0.45
1:A:1287:A:H2'	1:A:1288:A:H8	1.81	0.45
9:J:8:ILE:HG22	9:J:100:ILE:HG22	1.98	0.45
4:E:17:VAL:HA	4:E:33:THR:O	2.16	0.45
1:A:560:A:H5'	1:A:566:G:N2	2.32	0.45
1:A:1143:G:O2'	1:A:1144:G:H5'	2.17	0.45
3:D:25:ARG:HH11	3:D:25:ARG:CB	2.29	0.45
1:A:627:G:H2'	1:A:628:G:H8	1.82	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:903:G:H2'	1:A:904:U:H6	1.80	0.45
8:I:71:ILE:HG13	8:I:71:ILE:H	1.64	0.45
10:K:110:THR:HG22	21:U:4:LYS:HA	1.99	0.45
1:A:1330:U:H2'	1:A:1331:G:O4'	2.16	0.45
12:M:106:ARG:HH12	12:M:109:LYS:HD2	1.80	0.45
1:A:672:U:H2'	1:A:673:A:H8	1.79	0.45
20:B:101:THR:HG23	20:B:102:ASN:N	2.31	0.45
20:B:156:LEU:HG	20:B:157:PRO:HD2	1.99	0.45
20:B:95:TRP:HZ2	20:B:100:LEU:HD13	1.80	0.45
1:A:1131:G:H2'	1:A:1132:C:H5'	1.97	0.45
1:A:619:U:H3	3:D:130:ASN:HD22	1.62	0.45
3:D:117:VAL:HG12	3:D:130:ASN:CA	2.46	0.45
15:P:40:ASN:HD21	15:P:42:ILE:CG1	2.28	0.45
16:Q:60:ILE:HB	16:Q:73:THR:O	2.16	0.45
17:R:20:ILE:HG23	17:R:20:ILE:O	2.17	0.45
1:A:1036:A:H2'	1:A:1037:C:O4'	2.16	0.45
1:A:22:G:H2'	1:A:23:C:H6	1.82	0.45
17:R:28:LEU:C	17:R:30:ASN:N	2.70	0.45
21:U:3:ILE:HD11	21:U:19:LYS:HD3	1.98	0.45
5:F:29:ILE:HG21	5:F:64:VAL:CG1	2.42	0.45
14:O:70:LYS:HB2	14:O:77:TYR:CG	2.51	0.45
20:B:102:ASN:HD21	20:B:105:THR:HB	1.82	0.45
8:I:122:ARG:HG2	8:I:122:ARG:HH11	1.81	0.45
1:A:767:A:H2'	1:A:768:A:C8	2.52	0.45
1:A:923:A:O2'	1:A:924:C:H5'	2.16	0.45
18:S:14:LEU:HD12	18:S:15:LEU:H	1.80	0.45
18:S:30:LEU:O	18:S:49:ALA:HB3	2.17	0.45
1:A:99:C:H2'	23:A:1855:HOH:O	2.16	0.45
1:A:402:G:H2'	1:A:403:C:H6	1.81	0.45
1:A:22:G:H2'	1:A:23:C:C6	2.52	0.45
6:G:74:VAL:HG21	6:G:143:MET:HG2	1.99	0.45
1:A:666:G:H5'	1:A:726:C:H1'	1.98	0.45
2:C:29:ALA:HB2	13:N:75:LYS:O	2.17	0.45
1:A:232:G:H2'	1:A:233:C:O4'	2.16	0.45
1:A:255:G:H5'	16:Q:17:GLU:O	2.17	0.45
21:U:33:ARG:HB3	21:U:34:ARG:H	1.60	0.45
4:E:108:GLY:O	4:E:111:ARG:HB3	2.16	0.45
15:P:28:ARG:C	15:P:30:GLY:H	2.20	0.45
1:A:1135:U:H4'	1:A:1136:C:OP1	2.16	0.45
6:G:113:LYS:HA	6:G:113:LYS:HE2	1.98	0.45
9:J:15:HIS:O	9:J:18:ILE:HG22	2.16	0.45
2:C:143:LEU:HD22	2:C:143:LEU:H	1.80	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:426:U:H2'	1:A:427:U:C6	2.52	0.45
1:A:5:U:H1'	1:A:6:G:C2	2.52	0.45
1:A:1503:A:C8	1:A:1531:A:H1'	2.51	0.45
1:A:687:A:C2	1:A:704:A:C5	3.05	0.45
1:A:1528:U:H2'	21:U:46:ARG:HH22	1.81	0.45
4:E:45:VAL:O	4:E:71:ILE:HG22	2.17	0.45
1:A:619:U:O2	3:D:129:VAL:HG13	2.17	0.45
8:I:8:THR:OG1	8:I:9:GLY:N	2.50	0.45
4:E:156:ARG:HH22	7:H:100:ILE:HG23	1.82	0.45
19:T:73:ARG:O	19:T:74:HIS:C	2.54	0.45
16:Q:7:LEU:HD23	16:Q:7:LEU:N	2.32	0.45
12:M:102:LYS:HE3	12:M:103:THR:HG23	1.98	0.45
6:G:91:ARG:CB	6:G:92:PRO:HD2	2.47	0.45
4:E:24:VAL:HG22	4:E:29:ILE:HD11	1.99	0.45
1:A:902:G:H2'	1:A:903:G:H8	1.82	0.45
1:A:1414:U:O2'	1:A:1415:G:H5'	2.17	0.45
1:A:155:A:H2'	1:A:156:C:O4'	2.16	0.45
1:A:1522:U:O2'	1:A:1523:G:H5'	2.17	0.45
1:A:255:G:H2'	1:A:256:U:H6	1.81	0.45
14:O:69:LEU:HD12	14:O:77:TYR:N	2.32	0.45
18:S:21:ALA:HA	18:S:24:SER:OG	2.17	0.45
9:J:7:ARG:O	9:J:100:ILE:HA	2.17	0.45
13:N:50:LEU:CD1	13:N:51:PRO:HD3	2.46	0.45
8:I:49:GLN:O	8:I:53:LEU:HD23	2.17	0.45
1:A:1275:A:H2'	1:A:1276:G:C8	2.51	0.45
2:C:52:SER:O	2:C:53:ARG:HG3	2.17	0.45
1:A:123:U:OP1	1:A:312:C:H5'	2.17	0.45
1:A:598:U:H2'	1:A:599:C:C6	2.51	0.45
2:C:51:VAL:HG11	2:C:67:ILE:HD11	1.99	0.45
16:Q:32:ILE:O	16:Q:32:ILE:HG12	2.17	0.45
1:A:554:A:H2'	1:A:555:U:C6	2.52	0.45
1:A:591:U:H2'	1:A:592:G:H8	1.81	0.45
6:G:95:ARG:O	6:G:99:ALA:HB2	2.16	0.45
1:A:1297:G:H4'	1:A:1298:U:H5'	1.98	0.45
1:A:175:C:H2'	1:A:176:C:H6	1.81	0.45
1:A:147:G:H2'	1:A:148:G:C8	2.52	0.45
10:K:59:PRO:HA	10:K:91:GLY:N	2.32	0.45
9:J:46:LYS:HA	9:J:68:ARG:HA	1.99	0.45
1:A:1382:C:H2'	1:A:1383:C:C6	2.52	0.45
15:P:48:GLU:HG2	15:P:49:GLY:N	2.32	0.45
1:A:382:A:H2'	1:A:383:A:C8	2.51	0.45
20:B:61:SER:HG	20:B:62:ARG:HH11	1.64	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:F:25:TYR:O	5:F:29:ILE:HG13	2.18	0.44
1:A:374:A:H2'	1:A:375:U:C6	2.52	0.44
14:O:80:LEU:O	14:O:84:LEU:HD13	2.17	0.44
9:J:7:ARG:HD2	9:J:101:SER:OG	2.17	0.44
4:E:146:MET:N	4:E:146:MET:SD	2.90	0.44
11:L:73:LEU:HA	11:L:77:SER:OG	2.17	0.44
1:A:90:C:H2'	1:A:91:U:H6	1.81	0.44
2:C:53:ARG:HA	2:C:113:LYS:CE	2.46	0.44
2:C:54:ILE:HB	2:C:67:ILE:CD1	2.47	0.44
1:A:84:U:O2'	1:A:86:G:N2	2.50	0.44
3:D:30:LYS:HD3	3:D:30:LYS:N	2.31	0.44
3:D:53:GLN:HB3	3:D:202:LEU:HB2	1.99	0.44
1:A:1405:G:O2'	1:A:1406:U:H5'	2.17	0.44
3:D:44:LYS:HZ2	3:D:45:PRO:C	2.21	0.44
1:A:778:G:O2'	1:A:779:C:H5'	2.17	0.44
19:T:63:LYS:HD3	19:T:63:LYS:O	2.17	0.44
10:K:80:ASN:OD1	10:K:80:ASN:N	2.50	0.44
12:M:56:ARG:CZ	12:M:56:ARG:HB2	2.47	0.44
1:A:1271:A:H2'	1:A:1272:G:H8	1.81	0.44
13:N:53:ASP:HA	13:N:58:ARG:HD2	2.00	0.44
5:F:12:PRO:HD3	5:F:56:LYS:O	2.17	0.44
12:M:96:VAL:C	12:M:98:GLY:H	2.20	0.44
9:J:33:GLY:O	9:J:34:ALA:HB2	2.16	0.44
20:B:69:VAL:O	20:B:162:VAL:HA	2.17	0.44
1:A:25:C:H2'	1:A:26:A:C8	2.52	0.44
9:J:82:LYS:HD2	9:J:82:LYS:N	2.31	0.44
3:D:28:ASP:HB3	3:D:33:ILE:HB	2.00	0.44
1:A:448:A:H2'	1:A:449:G:C8	2.52	0.44
1:A:844:G:H2'	1:A:845:A:H5''	1.99	0.44
1:A:735:C:OP1	17:R:56:ARG:CZ	2.65	0.44
19:T:20:ASN:O	19:T:24:ARG:HB2	2.18	0.44
1:A:1187:G:H2'	1:A:1188:A:O4'	2.17	0.44
1:A:834:U:H2'	1:A:835:U:C6	2.52	0.44
19:T:43:LYS:HB3	19:T:86:ALA:HB3	2.00	0.44
1:A:489:C:H2'	1:A:490:C:C6	2.52	0.44
1:A:71:A:O2'	1:A:72:A:H5''	2.17	0.44
10:K:113:THR:HG21	21:U:28:LEU:CD1	2.32	0.44
1:A:1308:U:OP2	12:M:97:ARG:HD3	2.17	0.44
1:A:1343:G:H4'	8:I:123:ARG:O	2.18	0.44
18:S:43:MET:O	18:S:61:VAL:HB	2.17	0.44
4:E:87:VAL:O	4:E:88:HIS:HB3	2.18	0.44
12:M:80:MET:HA	12:M:87:GLY:CA	2.48	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:412:A:H1'	1:A:413:G:C8	2.43	0.44
1:A:471:U:H2'	1:A:472:U:C6	2.51	0.44
14:O:65:LEU:O	14:O:68:TYR:HB3	2.18	0.44
1:A:86:G:O2'	1:A:87:C:P	2.75	0.44
1:A:392:C:H2'	1:A:393:A:H8	1.82	0.44
1:A:828:U:H2'	1:A:829:G:O5'	2.18	0.44
2:C:123:LEU:HD23	2:C:195:ILE:HD12	1.98	0.44
17:R:52:ARG:O	17:R:56:ARG:HG3	2.17	0.44
3:D:6:PRO:HG2	3:D:9:LYS:HE2	2.00	0.44
1:A:1250:A:H2'	1:A:1251:A:H8	1.81	0.44
16:Q:10:ARG:HH22	16:Q:54:ILE:HA	1.82	0.44
1:A:1525:G:O2'	1:A:1526:G:H5'	2.17	0.44
9:J:59:LYS:C	9:J:61:ALA:H	2.20	0.44
3:D:121:ALA:C	3:D:145:ARG:HG3	2.38	0.44
1:A:677:U:H2'	1:A:678:U:H6	1.82	0.44
1:A:491:G:H2'	1:A:492:C:C6	2.52	0.44
3:D:33:ILE:O	3:D:34:GLU:C	2.55	0.44
4:E:32:PHE:CE2	4:E:55:VAL:HG22	2.53	0.44
1:A:691:G:H2'	1:A:692:U:C6	2.53	0.44
1:A:992:U:H1'	1:A:993:G:C2	2.52	0.44
1:A:386:C:C2'	1:A:387:U:H5'	2.47	0.44
1:A:975:A:H4'	1:A:975:A:OP2	2.18	0.44
20:B:31:PHE:N	20:B:41:ASN:HB2	2.32	0.44
1:A:1329:A:O2'	1:A:1330:U:H5'	2.18	0.44
9:J:55:PRO:O	9:J:56:HIS:HB3	2.16	0.44
1:A:673:A:H1'	17:R:63:TYR:HE1	1.81	0.44
6:G:107:ALA:O	6:G:118:ARG:HD2	2.18	0.44
1:A:502:A:OP1	11:L:114:SER:HB2	2.17	0.44
1:A:473:U:C2	1:A:474:G:N7	2.86	0.44
1:A:875:U:O2'	7:H:14:ARG:HD2	2.18	0.44
1:A:677:U:H2'	1:A:678:U:C6	2.53	0.44
2:C:33:ASP:OD1	2:C:37:LYS:HE2	2.17	0.44
20:B:104:LYS:NZ	20:B:104:LYS:HB2	2.33	0.44
2:C:107:LYS:O	2:C:110:LEU:HD23	2.18	0.44
1:A:1162:C:H2'	1:A:1163:A:C8	2.51	0.44
20:B:35:ASN:O	20:B:36:LYS:HB2	2.18	0.44
8:I:109:GLN:HE21	8:I:109:GLN:HB3	1.57	0.44
1:A:233:C:O2'	1:A:234:C:H5'	2.18	0.44
1:A:1102:A:O2'	1:A:1103:C:H5'	2.18	0.44
1:A:768:A:H5'	1:A:1524:C:H1'	1.99	0.44
4:E:87:VAL:CG2	4:E:88:HIS:H	2.23	0.44
11:L:97:VAL:HG23	11:L:97:VAL:O	2.17	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
19:T:27:MET:O	19:T:31:ILE:HG13	2.17	0.44
13:N:62:ARG:N	13:N:72:PHE:CZ	2.82	0.44
4:E:95:MET:HA	4:E:124:ALA:CB	2.44	0.44
16:Q:35:LYS:O	16:Q:35:LYS:HG3	2.17	0.44
1:A:119:A:H4'	1:A:120:A:O4'	2.18	0.44
18:S:62:THR:OG1	18:S:63:ASP:N	2.48	0.44
1:A:737:C:H5'	5:F:89:VAL:O	2.18	0.44
1:A:488:C:H2'	1:A:489:C:H6	1.83	0.44
1:A:705:G:N2	10:K:43:TRP:CE3	2.85	0.44
1:A:682:G:O2'	1:A:683:G:H5'	2.18	0.44
1:A:1308:U:H2'	1:A:1309:G:H8	1.82	0.44
1:A:1342:C:H4'	8:I:126:PHE:O	2.18	0.44
6:G:12:LEU:HD13	6:G:13:PRO:CD	2.47	0.44
13:N:52:ARG:O	13:N:58:ARG:HD2	2.18	0.44
15:P:28:ARG:N	15:P:28:ARG:HD2	2.33	0.44
1:A:812:G:OP1	1:A:812:G:H4'	2.17	0.44
11:L:65:TYR:HB3	11:L:95:HIS:HD2	1.82	0.44
4:E:17:VAL:O	4:E:17:VAL:HG13	2.17	0.44
10:K:70:ALA:O	10:K:72:ALA:N	2.50	0.44
3:D:171:GLU:HG3	3:D:182:LYS:CD	2.46	0.44
16:Q:58:VAL:HB	16:Q:74:LEU:CD2	2.48	0.44
14:O:31:LEU:HA	14:O:34:GLN:OE1	2.17	0.44
1:A:963:G:H2'	1:A:964:A:C8	2.51	0.44
1:A:143:A:H2	1:A:220:G:H22	1.64	0.44
1:A:284:C:H2'	1:A:285:C:H6	1.82	0.44
1:A:965:U:OP1	1:A:1198:G:H5''	2.18	0.44
1:A:1432:G:H8	1:A:1432:G:OP2	2.00	0.44
20:B:119:GLN:O	20:B:125:PHE:HB3	2.18	0.44
1:A:861:G:O2'	1:A:862:C:H5'	2.17	0.44
3:D:66:VAL:HG22	3:D:71:PHE:HB2	2.00	0.44
1:A:397:A:N3	1:A:397:A:H3'	2.33	0.44
4:E:28:ARG:NH2	4:E:30:PHE:HB3	2.33	0.44
1:A:1216:A:OP1	13:N:4:SER:HB3	2.18	0.44
1:A:1414:U:H2'	1:A:1415:G:C8	2.53	0.44
1:A:250:A:H1'	1:A:252:U:C5	2.53	0.44
6:G:49:LEU:HA	6:G:52:ARG:HG3	1.99	0.44
6:G:78:ARG:HD2	6:G:81:GLY:H	1.83	0.44
3:D:77:GLU:C	3:D:79:ALA:H	2.20	0.44
1:A:771:G:H2'	1:A:772:U:C6	2.52	0.44
1:A:295:C:H2'	1:A:296:U:C6	2.53	0.44
11:L:17:LYS:NZ	11:L:17:LYS:HB2	2.33	0.44
1:A:950:U:H2'	1:A:951:G:H8	1.83	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
19:T:66:ILE:HG23	19:T:70:LYS:HG3	2.00	0.44
1:A:921:U:H2'	1:A:922:G:O4'	2.17	0.44
2:C:32:LEU:O	2:C:35:ASP:HB3	2.18	0.44
12:M:17:ALA:O	12:M:20:SER:HB2	2.18	0.44
7:H:31:LEU:O	7:H:35:ILE:HG13	2.17	0.44
3:D:81:LEU:HB2	3:D:88:ASN:ND2	2.33	0.44
1:A:373:A:H1'	1:A:481:G:H1'	1.99	0.44
14:O:88:ARG:HG3	14:O:88:ARG:NH1	2.32	0.44
1:A:614:C:OP1	3:D:82:LYS:HE3	2.18	0.44
1:A:1493:A:C2'	1:A:1494:G:OP2	2.65	0.44
1:A:113:G:O4'	1:A:354:G:H4'	2.18	0.44
1:A:1049:U:H1'	1:A:1201:A:N7	2.33	0.44
14:O:67:ASP:O	14:O:71:ARG:HB2	2.17	0.44
1:A:706:A:H2	10:K:40:ALA:HB2	1.83	0.44
1:A:442:G:H2'	1:A:443:C:C6	2.53	0.44
13:N:56:PRO:HG2	13:N:57:SER:H	1.83	0.44
13:N:13:VAL:HG22	13:N:59:GLN:CD	2.38	0.44
20:B:78:ALA:CB	20:B:213:LEU:HD13	2.47	0.43
5:F:3:HIS:CE1	5:F:95:ALA:HB2	2.53	0.43
12:M:3:ILE:HA	12:M:56:ARG:NH1	2.32	0.43
1:A:1307:U:H2'	1:A:1308:U:O4'	2.18	0.43
8:I:35:GLU:O	8:I:39:GLY:HA2	2.18	0.43
20:B:33:ALA:HA	20:B:39:ILE:HG12	2.00	0.43
1:A:1319:A:P	18:S:4:LEU:HD11	2.58	0.43
16:Q:66:LEU:O	16:Q:67:SER:HB2	2.18	0.43
10:K:60:PHE:CE1	10:K:64:VAL:HG11	2.52	0.43
4:E:148:SER:HB2	4:E:149:PRO:HD2	2.00	0.43
1:A:336:A:O2'	1:A:337:G:H5'	2.18	0.43
18:S:44:ILE:HG23	18:S:62:THR:O	2.18	0.43
9:J:68:ARG:HD3	9:J:70:HIS:NE2	2.34	0.43
1:A:777:A:H2'	1:A:778:G:C8	2.52	0.43
1:A:29:U:H5'	1:A:296:U:OP1	2.18	0.43
8:I:11:ARG:HD2	8:I:12:LYS:HG3	2.00	0.43
13:N:45:LEU:O	13:N:48:GLN:HG3	2.18	0.43
18:S:66:VAL:HG23	18:S:67:GLY:H	1.82	0.43
1:A:1294:G:H2'	1:A:1295:U:C6	2.53	0.43
18:S:18:VAL:HG13	18:S:42:ASN:ND2	2.34	0.43
1:A:1512:U:H2'	1:A:1513:A:C8	2.54	0.43
1:A:818:G:C3'	1:A:819:A:H5''	2.47	0.43
1:A:538:G:H2'	1:A:539:A:H8	1.83	0.43
2:C:42:LEU:O	2:C:46:LEU:HG	2.18	0.43
15:P:13:LYS:O	15:P:15:PRO:HD3	2.17	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:B:104:LYS:HZ2	20:B:104:LYS:CB	2.31	0.43
1:A:607:A:H2'	1:A:608:A:H8	1.83	0.43
1:A:541:G:H2'	1:A:542:G:H8	1.82	0.43
1:A:644:U:O2'	1:A:645:G:H5'	2.18	0.43
1:A:1206:G:H2'	1:A:1207:G:O4'	2.18	0.43
13:N:76:PHE:O	13:N:78:LEU:HD13	2.18	0.43
5:F:92:THR:CG2	5:F:93:LYS:H	2.31	0.43
12:M:15:VAL:HG13	12:M:33:LEU:HD12	1.99	0.43
1:A:1366:C:H2'	1:A:1367:C:H6	1.83	0.43
5:F:85:ILE:HG22	5:F:86:ARG:N	2.32	0.43
18:S:35:ARG:HB2	18:S:71:GLY:CA	2.48	0.43
11:L:97:VAL:O	11:L:99:GLY:N	2.50	0.43
6:G:14:ASP:CB	6:G:19:SER:H	2.32	0.43
7:H:6:ILE:HD11	7:H:31:LEU:HD23	2.00	0.43
19:T:56:ILE:O	19:T:60:GLN:HG2	2.19	0.43
1:A:1142:G:H2'	1:A:1143:G:C8	2.52	0.43
20:B:202:ASN:ND2	20:B:203:ASP:N	2.64	0.43
8:I:33:SER:HB2	8:I:36:GLN:CG	2.48	0.43
1:A:746:A:H2'	1:A:747:A:H8	1.83	0.43
1:A:645:G:O2'	1:A:646:G:H5'	2.19	0.43
12:M:13:HIS:HA	12:M:43:LYS:HA	2.00	0.43
19:T:32:LYS:O	19:T:35:TYR:N	2.51	0.43
21:U:14:ALA:N	21:U:16:ARG:HH22	2.04	0.43
12:M:22:TYR:O	12:M:24:VAL:N	2.50	0.43
8:I:115:VAL:HG22	8:I:116:GLY:N	2.33	0.43
8:I:56:MET:HA	8:I:59:LYS:HB2	2.01	0.43
9:J:6:ILE:HD12	9:J:76:ILE:O	2.19	0.43
1:A:1526:G:H2'	1:A:1527:U:C6	2.53	0.43
15:P:6:LEU:CD1	15:P:71:VAL:HB	2.49	0.43
9:J:8:ILE:CG1	9:J:75:ASP:H	2.31	0.43
8:I:9:GLY:O	8:I:16:ALA:HB3	2.17	0.43
2:C:35:ASP:O	2:C:39:ARG:HG3	2.18	0.43
20:B:138:ARG:HA	20:B:141:GLU:CD	2.39	0.43
6:G:70:PRO:HD3	6:G:102:TRP:HZ3	1.83	0.43
11:L:14:LYS:HE2	11:L:16:ALA:CB	2.47	0.43
3:D:88:ASN:O	3:D:92:LEU:N	2.51	0.43
2:C:76:ILE:HA	2:C:83:VAL:CG2	2.49	0.43
1:A:796:C:O2'	1:A:797:C:H5'	2.17	0.43
1:A:394:G:H2'	1:A:395:C:H6	1.83	0.43
1:A:1420:U:O2'	1:A:1421:G:H5'	2.19	0.43
5:F:40:GLU:H	5:F:61:LEU:HB2	1.82	0.43
12:M:33:LEU:HB3	12:M:38:ILE:HB	1.99	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:948:C:OP1	12:M:105:ALA:HA	2.18	0.43
5:F:57:ALA:HB3	5:F:59:TYR:HE1	1.84	0.43
13:N:41:TRP:HD1	13:N:43:ALA:HB2	1.82	0.43
1:A:429:U:H4'	1:A:430:A:O5'	2.18	0.43
4:E:87:VAL:CG1	4:E:88:HIS:N	2.75	0.43
10:K:70:ALA:N	10:K:73:VAL:HG22	2.33	0.43
2:C:61:LYS:HE2	2:C:61:LYS:HB3	1.89	0.43
1:A:191:G:H2'	1:A:192:A:C8	2.53	0.43
1:A:24:U:O2'	1:A:25:C:H5'	2.18	0.43
19:T:21:ALA:O	19:T:25:SER:HB2	2.18	0.43
1:A:984:C:H2'	1:A:985:C:C6	2.54	0.43
1:A:415:A:N3	1:A:415:A:O4'	2.52	0.43
1:A:709:U:H2'	1:A:710:G:H8	1.84	0.43
1:A:1121:U:O2'	1:A:1122:U:H5'	2.18	0.43
10:K:35:ASP:N	10:K:41:LEU:HD11	2.34	0.43
1:A:11:G:H2'	1:A:12:U:C6	2.54	0.43
2:C:10:ARG:HH11	2:C:10:ARG:HG2	1.84	0.43
2:C:9:ILE:HG23	2:C:10:ARG:HG2	2.00	0.43
11:L:28:GLN:HE21	11:L:28:GLN:HB3	1.58	0.43
1:A:953:G:H3'	1:A:954:G:H8	1.83	0.43
1:A:1330:U:OP1	12:M:22:TYR:O	2.36	0.43
11:L:20:VAL:HA	11:L:94:TYR:HE2	1.83	0.43
4:E:104:ILE:HD13	4:E:104:ILE:C	2.38	0.43
7:H:74:ILE:O	7:H:74:ILE:HG23	2.18	0.43
1:A:643:C:H4'	7:H:31:LEU:HD22	2.00	0.43
1:A:91:U:H2'	1:A:92:U:C6	2.54	0.43
2:C:53:ARG:HA	2:C:113:LYS:HZ3	1.83	0.43
1:A:648:A:H2'	1:A:649:A:C8	2.54	0.43
1:A:484:G:H4'	1:A:485:U:H5'	2.00	0.43
1:A:1204:A:H2'	1:A:1205:U:C6	2.53	0.43
5:F:64:VAL:CG1	5:F:65:GLU:N	2.81	0.43
19:T:66:ILE:CA	19:T:70:LYS:HZ2	2.31	0.43
18:S:35:ARG:NH2	18:S:52:ASN:ND2	2.67	0.43
13:N:60:ARG:O	13:N:61:ASN:CB	2.62	0.43
8:I:46:VAL:O	8:I:49:GLN:HB2	2.19	0.43
1:A:813:U:O2'	1:A:814:A:H5'	2.19	0.43
10:K:69:CYS:O	10:K:73:VAL:N	2.51	0.43
6:G:14:ASP:HB3	6:G:18:GLY:H	1.79	0.43
1:A:1032:G:H2'	1:A:1033:G:C4'	2.49	0.43
12:M:63:VAL:HG12	12:M:68:LEU:HB2	2.01	0.43
1:A:1300:G:C2'	1:A:1301:U:OP2	2.67	0.43
1:A:177:G:O4'	1:A:177:G:N3	2.51	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:E:81:GLN:NE2	4:E:148:SER:HA	2.32	0.43
1:A:337:G:O2'	1:A:338:A:H5'	2.19	0.43
5:F:100:SER:N	17:R:23:LYS:NZ	2.66	0.43
1:A:93:U:H6	1:A:93:U:O5'	2.01	0.43
14:O:87:ARG:HA	14:O:87:ARG:NE	2.34	0.43
20:B:68:PHE:HA	20:B:161:PHE:O	2.19	0.43
19:T:44:ALA:O	19:T:48:LYS:HB3	2.18	0.43
1:A:463:U:H5'	1:A:464:U:OP2	2.18	0.43
10:K:81:LEU:HD22	10:K:104:PHE:CD1	2.54	0.43
8:I:91:GLU:CD	8:I:91:GLU:N	2.72	0.43
20:B:205:ALA:O	20:B:209:VAL:HG22	2.19	0.43
20:B:42:LEU:C	20:B:44:LYS:H	2.21	0.43
1:A:262:A:H5''	19:T:70:LYS:HD2	2.01	0.43
10:K:19:VAL:CG2	10:K:34:THR:HG22	2.36	0.43
16:Q:10:ARG:NE	16:Q:11:VAL:H	2.16	0.43
1:A:1125:U:OP1	9:J:37:ARG:NH1	2.52	0.43
9:J:65:TYR:CE1	13:N:84:ARG:HA	2.52	0.43
4:E:93:VAL:HG13	4:E:110:MET:SD	2.58	0.43
13:N:11:LYS:NZ	13:N:11:LYS:HA	2.34	0.43
5:F:12:PRO:HB3	5:F:56:LYS:O	2.19	0.43
8:I:80:HIS:HE1	8:I:103:VAL:O	2.01	0.43
2:C:129:PHE:O	2:C:133:MET:HG3	2.18	0.43
20:B:186:VAL:HG21	20:B:198:VAL:HG13	2.01	0.43
16:Q:35:LYS:O	16:Q:37:ILE:HG23	2.19	0.43
1:A:1151:A:O2'	1:A:1152:A:H8	2.02	0.43
1:A:902:G:H2'	1:A:903:G:C8	2.54	0.43
5:F:100:SER:H	17:R:23:LYS:HZ1	1.67	0.43
1:A:576:C:OP2	1:A:576:C:H3'	2.18	0.43
11:L:19:ASN:HB3	11:L:85:ARG:HD2	2.00	0.43
1:A:716:A:N3	10:K:118:ASN:O	2.51	0.43
1:A:178:C:O2'	1:A:179:A:H5'	2.19	0.43
1:A:367:U:OP1	1:A:395:C:H1'	2.19	0.43
1:A:394:G:H2'	1:A:395:C:C6	2.54	0.43
1:A:140:U:H2'	1:A:141:G:H8	1.84	0.43
18:S:10:ILE:HG22	18:S:37:SER:HB2	2.00	0.43
4:E:76:ASN:O	4:E:77:ASN:HB3	2.19	0.43
21:U:49:ALA:O	21:U:52:VAL:HG12	2.18	0.43
5:F:72:ASP:HA	5:F:75:GLU:HB3	2.00	0.43
21:U:14:ALA:N	21:U:16:ARG:NH2	2.54	0.43
8:I:27:ILE:HG21	8:I:34:LEU:HD13	2.00	0.43
13:N:42:ASN:CB	13:N:46:LYS:HE2	2.44	0.43
11:L:98:ARG:O	11:L:117:GLY:N	2.52	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:878:A:H2'	1:A:879:C:C6	2.54	0.43
10:K:60:PHE:CZ	10:K:64:VAL:HG11	2.54	0.43
1:A:1118:U:H6	1:A:1118:U:H5'	1.83	0.43
1:A:1190:G:P	2:C:4:VAL:HG12	2.58	0.43
1:A:384:G:H2'	1:A:385:C:H6	1.80	0.43
1:A:1427:C:H2'	1:A:1428:A:C8	2.53	0.43
1:A:231:U:P	15:P:31:ARG:HH12	2.41	0.43
15:P:43:ALA:C	15:P:45:GLU:H	2.21	0.43
1:A:144:G:H2'	1:A:145:G:O4'	2.19	0.43
21:U:4:LYS:O	21:U:5:VAL:HG23	2.18	0.43
5:F:38:ARG:NH2	5:F:63:ASN:ND2	2.67	0.43
1:A:661:G:O2'	1:A:662:U:H5'	2.19	0.43
4:E:152:VAL:HG12	4:E:156:ARG:HG2	2.01	0.43
20:B:48:MET:HB2	20:B:199:ILE:HG22	2.00	0.43
6:G:65:LEU:HD21	6:G:69:ARG:HH21	1.84	0.43
8:I:62:LEU:N	8:I:62:LEU:HD13	2.33	0.43
1:A:1458:G:O2'	1:A:1459:G:H5'	2.19	0.43
10:K:109:ILE:N	10:K:109:ILE:HD12	2.34	0.43
17:R:28:LEU:C	17:R:30:ASN:H	2.22	0.43
1:A:489:C:H2'	1:A:490:C:H6	1.84	0.43
1:A:421:U:H5'	1:A:422:C:C5	2.54	0.43
8:I:11:ARG:O	8:I:14:SER:HB2	2.18	0.42
1:A:1306:A:N6	1:A:1331:G:O2'	2.52	0.42
1:A:238:A:H3'	1:A:239:U:H5''	2.01	0.42
5:F:9:MET:HB2	5:F:57:ALA:HB1	2.00	0.42
11:L:86:VAL:HG22	11:L:95:HIS:HE2	1.83	0.42
10:K:70:ALA:O	10:K:74:LYS:HB2	2.18	0.42
1:A:1317:C:H2'	1:A:1318:A:O4'	2.19	0.42
4:E:152:VAL:HG21	7:H:98:LEU:HD13	2.01	0.42
4:E:52:ALA:HB3	4:E:58:ALA:HB2	2.01	0.42
1:A:1246:A:C6	1:A:1292:G:C6	3.06	0.42
12:M:102:LYS:NZ	12:M:103:THR:HG23	2.32	0.42
1:A:492:C:C2'	1:A:493:A:H5''	2.49	0.42
1:A:1163:A:H2'	1:A:1164:G:C8	2.52	0.42
1:A:512:U:H2'	1:A:513:C:C6	2.54	0.42
1:A:551:U:H2'	1:A:552:U:C6	2.54	0.42
1:A:968:A:H4'	1:A:969:A:OP2	2.19	0.42
2:C:75:VAL:HG11	2:C:102:ILE:HD13	2.01	0.42
4:E:144:GLU:HA	4:E:146:MET:SD	2.59	0.42
8:I:22:PRO:HA	8:I:60:LEU:HB3	2.00	0.42
8:I:86:LEU:HB3	8:I:93:LEU:CD1	2.49	0.42
2:C:129:PHE:CZ	2:C:156:LEU:HD13	2.55	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
19:T:69:ASN:N	19:T:69:ASN:ND2	2.57	0.42
3:D:195:ASN:HB3	3:D:197:HIS:CD2	2.54	0.42
1:A:113:G:H2'	1:A:114:U:C6	2.54	0.42
1:A:820:U:H4'	1:A:821:G:OP2	2.19	0.42
1:A:847:G:H2'	1:A:848:C:C6	2.53	0.42
7:H:117:GLN:HE21	7:H:117:GLN:HB3	1.62	0.42
13:N:69:PRO:O	13:N:71:GLY:N	2.52	0.42
5:F:36:ILE:HG12	5:F:64:VAL:HG22	2.00	0.42
9:J:51:VAL:CG2	13:N:80:ARG:HB2	2.36	0.42
5:F:54:LEU:HD13	5:F:55:HIS:H	1.85	0.42
18:S:26:ASP:OD1	18:S:46:LEU:HD13	2.18	0.42
7:H:76:ARG:HE	7:H:125:ILE:HG23	1.84	0.42
12:M:102:LYS:HG3	12:M:103:THR:N	2.35	0.42
19:T:55:PRO:HG2	19:T:56:ILE:HD12	2.00	0.42
1:A:601:G:H2'	1:A:602:A:C8	2.55	0.42
2:C:68:HIS:HA	2:C:103:ALA:CB	2.49	0.42
11:L:35:ARG:HH21	11:L:36:VAL:C	2.23	0.42
1:A:1105:A:O2'	1:A:1106:G:H5'	2.18	0.42
9:J:41:PRO:HA	9:J:72:ARG:CD	2.48	0.42
1:A:78:A:O2'	1:A:79:G:H5'	2.19	0.42
1:A:984:C:H2'	1:A:985:C:H6	1.83	0.42
2:C:143:LEU:HB2	2:C:144:GLY:H	1.65	0.42
1:A:736:C:H2'	1:A:737:C:H6	1.84	0.42
1:A:41:G:H2'	1:A:42:G:C8	2.54	0.42
1:A:69:G:H2'	1:A:70:U:C6	2.53	0.42
21:U:17:ARG:HA	21:U:20:ARG:HB2	2.01	0.42
10:K:113:THR:CG2	21:U:28:LEU:HD21	2.49	0.42
1:A:374:A:H5''	1:A:452:A:N1	2.33	0.42
8:I:51:LEU:CB	8:I:56:MET:HG2	2.39	0.42
3:D:54:LEU:O	3:D:58:GLN:HB2	2.20	0.42
18:S:14:LEU:HD23	18:S:32:THR:HG21	2.02	0.42
1:A:1030:U:O2'	1:A:1031:C:P	2.77	0.42
1:A:652:U:H1'	1:A:653:U:C5	2.53	0.42
1:A:1499:A:OP2	1:A:1500:A:OP2	2.38	0.42
1:A:1379:G:N7	6:G:2:ARG:CZ	2.82	0.42
10:K:127:ARG:HG3	10:K:127:ARG:NH1	2.34	0.42
18:S:62:THR:HG23	18:S:65:MET:HG2	2.00	0.42
12:M:48:SER:C	12:M:50:GLY:N	2.71	0.42
1:A:720:C:O4'	17:R:38:ILE:HG12	2.19	0.42
1:A:749:A:O2'	1:A:750:C:H5'	2.20	0.42
7:H:112:ASP:OD1	7:H:112:ASP:N	2.52	0.42
13:N:73:LEU:O	13:N:74:ARG:C	2.58	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:B:49:PHE:HB3	20:B:212:TYR:OH	2.20	0.42
16:Q:24:ILE:HD12	16:Q:24:ILE:N	2.34	0.42
13:N:40:ARG:HH12	18:S:6:LYS:N	2.17	0.42
9:J:11:LYS:HE3	9:J:99:GLN:HE22	1.85	0.42
17:R:50:TYR:O	17:R:54:LEU:HD12	2.19	0.42
3:D:21:LYS:O	3:D:23:GLY:N	2.52	0.42
1:A:203:G:N2	1:A:205:A:H61	2.18	0.42
1:A:1520:C:H2'	1:A:1521:C:H6	1.81	0.42
15:P:32:PHE:CD1	15:P:32:PHE:C	2.93	0.42
1:A:425:G:O2'	1:A:426:U:H5'	2.20	0.42
21:U:41:THR:CA	21:U:45:LYS:HD3	2.49	0.42
4:E:158:LYS:HB3	7:H:63:LYS:HE2	2.02	0.42
1:A:551:U:H2'	1:A:552:U:H6	1.84	0.42
13:N:55:SER:OG	13:N:56:PRO:HD2	2.19	0.42
1:A:755:G:OP2	14:O:64:LYS:HE2	2.19	0.42
1:A:761:G:H2'	1:A:762:U:C6	2.54	0.42
16:Q:23:ALA:HB1	16:Q:40:THR:CG2	2.50	0.42
2:C:69:THR:HG22	2:C:70:ALA:N	2.35	0.42
1:A:1000:A:H2'	1:A:1001:C:H6	1.78	0.42
8:I:7:GLY:HA3	8:I:81:GLY:O	2.19	0.42
11:L:100:ALA:O	11:L:101:LEU:O	2.37	0.42
3:D:74:TYR:HB3	3:D:89:LEU:HD12	2.00	0.42
1:A:1356:G:H2'	1:A:1357:A:C8	2.54	0.42
6:G:36:SER:OG	6:G:37:THR:N	2.52	0.42
1:A:611:C:H2'	1:A:612:C:H6	1.84	0.42
1:A:1248:A:H2'	1:A:1249:C:C6	2.55	0.42
1:A:551:U:O2'	1:A:552:U:H5'	2.19	0.42
10:K:18:GLY:O	10:K:81:LEU:HD12	2.19	0.42
1:A:1209:C:O2'	1:A:1210:C:H5'	2.20	0.42
20:B:41:ASN:ND2	20:B:44:LYS:HB2	2.35	0.42
1:A:238:A:C3'	1:A:239:U:H5''	2.49	0.42
19:T:66:ILE:HA	19:T:70:LYS:NZ	2.34	0.42
10:K:124:LYS:HD3	21:U:34:ARG:HH11	1.85	0.42
18:S:26:ASP:O	18:S:27:LYS:HB3	2.20	0.42
18:S:13:HIS:ND1	18:S:13:HIS:N	2.58	0.42
18:S:11:ASP:OD1	18:S:14:LEU:HD21	2.20	0.42
8:I:29:ILE:HD13	8:I:37:TYR:CD2	2.55	0.42
1:A:108:G:C6	19:T:9:ARG:HG2	2.54	0.42
2:C:156:LEU:CB	2:C:163:ARG:HD3	2.46	0.42
1:A:1172:C:H2'	1:A:1173:U:C6	2.54	0.42
1:A:562:U:H1'	11:L:11:ARG:HB3	2.02	0.42
1:A:148:G:N3	1:A:1446:A:H2	2.18	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
9:J:21:ALA:CB	9:J:96:VAL:HG11	2.49	0.42
1:A:512:U:O2'	1:A:513:C:H5'	2.20	0.42
7:H:17:GLN:HG2	7:H:62:LEU:HG	2.02	0.42
6:G:47:GLU:C	6:G:49:LEU:H	2.22	0.42
1:A:714:G:H2'	1:A:715:A:C8	2.54	0.42
1:A:928:G:O2'	1:A:929:G:H5'	2.20	0.42
20:B:31:PHE:HB3	20:B:32:GLY:H	1.71	0.42
1:A:237:G:H2'	1:A:238:A:C8	2.55	0.42
8:I:56:MET:C	8:I:58:GLU:N	2.73	0.42
18:S:39:ILE:HG12	18:S:68:HIS:O	2.19	0.42
18:S:43:MET:HB3	18:S:61:VAL:HG11	2.01	0.42
18:S:30:LEU:HB2	18:S:48:ILE:HA	2.01	0.42
8:I:6:TYR:CG	8:I:7:GLY:N	2.86	0.42
3:D:171:GLU:O	3:D:180:THR:HB	2.19	0.42
15:P:44:SER:HB3	15:P:46:LYS:HG2	2.02	0.42
1:A:167:A:H2'	1:A:168:G:H8	1.85	0.42
11:L:91:GLY:O	11:L:93:ARG:NE	2.52	0.42
15:P:78:VAL:HG13	15:P:78:VAL:O	2.19	0.42
1:A:709:U:H2'	1:A:710:G:C8	2.55	0.42
1:A:612:C:H2'	1:A:613:C:C6	2.54	0.42
1:A:792:A:H1'	1:A:794:A:N7	2.34	0.42
1:A:359:G:O2'	1:A:360:G:H5'	2.20	0.42
1:A:1349:A:H2'	1:A:1350:A:O4'	2.19	0.42
1:A:596:A:O2'	1:A:597:G:H5'	2.20	0.42
5:F:74:LEU:O	5:F:74:LEU:HD22	2.20	0.42
20:B:14:HIS:HB3	20:B:208:ALA:HB1	2.02	0.42
8:I:44:ARG:HB3	8:I:48:ARG:HH12	1.85	0.42
3:D:99:ASN:O	3:D:102:TYR:HB3	2.20	0.42
19:T:4:LYS:HE2	19:T:6:ALA:HB3	2.02	0.42
8:I:85:ALA:C	8:I:87:MET:N	2.73	0.42
7:H:125:ILE:HG22	7:H:126:CYS:SG	2.60	0.42
1:A:585:G:O2'	1:A:879:C:OP1	2.37	0.42
12:M:68:LEU:HD22	12:M:69:ARG:HH11	1.82	0.42
11:L:6:LEU:CD1	11:L:11:ARG:HE	2.29	0.42
16:Q:30:HIS:HB3	16:Q:33:TYR:HB2	2.01	0.42
5:F:19:PRO:HG2	5:F:20:GLY:H	1.84	0.42
4:E:28:ARG:HE	4:E:28:ARG:HB2	1.73	0.42
1:A:22:G:O2'	1:A:23:C:H5'	2.20	0.42
1:A:707:U:H2'	1:A:708:C:C6	2.55	0.42
1:A:893:C:H2'	1:A:894:G:H8	1.84	0.42
1:A:31:G:H2'	1:A:48:C:C5	2.54	0.42
1:A:28:A:H2'	1:A:29:U:O4'	2.20	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:41:G:H2'	1:A:42:G:H8	1.83	0.42
1:A:1058:G:H2'	1:A:1059:C:O4'	2.19	0.42
1:A:1486:G:H2'	1:A:1487:G:O4'	2.19	0.42
21:U:3:ILE:HB	21:U:18:PHE:CE2	2.54	0.42
12:M:1:ALA:O	12:M:3:ILE:HG13	2.20	0.42
3:D:169:TRP:CD2	3:D:185:PRO:HB3	2.55	0.42
19:T:66:ILE:CG2	19:T:67:HIS:N	2.81	0.42
12:M:79:LEU:HD22	12:M:86:ARG:HE	1.85	0.42
19:T:31:ILE:HD13	19:T:74:HIS:CE1	2.55	0.42
5:F:15:SER:HA	5:F:18:VAL:HG23	2.01	0.42
1:A:1119:C:O2'	1:A:1120:C:H5'	2.20	0.42
8:I:30:ASN:O	8:I:31:GLN:HB2	2.19	0.42
7:H:46:GLU:HA	7:H:63:LYS:HE3	2.01	0.42
1:A:1050:G:H2'	1:A:1051:C:C6	2.55	0.42
20:B:31:PHE:HB2	20:B:41:ASN:HA	2.01	0.41
21:U:24:LYS:CG	21:U:25:ALA:H	2.33	0.41
19:T:66:ILE:HG21	19:T:71:ALA:HB2	2.02	0.41
9:J:40:ILE:HG12	9:J:74:VAL:H	1.86	0.41
2:C:8:GLY:HA2	2:C:11:LEU:HG	2.02	0.41
16:Q:7:LEU:O	16:Q:59:GLU:HA	2.20	0.41
1:A:493:A:N3	1:A:493:A:O4'	2.52	0.41
1:A:1354:U:O2'	1:A:1355:G:H5'	2.20	0.41
20:B:96:LEU:O	20:B:99:MET:HG3	2.20	0.41
1:A:1284:C:C2	1:A:1285:A:N7	2.88	0.41
1:A:1284:C:H3'	1:A:1285:A:H8	1.84	0.41
1:A:1092:A:H5''	6:G:3:ARG:NH1	2.35	0.41
1:A:343:U:H2'	1:A:345:C:C5	2.55	0.41
20:B:121:GLN:NE2	20:B:122:ASP:N	2.67	0.41
7:H:51:GLU:OE2	7:H:59:GLU:HG3	2.20	0.41
1:A:754:C:H3'	1:A:754:C:O2	2.20	0.41
20:B:218:ALA:HA	20:B:221:ARG:HB3	2.02	0.41
21:U:4:LYS:HB2	21:U:4:LYS:HE3	1.89	0.41
20:B:115:ASP:O	20:B:119:GLN:HG2	2.20	0.41
12:M:51:GLN:O	12:M:55:LEU:HG	2.20	0.41
10:K:121:ARG:HH21	21:U:34:ARG:CD	2.33	0.41
1:A:1526:G:O5'	21:U:38:GLU:HB2	2.20	0.41
1:A:972:C:OP1	9:J:59:LYS:HD2	2.21	0.41
9:J:8:ILE:HD11	9:J:74:VAL:CG1	2.49	0.41
1:A:812:G:OP1	1:A:812:G:C4'	2.69	0.41
11:L:73:LEU:HD22	11:L:79:ILE:HG21	2.01	0.41
7:H:44:PHE:CE2	7:H:128:VAL:HG21	2.55	0.41
4:E:157:GLY:H	7:H:43:GLY:CA	2.31	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:D:156:ALA:O	3:D:160:LEU:HD12	2.20	0.41
1:A:1279:G:N2	9:J:45:ARG:HD2	2.35	0.41
4:E:28:ARG:O	4:E:29:ILE:HD13	2.19	0.41
1:A:265:G:H5'	16:Q:65:PRO:O	2.19	0.41
1:A:829:G:O2'	1:A:830:G:H5'	2.20	0.41
7:H:72:GLU:OE1	7:H:73:SER:N	2.52	0.41
1:A:958:A:C6	1:A:959:A:N1	2.88	0.41
1:A:1480:A:H2'	1:A:1481:U:H6	1.83	0.41
1:A:688:G:H5'	10:K:48:GLY:HA2	2.01	0.41
1:A:777:A:H2'	1:A:778:G:H8	1.84	0.41
1:A:323:U:H2'	1:A:324:G:O4'	2.20	0.41
2:C:64:ARG:HD3	2:C:101:ASN:ND2	2.35	0.41
1:A:261:U:H2'	1:A:263:A:OP2	2.20	0.41
5:F:73:GLU:O	5:F:77:THR:HG23	2.20	0.41
1:A:975:A:H2'	1:A:976:G:OP2	2.21	0.41
10:K:92:ARG:CG	10:K:92:ARG:HH11	2.28	0.41
10:K:110:THR:CG2	21:U:4:LYS:HA	2.50	0.41
5:F:93:LYS:O	5:F:94:HIS:HB2	2.20	0.41
8:I:38:PHE:HB2	8:I:44:ARG:HG3	2.02	0.41
15:P:54:LEU:HD22	15:P:80:LYS:NZ	2.35	0.41
18:S:24:SER:HB2	18:S:27:LYS:NZ	2.35	0.41
1:A:740:U:O2'	1:A:741:G:H5'	2.20	0.41
13:N:65:GLN:HG2	13:N:82:LYS:HG3	2.03	0.41
1:A:1070:U:H2'	1:A:1071:C:C6	2.55	0.41
1:A:1070:U:H2'	1:A:1071:C:H6	1.84	0.41
4:E:70:MET:HB3	4:E:71:ILE:H	1.60	0.41
16:Q:64:ARG:NH1	16:Q:64:ARG:HB3	2.32	0.41
8:I:46:VAL:HA	8:I:49:GLN:OE1	2.20	0.41
7:H:10:LEU:HD13	7:H:74:ILE:HG12	2.01	0.41
1:A:1238:A:O2'	1:A:1239:A:H5'	2.21	0.41
1:A:473:U:N3	1:A:474:G:N7	2.69	0.41
1:A:1434:A:H2'	1:A:1435:G:O4'	2.21	0.41
1:A:376:G:O2'	1:A:377:G:H5'	2.21	0.41
10:K:23:HIS:HB3	10:K:30:ILE:CG1	2.48	0.41
20:B:60:ALA:HB2	20:B:66:ILE:HD11	2.01	0.41
1:A:162:A:H2'	1:A:163:C:O4'	2.19	0.41
1:A:1492:A:N6	1:A:1494:G:C8	2.88	0.41
1:A:666:G:O2'	1:A:667:G:H5'	2.20	0.41
1:A:1321:U:H2'	1:A:1322:C:C5	2.55	0.41
12:M:28:ARG:O	12:M:32:ILE:HB	2.20	0.41
1:A:237:G:H2'	1:A:238:A:H8	1.85	0.41
19:T:61:ALA:HA	19:T:66:ILE:HG22	2.02	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
21:U:36:PHE:HB2	21:U:39:LYS:CB	2.47	0.41
4:E:110:MET:O	4:E:114:LEU:HG	2.20	0.41
3:D:129:VAL:HG12	3:D:131:ILE:H	1.86	0.41
13:N:96:LYS:HG2	13:N:97:LYS:N	2.27	0.41
11:L:113:ARG:CZ	11:L:120:ARG:HA	2.51	0.41
11:L:113:ARG:O	11:L:114:SER:C	2.58	0.41
20:B:199:ILE:HG13	20:B:199:ILE:O	2.19	0.41
2:C:52:SER:O	2:C:113:LYS:HD3	2.20	0.41
11:L:34:THR:HB	11:L:53:ARG:HB3	2.03	0.41
15:P:44:SER:HB3	15:P:46:LYS:NZ	2.34	0.41
1:A:628:G:O2'	1:A:629:A:H5'	2.21	0.41
1:A:373:A:C1'	1:A:481:G:H1'	2.50	0.41
1:A:65:A:N1	1:A:381:C:C2	2.88	0.41
1:A:1175:G:O2'	1:A:1176:A:H5'	2.19	0.41
1:A:1486:G:H2'	1:A:1487:G:C8	2.54	0.41
20:B:10:LYS:HB3	20:B:211:LEU:HD11	2.01	0.41
20:B:78:ALA:HB1	20:B:213:LEU:HD13	2.01	0.41
20:B:15:PHE:CA	20:B:42:LEU:HD21	2.50	0.41
2:C:140:ALA:HB3	2:C:148:ILE:HG21	2.02	0.41
8:I:48:ARG:O	8:I:52:GLU:HB2	2.20	0.41
5:F:10:VAL:HG12	5:F:11:HIS:H	1.85	0.41
17:R:51:GLN:NE2	17:R:54:LEU:HB2	2.36	0.41
3:D:121:ALA:CA	3:D:145:ARG:HG3	2.51	0.41
1:A:814:A:H5'	1:A:1511:G:C4'	2.44	0.41
10:K:70:ALA:HA	10:K:73:VAL:CG2	2.47	0.41
1:A:1276:G:H2'	1:A:1277:C:H6	1.86	0.41
3:D:61:ARG:HE	3:D:68:GLU:HA	1.86	0.41
1:A:797:C:OP1	10:K:125:LYS:HE2	2.21	0.41
20:B:79:VAL:HG12	20:B:90:PHE:HB2	2.02	0.41
1:A:1254:A:N6	1:A:1283:U:H3	2.17	0.41
1:A:94:G:H4'	1:A:95:C:O5'	2.18	0.41
1:A:1401:G:H2'	1:A:1402:C:O4'	2.20	0.41
1:A:1455:G:O2'	1:A:1456:A:H5'	2.20	0.41
1:A:1148:U:H2'	1:A:1149:C:O4'	2.20	0.41
1:A:1494:G:O2'	1:A:1495:U:H5'	2.21	0.41
1:A:847:G:H2'	1:A:848:C:H6	1.84	0.41
20:B:166:ASP:HB2	20:B:190:SER:OG	2.20	0.41
1:A:915:A:H2'	1:A:916:U:H5'	2.02	0.41
1:A:738:C:H2'	1:A:739:C:C6	2.56	0.41
1:A:738:C:H2'	1:A:739:C:H6	1.86	0.41
21:U:14:ALA:O	21:U:16:ARG:N	2.53	0.41
16:Q:22:VAL:O	16:Q:42:LYS:HA	2.20	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:G:12:LEU:HD13	6:G:13:PRO:HD2	2.02	0.41
4:E:104:ILE:HD11	4:E:111:ARG:HA	2.03	0.41
7:H:123:GLU:OE1	7:H:125:ILE:HG12	2.21	0.41
12:M:80:MET:HA	12:M:87:GLY:HA2	2.01	0.41
1:A:35:G:H2'	1:A:36:C:H6	1.86	0.41
11:L:100:ALA:O	11:L:103:CYS:SG	2.78	0.41
1:A:1241:G:H2'	1:A:1242:G:C8	2.49	0.41
16:Q:45:VAL:HA	16:Q:72:TRP:O	2.20	0.41
1:A:1053:G:O2'	1:A:1199:U:H5	2.04	0.41
6:G:100:MET:O	6:G:104:VAL:HG23	2.21	0.41
2:C:127:VAL:HG23	2:C:128:MET:N	2.35	0.41
17:R:47:ARG:HH12	17:R:49:LYS:H	1.67	0.41
17:R:19:GLU:O	17:R:21:ASP:N	2.53	0.41
1:A:1015:G:O2'	1:A:1016:A:H5'	2.21	0.41
1:A:56:U:O5'	1:A:56:U:H6	2.03	0.41
14:O:63:ARG:HD3	14:O:63:ARG:O	2.21	0.41
1:A:284:C:H2'	1:A:285:C:C6	2.56	0.41
1:A:1240:U:P	6:G:115:MET:H	2.44	0.41
1:A:949:A:O2'	1:A:950:U:H5'	2.20	0.41
16:Q:68:LYS:C	16:Q:70:LYS:N	2.74	0.41
13:N:43:ALA:O	13:N:47:LEU:HB2	2.20	0.41
21:U:39:LYS:N	21:U:40:PRO:HD2	2.31	0.41
4:E:37:VAL:HA	4:E:46:GLY:O	2.20	0.41
2:C:71:ARG:HG3	2:C:71:ARG:O	2.20	0.41
6:G:108:ARG:HA	6:G:118:ARG:NE	2.36	0.41
18:S:15:LEU:CA	18:S:18:VAL:HG12	2.44	0.41
1:A:1095:U:O2'	1:A:1096:C:H5'	2.20	0.41
6:G:61:PHE:CD2	6:G:65:LEU:HD13	2.55	0.41
20:B:93:HIS:O	20:B:94:ARG:C	2.58	0.41
1:A:192:A:O2'	1:A:193:C:H5'	2.21	0.41
8:I:26:LYS:HG3	8:I:61:ASP:OD2	2.20	0.41
1:A:219:U:H2'	1:A:220:G:H8	1.85	0.41
1:A:1492:A:N6	1:A:1494:G:N9	2.68	0.41
1:A:455:G:H2'	1:A:456:A:C8	2.55	0.41
2:C:15:LYS:HZ3	2:C:16:PRO:HD2	1.85	0.41
1:A:382:A:O2'	1:A:383:A:H5'	2.21	0.41
12:M:13:HIS:HB2	12:M:16:ILE:HG22	2.02	0.41
1:A:1349:A:H1'	1:A:1374:A:N6	2.35	0.41
1:A:669:G:O2'	1:A:670:G:H5'	2.21	0.41
21:U:23:GLU:HB3	21:U:24:LYS:H	1.67	0.41
8:I:70:GLY:O	8:I:74:GLN:N	2.53	0.41
1:A:951:G:O2'	1:A:952:U:H5'	2.20	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:8:A:C8	4:E:105:ILE:HG23	2.56	0.41
16:Q:24:ILE:HD13	16:Q:43:LEU:CD1	2.50	0.41
3:D:64:TYR:CE2	3:D:93:LEU:HD13	2.56	0.41
15:P:57:ILE:O	15:P:61:VAL:HG23	2.21	0.41
4:E:35:LEU:CD1	4:E:133:ILE:HA	2.48	0.41
5:F:90:MET:HB3	5:F:91:ARG:H	1.68	0.41
8:I:20:ILE:CD1	8:I:86:LEU:HG	2.50	0.41
1:A:502:A:O2'	1:A:503:C:H5'	2.21	0.41
2:C:166:TRP:O	2:C:167:TYR:HB3	2.21	0.41
1:A:1318:A:H4'	18:S:9:PHE:CE2	2.56	0.41
15:P:16:PHE:CE2	15:P:40:ASN:HB2	2.55	0.41
4:E:52:ALA:C	4:E:54:GLU:N	2.74	0.41
16:Q:30:HIS:ND1	16:Q:31:PRO:HD2	2.36	0.41
20:B:80:LYS:HA	20:B:90:PHE:CZ	2.55	0.41
3:D:106:PHE:N	3:D:106:PHE:CD1	2.87	0.41
8:I:15:ALA:O	8:I:66:VAL:HG23	2.20	0.41
1:A:841:C:H3'	1:A:843:U:P	2.60	0.41
4:E:158:LYS:HB3	7:H:63:LYS:CD	2.50	0.41
1:A:967:C:O2'	8:I:129:ARG:HG3	2.21	0.41
9:J:44:THR:HG23	9:J:70:HIS:HA	2.01	0.41
1:A:1200:C:C3'	1:A:1201:A:H5'	2.50	0.41
8:I:91:GLU:H	8:I:91:GLU:CD	2.23	0.41
1:A:1058:G:OP1	2:C:198:LYS:HE3	2.20	0.41
1:A:1447:A:H5'	1:A:1448:C:H5	1.85	0.41
1:A:1111:A:H2'	1:A:1112:C:C6	2.56	0.41
16:Q:28:VAL:O	16:Q:36:PHE:HA	2.20	0.41
20:B:11:ALA:O	20:B:15:PHE:HD2	2.04	0.41
12:M:52:ILE:HG23	12:M:53:ASP:N	2.36	0.41
1:A:1369:C:H2'	1:A:1370:G:C8	2.55	0.41
11:L:106:VAL:CG1	11:L:109:ARG:HG3	2.51	0.41
1:A:947:G:H5''	12:M:106:ARG:HB2	2.03	0.41
1:A:236:A:H2'	1:A:237:G:H8	1.86	0.41
13:N:26:LEU:HA	13:N:29:ILE:CD1	2.47	0.41
10:K:16:SER:N	10:K:78:ILE:HA	2.35	0.41
1:A:1101:A:H61	20:B:101:THR:HG21	1.85	0.41
18:S:35:ARG:NH2	18:S:52:ASN:HD22	2.19	0.41
1:A:719:C:O2'	17:R:37:LYS:HE3	2.20	0.41
1:A:1080:A:O3'	4:E:20:VAL:HG21	2.20	0.41
1:A:781:A:H2'	1:A:782:A:C5'	2.45	0.41
8:I:87:MET:SD	8:I:88:GLU:N	2.93	0.41
1:A:1509:C:O2'	1:A:1510:C:H5'	2.21	0.41
3:D:2:ARG:O	3:D:3:TYR:CB	2.68	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:D:3:TYR:C	3:D:5:GLY:H	2.24	0.41
11:L:49:ARG:HD3	11:L:89:LEU:HD21	2.02	0.41
3:D:13:ARG:HG3	3:D:55:ARG:NH2	2.36	0.41
7:H:124:ILE:HD12	7:H:125:ILE:N	2.36	0.41
1:A:1386:G:O2'	1:A:1387:G:H5'	2.20	0.41
1:A:473:U:C2	1:A:474:G:C8	3.09	0.41
1:A:474:G:H2'	1:A:475:C:H6	1.82	0.41
16:Q:8:GLN:HA	16:Q:59:GLU:HA	2.03	0.41
4:E:95:MET:HE2	4:E:143:LEU:HD13	2.03	0.41
1:A:977:A:H1'	1:A:981:U:H3	1.86	0.41
1:A:1276:G:H2'	1:A:1277:C:C6	2.56	0.41
14:O:35:ILE:HD11	14:O:58:MET:CB	2.50	0.41
1:A:191:G:H2'	1:A:192:A:H8	1.85	0.41
1:A:861:G:H2'	1:A:862:C:H6	1.86	0.41
1:A:1192:C:OP2	2:C:3:LYS:NZ	2.53	0.41
1:A:202:G:H1'	1:A:468:A:H8	1.86	0.41
1:A:599:C:O2'	1:A:600:A:H5'	2.20	0.41
1:A:601:G:O2'	1:A:602:A:H5'	2.21	0.41
3:D:151:GLN:HG3	3:D:153:ARG:HB3	2.03	0.41
1:A:478:A:H2'	1:A:479:U:O4'	2.20	0.41
16:Q:30:HIS:CB	16:Q:33:TYR:HB2	2.51	0.41
1:A:557:G:H2'	1:A:558:G:O4'	2.20	0.41
1:A:1352:C:H2'	1:A:1353:G:C8	2.56	0.41
17:R:19:GLU:CD	17:R:20:ILE:N	2.74	0.41
1:A:210:C:H4'	1:A:211:G:H5''	2.02	0.41
1:A:637:C:H2'	1:A:638:U:C6	2.56	0.41
1:A:426:U:O2'	1:A:427:U:H5'	2.20	0.41
11:L:93:ARG:HD2	11:L:93:ARG:H	1.85	0.41
2:C:190:THR:HG22	2:C:191:THR:N	2.35	0.41
1:A:1158:C:O3'	20:B:131:LYS:HD3	2.20	0.41
4:E:158:LYS:CB	7:H:63:LYS:HD3	2.50	0.41
1:A:113:G:H21	1:A:353:A:H8	1.68	0.41
6:G:49:LEU:C	6:G:51:GLN:N	2.74	0.41
1:A:792:A:O2'	1:A:794:A:N7	2.49	0.41
11:L:107:LYS:O	11:L:108:ASP:HB2	2.20	0.41
11:L:107:LYS:HG2	11:L:108:ASP:N	2.34	0.41
1:A:1359:C:H6	1:A:1359:C:O5'	2.04	0.41
1:A:186:C:H2'	1:A:187:G:O4'	2.21	0.41
6:G:6:ILE:HG22	6:G:7:GLY:N	2.36	0.41
10:K:128:VAL:OXT	10:K:128:VAL:HG23	2.21	0.41
1:A:224:U:H2'	1:A:225:C:C6	2.56	0.41
12:M:47:LEU:HD12	12:M:51:GLN:HB2	2.02	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:B:163:ILE:CG2	20:B:164:ASP:H	2.21	0.41
11:L:98:ARG:HD2	11:L:104:SER:O	2.21	0.41
3:D:187:ARG:HH12	3:D:191:SER:CA	2.30	0.41
1:A:500:G:H2'	1:A:501:C:C6	2.56	0.41
1:A:1499:A:H1'	1:A:1520:C:H5'	2.03	0.41
11:L:36:VAL:HA	11:L:52:CYS:CB	2.51	0.41
1:A:399:G:H2'	1:A:400:C:H6	1.84	0.41
3:D:28:ASP:CB	3:D:33:ILE:HD12	2.50	0.41
1:A:1333:A:H2'	1:A:1334:G:O4'	2.21	0.41
1:A:633:G:H2'	1:A:634:C:H6	1.84	0.41
9:J:68:ARG:HB3	9:J:68:ARG:CZ	2.50	0.41
3:D:44:LYS:HZ2	3:D:46:ARG:HA	1.86	0.41
1:A:567:G:H2'	1:A:568:G:O4'	2.21	0.41
1:A:542:G:O2'	1:A:543:U:H5'	2.20	0.41
1:A:605:U:H2'	1:A:606:G:C8	2.56	0.41
5:F:3:HIS:CA	5:F:65:GLU:HG3	2.51	0.40
1:A:1305:G:HO2'	1:A:1306:A:H8	1.67	0.40
1:A:1368:A:OP1	8:I:112:ARG:NH2	2.54	0.40
14:O:28:VAL:O	14:O:32:THR:N	2.54	0.40
3:D:8:LEU:O	3:D:11:SER:HB2	2.20	0.40
1:A:1314:C:H2'	1:A:1315:U:C6	2.56	0.40
13:N:51:PRO:HG2	13:N:52:ARG:N	2.30	0.40
8:I:94:ARG:HH11	8:I:98:ARG:NH1	2.18	0.40
1:A:108:G:O4'	1:A:108:G:N3	2.54	0.40
1:A:35:G:H2'	1:A:36:C:C6	2.56	0.40
2:C:2:GLN:CA	2:C:2:GLN:HE21	2.34	0.40
6:G:68:VAL:HG12	6:G:134:VAL:HA	2.02	0.40
1:A:1118:U:O4'	1:A:1179:A:H1'	2.21	0.40
1:A:415:A:N1	1:A:428:G:O6	2.54	0.40
1:A:1149:C:O2'	1:A:1150:A:H5'	2.21	0.40
1:A:152:A:N6	1:A:170:U:C2	2.89	0.40
1:A:1250:A:H5''	8:I:68:GLY:HA2	2.03	0.40
5:F:84:VAL:HG22	5:F:85:ILE:N	2.36	0.40
1:A:918:A:H2'	1:A:919:A:H8	1.82	0.40
4:E:131:ASN:C	4:E:135:VAL:HG23	2.41	0.40
18:S:30:LEU:HB2	18:S:48:ILE:HG12	2.03	0.40
1:A:1510:C:H2'	1:A:1511:G:H8	1.86	0.40
19:T:69:ASN:H	19:T:69:ASN:HD22	1.66	0.40
1:A:1316:G:N2	1:A:1318:A:H3'	2.36	0.40
1:A:547:A:H4'	1:A:548:G:O5'	2.22	0.40
7:H:85:TYR:CD1	7:H:85:TYR:N	2.89	0.40
3:D:56:GLU:HG2	3:D:198:LEU:HD13	2.03	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
15:P:32:PHE:HD1	15:P:32:PHE:C	2.24	0.40
4:E:148:SER:O	4:E:151:MET:HB2	2.21	0.40
1:A:635:A:H2'	1:A:636:U:C6	2.56	0.40
15:P:56:ARG:O	15:P:59:HIS:HB3	2.22	0.40
3:D:37:PRO:CD	3:D:41:GLY:HA3	2.51	0.40
1:A:806:C:O2'	1:A:807:A:H5'	2.21	0.40
7:H:21:LYS:O	7:H:62:LEU:HD22	2.21	0.40
2:C:194:VAL:HG12	2:C:195:ILE:N	2.36	0.40
1:A:1261:A:N3	1:A:1261:A:H2'	2.36	0.40
1:A:358:U:H2'	1:A:359:G:C8	2.56	0.40
1:A:987:G:H2'	1:A:988:G:C8	2.55	0.40
1:A:1113:C:O2'	1:A:1114:C:H5'	2.21	0.40
10:K:19:VAL:N	10:K:34:THR:O	2.47	0.40
4:E:93:VAL:HG12	4:E:94:PHE:N	2.36	0.40
5:F:11:HIS:CD2	5:F:13:ASP:HB3	2.56	0.40
1:A:1510:C:H2'	1:A:1511:G:C8	2.57	0.40
16:Q:26:ARG:HH21	16:Q:39:ARG:HG2	1.86	0.40
1:A:411:A:C4	1:A:413:G:H1'	2.56	0.40
20:B:27:LYS:CB	20:B:28:PRO:HD3	2.44	0.40
4:E:24:VAL:HG23	4:E:26:GLY:H	1.86	0.40
7:H:23:ALA:HB1	7:H:60:LEU:O	2.21	0.40
1:A:321:A:H2'	1:A:322:C:H6	1.87	0.40
1:A:1176:A:H3'	1:A:1177:G:H8	1.86	0.40
10:K:116:PRO:C	10:K:118:ASN:H	2.24	0.40
20:B:132:GLU:HA	20:B:135:MET:CE	2.51	0.40
1:A:1248:A:H2	8:I:71:ILE:HD11	1.85	0.40
7:H:112:ASP:CG	7:H:113:ARG:H	2.24	0.40
1:A:896:C:O2'	1:A:897:C:H5'	2.21	0.40
1:A:521:G:OP1	11:L:69:GLU:HB3	2.20	0.40
7:H:4:ASP:HB2	7:H:80:PRO:HG3	2.04	0.40
9:J:28:THR:CG2	9:J:86:ALA:HB1	2.51	0.40
9:J:98:VAL:HG23	9:J:98:VAL:O	2.21	0.40
10:K:34:THR:HG21	10:K:38:GLY:HA2	2.04	0.40
3:D:18:LEU:HB3	3:D:20:LEU:HG	2.03	0.40
1:A:1271:A:H2'	1:A:1272:G:C8	2.57	0.40
13:N:66:THR:CG2	13:N:82:LYS:HD3	2.51	0.40
8:I:89:TYR:O	8:I:90:ASP:HB2	2.21	0.40
1:A:501:C:O2'	1:A:502:A:H5'	2.21	0.40
12:M:9:PRO:O	12:M:44:ILE:HG12	2.21	0.40
16:Q:45:VAL:HG12	16:Q:46:HIS:O	2.21	0.40
1:A:1279:G:N1	9:J:45:ARG:NH1	2.70	0.40
1:A:598:U:H2'	1:A:599:C:H6	1.86	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:994:A:C2	13:N:4:SER:HA	2.56	0.40
1:A:1067:A:H3'	1:A:1094:G:OP1	2.21	0.40
7:H:17:GLN:HG3	7:H:71:VAL:HG21	2.03	0.40
1:A:658:C:O2'	1:A:659:U:H5'	2.22	0.40
1:A:462:G:H2'	1:A:463:U:C6	2.56	0.40
7:H:29:SER:O	7:H:33:VAL:HG23	2.21	0.40
1:A:224:U:H2'	1:A:225:C:H6	1.85	0.40
20:B:123:GLY:O	20:B:124:THR:HB	2.22	0.40
10:K:108:ASN:OD1	10:K:110:THR:HG23	2.21	0.40
4:E:105:ILE:HD12	4:E:123:LEU:CD2	2.51	0.40
8:I:51:LEU:HD22	8:I:56:MET:HG2	2.02	0.40
4:E:137:ARG:HH11	4:E:137:ARG:HG2	1.87	0.40
1:A:438:U:H2'	1:A:494:G:O6	2.22	0.40
3:D:120:LYS:O	3:D:121:ALA:HB2	2.22	0.40
1:A:812:G:O2'	1:A:813:U:C6	2.72	0.40
11:L:89:LEU:HD22	11:L:89:LEU:N	2.36	0.40
1:A:1236:A:H2'	1:A:1237:C:C6	2.57	0.40
1:A:1031:C:H5'	1:A:1032:G:C4	2.57	0.40
1:A:525:C:H2'	1:A:526:C:C6	2.56	0.40
1:A:1023:U:H2'	1:A:1024:G:O4'	2.21	0.40
11:L:51:VAL:HG12	11:L:52:CYS:N	2.35	0.40
1:A:797:C:O2'	1:A:798:U:H5'	2.21	0.40
1:A:481:G:H4'	1:A:481:G:OP1	2.21	0.40
1:A:449:G:H2'	1:A:450:G:H8	1.86	0.40
18:S:44:ILE:HG23	18:S:63:ASP:HB2	2.03	0.40
2:C:143:LEU:H	2:C:143:LEU:HD13	1.86	0.40
1:A:893:C:H2'	1:A:894:G:C8	2.57	0.40
7:H:94:VAL:CG2	7:H:127:TYR:HB2	2.51	0.40
1:A:61:G:H2'	1:A:62:U:O4'	2.21	0.40
2:C:192:TYR:CD2	2:C:192:TYR:N	2.89	0.40
21:U:32:ARG:HG2	21:U:32:ARG:O	2.21	0.40
12:M:113:LYS:HD3	12:M:113:LYS:N	2.37	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	C	204/232 (88%)	139 (68%)	45 (22%)	20 (10%)	1	14
3	D	203/205 (99%)	137 (68%)	49 (24%)	17 (8%)	1	18
4	E	148/166 (89%)	108 (73%)	31 (21%)	9 (6%)	2	29
5	F	98/135 (73%)	65 (66%)	23 (24%)	10 (10%)	1	12
6	G	150/178 (84%)	101 (67%)	36 (24%)	13 (9%)	1	17
7	H	127/129 (98%)	90 (71%)	31 (24%)	6 (5%)	4	37
8	I	125/129 (97%)	82 (66%)	33 (26%)	10 (8%)	1	20
9	J	96/103 (93%)	58 (60%)	21 (22%)	17 (18%)	0	3
10	K	115/128 (90%)	78 (68%)	27 (24%)	10 (9%)	1	17
11	L	121/123 (98%)	75 (62%)	28 (23%)	18 (15%)	0	5
12	M	111/117 (95%)	79 (71%)	17 (15%)	15 (14%)	0	7
13	N	92/100 (92%)	53 (58%)	24 (26%)	15 (16%)	0	4
14	O	86/89 (97%)	67 (78%)	16 (19%)	3 (4%)	6	49
15	P	78/82 (95%)	52 (67%)	19 (24%)	7 (9%)	1	16
16	Q	79/83 (95%)	61 (77%)	13 (16%)	5 (6%)	2	28
17	R	53/74 (72%)	39 (74%)	11 (21%)	3 (6%)	3	31
18	S	78/91 (86%)	48 (62%)	17 (22%)	13 (17%)	0	4
19	T	83/86 (96%)	61 (74%)	16 (19%)	6 (7%)	2	24
20	B	216/240 (90%)	150 (69%)	36 (17%)	30 (14%)	0	6
21	U	49/71 (69%)	28 (57%)	15 (31%)	6 (12%)	1	9
All	All	2312/2561 (90%)	1571 (68%)	508 (22%)	233 (10%)	1	13

All (233) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	54	ILE
3	D	22	SER
3	D	24	VAL
3	D	121	ALA
4	E	23	THR
5	F	98	GLU
6	G	16	LYS
6	G	62	GLU

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Mol	Chain	Res	Type
7	H	66	GLN
7	H	82	LEU
9	J	34	ALA
9	J	57	VAL
9	J	61	ALA
9	J	67	ILE
11	L	10	PRO
11	L	32	VAL
11	L	33	CYS
11	L	43	LYS
11	L	88	ASP
11	L	101	LEU
11	L	111	GLN
11	L	117	GLY
11	L	121	PRO
12	M	105	ALA
13	N	29	ILE
13	N	50	LEU
14	O	3	SER
14	O	73	ASP
15	P	28	ARG
16	Q	56	ASP
18	S	62	THR
19	T	3	ILE
19	T	4	LYS
20	B	22	TRP
20	B	72	LYS
20	B	73	ARG
20	B	124	THR
20	B	206	ILE
20	B	208	ALA
21	U	37	TYR
2	C	25	THR
2	C	63	ILE
2	C	95	GLY
2	C	128	MET
2	C	145	ALA
2	C	153	SER
3	D	47	LEU
3	D	49	ASP
3	D	120	LYS
3	D	169	TRP

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Mol	Chain	Res	Type
3	D	191	SER
4	E	15	ILE
4	E	20	VAL
5	F	95	ALA
6	G	97	ALA
6	G	130	LYS
7	H	69	ALA
7	H	122	GLY
8	I	34	LEU
8	I	55	ASP
9	J	33	GLY
9	J	37	ARG
9	J	60	ASP
9	J	68	ARG
9	J	74	VAL
9	J	94	ALA
10	K	14	GLN
10	K	17	ASP
10	K	52	ARG
10	K	53	GLY
10	K	108	ASN
11	L	13	ARG
11	L	24	GLU
11	L	73	LEU
11	L	97	VAL
11	L	104	SER
12	M	3	ILE
12	M	21	ILE
12	M	23	GLY
12	M	62	PHE
12	M	65	GLU
13	N	51	PRO
13	N	70	HIS
15	P	46	LYS
15	P	47	GLU
15	P	79	ASN
16	Q	69	THR
17	R	21	ASP
18	S	8	PRO
18	S	22	VAL
18	S	27	LYS
20	B	18	GLN

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Mol	Chain	Res	Type
20	B	44	LYS
20	B	97	GLY
20	B	153	MET
20	B	188	THR
21	U	22	CYS
21	U	23	GLU
2	C	3	LYS
2	C	65	VAL
2	C	167	TYR
2	C	180	ASP
3	D	14	GLU
3	D	34	GLU
5	F	5	GLU
5	F	89	VAL
6	G	3	ARG
6	G	78	ARG
6	G	99	ALA
6	G	112	ASP
6	G	113	LYS
8	I	121	ARG
9	J	75	ASP
9	J	77	VAL
9	J	93	ALA
10	K	88	PRO
11	L	98	ARG
12	M	7	ASN
13	N	31	SER
13	N	52	ARG
13	N	69	PRO
13	N	73	LEU
14	O	19	ASN
15	P	27	ALA
15	P	44	SER
16	Q	28	VAL
16	Q	47	ASP
17	R	20	ILE
18	S	33	TRP
18	S	63	ASP
19	T	68	LYS
20	B	14	HIS
20	B	15	PHE
20	B	19	THR

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Mol	Chain	Res	Type
20	B	20	ARG
20	B	43	GLU
20	B	86	CYS
20	B	94	ARG
20	B	95	TRP
20	B	114	LYS
20	B	204	ASP
21	U	17	ARG
2	C	50	SER
2	C	59	PRO
2	C	110	LEU
3	D	166	LYS
3	D	203	TYR
4	E	78	GLY
4	E	87	VAL
4	E	107	GLY
4	E	146	MET
6	G	129	ASN
7	H	30	LYS
7	H	94	VAL
8	I	24	ASN
8	I	57	VAL
8	I	58	GLU
8	I	90	ASP
9	J	56	HIS
9	J	58	ASN
10	K	49	SER
10	K	71	ASP
11	L	23	LEU
12	M	14	ALA
12	M	22	TYR
12	M	97	ARG
12	M	102	LYS
12	M	104	ASN
13	N	18	LYS
13	N	21	ALA
17	R	63	TYR
18	S	5	LYS
19	T	67	HIS
20	B	96	LEU
20	B	128	LEU
20	B	167	HIS

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Mol	Chain	Res	Type
20	B	193	ASP
2	C	53	ARG
3	D	25	ARG
3	D	119	HIS
5	F	35	LYS
5	F	38	ARG
5	F	41	ASP
5	F	85	ILE
5	F	92	THR
6	G	55	LYS
6	G	66	GLU
9	J	36	VAL
12	M	49	GLU
12	M	100	ARG
13	N	43	ALA
13	N	61	ASN
13	N	74	ARG
15	P	55	ASP
18	S	13	HIS
18	S	29	PRO
18	S	53	GLY
18	S	61	VAL
20	B	172	ILE
20	B	205	ALA
2	C	26	LYS
2	C	144	GLY
3	D	68	GLU
4	E	17	VAL
5	F	53	LYS
11	L	99	GLY
13	N	62	ARG
19	T	44	ALA
19	T	76	ALA
20	B	200	PRO
2	C	107	LYS
8	I	9	GLY
20	B	163	ILE
21	U	39	LYS
2	C	76	ILE
2	C	127	VAL
4	E	90	GLY
10	K	15	VAL

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Mol	Chain	Res	Type
10	K	119	GLY
11	L	78	VAL
13	N	33	VAL
20	B	13	VAL
3	D	37	PRO
6	G	68	VAL
8	I	23	GLY
8	I	71	ILE
9	J	100	ILE
18	S	74	ALA
12	M	42	VAL
16	Q	32	ILE
18	S	10	ILE
3	D	27	ILE
21	U	13	VAL

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	C	170/189 (90%)	146 (86%)	24 (14%)	5	28
3	D	172/172 (100%)	137 (80%)	35 (20%)	2	10
4	E	113/125 (90%)	92 (81%)	21 (19%)	2	13
5	F	87/116 (75%)	74 (85%)	13 (15%)	4	25
6	G	125/146 (86%)	106 (85%)	19 (15%)	4	24
7	H	104/104 (100%)	85 (82%)	19 (18%)	2	13
8	I	105/106 (99%)	89 (85%)	16 (15%)	4	24
9	J	86/90 (96%)	78 (91%)	8 (9%)	13	51
10	K	90/98 (92%)	74 (82%)	16 (18%)	2	15
11	L	103/103 (100%)	79 (77%)	24 (23%)	1	6
12	M	91/95 (96%)	75 (82%)	16 (18%)	3	15
13	N	79/83 (95%)	68 (86%)	11 (14%)	5	28
14	O	76/77 (99%)	63 (83%)	13 (17%)	3	17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	P	65/65 (100%)	54 (83%)	11 (17%)	3	18
16	Q	75/77 (97%)	66 (88%)	9 (12%)	7	36
17	R	48/64 (75%)	41 (85%)	7 (15%)	5	26
18	S	71/78 (91%)	53 (75%)	18 (25%)	1	5
19	T	65/65 (100%)	51 (78%)	14 (22%)	1	8
20	B	180/198 (91%)	153 (85%)	27 (15%)	4	25
21	U	44/61 (72%)	30 (68%)	14 (32%)	0	3
All	All	1949/2112 (92%)	1614 (83%)	335 (17%)	3	17

All (335) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	2	GLN
2	C	13	ILE
2	C	19	SER
2	C	20	THR
2	C	25	THR
2	C	28	PHE
2	C	30	ASP
2	C	40	GLN
2	C	46	LEU
2	C	87	ARG
2	C	88	LYS
2	C	96	VAL
2	C	128	MET
2	C	129	PHE
2	C	130	ARG
2	C	134	LYS
2	C	143	LEU
2	C	164	THR
2	C	165	GLU
2	C	166	TRP
2	C	168	ARG
2	C	176	THR
2	C	181	ILE
2	C	206	ILE
3	D	2	ARG
3	D	16	THR
3	D	25	ARG
3	D	28	ASP

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Mol	Chain	Res	Type
3	D	30	LYS
3	D	39	GLN
3	D	46	ARG
3	D	47	LEU
3	D	48	SER
3	D	49	ASP
3	D	55	ARG
3	D	58	GLN
3	D	69	ARG
3	D	71	PHE
3	D	77	GLU
3	D	84	ASN
3	D	92	LEU
3	D	93	LEU
3	D	99	ASN
3	D	100	VAL
3	D	106	PHE
3	D	125	ASN
3	D	127	ARG
3	D	130	ASN
3	D	137	SER
3	D	146	GLU
3	D	147	LYS
3	D	154	VAL
3	D	160	LEU
3	D	162	GLU
3	D	164	ARG
3	D	170	LEU
3	D	186	GLU
3	D	196	GLU
3	D	199	ILE
4	E	9	GLU
4	E	11	GLN
4	E	14	LEU
4	E	21	SER
4	E	23	THR
4	E	25	LYS
4	E	28	ARG
4	E	30	PHE
4	E	55	VAL
4	E	61	LYS
4	E	89	THR

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Mol	Chain	Res	Type
4	E	92	ARG
4	E	95	MET
4	E	104	ILE
4	E	120	HIS
4	E	133	ILE
4	E	141	ASP
4	E	144	GLU
4	E	146	MET
4	E	147	ASN
4	E	151	MET
5	F	3	HIS
5	F	6	ILE
5	F	13	ASP
5	F	39	LEU
5	F	54	LEU
5	F	55	HIS
5	F	59	TYR
5	F	62	MET
5	F	72	ASP
5	F	76	THR
5	F	86	ARG
5	F	91	ARG
5	F	97	THR
6	G	2	ARG
6	G	8	GLN
6	G	10	LYS
6	G	26	VAL
6	G	46	LEU
6	G	56	SER
6	G	58	LEU
6	G	71	THR
6	G	75	LYS
6	G	78	ARG
6	G	84	TYR
6	G	89	GLU
6	G	98	LEU
6	G	108	ARG
6	G	110	ARG
6	G	115	MET
6	G	117	LEU
6	G	134	VAL
6	G	153	TYR

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Mol	Chain	Res	Type
7	H	6	ILE
7	H	8	ASP
7	H	14	ARG
7	H	28	SER
7	H	45	ILE
7	H	47	ASP
7	H	53	ASP
7	H	57	GLU
7	H	68	LYS
7	H	72	GLU
7	H	79	ARG
7	H	82	LEU
7	H	88	LYS
7	H	107	LYS
7	H	110	MET
7	H	117	GLN
7	H	123	GLU
7	H	124	ILE
7	H	128	VAL
8	I	4	GLN
8	I	6	TYR
8	I	26	LYS
8	I	27	ILE
8	I	37	TYR
8	I	45	MET
8	I	52	GLU
8	I	55	ASP
8	I	60	LEU
8	I	61	ASP
8	I	62	LEU
8	I	74	GLN
8	I	87	MET
8	I	109	GLN
8	I	121	ARG
8	I	122	ARG
9	J	32	THR
9	J	37	ARG
9	J	47	GLU
9	J	57	VAL
9	J	71	LEU
9	J	77	VAL
9	J	78	GLU

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Mol	Chain	Res	Type
9	J	92	LEU
10	K	16	SER
10	K	28	ASN
10	K	31	VAL
10	K	34	THR
10	K	45	THR
10	K	55	ARG
10	K	64	VAL
10	K	69	CYS
10	K	75	GLU
10	K	76	TYR
10	K	78	ILE
10	K	81	LEU
10	K	84	MET
10	K	97	ARG
10	K	109	ILE
10	K	112	VAL
11	L	8	ARG
11	L	14	LYS
11	L	17	LYS
11	L	26	CYS
11	L	28	GLN
11	L	33	CYS
11	L	34	THR
11	L	40	THR
11	L	42	LYS
11	L	46	SER
11	L	49	ARG
11	L	53	ARG
11	L	61	GLU
11	L	69	GLU
11	L	73	LEU
11	L	75	GLU
11	L	88	ASP
11	L	93	ARG
11	L	98	ARG
11	L	107	LYS
11	L	109	ARG
11	L	111	GLN
11	L	120	ARG
11	L	122	LYS
12	M	2	ARG

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Mol	Chain	Res	Type
12	M	15	VAL
12	M	40	GLU
12	M	45	SER
12	M	46	GLU
12	M	49	GLU
12	M	56	ARG
12	M	65	GLU
12	M	67	ASP
12	M	88	LEU
12	M	92	ARG
12	M	97	ARG
12	M	102	LYS
12	M	106	ARG
12	M	109	LYS
12	M	112	ARG
13	N	5	MET
13	N	17	ASP
13	N	19	TYR
13	N	23	ARG
13	N	31	SER
13	N	44	VAL
13	N	48	GLN
13	N	50	LEU
13	N	82	LYS
13	N	89	ARG
13	N	95	LEU
14	O	4	THR
14	O	39	GLN
14	O	44	GLU
14	O	50	HIS
14	O	51	SER
14	O	53	ARG
14	O	56	LEU
14	O	59	VAL
14	O	63	ARG
14	O	69	LEU
14	O	78	THR
14	O	80	LEU
14	O	83	ARG
15	P	5	ARG
15	P	19	VAL
15	P	23	ASP

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Mol	Chain	Res	Type
15	P	25	ARG
15	P	28	ARG
15	P	32	PHE
15	P	35	ARG
15	P	50	THR
15	P	57	ILE
15	P	67	ILE
15	P	68	SER
16	Q	5	ARG
16	Q	7	LEU
16	Q	20	ILE
16	Q	26	ARG
16	Q	39	ARG
16	Q	48	GLU
16	Q	60	ILE
16	Q	64	ARG
16	Q	80	LYS
17	R	23	LYS
17	R	25	ILE
17	R	35	SER
17	R	37	LYS
17	R	38	ILE
17	R	42	ARG
17	R	47	ARG
18	S	3	SER
18	S	5	LYS
18	S	10	ILE
18	S	11	ASP
18	S	12	LEU
18	S	13	HIS
18	S	20	LYS
18	S	26	ASP
18	S	27	LYS
18	S	28	LYS
18	S	33	TRP
18	S	36	ARG
18	S	38	THR
18	S	47	THR
18	S	52	ASN
18	S	62	THR
18	S	64	GLU
18	S	73	PHE

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Mol	Chain	Res	Type
19	T	9	ARG
19	T	11	ILE
19	T	25	SER
19	T	29	THR
19	T	35	TYR
19	T	47	GLN
19	T	48	LYS
19	T	51	ASN
19	T	53	MET
19	T	66	ILE
19	T	69	ASN
19	T	70	LYS
19	T	73	ARG
19	T	77	ASN
20	B	8	MET
20	B	9	LEU
20	B	22	TRP
20	B	23	ASN
20	B	35	ASN
20	B	36	LYS
20	B	37	VAL
20	B	46	VAL
20	B	53	LEU
20	B	57	ASN
20	B	62	ARG
20	B	65	LYS
20	B	84	LEU
20	B	94	ARG
20	B	116	LEU
20	B	121	GLN
20	B	139	GLU
20	B	143	LEU
20	B	145	ASN
20	B	168	GLU
20	B	176	ASN
20	B	207	ARG
20	B	211	LEU
20	B	213	LEU
20	B	219	THR
20	B	221	ARG
20	B	222	GLU
21	U	7	GLU

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Mol	Chain	Res	Type
21	U	8	ASN
21	U	16	ARG
21	U	17	ARG
21	U	20	ARG
21	U	22	CYS
21	U	24	LYS
21	U	33	ARG
21	U	35	GLU
21	U	36	PHE
21	U	37	TYR
21	U	38	GLU
21	U	42	THR
21	U	48	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (60) such sidechains are listed below:

Mol	Chain	Res	Type
2	C	2	GLN
2	C	101	ASN
2	C	184	ASN
2	C	189	HIS
3	D	39	GLN
3	D	53	GLN
3	D	58	GLN
3	D	99	ASN
3	D	115	GLN
3	D	119	HIS
3	D	130	ASN
3	D	135	GLN
3	D	151	GLN
4	E	42	ASN
4	E	72	ASN
4	E	145	ASN
5	F	17	GLN
5	F	46	GLN
5	F	63	ASN
6	G	8	GLN
6	G	27	ASN
6	G	121	ASN
7	H	3	GLN
7	H	17	GLN
7	H	37	ASN

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Mol	Chain	Res	Type
7	H	75	GLN
7	H	117	GLN
8	I	80	HIS
8	I	109	GLN
9	J	58	ASN
9	J	99	GLN
10	K	28	ASN
10	K	37	GLN
10	K	63	GLN
10	K	108	ASN
10	K	118	ASN
11	L	28	GLN
11	L	45	ASN
11	L	71	HIS
12	M	7	ASN
13	N	34	ASN
13	N	61	ASN
14	O	36	ASN
15	P	40	ASN
15	P	63	GLN
16	Q	8	GLN
17	R	51	GLN
18	S	42	ASN
18	S	52	ASN
19	T	2	ASN
19	T	69	ASN
19	T	74	HIS
19	T	83	ASN
20	B	23	ASN
20	B	50	ASN
20	B	108	GLN
20	B	119	GLN
20	B	121	GLN
20	B	145	ASN
20	B	202	ASN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1529/1542 (99%)	249 (16%)	26 (1%)

All (249) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	7	A
1	A	9	G
1	A	14	U
1	A	31	G
1	A	32	A
1	A	39	G
1	A	47	C
1	A	48	C
1	A	51	A
1	A	52	C
1	A	55	A
1	A	61	G
1	A	71	A
1	A	72	A
1	A	83	C
1	A	85	U
1	A	87	C
1	A	92	U
1	A	93	U
1	A	94	G
1	A	108	G
1	A	121	U
1	A	122	G
1	A	131	A
1	A	151	A
1	A	164	G
1	A	182	A
1	A	183	C
1	A	197	A
1	A	209	U
1	A	210	C
1	A	239	U
1	A	240	G
1	A	243	A
1	A	244	U
1	A	245	U
1	A	247	G
1	A	250	A
1	A	251	G
1	A	253	A
1	A	257	G
1	A	258	G
1	A	266	G

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Mol	Chain	Res	Type
1	A	267	C
1	A	280	C
1	A	289	G
1	A	316	C
1	A	324	G
1	A	328	C
1	A	329	A
1	A	330	C
1	A	332	G
1	A	345	C
1	A	352	C
1	A	354	G
1	A	367	U
1	A	372	C
1	A	373	A
1	A	382	A
1	A	397	A
1	A	398	U
1	A	406	G
1	A	408	A
1	A	411	A
1	A	412	A
1	A	414	A
1	A	415	A
1	A	421	U
1	A	422	C
1	A	424	G
1	A	429	U
1	A	430	A
1	A	434	U
1	A	435	A
1	A	438	U
1	A	459	A
1	A	461	A
1	A	462	G
1	A	463	U
1	A	464	U
1	A	465	A
1	A	466	A
1	A	467	U
1	A	468	A
1	A	469	C

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Mol	Chain	Res	Type
1	A	476	U
1	A	479	U
1	A	481	G
1	A	482	A
1	A	484	G
1	A	485	U
1	A	493	A
1	A	500	G
1	A	511	C
1	A	518	C
1	A	522	C
1	A	527	G
1	A	531	U
1	A	532	A
1	A	547	A
1	A	559	A
1	A	562	U
1	A	572	A
1	A	573	A
1	A	576	C
1	A	577	G
1	A	607	A
1	A	639	G
1	A	650	G
1	A	653	U
1	A	665	A
1	A	693	G
1	A	700	G
1	A	721	G
1	A	724	G
1	A	731	G
1	A	733	G
1	A	747	A
1	A	748	G
1	A	755	G
1	A	781	A
1	A	782	A
1	A	793	U
1	A	794	A
1	A	812	G
1	A	815	A
1	A	817	C

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Mol	Chain	Res	Type
1	A	818	G
1	A	819	A
1	A	828	U
1	A	829	G
1	A	841	C
1	A	842	U
1	A	843	U
1	A	844	G
1	A	845	A
1	A	907	A
1	A	914	A
1	A	926	G
1	A	927	G
1	A	934	C
1	A	935	A
1	A	945	G
1	A	961	U
1	A	966	G
1	A	969	A
1	A	974	A
1	A	976	G
1	A	977	A
1	A	981	U
1	A	984	C
1	A	991	U
1	A	992	U
1	A	993	G
1	A	1004	A
1	A	1009	U
1	A	1010	U
1	A	1020	G
1	A	1022	A
1	A	1023	U
1	A	1025	U
1	A	1031	C
1	A	1033	G
1	A	1034	G
1	A	1036	A
1	A	1044	A
1	A	1050	G
1	A	1053	G
1	A	1054	C

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Mol	Chain	Res	Type
1	A	1063	C
1	A	1065	U
1	A	1066	C
1	A	1091	U
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	1118	U
1	A	1129	C
1	A	1130	A
1	A	1135	U
1	A	1136	C
1	A	1137	C
1	A	1138	G
1	A	1139	G
1	A	1140	C
1	A	1144	G
1	A	1159	U
1	A	1160	G
1	A	1166	G
1	A	1178	G
1	A	1184	G
1	A	1188	A
1	A	1190	G
1	A	1196	A
1	A	1197	A
1	A	1201	A
1	A	1202	U
1	A	1212	U
1	A	1213	A
1	A	1214	C
1	A	1225	A
1	A	1226	C
1	A	1227	A
1	A	1241	G
1	A	1250	A
1	A	1256	A
1	A	1257	A
1	A	1258	G
1	A	1279	G
1	A	1280	A
1	A	1281	C

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Mol	Chain	Res	Type
1	A	1282	C
1	A	1285	A
1	A	1298	U
1	A	1300	G
1	A	1301	U
1	A	1302	C
1	A	1303	C
1	A	1305	G
1	A	1317	C
1	A	1318	A
1	A	1320	C
1	A	1331	G
1	A	1362	A
1	A	1363	A
1	A	1364	U
1	A	1380	U
1	A	1397	C
1	A	1398	A
1	A	1400	C
1	A	1401	G
1	A	1419	G
1	A	1426	G
1	A	1432	G
1	A	1446	A
1	A	1451	U
1	A	1452	C
1	A	1491	G
1	A	1493	A
1	A	1497	G
1	A	1503	A
1	A	1506	U
1	A	1507	A
1	A	1517	G
1	A	1520	C
1	A	1529	G
1	A	1530	G
1	A	1533	C
1	A	1534	A

All (26) RNA pucker outliers are listed below:

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Mol	Chain	Res	Type
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Mol	Chain	Res	Type
1	A	51	A
1	A	60	A
1	A	243	A
1	A	279	A
1	A	328	C
1	A	366	A
1	A	372	C
1	A	428	G
1	A	429	U
1	A	484	G
1	A	960	U
1	A	975	A
1	A	1030	U
1	A	1049	U
1	A	1064	G
1	A	1065	U
1	A	1135	U
1	A	1201	A
1	A	1224	U
1	A	1226	C
1	A	1300	G
1	A	1301	U
1	A	1302	C
1	A	1319	A
1	A	1397	C
1	A	1451	U

## 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 62 ligands modelled in this entry, 62 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	1530/1542 (99%)	-0.23	22 (1%) 72 37	11, 49, 119, 180	0
2	C	206/232 (88%)	0.36	13 (6%) 19 8	13, 68, 122, 154	0
3	D	205/205 (100%)	0.01	4 (1%) 62 29	5, 49, 103, 156	0
4	E	150/166 (90%)	0.34	8 (5%) 25 10	5, 49, 101, 167	0
5	F	100/135 (74%)	0.91	10 (10%) 8 5	10, 65, 113, 147	0
6	G	152/178 (85%)	0.46	12 (7%) 13 7	22, 83, 132, 166	0
7	H	129/129 (100%)	0.02	3 (2%) 57 26	5, 49, 104, 154	0
8	I	127/129 (98%)	-0.30	0 100 100	23, 81, 135, 161	0
9	J	98/103 (95%)	-0.24	0 100 100	27, 78, 122, 143	0
10	K	117/128 (91%)	0.28	1 (0%) 81 49	5, 44, 95, 117	0
11	L	123/123 (100%)	-0.09	2 (1%) 68 33	5, 34, 109, 141	0
12	M	113/117 (96%)	0.85	17 (15%) 3 2	19, 92, 143, 180	0
13	N	96/100 (96%)	-0.18	0 100 100	32, 73, 130, 160	0
14	O	88/89 (98%)	0.13	5 (5%) 23 9	5, 46, 113, 136	0
15	P	80/82 (97%)	0.59	10 (12%) 5 3	5, 42, 126, 137	0
16	Q	81/83 (97%)	-0.09	0 100 100	11, 52, 113, 155	0
17	R	55/74 (74%)	0.54	4 (7%) 15 7	17, 45, 118, 139	0
18	S	80/91 (87%)	-0.15	1 (1%) 74 39	47, 99, 151, 161	0
19	T	85/86 (98%)	-0.29	0 100 100	9, 49, 103, 139	0
20	B	218/240 (90%)	0.29	8 (3%) 39 16	13, 90, 135, 162	0
21	U	51/71 (71%)	0.37	2 (3%) 37 16	34, 73, 112, 140	0
All	All	3884/4103 (94%)	0.03	122 (3%) 47 21	5, 58, 125, 180	0

All (122) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1492	A	7.9
12	M	47	LEU	6.8
12	M	48	SER	5.6
12	M	11	HIS	5.5
1	A	844	G	5.3
15	P	80	LYS	5.2
5	F	35	LYS	5.1
6	G	152	HIS	4.7
4	E	60	GLN	4.6
3	D	82	LYS	4.6
12	M	46	GLU	4.3
5	F	69	GLU	4.2
17	R	19	GLU	4.1
12	M	51	GLN	4.0
4	E	12	GLU	4.0
1	A	847	G	4.0
1	A	845	A	3.9
2	C	133	MET	3.8
1	A	1493	A	3.8
6	G	109	LYS	3.8
1	A	461	A	3.7
1	A	1491	G	3.7
15	P	48	GLU	3.7
2	C	126	ARG	3.7
12	M	9	PRO	3.6
1	A	464	U	3.6
3	D	184	LYS	3.6
15	P	43	ALA	3.6
20	B	43	GLU	3.6
5	F	93	LYS	3.5
15	P	79	ASN	3.5
12	M	112	ARG	3.5
6	G	151	ALA	3.5
1	A	1204	A	3.5
2	C	189	HIS	3.5
5	F	2	ARG	3.5
15	P	45	GLU	3.4
15	P	47	GLU	3.3
1	A	1030	U	3.3
5	F	79	ARG	3.2
17	R	73	HIS	3.2
2	C	198	LYS	3.2
5	F	32	ALA	3.2

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Mol	Chain	Res	Type	RSRZ
2	C	124	GLU	3.1
1	A	846	G	3.0
4	E	54	GLU	3.0
15	P	77	GLU	3.0
6	G	153	TYR	2.9
5	F	94	HIS	2.9
6	G	54	GLY	2.9
1	A	1298	U	2.9
17	R	50	TYR	2.8
20	B	158	ASP	2.8
11	L	123	ALA	2.8
1	A	1296	C	2.8
7	H	89	ASP	2.8
4	E	53	ARG	2.8
20	B	73	ARG	2.8
12	M	61	LYS	2.8
12	M	111	PRO	2.8
18	S	78	THR	2.7
1	A	466	A	2.7
2	C	151	GLU	2.7
1	A	5	U	2.7
20	B	123	GLY	2.7
20	B	108	GLN	2.6
2	C	191	THR	2.6
3	D	185	PRO	2.6
7	H	41	GLU	2.6
6	G	117	LEU	2.6
20	B	154	GLY	2.6
14	O	16	ARG	2.6
2	C	125	ARG	2.5
4	E	11	GLN	2.5
6	G	105	GLU	2.5
7	H	42	GLU	2.5
15	P	42	ILE	2.5
1	A	1297	G	2.4
17	R	69	TYR	2.4
2	C	165	GLU	2.4
14	O	83	ARG	2.4
12	M	43	LYS	2.4
12	M	35	ALA	2.4
1	A	250	A	2.4
1	A	747	A	2.4

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Mol	Chain	Res	Type	RSRZ
21	U	3	ILE	2.4
14	O	9	LYS	2.3
14	O	8	ALA	2.3
2	C	185	THR	2.3
1	A	1295	U	2.3
1	A	663	A	2.3
2	C	167	TYR	2.3
12	M	109	LYS	2.3
20	B	159	ALA	2.3
12	M	110	GLY	2.3
5	F	33	GLU	2.3
15	P	62	GLY	2.3
12	M	8	ILE	2.2
2	C	166	TRP	2.2
6	G	108	ARG	2.2
6	G	130	LYS	2.2
2	C	187	GLU	2.2
15	P	46	LYS	2.2
4	E	55	VAL	2.2
5	F	1	MET	2.2
5	F	28	ALA	2.2
20	B	153	MET	2.2
12	M	52	ILE	2.2
1	A	463	U	2.2
4	E	13	LYS	2.2
4	E	158	LYS	2.2
14	O	88	ARG	2.1
11	L	43	LYS	2.1
6	G	116	ALA	2.1
21	U	37	TYR	2.1
6	G	127	ALA	2.1
10	K	59	PRO	2.1
12	M	10	ASP	2.0
3	D	43	ARG	2.0
12	M	57	ASP	2.0
6	G	73	GLU	2.0
1	A	215	C	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	1570	1/1	1.05	55.97	55,55,55,55	1
22	MG	A	1572	1/1	0.27	37.57	5,5,5,5	1
22	MG	A	1565	1/1	0.49	22.95	151,151,151,151	0
22	MG	A	1574	1/1	0.26	13.35	61,61,61,61	0
22	MG	A	1557	1/1	0.34	5.05	101,101,101,101	0
22	MG	A	1544	1/1	0.18	2.97	32,32,32,32	0
22	MG	A	1583	1/1	0.22	2.17	92,92,92,92	0
22	MG	A	1564	1/1	0.15	1.65	67,67,67,67	0
22	MG	A	1598	1/1	0.18	1.60	48,48,48,48	0
22	MG	A	1599	1/1	0.19	0.67	37,37,37,37	0
22	MG	A	1546	1/1	0.16	0.65	18,18,18,18	0
22	MG	A	1547	1/1	0.18	0.33	18,18,18,18	0
22	MG	A	1563	1/1	0.14	-0.09	113,113,113,113	0
22	MG	A	1596	1/1	0.17	-0.25	40,40,40,40	0
22	MG	A	1580	1/1	0.14	-0.59	37,37,37,37	0
22	MG	A	1589	1/1	0.14	-0.73	32,32,32,32	0
22	MG	A	1558	1/1	0.14	-0.84	68,68,68,68	0
22	MG	A	1585	1/1	0.16	-1.01	41,41,41,41	0
22	MG	A	1577	1/1	0.16	-1.28	20,20,20,20	0
22	MG	A	1556	1/1	0.11	-1.40	47,47,47,47	0
22	MG	A	1584	1/1	0.15	-1.41	45,45,45,45	0
22	MG	A	1553	1/1	0.10	-1.49	71,71,71,71	0
22	MG	A	1604	1/1	0.07	-1.58	26,26,26,26	0
22	MG	A	1579	1/1	0.12	-1.66	68,68,68,68	0
22	MG	A	1594	1/1	0.10	-1.71	44,44,44,44	0
22	MG	A	1555	1/1	0.10	-1.76	78,78,78,78	0
22	MG	A	1576	1/1	0.07	-1.88	61,61,61,61	0
22	MG	A	1581	1/1	0.12	-1.95	117,117,117,117	0
22	MG	A	1562	1/1	0.10	-1.95	35,35,35,35	0
22	MG	A	1578	1/1	0.14	-1.95	51,51,51,51	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
22	MG	A	1554	1/1	0.08	-2.37	29,29,29,29	0
22	MG	A	1573	1/1	0.08	-2.69	36,36,36,36	0
22	MG	A	1567	1/1	0.06	-2.96	26,26,26,26	0
22	MG	A	1545	1/1	0.10	-3.01	69,69,69,69	0
22	MG	A	1595	1/1	0.09	-3.24	45,45,45,45	0
22	MG	A	1552	1/1	0.09	-3.38	34,34,34,34	0
22	MG	A	1550	1/1	0.08	-3.43	110,110,110,110	0
22	MG	A	1597	1/1	0.07	-3.53	48,48,48,48	0
22	MG	A	1587	1/1	0.09	-3.53	82,82,82,82	0
22	MG	A	1575	1/1	0.07	-3.73	47,47,47,47	0
22	MG	A	1591	1/1	0.08	-3.81	88,88,88,88	0
22	MG	A	1593	1/1	0.08	-3.97	14,14,14,14	0
22	MG	A	1559	1/1	0.09	-4.01	9,9,9,9	0
22	MG	A	1566	1/1	0.10	-4.19	48,48,48,48	0
22	MG	A	1551	1/1	0.09	-4.38	45,45,45,45	0
22	MG	A	1548	1/1	0.11	-4.59	74,74,74,74	0
22	MG	A	1602	1/1	0.06	-4.74	65,65,65,65	0
22	MG	A	1561	1/1	0.07	-4.75	26,26,26,26	0
22	MG	A	1600	1/1	0.07	-5.35	38,38,38,38	0
22	MG	A	1586	1/1	0.07	-5.70	29,29,29,29	0
22	MG	A	1603	1/1	0.07	-5.94	62,62,62,62	0
22	MG	A	1588	1/1	0.07	-8.16	42,42,42,42	0
22	MG	A	1582	1/1	0.07	-8.49	11,11,11,11	0
22	MG	A	1560	1/1	0.06	-8.70	5,5,5,5	0
22	MG	A	1590	1/1	0.04	-9.16	56,56,56,56	0
22	MG	A	1549	1/1	0.08	-9.34	18,18,18,18	0
22	MG	A	1543	1/1	0.04	-9.68	5,5,5,5	0
22	MG	A	1601	1/1	0.08	-10.21	48,48,48,48	0
22	MG	A	1571	1/1	0.08	-15.25	45,45,45,45	0
22	MG	A	1568	1/1	0.11	-43.64	73,73,73,73	0
22	MG	A	1592	1/1	0.10	-83.00	82,82,82,82	0
22	MG	A	1569	1/1	0.12	-	29,29,29,29	1

## 6.5 Other polymers ⓘ

There are no such residues in this entry.