



# Full wwPDB X-ray Structure Validation Report ⓘ

Dec 13, 2023 – 12:06 pm GMT

PDB ID : 4B3R  
Title : Crystal structure of the 30S ribosome in complex with compound 30  
Authors : Ng, C.L.; Lang, K.; Shcherbakov, D.; Matt, T.; Perez-Fernandez, D.; Patak, R.; Meyer, M.; Duscha, S.; Akbergenov, R.; Boukari, H.; Freihof, P.; Kudyba, I.; Reddy, M.S.K.; Nandurikar, R.S.; Ramakrishnan, V.; Vasella, A.; Bottger, E.C.  
Deposited on : 2012-07-26  
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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The following versions of software and data (see [references](#) ①) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.4, CSD as541be (2020)  
Xtrriage (Phenix) : 1.13  
EDS : 2.36  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

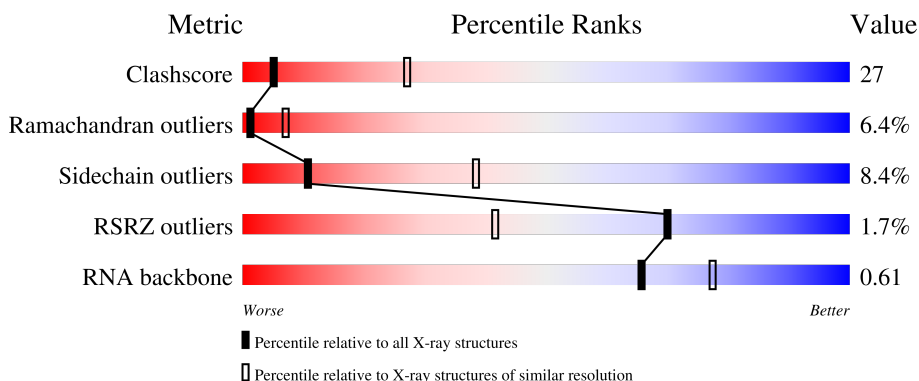
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.00 Å.

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






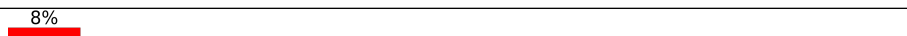
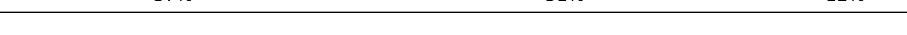
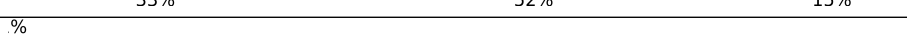
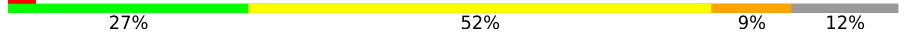

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)
RNA backbone	3102	1173 (3.30-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	1521	
2	B	256	
3	C	239	
4	D	208	
5	E	161	

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Mol	Chain	Length	Quality of chain
6	F	101	
7	G	155	
8	H	138	
9	I	128	
10	J	104	
11	K	129	
12	L	132	
13	M	126	
14	N	60	
15	O	88	
16	P	88	
17	Q	104	
18	R	88	
19	S	92	
20	T	106	
21	V	26	
22	W	6	
23	Z	16	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
24	MG	A	2549	-	-	-	X
24	MG	A	2551	-	-	-	X
24	MG	A	2568	-	-	-	X
24	MG	A	2570	-	-	-	X
24	MG	A	2571	-	-	-	X
24	MG	A	2593	-	-	-	X
24	MG	A	2595	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
24	MG	A	2644	-	-	-	X
24	MG	A	2657	-	-	-	X
24	MG	A	2679	-	-	-	X
24	MG	A	2680	-	-	-	X
24	MG	A	2681	-	-	-	X
24	MG	A	2687	-	-	-	X
24	MG	A	2694	-	-	-	X
24	MG	A	2697	-	-	-	X
24	MG	A	2698	-	-	-	X
24	MG	A	2700	-	-	-	X
24	MG	A	2707	-	-	-	X
24	MG	A	2727	-	-	-	X
24	MG	A	2728	-	-	-	X
24	MG	A	2732	-	-	-	X

## 2 Entry composition [i](#)

There are 28 unique types of molecules in this entry. The entry contains 52404 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 16S RIBOSOMAL RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
1	A	1512	32486	14462	6011	10503	1510	0	0	0

- Molecule 2 is a protein called 30S RIBOSOMAL PROTEIN S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	235	1901	1213	342	341	5	0	0	1

- Molecule 3 is a protein called 30S RIBOSOMAL PROTEIN S3.

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

- Molecule 4 is a protein called 30S RIBOSOMAL PROTEIN S4.

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

- Molecule 5 is a protein called 30S RIBOSOMAL PROTEIN S5.

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

- Molecule 6 is a protein called 30S RIBOSOMAL PROTEIN S6.

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

- Molecule 7 is a protein called 30S RIBOSOMAL PROTEIN S7.

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

- Molecule 8 is a protein called 30S RIBOSOMAL PROTEIN S8.

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

- Molecule 9 is a protein called 30S RIBOSOMAL PROTEIN S9.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
9	I	127	1011	639	198	174	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	57	ARG	HIS	conflict	UNP P80374

- Molecule 10 is a protein called 30S RIBOSOMAL PROTEIN S10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
10	J	99	795	499	157	138	1	0	0	1

- Molecule 11 is a protein called 30S RIBOSOMAL PROTEIN S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
11	K	119	885	549	168	165	3	0	0	0

- Molecule 12 is a protein called 30S RIBOSOMAL PROTEIN S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
12	L	125	971	611	196	163	1	0	0	1

- Molecule 13 is a protein called 30S RIBOSOMAL PROTEIN S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
13	M	125	997	617	207	171	2	0	0	0

- Molecule 14 is a protein called 30S RIBOSOMAL PROTEIN S14 TYPE Z.

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

- Molecule 15 is a protein called 30S RIBOSOMAL PROTEIN S15.

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

- Molecule 16 is a protein called 30S RIBOSOMAL PROTEIN S16.

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

- Molecule 17 is a protein called 30S RIBOSOMAL PROTEIN S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
17	Q	104	857	547	161	147	2	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	95	GLN	GLU	conflict	UNP Q5SHP7

- Molecule 18 is a protein called 30S RIBOSOMAL PROTEIN S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
18	R	73	597	380	118	99	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	45	GLY	ALA	conflict	UNP Q5SLQ0



- Molecule 19 is a protein called 30S RIBOSOMAL PROTEIN S19.

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

- Molecule 20 is a protein called 30S RIBOSOMAL PROTEIN S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
20	T	99	762	469	162	129	2	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
T	34	VAL	ILE	conflict	UNP P80380

- Molecule 21 is a protein called 30S RIBOSOMAL PROTEIN THX.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
22	W	4	79	37	12	27	3	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
23	Z	15	319	144	60	101	14	0	0	0

- Molecule 24 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
24	A	192	Total	Mg	0	0
			192	192		
24	B	2	Total	Mg	0	0
			2	2		

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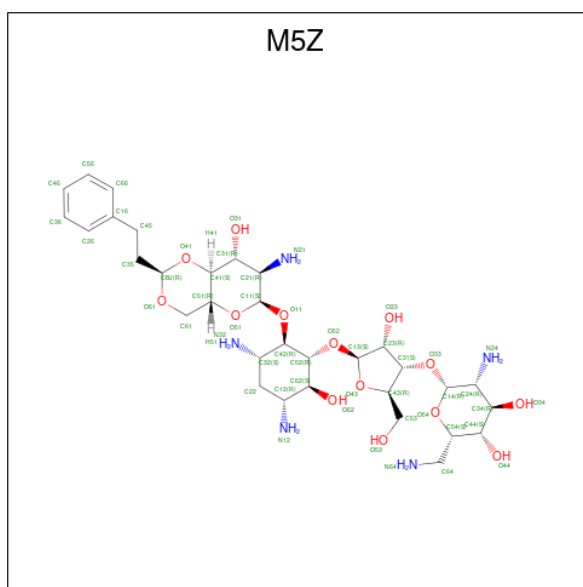
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
24	D	1	Total Mg 1 1	0	0
24	E	2	Total Mg 2 2	0	0
24	F	1	Total Mg 1 1	0	0
24	H	2	Total Mg 2 2	0	0
24	J	1	Total Mg 1 1	0	0
24	K	1	Total Mg 1 1	0	0
24	L	1	Total Mg 1 1	0	0
24	M	1	Total Mg 1 1	0	0
24	N	1	Total Mg 1 1	0	0
24	Q	2	Total Mg 2 2	0	0

- Molecule 25 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
25	A	14	Total K 14 14	0	0

- Molecule 26 is (1R,2R,3S,4R,6S)-4,6-diamino-2-{{3-O-(2,6-diamino-2,6-dideoxy-beta-L-idopyranosyl)-beta-D-ribofuranosyl]oxy}-3-hydroxycyclohexyl 2-amino-2-deoxy-4,6-O-[(1R)-3-phenylpropylidene]-alpha-D-glucopyranoside (three-letter code: M5Z) (formula: C<sub>32</sub>H<sub>53</sub>N<sub>5</sub>O<sub>14</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
26	A	1	51	32	5	14	0	0

- Molecule 27 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 28 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
28	A	7	7	7	0	0

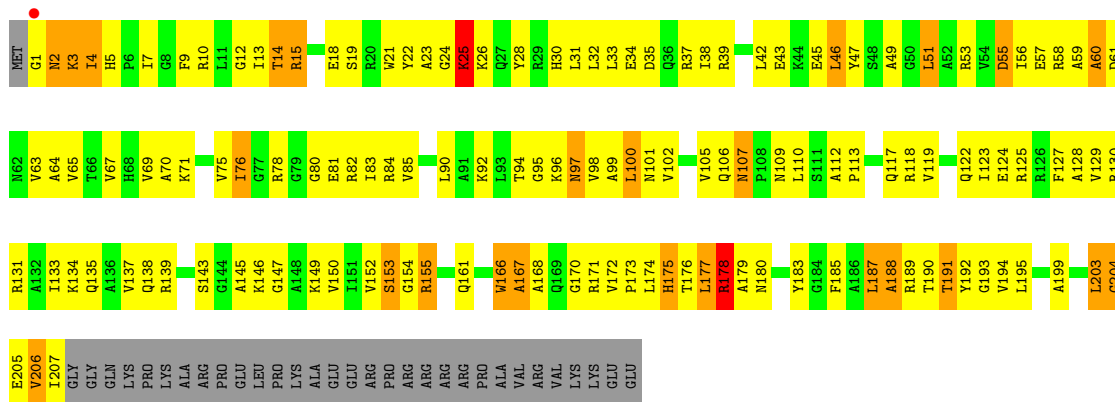






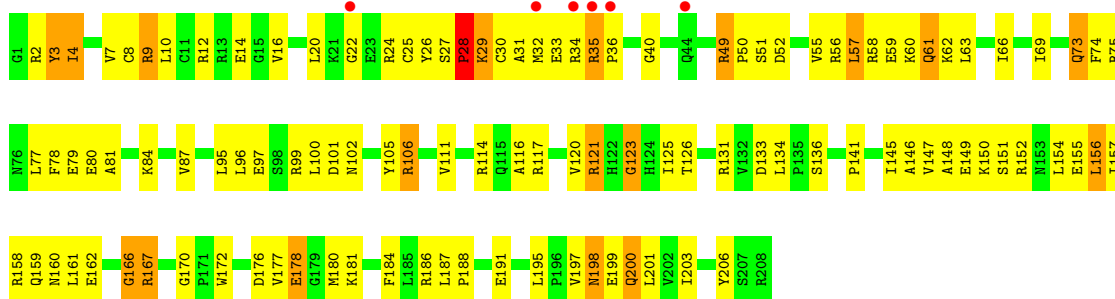
- Molecule 3: 30S RIBOSOMAL PROTEIN S3

Chain C: 28% 47% 10% 13%



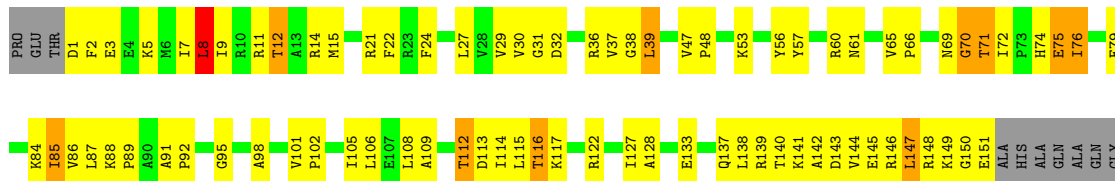
- Molecule 4: 30S RIBOSOMAL PROTEIN S4

Chain D: 3% 46% 45% 9%



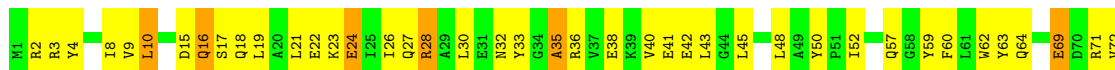
- Molecule 5: 30S RIBOSOMAL PROTEIN S5

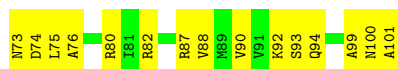
Chain E: 43% 43% 6% 6%



- Molecule 6: 30S RIBOSOMAL PROTEIN S6

Chain F: 45% 50% 6%





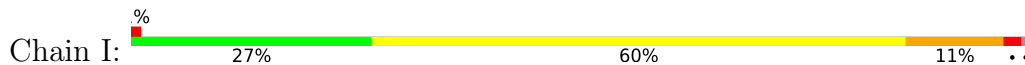
- Molecule 7: 30S RIBOSOMAL PROTEIN S7



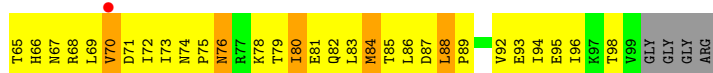
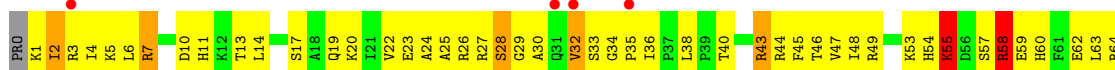
- Molecule 8: 30S RIBOSOMAL PROTEIN S8



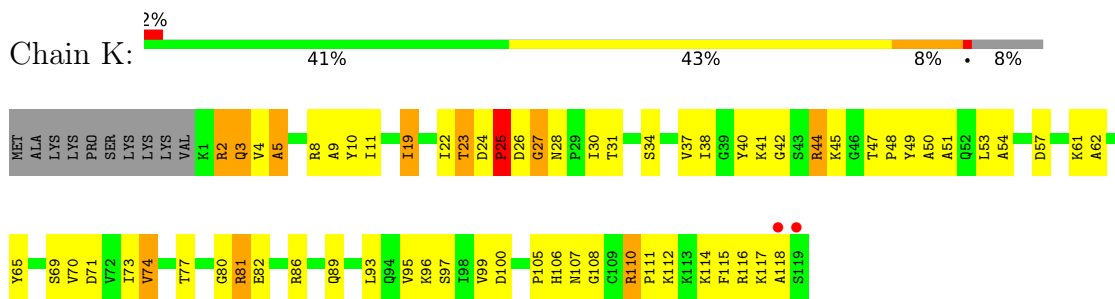
- Molecule 9: 30S RIBOSOMAL PROTEIN S9



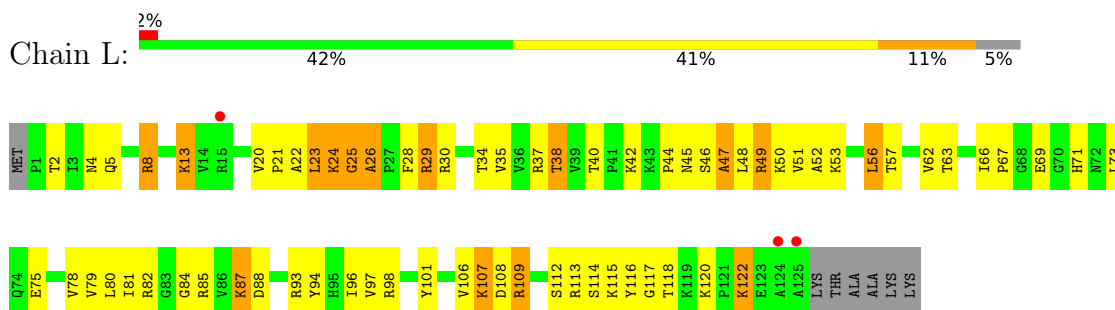
- Molecule 10: 30S RIBOSOMAL PROTEIN S10



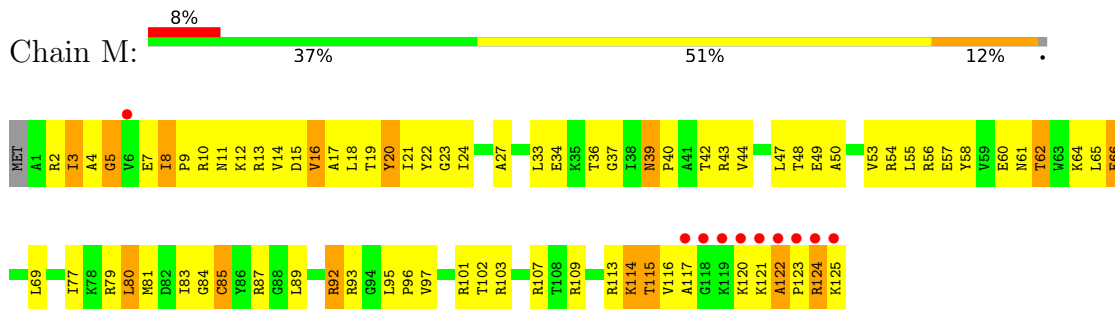
- Molecule 11: 30S RIBOSOMAL PROTEIN S11



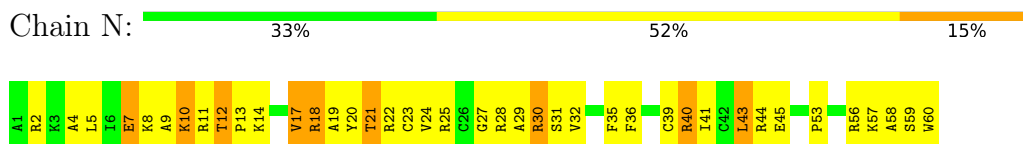
- Molecule 12: 30S RIBOSOMAL PROTEIN S12



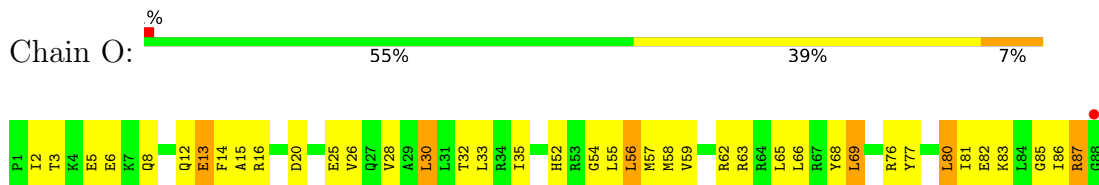
- Molecule 13: 30S RIBOSOMAL PROTEIN S13



- Molecule 14: 30S RIBOSOMAL PROTEIN S14 TYPE Z



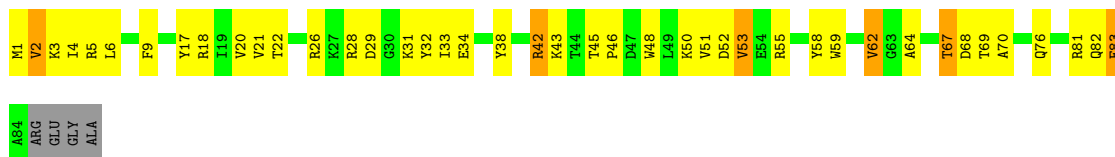
- Molecule 15: 30S RIBOSOMAL PROTEIN S15



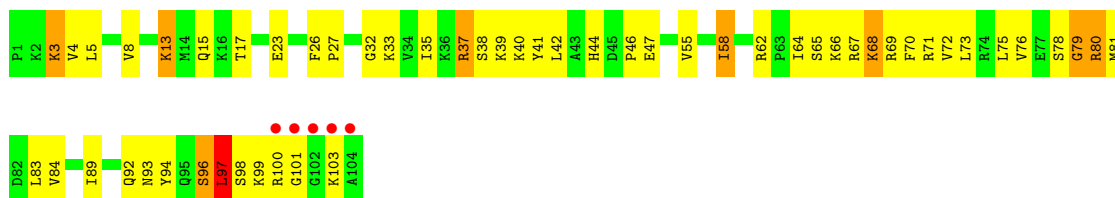
- Molecule 16: 30S RIBOSOMAL PROTEIN S16



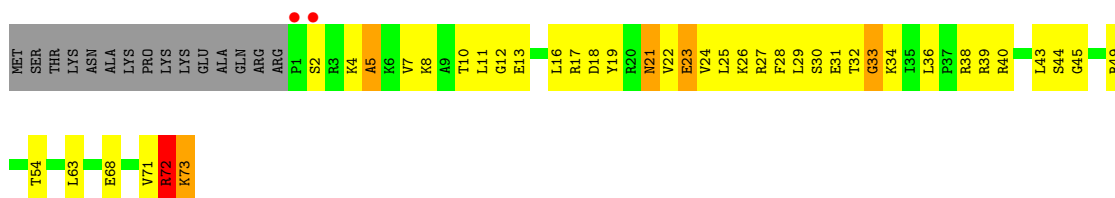




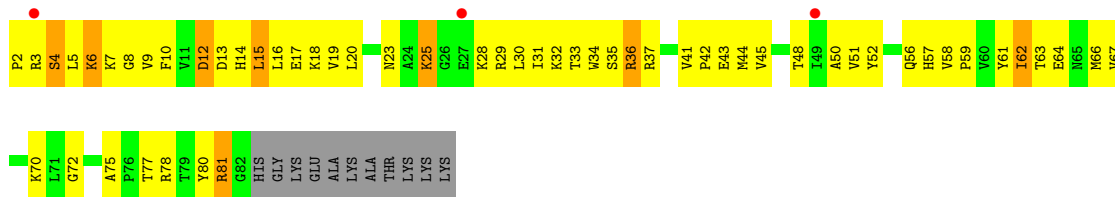
- Molecule 17: 30S RIBOSOMAL PROTEIN S17



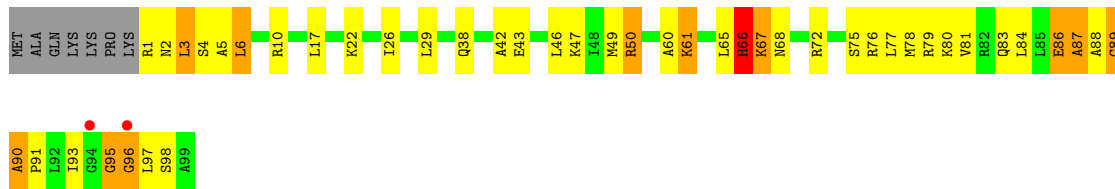
- Molecule 18: 30S RIBOSOMAL PROTEIN S18



- Molecule 19: 30S RIBOSOMAL PROTEIN S19



- Molecule 20: 30S RIBOSOMAL PROTEIN S20

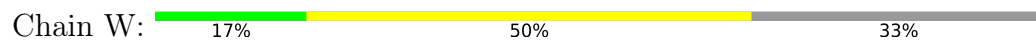


- Molecule 21: 30S RIBOSOMAL PROTEIN THX

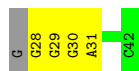




- Molecule 22: 5'-R(\*UP\*UP\*CP\*AP\*AP\*AP)-3'



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



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	402.48Å 402.48Å 174.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 3.00 39.82 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.3 (40.00-3.00) 99.3 (39.82-3.00)	Depositor EDS
$R_{merge}$	0.13	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.14 (at 3.01Å)	Xtrriage
Refinement program	CNS 1.2	Depositor
R, $R_{free}$	0.214 , 0.248 0.217 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	73.3	Xtrriage
Anisotropy	0.192	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 76.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	52404	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	82.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.56% of the height of the origin peak. No significant pseudotranslation is detected.*

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

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

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, M5Z, K, 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	0.46	0/36362	0.78	76/56750 (0.1%)
2	B	0.36	0/1936	0.64	0/2611
3	C	0.40	0/1637	0.65	0/2207
4	D	0.38	0/1733	0.60	0/2318
5	E	0.46	0/1163	0.71	1/1566 (0.1%)
6	F	0.34	0/856	0.62	0/1154
7	G	0.38	0/1276	0.60	0/1709
8	H	0.44	0/1136	0.72	0/1527
9	I	0.39	0/1029	0.65	0/1378
10	J	0.38	0/808	0.67	0/1087
11	K	0.41	0/900	0.67	1/1213 (0.1%)
12	L	0.48	0/987	0.74	0/1322
13	M	0.36	0/1008	0.62	0/1347
14	N	0.49	0/501	0.69	0/664
15	O	0.35	0/745	0.59	0/992
16	P	0.44	0/717	0.74	0/965
17	Q	0.45	0/870	0.73	0/1159
18	R	0.34	0/603	0.61	0/799
19	S	0.38	0/662	0.68	0/892
20	T	0.40	0/764	0.71	1/1006 (0.1%)
21	V	0.50	0/213	0.62	0/279
22	W	0.44	0/87	0.80	0/133
23	Z	0.40	0/357	0.65	0/555
All	All	0.44	0/56350	0.74	79/83633 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	47	38

There are no bond length outliers.

All (79) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	925	G	N9-C1'-C2'	14.23	132.50	114.00
1	A	573	A	N9-C1'-C2'	13.04	130.95	114.00
1	A	871	U	N1-C1'-C2'	11.46	128.89	114.00
1	A	189(H)	G	N9-C1'-C2'	11.32	128.71	114.00
1	A	1042	G	N9-C1'-C2'	10.97	128.26	114.00
1	A	925	G	C2'-C3'-O3'	10.71	133.05	109.50
1	A	189(H)	G	O4'-C4'-C3'	-10.45	93.55	104.00
1	A	753	A	N9-C1'-C2'	10.40	127.52	114.00
1	A	366	C	N1-C1'-C2'	9.92	126.90	114.00
1	A	1049	U	N1-C1'-C2'	9.87	126.83	114.00
1	A	925	G	C5'-C4'-O4'	9.79	120.85	109.10
1	A	1400	C	C2'-C3'-O3'	9.68	130.81	109.50
1	A	884	U	C2'-C3'-O3'	9.62	130.67	109.50
1	A	925	G	O4'-C1'-N9	-9.50	100.60	108.20
1	A	60	A	N9-C1'-C2'	9.46	126.29	114.00
1	A	1452	C	C2'-C3'-O3'	9.32	130.01	109.50
1	A	351	G	N9-C1'-C2'	9.30	126.09	114.00
1	A	305	G	C2'-C3'-O3'	9.21	129.77	109.50
1	A	189(G)	G	C2'-C3'-O3'	9.10	129.52	109.50
1	A	573	A	C5'-C4'-O4'	9.04	119.94	109.10
1	A	1122	U	N1-C1'-C2'	9.01	125.71	114.00
1	A	872	A	C2'-C3'-O3'	8.98	129.27	109.50
1	A	109	A	C2'-C3'-O3'	8.75	128.76	109.50
1	A	1067	A	N9-C1'-C2'	8.67	125.27	114.00
1	A	189(H)	G	O4'-C1'-N9	-8.49	101.41	108.20
1	A	189(H)	G	C2'-C3'-O3'	8.46	128.12	109.50
1	A	721	G	N9-C1'-C2'	8.46	124.99	114.00
1	A	474	G	N9-C1'-C2'	8.32	124.81	114.00
1	A	277	C	C2'-C3'-O3'	8.08	127.27	109.50
1	A	119	A	C5'-C4'-C3'	-8.05	103.12	116.00
1	A	730	G	C2'-C3'-O3'	7.90	126.89	109.50
1	A	1364	U	N1-C1'-C2'	7.64	123.93	114.00
1	A	573	A	C2'-C3'-O3'	7.51	126.02	109.50
1	A	871	U	C5'-C4'-O4'	7.43	118.02	109.10
1	A	721	G	C2'-C3'-O3'	7.40	125.78	109.50
1	A	925	G	O4'-C4'-C3'	-7.39	96.61	104.00
1	A	189(H)	G	C5'-C4'-O4'	7.35	117.92	109.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	992	U	C5'-C4'-O4'	7.28	117.84	109.10
1	A	820	U	C2'-C3'-O3'	7.20	125.34	109.50
1	A	35	G	N9-C1'-C2'	-7.20	104.08	112.00
1	A	721	G	C5'-C4'-C3'	6.96	127.13	116.00
1	A	1301	U	N1-C1'-C2'	6.69	122.69	114.00
1	A	573	A	O4'-C1'-N9	-6.62	102.90	108.20
1	A	1018	C	C2'-C3'-O3'	6.59	124.24	113.70
1	A	1364	U	C2'-C3'-O3'	6.54	124.16	113.70
1	A	366	C	C5'-C4'-O4'	6.52	116.92	109.10
1	A	792	A	N9-C1'-C2'	6.45	122.38	114.00
1	A	753	A	C5'-C4'-O4'	6.44	116.83	109.10
1	A	992	U	C5'-C4'-C3'	6.36	126.18	116.00
1	A	1299	A	N9-C1'-C2'	6.29	122.18	114.00
1	A	1042	G	C2'-C3'-O3'	6.21	123.63	113.70
1	A	60	A	C5'-C4'-O4'	6.15	116.48	109.10
1	A	992	U	N1-C1'-C2'	6.02	121.83	114.00
1	A	1502	A	N9-C1'-C2'	5.98	121.77	114.00
1	A	792	A	C5'-C4'-O4'	5.88	116.16	109.10
1	A	1042	G	C5'-C4'-C3'	5.84	125.34	116.00
1	A	60	A	O4'-C1'-N9	5.64	112.71	108.20
1	A	328	C	N1-C1'-C2'	5.61	121.29	114.00
20	T	6	LEU	N-CA-C	-5.59	95.89	111.00
1	A	189(G)	G	C4'-C3'-O3'	5.55	124.11	113.00
1	A	474	G	C2'-C3'-O3'	5.52	122.54	113.70
1	A	820	U	C4'-C3'-O3'	-5.51	97.83	109.40
1	A	7	G	C5'-C4'-C3'	-5.46	107.26	116.00
1	A	51	A	N9-C1'-C2'	5.43	121.06	114.00
1	A	1017	G	C2'-C3'-O3'	5.40	122.34	113.70
1	A	281	G	C5'-C4'-C3'	-5.33	107.46	116.00
1	A	601	C	C5'-C4'-C3'	-5.31	107.50	116.00
1	A	1053	G	C2'-C3'-O3'	5.30	122.18	113.70
1	A	974	A	N9-C1'-C2'	5.29	120.88	114.00
1	A	707	C	C5'-C4'-C3'	-5.27	107.57	116.00
1	A	1122	U	C2'-C3'-O3'	5.27	122.13	113.70
5	E	8	LEU	CA-CB-CG	5.23	127.33	115.30
11	K	27	GLY	N-CA-C	5.20	126.09	113.10
1	A	1067	A	C1'-O4'-C4'	-5.19	105.75	109.90
1	A	305	G	C4'-C3'-O3'	5.14	123.29	113.00
1	A	109	A	C4'-C3'-C2'	5.13	107.73	102.60
1	A	872	A	C4'-C3'-O3'	5.12	123.24	113.00
1	A	871	U	O4'-C1'-N1	5.07	112.25	108.20
1	A	1452	C	C4'-C3'-O3'	5.02	123.04	113.00

All (47) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	60	A	C4',C3',C1'
1	A	109	A	C3'
1	A	189(G)	G	C3'
1	A	189(H)	G	C4',C1'
1	A	277	C	C3'
1	A	305	G	C3'
1	A	351	G	C4'
1	A	366	C	C4',C3',C1'
1	A	474	G	C4',C3',C1'
1	A	573	A	C4',C1'
1	A	721	G	C4'
1	A	730	G	C3'
1	A	753	A	C4',C3',C1'
1	A	792	A	C4'
1	A	871	U	C4',C3',C1'
1	A	872	A	C3'
1	A	884	U	C3'
1	A	925	G	C4',C1'
1	A	992	U	C4'
1	A	1018	C	C3'
1	A	1042	G	C4',C3',C1'
1	A	1049	U	C4',C3',C1'
1	A	1067	A	C4'
1	A	1122	U	C4',C3',C1'
1	A	1346	A	C4'
1	A	1364	U	C4',C3'
1	A	1452	C	C3'

All (38) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1048	G	Sidechain
1	A	1077	G	Sidechain
1	A	1079	G	Sidechain
1	A	1094	G	Sidechain
1	A	112	G	Sidechain
1	A	1226	C	Sidechain
1	A	1288	A	Sidechain
1	A	1331	G	Sidechain
1	A	1346	A	Sidechain
1	A	1401	G	Sidechain
1	A	1406	U	Sidechain

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Mol	Chain	Res	Type	Group
1	A	1414	U	Sidechain
1	A	1457	G	Sidechain
1	A	1519	A	Sidechain
1	A	189(H)	G	Sidechain
1	A	195	A	Sidechain
1	A	229	U	Sidechain
1	A	297	G	Sidechain
1	A	317	G	Sidechain
1	A	35	G	Sidechain
1	A	380	G	Sidechain
1	A	474	G	Sidechain
1	A	529	G	Sidechain
1	A	560	U	Sidechain
1	A	573	A	Sidechain
1	A	587	G	Sidechain
1	A	664	G	Sidechain
1	A	727	G	Sidechain
1	A	73	G	Sidechain
1	A	753	A	Sidechain
1	A	871	U	Sidechain
1	A	879	C	Sidechain
1	A	883	C	Sidechain
1	A	898	G	Sidechain
1	A	925	G	Sidechain
1	A	940	C	Sidechain
1	A	946	A	Sidechain
1	A	974	A	Sidechain

## 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32486	0	16402	875	0
2	B	1901	0	1954	208	1
3	C	1613	0	1680	196	0
4	D	1703	0	1767	121	0
5	E	1147	0	1210	78	0
6	F	843	0	857	74	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	G	1257	0	1299	83	0
8	H	1116	0	1177	71	0
9	I	1011	0	1046	109	0
10	J	795	0	843	137	0
11	K	885	0	907	76	0
12	L	971	0	1059	94	0
13	M	997	0	1075	98	0
14	N	492	0	533	56	0
15	O	734	0	773	37	0
16	P	701	0	720	38	0
17	Q	857	0	932	59	0
18	R	597	0	670	66	0
19	S	648	0	673	88	0
20	T	762	0	862	54	0
21	V	209	0	221	10	0
22	W	79	0	44	2	0
23	Z	319	0	164	5	0
24	A	192	0	0	0	0
24	B	2	0	0	0	0
24	D	1	0	0	0	0
24	E	2	0	0	0	0
24	F	1	0	0	0	0
24	H	2	0	0	0	0
24	J	1	0	0	0	0
24	K	1	0	0	0	0
24	L	1	0	0	0	0
24	M	1	0	0	0	0
24	N	1	0	0	0	0
24	Q	2	0	0	0	0
25	A	14	0	0	0	0
26	A	51	0	53	3	0
27	D	1	0	0	0	0
27	N	1	0	0	0	0
28	A	7	0	0	1	0
All	All	52404	0	36921	2399	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 27.

All (2399) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:972:C:H4'	10:J:55:LYS:HG2	1.24	1.13
1:A:177:C:H2'	1:A:178:C:H5''	1.27	1.12
6:F:28:ARG:HH11	6:F:28:ARG:HB2	1.10	1.09
10:J:43:ARG:HB3	10:J:43:ARG:HH11	1.04	1.09
1:A:188:C:H2'	1:A:189:G:H5''	1.27	1.09
1:A:1286:A:H3'	1:A:1287:A:H5''	1.34	1.09
3:C:2:ASN:HD22	3:C:2:ASN:N	1.47	1.09
3:C:25:LYS:H	3:C:25:LYS:HE2	1.04	1.09
19:S:33:THR:HG22	19:S:35:SER:H	1.13	1.09
12:L:37:ARG:HG2	12:L:38:THR:H	1.08	1.08
1:A:402:G:H2'	1:A:403:C:H5''	1.32	1.08
3:C:13:ILE:HG22	3:C:14:THR:H	1.19	1.07
1:A:1474:G:H3'	1:A:1475:G:H5''	1.38	1.05
12:L:87:LYS:HA	12:L:87:LYS:HE3	1.37	1.05
1:A:177:C:C2'	1:A:178:C:H5''	1.86	1.05
13:M:116:VAL:HG12	13:M:117:ALA:H	1.18	1.03
1:A:1543:C:H2'	1:A:1544:U:H5''	1.37	1.03
1:A:1014:A:H4'	19:S:14:HIS:HD2	1.20	1.02
2:B:78:GLU:HB3	2:B:213:VAL:HG21	1.40	1.02
1:A:1029:C:H2'	1:A:1030:C:H5''	1.39	1.02
2:B:55:LEU:HD22	2:B:60:GLY:HA3	1.40	1.01
2:B:106:VAL:HG13	2:B:147:ARG:HG2	1.42	0.99
1:A:1041:A:H2'	1:A:1042:G:H5''	1.43	0.99
11:K:44:ARG:O	11:K:47:THR:HG22	1.63	0.99
4:D:61:GLN:HA	4:D:61:GLN:HE21	1.24	0.98
2:B:63:LEU:HD22	2:B:149:LEU:HD11	1.45	0.98
2:B:74:ILE:HD11	2:B:202:ILE:HG23	1.42	0.98
1:A:188:C:C2'	1:A:189:G:H5''	1.93	0.98
10:J:43:ARG:HB3	10:J:43:ARG:NH1	1.79	0.97
1:A:1287:A:HO2'	1:A:1288:A:H8	1.03	0.96
2:B:159:VAL:HG23	2:B:160:ASP:H	1.30	0.96
1:A:1060:C:C5	3:C:1:GLY:HA3	2.01	0.96
1:A:1101:A:H4'	1:A:1102:A:O5'	1.64	0.95
1:A:1247:U:H2'	1:A:1248:A:H5''	1.48	0.95
11:K:44:ARG:HB3	11:K:44:ARG:HH11	1.31	0.95
19:S:28:LYS:HG2	19:S:29:ARG:H	1.32	0.95
8:H:64:LYS:HG2	8:H:79:VAL:HG21	1.50	0.94
1:A:1187:G:H5'	9:I:112:LYS:HE3	1.47	0.94
1:A:647:C:C2'	1:A:648:A:H5''	1.98	0.94
1:A:647:C:H2'	1:A:648:A:H5''	1.45	0.94
1:A:35:G:HO2'	1:A:36:C:H6	1.14	0.93
1:A:870:U:H4'	1:A:871:U:H5'	1.48	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:25:LYS:H	3:C:25:LYS:CE	1.81	0.93
7:G:112:GLU:HG2	7:G:118:ARG:HG2	1.49	0.93
9:I:7:GLY:HA2	9:I:78:LEU:HD12	1.51	0.93
11:K:38:ILE:HD11	11:K:54:ALA:HA	1.51	0.93
6:F:10:LEU:HD12	6:F:59:TYR:HB3	1.52	0.92
23:Z:29:G:H2'	23:Z:30:G:H8	1.35	0.92
1:A:975:A:H4'	1:A:976:G:H5''	1.52	0.91
3:C:2:ASN:H	3:C:2:ASN:ND2	1.68	0.91
13:M:9:PRO:HB2	13:M:17:ALA:HB1	1.51	0.91
3:C:130:ARG:HG2	3:C:134:LYS:HE3	1.50	0.91
4:D:186:ARG:HE	4:D:187:LEU:H	1.05	0.91
3:C:107:ASN:HD21	3:C:143:SER:HB2	1.34	0.91
1:A:664:G:H22	1:A:741:G:H1	1.19	0.90
10:J:19:GLN:HA	10:J:22:VAL:HG12	1.50	0.90
1:A:1014:A:H4'	19:S:14:HIS:CD2	2.05	0.90
1:A:402:G:C2'	1:A:403:C:H5''	2.02	0.90
6:F:100:ASN:HD22	18:R:8:LYS:HG2	1.38	0.89
1:A:870:U:H4'	1:A:871:U:C5'	2.01	0.89
4:D:34:ARG:O	4:D:35:ARG:HB2	1.71	0.89
1:A:1127:G:H1	1:A:1144:G:H1	0.92	0.89
1:A:1086:U:H3	1:A:1099:G:H22	1.20	0.89
12:L:37:ARG:HG2	12:L:38:THR:N	1.87	0.89
15:O:15:ALA:HB1	15:O:20:ASP:HB3	1.53	0.88
20:T:50:ARG:HE	20:T:93:ILE:HG21	1.38	0.88
1:A:939:G:H5''	7:G:101:ARG:NH2	1.89	0.88
3:C:190:THR:HG22	3:C:192:TYR:H	1.38	0.88
3:C:25:LYS:HE2	3:C:25:LYS:N	1.90	0.87
6:F:36:ARG:HH12	6:F:38:GLU:HG2	1.39	0.87
1:A:457:C:H2'	1:A:458:C:H6	1.39	0.87
1:A:167:G:C2'	1:A:168:G:H5''	2.05	0.86
13:M:87:ARG:HH11	19:S:3:ARG:HH21	1.20	0.86
1:A:277:C:H5''	17:Q:67:ARG:HH21	1.40	0.86
6:F:94:GLN:HE21	18:R:17:ARG:HH11	1.23	0.86
10:J:62:GLU:HG2	14:N:58:ALA:HB2	1.57	0.86
3:C:118:ARG:HG2	3:C:139:ARG:HH12	1.42	0.85
19:S:33:THR:HG22	19:S:35:SER:N	1.92	0.85
2:B:194:ILE:H	2:B:194:ILE:HD12	1.40	0.85
1:A:1029:C:C2'	1:A:1030:C:H5''	2.07	0.85
1:A:1190:G:OP1	3:C:3:LYS:HA	1.76	0.85
6:F:28:ARG:HB2	6:F:28:ARG:NH1	1.90	0.85
13:M:2:ARG:HG2	13:M:8:ILE:HD12	1.59	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:88:ASN:HD22	2:B:88:ASN:H	1.22	0.85
3:C:33:LEU:HD12	14:N:24:VAL:HG21	1.58	0.84
17:Q:94:TYR:HA	17:Q:97:LEU:HD11	1.58	0.84
1:A:1367:C:H5'	10:J:58:ARG:HH12	1.42	0.84
4:D:25:CYS:HA	4:D:30:CYS:HB2	1.60	0.84
11:K:38:ILE:HD11	11:K:54:ALA:CA	2.07	0.84
3:C:2:ASN:N	3:C:2:ASN:ND2	2.22	0.84
5:E:70:GLY:HA3	5:E:112:THR:HG22	1.59	0.84
2:B:166:ILE:HD12	2:B:166:ILE:H	1.43	0.84
9:I:69:LYS:O	9:I:73:ILE:HG12	1.77	0.84
1:A:1223:C:P	19:S:78:ARG:HH12	2.00	0.83
1:A:1474:G:C3'	1:A:1475:G:H5''	2.07	0.83
8:H:60:ARG:HH11	8:H:60:ARG:HG3	1.41	0.83
18:R:23:GLU:HA	18:R:26:LYS:HE2	1.59	0.83
11:K:70:VAL:HG21	11:K:93:LEU:HD13	1.59	0.83
18:R:11:LEU:HD12	18:R:12:GLY:H	1.41	0.83
12:L:56:LEU:HD11	12:L:81:ILE:HD12	1.60	0.83
21:V:10:ARG:HH11	21:V:10:ARG:HG3	1.43	0.83
18:R:21:ASN:HD21	18:R:23:GLU:HG2	1.41	0.83
13:M:77:ILE:HA	13:M:80:LEU:HD11	1.59	0.82
6:F:94:GLN:NE2	18:R:17:ARG:HD3	1.93	0.82
4:D:198:ASN:HD21	4:D:200:GLN:HB2	1.44	0.82
12:L:24:LYS:O	12:L:26:ALA:N	2.12	0.82
13:M:39:ASN:HD22	13:M:40:PRO:HD2	1.42	0.82
1:A:35:G:O2'	1:A:36:C:H6	1.62	0.82
1:A:167:G:H2'	1:A:168:G:H5''	1.59	0.82
1:A:1288:A:HO2'	1:A:1289:A:H8	1.28	0.82
3:C:2:ASN:HD22	3:C:2:ASN:H	0.86	0.82
7:G:53:THR:HG22	7:G:55:GLN:H	1.44	0.82
1:A:925:G:H4'	1:A:926:G:OP2	1.78	0.82
1:A:1543:C:C2'	1:A:1544:U:H5''	2.10	0.81
18:R:21:ASN:ND2	18:R:23:GLU:HG2	1.96	0.81
1:A:946:A:H2'	1:A:947:G:C8	2.15	0.81
1:A:939:G:H5''	7:G:101:ARG:HH22	1.45	0.81
1:A:1286:A:H3'	1:A:1287:A:C5'	2.10	0.81
1:A:1435:G:H2'	1:A:1436:U:C6	2.14	0.81
3:C:90:LEU:HB3	3:C:98:VAL:HG11	1.63	0.81
11:K:8:ARG:HB2	11:K:23:THR:HG23	1.62	0.81
1:A:190:U:O2	20:T:98:SER:HB2	1.81	0.81
12:L:24:LYS:C	12:L:26:ALA:H	1.80	0.80
2:B:85:PRO:HG3	2:B:148:LEU:HB2	1.62	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:123:GLY:HA3	4:D:131:ARG:HD2	1.63	0.80
13:M:53:VAL:O	13:M:57:GLU:HG2	1.82	0.80
5:E:5:LYS:HG3	5:E:108:LEU:HD11	1.62	0.80
10:J:47:VAL:HG13	14:N:40:ARG:HB2	1.63	0.80
1:A:60:A:H2'	1:A:61:G:O4'	1.82	0.80
1:A:1095:U:H2'	1:A:1096:C:C6	2.16	0.80
10:J:47:VAL:O	10:J:58:ARG:HA	1.82	0.80
1:A:1127:G:H2'	1:A:1127:G:N3	1.95	0.80
8:H:90:GLY:O	8:H:91:ARG:HB2	1.80	0.80
3:C:173:PRO:HB2	3:C:176:THR:HG22	1.64	0.80
15:O:16:ARG:HH11	15:O:16:ARG:HG3	1.47	0.80
3:C:14:THR:O	3:C:15:ARG:HB2	1.82	0.79
3:C:12:GLY:HA3	14:N:56:ARG:HH21	1.47	0.79
3:C:190:THR:HG22	3:C:191:THR:N	1.97	0.79
1:A:1502:A:H2	1:A:1505:G:N1	1.80	0.79
19:S:5:LEU:O	19:S:6:LYS:HB2	1.82	0.79
1:A:192:U:H1'	20:T:96:GLY:HA2	1.63	0.79
20:T:38:GLN:HA	20:T:84:LEU:HD22	1.65	0.79
13:M:14:VAL:HG21	13:M:47:LEU:HD21	1.64	0.79
18:R:31:GLU:CD	18:R:31:GLU:H	1.86	0.79
1:A:404:U:H2'	1:A:405:U:H6	1.48	0.79
1:A:1057:G:H5''	3:C:153:SER:HB2	1.65	0.78
10:J:1:LYS:HA	10:J:73:ILE:HA	1.65	0.78
10:J:29:GLY:HA2	10:J:76:ASN:ND2	1.98	0.78
8:H:113:SER:HB2	8:H:134:ILE:HD11	1.65	0.78
9:I:99:GLY:O	9:I:101:LEU:N	2.16	0.78
21:V:6:ARG:NH1	21:V:15:ARG:HH12	1.81	0.78
11:K:77:THR:HA	11:K:81:ARG:HH21	1.49	0.78
1:A:1121:U:H2'	1:A:1122:U:H5''	1.64	0.78
1:A:1234:C:H4'	1:A:1364:U:H2'	1.65	0.78
10:J:25:ALA:HB1	10:J:79:THR:HG23	1.65	0.78
12:L:66:ILE:HD13	12:L:73:LEU:HD12	1.65	0.78
1:A:1001:A:O2'	1:A:1001(A):G:H5'	1.82	0.78
1:A:673:G:H2'	1:A:674:G:C8	2.17	0.78
1:A:1502:A:H2	1:A:1505:G:H1	1.27	0.78
3:C:33:LEU:HD23	3:C:33:LEU:C	2.03	0.78
8:H:63:LEU:HD22	8:H:63:LEU:H	1.49	0.78
1:A:647:C:H2'	1:A:648:A:C5'	2.13	0.78
1:A:993:G:H4'	1:A:994:A:OP2	1.83	0.78
3:C:57:GLU:HB2	3:C:64:ALA:HB3	1.65	0.78
1:A:522:C:H41	12:L:49:ARG:HH22	1.29	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:71:HIS:HD2	12:L:73:LEU:H	1.31	0.77
1:A:573:A:H4'	1:A:574:A:O5'	1.85	0.77
6:F:101:ALA:HB2	18:R:13:GLU:HB3	1.65	0.77
5:E:88:LYS:HB3	5:E:115:LEU:HB2	1.66	0.77
1:A:972:C:H4'	10:J:55:LYS:CG	2.11	0.77
3:C:69:VAL:HG12	3:C:70:ALA:N	2.00	0.77
4:D:148:ALA:HB3	4:D:151:SER:HB2	1.65	0.77
1:A:1182:G:H4'	1:A:1183:A:H5'	1.65	0.77
3:C:43:GLU:HA	3:C:51:LEU:HD11	1.67	0.77
16:P:43:LYS:HG3	16:P:48:TRP:CD2	2.20	0.77
11:K:69:SER:HB3	11:K:96:LYS:HD2	1.66	0.77
1:A:159:G:H3'	1:A:160:A:H5''	1.65	0.76
4:D:61:GLN:HA	4:D:61:GLN:NE2	2.00	0.76
1:A:35:G:O2'	1:A:36:C:C6	2.36	0.76
1:A:1226:C:H4'	1:A:1227:A:OP1	1.82	0.76
23:Z:29:G:H2'	23:Z:30:G:C8	2.18	0.76
1:A:733:A:H4'	1:A:734:G:OP1	1.85	0.76
2:B:47:ARG:HG2	2:B:47:ARG:HH11	1.49	0.76
12:L:23:LEU:O	12:L:25:GLY:N	2.19	0.76
1:A:1247:U:C2'	1:A:1248:A:H5''	2.16	0.76
7:G:22:VAL:O	7:G:26:ILE:HG13	1.85	0.76
10:J:25:ALA:HB2	10:J:83:LEU:HD11	1.68	0.76
10:J:32:VAL:HG22	10:J:72:ILE:HG23	1.68	0.76
11:K:9:ALA:HB2	11:K:70:VAL:HG11	1.67	0.76
19:S:77:THR:HG22	19:S:78:ARG:HG3	1.68	0.76
2:B:118:SER:O	2:B:121:ILE:HG13	1.86	0.76
3:C:69:VAL:HG12	3:C:71:LYS:H	1.50	0.76
4:D:156:LEU:HD22	4:D:160:ASN:HD21	1.52	0.75
1:A:247:G:OP2	17:Q:99:LYS:HG3	1.86	0.75
12:L:34:THR:HG22	12:L:35:VAL:HG23	1.68	0.75
1:A:1352:C:H2'	1:A:1353:G:C8	2.21	0.75
2:B:12:GLY:HA2	2:B:35:ILE:HA	1.67	0.75
1:A:168:G:H5'	1:A:168:G:H8	1.52	0.75
1:A:991:U:C4	1:A:1212:U:H1'	2.22	0.75
1:A:1420:C:H2'	1:A:1421:G:H8	1.51	0.75
13:M:87:ARG:HD2	13:M:97:VAL:HG12	1.68	0.75
1:A:327:A:O2'	1:A:329:A:H5''	1.87	0.75
1:A:460:G:H3'	1:A:461:A:C5'	2.16	0.75
1:A:1002:G:H2'	1:A:1003:G:C8	2.22	0.75
19:S:81:ARG:O	19:S:81:ARG:HG2	1.87	0.74
3:C:33:LEU:HD21	3:C:37:ARG:CZ	2.17	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:37:ARG:HH22	12:L:53:LYS:NZ	1.85	0.74
1:A:1216:G:O2'	1:A:1217:C:H5'	1.87	0.74
11:K:10:TYR:HD1	11:K:73:ILE:HB	1.52	0.74
1:A:451:A:H61	1:A:481:G:H5'	1.52	0.74
1:A:648:A:H5'	1:A:648:A:H8	1.52	0.74
2:B:209:LEU:O	2:B:213:VAL:HG23	1.86	0.74
1:A:707:C:H4'	11:K:10:TYR:CD2	2.22	0.74
2:B:12:GLY:HA2	2:B:34:HIS:O	1.88	0.74
2:B:82:ALA:CB	2:B:84:MET:HG2	2.18	0.74
4:D:186:ARG:HE	4:D:187:LEU:N	1.84	0.74
1:A:1313:U:H5	19:S:4:SER:HB2	1.50	0.74
1:A:1287:A:O2'	1:A:1288:A:H8	1.71	0.74
13:M:16:VAL:O	13:M:19:THR:HB	1.87	0.74
16:P:81:ARG:NH1	16:P:81:ARG:HB2	2.02	0.74
3:C:118:ARG:HG2	3:C:139:ARG:NH1	2.03	0.74
1:A:1222:G:OP1	19:S:77:THR:HG21	1.88	0.74
1:A:1391:U:H2'	1:A:1392:G:C8	2.23	0.74
1:A:404:U:H2'	1:A:405:U:C6	2.23	0.73
2:B:133:LYS:O	2:B:137:GLU:HG2	1.89	0.73
16:P:81:ARG:HB2	16:P:81:ARG:HH11	1.53	0.73
1:A:596:C:H6	1:A:596:C:H5'	1.52	0.73
9:I:110:ARG:HD2	14:N:60:TRP:OXT	1.88	0.73
8:H:120:THR:OG1	8:H:123:GLU:HG3	1.88	0.73
11:K:10:TYR:CD1	11:K:73:ILE:HB	2.23	0.73
1:A:967:C:H4'	9:I:127:ARG:HG3	1.70	0.73
1:A:977:A:H2'	1:A:978:A:H5''	1.70	0.73
16:P:22:THR:HA	16:P:33:ILE:HG12	1.68	0.73
5:E:53:LYS:HG2	5:E:57:TYR:CE2	2.24	0.73
1:A:457:C:H2'	1:A:458:C:C6	2.23	0.73
1:A:1421:G:H1	1:A:1479:C:H42	1.36	0.72
5:E:140:THR:HG22	5:E:142:ALA:H	1.52	0.72
1:A:159:G:C3'	1:A:160:A:H5''	2.19	0.72
1:A:547:A:H4'	1:A:548:G:H5'	1.71	0.72
3:C:129:VAL:O	3:C:133:ILE:HG12	1.89	0.72
11:K:100:ASP:HB2	18:R:73:LYS:HE3	1.70	0.72
1:A:613:C:O2'	1:A:614:A:H5'	1.88	0.72
1:A:1030(C):G:H2'	1:A:1030(D):A:C8	2.25	0.72
1:A:1260:C:OP1	1:A:1284:C:H4'	1.88	0.72
1:A:277:C:H5''	17:Q:67:ARG:NH2	2.05	0.72
13:M:2:ARG:HA	13:M:7:GLU:O	1.89	0.72
3:C:31:LEU:O	3:C:35:ASP:HB2	1.89	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:37:ARG:NH2	12:L:53:LYS:NZ	2.37	0.72
2:B:19:ASN:C	2:B:19:ASN:HD22	1.93	0.72
1:A:1228:C:H4'	13:M:115:THR:HA	1.71	0.72
3:C:187:LEU:HD13	3:C:188:ALA:H	1.54	0.72
1:A:1041:A:C2'	1:A:1042:G:H5''	2.18	0.72
1:A:1189:C:P	10:J:49:ARG:HH22	2.12	0.72
2:B:128:GLU:HG2	2:B:131:ARG:NH2	2.05	0.72
6:F:4:TYR:CE1	6:F:92:LYS:HG2	2.25	0.72
10:J:7:ARG:HB3	10:J:7:ARG:NH1	2.04	0.72
10:J:38:LEU:HB2	10:J:67:ASN:HB2	1.72	0.72
10:J:22:VAL:HG13	10:J:23:GLU:H	1.54	0.71
17:Q:42:LEU:HG	17:Q:67:ARG:NH1	2.05	0.71
17:Q:94:TYR:HA	17:Q:97:LEU:CD1	2.20	0.71
16:P:28:ARG:HG2	16:P:28:ARG:HH11	1.54	0.71
1:A:353:A:H5'	1:A:353:A:H8	1.54	0.71
1:A:580:U:H2'	1:A:581:G:O4'	1.89	0.71
1:A:573:A:H5'	1:A:574:A:OP2	1.89	0.71
12:L:37:ARG:NH1	12:L:37:ARG:HB3	2.05	0.71
13:M:116:VAL:HG12	13:M:117:ALA:N	1.98	0.71
1:A:273:A:H1'	17:Q:15:GLN:NE2	2.06	0.71
3:C:133:ILE:O	3:C:137:VAL:HG23	1.90	0.71
10:J:1:LYS:H1	10:J:74:ASN:N	1.89	0.71
13:M:58:TYR:O	13:M:62:THR:HG22	1.91	0.71
1:A:720:C:H3'	1:A:721:G:O4'	1.90	0.71
6:F:33:TYR:HA	6:F:71:ARG:NH2	2.06	0.71
2:B:42:MET:HA	2:B:45:LEU:HD12	1.72	0.71
3:C:190:THR:CG2	3:C:191:THR:N	2.53	0.71
19:S:28:LYS:HG2	19:S:29:ARG:N	2.05	0.71
1:A:1047:G:C2'	1:A:1048:G:H5'	2.21	0.71
2:B:81:ARG:NH1	2:B:227:SER:HA	2.06	0.71
1:A:254:G:OP1	17:Q:66:LYS:O	2.09	0.70
10:J:29:GLY:HA2	10:J:76:ASN:HD22	1.54	0.70
1:A:60:A:H5''	1:A:331:G:H22	1.56	0.70
2:B:212:ALA:O	2:B:216:ILE:HG13	1.91	0.70
12:L:106:VAL:O	12:L:118:THR:HG21	1.91	0.70
1:A:1049:U:H5''	14:N:2:ARG:CG	2.21	0.70
2:B:225:GLU:HB3	2:B:226:PRO:HD2	1.72	0.70
1:A:738:C:OP1	6:F:92:LYS:HD3	1.91	0.70
9:I:15:ARG:HB2	9:I:63:THR:HB	1.74	0.70
14:N:43:LEU:C	14:N:43:LEU:HD12	2.12	0.70
1:A:1127:G:H22	1:A:1144:G:N2	1.90	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:13:ILE:HG22	3:C:14:THR:N	2.00	0.70
9:I:125:SER:O	9:I:127:ARG:N	2.25	0.70
12:L:106:VAL:HG22	12:L:116:TYR:HB3	1.73	0.70
18:R:23:GLU:H	18:R:23:GLU:CD	1.94	0.70
13:M:87:ARG:NH1	19:S:3:ARG:HH21	1.89	0.70
1:A:888:G:H3'	1:A:889:A:H5''	1.74	0.69
1:A:189(H):G:H4'	1:A:189(I):G:O5'	1.92	0.69
1:A:731:G:OP1	1:A:766:A:H1'	1.92	0.69
3:C:13:ILE:CG2	3:C:14:THR:H	2.02	0.69
10:J:36:ILE:HD12	10:J:69:LEU:HD12	1.73	0.69
3:C:46:LEU:HD23	3:C:67:VAL:HG11	1.74	0.69
1:A:159:G:H5'	1:A:160:A:OP2	1.91	0.69
1:A:1108:G:H2'	1:A:1109:C:H5''	1.73	0.69
10:J:10:ASP:HB3	10:J:13:THR:HB	1.75	0.69
1:A:159:G:H3'	1:A:160:A:C5'	2.22	0.69
3:C:176:THR:HG23	3:C:179:ALA:HB2	1.75	0.69
5:E:140:THR:HG22	5:E:142:ALA:N	2.06	0.69
7:G:14:ASP:HB3	7:G:19:ASP:H	1.57	0.69
20:T:46:LEU:HD12	20:T:93:ILE:HB	1.74	0.69
1:A:1062:U:H2'	1:A:1063:C:C6	2.28	0.69
5:E:47:VAL:HB	5:E:48:PRO:HD3	1.73	0.69
6:F:2:ARG:NE	6:F:69:GLU:HG2	2.07	0.69
7:G:44:ASP:O	7:G:48:ILE:HG12	1.91	0.69
1:A:539:A:H2'	1:A:540:G:C8	2.28	0.69
2:B:13:HIS:CE1	2:B:200:ASP:HB3	2.27	0.69
2:B:54:ASP:O	2:B:58:ARG:HG3	1.92	0.69
4:D:186:ARG:NE	4:D:187:LEU:H	1.86	0.69
10:J:83:LEU:O	10:J:86:LEU:HD13	1.91	0.69
13:M:116:VAL:CG1	13:M:117:ALA:H	2.03	0.69
1:A:762:C:H4'	17:Q:103:LYS:NZ	2.07	0.69
2:B:63:LEU:HD12	2:B:64:PHE:N	2.07	0.69
2:B:137:GLU:O	2:B:141:LYS:HG3	1.93	0.69
9:I:96:LYS:HB3	9:I:97:PRO:HD3	1.73	0.69
10:J:1:LYS:CA	10:J:73:ILE:HA	2.22	0.69
13:M:96:PRO:HA	13:M:109:ARG:HD3	1.73	0.69
1:A:167:G:H2'	1:A:168:G:C5'	2.23	0.68
12:L:79:VAL:HG21	12:L:96:ILE:HG23	1.75	0.68
3:C:82:ARG:C	3:C:84:ARG:H	1.94	0.68
20:T:50:ARG:HE	20:T:93:ILE:CG2	2.07	0.68
1:A:650:G:O2'	1:A:651:C:H5'	1.93	0.68
1:A:1263:C:H2'	1:A:1264:C:C6	2.28	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1381:U:O2'	1:A:1382:C:H5'	1.92	0.68
2:B:13:HIS:HD2	2:B:183:ASP:OD2	1.77	0.68
7:G:134:VAL:O	7:G:138:GLU:HG3	1.92	0.68
8:H:86:ILE:HG21	8:H:133:LEU:HD13	1.76	0.68
3:C:55:ASP:O	3:C:56:ILE:HD13	1.93	0.68
2:B:78:GLU:OE1	2:B:210:SER:HA	1.94	0.68
4:D:198:ASN:ND2	4:D:200:GLN:HB2	2.08	0.68
10:J:4:ILE:HG22	10:J:96:ILE:HG12	1.74	0.68
15:O:69:LEU:HD13	15:O:77:TYR:HA	1.75	0.68
17:Q:73:LEU:O	17:Q:73:LEU:HD23	1.93	0.68
12:L:79:VAL:HG21	12:L:96:ILE:CG2	2.23	0.68
1:A:865:A:H5'	1:A:1078:U:O4	1.94	0.68
1:A:1143:G:H2'	1:A:1144:G:H8	1.59	0.67
10:J:7:ARG:HB3	10:J:7:ARG:HH11	1.59	0.67
2:B:159:VAL:HG23	2:B:160:ASP:N	2.08	0.67
7:G:49:ILE:O	7:G:53:THR:HB	1.94	0.67
3:C:180:ASN:ND2	3:C:203:LEU:HD12	2.10	0.67
8:H:20:TYR:CE1	8:H:76:PRO:HG2	2.29	0.67
13:M:8:ILE:HD13	13:M:8:ILE:N	2.10	0.67
1:A:60:A:H5''	1:A:331:G:N2	2.10	0.67
1:A:1363(A):A:H4'	1:A:1364:U:H5''	1.75	0.67
1:A:994:A:H5'	1:A:995:C:OP2	1.94	0.67
2:B:108:ARG:HD3	2:B:112:LEU:HG	1.75	0.67
3:C:81:GLU:O	3:C:85:VAL:HG23	1.95	0.67
19:S:33:THR:CG2	19:S:35:SER:H	1.99	0.67
19:S:63:THR:O	19:S:66:MET:HG2	1.95	0.67
1:A:177:C:H2'	1:A:178:C:C5'	2.16	0.67
1:A:235:C:H5'	17:Q:69:ARG:HG2	1.75	0.67
2:B:91:TRP:HZ2	2:B:96:LEU:HD13	1.59	0.67
2:B:217:ILE:HG21	2:B:224:VAL:HG23	1.77	0.67
8:H:127:LEU:N	8:H:127:LEU:HD23	2.10	0.67
10:J:58:ARG:HG2	10:J:58:ARG:HH11	1.60	0.67
17:Q:58:ILE:HG23	17:Q:70:PHE:CD1	2.29	0.67
17:Q:66:LYS:HA	17:Q:69:ARG:HH12	1.59	0.67
2:B:82:ALA:HB1	2:B:84:MET:HG2	1.75	0.67
3:C:18:GLU:O	3:C:39:ARG:NH2	2.28	0.67
5:E:76:ILE:CD1	5:E:87:LEU:HB2	2.25	0.67
5:E:149:LYS:O	5:E:151:GLU:N	2.28	0.67
20:T:47:LYS:HE3	20:T:93:ILE:HD11	1.77	0.67
4:D:35:ARG:H	4:D:36:PRO:HD3	1.60	0.66
5:E:76:ILE:HD13	5:E:87:LEU:HB2	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:36:ARG:NH1	6:F:38:GLU:HG2	2.10	0.66
20:T:43:GLU:HA	20:T:93:ILE:HG12	1.76	0.66
1:A:1143:G:H2'	1:A:1144:G:C8	2.30	0.66
1:A:1288:A:O2'	1:A:1289:A:H8	1.77	0.66
10:J:22:VAL:HG13	10:J:23:GLU:N	2.10	0.66
12:L:82:ARG:HG2	12:L:82:ARG:HH11	1.61	0.66
1:A:402:G:H2'	1:A:403:C:C5'	2.19	0.66
1:A:1067:A:H2'	1:A:1068:G:O4'	1.94	0.66
3:C:49:ALA:HB1	3:C:69:VAL:HG11	1.76	0.66
20:T:43:GLU:O	20:T:93:ILE:HG13	1.96	0.66
1:A:1127:G:H21	1:A:1146:A:N6	1.94	0.66
1:A:1129:C:O5'	1:A:1130:A:H5'	1.96	0.66
2:B:82:ALA:C	2:B:84:MET:H	1.98	0.66
2:B:172:ARG:HH11	2:B:172:ARG:HG3	1.59	0.66
11:K:8:ARG:HB2	11:K:23:THR:CG2	2.25	0.66
18:R:21:ASN:C	18:R:21:ASN:HD22	1.96	0.66
1:A:575:G:O2'	1:A:821:G:H5'	1.95	0.66
3:C:69:VAL:HG12	3:C:70:ALA:H	1.59	0.66
2:B:194:ILE:HD12	2:B:194:ILE:N	2.10	0.66
10:J:10:ASP:O	10:J:13:THR:HG22	1.96	0.66
10:J:20:LYS:HD2	10:J:88:LEU:HD12	1.78	0.66
1:A:1127:G:N2	1:A:1144:G:H22	1.93	0.66
14:N:8:LYS:HD3	14:N:9:ALA:N	2.11	0.66
3:C:69:VAL:O	3:C:105:VAL:HG23	1.95	0.66
6:F:4:TYR:HE1	6:F:92:LYS:HG2	1.59	0.66
1:A:1001:A:H2'	1:A:1001:A:N3	2.10	0.65
1:A:1057:G:H5''	3:C:153:SER:CB	2.25	0.65
1:A:1392:G:N2	1:A:1502:A:H8	1.94	0.65
1:A:1420:C:H2'	1:A:1421:G:C8	2.31	0.65
1:A:975:A:H4'	1:A:976:G:C5'	2.24	0.65
4:D:149:GLU:HB3	4:D:150:LYS:HD2	1.78	0.65
10:J:2:ILE:CD1	10:J:72:ILE:HB	2.26	0.65
11:K:44:ARG:HB3	11:K:44:ARG:NH1	2.07	0.65
1:A:275:G:H5''	17:Q:13:LYS:CB	2.25	0.65
4:D:148:ALA:HB3	4:D:151:SER:CB	2.26	0.65
15:O:52:HIS:CE1	15:O:56:LEU:HD13	2.31	0.65
18:R:11:LEU:HD12	18:R:12:GLY:N	2.11	0.65
2:B:166:ILE:HD12	2:B:166:ILE:N	2.11	0.65
2:B:230:TYR:O	2:B:233:VAL:HG22	1.96	0.65
4:D:63:LEU:HB2	4:D:197:VAL:HG11	1.79	0.65
19:S:30:LEU:O	19:S:31:ILE:HD13	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:85:THR:C	10:J:86:LEU:HD12	2.17	0.65
21:V:10:ARG:HG3	21:V:10:ARG:NH1	2.07	0.65
6:F:94:GLN:NE2	18:R:17:ARG:HH11	1.92	0.65
12:L:79:VAL:CG2	12:L:96:ILE:HG23	2.26	0.65
1:A:1127:G:H21	1:A:1146:A:H62	1.44	0.65
2:B:13:HIS:HB2	2:B:198:ASN:OD1	1.97	0.65
7:G:61:PHE:HA	7:G:123:LEU:HD21	1.77	0.65
19:S:28:LYS:CG	19:S:29:ARG:H	2.09	0.65
1:A:1127:G:N2	1:A:1144:G:N2	2.44	0.65
3:C:98:VAL:HG22	3:C:99:ALA:O	1.95	0.65
3:C:147:GLY:HA3	3:C:171:ARG:O	1.96	0.65
14:N:30:ARG:HH11	14:N:30:ARG:HG3	1.62	0.65
1:A:275:G:H5''	17:Q:13:LYS:HB2	1.77	0.65
1:A:539:A:H2'	1:A:540:G:H8	1.61	0.65
2:B:69:LYS:HE3	2:B:72:GLN:OE1	1.97	0.65
20:T:61:LYS:HA	20:T:61:LYS:HE3	1.78	0.65
1:A:1263:C:H2'	1:A:1264:C:H6	1.61	0.65
6:F:100:ASN:ND2	18:R:8:LYS:HG2	2.10	0.65
12:L:71:HIS:CD2	12:L:73:LEU:H	2.15	0.65
1:A:181:G:H2'	1:A:183:G:C6	2.31	0.64
1:A:353:A:H5'	1:A:353:A:C8	2.32	0.64
1:A:1132:C:H2'	1:A:1133:G:H8	1.61	0.64
1:A:1363(A):A:C4'	1:A:1364:U:H5''	2.27	0.64
2:B:53:GLU:HG3	2:B:215:LEU:HD11	1.77	0.64
10:J:5:LYS:HB3	10:J:95:GLU:HB2	1.78	0.64
1:A:45:U:H2'	1:A:46:G:C8	2.33	0.64
1:A:1330:U:H2'	1:A:1331:G:H5'	1.78	0.64
4:D:156:LEU:HD22	4:D:160:ASN:ND2	2.12	0.64
18:R:71:VAL:O	18:R:72:ARG:HG2	1.97	0.64
20:T:89:GLY:O	20:T:90:ALA:HB3	1.96	0.64
2:B:22:PHE:CZ	2:B:183:ASP:HA	2.32	0.64
12:L:37:ARG:HH22	12:L:53:LYS:CE	2.11	0.64
1:A:1367:C:C5'	10:J:58:ARG:HH12	2.11	0.64
3:C:206:VAL:HG12	3:C:207:ILE:N	2.12	0.64
5:E:76:ILE:HD11	5:E:87:LEU:HD12	1.78	0.64
10:J:43:ARG:HH11	10:J:43:ARG:CB	1.95	0.64
23:Z:30:G:H2'	23:Z:31:A:H8	1.62	0.64
1:A:287:U:O2'	1:A:288:A:H5'	1.98	0.64
1:A:1037:C:H2'	1:A:1038:C:C6	2.33	0.64
1:A:1323:G:H2'	1:A:1324:A:C8	2.32	0.64
14:N:11:ARG:O	14:N:13:PRO:HD3	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:34:GLU:OE2	16:P:55:ARG:HD3	1.97	0.64
19:S:64:GLU:O	19:S:67:VAL:HG23	1.96	0.64
17:Q:42:LEU:HG	17:Q:67:ARG:HH12	1.63	0.64
3:C:190:THR:HG21	3:C:192:TYR:CE1	2.33	0.64
6:F:30:LEU:HB3	6:F:35:ALA:HB3	1.80	0.64
13:M:49:GLU:O	13:M:53:VAL:HG23	1.97	0.64
15:O:26:VAL:O	15:O:30:LEU:HD22	1.98	0.64
1:A:1406:U:O2'	1:A:1407:C:H5'	1.98	0.64
9:I:8:ARG:HG2	9:I:13:VAL:HG22	1.80	0.64
10:J:88:LEU:H	10:J:89:PRO:HD2	1.61	0.64
10:J:92:VAL:HG12	10:J:93:GLU:N	2.12	0.64
1:A:743:U:H2'	1:A:744:C:C6	2.32	0.64
9:I:117:LYS:O	9:I:118:ALA:HB3	1.98	0.64
21:V:6:ARG:CZ	21:V:15:ARG:HH12	2.11	0.64
2:B:116:PHE:HE2	2:B:133:LYS:HG2	1.63	0.63
9:I:47:GLU:N	9:I:48:PRO:HD2	2.14	0.63
17:Q:17:THR:HG23	17:Q:68:LYS:HE3	1.78	0.63
1:A:293:G:H5'	1:A:609:A:H61	1.64	0.63
1:A:1049:U:H5''	14:N:2:ARG:HD2	1.81	0.63
4:D:57:LEU:HD22	4:D:61:GLN:HG2	1.80	0.63
9:I:16:VAL:HG22	9:I:62:ILE:HD12	1.80	0.63
1:A:1305:G:N2	1:A:1331:G:H1'	2.12	0.63
1:A:1369:C:H2'	1:A:1370:G:C8	2.33	0.63
4:D:62:LYS:HE3	4:D:197:VAL:HG22	1.80	0.63
1:A:189:G:H5'	1:A:189:G:H8	1.63	0.63
1:A:818:G:O2'	1:A:819:A:H5''	1.98	0.63
16:P:67:THR:HG22	16:P:70:ALA:H	1.63	0.63
18:R:32:THR:O	18:R:34:LYS:N	2.31	0.63
1:A:17:U:H2'	1:A:18:C:C6	2.33	0.63
7:G:144:ALA:O	7:G:146:ALA:N	2.30	0.63
10:J:47:VAL:HG13	14:N:40:ARG:HD2	1.79	0.63
16:P:43:LYS:HG3	16:P:48:TRP:CE2	2.34	0.63
1:A:653:A:H5'	8:H:56:LYS:HE3	1.78	0.63
1:A:997:U:H2'	1:A:998:G:H5''	1.81	0.63
9:I:105:ALA:O	9:I:107:VAL:HG13	1.97	0.63
12:L:67:PRO:O	12:L:98:ARG:HD2	1.98	0.63
12:L:106:VAL:H	12:L:118:THR:CG2	2.10	0.63
6:F:43:LEU:HD22	6:F:43:LEU:N	2.12	0.63
1:A:1132:C:H2'	1:A:1133:G:C8	2.34	0.63
5:E:71:THR:HG23	5:E:72:ILE:N	2.14	0.63
5:E:140:THR:HB	5:E:143:ASP:OD2	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:15:LEU:HA	19:S:18:LYS:HB3	1.79	0.63
1:A:702:A:H4'	1:A:703:G:OP2	1.98	0.62
10:J:19:GLN:HA	10:J:22:VAL:CG1	2.26	0.62
11:K:81:ARG:HH11	18:R:73:LYS:HD3	1.63	0.62
17:Q:67:ARG:HG2	17:Q:67:ARG:HH11	1.62	0.62
1:A:1216:G:H5''	14:N:4:ALA:HB2	1.82	0.62
2:B:89:GLN:HG3	2:B:141:LYS:O	1.99	0.62
1:A:91:C:H2'	1:A:92:C:H6	1.64	0.62
1:A:542:G:H2'	1:A:543:C:H6	1.63	0.62
1:A:1330:U:C2'	1:A:1331:G:H5'	2.28	0.62
1:A:1367:C:C5'	10:J:58:ARG:NH1	2.62	0.62
5:E:39:LEU:HD11	5:E:128:ALA:HB1	1.81	0.62
8:H:82:HIS:HD2	8:H:83:ILE:N	1.98	0.62
2:B:181:LEU:HD23	2:B:195:ILE:O	1.99	0.62
3:C:75:VAL:O	3:C:82:ARG:HB2	2.00	0.62
16:P:9:PHE:CD1	16:P:18:ARG:HG3	2.35	0.62
1:A:105:G:H2'	1:A:106:C:C6	2.35	0.62
1:A:1499:A:H1'	1:A:1520:G:H5'	1.81	0.62
4:D:150:LYS:HD2	4:D:150:LYS:N	2.14	0.62
9:I:86:GLN:HE21	9:I:86:GLN:HA	1.63	0.62
11:K:38:ILE:HD11	11:K:54:ALA:N	2.14	0.62
20:T:83:GLN:O	20:T:86:GLU:HB2	1.99	0.62
1:A:818:G:C2'	1:A:819:A:H5''	2.30	0.62
1:A:1190:G:OP1	3:C:4:ILE:HD12	2.00	0.62
1:A:1216:G:H5''	14:N:4:ALA:CB	2.30	0.62
7:G:61:PHE:HA	7:G:123:LEU:CD2	2.30	0.62
8:H:65:TYR:HA	8:H:79:VAL:HG23	1.82	0.62
19:S:15:LEU:HA	19:S:18:LYS:HE2	1.81	0.62
1:A:1187:G:C5'	9:I:112:LYS:HE3	2.27	0.62
3:C:123:ILE:HD12	3:C:129:VAL:HG22	1.81	0.62
5:E:145:GLU:O	5:E:149:LYS:HB2	1.99	0.62
10:J:46:THR:OG1	10:J:60:HIS:CD2	2.53	0.62
1:A:280:C:O2	17:Q:37:ARG:HG3	2.00	0.62
2:B:11:PHE:HD1	2:B:12:GLY:N	1.96	0.62
4:D:61:GLN:HE21	4:D:61:GLN:CA	2.07	0.62
1:A:1368:G:O2'	1:A:1369:C:H5'	1.99	0.62
8:H:4:ASP:CG	8:H:85:ARG:HH11	2.03	0.62
10:J:28:SER:CB	10:J:82:GLN:HE21	2.13	0.62
13:M:12:LYS:HA	13:M:43:ARG:HH11	1.64	0.62
18:R:18:ASP:OD2	18:R:21:ASN:HB2	2.00	0.62
21:V:5:ASP:O	21:V:11:GLY:HA3	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:246:A:H4'	1:A:247:G:OP1	2.00	0.61
1:A:327:A:HO2'	1:A:329:A:H8	1.46	0.61
7:G:115:ALA:O	7:G:119:ILE:HD12	2.00	0.61
3:C:107:ASN:ND2	3:C:143:SER:HB2	2.09	0.61
3:C:205:GLU:O	3:C:206:VAL:O	2.17	0.61
7:G:148:ARG:HD2	11:K:49:TYR:CE1	2.35	0.61
10:J:27:ARG:HB2	10:J:27:ARG:NH1	2.14	0.61
13:M:2:ARG:CG	13:M:8:ILE:HG23	2.30	0.61
1:A:1342:C:O2'	1:A:1343:G:H5'	1.99	0.61
1:A:152:A:H5'	1:A:153:C:OP2	2.00	0.61
7:G:71:ARG:HG2	7:G:141:GLU:OE2	2.00	0.61
13:M:10:ARG:HG2	13:M:11:ASN:N	2.14	0.61
18:R:19:TYR:HA	18:R:54:THR:HG23	1.80	0.61
8:H:24:THR:HG22	8:H:63:LEU:HD21	1.81	0.61
15:O:8:GLN:O	15:O:12:GLN:HG2	2.00	0.61
18:R:38:ARG:NH1	18:R:44:SER:HA	2.15	0.61
26:A:2733:M5Z:O52	26:A:2733:M5Z:H11	2.00	0.61
4:D:156:LEU:CD2	4:D:160:ASN:HD21	2.13	0.61
1:A:518:C:H2'	1:A:530:G:N3	2.15	0.61
1:A:1075:C:H5'	2:B:97:THR:HG21	1.82	0.61
2:B:133:LYS:O	2:B:133:LYS:HD3	2.00	0.61
3:C:33:LEU:HD23	3:C:33:LEU:O	1.98	0.61
10:J:27:ARG:HB2	10:J:27:ARG:HH11	1.65	0.61
15:O:35:ILE:HG12	15:O:58:MET:HE3	1.82	0.61
4:D:35:ARG:H	4:D:36:PRO:CD	2.13	0.61
4:D:106:ARG:HD2	4:D:172:TRP:HZ2	1.66	0.61
8:H:119:LEU:HD12	8:H:124:ALA:HA	1.82	0.61
10:J:2:ILE:HD11	10:J:72:ILE:HB	1.82	0.61
13:M:95:LEU:HB3	13:M:96:PRO:HD2	1.82	0.61
1:A:190:U:C2	20:T:98:SER:HB2	2.34	0.61
1:A:1127:G:N2	1:A:1146:A:H62	1.99	0.61
2:B:9:VAL:HG12	2:B:204:SER:OG	2.01	0.61
3:C:109:ASN:O	3:C:110:LEU:HD23	2.00	0.61
3:C:192:TYR:HE1	3:C:195:LEU:HD21	1.66	0.61
3:C:7:ILE:HG23	3:C:15:ARG:HG2	1.82	0.61
10:J:6:LEU:HB2	10:J:68:ARG:HB2	1.82	0.61
10:J:67:ASN:O	10:J:68:ARG:HD3	2.00	0.61
12:L:37:ARG:CG	12:L:38:THR:H	1.96	0.61
14:N:17:VAL:HG23	14:N:18:ARG:H	1.66	0.61
1:A:181:G:H5'	1:A:182:U:OP1	2.01	0.60
1:A:794:A:H2'	1:A:795:C:C6	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:21:LYS:HD3	2:B:189:ASP:OD2	2.00	0.60
2:B:207:LEU:O	2:B:210:SER:HB3	2.01	0.60
6:F:28:ARG:HH11	6:F:28:ARG:CB	2.01	0.60
1:A:1168:A:O2'	1:A:1169:A:C8	2.54	0.60
2:B:108:ARG:HD3	2:B:108:ARG:O	2.01	0.60
3:C:153:SER:OG	3:C:154:GLY:N	2.33	0.60
3:C:190:THR:HG21	3:C:192:TYR:CZ	2.36	0.60
5:E:85:ILE:HD13	5:E:86:VAL:N	2.16	0.60
7:G:14:ASP:OD1	7:G:43:TYR:OH	2.19	0.60
8:H:56:LYS:HD2	8:H:56:LYS:N	2.15	0.60
13:M:79:ARG:NH1	13:M:79:ARG:HB3	2.16	0.60
1:A:1495:U:H2'	1:A:1496:C:H6	1.66	0.60
2:B:134:HIS:O	2:B:137:GLU:HB2	2.01	0.60
7:G:121:HIS:O	7:G:125:ASP:HB2	2.02	0.60
11:K:38:ILE:O	11:K:38:ILE:HG22	2.00	0.60
1:A:109:A:H2'	1:A:326:G:N2	2.16	0.60
1:A:818:G:C3'	1:A:819:A:H5''	2.31	0.60
3:C:190:THR:HB	3:C:193:GLY:O	2.01	0.60
10:J:80:ILE:O	10:J:84:MET:HB2	2.02	0.60
15:O:86:ILE:O	15:O:87:ARG:HB2	2.01	0.60
1:A:1313:U:C5	19:S:4:SER:HB2	2.36	0.60
1:A:1442:G:N3	1:A:1442:G:H2'	2.16	0.60
2:B:88:ASN:HD22	2:B:88:ASN:N	1.90	0.60
2:B:173:LYS:HA	8:H:72:PRO:HD3	1.83	0.60
3:C:154:GLY:O	3:C:155:ARG:HB2	2.01	0.60
17:Q:3:LYS:HD3	17:Q:5:LEU:HD21	1.82	0.60
1:A:149:A:H2'	1:A:150:C:C6	2.36	0.60
2:B:81:ARG:HD3	2:B:228:PRO:HD2	1.81	0.60
3:C:4:ILE:CD1	3:C:4:ILE:H	2.14	0.60
4:D:7:VAL:C	4:D:9:ARG:H	2.05	0.60
16:P:45:THR:HB	16:P:46:PRO:HD2	1.83	0.60
1:A:537:G:OP1	12:L:109:ARG:NH2	2.34	0.60
1:A:1347:G:N2	1:A:1373:G:H2'	2.16	0.60
4:D:2:ARG:NH1	4:D:117:ARG:HH12	1.99	0.60
11:K:77:THR:HG22	11:K:81:ARG:NH2	2.17	0.60
12:L:71:HIS:HA	12:L:98:ARG:HH22	1.66	0.60
15:O:25:GLU:OE2	15:O:76:ARG:HD2	2.02	0.60
19:S:8:GLY:O	19:S:10:PHE:N	2.35	0.60
19:S:16:LEU:O	19:S:19:VAL:HG12	2.02	0.60
1:A:1029:C:H2'	1:A:1030:C:C5'	2.22	0.60
1:A:1163:C:H2'	1:A:1164:G:H8	1.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1368:G:OP2	9:I:111:LYS:HD2	2.01	0.60
7:G:36:ASN:ND2	9:I:40:VAL:HG23	2.16	0.60
8:H:104:ARG:HG2	8:H:104:ARG:HH11	1.67	0.60
12:L:24:LYS:C	12:L:26:ALA:N	2.49	0.60
15:O:16:ARG:HG3	15:O:16:ARG:NH1	2.17	0.60
1:A:424:G:O2'	1:A:425:G:H5'	2.02	0.60
1:A:1366:C:H2'	1:A:1367:C:H6	1.66	0.60
6:F:101:ALA:CB	18:R:13:GLU:HB3	2.30	0.60
12:L:122:LYS:N	12:L:122:LYS:HE2	2.17	0.60
1:A:530:G:O6	22:W:3:C:H1'	2.02	0.59
1:A:1333:A:H2'	1:A:1334:G:O4'	2.02	0.59
10:J:1:LYS:N	10:J:73:ILE:HA	2.17	0.59
13:M:33:LEU:HD13	13:M:40:PRO:HA	1.84	0.59
1:A:1021:G:H2'	1:A:1022:G:O4'	2.02	0.59
3:C:99:ALA:O	3:C:100:LEU:HB2	2.02	0.59
3:C:133:ILE:HD11	3:C:152:VAL:HG21	1.84	0.59
17:Q:67:ARG:N	17:Q:69:ARG:NH1	2.49	0.59
1:A:250:A:H4'	1:A:250:A:OP1	2.02	0.59
1:A:403:C:H6	1:A:403:C:H5'	1.68	0.59
4:D:56:ARG:HH11	4:D:56:ARG:HG3	1.67	0.59
19:S:29:ARG:O	19:S:30:LEU:HB2	2.01	0.59
3:C:119:VAL:O	3:C:123:ILE:HG12	2.01	0.59
19:S:33:THR:HG22	19:S:34:TRP:N	2.16	0.59
1:A:1283:G:O2'	1:A:1284:C:H5'	2.02	0.59
3:C:34:GLU:HG3	3:C:94:THR:HG21	1.84	0.59
6:F:48:LEU:HD13	6:F:52:ILE:HG13	1.83	0.59
7:G:154:ARG:O	7:G:155:TRP:HB3	2.03	0.59
11:K:19:ILE:C	11:K:19:ILE:HD13	2.22	0.59
1:A:1125:U:O4	10:J:3:ARG:HD2	2.03	0.59
1:A:1241:G:H2'	1:A:1242:C:C6	2.37	0.59
2:B:12:GLY:CA	2:B:35:ILE:HA	2.31	0.59
2:B:13:HIS:NE2	2:B:200:ASP:HB3	2.17	0.59
3:C:18:GLU:HB3	3:C:39:ARG:NH2	2.16	0.59
5:E:11:ARG:HD3	5:E:22:PHE:CD2	2.37	0.59
10:J:30:ALA:HB2	10:J:74:ASN:OD1	2.02	0.59
17:Q:100:ARG:NE	17:Q:100:ARG:HA	2.17	0.59
2:B:117:ALA:CA	2:B:121:ILE:HD11	2.32	0.59
7:G:109:GLN:HA	7:G:109:GLN:OE1	2.01	0.59
13:M:50:ALA:O	13:M:54:ARG:HG3	2.02	0.59
1:A:1145:C:O2'	1:A:1146:A:H8	1.86	0.59
1:A:1459:C:O2'	1:A:1460:A:H5'	2.03	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:24:GLY:O	3:C:26:LYS:N	2.36	0.59
11:K:96:LYS:NZ	11:K:96:LYS:HB3	2.18	0.59
19:S:32:LYS:HA	19:S:50:ALA:HB3	1.83	0.59
1:A:1047:G:H2'	1:A:1048:G:H5'	1.84	0.59
1:A:1222:G:P	19:S:77:THR:HG21	2.43	0.59
1:A:1229:A:H2'	1:A:1230:C:H6	1.68	0.59
6:F:101:ALA:HA	18:R:13:GLU:HG2	1.82	0.59
9:I:10:LYS:O	9:I:10:LYS:HG2	2.03	0.59
11:K:19:ILE:HD13	11:K:19:ILE:O	2.02	0.59
2:B:70:GLN:HG3	2:B:200:ASP:OD1	2.03	0.59
17:Q:58:ILE:HD12	17:Q:72:VAL:HA	1.83	0.59
1:A:974:A:OP2	14:N:40:ARG:NH1	2.35	0.58
1:A:1305:G:H5''	21:V:4:GLY:HA3	1.85	0.58
1:A:1392:G:H21	1:A:1502:A:H8	1.50	0.58
1:A:1512:U:O2'	1:A:1513:A:H5'	2.03	0.58
2:B:106:VAL:CG1	2:B:147:ARG:HG2	2.26	0.58
11:K:111:PRO:HG2	11:K:116:ARG:CG	2.32	0.58
1:A:1154:G:O2'	1:A:1155:G:H5'	2.03	0.58
14:N:40:ARG:HG2	14:N:40:ARG:HH11	1.68	0.58
1:A:460:G:H2'	1:A:461:A:H5''	1.85	0.58
1:A:620:C:N1	4:D:134:LEU:HD13	2.18	0.58
3:C:135:GLN:O	3:C:138:GLN:HB2	2.02	0.58
12:L:37:ARG:NH2	12:L:53:LYS:HZ1	2.00	0.58
12:L:122:LYS:HE2	12:L:122:LYS:O	2.04	0.58
13:M:2:ARG:HG2	13:M:8:ILE:HG23	1.84	0.58
15:O:13:GLU:HG3	15:O:14:PHE:CD1	2.38	0.58
1:A:686:U:O2'	1:A:687:A:H8	1.86	0.58
1:A:1148:U:H2'	1:A:1149:C:O4'	2.03	0.58
1:A:1470:G:O2'	1:A:1471:G:H5'	2.03	0.58
10:J:7:ARG:HH11	10:J:7:ARG:CB	2.16	0.58
1:A:918:A:H2'	1:A:919:A:C8	2.38	0.58
1:A:1286:A:C8	1:A:1287:A:H4'	2.38	0.58
2:B:172:ARG:HG3	2:B:172:ARG:NH1	2.16	0.58
2:B:225:GLU:H	2:B:225:GLU:CD	2.05	0.58
1:A:1065:U:C5	1:A:1190:G:H1'	2.39	0.58
1:A:1314:C:C5	19:S:6:LYS:HE2	2.39	0.58
4:D:77:LEU:HD22	4:D:95:LEU:HB3	1.84	0.58
1:A:818:G:H3'	1:A:819:A:C5'	2.34	0.58
2:B:51:PHE:O	2:B:54:ASP:HB3	2.03	0.58
2:B:126:LYS:O	2:B:130:VAL:HG23	2.02	0.58
2:B:161:PRO:HG3	2:B:182:ALA:HB2	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:86:ILE:HG12	8:H:135:CYS:HA	1.85	0.58
20:T:49:MET:CE	20:T:81:VAL:HG11	2.33	0.58
1:A:1029:C:C3'	1:A:1030:C:H5''	2.33	0.58
6:F:43:LEU:HD22	6:F:43:LEU:H	1.69	0.58
9:I:16:VAL:HG11	9:I:80:ILE:HA	1.85	0.58
20:T:46:LEU:HD22	20:T:49:MET:HE3	1.84	0.58
1:A:596:C:H5'	1:A:596:C:C6	2.34	0.58
1:A:861:G:O2'	1:A:862:C:H5'	2.04	0.58
1:A:1226:C:N4	13:M:103:ARG:HG3	2.18	0.58
1:A:1363(A):A:H4'	1:A:1364:U:C5'	2.34	0.58
2:B:92:LEU:O	2:B:95:MET:HG3	2.04	0.58
2:B:124:ARG:HB3	2:B:125:PRO:HD2	1.86	0.58
4:D:120:VAL:O	4:D:133:ASP:HA	2.04	0.58
5:E:7:ILE:HB	5:E:27:LEU:HB3	1.84	0.58
18:R:32:THR:HA	18:R:68:GLU:HB2	1.85	0.58
1:A:1090:U:H2'	1:A:1091:U:H6	1.68	0.58
6:F:30:LEU:HB3	6:F:35:ALA:CB	2.34	0.58
17:Q:39:LYS:HD2	17:Q:41:TYR:CZ	2.39	0.58
1:A:460:G:C6	1:A:470:C:H5''	2.39	0.57
1:A:1002:G:H22	1:A:1040:U:H1'	1.69	0.57
2:B:53:GLU:O	2:B:57:MET:HG2	2.04	0.57
15:O:35:ILE:CG1	15:O:58:MET:HE3	2.33	0.57
18:R:40:ARG:NH1	18:R:40:ARG:HB3	2.19	0.57
19:S:50:ALA:HB1	19:S:57:HIS:HB3	1.85	0.57
1:A:192:U:C1'	20:T:96:GLY:HA2	2.34	0.57
2:B:166:ILE:H	2:B:166:ILE:CD1	2.15	0.57
5:E:29:VAL:HG11	5:E:105:ILE:HA	1.87	0.57
12:L:13:LYS:HA	12:L:13:LYS:HE3	1.86	0.57
14:N:28:ARG:HG2	14:N:28:ARG:HH11	1.69	0.57
15:O:2:ILE:N	15:O:2:ILE:HD12	2.19	0.57
16:P:67:THR:HG22	16:P:69:THR:N	2.19	0.57
3:C:146:LYS:HE2	3:C:204:GLY:H	1.67	0.57
11:K:89:GLN:HG2	11:K:95:VAL:HG21	1.85	0.57
1:A:115:G:H1'	1:A:116:A:N7	2.19	0.57
1:A:1014:A:H2'	1:A:1015:A:C8	2.39	0.57
7:G:77:ARG:HB2	7:G:155:TRP:HZ3	1.69	0.57
7:G:85:GLN:HE21	7:G:143:MET:CE	2.17	0.57
9:I:43:VAL:HG12	9:I:50:ARG:HH22	1.70	0.57
10:J:59:GLU:OE1	14:N:44:ARG:NH1	2.35	0.57
13:M:3:ILE:HG23	13:M:56:ARG:HA	1.86	0.57
19:S:25:LYS:H	19:S:25:LYS:HD2	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:3:LEU:O	20:T:6:LEU:HD12	2.03	0.57
1:A:189(A):C:O2'	1:A:189(B):C:H5'	2.03	0.57
1:A:197:A:H4'	1:A:198:G:OP1	2.05	0.57
1:A:632:A:O2'	1:A:633:G:H5'	2.05	0.57
1:A:939:G:H2'	1:A:940:C:C6	2.38	0.57
1:A:1168:A:O2'	1:A:1169:A:H8	1.88	0.57
1:A:1320:C:N3	19:S:36:ARG:HG3	2.20	0.57
5:E:72:ILE:HG23	5:E:138:LEU:HD13	1.86	0.57
5:E:133:GLU:O	5:E:137:GLN:HG3	2.04	0.57
7:G:77:ARG:HB2	7:G:155:TRP:CZ3	2.39	0.57
9:I:126:LYS:H	9:I:126:LYS:HD2	1.69	0.57
13:M:3:ILE:HG22	13:M:4:ALA:N	2.19	0.57
20:T:17:LEU:HD12	20:T:17:LEU:O	2.03	0.57
20:T:43:GLU:HA	20:T:93:ILE:CG1	2.35	0.57
1:A:677:U:H3	1:A:713:G:H22	1.51	0.57
3:C:45:GLU:O	3:C:47:TYR:N	2.37	0.57
13:M:39:ASN:HB3	13:M:42:THR:HG23	1.87	0.57
1:A:489:C:H2'	1:A:490:G:H8	1.69	0.57
1:A:1037:C:H2'	1:A:1038:C:H6	1.70	0.57
2:B:82:ALA:HB3	2:B:84:MET:HG2	1.86	0.57
6:F:15:ASP:H	6:F:18:GLN:NE2	2.03	0.57
8:H:60:ARG:HG3	8:H:60:ARG:NH1	2.12	0.57
10:J:6:LEU:HD23	10:J:94:ILE:HG12	1.87	0.57
13:M:44:VAL:HA	13:M:47:LEU:HG	1.86	0.57
20:T:95:GLY:O	20:T:97:LEU:N	2.37	0.57
1:A:189(H):G:H5''	1:A:189(H):G:C8	2.40	0.57
2:B:6:GLU:OE1	2:B:6:GLU:HA	2.04	0.57
4:D:7:VAL:O	4:D:9:ARG:N	2.32	0.57
4:D:126:THR:HG23	4:D:146:ALA:HB3	1.87	0.57
4:D:141:PRO:HA	4:D:184:PHE:HD2	1.70	0.57
10:J:46:THR:HG1	10:J:60:HIS:CD2	2.22	0.57
13:M:77:ILE:O	13:M:80:LEU:HD12	2.05	0.57
1:A:200:G:H2'	1:A:201:C:O4'	2.05	0.57
2:B:1:VAL:HG21	2:B:215:LEU:HD23	1.87	0.57
4:D:10:LEU:O	4:D:14:GLU:HG2	2.05	0.57
4:D:34:ARG:O	4:D:35:ARG:CB	2.49	0.57
1:A:100:C:H2'	1:A:101:A:C8	2.40	0.57
1:A:573:A:H3'	1:A:574:A:H5'	1.85	0.57
1:A:664:G:OP1	18:R:49:ARG:HD2	2.05	0.57
15:O:86:ILE:O	15:O:87:ARG:CB	2.53	0.57
1:A:824:C:H2'	1:A:825:G:H8	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:994:A:N7	1:A:1216:G:H4'	2.20	0.56
2:B:91:TRP:CZ2	2:B:96:LEU:HD13	2.40	0.56
3:C:21:TRP:HB3	3:C:58:ARG:HB2	1.87	0.56
11:K:4:VAL:O	11:K:5:ALA:HB3	2.04	0.56
17:Q:39:LYS:HG2	17:Q:40:LYS:N	2.19	0.56
1:A:328:C:O2	1:A:328:C:H2'	2.05	0.56
1:A:491:G:H2'	1:A:492:G:H8	1.70	0.56
1:A:1228:C:H2'	1:A:1229:A:H8	1.69	0.56
1:A:1457:G:H2'	1:A:1458:G:H8	1.70	0.56
3:C:69:VAL:CG1	3:C:70:ALA:N	2.68	0.56
3:C:75:VAL:HG11	3:C:102:VAL:CG2	2.35	0.56
9:I:110:ARG:HG2	9:I:111:LYS:N	2.20	0.56
9:I:126:LYS:HB2	13:M:125:LYS:HZ2	1.70	0.56
1:A:501:C:O2'	1:A:502:G:H5'	2.06	0.56
1:A:627:G:H2'	1:A:628:G:H8	1.70	0.56
1:A:1286:A:H8	1:A:1287:A:H5''	1.70	0.56
1:A:1287:A:H2	1:A:1353:G:H1'	1.71	0.56
1:A:1412:C:H2'	1:A:1413:A:C8	2.39	0.56
2:B:200:ASP:O	2:B:201:ALA:CB	2.54	0.56
3:C:12:GLY:CA	14:N:56:ARG:HH21	2.17	0.56
3:C:133:ILE:HG22	3:C:167:ALA:HB3	1.86	0.56
8:H:38:ILE:HD11	8:H:118:VAL:HG12	1.86	0.56
9:I:7:GLY:HA2	9:I:78:LEU:CD1	2.30	0.56
12:L:30:ARG:O	12:L:57:THR:HG23	2.05	0.56
15:O:86:ILE:CG2	15:O:87:ARG:N	2.68	0.56
15:O:86:ILE:HG22	15:O:87:ARG:N	2.20	0.56
16:P:28:ARG:HG2	16:P:28:ARG:NH1	2.20	0.56
17:Q:80:ARG:HG3	17:Q:80:ARG:O	2.05	0.56
19:S:42:PRO:O	19:S:45:VAL:HG23	2.05	0.56
1:A:1442(A):G:C4'	1:A:1442(B):A:H5'	2.35	0.56
2:B:2:LYS:O	2:B:3:GLU:HB2	2.06	0.56
3:C:146:LYS:HE2	3:C:204:GLY:N	2.20	0.56
4:D:7:VAL:HB	4:D:20:LEU:HD12	1.87	0.56
8:H:103:VAL:HG21	8:H:109:ILE:O	2.06	0.56
11:K:111:PRO:HG2	11:K:116:ARG:HG2	1.85	0.56
12:L:37:ARG:HH22	12:L:53:LYS:HE3	1.70	0.56
1:A:714:G:H2'	1:A:715:A:C8	2.40	0.56
1:A:1060:C:C4	3:C:1:GLY:HA3	2.40	0.56
1:A:1206:G:H1'	3:C:192:TYR:O	2.06	0.56
1:A:1343:G:H2'	1:A:1344:C:C6	2.41	0.56
7:G:64:ALA:O	7:G:68:VAL:HG23	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:24:ASP:OD2	11:K:28:ASN:HB2	2.05	0.56
19:S:63:THR:HG22	19:S:64:GLU:N	2.21	0.56
2:B:19:ASN:HD22	2:B:20:PRO:N	2.03	0.56
2:B:19:ASN:ND2	2:B:21:LYS:H	2.03	0.56
3:C:10:ARG:O	3:C:13:ILE:O	2.24	0.56
8:H:111:ILE:O	8:H:134:ILE:HB	2.04	0.56
11:K:2:ARG:O	11:K:3:GLN:O	2.23	0.56
18:R:21:ASN:CG	18:R:24:VAL:HG12	2.26	0.56
19:S:62:ILE:C	19:S:62:ILE:HD13	2.25	0.56
5:E:140:THR:O	5:E:144:VAL:HG23	2.06	0.56
11:K:38:ILE:HD13	11:K:53:LEU:CB	2.35	0.56
1:A:1054:C:OP1	1:A:1197:G:OP1	2.23	0.56
1:A:1346:A:H2'	1:A:1348:U:C6	2.40	0.56
4:D:75:ARG:O	4:D:79:GLU:HG2	2.05	0.56
1:A:422:C:O2	1:A:422:C:H2'	2.06	0.56
1:A:1038:C:H2'	1:A:1039:C:H6	1.70	0.56
1:A:1540:U:OP2	1:A:1540:U:H4'	2.06	0.56
3:C:4:ILE:HG12	3:C:9:PHE:HB2	1.87	0.56
3:C:31:LEU:HD12	3:C:31:LEU:N	2.21	0.56
4:D:2:ARG:O	4:D:4:ILE:HG12	2.05	0.56
9:I:39:LEU:O	9:I:41:ARG:N	2.39	0.56
10:J:40:THR:HG23	10:J:65:THR:O	2.05	0.56
12:L:53:LYS:CD	12:L:63:THR:HG22	2.36	0.56
1:A:35:G:O2'	1:A:36:C:P	2.64	0.56
1:A:746:A:O2'	1:A:747:C:H5'	2.05	0.56
1:A:1047:G:O2'	1:A:1048:G:H5'	2.05	0.56
1:A:1136:U:H5''	1:A:1137:C:OP2	2.06	0.56
1:A:1392:G:O2'	1:A:1393:U:H5'	2.07	0.56
1:A:1442(A):G:C3'	1:A:1442(B):A:H5'	2.36	0.56
3:C:173:PRO:HB2	3:C:176:THR:CG2	2.34	0.56
8:H:83:ILE:HG23	8:H:83:ILE:O	2.06	0.56
11:K:107:ASN:HD22	11:K:107:ASN:N	2.04	0.56
16:P:59:TRP:HB3	16:P:64:ALA:HB2	1.87	0.56
20:T:60:ALA:HA	20:T:66:HIS:H	1.70	0.56
1:A:343:U:H3'	1:A:345:C:H41	1.71	0.55
1:A:733:A:O2'	1:A:734:G:H5''	2.06	0.55
1:A:967:C:C4'	9:I:127:ARG:HG3	2.36	0.55
2:B:9:VAL:CG2	2:B:203:ARG:HG3	2.36	0.55
3:C:22:TYR:CD1	3:C:23:ALA:N	2.73	0.55
4:D:80:GLU:O	4:D:84:LYS:HG3	2.05	0.55
19:S:16:LEU:C	19:S:18:LYS:H	2.10	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1072:G:H2'	1:A:1073:U:C6	2.40	0.55
3:C:31:LEU:HD12	3:C:31:LEU:H	1.70	0.55
3:C:46:LEU:H	3:C:46:LEU:CD1	2.19	0.55
12:L:107:LYS:O	12:L:108:ASP:HB2	2.06	0.55
17:Q:23:GLU:HG2	17:Q:38:SER:HB3	1.87	0.55
1:A:345:C:H4'	1:A:346:G:H5''	1.88	0.55
1:A:1141:C:H2'	1:A:1142:G:H8	1.71	0.55
1:A:1504:G:OP1	1:A:1507:A:H4'	2.06	0.55
3:C:82:ARG:C	3:C:84:ARG:N	2.60	0.55
6:F:33:TYR:HA	6:F:71:ARG:HH21	1.72	0.55
9:I:9:ARG:HG2	9:I:74:ASP:HB2	1.87	0.55
10:J:85:THR:O	10:J:86:LEU:HD12	2.06	0.55
10:J:92:VAL:CG1	10:J:93:GLU:N	2.70	0.55
13:M:56:ARG:HG3	13:M:60:GLU:OE2	2.07	0.55
16:P:38:TYR:CE2	16:P:50:LYS:HD3	2.42	0.55
17:Q:8:VAL:HG21	17:Q:83:LEU:HD13	1.88	0.55
1:A:21:G:H2'	1:A:22:G:C8	2.42	0.55
1:A:155:C:O2'	1:A:156:G:H5'	2.07	0.55
10:J:79:THR:C	10:J:81:GLU:H	2.09	0.55
1:A:477:A:O2'	1:A:479:C:H5'	2.06	0.55
1:A:1109:C:H6	1:A:1109:C:H5'	1.70	0.55
7:G:25:PHE:O	7:G:29:ILE:HG13	2.06	0.55
12:L:53:LYS:HD3	12:L:63:THR:HG22	1.87	0.55
1:A:994:A:H2'	1:A:994:A:N3	2.20	0.55
1:A:1095:U:H2'	1:A:1096:C:H6	1.69	0.55
2:B:156:ILE:HG22	2:B:158:VAL:HG23	1.87	0.55
3:C:13:ILE:O	3:C:15:ARG:N	2.40	0.55
4:D:63:LEU:HD12	4:D:74:PHE:CZ	2.42	0.55
9:I:32:PHE:HZ	9:I:45:ALA:HB3	1.71	0.55
11:K:116:ARG:C	11:K:118:ALA:H	2.09	0.55
1:A:533:A:H4'	1:A:534:U:OP1	2.07	0.55
1:A:737:A:H1'	6:F:73:ASN:OD1	2.07	0.55
1:A:1049:U:H5''	14:N:2:ARG:CD	2.36	0.55
1:A:1182:G:C4'	1:A:1183:A:H5'	2.35	0.55
4:D:2:ARG:CZ	4:D:117:ARG:HH22	2.19	0.55
4:D:145:ILE:HD12	4:D:145:ILE:N	2.22	0.55
7:G:85:GLN:HE21	7:G:143:MET:HE3	1.70	0.55
10:J:25:ALA:CB	10:J:79:THR:HG23	2.36	0.55
1:A:386:C:C2'	1:A:387:U:H5'	2.37	0.55
1:A:518:C:H5''	1:A:519:C:C6	2.41	0.55
1:A:870:U:H4'	1:A:871:U:H5''	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:40:VAL:HG22	6:F:41:GLU:N	2.22	0.55
10:J:2:ILE:HG22	10:J:98:THR:HB	1.89	0.55
11:K:30:ILE:HG22	11:K:31:THR:HG23	1.89	0.55
12:L:22:ALA:O	12:L:23:LEU:O	2.24	0.55
18:R:22:VAL:HG22	18:R:63:LEU:HB3	1.88	0.55
20:T:47:LYS:HA	20:T:50:ARG:HD2	1.89	0.55
1:A:1142:G:H2'	1:A:1143:G:O4'	2.06	0.55
1:A:1229:A:H2'	1:A:1230:C:C6	2.42	0.55
11:K:38:ILE:HD13	11:K:53:LEU:HB3	1.88	0.55
11:K:70:VAL:CG2	11:K:93:LEU:HD13	2.35	0.55
11:K:116:ARG:C	11:K:118:ALA:N	2.57	0.55
3:C:18:GLU:HB3	3:C:39:ARG:HH21	1.72	0.55
11:K:47:THR:HG23	11:K:50:ALA:H	1.71	0.55
13:M:89:LEU:O	13:M:92:ARG:HB2	2.07	0.55
13:M:93:ARG:HH22	19:S:81:ARG:NH1	2.03	0.55
1:A:168:G:H5'	1:A:168:G:C8	2.38	0.54
1:A:273:A:H1'	17:Q:15:GLN:HE21	1.71	0.54
1:A:345:C:H4'	1:A:346:G:C5'	2.37	0.54
1:A:538:G:O2'	1:A:539:A:H5'	2.07	0.54
1:A:1314:C:H5''	19:S:6:LYS:NZ	2.22	0.54
2:B:178:VAL:N	2:B:192:ASP:OD2	2.38	0.54
3:C:122:GLN:HE22	3:C:139:ARG:HH22	1.54	0.54
10:J:22:VAL:O	10:J:26:ARG:HB2	2.07	0.54
1:A:992:U:O4	1:A:1044:A:N7	2.40	0.54
7:G:45:ALA:O	7:G:49:ILE:HG13	2.08	0.54
14:N:43:LEU:HD12	14:N:43:LEU:O	2.05	0.54
13:M:36:THR:HG22	13:M:36:THR:O	2.08	0.54
1:A:1510:U:H2'	1:A:1511:G:C8	2.43	0.54
10:J:36:ILE:HD12	10:J:69:LEU:CD1	2.37	0.54
13:M:87:ARG:NH1	19:S:3:ARG:NH2	2.53	0.54
16:P:58:TYR:O	16:P:62:VAL:HG22	2.08	0.54
18:R:32:THR:C	18:R:34:LYS:H	2.10	0.54
19:S:16:LEU:O	19:S:20:LEU:HG	2.08	0.54
1:A:181:G:O2'	1:A:182:U:H5	1.90	0.54
1:A:403:C:O2'	1:A:404:U:H5'	2.08	0.54
1:A:460:G:C3'	1:A:461:A:C5'	2.84	0.54
7:G:112:GLU:HG2	7:G:118:ARG:CG	2.29	0.54
12:L:51:VAL:HG12	12:L:52:ALA:N	2.23	0.54
14:N:7:GLU:C	14:N:7:GLU:OE1	2.46	0.54
16:P:4:ILE:HA	16:P:20:VAL:O	2.07	0.54
1:A:625:G:H2'	1:A:626:U:C6	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1112:C:O2	3:C:178:ARG:HG3	2.08	0.54
2:B:3:GLU:OE1	2:B:4:LEU:N	2.37	0.54
4:D:16:VAL:N	4:D:32:MET:HE2	2.23	0.54
5:E:98:ALA:CB	5:E:116:THR:HG21	2.37	0.54
10:J:44:ARG:HH11	10:J:44:ARG:HG2	1.71	0.54
11:K:40:TYR:HB3	11:K:44:ARG:HB2	1.89	0.54
13:M:58:TYR:O	13:M:62:THR:CG2	2.56	0.54
2:B:47:ARG:HG2	2:B:47:ARG:NH1	2.21	0.54
4:D:55:VAL:HG12	4:D:201:LEU:HD13	1.89	0.54
4:D:63:LEU:HD12	4:D:74:PHE:HZ	1.72	0.54
4:D:125:ILE:HG22	4:D:126:THR:N	2.22	0.54
10:J:6:LEU:CD2	10:J:94:ILE:HG12	2.38	0.54
3:C:133:ILE:CG2	3:C:167:ALA:HB3	2.38	0.54
5:E:101:VAL:HB	5:E:102:PRO:HD3	1.89	0.54
11:K:81:ARG:HD3	18:R:73:LYS:NZ	2.23	0.54
13:M:13:ARG:NH1	13:M:15:ASP:OD2	2.36	0.54
13:M:84:GLY:O	13:M:85:CYS:O	2.26	0.54
13:M:121:LYS:NZ	13:M:122:ALA:HB2	2.22	0.54
19:S:5:LEU:O	19:S:6:LYS:CB	2.54	0.54
1:A:250:A:H1'	1:A:252:U:C6	2.43	0.54
1:A:1391:U:H2'	1:A:1392:G:H8	1.71	0.54
2:B:207:LEU:HD23	2:B:207:LEU:C	2.27	0.54
3:C:4:ILE:HD12	3:C:4:ILE:H	1.72	0.54
3:C:46:LEU:N	3:C:46:LEU:HD12	2.23	0.54
18:R:38:ARG:HH11	18:R:44:SER:HA	1.71	0.54
1:A:1230:C:O2'	13:M:125:LYS:HG2	2.08	0.54
1:A:1480:G:H3'	1:A:1481:U:H6	1.71	0.54
3:C:5:HIS:HD2	3:C:7:ILE:H	1.54	0.54
3:C:128:ALA:HB3	3:C:131:ARG:CD	2.38	0.54
5:E:56:TYR:HE1	5:E:60:ARG:NH2	2.06	0.54
11:K:48:PRO:O	11:K:51:ALA:HB3	2.08	0.54
1:A:164:U:O2'	1:A:165:C:H5'	2.08	0.53
1:A:1231:G:O3'	9:I:125:SER:HB3	2.08	0.53
3:C:25:LYS:CE	3:C:25:LYS:N	2.61	0.53
9:I:18:LEU:O	9:I:19:ARG:HG3	2.09	0.53
9:I:46:LEU:C	9:I:48:PRO:HD2	2.28	0.53
15:O:3:THR:OG1	15:O:6:GLU:HB2	2.07	0.53
1:A:181:G:O2'	1:A:182:U:C5	2.62	0.53
1:A:339:C:H2'	1:A:340:U:C6	2.44	0.53
1:A:1226:C:H5''	13:M:102:THR:HB	1.91	0.53
2:B:200:ASP:O	2:B:201:ALA:HB3	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:10:ARG:O	3:C:15:ARG:HB3	2.07	0.53
3:C:63:VAL:HG12	3:C:65:VAL:HG23	1.90	0.53
3:C:190:THR:CG2	3:C:191:THR:H	2.19	0.53
4:D:3:TYR:CE2	4:D:10:LEU:HD11	2.43	0.53
5:E:148:ARG:NH2	8:H:107:LEU:O	2.42	0.53
9:I:35:TYR:CD2	9:I:36:PHE:CE1	2.96	0.53
11:K:74:VAL:HG23	11:K:100:ASP:HA	1.89	0.53
18:R:21:ASN:ND2	18:R:21:ASN:C	2.61	0.53
1:A:1126:U:C2	1:A:1127:G:C8	2.96	0.53
4:D:69:ILE:HD11	4:D:99:ARG:NE	2.23	0.53
4:D:106:ARG:HD2	4:D:172:TRP:CZ2	2.43	0.53
12:L:82:ARG:HG2	12:L:82:ARG:NH1	2.23	0.53
14:N:28:ARG:HG2	14:N:28:ARG:NH1	2.24	0.53
17:Q:89:ILE:O	17:Q:92:GLN:HB3	2.08	0.53
1:A:197:A:N1	1:A:220:G:O2'	2.36	0.53
1:A:647:C:O2'	1:A:648:A:H5''	2.08	0.53
1:A:1245:A:H61	1:A:1292:U:H3	1.57	0.53
2:B:68:LYS:HE2	2:B:200:ASP:HB2	1.89	0.53
3:C:106:GLN:O	3:C:107:ASN:CB	2.56	0.53
6:F:19:LEU:C	6:F:19:LEU:HD23	2.29	0.53
7:G:50:GLN:HG2	7:G:57:PRO:HD3	1.91	0.53
8:H:104:ARG:HG2	8:H:104:ARG:NH1	2.23	0.53
18:R:2:SER:HB2	18:R:39:ARG:NH2	2.24	0.53
20:T:49:MET:HE2	20:T:81:VAL:HG11	1.90	0.53
1:A:530:G:H5'	1:A:531:U:H5'	1.89	0.53
1:A:972:C:C4'	10:J:55:LYS:HG2	2.17	0.53
1:A:1206:G:O2'	1:A:1207:G:H5'	2.08	0.53
6:F:4:TYR:HD1	6:F:92:LYS:HA	1.73	0.53
12:L:82:ARG:HB2	12:L:97:VAL:HG23	1.90	0.53
16:P:4:ILE:HG13	16:P:64:ALA:HB1	1.90	0.53
18:R:40:ARG:HH11	18:R:40:ARG:CA	2.22	0.53
1:A:427:U:OP1	4:D:12:ARG:NH2	2.42	0.53
1:A:1468:A:H2'	1:A:1469:G:O4'	2.09	0.53
3:C:166:TRP:O	3:C:167:ALA:HB3	2.08	0.53
15:O:5:GLU:H	15:O:5:GLU:CD	2.11	0.53
19:S:15:LEU:HD12	19:S:15:LEU:H	1.74	0.53
1:A:299:G:H2'	1:A:300:A:C8	2.44	0.53
1:A:328:C:O2	1:A:328:C:C2'	2.57	0.53
1:A:408:A:O2'	1:A:409:G:H5'	2.08	0.53
1:A:818:G:C3'	1:A:819:A:C5'	2.86	0.53
1:A:1346:A:N6	1:A:1374:A:H5'	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1:VAL:HG11	2:B:215:LEU:HB2	1.90	0.53
3:C:75:VAL:HG11	3:C:102:VAL:HG21	1.90	0.53
6:F:80:ARG:NH1	6:F:88:VAL:HB	2.24	0.53
9:I:78:LEU:HD23	9:I:100:PHE:O	2.09	0.53
12:L:106:VAL:H	12:L:118:THR:HG22	1.73	0.53
14:N:56:ARG:HG2	14:N:57:LYS:H	1.74	0.53
1:A:177:C:C3'	1:A:178:C:H5''	2.37	0.53
1:A:607:A:H5'	1:A:607:A:H8	1.74	0.53
1:A:1134:G:H2'	1:A:1134:G:N3	2.23	0.53
1:A:1254:C:OP1	10:J:43:ARG:HD2	2.08	0.53
1:A:1321:C:H42	19:S:37:ARG:HH12	1.57	0.53
2:B:124:ARG:HB3	2:B:128:GLU:OE1	2.09	0.53
8:H:10:LEU:HD12	8:H:85:ARG:HG3	1.91	0.53
10:J:3:ARG:HA	10:J:71:ASP:OD1	2.09	0.53
17:Q:96:SER:HA	17:Q:101:GLY:O	2.08	0.53
19:S:17:GLU:HA	19:S:20:LEU:HG	1.91	0.53
1:A:542:G:OP1	4:D:9:ARG:NH2	2.42	0.53
5:E:139:ARG:NH1	8:H:77:GLU:OE2	2.41	0.53
6:F:15:ASP:OD1	6:F:17:SER:HB2	2.08	0.53
13:M:120:LYS:N	13:M:120:LYS:HD2	2.24	0.53
14:N:11:ARG:O	14:N:13:PRO:CD	2.57	0.53
19:S:80:TYR:O	19:S:81:ARG:C	2.47	0.53
1:A:355:C:H1'	1:A:388:G:H2'	1.90	0.53
2:B:42:MET:O	2:B:45:LEU:HB2	2.09	0.53
8:H:4:ASP:OD2	8:H:85:ARG:NH1	2.42	0.53
8:H:10:LEU:HD22	8:H:83:ILE:HD11	1.91	0.53
9:I:3:TYR:CE2	9:I:87:TYR:HA	2.43	0.53
10:J:28:SER:HB3	10:J:82:GLN:HE21	1.71	0.53
10:J:87:ASP:O	10:J:88:LEU:HD23	2.09	0.53
12:L:25:GLY:O	12:L:26:ALA:O	2.27	0.53
14:N:5:LEU:C	14:N:7:GLU:H	2.11	0.53
18:R:72:ARG:HG2	18:R:72:ARG:HH11	1.74	0.53
1:A:1251:A:H4'	9:I:11:GLU:OE2	2.08	0.52
3:C:47:TYR:HE1	3:C:117:GLN:HE21	1.57	0.52
3:C:69:VAL:CG1	3:C:70:ALA:H	2.21	0.52
17:Q:78:SER:O	17:Q:79:GLY:O	2.28	0.52
1:A:101:A:O2'	1:A:102:G:H5'	2.08	0.52
1:A:181:G:H4'	1:A:182:U:OP1	2.09	0.52
1:A:384:G:H2'	1:A:385:C:C6	2.44	0.52
1:A:1259:C:H5'	1:A:1260:C:OP2	2.09	0.52
1:A:1367:C:H5''	10:J:58:ARG:NH1	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:24:ARG:HG3	2:B:25:TYR:CD1	2.45	0.52
20:T:47:LYS:HA	20:T:50:ARG:CD	2.39	0.52
1:A:824:C:H2'	1:A:825:G:C8	2.43	0.52
1:A:1049:U:H2'	1:A:1201:A:C8	2.45	0.52
3:C:4:ILE:CD1	3:C:4:ILE:N	2.72	0.52
3:C:118:ARG:CG	3:C:139:ARG:HH12	2.16	0.52
4:D:121:ARG:NH2	4:D:133:ASP:OD2	2.41	0.52
8:H:6:ILE:O	8:H:10:LEU:HG	2.09	0.52
8:H:11:THR:HA	8:H:14:ARG:NH1	2.25	0.52
12:L:56:LEU:HD11	12:L:81:ILE:CD1	2.37	0.52
1:A:154:C:O2'	1:A:155:C:H5'	2.10	0.52
1:A:432:A:H3'	1:A:433:C:H6	1.73	0.52
1:A:1179:A:O3'	9:I:102:THR:HG23	2.09	0.52
1:A:1423:G:H2'	1:A:1424:C:C6	2.45	0.52
1:A:1427:U:H2'	1:A:1428:A:C8	2.45	0.52
3:C:38:ILE:HG23	3:C:42:LEU:HD12	1.91	0.52
19:S:14:HIS:O	19:S:18:LYS:HE2	2.10	0.52
1:A:106:C:O2	1:A:379:C:H4'	2.09	0.52
1:A:757:U:H2'	1:A:758:G:O4'	2.10	0.52
1:A:984:C:H2'	1:A:985:C:H6	1.74	0.52
1:A:1152:A:H4'	10:J:11:HIS:HD2	1.75	0.52
1:A:1231:G:H4'	9:I:125:SER:OG	2.10	0.52
1:A:1366:C:H2'	1:A:1367:C:C6	2.44	0.52
19:S:77:THR:HG22	19:S:78:ARG:N	2.23	0.52
20:T:22:LYS:O	20:T:26:ILE:HG13	2.10	0.52
1:A:1230:C:O2'	1:A:1231:G:H5'	2.10	0.52
1:A:1367:C:H5'	10:J:58:ARG:NH1	2.15	0.52
5:E:92:PRO:HA	5:E:113:ASP:OD2	2.10	0.52
9:I:36:PHE:CZ	9:I:73:ILE:HD13	2.44	0.52
12:L:56:LEU:CD2	12:L:62:VAL:HG22	2.39	0.52
13:M:77:ILE:HA	13:M:80:LEU:CD1	2.34	0.52
16:P:51:VAL:O	16:P:53:VAL:N	2.43	0.52
1:A:188:C:H2'	1:A:189:G:C5'	2.19	0.52
1:A:556:C:O2'	1:A:557:G:H5'	2.10	0.52
1:A:952:U:H2'	1:A:953:G:H8	1.73	0.52
1:A:1060:C:O2'	1:A:1061:G:H5'	2.09	0.52
1:A:1126:U:C2'	1:A:1127:G:OP1	2.58	0.52
1:A:1447:A:OP2	1:A:1452:C:H5	1.92	0.52
9:I:96:LYS:O	9:I:99:GLY:N	2.40	0.52
1:A:720:C:H3'	1:A:721:G:C4'	2.39	0.52
1:A:1064:G:H21	1:A:1190:G:H2'	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1524:C:OP1	11:K:110:ARG:NH1	2.42	0.52
4:D:34:ARG:HH11	4:D:34:ARG:HG3	1.75	0.52
7:G:53:THR:HG22	7:G:55:GLN:N	2.21	0.52
8:H:60:ARG:NH1	8:H:60:ARG:CG	2.71	0.52
8:H:63:LEU:HD22	8:H:63:LEU:N	2.21	0.52
13:M:124:ARG:HH11	13:M:124:ARG:HG3	1.74	0.52
20:T:79:ARG:O	20:T:83:GLN:HG3	2.10	0.52
1:A:130:A:C8	17:Q:62:ARG:HG3	2.45	0.52
1:A:631:G:C2'	1:A:632:A:H5'	2.40	0.52
26:A:2733:M5Z:C56	12:L:40:THR:HG21	2.39	0.52
12:L:106:VAL:CG2	12:L:116:TYR:HB3	2.38	0.52
13:M:48:THR:HG22	13:M:50:ALA:H	1.74	0.52
15:O:54:GLY:HA2	15:O:57:MET:CE	2.40	0.52
1:A:445:G:O2'	1:A:446:G:H5'	2.10	0.52
1:A:706:A:H1'	11:K:19:ILE:HD11	1.92	0.52
1:A:1174:G:H2'	1:A:1175:G:H8	1.75	0.52
1:A:1225:A:H2'	1:A:1225:A:N3	2.25	0.52
2:B:159:VAL:O	2:B:181:LEU:O	2.28	0.52
10:J:32:VAL:HG12	10:J:33:SER:N	2.25	0.52
12:L:78:VAL:O	12:L:101:TYR:HB3	2.10	0.52
17:Q:94:TYR:N	17:Q:94:TYR:CD1	2.77	0.52
18:R:24:VAL:HG13	18:R:25:LEU:N	2.25	0.52
20:T:1:ARG:O	20:T:2:ASN:HB2	2.10	0.52
1:A:1068:G:OP2	1:A:1094:G:H5'	2.10	0.51
2:B:95:MET:HA	2:B:102:ILE:HD12	1.92	0.51
11:K:3:GLN:HA	11:K:65:TYR:O	2.10	0.51
1:A:181:G:H2'	1:A:183:G:C5	2.44	0.51
1:A:762:C:H4'	17:Q:103:LYS:HZ1	1.74	0.51
1:A:1232:U:OP1	9:I:123:GLN:HG2	2.10	0.51
2:B:105:ARG:HB3	2:B:143:LEU:HD11	1.92	0.51
3:C:109:ASN:C	3:C:110:LEU:HD23	2.31	0.51
4:D:2:ARG:NH2	4:D:73:GLN:HG3	2.25	0.51
11:K:22:ILE:HD12	11:K:62:ALA:HB2	1.91	0.51
17:Q:67:ARG:H	17:Q:69:ARG:NH1	2.08	0.51
18:R:4:LYS:O	18:R:5:ALA:HB2	2.10	0.51
18:R:32:THR:HG23	18:R:68:GLU:H	1.76	0.51
1:A:56:U:H2'	1:A:57:G:C8	2.46	0.51
2:B:55:LEU:HD11	2:B:154:ASP:HB2	1.92	0.51
2:B:180:ALA:HB3	2:B:191:VAL:HG11	1.92	0.51
4:D:49:ARG:HH11	4:D:49:ARG:HG3	1.75	0.51
6:F:33:TYR:CD2	6:F:75:LEU:HD23	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:24:ILE:CD1	13:M:65:LEU:HD13	2.39	0.51
1:A:229:U:O2'	1:A:230:G:H5'	2.10	0.51
1:A:1004:A:N7	1:A:1037:C:N3	2.59	0.51
1:A:1300:G:HO2'	1:A:1301:U:H6	1.55	0.51
6:F:22:GLU:O	6:F:26:ILE:HG12	2.09	0.51
6:F:40:VAL:CG2	6:F:41:GLU:N	2.74	0.51
8:H:82:HIS:CD2	8:H:83:ILE:N	2.78	0.51
14:N:10:LYS:O	14:N:11:ARG:C	2.49	0.51
1:A:430:A:H2'	1:A:431:A:H5'	1.93	0.51
1:A:1125:U:H3	10:J:3:ARG:NH1	2.08	0.51
1:A:1407:C:O2'	1:A:1408:A:H5'	2.10	0.51
2:B:88:ASN:H	2:B:88:ASN:ND2	2.00	0.51
2:B:224:VAL:HG12	2:B:225:GLU:N	2.26	0.51
5:E:95:GLY:O	5:E:113:ASP:HA	2.10	0.51
1:A:357:G:O2'	1:A:358:U:H5'	2.11	0.51
1:A:514:C:O2'	1:A:515:G:H5'	2.10	0.51
1:A:1019:C:H5'	1:A:1020:U:OP2	2.10	0.51
1:A:1049:U:H5''	14:N:2:ARG:HG3	1.92	0.51
9:I:35:TYR:HD2	9:I:36:PHE:CE1	2.29	0.51
10:J:48:ILE:HD12	10:J:48:ILE:N	2.26	0.51
12:L:2:THR:OG1	12:L:5:GLN:HG3	2.10	0.51
16:P:82:GLN:O	16:P:83:GLU:C	2.49	0.51
17:Q:67:ARG:NH1	17:Q:67:ARG:HG2	2.26	0.51
20:T:87:ALA:O	20:T:88:ALA:HB3	2.10	0.51
1:A:1291:G:H4'	9:I:37:GLN:O	2.10	0.51
2:B:58:ARG:HG2	2:B:58:ARG:HH11	1.76	0.51
3:C:107:ASN:HD21	3:C:143:SER:CB	2.16	0.51
4:D:116:ALA:O	4:D:120:VAL:HG23	2.10	0.51
1:A:188:C:C3'	1:A:189:G:H5''	2.40	0.51
1:A:457:C:O2'	1:A:458:C:H5'	2.10	0.51
1:A:1187:G:OP1	9:I:112:LYS:HE2	2.11	0.51
1:A:1457:G:O2'	1:A:1458:G:H5'	2.11	0.51
1:A:1499:A:C1'	1:A:1520:G:H5'	2.40	0.51
2:B:88:ASN:N	2:B:88:ASN:ND2	2.58	0.51
3:C:24:GLY:C	3:C:26:LYS:H	2.13	0.51
7:G:61:PHE:HD1	7:G:123:LEU:HD11	1.75	0.51
18:R:23:GLU:HA	18:R:26:LYS:CE	2.37	0.51
1:A:442:C:H2'	1:A:443:C:C6	2.45	0.51
1:A:632:A:C2'	1:A:633:G:H5'	2.40	0.51
3:C:31:LEU:H	3:C:31:LEU:CD1	2.24	0.51
4:D:176:ASP:OD1	4:D:178:GLU:HB2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:45:PHE:CZ	14:N:36:PHE:HE2	2.29	0.51
17:Q:66:LYS:CA	17:Q:69:ARG:HH12	2.23	0.51
1:A:59:A:H3'	1:A:331:G:H22	1.76	0.51
1:A:502:G:OP1	12:L:114:SER:CB	2.59	0.51
1:A:642:A:O2'	1:A:643:C:H5'	2.10	0.51
1:A:1187:G:H5'	9:I:112:LYS:CE	2.31	0.51
1:A:1480:G:H3'	1:A:1481:U:C6	2.45	0.51
26:A:2733:M5Z:H56	12:L:40:THR:HG21	1.93	0.51
2:B:11:PHE:CD1	2:B:12:GLY:N	2.77	0.51
5:E:8:LEU:CD1	5:E:27:LEU:HB2	2.41	0.51
8:H:20:TYR:HE1	8:H:76:PRO:HG2	1.72	0.51
8:H:118:VAL:C	8:H:119:LEU:HD23	2.31	0.51
13:M:79:ARG:HB3	13:M:79:ARG:HH11	1.73	0.51
1:A:627:G:O2'	1:A:628:G:H5'	2.10	0.50
1:A:1262:C:O2'	1:A:1263:C:H5'	2.11	0.50
1:A:1298:C:H4'	1:A:1299:A:O4'	2.10	0.50
1:A:1435:G:H2'	1:A:1436:U:H6	1.75	0.50
2:B:71:ALA:CB	2:B:205:ILE:HG21	2.41	0.50
2:B:82:ALA:C	2:B:84:MET:N	2.64	0.50
3:C:82:ARG:O	3:C:84:ARG:N	2.44	0.50
6:F:3:ARG:HG2	6:F:93:SER:OG	2.10	0.50
17:Q:44:HIS:HB3	17:Q:71:ARG:HG2	1.93	0.50
1:A:189:G:H5'	1:A:189:G:C8	2.45	0.50
1:A:979:C:H2'	1:A:980:C:H5'	1.92	0.50
1:A:1118:C:O5'	1:A:1118:C:H6	1.93	0.50
1:A:1264:C:H2'	1:A:1265:G:C8	2.46	0.50
5:E:75:GLU:O	8:H:104:ARG:CZ	2.58	0.50
8:H:72:PRO:O	8:H:73:ASP:HB3	2.11	0.50
1:A:41:G:H2'	1:A:42:G:C8	2.46	0.50
1:A:1026:G:H3'	1:A:1027:C:H5'	1.93	0.50
1:A:1227:A:O3'	13:M:114:LYS:HE3	2.10	0.50
1:A:1311:G:O6	19:S:2:PRO:HB3	2.11	0.50
1:A:1472:U:O2'	1:A:1473:A:H5'	2.12	0.50
2:B:109:LEU:C	2:B:109:LEU:HD23	2.31	0.50
3:C:9:PHE:CE2	3:C:177:LEU:HD13	2.45	0.50
4:D:161:LEU:CD1	4:D:180:MET:HE2	2.42	0.50
7:G:27:ASN:OD1	7:G:35:LYS:NZ	2.44	0.50
8:H:112:LEU:HD12	8:H:112:LEU:N	2.27	0.50
12:L:37:ARG:HB3	12:L:37:ARG:HH11	1.75	0.50
1:A:293:G:O2'	1:A:294:U:H5'	2.12	0.50
1:A:430:A:C2'	1:A:431:A:H5'	2.40	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1103:C:OP1	2:B:90:ARG:NH2	2.43	0.50
1:A:1109:C:H2'	1:A:1110:A:O4'	2.10	0.50
1:A:1381:U:H2'	1:A:1382:C:H6	1.77	0.50
12:L:20:VAL:HG12	12:L:20:VAL:O	2.12	0.50
15:O:63:ARG:NH1	15:O:63:ARG:HB3	2.25	0.50
19:S:51:VAL:O	19:S:58:VAL:HG22	2.12	0.50
1:A:81:U:H2'	1:A:83:U:OP2	2.11	0.50
1:A:628:G:H2'	1:A:629:G:C8	2.46	0.50
3:C:96:LYS:O	3:C:97:ASN:C	2.50	0.50
3:C:133:ILE:HG21	3:C:166:TRP:O	2.11	0.50
3:C:137:VAL:HG22	3:C:150:VAL:HG23	1.93	0.50
4:D:28:PRO:O	4:D:29:LYS:HG3	2.10	0.50
12:L:84:GLY:H	12:L:94:TYR:HA	1.76	0.50
14:N:17:VAL:O	14:N:19:ALA:N	2.44	0.50
17:Q:75:LEU:HD12	17:Q:76:VAL:N	2.27	0.50
1:A:445:G:H2'	1:A:446:G:H8	1.77	0.50
1:A:946:A:H2'	1:A:947:G:H8	1.72	0.50
3:C:173:PRO:O	3:C:176:THR:HG22	2.11	0.50
4:D:29:LYS:C	4:D:31:ALA:H	2.13	0.50
6:F:21:LEU:O	6:F:24:GLU:HG3	2.10	0.50
9:I:24:LYS:HB2	9:I:59:ASP:OD1	2.11	0.50
13:M:107:ARG:HD3	13:M:113:ARG:NH1	2.27	0.50
15:O:26:VAL:HG12	15:O:30:LEU:CD2	2.41	0.50
1:A:1039:C:O2	1:A:1039:C:H2'	2.12	0.50
1:A:1256:A:H62	1:A:1278:U:H5'	1.76	0.50
1:A:1264:C:H2'	1:A:1265:G:H8	1.77	0.50
2:B:80:GLU:C	2:B:82:ALA:H	2.15	0.50
4:D:66:ILE:HD13	4:D:195:LEU:HD22	1.93	0.50
5:E:79:GLU:HG2	5:E:84:LYS:HD2	1.94	0.50
10:J:25:ALA:HB2	10:J:83:LEU:HD21	1.93	0.50
1:A:248:C:O2'	1:A:249:U:H5'	2.11	0.50
1:A:1301:U:O2	1:A:1301:U:H2'	2.12	0.50
1:A:1414:U:H2'	1:A:1415:G:H8	1.77	0.50
1:A:1488:G:O2'	1:A:1489:G:H5'	2.12	0.50
13:M:97:VAL:HG12	13:M:97:VAL:O	2.11	0.50
1:A:668:G:O2'	1:A:669:U:H5'	2.11	0.50
1:A:920:U:H2'	1:A:921:U:C6	2.47	0.50
1:A:972:C:O5'	10:J:55:LYS:HE2	2.12	0.50
1:A:1026:G:H3'	1:A:1027:C:C5'	2.42	0.50
1:A:1030:C:H42	1:A:1031:G:H1	1.60	0.50
1:A:1442(A):G:H5''	1:A:1442(B):A:H5'	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1495:U:H2'	1:A:1496:C:C6	2.46	0.50
3:C:107:ASN:OD1	3:C:109:ASN:HB2	2.12	0.50
6:F:2:ARG:CD	6:F:69:GLU:HG2	2.42	0.50
12:L:79:VAL:HG22	12:L:80:LEU:N	2.26	0.50
13:M:7:GLU:C	13:M:8:ILE:HD13	2.32	0.50
13:M:33:LEU:HD23	13:M:55:LEU:HD21	1.93	0.50
1:A:630:G:O3'	1:A:631:G:H8	1.95	0.49
1:A:1400:C:O5'	1:A:1400:C:H6	1.95	0.49
2:B:1:VAL:CG2	2:B:215:LEU:HD23	2.42	0.49
5:E:116:THR:HG23	5:E:117:LYS:N	2.26	0.49
7:G:113:ARG:HG2	7:G:113:ARG:HH11	1.76	0.49
16:P:20:VAL:CG1	16:P:21:VAL:N	2.75	0.49
17:Q:26:PHE:CE2	17:Q:35:ILE:HD11	2.47	0.49
1:A:1316:G:N2	1:A:1318:A:H3'	2.26	0.49
7:G:119:ILE:HD12	7:G:119:ILE:H	1.77	0.49
11:K:38:ILE:CD1	11:K:54:ALA:N	2.75	0.49
20:T:50:ARG:NH1	20:T:50:ARG:HG2	2.26	0.49
1:A:153:C:O2'	1:A:154:C:H5'	2.12	0.49
1:A:420:U:O2'	1:A:421:U:H5''	2.11	0.49
1:A:954:G:H2'	1:A:955:U:H6	1.77	0.49
4:D:146:ALA:HA	4:D:181:LYS:HA	1.94	0.49
6:F:100:ASN:OD1	6:F:100:ASN:O	2.30	0.49
7:G:5:ARG:O	7:G:6:ALA:O	2.29	0.49
12:L:115:LYS:O	12:L:116:TYR:HB2	2.12	0.49
19:S:52:TYR:HA	19:S:56:GLN:O	2.12	0.49
20:T:3:LEU:O	20:T:5:ALA:N	2.45	0.49
1:A:599:C:O2'	1:A:600:C:H5'	2.12	0.49
1:A:849:C:O2'	1:A:850:U:H5'	2.12	0.49
1:A:1081:G:P	5:E:12:THR:OG1	2.71	0.49
2:B:163:LYS:O	2:B:163:LYS:HD3	2.11	0.49
9:I:94:LYS:O	9:I:98:LEU:HD23	2.12	0.49
16:P:28:ARG:HG2	16:P:29:ASP:OD1	2.12	0.49
1:A:686:U:O2'	1:A:687:A:C8	2.58	0.49
1:A:1115:C:O2'	1:A:1116:C:H5'	2.13	0.49
1:A:1314:C:H5''	19:S:6:LYS:HZ2	1.78	0.49
1:A:1399:C:O2	1:A:1401:G:C5	2.66	0.49
3:C:10:ARG:NH1	3:C:176:THR:O	2.46	0.49
5:E:75:GLU:HG3	5:E:89:PRO:CD	2.42	0.49
9:I:126:LYS:CB	13:M:125:LYS:NZ	2.76	0.49
16:P:81:ARG:HH11	16:P:81:ARG:CB	2.25	0.49
1:A:961:U:C2'	1:A:962:C:H5'	2.43	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1026:G:H2'	1:A:1026:G:N3	2.28	0.49
1:A:1379:G:OP2	7:G:5:ARG:CZ	2.60	0.49
2:B:63:LEU:HB3	2:B:156:ILE:HD13	1.94	0.49
17:Q:26:PHE:CZ	17:Q:35:ILE:HD11	2.48	0.49
19:S:41:VAL:HB	19:S:42:PRO:HD2	1.94	0.49
20:T:50:ARG:HG2	20:T:50:ARG:HH11	1.77	0.49
1:A:376:G:H5''	16:P:5:ARG:HB2	1.93	0.49
1:A:519:C:H2'	1:A:520:A:C8	2.47	0.49
1:A:954:G:H2'	1:A:955:U:C6	2.47	0.49
1:A:990:C:H4'	1:A:1018:C:OP1	2.13	0.49
3:C:112:ALA:HB3	3:C:113:PRO:HD3	1.93	0.49
4:D:97:GLU:HG2	4:D:188:PRO:HG3	1.95	0.49
8:H:38:ILE:CD1	8:H:118:VAL:HG12	2.42	0.49
9:I:113:TYR:CE1	10:J:57:SER:O	2.66	0.49
10:J:28:SER:OG	10:J:79:THR:HA	2.13	0.49
12:L:106:VAL:HG21	12:L:109:ARG:HD2	1.94	0.49
13:M:39:ASN:HD22	13:M:40:PRO:CD	2.19	0.49
1:A:105:G:H2'	1:A:106:C:H6	1.75	0.49
1:A:189(H):G:C4'	1:A:189(I):G:O5'	2.59	0.49
1:A:501:C:H2'	1:A:502:G:H8	1.77	0.49
1:A:1102:A:H2'	1:A:1103:C:C6	2.48	0.49
1:A:1128:C:C2'	1:A:1129:C:H5''	2.42	0.49
1:A:1371:G:OP1	9:I:10:LYS:HG2	2.12	0.49
2:B:175:PHE:HD2	8:H:70:GLN:HB3	1.78	0.49
3:C:78:ARG:HE	3:C:81:GLU:HG2	1.77	0.49
3:C:187:LEU:CD1	3:C:188:ALA:H	2.25	0.49
6:F:48:LEU:HG	6:F:57:GLN:HA	1.95	0.49
15:O:81:ILE:O	15:O:85:GLY:N	2.43	0.49
1:A:275:G:H5''	17:Q:13:LYS:HB3	1.93	0.49
3:C:45:GLU:C	3:C:47:TYR:H	2.16	0.49
5:E:32:ASP:OD2	5:E:36:ARG:HB2	2.13	0.49
7:G:67:ASN:HD22	7:G:127:ALA:HA	1.76	0.49
9:I:57:ARG:HH11	9:I:57:ARG:HG3	1.78	0.49
13:M:64:LYS:O	13:M:65:LEU:HD23	2.13	0.49
13:M:80:LEU:O	13:M:85:CYS:HB3	2.13	0.49
15:O:63:ARG:NH1	15:O:63:ARG:CB	2.75	0.49
17:Q:79:GLY:O	17:Q:80:ARG:HB3	2.13	0.49
18:R:38:ARG:HD2	18:R:43:LEU:O	2.13	0.49
1:A:432:A:H3'	1:A:433:C:C6	2.47	0.49
1:A:551:U:H2'	1:A:552:U:C6	2.47	0.49
1:A:627:G:H2'	1:A:628:G:C8	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1249:C:O2'	9:I:72:GLN:NE2	2.46	0.49
1:A:1312:G:O2'	1:A:1313:U:H5'	2.13	0.49
3:C:39:ARG:O	3:C:43:GLU:HG3	2.13	0.49
3:C:173:PRO:CB	3:C:176:THR:HG22	2.40	0.49
4:D:7:VAL:C	4:D:9:ARG:N	2.66	0.49
7:G:67:ASN:ND2	7:G:127:ALA:HA	2.28	0.49
10:J:74:ASN:O	10:J:76:ASN:N	2.39	0.49
1:A:191:G:C4	20:T:98:SER:HB3	2.47	0.48
1:A:243:A:N6	1:A:281:G:O2'	2.31	0.48
1:A:488:C:O2'	1:A:489:C:H5'	2.13	0.48
1:A:676:A:H1'	11:K:105:PRO:HB3	1.95	0.48
1:A:997:U:H2'	1:A:998:G:O4'	2.13	0.48
1:A:1128:C:H4'	1:A:1129:C:OP1	2.13	0.48
1:A:1354:C:O2'	1:A:1355:G:H5'	2.13	0.48
2:B:175:PHE:CD2	8:H:70:GLN:HB3	2.48	0.48
3:C:33:LEU:CD1	14:N:24:VAL:HG21	2.37	0.48
4:D:105:TYR:CE2	4:D:111:VAL:O	2.66	0.48
4:D:126:THR:CG2	4:D:146:ALA:HB3	2.43	0.48
5:E:1:ASP:CG	5:E:2:PHE:H	2.17	0.48
5:E:72:ILE:HD12	5:E:138:LEU:CD1	2.42	0.48
6:F:60:PHE:CE2	18:R:63:LEU:HD21	2.48	0.48
6:F:72:VAL:CG1	6:F:90:VAL:HG11	2.43	0.48
13:M:120:LYS:HD2	13:M:120:LYS:H	1.77	0.48
1:A:181:G:C4'	1:A:182:U:OP1	2.60	0.48
1:A:518:C:H2'	1:A:530:G:C4	2.48	0.48
1:A:997:U:C3'	1:A:998:G:H5''	2.44	0.48
1:A:1122:U:H4'	1:A:1123:A:OP2	2.13	0.48
1:A:1357:A:N7	1:A:1358:U:C5	2.81	0.48
1:A:1410:G:H2'	1:A:1411:C:C6	2.47	0.48
2:B:1:VAL:HG13	2:B:218:GLN:HE22	1.77	0.48
6:F:76:ALA:O	6:F:80:ARG:HG3	2.13	0.48
7:G:51:GLU:O	7:G:53:THR:N	2.47	0.48
7:G:115:ALA:HA	7:G:118:ARG:CZ	2.42	0.48
18:R:28:PHE:HA	18:R:36:LEU:HD12	1.94	0.48
1:A:189(J):G:O2'	1:A:189(K):U:H5'	2.13	0.48
1:A:652:U:O4	1:A:752:G:O2'	2.27	0.48
3:C:138:GLN:HA	3:C:138:GLN:NE2	2.27	0.48
4:D:123:GLY:CA	4:D:131:ARG:HD2	2.38	0.48
5:E:56:TYR:HE1	5:E:60:ARG:HH21	1.59	0.48
5:E:140:THR:CG2	5:E:141:LYS:N	2.76	0.48
5:E:146:ARG:HB2	5:E:146:ARG:NH1	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:62:TRP:CH2	6:F:64:GLN:HB2	2.49	0.48
10:J:47:VAL:CG1	14:N:40:ARG:HD2	2.43	0.48
19:S:50:ALA:HA	19:S:58:VAL:O	2.13	0.48
19:S:52:TYR:HB2	19:S:57:HIS:CE1	2.49	0.48
1:A:663:A:H5'	1:A:836:G:OP1	2.13	0.48
1:A:762:C:H4'	17:Q:103:LYS:HZ2	1.76	0.48
3:C:34:GLU:CD	3:C:94:THR:HG21	2.33	0.48
3:C:133:ILE:HD11	3:C:152:VAL:CG2	2.42	0.48
4:D:31:ALA:C	4:D:33:GLU:N	2.66	0.48
11:K:34:SER:H	11:K:37:VAL:HB	1.78	0.48
15:O:59:VAL:O	15:O:63:ARG:HG3	2.12	0.48
16:P:59:TRP:HA	16:P:62:VAL:HG23	1.96	0.48
20:T:89:GLY:O	20:T:90:ALA:CB	2.59	0.48
1:A:1152:A:OP1	10:J:66:HIS:ND1	2.47	0.48
1:A:1207:G:H2'	1:A:1208:C:H6	1.78	0.48
1:A:1316:G:H2'	1:A:1317:C:H5''	1.95	0.48
2:B:95:MET:O	2:B:99:PHE:HA	2.12	0.48
3:C:38:ILE:CG2	3:C:42:LEU:HD12	2.43	0.48
4:D:155:GLU:C	4:D:155:GLU:OE1	2.52	0.48
5:E:31:GLY:HA3	5:E:108:LEU:HB3	1.96	0.48
7:G:145:GLU:OE2	7:G:148:ARG:NH2	2.46	0.48
13:M:14:VAL:HG23	13:M:42:THR:O	2.12	0.48
1:A:501:C:H2'	1:A:502:G:C8	2.49	0.48
1:A:1131:G:H2'	1:A:1132:C:C6	2.47	0.48
2:B:11:PHE:CD1	2:B:11:PHE:C	2.87	0.48
2:B:194:ILE:H	2:B:194:ILE:CD1	2.17	0.48
4:D:176:ASP:O	4:D:178:GLU:N	2.46	0.48
7:G:74:VAL:CG1	7:G:144:ALA:HA	2.42	0.48
9:I:117:LYS:O	9:I:118:ALA:CB	2.62	0.48
1:A:531:U:O2'	1:A:532:A:H4'	2.13	0.48
1:A:953:G:O2'	1:A:954:G:H5'	2.14	0.48
2:B:76:ARG:O	2:B:80:GLU:HG3	2.13	0.48
5:E:3:GLU:O	5:E:30:VAL:HA	2.14	0.48
17:Q:65:SER:O	17:Q:69:ARG:NH1	2.47	0.48
1:A:1252:A:H61	1:A:1285:A:H61	1.62	0.48
2:B:213:VAL:HA	2:B:216:ILE:HD12	1.94	0.48
5:E:147:LEU:HD22	8:H:79:VAL:HA	1.95	0.48
7:G:21:LEU:HD12	7:G:100:LEU:HD11	1.95	0.48
10:J:32:VAL:HG22	10:J:72:ILE:HG12	1.96	0.48
13:M:4:ALA:O	13:M:5:GLY:C	2.52	0.48
20:T:46:LEU:O	20:T:50:ARG:HD2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:88:ALA:O	20:T:89:GLY:C	2.52	0.48
1:A:7:G:O2'	5:E:116:THR:O	2.31	0.48
1:A:304:U:H2'	1:A:305:G:C8	2.49	0.48
2:B:108:ARG:HG2	2:B:108:ARG:HH11	1.79	0.48
3:C:187:LEU:O	3:C:188:ALA:HB2	2.12	0.48
11:K:2:ARG:O	11:K:2:ARG:HG2	2.12	0.48
11:K:99:VAL:HG22	18:R:71:VAL:HA	1.95	0.48
18:R:31:GLU:CD	18:R:31:GLU:N	2.63	0.48
1:A:647:C:C2'	1:A:648:A:C5'	2.80	0.48
1:A:1014:A:C2	1:A:1219:U:H1'	2.49	0.48
6:F:8:ILE:HD13	6:F:26:ILE:HD12	1.95	0.48
8:H:68:ARG:HG3	8:H:74:PRO:HB2	1.96	0.48
9:I:31:ASP:O	9:I:34:GLU:N	2.47	0.48
9:I:54:ALA:C	9:I:56:GLY:H	2.16	0.48
9:I:70:SER:HA	9:I:73:ILE:CG1	2.44	0.48
10:J:24:ALA:HB3	10:J:83:LEU:CD2	2.44	0.48
12:L:45:ASN:OD1	12:L:88:ASP:OD2	2.32	0.48
13:M:2:ARG:HG2	13:M:8:ILE:CD1	2.37	0.48
13:M:10:ARG:HA	13:M:44:VAL:HB	1.96	0.48
15:O:54:GLY:HA2	15:O:57:MET:HE3	1.96	0.48
1:A:1474:G:H2'	1:A:1475:G:O4'	2.14	0.47
2:B:44:GLU:HB3	2:B:194:ILE:O	2.14	0.47
4:D:30:CYS:C	4:D:32:MET:H	2.17	0.47
10:J:38:LEU:HB2	10:J:67:ASN:CB	2.41	0.47
10:J:69:LEU:O	10:J:70:VAL:HB	2.14	0.47
14:N:35:PHE:O	14:N:35:PHE:CD1	2.67	0.47
1:A:385:C:O2'	1:A:386:C:H5'	2.14	0.47
1:A:559:A:P	5:E:122:ARG:HH22	2.36	0.47
1:A:640:A:O2'	1:A:641:U:H5'	2.14	0.47
1:A:1147:C:O2'	1:A:1148:U:H5'	2.14	0.47
3:C:34:GLU:CG	3:C:94:THR:HG21	2.44	0.47
3:C:174:LEU:HD23	3:C:174:LEU:N	2.29	0.47
4:D:99:ARG:HH12	4:D:136:SER:CB	2.27	0.47
9:I:111:LYS:HG2	9:I:117:LYS:HA	1.95	0.47
1:A:370:C:H2'	1:A:371:G:C8	2.49	0.47
1:A:382:A:H2'	1:A:383:A:C8	2.50	0.47
1:A:933:G:OP2	7:G:2:ARG:HB3	2.15	0.47
1:A:1057:G:H2'	1:A:1058:G:O4'	2.14	0.47
1:A:1423:G:O2'	1:A:1424:C:H5'	2.14	0.47
3:C:33:LEU:C	3:C:33:LEU:CD2	2.76	0.47
3:C:56:ILE:HD12	3:C:65:VAL:HG22	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:4:ASP:OD1	8:H:85:ARG:NH1	2.47	0.47
9:I:98:LEU:HD22	9:I:98:LEU:N	2.30	0.47
10:J:33:SER:HB2	10:J:70:VAL:O	2.15	0.47
18:R:39:ARG:HH11	18:R:39:ARG:HG3	1.79	0.47
1:A:460:G:C3'	1:A:461:A:H5''	2.43	0.47
4:D:24:ARG:HE	4:D:29:LYS:HB3	1.80	0.47
7:G:106:ALA:O	7:G:109:GLN:HB2	2.15	0.47
9:I:83:ALA:O	9:I:86:GLN:HB3	2.14	0.47
11:K:80:GLY:O	11:K:81:ARG:C	2.52	0.47
11:K:114:LYS:HG3	11:K:115:PHE:CD2	2.49	0.47
1:A:1206:G:C6	1:A:1207:G:C5	3.03	0.47
7:G:68:VAL:HG21	7:G:103:LEU:HD21	1.96	0.47
8:H:84:ARG:HG2	8:H:85:ARG:N	2.29	0.47
11:K:81:ARG:HD3	18:R:73:LYS:HD3	1.96	0.47
19:S:33:THR:CG2	19:S:34:TRP:N	2.77	0.47
1:A:543:C:O2'	1:A:544:G:H5'	2.14	0.47
1:A:573:A:C4'	1:A:574:A:O5'	2.59	0.47
1:A:977:A:C2'	1:A:978:A:H5''	2.43	0.47
1:A:1026:G:H2'	1:A:1027:C:H5''	1.97	0.47
1:A:1198:G:H2'	1:A:1199:U:C6	2.49	0.47
1:A:1308:U:O2'	1:A:1309:G:H5'	2.15	0.47
1:A:1539:C:O2	1:A:1539:C:O4'	2.31	0.47
12:L:23:LEU:C	12:L:25:GLY:N	2.68	0.47
14:N:43:LEU:C	14:N:43:LEU:CD1	2.83	0.47
15:O:63:ARG:CB	15:O:63:ARG:HH11	2.28	0.47
20:T:50:ARG:HH21	20:T:93:ILE:CG2	2.28	0.47
21:V:14:TRP:HZ3	21:V:15:ARG:HE	1.62	0.47
1:A:73:G:O2'	1:A:76:C:H5'	2.14	0.47
1:A:489:C:H2'	1:A:490:G:C8	2.48	0.47
1:A:1002:G:H2'	1:A:1003:G:H8	1.79	0.47
1:A:1067:A:H4'	1:A:1093:A:O3'	2.15	0.47
1:A:1188:A:C2'	1:A:1189:C:H5'	2.44	0.47
2:B:2:LYS:O	2:B:211:ARG:NH1	2.48	0.47
2:B:19:ASN:C	2:B:19:ASN:ND2	2.64	0.47
3:C:35:ASP:OD1	3:C:56:ILE:HG13	2.15	0.47
3:C:46:LEU:CD1	3:C:46:LEU:N	2.78	0.47
3:C:149:LYS:HG3	3:C:168:ALA:HB2	1.96	0.47
3:C:183:TYR:HA	3:C:199:ALA:O	2.14	0.47
3:C:187:LEU:HD13	3:C:194:VAL:HG13	1.96	0.47
9:I:8:ARG:HG3	9:I:13:VAL:HG13	1.95	0.47
9:I:78:LEU:HD13	9:I:82:ARG:HD2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:85:VAL:HG13	9:I:89:PRO:HA	1.97	0.47
9:I:124:TYR:CE2	9:I:127:ARG:NE	2.83	0.47
10:J:55:LYS:HD2	10:J:55:LYS:O	2.15	0.47
10:J:58:ARG:HG2	10:J:58:ARG:NH1	2.26	0.47
11:K:24:ASP:C	11:K:24:ASP:OD1	2.53	0.47
11:K:77:THR:CA	11:K:81:ARG:HH21	2.23	0.47
15:O:14:PHE:CZ	15:O:83:LYS:HE2	2.49	0.47
15:O:63:ARG:HH11	15:O:63:ARG:HB2	1.80	0.47
18:R:10:THR:O	18:R:11:LEU:HB2	2.15	0.47
1:A:216:G:H2'	1:A:217:C:C6	2.50	0.47
1:A:648:A:H5'	1:A:648:A:C8	2.41	0.47
1:A:720:C:P	1:A:721:G:H4'	2.55	0.47
2:B:128:GLU:HG2	2:B:131:ARG:HH21	1.77	0.47
7:G:17:TYR:CE2	7:G:58:LEU:HB2	2.50	0.47
7:G:75:ARG:CD	7:G:88:MET:HG3	2.45	0.47
19:S:45:VAL:HA	19:S:62:ILE:HD12	1.97	0.47
1:A:232:G:H1'	1:A:262:A:N1	2.29	0.47
1:A:287:U:C2'	1:A:288:A:H5'	2.45	0.47
2:B:17:ARG:O	2:B:18:TRP:O	2.33	0.47
2:B:54:ASP:HA	2:B:58:ARG:NH2	2.29	0.47
2:B:78:GLU:HB3	2:B:213:VAL:CG2	2.28	0.47
2:B:166:ILE:O	2:B:170:GLU:HG3	2.15	0.47
3:C:176:THR:HG23	3:C:176:THR:O	2.14	0.47
4:D:157:ILE:O	4:D:161:LEU:HB2	2.14	0.47
17:Q:44:HIS:CD2	17:Q:46:PRO:HG3	2.50	0.47
18:R:11:LEU:HD21	18:R:24:VAL:CG2	2.45	0.47
1:A:422:C:O2	1:A:422:C:C2'	2.63	0.47
1:A:882:C:O2'	1:A:883:C:H5'	2.15	0.47
2:B:68:LYS:CE	2:B:200:ASP:HB2	2.45	0.47
3:C:21:TRP:CB	3:C:58:ARG:HB2	2.45	0.47
5:E:14:ARG:HG2	5:E:15:MET:N	2.29	0.47
6:F:23:LYS:NZ	6:F:42:GLU:OE1	2.45	0.47
6:F:32:ASN:N	6:F:32:ASN:ND2	2.63	0.47
10:J:27:ARG:NH1	10:J:82:GLN:OE1	2.44	0.47
14:N:41:ILE:O	14:N:45:GLU:HG3	2.15	0.47
1:A:443:C:H2'	1:A:444:C:H6	1.78	0.46
1:A:1008:C:H2'	1:A:1009:G:H8	1.79	0.46
3:C:206:VAL:CG1	3:C:207:ILE:N	2.77	0.46
4:D:3:TYR:O	4:D:4:ILE:HB	2.15	0.46
12:L:113:ARG:NH2	12:L:120:LYS:HB2	2.30	0.46
14:N:22:ARG:NH1	14:N:29:ALA:HB2	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:3:LEU:CD1	20:T:5:ALA:HB3	2.45	0.46
1:A:34:C:H1'	12:L:28:PHE:CZ	2.50	0.46
1:A:167:G:O2'	1:A:168:G:H5''	2.13	0.46
1:A:997:U:C2'	1:A:998:G:H5''	2.44	0.46
1:A:1474:G:H3'	1:A:1475:G:C5'	2.27	0.46
3:C:46:LEU:H	3:C:46:LEU:HD12	1.80	0.46
4:D:7:VAL:CG1	4:D:114:ARG:NH1	2.78	0.46
5:E:9:ILE:O	5:E:9:ILE:HG13	2.14	0.46
6:F:22:GLU:OE1	6:F:22:GLU:HA	2.15	0.46
9:I:6:THR:O	9:I:14:ALA:O	2.33	0.46
10:J:14:LEU:HD23	10:J:92:VAL:HG22	1.98	0.46
12:L:20:VAL:N	12:L:21:PRO:HD3	2.30	0.46
12:L:29:ARG:HD3	12:L:29:ARG:HA	1.78	0.46
1:A:386:C:O2'	1:A:387:U:H5'	2.14	0.46
1:A:952:U:O2'	1:A:953:G:H5'	2.15	0.46
1:A:1092:A:H5''	7:G:3:ARG:CZ	2.45	0.46
1:A:1410:G:H2'	1:A:1411:C:H6	1.80	0.46
1:A:1425:U:O2	1:A:1425:U:H2'	2.15	0.46
9:I:32:PHE:CE2	9:I:46:LEU:HD11	2.51	0.46
13:M:24:ILE:HD11	13:M:65:LEU:CD1	2.46	0.46
13:M:114:LYS:HD3	13:M:114:LYS:N	2.30	0.46
17:Q:8:VAL:HG21	17:Q:83:LEU:CD1	2.45	0.46
19:S:20:LEU:HA	19:S:23:ASN:ND2	2.29	0.46
1:A:167:G:C2'	1:A:168:G:C5'	2.86	0.46
1:A:418:C:H2'	1:A:419:C:H6	1.80	0.46
1:A:1074:G:O3'	2:B:97:THR:CG2	2.63	0.46
1:A:1127:G:C8	1:A:1127:G:H5''	2.51	0.46
3:C:106:GLN:NE2	3:C:106:GLN:H	2.14	0.46
8:H:119:LEU:CD1	8:H:124:ALA:HA	2.46	0.46
12:L:122:LYS:CE	12:L:122:LYS:H	2.29	0.46
15:O:28:VAL:HG11	15:O:66:LEU:HD21	1.98	0.46
18:R:38:ARG:HH11	18:R:44:SER:CA	2.28	0.46
1:A:620:C:H2'	1:A:621:A:O4'	2.15	0.46
1:A:635:G:O2'	1:A:636:U:H5'	2.16	0.46
1:A:649:G:O2'	1:A:650:G:H5'	2.15	0.46
1:A:1096:C:O2'	1:A:1097:C:H5'	2.14	0.46
1:A:1320:C:O2	19:S:72:GLY:HA3	2.15	0.46
1:A:1392:G:N2	1:A:1502:A:C8	2.81	0.46
2:B:22:PHE:CD2	2:B:184:THR:HA	2.51	0.46
2:B:55:LEU:HD21	2:B:154:ASP:HB3	1.97	0.46
2:B:232:LEU:C	2:B:234:GLN:H	2.18	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:76:ILE:O	3:C:82:ARG:HB2	2.15	0.46
5:E:38:GLY:HA2	5:E:61:ASN:O	2.15	0.46
9:I:4:TYR:OH	9:I:15:ARG:HG2	2.16	0.46
11:K:24:ASP:HB2	11:K:25:PRO:HD2	1.97	0.46
1:A:178:C:H5'	1:A:178:C:H6	1.80	0.46
1:A:1492:A:OP1	12:L:42:LYS:HB2	2.16	0.46
2:B:172:ARG:HH22	8:H:74:PRO:HB3	1.80	0.46
4:D:7:VAL:HB	4:D:20:LEU:CD1	2.45	0.46
4:D:78:PHE:HE1	4:D:203:ILE:HG12	1.79	0.46
4:D:161:LEU:HD13	4:D:180:MET:HE2	1.98	0.46
8:H:103:VAL:HG21	8:H:109:ILE:C	2.35	0.46
16:P:67:THR:CG2	16:P:68:ASP:N	2.78	0.46
20:T:80:LYS:HE3	20:T:80:LYS:HB2	1.75	0.46
1:A:393:A:C2'	1:A:394:G:H5'	2.46	0.46
1:A:975:A:C4'	1:A:976:G:H5''	2.36	0.46
1:A:1421:G:H1	1:A:1479:C:N4	2.10	0.46
2:B:14:GLU:O	2:B:33:ILE:HG23	2.16	0.46
2:B:58:ARG:HH11	2:B:58:ARG:CG	2.28	0.46
4:D:4:ILE:HG22	4:D:4:ILE:O	2.14	0.46
17:Q:94:TYR:N	17:Q:94:TYR:HD1	2.12	0.46
20:T:3:LEU:HD12	20:T:5:ALA:HB3	1.98	0.46
1:A:370:C:H2'	1:A:371:G:H8	1.81	0.46
1:A:386:C:H2'	1:A:387:U:H5'	1.97	0.46
1:A:392:G:H2'	1:A:393:A:C8	2.51	0.46
1:A:434:U:H2'	1:A:435:C:C6	2.51	0.46
1:A:697:U:H2'	1:A:698:G:H5'	1.96	0.46
1:A:1051:C:O2'	1:A:1052:U:H5'	2.15	0.46
1:A:1168:A:O2'	1:A:1169:A:P	2.74	0.46
1:A:1188:A:H2'	1:A:1189:C:H5'	1.98	0.46
2:B:72:GLN:HG3	2:B:88:ASN:O	2.16	0.46
2:B:73:ASP:O	2:B:76:ARG:HG3	2.16	0.46
2:B:108:ARG:CZ	2:B:112:LEU:HD21	2.45	0.46
2:B:108:ARG:HE	2:B:135:GLU:CD	2.19	0.46
2:B:126:LYS:HA	2:B:129:GLN:HB2	1.97	0.46
4:D:2:ARG:HG3	4:D:117:ARG:CZ	2.46	0.46
4:D:59:GLU:OE1	4:D:62:LYS:HE2	2.16	0.46
5:E:24:PHE:CD2	5:E:47:VAL:HG22	2.50	0.46
13:M:18:LEU:HD11	13:M:33:LEU:HD21	1.98	0.46
18:R:38:ARG:NH1	18:R:45:GLY:N	2.63	0.46
1:A:279:A:H4'	1:A:281:G:C8	2.51	0.46
1:A:769:G:H4'	1:A:1513:A:H4'	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:961:U:H2'	1:A:962:C:H5'	1.96	0.46
1:A:1109:C:P	3:C:175:HIS:HD2	2.39	0.46
1:A:1313:U:H5	19:S:4:SER:CB	2.24	0.46
2:B:11:PHE:HA	2:B:36:ILE:HB	1.98	0.46
2:B:17:ARG:NH1	2:B:18:TRP:HA	2.31	0.46
3:C:7:ILE:O	3:C:10:ARG:N	2.46	0.46
4:D:9:ARG:HG2	4:D:10:LEU:N	2.31	0.46
5:E:72:ILE:HG23	5:E:138:LEU:CD1	2.46	0.46
10:J:82:GLN:O	10:J:86:LEU:HD22	2.16	0.46
11:K:42:GLY:O	11:K:45:LYS:HG3	2.16	0.46
13:M:2:ARG:HG3	13:M:8:ILE:HG23	1.98	0.46
16:P:2:VAL:CG2	16:P:3:LYS:N	2.78	0.46
16:P:55:ARG:O	16:P:58:TYR:HB3	2.15	0.46
1:A:337:C:H2'	1:A:338:A:C8	2.51	0.46
1:A:587:G:OP1	8:H:89:PRO:HB3	2.16	0.46
1:A:835:U:OP1	18:R:49:ARG:NH2	2.31	0.46
1:A:877:C:O2'	1:A:878:G:H5'	2.15	0.46
1:A:959:A:C2	1:A:1222:G:O4'	2.69	0.46
1:A:1371:G:O2'	1:A:1372:U:H5'	2.15	0.46
1:A:1487:G:O2'	1:A:1488:G:H5'	2.16	0.46
2:B:49:PHE:O	2:B:52:ILE:HB	2.16	0.46
2:B:81:ARG:O	2:B:217:ILE:HD11	2.16	0.46
2:B:91:TRP:CZ3	2:B:170:GLU:OE2	2.69	0.46
2:B:181:LEU:HA	2:B:195:ILE:HB	1.98	0.46
3:C:128:ALA:HB3	3:C:131:ARG:HD2	1.97	0.46
5:E:11:ARG:CD	5:E:22:PHE:CD2	2.99	0.46
10:J:28:SER:HB3	10:J:82:GLN:NE2	2.30	0.46
1:A:783:C:O2'	1:A:784:C:H5'	2.16	0.45
1:A:1010:G:O2'	1:A:1011:G:H5'	2.15	0.45
5:E:85:ILE:HD13	5:E:86:VAL:H	1.81	0.45
6:F:32:ASN:N	6:F:32:ASN:HD22	2.14	0.45
18:R:24:VAL:CG1	18:R:25:LEU:N	2.80	0.45
18:R:29:LEU:HD22	18:R:33:GLY:O	2.17	0.45
20:T:95:GLY:C	20:T:97:LEU:H	2.19	0.45
21:V:10:ARG:NH1	21:V:10:ARG:CG	2.78	0.45
1:A:997:U:H2'	1:A:998:G:C5'	2.46	0.45
1:A:1131:G:O2'	1:A:1132:C:H5'	2.17	0.45
1:A:1522:U:O2'	1:A:1523:G:H5'	2.17	0.45
2:B:9:VAL:HG11	2:B:203:ARG:C	2.37	0.45
2:B:36:ILE:HD12	2:B:197:GLY:HA2	1.98	0.45
3:C:122:GLN:NE2	3:C:139:ARG:HH22	2.14	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:166:TRP:O	3:C:167:ALA:CB	2.65	0.45
5:E:27:LEU:HD23	5:E:27:LEU:HA	1.77	0.45
7:G:74:VAL:HG21	7:G:143:MET:CE	2.46	0.45
7:G:125:ASP:OD1	7:G:130:LYS:HE3	2.15	0.45
8:H:86:ILE:HB	8:H:133:LEU:O	2.16	0.45
10:J:20:LYS:CD	10:J:88:LEU:HD12	2.45	0.45
13:M:10:ARG:CG	13:M:11:ASN:N	2.77	0.45
13:M:24:ILE:HD11	13:M:65:LEU:HD13	1.97	0.45
15:O:69:LEU:HD12	15:O:80:LEU:HD12	1.97	0.45
17:Q:73:LEU:HD23	17:Q:73:LEU:C	2.36	0.45
18:R:30:SER:C	18:R:32:THR:N	2.67	0.45
1:A:41:G:H2'	1:A:42:G:H8	1.80	0.45
1:A:52:G:O2'	1:A:53:A:H5'	2.16	0.45
1:A:456:C:H2'	1:A:457:C:C6	2.50	0.45
1:A:828:A:H2'	1:A:829:G:O4'	2.17	0.45
2:B:49:PHE:HA	2:B:52:ILE:CG1	2.47	0.45
3:C:46:LEU:CD2	3:C:67:VAL:HG11	2.44	0.45
4:D:178:GLU:C	4:D:180:MET:H	2.19	0.45
5:E:72:ILE:HD12	5:E:138:LEU:HD11	1.99	0.45
5:E:112:THR:HG23	5:E:113:ASP:OD2	2.17	0.45
10:J:10:ASP:HB3	10:J:13:THR:CB	2.44	0.45
10:J:10:ASP:HB3	10:J:13:THR:CG2	2.47	0.45
11:K:23:THR:OG1	11:K:27:GLY:CA	2.64	0.45
14:N:30:ARG:HH11	14:N:30:ARG:CG	2.29	0.45
19:S:12:ASP:O	19:S:15:LEU:HD12	2.16	0.45
1:A:189:G:H8	1:A:189:G:C5'	2.29	0.45
1:A:432:A:H5''	1:A:433:C:H5	1.81	0.45
1:A:789:U:H2'	1:A:791:G:OP2	2.15	0.45
1:A:1343:G:OP1	9:I:124:TYR:HE1	1.99	0.45
2:B:117:ALA:N	2:B:121:ILE:HD11	2.30	0.45
2:B:159:VAL:CG2	2:B:160:ASP:H	2.14	0.45
8:H:63:LEU:H	8:H:63:LEU:CD2	2.24	0.45
9:I:43:VAL:O	9:I:50:ARG:NH2	2.48	0.45
10:J:48:ILE:HD12	10:J:48:ILE:H	1.81	0.45
11:K:38:ILE:O	11:K:38:ILE:CG2	2.65	0.45
1:A:19:C:H2'	1:A:20:U:H6	1.81	0.45
1:A:1124:G:O2'	1:A:1125:U:P	2.75	0.45
1:A:1176:A:H2'	1:A:1177:G:C8	2.52	0.45
1:A:1197:G:H5'	1:A:1197:G:H8	1.82	0.45
1:A:1388:C:H2'	1:A:1389:C:C6	2.52	0.45
2:B:41:THR:HA	2:B:196:PRO:HG2	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:194:VAL:C	3:C:195:LEU:HD22	2.37	0.45
4:D:63:LEU:HD11	4:D:96:LEU:HD11	1.99	0.45
5:E:76:ILE:HD11	5:E:87:LEU:HB2	1.97	0.45
9:I:9:ARG:HD2	9:I:10:LYS:H	1.81	0.45
9:I:16:VAL:HA	9:I:62:ILE:CD1	2.46	0.45
10:J:1:LYS:N	10:J:75:PRO:HD3	2.32	0.45
12:L:79:VAL:HG21	12:L:96:ILE:HG21	1.97	0.45
18:R:22:VAL:CG2	18:R:63:LEU:HB3	2.46	0.45
1:A:67:C:O2'	1:A:171:A:H1'	2.16	0.45
1:A:181:G:C5'	1:A:182:U:OP1	2.64	0.45
1:A:738:C:P	6:F:92:LYS:HD3	2.56	0.45
1:A:924:C:H2'	1:A:925:G:H8	1.81	0.45
1:A:962:C:H2'	1:A:963:G:O4'	2.17	0.45
1:A:1203:C:O5'	1:A:1203:C:H6	1.99	0.45
1:A:1272:G:O2'	1:A:1273:G:H5'	2.16	0.45
1:A:1320:C:H41	19:S:37:ARG:HD3	1.81	0.45
2:B:105:ARG:NE	2:B:105:ARG:HA	2.32	0.45
9:I:117:LYS:HG3	9:I:120:ARG:HB3	1.99	0.45
12:L:109:ARG:HH12	12:L:112:SER:H	1.64	0.45
13:M:79:ARG:HH11	13:M:79:ARG:CB	2.30	0.45
16:P:26:ARG:HH21	16:P:31:LYS:HD2	1.81	0.45
17:Q:4:VAL:HA	17:Q:58:ILE:O	2.17	0.45
19:S:80:TYR:CE2	19:S:81:ARG:HB3	2.52	0.45
1:A:220:G:O2'	1:A:221:C:H5'	2.17	0.45
1:A:376:G:O3'	16:P:5:ARG:HD2	2.16	0.45
1:A:640:A:C2'	1:A:641:U:H5'	2.47	0.45
1:A:736:C:H2'	1:A:737:A:C8	2.51	0.45
1:A:968:A:H4'	1:A:969:A:OP2	2.17	0.45
1:A:976:G:H5'	1:A:1358:U:O2'	2.17	0.45
1:A:1127:G:H1'	1:A:1148:U:N3	2.32	0.45
2:B:85:PRO:HG2	2:B:149:LEU:CD2	2.47	0.45
2:B:217:ILE:HG21	2:B:224:VAL:CG2	2.44	0.45
3:C:43:GLU:HA	3:C:51:LEU:CD1	2.42	0.45
5:E:146:ARG:CB	5:E:146:ARG:HH11	2.30	0.45
6:F:45:LEU:HD23	6:F:59:TYR:HD1	1.81	0.45
1:A:116:A:H2'	1:A:117:G:O4'	2.17	0.45
1:A:300:A:H8	1:A:300:A:O5'	2.00	0.45
1:A:1346:A:C4	7:G:9:ARG:NH2	2.84	0.45
2:B:27:TYR:HB3	2:B:35:ILE:O	2.17	0.45
2:B:194:ILE:HG22	2:B:195:ILE:N	2.32	0.45
3:C:19:SER:O	14:N:53:PRO:HB3	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:22:TYR:CG	3:C:23:ALA:N	2.84	0.45
9:I:126:LYS:HG2	13:M:125:LYS:HD3	1.98	0.45
10:J:20:LYS:CE	10:J:88:LEU:HD12	2.46	0.45
12:L:24:LYS:HD3	12:L:29:ARG:HH22	1.81	0.45
12:L:85:ARG:NH2	12:L:93:ARG:HE	2.15	0.45
1:A:271:C:O2'	1:A:272:C:H5'	2.17	0.45
1:A:650:G:C2'	1:A:651:C:H5'	2.46	0.45
1:A:689:C:H2'	1:A:690:G:O4'	2.16	0.45
1:A:1118:C:H1'	1:A:1179:A:C4	2.51	0.45
1:A:1298:C:OP2	7:G:113:ARG:NH2	2.49	0.45
6:F:94:GLN:NE2	18:R:17:ARG:NH1	2.62	0.45
9:I:6:THR:H	9:I:79:GLY:HA2	1.81	0.45
11:K:44:ARG:HH11	11:K:44:ARG:CB	2.14	0.45
12:L:49:ARG:N	12:L:49:ARG:HD2	2.32	0.45
14:N:7:GLU:O	14:N:10:LYS:HB3	2.17	0.45
1:A:204:U:O2	1:A:204:U:H2'	2.16	0.45
1:A:818:G:H3'	1:A:819:A:H5''	1.99	0.45
1:A:1320:C:OP1	19:S:70:LYS:HE2	2.17	0.45
1:A:1321:C:H42	19:S:37:ARG:NH1	2.14	0.45
8:H:97:VAL:HG21	8:H:128:GLY:HA2	1.97	0.45
9:I:15:ARG:NH1	9:I:63:THR:HG21	2.32	0.45
1:A:389:A:C6	1:A:390:C:H1'	2.52	0.44
1:A:631:G:H2'	1:A:632:A:H5'	1.99	0.44
1:A:742:G:O2'	1:A:743:U:H5'	2.17	0.44
1:A:959:A:H5''	1:A:960:U:OP2	2.17	0.44
1:A:975:A:H5'	1:A:975:A:H8	1.83	0.44
1:A:1234:C:H4'	1:A:1364:U:C2'	2.42	0.44
1:A:1287:A:O2'	1:A:1288:A:P	2.74	0.44
4:D:56:ARG:HG3	4:D:56:ARG:NH1	2.31	0.44
4:D:58:ARG:NH2	4:D:61:GLN:HG3	2.30	0.44
5:E:21:ARG:HG3	5:E:21:ARG:HH11	1.82	0.44
7:G:91:SER:O	7:G:95:GLN:HG3	2.17	0.44
19:S:17:GLU:HA	19:S:20:LEU:CG	2.47	0.44
1:A:256:U:O2'	1:A:257:G:H5'	2.17	0.44
1:A:639:G:O2'	1:A:640:A:H5'	2.17	0.44
1:A:921:U:O2	5:E:15:MET:HB2	2.17	0.44
1:A:922:G:C6	1:A:923:A:C6	3.05	0.44
1:A:1091:U:O2	1:A:1093:A:C8	2.70	0.44
10:J:2:ILE:HA	10:J:98:THR:CB	2.47	0.44
14:N:32:VAL:HA	14:N:39:CYS:HA	1.99	0.44
1:A:107:G:C2'	1:A:108:G:H5'	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:163:C:O2'	1:A:164:U:H5'	2.17	0.44
1:A:414:A:H2'	1:A:415:A:C8	2.52	0.44
2:B:10:HIS:HB3	2:B:11:PHE:H	1.47	0.44
2:B:171:ALA:O	2:B:174:LEU:N	2.48	0.44
3:C:14:THR:HG21	3:C:178:ARG:HA	1.99	0.44
6:F:69:GLU:O	6:F:72:VAL:HG23	2.17	0.44
12:L:122:LYS:N	12:L:122:LYS:CE	2.80	0.44
20:T:60:ALA:O	20:T:66:HIS:ND1	2.51	0.44
1:A:107:G:H2'	1:A:108:G:H5'	2.00	0.44
1:A:573:A:O5'	1:A:573:A:O2'	2.20	0.44
1:A:1049:U:C5'	14:N:2:ARG:HD2	2.47	0.44
1:A:1166:G:H5'	1:A:1168:A:OP2	2.17	0.44
1:A:1321:C:N4	19:S:37:ARG:HH12	2.15	0.44
1:A:1381:U:HO2'	1:A:1382:C:H5'	1.82	0.44
1:A:1480:G:H2'	1:A:1480:G:N3	2.33	0.44
4:D:27:SER:O	4:D:29:LYS:N	2.51	0.44
4:D:198:ASN:HD22	4:D:198:ASN:C	2.21	0.44
6:F:16:GLN:HE21	6:F:16:GLN:CA	2.30	0.44
6:F:48:LEU:HD13	6:F:52:ILE:CG1	2.46	0.44
7:G:43:TYR:O	7:G:46:CYS:HB2	2.18	0.44
8:H:24:THR:CG2	8:H:63:LEU:HD21	2.44	0.44
10:J:2:ILE:HA	10:J:98:THR:OG1	2.18	0.44
16:P:6:LEU:HB3	16:P:17:TYR:CD2	2.52	0.44
1:A:319:G:O2'	1:A:320:C:H5'	2.18	0.44
1:A:460:G:C2'	1:A:461:A:H5''	2.46	0.44
1:A:1086:U:H3	1:A:1099:G:N2	2.02	0.44
1:A:1230:C:H1'	13:M:125:LYS:HA	1.98	0.44
1:A:1379:G:OP2	7:G:5:ARG:NE	2.51	0.44
5:E:147:LEU:CD2	8:H:79:VAL:HG22	2.48	0.44
6:F:69:GLU:HA	6:F:72:VAL:CG2	2.48	0.44
19:S:19:VAL:HG13	19:S:20:LEU:N	2.33	0.44
1:A:22:G:H4'	1:A:885:G:C8	2.52	0.44
1:A:61:G:H2'	1:A:62:U:O4'	2.18	0.44
1:A:190:U:O2'	1:A:191:G:H5'	2.17	0.44
1:A:433:C:H2'	1:A:434:U:C6	2.53	0.44
1:A:631:G:O2'	1:A:632:A:H5'	2.18	0.44
1:A:1352:C:H2'	1:A:1353:G:H8	1.74	0.44
1:A:1427:U:H2'	1:A:1428:A:H8	1.82	0.44
4:D:22:GLY:O	4:D:26:TYR:HD2	2.00	0.44
4:D:150:LYS:N	4:D:150:LYS:CD	2.80	0.44
5:E:76:ILE:HD13	5:E:76:ILE:N	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:32:VAL:HG22	10:J:72:ILE:CG2	2.43	0.44
10:J:62:GLU:HG2	14:N:58:ALA:CB	2.37	0.44
12:L:46:SER:O	12:L:47:ALA:HB2	2.17	0.44
19:S:3:ARG:O	19:S:4:SER:HB3	2.17	0.44
19:S:58:VAL:HA	19:S:59:PRO:HD3	1.81	0.44
1:A:91:C:H2'	1:A:92:C:C6	2.50	0.44
1:A:524:G:H2'	1:A:525:C:C6	2.53	0.44
1:A:542:G:H2'	1:A:543:C:C6	2.47	0.44
1:A:888:G:C3'	1:A:889:A:H5''	2.47	0.44
1:A:1126:U:H2'	1:A:1127:G:H8	1.83	0.44
3:C:123:ILE:CD1	3:C:129:VAL:HG22	2.48	0.44
3:C:187:LEU:HD22	3:C:187:LEU:HA	1.69	0.44
7:G:71:ARG:NH1	7:G:141:GLU:OE2	2.50	0.44
7:G:115:ALA:HA	7:G:118:ARG:NH2	2.33	0.44
9:I:8:ARG:CG	9:I:13:VAL:HG22	2.47	0.44
9:I:47:GLU:N	9:I:48:PRO:CD	2.81	0.44
12:L:25:GLY:O	12:L:26:ALA:C	2.55	0.44
12:L:49:ARG:HD2	12:L:49:ARG:H	1.83	0.44
13:M:57:GLU:HA	13:M:57:GLU:OE1	2.18	0.44
19:S:13:ASP:HA	19:S:16:LEU:HB3	1.99	0.44
19:S:36:ARG:NH2	19:S:75:ALA:HB3	2.32	0.44
1:A:341:C:O2'	1:A:342:C:H5'	2.18	0.44
1:A:476:G:H2'	1:A:477:A:C8	2.53	0.44
1:A:1109:C:OP1	3:C:175:HIS:HD2	2.01	0.44
2:B:6:GLU:OE2	2:B:9:VAL:HG23	2.18	0.44
2:B:55:LEU:HD21	2:B:154:ASP:CB	2.48	0.44
6:F:4:TYR:CZ	6:F:72:VAL:HG21	2.52	0.44
7:G:36:ASN:HD21	9:I:40:VAL:HG23	1.81	0.44
7:G:119:ILE:O	7:G:123:LEU:HB2	2.17	0.44
9:I:56:GLY:O	9:I:57:ARG:HB2	2.18	0.44
10:J:25:ALA:N	10:J:83:LEU:HD21	2.33	0.44
12:L:87:LYS:HA	12:L:87:LYS:CE	2.25	0.44
15:O:13:GLU:HG3	15:O:14:PHE:CE1	2.52	0.44
1:A:129(A):G:N2	1:A:189(F):U:H5''	2.32	0.44
1:A:1123:A:H4'	10:J:35:PRO:HD2	2.00	0.44
1:A:1163:C:H2'	1:A:1164:G:C8	2.50	0.44
1:A:1190:G:P	3:C:4:ILE:HD12	2.58	0.44
1:A:1228:C:H2'	1:A:1229:A:C8	2.52	0.44
1:A:1402:C:O2	1:A:1500:A:N1	2.51	0.44
2:B:123:GLU:HG2	2:B:124:ARG:N	2.32	0.44
2:B:133:LYS:HD3	2:B:133:LYS:C	2.38	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:1:MET:HG2	8:H:2:LEU:N	2.33	0.44
19:S:3:ARG:O	19:S:4:SER:CB	2.66	0.44
1:A:204:U:O2	1:A:204:U:C2'	2.65	0.43
1:A:418:C:H2'	1:A:419:C:C6	2.52	0.43
1:A:613:C:C2'	1:A:614:A:H5'	2.48	0.43
1:A:976:G:OP1	14:N:31:SER:HA	2.17	0.43
2:B:11:PHE:O	2:B:12:GLY:C	2.57	0.43
2:B:48:THR:HG23	2:B:193:TYR:HB3	2.00	0.43
2:B:138:ARG:HA	2:B:141:LYS:CD	2.48	0.43
3:C:94:THR:O	3:C:94:THR:OG1	2.36	0.43
4:D:24:ARG:C	4:D:26:TYR:H	2.21	0.43
4:D:159:GLN:O	4:D:162:GLU:HB3	2.18	0.43
5:E:91:ALA:HB1	5:E:92:PRO:HD2	2.00	0.43
7:G:51:GLU:C	7:G:53:THR:H	2.21	0.43
9:I:17:PHE:HD2	9:I:61:TYR:HD2	1.66	0.43
10:J:32:VAL:HG13	10:J:72:ILE:HG12	1.98	0.43
10:J:69:LEU:HD23	10:J:69:LEU:HA	1.86	0.43
11:K:24:ASP:O	11:K:26:ASP:N	2.50	0.43
20:T:78:MET:HB3	20:T:97:LEU:CD2	2.48	0.43
1:A:355:C:C1'	1:A:388:G:H2'	2.47	0.43
1:A:413:G:H21	1:A:428:G:H1'	1.83	0.43
1:A:1327:C:O2'	1:A:1328:C:H5'	2.18	0.43
1:A:1474:G:H5'	1:A:1475:G:OP2	2.18	0.43
3:C:59:ALA:O	3:C:60:ALA:HB2	2.18	0.43
4:D:120:VAL:HG22	4:D:125:ILE:HG13	2.00	0.43
7:G:77:ARG:O	7:G:83:ASN:HA	2.19	0.43
10:J:64:ARG:HE	10:J:64:ARG:HB3	1.65	0.43
11:K:57:ASP:OD1	11:K:61:LYS:HE3	2.18	0.43
15:O:77:TYR:O	15:O:81:ILE:HG12	2.18	0.43
1:A:559:A:OP1	5:E:122:ARG:NH2	2.51	0.43
1:A:1288:A:C2	1:A:1289:A:C4	3.06	0.43
1:A:1346:A:H61	1:A:1374:A:H5'	1.83	0.43
1:A:1447:A:O2'	1:A:1452:C:OP1	2.32	0.43
2:B:63:LEU:HD12	2:B:63:LEU:C	2.38	0.43
2:B:233:VAL:HG23	2:B:233:VAL:O	2.17	0.43
3:C:138:GLN:NE2	3:C:138:GLN:CA	2.80	0.43
6:F:69:GLU:OE1	6:F:69:GLU:N	2.50	0.43
8:H:8:ASP:O	8:H:12:ARG:HG3	2.17	0.43
11:K:96:LYS:O	11:K:97:SER:HB3	2.18	0.43
1:A:1287:A:C2	1:A:1353:G:H1'	2.51	0.43
6:F:26:ILE:HG21	6:F:63:TYR:CE2	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:14:ASP:CB	7:G:19:ASP:H	2.28	0.43
12:L:24:LYS:HD3	12:L:29:ARG:NH2	2.32	0.43
12:L:38:THR:HG21	12:L:48:LEU:HD22	1.99	0.43
19:S:36:ARG:NH2	19:S:75:ALA:O	2.48	0.43
1:A:262:A:C6	1:A:263:A:C6	3.05	0.43
1:A:1039:C:H2'	1:A:1040:U:C6	2.53	0.43
1:A:1329:A:P	13:M:27:ALA:HB3	2.59	0.43
2:B:85:PRO:HG2	2:B:149:LEU:HD23	2.01	0.43
4:D:75:ARG:HH11	4:D:75:ARG:HG2	1.84	0.43
7:G:74:VAL:HG21	7:G:143:MET:HE3	1.99	0.43
9:I:54:ALA:O	9:I:56:GLY:N	2.44	0.43
9:I:62:ILE:HG21	9:I:76:ILE:HG12	2.01	0.43
15:O:77:TYR:OH	15:O:87:ARG:NH2	2.51	0.43
19:S:30:LEU:HD23	19:S:48:THR:HG22	2.00	0.43
20:T:65:LEU:HD23	20:T:65:LEU:HA	1.80	0.43
20:T:75:SER:O	20:T:79:ARG:HB2	2.18	0.43
1:A:103:C:P	20:T:10:ARG:HH11	2.42	0.43
1:A:421:U:O2'	1:A:422:C:P	2.77	0.43
1:A:502:G:OP1	12:L:114:SER:HB3	2.18	0.43
1:A:513:C:H2'	1:A:514:C:C6	2.54	0.43
1:A:865:A:H5'	1:A:1078:U:C4	2.53	0.43
1:A:1428:A:H2'	1:A:1429:C:C6	2.54	0.43
2:B:47:ARG:NH1	2:B:47:ARG:CG	2.78	0.43
10:J:47:VAL:CG1	14:N:40:ARG:HB2	2.43	0.43
12:L:85:ARG:CZ	12:L:93:ARG:HG2	2.48	0.43
15:O:32:THR:HG23	15:O:62:ARG:HH12	1.83	0.43
20:T:76:ARG:O	20:T:80:LYS:HE3	2.19	0.43
1:A:716:A:N3	11:K:107:ASN:O	2.51	0.43
1:A:789:U:O2'	1:A:791:G:N7	2.46	0.43
1:A:969:A:H61	13:M:125:LYS:HE3	1.84	0.43
1:A:1089:G:C2'	1:A:1090:U:H5'	2.49	0.43
1:A:1128:C:O2'	1:A:1130:A:C8	2.67	0.43
1:A:1141:C:O2'	1:A:1142:G:H5'	2.19	0.43
2:B:229:SER:HB3	2:B:232:LEU:HD12	2.00	0.43
3:C:63:VAL:HB	3:C:98:VAL:HG23	2.00	0.43
3:C:185:PHE:CE2	3:C:187:LEU:HD23	2.53	0.43
7:G:14:ASP:OD1	7:G:15:LEU:N	2.51	0.43
7:G:30:MET:SD	7:G:33:GLY:HA2	2.58	0.43
9:I:17:PHE:HD2	9:I:61:TYR:CD2	2.37	0.43
9:I:27:VAL:O	9:I:28:ASN:HB2	2.18	0.43
10:J:2:ILE:HD12	10:J:72:ILE:O	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:71:HIS:HD2	12:L:73:LEU:N	2.08	0.43
19:S:28:LYS:CG	19:S:29:ARG:N	2.74	0.43
1:A:189(J):G:H2'	1:A:189(K):U:H6	1.83	0.43
1:A:392:G:H2'	1:A:393:A:H8	1.83	0.43
1:A:1197:G:H5'	1:A:1197:G:C8	2.54	0.43
1:A:1442(A):G:C5'	1:A:1442(B):A:H5'	2.48	0.43
1:A:1502:A:C2	1:A:1505:G:N1	2.61	0.43
3:C:130:ARG:O	3:C:134:LYS:HG3	2.19	0.43
3:C:171:ARG:O	3:C:172:VAL:CG2	2.66	0.43
4:D:101:ASP:OD1	4:D:102:ASN:N	2.51	0.43
4:D:198:ASN:ND2	4:D:198:ASN:C	2.72	0.43
8:H:119:LEU:HD12	8:H:124:ALA:CA	2.48	0.43
14:N:56:ARG:HG2	14:N:57:LYS:N	2.33	0.43
1:A:57:G:O2'	1:A:58:C:H5'	2.18	0.43
1:A:88:A:H2'	1:A:89:C:O4'	2.19	0.43
1:A:148:G:H2'	1:A:149:A:C8	2.54	0.43
1:A:448:A:C4	1:A:487:A:C2	3.07	0.43
1:A:945:G:H2'	1:A:945:G:N3	2.34	0.43
1:A:1109:C:OP1	3:C:175:HIS:CD2	2.72	0.43
1:A:1128:C:O2'	1:A:1129:C:H5''	2.18	0.43
1:A:1223:C:P	19:S:78:ARG:NH1	2.81	0.43
3:C:81:GLU:O	3:C:84:ARG:HB3	2.19	0.43
10:J:17:SER:HB2	10:J:89:PRO:HG3	2.00	0.43
11:K:23:THR:OG1	11:K:28:ASN:N	2.52	0.43
11:K:77:THR:HG22	11:K:81:ARG:HH21	1.84	0.43
12:L:107:LYS:H	12:L:107:LYS:HD2	1.83	0.43
14:N:22:ARG:C	14:N:32:VAL:HG11	2.39	0.43
1:A:992:U:O2	1:A:992:U:H2'	2.18	0.43
1:A:1543:C:C3'	1:A:1544:U:H5''	2.49	0.43
2:B:96:LEU:N	2:B:96:LEU:CD1	2.82	0.43
2:B:222:GLY:O	2:B:223:VAL:O	2.37	0.43
9:I:85:VAL:HG11	9:I:92:ARG:HG3	2.01	0.43
22:W:1:U:O2'	22:W:2:U:H5'	2.19	0.43
1:A:263:A:OP2	20:T:72:ARG:NH1	2.51	0.42
1:A:389:A:H2'	1:A:389:A:N3	2.34	0.42
1:A:512:U:H2'	1:A:513:C:C6	2.54	0.42
1:A:542:G:H5'	4:D:40:GLY:HA3	2.00	0.42
1:A:1218:C:H2'	1:A:1219:U:C6	2.54	0.42
1:A:1277:C:H5'	1:A:1278:U:OP2	2.18	0.42
1:A:1345:U:C4	1:A:1377:A:C2	3.07	0.42
2:B:9:VAL:HG21	2:B:203:ARG:HG3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:91:TRP:HZ3	2:B:170:GLU:OE2	2.01	0.42
3:C:34:GLU:O	3:C:37:ARG:N	2.52	0.42
3:C:154:GLY:O	3:C:155:ARG:CB	2.67	0.42
6:F:4:TYR:CD1	6:F:92:LYS:HG2	2.53	0.42
7:G:68:VAL:HG12	7:G:68:VAL:O	2.19	0.42
9:I:16:VAL:HG21	9:I:79:GLY:HA3	2.01	0.42
10:J:73:ILE:O	10:J:74:ASN:HB2	2.18	0.42
11:K:23:THR:OG1	11:K:27:GLY:C	2.58	0.42
13:M:92:ARG:HH11	13:M:92:ARG:HG3	1.84	0.42
15:O:52:HIS:O	15:O:55:LEU:HB3	2.20	0.42
19:S:13:ASP:O	19:S:17:GLU:HG2	2.19	0.42
1:A:662:G:H2'	1:A:663:A:C8	2.54	0.42
1:A:1109:C:P	3:C:175:HIS:CD2	3.12	0.42
18:R:32:THR:HG23	18:R:68:GLU:O	2.18	0.42
1:A:17:U:H1'	1:A:1080:A:N3	2.34	0.42
1:A:438:G:H4'	1:A:439:A:OP1	2.19	0.42
1:A:631:G:H2'	1:A:632:A:C5'	2.50	0.42
1:A:1030(C):G:H2'	1:A:1030(D):A:H8	1.80	0.42
1:A:1128:C:H2'	1:A:1139:G:N7	2.35	0.42
1:A:1360:A:H2'	1:A:1361:G:O4'	2.19	0.42
5:E:8:LEU:HD13	5:E:27:LEU:HB2	2.00	0.42
5:E:65:VAL:HG21	5:E:109:ALA:HB1	2.00	0.42
9:I:9:ARG:HG2	9:I:74:ASP:CB	2.49	0.42
9:I:92:ARG:O	9:I:94:LYS:N	2.52	0.42
10:J:76:ASN:HB2	10:J:79:THR:OG1	2.19	0.42
12:L:109:ARG:NH1	12:L:112:SER:H	2.17	0.42
13:M:93:ARG:HH22	19:S:81:ARG:HH11	1.65	0.42
17:Q:81:MET:HE3	17:Q:84:VAL:HG21	2.02	0.42
19:S:16:LEU:C	19:S:18:LYS:N	2.72	0.42
1:A:192:U:O2'	1:A:193:C:H5'	2.20	0.42
1:A:530:G:H5'	1:A:531:U:C5'	2.49	0.42
1:A:593:G:O2'	1:A:594:G:H5'	2.20	0.42
1:A:674:G:H5'	6:F:50:TYR:CE2	2.55	0.42
1:A:739:C:P	6:F:2:ARG:HH22	2.42	0.42
1:A:807:A:H2'	1:A:808:C:C6	2.54	0.42
1:A:841:U:C5	1:A:848:C:H1'	2.53	0.42
1:A:1223:C:OP1	19:S:78:ARG:NH1	2.51	0.42
1:A:1314:C:OP2	19:S:6:LYS:HD3	2.18	0.42
1:A:1350:A:C2	1:A:1351:U:C2	3.07	0.42
2:B:49:PHE:HA	2:B:52:ILE:HG13	2.01	0.42
2:B:71:ALA:HB1	2:B:205:ILE:HG21	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:178:GLU:OE1	4:D:178:GLU:HA	2.19	0.42
5:E:11:ARG:HD3	5:E:22:PHE:HB3	2.02	0.42
7:G:74:VAL:O	7:G:74:VAL:HG23	2.20	0.42
8:H:112:LEU:HD12	8:H:112:LEU:H	1.83	0.42
10:J:26:ARG:HG2	10:J:26:ARG:HH11	1.84	0.42
13:M:9:PRO:HB3	13:M:17:ALA:O	2.20	0.42
17:Q:8:VAL:HG22	17:Q:55:VAL:HG22	2.01	0.42
1:A:232:G:H2'	1:A:233:C:O4'	2.20	0.42
1:A:555:C:H2'	1:A:556:C:C6	2.53	0.42
1:A:902:G:H2'	1:A:903:G:H8	1.84	0.42
1:A:1015:A:N3	1:A:1218:C:O2'	2.48	0.42
1:A:1151:A:O2'	1:A:1152:A:H8	2.03	0.42
1:A:1222:G:O2'	1:A:1223:C:H5'	2.20	0.42
2:B:77:MET:O	2:B:80:GLU:N	2.49	0.42
2:B:96:LEU:N	2:B:96:LEU:HD12	2.35	0.42
4:D:78:PHE:O	4:D:81:ALA:HB3	2.19	0.42
7:G:53:THR:HG22	7:G:54:GLY:N	2.34	0.42
8:H:58:TYR:O	8:H:59:LEU:HD23	2.20	0.42
9:I:16:VAL:HG11	9:I:80:ILE:CA	2.48	0.42
9:I:43:VAL:HG12	9:I:50:ARG:NH2	2.33	0.42
12:L:50:LYS:HD2	12:L:50:LYS:N	2.33	0.42
13:M:79:ARG:C	13:M:81:MET:N	2.73	0.42
1:A:178:C:C5'	1:A:178:C:H6	2.32	0.42
1:A:190:U:H3	20:T:98:SER:CB	2.32	0.42
1:A:479:C:O2'	1:A:480:U:H5'	2.19	0.42
1:A:620:C:C1'	4:D:134:LEU:HD13	2.49	0.42
1:A:883:C:O2'	1:A:884:U:H5'	2.20	0.42
1:A:1118:C:OP1	9:I:103:ARG:HD2	2.20	0.42
2:B:55:LEU:HD23	2:B:55:LEU:HA	1.82	0.42
2:B:82:ALA:O	2:B:84:MET:N	2.53	0.42
3:C:138:GLN:CA	3:C:138:GLN:HE21	2.31	0.42
5:E:127:ILE:HD13	5:E:127:ILE:HA	1.89	0.42
6:F:16:GLN:NE2	6:F:16:GLN:HA	2.34	0.42
6:F:36:ARG:HG2	6:F:36:ARG:HH11	1.85	0.42
8:H:17:THR:HB	8:H:78:GLN:OE1	2.20	0.42
9:I:116:HIS:O	9:I:117:LYS:HB3	2.20	0.42
10:J:20:LYS:HE2	10:J:20:LYS:HB2	1.92	0.42
12:L:37:ARG:NH2	12:L:53:LYS:HZ2	2.18	0.42
12:L:106:VAL:N	12:L:118:THR:HG22	2.35	0.42
13:M:121:LYS:HZ3	13:M:122:ALA:HB2	1.85	0.42
18:R:73:LYS:HD2	18:R:73:LYS:C	2.39	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:Z:30:G:H2'	23:Z:31:A:C8	2.50	0.42
2:B:6:GLU:HG3	2:B:6:GLU:O	2.19	0.42
2:B:76:ARG:HB3	2:B:88:ASN:OD1	2.18	0.42
3:C:13:ILE:O	3:C:14:THR:C	2.57	0.42
4:D:60:LYS:HD2	4:D:206:TYR:OH	2.19	0.42
5:E:75:GLU:H	5:E:75:GLU:CD	2.23	0.42
7:G:30:MET:HB2	7:G:38:ALA:HB2	2.01	0.42
7:G:56:GLU:H	7:G:56:GLU:HG2	1.58	0.42
14:N:11:ARG:O	14:N:13:PRO:N	2.53	0.42
14:N:23:CYS:HB3	14:N:27:GLY:H	1.85	0.42
20:T:50:ARG:HH11	20:T:50:ARG:CG	2.32	0.42
1:A:189(J):G:H2'	1:A:189(K):U:C6	2.54	0.42
1:A:267:C:OP1	17:Q:66:LYS:HB2	2.20	0.42
1:A:730:G:C5	1:A:731:G:H1'	2.55	0.42
1:A:1006:C:H42	1:A:1024:G:H21	1.67	0.42
1:A:1236:A:H2'	1:A:1237:C:C6	2.54	0.42
1:A:1246:C:H2'	1:A:1247:U:C6	2.55	0.42
2:B:6:GLU:C	2:B:8:GLY:H	2.22	0.42
2:B:218:GLN:HG2	2:B:219:ALA:N	2.33	0.42
3:C:172:VAL:N	3:C:173:PRO:CD	2.82	0.42
4:D:22:GLY:HA3	4:D:111:VAL:HG12	2.01	0.42
4:D:147:VAL:O	4:D:148:ALA:C	2.57	0.42
5:E:74:HIS:CE1	5:E:76:ILE:CG2	3.03	0.42
7:G:17:TYR:CD2	7:G:58:LEU:HB2	2.54	0.42
19:S:42:PRO:C	19:S:44:MET:H	2.23	0.42
1:A:412:A:C2'	1:A:413:G:OP2	2.68	0.42
1:A:491:G:H2'	1:A:492:G:C8	2.52	0.42
1:A:1032:G:O2'	1:A:1033:G:H5'	2.19	0.42
1:A:1121:U:C2'	1:A:1122:U:H5''	2.43	0.42
1:A:1402:C:H2'	1:A:1403:C:O4'	2.20	0.42
3:C:30:HIS:C	3:C:32:LEU:N	2.73	0.42
7:G:71:ARG:O	7:G:72:MET:HG2	2.20	0.42
9:I:15:ARG:NH1	9:I:15:ARG:HG3	2.35	0.42
9:I:126:LYS:HB3	13:M:125:LYS:HZ3	1.85	0.42
10:J:28:SER:OG	10:J:82:GLN:NE2	2.48	0.42
10:J:43:ARG:NH2	14:N:35:PHE:CD2	2.88	0.42
13:M:20:TYR:N	13:M:20:TYR:CD1	2.88	0.42
14:N:8:LYS:HD3	14:N:8:LYS:C	2.40	0.42
1:A:19:C:H2'	1:A:20:U:C6	2.54	0.42
1:A:437:U:H5''	4:D:154:LEU:HD22	2.00	0.42
1:A:636:U:H2'	1:A:637:G:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:721:G:H5'	1:A:722:A:OP1	2.20	0.42
1:A:977:A:O2'	1:A:979:C:OP2	2.32	0.42
1:A:1129:C:OP2	9:I:61:TYR:HE2	2.03	0.42
1:A:1164:G:O2'	1:A:1165:C:H5'	2.20	0.42
1:A:1196:U:H3	3:C:161:GLN:NE2	2.18	0.42
1:A:1226:C:C5	13:M:103:ARG:HA	2.54	0.42
1:A:1353:G:O2'	1:A:1354:C:H5'	2.20	0.42
1:A:1368:G:H5''	9:I:111:LYS:HB3	2.01	0.42
1:A:1406:U:C2'	1:A:1407:C:H5'	2.49	0.42
2:B:116:PHE:CE2	2:B:133:LYS:HG2	2.49	0.42
2:B:117:ALA:HA	2:B:121:ILE:HD11	2.02	0.42
10:J:4:ILE:HG13	10:J:69:LEU:O	2.20	0.42
10:J:17:SER:CB	10:J:89:PRO:HG3	2.50	0.42
10:J:20:LYS:NZ	10:J:88:LEU:HD12	2.35	0.42
12:L:106:VAL:O	12:L:106:VAL:HG23	2.20	0.42
16:P:59:TRP:HB3	16:P:64:ALA:CB	2.50	0.42
20:T:83:GLN:O	20:T:86:GLU:N	2.49	0.42
1:A:103:C:OP2	20:T:10:ARG:NH1	2.53	0.41
1:A:794:A:C5	1:A:795:C:C4	3.08	0.41
1:A:881:G:P	12:L:8:ARG:NH2	2.93	0.41
1:A:1033:G:H2'	1:A:1034:G:O4'	2.19	0.41
1:A:1179:A:H2'	1:A:1180:A:O4'	2.20	0.41
1:A:1250:A:C2	1:A:1370:G:H1'	2.55	0.41
2:B:45:LEU:HD22	2:B:49:PHE:CE1	2.55	0.41
4:D:148:ALA:O	4:D:152:ARG:HG3	2.20	0.41
8:H:7:ALA:HB2	8:H:85:ARG:HD2	2.02	0.41
12:L:56:LEU:HD21	12:L:81:ILE:HD12	2.01	0.41
13:M:93:ARG:HH12	19:S:81:ARG:NH1	2.18	0.41
14:N:10:LYS:O	14:N:10:LYS:HG2	2.20	0.41
15:O:65:LEU:O	15:O:68:TYR:HB3	2.20	0.41
16:P:1:MET:CE	16:P:3:LYS:HD2	2.50	0.41
16:P:42:ARG:O	16:P:43:LYS:C	2.59	0.41
1:A:791:G:C6	1:A:792:A:N7	2.88	0.41
1:A:1313:U:C5	19:S:4:SER:CB	3.02	0.41
2:B:224:VAL:CG1	2:B:225:GLU:N	2.83	0.41
2:B:230:TYR:O	2:B:230:TYR:CD1	2.73	0.41
4:D:7:VAL:HG11	4:D:114:ARG:NH1	2.35	0.41
7:G:81:GLY:O	7:G:82:ALA:HB2	2.20	0.41
7:G:119:ILE:HD12	7:G:119:ILE:N	2.35	0.41
13:M:7:GLU:HG3	13:M:21:ILE:HG23	2.02	0.41
13:M:19:THR:C	13:M:21:ILE:H	2.22	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:59:SER:O	14:N:60:TRP:HB3	2.19	0.41
1:A:401:C:H1'	1:A:622:A:H1'	2.01	0.41
1:A:775:G:O2'	1:A:776:G:H5'	2.20	0.41
1:A:951:G:O2'	1:A:952:U:H5'	2.21	0.41
1:A:1126:U:N3	1:A:1127:G:N7	2.68	0.41
1:A:1346:A:N6	1:A:1374:A:H3'	2.35	0.41
2:B:6:GLU:O	2:B:6:GLU:CG	2.69	0.41
2:B:54:ASP:OD1	2:B:55:LEU:N	2.54	0.41
2:B:108:ARG:CD	2:B:112:LEU:HG	2.48	0.41
2:B:127:LYS:O	2:B:131:ARG:HG3	2.21	0.41
4:D:105:TYR:HE2	4:D:111:VAL:O	2.03	0.41
7:G:110:ARG:HB3	7:G:112:GLU:OE1	2.20	0.41
9:I:94:LYS:O	9:I:98:LEU:CD2	2.68	0.41
13:M:34:GLU:C	13:M:36:THR:H	2.23	0.41
16:P:6:LEU:HD12	16:P:6:LEU:N	2.35	0.41
1:A:270:A:H2'	1:A:271:C:C6	2.55	0.41
1:A:377:G:OP1	16:P:3:LYS:HD3	2.20	0.41
2:B:197:GLY:O	2:B:198:ASN:C	2.57	0.41
2:B:206:GLN:O	2:B:210:SER:CB	2.68	0.41
3:C:24:GLY:C	3:C:26:LYS:N	2.73	0.41
3:C:69:VAL:HG12	3:C:71:LYS:N	2.26	0.41
4:D:100:LEU:HD23	4:D:120:VAL:HG11	2.01	0.41
6:F:99:ALA:HB2	18:R:16:LEU:CD1	2.50	0.41
7:G:64:ALA:HB1	7:G:126:ALA:HB3	2.01	0.41
8:H:138:TRP:CE3	8:H:138:TRP:OXT	2.73	0.41
9:I:31:ASP:O	9:I:34:GLU:HB3	2.21	0.41
11:K:11:ILE:HB	11:K:74:VAL:HG12	2.03	0.41
11:K:106:HIS:O	11:K:107:ASN:HB2	2.21	0.41
13:M:56:ARG:CG	13:M:60:GLU:OE2	2.69	0.41
16:P:20:VAL:HG11	16:P:32:TYR:HB3	2.01	0.41
19:S:19:VAL:CG1	19:S:20:LEU:N	2.84	0.41
1:A:344:A:O5'	1:A:345:C:H5	2.03	0.41
1:A:390:C:O3'	16:P:28:ARG:NH2	2.54	0.41
1:A:908:A:O2'	1:A:909:A:H5'	2.20	0.41
1:A:1001:A:N1	1:A:1002:G:C6	2.89	0.41
1:A:1245:A:N6	1:A:1292:U:H3	2.19	0.41
3:C:4:ILE:N	3:C:4:ILE:HD13	2.35	0.41
3:C:94:THR:O	3:C:96:LYS:N	2.54	0.41
4:D:51:SER:O	4:D:52:ASP:C	2.59	0.41
4:D:161:LEU:HD13	4:D:180:MET:HG2	2.02	0.41
5:E:75:GLU:HG3	5:E:89:PRO:HD3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:106:LEU:HD13	5:E:114:ILE:HG21	2.01	0.41
7:G:47:LYS:HA	7:G:50:GLN:HB2	2.02	0.41
8:H:56:LYS:N	8:H:56:LYS:CD	2.83	0.41
10:J:22:VAL:HG22	10:J:26:ARG:HD3	2.03	0.41
13:M:124:ARG:HD2	13:M:124:ARG:C	2.41	0.41
18:R:40:ARG:HH11	18:R:40:ARG:CB	2.33	0.41
19:S:17:GLU:HA	19:S:20:LEU:HD11	2.01	0.41
19:S:17:GLU:HA	19:S:20:LEU:CD1	2.50	0.41
1:A:123:C:OP1	1:A:312:C:H5'	2.21	0.41
1:A:781:A:C5	1:A:802:A:C2	3.09	0.41
2:B:1:VAL:HG13	2:B:218:GLN:NE2	2.36	0.41
2:B:33:ILE:HG22	2:B:34:HIS:N	2.34	0.41
3:C:38:ILE:HG22	3:C:39:ARG:N	2.35	0.41
7:G:56:GLU:O	7:G:60:VAL:HG23	2.20	0.41
7:G:143:MET:C	7:G:144:ALA:O	2.58	0.41
1:A:246:A:N6	1:A:281:G:H1'	2.36	0.41
1:A:253:U:H2'	1:A:254:G:C8	2.55	0.41
1:A:502:G:C2	1:A:503:C:C2	3.08	0.41
1:A:1159:U:C5	1:A:1182:G:C4	3.09	0.41
1:A:1276:G:H2'	1:A:1277:C:C6	2.56	0.41
1:A:1349:A:H2'	1:A:1350:A:H8	1.86	0.41
2:B:86:TYR:CD1	2:B:86:TYR:C	2.93	0.41
2:B:230:TYR:CE1	2:B:233:VAL:HG21	2.55	0.41
3:C:92:LYS:HA	3:C:92:LYS:HD3	1.84	0.41
3:C:125:ARG:HD2	3:C:127:PHE:CE1	2.55	0.41
3:C:194:VAL:HG12	3:C:195:LEU:N	2.35	0.41
4:D:34:ARG:HG3	4:D:34:ARG:NH1	2.36	0.41
4:D:63:LEU:HD11	4:D:96:LEU:CD1	2.50	0.41
8:H:127:LEU:O	8:H:129:VAL:HG13	2.20	0.41
9:I:57:ARG:HG3	9:I:57:ARG:NH1	2.35	0.41
10:J:53:LYS:HG3	10:J:54:HIS:N	2.35	0.41
10:J:55:LYS:HD2	10:J:55:LYS:C	2.40	0.41
12:L:115:LYS:C	12:L:117:GLY:H	2.24	0.41
13:M:64:LYS:O	13:M:69:LEU:HG	2.20	0.41
13:M:124:ARG:HG3	13:M:124:ARG:NH1	2.36	0.41
17:Q:26:PHE:HB2	17:Q:27:PRO:HD2	2.02	0.41
1:A:965:A:C2	1:A:969:A:C2	3.09	0.41
2:B:189:ASP:O	8:H:74:PRO:HG3	2.20	0.41
5:E:71:THR:HG23	5:E:72:ILE:O	2.21	0.41
5:E:74:HIS:HD2	8:H:107:LEU:HD12	1.84	0.41
6:F:10:LEU:HD11	6:F:59:TYR:HD2	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:9:ARG:O	9:I:10:LYS:C	2.59	0.41
10:J:2:ILE:CG2	10:J:98:THR:HB	2.50	0.41
10:J:43:ARG:O	10:J:62:GLU:HA	2.20	0.41
11:K:116:ARG:O	11:K:117:LYS:HB2	2.20	0.41
12:L:38:THR:CG2	12:L:48:LEU:HD22	2.51	0.41
13:M:61:ASN:O	13:M:62:THR:HB	2.21	0.41
21:V:3:LYS:HB3	21:V:14:TRP:CG	2.55	0.41
1:A:136:C:H2'	1:A:137:C:H6	1.86	0.41
1:A:175:C:H2'	1:A:176:C:H6	1.85	0.41
1:A:359:U:O2'	1:A:360:A:H5'	2.20	0.41
1:A:632:A:H2'	1:A:633:G:H5'	2.03	0.41
1:A:782:A:H2'	1:A:783:C:O4'	2.21	0.41
1:A:1003:G:N2	1:A:1004:A:H1'	2.36	0.41
1:A:1069:C:O2'	1:A:1192:C:H1'	2.21	0.41
1:A:1111:A:N1	3:C:176:THR:HB	2.36	0.41
1:A:1123:A:H4'	10:J:34:GLY:HA3	2.03	0.41
1:A:1157:A:H4'	1:A:1158:C:C5'	2.51	0.41
1:A:1178:G:N2	1:A:1180:A:H3'	2.36	0.41
1:A:1237:C:H4'	1:A:1334:G:N2	2.36	0.41
1:A:1289:A:N1	1:A:1371:G:O2'	2.50	0.41
2:B:161:PRO:HG2	2:B:186:SER:OG	2.21	0.41
2:B:190:LEU:HD23	2:B:190:LEU:HA	1.79	0.41
2:B:194:ILE:N	2:B:194:ILE:CD1	2.78	0.41
3:C:60:ALA:O	3:C:61:ASP:HB2	2.21	0.41
4:D:155:GLU:O	4:D:158:ARG:HB2	2.21	0.41
4:D:166:GLY:O	4:D:167:ARG:HB2	2.21	0.41
5:E:65:VAL:HA	5:E:66:PRO:HD3	1.92	0.41
5:E:92:PRO:HA	5:E:113:ASP:CG	2.41	0.41
6:F:8:ILE:CD1	6:F:26:ILE:HD12	2.51	0.41
6:F:19:LEU:HD21	6:F:23:LYS:HD2	2.03	0.41
6:F:27:GLN:HA	6:F:27:GLN:HE21	1.86	0.41
8:H:78:GLN:O	8:H:81:HIS:CE1	2.74	0.41
9:I:5:GLY:O	9:I:6:THR:OG1	2.38	0.41
10:J:28:SER:HB2	10:J:78:LYS:C	2.41	0.41
11:K:41:LYS:HE2	11:K:41:LYS:HB3	1.78	0.41
12:L:23:LEU:C	12:L:25:GLY:H	2.24	0.41
12:L:23:LEU:HG	12:L:24:LYS:H	1.86	0.41
13:M:23:GLY:HA3	13:M:65:LEU:HD22	2.02	0.41
16:P:43:LYS:CG	16:P:48:TRP:CE2	3.02	0.41
18:R:40:ARG:NH1	18:R:40:ARG:CB	2.84	0.41
1:A:223:U:H5''	20:T:61:LYS:NZ	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:521:G:OP1	12:L:69:GLU:O	2.39	0.41
1:A:927:G:H4'	1:A:1503:A:N7	2.36	0.41
1:A:975:A:H4'	1:A:976:G:OP2	2.20	0.41
1:A:984:C:H2'	1:A:985:C:C6	2.54	0.41
1:A:1081:G:P	5:E:12:THR:HG1	2.42	0.41
1:A:1126:U:H6	1:A:1126:U:P	2.44	0.41
1:A:1127:G:O2'	9:I:15:ARG:NH2	2.54	0.41
1:A:1241:G:H2'	1:A:1242:C:H6	1.83	0.41
2:B:4:LEU:HA	2:B:42:MET:HE1	2.02	0.41
2:B:126:LYS:HA	2:B:129:GLN:CB	2.52	0.41
4:D:7:VAL:HG23	4:D:8:CYS:N	2.36	0.41
7:G:21:LEU:CD1	7:G:100:LEU:HD11	2.51	0.41
8:H:90:GLY:O	8:H:91:ARG:CB	2.62	0.41
9:I:42:ALA:O	9:I:43:VAL:C	2.59	0.41
11:K:49:TYR:CE2	11:K:53:LEU:HD11	2.55	0.41
11:K:100:ASP:C	11:K:100:ASP:OD1	2.60	0.41
11:K:100:ASP:OD2	18:R:73:LYS:CE	2.69	0.41
12:L:4:ASN:O	12:L:8:ARG:HB2	2.21	0.41
14:N:20:TYR:HD2	14:N:21:THR:O	2.03	0.41
17:Q:93:ASN:O	17:Q:94:TYR:C	2.59	0.41
23:Z:28:G:H2'	23:Z:28:G:N3	2.35	0.41
1:A:426:G:O2'	1:A:427:U:H5'	2.20	0.40
1:A:644:G:C5	1:A:645:C:C5	3.09	0.40
1:A:1234:C:C4'	1:A:1364:U:H2'	2.45	0.40
1:A:1300:G:O2'	1:A:1301:U:O5'	2.39	0.40
1:A:1347:G:H22	1:A:1373:G:H2'	1.86	0.40
2:B:109:LEU:C	2:B:109:LEU:CD2	2.89	0.40
3:C:33:LEU:HD21	3:C:37:ARG:NE	2.34	0.40
6:F:9:VAL:HB	6:F:87:ARG:HB2	2.03	0.40
6:F:101:ALA:HA	18:R:13:GLU:CG	2.48	0.40
7:G:154:ARG:HA	7:G:154:ARG:HD3	1.84	0.40
9:I:7:GLY:CA	9:I:78:LEU:HB3	2.51	0.40
9:I:48:PRO:O	9:I:51:ALA:HB3	2.22	0.40
9:I:49:LEU:HD23	9:I:84:LEU:HD11	2.03	0.40
10:J:2:ILE:HA	10:J:98:THR:HB	2.03	0.40
15:O:87:ARG:HD3	15:O:87:ARG:HA	1.91	0.40
17:Q:44:HIS:HB2	17:Q:64:ILE:CD1	2.51	0.40
18:R:40:ARG:HH11	18:R:40:ARG:HA	1.84	0.40
1:A:189(F):U:O2'	1:A:189(G):G:OP1	2.37	0.40
1:A:381:C:H2'	1:A:382:A:O4'	2.21	0.40
1:A:532:A:C2'	1:A:533:A:OP1	2.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1027:C:N3	1:A:1034:G:O6	2.55	0.40
1:A:1320:C:C2	19:S:72:GLY:HA3	2.57	0.40
1:A:1346:A:OP1	9:I:119:ARG:NH1	2.38	0.40
2:B:1:VAL:O	2:B:2:LYS:HB3	2.21	0.40
3:C:47:TYR:HE1	3:C:117:GLN:NE2	2.19	0.40
3:C:78:ARG:HG3	3:C:78:ARG:O	2.22	0.40
3:C:124:GLU:HG2	3:C:189:ARG:O	2.21	0.40
4:D:49:ARG:HA	4:D:50:PRO:HD3	1.94	0.40
6:F:26:ILE:O	6:F:30:LEU:HG	2.21	0.40
6:F:27:GLN:HA	6:F:27:GLN:NE2	2.35	0.40
9:I:32:PHE:CE1	9:I:36:PHE:CE2	3.09	0.40
10:J:28:SER:CB	10:J:82:GLN:NE2	2.82	0.40
10:J:44:ARG:HH11	10:J:44:ARG:CG	2.34	0.40
13:M:22:TYR:HB3	13:M:66:GLU:HA	2.03	0.40
14:N:11:ARG:O	14:N:12:THR:C	2.59	0.40
18:R:7:VAL:HG13	18:R:27:ARG:HG2	2.04	0.40
1:A:191:G:H1'	20:T:98:SER:HA	2.03	0.40
1:A:327:A:O2'	1:A:329:A:C5'	2.65	0.40
1:A:718:G:O4'	11:K:106:HIS:HA	2.21	0.40
1:A:720:C:O5'	1:A:721:G:H4'	2.20	0.40
1:A:953:G:H5'	1:A:965:A:H61	1.86	0.40
3:C:18:GLU:HG2	3:C:53:ARG:HE	1.86	0.40
4:D:199:GLU:HG2	4:D:200:GLN:N	2.36	0.40
9:I:27:VAL:HG22	9:I:62:ILE:HB	2.04	0.40
10:J:14:LEU:HD23	10:J:14:LEU:HA	1.94	0.40
10:J:73:ILE:HG22	10:J:74:ASN:N	2.36	0.40
10:J:79:THR:O	10:J:81:GLU:N	2.53	0.40
11:K:114:LYS:HE2	11:K:115:PHE:CZ	2.57	0.40
13:M:83:ILE:HG13	13:M:85:CYS:HB2	2.02	0.40
20:T:67:LYS:HE2	20:T:67:LYS:HB2	1.94	0.40
1:A:277:C:OP1	17:Q:67:ARG:NH2	2.53	0.40
1:A:333:G:H2'	1:A:334:C:C6	2.56	0.40
1:A:410:G:OP2	4:D:24:ARG:HD2	2.21	0.40
1:A:620:C:C6	4:D:134:LEU:HD13	2.57	0.40
1:A:1286:A:H2'	1:A:1287:A:O3'	2.22	0.40
1:A:1350:A:H2'	1:A:1351:U:C6	2.57	0.40
1:A:1388:C:H2'	1:A:1389:C:H6	1.87	0.40
1:A:1457:G:H2'	1:A:1458:G:C8	2.53	0.40
6:F:4:TYR:CE2	6:F:72:VAL:CG2	3.04	0.40
7:G:74:VAL:HG13	7:G:144:ALA:HA	2.03	0.40
8:H:24:THR:HG23	8:H:24:THR:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:87:ASP:OD1	10:J:88:LEU:N	2.55	0.40
10:J:88:LEU:N	10:J:89:PRO:HD2	2.34	0.40
17:Q:96:SER:O	17:Q:97:LEU:C	2.60	0.40
18:R:28:PHE:C	18:R:36:LEU:HD12	2.42	0.40
1:A:488:C:H6	1:A:488:C:O5'	2.04	0.40
1:A:538:G:H2'	1:A:539:A:C8	2.57	0.40
1:A:573:A:C3'	1:A:574:A:H5'	2.50	0.40
1:A:655:A:H2'	1:A:656:C:H6	1.87	0.40
1:A:730:G:H2'	1:A:731:G:H5'	2.04	0.40
1:A:731:G:O2'	1:A:732:C:H5'	2.22	0.40
1:A:969:A:N6	13:M:125:LYS:HE3	2.36	0.40
1:A:1067:A:O5'	1:A:1067:A:H1'	2.22	0.40
1:A:1127:G:N3	1:A:1127:G:C2'	2.75	0.40
1:A:1305:G:OP2	21:V:2:GLY:N	2.55	0.40
1:A:1493:A:H3'	28:A:2007:HOH:O	2.21	0.40
2:B:153:PRO:HG3	2:B:156:ILE:HD11	2.02	0.40
4:D:49:ARG:HG3	4:D:49:ARG:NH1	2.36	0.40
5:E:98:ALA:HB1	5:E:116:THR:HG21	2.04	0.40
9:I:9:ARG:HD2	9:I:10:LYS:N	2.37	0.40
14:N:13:PRO:O	14:N:14:LYS:CB	2.69	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:151:ARG:NH1	2:B:151:ARG:NH1[7_555]	1.88	0.32

## 5.3 Torsion angles [i](#)

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

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	B	233/256 (91%)	163 (70%)	43 (18%)	27 (12%)	<b>0</b> <b>1</b>

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	205/239 (86%)	143 (70%)	38 (18%)	24 (12%)	0	1
4	D	206/208 (99%)	173 (84%)	21 (10%)	12 (6%)	1	10
5	E	149/161 (92%)	138 (93%)	9 (6%)	2 (1%)	12	45
6	F	99/101 (98%)	81 (82%)	15 (15%)	3 (3%)	4	24
7	G	153/155 (99%)	125 (82%)	24 (16%)	4 (3%)	5	27
8	H	136/138 (99%)	117 (86%)	16 (12%)	3 (2%)	6	31
9	I	125/128 (98%)	97 (78%)	14 (11%)	14 (11%)	0	2
10	J	97/104 (93%)	70 (72%)	18 (19%)	9 (9%)	0	3
11	K	117/129 (91%)	100 (86%)	11 (9%)	6 (5%)	2	12
12	L	123/132 (93%)	100 (81%)	17 (14%)	6 (5%)	2	13
13	M	123/126 (98%)	91 (74%)	22 (18%)	10 (8%)	1	4
14	N	58/60 (97%)	44 (76%)	11 (19%)	3 (5%)	2	12
15	O	86/88 (98%)	81 (94%)	3 (4%)	2 (2%)	6	30
16	P	82/88 (93%)	77 (94%)	3 (4%)	2 (2%)	6	29
17	Q	102/104 (98%)	86 (84%)	8 (8%)	8 (8%)	1	4
18	R	71/88 (81%)	58 (82%)	10 (14%)	3 (4%)	3	16
19	S	79/92 (86%)	56 (71%)	18 (23%)	5 (6%)	1	7
20	T	97/106 (92%)	70 (72%)	18 (19%)	9 (9%)	0	3
21	V	23/26 (88%)	18 (78%)	5 (22%)	0	100	100
All	All	2364/2529 (94%)	1888 (80%)	324 (14%)	152 (6%)	1	7

All (152) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	10	HIS
2	B	12	GLY
2	B	15	ARG
2	B	18	TRP
2	B	184	THR
3	C	3	LYS
3	C	14	THR
3	C	15	ARG
3	C	25	LYS
3	C	46	LEU
3	C	60	ALA

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
3	C	100	LEU
3	C	153	SER
3	C	155	ARG
3	C	188	ALA
3	C	206	VAL
4	D	28	PRO
4	D	35	ARG
5	E	150	GLY
7	G	6	ALA
8	H	91	ARG
9	I	40	VAL
9	I	54	ALA
9	I	57	ARG
9	I	100	PHE
9	I	117	LYS
9	I	126	LYS
10	J	32	VAL
10	J	58	ARG
11	K	2	ARG
11	K	3	GLN
12	L	23	LEU
12	L	24	LYS
12	L	26	ALA
13	M	62	THR
13	M	66	GLU
13	M	85	CYS
15	O	87	ARG
16	P	83	GLU
17	Q	79	GLY
17	Q	80	ARG
17	Q	98	SER
19	S	6	LYS
19	S	9	VAL
20	T	89	GLY
2	B	3	GLU
2	B	5	LEU
2	B	9	VAL
2	B	14	GLU
2	B	117	ALA
2	B	201	ALA
2	B	223	VAL
2	B	233	VAL

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
3	C	107	ASN
3	C	167	ALA
3	C	204	GLY
4	D	3	TYR
4	D	87	VAL
4	D	167	ARG
4	D	170	GLY
4	D	177	VAL
5	E	70	GLY
6	F	16	GLN
7	G	52	LYS
7	G	154	ARG
8	H	24	THR
9	I	42	ALA
9	I	93	ALA
10	J	28	SER
10	J	76	ASN
10	J	80	ILE
10	J	84	MET
14	N	10	LYS
14	N	18	ARG
18	R	5	ALA
18	R	33	GLY
18	R	72	ARG
19	S	43	GLU
20	T	4	SER
20	T	95	GLY
20	T	96	GLY
2	B	11	PHE
2	B	71	ALA
2	B	189	ASP
2	B	198	ASN
3	C	28	TYR
3	C	80	GLY
3	C	83	ILE
3	C	97	ASN
3	C	101	ASN
3	C	145	ALA
9	I	6	THR
9	I	37	GLN
10	J	70	VAL
10	J	88	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
12	L	75	GLU
13	M	37	GLY
17	Q	68	LYS
17	Q	96	SER
17	Q	97	LEU
19	S	4	SER
20	T	87	ALA
2	B	54	ASP
2	B	57	MET
2	B	210	SER
2	B	222	GLY
3	C	178	ARG
4	D	123	GLY
6	F	35	ALA
6	F	82	ARG
9	I	23	GLY
9	I	118	ALA
11	K	5	ALA
11	K	81	ARG
11	K	108	GLY
12	L	25	GLY
13	M	123	PRO
17	Q	13	LYS
20	T	42	ALA
20	T	66	HIS
2	B	56	ALA
4	D	29	LYS
4	D	178	GLU
7	G	82	ALA
12	L	47	ALA
13	M	20	TYR
13	M	115	THR
16	P	52	ASP
19	S	81	ARG
20	T	91	PRO
2	B	2	LYS
3	C	95	GLY
4	D	4	ILE
4	D	166	GLY
8	H	83	ILE
10	J	55	LYS
15	O	13	GLU

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Mol	Chain	Res	Type
20	T	90	ALA
3	C	76	ILE
11	K	25	PRO
13	M	5	GLY
14	N	12	THR
9	I	7	GLY
2	B	159	VAL
2	B	208	ILE
3	C	170	GLY
17	Q	32	GLY
2	B	188	PRO
9	I	43	VAL
13	M	3	ILE
2	B	145	GLY
13	M	122	ALA

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	202/220 (92%)	181 (90%)	21 (10%)	7	27
3	C	160/188 (85%)	148 (92%)	12 (8%)	13	43
4	D	180/180 (100%)	168 (93%)	12 (7%)	16	49
5	E	115/122 (94%)	103 (90%)	12 (10%)	7	27
6	F	90/90 (100%)	85 (94%)	5 (6%)	21	56
7	G	126/126 (100%)	122 (97%)	4 (3%)	39	74
8	H	119/119 (100%)	108 (91%)	11 (9%)	9	34
9	I	98/99 (99%)	87 (89%)	11 (11%)	6	24
10	J	88/91 (97%)	82 (93%)	6 (7%)	16	48
11	K	90/99 (91%)	80 (89%)	10 (11%)	6	25
12	L	104/109 (95%)	93 (89%)	11 (11%)	6	26
13	M	100/101 (99%)	92 (92%)	8 (8%)	12	40

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	N	49/49 (100%)	42 (86%)	7 (14%)	3	15
15	O	79/79 (100%)	73 (92%)	6 (8%)	13	43
16	P	72/74 (97%)	66 (92%)	6 (8%)	11	39
17	Q	96/96 (100%)	90 (94%)	6 (6%)	18	51
18	R	64/77 (83%)	60 (94%)	4 (6%)	18	51
19	S	71/79 (90%)	64 (90%)	7 (10%)	8	30
20	T	76/82 (93%)	67 (88%)	9 (12%)	5	22
21	V	19/21 (90%)	19 (100%)	0	100	100
All	All	1998/2101 (95%)	1830 (92%)	168 (8%)	11	38

All (168) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	2	LYS
2	B	3	GLU
2	B	17	ARG
2	B	18	TRP
2	B	19	ASN
2	B	46	GLU
2	B	47	ARG
2	B	54	ASP
2	B	55	LEU
2	B	63	LEU
2	B	76	ARG
2	B	88	ASN
2	B	90	ARG
2	B	107	HIS
2	B	108	ARG
2	B	151	ARG
2	B	172	ARG
2	B	181	LEU
2	B	189	ASP
2	B	194	ILE
2	B	205	ILE
3	C	2	ASN
3	C	4	ILE
3	C	25	LYS
3	C	51	LEU
3	C	55	ASP

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
3	C	166	TRP
3	C	175	HIS
3	C	177	LEU
3	C	178	ARG
3	C	187	LEU
3	C	191	THR
3	C	203	LEU
4	D	9	ARG
4	D	28	PRO
4	D	49	ARG
4	D	57	LEU
4	D	61	GLN
4	D	73	GLN
4	D	106	ARG
4	D	121	ARG
4	D	156	LEU
4	D	191	GLU
4	D	198	ASN
4	D	200	GLN
5	E	8	LEU
5	E	12	THR
5	E	37	VAL
5	E	39	LEU
5	E	69	ASN
5	E	71	THR
5	E	75	GLU
5	E	76	ILE
5	E	85	ILE
5	E	112	THR
5	E	116	THR
5	E	147	LEU
6	F	10	LEU
6	F	24	GLU
6	F	28	ARG
6	F	69	GLU
6	F	74	ASP
7	G	7	GLU
7	G	50	GLN
7	G	123	LEU
7	G	139	ASP
8	H	26	VAL
8	H	39	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
8	H	52	ASP
8	H	85	ARG
8	H	91	ARG
8	H	102	ARG
8	H	104	ARG
8	H	112	LEU
8	H	119	LEU
8	H	127	LEU
8	H	133	LEU
9	I	2	GLN
9	I	22	ASN
9	I	37	GLN
9	I	55	LEU
9	I	57	ARG
9	I	59	ASP
9	I	78	LEU
9	I	86	GLN
9	I	90	ASP
9	I	103	ARG
9	I	104	ASP
10	J	2	ILE
10	J	7	ARG
10	J	43	ARG
10	J	55	LYS
10	J	58	ARG
10	J	63	LEU
11	K	19	ILE
11	K	23	THR
11	K	25	PRO
11	K	44	ARG
11	K	71	ASP
11	K	74	VAL
11	K	82	GLU
11	K	86	ARG
11	K	110	ARG
11	K	112	LYS
12	L	8	ARG
12	L	13	LYS
12	L	29	ARG
12	L	38	THR
12	L	44	PRO
12	L	49	ARG

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
12	L	56	LEU
12	L	87	LYS
12	L	107	LYS
12	L	109	ARG
12	L	122	LYS
13	M	8	ILE
13	M	16	VAL
13	M	39	ASN
13	M	80	LEU
13	M	92	ARG
13	M	101	ARG
13	M	114	LYS
13	M	124	ARG
14	N	7	GLU
14	N	17	VAL
14	N	21	THR
14	N	25	ARG
14	N	30	ARG
14	N	40	ARG
14	N	43	LEU
15	O	30	LEU
15	O	33	LEU
15	O	56	LEU
15	O	69	LEU
15	O	80	LEU
15	O	82	GLU
16	P	2	VAL
16	P	42	ARG
16	P	53	VAL
16	P	62	VAL
16	P	67	THR
16	P	76	GLN
17	Q	3	LYS
17	Q	33	LYS
17	Q	37	ARG
17	Q	47	GLU
17	Q	58	ILE
17	Q	97	LEU
18	R	21	ASN
18	R	23	GLU
18	R	72	ARG
18	R	73	LYS

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Mol	Chain	Res	Type
19	S	7	LYS
19	S	12	ASP
19	S	15	LEU
19	S	25	LYS
19	S	36	ARG
19	S	61	TYR
19	S	62	ILE
20	T	3	LEU
20	T	29	LEU
20	T	50	ARG
20	T	61	LYS
20	T	66	HIS
20	T	67	LYS
20	T	68	ASN
20	T	77	LEU
20	T	86	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (53) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	13	HIS
2	B	19	ASN
2	B	88	ASN
2	B	140	GLN
2	B	218	GLN
3	C	2	ASN
3	C	5	HIS
3	C	36	GLN
3	C	106	GLN
3	C	122	GLN
3	C	138	GLN
3	C	161	GLN
3	C	175	HIS
3	C	180	ASN
4	D	41	GLN
4	D	61	GLN
4	D	122	HIS
4	D	160	ASN
4	D	198	ASN
5	E	16	GLN
5	E	69	ASN
6	F	16	GLN

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Mol	Chain	Res	Type
6	F	18	GLN
6	F	27	GLN
6	F	32	ASN
6	F	94	GLN
6	F	100	ASN
7	G	36	ASN
7	G	63	GLN
7	G	67	ASN
7	G	85	GLN
7	G	95	GLN
9	I	22	ASN
9	I	72	GLN
9	I	86	GLN
9	I	88	ASN
10	J	11	HIS
10	J	54	HIS
10	J	60	HIS
10	J	76	ASN
11	K	52	GLN
11	K	83	GLN
11	K	107	ASN
12	L	45	ASN
12	L	71	HIS
13	M	11	ASN
13	M	39	ASN
15	O	36	ASN
15	O	45	HIS
15	O	52	HIS
17	Q	15	GLN
18	R	21	ASN
19	S	14	HIS

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1510/1521 (99%)	247 (16%)	60 (3%)
22	W	3/6 (50%)	0	0
23	Z	14/16 (87%)	0	0
All	All	1527/1543 (98%)	247 (16%)	60 (3%)

All (247) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	6	G
1	A	9	G
1	A	32	A
1	A	33	A
1	A	36	C
1	A	39	G
1	A	47	C
1	A	48	C
1	A	51	A
1	A	52	G
1	A	60	A
1	A	61	G
1	A	101	A
1	A	110	C
1	A	121	C
1	A	131	C
1	A	160	A
1	A	163	C
1	A	168	G
1	A	174	C
1	A	178	C
1	A	182	U
1	A	189	G
1	A	189(G)	G
1	A	189(H)	G
1	A	189(I)	G
1	A	195	A
1	A	197	A
1	A	198	G
1	A	202	U
1	A	203	U
1	A	204	U
1	A	216	G
1	A	246	A
1	A	247	G
1	A	250	A
1	A	266	G
1	A	267	C
1	A	277	C
1	A	278	G
1	A	281	G
1	A	289	G
1	A	306	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	321	A
1	A	328	C
1	A	329	A
1	A	345	C
1	A	351	G
1	A	352	C
1	A	353	A
1	A	354	G
1	A	366	C
1	A	367	U
1	A	368	U
1	A	373	A
1	A	388	G
1	A	393	A
1	A	403	C
1	A	406	G
1	A	411	A
1	A	412	A
1	A	413	G
1	A	421	U
1	A	422	C
1	A	423	G
1	A	429	U
1	A	439	A
1	A	448	A
1	A	452	A
1	A	453	A
1	A	461	A
1	A	470	C
1	A	474	G
1	A	475	G
1	A	496	A
1	A	498	U
1	A	511	C
1	A	512	U
1	A	518	C
1	A	519	C
1	A	531	U
1	A	532	A
1	A	533	A
1	A	534	U
1	A	535	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	547	A
1	A	548	G
1	A	559	A
1	A	572	A
1	A	573	A
1	A	574	A
1	A	575	G
1	A	576	G
1	A	577	G
1	A	588	G
1	A	596	C
1	A	607	A
1	A	608	A
1	A	648	A
1	A	653	A
1	A	665	A
1	A	686	U
1	A	687	A
1	A	688	G
1	A	701	C
1	A	702	A
1	A	703	G
1	A	721	G
1	A	722	A
1	A	723	U
1	A	730	G
1	A	731	G
1	A	734	G
1	A	753	A
1	A	754	C
1	A	755	G
1	A	777	A
1	A	792	A
1	A	793	U
1	A	794	A
1	A	817	C
1	A	819	A
1	A	820	U
1	A	821	G
1	A	828	A
1	A	840	C
1	A	841	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	859	A
1	A	870	U
1	A	871	U
1	A	872	A
1	A	873	A
1	A	885	G
1	A	889	A
1	A	902	G
1	A	914	A
1	A	925	G
1	A	926	G
1	A	927	G
1	A	934	C
1	A	935	A
1	A	960	U
1	A	969	A
1	A	971	G
1	A	974	A
1	A	975	A
1	A	976	G
1	A	977	A
1	A	992	U
1	A	993	G
1	A	994	A
1	A	998	G
1	A	1001	A
1	A	1001(A)	G
1	A	1002	G
1	A	1018	C
1	A	1019	C
1	A	1020	U
1	A	1026	G
1	A	1027	C
1	A	1030	C
1	A	1042	G
1	A	1043	C
1	A	1049	U
1	A	1050	G
1	A	1053	G
1	A	1054	C
1	A	1065	U
1	A	1067	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	1068	G
1	A	1081	G
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	1102	A
1	A	1109	C
1	A	1122	U
1	A	1123	A
1	A	1124	G
1	A	1125	U
1	A	1126	U
1	A	1127	G
1	A	1129	C
1	A	1130	A
1	A	1131	G
1	A	1137	C
1	A	1138	G
1	A	1139	G
1	A	1140	C
1	A	1145	C
1	A	1157	A
1	A	1159	U
1	A	1160	G
1	A	1169	A
1	A	1183	A
1	A	1184	G
1	A	1190	G
1	A	1196	U
1	A	1197	G
1	A	1212	U
1	A	1213	A
1	A	1225	A
1	A	1226	C
1	A	1227	A
1	A	1238	A
1	A	1248	A
1	A	1253	G
1	A	1257	U
1	A	1260	C
1	A	1277	C
1	A	1280	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	1287	A
1	A	1288	A
1	A	1289	A
1	A	1300	G
1	A	1317	C
1	A	1320	C
1	A	1346	A
1	A	1347	G
1	A	1353	G
1	A	1364	U
1	A	1365	G
1	A	1374	A
1	A	1379	G
1	A	1381	U
1	A	1401	G
1	A	1419	G
1	A	1442	G
1	A	1442(A)	G
1	A	1442(B)	A
1	A	1447	A
1	A	1452	C
1	A	1456	G
1	A	1475	G
1	A	1480	G
1	A	1481	U
1	A	1492	A
1	A	1494	G
1	A	1497	G
1	A	1504	G
1	A	1506	U
1	A	1517	G
1	A	1520	G
1	A	1529	G
1	A	1530	G
1	A	1533	C
1	A	1540	U

All (60) RNA pucker outliers are listed below:

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	35	G
1	A	51	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	60	A
1	A	109	A
1	A	181	G
1	A	189(F)	U
1	A	189(G)	G
1	A	189(H)	G
1	A	246	A
1	A	277	C
1	A	305	G
1	A	351	G
1	A	353	A
1	A	366	C
1	A	367	U
1	A	412	A
1	A	421	U
1	A	438	G
1	A	474	G
1	A	518	C
1	A	532	A
1	A	533	A
1	A	573	A
1	A	575	G
1	A	687	A
1	A	701	C
1	A	702	A
1	A	721	G
1	A	730	G
1	A	733	A
1	A	753	A
1	A	792	A
1	A	793	U
1	A	871	U
1	A	872	A
1	A	884	U
1	A	925	G
1	A	974	A
1	A	975	A
1	A	992	U
1	A	1001	A
1	A	1017	G
1	A	1018	C
1	A	1042	G

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Mol	Chain	Res	Type
1	A	1049	U
1	A	1053	G
1	A	1067	A
1	A	1101	A
1	A	1122	U
1	A	1124	G
1	A	1127	G
1	A	1128	C
1	A	1182	G
1	A	1183	A
1	A	1226	C
1	A	1346	A
1	A	1364	U
1	A	1400	C
1	A	1447	A
1	A	1452	C

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 224 ligands modelled in this entry, 223 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
26	M5Z	A	2733	24	56,56,56	1.36	11 (19%)	77,82,82	0.92	3 (3%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
26	M5Z	A	2733	24	-	6/21/106/106	0/6/6/6

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	A	2733	M5Z	C26-C16	3.28	1.45	1.38
26	A	2733	M5Z	C52-C42	2.67	1.57	1.52
26	A	2733	M5Z	O54-C14	2.47	1.48	1.41
26	A	2733	M5Z	C56-C46	2.45	1.44	1.38
26	A	2733	M5Z	O61-CBJ	2.35	1.48	1.41
26	A	2733	M5Z	C56-C66	2.18	1.43	1.38
26	A	2733	M5Z	C66-C16	2.16	1.43	1.38
26	A	2733	M5Z	C36-C26	2.08	1.43	1.38
26	A	2733	M5Z	O11-C42	2.07	1.49	1.43
26	A	2733	M5Z	C14-C24	2.06	1.56	1.52
26	A	2733	M5Z	O51-C11	2.02	1.47	1.41

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	A	2733	M5Z	C14-O33-C3'	-2.64	111.42	117.96
26	A	2733	M5Z	O54-C54-C64	2.31	110.31	106.01
26	A	2733	M5Z	O11-C42-C52	2.00	112.57	107.48

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
26	A	2733	M5Z	C52-C42-O11-C11
26	A	2733	M5Z	C32-C42-O11-C11
26	A	2733	M5Z	O54-C14-O33-C3'
26	A	2733	M5Z	C26-C16-C45-C35
26	A	2733	M5Z	C66-C16-C45-C35
26	A	2733	M5Z	C42-C52-O52-C13

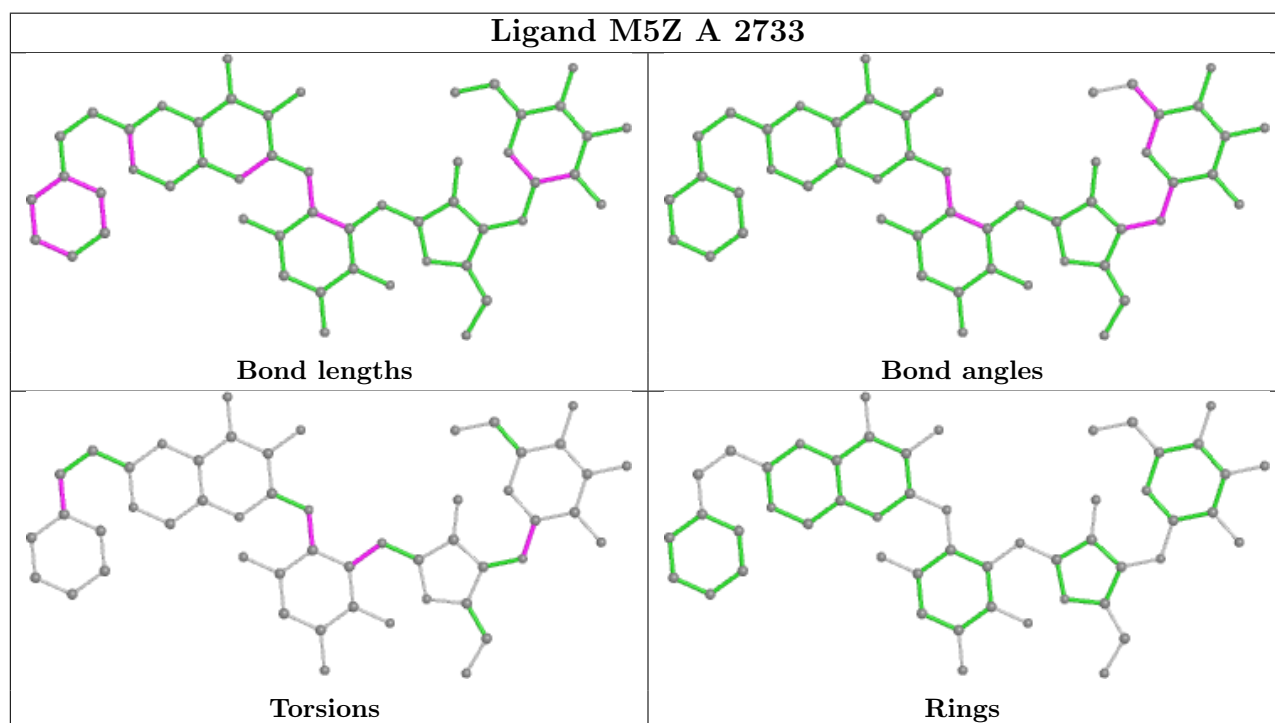
There are no ring outliers.

1 monomer is involved in 3 short contacts:



Mol	Chain	Res	Type	Clashes	Symm-Clashes
26	A	2733	M5Z	3	0

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



## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data i

### 6.1 Protein, DNA and RNA chains i

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	1512/1521 (99%)	-0.18	12 (0%) 86 65	38, 71, 142, 200	0
2	B	235/256 (91%)	-0.02	10 (4%) 35 13	54, 100, 159, 182	0
3	C	207/239 (86%)	-0.22	1 (0%) 91 75	53, 90, 134, 166	0
4	D	208/208 (100%)	-0.23	6 (2%) 51 23	54, 87, 138, 186	0
5	E	151/161 (93%)	-0.45	0 100 100	39, 62, 98, 156	0
6	F	101/101 (100%)	-0.25	0 100 100	69, 97, 133, 160	0
7	G	155/155 (100%)	-0.35	2 (1%) 77 51	56, 85, 136, 172	0
8	H	138/138 (100%)	-0.48	0 100 100	40, 61, 92, 139	0
9	I	127/128 (99%)	-0.12	1 (0%) 86 65	46, 100, 135, 185	0
10	J	99/104 (95%)	0.48	5 (5%) 28 10	49, 121, 182, 196	0
11	K	119/129 (92%)	-0.16	2 (1%) 70 41	41, 74, 113, 163	0
12	L	125/132 (94%)	-0.23	3 (2%) 59 30	37, 67, 111, 196	0
13	M	125/126 (99%)	0.40	10 (8%) 12 4	60, 88, 153, 184	0
14	N	60/60 (100%)	-0.08	0 100 100	51, 81, 113, 176	0
15	O	88/88 (100%)	-0.27	1 (1%) 80 56	51, 76, 120, 170	0
16	P	84/88 (95%)	-0.40	0 100 100	48, 66, 96, 173	0
17	Q	104/104 (100%)	0.03	5 (4%) 30 11	42, 71, 123, 201	0
18	R	73/88 (82%)	-0.18	2 (2%) 54 26	53, 82, 137, 194	0
19	S	81/92 (88%)	0.07	3 (3%) 41 17	67, 106, 154, 188	0
20	T	99/106 (93%)	-0.23	2 (2%) 65 36	45, 75, 112, 200	0
21	V	25/26 (96%)	0.01	0 100 100	51, 76, 111, 146	0
22	W	4/6 (66%)	-0.16	0 100 100	79, 80, 80, 105	0
23	Z	15/16 (93%)	0.12	0 100 100	74, 110, 176, 185	0
All	All	3935/4072 (96%)	-0.16	65 (1%) 70 41	37, 77, 147, 201	0

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
13	M	122	ALA	14.2
11	K	119	SER	12.5
13	M	120	LYS	11.8
13	M	121	LYS	9.4
17	Q	104	ALA	9.2
17	Q	102	GLY	9.0
13	M	123	PRO	8.9
12	L	125	ALA	8.9
17	Q	101	GLY	8.9
17	Q	103	LYS	8.9
13	M	119	LYS	7.7
13	M	124	ARG	7.3
1	A	1001(A)	G	6.7
13	M	125	LYS	6.5
2	B	128	GLU	5.2
1	A	1540	U	4.9
2	B	125	PRO	4.9
4	D	34	ARG	4.6
13	M	6	VAL	4.6
4	D	36	PRO	4.4
10	J	70	VAL	4.3
1	A	1533	C	4.1
1	A	1129	C	3.6
1	A	202	U	3.6
1	A	1539	C	3.5
13	M	118	GLY	3.5
10	J	32	VAL	3.5
2	B	127	LYS	3.5
19	S	3	ARG	3.4
12	L	124	ALA	3.4
2	B	129	GLN	3.4
7	G	155	TRP	3.3
11	K	118	ALA	3.0
10	J	31	GLN	3.0
10	J	3	ARG	2.9
1	A	1442(B)	A	2.8
10	J	35	PRO	2.8
13	M	117	ALA	2.7
1	A	723	U	2.7
17	Q	100	ARG	2.7
20	T	96	GLY	2.6
9	I	127	ARG	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	1257	U	2.6
4	D	22	GLY	2.6
18	R	1	PRO	2.5
4	D	35	ARG	2.5
2	B	116	PHE	2.5
4	D	32	MET	2.5
19	S	49	ILE	2.5
20	T	94	GLY	2.4
18	R	2	SER	2.4
1	A	1031	G	2.4
1	A	1003	G	2.4
12	L	15	ARG	2.3
19	S	27	GLU	2.3
4	D	44	GLN	2.3
2	B	29	GLU	2.3
15	O	88	GLY	2.3
2	B	232	LEU	2.2
2	B	122	GLU	2.2
7	G	80	GLY	2.1
1	A	1034	G	2.1
2	B	126	LYS	2.1
2	B	124	ARG	2.1
3	C	1	GLY	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

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

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
24	MG	A	2687	1/1	0.10	0.47	95,95,95,95	0
24	MG	A	2694	1/1	0.36	0.68	81,81,81,81	0
24	MG	A	2728	1/1	0.37	0.47	99,99,99,99	0
24	MG	A	2644	1/1	0.39	0.85	95,95,95,95	0
24	MG	A	2589	1/1	0.39	0.23	86,86,86,86	0
24	MG	A	2697	1/1	0.45	0.81	72,72,72,72	0
24	MG	F	1102	1/1	0.46	0.12	80,80,80,80	0
24	MG	A	2545	1/1	0.48	0.19	66,66,66,66	0
24	MG	A	2615	1/1	0.48	0.29	68,68,68,68	0
24	MG	A	2657	1/1	0.51	0.53	61,61,61,61	0
24	MG	A	2717	1/1	0.51	0.25	92,92,92,92	0
24	MG	A	2645	1/1	0.53	0.33	72,72,72,72	0
24	MG	A	2716	1/1	0.54	0.22	81,81,81,81	0
24	MG	A	2654	1/1	0.58	0.19	66,66,66,66	0
24	MG	A	2681	1/1	0.59	0.54	74,74,74,74	0
25	K	A	2668	1/1	0.60	0.22	111,111,111,111	0
24	MG	A	2613	1/1	0.61	0.26	79,79,79,79	0
24	MG	A	2549	1/1	0.62	0.48	81,81,81,81	0
24	MG	A	2708	1/1	0.63	0.29	75,75,75,75	0
24	MG	A	2656	1/1	0.63	0.40	67,67,67,67	0
24	MG	A	2689	1/1	0.63	0.33	86,86,86,86	0
24	MG	A	2727	1/1	0.64	0.69	77,77,77,77	0
24	MG	A	2679	1/1	0.65	0.47	72,72,72,72	0
24	MG	A	2732	1/1	0.65	0.44	76,76,76,76	0
25	K	A	2675	1/1	0.65	0.27	116,116,116,116	0
24	MG	A	2554	1/1	0.66	0.30	69,69,69,69	0
24	MG	A	2688	1/1	0.66	0.28	68,68,68,68	0
24	MG	A	2580	1/1	0.67	0.18	65,65,65,65	0
24	MG	A	2611	1/1	0.68	0.19	52,52,52,52	0
24	MG	A	2643	1/1	0.68	0.20	48,48,48,48	0
24	MG	A	2704	1/1	0.68	0.17	55,55,55,55	0
25	K	A	2670	1/1	0.68	0.15	89,89,89,89	0
24	MG	A	2553	1/1	0.68	0.23	41,41,41,41	0
24	MG	A	2712	1/1	0.69	0.23	55,55,55,55	0
24	MG	A	2623	1/1	0.70	0.12	49,49,49,49	0
24	MG	A	2700	1/1	0.70	0.44	77,77,77,77	0
25	K	A	2676	1/1	0.70	0.20	106,106,106,106	0
24	MG	A	2551	1/1	0.71	0.73	68,68,68,68	0
24	MG	A	2572	1/1	0.72	0.39	76,76,76,76	0
24	MG	A	2570	1/1	0.72	0.46	76,76,76,76	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
24	MG	A	2707	1/1	0.72	0.44	80,80,80,80	0
25	K	A	2677	1/1	0.72	0.22	126,126,126,126	0
24	MG	A	2599	1/1	0.73	0.29	66,66,66,66	0
24	MG	A	2560	1/1	0.73	0.19	64,64,64,64	0
24	MG	A	2685	1/1	0.73	0.24	77,77,77,77	0
24	MG	A	2646	1/1	0.73	0.30	76,76,76,76	0
25	K	A	2674	1/1	0.74	0.13	105,105,105,105	0
24	MG	N	1062	1/1	0.74	0.34	60,60,60,60	0
24	MG	A	2698	1/1	0.74	0.41	78,78,78,78	0
24	MG	A	2628	1/1	0.74	0.31	65,65,65,65	0
24	MG	A	2726	1/1	0.75	0.37	74,74,74,74	0
24	MG	A	2571	1/1	0.75	0.75	72,72,72,72	0
24	MG	A	2663	1/1	0.75	0.28	65,65,65,65	0
24	MG	A	2575	1/1	0.75	0.35	50,50,50,50	0
24	MG	A	2563	1/1	0.76	0.38	62,62,62,62	0
25	K	A	2678	1/1	0.76	0.32	93,93,93,93	0
24	MG	A	2633	1/1	0.77	0.32	51,51,51,51	0
24	MG	A	2719	1/1	0.77	0.36	62,62,62,62	0
24	MG	A	2593	1/1	0.77	0.51	73,73,73,73	0
24	MG	A	2631	1/1	0.78	0.21	58,58,58,58	0
24	MG	A	2705	1/1	0.78	0.31	66,66,66,66	0
24	MG	B	1236	1/1	0.78	0.24	76,76,76,76	0
24	MG	A	2680	1/1	0.79	0.63	71,71,71,71	0
25	K	A	2667	1/1	0.80	0.23	112,112,112,112	0
24	MG	A	2652	1/1	0.80	0.19	79,79,79,79	0
24	MG	A	2662	1/1	0.80	0.29	75,75,75,75	0
24	MG	A	2568	1/1	0.80	0.59	73,73,73,73	0
24	MG	A	2714	1/1	0.80	0.26	61,61,61,61	0
24	MG	A	2655	1/1	0.80	0.14	57,57,57,57	0
24	MG	A	2595	1/1	0.80	0.81	92,92,92,92	0
24	MG	A	2691	1/1	0.80	0.28	66,66,66,66	0
24	MG	A	2624	1/1	0.81	0.33	53,53,53,53	0
24	MG	A	2555	1/1	0.81	0.41	81,81,81,81	0
24	MG	A	2622	1/1	0.81	0.36	64,64,64,64	0
24	MG	Q	1105	1/1	0.81	0.08	67,67,67,67	0
24	MG	A	2729	1/1	0.81	1.13	66,66,66,66	0
24	MG	A	2586	1/1	0.81	0.27	87,87,87,87	0
24	MG	A	2642	1/1	0.82	0.20	58,58,58,58	0
24	MG	A	2562	1/1	0.82	0.49	46,46,46,46	0
24	MG	A	2650	1/1	0.82	0.44	77,77,77,77	0
24	MG	A	2620	1/1	0.82	0.20	52,52,52,52	0
24	MG	A	2660	1/1	0.82	0.34	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
24	MG	A	2612	1/1	0.83	0.26	60,60,60,60	0
24	MG	A	2616	1/1	0.83	0.19	50,50,50,50	0
24	MG	A	2617	1/1	0.83	0.27	51,51,51,51	0
24	MG	Q	2001	1/1	0.83	0.22	64,64,64,64	0
24	MG	E	1152	1/1	0.84	0.19	64,64,64,64	0
24	MG	A	2693	1/1	0.84	1.21	71,71,71,71	0
25	K	A	2672	1/1	0.84	0.63	139,139,139,139	0
24	MG	H	1139	1/1	0.84	0.22	59,59,59,59	0
24	MG	A	2559	1/1	0.84	0.36	73,73,73,73	0
24	MG	A	2635	1/1	0.84	0.26	41,41,41,41	0
24	MG	A	2603	1/1	0.84	0.20	95,95,95,95	0
24	MG	D	1210	1/1	0.84	0.13	54,54,54,54	0
24	MG	A	2701	1/1	0.85	0.35	67,67,67,67	0
25	K	A	2671	1/1	0.85	0.15	109,109,109,109	0
24	MG	A	2638	1/1	0.85	0.31	68,68,68,68	0
24	MG	A	2721	1/1	0.85	0.14	78,78,78,78	0
24	MG	A	2607	1/1	0.86	0.60	61,61,61,61	0
24	MG	A	2625	1/1	0.86	0.14	61,61,61,61	0
24	MG	A	2557	1/1	0.86	0.68	78,78,78,78	0
24	MG	A	2744	1/1	0.86	0.54	75,75,75,75	0
24	MG	A	2699	1/1	0.86	0.23	46,46,46,46	0
24	MG	A	2578	1/1	0.86	0.53	60,60,60,60	0
24	MG	E	1151	1/1	0.86	0.46	71,71,71,71	0
24	MG	A	2621	1/1	0.86	0.13	42,42,42,42	0
24	MG	A	2648	1/1	0.86	0.19	65,65,65,65	0
24	MG	A	2558	1/1	0.86	0.44	63,63,63,63	0
24	MG	M	1126	1/1	0.86	0.12	61,61,61,61	0
24	MG	A	2606	1/1	0.86	0.20	48,48,48,48	0
24	MG	A	2636	1/1	0.87	0.18	48,48,48,48	0
24	MG	A	2684	1/1	0.87	1.34	89,89,89,89	0
24	MG	A	2647	1/1	0.87	0.22	58,58,58,58	0
24	MG	A	2659	1/1	0.87	0.25	60,60,60,60	0
24	MG	A	2601	1/1	0.87	0.13	45,45,45,45	0
24	MG	A	2702	1/1	0.87	0.25	98,98,98,98	0
24	MG	A	2725	1/1	0.87	0.28	79,79,79,79	0
24	MG	A	2550	1/1	0.87	0.36	65,65,65,65	0
24	MG	A	2547	1/1	0.87	0.67	61,61,61,61	0
24	MG	A	2597	1/1	0.87	0.29	44,44,44,44	0
24	MG	A	2552	1/1	0.87	0.17	61,61,61,61	0
24	MG	A	2696	1/1	0.88	0.18	74,74,74,74	0
24	MG	A	2610	1/1	0.88	0.52	63,63,63,63	0
24	MG	A	2626	1/1	0.88	0.31	90,90,90,90	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
24	MG	A	2743	1/1	0.88	0.89	70,70,70,70	0
24	MG	A	2576	1/1	0.88	0.60	65,65,65,65	0
24	MG	A	2649	1/1	0.89	0.19	52,52,52,52	0
24	MG	A	2573	1/1	0.89	0.30	38,38,38,38	0
24	MG	A	2748	1/1	0.89	0.71	64,64,64,64	0
25	K	A	2673	1/1	0.89	0.18	96,96,96,96	0
24	MG	A	2751	1/1	0.89	0.73	69,69,69,69	0
24	MG	A	2548	1/1	0.89	0.31	20,20,20,20	0
24	MG	A	2564	1/1	0.89	0.50	60,60,60,60	0
24	MG	A	2692	1/1	0.89	0.22	55,55,55,55	0
24	MG	A	2741	1/1	0.89	0.83	66,66,66,66	0
24	MG	A	2742	1/1	0.90	0.34	69,69,69,69	0
24	MG	A	2724	1/1	0.90	1.11	51,51,51,51	0
24	MG	A	2658	1/1	0.90	0.40	48,48,48,48	0
24	MG	A	2594	1/1	0.90	0.23	57,57,57,57	0
24	MG	A	2740	1/1	0.90	0.35	74,74,74,74	0
24	MG	J	1099	1/1	0.90	0.23	61,61,61,61	0
24	MG	A	2722	1/1	0.90	0.25	75,75,75,75	0
24	MG	A	2730	1/1	0.91	0.62	69,69,69,69	0
24	MG	A	2556	1/1	0.91	0.54	55,55,55,55	0
24	MG	A	2737	1/1	0.91	0.64	64,64,64,64	0
24	MG	A	2579	1/1	0.91	0.46	63,63,63,63	0
24	MG	A	2619	1/1	0.91	0.10	49,49,49,49	0
24	MG	A	2629	1/1	0.91	0.20	63,63,63,63	0
24	MG	A	2641	1/1	0.91	0.27	35,35,35,35	0
24	MG	A	2600	1/1	0.91	0.42	60,60,60,60	0
24	MG	A	2546	1/1	0.92	0.90	80,80,80,80	0
24	MG	A	2709	1/1	0.92	0.44	66,66,66,66	0
25	K	A	2669	1/1	0.92	0.16	92,92,92,92	0
24	MG	A	2632	1/1	0.92	0.23	55,55,55,55	0
24	MG	A	2577	1/1	0.92	0.32	46,46,46,46	0
24	MG	A	2609	1/1	0.92	0.19	43,43,43,43	0
24	MG	A	2682	1/1	0.92	0.47	56,56,56,56	0
24	MG	K	1120	1/1	0.92	0.16	62,62,62,62	0
24	MG	A	2718	1/1	0.92	0.23	88,88,88,88	0
24	MG	A	2749	1/1	0.92	0.37	72,72,72,72	0
24	MG	A	2706	1/1	0.92	0.34	72,72,72,72	0
24	MG	A	2587	1/1	0.92	0.24	51,51,51,51	0
24	MG	A	2750	1/1	0.93	0.79	63,63,63,63	0
25	K	A	2666	1/1	0.93	0.14	87,87,87,87	0
24	MG	A	2590	1/1	0.93	0.14	66,66,66,66	0
24	MG	A	2695	1/1	0.93	0.28	101,101,101,101	0

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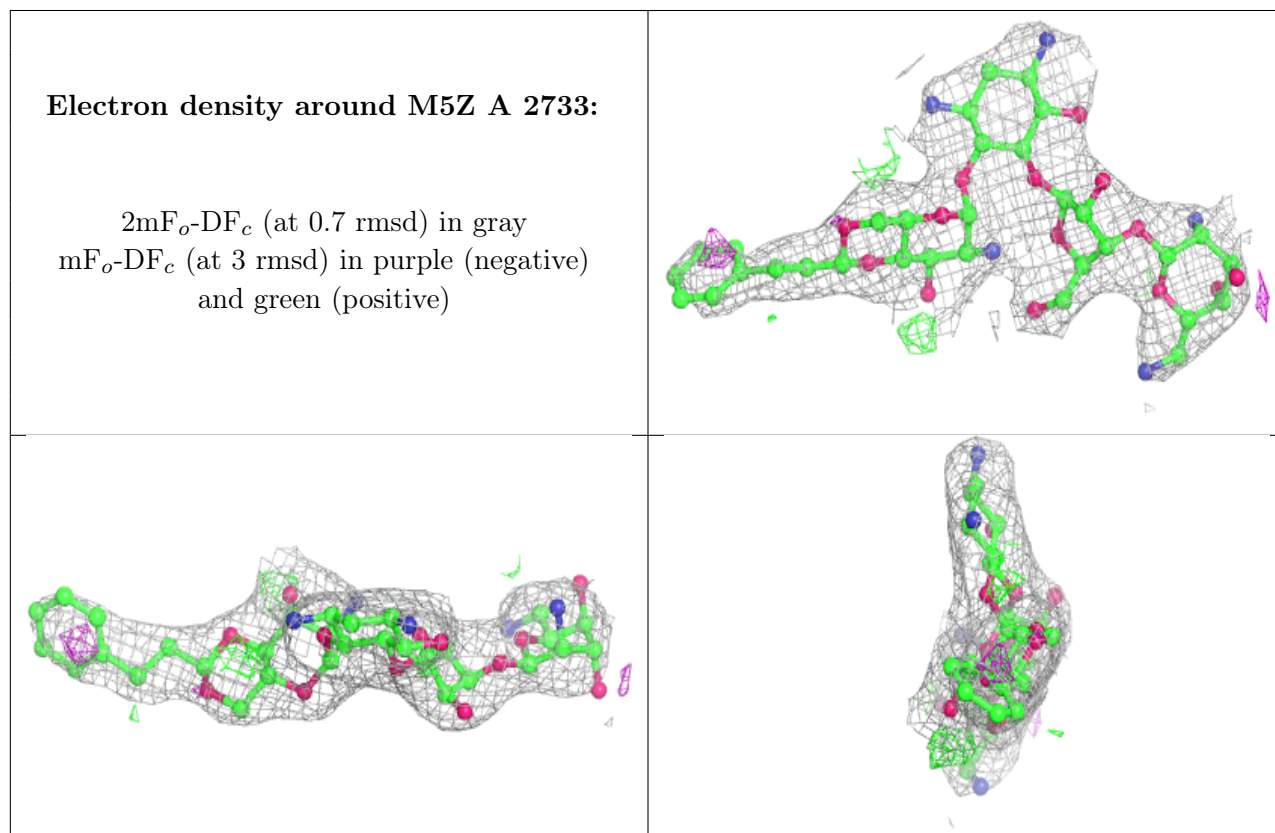
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
24	MG	A	2661	1/1	0.93	0.24	48,48,48,48	0
24	MG	A	2627	1/1	0.93	0.10	34,34,34,34	0
24	MG	A	2739	1/1	0.93	0.35	57,57,57,57	0
24	MG	A	2565	1/1	0.93	0.34	54,54,54,54	0
24	MG	A	2723	1/1	0.93	1.03	58,58,58,58	0
24	MG	A	2569	1/1	0.93	0.44	53,53,53,53	0
24	MG	A	2630	1/1	0.93	0.98	73,73,73,73	0
24	MG	A	2713	1/1	0.93	0.25	75,75,75,75	0
24	MG	A	2584	1/1	0.93	0.28	63,63,63,63	0
24	MG	A	2614	1/1	0.93	0.11	56,56,56,56	0
24	MG	A	2686	1/1	0.94	0.30	8,8,8,8	0
24	MG	A	2640	1/1	0.94	0.28	53,53,53,53	0
24	MG	A	2582	1/1	0.94	0.20	44,44,44,44	0
24	MG	A	2683	1/1	0.94	0.59	55,55,55,55	0
24	MG	A	2734	1/1	0.94	0.48	42,42,42,42	0
24	MG	A	2747	1/1	0.94	0.19	75,75,75,75	0
25	K	A	2665	1/1	0.94	0.13	87,87,87,87	0
24	MG	A	2574	1/1	0.94	0.41	49,49,49,49	0
24	MG	A	2634	1/1	0.94	0.30	62,62,62,62	0
24	MG	H	2001	1/1	0.94	0.58	74,74,74,74	0
26	M5Z	A	2733	51/51	0.94	0.23	51,61,76,78	0
24	MG	A	2736	1/1	0.95	0.53	65,65,65,65	0
24	MG	A	2710	1/1	0.95	0.56	68,68,68,68	0
24	MG	A	2711	1/1	0.95	0.21	70,70,70,70	0
24	MG	A	2639	1/1	0.95	0.19	37,37,37,37	0
24	MG	A	2604	1/1	0.95	0.19	48,48,48,48	0
24	MG	A	2664	1/1	0.95	0.35	64,64,64,64	0
24	MG	A	2715	1/1	0.95	0.23	52,52,52,52	0
24	MG	A	2605	1/1	0.95	0.48	50,50,50,50	0
24	MG	A	2745	1/1	0.95	0.64	62,62,62,62	0
24	MG	A	2583	1/1	0.95	0.23	41,41,41,41	0
24	MG	A	2581	1/1	0.95	0.58	53,53,53,53	0
24	MG	A	2731	1/1	0.95	0.73	66,66,66,66	0
24	MG	A	2618	1/1	0.95	0.10	34,34,34,34	0
24	MG	A	2608	1/1	0.95	0.18	43,43,43,43	0
24	MG	A	2746	1/1	0.96	0.94	57,57,57,57	0
24	MG	B	1235	1/1	0.96	0.19	74,74,74,74	0
24	MG	A	2567	1/1	0.96	0.37	56,56,56,56	0
24	MG	A	2690	1/1	0.96	0.28	72,72,72,72	0
24	MG	A	2596	1/1	0.96	0.23	33,33,33,33	0
24	MG	A	2591	1/1	0.96	0.52	50,50,50,50	0
24	MG	A	2720	1/1	0.97	0.12	61,61,61,61	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
24	MG	A	2588	1/1	0.97	0.34	54,54,54,54	0
24	MG	A	2566	1/1	0.97	0.38	49,49,49,49	0
24	MG	A	2651	1/1	0.97	0.14	71,71,71,71	0
24	MG	A	2585	1/1	0.97	0.72	62,62,62,62	0
24	MG	A	2703	1/1	0.97	0.30	55,55,55,55	0
24	MG	A	2653	1/1	0.97	0.23	28,28,28,28	0
24	MG	L	1125	1/1	0.97	0.17	55,55,55,55	0
24	MG	A	2598	1/1	0.97	0.42	69,69,69,69	0
24	MG	A	2637	1/1	0.98	0.08	19,19,19,19	0
24	MG	A	2738	1/1	0.98	0.66	51,51,51,51	0
24	MG	A	2592	1/1	0.98	0.14	47,47,47,47	0
24	MG	A	2735	1/1	0.98	0.35	41,41,41,41	0
24	MG	A	2561	1/1	0.98	0.41	38,38,38,38	0
27	ZN	D	1209	1/1	0.98	0.24	108,108,108,108	0
24	MG	A	2602	1/1	0.99	0.26	44,44,44,44	0
27	ZN	N	1061	1/1	0.99	0.13	124,124,124,124	0

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



## 6.5 Other polymers [i](#)

There are no such residues in this entry.