Full wwPDB X-ray Structure Validation Report (i)

Mar 23, 2024 – 04:26 PM EDT

PDB ID	:	1XNR
Title	:	Crystal Structure of an Inosine-Cytosine Wobble Base Pair in the Context of the Decoding Center
Authors	:	Murphy, F.V.; Ramakrishnan, V.
Deposited on	:	2004-10-05
Resolution	:	3.10 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

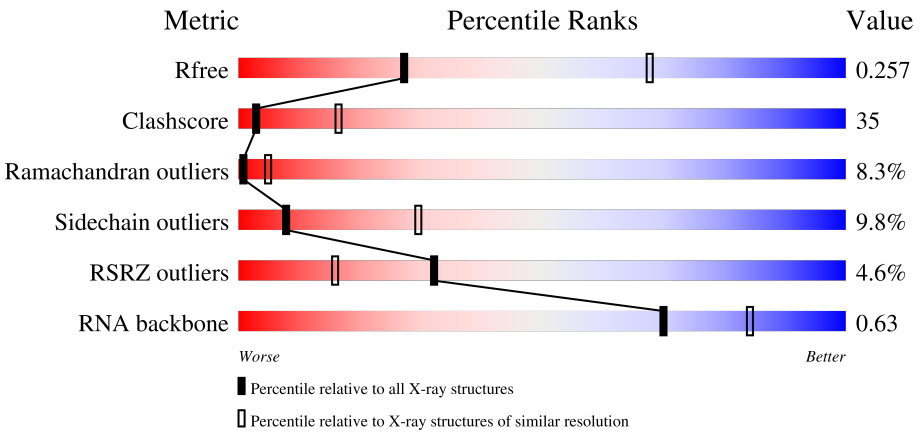
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1094 (3.10-3.10)
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)
RSRZ outliers	127900	1067 (3.10-3.10)
RNA backbone	3102	1116 (3.40-2.80)

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

Mol	Chain	Length	Quality of chain
1	A	1522	2% 32% 53% 12% • •
2	X	11	9% 64% 36%
3	W	4	25% 50% 50%
4	B	256	5% 16% 61% 12% • 9%

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Mol	Chain	Length	Quality of chain
5	C	239	3% 23% 49% 12% 14%
6	D	209	4% 44% 48% 7%
7	E	162	4% 28% 56% 9% 7%
8	F	101	% 44% 45% 11%
9	G	156	4% 30% 60% 8%
10	H	138	3% 43% 45% 10%
11	I	128	13% 23% 63% 12%
12	J	105	16% 16% 60% 14% 7%
13	K	129	3% 42% 43% 6% 8%
14	L	135	4% 28% 50% 13% 8%
15	M	126	9% 33% 48% 19%
16	N	61	21% 15% 69% 13%
17	O	89	2% 35% 48% 13%
18	P	88	10% 26% 61% 6% 6%
19	Q	105	6% 47% 41% 11%
20	R	88	2% 27% 50% 6% 17%
21	S	93	% 31% 49% 5% 14%
22	T	106	9% 38% 45% 10% 7%
23	V	27	22% 30% 44% 15% 11%

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
25	MG	A	1564	-	-	-	X
25	MG	A	1594	-	-	-	X
25	MG	A	1621	-	-	-	X
25	MG	X	500	-	-	-	X
25	MG	X	502	-	-	-	X

2 Entry composition (i)

There are 26 unique types of molecules in this entry. The entry contains 52075 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	1507	32380	14414	5990	10470	1506	0	0	0

- Molecule 2 is a RNA chain called Anticodon tRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
2	X	11	232	105	43	74	10	0	0	0

- Molecule 3 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
3	W	4	82	38	16	25	3	0	0	0

- Molecule 4 is a protein called 16S Ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	B	234	1900	1213	341	341	5	0	0	0

- Molecule 5 is a protein called 16S Ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
5	C	206	1612	1016	314	281	1	0	0	0

- Molecule 6 is a protein called 16S Ribosomal protein S4.

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

- Molecule 7 is a protein called 16S Ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
7	E	150	1146	724	217	201	4	0	0	0

- Molecule 8 is a protein called 16S Ribosomal protein S6.

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

- Molecule 9 is a protein called 16S Ribosomal protein S7.

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

- Molecule 10 is a protein called 16S Ribosomal protein S8.

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

- Molecule 11 is a protein called 16S Ribosomal protein S9.

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

- Molecule 12 is a protein called 16S Ribosomal protein S10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
12	J	98	792	498	156	137	1	0	0	0

- Molecule 13 is a protein called 16S Ribosomal protein S11.

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

- Molecule 14 is a protein called 16S Ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
14	L	124	970	611	195	163	1	0	0	0

- Molecule 15 is a protein called 16S Ribosomal protein S13.

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

- Molecule 16 is a protein called 16S Ribosomal protein S14.

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

- Molecule 17 is a protein called 16S Ribosomal protein S15.

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

- Molecule 18 is a protein called 16S Ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
18	P	83	700	443	139	117	1	0	0	0

- Molecule 19 is a protein called 16S Ribosomal protein S17.

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

- Molecule 20 is a protein called 16S Ribosomal protein S18.

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

- Molecule 21 is a protein called 16S Ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
21	S	80	647	414	119	112	2	0	0	0

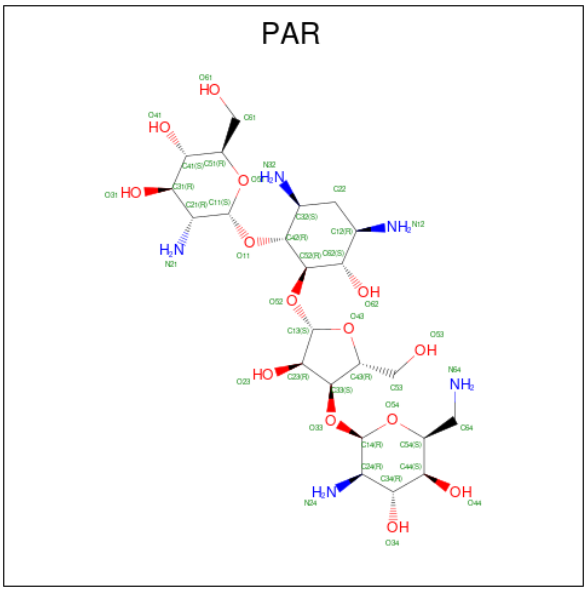
- Molecule 22 is a protein called 16S Ribosomal protein S20.

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

- Molecule 23 is a protein called 16S Ribosomal protein THX.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
23	V	24	208	128	50	30	0	0	0

- Molecule 24 is PAROMOMYCIN (three-letter code: PAR) (formula: $C_{23}H_{45}N_5O_{14}$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
24	A	1	42	23	5	14	0	0

- Molecule 25 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
25	A	104	104	104	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
25	X	3	3	3	0	0
			Total	Mg		
25	J	1	1	1	0	0

- Molecule 26 is ZINC ION (three-letter code: ZN) (formula: Zn).

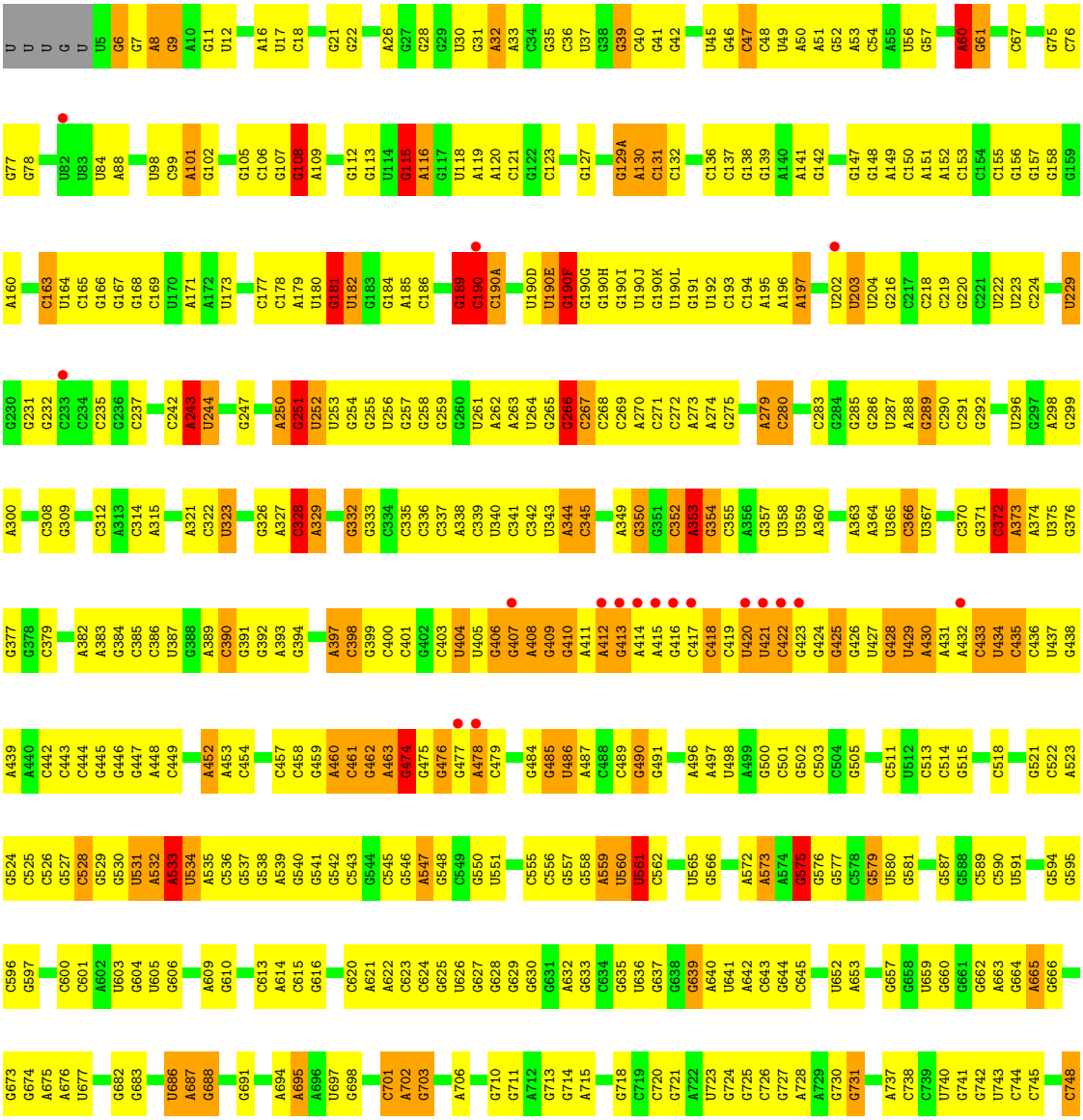
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
26	D	1	1	1	0	0
			Total	Zn		
26	N	1	1	1	0	0

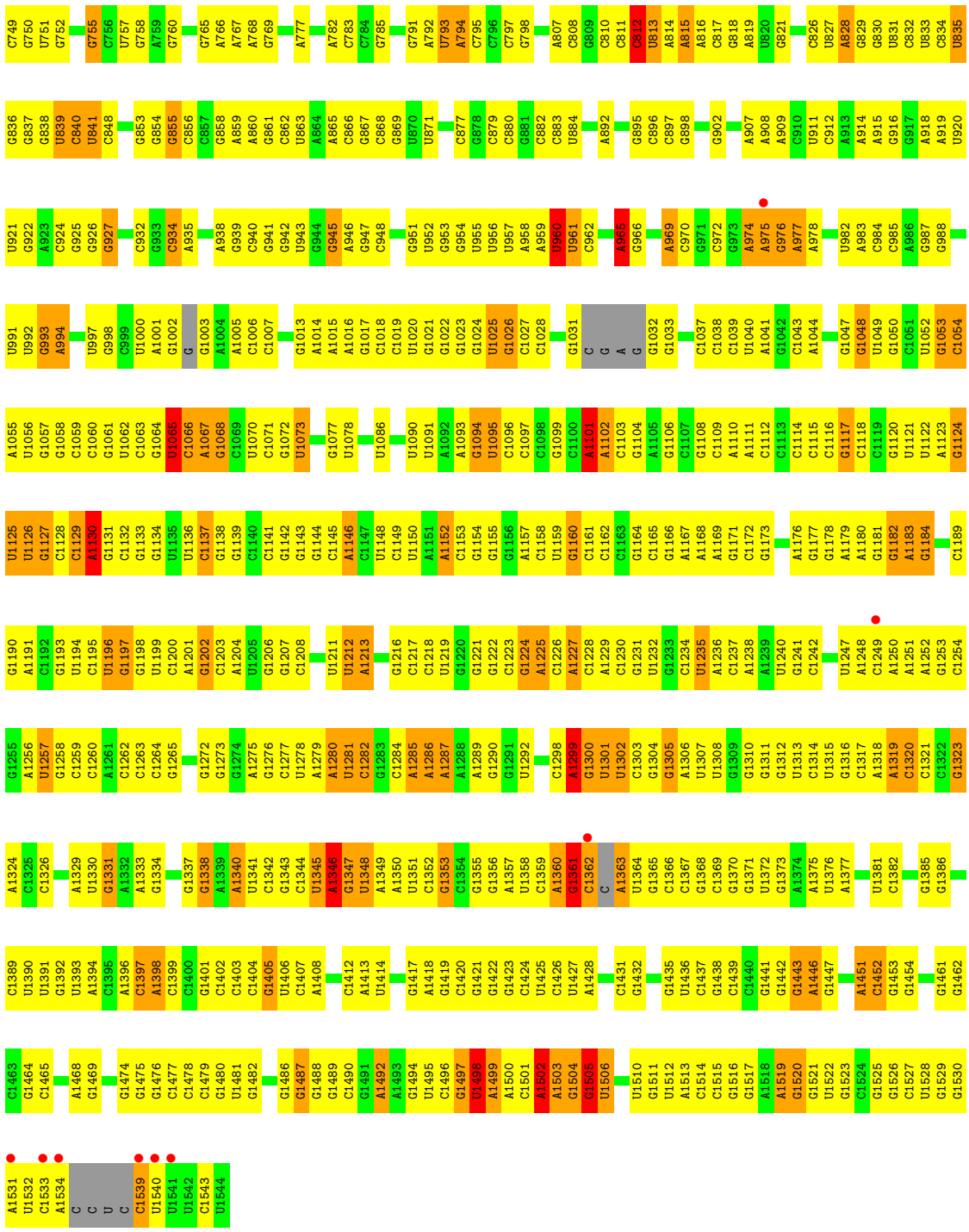
3 Residue-property plots (i)

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

- Molecule 1: 16S Ribosomal RNA

Chain A:





- Molecule 2: Anticodon tRNA

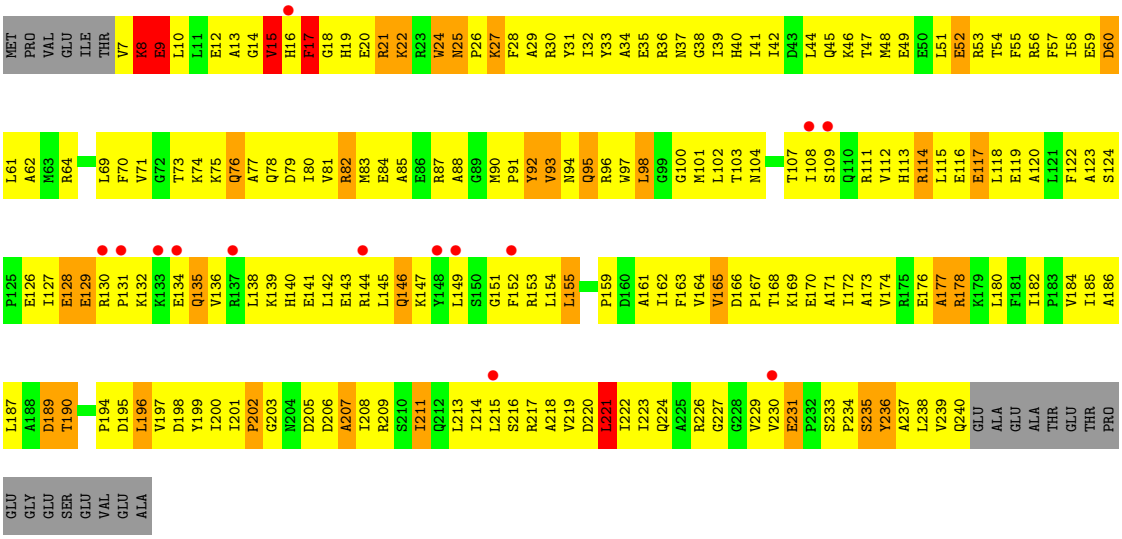
Chain X:

- Molecule 3: mRNA

Chain W: 25% 50% 50%

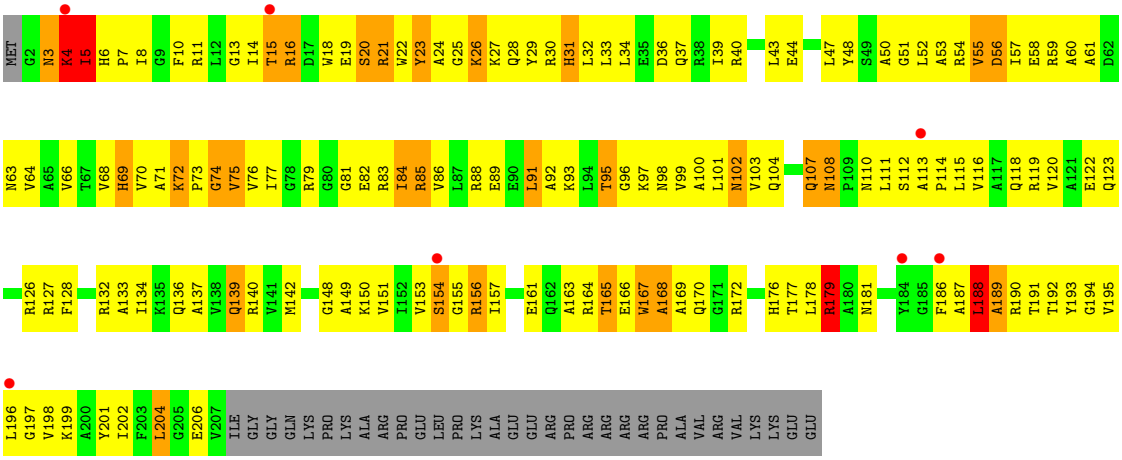
• Molecule 4: 16S Ribosomal protein S2

Chain B: 5% 16% 61% 12% • 9%



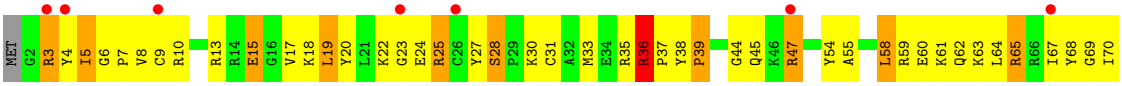
• Molecule 5: 16S Ribosomal protein S3

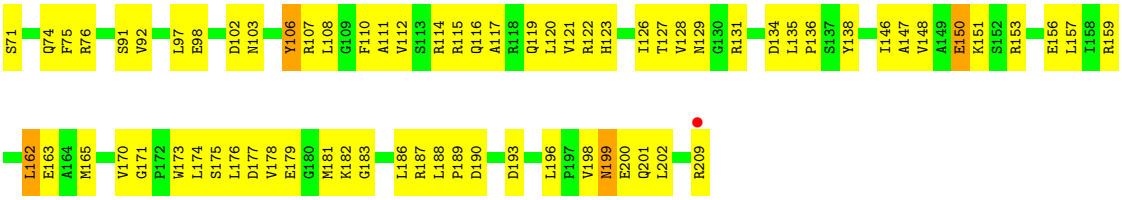
Chain C: 3% 23% 49% 12% • 14%



• Molecule 6: 16S Ribosomal protein S4

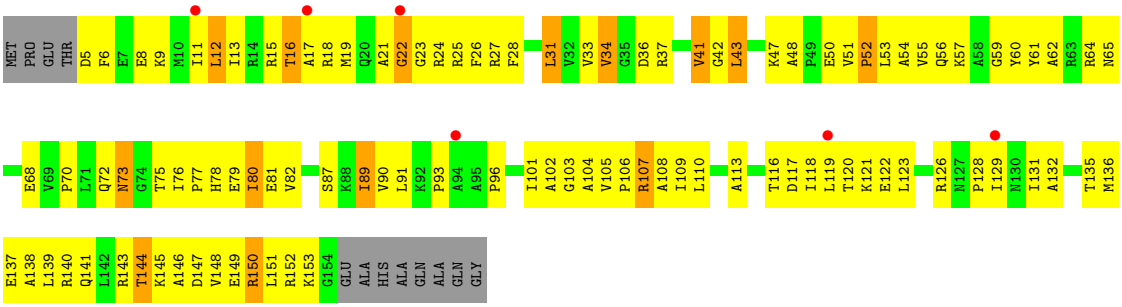
Chain D: 4% 44% 48% 7%





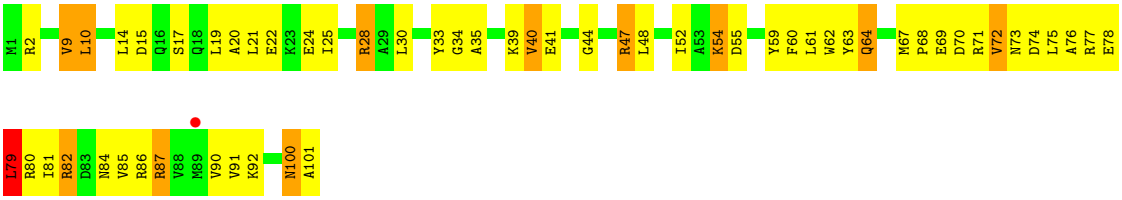
- Molecule 7: 16S Ribosomal protein S5

Chain E:



- Molecule 8: 16S Ribosomal protein S6

Chain F:

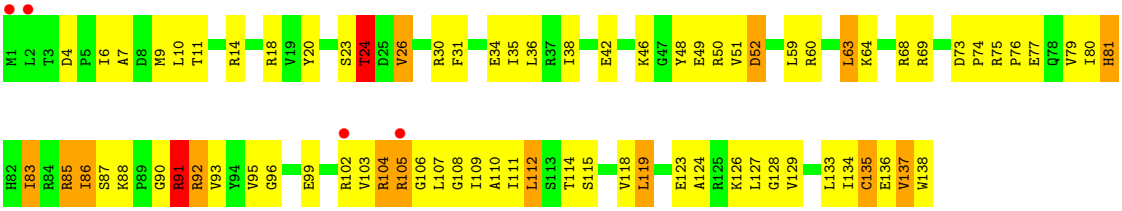


- Molecule 9: 16S Ribosomal protein S7

Chain G:

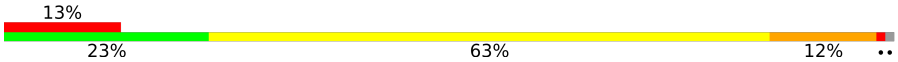
- Molecule 10: 16S Ribosomal protein S8

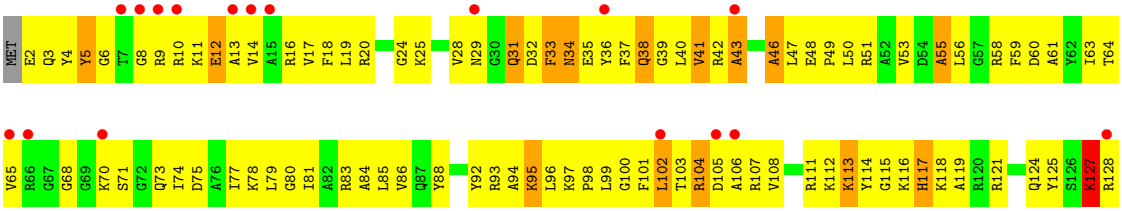
Chain H:



- Molecule 11: 16S Ribosomal protein S9

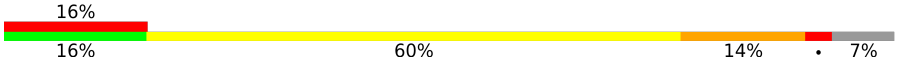
Chain I:

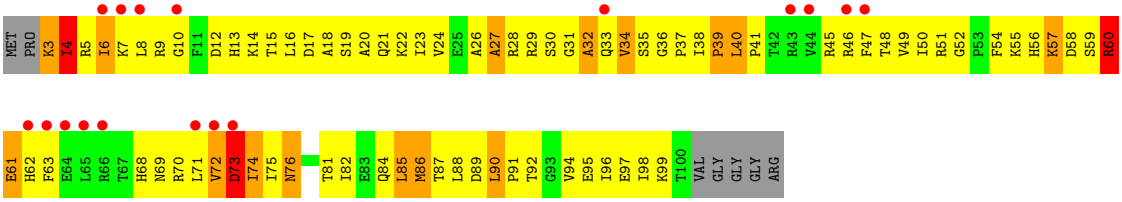




- Molecule 12: 16S Ribosomal protein S10

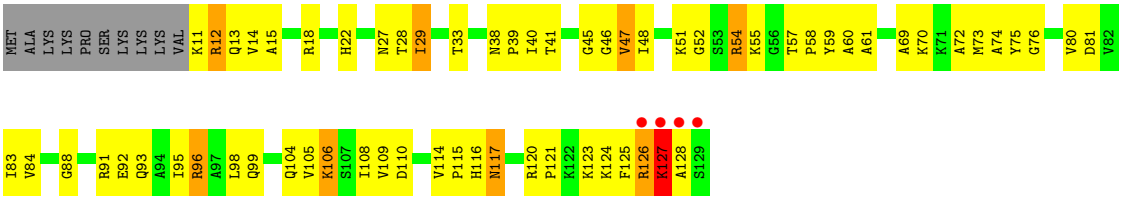
Chain J:





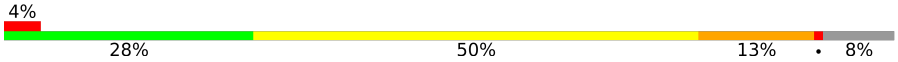
- Molecule 13: 16S Ribosomal protein S11

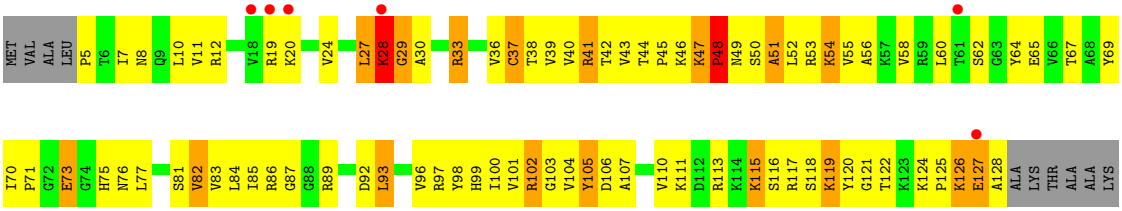
Chain K:



- Molecule 14: 16S Ribosomal protein S12

Chain L:

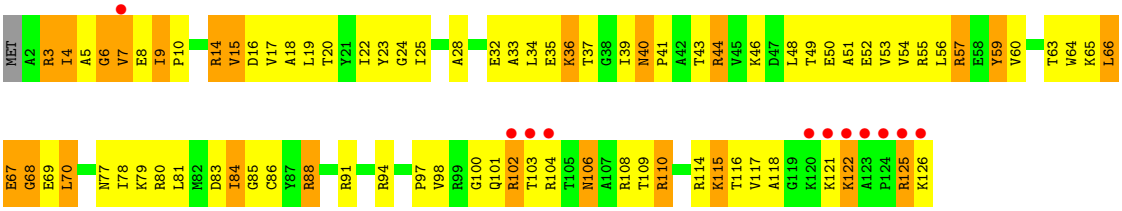




LYS

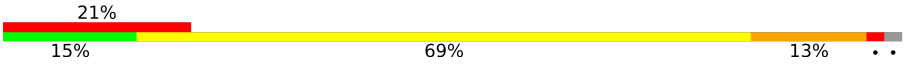
- Molecule 15: 16S Ribosomal protein S13

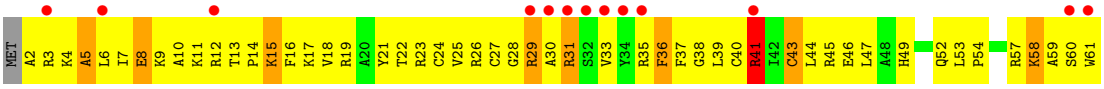
Chain M:



- Molecule 16: 16S Ribosomal protein S14

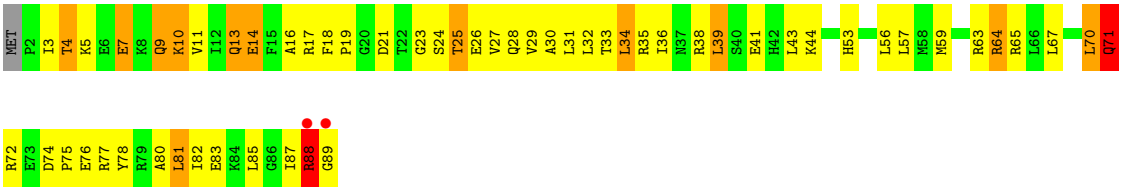
Chain N:





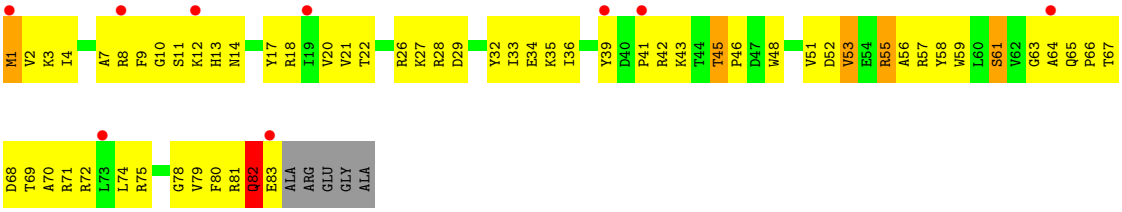
- Molecule 17: 16S Ribosomal protein S15

Chain O:



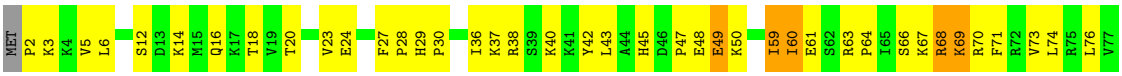
- Molecule 18: 16S Ribosomal protein S16

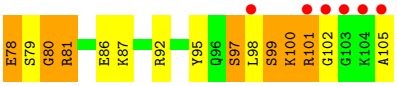
Chain P:



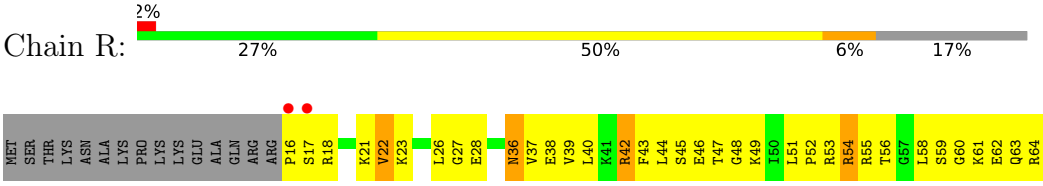
- Molecule 19: 16S Ribosomal protein S17

Chain Q:

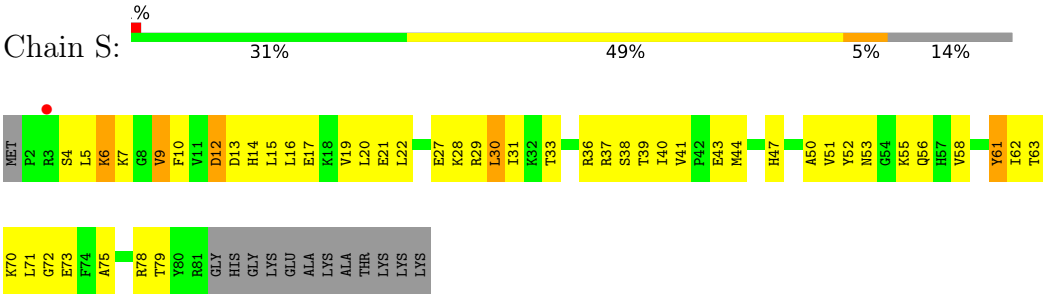




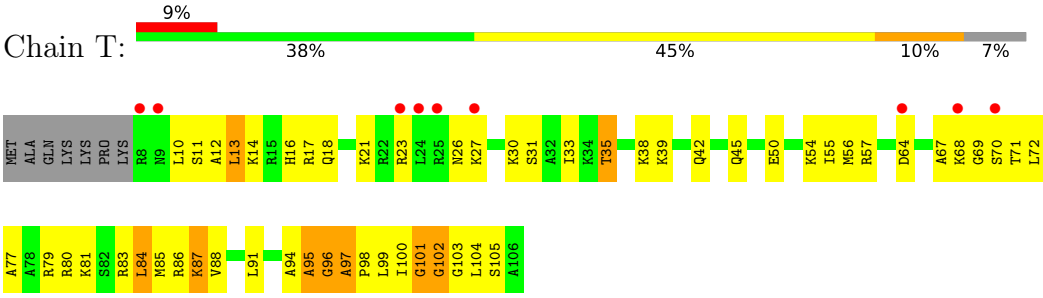
• Molecule 20: 16S Ribosomal protein S18



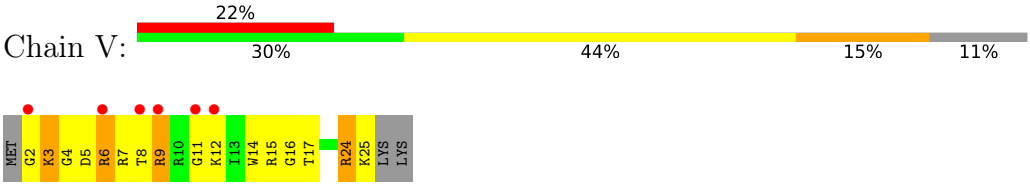
• Molecule 21: 16S Ribosomal protein S19



• Molecule 22: 16S Ribosomal protein S20



• Molecule 23: 16S Ribosomal protein THX



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	401.12Å 401.12Å 175.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	99.00 – 3.10 283.64 – 3.10	Depositor EDS
% Data completeness (in resolution range)	(Not available) (99.00-3.10) 91.7 (283.64-3.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.22 (at 3.07Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.227 , 0.273 0.216 , 0.257	Depositor DCC
R_{free} test set	12553 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å^2)	76.3	Xtriage
Anisotropy	0.284	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.27 , 87.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.86	EDS
Total number of atoms	52075	wwPDB-VP
Average B, all atoms (Å^2)	77.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.46% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, PAR, 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	0.55	2/36244 (0.0%)	0.74	31/56567 (0.1%)
2	X	0.64	0/258	0.85	0/398
3	W	0.56	0/91	0.70	0/140
4	B	0.34	0/1935	0.62	0/2609
5	C	0.38	0/1636	0.63	0/2205
6	D	0.38	0/1733	0.63	0/2318
7	E	0.47	0/1162	0.72	0/1564
8	F	0.31	0/856	0.59	0/1154
9	G	0.36	0/1276	0.62	0/1709
10	H	0.44	0/1136	0.76	0/1527
11	I	0.36	0/1029	0.67	0/1378
12	J	0.36	0/805	0.67	1/1082 (0.1%)
13	K	0.41	0/900	0.67	0/1213
14	L	0.42	0/986	0.76	1/1320 (0.1%)
15	M	0.34	0/1008	0.66	0/1347
16	N	0.41	0/501	0.68	0/664
17	O	0.36	0/745	0.60	0/992
18	P	0.46	0/716	0.80	0/963
19	Q	0.46	0/870	0.76	0/1159
20	R	0.35	0/603	0.60	0/799
21	S	0.31	0/661	0.62	0/890
22	T	0.41	0/764	0.67	0/1006
23	V	0.45	0/212	0.61	0/277
All	All	0.50	2/56127 (0.0%)	0.72	33/83281 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	2	53

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1543	C	N1-C2	5.57	1.45	1.40
1	A	815	A	C5-C6	-5.01	1.36	1.41

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1498	U	C2'-C3'-O3'	9.40	130.17	109.50
1	A	115	G	C2'-C3'-O3'	9.34	130.06	109.50
1	A	243	A	C2'-C3'-O3'	9.28	129.91	109.50
1	A	559	A	C2'-C3'-O3'	9.04	129.40	109.50
1	A	575	G	C2'-C3'-O3'	8.76	128.76	109.50
1	A	181	G	C2'-C3'-O3'	8.36	127.90	109.50
1	A	366	C	C2'-C3'-O3'	8.29	127.74	109.50
1	A	960	U	C2'-C3'-O3'	7.73	126.51	109.50
1	A	812	C	C2'-C3'-O3'	7.72	126.50	109.50
1	A	1505	G	C2'-C3'-O3'	7.42	125.83	109.50
1	A	965	A	C2'-C3'-O3'	7.40	125.79	109.50
1	A	328	C	C2'-C3'-O3'	7.13	125.18	109.50
1	A	60	A	C2'-C3'-O3'	7.01	124.93	109.50
1	A	1299	A	N9-C1'-C2'	7.01	123.11	114.00
1	A	353	A	C5'-C4'-O4'	-6.76	100.99	109.10
1	A	1503	A	C2'-C3'-O3'	6.38	123.90	113.70
1	A	1502	A	N9-C1'-C2'	6.26	122.14	114.00
1	A	266	G	C2'-C3'-O3'	5.92	123.18	113.70
1	A	533	A	C2'-C3'-O3'	5.90	123.15	113.70
1	A	1346	A	C2'-C3'-O3'	5.80	122.99	113.70
1	A	372	C	C2'-C3'-O3'	5.66	122.75	113.70
12	J	60	ARG	N-CA-C	5.39	125.57	111.00
1	A	108	G	O4'-C4'-C3'	-5.28	98.72	104.00
1	A	686	U	N1-C1'-C2'	5.27	120.85	114.00
1	A	474	G	N9-C1'-C2'	5.26	120.84	114.00
1	A	1101	A	C2'-C3'-O3'	5.22	122.05	113.70
1	A	1065	U	C1'-O4'-C4'	-5.18	105.75	109.90
1	A	1490	C	C5'-C4'-C3'	-5.15	107.76	116.00
1	A	1124	G	N9-C1'-C2'	5.13	120.67	114.00
14	L	119	LYS	N-CA-C	-5.11	97.22	111.00
1	A	115	G	C4'-C3'-C2'	5.06	107.66	102.60
1	A	366	C	C4'-C3'-O3'	5.04	123.08	113.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	190	C	O4'-C1'-N1	5.01	112.20	108.20

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	243	A	C3'
1	A	366	C	C3'

All (53) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1013	G	Sidechain
1	A	1048	G	Sidechain
1	A	1073	U	Sidechain
1	A	1077	G	Sidechain
1	A	108	G	Sidechain
1	A	1130	A	Sidechain
1	A	1235	U	Sidechain
1	A	1299	A	Sidechain
1	A	1331	G	Sidechain
1	A	1340	A	Sidechain
1	A	1345	U	Sidechain
1	A	1361	G	Sidechain
1	A	1396	A	Sidechain
1	A	1405	G	Sidechain
1	A	1414	U	Sidechain
1	A	1492	A	Sidechain
1	A	1498	U	Sidechain
1	A	1506	U	Sidechain
1	A	1519	A	Sidechain
1	A	173	U	Sidechain
1	A	189	G	Sidechain
1	A	190(F)	G	Sidechain
1	A	197	A	Sidechain
1	A	203	U	Sidechain
1	A	229	U	Sidechain
1	A	251	G	Sidechain
1	A	265	G	Sidechain
1	A	283	C	Sidechain
1	A	290	C	Sidechain
1	A	323	U	Sidechain
1	A	39	G	Sidechain

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Mol	Chain	Res	Type	Group
1	A	404	U	Sidechain
1	A	474	G	Sidechain
1	A	490	G	Sidechain
1	A	528	C	Sidechain
1	A	529	G	Sidechain
1	A	561	U	Sidechain
1	A	565	U	Sidechain
1	A	573	A	Sidechain
1	A	575	G	Sidechain
1	A	587	G	Sidechain
1	A	639	G	Sidechain
1	A	727	G	Sidechain
1	A	785	G	Sidechain
1	A	813	U	Sidechain
1	A	835	U	Sidechain
1	A	855	G	Sidechain
1	A	871	U	Sidechain
1	A	879	C	Sidechain
1	A	880	C	Sidechain
1	A	898	G	Sidechain
1	A	922	G	Sidechain
1	A	982	U	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	32380	0	16346	1091	0
2	X	232	0	121	3	0
3	W	82	0	46	1	0
4	B	1900	0	1951	284	0
5	C	1612	0	1677	248	0
6	D	1703	0	1764	146	0
7	E	1146	0	1207	126	0
8	F	843	0	857	89	0
9	G	1257	0	1296	120	0
10	H	1116	0	1177	110	0
11	I	1011	0	1043	141	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	J	792	0	835	139	0
13	K	885	0	904	73	0
14	L	970	0	1057	124	0
15	M	997	0	1072	111	0
16	N	492	0	529	82	0
17	O	734	0	771	67	0
18	P	700	0	720	71	0
19	Q	857	0	930	73	0
20	R	597	0	668	74	0
21	S	647	0	673	76	0
22	T	762	0	856	77	0
23	V	208	0	221	21	0
24	A	42	0	45	0	0
25	A	104	0	0	0	0
25	J	1	0	0	0	0
25	X	3	0	0	0	0
26	D	1	0	0	0	0
26	N	1	0	0	0	0
All	All	52075	0	36766	3094	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 35.

All (3094) 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)
16:N:26:ARG:HH12	16:N:47:LEU:HD21	1.03	1.17
1:A:1443:G:H5”	1:A:1446:A:H5”	1.27	1.14
5:C:64:VAL:HG23	5:C:99:VAL:HG11	1.36	1.08
1:A:1250:A:H4’	11:I:68:GLY:H	1.18	1.08
12:J:38:ILE:HB	12:J:71:LEU:HB2	1.33	1.08
13:K:40:ILE:HG22	13:K:41:THR:HG23	1.30	1.07
4:B:69:LEU:HD12	4:B:155:LEU:HD11	1.37	1.07
6:D:19:LEU:HD21	6:D:67:ILE:HG12	1.38	1.05
14:L:47:LYS:HB3	14:L:48:PRO:HD3	1.38	1.05
1:A:1116:C:H2’	1:A:1117:G:H5”	1.37	1.04
4:B:15:VAL:HG11	4:B:209:ARG:HB3	1.39	1.03
7:E:80:ILE:CD1	7:E:91:LEU:HB2	1.86	1.03
6:D:36:ARG:H	6:D:37:PRO:HD3	1.21	1.02
18:P:82:GLN:NE2	18:P:82:GLN:H	1.57	1.02
12:J:90:LEU:H	12:J:91:PRO:HD2	1.22	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:27:LEU:O	14:L:29:GLY:N	1.92	1.02
11:I:10:ARG:HD3	11:I:75:ASP:HB3	1.40	1.00
4:B:77:ALA:HB2	4:B:211:ILE:HD13	1.44	0.99
16:N:26:ARG:NH1	16:N:47:LEU:HD21	1.77	0.99
14:L:55:VAL:HG12	14:L:56:ALA:H	1.26	0.98
1:A:972:C:H4'	12:J:57:LYS:HD3	1.46	0.98
1:A:1190:G:H3'	5:C:3:ASN:OD1	1.63	0.97
4:B:25:ASN:ND2	4:B:27:LYS:H	1.63	0.97
1:A:1064:G:H4'	1:A:1065:U:H5'	1.44	0.96
7:E:41:VAL:HG22	7:E:113:ALA:HA	1.44	0.96
14:L:89:ARG:HA	14:L:97:ARG:HA	1.48	0.95
11:I:8:GLY:HA2	11:I:79:LEU:HD13	1.48	0.95
5:C:23:TYR:HD2	5:C:24:ALA:N	1.63	0.95
1:A:243:A:H4'	1:A:244:U:H5'	1.47	0.95
1:A:1057:G:H5"	5:C:154:SER:HB2	1.49	0.95
14:L:126:LYS:H	14:L:126:LYS:HD2	1.29	0.94
10:H:104:ARG:HG2	10:H:104:ARG:HH11	1.32	0.94
1:A:1305:G:O2'	1:A:1306:A:H8	1.50	0.93
1:A:1250:A:H4'	11:I:68:GLY:N	1.84	0.93
12:J:6:ILE:HA	12:J:98:ILE:HG22	1.50	0.93
1:A:664:G:H22	1:A:741:G:H1	1.10	0.93
1:A:1316:G:H5"	16:N:17:LYS:HE3	1.50	0.92
1:A:1124:G:H5'	12:J:35:SER:O	1.70	0.92
5:C:3:ASN:HD22	5:C:3:ASN:H	0.98	0.92
4:B:178:ARG:HH11	4:B:178:ARG:HG3	1.32	0.92
4:B:18:GLY:HA2	4:B:41:ILE:HA	1.50	0.91
11:I:106:ALA:O	11:I:108:VAL:HG23	1.71	0.91
4:B:229:VAL:HG12	4:B:231:GLU:HG3	1.52	0.91
4:B:197:VAL:HB	4:B:200:ILE:HG23	1.51	0.91
13:K:127:LYS:HA	13:K:127:LYS:HE3	1.51	0.91
1:A:477:G:H3'	1:A:478:A:H4'	1.53	0.90
14:L:124:LYS:HD2	14:L:125:PRO:HD2	1.52	0.90
20:R:22:VAL:HG13	20:R:42:ARG:HD2	1.53	0.90
1:A:349:A:H2'	1:A:350:G:H5"	1.51	0.90
11:I:116:LYS:HB3	11:I:119:ALA:O	1.72	0.90
14:L:27:LEU:HB3	14:L:33:ARG:HH12	1.38	0.89
14:L:47:LYS:HB3	14:L:48:PRO:CD	2.02	0.89
12:J:49:VAL:HG23	16:N:41:ARG:HB2	1.53	0.89
18:P:82:GLN:HE21	18:P:82:GLN:N	1.69	0.89
1:A:1116:C:C2'	1:A:1117:G:H5"	2.03	0.89
11:I:6:GLY:N	11:I:84:ALA:HB2	1.87	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:90:LEU:H	12:J:91:PRO:CD	1.86	0.89
9:G:50:ILE:O	9:G:54:THR:HB	1.72	0.89
1:A:1356:G:H2'	1:A:1357:A:C8	2.07	0.88
4:B:132:LYS:HA	4:B:135:GLN:HB2	1.55	0.88
1:A:266:G:H5'	1:A:266:G:C8	2.08	0.88
11:I:127:LYS:HB2	15:M:126:LYS:NZ	1.89	0.88
6:D:128:VAL:HG12	6:D:129:ASN:ND2	1.87	0.88
1:A:1367:C:H5'	12:J:60:ARG:NH1	1.88	0.88
4:B:20:GLU:O	4:B:39:ILE:HG23	1.74	0.88
18:P:82:GLN:H	18:P:82:GLN:HE21	0.91	0.87
15:M:10:PRO:HB2	15:M:18:ALA:HB1	1.57	0.87
1:A:1391:U:H2'	1:A:1392:G:C8	2.10	0.86
5:C:50:ALA:HB1	5:C:70:VAL:HG11	1.56	0.86
16:N:24:CYS:HB3	16:N:28:GLY:H	1.40	0.86
14:L:38:THR:HG22	14:L:39:VAL:HG23	1.57	0.86
5:C:91:LEU:HD21	5:C:99:VAL:HG22	1.56	0.85
7:E:144:THR:HG22	7:E:147:ASP:H	1.41	0.85
13:K:106:LYS:HA	13:K:106:LYS:NZ	1.92	0.85
4:B:71:VAL:O	4:B:165:VAL:HG23	1.77	0.85
5:C:19:GLU:HG2	5:C:40:ARG:HH21	1.42	0.85
1:A:1443:G:C5'	1:A:1446:A:H5"	2.06	0.85
9:G:113:GLU:HG2	9:G:119:ARG:HG2	1.60	0.84
18:P:28:ARG:HG2	18:P:28:ARG:HH11	1.42	0.84
1:A:1223:C:P	21:S:78:ARG:HH12	1.99	0.84
5:C:191:THR:HG22	5:C:193:TYR:H	1.40	0.84
11:I:104:ARG:HD3	11:I:105:ASP:N	1.91	0.84
17:O:4:THR:OG1	17:O:7:GLU:HB2	1.77	0.84
1:A:478:A:O2'	1:A:479:C:H5'	1.77	0.83
11:I:10:ARG:HD3	11:I:75:ASP:CB	2.09	0.83
1:A:409:G:H2'	1:A:409:G:N3	1.93	0.83
4:B:25:ASN:HD22	4:B:26:PRO:N	1.75	0.83
14:L:47:LYS:CB	14:L:48:PRO:HD3	2.08	0.83
4:B:21:ARG:O	4:B:22:LYS:HD2	1.78	0.83
5:C:178:LEU:O	5:C:179:ARG:HB3	1.77	0.83
9:G:15:ASP:HB3	9:G:19:GLY:N	1.94	0.83
5:C:3:ASN:H	5:C:3:ASN:ND2	1.76	0.82
7:E:13:ILE:HD12	7:E:13:ILE:O	1.79	0.82
1:A:1065:U:H4'	1:A:1066:C:O5'	1.80	0.82
21:S:9:VAL:HG12	21:S:10:PHE:H	1.42	0.82
6:D:62:GLN:HE22	6:D:65:ARG:HH12	1.26	0.82
11:I:102:LEU:HD23	11:I:102:LEU:H	1.44	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:101:ILE:O	7:E:120:THR:HG22	1.80	0.82
6:D:176:LEU:HA	6:D:183:GLY:HA2	1.62	0.82
7:E:50:GLU:HG3	7:E:52:PRO:HD2	1.59	0.82
12:J:75:ILE:H	12:J:75:ILE:HD12	1.45	0.81
1:A:420:U:H3'	1:A:421:U:C5'	2.10	0.81
7:E:102:ALA:HB2	7:E:120:THR:HG21	1.61	0.81
14:L:89:ARG:HG2	14:L:97:ARG:HB3	1.61	0.81
23:V:24:ARG:HG2	23:V:24:ARG:HH11	1.44	0.81
1:A:1128:C:HO2'	1:A:1130:A:H8	0.83	0.81
15:M:4:ILE:HG22	15:M:5:ALA:N	1.95	0.81
10:H:10:LEU:HD22	10:H:83:ILE:HD11	1.61	0.81
1:A:462:G:H22	18:P:82:GLN:HB3	1.46	0.81
20:R:47:THR:HG23	20:R:83:GLU:H	1.46	0.80
1:A:706:A:O2'	13:K:29:ILE:HD11	1.81	0.80
1:A:1152:A:H5"	12:J:13:HIS:CD2	2.16	0.80
6:D:119:GLN:HG2	6:D:123:HIS:CD2	2.15	0.80
1:A:371:G:O2'	1:A:372:C:H5'	1.81	0.80
20:R:38:GLU:H	20:R:38:GLU:CD	1.85	0.80
1:A:737:A:H1'	8:F:73:ASN:HD21	1.46	0.80
17:O:39:LEU:HD13	17:O:56:LEU:HB2	1.62	0.80
5:C:31:HIS:CD2	5:C:31:HIS:H	2.00	0.80
17:O:71:GLN:HG3	17:O:71:GLN:O	1.80	0.80
1:A:489:C:H2'	1:A:490:G:H8	1.46	0.80
1:A:1502:A:H2	1:A:1505:G:H1	1.29	0.80
4:B:14:GLY:O	4:B:15:VAL:HG13	1.81	0.80
4:B:92:TYR:CD1	4:B:151:GLY:HA3	2.17	0.80
9:G:147:ALA:C	9:G:148:ASN:HD22	1.85	0.80
14:L:55:VAL:HG12	14:L:56:ALA:N	1.96	0.80
4:B:218:ALA:O	4:B:222:ILE:HG13	1.82	0.80
7:E:51:VAL:O	7:E:54:ALA:HB3	1.81	0.80
5:C:191:THR:HG21	5:C:193:TYR:CZ	2.17	0.80
1:A:190:C:H4'	1:A:190(A):C:OP1	1.82	0.80
6:D:127:THR:HG23	6:D:147:ALA:HB3	1.63	0.80
16:N:26:ARG:HH12	16:N:47:LEU:CD2	1.90	0.79
1:A:420:U:H3'	1:A:421:U:H5'	1.65	0.79
1:A:738:C:H5"	8:F:69:GLU:HB3	1.65	0.79
1:A:1128:C:O2'	1:A:1130:A:H8	1.65	0.79
6:D:187:ARG:HD2	6:D:188:LEU:H	1.48	0.79
20:R:36:ASN:ND2	20:R:38:GLU:HG2	1.97	0.79
4:B:18:GLY:CA	4:B:41:ILE:HA	2.11	0.79
8:F:72:VAL:HG23	8:F:73:ASN:H	1.47	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:3:ARG:NH1	15:M:3:ARG:HB2	1.97	0.79
1:A:547:A:H4'	1:A:548:G:O5'	1.82	0.79
1:A:694:A:H3'	1:A:695:A:H5"	1.65	0.79
1:A:1250:A:C4'	11:I:68:GLY:H	1.94	0.79
14:L:38:THR:HG22	14:L:39:VAL:N	1.97	0.79
1:A:969:A:H61	15:M:126:LYS:HG3	1.47	0.79
1:A:1314:C:OP2	21:S:6:LYS:HG2	1.83	0.79
5:C:3:ASN:HD22	5:C:3:ASN:N	1.76	0.79
10:H:133:LEU:HD23	10:H:134:ILE:N	1.98	0.79
11:I:6:GLY:H	11:I:84:ALA:HB2	1.45	0.79
1:A:840:C:H5"	1:A:841:U:OP1	1.83	0.78
1:A:946:A:H2'	1:A:947:G:C8	2.18	0.78
1:A:1095:U:H2'	1:A:1096:C:C6	2.17	0.78
9:G:15:ASP:HB3	9:G:19:GLY:H	1.47	0.78
10:H:31:PHE:HZ	10:H:134:ILE:HD11	1.48	0.78
1:A:1435:G:H2'	1:A:1436:U:H6	1.48	0.78
5:C:23:TYR:CD2	5:C:24:ALA:N	2.50	0.78
1:A:1313:U:P	21:S:6:LYS:HB3	2.24	0.78
15:M:40:ASN:HD22	15:M:41:PRO:CD	1.95	0.78
6:D:62:GLN:HE22	6:D:65:ARG:NH1	1.82	0.78
1:A:1154:G:H2'	1:A:1155:G:H8	1.48	0.78
6:D:151:LYS:H	6:D:151:LYS:HD2	1.48	0.78
1:A:235:C:H5'	19:Q:70:ARG:HG2	1.64	0.77
1:A:1281:U:H5'	1:A:1282:C:H5	1.47	0.77
16:N:16:PHE:HB2	16:N:18:VAL:HG22	1.66	0.77
4:B:71:VAL:CG2	4:B:164:VAL:HA	2.14	0.77
6:D:36:ARG:N	6:D:37:PRO:HD3	1.99	0.77
16:N:9:LYS:C	16:N:11:LYS:H	1.86	0.77
18:P:18:ARG:O	18:P:20:VAL:HG23	1.83	0.77
1:A:1086:U:H3	1:A:1099:G:H22	1.32	0.77
1:A:1152:A:H2'	1:A:1153:C:C6	2.18	0.77
1:A:1224:G:H1	1:A:1362:C:H42	1.33	0.77
1:A:1343:G:H2'	1:A:1344:C:C6	2.20	0.77
1:A:556:C:O2'	1:A:557:G:H5'	1.84	0.77
17:O:64:ARG:HB3	17:O:64:ARG:HH11	1.50	0.77
1:A:250:A:H4'	1:A:251:G:O5'	1.82	0.77
8:F:19:LEU:HD23	8:F:20:ALA:N	2.00	0.77
1:A:1226:C:N4	15:M:104:ARG:HD3	2.00	0.77
21:S:40:ILE:HD13	21:S:62:ILE:HD13	1.65	0.77
4:B:97:TRP:HZ2	4:B:102:LEU:HD13	1.50	0.76
11:I:93:ARG:NH1	11:I:93:ARG:HB3	1.99	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:195:VAL:O	5:C:196:LEU:HD22	1.85	0.76
1:A:687:A:H4'	1:A:688:G:O5'	1.85	0.76
7:E:11:ILE:HB	7:E:31:LEU:HB3	1.66	0.76
12:J:6:ILE:HD13	12:J:72:VAL:HB	1.68	0.76
4:B:71:VAL:HG21	4:B:164:VAL:HG22	1.68	0.76
1:A:839:U:H5'	1:A:840:C:H5	1.51	0.76
4:B:84:GLU:OE1	4:B:216:SER:HA	1.85	0.76
7:E:79:GLU:HG3	7:E:93:PRO:HD2	1.67	0.76
1:A:349:A:C2'	1:A:350:G:H5"	2.16	0.75
1:A:1125:U:H3	12:J:5:ARG:NH2	1.84	0.75
1:A:1057:G:H5"	5:C:154:SER:CB	2.17	0.75
1:A:1161:C:H2'	1:A:1162:C:C6	2.21	0.75
1:A:1281:U:H5'	1:A:1282:C:C5	2.21	0.75
4:B:61:LEU:HA	4:B:64:ARG:HD2	1.69	0.75
15:M:3:ARG:HB2	15:M:3:ARG:HH11	1.48	0.75
1:A:975:A:O5'	1:A:976:G:H5'	1.85	0.75
1:A:1497:G:C2'	1:A:1498:U:H5'	2.17	0.75
6:D:64:LEU:C	6:D:64:LEU:HD13	2.07	0.75
7:E:53:LEU:H	7:E:53:LEU:HD12	1.51	0.75
1:A:677:U:H3	1:A:713:G:H22	1.32	0.75
1:A:1106:G:H5"	5:C:172:ARG:HG2	1.69	0.75
1:A:1125:U:H3	12:J:5:ARG:HH21	1.35	0.75
1:A:1435:G:H2'	1:A:1436:U:C6	2.22	0.74
1:A:328:C:O2	1:A:328:C:H2'	1.87	0.74
12:J:6:ILE:HD12	12:J:6:ILE:N	2.02	0.74
13:K:106:LYS:HA	13:K:106:LYS:HZ3	1.49	0.74
18:P:67:THR:HG22	18:P:68:ASP:N	2.00	0.74
11:I:100:GLY:O	11:I:102:LEU:HD23	1.87	0.74
18:P:4:ILE:HG13	18:P:64:ALA:HB1	1.68	0.74
1:A:189:G:H5"	1:A:189:G:H8	1.50	0.74
1:A:390:C:H2'	1:A:391:G:C8	2.22	0.74
9:G:52:GLU:C	9:G:53:LYS:HD2	2.08	0.74
14:L:126:LYS:HD2	14:L:126:LYS:N	2.01	0.74
1:A:1031:G:H4'	1:A:1032:G:C8	2.23	0.74
10:H:24:THR:HG22	10:H:63:LEU:HD21	1.70	0.74
21:S:62:ILE:HD12	21:S:66:MET:HG3	1.69	0.74
4:B:60:ASP:O	4:B:64:ARG:HG3	1.87	0.74
1:A:463:A:H1'	1:A:474:G:N2	2.03	0.74
1:A:1347:G:N2	1:A:1373:G:H2'	2.02	0.74
18:P:11:SER:HB3	18:P:14:ASN:HB3	1.68	0.74
20:R:53:ARG:HH11	20:R:59:SER:HA	1.51	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:376:G:OP2	18:P:67:THR:HG21	1.88	0.74
4:B:102:LEU:HD21	4:B:162:ILE:HD11	1.69	0.74
14:L:27:LEU:HB3	14:L:33:ARG:NH1	2.03	0.74
1:A:406:G:H21	6:D:119:GLN:HE22	1.34	0.73
15:M:3:ARG:HA	15:M:8:GLU:O	1.88	0.73
1:A:1168:A:H2'	1:A:1169:A:C8	2.23	0.73
9:G:16:LEU:H	9:G:16:LEU:HD22	1.53	0.73
10:H:31:PHE:HZ	10:H:134:ILE:CD1	2.01	0.73
4:B:166:ASP:OD2	4:B:169:LYS:HB2	1.89	0.73
18:P:74:LEU:O	18:P:79:VAL:HG23	1.89	0.73
4:B:77:ALA:CB	4:B:211:ILE:HG21	2.17	0.73
1:A:1015:A:H2'	1:A:1016:A:C8	2.23	0.73
1:A:1038:C:H2'	1:A:1039:C:C6	2.22	0.73
4:B:51:LEU:HD22	4:B:55:PHE:HE2	1.52	0.73
4:B:71:VAL:HG12	4:B:93:VAL:HG21	1.69	0.73
5:C:64:VAL:HB	5:C:99:VAL:HG21	1.71	0.73
1:A:1417:G:H2'	1:A:1482:G:H22	1.54	0.73
15:M:79:LYS:HG2	15:M:83:ASP:OD2	1.89	0.73
14:L:46:LYS:HE2	14:L:47:LYS:HB2	1.69	0.73
1:A:390:C:H2'	1:A:391:G:H8	1.53	0.73
1:A:1230:C:H1'	15:M:126:LYS:HA	1.69	0.73
4:B:71:VAL:HG12	4:B:93:VAL:CG2	2.19	0.72
7:E:24:ARG:HG2	7:E:24:ARG:HH11	1.53	0.72
9:G:78:ARG:HB2	9:G:156:TRP:HZ3	1.53	0.72
4:B:55:PHE:HE1	4:B:218:ALA:HA	1.54	0.72
8:F:69:GLU:O	8:F:72:VAL:HG22	1.89	0.72
8:F:101:ALA:HA	20:R:28:GLU:HG3	1.71	0.72
15:M:15:VAL:HG23	15:M:43:THR:O	1.90	0.72
1:A:1343:G:H2'	1:A:1344:C:H6	1.54	0.72
7:E:102:ALA:CB	7:E:120:THR:HG21	2.19	0.72
1:A:1032:G:H2'	1:A:1033:G:O4'	1.88	0.72
1:A:1141:C:H2'	1:A:1142:G:H8	1.54	0.72
1:A:1152:A:H5"	12:J:13:HIS:HD2	1.54	0.72
12:J:49:VAL:O	12:J:60:ARG:O	2.06	0.72
1:A:1054:C:N4	2:X:34:I:H1'	2.05	0.72
4:B:17:PHE:HB3	4:B:44:LEU:HD21	1.70	0.72
22:T:57:ARG:NH1	22:T:102:GLY:HA3	2.05	0.72
12:J:19:SER:HA	12:J:22:LYS:NZ	2.04	0.72
12:J:60:ARG:HD2	12:J:60:ARG:N	2.04	0.72
12:J:94:VAL:HG12	12:J:95:GLU:N	2.04	0.72
20:R:47:THR:HA	20:R:83:GLU:HB2	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1441:G:H4'	1:A:1442:G:C5	2.25	0.71
6:D:3:ARG:HH21	6:D:71:SER:HB3	1.53	0.71
4:B:74:LYS:HZ1	4:B:206:ASP:HB2	1.54	0.71
5:C:14:ILE:HG22	5:C:15:THR:N	2.05	0.71
1:A:462:G:N2	18:P:82:GLN:HB3	2.04	0.71
1:A:1363:A:H1'	1:A:1365:G:N7	2.04	0.71
1:A:1024:G:H2'	1:A:1025:U:H5"	1.71	0.71
4:B:32:ILE:HD13	4:B:40:HIS:CD2	2.24	0.71
5:C:91:LEU:HD23	5:C:92:ALA:N	2.04	0.71
8:F:72:VAL:HG23	8:F:73:ASN:N	2.05	0.71
8:F:75:LEU:HD11	8:F:79:LEU:HD12	1.73	0.71
4:B:51:LEU:HD22	4:B:55:PHE:CE2	2.25	0.71
11:I:47:LEU:C	11:I:49:PRO:HD2	2.11	0.71
12:J:32:ALA:HB2	12:J:76:ASN:OD1	1.90	0.71
16:N:24:CYS:HB3	16:N:28:GLY:N	2.06	0.71
6:D:126:ILE:HG22	6:D:127:THR:N	2.06	0.71
7:E:8:GLU:HB3	7:E:34:VAL:HG23	1.72	0.71
15:M:8:GLU:OE1	15:M:22:ILE:HA	1.91	0.71
5:C:204:LEU:HD12	5:C:204:LEU:O	1.90	0.71
22:T:57:ARG:NH1	22:T:57:ARG:HB2	2.05	0.71
1:A:463:A:C2	18:P:82:GLN:HB2	2.25	0.71
5:C:134:ILE:HD11	5:C:153:VAL:HG23	1.73	0.71
4:B:77:ALA:HB1	4:B:211:ILE:HG21	1.73	0.71
4:B:178:ARG:HH21	4:B:196:LEU:C	1.93	0.71
1:A:275:G:H5'	19:Q:14:LYS:HE2	1.73	0.71
10:H:86:ILE:HG22	10:H:87:SER:N	2.05	0.71
11:I:48:GLU:N	11:I:49:PRO:HD2	2.05	0.71
12:J:38:ILE:HB	12:J:71:LEU:CB	2.18	0.71
15:M:49:THR:HG22	15:M:51:ALA:H	1.56	0.71
16:N:8:GLU:O	16:N:11:LYS:HB2	1.91	0.71
1:A:1367:C:H5'	12:J:60:ARG:HH12	1.54	0.70
14:L:48:PRO:C	14:L:49:ASN:HD22	1.93	0.70
14:L:58:VAL:O	14:L:65:GLU:HA	1.91	0.70
19:Q:68:ARG:N	19:Q:70:ARG:NH1	2.38	0.70
4:B:35:GLU:HA	4:B:39:ILE:O	1.91	0.70
12:J:39:PRO:O	12:J:40:LEU:HB2	1.91	0.70
22:T:30:LYS:HE2	22:T:72:LEU:HD21	1.73	0.70
4:B:25:ASN:HD22	4:B:25:ASN:C	1.92	0.70
21:S:51:VAL:HG21	21:S:71:LEU:HB3	1.74	0.70
1:A:243:A:C4'	1:A:244:U:H5'	2.19	0.70
4:B:141:GLU:O	4:B:145:LEU:HG	1.92	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:92:TYR:O	11:I:96:LEU:HD13	1.92	0.70
4:B:59:GLU:HB3	4:B:221:LEU:HD11	1.74	0.70
6:D:146:ILE:N	6:D:146:ILE:HD12	2.06	0.70
8:F:9:VAL:HG23	8:F:87:ARG:HB2	1.73	0.70
10:H:35:ILE:HG23	10:H:111:ILE:HG21	1.74	0.70
11:I:43:ALA:HA	11:I:74:ILE:HD13	1.72	0.70
14:L:117:ARG:NH2	14:L:124:LYS:HA	2.06	0.70
4:B:25:ASN:HD22	4:B:27:LYS:H	1.38	0.70
6:D:36:ARG:HG3	6:D:38:TYR:CE2	2.27	0.70
1:A:1497:G:O2'	1:A:1498:U:H5'	1.92	0.70
5:C:23:TYR:HD2	5:C:23:TYR:C	1.94	0.70
1:A:673:G:H2'	1:A:674:G:C8	2.27	0.70
13:K:29:ILE:C	13:K:29:ILE:HD12	2.12	0.70
17:O:26:GLU:OE1	17:O:77:ARG:HD2	1.92	0.70
6:D:173:TRP:CD2	6:D:189:PRO:HB3	2.27	0.69
22:T:57:ARG:HB2	22:T:57:ARG:HH11	1.57	0.69
1:A:983:A:H5'	1:A:984:C:OP2	1.92	0.69
1:A:984:C:H2'	1:A:985:C:H6	1.57	0.69
4:B:112:VAL:C	4:B:114:ARG:H	1.94	0.69
4:B:186:ALA:HB3	4:B:197:VAL:HG11	1.74	0.69
5:C:107:GLN:O	5:C:108:ASN:HB2	1.91	0.69
1:A:539:A:H2'	1:A:540:G:C8	2.28	0.69
4:B:97:TRP:CZ2	4:B:102:LEU:HD13	2.27	0.69
7:E:18:ARG:HG2	7:E:25:ARG:HB2	1.73	0.69
10:H:104:ARG:HH11	10:H:104:ARG:CG	2.02	0.69
15:M:37:THR:HG23	15:M:55:ARG:HD2	1.74	0.69
1:A:1370:G:O2'	1:A:1371:G:H5'	1.92	0.69
10:H:63:LEU:HD22	10:H:63:LEU:H	1.57	0.69
15:M:19:LEU:O	15:M:22:ILE:HD13	1.92	0.69
4:B:30:ARG:HG3	4:B:31:TYR:CD2	2.27	0.69
9:G:155:ARG:O	9:G:156:TRP:HB2	1.92	0.69
10:H:92:ARG:HG2	10:H:92:ARG:HH11	1.57	0.69
1:A:190(L):U:O2	22:T:105:SER:HB2	1.93	0.69
5:C:20:SER:HB3	5:C:22:TRP:NE1	2.08	0.69
7:E:43:LEU:HD11	7:E:132:ALA:HB1	1.75	0.69
19:Q:68:ARG:HG3	19:Q:68:ARG:O	1.93	0.69
1:A:254:G:OP1	19:Q:67:LYS:O	2.10	0.69
1:A:421:U:O2'	1:A:422:C:H3'	1.92	0.69
1:A:639:G:O2'	1:A:640:A:H5'	1.93	0.69
1:A:939:G:H2'	1:A:940:C:C6	2.28	0.69
16:N:9:LYS:HE3	16:N:21:TYR:O	1.93	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:397:A:H5'	1:A:398:C:OP1	1.91	0.69
1:A:458:C:H42	1:A:463:A:H3'	1.57	0.69
1:A:523:A:H61	14:L:92:ASP:HB2	1.58	0.69
1:A:1251:A:H4'	11:I:12:GLU:OE2	1.92	0.69
1:A:1133:G:H2'	1:A:1134:G:H8	1.58	0.69
5:C:155:GLY:O	5:C:156:ARG:HB2	1.93	0.69
1:A:620:C:N1	6:D:135:LEU:HD13	2.07	0.68
20:R:36:ASN:HD21	20:R:38:GLU:HG2	1.57	0.68
1:A:532:A:H5"	5:C:161:GLU:OE1	1.93	0.68
1:A:877:C:OP1	10:H:88:LYS:HE2	1.91	0.68
5:C:150:LYS:HG3	5:C:169:ALA:HB2	1.75	0.68
5:C:195:VAL:HG12	5:C:196:LEU:N	2.05	0.68
13:K:58:PRO:O	13:K:61:ALA:HB3	1.93	0.68
1:A:1121:U:H2'	1:A:1122:U:H6	1.58	0.68
9:G:120:ILE:O	9:G:124:LEU:HB2	1.93	0.68
1:A:501:C:H2'	1:A:502:G:H8	1.57	0.68
7:E:51:VAL:HB	7:E:52:PRO:HD3	1.76	0.68
11:I:127:LYS:HB2	15:M:126:LYS:HZ1	1.56	0.68
1:A:344:A:H5"	1:A:345:C:H5	1.57	0.68
1:A:1190:G:C3'	5:C:3:ASN:OD1	2.40	0.68
17:O:70:LEU:HD12	17:O:78:TYR:HB2	1.74	0.68
17:O:88:ARG:HH11	17:O:88:ARG:HA	1.58	0.68
21:S:40:ILE:HG21	21:S:62:ILE:HD11	1.76	0.68
1:A:838:G:H2'	1:A:839:U:H5"	1.75	0.68
5:C:112:SER:HB3	5:C:115:LEU:HD12	1.75	0.68
8:F:75:LEU:CD1	8:F:79:LEU:HD12	2.24	0.68
1:A:960:U:O2	1:A:960:U:H2'	1.94	0.67
1:A:1391:U:H2'	1:A:1392:G:H8	1.59	0.67
4:B:60:ASP:HB3	4:B:64:ARG:HH21	1.58	0.67
6:D:33:MET:O	6:D:37:PRO:HG3	1.93	0.67
6:D:151:LYS:HD2	6:D:151:LYS:N	2.09	0.67
1:A:834:C:H2'	1:A:835:U:H6	1.59	0.67
4:B:21:ARG:HB3	4:B:38:GLY:O	1.94	0.67
5:C:63:ASN:HA	5:C:99:VAL:HG12	1.74	0.67
6:D:111:ALA:HB2	6:D:120:LEU:HD12	1.75	0.67
10:H:112:LEU:C	10:H:112:LEU:HD12	2.15	0.67
11:I:4:TYR:CE2	11:I:88:TYR:HA	2.29	0.67
14:L:101:VAL:O	14:L:101:VAL:HG12	1.94	0.67
6:D:47:ARG:HB3	6:D:47:ARG:HH11	1.58	0.67
18:P:34:GLU:OE2	18:P:55:ARG:HD3	1.94	0.67
5:C:39:ILE:HG21	5:C:57:ILE:HD11	1.76	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:82:VAL:HG21	7:E:138:ALA:HA	1.77	0.67
9:G:102:ARG:O	9:G:106:GLN:HG3	1.95	0.67
1:A:190(L):U:C2	22:T:105:SER:HB2	2.29	0.67
14:L:55:VAL:CG1	14:L:56:ALA:H	2.04	0.67
12:J:90:LEU:O	12:J:90:LEU:HD23	1.93	0.67
21:S:13:ASP:HA	21:S:16:LEU:HB3	1.76	0.67
4:B:38:GLY:C	4:B:39:ILE:HD12	2.14	0.67
5:C:23:TYR:CD2	5:C:23:TYR:C	2.68	0.67
5:C:24:ALA:HB2	5:C:32:LEU:HD13	1.75	0.67
1:A:1207:G:H2'	1:A:1208:C:H6	1.60	0.67
1:A:1356:G:H2'	1:A:1357:A:H8	1.55	0.67
7:E:126:ARG:HG3	7:E:126:ARG:HH11	1.58	0.67
11:I:58:ARG:HE	11:I:59:PHE:HE1	1.43	0.67
19:Q:27:PHE:CZ	19:Q:36:ILE:HD11	2.29	0.67
1:A:853:G:O2'	1:A:854:G:H5'	1.95	0.67
1:A:1182:G:O2'	1:A:1183:A:OP2	2.12	0.67
12:J:6:ILE:HD12	12:J:6:ILE:H	1.60	0.67
14:L:126:LYS:H	14:L:126:LYS:CD	2.05	0.67
22:T:87:LYS:O	22:T:91:LEU:HG	1.95	0.67
23:V:24:ARG:HG2	23:V:24:ARG:NH1	2.10	0.67
1:A:403:C:O2'	1:A:404:U:H5'	1.94	0.66
1:A:424:G:H3'	1:A:424:G:N3	2.09	0.66
1:A:1412:C:H2'	1:A:1413:A:C8	2.31	0.66
22:T:21:LYS:HB2	22:T:21:LYS:NZ	2.09	0.66
1:A:243:A:H4'	1:A:244:U:C5'	2.22	0.66
5:C:55:VAL:O	5:C:55:VAL:HG12	1.94	0.66
5:C:191:THR:HB	5:C:194:GLY:O	1.95	0.66
7:E:41:VAL:CG2	7:E:113:ALA:HA	2.22	0.66
1:A:476:G:H2'	1:A:476:G:N3	2.10	0.66
1:A:579:G:H5'	1:A:728:A:H1'	1.77	0.66
4:B:95:GLN:O	4:B:96:ARG:HD2	1.94	0.66
4:B:102:LEU:N	4:B:102:LEU:HD12	2.10	0.66
4:B:229:VAL:CG1	4:B:231:GLU:HG3	2.23	0.66
9:G:146:GLU:HG2	9:G:149:ARG:HH21	1.58	0.66
1:A:115:G:H1'	1:A:116:A:N7	2.10	0.66
4:B:71:VAL:HG22	4:B:164:VAL:HA	1.77	0.66
4:B:161:ALA:HB1	4:B:185:ILE:HD11	1.76	0.66
5:C:139:GLN:CA	5:C:139:GLN:HE21	2.08	0.66
21:S:41:VAL:HG23	21:S:43:GLU:HG2	1.76	0.66
22:T:83:ARG:HB3	22:T:87:LYS:NZ	2.10	0.66
1:A:255:G:H1'	19:Q:16:GLN:NE2	2.10	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:33:VAL:HG21	7:E:109:ILE:HG12	1.77	0.66
7:E:87:SER:HB3	7:E:131:ILE:HD13	1.76	0.66
1:A:1251:A:H2'	1:A:1252:A:C8	2.30	0.66
1:A:1277:C:O2'	1:A:1279:A:H1'	1.96	0.66
4:B:15:VAL:CG1	4:B:209:ARG:HB3	2.23	0.66
5:C:139:GLN:HE21	5:C:139:GLN:HA	1.60	0.66
11:I:81:ILE:O	11:I:85:LEU:HB2	1.96	0.66
21:S:40:ILE:HG21	21:S:62:ILE:CD1	2.26	0.66
4:B:12:GLU:OE2	4:B:213:LEU:HD11	1.96	0.66
4:B:142:LEU:O	4:B:146:GLN:HG2	1.96	0.66
5:C:107:GLN:NE2	5:C:107:GLN:H	1.93	0.66
8:F:10:LEU:CD1	8:F:59:TYR:HB3	2.25	0.66
11:I:127:LYS:HB2	15:M:126:LYS:HZ3	1.61	0.66
15:M:85:GLY:O	15:M:86:CYS:HB3	1.95	0.66
1:A:524:G:H2'	1:A:525:C:C6	2.30	0.66
1:A:1352:C:H2'	1:A:1353:G:C8	2.31	0.66
8:F:61:LEU:HB3	8:F:63:TYR:HE1	1.61	0.66
12:J:84:GLN:O	12:J:88:LEU:HD12	1.96	0.66
16:N:36:PHE:O	16:N:36:PHE:CD1	2.49	0.66
12:J:49:VAL:CG2	16:N:41:ARG:HB2	2.25	0.66
1:A:129(A):G:HO2'	1:A:190(E):U:H2'	1.61	0.65
1:A:383:A:H2'	1:A:384:G:H5'	1.78	0.65
1:A:1286:A:H2'	1:A:1287:A:H4'	1.77	0.65
7:E:80:ILE:HD11	7:E:91:LEU:HB2	1.73	0.65
21:S:30:LEU:O	21:S:31:ILE:HD13	1.96	0.65
1:A:1368:G:O2'	1:A:1369:C:H5'	1.96	0.65
14:L:120:TYR:O	14:L:122:THR:HG23	1.97	0.65
15:M:36:LYS:HD3	15:M:59:TYR:OH	1.96	0.65
4:B:178:ARG:HG3	4:B:178:ARG:NH1	2.09	0.65
5:C:64:VAL:CG2	5:C:99:VAL:HG11	2.19	0.65
6:D:25:ARG:C	6:D:27:TYR:H	1.98	0.65
10:H:103:VAL:HG21	10:H:109:ILE:O	1.96	0.65
12:J:38:ILE:CB	12:J:71:LEU:HB2	2.19	0.65
5:C:179:ARG:C	5:C:179:ARG:HD3	2.15	0.65
7:E:121:LYS:HD2	7:E:122:GLU:H	1.62	0.65
14:L:36:VAL:HG22	14:L:82:VAL:HG23	1.77	0.65
1:A:502:G:H2'	1:A:503:C:C6	2.32	0.65
1:A:1263:C:H2'	1:A:1264:C:C6	2.31	0.65
1:A:1347:G:O2'	1:A:1348:U:P	2.54	0.65
4:B:74:LYS:NZ	4:B:206:ASP:HB2	2.11	0.65
4:B:76:GLN:HG3	4:B:206:ASP:OD1	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:52:LEU:HD23	5:C:52:LEU:H	1.62	0.65
6:D:62:GLN:NE2	6:D:65:ARG:HH12	1.94	0.65
11:I:9:ARG:HG3	11:I:14:VAL:HG13	1.79	0.65
5:C:70:VAL:HG12	5:C:71:ALA:N	2.12	0.65
1:A:1240:U:P	9:G:116:ALA:HB2	2.37	0.65
1:A:1417:G:H2'	1:A:1482:G:N2	2.12	0.65
7:E:51:VAL:O	7:E:55:VAL:HG23	1.97	0.65
8:F:55:ASP:CB	8:F:86:ARG:HH12	2.10	0.65
1:A:957:U:H3	1:A:960:U:H5"	1.61	0.65
1:A:1195:C:H3'	1:A:1196:U:H5"	1.77	0.65
4:B:144:ARG:O	4:B:147:LYS:HB2	1.96	0.65
19:Q:48:GLU:O	19:Q:50:LYS:N	2.30	0.65
1:A:353:A:H5'	1:A:353:A:C8	2.32	0.64
1:A:921:U:O2	7:E:19:MET:HB2	1.97	0.64
4:B:178:ARG:HH11	4:B:178:ARG:CG	2.06	0.64
20:R:58:LEU:HD22	20:R:62:GLU:HB3	1.80	0.64
5:C:134:ILE:HD11	5:C:153:VAL:CG2	2.27	0.64
18:P:28:ARG:HG2	18:P:28:ARG:NH1	2.12	0.64
22:T:71:THR:O	22:T:72:LEU:HD23	1.97	0.64
1:A:427:U:OP1	6:D:13:ARG:NH2	2.29	0.64
1:A:939:G:H5"	9:G:102:ARG:NH2	2.12	0.64
7:E:102:ALA:HB2	7:E:120:THR:CG2	2.26	0.64
13:K:51:LYS:HD3	13:K:52:GLY:N	2.12	0.64
14:L:50:SER:O	14:L:51:ALA:HB2	1.96	0.64
14:L:83:VAL:CG2	14:L:100:ILE:HG23	2.28	0.64
16:N:58:LYS:HZ2	16:N:58:LYS:HB3	1.62	0.64
19:Q:76:LEU:C	19:Q:76:LEU:HD23	2.17	0.64
1:A:502:G:H2'	1:A:503:C:H6	1.63	0.64
1:A:1247:U:O2'	1:A:1248:A:H5'	1.97	0.64
9:G:21:VAL:HG23	9:G:22:LEU:N	2.13	0.64
9:G:116:ALA:HA	9:G:119:ARG:NH2	2.13	0.64
10:H:86:ILE:HD11	10:H:136:GLU:HG3	1.78	0.64
13:K:121:PRO:HG2	13:K:126:ARG:HG3	1.78	0.64
14:L:83:VAL:HG21	14:L:100:ILE:HG23	1.79	0.64
10:H:87:SER:HB2	10:H:93:VAL:HB	1.79	0.64
17:O:17:ARG:HG3	17:O:17:ARG:HH11	1.61	0.64
22:T:38:LYS:HB2	22:T:38:LYS:NZ	2.13	0.64
22:T:76:ALA:O	22:T:80:ARG:HG3	1.98	0.64
1:A:701:C:H5"	1:A:703:G:O4'	1.98	0.64
5:C:32:LEU:HD21	5:C:59:ARG:HD2	1.79	0.64
1:A:629:G:O2'	1:A:630:G:H5'	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:664:G:OP1	20:R:64:ARG:HD2	1.98	0.64
1:A:1427:U:H2'	1:A:1428:A:H8	1.61	0.64
11:I:115:GLY:O	11:I:116:LYS:HD3	1.97	0.64
13:K:84:VAL:HG21	13:K:95:ILE:HD11	1.80	0.64
20:R:22:VAL:O	20:R:22:VAL:HG12	1.97	0.64
5:C:110:ASN:O	5:C:111:LEU:HD23	1.97	0.64
12:J:82:ILE:HG22	12:J:86:MET:SD	2.38	0.64
14:L:60:LEU:HD11	14:L:85:ILE:HD12	1.79	0.64
16:N:35:ARG:C	16:N:37:PHE:H	1.99	0.64
21:S:4:SER:O	21:S:5:LEU:HB2	1.97	0.64
1:A:35:G:H2'	1:A:36:C:C6	2.32	0.64
1:A:865:A:H5'	1:A:1078:U:O4	1.98	0.64
1:A:1117:G:H21	1:A:1180:A:H1'	1.63	0.64
1:A:353:A:H5'	1:A:353:A:H8	1.63	0.64
1:A:580:U:H2'	1:A:581:G:O4'	1.98	0.64
5:C:10:PHE:CZ	5:C:178:LEU:HD13	2.32	0.64
5:C:139:GLN:HA	5:C:139:GLN:NE2	2.13	0.64
9:G:75:VAL:HG13	9:G:75:VAL:O	1.98	0.64
15:M:77:ASN:O	15:M:80:ARG:HB2	1.97	0.64
4:B:16:HIS:NE2	4:B:214:ILE:HD11	2.12	0.63
14:L:41:ARG:HG2	14:L:42:THR:H	1.63	0.63
8:F:78:GLU:O	8:F:81:ILE:HG22	1.99	0.63
1:A:392:G:H2'	1:A:393:A:H8	1.63	0.63
1:A:1497:G:H2'	1:A:1498:U:H5'	1.81	0.63
4:B:101:MET:HA	4:B:108:ILE:HG13	1.81	0.63
5:C:164:ARG:HG2	5:C:165:THR:H	1.63	0.63
6:D:177:ASP:OD1	6:D:179:GLU:HB2	1.98	0.63
13:K:84:VAL:HG11	13:K:91:ARG:HG3	1.81	0.63
1:A:984:C:H2'	1:A:985:C:C6	2.33	0.63
7:E:144:THR:HG23	7:E:146:ALA:H	1.64	0.63
9:G:26:PHE:CE2	9:G:30:ILE:HD11	2.34	0.63
13:K:124:LYS:HD2	13:K:125:PHE:CZ	2.34	0.63
14:L:75:HIS:HD2	14:L:77:LEU:H	1.45	0.63
18:P:8:ARG:HG2	18:P:8:ARG:HH11	1.64	0.63
1:A:1342:C:O2'	1:A:1343:G:H5'	1.98	0.63
1:A:1495:U:H2'	1:A:1496:C:H6	1.62	0.63
4:B:87:ARG:HD3	4:B:234:PRO:HD2	1.80	0.63
1:A:279:A:C4	19:Q:98:LEU:HD23	2.34	0.63
1:A:1316:G:N2	1:A:1318:A:H3'	2.14	0.63
6:D:62:GLN:NE2	6:D:65:ARG:NH1	2.47	0.63
6:D:121:VAL:O	6:D:134:ASP:HA	1.97	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:Q:18:THR:HG23	19:Q:69:LYS:HE3	1.80	0.63
20:R:52:PRO:HB2	20:R:54:ARG:HD2	1.81	0.63
21:S:20:LEU:HD12	21:S:21:GLU:N	2.13	0.63
1:A:382:A:H2'	1:A:383:A:C8	2.33	0.63
1:A:393:A:O2'	1:A:394:G:H5'	1.98	0.63
4:B:116:GLU:HA	4:B:119:GLU:OE1	1.99	0.63
17:O:9:GLN:HG3	17:O:13:GLN:HE22	1.64	0.63
11:I:111:ARG:HG2	11:I:112:LYS:N	2.14	0.63
13:K:126:ARG:C	13:K:128:ALA:H	2.01	0.63
1:A:149:A:H2'	1:A:150:C:C6	2.34	0.62
1:A:474:G:OP1	1:A:474:G:H4'	1.97	0.62
1:A:1118:C:H1'	1:A:1179:A:C4	2.34	0.62
1:A:1381:U:O2'	1:A:1382:C:H5'	1.99	0.62
19:Q:43:LEU:O	19:Q:69:LYS:HG3	1.99	0.62
12:J:75:ILE:HD12	12:J:75:ILE:N	2.14	0.62
12:J:89:ASP:HB2	12:J:91:PRO:HD2	1.81	0.62
16:N:58:LYS:HB3	16:N:58:LYS:NZ	2.14	0.62
1:A:1129:C:H1'	1:A:1132:C:H5	1.64	0.62
4:B:172:ILE:N	4:B:172:ILE:HD12	2.14	0.62
5:C:6:HIS:CD2	5:C:8:ILE:HB	2.34	0.62
5:C:52:LEU:H	5:C:52:LEU:CD2	2.11	0.62
10:H:4:ASP:OD1	10:H:85:ARG:NH1	2.33	0.62
12:J:35:SER:HB2	12:J:72:VAL:O	2.00	0.62
17:O:16:ALA:HB1	17:O:21:ASP:HB3	1.79	0.62
19:Q:60:ILE:HD13	19:Q:61:GLU:N	2.14	0.62
4:B:10:LEU:HD12	4:B:10:LEU:N	2.15	0.62
4:B:102:LEU:HD21	4:B:162:ILE:CD1	2.29	0.62
4:B:139:LYS:O	4:B:139:LYS:HD3	1.99	0.62
15:M:37:THR:HG22	15:M:39:ILE:HG13	1.81	0.62
16:N:37:PHE:CE2	16:N:53:LEU:HD13	2.34	0.62
1:A:113:G:H1'	1:A:354:G:H5'	1.81	0.62
1:A:539:A:H2'	1:A:540:G:H8	1.65	0.62
18:P:67:THR:CG2	18:P:68:ASP:N	2.62	0.62
1:A:1277:C:H2'	1:A:1278:U:H5'	1.81	0.62
10:H:4:ASP:OD1	10:H:7:ALA:HB2	2.00	0.62
1:A:357:G:O2'	1:A:358:U:H5'	2.00	0.62
1:A:939:G:H2'	1:A:940:C:H6	1.62	0.62
1:A:1300:G:O2'	1:A:1301:U:H6	1.81	0.62
1:A:1347:G:H2'	1:A:1373:G:H1	1.65	0.62
4:B:21:ARG:C	4:B:22:LYS:HD2	2.19	0.62
18:P:43:LYS:HB3	18:P:48:TRP:CD1	2.35	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:R:47:THR:HG22	20:R:48:GLY:N	2.13	0.62
1:A:560:U:H4'	1:A:561:U:H5"	1.82	0.62
1:A:1064:G:C4'	1:A:1065:U:H5'	2.26	0.62
1:A:1104:G:OP1	4:B:111:ARG:HD2	1.99	0.62
1:A:1117:G:N2	1:A:1180:A:H1'	2.14	0.62
5:C:6:HIS:HD2	5:C:8:ILE:H	1.48	0.62
5:C:22:TRP:HB2	5:C:59:ARG:HB2	1.82	0.62
10:H:134:ILE:O	10:H:135:CYS:HB3	1.99	0.62
11:I:12:GLU:HG3	11:I:12:GLU:O	2.00	0.62
20:R:17:SER:OG	20:R:54:ARG:HB2	2.00	0.62
1:A:974:A:OP1	16:N:31:ARG:HD3	2.00	0.62
4:B:219:VAL:C	4:B:221:LEU:H	2.02	0.62
6:D:187:ARG:HD2	6:D:188:LEU:N	2.14	0.62
9:G:155:ARG:CZ	9:G:155:ARG:HA	2.30	0.62
11:I:5:TYR:HA	11:I:17:VAL:O	2.00	0.62
1:A:1371:G:OP1	11:I:12:GLU:HB3	2.00	0.61
1:A:266:G:H5"	1:A:268:C:H41	1.65	0.61
1:A:501:C:H2'	1:A:502:G:C8	2.34	0.61
1:A:1510:U:H2'	1:A:1511:G:C8	2.35	0.61
7:E:87:SER:HB3	7:E:131:ILE:CD1	2.29	0.61
14:L:83:VAL:HG22	14:L:84:LEU:N	2.14	0.61
1:A:434:U:H2'	1:A:435:C:C6	2.36	0.61
1:A:993:G:H4'	1:A:994:A:OP2	1.99	0.61
4:B:45:GLN:O	4:B:49:GLU:HG3	1.99	0.61
4:B:162:ILE:HG22	4:B:164:VAL:HG23	1.83	0.61
7:E:33:VAL:HG11	7:E:109:ILE:HA	1.82	0.61
11:I:118:LYS:NZ	11:I:118:LYS:HB3	2.14	0.61
18:P:74:LEU:HD22	18:P:79:VAL:HG21	1.82	0.61
20:R:43:PHE:O	20:R:51:LEU:HD12	1.99	0.61
1:A:409:G:C6	1:A:433:C:H5'	2.35	0.61
4:B:7:VAL:HG12	4:B:221:LEU:HD23	1.81	0.61
6:D:8:VAL:C	6:D:10:ARG:H	2.04	0.61
7:E:148:VAL:O	7:E:152:ARG:HG3	2.00	0.61
8:F:30:LEU:O	8:F:35:ALA:HB3	2.01	0.61
8:F:67:MET:HE2	8:F:71:ARG:HB2	1.81	0.61
15:M:94:ARG:HH11	15:M:94:ARG:HG3	1.63	0.61
21:S:9:VAL:HG12	21:S:10:PHE:N	2.13	0.61
21:S:12:ASP:HB3	21:S:14:HIS:CE1	2.36	0.61
4:B:47:THR:HA	4:B:202:PRO:HG2	1.83	0.61
4:B:69:LEU:C	4:B:69:LEU:HD23	2.20	0.61
1:A:131:C:H2'	1:A:132:C:C6	2.35	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1189:C:P	12:J:51:ARG:HH22	2.22	0.61
9:G:75:VAL:HG23	9:G:87:VAL:C	2.20	0.61
21:S:50:ALA:HA	21:S:58:VAL:O	2.00	0.61
1:A:462:G:N2	18:P:82:GLN:NE2	2.49	0.61
1:A:477:G:H3'	1:A:478:A:C4'	2.30	0.61
1:A:657:G:H4'	17:O:28:GLN:HG2	1.81	0.61
1:A:1468:A:H2'	1:A:1469:G:O4'	2.00	0.61
7:E:81:GLU:HG2	7:E:90:VAL:HG13	1.82	0.61
10:H:104:ARG:O	10:H:106:GLY:N	2.32	0.61
11:I:51:ARG:HG2	11:I:56:LEU:HD12	1.81	0.61
14:L:62:SER:O	14:L:64:TYR:HD1	1.83	0.61
20:R:55:ARG:NH1	20:R:55:ARG:HB3	2.16	0.61
21:S:17:GLU:O	21:S:20:LEU:HG	1.99	0.61
1:A:625:G:H2'	1:A:626:U:C6	2.36	0.61
1:A:1486:G:H2'	1:A:1487:G:O4'	2.01	0.61
4:B:95:GLN:C	4:B:96:ARG:HD2	2.21	0.61
4:B:167:PRO:O	4:B:171:ALA:N	2.34	0.61
6:D:98:GLU:HG2	6:D:189:PRO:HG3	1.82	0.61
15:M:86:CYS:HA	21:S:73:GLU:O	2.01	0.61
22:T:35:THR:HA	22:T:38:LYS:NZ	2.16	0.61
1:A:918:A:H2'	1:A:919:A:C8	2.36	0.61
1:A:974:A:P	16:N:29:ARG:HH22	2.22	0.61
1:A:1229:A:H2'	1:A:1230:C:H6	1.65	0.61
5:C:36:ASP:OD1	5:C:57:ILE:HG21	2.01	0.61
5:C:64:VAL:H	5:C:99:VAL:HB	1.66	0.61
8:F:19:LEU:HD23	8:F:19:LEU:C	2.21	0.61
10:H:137:VAL:O	10:H:137:VAL:HG12	2.00	0.61
13:K:110:ASP:HB2	20:R:88:LYS:CE	2.31	0.61
22:T:38:LYS:HB2	22:T:38:LYS:HZ2	1.66	0.61
1:A:8:A:N6	6:D:209:ARG:HB2	2.16	0.61
1:A:1488:G:O2'	1:A:1489:G:H5'	2.00	0.61
5:C:134:ILE:HG23	5:C:151:VAL:HB	1.83	0.61
5:C:191:THR:HG21	5:C:193:TYR:CE1	2.35	0.61
6:D:151:LYS:H	6:D:151:LYS:CD	2.13	0.61
11:I:55:ALA:O	11:I:56:LEU:HB3	2.00	0.61
1:A:193:C:H2'	1:A:194:C:C6	2.35	0.60
6:D:127:THR:CG2	6:D:147:ALA:HB3	2.31	0.60
14:L:53:ARG:HG3	14:L:93:LEU:HD21	1.83	0.60
14:L:86:ARG:HG3	14:L:87:GLY:O	2.01	0.60
17:O:87:ILE:HG22	17:O:88:ARG:NH1	2.15	0.60
18:P:4:ILE:CG1	18:P:64:ALA:HB1	2.31	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:328:C:O2	1:A:328:C:C2'	2.49	0.60
11:I:10:ARG:HG2	11:I:10:ARG:HH11	1.65	0.60
13:K:74:ALA:C	13:K:76:GLY:H	2.03	0.60
14:L:110:VAL:O	14:L:122:THR:HG22	2.00	0.60
18:P:20:VAL:HG11	18:P:32:TYR:CB	2.31	0.60
1:A:109:A:H2'	1:A:326:G:N2	2.16	0.60
1:A:1521:G:H2'	1:A:1522:U:C6	2.36	0.60
5:C:96:GLY:O	5:C:97:LYS:HD3	2.01	0.60
6:D:5:ILE:HG22	6:D:5:ILE:O	2.01	0.60
6:D:8:VAL:O	6:D:10:ARG:N	2.28	0.60
6:D:150:GLU:HA	6:D:153:ARG:HG2	1.82	0.60
7:E:24:ARG:HG2	7:E:24:ARG:NH1	2.16	0.60
17:O:56:LEU:C	17:O:56:LEU:HD23	2.21	0.60
20:R:46:GLU:H	20:R:46:GLU:CD	2.05	0.60
5:C:10:PHE:CE2	5:C:178:LEU:HD13	2.36	0.60
5:C:20:SER:O	16:N:54:PRO:HB3	2.02	0.60
5:C:191:THR:HG21	5:C:193:TYR:CE2	2.36	0.60
7:E:79:GLU:OE1	10:H:105:ARG:HG2	2.02	0.60
9:G:48:LYS:O	9:G:51:GLN:HB2	2.01	0.60
14:L:71:PRO:O	14:L:102:ARG:HG3	2.02	0.60
1:A:130:A:OP2	1:A:190(E):U:H2'	2.01	0.60
4:B:216:SER:O	4:B:219:VAL:N	2.34	0.60
12:J:24:VAL:O	12:J:28:ARG:HB2	2.02	0.60
14:L:93:LEU:O	14:L:96:VAL:HG23	2.02	0.60
23:V:5:ASP:O	23:V:11:GLY:HA3	2.01	0.60
1:A:409:G:N1	1:A:433:C:OP1	2.35	0.60
4:B:87:ARG:HH21	4:B:219:VAL:HB	1.67	0.60
5:C:115:LEU:HD23	5:C:118:GLN:OE1	2.02	0.60
7:E:80:ILE:HD13	7:E:91:LEU:HB2	1.82	0.60
20:R:56:THR:HB	20:R:58:LEU:HD12	1.83	0.60
1:A:179:A:H2'	1:A:180:U:C6	2.36	0.60
1:A:477:G:C3'	1:A:478:A:H4'	2.30	0.60
1:A:1281:U:H4'	1:A:1282:C:OP2	2.01	0.60
8:F:69:GLU:H	8:F:69:GLU:CD	2.05	0.60
10:H:118:VAL:C	10:H:119:LEU:HD23	2.21	0.60
13:K:33:THR:HG22	13:K:39:PRO:HA	1.82	0.60
1:A:640:A:O2'	1:A:641:U:H5'	2.02	0.60
5:C:14:ILE:HG22	5:C:15:THR:HG23	1.83	0.60
9:G:124:LEU:O	9:G:127:ALA:HB3	2.01	0.60
14:L:27:LEU:HG	14:L:28:LYS:H	1.65	0.60
1:A:977:A:H2'	1:A:978:A:H5"	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1047:G:H5"	16:N:4:LYS:HG3	1.82	0.60
4:B:71:VAL:HA	4:B:93:VAL:HG23	1.83	0.60
5:C:15:THR:OG1	5:C:179:ARG:HA	2.01	0.60
12:J:62:HIS:HB3	16:N:59:ALA:HB3	1.83	0.60
22:T:54:LYS:HA	22:T:57:ARG:NH2	2.17	0.60
1:A:112:G:H21	1:A:354:G:H5'	1.67	0.60
1:A:340:U:H2'	1:A:341:C:C6	2.37	0.60
1:A:384:G:H2'	1:A:385:C:C6	2.37	0.60
1:A:459:G:H3'	1:A:460:A:H5"	1.83	0.60
1:A:730:G:H21	1:A:765:G:H5"	1.67	0.60
5:C:191:THR:HG22	5:C:192:THR:N	2.16	0.60
6:D:36:ARG:H	6:D:37:PRO:CD	2.06	0.60
21:S:15:LEU:HD12	21:S:16:LEU:N	2.16	0.60
1:A:26:A:N6	1:A:558:G:H1'	2.17	0.59
1:A:1323:G:H2'	1:A:1324:A:C8	2.37	0.59
7:E:103:GLY:O	7:E:106:PRO:HD2	2.02	0.59
12:J:49:VAL:HG21	16:N:41:ARG:O	2.02	0.59
22:T:35:THR:HA	22:T:38:LYS:HZ2	1.66	0.59
1:A:710:G:OP1	8:F:54:LYS:HD2	2.02	0.59
1:A:1133:G:H2'	1:A:1134:G:C8	2.37	0.59
1:A:1236:A:H2'	1:A:1237:C:C6	2.37	0.59
6:D:7:PRO:HG2	6:D:10:ARG:HD2	1.84	0.59
12:J:19:SER:HA	12:J:22:LYS:HZ3	1.67	0.59
14:L:40:VAL:O	14:L:40:VAL:HG12	2.03	0.59
17:O:26:GLU:HA	17:O:81:LEU:HD11	1.85	0.59
1:A:107:G:C2'	1:A:108:G:H5'	2.32	0.59
1:A:355:C:H5'	1:A:389:A:OP2	2.02	0.59
1:A:1330:U:H2'	1:A:1331:G:H5'	1.83	0.59
4:B:81:VAL:O	4:B:81:VAL:HG12	2.03	0.59
5:C:178:LEU:O	5:C:179:ARG:CB	2.48	0.59
16:N:9:LYS:C	16:N:11:LYS:N	2.56	0.59
18:P:75:ARG:O	18:P:78:GLY:N	2.33	0.59
1:A:1056:U:H5'	5:C:163:ALA:HB2	1.84	0.59
4:B:24:TRP:CZ2	4:B:26:PRO:HG3	2.37	0.59
5:C:86:VAL:O	5:C:89:GLU:HB3	2.01	0.59
7:E:150:ARG:HG3	7:E:150:ARG:HH11	1.67	0.59
8:F:10:LEU:HD12	8:F:59:TYR:HB3	1.81	0.59
14:L:75:HIS:CD2	14:L:77:LEU:H	2.20	0.59
1:A:1360:A:H2'	1:A:1361:G:C8	2.36	0.59
4:B:140:HIS:HA	4:B:143:GLU:HG2	1.84	0.59
6:D:36:ARG:HG2	6:D:36:ARG:O	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:103:VAL:HB	10:H:108:GLY:O	2.01	0.59
11:I:97:LYS:HB3	11:I:98:PRO:HD3	1.84	0.59
11:I:105:ASP:OD1	11:I:107:ARG:HB2	2.03	0.59
12:J:16:LEU:O	12:J:19:SER:N	2.36	0.59
13:K:127:LYS:O	13:K:127:LYS:HD3	2.02	0.59
20:R:26:LEU:HD12	20:R:27:GLY:H	1.68	0.59
1:A:1316:G:H5"	16:N:17:LYS:CE	2.30	0.59
4:B:209:ARG:CZ	4:B:239:VAL:HG11	2.32	0.59
5:C:85:ARG:HH21	5:C:88:ARG:HD3	1.66	0.59
16:N:21:TYR:HD2	16:N:22:THR:O	1.86	0.59
19:Q:68:ARG:H	19:Q:70:ARG:NH1	2.01	0.59
21:S:28:LYS:HG3	21:S:29:ARG:N	2.17	0.59
1:A:605:U:O2'	1:A:606:G:H5'	2.02	0.59
6:D:103:ASN:OD1	6:D:114:ARG:NH2	2.35	0.59
7:E:43:LEU:HB2	7:E:136:MET:HE2	1.84	0.59
8:F:33:TYR:HB2	8:F:75:LEU:HD23	1.83	0.59
1:A:437:U:C2'	1:A:438:G:H5'	2.33	0.59
1:A:760:G:H1	19:Q:105:ALA:CB	2.15	0.59
5:C:20:SER:HB3	5:C:22:TRP:HE1	1.66	0.59
5:C:85:ARG:HH11	5:C:85:ARG:HB2	1.67	0.59
9:G:50:ILE:HG21	9:G:61:VAL:HG21	1.84	0.59
14:L:27:LEU:HD22	14:L:62:SER:HB3	1.84	0.59
14:L:28:LYS:C	14:L:30:ALA:H	2.05	0.59
14:L:37:CYS:HB2	14:L:81:SER:O	2.03	0.59
16:N:3:ARG:NH1	16:N:6:LEU:HD11	2.17	0.59
20:R:37:VAL:CG2	20:R:78:LEU:HB3	2.33	0.59
1:A:129(A):G:O2'	1:A:130:A:OP2	2.20	0.59
1:A:958:A:N3	1:A:985:C:O2'	2.33	0.59
1:A:1279:A:H5"	1:A:1280:A:OP1	2.03	0.59
4:B:184:VAL:N	4:B:198:ASP:OD2	2.33	0.59
6:D:71:SER:OG	6:D:74:GLN:HG3	2.03	0.59
9:G:50:ILE:CG2	9:G:61:VAL:HG21	2.32	0.59
9:G:78:ARG:HB2	9:G:156:TRP:CZ3	2.38	0.59
13:K:121:PRO:HG2	13:K:126:ARG:CG	2.31	0.59
16:N:18:VAL:HG23	16:N:19:ARG:HG3	1.85	0.59
1:A:1137:C:H4'	1:A:1138:G:C2	2.38	0.59
4:B:82:ARG:HA	4:B:92:TYR:CE2	2.38	0.59
4:B:88:ALA:HB3	4:B:90:MET:HG2	1.84	0.59
5:C:191:THR:CG2	5:C:192:THR:N	2.66	0.59
6:D:176:LEU:H	6:D:176:LEU:HD23	1.68	0.59
11:I:17:VAL:HG11	11:I:81:ILE:HA	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:R:53:ARG:NH1	20:R:59:SER:HA	2.16	0.59
1:A:164:U:H2'	1:A:165:C:C6	2.37	0.58
1:A:409:G:N3	1:A:409:G:C2'	2.66	0.58
1:A:972:C:C4'	12:J:57:LYS:HD3	2.27	0.58
1:A:1112:C:O2	5:C:179:ARG:HD2	2.02	0.58
1:A:1202:G:O2'	1:A:1203:C:H5'	2.02	0.58
1:A:1212:U:H4'	1:A:1213:A:H5'	1.83	0.58
4:B:195:ASP:O	10:H:74:PRO:HG3	2.02	0.58
4:B:200:ILE:HD13	4:B:202:PRO:HD3	1.84	0.58
5:C:13:GLY:HA3	16:N:57:ARG:NH2	2.17	0.58
1:A:332:G:O2'	1:A:333:G:H5'	2.03	0.58
1:A:392:G:H2'	1:A:393:A:C8	2.38	0.58
1:A:409:G:H3'	1:A:431:A:H62	1.69	0.58
1:A:556:C:C2'	1:A:557:G:H5'	2.33	0.58
1:A:1154:G:H2'	1:A:1155:G:C8	2.35	0.58
1:A:1305:G:C5'	23:V:4:GLY:HA3	2.33	0.58
4:B:206:ASP:O	4:B:207:ALA:CB	2.50	0.58
14:L:8:ASN:O	14:L:12:ARG:HG3	2.03	0.58
1:A:141:A:H1'	1:A:182:U:O2	2.03	0.58
1:A:448:A:H2'	1:A:449:C:C6	2.38	0.58
4:B:12:GLU:C	4:B:14:GLY:H	2.07	0.58
4:B:88:ALA:HB2	4:B:219:VAL:HG13	1.83	0.58
11:I:93:ARG:CB	11:I:93:ARG:HH11	2.16	0.58
12:J:71:LEU:O	12:J:72:VAL:HB	2.02	0.58
14:L:115:LYS:O	14:L:117:ARG:N	2.36	0.58
16:N:29:ARG:HB3	16:N:40:CYS:CB	2.34	0.58
19:Q:101:ARG:CZ	19:Q:101:ARG:HA	2.33	0.58
1:A:1031:G:H4'	1:A:1032:G:N7	2.18	0.58
1:A:1096:C:H2'	1:A:1097:C:H6	1.67	0.58
4:B:28:PHE:CE2	4:B:190:THR:HA	2.37	0.58
5:C:69:HIS:H	5:C:69:HIS:CD2	2.21	0.58
12:J:7:LYS:HB2	12:J:97:GLU:O	2.04	0.58
16:N:16:PHE:CB	16:N:18:VAL:HG22	2.33	0.58
19:Q:27:PHE:HB2	19:Q:28:PRO:HD2	1.83	0.58
1:A:676:A:H1'	13:K:115:PRO:HB3	1.86	0.58
1:A:1278:U:H5"	1:A:1279:A:O4'	2.04	0.58
1:A:1329:A:P	15:M:28:ALA:HB3	2.43	0.58
4:B:102:LEU:N	4:B:102:LEU:CD1	2.67	0.58
8:F:39:LYS:HE3	8:F:64:GLN:NE2	2.18	0.58
20:R:43:PHE:C	20:R:51:LEU:HD12	2.23	0.58
1:A:60:A:H4'	1:A:61:G:O5'	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:3:ARG:N	6:D:3:ARG:NE	2.50	0.58
8:F:62:TRP:C	8:F:63:TYR:HD1	2.06	0.58
10:H:80:ILE:O	10:H:80:ILE:HG22	2.03	0.58
11:I:3:GLN:HG2	11:I:4:TYR:N	2.18	0.58
16:N:27:CYS:SG	16:N:29:ARG:HB2	2.43	0.58
1:A:112:G:N2	1:A:354:G:H5'	2.19	0.58
1:A:389:A:H2'	1:A:390:C:H5'	1.86	0.58
1:A:410:G:H2'	1:A:411:A:O4'	2.04	0.58
5:C:167:TRP:O	5:C:168:ALA:HB3	2.03	0.58
9:G:110:GLN:OE1	9:G:110:GLN:HA	2.03	0.58
14:L:77:LEU:HD21	14:L:107:ALA:HA	1.85	0.58
1:A:718:G:C8	13:K:116:HIS:HB3	2.38	0.58
17:O:35:ARG:C	17:O:59:MET:HE1	2.24	0.58
1:A:1349:A:H2'	1:A:1350:A:H8	1.69	0.58
1:A:1477:C:H2'	1:A:1478:C:C6	2.39	0.58
4:B:98:LEU:HD23	4:B:98:LEU:N	2.19	0.58
7:E:15:ARG:O	7:E:27:ARG:O	2.22	0.58
15:M:4:ILE:HG22	15:M:5:ALA:H	1.66	0.58
1:A:840:C:OP2	1:A:840:C:H3'	2.04	0.57
1:A:1057:G:O2'	1:A:1058:G:H5'	2.03	0.57
1:A:1176:A:H2'	1:A:1177:G:C8	2.39	0.57
1:A:1320:C:N3	21:S:36:ARG:HD3	2.19	0.57
1:A:1502:A:H2	1:A:1505:G:N1	2.01	0.57
4:B:26:PRO:C	4:B:28:PHE:H	2.06	0.57
6:D:76:ARG:HG2	6:D:76:ARG:HH11	1.69	0.57
11:I:118:LYS:O	11:I:119:ALA:HB3	2.04	0.57
12:J:34:VAL:HG22	12:J:74:ILE:HG23	1.84	0.57
17:O:29:VAL:HG11	17:O:67:LEU:HD21	1.86	0.57
18:P:28:ARG:HG2	18:P:29:ASP:OD2	2.03	0.57
1:A:352:C:H4'	1:A:354:G:OP1	2.04	0.57
1:A:1212:U:H1'	1:A:1213:A:OP2	2.03	0.57
1:A:1305:G:C8	1:A:1305:G:OP2	2.57	0.57
4:B:10:LEU:HG	4:B:48:MET:CE	2.35	0.57
7:E:28:PHE:O	7:E:47:LYS:HA	2.04	0.57
13:K:127:LYS:HA	13:K:127:LYS:CE	2.29	0.57
14:L:28:LYS:C	14:L:30:ALA:N	2.57	0.57
1:A:1305:G:N2	1:A:1331:G:H1'	2.19	0.57
1:A:1504:G:O2'	1:A:1505:G:OP2	2.20	0.57
6:D:170:VAL:HG13	6:D:174:LEU:HB2	1.86	0.57
8:F:76:ALA:O	8:F:80:ARG:HG3	2.04	0.57
9:G:137:LYS:O	9:G:141:VAL:HG23	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:34:VAL:HG12	12:J:35:SER:H	1.67	0.57
12:J:51:ARG:HB2	12:J:59:SER:HB3	1.85	0.57
12:J:90:LEU:N	12:J:91:PRO:CD	2.62	0.57
19:Q:24:GLU:CD	19:Q:37:LYS:HD3	2.24	0.57
1:A:834:C:H2'	1:A:835:U:C6	2.39	0.57
1:A:883:C:O2'	1:A:884:U:H5'	2.04	0.57
4:B:44:LEU:HA	4:B:47:THR:OG1	2.04	0.57
9:G:120:ILE:H	9:G:120:ILE:HD12	1.69	0.57
12:J:39:PRO:O	12:J:69:ASN:O	2.23	0.57
1:A:478:A:C2'	1:A:479:C:H5'	2.34	0.57
1:A:959:A:C2	1:A:1222:G:O4'	2.58	0.57
1:A:1061:G:O2'	1:A:1062:U:H5'	2.05	0.57
1:A:1226:C:H6	15:M:103:THR:OG1	1.87	0.57
5:C:14:ILE:HG22	5:C:15:THR:H	1.69	0.57
6:D:24:GLU:OE1	6:D:24:GLU:HA	2.04	0.57
12:J:4:ILE:HD11	12:J:74:ILE:HB	1.86	0.57
15:M:39:ILE:CD1	15:M:52:GLU:HB3	2.35	0.57
1:A:107:G:H2'	1:A:108:G:H5'	1.85	0.57
4:B:194:PRO:C	4:B:196:LEU:H	2.08	0.57
5:C:88:ARG:HG3	5:C:101:LEU:HB2	1.86	0.57
5:C:188:LEU:O	5:C:189:ALA:HB2	2.05	0.57
7:E:79:GLU:CD	7:E:79:GLU:H	2.07	0.57
8:F:91:VAL:HG21	20:R:72:ARG:NH1	2.20	0.57
22:T:64:ASP:OD1	22:T:81:LYS:HD2	2.04	0.57
1:A:1121:U:H2'	1:A:1122:U:C6	2.38	0.57
1:A:1152:A:H5'	12:J:70:ARG:HH22	1.70	0.57
6:D:126:ILE:CG2	6:D:127:THR:N	2.68	0.57
15:M:3:ARG:HH11	15:M:3:ARG:CB	2.17	0.57
19:Q:81:ARG:HG3	19:Q:81:ARG:O	2.05	0.57
1:A:489:C:H2'	1:A:490:G:C8	2.36	0.57
1:A:686:U:O4	1:A:703:G:H1'	2.04	0.57
1:A:1347:G:C2'	1:A:1373:G:H1	2.18	0.57
4:B:79:ASP:CB	4:B:238:LEU:HD21	2.35	0.57
5:C:18:TRP:HE3	5:C:18:TRP:H	1.51	0.57
1:A:76:C:O2'	1:A:77:G:H5'	2.05	0.57
5:C:15:THR:O	5:C:16:ARG:HB2	2.04	0.57
7:E:96:PRO:HA	7:E:117:ASP:OD2	2.04	0.57
7:E:146:ALA:O	7:E:149:GLU:HG2	2.04	0.57
9:G:153:HIS:C	9:G:155:ARG:H	2.07	0.57
10:H:69:ARG:NH1	10:H:75:ARG:O	2.37	0.57
17:O:29:VAL:HG21	17:O:67:LEU:HD23	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1196:U:OP1	1:A:1197:G:H5'	2.05	0.57
4:B:75:LYS:HE2	4:B:96:ARG:HH22	1.69	0.57
4:B:87:ARG:HH22	4:B:220:ASP:CG	2.08	0.57
4:B:111:ARG:HB3	4:B:149:LEU:HD11	1.86	0.57
5:C:107:GLN:H	5:C:107:GLN:CD	2.07	0.57
6:D:61:LYS:HZ1	6:D:62:GLN:NE2	2.03	0.57
8:F:55:ASP:HB3	8:F:86:ARG:HH12	1.68	0.57
13:K:52:GLY:H	13:K:55:LYS:HE3	1.68	0.57
19:Q:66:SER:O	19:Q:70:ARG:NH1	2.37	0.57
1:A:1365:G:H2'	1:A:1366:C:H6	1.69	0.56
4:B:53:ARG:O	4:B:56:ARG:HB3	2.04	0.56
4:B:91:PRO:HG3	4:B:154:LEU:HD12	1.86	0.56
6:D:153:ARG:HE	6:D:181:MET:CE	2.17	0.56
7:E:72:GLN:O	7:E:73:ASN:HB3	2.05	0.56
9:G:70:LYS:HB3	9:G:96:GLN:HG2	1.86	0.56
10:H:35:ILE:CG2	10:H:111:ILE:HD13	2.35	0.56
11:I:42:ARG:HG2	11:I:42:ARG:HH11	1.70	0.56
12:J:34:VAL:HG12	12:J:35:SER:N	2.19	0.56
14:L:89:ARG:HG2	14:L:97:ARG:CB	2.33	0.56
14:L:101:VAL:O	14:L:103:GLY:N	2.38	0.56
1:A:279:A:H4'	1:A:280:C:OP2	2.04	0.56
1:A:1202:G:C2'	1:A:1203:C:H5'	2.34	0.56
12:J:8:LEU:HD13	12:J:20:ALA:CB	2.35	0.56
18:P:63:GLY:O	18:P:64:ALA:C	2.42	0.56
21:S:19:VAL:HG13	21:S:20:LEU:N	2.20	0.56
1:A:163:C:O2'	1:A:164:U:H5'	2.05	0.56
1:A:258:G:H2'	1:A:259:G:H8	1.70	0.56
1:A:442:C:H2'	1:A:443:C:H6	1.69	0.56
1:A:627:G:H2'	1:A:628:G:H8	1.70	0.56
1:A:748:C:OP2	1:A:748:C:H6	1.86	0.56
1:A:1194:U:H4'	7:E:22:GLY:CA	2.36	0.56
1:A:1305:G:H5'	23:V:4:GLY:HA3	1.87	0.56
1:A:1313:U:OP1	21:S:6:LYS:HB3	2.04	0.56
1:A:1330:U:C2'	1:A:1331:G:H5'	2.34	0.56
1:A:1372:U:OP1	11:I:71:SER:HB3	2.05	0.56
5:C:34:LEU:HD23	5:C:34:LEU:O	2.06	0.56
5:C:179:ARG:HH11	5:C:179:ARG:HG3	1.71	0.56
8:F:2:ARG:NH2	8:F:69:GLU:HG2	2.20	0.56
8:F:33:TYR:HA	8:F:71:ARG:HH21	1.70	0.56
8:F:40:VAL:CG2	8:F:41:GLU:N	2.68	0.56
9:G:15:ASP:OD2	9:G:44:TYR:OH	2.22	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:14:ARG:O	10:H:18:ARG:HD3	2.04	0.56
10:H:92:ARG:HH11	10:H:92:ARG:CG	2.18	0.56
10:H:107:LEU:HD23	10:H:107:LEU:N	2.20	0.56
11:I:8:GLY:HA3	11:I:79:LEU:HB3	1.87	0.56
12:J:16:LEU:O	12:J:17:ASP:C	2.43	0.56
12:J:75:ILE:HG22	12:J:76:ASN:N	2.20	0.56
15:M:5:ALA:HB3	15:M:8:GLU:HG3	1.86	0.56
17:O:27:VAL:O	17:O:30:ALA:HB3	2.05	0.56
19:Q:67:LYS:HA	19:Q:70:ARG:HH12	1.69	0.56
1:A:1427:U:H2'	1:A:1428:A:C8	2.39	0.56
5:C:14:ILE:CG2	5:C:15:THR:N	2.68	0.56
10:H:23:SER:C	10:H:24:THR:HG22	2.25	0.56
11:I:85:LEU:O	11:I:92:TYR:HD1	1.88	0.56
13:K:54:ARG:O	13:K:57:THR:HG23	2.05	0.56
21:S:28:LYS:HG2	21:S:31:ILE:HD11	1.87	0.56
1:A:130:A:P	19:Q:63:ARG:HH21	2.27	0.56
1:A:192:U:C1'	22:T:103:GLY:HA2	2.34	0.56
1:A:259:G:OP1	22:T:87:LYS:HE2	2.06	0.56
7:E:50:GLU:HB3	7:E:53:LEU:HD13	1.87	0.56
11:I:28:VAL:O	11:I:28:VAL:HG23	2.05	0.56
11:I:31:GLN:OE1	11:I:36:TYR:HD1	1.88	0.56
1:A:285:G:O2'	1:A:286:G:H5'	2.06	0.56
1:A:349:A:C3'	1:A:350:G:H5"	2.35	0.56
1:A:521:G:OP1	14:L:73:GLU:O	2.23	0.56
1:A:603:U:H2'	1:A:604:G:H8	1.70	0.56
1:A:748:C:H1'	1:A:749:C:H5	1.71	0.56
4:B:213:LEU:HD23	4:B:213:LEU:C	2.26	0.56
5:C:54:ARG:HG3	5:C:55:VAL:H	1.71	0.56
8:F:47:ARG:N	8:F:47:ARG:HD3	2.21	0.56
15:M:53:VAL:O	15:M:57:ARG:HB2	2.06	0.56
1:A:191:G:C4	22:T:105:SER:HB3	2.41	0.56
1:A:229:U:H5"	18:P:33:ILE:HD13	1.88	0.56
1:A:590:C:O2'	1:A:591:U:H5'	2.06	0.56
1:A:1101:A:H4'	1:A:1102:A:O5'	2.06	0.56
1:A:1128:C:H1'	1:A:1130:A:C8	2.41	0.56
1:A:1226:C:H2'	15:M:103:THR:OG1	2.06	0.56
1:A:1260:C:O5'	1:A:1284:C:H4'	2.06	0.56
4:B:70:PHE:HE1	4:B:90:MET:HG3	1.70	0.56
8:F:60:PHE:C	8:F:61:LEU:HD12	2.26	0.56
9:G:42:ILE:HG23	9:G:117:ALA:HA	1.88	0.56
9:G:78:ARG:HG2	9:G:80:VAL:HG13	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:49:ASN:HD22	14:L:49:ASN:N	2.03	0.56
19:Q:3:LYS:HB3	19:Q:61:GLU:HB3	1.88	0.56
1:A:190(E):U:O2'	19:Q:63:ARG:NH2	2.38	0.56
1:A:1160:G:O2'	1:A:1161:C:H5'	2.06	0.56
6:D:157:LEU:O	6:D:157:LEU:HD22	2.05	0.56
7:E:60:TYR:O	7:E:64:ARG:HG2	2.06	0.56
9:G:116:ALA:HA	9:G:119:ARG:CZ	2.35	0.56
13:K:54:ARG:HA	13:K:57:THR:HG23	1.87	0.56
16:N:9:LYS:C	16:N:9:LYS:HD3	2.26	0.56
1:A:1407:C:O2'	1:A:1408:A:H5'	2.06	0.56
4:B:88:ALA:CB	4:B:90:MET:HG2	2.36	0.56
5:C:142:MET:HG3	5:C:170:GLN:HB2	1.88	0.56
7:E:148:VAL:HG21	10:H:107:LEU:HB3	1.86	0.56
10:H:69:ARG:HH11	10:H:69:ARG:HG3	1.71	0.56
12:J:94:VAL:CG1	12:J:95:GLU:N	2.69	0.56
14:L:113:ARG:HH11	14:L:113:ARG:HG2	1.70	0.56
19:Q:66:SER:OG	19:Q:69:LYS:HB3	2.05	0.56
1:A:1016:A:H2'	1:A:1017:G:O4'	2.06	0.56
4:B:197:VAL:CB	4:B:200:ILE:HG23	2.31	0.56
20:R:54:ARG:HD3	20:R:55:ARG:HG2	1.87	0.56
21:S:15:LEU:HD12	21:S:15:LEU:C	2.25	0.56
1:A:536:C:H2'	1:A:537:G:C8	2.40	0.55
4:B:127:ILE:HG13	4:B:128:GLU:OE2	2.06	0.55
5:C:84:ILE:O	5:C:84:ILE:HG12	2.06	0.55
9:G:22:LEU:O	9:G:25:ALA:HB3	2.06	0.55
10:H:9:MET:HG3	10:H:26:VAL:HG21	1.88	0.55
10:H:60:ARG:HH11	10:H:60:ARG:HG3	1.70	0.55
11:I:25:LYS:HB2	11:I:60:ASP:OD2	2.05	0.55
11:I:46:ALA:HB2	11:I:74:ILE:HG23	1.88	0.55
1:A:386:C:O2'	1:A:387:U:H5'	2.05	0.55
1:A:975:A:H5'	1:A:975:A:H8	1.71	0.55
1:A:1206:G:H1'	5:C:193:TYR:O	2.06	0.55
1:A:1241:G:H2'	1:A:1242:C:C6	2.41	0.55
4:B:81:VAL:HG22	4:B:215:LEU:HD21	1.88	0.55
7:E:21:ALA:O	7:E:23:GLY:N	2.37	0.55
7:E:146:ALA:HA	7:E:149:GLU:HG2	1.88	0.55
12:J:94:VAL:HG12	12:J:95:GLU:H	1.70	0.55
15:M:22:ILE:HG21	15:M:66:LEU:HD22	1.87	0.55
1:A:1142:G:H2'	1:A:1143:G:O4'	2.06	0.55
5:C:28:GLN:HA	5:C:31:HIS:CD2	2.40	0.55
10:H:119:LEU:HD12	10:H:124:ALA:HA	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:33:PHE:C	11:I:35:GLU:H	2.08	0.55
22:T:13:LEU:C	22:T:13:LEU:CD1	2.75	0.55
1:A:409:G:H5"	1:A:431:A:N7	2.21	0.55
1:A:1132:C:H2'	1:A:1133:G:C8	2.40	0.55
4:B:69:LEU:HD12	4:B:155:LEU:CD1	2.25	0.55
5:C:61:ALA:O	5:C:63:ASN:N	2.38	0.55
7:E:107:ARG:O	7:E:110:LEU:N	2.35	0.55
12:J:6:ILE:CD1	12:J:73:ASP:H	2.19	0.55
15:M:97:PRO:HB2	15:M:101:GLN:OE1	2.06	0.55
1:A:858:G:O2'	1:A:859:A:H5'	2.07	0.55
1:A:1495:U:H2'	1:A:1496:C:C6	2.41	0.55
6:D:3:ARG:NE	6:D:3:ARG:H	2.04	0.55
9:G:23:VAL:HG12	9:G:27:ILE:HD11	1.88	0.55
16:N:36:PHE:O	16:N:36:PHE:HD1	1.87	0.55
1:A:189:G:N2	1:A:190(J):U:O2	2.34	0.55
1:A:421:U:HO2'	1:A:422:C:H3'	1.72	0.55
1:A:458:C:H2'	1:A:459:G:H8	1.72	0.55
1:A:490:G:H2'	1:A:491:G:H8	1.70	0.55
1:A:1305:G:OP2	1:A:1305:G:H8	1.89	0.55
1:A:1333:A:H2'	1:A:1334:G:O4'	2.06	0.55
1:A:1478:C:H2'	1:A:1479:C:H6	1.72	0.55
4:B:39:ILE:HG22	4:B:40:HIS:O	2.07	0.55
6:D:61:LYS:NZ	6:D:62:GLN:NE2	2.55	0.55
11:I:128:ARG:HG2	11:I:128:ARG:OXT	2.07	0.55
13:K:27:ASN:OD1	13:K:28:THR:N	2.39	0.55
14:L:28:LYS:O	14:L:30:ALA:N	2.39	0.55
1:A:308:C:H2'	1:A:309:G:H8	1.72	0.55
1:A:713:G:H2'	1:A:714:G:C8	2.42	0.55
1:A:867:G:O2'	1:A:868:C:H5'	2.06	0.55
4:B:12:GLU:C	4:B:14:GLY:N	2.60	0.55
5:C:76:VAL:HG11	5:C:103:VAL:HG21	1.88	0.55
8:F:10:LEU:HD12	8:F:10:LEU:H	1.71	0.55
1:A:1014:A:H2'	1:A:1015:A:C8	2.41	0.55
4:B:136:VAL:HG12	4:B:140:HIS:NE2	2.21	0.55
7:E:11:ILE:HG22	7:E:12:LEU:HD12	1.88	0.55
10:H:48:TYR:HB2	10:H:60:ARG:O	2.06	0.55
11:I:10:ARG:HA	11:I:104:ARG:HE	1.71	0.55
21:S:6:LYS:H	21:S:6:LYS:HD2	1.71	0.55
1:A:1178:G:N2	1:A:1180:A:H3'	2.22	0.55
13:K:110:ASP:HB3	20:R:85:LEU:HB3	1.89	0.55
13:K:126:ARG:C	13:K:128:ALA:N	2.59	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:Q:100:LYS:HG3	19:Q:101:ARG:HG2	1.89	0.55
20:R:45:SER:OG	20:R:49:LYS:HB2	2.07	0.55
20:R:53:ARG:HG2	20:R:63:GLN:OE1	2.07	0.55
1:A:442:C:H2'	1:A:443:C:C6	2.42	0.55
1:A:1039:C:O2'	1:A:1040:U:H5'	2.07	0.55
6:D:199:ASN:ND2	6:D:201:GLN:HB2	2.22	0.55
8:F:71:ARG:O	8:F:73:ASN:N	2.40	0.55
12:J:36:GLY:O	12:J:72:VAL:HA	2.07	0.55
14:L:43:VAL:HG12	14:L:44:THR:N	2.21	0.55
14:L:119:LYS:O	14:L:120:TYR:HB2	2.07	0.55
1:A:291:C:O2'	1:A:292:G:H5'	2.06	0.54
1:A:408:A:H4'	1:A:429:U:O2	2.07	0.54
1:A:750:G:N3	17:O:23:GLY:HA3	2.22	0.54
1:A:1094:G:H5"	1:A:1095:U:H5	1.71	0.54
1:A:1367:C:C5'	12:J:60:ARG:NH1	2.68	0.54
1:A:1419:G:H2'	1:A:1420:C:C6	2.42	0.54
4:B:71:VAL:CG2	4:B:164:VAL:HG22	2.35	0.54
5:C:11:ARG:O	5:C:14:ILE:O	2.25	0.54
5:C:50:ALA:O	5:C:70:VAL:CG1	2.55	0.54
5:C:195:VAL:CG1	5:C:196:LEU:N	2.70	0.54
10:H:42:GLU:HG3	10:H:109:ILE:HG21	1.90	0.54
11:I:100:GLY:O	11:I:102:LEU:N	2.39	0.54
18:P:28:ARG:NH1	18:P:29:ASP:OD2	2.41	0.54
22:T:83:ARG:HB3	22:T:87:LYS:HZ3	1.72	0.54
1:A:287:U:O2'	1:A:288:A:H5'	2.06	0.54
1:A:1068:G:OP2	1:A:1068:G:H8	1.89	0.54
1:A:1090:U:H2'	1:A:1091:U:H6	1.72	0.54
4:B:190:THR:O	4:B:190:THR:HG23	2.08	0.54
10:H:104:ARG:NH2	10:H:138:TRP:CH2	2.75	0.54
11:I:19:LEU:HD23	11:I:61:ALA:HB2	1.88	0.54
12:J:32:ALA:HB2	12:J:75:ILE:HB	1.89	0.54
16:N:43:CYS:HA	16:N:46:GLU:HB2	1.90	0.54
21:S:63:THR:HG22	21:S:64:GLU:N	2.21	0.54
1:A:266:G:O2'	1:A:267:C:OP2	2.19	0.54
1:A:545:C:O2'	1:A:546:G:H5'	2.08	0.54
1:A:1225:A:H5'	1:A:1226:C:OP2	2.08	0.54
1:A:1312:G:O2'	1:A:1313:U:H5'	2.06	0.54
5:C:93:LYS:HD3	5:C:93:LYS:C	2.27	0.54
12:J:75:ILE:HG22	12:J:76:ASN:H	1.72	0.54
14:L:101:VAL:O	14:L:102:ARG:C	2.45	0.54
15:M:44:ARG:HB3	15:M:46:LYS:HG2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1241:G:H2'	1:A:1242:C:H6	1.73	0.54
4:B:178:ARG:NH1	4:B:178:ARG:CG	2.64	0.54
5:C:69:HIS:CD2	5:C:69:HIS:N	2.76	0.54
6:D:170:VAL:HG21	6:D:176:LEU:HD22	1.89	0.54
12:J:8:LEU:HD22	12:J:20:ALA:HB2	1.88	0.54
21:S:15:LEU:O	21:S:19:VAL:HG12	2.08	0.54
1:A:189:G:H5"	1:A:189:G:C8	2.38	0.54
1:A:445:G:O2'	1:A:446:G:H5'	2.07	0.54
1:A:1066:C:O2'	1:A:1067:A:H5'	2.07	0.54
4:B:60:ASP:HB3	4:B:64:ARG:NH2	2.23	0.54
13:K:11:LYS:O	13:K:12:ARG:HB2	2.06	0.54
15:M:77:ASN:O	15:M:80:ARG:N	2.41	0.54
1:A:222:U:H2'	1:A:223:U:C6	2.43	0.54
1:A:1091:U:O2	1:A:1093:A:C8	2.61	0.54
1:A:1138:G:H3'	1:A:1138:G:N3	2.22	0.54
1:A:1289:A:H2'	1:A:1290:G:H5'	1.89	0.54
4:B:145:LEU:O	4:B:147:LYS:N	2.41	0.54
5:C:54:ARG:HG3	5:C:55:VAL:N	2.22	0.54
6:D:39:PRO:O	6:D:44:GLY:HA3	2.08	0.54
9:G:50:ILE:O	9:G:50:ILE:HG22	2.07	0.54
12:J:46:ARG:HG2	12:J:46:ARG:HH11	1.72	0.54
15:M:66:LEU:N	15:M:66:LEU:HD12	2.23	0.54
1:A:45:U:H2'	1:A:46:G:C8	2.43	0.54
1:A:190(F):G:H4'	1:A:190(G):G:OP2	2.08	0.54
1:A:350:G:H5'	1:A:350:G:H8	1.73	0.54
1:A:1320:C:O2	21:S:72:GLY:HA3	2.07	0.54
4:B:60:ASP:HB3	4:B:64:ARG:HE	1.72	0.54
4:B:91:PRO:HG3	4:B:154:LEU:HB2	1.89	0.54
4:B:209:ARG:NE	4:B:239:VAL:HG11	2.22	0.54
5:C:28:GLN:HA	5:C:31:HIS:NE2	2.23	0.54
8:F:25:ILE:HD12	8:F:82:ARG:HH11	1.73	0.54
8:F:28:ARG:HA	8:F:28:ARG:HE	1.72	0.54
8:F:68:PRO:HB2	8:F:71:ARG:HG2	1.90	0.54
11:I:33:PHE:CE2	11:I:47:LEU:HD11	2.43	0.54
11:I:113:LYS:N	11:I:113:LYS:CD	2.71	0.54
20:R:48:GLY:O	20:R:74:ARG:NH2	2.40	0.54
1:A:560:U:H5'	1:A:566:G:N2	2.22	0.54
5:C:39:ILE:HG22	5:C:40:ARG:N	2.23	0.54
5:C:153:VAL:HA	5:C:197:GLY:O	2.07	0.54
8:F:22:GLU:CD	8:F:84:ASN:HD22	2.10	0.54
15:M:35:GLU:C	15:M:37:THR:H	2.10	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:88:ARG:HG3	15:M:98:VAL:HG11	1.90	0.54
20:R:17:SER:HB2	20:R:54:ARG:HE	1.73	0.54
20:R:37:VAL:HG22	20:R:78:LEU:HB3	1.89	0.54
20:R:52:PRO:HB2	20:R:54:ARG:CD	2.38	0.54
22:T:100:ILE:O	22:T:101:GLY:C	2.46	0.54
1:A:459:G:H3'	1:A:460:A:C5'	2.38	0.54
7:E:43:LEU:HB2	7:E:136:MET:CE	2.38	0.54
15:M:121:LYS:O	15:M:122:LYS:HB2	2.08	0.54
1:A:327:A:H3'	1:A:328:C:H5"	1.90	0.54
1:A:960:U:O2'	1:A:1223:C:H4'	2.08	0.54
1:A:975:A:H4'	1:A:976:G:O5'	2.07	0.54
1:A:1039:C:H2'	1:A:1040:U:H6	1.73	0.54
1:A:1347:G:C2'	1:A:1348:U:OP2	2.56	0.54
4:B:217:ARG:HA	4:B:220:ASP:HB2	1.89	0.54
7:E:80:ILE:N	7:E:80:ILE:HD12	2.23	0.54
14:L:85:ILE:CG2	14:L:98:TYR:HB3	2.38	0.54
14:L:93:LEU:N	14:L:93:LEU:HD23	2.23	0.54
15:M:94:ARG:HG3	15:M:94:ARG:NH1	2.20	0.54
20:R:44:LEU:HD11	20:R:79:LEU:HD13	1.89	0.54
1:A:17:U:H2'	1:A:18:C:C6	2.42	0.53
1:A:418:C:H5	1:A:425:G:O6	1.91	0.53
1:A:947:G:H2'	1:A:948:C:O4'	2.08	0.53
1:A:1531:A:H2'	1:A:1532:U:O4'	2.09	0.53
6:D:64:LEU:HB2	6:D:198:VAL:HG21	1.90	0.53
11:I:36:TYR:CD2	11:I:37:PHE:CE2	2.96	0.53
12:J:19:SER:HA	12:J:22:LYS:HZ2	1.72	0.53
12:J:56:HIS:O	12:J:58:ASP:N	2.41	0.53
21:S:52:TYR:HA	21:S:56:GLN:O	2.08	0.53
1:A:131:C:H2'	1:A:132:C:H6	1.73	0.53
1:A:314:C:O2'	1:A:315:A:H5'	2.08	0.53
1:A:644:G:O2'	1:A:645:C:H5'	2.07	0.53
1:A:818:G:O2'	1:A:819:A:H5'	2.09	0.53
1:A:1103:C:H5"	4:B:98:LEU:HD13	1.90	0.53
1:A:1250:A:H4'	11:I:68:GLY:CA	2.37	0.53
4:B:78:GLN:O	4:B:94:ASN:ND2	2.40	0.53
4:B:167:PRO:HG2	4:B:168:THR:H	1.72	0.53
9:G:77:SER:HB2	9:G:86:GLN:HE22	1.74	0.53
10:H:6:ILE:HD12	10:H:35:ILE:HD12	1.90	0.53
10:H:90:GLY:O	10:H:91:ARG:HB2	2.08	0.53
11:I:118:LYS:HZ2	11:I:118:LYS:CB	2.22	0.53
14:L:5:PRO:HB2	14:L:10:LEU:HG	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:V:6:ARG:NH1	23:V:7:ARG:HD2	2.24	0.53
1:A:264:U:H4'	19:Q:63:ARG:HD3	1.90	0.53
1:A:636:U:H2'	1:A:637:G:H8	1.74	0.53
1:A:826:C:H2'	1:A:827:U:H6	1.74	0.53
1:A:997:U:O2'	1:A:998:G:H5'	2.07	0.53
1:A:1300:G:HO2'	1:A:1301:U:H6	1.44	0.53
4:B:209:ARG:NH2	4:B:239:VAL:HG11	2.23	0.53
7:E:80:ILE:HD12	7:E:91:LEU:HB2	1.83	0.53
14:L:24:VAL:O	14:L:24:VAL:HG12	2.07	0.53
18:P:51:VAL:O	18:P:53:VAL:N	2.39	0.53
1:A:151:A:H2'	1:A:152:A:O4'	2.09	0.53
1:A:1062:U:H2'	1:A:1063:C:C6	2.43	0.53
1:A:1453:G:H2'	1:A:1454:G:O4'	2.09	0.53
5:C:85:ARG:HB2	5:C:85:ARG:NH1	2.23	0.53
7:E:110:LEU:O	7:E:113:ALA:HB3	2.09	0.53
9:G:148:ASN:HD22	9:G:148:ASN:N	2.04	0.53
10:H:31:PHE:O	10:H:35:ILE:HG13	2.09	0.53
11:I:4:TYR:CD2	11:I:88:TYR:HA	2.42	0.53
17:O:25:THR:HG22	17:O:25:THR:O	2.08	0.53
20:R:79:LEU:HD22	20:R:80:PRO:HD2	1.90	0.53
22:T:100:ILE:O	22:T:102:GLY:N	2.41	0.53
1:A:404:U:O2'	1:A:405:U:H5'	2.09	0.53
4:B:172:ILE:HD12	4:B:172:ILE:H	1.73	0.53
5:C:22:TRP:CZ3	5:C:32:LEU:HD22	2.44	0.53
6:D:31:CYS:O	6:D:31:CYS:SG	2.67	0.53
6:D:108:LEU:HB2	6:D:110:PHE:CE1	2.44	0.53
19:Q:48:GLU:O	19:Q:49:GLU:C	2.47	0.53
1:A:382:A:H2'	1:A:383:A:H8	1.74	0.53
1:A:410:G:P	1:A:410:G:O4'	2.67	0.53
1:A:413:G:H1'	1:A:417:C:OP1	2.09	0.53
1:A:627:G:O2'	1:A:628:G:H5'	2.08	0.53
1:A:1256:A:O3'	1:A:1257:U:H4'	2.08	0.53
4:B:25:ASN:ND2	4:B:27:LYS:N	2.45	0.53
5:C:14:ILE:O	5:C:16:ARG:N	2.42	0.53
7:E:43:LEU:N	7:E:136:MET:HE1	2.24	0.53
7:E:80:ILE:HD12	7:E:80:ILE:H	1.74	0.53
7:E:89:ILE:HD13	7:E:90:VAL:H	1.74	0.53
12:J:47:PHE:CE2	16:N:37:PHE:HE1	2.26	0.53
15:M:40:ASN:HD22	15:M:41:PRO:HD2	1.73	0.53
1:A:939:G:P	9:G:95:ARG:HH22	2.31	0.53
5:C:165:THR:O	5:C:165:THR:HG22	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:150:GLU:HA	6:D:153:ARG:CG	2.38	0.53
7:E:12:LEU:HD22	7:E:12:LEU:C	2.28	0.53
12:J:32:ALA:CB	12:J:75:ILE:HB	2.38	0.53
13:K:14:VAL:HG11	13:K:40:ILE:HD11	1.90	0.53
15:M:102:ARG:NH1	15:M:104:ARG:HB3	2.24	0.53
23:V:6:ARG:CZ	23:V:7:ARG:HD2	2.38	0.53
1:A:390:C:O3'	18:P:28:ARG:NH2	2.42	0.53
1:A:975:A:H5'	1:A:975:A:C8	2.44	0.53
5:C:113:ALA:HB2	5:C:202:ILE:HG13	1.90	0.53
11:I:48:GLU:N	11:I:49:PRO:CD	2.70	0.53
12:J:48:THR:OG1	12:J:62:HIS:CD2	2.62	0.53
14:L:54:LYS:HE2	14:L:54:LYS:N	2.23	0.53
15:M:23:TYR:CD2	15:M:70:LEU:HD13	2.44	0.53
17:O:25:THR:HG22	17:O:70:LEU:HD23	1.91	0.53
22:T:14:LYS:HG2	22:T:18:GLN:OE1	2.09	0.53
1:A:1043:C:O2'	1:A:1044:A:H5'	2.09	0.53
4:B:97:TRP:HZ2	4:B:102:LEU:CD1	2.22	0.53
5:C:21:ARG:N	5:C:21:ARG:HD2	2.23	0.53
5:C:58:GLU:HB3	12:J:92:THR:HG21	1.90	0.53
8:F:82:ARG:HA	8:F:82:ARG:HE	1.73	0.53
11:I:11:LYS:O	11:I:12:GLU:HB3	2.08	0.53
1:A:190:C:O2'	1:A:190(A):C:O5'	2.26	0.53
1:A:835:U:OP1	20:R:64:ARG:NH2	2.39	0.53
1:A:860:A:H2'	1:A:861:G:O4'	2.09	0.53
1:A:1499:A:O2'	1:A:1500:A:H5'	2.09	0.53
5:C:43:LEU:HD23	5:C:43:LEU:C	2.29	0.53
12:J:38:ILE:O	12:J:70:ARG:HA	2.09	0.53
14:L:124:LYS:CD	14:L:125:PRO:HD2	2.34	0.53
17:O:78:TYR:CZ	17:O:82:ILE:HD11	2.44	0.53
1:A:538:G:O2'	1:A:539:A:H5'	2.09	0.52
1:A:662:G:H2'	1:A:663:A:C8	2.45	0.52
1:A:1136:U:H5"	1:A:1137:C:H5	1.74	0.52
1:A:1329:A:O2'	1:A:1330:U:H5'	2.08	0.52
1:A:1442:G:H2'	1:A:1446:A:C8	2.45	0.52
4:B:185:ILE:H	4:B:185:ILE:HD12	1.75	0.52
4:B:221:LEU:HA	4:B:224:GLN:HB3	1.90	0.52
6:D:31:CYS:O	6:D:33:MET:N	2.42	0.52
6:D:199:ASN:HD21	6:D:201:GLN:HB2	1.74	0.52
10:H:73:ASP:OD2	10:H:75:ARG:HB2	2.08	0.52
16:N:14:PRO:O	16:N:15:LYS:CB	2.57	0.52
18:P:20:VAL:CG1	18:P:32:TYR:HB2	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:Q:24:GLU:OE2	19:Q:37:LYS:HD3	2.08	0.52
1:A:838:G:C2'	1:A:839:U:H5"	2.39	0.52
1:A:945:G:C2	1:A:946:A:C8	2.96	0.52
1:A:1292:U:OP2	9:G:41:ARG:NH2	2.42	0.52
1:A:1431:C:C2'	1:A:1432:G:H5'	2.39	0.52
4:B:87:ARG:HB2	4:B:219:VAL:HG11	1.91	0.52
6:D:148:VAL:O	6:D:153:ARG:HD3	2.09	0.52
9:G:79:ARG:HG2	9:G:79:ARG:HH11	1.73	0.52
11:I:36:TYR:HD2	11:I:37:PHE:CE2	2.27	0.52
1:A:184:G:C4'	1:A:224:C:H4'	2.39	0.52
1:A:1118:C:O5'	1:A:1118:C:H6	1.92	0.52
1:A:1402:C:H2'	1:A:1403:C:O4'	2.10	0.52
1:A:1480:G:H2'	1:A:1481:U:H6	1.73	0.52
7:E:72:GLN:O	7:E:73:ASN:CB	2.58	0.52
7:E:76:ILE:HG22	7:E:78:HIS:H	1.74	0.52
12:J:5:ARG:HD2	12:J:99:LYS:HB3	1.91	0.52
12:J:60:ARG:O	12:J:61:GLU:O	2.26	0.52
12:J:96:ILE:HG22	12:J:97:GLU:N	2.23	0.52
14:L:27:LEU:HD22	14:L:62:SER:CB	2.39	0.52
22:T:94:ALA:O	22:T:95:ALA:HB3	2.08	0.52
1:A:84:U:H2'	1:A:88:A:O4'	2.08	0.52
1:A:430:A:P	6:D:22:LYS:HZ1	2.33	0.52
1:A:476:G:C2	1:A:478:A:H5'	2.43	0.52
1:A:485:G:O2'	1:A:486:U:P	2.67	0.52
1:A:620:C:C2	6:D:135:LEU:HD13	2.44	0.52
1:A:1000:U:H2'	1:A:1001:A:O4'	2.09	0.52
1:A:1060:C:O2	1:A:1198:G:C2	2.62	0.52
4:B:53:ARG:CZ	4:B:53:ARG:HB3	2.40	0.52
5:C:52:LEU:HD23	5:C:52:LEU:N	2.24	0.52
9:G:155:ARG:HA	9:G:155:ARG:NH1	2.24	0.52
10:H:20:TYR:CE2	10:H:75:ARG:HD2	2.44	0.52
11:I:93:ARG:NH1	11:I:93:ARG:CB	2.71	0.52
17:O:87:ILE:HG22	17:O:88:ARG:HH12	1.74	0.52
21:S:41:VAL:O	21:S:44:MET:HG3	2.10	0.52
1:A:1366:C:H2'	1:A:1367:C:C6	2.45	0.52
5:C:43:LEU:HD11	5:C:68:VAL:HG21	1.92	0.52
6:D:102:ASP:OD2	6:D:103:ASN:N	2.42	0.52
13:K:110:ASP:HB2	20:R:88:LYS:HE2	1.91	0.52
16:N:22:THR:HB	16:N:33:VAL:HG21	1.92	0.52
16:N:29:ARG:O	16:N:33:VAL:HG13	2.10	0.52
17:O:88:ARG:HG3	17:O:89:GLY:H	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:P:7:ALA:O	18:P:17:TYR:HA	2.09	0.52
20:R:70:ILE:O	20:R:74:ARG:HG3	2.10	0.52
1:A:256:U:H2'	1:A:257:G:H8	1.75	0.52
1:A:353:A:H8	1:A:353:A:C5'	2.23	0.52
1:A:603:U:H2'	1:A:604:G:C8	2.44	0.52
1:A:760:G:H1	19:Q:105:ALA:HB2	1.73	0.52
1:A:1366:C:H2'	1:A:1367:C:H6	1.74	0.52
1:A:1451:A:O2'	1:A:1452:C:OP1	2.25	0.52
4:B:79:ASP:HB2	4:B:238:LEU:HD21	1.90	0.52
8:F:91:VAL:HG21	20:R:72:ARG:CZ	2.39	0.52
10:H:103:VAL:CG2	10:H:110:ALA:HB2	2.39	0.52
10:H:126:LYS:C	10:H:128:GLY:H	2.13	0.52
13:K:14:VAL:HG21	13:K:40:ILE:HD11	1.92	0.52
13:K:126:ARG:O	13:K:128:ALA:N	2.42	0.52
15:M:48:LEU:HD13	15:M:53:VAL:HG22	1.91	0.52
19:Q:40:LYS:HD3	19:Q:42:TYR:OH	2.09	0.52
1:A:192:U:O4'	22:T:103:GLY:HA2	2.10	0.52
1:A:666:G:H5'	1:A:726:C:H1'	1.91	0.52
4:B:91:PRO:HG2	4:B:155:LEU:HD23	1.91	0.52
5:C:14:ILE:CG2	5:C:15:THR:H	2.21	0.52
6:D:107:ARG:HB3	6:D:174:LEU:HD11	1.91	0.52
7:E:17:ALA:HB2	7:E:26:PHE:HD2	1.74	0.52
14:L:85:ILE:HG22	14:L:86:ARG:N	2.25	0.52
15:M:34:LEU:HG	15:M:41:PRO:HB3	1.90	0.52
17:O:33:THR:HG23	17:O:63:ARG:NH1	2.24	0.52
20:R:53:ARG:NH1	20:R:60:GLY:N	2.58	0.52
1:A:408:A:N3	1:A:408:A:H2'	2.25	0.52
1:A:831:U:H2'	1:A:832:C:H6	1.75	0.52
1:A:1090:U:H2'	1:A:1091:U:C6	2.44	0.52
4:B:16:HIS:O	4:B:17:PHE:O	2.28	0.52
5:C:151:VAL:HA	5:C:199:LYS:O	2.10	0.52
7:E:15:ARG:HD3	7:E:26:PHE:CG	2.45	0.52
11:I:10:ARG:HG2	11:I:10:ARG:NH1	2.25	0.52
16:N:18:VAL:HG23	16:N:19:ARG:N	2.24	0.52
1:A:861:G:O2'	1:A:862:C:H5'	2.09	0.52
5:C:34:LEU:HG	16:N:25:VAL:HG21	1.92	0.52
8:F:75:LEU:C	8:F:75:LEU:HD13	2.30	0.52
11:I:46:ALA:HA	11:I:78:LYS:HB2	1.92	0.52
14:L:115:LYS:O	14:L:117:ARG:HG3	2.09	0.52
22:T:96:GLY:O	22:T:97:ALA:HB3	2.10	0.52
1:A:105:G:H2'	1:A:106:C:C6	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:269:C:H2'	1:A:270:A:C8	2.44	0.52
1:A:575:G:OP1	1:A:575:G:H4'	2.10	0.52
1:A:1224:G:H1	1:A:1362:C:N4	2.06	0.52
1:A:1431:C:H2'	1:A:1432:G:H5'	1.91	0.52
4:B:115:LEU:HG	4:B:116:GLU:N	2.25	0.52
7:E:106:PRO:O	7:E:110:LEU:HG	2.09	0.52
8:F:44:GLY:HA2	8:F:59:TYR:CE1	2.45	0.52
9:G:52:GLU:O	9:G:53:LYS:HD2	2.10	0.52
12:J:18:ALA:O	12:J:21:GLN:HB3	2.09	0.52
13:K:22:HIS:HB3	13:K:29:ILE:HG13	1.92	0.52
14:L:85:ILE:HG23	14:L:98:TYR:HB3	1.91	0.52
15:M:125:ARG:HD2	15:M:125:ARG:C	2.30	0.52
1:A:462:G:H22	18:P:82:GLN:NE2	2.08	0.51
1:A:1114:C:H2'	1:A:1115:C:H6	1.75	0.51
1:A:1221:G:C2'	1:A:1222:G:H5'	2.40	0.51
1:A:1424:C:O2'	1:A:1425:U:H5'	2.10	0.51
4:B:180:LEU:O	4:B:182:ILE:HG13	2.10	0.51
9:G:50:ILE:HD11	9:G:121:ALA:HA	1.92	0.51
10:H:31:PHE:CZ	10:H:134:ILE:CD1	2.90	0.51
11:I:8:GLY:CA	11:I:79:LEU:HB3	2.40	0.51
12:J:28:ARG:NH2	12:J:33:GLN:HE21	2.09	0.51
16:N:3:ARG:O	16:N:7:ILE:HG13	2.10	0.51
1:A:432:A:H4'	1:A:433:C:C2	2.45	0.51
1:A:1110:A:H8	1:A:1110:A:O5'	1.93	0.51
1:A:1326:C:OP1	23:V:12:LYS:NZ	2.37	0.51
4:B:10:LEU:HG	4:B:48:MET:HE2	1.91	0.51
4:B:103:THR:HG23	4:B:176:GLU:HB3	1.92	0.51
5:C:28:GLN:O	5:C:31:HIS:HD2	1.93	0.51
7:E:135:THR:O	7:E:138:ALA:HB3	2.10	0.51
7:E:139:LEU:O	7:E:141:GLN:N	2.44	0.51
21:S:28:LYS:CG	21:S:29:ARG:N	2.73	0.51
22:T:72:LEU:O	22:T:73:HIS:C	2.47	0.51
1:A:364:A:N6	14:L:28:LYS:HE2	2.26	0.51
1:A:437:U:H2'	1:A:438:G:H5'	1.93	0.51
1:A:445:G:H2'	1:A:446:G:H8	1.75	0.51
1:A:1065:U:O2'	1:A:1066:C:OP2	2.25	0.51
1:A:1203:C:OP1	16:N:2:ALA:HB3	2.10	0.51
1:A:1216:G:O3'	16:N:5:ALA:HB1	2.10	0.51
1:A:1249:C:H2'	1:A:1250:A:H5'	1.92	0.51
4:B:88:ALA:C	4:B:90:MET:H	2.13	0.51
4:B:128:GLU:HA	4:B:135:GLN:HE22	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:91:LEU:O	5:C:95:THR:HG23	2.11	0.51
7:E:76:ILE:HG23	7:E:77:PRO:HD2	1.93	0.51
10:H:138:TRP:CE3	10:H:138:TRP:OXT	2.64	0.51
19:Q:59:ILE:HD13	19:Q:73:VAL:HA	1.92	0.51
22:T:39:LYS:HD3	22:T:55:ILE:HD13	1.92	0.51
1:A:371:G:C2'	1:A:372:C:H5'	2.40	0.51
1:A:406:G:H1	1:A:436:C:N4	2.07	0.51
1:A:1152:A:H2'	1:A:1153:C:H6	1.71	0.51
1:A:1480:G:H2'	1:A:1481:U:C6	2.45	0.51
5:C:4:LYS:HA	5:C:4:LYS:HZ3	1.75	0.51
5:C:58:GLU:O	5:C:64:VAL:HG13	2.11	0.51
9:G:12:LEU:HD22	9:G:12:LEU:N	2.25	0.51
10:H:103:VAL:HG21	10:H:110:ALA:HB2	1.93	0.51
13:K:84:VAL:HG11	13:K:91:ARG:CD	2.40	0.51
13:K:105:VAL:O	13:K:105:VAL:HG12	2.09	0.51
23:V:2:GLY:C	23:V:4:GLY:H	2.12	0.51
1:A:1038:C:H2'	1:A:1039:C:C5	2.44	0.51
1:A:1286:A:C8	1:A:1287:A:H4'	2.44	0.51
10:H:119:LEU:HD23	10:H:119:LEU:N	2.25	0.51
12:J:6:ILE:HD13	12:J:73:ASP:H	1.75	0.51
21:S:53:ASN:HD22	21:S:58:VAL:CG2	2.23	0.51
22:T:13:LEU:H	22:T:13:LEU:HD12	1.74	0.51
1:A:177:C:H2'	1:A:178:C:H6	1.76	0.51
1:A:1349:A:H2'	1:A:1350:A:C8	2.45	0.51
1:A:1442:G:N2	1:A:1446:A:H2'	2.25	0.51
4:B:13:ALA:C	4:B:15:VAL:H	2.13	0.51
4:B:112:VAL:C	4:B:114:ARG:N	2.63	0.51
5:C:179:ARG:HG3	5:C:179:ARG:NH1	2.26	0.51
6:D:36:ARG:N	6:D:37:PRO:CD	2.72	0.51
8:F:9:VAL:CG2	8:F:87:ARG:HB2	2.39	0.51
1:A:418:C:H2'	1:A:419:C:C6	2.46	0.51
1:A:476:G:C5'	1:A:477:G:H5"	2.40	0.51
1:A:682:G:O2'	1:A:683:G:H5'	2.11	0.51
1:A:1053:G:C3'	1:A:1054:C:H5'	2.41	0.51
1:A:1229:A:H2'	1:A:1230:C:C6	2.44	0.51
7:E:105:VAL:HB	7:E:106:PRO:HD3	1.93	0.51
9:G:16:LEU:HD22	9:G:16:LEU:N	2.23	0.51
10:H:20:TYR:HE2	10:H:75:ARG:HD2	1.76	0.51
15:M:40:ASN:ND2	15:M:41:PRO:CD	2.71	0.51
17:O:71:GLN:O	17:O:71:GLN:CG	2.57	0.51
18:P:55:ARG:O	18:P:58:TYR:HB3	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1319:A:OP1	21:S:5:LEU:HD11	2.11	0.51
1:A:1320:C:H41	21:S:37:ARG:HD3	1.75	0.51
5:C:75:VAL:O	5:C:83:ARG:HG2	2.11	0.51
5:C:85:ARG:NH2	5:C:88:ARG:HD3	2.26	0.51
5:C:119:ARG:O	5:C:122:GLU:HB2	2.09	0.51
6:D:19:LEU:HD23	6:D:20:TYR:H	1.76	0.51
10:H:51:VAL:HG21	10:H:60:ARG:NH1	2.24	0.51
11:I:127:LYS:CB	15:M:126:LYS:HZ3	2.23	0.51
12:J:82:ILE:O	12:J:86:MET:HB2	2.11	0.51
13:K:74:ALA:C	13:K:76:GLY:N	2.63	0.51
14:L:125:PRO:C	14:L:127:GLU:H	2.14	0.51
22:T:54:LYS:HA	22:T:57:ARG:HH22	1.75	0.51
1:A:142:G:N3	1:A:196:A:H2	2.09	0.51
1:A:232:G:H1'	1:A:262:A:N1	2.26	0.51
1:A:794:A:H2'	1:A:795:C:C6	2.46	0.51
1:A:1305:G:O2'	1:A:1306:A:C8	2.38	0.51
1:A:1372:U:H2'	1:A:1373:G:O4'	2.11	0.51
8:F:63:TYR:N	8:F:63:TYR:CD1	2.78	0.51
9:G:146:GLU:CG	9:G:149:ARG:HH21	2.22	0.51
15:M:19:LEU:O	15:M:22:ILE:CD1	2.57	0.51
19:Q:59:ILE:HG23	19:Q:71:PHE:HB3	1.93	0.51
1:A:160:A:H1'	1:A:344:A:N7	2.26	0.51
1:A:636:U:H2'	1:A:637:G:C8	2.46	0.51
9:G:58:PRO:HG2	9:G:59:LEU:H	1.75	0.51
14:L:54:LYS:HG2	14:L:75:HIS:CE1	2.46	0.51
17:O:3:ILE:HG12	17:O:38:ARG:NH1	2.26	0.51
17:O:33:THR:HG23	17:O:63:ARG:HH12	1.76	0.51
18:P:12:LYS:O	18:P:13:HIS:HB2	2.09	0.51
1:A:404:U:H2'	1:A:405:U:H6	1.76	0.50
1:A:1072:G:H2'	1:A:1073:U:C6	2.45	0.50
1:A:1397:C:H4'	1:A:1398:A:OP2	2.10	0.50
4:B:59:GLU:O	4:B:62:ALA:HB3	2.11	0.50
4:B:77:ALA:HB2	4:B:211:ILE:HG21	1.89	0.50
4:B:85:ALA:HB3	4:B:92:TYR:HD2	1.75	0.50
4:B:112:VAL:O	4:B:114:ARG:N	2.42	0.50
6:D:162:LEU:HD13	6:D:181:MET:SD	2.51	0.50
8:F:10:LEU:HD11	8:F:61:LEU:HD11	1.93	0.50
8:F:39:LYS:HE3	8:F:64:GLN:HE22	1.74	0.50
9:G:62:PHE:HA	9:G:124:LEU:HD21	1.93	0.50
1:A:67:C:O2'	1:A:171:A:H1'	2.11	0.50
1:A:231:G:O2'	1:A:232:G:H5'	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:555:C:H2'	1:A:556:C:C6	2.46	0.50
1:A:1047:G:O2'	1:A:1048:G:H5'	2.11	0.50
1:A:1120:G:H2'	1:A:1121:U:C6	2.46	0.50
4:B:9:GLU:OE2	4:B:12:GLU:HA	2.12	0.50
5:C:44:GLU:HA	5:C:52:LEU:HD11	1.92	0.50
5:C:186:PHE:CG	5:C:187:ALA:N	2.80	0.50
6:D:35:ARG:O	6:D:36:ARG:CB	2.58	0.50
10:H:38:ILE:N	10:H:38:ILE:HD12	2.25	0.50
15:M:91:ARG:HB2	15:M:98:VAL:HG13	1.93	0.50
1:A:129(A):G:O2'	1:A:190(E):U:H2'	2.10	0.50
1:A:190(L):U:H3	22:T:105:SER:CB	2.23	0.50
1:A:532:A:C2'	1:A:533:A:OP1	2.59	0.50
1:A:925:G:C2	1:A:927:G:C8	3.00	0.50
1:A:1095:U:H2'	1:A:1096:C:H6	1.75	0.50
1:A:1525:G:O2'	1:A:1526:G:H5'	2.11	0.50
4:B:91:PRO:HB3	4:B:151:GLY:O	2.12	0.50
6:D:58:LEU:HD22	6:D:62:GLN:HG2	1.92	0.50
11:I:18:PHE:O	11:I:61:ALA:HA	2.11	0.50
16:N:29:ARG:HB3	16:N:40:CYS:HB3	1.93	0.50
18:P:59:TRP:HB3	18:P:64:ALA:HB2	1.93	0.50
1:A:1527:C:O2'	1:A:1528:U:H5'	2.11	0.50
7:E:75:THR:HG23	7:E:76:ILE:N	2.25	0.50
12:J:51:ARG:HB2	12:J:59:SER:CB	2.42	0.50
15:M:17:VAL:O	15:M:20:THR:HB	2.11	0.50
15:M:39:ILE:HD11	15:M:52:GLU:HB3	1.93	0.50
15:M:102:ARG:HH12	15:M:104:ARG:HB3	1.77	0.50
16:N:18:VAL:HG23	16:N:19:ARG:CG	2.41	0.50
1:A:130:A:H5'	19:Q:63:ARG:CZ	2.42	0.50
1:A:376:G:O2'	1:A:377:G:H5'	2.12	0.50
1:A:624:C:H2'	1:A:625:G:H8	1.76	0.50
1:A:731:G:OP1	1:A:766:A:H1'	2.11	0.50
1:A:961:U:O2'	1:A:962:C:H5'	2.11	0.50
1:A:974:A:OP2	16:N:41:ARG:NH1	2.45	0.50
1:A:1112:C:N3	5:C:178:LEU:N	2.58	0.50
5:C:91:LEU:CD2	5:C:92:ALA:N	2.73	0.50
6:D:64:LEU:HD12	6:D:75:PHE:CZ	2.47	0.50
8:F:63:TYR:HD1	8:F:63:TYR:N	2.08	0.50
15:M:23:TYR:CE2	15:M:70:LEU:HD13	2.46	0.50
16:N:35:ARG:C	16:N:37:PHE:N	2.65	0.50
16:N:35:ARG:O	16:N:37:PHE:N	2.45	0.50
16:N:44:LEU:HD23	16:N:44:LEU:C	2.31	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:T:86:ARG:HH11	22:T:86:ARG:HG2	1.76	0.50
1:A:514:C:O2'	1:A:515:G:H5'	2.12	0.50
1:A:782:A:H2'	1:A:783:C:O4'	2.12	0.50
1:A:1094:G:OP2	1:A:1095:U:C5	2.64	0.50
5:C:70:VAL:HG12	5:C:71:ALA:H	1.77	0.50
5:C:92:ALA:HA	5:C:96:GLY:H	1.76	0.50
11:I:32:ASP:O	11:I:35:GLU:N	2.44	0.50
12:J:8:LEU:HD13	12:J:20:ALA:HB2	1.93	0.50
14:L:47:LYS:CG	14:L:48:PRO:HD3	2.42	0.50
17:O:17:ARG:HG3	17:O:17:ARG:NH1	2.26	0.50
22:T:56:MET:HE1	22:T:104:LEU:HG	1.94	0.50
1:A:149:A:H2'	1:A:150:C:H6	1.76	0.50
4:B:189:ASP:OD1	4:B:205:ASP:HB3	2.12	0.50
6:D:150:GLU:OE1	6:D:153:ARG:HG3	2.10	0.50
7:E:79:GLU:O	10:H:104:ARG:NH1	2.45	0.50
16:N:8:GLU:OE1	16:N:8:GLU:C	2.50	0.50
20:R:21:LYS:O	20:R:23:LYS:N	2.45	0.50
20:R:39:VAL:HG13	20:R:40:LEU:N	2.26	0.50
1:A:383:A:C2'	1:A:384:G:H5'	2.42	0.50
1:A:386:C:C2'	1:A:387:U:H5'	2.42	0.50
1:A:446:G:C2'	1:A:447:G:H5'	2.42	0.50
1:A:1249:C:H4'	11:I:73:GLN:HE22	1.76	0.50
1:A:1286:A:H8	1:A:1287:A:H4'	1.77	0.50
5:C:18:TRP:O	5:C:54:ARG:NH2	2.45	0.50
5:C:179:ARG:C	5:C:181:ASN:H	2.15	0.50
6:D:162:LEU:HD13	6:D:181:MET:CG	2.41	0.50
12:J:94:VAL:CG1	12:J:95:GLU:H	2.25	0.50
14:L:93:LEU:HB2	14:L:96:VAL:HG21	1.94	0.50
1:A:147:G:O2'	1:A:148:G:H5'	2.12	0.50
1:A:186:C:H1'	22:T:85:MET:CE	2.42	0.50
1:A:382:A:C2	1:A:383:A:C4	3.00	0.50
1:A:768:A:H2'	1:A:769:G:O4'	2.11	0.50
7:E:109:ILE:O	7:E:113:ALA:HB2	2.12	0.50
8:F:64:GLN:O	8:F:64:GLN:HG2	2.10	0.50
13:K:96:ARG:HG2	13:K:96:ARG:HH11	1.76	0.50
14:L:40:VAL:HG21	14:L:77:LEU:O	2.12	0.50
1:A:579:G:H2'	1:A:580:U:C6	2.46	0.49
1:A:797:C:O2'	1:A:798:G:H5'	2.11	0.49
1:A:826:C:H2'	1:A:827:U:C6	2.47	0.49
1:A:1073:U:H3	1:A:1102:A:H61	1.60	0.49
1:A:1315:U:H2'	1:A:1316:G:O4'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:21:ARG:HD2	5:C:21:ARG:H	1.76	0.49
5:C:114:PRO:O	5:C:118:GLN:HG3	2.12	0.49
6:D:8:VAL:C	6:D:10:ARG:N	2.66	0.49
6:D:13:ARG:NH1	6:D:38:TYR:O	2.45	0.49
11:I:49:PRO:O	11:I:53:VAL:HG23	2.11	0.49
13:K:48:ILE:O	13:K:48:ILE:HG22	2.12	0.49
14:L:119:LYS:O	14:L:120:TYR:CB	2.60	0.49
1:A:192:U:H1'	22:T:103:GLY:HA2	1.94	0.49
1:A:462:G:N2	18:P:82:GLN:CD	2.66	0.49
1:A:640:A:C2'	1:A:641:U:H5'	2.42	0.49
1:A:952:U:O2'	1:A:953:G:H5'	2.10	0.49
1:A:974:A:OP1	1:A:974:A:H8	1.95	0.49
1:A:1225:A:H2'	1:A:1225:A:N3	2.27	0.49
1:A:1351:U:O2'	1:A:1352:C:H5'	2.12	0.49
1:A:1358:U:H3'	1:A:1359:C:C6	2.47	0.49
1:A:1423:G:O2'	1:A:1424:C:H5'	2.12	0.49
4:B:19:HIS:NE2	4:B:20:GLU:OE1	2.45	0.49
4:B:53:ARG:HB3	4:B:53:ARG:NH1	2.27	0.49
9:G:135:VAL:O	9:G:139:GLU:HG3	2.12	0.49
11:I:63:ILE:HG22	11:I:64:THR:N	2.27	0.49
16:N:60:SER:O	16:N:61:TRP:HB3	2.11	0.49
17:O:10:LYS:O	17:O:10:LYS:HD2	2.12	0.49
17:O:64:ARG:HB3	17:O:64:ARG:NH1	2.24	0.49
17:O:74:ASP:C	17:O:76:GLU:H	2.16	0.49
19:Q:97:SER:HA	19:Q:102:GLY:O	2.12	0.49
1:A:190:C:N4	1:A:190(J):U:O2'	2.45	0.49
1:A:485:G:C2'	1:A:486:U:OP2	2.60	0.49
1:A:792:A:H4'	1:A:793:U:H5"	1.93	0.49
1:A:1056:U:H5'	5:C:163:ALA:CB	2.42	0.49
1:A:1474:G:O2'	1:A:1475:G:H5'	2.11	0.49
4:B:126:GLU:HB3	4:B:129:GLU:OE2	2.12	0.49
4:B:159:PRO:HB2	4:B:161:ALA:O	2.11	0.49
5:C:85:ARG:HA	5:C:85:ARG:CZ	2.42	0.49
6:D:173:TRP:HB2	6:D:187:ARG:O	2.12	0.49
8:F:86:ARG:O	8:F:87:ARG:HG2	2.12	0.49
9:G:18:TYR:HE2	9:G:58:PRO:HG2	1.76	0.49
9:G:36:LYS:O	9:G:36:LYS:HG2	2.12	0.49
9:G:111:ARG:HB3	9:G:113:GLU:OE2	2.12	0.49
11:I:118:LYS:NZ	11:I:118:LYS:CB	2.74	0.49
12:J:6:ILE:HG23	12:J:98:ILE:CG2	2.42	0.49
13:K:99:GLN:HG2	13:K:105:VAL:HG21	1.92	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:S:22:LEU:HD13	21:S:28:LYS:CG	2.43	0.49
1:A:129(A):G:N3	1:A:190(E):U:H5'	2.27	0.49
1:A:192:U:O3'	22:T:57:ARG:HD2	2.13	0.49
1:A:828:A:H2'	1:A:829:G:O4'	2.12	0.49
4:B:83:MET:CE	4:B:238:LEU:HD22	2.43	0.49
5:C:102:ASN:N	5:C:102:ASN:HD22	2.09	0.49
5:C:148:GLY:HA3	5:C:172:ARG:O	2.12	0.49
9:G:21:VAL:HG23	9:G:22:LEU:H	1.76	0.49
10:H:51:VAL:HG12	10:H:52:ASP:N	2.27	0.49
13:K:14:VAL:HG21	13:K:40:ILE:CD1	2.42	0.49
22:T:30:LYS:HE2	22:T:72:LEU:CD2	2.40	0.49
1:A:32:A:H2'	1:A:33:A:C8	2.47	0.49
1:A:270:A:H2'	1:A:271:C:C6	2.48	0.49
1:A:528:C:H5'	1:A:535:A:C6	2.47	0.49
1:A:830:G:O2'	1:A:831:U:H5'	2.12	0.49
1:A:1059:C:O2'	1:A:1060:C:H5'	2.12	0.49
1:A:1149:C:H2'	1:A:1150:U:C6	2.47	0.49
1:A:1513:A:H2'	1:A:1514:C:C6	2.48	0.49
4:B:118:LEU:C	4:B:120:ALA:N	2.64	0.49
4:B:219:VAL:C	4:B:221:LEU:N	2.65	0.49
6:D:129:ASN:HB2	6:D:131:ARG:HH12	1.77	0.49
11:I:56:LEU:HD23	11:I:56:LEU:C	2.33	0.49
12:J:8:LEU:HB2	12:J:70:ARG:HB2	1.93	0.49
16:N:26:ARG:NH1	16:N:47:LEU:CD2	2.62	0.49
23:V:2:GLY:O	23:V:4:GLY:N	2.45	0.49
1:A:28:G:O2'	1:A:296:U:OP1	2.28	0.49
1:A:344:A:C5'	1:A:345:C:H5	2.23	0.49
1:A:460:A:N6	1:A:463:A:N6	2.60	0.49
1:A:1251:A:H2'	1:A:1252:A:H8	1.77	0.49
4:B:12:GLU:CD	4:B:213:LEU:HD11	2.32	0.49
4:B:100:GLY:O	4:B:104:ASN:N	2.46	0.49
6:D:64:LEU:C	6:D:64:LEU:CD1	2.81	0.49
6:D:64:LEU:HD13	6:D:64:LEU:O	2.12	0.49
8:F:15:ASP:OD1	8:F:17:SER:HB2	2.13	0.49
9:G:49:ILE:C	9:G:51:GLN:H	2.14	0.49
10:H:138:TRP:OXT	10:H:138:TRP:HE3	1.96	0.49
11:I:116:LYS:O	11:I:117:HIS:C	2.50	0.49
12:J:6:ILE:HG23	12:J:98:ILE:HG21	1.95	0.49
19:Q:78:GLU:CD	19:Q:81:ARG:HD2	2.33	0.49
20:R:36:ASN:O	20:R:39:VAL:HG12	2.12	0.49
1:A:98:U:O2'	1:A:99:C:H5'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:308:C:H2'	1:A:309:G:C8	2.48	0.49
1:A:620:C:C1'	6:D:135:LEU:HD13	2.42	0.49
1:A:791:G:C6	1:A:792:A:N7	2.81	0.49
1:A:810:C:H2'	1:A:811:C:H6	1.78	0.49
1:A:1091:U:O2	1:A:1093:A:H8	1.96	0.49
1:A:1262:C:O2'	1:A:1263:C:H5'	2.12	0.49
6:D:106:TYR:C	6:D:106:TYR:CD2	2.85	0.49
9:G:25:ALA:O	9:G:28:ASN:HB2	2.11	0.49
10:H:81:HIS:ND1	10:H:81:HIS:N	2.61	0.49
11:I:20:ARG:O	11:I:60:ASP:N	2.46	0.49
16:N:21:TYR:HE2	16:N:23:ARG:HG3	1.77	0.49
22:T:64:ASP:OD1	22:T:81:LYS:NZ	2.44	0.49
1:A:189:G:N2	1:A:190(K):G:C5	2.81	0.49
4:B:80:ILE:HD12	4:B:80:ILE:N	2.27	0.49
4:B:118:LEU:C	4:B:120:ALA:H	2.16	0.49
5:C:58:GLU:HB3	12:J:92:THR:CG2	2.43	0.49
5:C:88:ARG:CA	5:C:101:LEU:HD12	2.42	0.49
7:E:121:LYS:HD2	7:E:122:GLU:N	2.27	0.49
9:G:115:ARG:HB2	9:G:118:VAL:CG2	2.42	0.49
10:H:86:ILE:HD12	10:H:133:LEU:CD2	2.43	0.49
20:R:53:ARG:HH11	20:R:59:SER:CA	2.22	0.49
1:A:255:G:H1'	19:Q:16:GLN:HE22	1.77	0.49
1:A:920:U:H2'	1:A:921:U:C6	2.47	0.49
5:C:74:GLY:O	5:C:77:ILE:N	2.45	0.49
8:F:90:VAL:O	8:F:90:VAL:HG12	2.12	0.49
9:G:69:VAL:HG12	9:G:100:ALA:HA	1.93	0.49
10:H:64:LYS:HB2	10:H:79:VAL:HG21	1.95	0.49
11:I:9:ARG:CG	11:I:14:VAL:HG22	2.43	0.49
12:J:48:THR:HG1	12:J:62:HIS:CD2	2.31	0.49
18:P:1:MET:CE	18:P:1:MET:H3	2.26	0.49
1:A:721:G:H8	1:A:721:G:OP1	1.95	0.49
1:A:730:G:N2	1:A:765:G:H5"	2.27	0.49
1:A:1064:G:H4'	1:A:1065:U:C5'	2.30	0.49
1:A:1232:U:H5"	11:I:124:GLN:O	2.12	0.49
4:B:78:GLN:O	4:B:94:ASN:OD1	2.31	0.49
4:B:223:ILE:O	4:B:226:ARG:N	2.45	0.49
5:C:13:GLY:O	5:C:14:ILE:HD13	2.12	0.49
5:C:37:GLN:OE1	16:N:52:GLN:OE1	2.31	0.49
5:C:72:LYS:NZ	5:C:72:LYS:HB3	2.28	0.49
5:C:83:ARG:C	5:C:85:ARG:H	2.17	0.49
5:C:178:LEU:O	5:C:179:ARG:HD2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:2:ARG:CZ	8:F:69:GLU:HG2	2.43	0.49
8:F:9:VAL:HG13	8:F:60:PHE:CD2	2.48	0.49
12:J:54:PHE:O	12:J:55:LYS:HG2	2.12	0.49
12:J:75:ILE:H	12:J:75:ILE:CD1	2.21	0.49
13:K:84:VAL:HG11	13:K:91:ARG:CG	2.42	0.49
15:M:53:VAL:O	15:M:53:VAL:HG12	2.12	0.49
1:A:185:A:H61	1:A:192:U:H3	1.61	0.48
1:A:1056:U:C5'	5:C:163:ALA:HB2	2.43	0.48
1:A:1251:A:H1'	1:A:1369:C:O2'	2.13	0.48
9:G:95:ARG:HG3	9:G:95:ARG:HH11	1.78	0.48
14:L:83:VAL:HG21	14:L:100:ILE:CG2	2.42	0.48
15:M:8:GLU:C	15:M:9:ILE:HG13	2.33	0.48
20:R:16:PRO:O	20:R:17:SER:HB3	2.13	0.48
21:S:5:LEU:HA	21:S:6:LYS:HZ2	1.76	0.48
1:A:447:G:H2'	1:A:485:G:N2	2.29	0.48
1:A:530:G:H3'	1:A:531:U:C5'	2.43	0.48
1:A:1197:G:O2'	1:A:1198:G:H5'	2.12	0.48
1:A:1494:G:O2'	1:A:1495:U:H5'	2.12	0.48
4:B:80:ILE:HD11	4:B:208:ILE:HG23	1.94	0.48
4:B:194:PRO:C	4:B:196:LEU:N	2.66	0.48
6:D:3:ARG:NH2	6:D:71:SER:HB3	2.24	0.48
6:D:182:LYS:HG3	6:D:182:LYS:O	2.13	0.48
7:E:126:ARG:HG3	7:E:126:ARG:NH1	2.25	0.48
11:I:85:LEU:O	11:I:92:TYR:CD1	2.66	0.48
15:M:66:LEU:HD12	15:M:66:LEU:H	1.77	0.48
17:O:70:LEU:HD12	17:O:78:TYR:CB	2.42	0.48
21:S:13:ASP:O	21:S:17:GLU:HG3	2.13	0.48
22:T:97:ALA:O	22:T:99:LEU:N	2.46	0.48
1:A:273:A:N6	1:A:274:A:C6	2.81	0.48
1:A:448:A:H2'	1:A:449:C:H6	1.79	0.48
1:A:994:A:H2'	1:A:994:A:N3	2.29	0.48
1:A:1248:A:N3	11:I:70:LYS:HE3	2.28	0.48
5:C:73:PRO:O	5:C:76:VAL:HB	2.13	0.48
5:C:113:ALA:HB3	5:C:114:PRO:HD3	1.96	0.48
11:I:28:VAL:O	11:I:29:ASN:C	2.51	0.48
14:L:43:VAL:CG1	14:L:44:THR:N	2.75	0.48
22:T:23:ARG:HG2	22:T:23:ARG:HH11	1.78	0.48
1:A:372:C:H4'	1:A:373:A:O5'	2.13	0.48
1:A:941:G:C2'	1:A:942:G:O5'	2.62	0.48
1:A:1165:C:C2'	1:A:1166:G:H5'	2.44	0.48
1:A:1202:G:H2'	1:A:1203:C:C5'	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1305:G:HO2'	1:A:1306:A:H8	0.69	0.48
4:B:13:ALA:C	4:B:15:VAL:N	2.67	0.48
7:E:122:GLU:O	7:E:123:LEU:HD23	2.13	0.48
8:F:69:GLU:O	8:F:71:ARG:N	2.46	0.48
9:G:50:ILE:HD12	9:G:50:ILE:N	2.28	0.48
14:L:56:ALA:O	14:L:67:THR:HA	2.14	0.48
22:T:23:ARG:HG2	22:T:23:ARG:NH1	2.27	0.48
1:A:77:G:O2'	1:A:78:G:H5'	2.12	0.48
1:A:1108:G:H5'	1:A:1191:A:H4'	1.96	0.48
1:A:1223:C:P	21:S:78:ARG:NH1	2.79	0.48
1:A:1263:C:H2'	1:A:1264:C:H6	1.74	0.48
1:A:1353:G:OP1	23:V:3:LYS:HE2	2.14	0.48
1:A:1355:G:H2'	1:A:1356:G:H8	1.78	0.48
1:A:1365:G:O2'	1:A:1366:C:H5'	2.14	0.48
5:C:54:ARG:HG2	5:C:54:ARG:NH1	2.27	0.48
6:D:196:LEU:C	6:D:198:VAL:H	2.16	0.48
7:E:18:ARG:NH1	7:E:25:ARG:HB3	2.29	0.48
10:H:104:ARG:CG	10:H:104:ARG:NH1	2.68	0.48
15:M:59:TYR:CZ	15:M:63:THR:HG21	2.49	0.48
22:T:83:ARG:HB3	22:T:87:LYS:HZ2	1.78	0.48
1:A:344:A:H4'	1:A:345:C:OP2	2.14	0.48
1:A:701:C:O2'	1:A:702:A:P	2.71	0.48
1:A:1006:C:H2'	1:A:1007:C:H6	1.78	0.48
1:A:1221:G:O2'	1:A:1222:G:H5'	2.13	0.48
4:B:25:ASN:ND2	4:B:25:ASN:C	2.64	0.48
4:B:44:LEU:O	4:B:47:THR:N	2.46	0.48
4:B:207:ALA:O	4:B:211:ILE:HG13	2.13	0.48
7:E:144:THR:HB	7:E:147:ASP:OD2	2.13	0.48
9:G:155:ARG:O	9:G:156:TRP:CB	2.59	0.48
10:H:134:ILE:HG22	10:H:135:CYS:SG	2.53	0.48
11:I:2:GLU:N	11:I:2:GLU:OE2	2.47	0.48
11:I:48:GLU:HA	11:I:51:ARG:HE	1.79	0.48
12:J:28:ARG:HG2	12:J:28:ARG:HH11	1.77	0.48
14:L:37:CYS:CB	14:L:81:SER:O	2.61	0.48
18:P:10:GLY:HA3	18:P:14:ASN:O	2.13	0.48
21:S:62:ILE:HD12	21:S:63:THR:H	1.79	0.48
1:A:537:G:OP1	14:L:113:ARG:NH2	2.47	0.48
1:A:625:G:H2'	1:A:626:U:H6	1.77	0.48
1:A:643:C:H2'	1:A:644:G:H8	1.79	0.48
1:A:767:A:H2'	1:A:768:A:O4'	2.13	0.48
1:A:1144:G:H21	1:A:1146:A:H62	1.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1305:G:H5"	23:V:4:GLY:C	2.34	0.48
9:G:78:ARG:O	9:G:80:VAL:HG13	2.14	0.48
13:K:54:ARG:HA	13:K:57:THR:CG2	2.43	0.48
13:K:127:LYS:HE3	13:K:127:LYS:CA	2.35	0.48
14:L:38:THR:HG22	14:L:39:VAL:CG2	2.36	0.48
14:L:93:LEU:HB2	14:L:96:VAL:CG2	2.43	0.48
15:M:108:ARG:O	15:M:109:THR:C	2.50	0.48
19:Q:63:ARG:HG2	19:Q:64:PRO:HD2	1.94	0.48
20:R:55:ARG:HB3	20:R:55:ARG:CZ	2.44	0.48
1:A:462:G:OP2	1:A:462:G:C8	2.66	0.48
1:A:476:G:H5'	1:A:477:G:H5"	1.96	0.48
1:A:674:G:O2'	1:A:675:A:H5'	2.14	0.48
1:A:751:U:H4'	17:O:24:SER:HA	1.95	0.48
1:A:1249:C:C2'	1:A:1250:A:H5'	2.44	0.48
1:A:1250:A:H5"	11:I:68:GLY:N	2.29	0.48
1:A:1302:U:C5	15:M:17:VAL:HG21	2.49	0.48
4:B:92:TYR:HD1	4:B:92:TYR:C	2.17	0.48
5:C:64:VAL:O	5:C:99:VAL:HB	2.13	0.48
6:D:107:ARG:HB3	6:D:174:LEU:CD1	2.44	0.48
12:J:45:ARG:NH1	12:J:45:ARG:HB2	2.29	0.48
18:P:39:TYR:CZ	18:P:41:PRO:HA	2.49	0.48
21:S:30:LEU:HD12	21:S:30:LEU:N	2.29	0.48
22:T:10:LEU:HD11	22:T:12:ALA:HB3	1.96	0.48
1:A:353:A:C8	1:A:353:A:C5'	2.97	0.48
1:A:376:G:P	18:P:67:THR:HG21	2.52	0.48
1:A:635:G:O2'	1:A:636:U:H5'	2.13	0.48
1:A:697:U:H2'	1:A:698:G:H5'	1.96	0.48
1:A:1054:C:C4	2:X:34:I:H1'	2.49	0.48
1:A:1112:C:O2	5:C:178:LEU:O	2.31	0.48
1:A:1399:C:C2	1:A:1502:A:N6	2.82	0.48
4:B:200:ILE:HD12	4:B:200:ILE:O	2.13	0.48
5:C:19:GLU:O	5:C:40:ARG:NH2	2.47	0.48
5:C:126:ARG:O	5:C:127:ARG:HB2	2.14	0.48
11:I:5:TYR:O	11:I:5:TYR:CD1	2.67	0.48
11:I:70:LYS:O	11:I:74:ILE:HG13	2.14	0.48
14:L:53:ARG:HG3	14:L:53:ARG:HH11	1.77	0.48
19:Q:45:HIS:CD2	19:Q:47:PRO:HG3	2.49	0.48
19:Q:68:ARG:O	19:Q:68:ARG:CG	2.61	0.48
1:A:428:G:H4'	1:A:429:U:O5'	2.14	0.48
1:A:541:G:O2'	1:A:542:G:H5'	2.14	0.48
1:A:951:G:O2'	1:A:952:U:H5'	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:975:A:O2'	1:A:976:G:OP2	2.27	0.48
1:A:1052:U:O2'	1:A:1055:A:OP2	2.29	0.48
1:A:1103:C:C5'	4:B:98:LEU:HD13	2.44	0.48
1:A:1150:U:O3'	12:J:41:PRO:HA	2.14	0.48
1:A:1153:C:O2'	1:A:1154:G:H5'	2.14	0.48
1:A:1212:U:H4'	1:A:1213:A:C5'	2.43	0.48
1:A:1290:G:H21	11:I:70:LYS:NZ	2.11	0.48
1:A:1365:G:H2'	1:A:1366:C:C6	2.48	0.48
4:B:36:ARG:O	4:B:37:ASN:HB2	2.14	0.48
4:B:154:LEU:O	4:B:155:LEU:C	2.51	0.48
5:C:20:SER:HB3	5:C:22:TRP:CD1	2.48	0.48
5:C:74:GLY:O	5:C:76:VAL:N	2.47	0.48
7:E:61:TYR:O	7:E:64:ARG:HB2	2.14	0.48
8:F:25:ILE:CD1	8:F:82:ARG:HD2	2.43	0.48
9:G:31:MET:HG3	9:G:36:LYS:HA	1.96	0.48
10:H:34:GLU:OE2	10:H:34:GLU:HA	2.14	0.48
10:H:35:ILE:HG23	10:H:111:ILE:HD13	1.95	0.48
11:I:104:ARG:HD3	11:I:104:ARG:C	2.31	0.48
1:A:242:C:H2'	1:A:243:A:H5'	1.94	0.47
11:I:32:ASP:O	11:I:33:PHE:C	2.51	0.47
14:L:38:THR:CG2	14:L:39:VAL:N	2.68	0.47
19:Q:23:VAL:O	19:Q:23:VAL:HG12	2.14	0.47
23:V:25:LYS:HB3	23:V:25:LYS:NZ	2.29	0.47
1:A:112:G:O2'	1:A:113:G:H5'	2.14	0.47
1:A:1392:G:H21	1:A:1502:A:H8	1.61	0.47
1:A:1539:C:H2'	1:A:1540:U:H5'	1.94	0.47
4:B:174:VAL:O	4:B:177:ALA:HB3	2.14	0.47
5:C:70:VAL:CG1	5:C:71:ALA:N	2.77	0.47
9:G:95:ARG:HG3	9:G:95:ARG:NH1	2.29	0.47
10:H:6:ILE:O	10:H:10:LEU:HG	2.14	0.47
21:S:51:VAL:O	21:S:58:VAL:N	2.46	0.47
1:A:406:G:H1	1:A:436:C:H42	1.63	0.47
1:A:460:A:N6	1:A:463:A:H61	2.11	0.47
1:A:961:U:H2'	1:A:962:C:O4'	2.14	0.47
1:A:1171:G:H2'	1:A:1172:C:C6	2.49	0.47
2:X:30:G:O2'	2:X:31:G:H5'	2.15	0.47
5:C:54:ARG:HG2	5:C:54:ARG:HH11	1.78	0.47
9:G:15:ASP:CB	9:G:20:ASP:H	2.27	0.47
12:J:71:LEU:O	12:J:72:VAL:CB	2.62	0.47
13:K:57:THR:HB	13:K:58:PRO:HD2	1.96	0.47
14:L:33:ARG:HD2	14:L:33:ARG:HA	1.56	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:R:18:ARG:NH2	20:R:21:LYS:HE2	2.28	0.47
20:R:47:THR:CG2	20:R:48:GLY:N	2.77	0.47
1:A:256:U:H2'	1:A:257:G:C8	2.49	0.47
1:A:444:C:O2'	1:A:445:G:H5'	2.14	0.47
1:A:1039:C:H2'	1:A:1040:U:C6	2.49	0.47
1:A:1190:G:OP1	5:C:4:LYS:HA	2.14	0.47
1:A:1300:G:O4'	1:A:1300:G:OP2	2.31	0.47
1:A:1405:G:O4'	1:A:1519:A:H4'	2.14	0.47
4:B:84:GLU:O	4:B:219:VAL:HG21	2.13	0.47
4:B:92:TYR:CD1	4:B:92:TYR:C	2.88	0.47
5:C:22:TRP:CE3	5:C:32:LEU:HD22	2.48	0.47
6:D:129:ASN:HB2	6:D:131:ARG:NH1	2.30	0.47
14:L:77:LEU:HD21	14:L:107:ALA:CA	2.44	0.47
15:M:52:GLU:C	15:M:54:VAL:N	2.66	0.47
17:O:25:THR:CG2	17:O:70:LEU:HD23	2.45	0.47
22:T:73:HIS:O	22:T:74:LYS:C	2.51	0.47
1:A:129(A):G:C2	1:A:190(E):U:H5'	2.49	0.47
1:A:136:C:H2'	1:A:137:C:H6	1.79	0.47
1:A:299:G:H2'	1:A:300:A:C8	2.49	0.47
1:A:407:G:H2'	1:A:431:A:OP1	2.15	0.47
1:A:502:G:H4'	1:A:550:G:H4'	1.95	0.47
1:A:621:A:H2'	1:A:622:A:C8	2.49	0.47
1:A:1218:C:H2'	1:A:1219:U:C6	2.50	0.47
4:B:22:LYS:HZ2	4:B:22:LYS:HB3	1.80	0.47
4:B:131:PRO:O	4:B:135:GLN:HG2	2.15	0.47
7:E:110:LEU:HD13	7:E:118:ILE:HG21	1.95	0.47
7:E:144:THR:HG23	7:E:146:ALA:N	2.29	0.47
12:J:26:ALA:O	12:J:27:ALA:HB2	2.15	0.47
18:P:43:LYS:HA	18:P:48:TRP:CB	2.44	0.47
19:Q:66:SER:OG	19:Q:69:LYS:CB	2.62	0.47
1:A:977:A:C2'	1:A:978:A:H5"	2.43	0.47
1:A:1179:A:O3'	11:I:103:THR:HG23	2.15	0.47
5:C:79:ARG:HB2	5:C:79:ARG:HH11	1.79	0.47
5:C:154:SER:O	5:C:165:THR:HA	2.14	0.47
7:E:78:HIS:HD2	10:H:107:LEU:HD12	1.80	0.47
8:F:72:VAL:O	8:F:75:LEU:HB3	2.13	0.47
10:H:127:LEU:O	10:H:129:VAL:HG13	2.14	0.47
15:M:52:GLU:C	15:M:54:VAL:H	2.18	0.47
17:O:87:ILE:O	17:O:88:ARG:CB	2.63	0.47
19:Q:5:VAL:HG22	19:Q:60:ILE:HG12	1.96	0.47
20:R:47:THR:C	20:R:49:LYS:H	2.17	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:75:G:O2'	1:A:76:C:H5'	2.15	0.47
1:A:190(A):C:H42	1:A:190(H):G:H1	1.61	0.47
1:A:406:G:H5'	6:D:5:ILE:HG21	1.95	0.47
1:A:604:G:C5	1:A:605:U:C5	3.03	0.47
1:A:1006:C:H2'	1:A:1007:C:C6	2.49	0.47
1:A:1128:C:H5'	11:I:16:ARG:HH12	1.80	0.47
1:A:1298:C:OP2	9:G:114:ARG:NH2	2.48	0.47
4:B:124:SER:O	4:B:127:ILE:HG23	2.15	0.47
4:B:145:LEU:O	4:B:146:GLN:C	2.52	0.47
5:C:77:ILE:O	5:C:83:ARG:HB3	2.15	0.47
6:D:134:ASP:O	6:D:136:PRO:HD3	2.14	0.47
7:E:8:GLU:CB	7:E:34:VAL:HG23	2.42	0.47
8:F:22:GLU:OE1	8:F:82:ARG:HD3	2.15	0.47
8:F:74:ASP:O	8:F:77:ARG:HB3	2.15	0.47
9:G:69:VAL:O	9:G:138:LYS:HG3	2.15	0.47
14:L:19:ARG:HH11	14:L:19:ARG:HG3	1.79	0.47
14:L:27:LEU:C	14:L:29:GLY:N	2.67	0.47
15:M:78:ILE:HA	15:M:81:LEU:HG	1.96	0.47
17:O:74:ASP:O	17:O:76:GLU:N	2.47	0.47
19:Q:92:ARG:O	19:Q:95:TYR:HB2	2.14	0.47
20:R:51:LEU:HA	20:R:52:PRO:HD3	1.71	0.47
21:S:44:MET:O	21:S:47:HIS:HB2	2.14	0.47
1:A:190:C:HO2'	1:A:190(A):C:C4'	2.28	0.47
1:A:261:U:O2	1:A:263:A:C8	2.68	0.47
1:A:1488:G:H2'	1:A:1489:G:H8	1.79	0.47
4:B:47:THR:O	4:B:51:LEU:HG	2.15	0.47
4:B:213:LEU:HD22	4:B:214:ILE:HD13	1.95	0.47
6:D:108:LEU:CB	6:D:110:PHE:CE1	2.98	0.47
6:D:190:ASP:O	6:D:193:ASP:HB2	2.15	0.47
13:K:52:GLY:N	13:K:55:LYS:HE3	2.30	0.47
20:R:47:THR:HG22	20:R:48:GLY:H	1.77	0.47
21:S:28:LYS:CG	21:S:29:ARG:H	2.28	0.47
22:T:21:LYS:HB2	22:T:21:LYS:HZ2	1.77	0.47
1:A:190(I):G:H2'	1:A:190(J):U:C6	2.50	0.47
1:A:560:U:O2'	1:A:561:U:OP2	2.25	0.47
1:A:965:A:H5'	1:A:969:A:O4'	2.14	0.47
1:A:1223:C:H3'	1:A:1224:G:H5"	1.96	0.47
4:B:22:LYS:HA	4:B:22:LYS:NZ	2.29	0.47
5:C:15:THR:HG21	5:C:179:ARG:O	2.15	0.47
9:G:120:ILE:HD12	9:G:120:ILE:N	2.30	0.47
10:H:51:VAL:HG21	10:H:60:ARG:HG3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:91:ARG:CG	14:L:7:ILE:HG13	2.45	0.47
11:I:99:LEU:HD22	11:I:99:LEU:N	2.30	0.47
16:N:29:ARG:HG2	16:N:29:ARG:HH11	1.80	0.47
19:Q:79:SER:O	19:Q:80:GLY:O	2.33	0.47
21:S:63:THR:HG21	21:S:65:ASN:ND2	2.30	0.47
1:A:190(L):U:N3	22:T:105:SER:HB2	2.29	0.47
1:A:613:C:O2'	1:A:614:A:H5'	2.14	0.47
1:A:1355:G:O2'	1:A:1356:G:H5'	2.15	0.47
4:B:124:SER:C	4:B:126:GLU:H	2.18	0.47
5:C:195:VAL:HG12	5:C:196:LEU:H	1.76	0.47
6:D:112:VAL:HG22	6:D:116:GLN:OE1	2.14	0.47
6:D:190:ASP:HB2	6:D:193:ASP:OD2	2.14	0.47
7:E:12:LEU:HD13	7:E:31:LEU:HB2	1.97	0.47
7:E:57:LYS:HG2	7:E:61:TYR:CE2	2.50	0.47
7:E:76:ILE:HD13	7:E:118:ILE:HD12	1.97	0.47
9:G:65:ALA:CB	9:G:124:LEU:HD23	2.45	0.47
10:H:91:ARG:HG2	14:L:7:ILE:HG13	1.96	0.47
11:I:103:THR:O	11:I:104:ARG:C	2.53	0.47
1:A:56:U:H2'	1:A:57:G:C8	2.51	0.46
1:A:338:A:H2'	1:A:339:C:C6	2.50	0.46
1:A:411:A:C2	1:A:417:C:O2	2.68	0.46
1:A:660:G:OP1	17:O:5:LYS:HD3	2.15	0.46
1:A:694:A:C3'	1:A:695:A:H5"	2.41	0.46
1:A:1320:C:C2	21:S:72:GLY:HA3	2.50	0.46
7:E:144:THR:O	7:E:145:LYS:C	2.53	0.46
14:L:38:THR:HG22	14:L:39:VAL:H	1.77	0.46
17:O:88:ARG:NH1	17:O:88:ARG:CA	2.78	0.46
1:A:622:A:C8	1:A:623:C:C6	3.03	0.46
1:A:1007:C:H1'	1:A:1023:G:N1	2.31	0.46
1:A:1026:G:H2'	1:A:1026:G:N3	2.30	0.46
4:B:140:HIS:HA	4:B:143:GLU:CG	2.44	0.46
5:C:3:ASN:ND2	5:C:3:ASN:N	2.47	0.46
6:D:173:TRP:O	6:D:186:LEU:HB2	2.14	0.46
9:G:23:VAL:HG13	9:G:43:PHE:CE2	2.51	0.46
12:J:6:ILE:N	12:J:6:ILE:CD1	2.71	0.46
12:J:27:ALA:HB2	12:J:85:LEU:HG	1.97	0.46
15:M:37:THR:CG2	15:M:55:ARG:HD2	2.43	0.46
1:A:1021:G:O2'	1:A:1022:G:H5'	2.15	0.46
1:A:1024:G:C2'	1:A:1025:U:H5"	2.43	0.46
1:A:1126:U:N3	1:A:1127:G:C2	2.83	0.46
1:A:1202:G:H2'	1:A:1203:C:H5'	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1285:A:H1'	1:A:1286:A:OP2	2.15	0.46
1:A:1347:G:O2'	1:A:1348:U:OP2	2.33	0.46
1:A:1347:G:C8	11:I:107:ARG:HB3	2.50	0.46
4:B:12:GLU:HA	4:B:12:GLU:OE1	2.14	0.46
4:B:46:LYS:HA	4:B:49:GLU:HB2	1.97	0.46
4:B:206:ASP:O	4:B:207:ALA:HB2	2.14	0.46
5:C:116:VAL:O	5:C:120:VAL:HG23	2.15	0.46
6:D:15:GLU:OE2	6:D:59:ARG:NE	2.43	0.46
6:D:153:ARG:HB3	6:D:181:MET:HE3	1.97	0.46
12:J:24:VAL:CG1	12:J:28:ARG:HD2	2.46	0.46
1:A:262:A:C6	1:A:263:A:C6	3.03	0.46
1:A:1250:A:C5'	11:I:68:GLY:N	2.78	0.46
4:B:21:ARG:N	4:B:21:ARG:HD2	2.30	0.46
4:B:178:ARG:HH21	4:B:196:LEU:CA	2.28	0.46
5:C:83:ARG:O	5:C:85:ARG:N	2.48	0.46
6:D:108:LEU:CD2	6:D:174:LEU:HD13	2.46	0.46
7:E:122:GLU:C	7:E:123:LEU:HD23	2.36	0.46
9:G:31:MET:SD	9:G:34:GLY:HA2	2.55	0.46
10:H:102:ARG:HG3	10:H:102:ARG:O	2.16	0.46
10:H:104:ARG:O	10:H:105:ARG:C	2.54	0.46
11:I:3:GLN:CG	11:I:4:TYR:N	2.77	0.46
11:I:9:ARG:HG3	11:I:14:VAL:HA	1.97	0.46
15:M:40:ASN:ND2	15:M:41:PRO:HD2	2.30	0.46
19:Q:68:ARG:N	19:Q:70:ARG:HH11	2.11	0.46
21:S:22:LEU:HD13	21:S:28:LYS:HG2	1.96	0.46
1:A:47:C:H5"	1:A:365:U:C6	2.50	0.46
1:A:437:U:O2'	1:A:438:G:H5'	2.16	0.46
1:A:446:G:H2'	1:A:447:G:H5'	1.97	0.46
1:A:542:G:H2'	1:A:543:C:H6	1.81	0.46
1:A:1236:A:H4'	1:A:1304:G:H4'	1.97	0.46
1:A:1279:A:O2'	1:A:1281:U:OP2	2.32	0.46
1:A:1350:A:C2	1:A:1351:U:C2	3.02	0.46
4:B:79:ASP:HB3	4:B:238:LEU:HD21	1.97	0.46
5:C:19:GLU:HG2	5:C:19:GLU:O	2.16	0.46
6:D:7:PRO:CG	6:D:10:ARG:HD2	2.44	0.46
7:E:5:ASP:CG	7:E:6:PHE:H	2.19	0.46
8:F:48:LEU:HD13	8:F:52:ILE:HD12	1.97	0.46
8:F:61:LEU:HD12	8:F:61:LEU:N	2.31	0.46
9:G:16:LEU:H	9:G:16:LEU:CD2	2.27	0.46
9:G:22:LEU:HG	9:G:62:PHE:HE2	1.80	0.46
10:H:46:LYS:HG2	10:H:64:LYS:HG2	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:48:TYR:CD1	10:H:49:GLU:N	2.84	0.46
16:N:5:ALA:O	16:N:6:LEU:HD23	2.16	0.46
17:O:17:ARG:NH1	17:O:77:ARG:NH1	2.64	0.46
20:R:39:VAL:CG1	20:R:40:LEU:N	2.78	0.46
20:R:66:LEU:O	20:R:69:THR:N	2.49	0.46
23:V:2:GLY:C	23:V:4:GLY:N	2.68	0.46
1:A:142:G:O2'	1:A:196:A:N1	2.43	0.46
1:A:166:G:H2'	1:A:167:G:H8	1.81	0.46
1:A:192:U:O2'	1:A:193:C:H5'	2.16	0.46
1:A:376:G:H2'	1:A:377:G:H8	1.80	0.46
1:A:940:C:O2'	1:A:941:G:H5'	2.15	0.46
1:A:954:G:H21	1:A:1227:A:H62	1.64	0.46
1:A:1117:G:H5'	1:A:1117:G:H8	1.81	0.46
1:A:1216:G:H5"	16:N:5:ALA:HB2	1.97	0.46
1:A:1307:U:H2'	1:A:1308:U:C6	2.51	0.46
1:A:1364:U:O2'	1:A:1365:G:H5'	2.15	0.46
4:B:42:ILE:CD1	4:B:203:GLY:O	2.64	0.46
7:E:36:ASP:O	7:E:37:ARG:HB2	2.15	0.46
9:G:62:PHE:HA	9:G:124:LEU:CD2	2.46	0.46
10:H:24:THR:CG2	10:H:63:LEU:HD21	2.41	0.46
11:I:102:LEU:H	11:I:102:LEU:CD2	2.23	0.46
12:J:4:ILE:CD1	12:J:74:ILE:O	2.64	0.46
12:J:82:ILE:CG2	12:J:86:MET:SD	3.03	0.46
21:S:28:LYS:CD	21:S:29:ARG:H	2.29	0.46
21:S:31:ILE:O	21:S:33:THR:HG22	2.16	0.46
1:A:130:A:H5'	19:Q:63:ARG:NE	2.30	0.46
1:A:1237:C:H4'	1:A:1334:G:N2	2.31	0.46
6:D:146:ILE:N	6:D:146:ILE:CD1	2.75	0.46
7:E:81:GLU:HG2	7:E:90:VAL:HG22	1.98	0.46
7:E:144:THR:CG2	7:E:146:ALA:HB3	2.46	0.46
9:G:108:ALA:C	9:G:110:GLN:H	2.18	0.46
10:H:85:ARG:NE	10:H:87:SER:O	2.49	0.46
11:I:17:VAL:HG21	11:I:81:ILE:N	2.30	0.46
13:K:95:ILE:O	13:K:99:GLN:HG3	2.15	0.46
17:O:82:ILE:HG22	17:O:83:GLU:N	2.31	0.46
1:A:344:A:H5"	1:A:345:C:C5	2.45	0.46
1:A:663:A:O2'	1:A:664:G:H5'	2.16	0.46
1:A:882:C:O2'	1:A:883:C:H5'	2.15	0.46
1:A:924:C:H2'	1:A:925:G:C8	2.50	0.46
1:A:1195:C:H3'	1:A:1196:U:C5'	2.45	0.46
1:A:1258:G:O2'	1:A:1259:C:H5'	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1264:C:H2'	1:A:1265:G:H8	1.79	0.46
5:C:33:LEU:HD21	16:N:53:LEU:HD21	1.98	0.46
5:C:136:GLN:O	5:C:139:GLN:N	2.48	0.46
5:C:155:GLY:O	5:C:156:ARG:CB	2.61	0.46
5:C:167:TRP:O	5:C:168:ALA:CB	2.63	0.46
9:G:144:MET:O	9:G:147:ALA:HB3	2.16	0.46
12:J:4:ILE:HD11	12:J:74:ILE:O	2.16	0.46
12:J:10:GLY:H	12:J:16:LEU:HD11	1.80	0.46
15:M:33:ALA:HB2	15:M:64:TRP:CH2	2.51	0.46
15:M:60:VAL:HG22	15:M:64:TRP:CZ3	2.51	0.46
16:N:9:LYS:O	16:N:11:LYS:N	2.48	0.46
17:O:14:GLU:CG	17:O:14:GLU:O	2.64	0.46
17:O:88:ARG:HH11	17:O:88:ARG:CA	2.26	0.46
21:S:36:ARG:NH2	21:S:75:ALA:HB3	2.30	0.46
1:A:258:G:H2'	1:A:259:G:C8	2.51	0.46
1:A:460:A:H2'	1:A:461:C:H5"	1.98	0.46
1:A:858:G:O6	1:A:869:G:H3'	2.14	0.46
1:A:1148:U:H2'	1:A:1149:C:O4'	2.16	0.46
1:A:1228:C:H2'	1:A:1229:A:H8	1.80	0.46
1:A:1320:C:O2'	1:A:1321:C:H5'	2.15	0.46
1:A:1329:A:C2'	1:A:1330:U:H5'	2.46	0.46
1:A:1372:U:O2'	1:A:1373:G:H5'	2.15	0.46
4:B:53:ARG:HH12	4:B:199:TYR:HD2	1.62	0.46
5:C:56:ASP:OD1	5:C:57:ILE:N	2.49	0.46
5:C:137:ALA:HA	5:C:140:ARG:HE	1.80	0.46
7:E:53:LEU:H	7:E:53:LEU:CD1	2.24	0.46
8:F:101:ALA:CA	20:R:28:GLU:HG3	2.44	0.46
9:G:65:ALA:HB2	9:G:124:LEU:HD23	1.97	0.46
11:I:97:LYS:N	11:I:98:PRO:CD	2.79	0.46
13:K:93:GLN:OE1	13:K:93:GLN:HA	2.16	0.46
14:L:50:SER:O	14:L:51:ALA:CB	2.61	0.46
14:L:104:VAL:O	14:L:105:TYR:HB2	2.15	0.46
1:A:370:C:O2'	1:A:371:G:H5'	2.16	0.46
1:A:393:A:C2'	1:A:394:G:H5'	2.46	0.46
1:A:1303:C:N4	1:A:1304:G:C6	2.84	0.46
1:A:1310:G:O2'	1:A:1311:G:H5'	2.16	0.46
4:B:20:GLU:HB2	4:B:190:THR:CG2	2.46	0.46
5:C:76:VAL:HG11	5:C:103:VAL:CG2	2.46	0.46
5:C:107:GLN:CD	5:C:107:GLN:N	2.68	0.46
6:D:36:ARG:O	6:D:36:ARG:CG	2.63	0.46
8:F:68:PRO:HB2	8:F:71:ARG:CG	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:K:126:ARG:HB3	13:K:126:ARG:NH1	2.31	0.46
14:L:85:ILE:CG2	14:L:86:ARG:N	2.79	0.46
15:M:14:ARG:O	15:M:14:ARG:HG2	2.15	0.46
15:M:88:ARG:NH1	15:M:88:ARG:HG2	2.30	0.46
18:P:67:THR:CG2	18:P:68:ASP:H	2.28	0.46
1:A:252:U:H2'	1:A:253:U:C6	2.50	0.45
1:A:279:A:H5"	1:A:280:C:H3'	1.99	0.45
1:A:934:C:C4	1:A:1345:U:C5	3.04	0.45
1:A:938:A:C6	1:A:939:G:C5	3.04	0.45
1:A:1300:G:O2'	1:A:1301:U:P	2.74	0.45
4:B:71:VAL:HG23	4:B:164:VAL:HA	1.93	0.45
5:C:22:TRP:HZ3	5:C:24:ALA:HB2	1.82	0.45
6:D:60:GLU:HG2	6:D:202:LEU:HB2	1.96	0.45
7:E:15:ARG:C	7:E:16:THR:HG23	2.36	0.45
9:G:49:ILE:C	9:G:51:GLN:N	2.69	0.45
12:J:47:PHE:CZ	16:N:37:PHE:HE1	2.33	0.45
15:M:15:VAL:O	15:M:19:LEU:HG	2.16	0.45
15:M:23:TYR:HB2	15:M:67:GLU:OE2	2.16	0.45
15:M:33:ALA:O	15:M:37:THR:HB	2.16	0.45
17:O:64:ARG:HH11	17:O:64:ARG:CB	2.23	0.45
1:A:452:A:O2'	1:A:453:A:H8	1.99	0.45
1:A:737:A:H2'	1:A:738:C:C6	2.50	0.45
1:A:865:A:H5'	1:A:1078:U:C4	2.51	0.45
1:A:1061:G:H1'	12:J:56:HIS:CE1	2.51	0.45
1:A:1106:G:H5"	5:C:172:ARG:CG	2.41	0.45
1:A:1317:C:H2'	1:A:1318:A:O4'	2.16	0.45
4:B:185:ILE:HD12	4:B:185:ILE:N	2.31	0.45
6:D:24:GLU:O	6:D:25:ARG:CB	2.65	0.45
7:E:11:ILE:HG23	7:E:105:VAL:HG22	1.97	0.45
7:E:17:ALA:HB2	7:E:26:PHE:CD2	2.51	0.45
7:E:53:LEU:O	7:E:57:LYS:HB2	2.15	0.45
10:H:64:LYS:CB	10:H:79:VAL:HG21	2.46	0.45
11:I:24:GLY:HA2	11:I:59:PHE:O	2.16	0.45
11:I:83:ARG:O	11:I:86:VAL:HB	2.16	0.45
12:J:55:LYS:HG3	12:J:56:HIS:N	2.31	0.45
12:J:69:ASN:O	12:J:70:ARG:HD3	2.17	0.45
15:M:100:GLY:O	15:M:101:GLN:HG3	2.16	0.45
18:P:26:ARG:HG3	18:P:27:LYS:N	2.31	0.45
21:S:28:LYS:HD2	21:S:29:ARG:H	1.81	0.45
1:A:35:G:H2'	1:A:36:C:H6	1.76	0.45
1:A:632:A:C2'	1:A:633:G:H5'	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:953:G:H1'	15:M:125:ARG:HA	1.98	0.45
1:A:1057:G:C4	1:A:1204:A:C2	3.05	0.45
1:A:1109:C:OP2	5:C:176:HIS:CD2	2.69	0.45
1:A:1221:G:H2'	1:A:1222:G:H5'	1.99	0.45
5:C:47:LEU:HD23	5:C:68:VAL:HG11	1.98	0.45
5:C:64:VAL:N	5:C:99:VAL:HB	2.30	0.45
6:D:25:ARG:C	6:D:27:TYR:N	2.67	0.45
6:D:150:GLU:CA	6:D:153:ARG:HG2	2.45	0.45
7:E:128:PRO:O	7:E:129:ILE:C	2.54	0.45
9:G:143:ARG:O	9:G:145:ALA:O	2.34	0.45
12:J:46:ARG:HH11	12:J:46:ARG:CG	2.28	0.45
22:T:14:LYS:O	22:T:17:ARG:HB2	2.15	0.45
1:A:409:G:C2	1:A:431:A:H2'	2.51	0.45
1:A:463:A:H1'	1:A:474:G:H21	1.79	0.45
1:A:1060:C:O2'	1:A:1061:G:H5'	2.15	0.45
4:B:115:LEU:HD21	4:B:153:ARG:NH1	2.30	0.45
5:C:77:ILE:C	5:C:83:ARG:HB3	2.36	0.45
6:D:25:ARG:NH2	6:D:30:LYS:HE2	2.32	0.45
6:D:67:ILE:HG22	6:D:68:TYR:CD1	2.52	0.45
7:E:59:GLY:O	7:E:60:TYR:C	2.55	0.45
7:E:107:ARG:O	7:E:108:ALA:C	2.55	0.45
8:F:67:MET:CE	8:F:71:ARG:HB2	2.46	0.45
9:G:24:THR:HA	9:G:27:ILE:HD12	1.98	0.45
13:K:120:ARG:HG3	13:K:126:ARG:HD2	1.98	0.45
14:L:55:VAL:O	14:L:70:ILE:HD11	2.17	0.45
17:O:43:LEU:HD11	17:O:53:HIS:HA	1.98	0.45
21:S:5:LEU:HA	21:S:6:LYS:NZ	2.32	0.45
22:T:23:ARG:HH12	22:T:27:LYS:NZ	2.14	0.45
22:T:86:ARG:O	22:T:88:VAL:N	2.50	0.45
1:A:454:C:N4	1:A:479:C:C5	2.84	0.45
1:A:462:G:H21	18:P:75:ARG:HH12	1.65	0.45
1:A:737:A:H2'	1:A:738:C:H6	1.81	0.45
1:A:1406:U:O2'	1:A:1407:C:H5'	2.16	0.45
4:B:18:GLY:H	4:B:42:ILE:H	1.63	0.45
4:B:189:ASP:OD1	4:B:189:ASP:N	2.49	0.45
5:C:115:LEU:O	5:C:116:VAL:C	2.55	0.45
10:H:31:PHE:CZ	10:H:134:ILE:HD11	2.40	0.45
13:K:104:GLN:HG2	13:K:106:LYS:HE2	1.98	0.45
14:L:82:VAL:N	14:L:106:ASP:OD1	2.40	0.45
15:M:108:ARG:NH2	15:M:114:ARG:HA	2.31	0.45
16:N:22:THR:HG22	16:N:23:ARG:H	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:N:36:PHE:O	16:N:37:PHE:CG	2.69	0.45
16:N:45:ARG:O	16:N:49:HIS:CD2	2.70	0.45
19:Q:59:ILE:CG2	19:Q:71:PHE:CD1	3.00	0.45
19:Q:86:GLU:O	19:Q:87:LYS:C	2.55	0.45
22:T:73:HIS:O	22:T:74:LYS:O	2.35	0.45
23:V:6:ARG:HH12	23:V:7:ARG:HH11	1.64	0.45
1:A:112:G:H21	1:A:354:G:C5'	2.29	0.45
1:A:218:C:H2'	1:A:219:C:C6	2.50	0.45
1:A:1222:G:O2'	1:A:1223:C:H5'	2.16	0.45
1:A:1330:U:OP1	15:M:23:TYR:O	2.35	0.45
1:A:1337:G:H5"	1:A:1338:G:OP1	2.17	0.45
4:B:55:PHE:O	4:B:58:ILE:HB	2.15	0.45
6:D:177:ASP:O	6:D:179:GLU:N	2.50	0.45
7:E:33:VAL:CG2	7:E:109:ILE:HG12	2.46	0.45
7:E:147:ASP:O	7:E:151:LEU:HD13	2.17	0.45
8:F:77:ARG:HD2	8:F:77:ARG:C	2.36	0.45
9:G:148:ASN:C	9:G:150:ALA:N	2.70	0.45
9:G:151:TYR:HA	9:G:153:HIS:CE1	2.51	0.45
14:L:83:VAL:CG2	14:L:84:LEU:N	2.79	0.45
17:O:74:ASP:OD1	17:O:76:GLU:HB3	2.17	0.45
20:R:86:VAL:O	20:R:87:ARG:HB2	2.16	0.45
21:S:6:LYS:HB2	21:S:7:LYS:HG3	1.99	0.45
21:S:16:LEU:C	21:S:19:VAL:HG12	2.36	0.45
21:S:63:THR:H	21:S:66:MET:CG	2.30	0.45
1:A:373:A:O2'	1:A:374:A:H5'	2.16	0.45
1:A:652:U:C5	1:A:752:G:C4	3.05	0.45
1:A:832:C:O2'	1:A:833:U:H5'	2.17	0.45
1:A:938:A:N6	1:A:939:G:C6	2.85	0.45
5:C:118:GLN:O	5:C:122:GLU:HG3	2.17	0.45
8:F:19:LEU:CD2	8:F:20:ALA:N	2.77	0.45
8:F:100:ASN:HB2	20:R:23:LYS:HZ2	1.82	0.45
11:I:58:ARG:HH11	11:I:58:ARG:HG3	1.82	0.45
13:K:92:GLU:O	13:K:96:ARG:HD3	2.16	0.45
14:L:126:LYS:O	14:L:128:ALA:N	2.50	0.45
17:O:10:LYS:HD2	17:O:10:LYS:C	2.36	0.45
21:S:53:ASN:HD22	21:S:58:VAL:HG23	1.82	0.45
22:T:57:ARG:NH1	22:T:57:ARG:CB	2.77	0.45
23:V:24:ARG:H	23:V:24:ARG:HD2	1.82	0.45
1:A:41:G:H2'	1:A:42:G:C8	2.52	0.45
1:A:181:G:H4'	1:A:182:U:H5'	1.98	0.45
1:A:263:A:OP2	22:T:79:ARG:NH1	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:579:G:H2'	1:A:580:U:H6	1.82	0.45
1:A:1153:C:H2'	1:A:1154:G:H8	1.82	0.45
1:A:1229:A:O2'	15:M:125:ARG:HD3	2.17	0.45
1:A:1253:G:H2'	1:A:1254:C:C6	2.52	0.45
4:B:19:HIS:CD2	4:B:20:GLU:HG2	2.52	0.45
4:B:55:PHE:HA	4:B:58:ILE:CG1	2.47	0.45
4:B:71:VAL:O	4:B:71:VAL:HG23	2.16	0.45
5:C:22:TRP:CD2	5:C:22:TRP:O	2.70	0.45
5:C:47:LEU:N	5:C:47:LEU:HD12	2.32	0.45
5:C:123:GLN:O	5:C:128:PHE:HB2	2.17	0.45
5:C:179:ARG:C	5:C:181:ASN:N	2.70	0.45
7:E:21:ALA:C	7:E:23:GLY:H	2.19	0.45
8:F:40:VAL:HG23	8:F:41:GLU:N	2.32	0.45
8:F:67:MET:HE1	8:F:75:LEU:HB2	1.97	0.45
8:F:72:VAL:CG2	8:F:73:ASN:N	2.76	0.45
9:G:21:VAL:CG2	9:G:22:LEU:N	2.79	0.45
19:Q:78:GLU:OE2	19:Q:81:ARG:HD2	2.16	0.45
20:R:79:LEU:HD23	20:R:79:LEU:HA	1.81	0.45
1:A:375:U:H4'	18:P:17:TYR:CE2	2.52	0.45
1:A:1037:C:H2'	1:A:1038:C:O4'	2.17	0.45
1:A:1206:G:C6	1:A:1207:G:C5	3.05	0.45
1:A:1216:G:O2'	1:A:1217:C:H5'	2.17	0.45
1:A:1228:C:H4'	15:M:116:THR:HA	1.97	0.45
4:B:37:ASN:O	4:B:39:ILE:HD12	2.17	0.45
5:C:47:LEU:N	5:C:47:LEU:CD1	2.80	0.45
9:G:23:VAL:O	9:G:27:ILE:HG13	2.17	0.45
10:H:119:LEU:HD12	10:H:124:ALA:CA	2.47	0.45
13:K:117:ASN:HD22	13:K:117:ASN:HA	1.47	0.45
19:Q:68:ARG:N	19:Q:70:ARG:HH12	2.14	0.45
1:A:460:A:H2'	1:A:461:C:C5'	2.47	0.45
1:A:604:G:C6	1:A:605:U:C4	3.05	0.45
1:A:740:U:O2'	1:A:741:G:H5'	2.17	0.45
1:A:1111:A:H61	5:C:177:THR:HA	1.82	0.45
1:A:1223:C:OP1	1:A:1224:G:H3'	2.17	0.45
1:A:1394:A:C5	1:A:1501:C:H4'	2.52	0.45
4:B:80:ILE:HG22	4:B:215:LEU:HD22	1.99	0.45
5:C:70:VAL:HG12	5:C:72:LYS:H	1.82	0.45
9:G:107:ALA:O	9:G:110:GLN:HB2	2.17	0.45
1:A:166:G:O2'	1:A:167:G:H5'	2.17	0.44
1:A:459:G:C3'	1:A:460:A:H5"	2.47	0.44
1:A:836:G:H2'	1:A:837:G:H8	1.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:915:A:H2'	1:A:916:G:O5'	2.17	0.44
1:A:954:G:H2'	1:A:955:U:C6	2.52	0.44
1:A:1123:A:H4'	12:J:37:PRO:HD2	1.99	0.44
1:A:1313:U:O4	21:S:4:SER:HA	2.17	0.44
1:A:1461:G:O2'	1:A:1462:G:H5'	2.16	0.44
4:B:69:LEU:HD23	4:B:70:PHE:N	2.32	0.44
4:B:138:LEU:C	4:B:140:HIS:N	2.70	0.44
5:C:14:ILE:O	5:C:15:THR:C	2.55	0.44
5:C:48:TYR:O	5:C:51:GLY:N	2.48	0.44
8:F:25:ILE:HD13	8:F:82:ARG:HD2	1.99	0.44
11:I:4:TYR:CZ	11:I:88:TYR:HD1	2.35	0.44
11:I:11:LYS:O	11:I:12:GLU:CB	2.65	0.44
12:J:5:ARG:CG	12:J:99:LYS:HB3	2.47	0.44
14:L:110:VAL:HG12	14:L:111:LYS:N	2.32	0.44
15:M:37:THR:HG22	15:M:37:THR:O	2.17	0.44
20:R:87:ARG:O	20:R:88:LYS:HB2	2.16	0.44
21:S:6:LYS:HD2	21:S:6:LYS:N	2.31	0.44
1:A:16:A:C2'	1:A:17:U:H5'	2.47	0.44
1:A:192:U:H5'	22:T:102:GLY:O	2.17	0.44
1:A:542:G:O2'	1:A:543:C:H5'	2.16	0.44
1:A:972:C:H4'	12:J:57:LYS:CD	2.33	0.44
1:A:1126:U:H3	1:A:1127:G:N2	2.14	0.44
1:A:1298:C:C5	9:G:114:ARG:HD3	2.52	0.44
1:A:1373:G:H5"	9:G:36:LYS:HD2	1.98	0.44
1:A:1405:G:O2'	1:A:1406:U:H5'	2.17	0.44
1:A:1522:U:O2'	1:A:1523:G:H5'	2.17	0.44
5:C:155:GLY:CA	5:C:164:ARG:H	2.31	0.44
7:E:37:ARG:HG2	7:E:37:ARG:HH11	1.82	0.44
8:F:44:GLY:O	8:F:59:TYR:HA	2.17	0.44
8:F:63:TYR:O	8:F:64:GLN:HB2	2.17	0.44
10:H:109:ILE:HG13	10:H:110:ALA:N	2.32	0.44
11:I:104:ARG:HD3	11:I:105:ASP:H	1.78	0.44
12:J:8:LEU:HD13	12:J:20:ALA:HB1	1.99	0.44
12:J:17:ASP:O	12:J:21:GLN:HB2	2.17	0.44
12:J:29:ARG:HD2	12:J:84:GLN:OE1	2.17	0.44
18:P:22:THR:HA	18:P:33:ILE:HG13	1.98	0.44
18:P:43:LYS:HA	18:P:48:TRP:HB3	1.99	0.44
20:R:17:SER:HB2	20:R:54:ARG:HH21	1.82	0.44
22:T:73:HIS:HB3	22:T:74:LYS:H	1.45	0.44
1:A:436:C:H2'	1:A:437:U:H6	1.81	0.44
1:A:831:U:H2'	1:A:832:C:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1150:U:O5'	1:A:1150:U:H6	2.00	0.44
1:A:1394:A:H8	1:A:1394:A:OP1	2.00	0.44
1:A:1394:A:C6	1:A:1501:C:H4'	2.52	0.44
4:B:230:VAL:HG12	4:B:230:VAL:O	2.16	0.44
5:C:104:GLN:OE1	5:C:104:GLN:HA	2.16	0.44
6:D:70:ILE:HG22	6:D:75:PHE:HB2	1.98	0.44
11:I:114:TYR:CE1	12:J:59:SER:O	2.71	0.44
17:O:87:ILE:HG22	17:O:88:ARG:CZ	2.48	0.44
21:S:44:MET:HA	21:S:47:HIS:HD2	1.82	0.44
21:S:61:TYR:CD1	21:S:61:TYR:C	2.91	0.44
1:A:769:G:H4'	1:A:1513:A:H4'	2.00	0.44
1:A:1153:C:P	12:J:13:HIS:HE2	2.39	0.44
1:A:1264:C:H2'	1:A:1265:G:C8	2.52	0.44
1:A:1329:A:H5"	15:M:24:GLY:O	2.16	0.44
1:A:1437:C:H2'	1:A:1438:G:H8	1.82	0.44
1:A:1476:G:O2'	1:A:1477:C:H5'	2.17	0.44
4:B:54:THR:O	4:B:57:PHE:HB3	2.18	0.44
4:B:95:GLN:OE1	4:B:95:GLN:HA	2.17	0.44
7:E:102:ALA:CB	7:E:120:THR:CG2	2.88	0.44
10:H:133:LEU:HD23	10:H:134:ILE:H	1.78	0.44
12:J:10:GLY:N	12:J:16:LEU:HD11	2.32	0.44
17:O:57:LEU:HD12	17:O:57:LEU:HA	1.70	0.44
23:V:6:ARG:HB3	23:V:15:ARG:NH1	2.32	0.44
1:A:6:G:H3'	1:A:6:G:N3	2.32	0.44
1:A:743:U:H2'	1:A:744:C:C6	2.52	0.44
1:A:1027:C:H2'	1:A:1028:C:C6	2.51	0.44
1:A:1054:C:O2	1:A:1054:C:O4'	2.34	0.44
1:A:1165:C:O2'	1:A:1166:G:H5'	2.17	0.44
1:A:1298:C:H4'	1:A:1299:A:O4'	2.18	0.44
1:A:1355:G:H2'	1:A:1356:G:C8	2.53	0.44
4:B:97:TRP:CH2	4:B:173:ALA:HA	2.52	0.44
5:C:148:GLY:HA3	5:C:172:ARG:H	1.81	0.44
12:J:3:LYS:HD2	12:J:3:LYS:C	2.38	0.44
12:J:50:ILE:HG22	12:J:52:GLY:O	2.17	0.44
14:L:54:LYS:HE2	14:L:54:LYS:H	1.80	0.44
18:P:59:TRP:HB3	18:P:64:ALA:CB	2.48	0.44
18:P:81:ARG:C	18:P:83:GLU:H	2.17	0.44
1:A:26:A:H61	1:A:558:G:H1'	1.82	0.44
1:A:389:A:H2'	1:A:390:C:C5'	2.47	0.44
1:A:444:C:H2'	1:A:445:G:H8	1.82	0.44
1:A:942:G:C2	1:A:943:U:C6	3.06	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1108:G:H4'	1:A:1191:A:O4'	2.17	0.44
5:C:5:ILE:HB	5:C:6:HIS:H	1.23	0.44
5:C:59:ARG:HG2	5:C:64:VAL:HG13	1.98	0.44
5:C:119:ARG:HG2	5:C:140:ARG:HH12	1.83	0.44
5:C:188:LEU:HB3	5:C:189:ALA:H	1.67	0.44
8:F:67:MET:HB2	8:F:68:PRO:CD	2.47	0.44
10:H:23:SER:O	10:H:24:THR:HG22	2.17	0.44
18:P:21:VAL:HG21	18:P:59:TRP:CD1	2.52	0.44
1:A:328:C:H4'	1:A:329:A:H5'	1.99	0.44
1:A:342:C:H2'	1:A:343:U:O4'	2.17	0.44
1:A:895:G:H2'	1:A:896:C:C6	2.53	0.44
1:A:1320:C:O2	21:S:36:ARG:NH1	2.51	0.44
1:A:1426:C:H2'	1:A:1427:U:C6	2.53	0.44
4:B:20:GLU:HB2	4:B:190:THR:HG22	1.99	0.44
4:B:90:MET:HA	4:B:91:PRO:HD3	1.70	0.44
6:D:54:TYR:O	6:D:55:ALA:C	2.55	0.44
7:E:137:GLU:O	7:E:141:GLN:HG3	2.17	0.44
13:K:18:ARG:CA	13:K:80:VAL:HG23	2.47	0.44
13:K:54:ARG:H	13:K:54:ARG:HG2	1.45	0.44
15:M:52:GLU:O	15:M:54:VAL:N	2.50	0.44
22:T:30:LYS:O	22:T:33:ILE:HB	2.17	0.44
1:A:106:C:O2	1:A:379:C:H4'	2.18	0.44
1:A:116:A:O5'	1:A:116:A:H8	2.01	0.44
1:A:142:G:N3	1:A:196:A:C2	2.86	0.44
1:A:268:C:O2'	1:A:269:C:H5'	2.17	0.44
1:A:337:C:H2'	1:A:338:A:C8	2.53	0.44
1:A:409:G:N1	1:A:433:C:H5'	2.33	0.44
1:A:513:C:O2'	1:A:514:C:H5'	2.18	0.44
1:A:642:A:C5	10:H:115:SER:HA	2.53	0.44
1:A:975:A:C5'	1:A:976:G:H5'	2.47	0.44
1:A:1116:C:H2'	1:A:1117:G:C5'	2.28	0.44
1:A:1132:C:H2'	1:A:1133:G:H8	1.81	0.44
1:A:1143:G:H2'	1:A:1144:G:C8	2.52	0.44
1:A:1275:A:H2'	1:A:1276:G:O4'	2.17	0.44
1:A:1488:G:H2'	1:A:1489:G:C8	2.52	0.44
4:B:136:VAL:HG12	4:B:140:HIS:CD2	2.53	0.44
4:B:178:ARG:NH2	4:B:196:LEU:O	2.49	0.44
6:D:103:ASN:O	6:D:106:TYR:N	2.51	0.44
6:D:153:ARG:NE	6:D:181:MET:HE3	2.32	0.44
8:F:44:GLY:HA2	8:F:59:TYR:CZ	2.53	0.44
10:H:75:ARG:HA	10:H:76:PRO:HD3	1.67	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:136:GLU:O	10:H:137:VAL:CG2	2.66	0.44
11:I:9:ARG:H	11:I:79:LEU:HD13	1.83	0.44
12:J:28:ARG:HH21	12:J:33:GLN:HE21	1.64	0.44
12:J:33:GLN:C	12:J:34:VAL:HG23	2.38	0.44
13:K:46:GLY:O	13:K:47:VAL:C	2.55	0.44
14:L:27:LEU:C	14:L:29:GLY:H	2.11	0.44
18:P:81:ARG:O	18:P:83:GLU:N	2.40	0.44
19:Q:80:GLY:O	19:Q:81:ARG:HB3	2.18	0.44
20:R:61:LYS:O	20:R:65:ILE:HG13	2.17	0.44
1:A:339:C:H2'	1:A:340:U:C6	2.52	0.44
1:A:627:G:H2'	1:A:628:G:C8	2.52	0.44
1:A:644:G:C5	1:A:645:C:C5	3.06	0.44
1:A:866:C:C2'	1:A:867:G:O5'	2.66	0.44
1:A:1193:G:O2'	1:A:1194:U:H5'	2.17	0.44
1:A:1424:C:H2'	1:A:1425:U:H6	1.83	0.44
4:B:115:LEU:C	4:B:115:LEU:HD12	2.38	0.44
4:B:127:ILE:HG13	4:B:128:GLU:CD	2.38	0.44
4:B:184:VAL:HG12	4:B:197:VAL:HG13	2.00	0.44
4:B:209:ARG:HH12	4:B:236:TYR:HE2	1.66	0.44
4:B:239:VAL:HB	4:B:240:GLN:NE2	2.33	0.44
6:D:117:ALA:O	6:D:121:VAL:HG23	2.17	0.44
11:I:79:LEU:O	11:I:80:GLY:C	2.56	0.44
12:J:61:GLU:OE1	16:N:45:ARG:HD2	2.18	0.44
13:K:12:ARG:HG2	13:K:12:ARG:O	2.18	0.44
17:O:76:GLU:O	17:O:77:ARG:C	2.55	0.44
17:O:78:TYR:C	17:O:80:ALA:N	2.71	0.44
17:O:88:ARG:HA	17:O:88:ARG:NH1	2.31	0.44
18:P:17:TYR:N	18:P:17:TYR:CD1	2.85	0.44
18:P:69:THR:O	18:P:70:ALA:C	2.56	0.44
19:Q:59:ILE:HD13	19:Q:59:ILE:HA	1.58	0.44
20:R:52:PRO:CB	20:R:54:ARG:HD2	2.46	0.44
20:R:66:LEU:HG	20:R:70:ILE:CD1	2.48	0.44
21:S:22:LEU:HD13	21:S:28:LYS:HD3	1.98	0.44
1:A:419:C:C4	1:A:425:G:C6	3.06	0.43
1:A:624:C:H2'	1:A:625:G:C8	2.53	0.43
1:A:941:G:H2'	1:A:942:G:O5'	2.18	0.43
1:A:1018:C:O5'	1:A:1018:C:H6	2.01	0.43
4:B:8:LYS:HB2	4:B:9:GLU:H	1.50	0.43
4:B:236:TYR:C	4:B:238:LEU:N	2.72	0.43
6:D:138:TYR:C	6:D:138:TYR:CD2	2.91	0.43
10:H:11:THR:HA	10:H:14:ARG:NH1	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:14:LYS:C	12:J:16:LEU:H	2.22	0.43
18:P:45:THR:OG1	18:P:46:PRO:HD2	2.18	0.43
19:Q:6:LEU:O	19:Q:59:ILE:N	2.44	0.43
21:S:55:LYS:HG2	21:S:56:GLN:HE21	1.83	0.43
1:A:35:G:O2'	14:L:118:SER:O	2.28	0.43
1:A:1207:G:H2'	1:A:1208:C:C6	2.49	0.43
1:A:1262:C:H2'	1:A:1263:C:H6	1.82	0.43
1:A:1438:G:H2'	1:A:1439:C:C6	2.53	0.43
4:B:122:PHE:CZ	4:B:139:LYS:HG2	2.53	0.43
5:C:73:PRO:O	5:C:74:GLY:C	2.56	0.43
5:C:88:ARG:HA	5:C:101:LEU:HD12	1.98	0.43
5:C:149:ALA:HA	5:C:201:TYR:O	2.18	0.43
6:D:199:ASN:HD22	6:D:199:ASN:C	2.22	0.43
9:G:8:GLU:OE1	9:G:8:GLU:N	2.52	0.43
9:G:15:ASP:HB2	9:G:20:ASP:H	1.84	0.43
10:H:68:ARG:HG2	10:H:68:ARG:HH11	1.83	0.43
11:I:9:ARG:HG2	11:I:13:ALA:O	2.18	0.43
15:M:10:PRO:HB3	15:M:18:ALA:O	2.19	0.43
19:Q:12:SER:HB3	19:Q:20:THR:HB	1.99	0.43
19:Q:74:LEU:O	19:Q:74:LEU:HD23	2.18	0.43
22:T:21:LYS:HB2	22:T:21:LYS:HZ3	1.82	0.43
22:T:57:ARG:NH2	22:T:100:ILE:HD13	2.33	0.43
1:A:16:A:O2'	1:A:17:U:H5'	2.18	0.43
1:A:383:A:H2'	1:A:384:G:C5'	2.45	0.43
1:A:755:G:OP2	17:O:65:ARG:HD2	2.18	0.43
1:A:814:A:N7	1:A:816:A:C4	2.87	0.43
1:A:987:G:O2'	1:A:988:G:H5'	2.18	0.43
1:A:998:G:N2	1:A:1043:C:O2	2.50	0.43
1:A:1182:G:H4'	1:A:1183:A:H5"	2.00	0.43
1:A:1256:A:H5'	1:A:1258:G:H1'	2.01	0.43
4:B:9:GLU:OE1	4:B:10:LEU:N	2.51	0.43
4:B:39:ILE:HD12	4:B:39:ILE:N	2.32	0.43
4:B:129:GLU:O	4:B:130:ARG:HB2	2.16	0.43
5:C:26:LYS:HD2	5:C:26:LYS:O	2.19	0.43
5:C:195:VAL:CG1	5:C:196:LEU:H	2.29	0.43
7:E:42:GLY:HA2	7:E:65:ASN:O	2.18	0.43
10:H:86:ILE:HD12	10:H:133:LEU:HD22	2.00	0.43
13:K:96:ARG:HG2	13:K:96:ARG:NH1	2.33	0.43
18:P:81:ARG:HD2	18:P:81:ARG:HA	1.74	0.43
1:A:401:C:H1'	1:A:622:A:H1'	1.99	0.43
1:A:969:A:N6	15:M:126:LYS:HG3	2.26	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1260:C:H4'	1:A:1284:C:H5'	2.00	0.43
1:A:1342:C:H1'	11:I:124:GLN:HG3	1.99	0.43
5:C:154:SER:OG	5:C:196:LEU:HA	2.18	0.43
7:E:18:ARG:NH1	7:E:25:ARG:CB	2.81	0.43
8:F:25:ILE:CD1	8:F:82:ARG:HH11	2.31	0.43
9:G:44:TYR:O	9:G:45:ASP:C	2.55	0.43
10:H:96:GLY:H	10:H:99:GLU:HB2	1.82	0.43
11:I:9:ARG:HE	11:I:9:ARG:HB2	1.71	0.43
12:J:96:ILE:CG2	12:J:97:GLU:N	2.80	0.43
13:K:84:VAL:HG23	13:K:109:VAL:O	2.17	0.43
14:L:45:PRO:HD3	14:L:51:ALA:O	2.19	0.43
15:M:5:ALA:O	15:M:6:GLY:C	2.54	0.43
19:Q:97:SER:HA	19:Q:102:GLY:C	2.38	0.43
20:R:22:VAL:O	20:R:22:VAL:CG1	2.65	0.43
1:A:153:C:O5'	1:A:153:C:H6	2.02	0.43
1:A:448:A:C4	1:A:487:A:C2	3.07	0.43
1:A:609:A:H2'	1:A:610:G:H5'	1.99	0.43
1:A:855:G:H2'	1:A:856:C:C6	2.54	0.43
1:A:897:C:H5'	19:Q:101:ARG:NH2	2.33	0.43
1:A:1230:C:O2'	1:A:1231:G:H5'	2.18	0.43
1:A:1250:A:H2'	1:A:1251:A:C8	2.53	0.43
1:A:1298:C:C4	9:G:114:ARG:HD3	2.54	0.43
1:A:1481:U:O2'	1:A:1482:G:H5'	2.18	0.43
4:B:53:ARG:NH1	4:B:53:ARG:CB	2.81	0.43
4:B:126:GLU:C	4:B:128:GLU:H	2.20	0.43
5:C:32:LEU:CD2	5:C:32:LEU:O	2.67	0.43
5:C:123:GLN:NE2	5:C:140:ARG:HH22	2.17	0.43
6:D:162:LEU:O	6:D:162:LEU:HD23	2.19	0.43
8:F:19:LEU:HD23	8:F:20:ALA:CA	2.48	0.43
9:G:15:ASP:O	9:G:19:GLY:HA2	2.18	0.43
10:H:69:ARG:HH12	10:H:76:PRO:C	2.20	0.43
11:I:55:ALA:O	11:I:56:LEU:CB	2.66	0.43
14:L:100:ILE:CG2	14:L:101:VAL:N	2.82	0.43
19:Q:29:HIS:CG	19:Q:30:PRO:HD2	2.54	0.43
19:Q:67:LYS:CA	19:Q:70:ARG:HH12	2.31	0.43
1:A:185:A:N6	1:A:192:U:H3	2.16	0.43
1:A:419:C:C4	1:A:424:G:C6	3.07	0.43
1:A:1168:A:H2'	1:A:1169:A:H8	1.76	0.43
1:A:1249:C:O2'	11:I:73:GLN:NE2	2.52	0.43
1:A:1402:C:O2	1:A:1500:A:N1	2.52	0.43
1:A:1499:A:H1'	1:A:1520:G:H5'	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1515:C:O2'	1:A:1516:G:H5'	2.19	0.43
4:B:21:ARG:N	4:B:21:ARG:CD	2.81	0.43
4:B:97:TRP:HH2	4:B:176:GLU:CD	2.21	0.43
5:C:83:ARG:C	5:C:85:ARG:N	2.72	0.43
6:D:3:ARG:N	6:D:3:ARG:CD	2.81	0.43
7:E:15:ARG:HD3	7:E:26:PHE:CD2	2.54	0.43
7:E:31:LEU:HD22	7:E:43:LEU:CD2	2.47	0.43
12:J:24:VAL:O	12:J:28:ARG:CB	2.65	0.43
13:K:95:ILE:CG2	13:K:108:ILE:HD13	2.48	0.43
15:M:22:ILE:HB	15:M:25:ILE:HD12	2.00	0.43
15:M:65:LYS:HE2	15:M:69:GLU:O	2.18	0.43
16:N:25:VAL:HG12	16:N:39:LEU:HD23	2.01	0.43
18:P:18:ARG:HD3	18:P:35:LYS:HD2	2.01	0.43
18:P:20:VAL:CG1	18:P:32:TYR:CB	2.96	0.43
18:P:42:ARG:C	18:P:43:LYS:HD2	2.39	0.43
21:S:28:LYS:HG3	21:S:29:ARG:H	1.83	0.43
22:T:67:ALA:HB2	22:T:77:ALA:HB2	2.01	0.43
22:T:69:GLY:O	22:T:73:HIS:CD2	2.72	0.43
1:A:127:G:H4'	19:Q:2:PRO:HD2	2.00	0.43
1:A:190(H):G:O2'	1:A:190(I):G:H5'	2.18	0.43
1:A:272:C:O2'	1:A:273:A:H5'	2.19	0.43
1:A:359:U:H2'	1:A:360:A:C8	2.54	0.43
1:A:659:U:O2'	1:A:660:G:H5'	2.18	0.43
1:A:1070:U:H2'	1:A:1071:C:H6	1.83	0.43
1:A:1168:A:C6	1:A:1169:A:C6	3.06	0.43
4:B:115:LEU:C	4:B:117:GLU:N	2.69	0.43
5:C:3:ASN:O	5:C:4:LYS:O	2.37	0.43
5:C:79:ARG:NH1	5:C:79:ARG:CB	2.82	0.43
13:K:109:VAL:HG13	20:R:85:LEU:O	2.18	0.43
14:L:92:ASP:C	14:L:93:LEU:HD23	2.39	0.43
18:P:52:ASP:CG	18:P:55:ARG:HG3	2.39	0.43
20:R:56:THR:CB	20:R:58:LEU:HD12	2.48	0.43
21:S:38:SER:O	21:S:70:LYS:HD2	2.18	0.43
1:A:1194:U:H4'	7:E:22:GLY:HA3	1.99	0.43
1:A:1318:A:H4'	21:S:10:PHE:CE1	2.54	0.43
1:A:1399:C:C2	1:A:1401:G:C5	3.06	0.43
4:B:111:ARG:HB3	4:B:149:LEU:CD1	2.48	0.43
5:C:4:LYS:HA	5:C:4:LYS:NZ	2.33	0.43
5:C:30:ARG:HG3	5:C:31:HIS:N	2.33	0.43
5:C:101:LEU:O	5:C:101:LEU:HD22	2.18	0.43
6:D:64:LEU:HB2	6:D:198:VAL:HG11	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:72:VAL:CG2	8:F:73:ASN:H	2.25	0.43
12:J:12:ASP:O	12:J:15:THR:HG22	2.18	0.43
12:J:19:SER:C	12:J:21:GLN:N	2.72	0.43
15:M:8:GLU:O	15:M:9:ILE:HG23	2.19	0.43
18:P:65:GLN:HA	18:P:66:PRO:HD2	1.85	0.43
20:R:79:LEU:CD2	20:R:80:PRO:HD2	2.48	0.43
20:R:86:VAL:O	20:R:87:ARG:CB	2.66	0.43
1:A:251:G:H4'	1:A:252:U:O5'	2.19	0.43
1:A:264:U:O2'	19:Q:64:PRO:HB2	2.18	0.43
1:A:335:C:H2'	1:A:336:C:C6	2.54	0.43
1:A:710:G:O2'	1:A:711:G:H5'	2.19	0.43
1:A:1249:C:H4'	11:I:36:TYR:OH	2.19	0.43
1:A:1404:C:H2'	1:A:1405:G:C8	2.54	0.43
4:B:22:LYS:HA	4:B:22:LYS:HZ3	1.84	0.43
4:B:69:LEU:HD21	4:B:93:VAL:HG22	2.00	0.43
5:C:112:SER:O	5:C:116:VAL:HG23	2.18	0.43
6:D:17:VAL:CG1	6:D:18:LYS:N	2.81	0.43
6:D:176:LEU:H	6:D:176:LEU:CD2	2.31	0.43
10:H:95:VAL:HB	10:H:99:GLU:HB2	2.00	0.43
11:I:46:ALA:O	11:I:78:LYS:HA	2.19	0.43
13:K:45:GLY:HA3	13:K:55:LYS:HG2	2.00	0.43
13:K:69:ALA:O	13:K:73:MET:HG2	2.19	0.43
13:K:123:LYS:O	13:K:125:PHE:N	2.52	0.43
15:M:9:ILE:HD12	15:M:9:ILE:N	2.34	0.43
15:M:110:ARG:HH11	15:M:110:ARG:CG	2.32	0.43
16:N:11:LYS:C	16:N:13:THR:H	2.22	0.43
16:N:24:CYS:HB2	16:N:40:CYS:HB3	1.99	0.43
21:S:16:LEU:O	21:S:19:VAL:HG12	2.19	0.43
1:A:193:C:H2'	1:A:194:C:H6	1.81	0.43
1:A:409:G:H5'	1:A:430:A:N6	2.34	0.43
1:A:976:G:N7	1:A:1358:U:C2	2.86	0.43
1:A:1000:U:O2'	1:A:1001:A:H5'	2.19	0.43
1:A:1001:A:H2'	1:A:1002:G:C8	2.54	0.43
1:A:1183:A:O2'	1:A:1184:G:P	2.77	0.43
1:A:1375:A:H2'	1:A:1376:U:O4'	2.19	0.43
1:A:1392:G:O2'	1:A:1502:A:H5"	2.19	0.43
1:A:1431:C:H2'	1:A:1432:G:C5'	2.49	0.43
4:B:29:ALA:HA	4:B:32:ILE:HD12	2.00	0.43
4:B:33:TYR:O	4:B:34:ALA:HB2	2.19	0.43
4:B:221:LEU:O	4:B:221:LEU:HD13	2.19	0.43
6:D:6:GLY:H	6:D:115:ARG:HH22	1.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:31:LEU:HD23	7:E:31:LEU:HA	1.73	0.43
8:F:10:LEU:HD11	8:F:61:LEU:CD1	2.48	0.43
9:G:59:LEU:HD11	9:G:63:LYS:HZ3	1.83	0.43
9:G:148:ASN:C	9:G:150:ALA:H	2.21	0.43
11:I:39:GLY:O	11:I:40:LEU:HD23	2.19	0.43
11:I:49:PRO:HG2	11:I:50:LEU:H	1.83	0.43
12:J:9:ARG:HA	12:J:16:LEU:HD11	2.01	0.43
16:N:37:PHE:HE2	16:N:53:LEU:HD13	1.83	0.43
18:P:9:PHE:CE1	18:P:18:ARG:CZ	3.02	0.43
21:S:62:ILE:HD12	21:S:63:THR:N	2.34	0.43
1:A:407:G:H4'	1:A:408:A:OP1	2.19	0.42
1:A:426:G:O2'	1:A:427:U:H5'	2.19	0.42
1:A:955:U:H2'	1:A:956:U:H6	1.84	0.42
1:A:1058:G:O2'	1:A:1059:C:H5'	2.19	0.42
1:A:1150:U:O2	12:J:39:PRO:HG3	2.19	0.42
1:A:1229:A:C2	1:A:1230:C:C5	3.07	0.42
1:A:1234:C:O2'	1:A:1235:U:H5'	2.19	0.42
1:A:1366:C:C2	1:A:1367:C:C5	3.07	0.42
5:C:101:LEU:O	5:C:101:LEU:CD2	2.66	0.42
7:E:82:VAL:CG2	7:E:138:ALA:HA	2.47	0.42
8:F:44:GLY:CA	8:F:59:TYR:CE1	3.02	0.42
8:F:69:GLU:C	8:F:71:ARG:H	2.22	0.42
9:G:125:MET:O	9:G:128:ALA:N	2.52	0.42
10:H:95:VAL:HB	10:H:99:GLU:CB	2.49	0.42
11:I:33:PHE:O	11:I:35:GLU:N	2.49	0.42
11:I:93:ARG:HB3	11:I:93:ARG:CZ	2.48	0.42
13:K:33:THR:HB	13:K:38:ASN:C	2.39	0.42
13:K:74:ALA:O	13:K:76:GLY:N	2.52	0.42
15:M:39:ILE:HG22	15:M:40:ASN:O	2.19	0.42
16:N:25:VAL:HG12	16:N:38:GLY:O	2.19	0.42
17:O:70:LEU:HD12	17:O:78:TYR:CA	2.48	0.42
19:Q:97:SER:O	19:Q:99:SER:N	2.50	0.42
21:S:30:LEU:N	21:S:30:LEU:CD1	2.82	0.42
22:T:30:LYS:O	22:T:31:SER:C	2.57	0.42
23:V:12:LYS:HG3	23:V:17:THR:OG1	2.19	0.42
1:A:792:A:H4'	1:A:793:U:C5'	2.49	0.42
1:A:862:C:O2'	1:A:863:U:H5'	2.19	0.42
4:B:26:PRO:C	4:B:28:PHE:N	2.72	0.42
6:D:25:ARG:NH1	6:D:30:LYS:O	2.49	0.42
6:D:60:GLU:OE1	6:D:60:GLU:HA	2.19	0.42
6:D:187:ARG:CD	6:D:188:LEU:N	2.81	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:14:LEU:HD13	8:F:19:LEU:HA	2.01	0.42
10:H:86:ILE:CG2	10:H:87:SER:N	2.75	0.42
14:L:76:ASN:O	14:L:76:ASN:CG	2.57	0.42
14:L:86:ARG:NH2	14:L:99:HIS:CD2	2.86	0.42
17:O:18:PHE:HB2	17:O:19:PRO:CD	2.48	0.42
20:R:36:ASN:HA	20:R:38:GLU:OE2	2.20	0.42
1:A:21:G:H2'	1:A:22:G:C8	2.54	0.42
1:A:52:G:O2'	1:A:53:A:H5'	2.18	0.42
1:A:589:C:O2'	1:A:590:C:H5'	2.19	0.42
1:A:807:A:H2'	1:A:808:C:C6	2.53	0.42
1:A:1370:G:C2	1:A:1371:G:N7	2.87	0.42
4:B:60:ASP:HB3	4:B:64:ARG:NE	2.34	0.42
4:B:143:GLU:O	4:B:144:ARG:C	2.58	0.42
4:B:145:LEU:C	4:B:147:LYS:N	2.72	0.42
5:C:179:ARG:O	5:C:179:ARG:HG2	2.19	0.42
9:G:51:GLN:NE2	9:G:56:GLN:O	2.47	0.42
10:H:96:GLY:N	10:H:99:GLU:HB2	2.34	0.42
12:J:14:LYS:C	12:J:16:LEU:N	2.72	0.42
12:J:22:LYS:O	12:J:24:VAL:N	2.52	0.42
12:J:28:ARG:HG2	12:J:28:ARG:NH1	2.34	0.42
13:K:69:ALA:O	13:K:72:ALA:N	2.53	0.42
15:M:50:GLU:O	15:M:54:VAL:HG23	2.19	0.42
17:O:18:PHE:HB2	17:O:19:PRO:HD2	2.00	0.42
19:Q:67:LYS:O	19:Q:68:ARG:C	2.57	0.42
22:T:56:MET:HE3	22:T:88:VAL:HG11	2.02	0.42
22:T:94:ALA:O	22:T:95:ALA:CB	2.67	0.42
1:A:37:U:O2'	1:A:500:G:H4'	2.18	0.42
1:A:408:A:H4'	1:A:429:U:H1'	2.00	0.42
1:A:477:G:H3'	1:A:478:A:C5'	2.50	0.42
1:A:536:C:H2'	1:A:537:G:H8	1.84	0.42
1:A:757:U:H2'	1:A:758:G:O4'	2.19	0.42
1:A:1371:G:OP1	11:I:11:LYS:O	2.37	0.42
1:A:1441:G:H4'	1:A:1442:G:C4	2.55	0.42
4:B:85:ALA:CB	4:B:92:TYR:HD2	2.32	0.42
4:B:103:THR:HG23	4:B:176:GLU:CB	2.49	0.42
5:C:119:ARG:HG2	5:C:140:ARG:NH1	2.35	0.42
6:D:153:ARG:NE	6:D:181:MET:CE	2.83	0.42
7:E:68:GLU:O	7:E:70:PRO:HD3	2.19	0.42
7:E:152:ARG:O	7:E:153:LYS:C	2.58	0.42
8:F:82:ARG:HB2	8:F:85:VAL:CG2	2.50	0.42
10:H:36:LEU:HD12	10:H:59:LEU:HD13	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:133:LEU:HD23	10:H:133:LEU:C	2.40	0.42
12:J:12:ASP:OD1	12:J:14:LYS:N	2.52	0.42
14:L:7:ILE:O	14:L:11:VAL:HG23	2.20	0.42
14:L:37:CYS:N	14:L:81:SER:O	2.43	0.42
15:M:100:GLY:C	15:M:101:GLN:HG3	2.40	0.42
15:M:108:ARG:N	15:M:108:ARG:HD2	2.34	0.42
18:P:67:THR:HG22	18:P:68:ASP:H	1.81	0.42
19:Q:76:LEU:C	19:Q:76:LEU:CD2	2.87	0.42
1:A:11:G:C6	1:A:12:U:C4	3.08	0.42
1:A:322:C:H2'	1:A:323:U:C6	2.54	0.42
1:A:332:G:OP2	22:T:10:LEU:HD23	2.19	0.42
1:A:457:C:H2'	1:A:458:C:H6	1.84	0.42
1:A:532:A:H2'	1:A:533:A:OP1	2.19	0.42
1:A:596:C:O2'	1:A:597:G:H5'	2.18	0.42
1:A:600:C:O2'	1:A:601:C:H5'	2.19	0.42
1:A:662:G:H2'	1:A:663:A:H8	1.84	0.42
1:A:742:G:H2'	1:A:743:U:O4'	2.19	0.42
1:A:959:A:H2'	1:A:960:U:O4'	2.19	0.42
1:A:1182:G:H4'	1:A:1183:A:C5'	2.50	0.42
1:A:1280:A:O4'	12:J:41:PRO:HG3	2.20	0.42
1:A:1525:G:OP1	13:K:120:ARG:NH2	2.52	0.42
3:W:2:G:O2'	3:W:3:C:H5'	2.20	0.42
4:B:130:ARG:HB3	4:B:131:PRO:HD2	2.01	0.42
5:C:25:GLY:C	5:C:27:LYS:H	2.23	0.42
5:C:43:LEU:HD21	5:C:47:LEU:HD22	2.01	0.42
5:C:116:VAL:HG21	5:C:202:ILE:HD11	2.01	0.42
10:H:60:ARG:HG3	10:H:60:ARG:NH1	2.33	0.42
10:H:123:GLU:O	10:H:124:ALA:C	2.58	0.42
14:L:52:LEU:N	14:L:52:LEU:HD22	2.34	0.42
16:N:24:CYS:SG	16:N:43:CYS:SG	3.17	0.42
18:P:20:VAL:HG11	18:P:32:TYR:HB3	2.00	0.42
1:A:118:U:O4	1:A:289:G:H4'	2.19	0.42
1:A:155:C:O2'	1:A:156:G:H5'	2.19	0.42
1:A:267:C:H2'	1:A:268:C:C6	2.55	0.42
1:A:1067:A:N3	1:A:1068:G:H1'	2.35	0.42
1:A:1190:G:OP1	5:C:5:ILE:HG13	2.19	0.42
1:A:1256:A:H2	1:A:1277:C:N4	2.17	0.42
1:A:1340:A:O2'	1:A:1341:U:H5'	2.19	0.42
1:A:1375:A:O2'	1:A:1376:U:H5'	2.19	0.42
1:A:1422:G:H2'	1:A:1423:G:H8	1.85	0.42
4:B:81:VAL:HG22	4:B:215:LEU:CD2	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:178:ARG:HH21	4:B:196:LEU:HA	1.85	0.42
6:D:76:ARG:HG2	6:D:76:ARG:NH1	2.35	0.42
8:F:30:LEU:HD23	8:F:75:LEU:HD21	2.02	0.42
12:J:16:LEU:O	12:J:20:ALA:N	2.51	0.42
15:M:115:LYS:HB2	15:M:115:LYS:NZ	2.33	0.42
16:N:23:ARG:NH1	16:N:30:ALA:HB2	2.35	0.42
1:A:327:A:O2'	1:A:328:C:O4'	2.32	0.42
1:A:399:G:H2'	1:A:400:C:C6	2.55	0.42
1:A:505:G:C6	1:A:535:A:C2	3.07	0.42
1:A:860:A:O2'	1:A:861:G:H5'	2.20	0.42
1:A:1048:G:OP1	16:N:3:ARG:HA	2.20	0.42
1:A:1058:G:OP1	5:C:199:LYS:NZ	2.53	0.42
1:A:1157:A:H1'	1:A:1181:G:N2	2.34	0.42
1:A:1373:G:H5"	9:G:36:LYS:CB	2.50	0.42
5:C:188:LEU:HD22	5:C:188:LEU:HA	1.88	0.42
8:F:10:LEU:HD12	8:F:59:TYR:O	2.19	0.42
9:G:40:ALA:CB	11:I:41:VAL:HG21	2.50	0.42
10:H:69:ARG:NH1	10:H:69:ARG:HG3	2.34	0.42
18:P:55:ARG:O	18:P:56:ALA:C	2.57	0.42
1:A:279:A:C5	19:Q:98:LEU:HD23	2.54	0.42
1:A:406:G:C5'	6:D:5:ILE:HG21	2.50	0.42
1:A:448:A:OP2	1:A:485:G:N2	2.36	0.42
1:A:550:G:O2'	1:A:551:U:H5'	2.20	0.42
1:A:609:A:C2'	1:A:610:G:H5'	2.49	0.42
1:A:1111:A:N6	5:C:177:THR:HA	2.35	0.42
1:A:1347:G:H22	1:A:1373:G:H2'	1.80	0.42
4:B:16:HIS:HB3	4:B:17:PHE:H	1.52	0.42
4:B:88:ALA:O	4:B:90:MET:N	2.53	0.42
5:C:79:ARG:HB2	5:C:79:ARG:NH1	2.35	0.42
5:C:91:LEU:HD11	5:C:99:VAL:HG23	2.01	0.42
6:D:108:LEU:HB2	6:D:110:PHE:CD1	2.54	0.42
10:H:4:ASP:CG	10:H:85:ARG:NH1	2.73	0.42
11:I:32:ASP:O	11:I:34:ASN:N	2.53	0.42
14:L:117:ARG:NH2	14:L:124:LYS:CA	2.81	0.42
21:S:61:TYR:C	21:S:61:TYR:HD1	2.23	0.42
1:A:12:U:H4'	1:A:526:C:H4'	2.01	0.42
1:A:123:C:OP1	1:A:312:C:H5'	2.20	0.42
1:A:522:C:O2'	1:A:523:A:H5'	2.19	0.42
1:A:534:U:OP1	1:A:535:A:OP2	2.38	0.42
1:A:957:U:H3	1:A:960:U:C5'	2.31	0.42
1:A:1006:C:O5'	1:A:1006:C:H6	2.03	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1348:U:H2'	1:A:1349:A:H8	1.85	0.42
1:A:1480:G:O2'	1:A:1481:U:H5'	2.19	0.42
4:B:73:THR:O	4:B:74:LYS:C	2.58	0.42
4:B:83:MET:HE3	4:B:238:LEU:HD22	2.02	0.42
4:B:97:TRP:CH2	4:B:176:GLU:OE2	2.73	0.42
5:C:15:THR:CG2	5:C:179:ARG:HB2	2.50	0.42
5:C:70:VAL:CG1	5:C:71:ALA:H	2.32	0.42
5:C:100:ALA:HB1	5:C:102:ASN:ND2	2.35	0.42
6:D:7:PRO:HG2	6:D:10:ARG:CD	2.47	0.42
6:D:38:TYR:CD1	6:D:45:GLN:HG3	2.54	0.42
7:E:51:VAL:CB	7:E:52:PRO:HD3	2.48	0.42
9:G:69:VAL:O	9:G:71:PRO:HD3	2.20	0.42
9:G:118:VAL:O	9:G:121:ALA:HB3	2.19	0.42
10:H:51:VAL:CG1	10:H:52:ASP:N	2.82	0.42
11:I:127:LYS:CG	15:M:126:LYS:HZ3	2.33	0.42
11:I:127:LYS:HD2	15:M:126:LYS:NZ	2.34	0.42
14:L:102:ARG:NH2	14:L:110:VAL:HA	2.34	0.42
14:L:113:ARG:HG2	14:L:113:ARG:NH1	2.34	0.42
18:P:58:TYR:O	18:P:61:SER:N	2.53	0.42
20:R:21:LYS:C	20:R:23:LYS:H	2.22	0.42
20:R:44:LEU:CD1	20:R:79:LEU:HD22	2.49	0.42
23:V:14:TRP:C	23:V:16:GLY:H	2.22	0.42
1:A:866:C:H2'	1:A:867:G:O4'	2.20	0.42
1:A:1240:U:C4'	9:G:38:LEU:HD21	2.50	0.42
1:A:1531:A:O5'	1:A:1531:A:H8	2.02	0.42
4:B:10:LEU:HG	4:B:48:MET:HE1	2.01	0.42
5:C:64:VAL:HB	5:C:99:VAL:CG2	2.44	0.42
5:C:132:ARG:O	5:C:133:ALA:C	2.58	0.42
13:K:84:VAL:HG11	13:K:91:ARG:HD2	2.01	0.42
14:L:69:TYR:HE2	14:L:71:PRO:HA	1.84	0.42
15:M:40:ASN:HD22	15:M:41:PRO:N	2.17	0.42
15:M:117:VAL:HB	15:M:118:ALA:H	1.75	0.42
16:N:53:LEU:HD23	16:N:53:LEU:HA	1.89	0.42
17:O:24:SER:OG	17:O:27:VAL:HG23	2.20	0.42
17:O:41:GLU:O	17:O:44:LYS:HB3	2.20	0.42
19:Q:59:ILE:CD1	19:Q:73:VAL:HA	2.50	0.42
22:T:70:SER:HA	22:T:73:HIS:CD2	2.54	0.42
1:A:53:A:H2'	1:A:54:C:O5'	2.19	0.41
1:A:191:G:N2	22:T:103:GLY:O	2.35	0.41
1:A:591:U:OP1	10:H:30:ARG:CZ	2.67	0.41
1:A:662:G:O2'	1:A:663:A:H5'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:686:U:C2	1:A:687:A:N7	2.88	0.41
1:A:811:C:C5	1:A:812:C:N4	2.88	0.41
1:A:1003:G:H2'	1:A:1003:G:N3	2.35	0.41
1:A:1020:U:H2'	1:A:1021:G:C8	2.55	0.41
1:A:1152:A:OP1	12:J:68:HIS:ND1	2.53	0.41
1:A:1226:C:H2'	15:M:103:THR:CB	2.50	0.41
1:A:1385:G:H2'	1:A:1386:G:O4'	2.19	0.41
4:B:73:THR:HG23	4:B:95:GLN:O	2.20	0.41
4:B:132:LYS:HA	4:B:132:LYS:HD3	1.90	0.41
4:B:215:LEU:O	4:B:218:ALA:HB3	2.20	0.41
8:F:21:LEU:O	8:F:24:GLU:HB3	2.20	0.41
8:F:55:ASP:HB2	8:F:86:ARG:HH12	1.84	0.41
10:H:119:LEU:HD12	10:H:124:ALA:N	2.35	0.41
11:I:125:TYR:CE1	11:I:128:ARG:NE	2.88	0.41
21:S:39:THR:HG22	21:S:40:ILE:N	2.34	0.41
22:T:16:HIS:O	22:T:17:ARG:C	2.59	0.41
22:T:26:ASN:O	22:T:27:LYS:C	2.58	0.41
1:A:8:A:H5'	7:E:101:ILE:HG22	2.01	0.41
1:A:287:U:C2'	1:A:288:A:H5'	2.50	0.41
1:A:490:G:H2'	1:A:491:G:C8	2.53	0.41
1:A:614:A:C2	1:A:627:G:C2	3.08	0.41
1:A:792:A:C4	1:A:794:A:C6	3.09	0.41
1:A:1116:C:C3'	1:A:1117:G:H5"	2.51	0.41
1:A:1183:A:C2'	1:A:1184:G:OP1	2.68	0.41
1:A:1464:G:O2'	1:A:1465:C:H5'	2.20	0.41
4:B:25:ASN:HD22	4:B:27:LYS:N	2.10	0.41
4:B:42:ILE:HD12	4:B:203:GLY:O	2.20	0.41
4:B:172:ILE:N	4:B:172:ILE:CD1	2.82	0.41
6:D:126:ILE:CG2	6:D:127:THR:H	2.32	0.41
6:D:163:GLU:C	6:D:165:MET:H	2.24	0.41
11:I:42:ARG:O	11:I:43:ALA:C	2.57	0.41
13:K:59:TYR:O	13:K:60:ALA:C	2.58	0.41
14:L:125:PRO:O	14:L:127:GLU:HG2	2.21	0.41
17:O:9:GLN:C	17:O:11:VAL:N	2.74	0.41
20:R:17:SER:HB2	20:R:54:ARG:NE	2.33	0.41
21:S:22:LEU:HD13	21:S:28:LYS:CD	2.50	0.41
22:T:57:ARG:HH22	22:T:100:ILE:HD13	1.85	0.41
1:A:168:G:O2'	1:A:169:C:H5'	2.20	0.41
1:A:691:G:O2'	1:A:797:C:H4'	2.20	0.41
1:A:720:C:H2'	1:A:721:G:C8	2.55	0.41
1:A:723:U:H5"	1:A:724:G:OP2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1157:A:H4'	1:A:1158:C:O5'	2.20	0.41
1:A:1349:A:OP2	11:I:118:LYS:NZ	2.54	0.41
4:B:91:PRO:CG	4:B:154:LEU:HB2	2.50	0.41
4:B:177:ALA:O	4:B:180:LEU:N	2.39	0.41
4:B:187:LEU:HD12	4:B:201:ILE:O	2.20	0.41
4:B:197:VAL:HB	4:B:200:ILE:CG2	2.37	0.41
6:D:153:ARG:HE	6:D:181:MET:HE3	1.83	0.41
6:D:159:ARG:HH11	6:D:159:ARG:HG3	1.85	0.41
6:D:163:GLU:C	6:D:165:MET:N	2.73	0.41
9:G:115:ARG:HB2	9:G:118:VAL:HG23	2.02	0.41
12:J:87:THR:O	12:J:88:LEU:HD23	2.20	0.41
15:M:80:ARG:HB3	15:M:80:ARG:CZ	2.49	0.41
18:P:20:VAL:HG12	18:P:21:VAL:N	2.34	0.41
19:Q:48:GLU:C	19:Q:50:LYS:N	2.71	0.41
1:A:40:C:O2'	1:A:41:G:H5'	2.20	0.41
1:A:273:A:N6	1:A:274:A:N6	2.69	0.41
1:A:615:C:O2'	1:A:616:G:H5'	2.20	0.41
1:A:969:A:C2'	1:A:970:C:H5'	2.51	0.41
1:A:976:G:C8	1:A:1358:U:O2	2.73	0.41
1:A:1020:U:H2'	1:A:1021:G:H8	1.84	0.41
4:B:145:LEU:N	4:B:145:LEU:HD23	2.34	0.41
4:B:235:SER:O	4:B:237:ALA:N	2.46	0.41
6:D:24:GLU:O	6:D:25:ARG:HB2	2.20	0.41
6:D:91:SER:O	6:D:92:VAL:C	2.58	0.41
7:E:48:ALA:HB2	7:E:57:LYS:HE2	2.01	0.41
9:G:72:ARG:HA	9:G:72:ARG:HD3	1.87	0.41
9:G:108:ALA:O	9:G:110:GLN:N	2.53	0.41
14:L:49:ASN:N	14:L:49:ASN:ND2	2.67	0.41
15:M:84:ILE:O	15:M:85:GLY:C	2.58	0.41
17:O:74:ASP:C	17:O:76:GLU:N	2.73	0.41
19:Q:27:PHE:CE1	19:Q:36:ILE:HD11	2.55	0.41
19:Q:81:ARG:HE	19:Q:81:ARG:HB2	1.53	0.41
21:S:53:ASN:ND2	21:S:58:VAL:HG23	2.36	0.41
23:V:6:ARG:HB3	23:V:15:ARG:HH11	1.84	0.41
1:A:46:G:O2'	1:A:365:U:H1'	2.20	0.41
1:A:337:C:H2'	1:A:338:A:H8	1.85	0.41
1:A:384:G:H2'	1:A:385:C:H6	1.84	0.41
1:A:1094:G:OP2	1:A:1095:U:H5	2.02	0.41
1:A:1256:A:H2	1:A:1277:C:H42	1.69	0.41
5:C:22:TRP:CB	5:C:59:ARG:HB2	2.50	0.41
5:C:30:ARG:O	5:C:33:LEU:HB3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:66:VAL:O	5:C:66:VAL:HG12	2.21	0.41
6:D:36:ARG:HA	6:D:38:TYR:CD2	2.56	0.41
7:E:144:THR:O	7:E:148:VAL:HG23	2.20	0.41
9:G:99:LEU:HD23	9:G:102:ARG:NH1	2.35	0.41
11:I:3:GLN:HB2	11:I:19:LEU:O	2.20	0.41
17:O:39:LEU:HD13	17:O:56:LEU:CB	2.44	0.41
17:O:81:LEU:HD22	17:O:85:LEU:CD1	2.51	0.41
18:P:71:ARG:O	18:P:72:ARG:C	2.59	0.41
21:S:62:ILE:CD1	21:S:66:MET:HG3	2.46	0.41
22:T:68:LYS:HD2	22:T:68:LYS:HA	1.90	0.41
1:A:9:G:OP1	7:E:122:GLU:HG3	2.20	0.41
1:A:113:G:C1'	1:A:354:G:H5'	2.49	0.41
1:A:738:C:OP2	8:F:92:LYS:NZ	2.45	0.41
1:A:892:A:C2	1:A:907:A:C4	3.09	0.41
1:A:951:G:C2	1:A:1231:G:C4	3.09	0.41
1:A:955:U:H2'	1:A:956:U:C6	2.56	0.41
1:A:1000:U:C2'	1:A:1001:A:H5'	2.51	0.41
1:A:1053:G:H4'	1:A:1054:C:H5'	2.01	0.41
1:A:1368:G:OP2	11:I:112:LYS:HD3	2.20	0.41
4:B:88:ALA:C	4:B:90:MET:N	2.72	0.41
5:C:32:LEU:O	5:C:32:LEU:HD23	2.21	0.41
6:D:28:SER:OG	6:D:30:LYS:HG2	2.21	0.41
6:D:196:LEU:HD23	6:D:196:LEU:HA	1.93	0.41
9:G:54:THR:HG22	9:G:56:GLN:H	1.86	0.41
10:H:112:LEU:HD11	10:H:114:THR:HG22	2.02	0.41
11:I:9:ARG:HD3	11:I:14:VAL:HG22	2.03	0.41
15:M:3:ARG:HA	15:M:9:ILE:HG23	2.02	0.41
15:M:60:VAL:HG22	15:M:64:TRP:HZ3	1.86	0.41
17:O:32:LEU:O	17:O:36:ILE:HG13	2.20	0.41
1:A:410:G:OP1	1:A:431:A:N6	2.54	0.41
1:A:665:A:H2'	1:A:725:G:N2	2.36	0.41
1:A:908:A:H2'	1:A:909:A:C8	2.55	0.41
1:A:1018:C:H2'	1:A:1019:C:O4'	2.21	0.41
1:A:1025:U:HO2'	1:A:1026:G:H8	1.68	0.41
1:A:1040:U:H2'	1:A:1041:A:C8	2.56	0.41
1:A:1406:U:H2'	1:A:1407:C:O4'	2.20	0.41
4:B:162:ILE:O	4:B:185:ILE:HD12	2.20	0.41
5:C:29:TYR:OH	16:N:54:PRO:HG2	2.21	0.41
5:C:179:ARG:C	5:C:179:ARG:CD	2.83	0.41
6:D:68:TYR:CE2	6:D:97:LEU:HB3	2.56	0.41
7:E:101:ILE:HD12	7:E:119:LEU:CD2	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:F:62:TRP:C	8:F:63:TYR:CD1	2.91	0.41
10:H:92:ARG:CG	10:H:92:ARG:NH1	2.78	0.41
14:L:65:GLU:CD	14:L:65:GLU:N	2.74	0.41
15:M:67:GLU:O	15:M:68:GLY:C	2.59	0.41
17:O:11:VAL:HG21	17:O:34:LEU:HD12	2.02	0.41
18:P:3:LYS:O	18:P:21:VAL:HA	2.20	0.41
18:P:4:ILE:HG23	18:P:36:ILE:HD11	2.03	0.41
18:P:56:ALA:O	18:P:57:ARG:C	2.58	0.41
21:S:51:VAL:HG22	21:S:71:LEU:HD23	2.02	0.41
1:A:190(I):G:H2'	1:A:190(J):U:H6	1.86	0.41
1:A:363:A:O2'	1:A:364:A:H5'	2.20	0.41
1:A:1405:G:H1'	1:A:1519:A:O4'	2.20	0.41
1:A:1420:C:H2'	1:A:1421:G:C8	2.56	0.41
4:B:107:THR:C	4:B:109:SER:N	2.74	0.41
4:B:222:ILE:HG22	4:B:226:ARG:NH2	2.36	0.41
5:C:6:HIS:CD2	5:C:8:ILE:H	2.35	0.41
5:C:13:GLY:HA3	16:N:57:ARG:HH21	1.84	0.41
5:C:120:VAL:HB	5:C:198:VAL:HG11	2.03	0.41
6:D:68:TYR:CD1	6:D:68:TYR:N	2.89	0.41
7:E:143:ARG:NH1	10:H:77:GLU:CD	2.74	0.41
12:J:12:ASP:HB3	12:J:15:THR:HG22	2.03	0.41
14:L:46:LYS:O	14:L:47:LYS:C	2.59	0.41
15:M:49:THR:C	15:M:51:ALA:N	2.73	0.41
16:N:53:LEU:HA	16:N:54:PRO:HD2	1.93	0.41
19:Q:69:LYS:C	19:Q:70:ARG:HD2	2.40	0.41
1:A:186:C:H1'	22:T:85:MET:HE1	2.02	0.41
1:A:298:A:H2'	1:A:299:G:O4'	2.21	0.41
1:A:363:A:OP1	14:L:33:ARG:HD2	2.21	0.41
1:A:401:C:O2'	1:A:621:A:H1'	2.20	0.41
1:A:485:G:O2'	1:A:486:U:OP2	2.39	0.41
1:A:538:G:OP2	14:L:115:LYS:HD2	2.21	0.41
1:A:625:G:O2'	1:A:626:U:H5'	2.21	0.41
1:A:628:G:H2'	1:A:629:G:C8	2.56	0.41
1:A:744:C:H2'	1:A:745:C:C6	2.55	0.41
1:A:748:C:OP2	1:A:748:C:C6	2.71	0.41
1:A:911:U:H2'	1:A:912:C:C6	2.56	0.41
1:A:1055:A:C2	1:A:1056:U:H1'	2.56	0.41
1:A:1347:G:C6	11:I:107:ARG:NH2	2.78	0.41
1:A:1392:G:H2'	1:A:1393:U:H6	1.86	0.41
1:A:1418:A:H2'	1:A:1419:G:H5'	2.02	0.41
1:A:1442:G:C4	1:A:1446:A:N7	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:7:VAL:HG23	4:B:7:VAL:O	2.21	0.41
5:C:31:HIS:CD2	5:C:31:HIS:N	2.75	0.41
5:C:77:ILE:HG23	5:C:81:GLY:HA2	2.02	0.41
5:C:113:ALA:N	5:C:114:PRO:CD	2.84	0.41
7:E:50:GLU:O	7:E:51:VAL:C	2.59	0.41
9:G:51:GLN:C	9:G:53:LYS:H	2.24	0.41
9:G:57:GLU:HB3	9:G:58:PRO:HD2	2.02	0.41
10:H:35:ILE:HG22	10:H:111:ILE:HD13	2.01	0.41
10:H:48:TYR:CD1	10:H:48:TYR:C	2.95	0.41
12:J:19:SER:C	12:J:21:GLN:H	2.24	0.41
12:J:30:SER:OG	12:J:81:THR:HA	2.21	0.41
13:K:18:ARG:HD2	13:K:83:ILE:HD11	2.02	0.41
14:L:46:LYS:CE	14:L:47:LYS:HB2	2.45	0.41
15:M:6:GLY:O	15:M:7:VAL:HG22	2.20	0.41
16:N:18:VAL:CG2	16:N:19:ARG:N	2.84	0.41
16:N:39:LEU:HD23	16:N:39:LEU:HA	1.93	0.41
20:R:53:ARG:HA	20:R:56:THR:OG1	2.20	0.41
20:R:59:SER:O	20:R:60:GLY:C	2.58	0.41
1:A:427:U:P	6:D:13:ARG:HH22	2.44	0.41
1:A:1047:G:C2'	1:A:1048:G:H5'	2.51	0.41
1:A:1063:C:H3'	1:A:1064:G:H2'	2.03	0.41
1:A:1272:G:O2'	1:A:1273:G:H5'	2.21	0.41
1:A:1272:G:H2'	1:A:1273:G:O4'	2.20	0.41
4:B:28:PHE:CD2	4:B:190:THR:HA	2.56	0.41
4:B:32:ILE:HG21	4:B:40:HIS:HD2	1.86	0.41
4:B:33:TYR:HB3	4:B:41:ILE:O	2.21	0.41
5:C:153:VAL:HG12	5:C:196:LEU:HD12	2.02	0.41
5:C:188:LEU:O	5:C:189:ALA:CB	2.69	0.41
6:D:200:GLU:O	6:D:201:GLN:C	2.59	0.41
7:E:53:LEU:HD12	7:E:53:LEU:N	2.27	0.41
8:F:9:VAL:O	8:F:86:ARG:HB2	2.21	0.41
9:G:40:ALA:O	9:G:44:TYR:CD1	2.74	0.41
9:G:41:ARG:O	9:G:42:ILE:C	2.59	0.41
9:G:66:VAL:O	9:G:68:ASN:N	2.54	0.41
10:H:126:LYS:C	10:H:128:GLY:N	2.75	0.41
11:I:63:ILE:CG2	11:I:64:THR:N	2.83	0.41
11:I:93:ARG:O	11:I:95:LYS:N	2.42	0.41
14:L:27:LEU:HD23	14:L:33:ARG:HH22	1.85	0.41
16:N:47:LEU:HA	16:N:47:LEU:HD23	1.83	0.41
22:T:13:LEU:C	22:T:13:LEU:HD12	2.41	0.41
1:A:237:C:OP2	19:Q:40:LYS:NZ	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:263:A:H2'	1:A:264:U:C6	2.56	0.40
1:A:1153:C:C2	1:A:1154:G:C8	3.09	0.40
1:A:1158:C:C4	1:A:1160:G:C8	3.09	0.40
1:A:1164:G:C6	1:A:1173:G:C6	3.09	0.40
1:A:1167:A:C6	1:A:1168:A:C6	3.10	0.40
1:A:1229:A:C2	1:A:1230:C:C4	3.09	0.40
1:A:1345:U:C4	1:A:1377:A:N3	2.90	0.40
1:A:1502:A:H2	1:A:1505:G:H22	1.67	0.40
4:B:19:HIS:HD2	4:B:189:ASP:HB2	1.86	0.40
5:C:193:TYR:CD1	5:C:194:GLY:N	2.89	0.40
9:G:136:LYS:O	9:G:137:LYS:C	2.60	0.40
9:G:153:HIS:C	9:G:155:ARG:N	2.73	0.40
11:I:65:VAL:HG11	11:I:77:ILE:HD11	2.04	0.40
20:R:38:GLU:CD	20:R:38:GLU:N	2.64	0.40
1:A:138:G:O2'	1:A:139:G:H5'	2.22	0.40
1:A:157:G:C2	1:A:158:G:C8	3.09	0.40
1:A:191:G:N3	22:T:105:SER:HB3	2.36	0.40
1:A:254:G:O2'	1:A:255:G:H5'	2.21	0.40
1:A:975:A:H4'	1:A:976:G:C5'	2.50	0.40
1:A:1052:U:N3	1:A:1200:C:N3	2.69	0.40
1:A:1053:G:O2'	1:A:1199:U:H5	2.04	0.40
4:B:108:ILE:HD13	4:B:108:ILE:HA	1.94	0.40
4:B:213:LEU:HD23	4:B:213:LEU:O	2.21	0.40
7:E:52:PRO:O	7:E:53:LEU:C	2.57	0.40
9:G:11:GLN:C	9:G:12:LEU:HD22	2.42	0.40
9:G:39:ALA:O	9:G:40:ALA:C	2.60	0.40
9:G:50:ILE:O	9:G:50:ILE:CG2	2.69	0.40
11:I:46:ALA:O	11:I:49:PRO:HD2	2.21	0.40
14:L:38:THR:CG2	14:L:39:VAL:HG23	2.39	0.40
15:M:4:ILE:CG2	15:M:5:ALA:N	2.67	0.40
15:M:16:ASP:OD1	15:M:16:ASP:N	2.51	0.40
15:M:23:TYR:HB3	15:M:67:GLU:HA	2.04	0.40
1:A:101:A:C2'	1:A:102:G:H5'	2.51	0.40
1:A:407:G:O2'	1:A:408:A:P	2.79	0.40
1:A:1053:G:C4	1:A:1199:U:C5	3.09	0.40
1:A:1061:G:C1'	12:J:56:HIS:CE1	3.05	0.40
1:A:1303:C:C4	1:A:1304:G:C5	3.09	0.40
1:A:1389:C:H2'	1:A:1390:U:O4'	2.21	0.40
7:E:59:GLY:O	7:E:62:ALA:HB3	2.21	0.40
9:G:155:ARG:NH1	9:G:155:ARG:CA	2.84	0.40
10:H:46:LYS:CG	10:H:64:LYS:HG2	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:10:ARG:CD	11:I:75:ASP:HB3	2.30	0.40
11:I:92:TYR:O	11:I:93:ARG:C	2.59	0.40
12:J:6:ILE:HD13	12:J:71:LEU:O	2.21	0.40
13:K:84:VAL:CG1	13:K:91:ARG:HG3	2.47	0.40
16:N:43:CYS:O	16:N:44:LEU:C	2.59	0.40
1:A:332:G:P	22:T:10:LEU:HD23	2.61	0.40
1:A:714:G:H2'	1:A:715:A:C8	2.57	0.40
1:A:1061:G:C2'	1:A:1062:U:H5'	2.51	0.40
1:A:1352:C:N3	1:A:1371:G:C6	2.89	0.40
1:A:1511:G:H2'	1:A:1512:U:O4'	2.21	0.40
4:B:108:ILE:HG22	4:B:152:PHE:CE2	2.56	0.40
6:D:170:VAL:O	6:D:171:GLY:C	2.60	0.40
7:E:79:GLU:CD	7:E:79:GLU:N	2.74	0.40
8:F:81:ILE:HG23	8:F:82:ARG:N	2.37	0.40
11:I:20:ARG:O	11:I:60:ASP:HB3	2.22	0.40
12:J:17:ASP:O	12:J:21:GLN:N	2.54	0.40
12:J:71:LEU:HA	12:J:71:LEU:HD23	1.83	0.40
15:M:86:CYS:SG	15:M:88:ARG:HB3	2.61	0.40
17:O:14:GLU:OE2	17:O:14:GLU:HA	2.21	0.40
17:O:70:LEU:C	17:O:72:ARG:H	2.24	0.40
18:P:20:VAL:CG1	18:P:21:VAL:N	2.85	0.40
19:Q:3:LYS:HB2	19:Q:60:ILE:HD11	2.03	0.40
22:T:38:LYS:NZ	22:T:38:LYS:CB	2.83	0.40
23:V:8:THR:HG22	23:V:9:ARG:N	2.36	0.40
1:A:404:U:H2'	1:A:405:U:C6	2.56	0.40
1:A:409:G:OP2	1:A:431:A:H8	2.04	0.40
1:A:412:A:N3	1:A:412:A:H2'	2.35	0.40
1:A:594:G:H2'	1:A:595:G:H5'	2.03	0.40
1:A:831:U:O2'	1:A:832:C:H5'	2.21	0.40
1:A:855:G:C6	1:A:856:C:C4	3.09	0.40
1:A:939:G:C4	1:A:940:C:C5	3.10	0.40
1:A:1153:C:H2'	1:A:1154:G:C8	2.57	0.40
1:A:1346:A:C5	9:G:10:ARG:CZ	3.05	0.40
4:B:87:ARG:NH1	4:B:233:SER:HA	2.36	0.40
4:B:236:TYR:C	4:B:238:LEU:H	2.24	0.40
9:G:136:LYS:O	9:G:139:GLU:N	2.55	0.40
11:I:113:LYS:N	11:I:113:LYS:HD2	2.36	0.40
12:J:63:PHE:CE1	16:N:45:ARG:HG3	2.56	0.40
13:K:69:ALA:O	13:K:70:LYS:C	2.60	0.40
13:K:80:VAL:HG22	13:K:81:ASP:N	2.37	0.40
14:L:39:VAL:HG12	14:L:40:VAL:N	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:70:ILE:HD13	14:L:77:LEU:HD12	2.03	0.40
17:O:29:VAL:HG21	17:O:67:LEU:CD2	2.50	0.40
20:R:22:VAL:HB	20:R:56:THR:HA	2.04	0.40
22:T:56:MET:HG2	22:T:84:LEU:HD13	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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
4	B	232/256 (91%)	146 (63%)	65 (28%)	21 (9%)	1 4
5	C	204/239 (85%)	132 (65%)	47 (23%)	25 (12%)	0 1
6	D	206/209 (99%)	157 (76%)	38 (18%)	11 (5%)	2 12
7	E	148/162 (91%)	121 (82%)	21 (14%)	6 (4%)	3 16
8	F	99/101 (98%)	74 (75%)	20 (20%)	5 (5%)	2 13
9	G	153/156 (98%)	104 (68%)	33 (22%)	16 (10%)	0 3
10	H	136/138 (99%)	112 (82%)	17 (12%)	7 (5%)	2 13
11	I	125/128 (98%)	79 (63%)	32 (26%)	14 (11%)	0 2
12	J	96/105 (91%)	61 (64%)	19 (20%)	16 (17%)	0 0
13	K	117/129 (91%)	92 (79%)	17 (14%)	8 (7%)	1 7
14	L	122/135 (90%)	88 (72%)	19 (16%)	15 (12%)	0 1
15	M	123/126 (98%)	67 (54%)	41 (33%)	15 (12%)	0 1
16	N	58/61 (95%)	47 (81%)	5 (9%)	6 (10%)	0 3
17	O	86/89 (97%)	65 (76%)	16 (19%)	5 (6%)	1 10
18	P	81/88 (92%)	65 (80%)	15 (18%)	1 (1%)	13 44
19	Q	102/105 (97%)	85 (83%)	10 (10%)	7 (7%)	1 7

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
20	R	71/88 (81%)	57 (80%)	12 (17%)	2 (3%)	5 25
21	S	78/93 (84%)	59 (76%)	16 (20%)	3 (4%)	3 19
22	T	97/106 (92%)	60 (62%)	26 (27%)	11 (11%)	0 2
23	V	22/27 (82%)	15 (68%)	5 (23%)	2 (9%)	1 4
All	All	2356/2541 (93%)	1686 (72%)	474 (20%)	196 (8%)	1 5

All (196) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	B	15	VAL
4	B	17	PHE
4	B	95	GLN
4	B	207	ALA
4	B	235	SER
5	C	4	LYS
5	C	5	ILE
5	C	15	THR
5	C	102	ASN
5	C	108	ASN
5	C	154	SER
5	C	179	ARG
5	C	189	ALA
6	D	36	ARG
8	F	64	GLN
8	F	72	VAL
9	G	147	ALA
9	G	155	ARG
10	H	91	ARG
10	H	105	ARG
11	I	33	PHE
11	I	38	GLN
11	I	55	ALA
11	I	117	HIS
12	J	27	ALA
12	J	34	VAL
12	J	39	PRO
12	J	57	LYS
12	J	61	GLU
12	J	90	LEU
13	K	12	ARG
14	L	28	LYS

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Mol	Chain	Res	Type
14	L	41	ARG
14	L	47	LYS
14	L	48	PRO
14	L	116	SER
15	M	15	VAL
15	M	67	GLU
15	M	122	LYS
19	Q	49	GLU
19	Q	69	LYS
19	Q	80	GLY
19	Q	81	ARG
19	Q	99	SER
20	R	22	VAL
21	S	9	VAL
21	S	27	GLU
22	T	74	LYS
22	T	98	PRO
4	B	8	LYS
4	B	52	GLU
4	B	123	ALA
4	B	146	GLN
4	B	227	GLY
5	C	16	ARG
5	C	60	ALA
5	C	74	GLY
5	C	75	VAL
5	C	91	LEU
5	C	157	ILE
5	C	188	LEU
6	D	25	ARG
6	D	39	PRO
6	D	178	VAL
7	E	104	ALA
7	E	140	ARG
8	F	70	ASP
9	G	42	ILE
9	G	69	VAL
10	H	24	THR
10	H	137	VAL
11	I	31	GLN
11	I	43	ALA
11	I	101	PHE

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Mol	Chain	Res	Type
11	I	127	LYS
12	J	31	GLY
12	J	85	LEU
12	J	86	MET
13	K	47	VAL
13	K	88	GLY
14	L	27	LEU
14	L	102	ARG
14	L	121	GLY
14	L	127	GLU
15	M	3	ARG
15	M	14	ARG
15	M	106	ASN
16	N	29	ARG
16	N	36	PHE
17	O	14	GLU
22	T	102	GLY
4	B	113	HIS
4	B	165	VAL
4	B	177	ALA
4	B	221	LEU
5	C	84	ILE
5	C	156	ARG
5	C	168	ALA
7	E	73	ASN
7	E	107	ARG
9	G	67	GLU
10	H	135	CYS
11	I	34	ASN
11	I	41	VAL
11	I	94	ALA
11	I	95	LYS
12	J	32	ALA
12	J	72	VAL
12	J	73	ASP
13	K	15	ALA
13	K	127	LYS
14	L	51	ALA
14	L	126	LYS
15	M	59	TYR
16	N	10	ALA
16	N	15	LYS

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Mol	Chain	Res	Type
16	N	41	ARG
18	P	82	GLN
19	Q	97	SER
22	T	50	GLU
22	T	73	HIS
22	T	95	ALA
22	T	101	GLY
23	V	3	LYS
4	B	27	LYS
4	B	60	ASP
4	B	155	LEU
5	C	53	ALA
5	C	98	ASN
6	D	63	LYS
8	F	79	LEU
9	G	6	ARG
9	G	109	ASN
9	G	134	ALA
10	H	83	ILE
11	I	12	GLU
12	J	23	ILE
12	J	40	LEU
14	L	105	TYR
15	M	57	ARG
17	O	71	GLN
17	O	88	ARG
20	R	87	ARG
22	T	11	SER
22	T	87	LYS
4	B	135	GLN
4	B	202	PRO
5	C	190	ARG
6	D	9	CYS
6	D	175	SER
9	G	4	ARG
9	G	41	ARG
12	J	76	ASN
13	K	13	GLN
14	L	29	GLY
14	L	115	LYS
15	M	4	ILE
15	M	32	GLU

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Mol	Chain	Res	Type
15	M	36	LYS
15	M	84	ILE
16	N	5	ALA
17	O	25	THR
17	O	75	PRO
21	S	30	LEU
22	T	97	ALA
23	V	9	ARG
4	B	9	GLU
5	C	20	SER
5	C	55	VAL
5	C	56	ASP
6	D	4	TYR
6	D	5	ILE
6	D	23	GLY
7	E	52	PRO
9	G	38	LEU
9	G	63	LYS
11	I	46	ALA
13	K	75	TYR
13	K	126	ARG
14	L	73	GLU
15	M	6	GLY
19	Q	68	ARG
22	T	96	GLY
8	F	34	GLY
9	G	14	PRO
9	G	112	PRO
12	J	4	ILE
4	B	211	ILE
7	E	22	GLY
9	G	58	PRO
10	H	86	ILE
15	M	7	VAL
5	C	7	PRO
6	D	69	GLY
9	G	81	GLY
15	M	68	GLY

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	
4	B	202/220 (92%)	174 (86%)	28 (14%)	3	15
5	C	160/188 (85%)	139 (87%)	21 (13%)	4	17
6	D	180/181 (99%)	166 (92%)	14 (8%)	12	40
7	E	115/123 (94%)	102 (89%)	13 (11%)	6	23
8	F	90/90 (100%)	80 (89%)	10 (11%)	6	24
9	G	126/127 (99%)	117 (93%)	9 (7%)	14	44
10	H	119/119 (100%)	107 (90%)	12 (10%)	7	28
11	I	98/99 (99%)	91 (93%)	7 (7%)	14	44
12	J	87/92 (95%)	81 (93%)	6 (7%)	15	45
13	K	90/99 (91%)	82 (91%)	8 (9%)	9	34
14	L	104/111 (94%)	96 (92%)	8 (8%)	13	41
15	M	100/101 (99%)	88 (88%)	12 (12%)	5	20
16	N	49/50 (98%)	43 (88%)	6 (12%)	5	19
17	O	79/80 (99%)	66 (84%)	13 (16%)	2	10
18	P	72/74 (97%)	64 (89%)	8 (11%)	6	24
19	Q	96/97 (99%)	90 (94%)	6 (6%)	18	48
20	R	64/77 (83%)	61 (95%)	3 (5%)	26	59
21	S	71/80 (89%)	67 (94%)	4 (6%)	21	52
22	T	75/82 (92%)	69 (92%)	6 (8%)	12	40
23	V	19/22 (86%)	17 (90%)	2 (10%)	7	26
All	All	1996/2112 (94%)	1800 (90%)	196 (10%)	8	29

All (196) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	B	8	LYS
4	B	9	GLU
4	B	15	VAL

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Mol	Chain	Res	Type
4	B	17	PHE
4	B	21	ARG
4	B	22	LYS
4	B	24	TRP
4	B	25	ASN
4	B	52	GLU
4	B	76	GLN
4	B	82	ARG
4	B	92	TYR
4	B	93	VAL
4	B	98	LEU
4	B	114	ARG
4	B	117	GLU
4	B	128	GLU
4	B	129	GLU
4	B	134	GLU
4	B	163	PHE
4	B	170	GLU
4	B	178	ARG
4	B	189	ASP
4	B	190	THR
4	B	196	LEU
4	B	221	LEU
4	B	231	GLU
4	B	236	TYR
5	C	3	ASN
5	C	4	LYS
5	C	5	ILE
5	C	21	ARG
5	C	23	TYR
5	C	26	LYS
5	C	31	HIS
5	C	69	HIS
5	C	72	LYS
5	C	82	GLU
5	C	85	ARG
5	C	95	THR
5	C	107	GLN
5	C	139	GLN
5	C	165	THR
5	C	166	GLU
5	C	167	TRP

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Mol	Chain	Res	Type
5	C	179	ARG
5	C	188	LEU
5	C	204	LEU
5	C	206	GLU
6	D	3	ARG
6	D	15	GLU
6	D	19	LEU
6	D	28	SER
6	D	36	ARG
6	D	47	ARG
6	D	58	LEU
6	D	65	ARG
6	D	106	TYR
6	D	122	ARG
6	D	150	GLU
6	D	156	GLU
6	D	162	LEU
6	D	199	ASN
7	E	9	LYS
7	E	12	LEU
7	E	16	THR
7	E	31	LEU
7	E	34	VAL
7	E	41	VAL
7	E	43	LEU
7	E	56	GLN
7	E	80	ILE
7	E	89	ILE
7	E	116	THR
7	E	144	THR
7	E	150	ARG
8	F	9	VAL
8	F	10	LEU
8	F	28	ARG
8	F	40	VAL
8	F	47	ARG
8	F	54	LYS
8	F	79	LEU
8	F	82	ARG
8	F	87	ARG
8	F	100	ASN
9	G	8	GLU

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Mol	Chain	Res	Type
9	G	11	GLN
9	G	16	LEU
9	G	79	ARG
9	G	109	ASN
9	G	124	LEU
9	G	126	ASP
9	G	140	ASP
9	G	155	ARG
10	H	24	THR
10	H	26	VAL
10	H	50	ARG
10	H	52	ASP
10	H	63	LEU
10	H	81	HIS
10	H	85	ARG
10	H	91	ARG
10	H	92	ARG
10	H	104	ARG
10	H	112	LEU
10	H	119	LEU
11	I	5	TYR
11	I	38	GLN
11	I	102	LEU
11	I	104	ARG
11	I	113	LYS
11	I	121	ARG
11	I	127	LYS
12	J	3	LYS
12	J	4	ILE
12	J	6	ILE
12	J	60	ARG
12	J	73	ASP
12	J	74	ILE
13	K	29	ILE
13	K	54	ARG
13	K	96	ARG
13	K	98	LEU
13	K	106	LYS
13	K	114	VAL
13	K	117	ASN
13	K	127	LYS
14	L	20	LYS

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Mol	Chain	Res	Type
14	L	28	LYS
14	L	33	ARG
14	L	37	CYS
14	L	48	PRO
14	L	54	LYS
14	L	82	VAL
14	L	93	LEU
15	M	9	ILE
15	M	40	ASN
15	M	44	ARG
15	M	56	LEU
15	M	66	LEU
15	M	70	LEU
15	M	88	ARG
15	M	102	ARG
15	M	106	ASN
15	M	110	ARG
15	M	115	LYS
15	M	125	ARG
16	N	8	GLU
16	N	12	ARG
16	N	31	ARG
16	N	41	ARG
16	N	43	CYS
16	N	58	LYS
17	O	4	THR
17	O	7	GLU
17	O	9	GLN
17	O	10	LYS
17	O	13	GLN
17	O	31	LEU
17	O	34	LEU
17	O	39	LEU
17	O	64	ARG
17	O	70	LEU
17	O	71	GLN
17	O	81	LEU
17	O	88	ARG
18	P	1	MET
18	P	2	VAL
18	P	45	THR
18	P	53	VAL

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Mol	Chain	Res	Type
18	P	55	ARG
18	P	61	SER
18	P	80	PHE
18	P	82	GLN
19	Q	38	ARG
19	Q	59	ILE
19	Q	60	ILE
19	Q	78	GLU
19	Q	100	LYS
19	Q	101	ARG
20	R	36	ASN
20	R	42	ARG
20	R	54	ARG
21	S	6	LYS
21	S	12	ASP
21	S	61	TYR
21	S	79	THR
22	T	13	LEU
22	T	35	THR
22	T	42	GLN
22	T	45	GLN
22	T	75	ASN
22	T	84	LEU
23	V	6	ARG
23	V	24	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (57) such sidechains are listed below:

Mol	Chain	Res	Type
4	B	25	ASN
4	B	40	HIS
4	B	45	GLN
4	B	135	GLN
4	B	212	GLN
4	B	240	GLN
5	C	3	ASN
5	C	31	HIS
5	C	37	GLN
5	C	69	HIS
5	C	102	ASN
5	C	107	GLN
5	C	123	GLN

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Mol	Chain	Res	Type
5	C	139	GLN
5	C	170	GLN
6	D	62	GLN
6	D	119	GLN
6	D	123	HIS
6	D	199	ASN
7	E	73	ASN
8	F	18	GLN
8	F	57	GLN
8	F	64	GLN
8	F	73	ASN
8	F	84	ASN
9	G	28	ASN
9	G	37	ASN
9	G	51	GLN
9	G	86	GLN
9	G	109	ASN
9	G	122	HIS
9	G	148	ASN
11	I	73	GLN
11	I	117	HIS
12	J	33	GLN
12	J	56	HIS
13	K	117	ASN
14	L	49	ASN
14	L	75	HIS
15	M	40	ASN
15	M	62	ASN
15	M	77	ASN
15	M	106	ASN
17	O	9	GLN
17	O	13	GLN
17	O	37	ASN
17	O	46	HIS
18	P	82	GLN
19	Q	16	GLN
19	Q	26	GLN
19	Q	96	GLN
20	R	36	ASN
21	S	14	HIS
21	S	47	HIS
21	S	56	GLN

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Mol	Chain	Res	Type
21	S	65	ASN
22	T	45	GLN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1506/1522 (98%)	234 (15%)	66 (4%)
2	X	10/11 (90%)	1 (10%)	0
3	W	3/4 (75%)	0	0
All	All	1519/1537 (98%)	235 (15%)	66 (4%)

All (235) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	6	G
1	A	7	G
1	A	8	A
1	A	9	G
1	A	31	G
1	A	32	A
1	A	39	G
1	A	47	C
1	A	48	C
1	A	49	U
1	A	50	A
1	A	51	A
1	A	61	G
1	A	101	A
1	A	116	A
1	A	120	A
1	A	121	C
1	A	129(A)	G
1	A	130	A
1	A	131	C
1	A	163	C
1	A	182	U
1	A	189	G
1	A	190	C
1	A	190(A)	C
1	A	190(D)	U
1	A	190(E)	U

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Mol	Chain	Res	Type
1	A	190(F)	G
1	A	195	A
1	A	197	A
1	A	202	U
1	A	203	U
1	A	204	U
1	A	216	G
1	A	220	G
1	A	244	U
1	A	247	G
1	A	251	G
1	A	252	U
1	A	266	G
1	A	267	C
1	A	280	C
1	A	289	G
1	A	321	A
1	A	328	C
1	A	329	A
1	A	332	G
1	A	345	C
1	A	350	G
1	A	352	C
1	A	353	A
1	A	354	G
1	A	367	U
1	A	373	A
1	A	390	C
1	A	397	A
1	A	398	C
1	A	406	G
1	A	407	G
1	A	408	A
1	A	409	G
1	A	410	G
1	A	412	A
1	A	413	G
1	A	414	A
1	A	415	A
1	A	416	G
1	A	418	C
1	A	420	U

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Mol	Chain	Res	Type
1	A	421	U
1	A	422	C
1	A	423	G
1	A	425	G
1	A	429	U
1	A	430	A
1	A	433	C
1	A	434	U
1	A	435	C
1	A	439	A
1	A	452	A
1	A	460	A
1	A	461	C
1	A	462	G
1	A	463	A
1	A	474	G
1	A	475	G
1	A	476	G
1	A	478	A
1	A	484	G
1	A	485	G
1	A	486	U
1	A	497	A
1	A	498	U
1	A	511	C
1	A	518	C
1	A	527	G
1	A	531	U
1	A	532	A
1	A	533	A
1	A	534	U
1	A	547	A
1	A	559	A
1	A	560	U
1	A	561	U
1	A	562	C
1	A	572	A
1	A	573	A
1	A	575	G
1	A	576	G
1	A	577	G
1	A	579	G

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Mol	Chain	Res	Type
1	A	653	A
1	A	665	A
1	A	688	G
1	A	695	A
1	A	701	C
1	A	702	A
1	A	703	G
1	A	731	G
1	A	748	C
1	A	755	G
1	A	777	A
1	A	793	U
1	A	794	A
1	A	813	U
1	A	815	A
1	A	817	C
1	A	821	G
1	A	828	A
1	A	839	U
1	A	840	C
1	A	841	U
1	A	848	C
1	A	902	G
1	A	914	A
1	A	926	G
1	A	927	G
1	A	932	C
1	A	934	C
1	A	935	A
1	A	945	G
1	A	960	U
1	A	961	U
1	A	965	A
1	A	966	G
1	A	969	A
1	A	974	A
1	A	975	A
1	A	976	G
1	A	977	A
1	A	991	U
1	A	992	U
1	A	994	A

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Mol	Chain	Res	Type
1	A	1005	A
1	A	1025	U
1	A	1026	G
1	A	1050	G
1	A	1053	G
1	A	1054	C
1	A	1065	U
1	A	1066	C
1	A	1068	G
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	1102	A
1	A	1117	G
1	A	1125	U
1	A	1127	G
1	A	1129	C
1	A	1130	A
1	A	1131	G
1	A	1137	C
1	A	1139	G
1	A	1146	A
1	A	1152	A
1	A	1159	U
1	A	1160	G
1	A	1183	A
1	A	1184	G
1	A	1196	U
1	A	1197	G
1	A	1201	A
1	A	1202	G
1	A	1211	U
1	A	1212	U
1	A	1213	A
1	A	1224	G
1	A	1225	A
1	A	1227	A
1	A	1238	A
1	A	1257	U
1	A	1280	A
1	A	1281	U
1	A	1282	C

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Mol	Chain	Res	Type
1	A	1286	A
1	A	1287	A
1	A	1300	G
1	A	1301	U
1	A	1302	U
1	A	1305	G
1	A	1319	A
1	A	1320	C
1	A	1323	G
1	A	1338	G
1	A	1346	A
1	A	1347	G
1	A	1348	U
1	A	1353	G
1	A	1360	A
1	A	1361	G
1	A	1362	C
1	A	1363	A
1	A	1398	A
1	A	1443	G
1	A	1446	A
1	A	1447	G
1	A	1452	C
1	A	1487	G
1	A	1492	A
1	A	1497	G
1	A	1499	A
1	A	1502	A
1	A	1503	A
1	A	1504	G
1	A	1505	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	1534	A
1	A	1539	C
2	X	33	U

All (66) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	7	G
1	A	30	U
1	A	60	A
1	A	115	G
1	A	119	A
1	A	129(A)	G
1	A	181	G
1	A	190	C
1	A	203	U
1	A	243	A
1	A	250	A
1	A	251	G
1	A	266	G
1	A	279	A
1	A	328	C
1	A	344	A
1	A	350	G
1	A	353	A
1	A	366	C
1	A	372	C
1	A	407	G
1	A	418	C
1	A	428	G
1	A	429	U
1	A	484	G
1	A	485	G
1	A	496	A
1	A	532	A
1	A	533	A
1	A	559	A
1	A	560	U
1	A	575	G
1	A	687	A
1	A	701	C
1	A	793	U
1	A	812	C
1	A	840	C
1	A	945	G
1	A	960	U
1	A	965	A
1	A	975	A
1	A	993	G
1	A	1049	U

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Mol	Chain	Res	Type
1	A	1065	U
1	A	1067	A
1	A	1101	A
1	A	1126	U
1	A	1145	C
1	A	1182	G
1	A	1183	A
1	A	1201	A
1	A	1212	U
1	A	1224	G
1	A	1281	U
1	A	1285	A
1	A	1300	G
1	A	1319	A
1	A	1346	A
1	A	1347	G
1	A	1397	C
1	A	1451	A
1	A	1498	U
1	A	1502	A
1	A	1503	A
1	A	1504	G
1	A	1505	G

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 111 ligands modelled in this entry, 110 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	$\#\|Z\| > 2$
24	PAR	A	1545	-	45,45,45	1.55	8 (17%)	64,67,67	1.27	7 (10%)

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
24	PAR	A	1545	-	-	2/18/94/94	0/4/4/4

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	A	1545	PAR	C64-C54	5.21	1.59	1.52
24	A	1545	PAR	O54-C14	3.24	1.50	1.41
24	A	1545	PAR	C11-C21	2.52	1.57	1.52
24	A	1545	PAR	C14-C24	2.49	1.57	1.52
24	A	1545	PAR	C52-C42	2.44	1.57	1.52
24	A	1545	PAR	O51-C11	2.25	1.47	1.41
24	A	1545	PAR	C31-C21	2.23	1.56	1.53
24	A	1545	PAR	O54-C54	2.20	1.49	1.44

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
24	A	1545	PAR	O33-C14-C24	4.17	115.39	108.22
24	A	1545	PAR	O54-C54-C64	3.55	112.62	106.01
24	A	1545	PAR	C14-O54-C54	3.34	120.23	113.69
24	A	1545	PAR	O52-C13-C23	3.24	114.67	107.96
24	A	1545	PAR	O52-C13-O43	-3.09	108.09	111.43
24	A	1545	PAR	O11-C11-C21	2.20	112.01	108.22
24	A	1545	PAR	C11-O51-C51	2.01	117.64	113.69

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
24	A	1545	PAR	C23-C13-O52-C52

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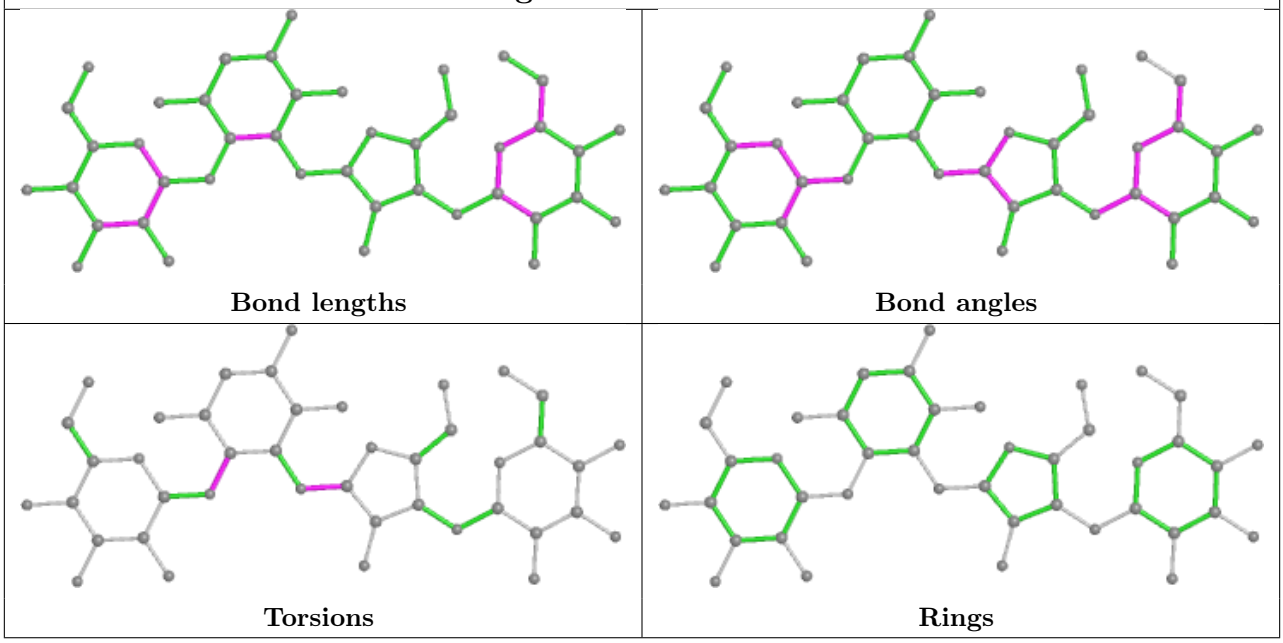
Mol	Chain	Res	Type	Atoms
24	A	1545	PAR	C52-C42-O11-C11

There are no ring outliers.

No monomer is involved in short contacts.

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 then 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.

Ligand PAR A 1545



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, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	1507/1522 (99%)	0.45	27 (1%)	68	47	25, 61, 150, 200	0
2	X	10/11 (90%)	1.07	1 (10%)	7	2	75, 104, 168, 174	0
3	W	4/4 (100%)	1.58	1 (25%)	0	0	53, 57, 58, 85	0
4	B	234/256 (91%)	0.31	14 (5%)	21	10	34, 99, 168, 200	0
5	C	206/239 (86%)	0.30	7 (3%)	45	24	37, 88, 159, 192	0
6	D	208/209 (99%)	0.37	8 (3%)	40	20	31, 72, 145, 200	0
7	E	150/162 (92%)	0.37	6 (4%)	38	19	28, 55, 110, 148	0
8	F	101/101 (100%)	-0.18	1 (0%)	82	67	53, 95, 150, 176	0
9	G	155/156 (99%)	0.15	7 (4%)	33	16	41, 78, 143, 174	0
10	H	138/138 (100%)	0.45	4 (2%)	51	28	23, 52, 103, 144	0
11	I	127/128 (99%)	0.80	17 (13%)	3	1	40, 90, 149, 178	0
12	J	98/105 (93%)	0.67	17 (17%)	1	0	35, 122, 185, 200	0
13	K	119/129 (92%)	0.56	4 (3%)	45	24	26, 61, 122, 179	0
14	L	124/135 (91%)	0.47	6 (4%)	30	14	20, 65, 141, 180	0
15	M	125/126 (99%)	1.03	11 (8%)	10	4	49, 87, 157, 200	0
16	N	60/61 (98%)	1.09	13 (21%)	0	0	48, 79, 155, 185	0
17	O	88/89 (98%)	0.14	2 (2%)	60	39	28, 67, 136, 187	0
18	P	83/88 (94%)	0.83	9 (10%)	5	2	30, 51, 97, 166	0
19	Q	104/105 (99%)	0.96	6 (5%)	23	10	29, 51, 136, 200	0
20	R	73/88 (82%)	0.13	2 (2%)	54	31	44, 76, 169, 198	0
21	S	80/93 (86%)	-0.06	1 (1%)	77	59	58, 105, 166, 193	0
22	T	99/106 (93%)	0.75	10 (10%)	7	2	33, 62, 134, 189	0
23	V	24/27 (88%)	1.36	6 (25%)	0	0	49, 66, 127, 174	0
All	All	3917/4078 (96%)	0.46	180 (4%)	32	16	20, 70, 156, 200	0

All (180) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
13	K	129	SER	25.3
15	M	124	PRO	20.4
1	A	422	C	19.6
15	M	123	ALA	19.6
1	A	1534	A	17.3
1	A	416	G	16.0
19	Q	102	GLY	15.6
15	M	122	LYS	14.6
1	A	1533	C	14.6
1	A	414	A	13.8
1	A	413	G	13.6
15	M	125	ARG	11.8
1	A	423	G	11.6
15	M	121	LYS	11.4
19	Q	105	ALA	11.0
1	A	421	U	10.6
1	A	415	A	10.5
19	Q	103	GLY	10.5
11	I	128	ARG	10.4
13	K	128	ALA	9.9
19	Q	104	LYS	8.8
15	M	120	LYS	7.6
1	A	432	A	6.6
21	S	3	ARG	6.5
10	H	1	MET	6.4
1	A	407	G	6.2
15	M	126	LYS	6.2
11	I	105	ASP	6.1
2	X	33	U	5.6
1	A	1539	C	5.5
14	L	19	ARG	5.4
12	J	64	GLU	5.3
4	B	133	LYS	5.2
23	V	6	ARG	5.0
11	I	7	THR	5.0
17	O	89	GLY	4.9
13	K	127	LYS	4.8
9	G	13	GLN	4.6
14	L	20	LYS	4.4
19	Q	101	ARG	4.4
4	B	148	TYR	4.3
4	B	215	LEU	4.2

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Mol	Chain	Res	Type	RSRZ
16	N	6	LEU	4.2
12	J	46	ARG	4.2
11	I	14	VAL	4.1
1	A	412	A	4.1
20	R	17	SER	4.0
10	H	2	LEU	4.0
6	D	209	ARG	3.9
14	L	18	VAL	3.9
4	B	130	ARG	3.8
4	B	16	HIS	3.8
9	G	81	GLY	3.7
15	M	7	VAL	3.7
23	V	2	GLY	3.7
11	I	66	ARG	3.7
22	T	9	ASN	3.6
1	A	1540	U	3.5
16	N	29	ARG	3.5
12	J	47	PHE	3.4
4	B	134	GLU	3.4
16	N	60	SER	3.4
1	A	202	U	3.4
23	V	9	ARG	3.4
11	I	65	VAL	3.4
1	A	190	C	3.3
12	J	63	PHE	3.3
15	M	104	ARG	3.2
23	V	11	GLY	3.2
16	N	30	ALA	3.2
18	P	83	GLU	3.2
22	T	68	LYS	3.2
11	I	9	ARG	3.1
16	N	32	SER	3.1
11	I	15	ALA	3.1
12	J	72	VAL	3.1
16	N	61	TRP	3.0
12	J	43	ARG	3.0
11	I	70	LYS	3.0
12	J	10	GLY	3.0
5	C	4	LYS	3.0
12	J	6	ILE	3.0
15	M	102	ARG	3.0
4	B	131	PRO	2.9

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Mol	Chain	Res	Type	RSRZ
6	D	23	GLY	2.9
4	B	152	PHE	2.9
12	J	62	HIS	2.8
7	E	17	ALA	2.7
16	N	34	TYR	2.7
3	W	4	A	2.7
11	I	29	ASN	2.7
1	A	478	A	2.7
18	P	1	MET	2.7
4	B	109	SER	2.7
9	G	5	ARG	2.6
7	E	119	LEU	2.6
16	N	33	VAL	2.6
7	E	129	ILE	2.6
22	T	24	LEU	2.6
22	T	64	ASP	2.6
1	A	417	C	2.6
8	F	89	MET	2.6
12	J	7	LYS	2.6
12	J	66	ARG	2.6
15	M	103	THR	2.6
11	I	36	TYR	2.6
18	P	64	ALA	2.6
5	C	154	SER	2.6
11	I	10	ARG	2.6
16	N	3	ARG	2.5
11	I	13	ALA	2.5
9	G	12	LEU	2.5
12	J	33	GLN	2.5
12	J	71	LEU	2.5
22	T	8	ARG	2.5
14	L	127	GLU	2.5
11	I	43	ALA	2.5
18	P	41	PRO	2.5
5	C	184	TYR	2.4
6	D	3	ARG	2.4
13	K	126	ARG	2.4
12	J	65	LEU	2.4
9	G	83	ALA	2.4
18	P	12	LYS	2.4
9	G	8	GLU	2.4
6	D	47	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
7	E	22	GLY	2.4
6	D	67	ILE	2.4
5	C	15	THR	2.4
4	B	144	ARG	2.3
14	L	61	THR	2.3
4	B	108	ILE	2.3
18	P	73	LEU	2.3
22	T	73	HIS	2.3
10	H	102	ARG	2.3
6	D	4	TYR	2.3
11	I	8	GLY	2.3
11	I	102	LEU	2.3
12	J	8	LEU	2.3
5	C	196	LEU	2.2
1	A	1249	C	2.2
12	J	73	ASP	2.2
6	D	9	CYS	2.2
18	P	8	ARG	2.2
1	A	82	U	2.2
12	J	44	VAL	2.2
16	N	35	ARG	2.2
5	C	186	PHE	2.2
23	V	8	THR	2.2
22	T	23	ARG	2.1
19	Q	98	LEU	2.1
7	E	11	ILE	2.1
1	A	420	U	2.1
18	P	19	ILE	2.1
4	B	149	LEU	2.1
16	N	12	ARG	2.1
23	V	12	LYS	2.1
4	B	230	VAL	2.1
16	N	31	ARG	2.1
4	B	137	ARG	2.1
22	T	27	LYS	2.1
17	O	88	ARG	2.1
1	A	1531	A	2.1
1	A	1541	U	2.1
10	H	105	ARG	2.1
22	T	25	ARG	2.1
22	T	70	SER	2.1
6	D	26	CYS	2.1

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Mol	Chain	Res	Type	RSRZ
9	G	85	TYR	2.1
1	A	233	C	2.0
1	A	1362	C	2.0
7	E	94	ALA	2.0
20	R	16	PRO	2.0
16	N	41	ARG	2.0
1	A	975	A	2.0
18	P	39	TYR	2.0
1	A	477	G	2.0
5	C	113	ALA	2.0
11	I	106	ALA	2.0
14	L	28	LYS	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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
25	MG	X	502	1/1	0.42	1.92	65,65,65,65	1
25	MG	A	1619	1/1	0.60	0.27	65,65,65,65	0
25	MG	A	1601	1/1	0.60	0.29	65,65,65,65	0
25	MG	X	500	1/1	0.64	0.91	65,65,65,65	1
25	MG	A	1587	1/1	0.64	0.33	65,65,65,65	0
25	MG	A	1592	1/1	0.67	0.35	65,65,65,65	0
25	MG	A	1583	1/1	0.68	0.28	65,65,65,65	0
25	MG	A	210	1/1	0.68	0.22	65,65,65,65	0
25	MG	A	1548	1/1	0.68	0.17	65,65,65,65	0
25	MG	A	1621	1/1	0.71	0.43	65,65,65,65	0
25	MG	A	86	1/1	0.72	0.35	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
25	MG	A	1561	1/1	0.72	0.25	65,65,65,65	0
25	MG	A	1594	1/1	0.73	0.85	65,65,65,65	1
25	MG	A	1602	1/1	0.76	0.27	65,65,65,65	0
25	MG	A	1611	1/1	0.77	0.27	65,65,65,65	0
25	MG	A	471	1/1	0.77	0.18	65,65,65,65	0
25	MG	A	1620	1/1	0.78	0.22	65,65,65,65	0
25	MG	A	1564	1/1	0.78	0.51	65,65,65,65	0
25	MG	A	466	1/1	0.78	0.27	65,65,65,65	0
25	MG	A	1607	1/1	0.78	0.21	65,65,65,65	0
25	MG	A	1558	1/1	0.78	0.32	65,65,65,65	0
25	MG	A	1571	1/1	0.78	0.32	65,65,65,65	0
25	MG	A	1632	1/1	0.79	0.17	65,65,65,65	0
25	MG	A	1598	1/1	0.79	0.23	65,65,65,65	0
25	MG	A	1610	1/1	0.79	0.23	65,65,65,65	1
25	MG	A	1630	1/1	0.80	0.20	65,65,65,65	0
25	MG	A	1608	1/1	0.80	0.37	65,65,65,65	0
25	MG	X	503	1/1	0.80	0.17	50,50,50,50	1
25	MG	A	469	1/1	0.81	0.23	65,65,65,65	1
25	MG	A	1590	1/1	0.81	0.41	65,65,65,65	0
25	MG	A	1595	1/1	0.81	0.34	65,65,65,65	0
25	MG	A	1574	1/1	0.82	0.32	65,65,65,65	0
25	MG	A	441	1/1	0.83	0.27	65,65,65,65	0
25	MG	A	1550	1/1	0.84	0.40	65,65,65,65	0
25	MG	A	1624	1/1	0.84	0.43	65,65,65,65	0
25	MG	A	1585	1/1	0.85	0.39	65,65,65,65	0
25	MG	A	467	1/1	0.85	0.26	65,65,65,65	0
25	MG	A	1586	1/1	0.85	0.43	65,65,65,65	0
25	MG	A	1578	1/1	0.85	0.33	65,65,65,65	0
25	MG	A	1547	1/1	0.86	0.37	65,65,65,65	0
25	MG	A	1582	1/1	0.86	0.31	65,65,65,65	0
25	MG	A	1603	1/1	0.86	0.17	65,65,65,65	0
25	MG	A	1633	1/1	0.86	0.25	65,65,65,65	1
25	MG	A	1613	1/1	0.86	0.46	65,65,65,65	0
25	MG	A	1606	1/1	0.86	0.56	65,65,65,65	1
25	MG	A	1575	1/1	0.86	0.32	65,65,65,65	0
25	MG	A	1614	1/1	0.87	0.23	65,65,65,65	0
25	MG	A	493	1/1	0.87	0.38	65,65,65,65	0
25	MG	A	1572	1/1	0.87	0.29	65,65,65,65	0
25	MG	A	211	1/1	0.87	0.40	65,65,65,65	0
25	MG	A	1604	1/1	0.87	0.49	65,65,65,65	0
25	MG	A	1627	1/1	0.88	0.15	65,65,65,65	0
25	MG	A	1546	1/1	0.88	0.31	65,65,65,65	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
25	MG	A	1634	1/1	0.88	0.36	65,65,65,65	0
25	MG	A	1568	1/1	0.88	0.41	65,65,65,65	0
25	MG	A	1596	1/1	0.88	0.16	65,65,65,65	0
25	MG	A	1615	1/1	0.88	0.28	65,65,65,65	0
25	MG	A	1617	1/1	0.88	0.25	65,65,65,65	0
25	MG	J	449	1/1	0.88	0.32	65,65,65,65	0
25	MG	A	1565	1/1	0.89	0.32	65,65,65,65	0
25	MG	A	1599	1/1	0.89	0.17	65,65,65,65	0
25	MG	A	1628	1/1	0.89	0.34	65,65,65,65	0
25	MG	A	1600	1/1	0.89	0.13	65,65,65,65	0
25	MG	A	1567	1/1	0.89	0.50	65,65,65,65	0
25	MG	A	1551	1/1	0.89	0.45	65,65,65,65	0
25	MG	A	1622	1/1	0.89	0.30	65,65,65,65	0
25	MG	A	1623	1/1	0.89	0.35	65,65,65,65	0
25	MG	A	1584	1/1	0.90	0.37	65,65,65,65	0
25	MG	A	1616	1/1	0.90	0.24	65,65,65,65	0
25	MG	A	1562	1/1	0.90	0.23	65,65,65,65	0
25	MG	A	214	1/1	0.90	0.25	65,65,65,65	0
25	MG	A	87	1/1	0.90	0.45	65,65,65,65	0
25	MG	A	1609	1/1	0.91	0.22	65,65,65,65	0
25	MG	A	1570	1/1	0.91	0.39	65,65,65,65	0
25	MG	A	1605	1/1	0.91	0.43	65,65,65,65	0
25	MG	A	1577	1/1	0.91	0.24	65,65,65,65	0
25	MG	A	1569	1/1	0.91	0.50	65,65,65,65	0
25	MG	A	1580	1/1	0.91	0.45	65,65,65,65	0
25	MG	A	1554	1/1	0.92	0.38	65,65,65,65	0
24	PAR	A	1545	42/42	0.92	0.29	65,65,65,65	0
25	MG	A	1559	1/1	0.92	0.36	65,65,65,65	0
25	MG	A	1612	1/1	0.92	0.37	65,65,65,65	0
25	MG	A	470	1/1	0.92	0.21	65,65,65,65	0
25	MG	A	1560	1/1	0.92	0.48	65,65,65,65	0
25	MG	A	1573	1/1	0.92	0.34	65,65,65,65	0
25	MG	A	1591	1/1	0.93	0.34	65,65,65,65	0
25	MG	A	1566	1/1	0.93	0.49	65,65,65,65	0
25	MG	A	1579	1/1	0.93	0.28	65,65,65,65	0
25	MG	A	1581	1/1	0.94	0.44	65,65,65,65	0
25	MG	A	1556	1/1	0.94	0.51	65,65,65,65	0
25	MG	A	1625	1/1	0.94	0.23	65,65,65,65	0
25	MG	A	1635	1/1	0.94	0.23	65,65,65,65	1
25	MG	A	1553	1/1	0.94	0.52	65,65,65,65	0
25	MG	A	1549	1/1	0.94	0.46	65,65,65,65	0
25	MG	A	473	1/1	0.94	0.14	65,65,65,65	1

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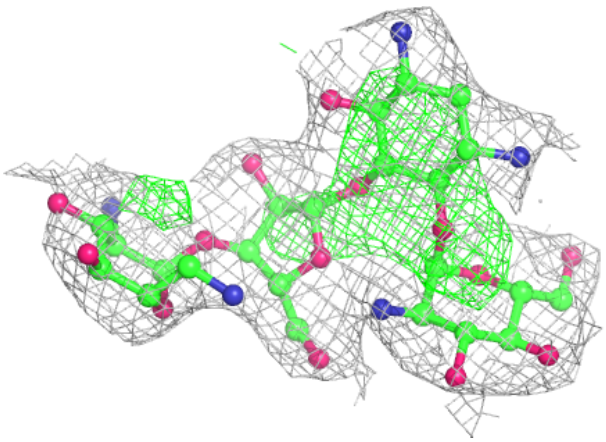
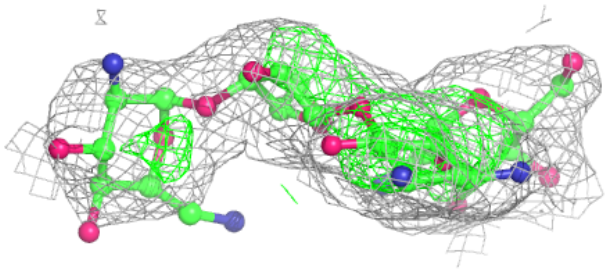
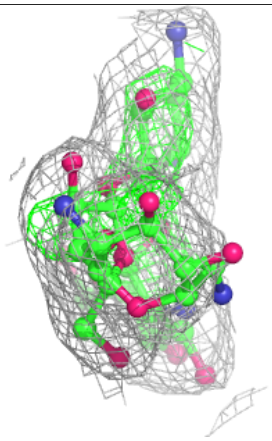
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
25	MG	A	1597	1/1	0.94	0.35	65,65,65,65	0
25	MG	A	1626	1/1	0.95	0.22	65,65,65,65	0
25	MG	A	1618	1/1	0.95	0.40	65,65,65,65	0
25	MG	A	1557	1/1	0.95	0.45	65,65,65,65	0
25	MG	A	1629	1/1	0.95	0.41	65,65,65,65	0
25	MG	A	1588	1/1	0.95	0.47	65,65,65,65	0
25	MG	A	1631	1/1	0.96	0.18	65,65,65,65	0
25	MG	A	71	1/1	0.96	0.40	65,65,65,65	0
25	MG	A	1563	1/1	0.97	0.46	65,65,65,65	0
25	MG	A	1589	1/1	0.97	0.58	65,65,65,65	0
25	MG	A	1555	1/1	0.98	0.49	65,65,65,65	0
25	MG	A	1593	1/1	0.98	0.48	65,65,65,65	0
25	MG	A	1552	1/1	0.98	0.53	65,65,65,65	0
25	MG	A	1576	1/1	0.98	0.36	65,65,65,65	0
26	ZN	D	306	1/1	0.98	0.46	65,65,65,65	0
26	ZN	N	307	1/1	0.99	0.20	65,65,65,65	0

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

Electron density around PAR A 1545: 2mF$_o$-DF$_c$ (at 0.7 rmsd) in gray mF$_o$-DF$_c$ (at 3 rmsd) in purple (negative) and green (positive)	
	

6.5 Other polymers (i)

There are no such residues in this entry.