



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 10:42 AM UTC

PDB ID : 4AQY / pdb_00004aqy
Title : Structure of ribosome-apramycin complexes
Authors : Matt, T.; Ng, C.L.; Lang, K.; Sha, S.H.; Akbergenov, R.; Shcherbakov, D.; Meyer, M.; Duscha, S.; Xie, J.; Dubbaka, S.R.; Perez-Fernandez, D.; Vasella, A.; Ramakrishnan, V.; Schacht, J.; Bottger, E.C.
Deposited on : 2012-04-20
Resolution : 3.50 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

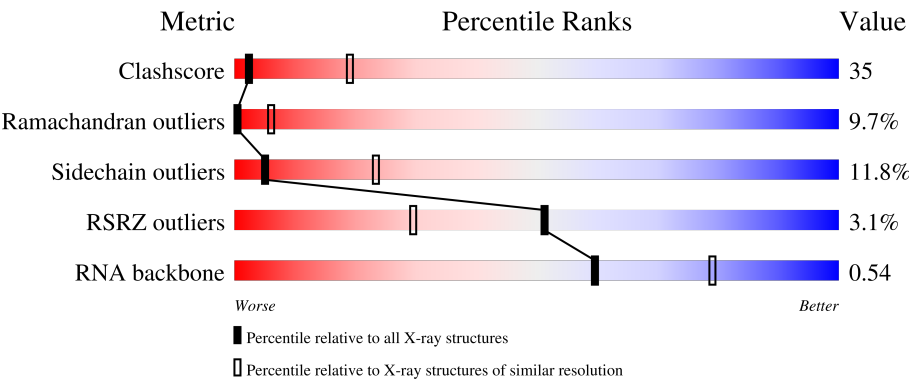
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	1140 (3.54-3.46)
Ramachandran outliers	187476	1113 (3.54-3.46)
Sidechain outliers	187428	1114 (3.54-3.46)
RSRZ outliers	180081	1084 (3.54-3.46)
RNA backbone	3983	1010 (3.98-3.02)

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

Mol	Chain	Length	Quality of chain
1	A	1522	2% 36% 51% 10% ..
2	B	256	2% 17% 53% 20% 9%
3	C	239	3% 19% 46% 19% 14%
4	D	208	5% 31% 50% 18% .

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Mol	Chain	Length	Quality of chain
5	E	161	
6	F	101	
7	G	155	
8	H	138	
9	I	128	
10	J	104	
11	K	129	
12	L	135	
13	M	126	
14	N	60	
15	O	88	
16	P	88	
17	Q	104	
18	R	88	
19	S	92	
20	T	106	
21	V	26	
22	W	6	
23	Z	15	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
24	MG	A	2548	-	-	-	X
24	MG	A	2554	-	-	-	X
24	MG	A	2587	-	-	-	X
24	MG	A	2590	-	-	-	X
24	MG	A	2603	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
24	MG	A	2609	-	-	-	X
24	MG	A	2618	-	-	-	X
24	MG	A	2626	-	-	-	X
24	MG	A	2683	-	-	-	X
24	MG	A	2687	-	-	-	X
24	MG	A	2688	-	-	-	X
24	MG	A	2720	-	-	-	X
24	MG	A	2721	-	-	-	X
24	MG	A	2729	-	-	-	X
24	MG	A	2734	-	-	-	X
24	MG	A	2743	-	-	-	X
24	MG	A	2745	-	-	-	X
24	MG	S	1143	-	-	-	X

2 Entry composition

There are 28 unique types of molecules in this entry. The entry contains 52514 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
1	A	1510	Total	C	N	O	P	0	0	0
			32446	14444	6006	10488	1508			

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	208	Total	C	N	O	S	0	0	0
			1702	1066	339	290	7			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	101	Total	C	N	O	S	0	0	0
			842	531	155	153	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	155	Total	C	N	O	S	0	0	0
			1256	781	252	217	6			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	138	Total	C	N	O	S	0	0	0
			1115	705	215	192	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	I	127	Total	C	N	O	S	0	0	0
			1010	639	198	173				

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	98	Total	C	N	O	S	0	0	0
			794	499	156	138	1			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	119	Total	C	N	O	S	0	0	0
			884	549	168	164	3			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	125	Total	C	N	O	S	0	0	0
			996	617	207	170	2			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	N	60	Total	C	N	O	S	0	0	0
			491	312	104	71	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	O	88	Total	C	N	O	S	0	0	0
			733	459	147	125	2			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	Q	104	Total	C	N	O	S	0	0	0
			856	547	161	146	2			

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	R	73	Total	C	N	O	0	0	0
			596	380	118	98			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	T	99	Total	C	N	O	S	0	0	0
			761	469	162	128	2			

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	W	6	Total	C	N	O	P	0	0	0
			123	57	22	39	5			

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

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

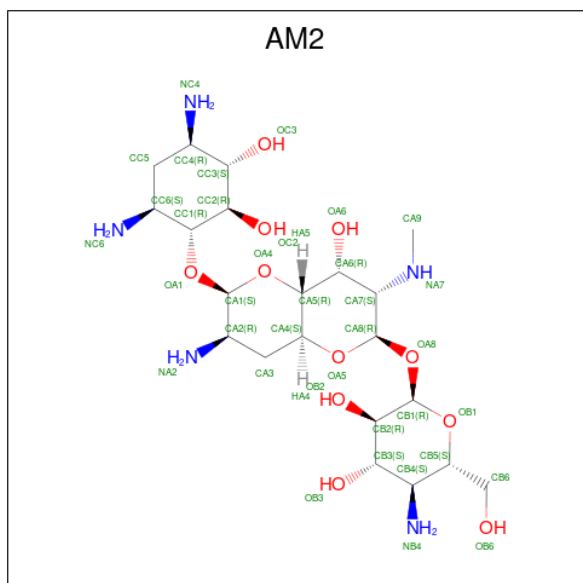
- Molecule 24 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
24	A	190	Total	Mg	0	0
			190	190		
24	D	1	Total	Mg	0	0
			1	1		
24	F	1	Total	Mg	0	0
			1	1		
24	G	2	Total	Mg	0	0
			2	2		
24	H	1	Total	Mg	0	0
			1	1		
24	J	1	Total	Mg	0	0
			1	1		
24	K	1	Total	Mg	0	0
			1	1		
24	L	1	Total	Mg	0	0
			1	1		
24	M	1	Total	Mg	0	0
			1	1		
24	S	1	Total	Mg	0	0
			1	1		
24	W	2	Total	Mg	0	0
			2	2		
24	Z	1	Total	Mg	0	0
			1	1		

- Molecule 25 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
25	A	14	Total K 14 14	0	0
25	V	1	Total K 1 1	0	0

- Molecule 26 is APRAMYCIN (CCD ID: AM2) (formula: C₂₁H₄₁N₅O₁₁).



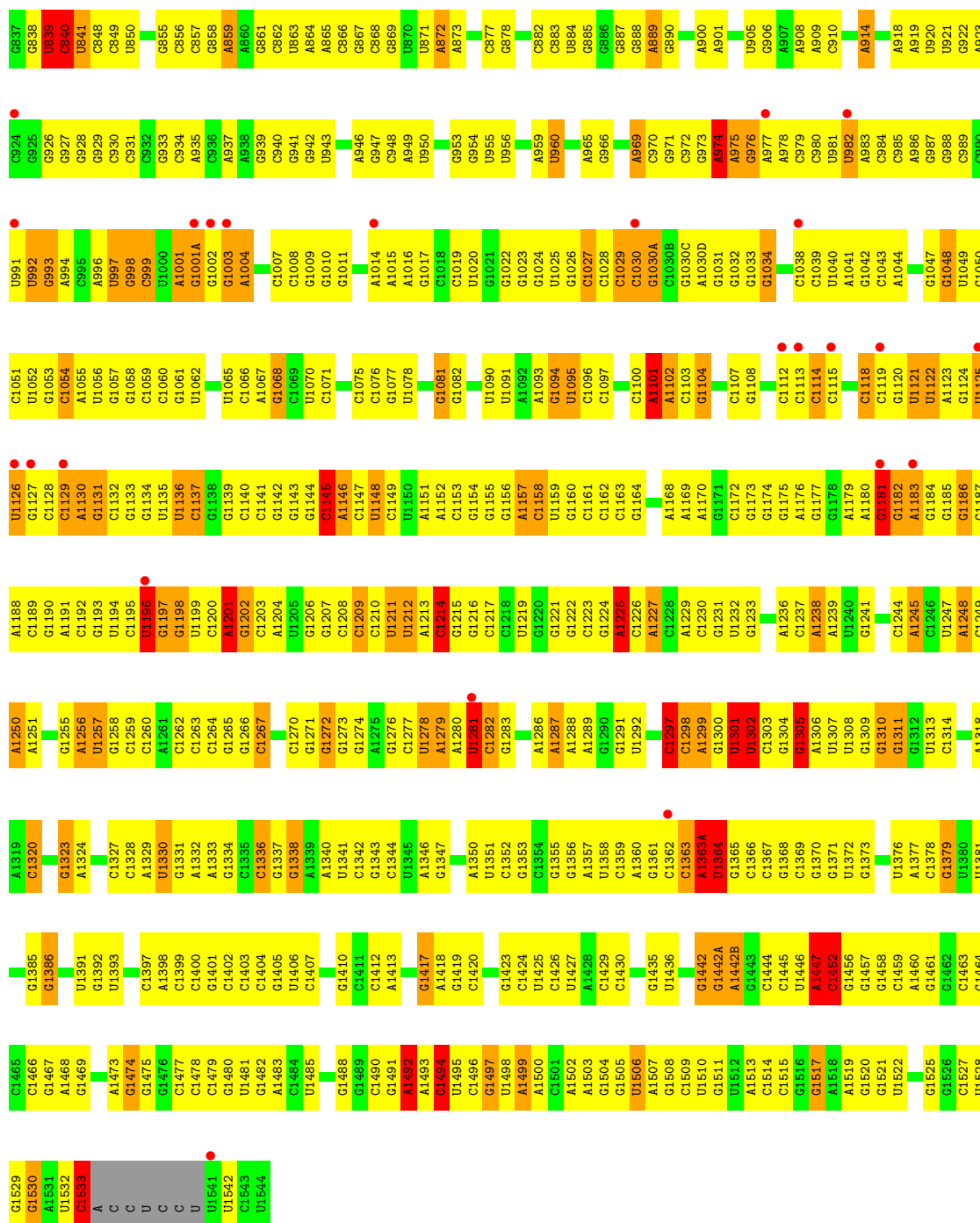
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
26	A	1	Total C N O 37 21 5 11	0	0
26	A	1	Total C N O 37 21 5 11	0	0
26	A	1	Total C N O 37 21 5 11	0	0
26	A	1	Total C N O 37 21 5 11	0	0
26	A	1	Total C N O 37 21 5 11	0	0

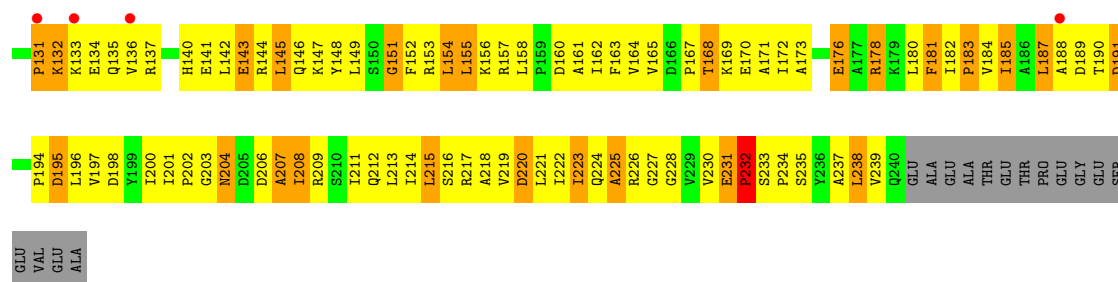
- Molecule 27 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

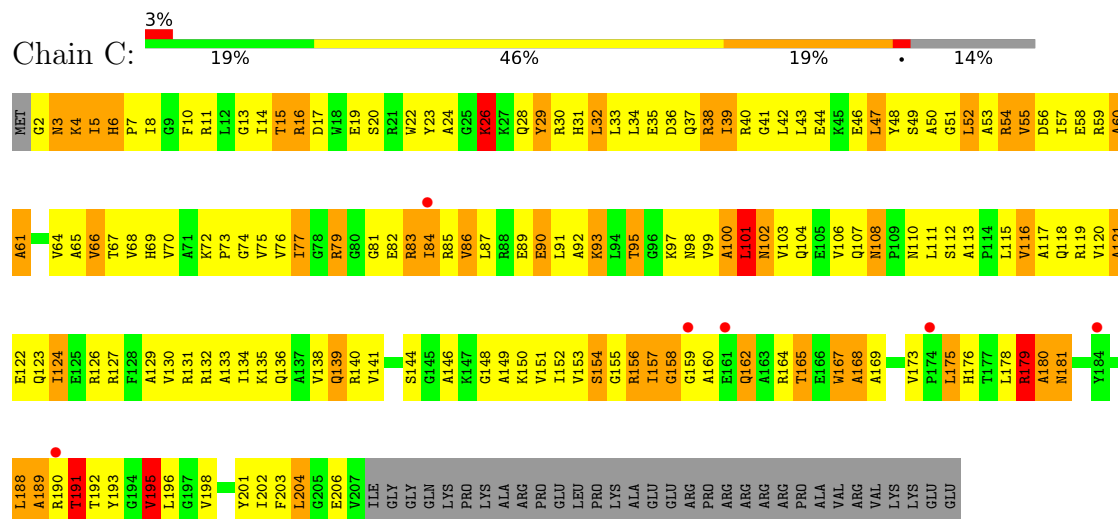
- Molecule 28 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
28	A	1	Total	O	0	0
			1	1		

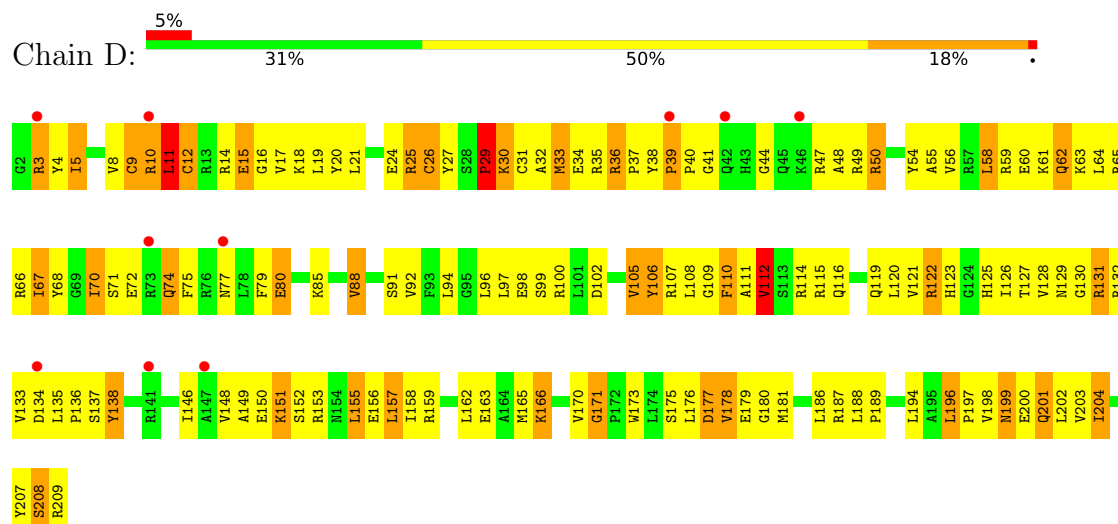




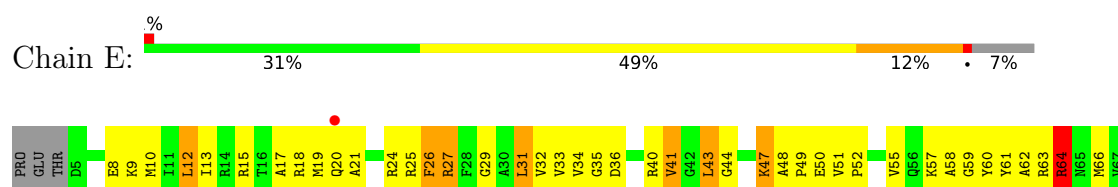
• Molecule 3: 30S RIBOSOMAL PROTEIN S3

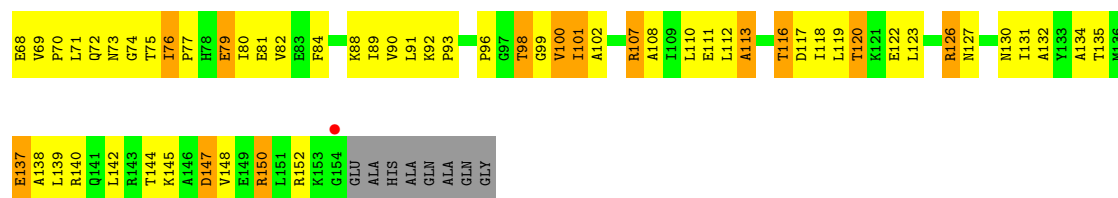


- Molecule 4: 30S RIBOSOMAL PROTEIN S4



● Molecule 5: 30S RIBOSOMAL PROTEIN S5

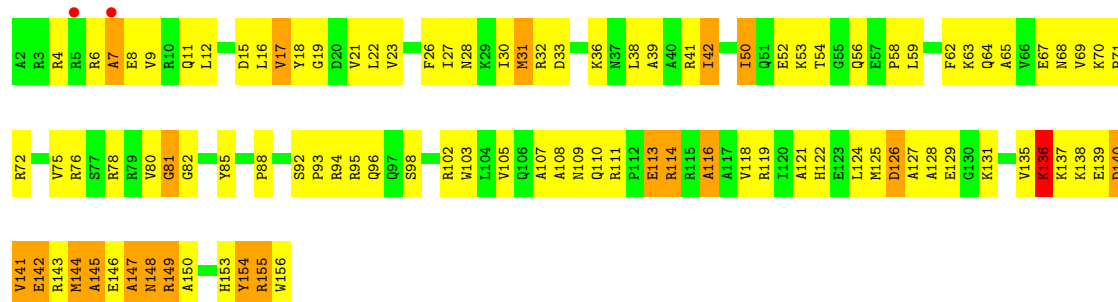




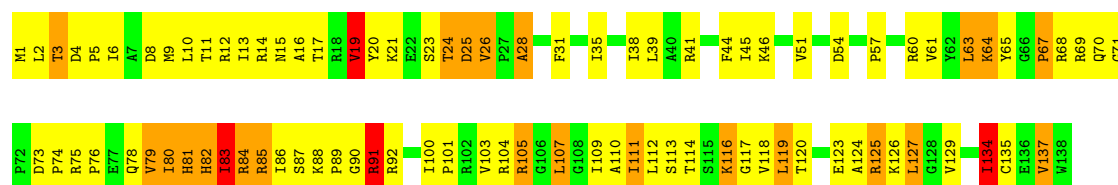
• Molecule 6: 30S RIBOSOMAL PROTEIN S6



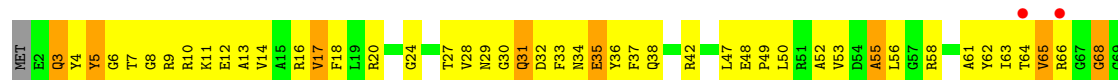
• Molecule 7: 30S RIBOSOMAL PROTEIN S7

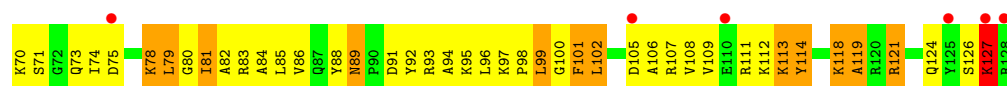


• Molecule 8: 30S RIBOSOMAL PROTEIN S8

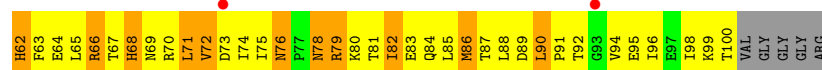
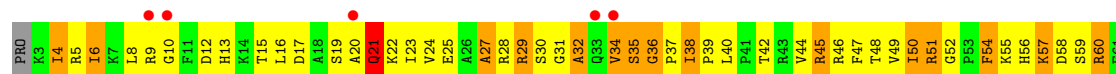
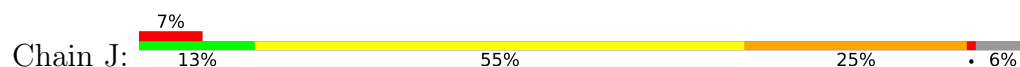


• Molecule 9: 30S RIBOSOMAL PROTEIN S9

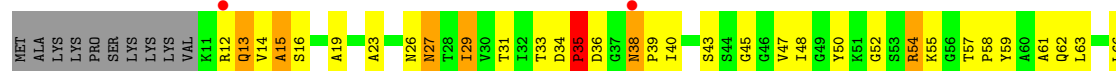




• Molecule 10: 30S RIBOSOMAL PROTEIN S10



• Molecule 11: 30S RIBOSOMAL PROTEIN S11



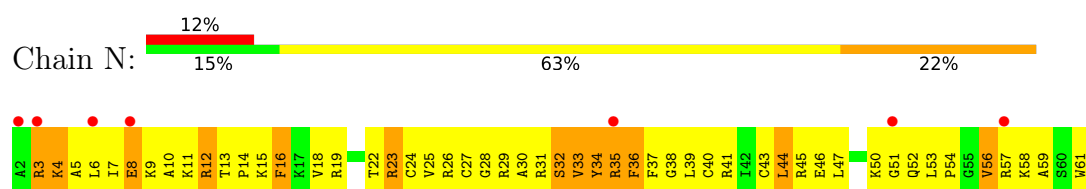
• Molecule 12: 30S RIBOSOMAL PROTEIN S12



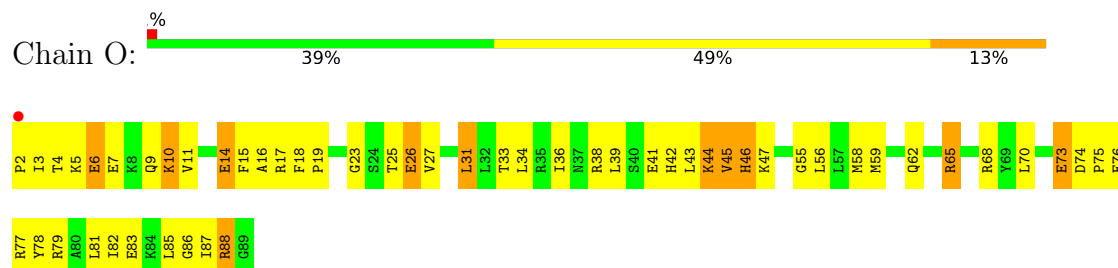
• Molecule 13: 30S RIBOSOMAL PROTEIN S13



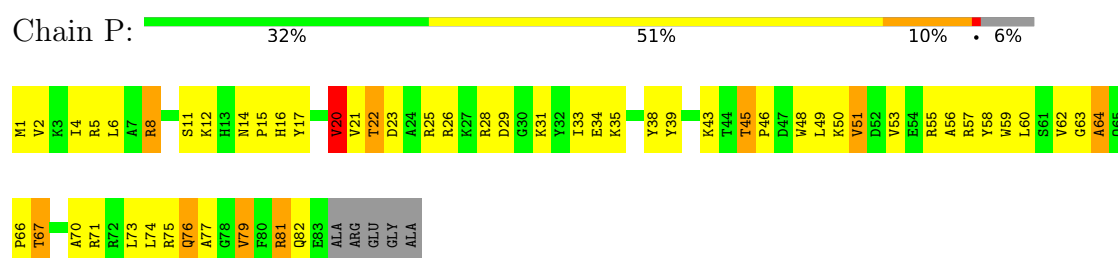
• Molecule 14: 30S RIBOSOMAL PROTEIN S14



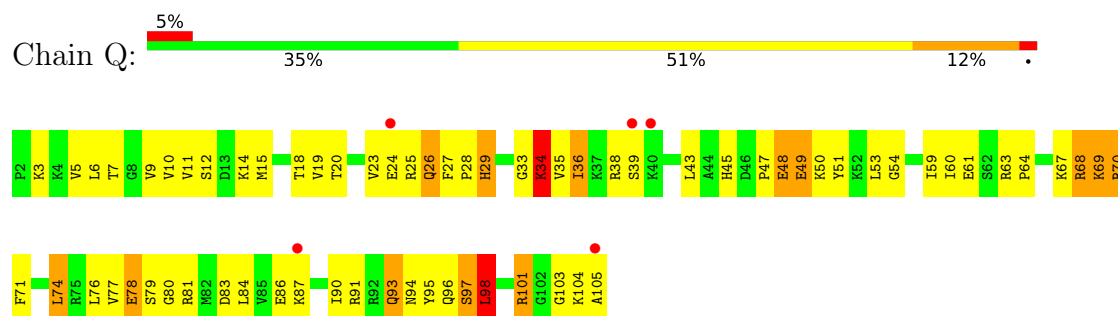
• Molecule 15: 30S RIBOSOMAL PROTEIN S15



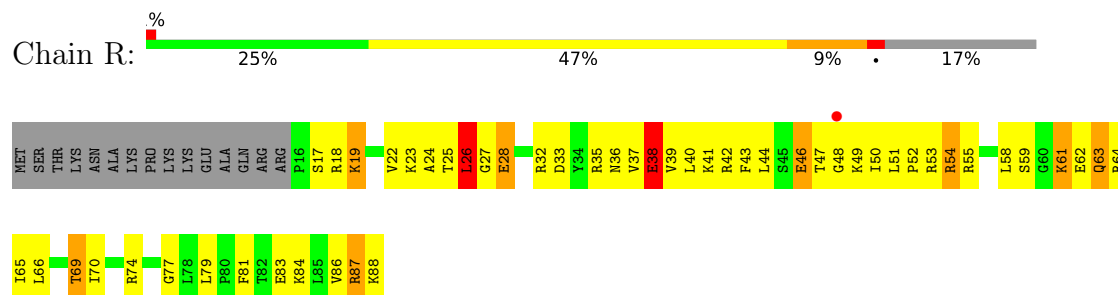
• Molecule 16: 30S RIBOSOMAL PROTEIN S16



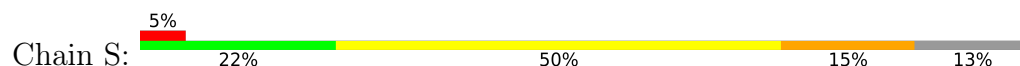
• Molecule 17: 30S RIBOSOMAL PROTEIN S17

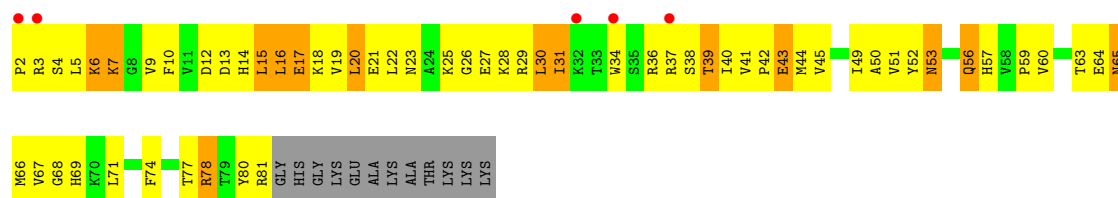


• Molecule 18: 30S RIBOSOMAL PROTEIN S18

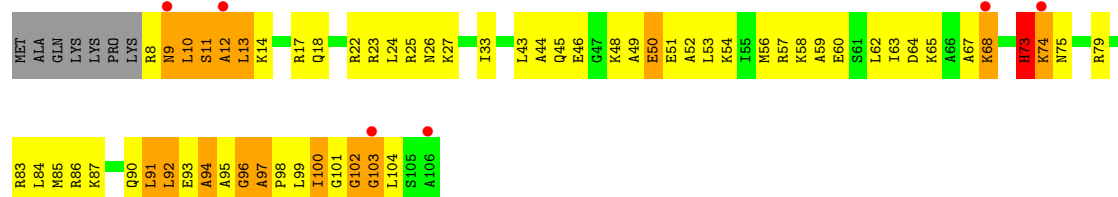


• Molecule 19: 30S RIBOSOMAL PROTEIN S19





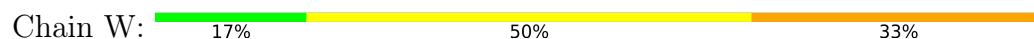
• Molecule 20: 30S RIBOSOMAL PROTEIN S20



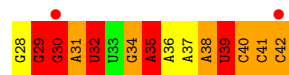
• Molecule 21: 30S RIBOSOMAL PROTEIN THX



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



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	402.18Å 402.18Å 175.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 3.50 40.00 – 3.50	Depositor EDS
% Data completeness (in resolution range)	99.8 (40.00-3.50) 99.7 (40.00-3.50)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.25 (at 3.48Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.193 , 0.235 0.198 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	119.8	Xtriage
Anisotropy	0.253	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 120.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	52514	wwPDB-VP
Average B, all atoms (Å ²)	126.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.45% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: K, AM2, ZN, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.45	2/36318 (0.0%)	0.69	44/56682 (0.1%)
2	B	0.45	0/1935	1.06	10/2609 (0.4%)
3	C	0.48	0/1636	1.03	10/2205 (0.5%)
4	D	0.44	0/1732	1.09	15/2318 (0.6%)
5	E	0.52	0/1162	1.11	4/1564 (0.3%)
6	F	0.41	0/855	1.00	7/1154 (0.6%)
7	G	0.45	0/1275	1.04	8/1709 (0.5%)
8	H	0.58	0/1135	1.17	12/1527 (0.8%)
9	I	0.43	0/1028	1.04	6/1378 (0.4%)
10	J	0.49	0/807	1.07	6/1085 (0.6%)
11	K	0.51	0/899	1.08	6/1213 (0.5%)
12	L	0.59	1/987 (0.1%)	1.05	5/1322 (0.4%)
13	M	0.48	0/1007	1.04	7/1347 (0.5%)
14	N	0.47	0/500	0.97	1/664 (0.2%)
15	O	0.47	0/744	0.85	1/992 (0.1%)
16	P	0.53	0/716	1.03	2/963 (0.2%)
17	Q	0.50	0/869	1.05	4/1159 (0.3%)
18	R	0.42	0/602	0.96	1/799 (0.1%)
19	S	0.43	0/661	1.05	5/890 (0.6%)
20	T	0.55	0/763	1.22	6/1006 (0.6%)
21	V	0.53	0/212	0.97	0/277
22	W	1.22	0/137	1.01	1/211 (0.5%)
23	Z	1.11	0/357	1.05	3/555 (0.5%)
All	All	0.47	3/56337 (0.0%)	0.83	164/83629 (0.2%)

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	8	22
22	W	0	1
23	Z	0	3
All	All	8	26

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1533	C	N1-C2	7.51	1.55	1.40
12	L	128	ALA	C-N	-5.28	1.25	1.33
1	A	1533	C	C4-C5	5.26	1.53	1.43

All (164) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1363(A)	A	C2'-C3'-O3'	14.53	131.30	109.50
1	A	243	A	C2'-C3'-O3'	13.20	129.30	109.50
1	A	1452	C	C2'-C3'-O3'	12.76	128.64	109.50
20	T	12	ALA	N-CA-C	-11.52	94.98	113.19
1	A	119	A	C2'-C3'-O3'	11.37	126.55	109.50
2	B	132	LYS	N-CA-C	-11.22	99.60	113.18
1	A	51	A	C2'-C3'-O3'	11.09	126.13	109.50
5	E	64	ARG	N-CA-C	-10.90	96.47	110.53
4	D	97	LEU	N-CA-C	-10.16	100.28	111.36
1	A	793	U	C2'-C3'-O3'	9.77	124.16	109.50
1	A	372	C	C2'-C3'-O3'	9.61	123.91	109.50
11	K	38	ASN	N-CA-C	9.49	121.25	109.57
1	A	410	G	C2'-C3'-O3'	9.38	127.78	113.70
20	T	13	LEU	N-CA-C	-9.11	100.97	112.90
1	A	1452	C	C4'-C3'-O3'	8.99	122.89	109.40
11	K	73	MET	N-CA-C	-8.74	102.62	113.38
1	A	119	A	C4'-C3'-O3'	8.73	122.49	109.40
5	E	76	ILE	CA-C-N	8.66	128.81	119.28
5	E	76	ILE	C-N-CA	8.66	128.81	119.28
4	D	26	CYS	N-CA-C	-8.58	102.36	113.17
1	A	243	A	C4'-C3'-O3'	8.49	122.13	109.40
7	G	147	ALA	N-CA-C	-8.10	102.18	114.16
14	N	8	GLU	N-CA-C	-8.03	103.38	113.02
1	A	1363(A)	A	C4'-C3'-O3'	8.00	121.41	109.40
8	H	100	ILE	CA-C-N	7.99	128.47	119.93
8	H	100	ILE	C-N-CA	7.99	128.47	119.93
7	G	148	ASN	N-CA-C	-7.88	101.28	113.02
4	D	204	ILE	N-CA-C	-7.87	103.02	110.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	120	ALA	N-CA-C	-7.78	102.88	111.36
1	A	30	U	N1-C1'-C2'	7.63	123.45	112.00
4	D	11	LEU	N-CA-C	-7.57	102.38	111.69
5	E	113	ALA	N-CA-C	-7.54	103.34	112.54
20	T	74	LYS	N-CA-C	7.54	119.16	108.00
1	A	992	U	C2'-C3'-O3'	7.50	120.75	109.50
4	D	33	MET	N-CA-C	-7.49	103.25	112.38
1	A	1145	C	C2'-C3'-O3'	7.49	120.73	109.50
9	I	99	LEU	N-CA-C	-7.48	104.39	113.97
1	A	428	G	C2'-C3'-O3'	7.42	120.63	109.50
4	D	14	ARG	N-CA-C	-7.35	103.47	114.64
1	A	974	A	C2'-C3'-O3'	7.33	120.49	109.50
10	J	21	GLN	N-CA-C	-7.32	104.87	114.31
22	W	6	A	C2'-C3'-O3'	7.26	124.59	113.70
10	J	62	HIS	N-CA-C	7.23	120.30	108.52
7	G	145	ALA	N-CA-C	-7.08	98.88	109.86
4	D	208	SER	N-CA-C	-7.07	104.78	113.19
9	I	68	GLY	N-CA-C	7.05	120.12	111.45
17	Q	29	HIS	CA-C-N	6.95	127.53	119.47
17	Q	29	HIS	C-N-CA	6.95	127.53	119.47
20	T	60	GLU	N-CA-C	-6.71	103.96	111.28
15	O	44	LYS	N-CA-C	-6.71	103.99	111.71
13	M	107	ALA	N-CA-C	-6.70	102.31	111.56
8	H	69	ARG	N-CA-C	6.65	119.27	109.69
1	A	1214	C	N1-C1'-C2'	6.64	121.96	112.00
2	B	14	GLY	N-CA-C	-6.64	107.37	114.67
19	S	10	PHE	N-CA-C	6.61	118.83	110.24
18	R	46	GLU	N-CA-C	-6.61	104.48	112.54
17	Q	79	SER	N-CA-C	6.60	120.38	110.14
7	G	154	TYR	N-CA-C	-6.54	105.69	113.21
12	L	26	ALA	N-CA-C	-6.52	102.42	111.81
8	H	19	VAL	N-CA-C	-6.50	106.66	112.90
3	C	124	ILE	N-CA-C	6.48	117.11	110.82
3	C	6	HIS	CA-C-N	6.48	127.94	119.84
3	C	6	HIS	C-N-CA	6.48	127.94	119.84
1	A	1305	G	N9-C1'-C2'	6.46	121.69	112.00
2	B	172	ILE	N-CA-C	-6.45	103.00	112.04
12	L	27	LEU	N-CA-C	6.42	124.47	110.80
2	B	214	ILE	N-CA-C	6.40	116.55	110.53
7	G	136	LYS	N-CA-C	-6.38	103.95	111.03
1	A	840	C	N1-C1'-C2'	6.30	121.45	112.00
4	D	163	GLU	N-CA-C	-6.29	104.34	111.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	90	GLU	N-CA-C	-6.29	104.43	111.28
13	M	84	ILE	N-CA-C	-6.27	103.13	110.21
6	F	27	GLN	N-CA-C	-6.26	104.37	111.07
1	A	1101	A	C2'-C3'-O3'	6.25	118.88	109.50
1	A	1533	C	C4'-C3'-O3'	6.25	122.37	113.00
12	L	119	LYS	N-CA-C	-6.24	101.28	110.52
1	A	1447	A	C4'-C3'-O3'	6.22	118.72	109.40
13	M	12	ASN	N-CA-C	6.20	124.00	110.80
1	A	30	U	C5'-C4'-C3'	6.14	125.21	116.00
1	A	1299	A	N9-C1'-C2'	6.14	121.21	112.00
10	J	66	ARG	N-CA-C	6.10	118.58	109.25
13	M	83	ASP	N-CA-C	-6.08	103.99	111.40
8	H	126	LYS	N-CA-C	-6.06	104.30	111.03
13	M	11	ARG	N-CA-C	6.06	123.70	110.80
1	A	1301	U	N1-C1'-C2'	6.02	121.03	112.00
1	A	839	U	N1-C1'-C2'	6.01	121.02	112.00
6	F	11	ASN	CA-C-N	5.92	127.02	120.45
6	F	11	ASN	C-N-CA	5.92	127.02	120.45
8	H	79	VAL	N-CA-C	-5.89	104.04	112.35
1	A	328	C	N1-C1'-C2'	5.89	122.84	114.00
9	I	35	GLU	N-CA-C	-5.88	106.02	113.43
12	L	60	LEU	N-CA-C	5.88	118.48	110.55
8	H	125	ARG	N-CA-C	-5.82	104.90	112.23
2	B	115	LEU	N-CA-C	-5.79	105.71	112.89
1	A	51	A	C4'-C3'-O3'	5.77	118.06	109.40
2	B	13	ALA	N-CA-C	-5.77	106.09	113.01
19	S	68	GLY	N-CA-C	-5.72	107.46	113.58
1	A	1488	G	C5'-C4'-C3'	-5.67	107.49	116.00
23	Z	35	A	C4'-C3'-O3'	-5.67	104.50	113.00
17	Q	74	LEU	N-CA-C	5.66	117.25	111.14
2	B	152	PHE	N-CA-C	-5.63	106.17	113.16
4	D	56	VAL	N-CA-C	5.63	115.76	110.30
1	A	1225	A	N9-C1'-C2'	5.61	120.42	112.00
7	G	128	ALA	N-CA-C	-5.61	105.93	112.89
11	K	38	ASN	CA-C-N	5.61	126.85	119.84
11	K	38	ASN	C-N-CA	5.61	126.85	119.84
3	C	83	ARG	N-CA-C	5.60	117.19	111.14
13	M	37	THR	N-CA-C	-5.60	106.44	113.72
4	D	38	TYR	CA-C-N	5.59	123.74	119.66
4	D	38	TYR	C-N-CA	5.59	123.74	119.66
1	A	428	G	N9-C1'-C2'	5.57	122.35	114.00
6	F	100	ASN	N-CA-C	-5.54	106.10	112.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1305	G	C2'-C3'-O3'	5.52	121.98	113.70
23	Z	39	U	C2'-C3'-O3'	5.52	117.78	109.50
1	A	1297	C	N1-C1'-C2'	5.52	120.28	112.00
7	G	141	VAL	N-CA-C	-5.51	105.74	111.58
1	A	749	C	N1-C1'-C2'	-5.50	105.74	114.00
1	A	577	G	C5'-C4'-C3'	-5.50	107.75	116.00
19	S	16	LEU	N-CA-C	-5.49	104.99	110.97
16	P	79	VAL	N-CA-C	-5.48	104.09	111.44
16	P	20	VAL	N-CA-C	5.46	117.96	108.90
3	C	26	LYS	N-CA-C	5.43	119.39	112.87
1	A	1302	U	N1-C1'-C2'	5.42	120.14	112.00
23	Z	30	G	C2'-C3'-O3'	5.40	121.80	113.70
19	S	56	GLN	N-CA-C	5.40	116.85	109.18
2	B	220	ASP	N-CA-C	-5.35	105.53	111.36
19	S	34	TRP	N-CA-C	-5.34	106.08	112.59
6	F	22	GLU	N-CA-C	-5.31	105.15	111.69
6	F	43	LEU	N-CA-C	-5.29	106.66	113.01
11	K	75	TYR	N-CA-C	-5.28	104.84	113.19
1	A	686	U	N1-C1'-C2'	5.28	121.92	114.00
4	D	112	VAL	N-CA-C	5.27	115.38	110.42
9	I	61	ALA	N-CA-C	5.27	117.76	108.75
7	G	116	ALA	N-CA-C	5.27	116.71	111.07
20	T	92	LEU	N-CA-C	-5.24	106.73	113.02
1	A	1181	G	N9-C1'-C2'	5.24	119.86	112.00
2	B	44	LEU	N-CA-C	5.24	116.99	111.28
8	H	116	LYS	N-CA-C	-5.21	106.16	112.88
4	D	196	LEU	CA-C-N	5.20	126.34	119.84
4	D	196	LEU	C-N-CA	5.20	126.34	119.84
10	J	22	LYS	N-CA-C	-5.19	107.12	113.50
8	H	134	ILE	N-CA-C	5.18	120.12	109.34
10	J	38	ILE	CA-C-N	5.18	128.07	120.46
10	J	38	ILE	C-N-CA	5.18	128.07	120.46
3	C	121	ALA	N-CA-C	-5.17	105.83	111.82
1	A	1201	A	C2'-C3'-O3'	5.16	117.24	109.50
3	C	126	ARG	N-CA-C	-5.16	106.83	113.02
1	A	1196	U	C2'-C3'-O3'	5.15	121.42	113.70
4	D	39	PRO	N-CA-C	5.14	115.41	110.47
20	T	74	LYS	CB-CA-C	-5.14	109.15	116.34
3	C	77	ILE	N-CA-C	5.14	115.80	110.82
1	A	1305	G	C5'-C4'-C3'	5.12	123.67	116.00
8	H	101	PRO	N-CA-C	5.11	119.59	111.26
13	M	15	VAL	N-CA-C	5.11	115.32	110.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	868	C	C5'-C4'-C3'	-5.09	108.36	116.00
9	I	17	VAL	N-CA-C	5.09	115.18	107.80
9	I	5	TYR	N-CA-C	5.08	117.85	109.72
11	K	70	LYS	N-CA-C	-5.07	104.74	112.04
8	H	28	ALA	N-CA-C	5.06	116.99	109.25
12	L	62	SER	N-CA-C	-5.02	107.00	112.72
8	H	137	VAL	CB-CA-C	-5.02	104.07	111.80
6	F	11	ASN	N-CA-C	5.01	115.73	109.57
1	A	722	A	C4'-C3'-O3'	-5.01	105.48	113.00
3	C	191	THR	N-CA-C	5.00	114.89	108.34

All (8) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	30	U	C4'
1	A	197	A	C4'
1	A	410	G	C3'
1	A	1181	G	C4'
1	A	1305	G	C4',C3'
1	A	1363(A)	A	C3'
1	A	1452	C	C3'

All (26) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1065	U	Sidechain
1	A	1094	G	Sidechain
1	A	112	G	Sidechain
1	A	1121	U	Sidechain
1	A	1186	G	Sidechain
1	A	1281	U	Sidechain
1	A	1310	G	Sidechain
1	A	1330	U	Sidechain
1	A	1364	U	Sidechain
1	A	1417	G	Sidechain
1	A	1492	A	Sidechain
1	A	1494	G	Sidechain
1	A	1533	C	Sidechain
1	A	239	U	Sidechain
1	A	250	A	Sidechain
1	A	251	G	Sidechain
1	A	424	G	Sidechain

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Mol	Chain	Res	Type	Group
1	A	516	U	Sidechain
1	A	529	G	Sidechain
1	A	575	G	Sidechain
1	A	740	U	Sidechain
1	A	773	G	Sidechain
22	W	1	U	Sidechain
23	Z	29	G	Sidechain
23	Z	32	U	Sidechain
23	Z	35	A	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32446	0	16380	1057	0
2	B	1900	0	1951	305	0
3	C	1612	0	1677	252	0
4	D	1702	0	1762	191	0
5	E	1146	0	1207	118	0
6	F	842	0	857	95	0
7	G	1256	0	1295	98	0
8	H	1115	0	1177	97	0
9	I	1010	0	1043	129	0
10	J	794	0	840	148	0
11	K	884	0	904	98	0
12	L	971	0	1057	98	0
13	M	996	0	1072	120	0
14	N	491	0	529	91	0
15	O	733	0	771	63	0
16	P	700	0	720	70	0
17	Q	856	0	930	72	0
18	R	596	0	668	86	0
19	S	647	0	673	88	0
20	T	761	0	859	72	0
21	V	208	0	221	15	0
22	W	123	0	66	5	0
23	Z	319	0	164	32	0
24	A	190	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	D	1	0	0	0	0
24	F	1	0	0	0	0
24	G	2	0	0	0	0
24	H	1	0	0	0	0
24	J	1	0	0	0	0
24	K	1	0	0	0	0
24	L	1	0	0	0	0
24	M	1	0	0	0	0
24	S	1	0	0	0	0
24	W	2	0	0	0	0
24	Z	1	0	0	0	0
25	A	14	0	0	0	0
25	V	1	0	0	0	0
26	A	185	0	205	7	0
27	D	1	0	0	0	0
27	N	1	0	0	0	0
28	A	1	0	0	0	0
All	All	52514	0	37028	3155	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 (3155) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1113:C:C2'	1:A:1114:C:H5'	1.60	1.28
1:A:1147:C:H2'	1:A:1148:U:H5''	1.25	1.12
4:D:98:GLU:HG2	4:D:189:PRO:HG3	1.32	1.11
1:A:1271:G:H2'	1:A:1272:G:H5''	1.22	1.11
1:A:972:C:H4'	10:J:57:LYS:HG2	1.30	1.10
1:A:1244:C:H2'	1:A:1245:A:H5''	1.28	1.10
4:D:62:GLN:HA	4:D:62:GLN:HE21	1.14	1.09
3:C:79:ARG:H	3:C:79:ARG:HD3	1.17	1.08
6:F:30:LEU:HB3	6:F:35:ALA:HB3	1.21	1.08
20:T:50:GLU:HA	20:T:100:ILE:HD11	1.27	1.08
1:A:243:A:H4'	1:A:244:U:H5'	1.29	1.07
2:B:91:PRO:HG3	2:B:154:LEU:HB2	1.30	1.07
1:A:1047:G:H2'	1:A:1048:G:H5''	1.35	1.07
14:N:26:ARG:HH12	14:N:47:LEU:HD21	1.18	1.07
19:S:39:THR:HG22	19:S:40:ILE:H	1.11	1.07
19:S:28:LYS:HG3	19:S:29:ARG:H	1.20	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:991:U:H3	1:A:1212:U:H1'	1.17	1.06
3:C:26:LYS:H	3:C:26:LYS:HD3	1.18	1.06
6:F:28:ARG:HH11	6:F:28:ARG:HB2	1.17	1.05
3:C:44:GLU:HA	3:C:52:LEU:HD21	1.35	1.05
1:A:1157:A:H5'	1:A:1158:C:C6	1.92	1.04
1:A:1047:G:C2'	1:A:1048:G:H5''	1.88	1.04
10:J:49:VAL:HG13	14:N:41:ARG:HB2	1.37	1.03
1:A:1029:C:H3'	1:A:1030:C:H5''	1.40	1.03
2:B:116:GLU:HA	2:B:153:ARG:HH22	1.18	1.02
5:E:101:ILE:HD13	5:E:119:LEU:HD23	1.40	1.02
4:D:187:ARG:NE	4:D:188:LEU:H	1.56	1.02
1:A:498:U:H2'	1:A:499:A:H5''	1.41	1.02
3:C:64:VAL:HB	3:C:99:VAL:HG21	1.43	1.01
1:A:1113:C:H2'	1:A:1114:C:H5'	1.01	1.00
2:B:18:GLY:HA2	2:B:42:ILE:HG12	1.40	0.99
3:C:91:LEU:HD11	3:C:99:VAL:HG23	1.44	0.99
1:A:1115:C:H42	1:A:1185:G:H1	1.05	0.99
4:D:187:ARG:HE	4:D:188:LEU:H	1.11	0.98
1:A:329:A:C5	1:A:332:G:C6	2.52	0.97
1:A:991:U:N3	1:A:1212:U:H1'	1.79	0.97
1:A:1113:C:C2'	1:A:1114:C:C5'	2.43	0.97
1:A:329:A:C8	1:A:332:G:O6	2.17	0.97
1:A:1314:C:OP2	19:S:6:LYS:HD3	1.65	0.97
1:A:223:U:H2'	1:A:224:C:H5''	1.42	0.97
9:I:127:LYS:H	9:I:127:LYS:HD2	1.28	0.96
18:R:38:GLU:HA	18:R:41:LYS:HE2	1.45	0.96
9:I:114:TYR:HD2	10:J:60:ARG:HB2	1.27	0.96
10:J:79:ARG:HH11	10:J:79:ARG:HA	1.30	0.96
10:J:8:LEU:HD12	10:J:20:ALA:HB2	1.45	0.96
3:C:83:ARG:HA	3:C:86:VAL:HG23	1.47	0.96
23:Z:30:G:H2'	23:Z:31:A:H8	1.31	0.96
4:D:3:ARG:HH21	4:D:74:GLN:HG3	1.30	0.95
1:A:1158:C:H3'	1:A:1158:C:O2	1.65	0.95
10:J:4:ILE:HD13	10:J:4:ILE:H	1.30	0.95
9:I:3:GLN:HA	9:I:3:GLN:HE21	1.32	0.95
1:A:998:G:H3'	1:A:999:C:H5''	1.46	0.94
1:A:1271:G:C2'	1:A:1272:G:H5''	1.96	0.94
1:A:1502:A:H2	1:A:1505:G:H1	1.14	0.94
1:A:996:A:H3'	1:A:997:U:H5''	1.50	0.93
3:C:14:ILE:HG22	3:C:15:THR:H	1.33	0.93
12:L:55:VAL:HG12	12:L:56:ALA:H	1.33	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1147:C:C2'	1:A:1148:U:H5''	1.99	0.93
1:A:141:A:H1'	1:A:182:U:O2	1.69	0.92
2:B:7:VAL:HG12	2:B:8:LYS:H	1.33	0.92
10:J:29:ARG:HB2	10:J:29:ARG:HH11	1.33	0.92
10:J:32:ALA:HB3	10:J:75:ILE:HG23	1.48	0.92
1:A:1129:C:O2'	1:A:1131:G:H5''	1.70	0.92
9:I:9:ARG:HG2	9:I:14:VAL:HG12	1.52	0.92
23:Z:30:G:H2'	23:Z:31:A:C8	2.04	0.91
2:B:103:THR:HG23	2:B:176:GLU:OE1	1.70	0.91
18:R:55:ARG:NH1	18:R:55:ARG:HB3	1.85	0.91
1:A:1115:C:O2'	14:N:61:TRP:HB2	1.68	0.91
23:Z:34:G:H2'	23:Z:35:A:C8	2.06	0.91
1:A:1115:C:H1'	14:N:61:TRP:HA	1.50	0.91
3:C:130:VAL:O	3:C:134:ILE:HG12	1.72	0.90
1:A:155:C:H2'	1:A:156:G:H5''	1.53	0.90
2:B:98:LEU:HD23	2:B:98:LEU:H	1.33	0.90
3:C:157:ILE:HG21	3:C:164:ARG:HH21	1.37	0.90
4:D:50:ARG:NH1	4:D:50:ARG:HB3	1.85	0.90
4:D:199:ASN:HD21	4:D:201:GLN:HB2	1.36	0.89
1:A:1244:C:C2'	1:A:1245:A:H5''	2.01	0.89
9:I:97:LYS:HA	9:I:102:LEU:HD13	1.54	0.89
1:A:586:C:H2'	1:A:587:G:H5''	1.54	0.89
18:R:59:SER:HB3	18:R:62:GLU:HG3	1.55	0.88
1:A:477:A:H2'	1:A:479:C:H5''	1.56	0.88
3:C:93:LYS:HE2	3:C:93:LYS:HA	1.55	0.88
9:I:17:VAL:HG22	9:I:63:ILE:HD12	1.52	0.88
1:A:1473:A:H2'	1:A:1474:G:H5''	1.56	0.88
13:M:117:VAL:HG12	13:M:118:ALA:H	1.37	0.88
2:B:82:ARG:HA	2:B:92:TYR:CE2	2.09	0.87
1:A:479:C:H5'	1:A:479:C:H6	1.39	0.87
4:D:121:VAL:HG22	4:D:126:ILE:HD12	1.55	0.87
4:D:150:GLU:HG2	4:D:153:ARG:NH2	1.90	0.87
1:A:1060:C:C5	3:C:2:GLY:HA3	2.09	0.87
2:B:218:ALA:O	2:B:222:ILE:HG13	1.75	0.87
1:A:1250:A:H4'	9:I:68:GLY:H	1.38	0.87
1:A:38:G:H22	1:A:397:A:H5'	1.40	0.86
1:A:135:C:O2	16:P:1:MET:HB2	1.73	0.86
1:A:329:A:N7	1:A:332:G:C6	2.43	0.86
1:A:1038:C:H2'	1:A:1039:C:C6	2.11	0.86
4:D:64:LEU:HD12	4:D:75:PHE:HZ	1.40	0.86
11:K:54:ARG:HB3	11:K:54:ARG:HH11	1.40	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1022:G:H2'	1:A:1023:G:H8	1.41	0.86
1:A:1301:U:H3'	1:A:1302:U:H5'	1.57	0.86
2:B:78:GLN:HE22	2:B:96:ARG:HH12	1.21	0.86
1:A:1103:C:H2'	1:A:1104:G:H5''	1.57	0.86
1:A:939:G:H5''	7:G:102:ARG:NH2	1.91	0.85
1:A:1144:G:H21	1:A:1146:A:H62	1.20	0.85
10:J:31:GLY:HA2	10:J:78:ASN:HD22	1.40	0.85
14:N:26:ARG:HG3	14:N:27:CYS:H	1.41	0.85
8:H:17:THR:HG22	8:H:63:LEU:HD13	1.56	0.85
3:C:108:ASN:HD21	3:C:144:SER:HB2	1.41	0.85
1:A:1314:C:C5	19:S:6:LYS:HE2	2.11	0.85
11:K:54:ARG:O	11:K:57:THR:HG22	1.77	0.85
19:S:42:PRO:O	19:S:45:VAL:HG23	1.77	0.85
3:C:79:ARG:HE	3:C:82:GLU:HG2	1.41	0.84
13:M:91:ARG:HB2	13:M:98:VAL:HG23	1.58	0.84
1:A:1132:C:H2'	1:A:1133:G:C8	2.11	0.84
7:G:54:THR:HG22	7:G:56:GLN:H	1.43	0.84
13:M:15:VAL:HG23	13:M:43:THR:O	1.76	0.84
1:A:1247:U:H2'	1:A:1248:A:H5''	1.58	0.84
10:J:94:VAL:HG12	10:J:95:GLU:H	1.42	0.84
18:R:47:THR:HA	18:R:83:GLU:HB2	1.58	0.84
1:A:1047:G:H2'	1:A:1048:G:C5'	2.08	0.83
11:K:54:ARG:HB3	11:K:54:ARG:NH1	1.93	0.83
12:L:83:VAL:HG21	12:L:100:ILE:HG23	1.60	0.83
1:A:877:C:O2	8:H:3:THR:HG21	1.76	0.83
1:A:1247:U:C2'	1:A:1248:A:H5''	2.07	0.83
5:E:15:ARG:HD3	5:E:26:PHE:CD1	2.13	0.83
5:E:43:LEU:HD11	5:E:132:ALA:HB1	1.60	0.83
9:I:127:LYS:HB2	13:M:126:LYS:NZ	1.93	0.83
16:P:6:LEU:HB3	16:P:17:TYR:HD2	1.42	0.83
1:A:838:G:H2'	1:A:839:U:H5''	1.60	0.83
13:M:34:LEU:HD13	13:M:41:PRO:HA	1.61	0.83
2:B:16:HIS:HA	2:B:204:ASN:OD1	1.79	0.83
20:T:50:GLU:O	20:T:100:ILE:HG13	1.79	0.83
1:A:1113:C:H2'	1:A:1114:C:C5'	1.98	0.82
4:D:105:VAL:HG21	4:D:126:ILE:HD13	1.60	0.82
4:D:153:ARG:HG2	4:D:181:MET:HE3	1.60	0.82
10:J:32:ALA:HB3	10:J:75:ILE:CG2	2.08	0.82
13:M:62:ASN:O	13:M:63:THR:HB	1.79	0.82
13:M:81:LEU:HD22	13:M:88:ARG:HH21	1.44	0.82
19:S:28:LYS:HG3	19:S:29:ARG:N	1.94	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:231:G:H2'	1:A:232:G:H5''	1.61	0.82
2:B:223:ILE:HG21	2:B:230:VAL:HG22	1.59	0.82
3:C:26:LYS:H	3:C:26:LYS:CD	1.90	0.82
1:A:1001(A):G:H2'	1:A:1002:G:O4'	1.80	0.82
1:A:9:G:OP1	5:E:122:GLU:HG3	1.79	0.82
1:A:62:U:O2'	1:A:379:C:H1'	1.80	0.82
2:B:76:GLN:HG3	2:B:206:ASP:OD1	1.79	0.82
3:C:59:ARG:HH12	3:C:97:LYS:HE2	1.44	0.82
6:F:26:ILE:HG21	6:F:63:TYR:CE2	2.15	0.82
10:J:27:ALA:HB2	10:J:85:LEU:HD21	1.62	0.82
19:S:52:TYR:HA	19:S:56:GLN:O	1.80	0.82
9:I:53:VAL:HG21	9:I:85:LEU:HD21	1.61	0.82
1:A:1163:C:H2'	1:A:1164:G:H8	1.42	0.82
2:B:116:GLU:HA	2:B:153:ARG:NH2	1.95	0.82
4:D:187:ARG:HE	4:D:188:LEU:N	1.77	0.82
19:S:28:LYS:CG	19:S:29:ARG:H	1.93	0.82
5:E:101:ILE:HD12	5:E:118:ILE:O	1.79	0.81
20:T:73:HIS:O	20:T:74:LYS:HG2	1.80	0.81
10:J:4:ILE:HD13	10:J:4:ILE:N	1.95	0.81
1:A:223:U:C2'	1:A:224:C:H5''	2.11	0.81
3:C:110:ASN:ND2	3:C:140:ARG:HB3	1.95	0.81
17:Q:78:GLU:OE2	17:Q:81:ARG:HD2	1.79	0.81
1:A:1101:A:H4'	1:A:1102:A:O5'	1.80	0.81
19:S:39:THR:HG22	19:S:40:ILE:N	1.91	0.81
3:C:155:GLY:O	3:C:156:ARG:HB2	1.78	0.81
10:J:6:ILE:HD11	10:J:73:ASP:H	1.44	0.81
3:C:131:ARG:O	3:C:135:LYS:HG3	1.81	0.81
1:A:718:G:H5'	11:K:117:ASN:ND2	1.95	0.81
21:V:6:ARG:NE	21:V:15:ARG:HH12	1.79	0.81
1:A:1210:C:H3'	1:A:1211:U:H5''	1.62	0.81
2:B:136:VAL:O	2:B:140:HIS:HB2	1.80	0.81
3:C:26:LYS:HD3	3:C:26:LYS:N	1.96	0.81
11:K:84:VAL:HG23	11:K:110:ASP:HA	1.63	0.80
2:B:19:HIS:NE2	2:B:206:ASP:HB3	1.95	0.80
2:B:116:GLU:HG2	2:B:153:ARG:NH1	1.96	0.80
10:J:94:VAL:HG12	10:J:95:GLU:N	1.96	0.80
3:C:79:ARG:H	3:C:79:ARG:CD	1.95	0.80
7:G:50:ILE:HA	7:G:125:MET:HE3	1.64	0.80
8:H:20:TYR:HE2	8:H:75:ARG:HD2	1.45	0.80
5:E:150:ARG:HH11	5:E:150:ARG:CB	1.95	0.80
1:A:1158:C:O2	1:A:1158:C:C3'	2.30	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:51:VAL:HG21	8:H:60:ARG:NH2	1.95	0.80
1:A:954:G:H2'	1:A:955:U:C6	2.17	0.80
1:A:1048:G:H5'	1:A:1048:G:H8	1.45	0.80
2:B:19:HIS:HE2	2:B:206:ASP:HB3	1.46	0.80
19:S:63:THR:HG22	19:S:64:GLU:H	1.46	0.79
1:A:1121:U:O2'	1:A:1122:U:H5'	1.80	0.79
20:T:56:MET:HG3	20:T:84:LEU:CD1	2.12	0.79
2:B:71:VAL:O	2:B:165:VAL:HG23	1.81	0.79
4:D:158:ILE:H	4:D:158:ILE:HD12	1.48	0.79
1:A:232:G:H5'	1:A:232:G:H8	1.46	0.79
1:A:243:A:C4'	1:A:244:U:H5'	2.12	0.79
1:A:1060:C:H5''	10:J:51:ARG:HG2	1.62	0.79
1:A:1115:C:H1'	14:N:61:TRP:CA	2.11	0.79
4:D:162:LEU:HD13	4:D:181:MET:HG2	1.63	0.79
12:L:117:ARG:HD2	12:L:123:LYS:O	1.82	0.79
1:A:1125:U:H5''	1:A:1126:U:H5	1.46	0.79
1:A:1157:A:H5'	1:A:1158:C:N1	1.96	0.79
12:L:110:VAL:HG21	12:L:113:ARG:HG3	1.63	0.79
17:Q:63:ARG:HG2	17:Q:64:PRO:HD2	1.65	0.79
1:A:1491:G:H21	26:A:3001:AM2:HB61	1.46	0.79
1:A:427:U:H3'	1:A:428:G:H5''	1.65	0.79
1:A:1163:C:H2'	1:A:1164:G:C8	2.18	0.79
9:I:99:LEU:HB3	9:I:101:PHE:HE1	1.48	0.79
9:I:114:TYR:CD2	10:J:60:ARG:HB2	2.16	0.79
3:C:132:ARG:HA	3:C:135:LYS:HE2	1.63	0.79
4:D:153:ARG:HG2	4:D:181:MET:CE	2.12	0.78
1:A:888:G:H3'	1:A:889:A:H5''	1.63	0.78
1:A:984:C:H2'	1:A:985:C:H6	1.49	0.78
14:N:32:SER:HB2	14:N:40:CYS:HB2	1.65	0.78
18:R:32:ARG:HH21	18:R:65:ILE:HD12	1.47	0.78
2:B:10:LEU:HD23	2:B:11:LEU:HG	1.65	0.78
14:N:26:ARG:NH1	14:N:47:LEU:HD21	1.97	0.78
2:B:219:VAL:HA	2:B:222:ILE:HD12	1.65	0.78
18:R:55:ARG:HB3	18:R:55:ARG:HH11	1.46	0.78
1:A:498:U:C2'	1:A:499:A:H5''	2.12	0.78
3:C:70:VAL:O	3:C:106:VAL:HG23	1.82	0.78
12:L:27:LEU:HG	12:L:28:LYS:H	1.49	0.78
1:A:1029:C:C3'	1:A:1030:C:H5''	2.12	0.78
5:E:127:ASN:HD22	5:E:130:ASN:ND2	1.81	0.78
1:A:129(A):G:O2'	1:A:189(F):U:H2'	1.84	0.77
20:T:68:LYS:HE3	20:T:68:LYS:HA	1.65	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:62:GLN:HA	4:D:62:GLN:NE2	1.96	0.77
4:D:176:LEU:HG	4:D:177:ASP:H	1.48	0.77
9:I:99:LEU:HB3	9:I:101:PHE:CE1	2.19	0.77
19:S:63:THR:HB	19:S:65:ASN:HD21	1.49	0.77
1:A:344:A:H3'	1:A:345:C:H5''	1.66	0.77
3:C:79:ARG:NE	3:C:82:GLU:HG2	2.00	0.77
18:R:25:THR:O	18:R:26:LEU:HB2	1.82	0.77
1:A:1113:C:O2'	1:A:1114:C:C5'	2.32	0.77
1:A:250:A:H1'	1:A:252:U:C6	2.20	0.77
1:A:231:G:C2'	1:A:232:G:H5''	2.14	0.77
4:D:64:LEU:HD12	4:D:75:PHE:CZ	2.18	0.77
9:I:70:LYS:O	9:I:74:ILE:HG13	1.84	0.77
16:P:74:LEU:O	16:P:79:VAL:HG23	1.84	0.77
5:E:34:VAL:HG12	5:E:66:MET:HE1	1.67	0.77
1:A:155:C:C2'	1:A:156:G:H5''	2.15	0.77
1:A:1125:U:H5''	1:A:1126:U:C5	2.20	0.77
6:F:37:VAL:HA	6:F:65:VAL:HG12	1.67	0.77
1:A:1226:C:N4	13:M:104:ARG:HD2	2.00	0.77
1:A:1115:C:N4	1:A:1185:G:H1	1.83	0.76
1:A:1502:A:H2	1:A:1505:G:N1	1.83	0.76
2:B:140:HIS:HA	2:B:143:GLU:HG2	1.67	0.76
4:D:112:VAL:HG23	4:D:116:GLN:OE1	1.82	0.76
3:C:83:ARG:C	3:C:85:ARG:H	1.91	0.76
3:C:179:ARG:O	3:C:181:ASN:N	2.18	0.76
7:G:26:PHE:CE2	7:G:30:ILE:HD11	2.21	0.76
1:A:1391:U:H2'	1:A:1392:G:C8	2.20	0.76
10:J:29:ARG:HB2	10:J:29:ARG:NH1	2.01	0.76
10:J:50:ILE:H	10:J:50:ILE:HD12	1.49	0.76
10:J:81:THR:C	10:J:83:GLU:H	1.91	0.76
1:A:329:A:N6	1:A:332:G:C2	2.54	0.76
1:A:1057:G:H5''	3:C:154:SER:OG	1.86	0.76
3:C:179:ARG:HG2	3:C:180:ALA:N	2.00	0.76
1:A:1263:C:H2'	1:A:1264:C:C6	2.20	0.76
1:A:989:C:H42	1:A:1216:G:H1	1.30	0.75
7:G:15:ASP:O	7:G:19:GLY:HA2	1.84	0.75
1:A:196:A:H2'	1:A:197:A:H5''	1.68	0.75
1:A:522:C:H41	12:L:53:ARG:HH22	1.32	0.75
4:D:79:PHE:HE1	4:D:204:ILE:HD13	1.52	0.75
1:A:1216:G:H5''	14:N:5:ALA:CB	2.16	0.75
4:D:3:ARG:NH2	4:D:70:ILE:HG13	2.02	0.75
8:H:51:VAL:HG11	8:H:60:ARG:HB2	1.67	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:80:ILE:N	8:H:80:ILE:HD12	2.01	0.75
1:A:385:C:H2'	1:A:386:C:H6	1.49	0.75
13:M:52:GLU:HG2	13:M:55:ARG:HH21	1.52	0.75
16:P:4:ILE:HG13	16:P:64:ALA:HB1	1.67	0.75
5:E:79:GLU:HG3	5:E:93:PRO:HD2	1.66	0.75
12:L:5:PRO:HG2	12:L:10:LEU:HD11	1.67	0.75
6:F:28:ARG:HB2	6:F:28:ARG:NH1	1.98	0.75
20:T:53:LEU:HD11	20:T:104:LEU:HD12	1.68	0.75
19:S:20:LEU:HA	19:S:23:ASN:HD22	1.50	0.75
1:A:1038:C:H2'	1:A:1039:C:H6	1.50	0.74
1:A:1142:G:H2'	1:A:1143:G:O4'	1.87	0.74
2:B:59:GLU:HB2	2:B:221:LEU:HD11	1.68	0.74
3:C:102:ASN:N	3:C:102:ASN:HD22	1.85	0.74
15:O:87:ILE:HG22	15:O:88:ARG:N	2.02	0.74
2:B:95:GLN:HE21	2:B:147:LYS:HG3	1.51	0.74
5:E:101:ILE:HD12	5:E:101:ILE:H	1.52	0.74
8:H:1:MET:HG2	8:H:2:LEU:H	1.52	0.74
3:C:64:VAL:CB	3:C:99:VAL:HG21	2.17	0.74
5:E:150:ARG:HH11	5:E:150:ARG:HB3	1.53	0.74
3:C:14:ILE:HG22	3:C:15:THR:N	2.02	0.74
1:A:1157:A:H4'	1:A:1158:C:O5'	1.86	0.74
5:E:81:GLU:HG3	5:E:90:VAL:HG22	1.68	0.74
23:Z:30:G:C2'	23:Z:31:A:H8	2.01	0.74
1:A:998:G:C3'	1:A:999:C:H5''	2.18	0.74
1:A:1250:A:H4'	9:I:68:GLY:N	2.02	0.74
1:A:1281:U:H5'	1:A:1282:C:H5	1.53	0.74
19:S:63:THR:HB	19:S:65:ASN:ND2	2.01	0.74
9:I:102:LEU:HD12	9:I:102:LEU:N	2.01	0.74
23:Z:34:G:H2'	23:Z:35:A:H8	1.50	0.74
2:B:111:ARG:HB3	2:B:149:LEU:HD11	1.69	0.74
14:N:12:ARG:O	14:N:14:PRO:HD3	1.87	0.74
10:J:8:LEU:HB3	10:J:16:LEU:HD22	1.69	0.74
1:A:720:C:H3'	1:A:721:G:H5''	1.68	0.73
1:A:1276:G:H2'	1:A:1277:C:H5''	1.70	0.73
1:A:1369:C:H2'	1:A:1370:G:C8	2.23	0.73
9:I:42:ARG:HH21	9:I:71:SER:HB2	1.52	0.73
17:Q:101:ARG:HA	17:Q:101:ARG:HE	1.52	0.73
1:A:1161:C:H2'	1:A:1162:C:C6	2.24	0.73
2:B:124:SER:O	2:B:127:ILE:HG13	1.87	0.73
5:E:69:VAL:HG21	5:E:113:ALA:HB1	1.70	0.73
11:K:124:LYS:HD3	11:K:125:PHE:HE1	1.53	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:Z:39:U:H2'	23:Z:40:C:C6	2.23	0.73
1:A:954:G:H2'	1:A:955:U:H6	1.54	0.73
4:D:50:ARG:HB3	4:D:50:ARG:HH11	1.52	0.73
5:E:101:ILE:CD1	5:E:119:LEU:HD23	2.16	0.73
6:F:48:LEU:HG	6:F:57:GLN:HA	1.70	0.73
1:A:984:C:H2'	1:A:985:C:C6	2.23	0.73
1:A:1132:C:H2'	1:A:1133:G:H8	1.53	0.73
3:C:42:LEU:O	3:C:42:LEU:HD23	1.88	0.73
3:C:180:ALA:O	3:C:181:ASN:HB3	1.87	0.73
11:K:23:ALA:HB1	11:K:88:GLY:HA3	1.71	0.73
3:C:64:VAL:HB	3:C:99:VAL:CG2	2.17	0.73
1:A:996:A:C3'	1:A:997:U:H5''	2.19	0.73
1:A:21:G:H2'	1:A:22:G:C8	2.23	0.73
2:B:118:LEU:HD12	2:B:142:LEU:HD21	1.69	0.73
10:J:37:PRO:HA	10:J:72:VAL:HG22	1.69	0.73
10:J:49:VAL:O	10:J:60:ARG:HA	1.88	0.73
17:Q:67:LYS:HA	17:Q:70:ARG:HH12	1.54	0.73
19:S:22:LEU:HD13	19:S:28:LYS:HG2	1.71	0.73
1:A:342:C:H3'	1:A:343:U:H5''	1.71	0.73
2:B:78:GLN:NE2	2:B:96:ARG:HH12	1.86	0.73
13:M:108:ARG:NH1	13:M:114:ARG:HG2	2.03	0.73
1:A:477:A:C2'	1:A:479:C:H5''	2.19	0.72
1:A:676:A:H1'	11:K:115:PRO:HB3	1.71	0.72
1:A:1157:A:H5'	1:A:1158:C:C5	2.23	0.72
26:A:3001:AM2:HA93	26:A:3001:AM2:HB5	1.69	0.72
2:B:69:LEU:HD23	2:B:70:PHE:N	2.04	0.72
3:C:34:LEU:O	3:C:38:ARG:HG3	1.89	0.72
1:A:428:G:H1'	1:A:430:A:C8	2.23	0.72
1:A:1133:G:H2'	1:A:1134:G:H8	1.54	0.72
1:A:1420:C:H42	1:A:1480:G:H1	1.37	0.72
2:B:217:ARG:HA	2:B:220:ASP:OD2	1.87	0.72
9:I:6:GLY:HA3	9:I:83:ARG:HB2	1.71	0.72
15:O:6:GLU:H	15:O:6:GLU:CD	1.94	0.72
18:R:46:GLU:H	18:R:46:GLU:CD	1.96	0.72
19:S:63:THR:HG22	19:S:64:GLU:N	2.04	0.72
1:A:718:G:H5'	11:K:117:ASN:HD22	1.53	0.72
4:D:3:ARG:HH21	4:D:74:GLN:CG	2.00	0.72
3:C:91:LEU:HD21	3:C:99:VAL:H	1.54	0.72
1:A:38:G:N2	1:A:397:A:H5'	2.04	0.72
1:A:1264:C:H2'	1:A:1265:G:C8	2.25	0.72
2:B:91:PRO:HG2	2:B:155:LEU:HG	1.70	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:30:LEU:HB3	6:F:35:ALA:CB	2.13	0.72
1:A:1151:A:HO2'	1:A:1152:A:H8	1.35	0.72
1:A:576:G:H3'	1:A:577:G:C5'	2.20	0.72
2:B:69:LEU:HD12	2:B:155:LEU:HD11	1.71	0.72
2:B:101:MET:HA	2:B:108:ILE:HG21	1.72	0.72
12:L:41:ARG:HG3	12:L:42:THR:N	2.01	0.72
14:N:23:ARG:NH1	14:N:30:ALA:HB2	2.04	0.72
1:A:1417:G:OP2	26:A:3005:AM2:NC6	2.22	0.72
2:B:68:ILE:HG13	2:B:161:ALA:HB3	1.72	0.72
12:L:28:LYS:C	12:L:30:ALA:H	1.98	0.72
18:R:26:LEU:HD13	18:R:27:GLY:H	1.54	0.72
2:B:80:ILE:HG21	2:B:211:ILE:HG22	1.70	0.71
20:T:49:ALA:O	20:T:53:LEU:HD23	1.90	0.71
1:A:1113:C:O2'	1:A:1114:C:H5''	1.90	0.71
1:A:1256:A:O3'	1:A:1257:U:H4'	1.90	0.71
1:A:1399:C:H4'	1:A:1400:C:H5''	1.71	0.71
8:H:103:VAL:HG21	8:H:109:ILE:O	1.91	0.71
15:O:18:PHE:HB2	15:O:19:PRO:HD2	1.72	0.71
1:A:1262:C:H2'	1:A:1263:C:C6	2.26	0.71
4:D:24:GLU:O	4:D:25:ARG:HB3	1.91	0.71
11:K:95:ILE:HD12	11:K:95:ILE:H	1.55	0.71
19:S:39:THR:CG2	19:S:40:ILE:H	1.94	0.71
20:T:73:HIS:C	20:T:74:LYS:HG2	2.15	0.71
4:D:110:PHE:HD1	4:D:110:PHE:H	1.37	0.71
16:P:76:GLN:O	16:P:76:GLN:HG2	1.90	0.71
1:A:269:C:H2'	1:A:270:A:H8	1.56	0.71
1:A:329:A:C8	1:A:332:G:C6	2.77	0.71
12:L:93:LEU:HD23	12:L:93:LEU:H	1.55	0.71
3:C:19:GLU:HG2	3:C:54:ARG:NH1	2.04	0.71
15:O:27:VAL:HG12	15:O:31:LEU:HD22	1.73	0.71
1:A:479:C:H6	1:A:479:C:C5'	2.01	0.71
2:B:132:LYS:HA	2:B:135:GLN:HB2	1.72	0.71
7:G:50:ILE:HG21	7:G:58:PRO:HA	1.72	0.71
10:J:5:ARG:O	10:J:98:ILE:HA	1.90	0.71
26:A:3005:AM2:HC61	26:A:3005:AM2:HA21	1.39	0.71
3:C:23:TYR:CD1	3:C:24:ALA:N	2.58	0.71
8:H:79:VAL:HB	8:H:80:ILE:HD12	1.73	0.71
11:K:78:GLN:O	11:K:103:LEU:HD23	1.90	0.71
1:A:376:G:H2'	1:A:377:G:H8	1.56	0.71
3:C:55:VAL:O	3:C:55:VAL:HG12	1.90	0.71
2:B:115:LEU:HD12	2:B:145:LEU:HD22	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:46:LYS:HG3	8:H:64:LYS:HB2	1.72	0.70
8:H:64:LYS:HG2	8:H:79:VAL:HG21	1.72	0.70
9:I:48:GLU:N	9:I:49:PRO:HD2	2.05	0.70
1:A:180:U:C2'	1:A:181:G:H5'	2.21	0.70
1:A:692:U:OP1	11:K:124:LYS:HE2	1.90	0.70
8:H:51:VAL:CG1	8:H:60:ARG:HB2	2.20	0.70
14:N:40:CYS:O	14:N:44:LEU:HB3	1.92	0.70
1:A:1297:C:O2	1:A:1297:C:H2'	1.89	0.70
3:C:43:LEU:HD21	3:C:68:VAL:HG21	1.73	0.70
10:J:62:HIS:HB3	14:N:59:ALA:HB3	1.73	0.70
13:M:10:PRO:HB2	13:M:18:ALA:HB1	1.72	0.70
12:L:24:VAL:O	12:L:24:VAL:HG12	1.91	0.70
1:A:329:A:C6	1:A:332:G:C2	2.79	0.70
1:A:840:C:H4'	1:A:841:U:H5	1.56	0.70
1:A:1264:C:H2'	1:A:1265:G:H8	1.57	0.70
14:N:26:ARG:HH12	14:N:47:LEU:CD2	1.99	0.70
1:A:421:U:H5'	1:A:422:C:OP2	1.92	0.70
1:A:1114:C:O2	1:A:1115:C:C6	2.45	0.70
4:D:155:LEU:HB3	4:D:158:ILE:HD13	1.73	0.70
2:B:97:TRP:HZ2	2:B:102:LEU:HD13	1.57	0.70
13:M:40:ASN:HD22	13:M:41:PRO:CD	2.05	0.70
1:A:1010:G:H2'	1:A:1011:G:H8	1.56	0.70
4:D:62:GLN:HE21	4:D:62:GLN:CA	1.97	0.70
6:F:50:TYR:CE1	18:R:77:GLY:HA2	2.27	0.70
9:I:127:LYS:HB2	13:M:126:LYS:HZ2	1.54	0.70
3:C:58:GLU:HB3	10:J:92:THR:HG21	1.73	0.69
3:C:129:ALA:HB3	3:C:132:ARG:NH1	2.06	0.69
4:D:63:LYS:HD2	4:D:198:VAL:HG22	1.74	0.69
12:L:83:VAL:CG2	12:L:100:ILE:HG23	2.21	0.69
19:S:77:THR:HG22	19:S:78:ARG:N	2.05	0.69
1:A:866:C:H2'	1:A:867:G:H5'	1.74	0.69
15:O:81:LEU:HD22	15:O:85:LEU:HD12	1.74	0.69
1:A:1196:U:H4'	1:A:1197:G:H5''	1.75	0.69
19:S:15:LEU:HA	19:S:18:LYS:HB2	1.72	0.69
2:B:116:GLU:HG2	2:B:153:ARG:HH12	1.55	0.69
1:A:586:C:C2'	1:A:587:G:H5''	2.22	0.69
1:A:1356:G:H2'	1:A:1357:A:C8	2.28	0.69
1:A:1532:U:H2'	1:A:1533:C:C6	2.27	0.69
10:J:38:ILE:HG13	10:J:71:LEU:HB3	1.73	0.69
2:B:90:MET:HE2	2:B:90:MET:HA	1.75	0.69
5:E:102:ALA:HB2	5:E:120:THR:HB	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:34:ASP:O	11:K:36:ASP:N	2.26	0.69
21:V:6:ARG:CZ	21:V:15:ARG:HH12	2.04	0.69
1:A:479:C:H5'	1:A:479:C:C6	2.27	0.69
7:G:52:GLU:O	7:G:54:THR:N	2.26	0.69
10:J:27:ALA:HB1	10:J:74:ILE:HD13	1.73	0.69
11:K:14:VAL:HG21	11:K:40:ILE:HD13	1.74	0.69
12:L:38:THR:HG22	12:L:39:VAL:HG23	1.75	0.69
16:P:34:GLU:OE2	16:P:55:ARG:HD3	1.91	0.69
1:A:371:G:O2'	1:A:372:C:H5'	1.92	0.69
1:A:1129:C:HO2'	1:A:1131:G:H5''	1.55	0.69
15:O:5:LYS:H	15:O:5:LYS:HD2	1.57	0.69
2:B:178:ARG:HB3	2:B:178:ARG:HH11	1.58	0.69
5:E:150:ARG:HH11	5:E:150:ARG:CG	2.05	0.69
8:H:113:SER:HB2	8:H:134:ILE:HD11	1.75	0.69
9:I:47:LEU:C	9:I:49:PRO:HD2	2.18	0.69
13:M:15:VAL:HG21	13:M:48:LEU:HD21	1.74	0.69
1:A:448:A:OP2	1:A:485:G:N2	2.27	0.68
1:A:1190:G:OP1	3:C:4:LYS:HA	1.93	0.68
9:I:9:ARG:CG	9:I:14:VAL:HG12	2.22	0.68
17:Q:33:GLY:O	17:Q:34:LYS:C	2.34	0.68
1:A:8:A:N6	4:D:209:ARG:HA	2.09	0.68
1:A:613:C:O2'	1:A:614:A:H5'	1.92	0.68
1:A:1347:G:N2	1:A:1373:G:H2'	2.09	0.68
1:A:229:U:H5''	16:P:33:ILE:HD13	1.75	0.68
1:A:576:G:H3'	1:A:577:G:H5'	1.74	0.68
1:A:1125:U:H3	10:J:5:ARG:HH21	1.40	0.68
1:A:1330:U:H2'	1:A:1331:G:H5'	1.74	0.68
1:A:1473:A:C2'	1:A:1474:G:H5''	2.23	0.68
11:K:14:VAL:HG21	11:K:40:ILE:CD1	2.22	0.68
17:Q:7:THR:O	17:Q:23:VAL:HG13	1.94	0.68
4:D:128:VAL:HG12	4:D:129:ASN:ND2	2.09	0.68
8:H:3:THR:HG23	8:H:4:ASP:H	1.59	0.68
19:S:30:LEU:HD11	19:S:50:ALA:HB2	1.76	0.68
2:B:7:VAL:HG21	2:B:220:ASP:HB2	1.76	0.68
5:E:81:GLU:CD	5:E:88:LYS:HE2	2.19	0.68
13:M:19:LEU:O	13:M:22:ILE:HG13	1.94	0.68
1:A:1113:C:O2'	1:A:1114:C:H5'	1.92	0.68
1:A:1022:G:H2'	1:A:1023:G:C8	2.28	0.68
14:N:14:PRO:O	14:N:15:LYS:HB2	1.93	0.68
20:T:96:GLY:O	20:T:97:ALA:HB3	1.95	0.68
1:A:1103:C:C2'	1:A:1104:G:H5''	2.25	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:134:ILE:HG23	3:C:151:VAL:HB	1.76	0.67
1:A:981:U:H3'	1:A:982:U:H5''	1.74	0.67
1:A:1491:G:H5''	12:L:46:LYS:HG3	1.76	0.67
3:C:118:GLN:O	3:C:122:GLU:HB2	1.93	0.67
20:T:85:MET:HE2	20:T:103:GLY:O	1.94	0.67
13:M:40:ASN:HD22	13:M:41:PRO:HD2	1.58	0.67
1:A:1039:C:H2'	1:A:1040:U:C6	2.29	0.67
1:A:1281:U:H5'	1:A:1282:C:C5	2.29	0.67
3:C:58:GLU:HB2	3:C:65:ALA:HB2	1.76	0.67
4:D:4:TYR:O	4:D:5:ILE:HB	1.94	0.67
13:M:117:VAL:HG12	13:M:118:ALA:N	2.09	0.67
16:P:6:LEU:HB3	16:P:17:TYR:CD2	2.29	0.67
1:A:291:C:O2'	1:A:292:G:H5'	1.95	0.67
1:A:1041:A:H2'	1:A:1042:G:H8	1.59	0.67
3:C:53:ALA:O	3:C:54:ARG:HB2	1.94	0.67
10:J:5:ARG:HA	10:J:73:ASP:OD1	1.94	0.67
20:T:14:LYS:O	20:T:18:GLN:HG3	1.94	0.67
4:D:189:PRO:HB2	4:D:194:LEU:HD21	1.76	0.67
8:H:85:ARG:HD3	8:H:86:ILE:N	2.09	0.67
1:A:369:C:O2	1:A:369:C:H2'	1.93	0.67
2:B:87:ARG:NH1	2:B:233:SER:HB3	2.09	0.67
2:B:95:GLN:C	2:B:96:ARG:HD2	2.20	0.67
3:C:8:ILE:HG23	3:C:16:ARG:HG2	1.76	0.67
3:C:59:ARG:NH1	3:C:97:LYS:HE2	2.10	0.67
4:D:187:ARG:NE	4:D:188:LEU:N	2.37	0.67
8:H:45:ILE:HD12	8:H:61:VAL:HG13	1.75	0.67
12:L:28:LYS:C	12:L:30:ALA:N	2.52	0.67
18:R:17:SER:HA	18:R:19:LYS:NZ	2.10	0.67
1:A:839:U:O2	1:A:839:U:H2'	1.94	0.67
13:M:49:THR:HG22	13:M:51:ALA:H	1.59	0.67
1:A:1210:C:C3'	1:A:1211:U:H5''	2.26	0.66
3:C:107:GLN:H	3:C:107:GLN:CD	2.01	0.66
19:S:3:ARG:HG2	19:S:3:ARG:HH11	1.59	0.66
19:S:12:ASP:H	19:S:38:SER:HB3	1.60	0.66
1:A:342:C:C3'	1:A:343:U:H5''	2.24	0.66
3:C:64:VAL:HG12	3:C:66:VAL:HG23	1.76	0.66
4:D:150:GLU:HA	4:D:153:ARG:HH21	1.59	0.66
13:M:81:LEU:O	13:M:86:CYS:HB3	1.95	0.66
23:Z:39:U:O2'	23:Z:40:C:H5'	1.95	0.66
1:A:1003:G:H2'	1:A:1003:G:N3	2.10	0.66
1:A:1040:U:H2'	1:A:1041:A:C8	2.29	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:47:LEU:H	3:C:47:LEU:HD12	1.60	0.66
7:G:144:MET:HA	7:G:144:MET:HE2	1.76	0.66
21:V:5:ASP:O	21:V:11:GLY:HA3	1.96	0.66
4:D:209:ARG:HG2	4:D:209:ARG:HH11	1.59	0.66
13:M:54:VAL:O	13:M:58:GLU:HG2	1.96	0.66
1:A:664:G:H22	1:A:741:G:H1	1.42	0.66
1:A:997:U:H3'	1:A:998:G:H5''	1.75	0.66
1:A:1009:G:O2'	1:A:1010:G:H5'	1.96	0.66
18:R:55:ARG:HH11	18:R:55:ARG:CB	2.08	0.66
20:T:10:LEU:H	20:T:13:LEU:HD11	1.60	0.66
1:A:389:A:H2'	1:A:390:C:H5'	1.77	0.66
1:A:628:G:H2'	1:A:629:G:C8	2.30	0.66
1:A:1051:C:H2'	1:A:1052:U:H6	1.61	0.66
2:B:9:GLU:CD	2:B:10:LEU:H	2.03	0.66
2:B:82:ARG:HA	2:B:92:TYR:HE2	1.57	0.66
6:F:50:TYR:HE1	18:R:77:GLY:HA2	1.61	0.66
8:H:13:ILE:O	8:H:17:THR:HG23	1.95	0.66
10:J:42:THR:HG23	10:J:67:THR:O	1.96	0.66
1:A:1310:G:O2'	1:A:1311:G:O5'	2.13	0.66
1:A:1366:C:H2'	1:A:1367:C:H6	1.61	0.66
2:B:142:LEU:HB3	2:B:146:GLN:OE1	1.95	0.66
8:H:86:ILE:HG22	8:H:87:SER:N	2.09	0.66
10:J:31:GLY:HA2	10:J:78:ASN:ND2	2.10	0.66
1:A:1255:G:H3'	1:A:1279:A:H61	1.59	0.66
2:B:67:THR:HA	2:B:90:MET:HE1	1.77	0.66
3:C:107:GLN:O	3:C:108:ASN:HB2	1.95	0.66
4:D:170:VAL:HG22	4:D:171:GLY:N	2.09	0.66
8:H:84:ARG:HH11	8:H:84:ARG:HG3	1.61	0.66
1:A:192:U:H2'	1:A:193:C:H6	1.59	0.66
1:A:343:U:H5'	1:A:343:U:H6	1.61	0.66
14:N:25:VAL:HG12	14:N:39:LEU:HD23	1.75	0.66
15:O:87:ILE:HG22	15:O:88:ARG:H	1.59	0.66
1:A:1039:C:H2'	1:A:1040:U:H6	1.60	0.65
2:B:115:LEU:HD23	2:B:153:ARG:HH21	1.61	0.65
7:G:85:TYR:HD2	7:G:154:TYR:HE2	1.44	0.65
21:V:2:GLY:C	21:V:4:GLY:H	2.03	0.65
1:A:329:A:N7	1:A:332:G:O6	2.26	0.65
1:A:1201:A:H4'	1:A:1202:G:O5'	1.95	0.65
2:B:15:VAL:HG12	2:B:16:HIS:H	1.60	0.65
2:B:24:TRP:HA	2:B:190:THR:HG22	1.77	0.65
6:F:48:LEU:HD13	6:F:52:ILE:HD12	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:51:LEU:HD22	2:B:55:PHE:HE1	1.62	0.65
3:C:43:LEU:CD2	3:C:47:LEU:HD22	2.26	0.65
19:S:4:SER:C	19:S:5:LEU:HD12	2.22	0.65
18:R:36:ASN:OD1	18:R:39:VAL:HG12	1.95	0.65
23:Z:28:G:H2'	23:Z:29:G:C5	2.31	0.65
1:A:1435:G:H2'	1:A:1436:U:C6	2.31	0.65
14:N:29:ARG:HG2	14:N:29:ARG:HH11	1.60	0.65
1:A:196:A:C2'	1:A:197:A:H5''	2.25	0.65
3:C:19:GLU:HB3	3:C:40:ARG:HH22	1.62	0.65
1:A:1123:A:H4'	10:J:37:PRO:HD2	1.79	0.65
9:I:66:ARG:HB3	9:I:66:ARG:NH1	2.11	0.65
10:J:50:ILE:HD12	10:J:50:ILE:N	2.11	0.65
1:A:165:C:H2'	1:A:166:G:H8	1.60	0.65
2:B:132:LYS:O	2:B:136:VAL:HG23	1.96	0.65
5:E:57:LYS:HG2	5:E:61:TYR:CE2	2.32	0.65
7:G:52:GLU:C	7:G:54:THR:H	2.04	0.65
17:Q:68:ARG:O	17:Q:69:LYS:HB2	1.95	0.65
1:A:269:C:H2'	1:A:270:A:C8	2.31	0.65
2:B:131:PRO:HB2	2:B:133:LYS:HB3	1.78	0.65
10:J:94:VAL:CG1	10:J:95:GLU:H	2.09	0.65
1:A:1193:G:O2'	1:A:1194:U:H5'	1.96	0.64
1:A:1292:U:P	7:G:41:ARG:HH22	2.21	0.64
2:B:102:LEU:N	2:B:102:LEU:HD12	2.12	0.64
3:C:134:ILE:O	3:C:138:VAL:HG23	1.97	0.64
7:G:54:THR:CG2	7:G:56:GLN:H	2.10	0.64
9:I:118:LYS:O	9:I:119:ALA:HB3	1.96	0.64
11:K:72:ALA:HB1	11:K:77:MET:HG3	1.79	0.64
12:L:25:PRO:C	12:L:27:LEU:H	2.05	0.64
1:A:1053:G:C3'	1:A:1054:C:H5'	2.27	0.64
1:A:1114:C:C2	1:A:1115:C:C5	2.85	0.64
6:F:40:VAL:HG22	6:F:41:GLU:N	2.12	0.64
7:G:153:HIS:C	7:G:155:ARG:H	2.04	0.64
16:P:63:GLY:O	16:P:64:ALA:C	2.39	0.64
2:B:7:VAL:N	2:B:221:LEU:HD23	2.12	0.64
2:B:167:PRO:HD3	2:B:188:ALA:HB2	1.79	0.64
16:P:11:SER:OG	16:P:14:ASN:HB3	1.98	0.64
1:A:9:G:H5''	5:E:122:GLU:OE1	1.96	0.64
1:A:946:A:H2'	1:A:947:G:C8	2.33	0.64
1:A:1001:A:O2'	1:A:1001(A):G:H5'	1.97	0.64
1:A:1014:A:C2	1:A:1219:U:H1'	2.33	0.64
1:A:1154:G:H2'	1:A:1155:G:H8	1.62	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:95:GLN:HE21	2:B:147:LYS:CG	2.10	0.64
3:C:110:ASN:HD21	3:C:140:ARG:HB3	1.59	0.64
4:D:150:GLU:HG2	4:D:153:ARG:HH21	1.61	0.64
5:E:122:GLU:CD	5:E:131:ILE:HD13	2.22	0.64
7:G:92:SER:O	7:G:96:GLN:HG3	1.97	0.64
9:I:111:ARG:HG2	9:I:112:LYS:N	2.12	0.64
12:L:41:ARG:HG2	12:L:41:ARG:HH11	1.62	0.64
17:Q:48:GLU:O	17:Q:49:GLU:C	2.40	0.64
1:A:537:G:OP1	12:L:113:ARG:NH2	2.31	0.64
1:A:1158:C:C5	1:A:1160:G:C8	2.85	0.64
1:A:1251:A:H4'	9:I:12:GLU:OE2	1.97	0.64
1:A:1533:C:O5'	1:A:1533:C:H6	1.81	0.64
16:P:43:LYS:HA	16:P:48:TRP:HB3	1.78	0.64
20:T:90:GLN:HA	20:T:93:GLU:HG2	1.79	0.64
1:A:840:C:H4'	1:A:841:U:C5	2.32	0.64
1:A:1048:G:H5'	1:A:1048:G:C8	2.29	0.64
3:C:47:LEU:HD23	3:C:68:VAL:HG11	1.78	0.64
4:D:8:VAL:C	4:D:10:ARG:H	2.05	0.64
11:K:69:ALA:O	11:K:73:MET:HG2	1.97	0.64
12:L:24:VAL:HG13	12:L:98:TYR:HE2	1.61	0.64
20:T:57:ARG:HH22	20:T:100:ILE:HG21	1.62	0.64
20:T:93:GLU:OE1	20:T:93:GLU:HA	1.97	0.64
23:Z:39:U:C3'	23:Z:40:C:H5'	2.27	0.64
1:A:272:C:O2'	1:A:273:A:H5'	1.97	0.64
1:A:1152:A:OP1	10:J:68:HIS:ND1	2.31	0.64
1:A:1168:A:H2'	1:A:1169:A:O4'	1.97	0.64
1:A:1314:C:C6	19:S:6:LYS:HE2	2.33	0.64
2:B:167:PRO:CD	2:B:188:ALA:HB2	2.28	0.64
6:F:10:LEU:CD1	6:F:59:TYR:HB3	2.28	0.64
9:I:79:LEU:O	9:I:83:ARG:HG3	1.98	0.64
19:S:13:ASP:HA	19:S:16:LEU:HB3	1.80	0.64
1:A:501:C:H2'	1:A:502:G:H8	1.62	0.64
1:A:1209:C:O2	1:A:1209:C:H2'	1.98	0.64
3:C:39:ILE:O	3:C:43:LEU:HB2	1.98	0.64
8:H:119:LEU:HD12	8:H:124:ALA:CA	2.28	0.64
8:H:119:LEU:HD12	8:H:124:ALA:HB2	1.78	0.64
12:L:110:VAL:CG2	12:L:113:ARG:HG3	2.28	0.64
20:T:102:GLY:O	20:T:104:LEU:N	2.30	0.64
1:A:155:C:C3'	1:A:156:G:H5''	2.28	0.63
1:A:1157:A:H5'	1:A:1158:C:C2	2.33	0.63
2:B:181:PHE:HD2	8:H:70:GLN:HB3	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:139:GLN:HA	3:C:139:GLN:NE2	2.12	0.63
11:K:26:ASN:O	11:K:27:ASN:HB2	1.98	0.63
1:A:587:G:H5'	1:A:587:G:H8	1.63	0.63
6:F:87:ARG:HH11	6:F:87:ARG:HG3	1.63	0.63
10:J:8:LEU:HD21	10:J:96:ILE:HG12	1.79	0.63
12:L:6:THR:O	12:L:10:LEU:HD12	1.98	0.63
1:A:489:C:H2'	1:A:490:G:H8	1.63	0.63
1:A:1222:G:OP1	19:S:77:THR:HG21	1.99	0.63
2:B:87:ARG:CZ	2:B:233:SER:HB3	2.28	0.63
3:C:123:GLN:HE22	3:C:140:ARG:HH22	1.47	0.63
7:G:148:ASN:C	7:G:150:ALA:H	2.04	0.63
8:H:31:PHE:O	8:H:35:ILE:HG12	1.98	0.63
1:A:189:G:H1	1:A:189(K):U:H3	1.44	0.63
10:J:51:ARG:HB3	10:J:59:SER:HB3	1.81	0.63
11:K:101:SER:C	11:K:103:LEU:H	2.06	0.63
14:N:32:SER:O	14:N:33:VAL:C	2.41	0.63
1:A:444:C:H2'	1:A:445:G:H8	1.63	0.63
1:A:1360:A:O2'	1:A:1361:G:H5'	1.97	0.63
2:B:95:GLN:HG3	2:B:147:LYS:O	1.98	0.63
6:F:101:ALA:HB2	18:R:28:GLU:HA	1.80	0.63
17:Q:36:ILE:H	17:Q:36:ILE:HD13	1.62	0.63
2:B:66:GLY:HA2	2:B:160:ASP:OD2	1.98	0.63
4:D:108:LEU:HB3	4:D:110:PHE:HE1	1.64	0.63
7:G:54:THR:HG22	7:G:56:GLN:N	2.13	0.63
9:I:97:LYS:HA	9:I:102:LEU:CD1	2.29	0.63
14:N:24:CYS:HB3	14:N:28:GLY:H	1.64	0.63
15:O:10:LYS:HE2	15:O:10:LYS:O	1.98	0.63
1:A:580:U:H2'	1:A:581:G:O4'	1.98	0.63
2:B:82:ARG:O	2:B:86:GLU:HG3	1.99	0.63
5:E:48:ALA:HB1	5:E:49:PRO:HD2	1.80	0.63
1:A:1423:G:O2'	1:A:1424:C:H5'	1.98	0.63
3:C:110:ASN:O	3:C:111:LEU:HD23	1.99	0.63
13:M:105:THR:O	13:M:107:ALA:N	2.30	0.63
1:A:1095:U:H6	1:A:1095:U:H5'	1.63	0.63
1:A:1385:G:H2'	1:A:1386:G:H5''	1.81	0.63
2:B:97:TRP:HH2	2:B:176:GLU:OE2	1.79	0.63
4:D:158:ILE:H	4:D:158:ILE:CD1	2.11	0.63
6:F:67:MET:SD	6:F:72:VAL:HG22	2.39	0.63
9:I:126:SER:HB2	9:I:127:LYS:HD2	1.81	0.63
1:A:339:C:H2'	1:A:340:U:H6	1.62	0.62
1:A:539:A:H2'	1:A:540:G:C8	2.34	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:178:ARG:HH22	8:H:74:PRO:HB3	1.63	0.62
5:E:79:GLU:CD	5:E:79:GLU:H	2.06	0.62
18:R:53:ARG:C	18:R:55:ARG:H	2.07	0.62
19:S:60:VAL:HG21	19:S:74:PHE:HB3	1.80	0.62
1:A:262:A:H4'	20:T:75:ASN:HD22	1.64	0.62
1:A:476:G:H2'	1:A:477:A:H8	1.63	0.62
1:A:1222:G:P	19:S:77:THR:HG21	2.38	0.62
8:H:118:VAL:C	8:H:119:LEU:HD23	2.24	0.62
10:J:30:SER:HB3	10:J:80:LYS:C	2.24	0.62
13:M:81:LEU:HD22	13:M:88:ARG:NH2	2.12	0.62
1:A:983:A:H5'	14:N:3:ARG:NH1	2.13	0.62
2:B:167:PRO:O	2:B:171:ALA:N	2.32	0.62
8:H:38:ILE:HG21	8:H:111:ILE:HG12	1.80	0.62
8:H:107:LEU:HD23	8:H:107:LEU:N	2.14	0.62
19:S:6:LYS:HB3	19:S:7:LYS:HE3	1.80	0.62
1:A:1114:C:C2'	1:A:1115:C:O5'	2.47	0.62
1:A:1405:G:O2'	1:A:1406:U:H5'	2.00	0.62
11:K:124:LYS:HD3	11:K:125:PHE:CE1	2.34	0.62
1:A:59:A:H1'	1:A:354:G:N2	2.15	0.62
1:A:178:C:O2'	1:A:179:A:H5'	2.00	0.62
1:A:759:A:H61	17:Q:94:ASN:HD21	1.47	0.62
1:A:872:A:O2'	1:A:873:A:H3'	1.99	0.62
2:B:114:ARG:O	2:B:114:ARG:HD3	2.00	0.62
16:P:75:ARG:C	16:P:77:ALA:H	2.08	0.62
19:S:30:LEU:HD12	19:S:31:ILE:H	1.65	0.62
1:A:35:G:H2'	1:A:36:C:C6	2.35	0.62
1:A:486:U:H2'	1:A:487:A:H8	1.65	0.62
1:A:545:C:H5''	4:D:72:GLU:HG3	1.81	0.62
6:F:2:ARG:NE	6:F:69:GLU:HG2	2.14	0.62
6:F:10:LEU:H	6:F:10:LEU:HD12	1.63	0.62
6:F:22:GLU:O	6:F:26:ILE:HG12	1.99	0.62
6:F:30:LEU:CB	6:F:35:ALA:HB3	2.14	0.62
6:F:38:GLU:O	6:F:39:LYS:C	2.41	0.62
23:Z:39:U:H2'	23:Z:40:C:C5	2.34	0.62
1:A:254:G:O2'	1:A:255:G:H5'	1.98	0.62
1:A:439:A:N6	1:A:496:A:H1'	2.14	0.62
5:E:15:ARG:HD3	5:E:26:PHE:HD1	1.62	0.62
10:J:56:HIS:C	10:J:58:ASP:H	2.08	0.62
2:B:10:LEU:CD2	2:B:11:LEU:HG	2.30	0.62
12:L:24:VAL:HG13	12:L:98:TYR:CE2	2.35	0.62
13:M:3:ARG:HA	13:M:8:GLU:O	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:23:TYR:HB2	13:M:67:GLU:OE2	2.00	0.62
15:O:17:ARG:HG3	15:O:17:ARG:HH11	1.64	0.62
1:A:235:C:H1'	17:Q:61:GLU:OE2	1.99	0.62
1:A:620:C:N1	4:D:135:LEU:HD13	2.14	0.62
1:A:976:G:H5''	1:A:1358:U:O2'	2.00	0.62
1:A:1031:G:H2'	1:A:1032:G:C8	2.34	0.62
1:A:1201:A:O2'	1:A:1202:G:OP2	2.18	0.62
4:D:105:VAL:HG21	4:D:126:ILE:CD1	2.30	0.62
1:A:1162:C:O2'	1:A:1163:C:H5'	2.00	0.62
9:I:33:PHE:CE2	9:I:47:LEU:HD11	2.35	0.62
9:I:102:LEU:HD12	9:I:102:LEU:H	1.65	0.62
14:N:22:THR:OG1	14:N:33:VAL:HG21	1.99	0.62
1:A:620:C:H6	1:A:620:C:H5'	1.65	0.61
1:A:985:C:H2'	1:A:986:A:C8	2.35	0.61
1:A:1276:G:C2'	1:A:1277:C:H5''	2.30	0.61
1:A:1327:C:O2'	1:A:1328:C:H5'	2.00	0.61
2:B:59:GLU:O	2:B:62:ALA:HB3	2.00	0.61
4:D:25:ARG:HH12	4:D:30:LYS:HD2	1.64	0.61
6:F:30:LEU:N	6:F:30:LEU:HD23	2.14	0.61
11:K:92:GLU:HA	11:K:95:ILE:HD13	1.82	0.61
12:L:55:VAL:HG12	12:L:56:ALA:N	2.10	0.61
14:N:11:LYS:C	14:N:13:THR:H	2.06	0.61
1:A:6:G:N2	5:E:98:THR:HG23	2.15	0.61
1:A:750:G:H21	15:O:23:GLY:HA3	1.64	0.61
1:A:862:C:O2'	1:A:863:U:H5'	2.00	0.61
1:A:1208:C:H2'	1:A:1209:C:H6	1.64	0.61
4:D:199:ASN:HD21	4:D:201:GLN:CB	2.11	0.61
4:D:207:TYR:C	4:D:209:ARG:H	2.08	0.61
6:F:25:ILE:HG23	6:F:28:ARG:HD2	1.82	0.61
1:A:243:A:H4'	1:A:244:U:C5'	2.19	0.61
1:A:1114:C:H2'	1:A:1115:C:O5'	2.00	0.61
3:C:103:VAL:HG12	3:C:104:GLN:N	2.13	0.61
7:G:65:ALA:HB1	7:G:127:ALA:HB3	1.81	0.61
7:G:92:SER:HB2	7:G:93:PRO:HD2	1.82	0.61
1:A:1457:G:O2'	1:A:1458:G:H5'	2.00	0.61
2:B:91:PRO:HG3	2:B:154:LEU:CB	2.20	0.61
4:D:29:PRO:O	4:D:30:LYS:HG3	2.00	0.61
8:H:16:ALA:O	8:H:21:LYS:HG2	2.00	0.61
11:K:34:ASP:OD2	11:K:38:ASN:HB2	2.00	0.61
16:P:28:ARG:HG2	16:P:29:ASP:OD1	2.00	0.61
17:Q:59:ILE:HG23	17:Q:71:PHE:HB3	1.83	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:954:G:H21	1:A:1227:A:H62	1.48	0.61
1:A:1010:G:H2'	1:A:1011:G:C8	2.34	0.61
1:A:1301:U:O2	1:A:1301:U:H2'	2.00	0.61
1:A:1444:C:H2'	1:A:1445:C:H6	1.65	0.61
3:C:91:LEU:CD2	3:C:99:VAL:H	2.14	0.61
7:G:65:ALA:O	7:G:69:VAL:HG23	2.00	0.61
9:I:65:VAL:HG21	9:I:73:GLN:HB3	1.81	0.61
14:N:26:ARG:CG	14:N:27:CYS:H	2.12	0.61
16:P:43:LYS:HG3	16:P:48:TRP:CD2	2.35	0.61
20:T:50:GLU:CA	20:T:100:ILE:HD11	2.17	0.61
5:E:101:ILE:HD13	5:E:119:LEU:HA	1.83	0.61
9:I:4:TYR:CE1	9:I:88:TYR:HA	2.35	0.61
10:J:17:ASP:O	10:J:21:GLN:HB2	2.00	0.61
1:A:1510:U:H2'	1:A:1511:G:C8	2.35	0.61
2:B:137:ARG:NH1	2:B:137:ARG:HB2	2.15	0.61
3:C:103:VAL:HG12	3:C:104:GLN:H	1.66	0.61
7:G:32:ARG:O	7:G:33:ASP:HB2	1.99	0.61
7:G:76:ARG:HH11	7:G:76:ARG:HG3	1.65	0.61
10:J:78:ASN:HB2	10:J:81:THR:OG1	2.00	0.61
10:J:81:THR:O	10:J:83:GLU:N	2.34	0.61
1:A:1157:A:O4'	1:A:1158:C:N3	2.34	0.61
15:O:74:ASP:CB	15:O:77:ARG:HD3	2.31	0.61
17:Q:76:LEU:C	17:Q:76:LEU:HD23	2.26	0.61
20:T:56:MET:HG3	20:T:84:LEU:HD11	1.81	0.61
1:A:1152:A:O2'	1:A:1153:C:H5'	2.01	0.61
9:I:7:THR:H	9:I:83:ARG:HD3	1.66	0.61
12:L:117:ARG:HG3	12:L:122:THR:HB	1.82	0.61
1:A:1053:G:H4'	1:A:1054:C:H5'	1.82	0.60
1:A:1103:C:H2'	1:A:1104:G:C5'	2.31	0.60
1:A:1208:C:H2'	1:A:1209:C:C6	2.36	0.60
2:B:91:PRO:HA	2:B:154:LEU:HD12	1.83	0.60
15:O:33:THR:HG21	15:O:85:LEU:HD22	1.81	0.60
15:O:41:GLU:OE1	15:O:44:LYS:HE2	2.01	0.60
16:P:81:ARG:HH11	16:P:81:ARG:HB2	1.65	0.60
18:R:26:LEU:CD1	18:R:27:GLY:H	2.13	0.60
1:A:1030(C):G:H2'	1:A:1030(D):A:C8	2.36	0.60
1:A:1157:A:C6	1:A:1180:A:C6	2.89	0.60
1:A:1239:A:H62	1:A:1299:A:N6	1.99	0.60
12:L:93:LEU:HD23	12:L:93:LEU:N	2.15	0.60
1:A:180:U:H2'	1:A:181:G:H5'	1.82	0.60
1:A:386:C:C2'	1:A:387:U:H5'	2.31	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1096:C:O2'	1:A:1097:C:H5'	2.01	0.60
11:K:52:GLY:O	11:K:55:LYS:HG3	2.01	0.60
17:Q:34:LYS:HG3	17:Q:34:LYS:O	2.01	0.60
17:Q:68:ARG:O	17:Q:68:ARG:CG	2.49	0.60
1:A:1114:C:C2	1:A:1115:C:C6	2.89	0.60
1:A:510:A:H5'	1:A:511:C:OP2	2.02	0.60
1:A:1481:U:O2'	1:A:1482:G:H5'	2.01	0.60
4:D:61:LYS:HD2	4:D:61:LYS:C	2.25	0.60
8:H:80:ILE:HD12	8:H:80:ILE:H	1.65	0.60
23:Z:30:G:C2	23:Z:41:C:C5	2.90	0.60
1:A:411:A:H62	1:A:413:G:H21	1.49	0.60
3:C:91:LEU:HD23	3:C:92:ALA:N	2.16	0.60
9:I:97:LYS:HB3	9:I:98:PRO:HD3	1.82	0.60
10:J:94:VAL:CG1	10:J:95:GLU:N	2.65	0.60
1:A:900:A:H2'	1:A:901:A:C8	2.37	0.60
1:A:1157:A:C4'	1:A:1158:C:C2	2.85	0.60
1:A:1263:C:H2'	1:A:1264:C:H6	1.62	0.60
6:F:4:TYR:HE1	6:F:92:LYS:HG2	1.66	0.60
9:I:127:LYS:HD2	9:I:127:LYS:N	2.08	0.60
1:A:189(C):C:H2'	1:A:189(D):C:O4'	2.02	0.60
1:A:619:U:H2'	1:A:620:C:H5''	1.83	0.60
4:D:108:LEU:HB3	4:D:110:PHE:CE1	2.37	0.60
10:J:19:SER:OG	10:J:91:PRO:HG3	2.02	0.60
15:O:81:LEU:O	15:O:85:LEU:HB2	2.02	0.60
1:A:329:A:C5	1:A:332:G:N1	2.69	0.60
1:A:1114:C:N3	1:A:1115:C:C5	2.70	0.60
1:A:1442(A):G:O5'	1:A:1442(B):A:H5'	2.01	0.60
2:B:213:LEU:O	2:B:217:ARG:HG2	2.02	0.60
3:C:43:LEU:HD21	3:C:47:LEU:HD22	1.83	0.60
3:C:49:SER:O	3:C:72:LYS:HD3	2.01	0.60
5:E:59:GLY:O	5:E:62:ALA:HB3	2.02	0.60
1:A:1014:A:H2'	1:A:1015:A:C8	2.37	0.60
1:A:1133:G:H2'	1:A:1134:G:C8	2.35	0.60
1:A:1368:G:O2'	1:A:1369:C:H5'	2.01	0.60
3:C:60:ALA:O	3:C:61:ALA:CB	2.49	0.60
4:D:24:GLU:O	4:D:25:ARG:CB	2.50	0.60
13:M:88:ARG:CG	13:M:98:VAL:HG22	2.31	0.60
1:A:1016:A:H2'	1:A:1017:G:O4'	2.01	0.59
3:C:68:VAL:HG12	3:C:70:VAL:HG13	1.84	0.59
10:J:79:ARG:HH12	10:J:82:ILE:HD12	1.67	0.59
12:L:43:VAL:HG12	12:L:44:THR:N	2.16	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:87:ILE:O	15:O:88:ARG:HB2	2.01	0.59
1:A:192:U:H1'	20:T:103:GLY:HA2	1.84	0.59
1:A:1010:G:N2	1:A:1020:U:H1'	2.17	0.59
2:B:69:LEU:HB3	2:B:162:ILE:HD13	1.85	0.59
4:D:35:ARG:O	4:D:36:ARG:HG3	2.02	0.59
5:E:131:ILE:O	5:E:135:THR:HG23	2.02	0.59
7:G:155:ARG:O	7:G:156:TRP:CB	2.50	0.59
10:J:38:ILE:CG1	10:J:71:LEU:HB3	2.31	0.59
23:Z:36:A:H2'	23:Z:37:A:C8	2.37	0.59
1:A:309:G:O2'	1:A:310:G:H5'	2.02	0.59
2:B:25:ASN:HD22	2:B:25:ASN:C	2.09	0.59
2:B:117:GLU:O	2:B:121:LEU:HD13	2.01	0.59
2:B:206:ASP:O	2:B:207:ALA:HB3	2.02	0.59
3:C:46:GLU:C	3:C:48:TYR:H	2.11	0.59
3:C:64:VAL:HG23	3:C:99:VAL:HG11	1.84	0.59
3:C:87:LEU:C	3:C:89:GLU:H	2.08	0.59
3:C:179:ARG:CG	3:C:180:ALA:N	2.64	0.59
4:D:158:ILE:HD12	4:D:158:ILE:N	2.16	0.59
8:H:120:THR:HG23	8:H:123:GLU:OE2	2.03	0.59
11:K:126:ARG:HG3	11:K:127:LYS:H	1.67	0.59
19:S:5:LEU:O	19:S:6:LYS:HG3	2.03	0.59
20:T:45:GLN:HA	20:T:91:LEU:HD22	1.84	0.59
1:A:1181:G:H2'	1:A:1181:G:N3	2.17	0.59
1:A:1279:A:H5'	10:J:9:ARG:NH2	2.16	0.59
2:B:118:LEU:HD12	2:B:142:LEU:CD2	2.32	0.59
5:E:72:GLN:C	5:E:74:GLY:H	2.11	0.59
1:A:718:G:C5'	11:K:117:ASN:ND2	2.64	0.59
1:A:1041:A:H2'	1:A:1042:G:C8	2.38	0.59
1:A:1248:A:H5'	1:A:1248:A:H8	1.68	0.59
1:A:1391:U:H2'	1:A:1392:G:H8	1.67	0.59
3:C:58:GLU:H	3:C:65:ALA:HB3	1.67	0.59
3:C:157:ILE:HG21	3:C:164:ARG:NH2	2.12	0.59
3:C:158:GLY:O	3:C:160:ALA:N	2.36	0.59
7:G:62:PHE:HA	7:G:124:LEU:HD22	1.83	0.59
8:H:20:TYR:CE1	8:H:76:PRO:HG2	2.37	0.59
14:N:12:ARG:C	14:N:14:PRO:HD3	2.27	0.59
15:O:36:ILE:HG12	15:O:59:MET:HE2	1.84	0.59
16:P:26:ARG:HD3	16:P:31:LYS:O	2.02	0.59
17:Q:29:HIS:HB2	17:Q:36:ILE:HD12	1.84	0.59
1:A:1276:G:C3'	1:A:1277:C:H5''	2.32	0.59
1:A:1532:U:H2'	1:A:1533:C:C5	2.38	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:44:LEU:HA	2:B:47:THR:OG1	2.01	0.59
4:D:3:ARG:NE	4:D:71:SER:H	2.00	0.59
4:D:31:CYS:O	4:D:32:ALA:HB3	2.02	0.59
17:Q:26:GLN:O	17:Q:27:PHE:HB3	2.02	0.59
1:A:189(I):G:O2'	1:A:189(J):G:H5'	2.02	0.59
1:A:342:C:H3'	1:A:343:U:C5'	2.33	0.59
1:A:1182:G:H4'	1:A:1183:A:H5'	1.83	0.59
4:D:165:MET:O	4:D:166:LYS:C	2.45	0.59
12:L:15:ARG:HG3	12:L:15:ARG:HH11	1.66	0.59
1:A:376:G:OP1	16:P:67:THR:HG21	2.03	0.59
1:A:1320:C:N3	19:S:36:ARG:HD3	2.18	0.59
2:B:37:ASN:O	2:B:39:ILE:N	2.36	0.59
2:B:100:GLY:C	2:B:108:ILE:HG13	2.28	0.59
3:C:100:ALA:O	3:C:101:LEU:HB2	2.03	0.59
10:J:6:ILE:CD1	10:J:73:ASP:H	2.15	0.59
6:F:75:LEU:C	6:F:75:LEU:HD13	2.28	0.59
8:H:19:VAL:HB	8:H:21:LYS:HD3	1.84	0.59
12:L:83:VAL:HG21	12:L:100:ILE:CG2	2.32	0.59
1:A:134:A:H61	16:P:25:ARG:NH1	2.00	0.59
1:A:650:G:O2'	1:A:651:C:H5'	2.03	0.59
1:A:1442(A):G:C4'	1:A:1442(B):A:H5'	2.33	0.59
4:D:187:ARG:HE	4:D:187:ARG:HA	1.67	0.59
23:Z:38:A:C4	23:Z:39:U:H1'	2.38	0.59
1:A:522:C:H41	12:L:53:ARG:NH2	2.01	0.58
1:A:1195:C:H5'	1:A:1196:U:OP2	2.02	0.58
1:A:1305:G:H4'	21:V:4:GLY:O	2.02	0.58
1:A:1363(A):A:H1'	1:A:1365:G:N7	2.18	0.58
2:B:163:PHE:HD1	2:B:185:ILE:HB	1.68	0.58
3:C:47:LEU:H	3:C:47:LEU:CD1	2.16	0.58
5:E:79:GLU:HG2	5:E:92:LYS:HG2	1.85	0.58
10:J:6:ILE:HD11	10:J:73:ASP:N	2.16	0.58
10:J:81:THR:C	10:J:83:GLU:N	2.60	0.58
12:L:110:VAL:HG22	12:L:120:TYR:HB3	1.84	0.58
21:V:2:GLY:O	21:V:4:GLY:N	2.35	0.58
4:D:199:ASN:ND2	4:D:201:GLN:HB2	2.13	0.58
5:E:57:LYS:HG2	5:E:61:TYR:HE2	1.68	0.58
6:F:4:TYR:CE2	6:F:72:VAL:HG21	2.38	0.58
1:A:179:A:O2'	1:A:180:U:H5'	2.03	0.58
1:A:974:A:OP2	14:N:41:ARG:NH1	2.36	0.58
1:A:1360:A:H2'	1:A:1361:G:O4'	2.04	0.58
1:A:1493:A:H5''	1:A:1494:G:OP2	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:55:PHE:HA	2:B:58:ILE:HD11	1.85	0.58
2:B:61:LEU:HD13	2:B:64:ARG:NH1	2.18	0.58
3:C:91:LEU:HD21	3:C:99:VAL:N	2.18	0.58
8:H:3:THR:HG23	8:H:4:ASP:N	2.18	0.58
10:J:49:VAL:HG11	14:N:41:ARG:O	2.03	0.58
10:J:69:ASN:O	10:J:70:ARG:HD3	2.03	0.58
1:A:314:C:O2'	1:A:315:A:H5'	2.03	0.58
1:A:858:G:O2'	1:A:859:A:H5''	2.04	0.58
2:B:48:MET:HA	2:B:51:LEU:HD12	1.86	0.58
2:B:115:LEU:CD2	2:B:153:ARG:HH21	2.16	0.58
3:C:14:ILE:CG2	3:C:15:THR:H	2.10	0.58
4:D:3:ARG:CZ	4:D:70:ILE:HG13	2.33	0.58
5:E:13:ILE:HG13	5:E:13:ILE:O	2.02	0.58
10:J:28:ARG:HG2	10:J:28:ARG:HH11	1.68	0.58
14:N:34:TYR:O	14:N:36:PHE:N	2.36	0.58
1:A:820:U:H4'	1:A:821:G:OP2	2.03	0.58
2:B:178:ARG:HB3	2:B:178:ARG:NH1	2.19	0.58
3:C:84:ILE:O	3:C:84:ILE:HG12	2.02	0.58
5:E:41:VAL:HG13	5:E:113:ALA:HA	1.86	0.58
12:L:50:SER:O	12:L:51:ALA:HB2	2.01	0.58
14:N:9:LYS:C	14:N:11:LYS:H	2.12	0.58
3:C:46:GLU:O	3:C:48:TYR:N	2.37	0.58
3:C:83:ARG:C	3:C:85:ARG:N	2.60	0.58
7:G:71:PRO:HD3	7:G:103:TRP:HZ3	1.67	0.58
2:B:184:VAL:HG12	2:B:197:VAL:HG13	1.85	0.58
3:C:47:LEU:HD12	3:C:47:LEU:N	2.18	0.58
8:H:111:ILE:O	8:H:134:ILE:HB	2.03	0.58
12:L:40:VAL:O	12:L:40:VAL:HG12	2.03	0.58
15:O:78:TYR:OH	15:O:88:ARG:HD2	2.03	0.58
1:A:134:A:H61	16:P:25:ARG:HH12	1.51	0.58
4:D:105:VAL:CG2	4:D:126:ILE:HD13	2.32	0.58
9:I:114:TYR:CD1	9:I:114:TYR:N	2.68	0.58
11:K:48:ILE:HD12	11:K:63:LEU:HB3	1.86	0.58
11:K:54:ARG:HH11	11:K:54:ARG:CB	2.12	0.58
1:A:386:C:H2'	1:A:387:U:H5'	1.85	0.58
1:A:424:G:O2'	1:A:425:G:H5'	2.03	0.58
1:A:1053:G:C4'	1:A:1054:C:H5'	2.34	0.58
1:A:1406:U:C5	1:A:1407:C:C5	2.91	0.58
1:A:1442(A):G:H5'	1:A:1442(A):G:C8	2.38	0.58
4:D:146:ILE:N	4:D:146:ILE:HD12	2.18	0.58
10:J:90:LEU:H	10:J:91:PRO:HD2	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:444:C:H2'	1:A:445:G:C8	2.39	0.58
1:A:1311:G:N7	19:S:2:PRO:HA	2.18	0.58
1:A:1399:C:H4'	1:A:1400:C:C5'	2.34	0.58
1:A:1514:C:O2'	1:A:1515:C:H5'	2.03	0.58
2:B:223:ILE:HD13	2:B:226:ARG:HE	1.69	0.58
3:C:39:ILE:C	3:C:41:GLY:H	2.10	0.58
4:D:5:ILE:HG22	4:D:5:ILE:O	2.04	0.58
6:F:94:GLN:HE21	18:R:32:ARG:HD3	1.68	0.58
18:R:46:GLU:CD	18:R:46:GLU:N	2.62	0.58
19:S:19:VAL:HG13	19:S:20:LEU:N	2.19	0.58
1:A:1216:G:H5''	14:N:5:ALA:HB1	1.85	0.57
3:C:44:GLU:HG2	3:C:52:LEU:HD22	1.86	0.57
5:E:32:VAL:HG22	5:E:58:ALA:HB1	1.86	0.57
5:E:71:LEU:C	5:E:72:GLN:HG2	2.29	0.57
10:J:39:PRO:HB3	10:J:70:ARG:NH1	2.19	0.57
1:A:103:C:P	20:T:17:ARG:HH11	2.28	0.57
1:A:882:C:O2'	1:A:883:C:H5'	2.04	0.57
1:A:922:G:N3	1:A:1398:A:H2	2.02	0.57
2:B:83:MET:HE3	2:B:234:PRO:O	2.05	0.57
3:C:83:ARG:HA	3:C:86:VAL:CG2	2.28	0.57
6:F:4:TYR:CE1	6:F:92:LYS:HG2	2.39	0.57
10:J:38:ILE:HD11	10:J:71:LEU:HD12	1.85	0.57
11:K:108:ILE:O	11:K:109:VAL:HG23	2.03	0.57
12:L:113:ARG:NH2	12:L:120:TYR:HE2	2.02	0.57
18:R:53:ARG:HA	18:R:63:GLN:OE1	2.04	0.57
1:A:344:A:C3'	1:A:345:C:H5''	2.33	0.57
1:A:375:U:H4'	16:P:17:TYR:CE2	2.39	0.57
8:H:120:THR:OG1	8:H:123:GLU:HG3	2.04	0.57
13:M:107:ALA:O	13:M:111:LYS:HB2	2.04	0.57
18:R:62:GLU:C	18:R:64:ARG:H	2.11	0.57
1:A:21:G:H2'	1:A:22:G:H8	1.65	0.57
1:A:1230:C:H2'	1:A:1231:G:H8	1.69	0.57
2:B:21:ARG:HA	2:B:39:ILE:HA	1.87	0.57
7:G:113:GLU:O	7:G:119:ARG:HD3	2.04	0.57
10:J:36:GLY:O	10:J:72:VAL:HA	2.05	0.57
16:P:21:VAL:HG11	16:P:59:TRP:CD2	2.39	0.57
1:A:989:C:N4	1:A:1216:G:H1	2.00	0.57
1:A:1301:U:H3'	1:A:1302:U:C5'	2.32	0.57
1:A:1342:C:O2'	1:A:1343:G:H5'	2.04	0.57
2:B:16:HIS:C	2:B:18:GLY:H	2.12	0.57
12:L:27:LEU:HG	12:L:28:LYS:N	2.18	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:28:LYS:O	12:L:30:ALA:N	2.37	0.57
20:T:48:LYS:O	20:T:52:ALA:HB2	2.05	0.57
3:C:32:LEU:O	3:C:36:ASP:HB2	2.03	0.57
3:C:139:GLN:CA	3:C:139:GLN:HE21	2.16	0.57
4:D:62:GLN:HE22	4:D:65:ARG:HH11	1.52	0.57
12:L:85:ILE:CD1	12:L:100:ILE:HD13	2.35	0.57
15:O:5:LYS:HD2	15:O:5:LYS:N	2.19	0.57
1:A:883:C:O2'	1:A:884:U:H5'	2.05	0.57
1:A:1239:A:H62	1:A:1299:A:H62	1.52	0.57
5:E:71:LEU:O	5:E:72:GLN:HG2	2.04	0.57
7:G:68:ASN:O	7:G:135:VAL:HG12	2.03	0.57
8:H:119:LEU:HD12	8:H:124:ALA:CB	2.35	0.57
10:J:4:ILE:N	10:J:4:ILE:CD1	2.66	0.57
1:A:165:C:H2'	1:A:166:G:C8	2.39	0.57
1:A:1001:A:H2'	1:A:1001:A:N3	2.19	0.57
1:A:1309:G:C2'	1:A:1310:G:H5'	2.35	0.57
13:M:49:THR:HB	13:M:52:GLU:HG3	1.87	0.57
1:A:1412:C:H2'	1:A:1413:A:C8	2.39	0.57
3:C:91:LEU:HD21	3:C:99:VAL:HG22	1.87	0.57
3:C:120:VAL:HG21	3:C:134:ILE:HD13	1.87	0.57
8:H:28:ALA:HB3	8:H:57:PRO:HB2	1.87	0.57
13:M:58:GLU:O	13:M:62:ASN:HB2	2.04	0.57
13:M:125:ARG:HD2	13:M:125:ARG:C	2.30	0.57
15:O:10:LYS:HE2	15:O:14:GLU:HB2	1.87	0.57
1:A:555:C:H2'	1:A:556:C:H6	1.68	0.57
5:E:122:GLU:OE2	5:E:131:ILE:HD13	2.05	0.57
9:I:17:VAL:HG22	9:I:63:ILE:CD1	2.30	0.57
10:J:87:THR:O	10:J:88:LEU:HG	2.04	0.57
16:P:67:THR:HG23	16:P:70:ALA:HB2	1.85	0.57
1:A:769:G:H4'	1:A:1513:A:H4'	1.87	0.56
1:A:1442(A):G:H4'	1:A:1442(B):A:H5'	1.86	0.56
2:B:115:LEU:HD12	2:B:145:LEU:HB3	1.86	0.56
3:C:157:ILE:CG2	3:C:164:ARG:HH21	2.14	0.56
6:F:19:LEU:C	6:F:19:LEU:HD23	2.30	0.56
8:H:116:LYS:HD3	8:H:127:LEU:HD12	1.87	0.56
9:I:100:GLY:C	9:I:102:LEU:H	2.12	0.56
11:K:27:ASN:HB2	11:K:55:LYS:HE2	1.87	0.56
15:O:36:ILE:CG1	15:O:59:MET:HE2	2.34	0.56
16:P:6:LEU:HD12	16:P:6:LEU:N	2.20	0.56
17:Q:97:SER:HB3	17:Q:103:GLY:HA3	1.87	0.56
9:I:66:ARG:HB3	9:I:66:ARG:HH11	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:8:LEU:CD2	10:J:96:ILE:HG12	2.36	0.56
17:Q:81:ARG:HG3	17:Q:81:ARG:O	2.05	0.56
1:A:279:A:H5''	1:A:280:C:H3'	1.85	0.56
1:A:344:A:H5''	1:A:345:C:C6	2.41	0.56
1:A:530:G:O6	22:W:3:C:H1'	2.05	0.56
1:A:691:G:O6	11:K:55:LYS:NZ	2.38	0.56
1:A:949:A:N7	13:M:106:ASN:ND2	2.53	0.56
1:A:983:A:H5'	14:N:3:ARG:HH12	1.70	0.56
1:A:1027:C:H2'	1:A:1028:C:C6	2.39	0.56
2:B:24:TRP:CG	2:B:25:ASN:H	2.22	0.56
2:B:25:ASN:ND2	2:B:27:LYS:H	2.02	0.56
2:B:102:LEU:N	2:B:102:LEU:CD1	2.68	0.56
2:B:112:VAL:CG1	2:B:153:ARG:HD3	2.35	0.56
4:D:3:ARG:NH2	4:D:74:GLN:HG3	2.12	0.56
4:D:187:ARG:HE	4:D:187:ARG:CA	2.18	0.56
5:E:20:GLN:O	5:E:21:ALA:C	2.48	0.56
8:H:91:ARG:HH11	8:H:91:ARG:HG2	1.69	0.56
10:J:21:GLN:O	10:J:25:GLU:HG2	2.06	0.56
14:N:29:ARG:HH22	14:N:41:ARG:HH12	1.53	0.56
19:S:80:TYR:O	19:S:81:ARG:C	2.48	0.56
23:Z:39:U:C2'	23:Z:40:C:H5'	2.35	0.56
1:A:101:A:O2'	1:A:102:G:H5'	2.05	0.56
1:A:861:G:O2'	1:A:862:C:H5'	2.04	0.56
1:A:887:G:H1	1:A:910:C:H42	1.53	0.56
2:B:25:ASN:C	2:B:25:ASN:ND2	2.63	0.56
2:B:71:VAL:HG23	2:B:164:VAL:HA	1.87	0.56
2:B:98:LEU:H	2:B:98:LEU:CD2	2.12	0.56
3:C:107:GLN:H	3:C:107:GLN:NE2	2.04	0.56
6:F:33:TYR:CD2	6:F:75:LEU:HA	2.40	0.56
9:I:30:GLY:O	9:I:31:GLN:O	2.23	0.56
1:A:437:U:H5''	4:D:155:LEU:HD21	1.87	0.56
1:A:486:U:H2'	1:A:487:A:C8	2.40	0.56
1:A:628:G:O2'	1:A:629:G:H5'	2.05	0.56
1:A:1352:C:H2'	1:A:1353:G:C8	2.41	0.56
2:B:98:LEU:O	2:B:101:MET:HG3	2.06	0.56
3:C:70:VAL:HG21	3:C:76:VAL:HG21	1.88	0.56
6:F:43:LEU:HD22	6:F:43:LEU:N	2.20	0.56
9:I:91:ASP:C	9:I:93:ARG:H	2.13	0.56
17:Q:53:LEU:C	17:Q:53:LEU:HD23	2.29	0.56
2:B:222:ILE:O	2:B:226:ARG:HB2	2.06	0.56
10:J:12:ASP:HB3	10:J:15:THR:CG2	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:124:PRO:C	13:M:126:LYS:H	2.13	0.56
18:R:39:VAL:HG13	18:R:40:LEU:HD23	1.87	0.56
1:A:26:A:H2'	1:A:27:G:H5'	1.87	0.56
1:A:1148:U:H2'	1:A:1149:C:O4'	2.06	0.56
1:A:1399:C:C2	1:A:1502:A:N6	2.74	0.56
3:C:60:ALA:O	3:C:61:ALA:HB3	2.05	0.56
8:H:9:MET:O	8:H:13:ILE:HG12	2.05	0.56
18:R:88:LYS:C	18:R:88:LYS:HD3	2.30	0.56
1:A:329:A:H4'	1:A:330:C:OP2	2.06	0.56
2:B:107:THR:HG23	2:B:110:GLN:OE1	2.06	0.56
3:C:11:ARG:O	3:C:14:ILE:O	2.24	0.56
10:J:50:ILE:H	10:J:50:ILE:CD1	2.15	0.56
10:J:56:HIS:O	10:J:58:ASP:N	2.39	0.56
12:L:34:ARG:O	12:L:61:THR:HG23	2.06	0.56
1:A:192:U:C1'	20:T:103:GLY:HA2	2.35	0.56
1:A:1095:U:H5'	1:A:1095:U:C6	2.41	0.56
1:A:1115:C:O2	1:A:1115:C:H2'	2.04	0.56
1:A:1216:G:H5''	14:N:5:ALA:HB2	1.88	0.56
2:B:58:ILE:O	2:B:62:ALA:HB2	2.05	0.56
2:B:137:ARG:NH1	2:B:137:ARG:CB	2.69	0.56
2:B:154:LEU:N	2:B:154:LEU:HD23	2.20	0.56
2:B:170:GLU:O	2:B:173:ALA:HB3	2.06	0.56
2:B:219:VAL:HA	2:B:222:ILE:CD1	2.36	0.56
3:C:55:VAL:O	3:C:57:ILE:HG13	2.06	0.56
4:D:18:LYS:HG3	4:D:31:CYS:SG	2.46	0.56
9:I:28:VAL:HG22	9:I:63:ILE:HB	1.88	0.56
13:M:49:THR:HG22	13:M:51:ALA:N	2.21	0.56
15:O:27:VAL:CG1	15:O:31:LEU:HD22	2.35	0.56
19:S:30:LEU:HD11	19:S:50:ALA:CB	2.36	0.56
1:A:939:G:H2'	1:A:940:C:C6	2.41	0.56
2:B:12:GLU:HG3	2:B:213:LEU:HD11	1.86	0.56
8:H:17:THR:CG2	8:H:63:LEU:HD13	2.34	0.56
8:H:103:VAL:HG21	8:H:110:ALA:HB2	1.88	0.56
11:K:62:GLN:O	11:K:66:LEU:HG	2.06	0.56
1:A:80:G:H2'	1:A:81:U:H5''	1.86	0.55
1:A:344:A:H5''	1:A:345:C:C5	2.41	0.55
1:A:1366:C:C2	1:A:1367:C:C5	2.94	0.55
1:A:1376:U:O2'	1:A:1377:A:H5'	2.07	0.55
1:A:1392:G:O2'	1:A:1393:U:H5'	2.06	0.55
2:B:23:ARG:C	2:B:23:ARG:HD3	2.31	0.55
2:B:92:TYR:CD1	2:B:151:GLY:HA3	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:33:LEU:HD21	14:N:53:LEU:CD2	2.36	0.55
5:E:9:LYS:HE3	5:E:112:LEU:HD21	1.89	0.55
11:K:126:ARG:O	11:K:128:ALA:N	2.39	0.55
13:M:88:ARG:HG2	13:M:98:VAL:HG22	1.87	0.55
17:Q:63:ARG:HG2	17:Q:64:PRO:CD	2.35	0.55
1:A:619:U:C2'	1:A:620:C:H5''	2.36	0.55
1:A:1153:C:H2'	1:A:1154:G:C8	2.41	0.55
1:A:1527:C:O2'	1:A:1528:U:H5'	2.05	0.55
2:B:23:ARG:HH12	2:B:191:ASP:HA	1.71	0.55
2:B:92:TYR:CE1	2:B:151:GLY:HA3	2.41	0.55
3:C:79:ARG:HD3	3:C:79:ARG:N	2.02	0.55
4:D:17:VAL:O	4:D:19:LEU:HD12	2.06	0.55
5:E:63:ARG:HG2	5:E:63:ARG:HH11	1.70	0.55
7:G:64:GLN:HA	7:G:64:GLN:NE2	2.22	0.55
9:I:100:GLY:O	9:I:102:LEU:N	2.40	0.55
10:J:30:SER:HB3	10:J:81:THR:HA	1.88	0.55
17:Q:9:VAL:HG21	17:Q:84:LEU:HD13	1.88	0.55
19:S:20:LEU:HD12	19:S:21:GLU:HG3	1.88	0.55
1:A:329:A:C5	1:A:332:G:C5	2.94	0.55
1:A:616:G:O2'	1:A:617:G:H5'	2.06	0.55
1:A:1176:A:O2'	1:A:1177:G:H5'	2.06	0.55
1:A:1237:C:H4'	1:A:1334:G:N2	2.21	0.55
2:B:142:LEU:HD22	2:B:146:GLN:HE22	1.69	0.55
3:C:92:ALA:HA	3:C:95:THR:O	2.07	0.55
3:C:116:VAL:O	3:C:119:ARG:HB3	2.06	0.55
4:D:107:ARG:HH12	4:D:114:ARG:NH2	2.04	0.55
9:I:48:GLU:N	9:I:49:PRO:CD	2.69	0.55
10:J:12:ASP:HB3	10:J:15:THR:HG22	1.88	0.55
13:M:105:THR:HG22	13:M:106:ASN:H	1.71	0.55
14:N:26:ARG:HH11	14:N:47:LEU:HD11	1.72	0.55
14:N:37:PHE:C	14:N:39:LEU:H	2.14	0.55
15:O:74:ASP:HB3	15:O:77:ARG:HD3	1.87	0.55
1:A:666:G:H5'	1:A:726:C:H1'	1.88	0.55
1:A:673:G:H5''	6:F:87:ARG:NH1	2.21	0.55
1:A:1103:C:C5'	2:B:98:LEU:HD12	2.36	0.55
1:A:1446:U:HO2'	1:A:1447:A:H8	1.54	0.55
3:C:204:LEU:HD12	3:C:204:LEU:N	2.21	0.55
4:D:62:GLN:HE22	4:D:65:ARG:NH1	2.03	0.55
13:M:88:ARG:CZ	19:S:3:ARG:HH21	2.20	0.55
1:A:329:A:C4	1:A:332:G:C5	2.94	0.55
2:B:82:ARG:HB3	2:B:94:ASN:HD22	1.70	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:118:LEU:HB3	2:B:142:LEU:HD21	1.87	0.55
2:B:165:VAL:O	2:B:187:LEU:O	2.24	0.55
2:B:223:ILE:HD13	2:B:226:ARG:HD2	1.89	0.55
4:D:3:ARG:HH11	4:D:3:ARG:HG3	1.72	0.55
4:D:121:VAL:O	4:D:134:ASP:HA	2.06	0.55
6:F:28:ARG:HH11	6:F:28:ARG:CB	2.04	0.55
11:K:33:THR:HG22	11:K:39:PRO:HA	1.88	0.55
15:O:87:ILE:CG2	15:O:88:ARG:N	2.69	0.55
1:A:1067:A:H4'	1:A:1068:G:OP1	2.05	0.55
1:A:1333:A:H2'	1:A:1334:G:O4'	2.05	0.55
3:C:47:LEU:CD2	3:C:68:VAL:HG11	2.37	0.55
6:F:76:ALA:O	6:F:80:ARG:HG3	2.05	0.55
12:L:119:LYS:O	12:L:120:TYR:HB2	2.07	0.55
18:R:74:ARG:HD3	18:R:81:PHE:CD1	2.42	0.55
19:S:51:VAL:HG21	19:S:71:LEU:HD22	1.88	0.55
1:A:587:G:H5'	1:A:587:G:C8	2.42	0.55
1:A:923:A:H8	1:A:923:A:O5'	1.90	0.55
1:A:1447:A:H4'	1:A:1452:C:OP2	2.04	0.55
3:C:87:LEU:HA	3:C:90:GLU:HG2	1.88	0.55
4:D:162:LEU:HD13	4:D:181:MET:CG	2.36	0.55
8:H:119:LEU:HD12	8:H:124:ALA:HA	1.88	0.55
9:I:112:LYS:HD3	9:I:118:LYS:HA	1.87	0.55
11:K:67:ASP:O	11:K:71:LYS:HG3	2.07	0.55
11:K:77:MET:O	11:K:78:GLN:HB2	2.07	0.55
1:A:1323:G:H2'	1:A:1324:A:C8	2.41	0.55
1:A:1368:G:OP2	9:I:112:LYS:HG3	2.07	0.55
9:I:10:ARG:HG2	9:I:10:ARG:HH11	1.72	0.55
15:O:87:ILE:CG2	15:O:88:ARG:H	2.20	0.55
17:Q:36:ILE:HD13	17:Q:36:ILE:N	2.21	0.55
1:A:494:U:H2'	1:A:495:A:H5'	1.89	0.55
1:A:849:C:O2'	1:A:850:U:H5'	2.06	0.55
2:B:79:ASP:O	2:B:80:ILE:C	2.48	0.55
7:G:148:ASN:C	7:G:150:ALA:N	2.64	0.55
14:N:26:ARG:NH1	14:N:47:LEU:HD11	2.22	0.55
1:A:103:C:OP1	20:T:17:ARG:HD2	2.07	0.55
1:A:477:A:C3'	1:A:479:C:H5''	2.37	0.55
1:A:590:C:O2'	1:A:591:U:H5'	2.07	0.55
1:A:639:G:O2'	1:A:640:A:H5'	2.06	0.55
2:B:69:LEU:CD1	2:B:155:LEU:HD11	2.37	0.55
2:B:71:VAL:HG21	2:B:164:VAL:HG22	1.89	0.55
5:E:72:GLN:O	5:E:73:ASN:HB3	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:50:LEU:HD21	9:I:81:ILE:HG22	1.89	0.55
10:J:6:ILE:HG13	10:J:71:LEU:O	2.07	0.55
1:A:629:G:H2'	1:A:630:G:O4'	2.06	0.54
2:B:112:VAL:O	2:B:116:GLU:HG3	2.07	0.54
9:I:114:TYR:N	9:I:114:TYR:HD1	2.05	0.54
1:A:189(A):C:H2'	1:A:189(B):C:H6	1.72	0.54
1:A:418:C:O2'	1:A:540:G:H1'	2.07	0.54
1:A:663:A:O2'	1:A:664:G:H5'	2.07	0.54
1:A:1004:A:H4'	1:A:1004:A:OP2	2.06	0.54
1:A:1227:A:H5'	13:M:111:LYS:NZ	2.22	0.54
3:C:93:LYS:HA	3:C:93:LYS:CE	2.32	0.54
3:C:155:GLY:HA3	3:C:164:ARG:O	2.07	0.54
7:G:23:VAL:O	7:G:27:ILE:HG13	2.06	0.54
10:J:12:ASP:O	10:J:15:THR:HG22	2.07	0.54
10:J:28:ARG:C	10:J:29:ARG:HD3	2.32	0.54
18:R:74:ARG:HB3	18:R:81:PHE:CE1	2.42	0.54
20:T:87:LYS:O	20:T:91:LEU:HB2	2.06	0.54
1:A:1028:C:H2'	1:A:1029:C:C6	2.42	0.54
2:B:98:LEU:HD21	2:B:101:MET:HE3	1.89	0.54
2:B:134:GLU:HG2	2:B:137:ARG:HH21	1.72	0.54
3:C:6:HIS:HD2	3:C:8:ILE:H	1.55	0.54
3:C:158:GLY:C	3:C:160:ALA:H	2.16	0.54
6:F:87:ARG:HG3	6:F:87:ARG:NH1	2.23	0.54
10:J:34:VAL:HG22	10:J:74:ILE:HG23	1.87	0.54
10:J:51:ARG:HB3	10:J:59:SER:CB	2.37	0.54
15:O:3:ILE:HA	15:O:7:GLU:OE2	2.07	0.54
17:Q:24:GLU:HG2	17:Q:39:SER:HB3	1.90	0.54
19:S:5:LEU:O	19:S:6:LYS:CB	2.55	0.54
19:S:16:LEU:O	19:S:20:LEU:HG	2.07	0.54
5:E:76:ILE:CG2	5:E:77:PRO:HD2	2.36	0.54
6:F:8:ILE:HG23	6:F:85:VAL:HG13	1.88	0.54
13:M:36:LYS:HD2	13:M:59:TYR:OH	2.07	0.54
13:M:105:THR:HG22	13:M:106:ASN:N	2.23	0.54
21:V:6:ARG:NE	21:V:15:ARG:NH1	2.53	0.54
1:A:231:G:H2'	1:A:232:G:C5'	2.34	0.54
1:A:390:C:H4'	16:P:28:ARG:NH2	2.23	0.54
2:B:211:ILE:H	2:B:211:ILE:HD12	1.73	0.54
3:C:50:ALA:HA	3:C:72:LYS:HB2	1.90	0.54
3:C:113:ALA:HB2	3:C:202:ILE:HG13	1.88	0.54
4:D:50:ARG:HB3	4:D:50:ARG:CZ	2.37	0.54
13:M:40:ASN:ND2	13:M:41:PRO:HD2	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:82:MET:HE3	13:M:93:ARG:HB2	1.89	0.54
17:Q:95:TYR:HA	17:Q:98:LEU:HD13	1.90	0.54
18:R:39:VAL:HG13	18:R:40:LEU:N	2.22	0.54
1:A:533:A:O2'	1:A:535:A:OP2	2.26	0.54
1:A:570:G:H2'	1:A:571:U:C6	2.42	0.54
1:A:838:G:C2'	1:A:839:U:H5''	2.34	0.54
1:A:1120:G:O2'	1:A:1121:U:H5'	2.07	0.54
3:C:54:ARG:NH1	3:C:56:ASP:OD1	2.40	0.54
3:C:83:ARG:O	3:C:85:ARG:N	2.40	0.54
15:O:74:ASP:OD1	15:O:76:GLU:HB3	2.07	0.54
17:Q:74:LEU:HD23	17:Q:74:LEU:C	2.33	0.54
21:V:2:GLY:C	21:V:4:GLY:N	2.63	0.54
1:A:448:A:O2'	1:A:449:C:H5'	2.08	0.54
1:A:864:A:H2'	1:A:865:A:C8	2.43	0.54
1:A:1026:G:H2'	1:A:1026:G:N3	2.22	0.54
1:A:1277:C:C5'	1:A:1277:C:H6	2.21	0.54
2:B:69:LEU:HD12	2:B:155:LEU:CD1	2.36	0.54
5:E:102:ALA:HB1	5:E:120:THR:HG21	1.90	0.54
9:I:9:ARG:HA	9:I:13:ALA:O	2.07	0.54
10:J:46:ARG:HG2	10:J:46:ARG:HH11	1.72	0.54
23:Z:31:A:H2'	23:Z:32:U:O4'	2.06	0.54
1:A:149:A:H2'	1:A:150:C:C6	2.43	0.54
1:A:323:U:H2'	1:A:324:G:O4'	2.07	0.54
1:A:953:G:H1'	13:M:125:ARG:HA	1.89	0.54
5:E:150:ARG:CG	5:E:150:ARG:NH1	2.68	0.54
7:G:137:LYS:O	7:G:141:VAL:HG23	2.08	0.54
18:R:36:ASN:O	18:R:40:LEU:HG	2.07	0.54
1:A:577:G:O2'	1:A:816:A:H2'	2.08	0.54
2:B:16:HIS:O	2:B:18:GLY:N	2.41	0.54
2:B:137:ARG:CB	2:B:137:ARG:HH11	2.21	0.54
3:C:13:GLY:O	3:C:14:ILE:HD13	2.07	0.54
8:H:119:LEU:HD23	8:H:119:LEU:N	2.23	0.54
15:O:75:PRO:O	15:O:78:TYR:HB3	2.07	0.54
17:Q:101:ARG:HA	17:Q:101:ARG:NE	2.20	0.54
1:A:223:U:C3'	1:A:224:C:H5''	2.38	0.54
1:A:998:G:H3'	1:A:999:C:C5'	2.30	0.54
1:A:1197:G:C2'	1:A:1198:G:H5''	2.38	0.54
2:B:24:TRP:CG	2:B:25:ASN:N	2.74	0.54
2:B:24:TRP:HB3	2:B:40:HIS:CE1	2.44	0.54
2:B:73:THR:HB	2:B:170:GLU:OE1	2.08	0.54
2:B:114:ARG:NH1	2:B:118:LEU:HG	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:171:GLY:C	4:D:173:TRP:H	2.16	0.54
5:E:18:ARG:HG2	5:E:19:MET:N	2.23	0.54
12:L:11:VAL:HG21	17:Q:34:LYS:HG2	1.90	0.54
12:L:41:ARG:HG2	12:L:41:ARG:NH1	2.22	0.54
13:M:3:ARG:O	13:M:3:ARG:HG3	2.07	0.54
18:R:25:THR:HG22	18:R:42:ARG:HH11	1.73	0.54
18:R:86:VAL:HG12	18:R:87:ARG:HG3	1.88	0.54
1:A:1004:A:N7	1:A:1026:G:C5	2.76	0.53
2:B:111:ARG:HB3	2:B:149:LEU:CD1	2.37	0.53
8:H:11:THR:HG22	8:H:15:ASN:ND2	2.23	0.53
10:J:10:GLY:H	10:J:16:LEU:HD11	1.73	0.53
11:K:48:ILE:HG21	11:K:63:LEU:HD12	1.89	0.53
19:S:3:ARG:HG2	19:S:3:ARG:NH1	2.22	0.53
19:S:22:LEU:HD13	19:S:28:LYS:CG	2.38	0.53
21:V:6:ARG:HB3	21:V:15:ARG:HH11	1.73	0.53
1:A:22:G:H2'	1:A:23:C:C6	2.44	0.53
1:A:251:G:H4'	1:A:252:U:O5'	2.08	0.53
3:C:189:ALA:O	3:C:191:THR:HG22	2.08	0.53
4:D:132:ARG:HB3	4:D:132:ARG:CZ	2.38	0.53
5:E:96:PRO:HA	5:E:117:ASP:OD2	2.09	0.53
13:M:8:GLU:O	13:M:10:PRO:CD	2.57	0.53
13:M:122:LYS:O	13:M:123:ALA:HB3	2.08	0.53
14:N:29:ARG:HG2	14:N:29:ARG:NH1	2.23	0.53
23:Z:36:A:H2'	23:Z:37:A:H8	1.73	0.53
1:A:320:C:H5'	1:A:321:A:OP2	2.09	0.53
1:A:692:U:OP1	11:K:124:LYS:CE	2.57	0.53
2:B:69:LEU:HD21	2:B:93:VAL:HG23	1.89	0.53
3:C:108:ASN:ND2	3:C:144:SER:HB2	2.17	0.53
6:F:62:TRP:CG	18:R:35:ARG:NH1	2.77	0.53
7:G:52:GLU:C	7:G:54:THR:N	2.64	0.53
8:H:11:THR:HA	8:H:14:ARG:NH1	2.22	0.53
10:J:50:ILE:HD13	14:N:41:ARG:CD	2.38	0.53
14:N:53:LEU:HB3	14:N:56:VAL:HG21	1.89	0.53
17:Q:68:ARG:O	17:Q:68:ARG:HG3	2.08	0.53
1:A:250:A:H5'	1:A:251:G:OP1	2.08	0.53
1:A:501:C:H2'	1:A:502:G:C8	2.43	0.53
3:C:188:LEU:O	3:C:189:ALA:HB2	2.08	0.53
5:E:74:GLY:HA3	5:E:116:THR:HG22	1.91	0.53
11:K:91:ARG:NH1	18:R:88:LYS:HZ3	2.07	0.53
15:O:4:THR:H	15:O:7:GLU:CD	2.17	0.53
18:R:53:ARG:NE	18:R:58:LEU:O	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:162:A:H2'	1:A:163:C:H5'	1.89	0.53
1:A:738:C:OP1	6:F:92:LYS:HD3	2.09	0.53
1:A:1251:A:H4'	9:I:12:GLU:CD	2.33	0.53
1:A:1258:G:O2'	1:A:1259:C:H5'	2.08	0.53
2:B:21:ARG:CD	2:B:21:ARG:H	2.22	0.53
2:B:60:ASP:C	2:B:62:ALA:H	2.15	0.53
2:B:158:LEU:H	2:B:158:LEU:HD22	1.73	0.53
3:C:154:SER:O	3:C:165:THR:HA	2.08	0.53
3:C:195:VAL:C	3:C:196:LEU:HD12	2.34	0.53
4:D:110:PHE:HD2	4:D:148:VAL:CG2	2.20	0.53
9:I:113:LYS:HD3	9:I:119:ALA:HA	1.90	0.53
15:O:65:ARG:O	15:O:68:ARG:HB3	2.09	0.53
2:B:140:HIS:HA	2:B:143:GLU:CG	2.38	0.53
2:B:168:THR:OG1	2:B:191:ASP:O	2.26	0.53
3:C:58:GLU:O	3:C:59:ARG:HG3	2.08	0.53
4:D:110:PHE:N	4:D:110:PHE:CD1	2.76	0.53
18:R:17:SER:HA	18:R:19:LYS:HZ3	1.74	0.53
1:A:866:C:C2'	1:A:867:G:H5'	2.39	0.53
1:A:972:C:C4'	10:J:57:LYS:HG2	2.20	0.53
1:A:1007:C:H2'	1:A:1008:C:C6	2.44	0.53
1:A:1237:C:C4'	1:A:1334:G:N2	2.71	0.53
2:B:91:PRO:CG	2:B:154:LEU:HB2	2.21	0.53
3:C:39:ILE:HG22	3:C:40:ARG:N	2.24	0.53
4:D:18:LYS:HE3	4:D:20:TYR:CE2	2.43	0.53
19:S:20:LEU:CD1	19:S:21:GLU:HG3	2.39	0.53
1:A:224:C:H6	1:A:224:C:H5'	1.74	0.53
1:A:418:C:HO2'	1:A:540:G:H1'	1.74	0.53
1:A:1060:C:O2'	1:A:1061:G:H5'	2.09	0.53
1:A:1153:C:H2'	1:A:1154:G:H8	1.72	0.53
1:A:1206:G:C6	1:A:1207:G:C5	2.97	0.53
2:B:22:LYS:HA	2:B:40:HIS:HE1	1.73	0.53
2:B:91:PRO:HB3	2:B:151:GLY:O	2.09	0.53
3:C:111:LEU:HD21	3:C:144:SER:O	2.08	0.53
7:G:16:LEU:N	7:G:16:LEU:HD12	2.24	0.53
9:I:88:TYR:O	9:I:89:ASN:HB2	2.09	0.53
12:L:115:LYS:O	12:L:117:ARG:N	2.38	0.53
1:A:1144:G:N2	1:A:1146:A:H62	1.98	0.53
2:B:113:HIS:HD2	2:B:116:GLU:OE1	1.92	0.53
12:L:53:ARG:HG2	12:L:53:ARG:HH11	1.74	0.53
1:A:192:U:H2'	1:A:193:C:C6	2.43	0.53
1:A:224:C:H6	1:A:224:C:C5'	2.22	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:339:C:H2'	1:A:340:U:C6	2.42	0.53
1:A:577:G:H1'	1:A:816:A:C4	2.44	0.53
1:A:706:A:H1'	11:K:29:ILE:HD11	1.91	0.53
1:A:857:C:H2'	1:A:858:G:O4'	2.09	0.53
1:A:939:G:H2'	1:A:940:C:H6	1.74	0.53
1:A:1001:A:H4'	1:A:1001(A):G:OP1	2.08	0.53
1:A:1002:G:C2	1:A:1003:G:N7	2.77	0.53
1:A:1222:G:O2'	1:A:1223:C:H5'	2.08	0.53
1:A:1310:G:N7	19:S:2:PRO:HG3	2.24	0.53
2:B:15:VAL:HG21	2:B:209:ARG:HG3	1.91	0.53
3:C:64:VAL:N	3:C:99:VAL:HG11	2.24	0.53
3:C:167:TRP:O	3:C:168:ALA:HB3	2.09	0.53
7:G:6:ARG:HG2	7:G:6:ARG:O	2.07	0.53
20:T:10:LEU:O	20:T:11:SER:C	2.52	0.53
1:A:866:C:H2'	1:A:867:G:C5'	2.36	0.52
1:A:1347:G:H22	1:A:1373:G:H2'	1.72	0.52
2:B:20:GLU:O	2:B:39:ILE:HG23	2.08	0.52
3:C:87:LEU:C	3:C:89:GLU:N	2.66	0.52
5:E:144:THR:N	5:E:147:ASP:OD1	2.38	0.52
6:F:80:ARG:HG2	6:F:80:ARG:HH11	1.73	0.52
8:H:20:TYR:CE2	8:H:75:ARG:HD2	2.36	0.52
9:I:7:THR:HB	9:I:83:ARG:NH1	2.23	0.52
10:J:10:GLY:N	10:J:16:LEU:HD11	2.25	0.52
11:K:108:ILE:HG22	11:K:109:VAL:N	2.23	0.52
12:L:27:LEU:C	12:L:29:GLY:H	2.17	0.52
14:N:3:ARG:HD3	14:N:6:LEU:HD12	1.90	0.52
14:N:57:ARG:HG2	14:N:58:LYS:N	2.25	0.52
1:A:427:U:C3'	1:A:428:G:H5''	2.37	0.52
1:A:471:G:H21	16:P:82:GLN:NE2	2.06	0.52
1:A:627:G:O2'	1:A:628:G:H5'	2.09	0.52
1:A:750:G:N2	15:O:23:GLY:HA3	2.23	0.52
1:A:781:A:H2	1:A:1514:C:O4'	1.92	0.52
1:A:877:C:H1'	8:H:3:THR:HG21	1.91	0.52
1:A:1297:C:O2	1:A:1297:C:C2'	2.57	0.52
1:A:1366:C:H2'	1:A:1367:C:C6	2.44	0.52
2:B:91:PRO:CA	2:B:154:LEU:HD12	2.39	0.52
3:C:35:GLU:O	3:C:39:ILE:HD13	2.10	0.52
12:L:86:ARG:HD3	12:L:101:VAL:HG22	1.92	0.52
16:P:39:TYR:HB2	16:P:49:LEU:HD13	1.90	0.52
17:Q:10:VAL:HG13	17:Q:19:VAL:HB	1.91	0.52
1:A:232:G:H5'	1:A:232:G:C8	2.36	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:833:U:H2'	1:A:834:C:C6	2.44	0.52
1:A:1103:C:C3'	1:A:1104:G:H5''	2.40	0.52
1:A:1197:G:H2'	1:A:1198:G:H5''	1.91	0.52
2:B:55:PHE:O	2:B:58:ILE:HG13	2.09	0.52
3:C:123:GLN:NE2	3:C:140:ARG:HH22	2.07	0.52
4:D:36:ARG:H	4:D:37:PRO:HD3	1.73	0.52
5:E:99:GLY:O	5:E:117:ASP:HA	2.09	0.52
6:F:10:LEU:HD12	6:F:59:TYR:HB3	1.92	0.52
7:G:26:PHE:O	7:G:30:ILE:HG13	2.08	0.52
8:H:11:THR:HG23	8:H:14:ARG:NH1	2.24	0.52
11:K:91:ARG:NH1	18:R:88:LYS:NZ	2.57	0.52
12:L:59:ARG:HD3	12:L:65:GLU:HG3	1.91	0.52
13:M:71:ARG:HG2	13:M:71:ARG:HH11	1.74	0.52
18:R:59:SER:HB3	18:R:62:GLU:CG	2.36	0.52
1:A:749:C:O2'	1:A:750:G:H8	1.92	0.52
1:A:974:A:OP1	14:N:31:ARG:HD3	2.09	0.52
1:A:1223:C:P	19:S:78:ARG:HH12	2.32	0.52
1:A:1281:U:H3'	1:A:1281:U:H6	1.74	0.52
1:A:1406:U:O2'	1:A:1407:C:H5'	2.09	0.52
2:B:112:VAL:HG11	2:B:153:ARG:HA	1.92	0.52
3:C:19:GLU:HG2	3:C:54:ARG:HH12	1.71	0.52
4:D:61:LYS:HG2	4:D:203:VAL:HG13	1.91	0.52
6:F:40:VAL:HG22	6:F:41:GLU:H	1.73	0.52
7:G:15:ASP:OD1	7:G:17:VAL:N	2.42	0.52
7:G:17:VAL:HG12	7:G:18:TYR:CD1	2.45	0.52
15:O:5:LYS:O	15:O:9:GLN:HG2	2.08	0.52
15:O:6:GLU:CD	15:O:6:GLU:N	2.67	0.52
18:R:25:THR:O	18:R:25:THR:HG22	2.10	0.52
19:S:5:LEU:O	19:S:6:LYS:CG	2.57	0.52
1:A:757:U:H2'	1:A:758:G:O4'	2.09	0.52
1:A:908:A:O2'	1:A:909:A:H5'	2.10	0.52
1:A:1019:C:O2'	1:A:1020:U:H5'	2.08	0.52
1:A:1201:A:H4'	1:A:1202:G:C5'	2.40	0.52
2:B:7:VAL:HG12	2:B:8:LYS:N	2.13	0.52
2:B:111:ARG:CB	2:B:149:LEU:HD11	2.37	0.52
2:B:181:PHE:CD2	8:H:70:GLN:HB3	2.44	0.52
16:P:4:ILE:HA	16:P:20:VAL:O	2.08	0.52
16:P:59:TRP:HB3	16:P:64:ALA:HB2	1.92	0.52
18:R:53:ARG:HB2	18:R:63:GLN:HG2	1.91	0.52
1:A:404:U:H5'	4:D:122:ARG:HD2	1.92	0.52
1:A:1141:C:H2'	1:A:1142:G:H8	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:158:LEU:H	2:B:158:LEU:CD2	2.22	0.52
4:D:60:GLU:HG2	4:D:202:LEU:HB2	1.91	0.52
9:I:3:GLN:NE2	9:I:20:ARG:HG2	2.24	0.52
11:K:66:LEU:CD2	11:K:97:ALA:HB1	2.39	0.52
14:N:23:ARG:HH12	14:N:30:ALA:HB2	1.72	0.52
19:S:41:VAL:O	19:S:44:MET:HG3	2.10	0.52
2:B:84:GLU:CG	2:B:216:SER:HA	2.39	0.52
3:C:173:VAL:O	3:C:175:LEU:HD23	2.09	0.52
3:C:190:ARG:CB	3:C:190:ARG:HH11	2.22	0.52
4:D:8:VAL:O	4:D:10:ARG:N	2.39	0.52
7:G:38:LEU:O	7:G:42:ILE:HG12	2.10	0.52
7:G:64:GLN:HA	7:G:64:GLN:HE21	1.74	0.52
10:J:50:ILE:HD13	14:N:41:ARG:HD3	1.92	0.52
13:M:71:ARG:HG2	13:M:71:ARG:NH1	2.24	0.52
1:A:349:A:O2'	1:A:350:G:H5'	2.09	0.52
1:A:1214:C:O2	1:A:1214:C:H2'	2.09	0.52
3:C:14:ILE:O	3:C:16:ARG:N	2.43	0.52
4:D:36:ARG:H	4:D:37:PRO:CD	2.23	0.52
8:H:112:LEU:C	8:H:112:LEU:HD12	2.35	0.52
9:I:97:LYS:O	9:I:100:GLY:N	2.40	0.52
12:L:26:ALA:HB2	12:L:98:TYR:CE2	2.45	0.52
14:N:8:GLU:O	14:N:11:LYS:HB2	2.09	0.52
14:N:16:PHE:HB2	14:N:18:VAL:HG22	1.91	0.52
20:T:23:ARG:HG2	20:T:23:ARG:HH11	1.74	0.52
1:A:605:U:O2'	1:A:606:G:H5'	2.10	0.52
1:A:965:A:C2	1:A:969:A:C2	2.97	0.52
3:C:115:LEU:HD23	3:C:118:GLN:OE1	2.10	0.52
4:D:170:VAL:CG2	4:D:171:GLY:N	2.72	0.52
4:D:176:LEU:CG	4:D:177:ASP:H	2.18	0.52
9:I:8:GLY:HA2	9:I:79:LEU:HD13	1.92	0.52
10:J:24:VAL:O	10:J:24:VAL:HG22	2.09	0.52
13:M:17:VAL:O	13:M:20:THR:HB	2.10	0.52
23:Z:31:A:H61	23:Z:39:U:H3	1.56	0.52
1:A:1473:A:H2'	1:A:1474:G:O4'	2.10	0.52
2:B:83:MET:HE2	2:B:238:LEU:HD11	1.92	0.52
2:B:173:ALA:O	2:B:176:GLU:HB2	2.10	0.52
4:D:196:LEU:C	4:D:198:VAL:H	2.18	0.52
7:G:93:PRO:HG2	7:G:94:ARG:H	1.76	0.52
10:J:76:ASN:C	10:J:78:ASN:H	2.17	0.52
11:K:115:PRO:C	11:K:117:ASN:H	2.18	0.52
17:Q:18:THR:HG22	17:Q:19:VAL:N	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:32:ARG:NH2	18:R:65:ILE:HD12	2.23	0.52
19:S:53:ASN:HD21	19:S:56:GLN:HB2	1.75	0.52
20:T:96:GLY:O	20:T:97:ALA:CB	2.58	0.52
1:A:1473:A:H2'	1:A:1474:G:C5'	2.37	0.51
4:D:209:ARG:HG2	4:D:209:ARG:NH1	2.25	0.51
7:G:6:ARG:O	7:G:7:ALA:C	2.52	0.51
7:G:110:GLN:OE1	7:G:110:GLN:HA	2.09	0.51
10:J:79:ARG:HH22	10:J:82:ILE:HD12	1.76	0.51
13:M:40:ASN:HB3	13:M:43:THR:HG23	1.92	0.51
14:N:26:ARG:HG3	14:N:27:CYS:N	2.19	0.51
16:P:21:VAL:HG11	16:P:59:TRP:CE3	2.45	0.51
19:S:17:GLU:HA	19:S:20:LEU:HD11	1.91	0.51
1:A:55:A:O2'	1:A:56:U:H5'	2.09	0.51
1:A:1055:A:C2	1:A:1056:U:H1'	2.45	0.51
1:A:1090:U:H2'	1:A:1091:U:H6	1.76	0.51
1:A:1237:C:H2'	1:A:1336:C:H5	1.76	0.51
2:B:206:ASP:O	2:B:207:ALA:CB	2.59	0.51
3:C:64:VAL:CG2	3:C:99:VAL:HG21	2.39	0.51
5:E:74:GLY:HA3	5:E:116:THR:CG2	2.40	0.51
6:F:33:TYR:HA	6:F:71:ARG:NH2	2.24	0.51
10:J:45:ARG:HH11	10:J:45:ARG:HB2	1.74	0.51
12:L:59:ARG:HG2	12:L:59:ARG:HH11	1.76	0.51
13:M:79:LYS:HG2	13:M:83:ASP:OD2	2.09	0.51
17:Q:45:HIS:O	17:Q:47:PRO:HD3	2.11	0.51
1:A:109:A:C8	1:A:326:G:H2'	2.45	0.51
1:A:474:G:O2'	1:A:475:G:H5'	2.11	0.51
1:A:1047:G:H5''	14:N:4:LYS:HD2	1.91	0.51
1:A:1309:G:O2'	1:A:1310:G:H5'	2.10	0.51
2:B:84:GLU:HB3	2:B:219:VAL:HG21	1.90	0.51
2:B:112:VAL:C	2:B:114:ARG:H	2.18	0.51
9:I:8:GLY:N	9:I:83:ARG:HH11	2.09	0.51
16:P:21:VAL:HG21	16:P:59:TRP:CD1	2.45	0.51
19:S:15:LEU:O	19:S:19:VAL:HG12	2.10	0.51
19:S:63:THR:CG2	19:S:64:GLU:H	2.19	0.51
19:S:63:THR:CG2	19:S:64:GLU:N	2.73	0.51
1:A:376:G:H2'	1:A:377:G:C8	2.43	0.51
1:A:625:G:H4'	16:P:16:HIS:CD2	2.45	0.51
1:A:1442(A):G:O5'	1:A:1442(B):A:C5'	2.57	0.51
2:B:79:ASP:O	2:B:82:ARG:N	2.42	0.51
6:F:62:TRP:CB	18:R:35:ARG:HH12	2.23	0.51
10:J:30:SER:HB3	10:J:80:LYS:O	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:72:VAL:O	10:J:73:ASP:HB2	2.10	0.51
11:K:108:ILE:HG22	11:K:109:VAL:H	1.75	0.51
12:L:119:LYS:O	12:L:120:TYR:CB	2.58	0.51
13:M:4:ILE:HG22	13:M:5:ALA:N	2.24	0.51
16:P:45:THR:OG1	16:P:46:PRO:HD2	2.11	0.51
18:R:61:LYS:O	18:R:65:ILE:HG12	2.10	0.51
1:A:818:G:O2'	1:A:819:A:H5'	2.10	0.51
1:A:1112:C:H1'	3:C:179:ARG:HH21	1.74	0.51
1:A:1337:G:H5''	1:A:1338:G:OP1	2.10	0.51
3:C:43:LEU:HD21	3:C:68:VAL:CG2	2.41	0.51
11:K:19:ALA:HB2	11:K:80:VAL:HG21	1.93	0.51
15:O:86:GLY:O	15:O:87:ILE:HD13	2.11	0.51
16:P:43:LYS:HA	16:P:48:TRP:CB	2.41	0.51
1:A:329:A:N6	1:A:332:G:N2	2.57	0.51
1:A:542:G:H5'	4:D:41:GLY:HA3	1.91	0.51
1:A:865:A:H5'	1:A:1078:U:O4	2.11	0.51
1:A:1425:U:H2'	1:A:1426:C:C6	2.46	0.51
2:B:55:PHE:HA	2:B:58:ILE:CD1	2.41	0.51
8:H:5:PRO:O	8:H:8:ASP:HB3	2.11	0.51
8:H:6:ILE:O	8:H:10:LEU:HG	2.10	0.51
9:I:5:TYR:O	9:I:84:ALA:HA	2.11	0.51
1:A:250:A:H4'	1:A:251:G:O5'	2.11	0.51
2:B:55:PHE:HA	2:B:58:ILE:CG1	2.41	0.51
3:C:112:SER:OG	3:C:115:LEU:HD12	2.10	0.51
5:E:100:VAL:HG13	5:E:118:ILE:HG22	1.92	0.51
6:F:2:ARG:CD	6:F:69:GLU:HG2	2.40	0.51
7:G:143:ARG:HB3	7:G:143:ARG:NH1	2.26	0.51
14:N:57:ARG:HG2	14:N:58:LYS:H	1.76	0.51
16:P:26:ARG:HG2	16:P:26:ARG:HH11	1.76	0.51
1:A:1081:G:O2'	1:A:1082:G:H5'	2.11	0.51
1:A:1131:G:OP1	1:A:1131:G:H4'	2.11	0.51
1:A:1327:C:H5''	21:V:20:LYS:HE3	1.91	0.51
2:B:55:PHE:HA	2:B:58:ILE:HG13	1.93	0.51
2:B:108:ILE:O	2:B:108:ILE:HG22	2.09	0.51
3:C:51:GLY:O	3:C:115:LEU:HD21	2.11	0.51
8:H:134:ILE:O	8:H:135:CYS:HB3	2.10	0.51
11:K:29:ILE:C	11:K:29:ILE:HD13	2.35	0.51
15:O:45:VAL:O	15:O:46:HIS:C	2.53	0.51
1:A:313:A:H2'	1:A:314:C:C6	2.46	0.51
1:A:718:G:C5'	11:K:117:ASN:HD22	2.20	0.51
1:A:1340:A:O2'	1:A:1341:U:H5'	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:51:LEU:O	2:B:55:PHE:HD1	1.93	0.51
2:B:82:ARG:NH1	2:B:82:ARG:HB2	2.26	0.51
2:B:97:TRP:CZ2	2:B:102:LEU:HD13	2.43	0.51
4:D:158:ILE:HG23	4:D:162:LEU:HD12	1.93	0.51
15:O:11:VAL:HG21	15:O:34:LEU:HD22	1.92	0.51
1:A:491:G:O2'	1:A:492:G:H5'	2.11	0.51
1:A:1053:G:O2'	1:A:1199:U:H5	1.93	0.51
1:A:1244:C:C3'	1:A:1245:A:H5''	2.41	0.51
2:B:161:ALA:HB1	2:B:185:ILE:HD11	1.92	0.51
2:B:162:ILE:HG22	2:B:164:VAL:HG23	1.92	0.51
5:E:12:LEU:HD12	5:E:12:LEU:O	2.11	0.51
5:E:110:LEU:O	5:E:111:GLU:C	2.54	0.51
9:I:17:VAL:CG1	9:I:81:ILE:HD13	2.41	0.51
13:M:29:ARG:O	13:M:32:GLU:HB3	2.11	0.51
15:O:39:LEU:O	15:O:43:LEU:HG	2.11	0.51
16:P:6:LEU:HD23	16:P:17:TYR:CD2	2.46	0.51
1:A:721:G:OP2	18:R:63:GLN:HG2	2.11	0.50
1:A:840:C:O2	1:A:840:C:H2'	2.10	0.50
1:A:1152:A:H4'	10:J:13:HIS:HD2	1.75	0.50
1:A:1197:G:C3'	1:A:1198:G:C5'	2.89	0.50
1:A:1364:U:O2'	1:A:1365:G:H5'	2.11	0.50
2:B:44:LEU:O	2:B:45:GLN:C	2.54	0.50
2:B:78:GLN:NE2	2:B:96:ARG:NH1	2.58	0.50
2:B:95:GLN:O	2:B:96:ARG:HD2	2.11	0.50
2:B:137:ARG:HH11	2:B:137:ARG:HB3	1.75	0.50
7:G:119:ARG:HH11	7:G:119:ARG:HG3	1.76	0.50
8:H:81:HIS:O	8:H:82:HIS:HB2	2.10	0.50
10:J:8:LEU:HB2	10:J:70:ARG:HB2	1.92	0.50
20:T:45:GLN:CB	20:T:91:LEU:HD22	2.41	0.50
1:A:1004:A:H5''	1:A:1025:U:O2	2.11	0.50
1:A:1352:C:O2	1:A:1371:G:C2	2.64	0.50
1:A:1473:A:C3'	1:A:1474:G:H5''	2.41	0.50
3:C:155:GLY:O	3:C:156:ARG:CB	2.57	0.50
9:I:8:GLY:H	9:I:83:ARG:HH11	1.59	0.50
16:P:5:ARG:C	16:P:6:LEU:HD12	2.36	0.50
1:A:329:A:C4	1:A:332:G:C6	2.98	0.50
1:A:979:C:H2'	1:A:980:C:H5'	1.93	0.50
1:A:1128:C:H1'	1:A:1146:A:H61	1.75	0.50
1:A:1128:C:C5'	9:I:16:ARG:HH12	2.23	0.50
1:A:1355:G:O2'	1:A:1356:G:H5'	2.10	0.50
2:B:167:PRO:O	2:B:168:THR:C	2.53	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:132:ARG:HA	3:C:135:LYS:CE	2.39	0.50
7:G:41:ARG:O	7:G:42:ILE:C	2.53	0.50
14:N:4:LYS:HA	14:N:7:ILE:HG13	1.92	0.50
16:P:56:ALA:C	16:P:58:TYR:H	2.20	0.50
18:R:66:LEU:HD11	18:R:70:ILE:HD11	1.92	0.50
20:T:43:LEU:HD13	20:T:51:GLU:HG3	1.92	0.50
1:A:248:C:O2'	1:A:249:U:H5'	2.11	0.50
1:A:1151:A:O2'	1:A:1152:A:H8	1.95	0.50
1:A:1206:G:C4	1:A:1207:G:C8	3.00	0.50
1:A:1495:U:H2'	1:A:1496:C:H6	1.76	0.50
2:B:216:SER:O	2:B:219:VAL:N	2.44	0.50
3:C:15:THR:O	3:C:16:ARG:HB2	2.10	0.50
3:C:31:HIS:C	3:C:33:LEU:H	2.19	0.50
3:C:82:GLU:O	3:C:86:VAL:HG23	2.12	0.50
11:K:16:SER:O	11:K:35:PRO:HG3	2.12	0.50
12:L:27:LEU:O	12:L:29:GLY:N	2.45	0.50
12:L:36:VAL:HG22	12:L:82:VAL:HG12	1.93	0.50
17:Q:60:ILE:C	17:Q:71:PHE:HD1	2.18	0.50
1:A:500:G:H5''	12:L:124:LYS:HE2	1.93	0.50
1:A:1049:U:H4'	1:A:1050:G:H5''	1.94	0.50
2:B:17:PHE:CD1	2:B:17:PHE:C	2.89	0.50
2:B:67:THR:HA	2:B:90:MET:CE	2.41	0.50
2:B:84:GLU:HG3	2:B:219:VAL:HG21	1.94	0.50
3:C:129:ALA:HB3	3:C:132:ARG:HH12	1.73	0.50
4:D:67:ILE:HG22	4:D:68:TYR:CD1	2.46	0.50
5:E:79:GLU:HB3	5:E:92:LYS:HA	1.94	0.50
11:K:114:VAL:O	11:K:114:VAL:HG13	2.10	0.50
16:P:75:ARG:HH11	16:P:75:ARG:HG3	1.75	0.50
1:A:179:A:H2'	1:A:180:U:C6	2.47	0.50
1:A:231:G:O2'	1:A:232:G:H5''	2.12	0.50
1:A:254:G:OP1	17:Q:67:LYS:O	2.28	0.50
1:A:275:G:OP1	17:Q:14:LYS:HD2	2.11	0.50
1:A:328:C:O2	1:A:328:C:C2'	2.59	0.50
1:A:443:C:O2'	1:A:444:C:H5'	2.10	0.50
1:A:538:G:OP2	12:L:115:LYS:HG3	2.12	0.50
1:A:976:G:N7	1:A:1358:U:C2	2.80	0.50
1:A:1330:U:OP1	13:M:23:TYR:O	2.29	0.50
1:A:1378:C:O2	1:A:1378:C:H2'	2.11	0.50
2:B:32:ILE:HD12	2:B:40:HIS:HB3	1.92	0.50
2:B:88:ALA:C	2:B:90:MET:H	2.19	0.50
4:D:19:LEU:O	4:D:21:LEU:HG	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:3:GLN:HA	9:I:3:GLN:NE2	2.14	0.50
14:N:23:ARG:NH1	14:N:28:GLY:O	2.45	0.50
14:N:36:PHE:O	14:N:36:PHE:CD1	2.65	0.50
17:Q:97:SER:C	17:Q:98:LEU:HD12	2.37	0.50
1:A:180:U:O2'	1:A:181:G:H5'	2.12	0.50
1:A:232:G:H1'	1:A:262:A:N1	2.26	0.50
1:A:501:C:O3'	12:L:118:SER:HB2	2.12	0.50
1:A:1001(A):G:C2	1:A:1002:G:H1'	2.47	0.50
1:A:1194:U:H2'	1:A:1195:C:C6	2.46	0.50
3:C:91:LEU:HD23	3:C:91:LEU:C	2.37	0.50
3:C:108:ASN:C	3:C:110:ASN:H	2.20	0.50
3:C:150:LYS:HB2	3:C:169:ALA:HB2	1.94	0.50
5:E:55:VAL:O	5:E:58:ALA:HB3	2.11	0.50
9:I:4:TYR:CZ	9:I:88:TYR:HD1	2.30	0.50
1:A:922:G:H5'	5:E:19:MET:O	2.12	0.50
1:A:978:A:N7	1:A:1361:G:N2	2.60	0.50
3:C:102:ASN:N	3:C:102:ASN:ND2	2.55	0.50
3:C:120:VAL:CG1	3:C:198:VAL:HG11	2.41	0.50
5:E:17:ALA:HA	5:E:26:PHE:HA	1.94	0.50
9:I:10:ARG:HD3	9:I:105:ASP:HB3	1.92	0.50
9:I:114:TYR:HD1	9:I:114:TYR:H	1.57	0.50
10:J:19:SER:O	10:J:23:ILE:HG12	2.11	0.50
10:J:42:THR:HG23	10:J:67:THR:C	2.37	0.50
10:J:68:HIS:N	10:J:68:HIS:CD2	2.78	0.50
18:R:33:ASP:OD2	18:R:36:ASN:HB2	2.12	0.50
1:A:473:G:H5''	16:P:81:ARG:CZ	2.42	0.50
1:A:1054:C:N3	23:Z:34:G:O4'	2.45	0.50
1:A:1260:C:H4'	1:A:1283:G:O2'	2.11	0.50
1:A:1360:A:C2'	1:A:1361:G:H5'	2.42	0.50
1:A:1403:C:O5'	1:A:1403:C:H6	1.93	0.50
1:A:1468:A:H2'	1:A:1469:G:O4'	2.12	0.50
7:G:21:VAL:HG23	7:G:22:LEU:N	2.26	0.50
11:K:34:ASP:C	11:K:36:ASP:H	2.19	0.50
11:K:109:VAL:HG22	18:R:86:VAL:HA	1.94	0.50
12:L:93:LEU:H	12:L:93:LEU:CD2	2.24	0.50
13:M:5:ALA:O	13:M:6:GLY:C	2.55	0.50
16:P:4:ILE:HG21	16:P:74:LEU:HD11	1.94	0.50
1:A:370:C:O2'	1:A:371:G:H5'	2.10	0.49
1:A:624:C:H2'	1:A:625:G:H8	1.75	0.49
1:A:673:G:H2'	1:A:674:G:C8	2.47	0.49
1:A:737:A:H1'	6:F:73:ASN:OD1	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:802:A:H2'	1:A:803:G:O4'	2.12	0.49
2:B:88:ALA:HB1	2:B:90:MET:HG2	1.93	0.49
3:C:39:ILE:C	3:C:41:GLY:N	2.70	0.49
4:D:207:TYR:C	4:D:209:ARG:N	2.66	0.49
5:E:79:GLU:HG3	5:E:93:PRO:CD	2.40	0.49
5:E:150:ARG:NH1	5:E:150:ARG:HG3	2.27	0.49
6:F:86:ARG:HH11	6:F:86:ARG:HG3	1.75	0.49
8:H:23:SER:O	8:H:24:THR:HB	2.11	0.49
13:M:3:ARG:HH11	13:M:3:ARG:HG2	1.77	0.49
20:T:10:LEU:O	20:T:12:ALA:N	2.45	0.49
1:A:262:A:C6	1:A:263:A:C6	2.99	0.49
1:A:555:C:H2'	1:A:556:C:C6	2.46	0.49
1:A:1030(A):G:N2	1:A:1030(C):G:H3'	2.26	0.49
2:B:69:LEU:HD23	2:B:69:LEU:C	2.36	0.49
2:B:84:GLU:CB	2:B:219:VAL:HG21	2.43	0.49
2:B:101:MET:C	2:B:102:LEU:HD12	2.37	0.49
9:I:113:LYS:N	9:I:113:LYS:CD	2.75	0.49
13:M:5:ALA:HB3	13:M:8:GLU:HG3	1.93	0.49
13:M:120:LYS:HE2	13:M:122:LYS:O	2.12	0.49
1:A:409:G:OP1	4:D:24:GLU:O	2.31	0.49
1:A:905:U:H5'	1:A:906:G:OP2	2.11	0.49
3:C:139:GLN:NE2	3:C:139:GLN:CA	2.70	0.49
4:D:64:LEU:O	4:D:64:LEU:HD13	2.13	0.49
4:D:151:LYS:N	4:D:151:LYS:HD2	2.26	0.49
5:E:99:GLY:N	5:E:117:ASP:OD1	2.45	0.49
9:I:118:LYS:O	9:I:119:ALA:CB	2.60	0.49
10:J:83:GLU:O	10:J:85:LEU:N	2.44	0.49
1:A:485:G:C2'	1:A:486:U:OP2	2.60	0.49
1:A:576:G:C3'	1:A:577:G:C5'	2.89	0.49
1:A:777:A:H2'	1:A:778:G:H8	1.78	0.49
1:A:959:A:C2	1:A:1222:G:O4'	2.65	0.49
1:A:1226:C:C5	13:M:104:ARG:HB2	2.47	0.49
2:B:83:MET:CB	2:B:235:SER:OG	2.60	0.49
2:B:178:ARG:O	8:H:71:GLY:HA2	2.12	0.49
4:D:199:ASN:ND2	4:D:199:ASN:C	2.69	0.49
12:L:27:LEU:C	12:L:29:GLY:N	2.70	0.49
13:M:3:ARG:HE	13:M:7:VAL:HA	1.76	0.49
18:R:18:ARG:HA	18:R:18:ARG:HE	1.78	0.49
23:Z:28:G:H2'	23:Z:29:G:N7	2.26	0.49
1:A:436:C:H5''	4:D:156:GLU:OE1	2.12	0.49
1:A:661:G:O2'	1:A:662:G:H5'	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:777:A:H2'	1:A:778:G:C8	2.47	0.49
1:A:832:C:O2'	1:A:833:U:H5'	2.12	0.49
1:A:1070:U:H2'	1:A:1071:C:H6	1.76	0.49
1:A:1115:C:H1'	14:N:61:TRP:CB	2.42	0.49
1:A:1329:A:C2'	1:A:1330:U:H5'	2.42	0.49
1:A:1329:A:O2'	1:A:1330:U:H5'	2.12	0.49
2:B:9:GLU:OE1	2:B:9:GLU:HA	2.12	0.49
3:C:67:THR:HG22	3:C:69:HIS:CD2	2.47	0.49
5:E:10:MET:HA	5:E:32:VAL:HG12	1.93	0.49
5:E:76:ILE:HG23	5:E:77:PRO:HD2	1.95	0.49
6:F:100:ASN:HB3	18:R:27:GLY:HA2	1.93	0.49
8:H:89:PRO:HA	8:H:92:ARG:NH1	2.28	0.49
10:J:8:LEU:CD1	10:J:20:ALA:HB2	2.29	0.49
10:J:37:PRO:CA	10:J:72:VAL:HG22	2.39	0.49
10:J:47:PHE:CZ	14:N:37:PHE:HE2	2.30	0.49
15:O:4:THR:O	15:O:7:GLU:HG2	2.12	0.49
16:P:33:ILE:O	16:P:34:GLU:HB2	2.13	0.49
1:A:129(A):G:O2'	1:A:189(F):U:C2'	2.57	0.49
1:A:922:G:O2'	1:A:1398:A:N1	2.44	0.49
1:A:975:A:H4'	1:A:976:G:O5'	2.11	0.49
1:A:1090:U:H2'	1:A:1091:U:C6	2.48	0.49
2:B:223:ILE:HD13	2:B:226:ARG:NE	2.27	0.49
6:F:21:LEU:O	6:F:25:ILE:HG13	2.12	0.49
9:I:53:VAL:CG2	9:I:85:LEU:HD21	2.38	0.49
9:I:63:ILE:HD11	9:I:81:ILE:HD11	1.94	0.49
9:I:93:ARG:O	9:I:95:LYS:N	2.46	0.49
15:O:36:ILE:HG23	15:O:56:LEU:HD11	1.95	0.49
19:S:49:ILE:O	19:S:60:VAL:HG12	2.13	0.49
21:V:5:ASP:C	21:V:7:ARG:H	2.21	0.49
1:A:394:G:H2'	1:A:395:C:C6	2.48	0.49
1:A:1047:G:O2'	1:A:1048:G:H5''	2.12	0.49
1:A:1203:C:O5'	1:A:1203:C:H6	1.94	0.49
3:C:193:TYR:HE1	3:C:196:LEU:HD11	1.77	0.49
4:D:110:PHE:CD2	4:D:148:VAL:CG2	2.96	0.49
5:E:80:ILE:HG22	8:H:104:ARG:NH1	2.27	0.49
7:G:76:ARG:HG3	7:G:76:ARG:NH1	2.28	0.49
15:O:76:GLU:O	15:O:77:ARG:C	2.55	0.49
16:P:4:ILE:CG1	16:P:64:ALA:HB1	2.38	0.49
1:A:197:A:H2'	1:A:198:G:O4'	2.13	0.49
1:A:421:U:C5	3:C:127:ARG:NH2	2.81	0.49
1:A:1057:G:H2'	1:A:1058:G:O4'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1191:A:P	3:C:3:ASN:ND2	2.85	0.49
1:A:1192:C:C5	1:A:1193:G:C8	3.00	0.49
2:B:91:PRO:O	2:B:92:TYR:HB3	2.13	0.49
2:B:211:ILE:HD12	2:B:211:ILE:N	2.28	0.49
4:D:3:ARG:NH1	4:D:70:ILE:HD12	2.28	0.49
7:G:12:LEU:HD12	7:G:12:LEU:N	2.28	0.49
14:N:25:VAL:HG12	14:N:39:LEU:CD2	2.43	0.49
18:R:62:GLU:C	18:R:64:ARG:N	2.70	0.49
1:A:1002:G:H2'	1:A:1003:G:H8	1.78	0.49
1:A:1255:G:H3'	1:A:1279:A:N6	2.26	0.49
2:B:17:PHE:O	2:B:41:ILE:HG23	2.13	0.49
2:B:87:ARG:HH21	2:B:219:VAL:HB	1.78	0.49
2:B:187:LEU:HA	2:B:201:ILE:HB	1.95	0.49
3:C:73:PRO:O	3:C:76:VAL:HB	2.12	0.49
4:D:3:ARG:O	4:D:5:ILE:HG13	2.12	0.49
4:D:61:LYS:HA	4:D:203:VAL:HG22	1.95	0.49
4:D:132:ARG:NH1	4:D:132:ARG:CB	2.76	0.49
9:I:82:ALA:HB1	9:I:96:LEU:HD21	1.94	0.49
13:M:42:ALA:O	13:M:43:THR:C	2.55	0.49
1:A:59:A:H2'	1:A:59:A:N3	2.28	0.49
1:A:162:A:C2'	1:A:163:C:H5'	2.43	0.49
1:A:697:U:H2'	1:A:698:G:H5'	1.94	0.49
1:A:1061:G:O2'	1:A:1062:U:H5'	2.13	0.49
1:A:1124:G:N7	1:A:1145:C:H2'	2.28	0.49
1:A:1128:C:H5'	9:I:16:ARG:HH12	1.77	0.49
2:B:237:ALA:C	2:B:239:VAL:H	2.20	0.49
3:C:23:TYR:CD1	3:C:23:TYR:C	2.91	0.49
9:I:106:ALA:O	9:I:108:VAL:HG23	2.12	0.49
11:K:50:TYR:HB3	11:K:54:ARG:HB2	1.93	0.49
13:M:115:LYS:O	13:M:116:THR:C	2.54	0.49
15:O:26:GLU:HA	15:O:81:LEU:HD11	1.95	0.49
1:A:175:C:H2'	1:A:176:C:H6	1.78	0.48
1:A:328:C:O2	1:A:328:C:H2'	2.13	0.48
1:A:1057:G:O2'	1:A:1058:G:H5'	2.13	0.48
1:A:1221:G:O3'	19:S:77:THR:HG21	2.12	0.48
1:A:1250:A:H2	1:A:1353:G:H21	1.61	0.48
4:D:8:VAL:HG21	4:D:115:ARG:HE	1.77	0.48
7:G:88:PRO:HB3	7:G:145:ALA:HB1	1.94	0.48
10:J:25:GLU:C	10:J:27:ALA:H	2.21	0.48
11:K:14:VAL:O	11:K:15:ALA:HB3	2.13	0.48
12:L:55:VAL:CG1	12:L:56:ALA:H	2.17	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:90:VAL:O	12:L:92:ASP:N	2.45	0.48
1:A:877:C:O2'	1:A:878:G:H5'	2.13	0.48
1:A:939:G:H5''	7:G:102:ARG:HH22	1.74	0.48
1:A:1091:U:O2	1:A:1093:A:C8	2.66	0.48
1:A:1216:G:O2'	1:A:1217:C:H5'	2.13	0.48
1:A:1309:G:H2'	1:A:1310:G:H5'	1.95	0.48
3:C:37:GLN:NE2	14:N:52:GLN:OE1	2.39	0.48
3:C:58:GLU:HB2	3:C:65:ALA:CB	2.42	0.48
3:C:91:LEU:CD1	3:C:99:VAL:HG23	2.31	0.48
6:F:19:LEU:C	6:F:21:LEU:H	2.21	0.48
7:G:38:LEU:O	7:G:38:LEU:HD12	2.13	0.48
10:J:34:VAL:C	10:J:36:GLY:H	2.21	0.48
1:A:920:U:H2'	1:A:921:U:C6	2.48	0.48
1:A:1115:C:H1'	14:N:61:TRP:HB2	1.95	0.48
6:F:3:ARG:HG2	6:F:3:ARG:HH11	1.79	0.48
6:F:43:LEU:HD22	6:F:43:LEU:H	1.78	0.48
7:G:107:ALA:O	7:G:110:GLN:HB2	2.13	0.48
8:H:68:ARG:HG2	8:H:68:ARG:HH11	1.77	0.48
9:I:5:TYR:OH	9:I:16:ARG:HG3	2.12	0.48
17:Q:95:TYR:N	17:Q:95:TYR:HD1	2.10	0.48
18:R:70:ILE:HG23	18:R:79:LEU:HD13	1.95	0.48
1:A:476:G:H2'	1:A:477:A:C8	2.46	0.48
1:A:1060:C:H5	3:C:2:GLY:HA3	1.72	0.48
2:B:77:ALA:CB	2:B:211:ILE:HG12	2.43	0.48
4:D:39:PRO:O	4:D:44:GLY:HA3	2.13	0.48
5:E:50:GLU:HG2	5:E:52:PRO:HD2	1.94	0.48
13:M:81:LEU:CD2	13:M:88:ARG:HH21	2.20	0.48
13:M:86:CYS:SG	13:M:87:TYR:N	2.86	0.48
1:A:250:A:H1'	1:A:252:U:C5	2.47	0.48
1:A:473:G:H5''	16:P:81:ARG:NH2	2.28	0.48
1:A:829:G:O2'	1:A:830:G:H5'	2.13	0.48
1:A:1077:G:H5'	1:A:1078:U:OP2	2.13	0.48
1:A:1273:G:C2	1:A:1274:G:H1'	2.49	0.48
1:A:1508:G:H2'	1:A:1509:C:H6	1.78	0.48
3:C:108:ASN:OD1	3:C:110:ASN:HB2	2.14	0.48
3:C:112:SER:O	3:C:115:LEU:HB2	2.13	0.48
4:D:133:VAL:HG11	4:D:138:TYR:CD2	2.48	0.48
7:G:148:ASN:O	7:G:150:ALA:N	2.46	0.48
11:K:69:ALA:HB1	11:K:103:LEU:HD12	1.95	0.48
17:Q:27:PHE:C	17:Q:35:VAL:HG23	2.39	0.48
20:T:57:ARG:NH1	20:T:102:GLY:CA	2.76	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:189(E):U:O2'	1:A:189(F):U:H5'	2.13	0.48
1:A:200:G:H2'	1:A:201:C:O4'	2.14	0.48
1:A:429:U:H1'	1:A:430:A:H5''	1.93	0.48
1:A:1118:C:H1'	1:A:1179:A:C4	2.49	0.48
1:A:1305:G:O2'	1:A:1332:A:N6	2.46	0.48
1:A:1420:C:N4	1:A:1480:G:H1	2.07	0.48
2:B:145:LEU:CD2	2:B:149:LEU:HD12	2.43	0.48
4:D:31:CYS:O	4:D:31:CYS:SG	2.71	0.48
4:D:80:GLU:OE1	4:D:80:GLU:HA	2.13	0.48
4:D:149:ALA:HB3	4:D:152:SER:OG	2.14	0.48
5:E:79:GLU:HB3	5:E:91:LEU:O	2.13	0.48
6:F:32:ASN:N	6:F:32:ASN:HD22	2.11	0.48
7:G:122:HIS:O	7:G:126:ASP:HB2	2.14	0.48
9:I:27:THR:OG1	9:I:62:TYR:HD1	1.96	0.48
9:I:31:GLN:HB3	9:I:35:GLU:HB3	1.94	0.48
9:I:100:GLY:C	9:I:102:LEU:N	2.69	0.48
12:L:10:LEU:HD21	12:L:15:ARG:HE	1.78	0.48
15:O:70:LEU:CD2	15:O:81:LEU:HD12	2.43	0.48
1:A:1305:G:P	21:V:2:GLY:N	2.87	0.48
2:B:74:LYS:NZ	2:B:206:ASP:HB2	2.28	0.48
3:C:19:GLU:HB3	3:C:40:ARG:NH2	2.28	0.48
3:C:148:GLY:O	3:C:149:ALA:HB2	2.14	0.48
4:D:15:GLU:C	4:D:17:VAL:H	2.22	0.48
5:E:96:PRO:HA	5:E:117:ASP:CG	2.38	0.48
6:F:19:LEU:HD23	6:F:20:ALA:N	2.29	0.48
10:J:79:ARG:O	10:J:83:GLU:HB2	2.13	0.48
11:K:77:MET:O	11:K:78:GLN:CB	2.61	0.48
13:M:117:VAL:CG1	13:M:118:ALA:H	2.17	0.48
14:N:31:ARG:HH11	14:N:31:ARG:HG3	1.79	0.48
16:P:76:GLN:O	16:P:76:GLN:CG	2.61	0.48
17:Q:74:LEU:HD23	17:Q:74:LEU:O	2.14	0.48
20:T:57:ARG:NH1	20:T:102:GLY:HA2	2.28	0.48
1:A:755:G:OP2	15:O:65:ARG:HD2	2.14	0.48
1:A:858:G:O6	1:A:869:G:C8	2.67	0.48
1:A:1271:G:C3'	1:A:1272:G:H5''	2.41	0.48
3:C:10:PHE:CZ	3:C:178:LEU:HD13	2.49	0.48
19:S:60:VAL:HG13	19:S:60:VAL:O	2.14	0.48
1:A:369:C:O2	1:A:369:C:C2'	2.62	0.48
1:A:1313:U:OP2	19:S:6:LYS:HA	2.14	0.48
3:C:149:ALA:HB1	3:C:201:TYR:O	2.14	0.48
10:J:19:SER:C	10:J:21:GLN:H	2.21	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:105:VAL:HG11	11:K:108:ILE:HD11	1.95	0.48
12:L:33:ARG:HD3	12:L:62:SER:HB3	1.96	0.48
14:N:44:LEU:C	14:N:44:LEU:HD12	2.38	0.48
17:Q:15:MET:HE1	17:Q:43:LEU:HD22	1.95	0.48
17:Q:95:TYR:N	17:Q:95:TYR:CD1	2.80	0.48
18:R:36:ASN:O	18:R:39:VAL:HG12	2.14	0.48
18:R:63:GLN:HG3	18:R:63:GLN:O	2.14	0.48
1:A:321:A:O2'	1:A:322:C:H5'	2.14	0.48
1:A:428:G:O2'	1:A:429:U:P	2.72	0.48
1:A:496:A:N3	1:A:496:A:H2'	2.29	0.48
1:A:965:A:C2	1:A:969:A:N1	2.81	0.48
1:A:1040:U:H2'	1:A:1041:A:H8	1.79	0.48
2:B:158:LEU:HD22	2:B:158:LEU:N	2.29	0.48
2:B:213:LEU:HD23	2:B:213:LEU:C	2.39	0.48
3:C:76:VAL:O	3:C:83:ARG:HB3	2.14	0.48
10:J:57:LYS:O	10:J:60:ARG:NH1	2.46	0.48
13:M:50:GLU:O	13:M:54:VAL:HG23	2.14	0.48
16:P:50:LYS:HD3	16:P:51:VAL:N	2.29	0.48
18:R:43:PHE:O	18:R:51:LEU:HD12	2.14	0.48
1:A:244:U:O4	1:A:906:G:H1'	2.14	0.47
1:A:855:G:C2'	1:A:856:C:H5'	2.44	0.47
1:A:1034:G:H2'	1:A:1034:G:N3	2.28	0.47
1:A:1115:C:N4	1:A:1186:G:C6	2.82	0.47
1:A:1196:U:O2	1:A:1196:U:H5''	2.14	0.47
1:A:1417:G:N2	1:A:1482:G:H2'	2.29	0.47
2:B:120:ALA:C	2:B:122:PHE:H	2.22	0.47
4:D:132:ARG:HB2	4:D:132:ARG:HH11	1.79	0.47
13:M:15:VAL:CG1	13:M:34:LEU:HD21	2.43	0.47
18:R:70:ILE:O	18:R:74:ARG:HG3	2.14	0.47
1:A:627:G:H2'	1:A:628:G:H8	1.78	0.47
1:A:707:C:O2'	1:A:708:C:H5'	2.14	0.47
1:A:1052:U:O2'	1:A:1055:A:OP2	2.32	0.47
1:A:1330:U:C2'	1:A:1331:G:H5'	2.43	0.47
2:B:132:LYS:HD3	2:B:135:GLN:NE2	2.29	0.47
3:C:134:ILE:HD11	3:C:153:VAL:CG2	2.44	0.47
4:D:3:ARG:CZ	4:D:70:ILE:HA	2.44	0.47
4:D:30:LYS:C	4:D:32:ALA:H	2.22	0.47
4:D:64:LEU:HD13	4:D:64:LEU:C	2.38	0.47
5:E:138:ALA:O	5:E:139:LEU:C	2.57	0.47
6:F:33:TYR:CE2	6:F:75:LEU:HA	2.49	0.47
7:G:121:ALA:O	7:G:125:MET:HG3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:80:ILE:N	8:H:80:ILE:CD1	2.71	0.47
10:J:27:ALA:HB2	10:J:85:LEU:CD2	2.39	0.47
12:L:50:SER:O	12:L:51:ALA:CB	2.62	0.47
12:L:90:VAL:O	12:L:91:LYS:C	2.57	0.47
16:P:64:ALA:O	16:P:66:PRO:HD3	2.14	0.47
19:S:65:ASN:HD22	19:S:65:ASN:N	2.12	0.47
23:Z:28:G:H3'	23:Z:29:G:C8	2.49	0.47
1:A:386:C:O2'	1:A:387:U:H5'	2.14	0.47
1:A:1128:C:H4'	9:I:16:ARG:HH12	1.78	0.47
1:A:1144:G:H21	1:A:1146:A:N6	2.01	0.47
1:A:1157:A:C6	1:A:1180:A:C5	3.02	0.47
1:A:1160:G:H2'	1:A:1160:G:N3	2.29	0.47
7:G:59:LEU:HD11	7:G:63:LYS:HE2	1.96	0.47
7:G:105:VAL:HG12	7:G:109:ASN:ND2	2.29	0.47
11:K:121:PRO:HG2	11:K:126:ARG:HB3	1.96	0.47
12:L:86:ARG:HH11	12:L:86:ARG:HG3	1.79	0.47
1:A:22:G:H2'	1:A:23:C:H6	1.78	0.47
1:A:226:G:O2'	1:A:227:G:H5'	2.15	0.47
1:A:248:C:C2'	1:A:249:U:H5'	2.44	0.47
1:A:329:A:N7	1:A:332:G:N1	2.62	0.47
1:A:663:A:C2'	1:A:664:G:H5'	2.43	0.47
1:A:986:A:N3	19:S:52:TYR:OH	2.43	0.47
4:D:130:GLY:O	4:D:131:ARG:O	2.31	0.47
5:E:84:PHE:HB3	5:E:134:ALA:HB2	1.96	0.47
8:H:11:THR:O	8:H:12:ARG:C	2.55	0.47
8:H:91:ARG:HH11	8:H:91:ARG:CG	2.27	0.47
11:K:59:TYR:CZ	11:K:63:LEU:HD21	2.50	0.47
11:K:126:ARG:C	11:K:128:ALA:N	2.73	0.47
15:O:73:GLU:O	15:O:75:PRO:HD3	2.14	0.47
17:Q:27:PHE:O	17:Q:36:ILE:HD13	2.14	0.47
17:Q:53:LEU:HD23	17:Q:54:GLY:N	2.28	0.47
19:S:30:LEU:C	19:S:31:ILE:HG13	2.39	0.47
23:Z:38:A:H2'	23:Z:39:U:O4'	2.14	0.47
1:A:181:G:O2'	1:A:182:U:C6	2.67	0.47
1:A:625:G:H2'	1:A:626:U:C6	2.50	0.47
1:A:1219:U:OP1	14:N:19:ARG:NH2	2.43	0.47
2:B:84:GLU:HG3	2:B:219:VAL:CG2	2.45	0.47
3:C:152:ILE:O	3:C:152:ILE:HG22	2.13	0.47
4:D:25:ARG:HH11	4:D:25:ARG:HG3	1.79	0.47
8:H:79:VAL:HB	8:H:80:ILE:CD1	2.41	0.47
9:I:75:ASP:O	9:I:78:LYS:HB3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:85:ILE:HG22	12:L:86:ARG:N	2.28	0.47
13:M:88:ARG:HG3	13:M:98:VAL:HG22	1.94	0.47
1:A:622:A:H2'	1:A:623:C:H5'	1.97	0.47
1:A:628:G:H2'	1:A:629:G:H8	1.79	0.47
1:A:1129:C:OP1	1:A:1130:A:H5''	2.15	0.47
1:A:1236:A:O2'	1:A:1304:G:H4'	2.14	0.47
7:G:28:ASN:OD1	7:G:36:LYS:HE2	2.15	0.47
7:G:116:ALA:HA	7:G:119:ARG:NH1	2.29	0.47
9:I:8:GLY:H	9:I:83:ARG:NH1	2.11	0.47
1:A:192:U:O2'	1:A:193:C:H5'	2.14	0.47
1:A:689:C:H2'	1:A:690:G:O4'	2.14	0.47
1:A:721:G:OP2	18:R:53:ARG:HB2	2.14	0.47
1:A:724:G:O2'	1:A:725:G:H5'	2.15	0.47
1:A:803:G:C6	1:A:804:U:C4	3.03	0.47
1:A:918:A:H2'	1:A:919:A:C8	2.49	0.47
1:A:1226:C:C4	13:M:104:ARG:HB2	2.49	0.47
1:A:1257:U:O2	1:A:1257:U:H2'	2.15	0.47
1:A:1279:A:H5'	10:J:9:ARG:HH22	1.79	0.47
1:A:1310:G:O2'	1:A:1311:G:H8	1.96	0.47
1:A:1496:C:H1'	1:A:1517:G:H22	1.80	0.47
2:B:21:ARG:H	2:B:21:ARG:HD3	1.79	0.47
2:B:70:PHE:CE2	2:B:215:LEU:HD21	2.49	0.47
2:B:97:TRP:HH2	2:B:176:GLU:CD	2.22	0.47
4:D:54:TYR:O	4:D:55:ALA:C	2.57	0.47
4:D:60:GLU:OE2	4:D:199:ASN:HB3	2.15	0.47
4:D:110:PHE:CE2	4:D:148:VAL:HG23	2.50	0.47
4:D:180:GLY:O	4:D:181:MET:HB2	2.14	0.47
5:E:35:GLY:HA3	5:E:112:LEU:HB3	1.97	0.47
5:E:148:VAL:O	5:E:152:ARG:HG3	2.14	0.47
6:F:4:TYR:CZ	6:F:72:VAL:HG21	2.49	0.47
9:I:86:VAL:HG22	9:I:92:TYR:O	2.15	0.47
9:I:111:ARG:HD2	14:N:61:TRP:O	2.14	0.47
12:L:83:VAL:HG22	12:L:84:LEU:N	2.28	0.47
13:M:96:LEU:O	13:M:110:ARG:NH1	2.48	0.47
13:M:122:LYS:HD2	13:M:123:ALA:H	1.78	0.47
14:N:37:PHE:O	14:N:39:LEU:N	2.48	0.47
14:N:43:CYS:O	14:N:46:GLU:HB2	2.15	0.47
16:P:26:ARG:HG2	16:P:26:ARG:NH1	2.29	0.47
17:Q:43:LEU:O	17:Q:69:LYS:HG3	2.13	0.47
17:Q:51:TYR:CD1	17:Q:51:TYR:N	2.82	0.47
18:R:40:LEU:C	18:R:42:ARG:N	2.72	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:19:VAL:HG13	19:S:20:LEU:H	1.79	0.47
1:A:413:G:H2'	1:A:428:G:N2	2.30	0.47
2:B:18:GLY:CA	2:B:42:ILE:HG12	2.29	0.47
2:B:36:ARG:O	2:B:37:ASN:HB3	2.15	0.47
2:B:82:ARG:CA	2:B:92:TYR:HE2	2.26	0.47
4:D:137:SER:O	4:D:138:TYR:C	2.58	0.47
11:K:103:LEU:HD23	11:K:104:GLN:H	1.80	0.47
12:L:87:GLY:HA2	12:L:98:TYR:HA	1.96	0.47
12:L:90:VAL:CG1	12:L:93:LEU:HD21	2.45	0.47
20:T:23:ARG:HG2	20:T:23:ARG:NH1	2.29	0.47
1:A:139:G:O2'	1:A:140:A:H5'	2.14	0.47
1:A:375:U:H4'	16:P:17:TYR:HE2	1.79	0.47
1:A:1186:G:N2	1:A:1187:G:H1'	2.29	0.47
1:A:1238:A:N7	1:A:1301:U:O4	2.48	0.47
1:A:1287:A:H2'	1:A:1288:A:C8	2.49	0.47
1:A:1305:G:OP1	21:V:2:GLY:N	2.48	0.47
3:C:6:HIS:CD2	3:C:8:ILE:H	2.33	0.47
8:H:65:TYR:N	8:H:65:TYR:CD1	2.83	0.47
11:K:27:ASN:OD1	11:K:45:GLY:HA3	2.14	0.47
11:K:128:ALA:O	11:K:129:SER:HB3	2.15	0.47
14:N:24:CYS:N	14:N:29:ARG:O	2.48	0.47
1:A:820:U:O4	26:A:3002:AM2:HA2	2.15	0.47
1:A:833:U:H2'	1:A:834:C:H6	1.80	0.47
1:A:1124:G:C2	1:A:1127:G:N2	2.83	0.47
1:A:1188:A:H2'	1:A:1189:C:H5'	1.97	0.47
1:A:1247:U:O2'	1:A:1248:A:H5''	2.15	0.47
1:A:1379:G:OP2	7:G:6:ARG:NE	2.48	0.47
2:B:16:HIS:HA	2:B:204:ASN:CG	2.38	0.47
3:C:6:HIS:NE2	3:C:8:ILE:HD12	2.30	0.47
3:C:180:ALA:O	3:C:181:ASN:CB	2.58	0.47
4:D:47:ARG:HG2	4:D:48:ALA:N	2.30	0.47
6:F:3:ARG:HG2	6:F:3:ARG:NH1	2.30	0.47
6:F:44:GLY:O	6:F:59:TYR:HA	2.14	0.47
10:J:13:HIS:HB3	10:J:68:HIS:CE1	2.50	0.47
11:K:101:SER:C	11:K:103:LEU:N	2.70	0.47
12:L:30:ALA:O	12:L:31:PRO:C	2.57	0.47
14:N:25:VAL:HG13	14:N:26:ARG:N	2.29	0.47
15:O:59:MET:O	15:O:62:GLN:HB3	2.15	0.47
17:Q:59:ILE:HG22	17:Q:71:PHE:CD1	2.50	0.47
18:R:69:THR:HG22	18:R:70:ILE:N	2.30	0.47
19:S:51:VAL:CG2	19:S:71:LEU:HD22	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:Z:34:G:C6	23:Z:35:A:C6	3.03	0.47
1:A:1004:A:N7	1:A:1026:G:C6	2.83	0.46
1:A:1054:C:OP1	1:A:1197:G:OP2	2.32	0.46
1:A:1136:U:H5''	1:A:1137:C:OP2	2.15	0.46
1:A:1157:A:H4'	1:A:1158:C:C2	2.49	0.46
1:A:1157:A:C5'	1:A:1158:C:C2	2.98	0.46
1:A:1190:G:C5'	3:C:176:HIS:NE2	2.77	0.46
1:A:1307:U:H2'	1:A:1308:U:C6	2.50	0.46
2:B:137:ARG:HB2	2:B:137:ARG:CZ	2.45	0.46
3:C:116:VAL:HG11	3:C:141:VAL:HG21	1.97	0.46
3:C:136:GLN:O	3:C:139:GLN:N	2.48	0.46
3:C:156:ARG:O	3:C:157:ILE:C	2.57	0.46
5:E:68:GLU:O	5:E:70:PRO:HD3	2.15	0.46
8:H:20:TYR:HD1	8:H:65:TYR:CD2	2.32	0.46
10:J:9:ARG:HG2	10:J:9:ARG:HH11	1.79	0.46
17:Q:12:SER:HB3	17:Q:20:THR:HB	1.98	0.46
17:Q:90:ILE:HG23	17:Q:91:ARG:N	2.30	0.46
1:A:393:A:OP2	16:P:12:LYS:HE2	2.15	0.46
1:A:439:A:C6	1:A:496:A:H1'	2.50	0.46
1:A:1404:C:H2'	1:A:1405:G:C8	2.51	0.46
2:B:16:HIS:C	2:B:18:GLY:N	2.72	0.46
3:C:87:LEU:HA	3:C:90:GLU:CG	2.44	0.46
6:F:52:ILE:O	6:F:53:ALA:HB3	2.14	0.46
9:I:99:LEU:CB	9:I:101:PHE:HE1	2.25	0.46
12:L:126:LYS:HD2	12:L:126:LYS:C	2.40	0.46
15:O:10:LYS:NZ	15:O:14:GLU:HG3	2.30	0.46
1:A:229:U:O2'	16:P:23:ASP:HB2	2.16	0.46
1:A:274:A:O2'	1:A:275:G:C8	2.69	0.46
1:A:642:A:N3	8:H:113:SER:OG	2.49	0.46
1:A:942:G:C2	1:A:943:U:C6	3.03	0.46
1:A:1051:C:C2	1:A:1052:U:C5	3.03	0.46
1:A:1053:G:N7	1:A:1200:C:H5''	2.31	0.46
1:A:1125:U:H3	10:J:5:ARG:NH2	2.11	0.46
1:A:1227:A:H5'	13:M:111:LYS:HZ3	1.81	0.46
2:B:76:GLN:NE2	2:B:208:ILE:H	2.13	0.46
2:B:81:VAL:HG12	2:B:92:TYR:HD2	1.80	0.46
2:B:92:TYR:CE1	2:B:151:GLY:CA	2.98	0.46
3:C:37:GLN:O	3:C:39:ILE:N	2.49	0.46
5:E:89:ILE:HG12	5:E:135:THR:HG22	1.96	0.46
6:F:1:MET:N	6:F:1:MET:HE3	2.31	0.46
11:K:52:GLY:C	11:K:54:ARG:N	2.73	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:63:THR:HG23	13:M:64:TRP:CD2	2.50	0.46
14:N:37:PHE:C	14:N:39:LEU:N	2.73	0.46
1:A:299:G:H2'	1:A:300:A:C8	2.50	0.46
1:A:1066:C:C5	1:A:1067:A:N6	2.83	0.46
1:A:1126:U:N3	1:A:1127:G:N2	2.63	0.46
1:A:1226:C:H42	13:M:104:ARG:HD2	1.79	0.46
1:A:1392:G:H21	1:A:1502:A:H8	1.63	0.46
3:C:23:TYR:CG	3:C:24:ALA:N	2.84	0.46
3:C:72:LYS:C	3:C:74:GLY:N	2.72	0.46
5:E:150:ARG:HH11	5:E:150:ARG:HG3	1.80	0.46
7:G:18:TYR:CD2	7:G:59:LEU:HB2	2.51	0.46
9:I:58:ARG:HB3	9:I:58:ARG:NH1	2.30	0.46
12:L:120:TYR:N	12:L:120:TYR:CD1	2.81	0.46
17:Q:61:GLU:HA	17:Q:71:PHE:CE1	2.50	0.46
19:S:5:LEU:O	19:S:6:LYS:HB2	2.15	0.46
19:S:78:ARG:HG2	19:S:78:ARG:HH11	1.79	0.46
20:T:59:ALA:O	20:T:63:ILE:HG13	2.16	0.46
1:A:438:G:O2'	1:A:494:U:O4	2.34	0.46
1:A:667:G:H2'	1:A:668:G:H8	1.79	0.46
1:A:760:G:H1	17:Q:105:ALA:CB	2.28	0.46
1:A:762:C:H5'	17:Q:104:LYS:HZ2	1.81	0.46
1:A:1147:C:C3'	1:A:1148:U:H5''	2.44	0.46
1:A:1272:G:H5'	1:A:1272:G:H8	1.80	0.46
1:A:1521:G:H2'	1:A:1522:U:C6	2.51	0.46
2:B:36:ARG:O	2:B:36:ARG:HG3	2.16	0.46
2:B:82:ARG:HB2	2:B:82:ARG:CZ	2.46	0.46
3:C:37:GLN:O	3:C:38:ARG:C	2.59	0.46
5:E:8:GLU:HA	5:E:33:VAL:O	2.15	0.46
5:E:110:LEU:HD21	5:E:139:LEU:HD21	1.97	0.46
8:H:19:VAL:HG23	8:H:21:LYS:HG2	1.97	0.46
13:M:66:LEU:O	13:M:67:GLU:C	2.59	0.46
16:P:28:ARG:HG2	16:P:28:ARG:HH11	1.81	0.46
1:A:308:C:H2'	1:A:309:G:H8	1.79	0.46
1:A:539:A:H2'	1:A:540:G:H8	1.78	0.46
1:A:956:U:O2	1:A:1225:A:C2	2.69	0.46
1:A:1256:A:N1	1:A:1278:U:O2	2.48	0.46
1:A:1318:A:O2'	19:S:37:ARG:HD2	2.15	0.46
2:B:9:GLU:CD	2:B:10:LEU:N	2.72	0.46
2:B:10:LEU:HD23	2:B:11:LEU:N	2.30	0.46
2:B:47:THR:HA	2:B:202:PRO:HG2	1.96	0.46
2:B:142:LEU:O	2:B:143:GLU:C	2.58	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:156:LYS:O	2:B:156:LYS:HD2	2.16	0.46
2:B:223:ILE:HD13	2:B:226:ARG:CD	2.45	0.46
3:C:31:HIS:C	3:C:33:LEU:N	2.74	0.46
5:E:64:ARG:H	5:E:64:ARG:HD2	1.81	0.46
6:F:62:TRP:CH2	6:F:64:GLN:HB2	2.50	0.46
10:J:92:THR:C	10:J:94:VAL:H	2.24	0.46
13:M:91:ARG:HH22	13:M:103:THR:HG21	1.81	0.46
14:N:4:LYS:CA	14:N:7:ILE:HG13	2.46	0.46
17:Q:68:ARG:H	17:Q:70:ARG:NH1	2.12	0.46
22:W:3:C:H2'	22:W:4:A:O4'	2.16	0.46
1:A:177:C:O2'	1:A:178:C:H5'	2.16	0.46
1:A:1286:A:C8	1:A:1287:A:H4'	2.51	0.46
1:A:1379:G:OP2	7:G:6:ARG:CZ	2.64	0.46
1:A:1426:C:O2'	1:A:1427:U:H5'	2.15	0.46
2:B:87:ARG:HD3	2:B:234:PRO:HD2	1.98	0.46
3:C:121:ALA:HB1	3:C:188:LEU:O	2.15	0.46
5:E:144:THR:O	5:E:145:LYS:C	2.58	0.46
7:G:119:ARG:HG3	7:G:119:ARG:NH1	2.31	0.46
8:H:104:ARG:O	8:H:105:ARG:C	2.59	0.46
11:K:12:ARG:HG2	11:K:12:ARG:O	2.15	0.46
11:K:126:ARG:O	11:K:127:LYS:C	2.58	0.46
12:L:41:ARG:HG3	12:L:42:THR:O	2.15	0.46
13:M:11:ARG:HG3	13:M:12:ASN:HB2	1.97	0.46
16:P:39:TYR:CD2	16:P:73:LEU:HD11	2.51	0.46
19:S:19:VAL:O	19:S:22:LEU:N	2.45	0.46
1:A:414:A:H2'	1:A:415:A:O4'	2.16	0.46
1:A:488:C:O5'	1:A:488:C:H6	1.98	0.46
1:A:1191:A:P	3:C:3:ASN:HD22	2.38	0.46
1:A:1229:A:O2'	13:M:125:ARG:NE	2.47	0.46
1:A:1249:C:H4'	9:I:36:TYR:OH	2.15	0.46
2:B:46:LYS:O	2:B:49:GLU:HB2	2.16	0.46
2:B:101:MET:HG2	2:B:108:ILE:HG21	1.98	0.46
4:D:8:VAL:HG21	4:D:115:ARG:NE	2.31	0.46
9:I:11:LYS:O	9:I:11:LYS:HG2	2.16	0.46
10:J:85:LEU:O	10:J:87:THR:N	2.49	0.46
12:L:75:HIS:HD2	12:L:77:LEU:HB2	1.81	0.46
14:N:32:SER:O	14:N:34:TYR:N	2.49	0.46
14:N:54:PRO:C	14:N:56:VAL:H	2.23	0.46
18:R:58:LEU:HB3	18:R:62:GLU:HB2	1.98	0.46
19:S:7:LYS:HG2	19:S:7:LYS:O	2.15	0.46
20:T:53:LEU:CD1	20:T:104:LEU:HD12	2.42	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:411:A:N6	1:A:413:G:H21	2.14	0.46
1:A:750:G:H21	15:O:23:GLY:CA	2.29	0.46
1:A:928:G:O2'	1:A:929:G:H5'	2.16	0.46
1:A:1418:A:H2'	1:A:1419:G:H5'	1.98	0.46
1:A:1497:G:C2'	1:A:1498:U:H5'	2.46	0.46
1:A:1530:G:H4'	1:A:1530:G:OP1	2.15	0.46
2:B:71:VAL:CG2	2:B:164:VAL:HG22	2.45	0.46
2:B:73:THR:HG22	2:B:169:LYS:HZ1	1.80	0.46
3:C:107:GLN:CD	3:C:107:GLN:N	2.70	0.46
3:C:107:GLN:NE2	3:C:107:GLN:N	2.64	0.46
5:E:43:LEU:HD11	5:E:132:ALA:CB	2.39	0.46
5:E:60:TYR:O	5:E:64:ARG:NE	2.48	0.46
6:F:19:LEU:C	6:F:21:LEU:N	2.73	0.46
10:J:47:PHE:N	10:J:63:PHE:O	2.45	0.46
15:O:38:ARG:HG3	15:O:38:ARG:NH1	2.31	0.46
17:Q:83:ASP:O	17:Q:86:GLU:HB2	2.15	0.46
19:S:13:ASP:HA	19:S:16:LEU:CB	2.45	0.46
1:A:982:U:OP1	1:A:982:U:H6	1.99	0.46
1:A:1288:A:H2'	1:A:1289:A:O4'	2.16	0.46
2:B:187:LEU:C	2:B:187:LEU:HD13	2.41	0.46
4:D:19:LEU:HB3	4:D:21:LEU:HD21	1.98	0.46
4:D:91:SER:O	4:D:94:LEU:HB2	2.16	0.46
5:E:36:ASP:OD1	5:E:40:ARG:HB2	2.15	0.46
7:G:6:ARG:O	7:G:7:ALA:O	2.33	0.46
11:K:95:ILE:HD12	11:K:95:ILE:N	2.29	0.46
13:M:52:GLU:HG2	13:M:55:ARG:NH2	2.26	0.46
13:M:87:TYR:C	13:M:89:GLY:N	2.72	0.46
15:O:31:LEU:HD12	15:O:31:LEU:HA	1.80	0.46
20:T:64:ASP:O	20:T:67:ALA:HB3	2.15	0.46
1:A:677:U:H3	1:A:713:G:H22	1.63	0.45
1:A:1070:U:P	5:E:25:ARG:HH12	2.39	0.45
4:D:31:CYS:C	4:D:33:MET:H	2.24	0.45
9:I:42:ARG:NH2	9:I:71:SER:HB2	2.27	0.45
10:J:75:ILE:O	10:J:76:ASN:HB2	2.16	0.45
13:M:7:VAL:HG23	13:M:7:VAL:O	2.16	0.45
13:M:8:GLU:O	13:M:10:PRO:HD3	2.16	0.45
15:O:38:ARG:HG3	15:O:38:ARG:HH11	1.81	0.45
17:Q:60:ILE:O	17:Q:71:PHE:HD1	1.98	0.45
20:T:8:ARG:O	20:T:9:ASN:HB2	2.16	0.45
20:T:26:ASN:O	20:T:27:LYS:C	2.58	0.45
20:T:43:LEU:CD1	20:T:51:GLU:HG3	2.45	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:538:G:O2'	1:A:539:A:H5'	2.17	0.45
1:A:1157:A:OP2	1:A:1157:A:H3'	2.16	0.45
1:A:1279:A:H2'	1:A:1279:A:N3	2.31	0.45
1:A:1362:C:H2'	1:A:1363:C:H5''	1.97	0.45
4:D:61:LYS:HE3	4:D:62:GLN:NE2	2.31	0.45
9:I:28:VAL:O	9:I:29:ASN:HB2	2.15	0.45
10:J:4:ILE:HD11	10:J:74:ILE:HB	1.98	0.45
11:K:58:PRO:O	11:K:61:ALA:HB3	2.17	0.45
11:K:82:VAL:HG23	11:K:105:VAL:HG13	1.99	0.45
11:K:128:ALA:O	11:K:129:SER:CB	2.63	0.45
12:L:105:TYR:C	12:L:107:ALA:H	2.24	0.45
14:N:11:LYS:C	14:N:13:THR:N	2.74	0.45
20:T:22:ARG:O	20:T:23:ARG:C	2.58	0.45
23:Z:29:G:H2'	23:Z:30:G:C5	2.51	0.45
1:A:26:A:C2'	1:A:27:G:H5'	2.46	0.45
1:A:794:A:H2'	1:A:795:C:C6	2.52	0.45
1:A:972:C:H4'	10:J:57:LYS:CG	2.23	0.45
1:A:1049:U:H4'	1:A:1050:G:C5'	2.46	0.45
1:A:1277:C:H6	1:A:1277:C:H5'	1.81	0.45
1:A:1343:G:H2'	1:A:1344:C:C6	2.52	0.45
3:C:115:LEU:O	3:C:116:VAL:C	2.58	0.45
4:D:19:LEU:O	4:D:21:LEU:N	2.49	0.45
4:D:64:LEU:HB2	4:D:198:VAL:HG11	1.99	0.45
5:E:15:ARG:HD2	5:E:15:ARG:O	2.16	0.45
5:E:99:GLY:HA2	5:E:116:THR:O	2.16	0.45
6:F:1:MET:H3	6:F:1:MET:CE	2.29	0.45
9:I:16:ARG:NH2	9:I:64:THR:HG21	2.31	0.45
10:J:47:PHE:HB2	10:J:63:PHE:HB2	1.97	0.45
15:O:88:ARG:HH11	15:O:88:ARG:HG2	1.81	0.45
18:R:53:ARG:O	18:R:55:ARG:N	2.48	0.45
1:A:620:C:H2'	1:A:621:A:O4'	2.16	0.45
1:A:1047:G:C3'	1:A:1048:G:H5''	2.44	0.45
1:A:1121:U:O2'	1:A:1122:U:H6	2.00	0.45
1:A:1250:A:H4'	9:I:68:GLY:CA	2.45	0.45
1:A:1309:G:H5'	13:M:78:ILE:HD11	1.97	0.45
1:A:1371:G:C6	1:A:1372:U:C4	3.05	0.45
2:B:28:PHE:CZ	2:B:189:ASP:HA	2.51	0.45
3:C:55:VAL:O	3:C:56:ASP:C	2.58	0.45
5:E:107:ARG:O	5:E:110:LEU:N	2.47	0.45
6:F:40:VAL:CG2	6:F:41:GLU:N	2.79	0.45
14:N:24:CYS:HB3	14:N:28:GLY:N	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:5:LYS:H	15:O:5:LYS:CD	2.27	0.45
17:Q:95:TYR:HA	17:Q:98:LEU:CD1	2.46	0.45
19:S:43:GLU:H	19:S:43:GLU:CD	2.24	0.45
20:T:45:GLN:CA	20:T:91:LEU:HD22	2.46	0.45
1:A:16:A:C2	1:A:920:U:O2	2.70	0.45
1:A:67:C:O2'	1:A:171:A:H1'	2.16	0.45
1:A:242:C:H2'	1:A:243:A:H5'	1.97	0.45
1:A:279:A:C5'	1:A:280:C:H3'	2.46	0.45
1:A:1060:C:C2	1:A:1198:G:C2	3.05	0.45
1:A:1103:C:H4'	2:B:98:LEU:HD12	1.98	0.45
1:A:1508:G:H2'	1:A:1509:C:C6	2.51	0.45
6:F:9:VAL:HG22	6:F:60:PHE:CD2	2.51	0.45
9:I:5:TYR:CD1	9:I:6:GLY:N	2.84	0.45
9:I:27:THR:OG1	9:I:62:TYR:HA	2.17	0.45
9:I:32:ASP:O	9:I:33:PHE:C	2.58	0.45
11:K:104:GLN:NE2	11:K:106:LYS:HE2	2.31	0.45
12:L:29:GLY:O	12:L:30:ALA:C	2.59	0.45
12:L:78:GLN:HB3	12:L:79:GLU:H	1.46	0.45
1:A:135:C:C2	16:P:1:MET:HB2	2.46	0.45
1:A:192:U:O4'	20:T:103:GLY:HA2	2.17	0.45
1:A:343:U:H6	1:A:343:U:C5'	2.28	0.45
1:A:599:C:O2'	1:A:600:C:H5'	2.17	0.45
1:A:792:A:H1'	1:A:794:A:N7	2.31	0.45
1:A:1397:C:O2'	22:W:5:A:N6	2.49	0.45
2:B:163:PHE:HA	2:B:185:ILE:O	2.17	0.45
3:C:132:ARG:NH1	3:C:132:ARG:HB3	2.32	0.45
3:C:188:LEU:HB3	3:C:189:ALA:H	1.55	0.45
3:C:195:VAL:HG23	3:C:196:LEU:N	2.30	0.45
4:D:29:PRO:HA	4:D:34:GLU:HG2	1.99	0.45
7:G:50:ILE:HD11	7:G:121:ALA:O	2.17	0.45
13:M:8:GLU:O	13:M:10:PRO:HD2	2.17	0.45
13:M:21:TYR:N	13:M:21:TYR:CD1	2.84	0.45
16:P:48:TRP:CD1	16:P:48:TRP:H	2.33	0.45
20:T:73:HIS:O	20:T:74:LYS:CG	2.60	0.45
1:A:90:U:O5'	1:A:90:U:H6	1.99	0.45
1:A:622:A:C8	1:A:623:C:C6	3.05	0.45
1:A:865:A:O5'	1:A:865:A:H8	1.99	0.45
1:A:987:G:H2'	1:A:988:G:C8	2.52	0.45
1:A:1298:C:N4	7:G:114:ARG:HG2	2.32	0.45
2:B:25:ASN:HD22	2:B:26:PRO:CD	2.29	0.45
2:B:197:VAL:HB	2:B:200:ILE:HG12	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:216:SER:C	2:B:218:ALA:N	2.73	0.45
4:D:60:GLU:OE1	4:D:60:GLU:HA	2.16	0.45
4:D:119:GLN:HG3	4:D:123:HIS:CD2	2.51	0.45
5:E:72:GLN:O	5:E:73:ASN:CB	2.65	0.45
5:E:110:LEU:O	5:E:113:ALA:N	2.47	0.45
13:M:108:ARG:NE	13:M:108:ARG:HA	2.32	0.45
14:N:3:ARG:O	14:N:5:ALA:N	2.49	0.45
18:R:88:LYS:C	18:R:88:LYS:CD	2.90	0.45
1:A:374:A:C6	1:A:375:U:C4	3.05	0.45
1:A:609:A:H2'	1:A:610:G:H5'	1.98	0.45
1:A:1197:G:H3'	1:A:1198:G:H5'	1.99	0.45
1:A:1214:C:O2	1:A:1214:C:C2'	2.65	0.45
1:A:1238:A:N7	1:A:1303:C:H1'	2.32	0.45
2:B:23:ARG:NH1	2:B:191:ASP:HA	2.31	0.45
3:C:165:THR:O	3:C:165:THR:HG22	2.15	0.45
4:D:8:VAL:C	4:D:10:ARG:N	2.69	0.45
4:D:170:VAL:HG22	4:D:171:GLY:H	1.78	0.45
8:H:51:VAL:HG11	8:H:60:ARG:NE	2.32	0.45
9:I:9:ARG:HG2	9:I:14:VAL:CG1	2.34	0.45
9:I:35:GLU:OE1	9:I:35:GLU:HA	2.16	0.45
12:L:54:LYS:N	12:L:54:LYS:HD2	2.31	0.45
13:M:82:MET:CE	13:M:93:ARG:HB2	2.46	0.45
16:P:56:ALA:C	16:P:58:TYR:N	2.72	0.45
18:R:47:THR:HG23	18:R:83:GLU:H	1.81	0.45
1:A:10:A:OP2	5:E:126:ARG:NH1	2.50	0.45
1:A:129:U:H5''	1:A:129(A):G:H5'	1.99	0.45
1:A:855:G:O2'	1:A:856:C:H5'	2.17	0.45
1:A:1103:C:H5'	2:B:98:LEU:HD12	1.99	0.45
1:A:1113:C:C3'	1:A:1114:C:H5'	2.38	0.45
1:A:1273:G:H2'	1:A:1274:G:O4'	2.16	0.45
1:A:1286:A:H2'	1:A:1287:A:H4'	1.98	0.45
1:A:1410:G:H1	1:A:1490:C:H42	1.65	0.45
1:A:1506:U:O2'	1:A:1507:A:H5'	2.17	0.45
4:D:3:ARG:HG3	4:D:3:ARG:NH1	2.31	0.45
4:D:111:ALA:HB2	4:D:120:LEU:CD1	2.47	0.45
4:D:125:HIS:C	4:D:126:ILE:HG13	2.42	0.45
5:E:101:ILE:CD1	5:E:119:LEU:HA	2.47	0.45
7:G:67:GLU:HA	7:G:67:GLU:OE1	2.17	0.45
7:G:118:VAL:O	7:G:121:ALA:HB3	2.17	0.45
15:O:2:PRO:HB2	15:O:3:ILE:H	1.65	0.45
16:P:14:ASN:N	16:P:15:PRO:CD	2.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:47:THR:C	18:R:49:LYS:H	2.24	0.45
19:S:41:VAL:HB	19:S:43:GLU:OE2	2.17	0.45
20:T:79:ARG:HD2	20:T:83:ARG:NH2	2.32	0.45
1:A:476:G:O2'	1:A:477:A:H5'	2.17	0.45
1:A:1141:C:O2'	1:A:1142:G:H5'	2.16	0.45
2:B:78:GLN:CG	2:B:94:ASN:OD1	2.65	0.45
2:B:97:TRP:CZ2	2:B:101:MET:HB2	2.51	0.45
2:B:142:LEU:HD22	2:B:146:GLN:NE2	2.31	0.45
2:B:223:ILE:HG22	2:B:224:GLN:N	2.32	0.45
4:D:12:CYS:SG	4:D:19:LEU:O	2.75	0.45
4:D:106:TYR:CD1	4:D:106:TYR:C	2.94	0.45
9:I:49:PRO:O	9:I:52:ALA:HB3	2.17	0.45
18:R:53:ARG:C	18:R:55:ARG:N	2.74	0.45
20:T:94:ALA:O	20:T:95:ALA:HB3	2.16	0.45
1:A:52:G:O2'	1:A:53:A:H5'	2.17	0.44
1:A:922:G:H2'	1:A:923:A:C8	2.52	0.44
1:A:981:U:C3'	1:A:982:U:H5''	2.44	0.44
1:A:1232:U:H5''	9:I:124:GLN:O	2.16	0.44
1:A:1291:G:H2'	1:A:1292:U:C6	2.51	0.44
1:A:1305:G:N2	1:A:1331:G:H1'	2.31	0.44
2:B:211:ILE:HG23	2:B:215:LEU:HD12	1.98	0.44
3:C:14:ILE:O	3:C:15:THR:C	2.59	0.44
3:C:190:ARG:HB3	3:C:190:ARG:NH1	2.32	0.44
4:D:170:VAL:CG2	4:D:171:GLY:H	2.30	0.44
4:D:196:LEU:HA	4:D:197:PRO:HD2	1.85	0.44
5:E:76:ILE:CG1	5:E:118:ILE:HD12	2.47	0.44
6:F:67:MET:HE3	6:F:75:LEU:HG	1.99	0.44
13:M:30:ALA:C	13:M:32:GLU:H	2.24	0.44
14:N:11:LYS:O	14:N:12:ARG:HB2	2.17	0.44
18:R:27:GLY:O	18:R:28:GLU:C	2.60	0.44
1:A:1176:A:H2'	1:A:1177:G:O4'	2.18	0.44
1:A:1366:C:O2'	10:J:60:ARG:NH2	2.50	0.44
1:A:1424:C:O2'	1:A:1425:U:H5'	2.18	0.44
2:B:23:ARG:C	2:B:23:ARG:CD	2.89	0.44
2:B:25:ASN:HD22	2:B:26:PRO:N	2.15	0.44
2:B:64:ARG:NH1	2:B:64:ARG:CB	2.81	0.44
2:B:82:ARG:HB3	2:B:94:ASN:ND2	2.31	0.44
2:B:180:LEU:C	2:B:182:ILE:H	2.24	0.44
3:C:173:VAL:HG12	3:C:175:LEU:CD2	2.47	0.44
8:H:125:ARG:HE	8:H:125:ARG:HB2	1.63	0.44
9:I:6:GLY:CA	9:I:83:ARG:HB2	2.44	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:26:LEU:HD22	18:R:26:LEU:HA	1.85	0.44
19:S:65:ASN:ND2	19:S:65:ASN:N	2.65	0.44
21:V:14:TRP:C	21:V:16:GLY:H	2.23	0.44
1:A:640:A:C2'	1:A:641:U:H5'	2.47	0.44
1:A:1477:C:H2'	1:A:1478:C:C6	2.52	0.44
6:F:48:LEU:HD13	6:F:52:ILE:CD1	2.47	0.44
7:G:108:ALA:C	7:G:110:GLN:N	2.75	0.44
18:R:48:GLY:O	18:R:74:ARG:NH2	2.50	0.44
20:T:54:LYS:HB3	20:T:54:LYS:HE2	1.87	0.44
23:Z:29:G:H22	23:Z:42:C:N4	2.15	0.44
1:A:373:A:C2	1:A:482:A:C6	3.06	0.44
1:A:997:U:H6	1:A:997:U:H5'	1.83	0.44
1:A:1100:C:O2'	1:A:1101:A:H5'	2.17	0.44
1:A:1112:C:H1'	3:C:179:ARG:NH2	2.32	0.44
1:A:1157:A:H5'	1:A:1158:C:C4	2.53	0.44
2:B:178:ARG:HH11	2:B:178:ARG:CB	2.29	0.44
3:C:20:SER:O	14:N:54:PRO:HB3	2.17	0.44
5:E:31:LEU:HD23	5:E:31:LEU:HA	1.87	0.44
9:I:93:ARG:C	9:I:95:LYS:N	2.74	0.44
11:K:29:ILE:HD13	11:K:29:ILE:O	2.17	0.44
13:M:63:THR:HG23	13:M:64:TRP:CG	2.52	0.44
20:T:24:LEU:HD12	20:T:24:LEU:HA	1.82	0.44
1:A:451:A:N6	1:A:480:U:H2'	2.32	0.44
1:A:644:G:C5	1:A:645:C:C5	3.05	0.44
1:A:940:C:H2'	1:A:941:G:C8	2.53	0.44
1:A:986:A:H2'	1:A:987:G:C8	2.53	0.44
1:A:1030:C:C1'	1:A:1032:G:H22	2.31	0.44
1:A:1463:C:O2'	1:A:1464:G:H5'	2.17	0.44
2:B:224:GLN:O	2:B:225:ALA:HB2	2.18	0.44
3:C:5:ILE:CD1	3:C:5:ILE:H	2.31	0.44
3:C:54:ARG:O	3:C:55:VAL:HG23	2.18	0.44
3:C:70:VAL:C	3:C:106:VAL:HG23	2.42	0.44
3:C:134:ILE:HG22	3:C:168:ALA:HB3	1.97	0.44
4:D:59:ARG:NH2	4:D:66:ARG:HH12	2.15	0.44
4:D:153:ARG:HG2	4:D:181:MET:SD	2.57	0.44
5:E:31:LEU:HD22	5:E:43:LEU:CD2	2.47	0.44
5:E:79:GLU:CG	5:E:93:PRO:HD2	2.42	0.44
8:H:17:THR:HB	8:H:78:GLN:OE1	2.18	0.44
9:I:18:PHE:HD2	9:I:62:TYR:CD2	2.36	0.44
9:I:97:LYS:C	9:I:99:LEU:H	2.25	0.44
10:J:63:PHE:HE2	14:N:45:ARG:HA	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:75:PRO:O	15:O:79:ARG:HG3	2.18	0.44
17:Q:59:ILE:CG2	17:Q:71:PHE:HB3	2.48	0.44
18:R:22:VAL:C	18:R:24:ALA:H	2.24	0.44
1:A:385:C:H2'	1:A:386:C:C6	2.40	0.44
1:A:545:C:O2'	1:A:546:G:H5'	2.17	0.44
1:A:1352:C:N3	1:A:1371:G:C6	2.86	0.44
2:B:216:SER:OG	2:B:217:ARG:N	2.51	0.44
3:C:14:ILE:HG22	3:C:15:THR:HG23	2.00	0.44
4:D:150:GLU:HG2	4:D:153:ARG:HH22	1.76	0.44
6:F:32:ASN:N	6:F:32:ASN:ND2	2.66	0.44
8:H:51:VAL:HG12	8:H:60:ARG:HB2	1.99	0.44
8:H:103:VAL:CG2	8:H:110:ALA:HB2	2.47	0.44
9:I:99:LEU:CB	9:I:101:PHE:CE1	2.97	0.44
10:J:48:THR:OG1	10:J:62:HIS:CD2	2.71	0.44
10:J:63:PHE:HA	14:N:57:ARG:O	2.17	0.44
12:L:48:PRO:O	12:L:49:ASN:ND2	2.45	0.44
18:R:50:ILE:CD1	18:R:70:ILE:HG21	2.47	0.44
1:A:81:U:H6	1:A:81:U:H5'	1.82	0.44
1:A:419:C:O2	1:A:419:C:H2'	2.18	0.44
1:A:750:G:N3	15:O:23:GLY:HA3	2.32	0.44
1:A:930:C:C2'	1:A:931:C:H5'	2.48	0.44
1:A:1182:G:O2'	1:A:1183:A:P	2.76	0.44
2:B:182:ILE:O	2:B:183:PRO:C	2.60	0.44
3:C:180:ALA:HB1	3:C:203:PHE:HE1	1.83	0.44
9:I:108:VAL:HG12	9:I:109:VAL:N	2.33	0.44
11:K:52:GLY:C	11:K:54:ARG:H	2.26	0.44
1:A:8:A:N7	4:D:208:SER:O	2.50	0.44
1:A:46:G:O2'	1:A:365:U:H1'	2.17	0.44
1:A:1402:C:H2'	1:A:1403:C:O4'	2.18	0.44
1:A:1496:C:H2'	1:A:1497:G:C8	2.52	0.44
2:B:78:GLN:HG2	2:B:94:ASN:OD1	2.17	0.44
3:C:10:PHE:CE2	3:C:178:LEU:HD13	2.53	0.44
3:C:29:TYR:OH	14:N:54:PRO:HG2	2.18	0.44
3:C:79:ARG:HE	3:C:82:GLU:CG	2.22	0.44
4:D:150:GLU:CA	4:D:153:ARG:HH21	2.27	0.44
5:E:81:GLU:CG	5:E:88:LYS:HE2	2.48	0.44
11:K:13:GLN:HA	11:K:75:TYR:O	2.18	0.44
15:O:76:GLU:C	15:O:78:TYR:N	2.75	0.44
16:P:6:LEU:N	16:P:6:LEU:CD1	2.80	0.44
1:A:38:G:C2	1:A:397:A:C2	3.06	0.44
1:A:107:G:H5'	1:A:108:G:OP2	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:329:A:C6	1:A:332:G:N1	2.85	0.44
1:A:1402:C:O2	1:A:1500:A:N1	2.51	0.44
2:B:75:LYS:HD2	2:B:78:GLN:OE1	2.18	0.44
2:B:95:GLN:OE1	2:B:95:GLN:HA	2.18	0.44
2:B:211:ILE:O	2:B:212:GLN:C	2.61	0.44
3:C:16:ARG:HD2	3:C:16:ARG:HA	1.88	0.44
4:D:98:GLU:C	4:D:100:ARG:H	2.26	0.44
4:D:194:LEU:HD22	4:D:194:LEU:N	2.33	0.44
6:F:16:GLN:NE2	6:F:16:GLN:O	2.51	0.44
7:G:16:LEU:O	7:G:17:VAL:HG23	2.18	0.44
10:J:62:HIS:O	14:N:59:ALA:N	2.44	0.44
15:O:25:THR:HG21	15:O:70:LEU:HB2	1.99	0.44
1:A:160:A:H2'	1:A:161:A:O4'	2.18	0.43
1:A:428:G:H1'	1:A:430:A:N7	2.33	0.43
1:A:520:A:H61	1:A:529:G:H1'	1.83	0.43
1:A:714:G:H2'	1:A:715:A:C8	2.52	0.43
1:A:840:C:O2'	1:A:848:C:N3	2.50	0.43
1:A:985:C:H2'	1:A:986:A:H8	1.82	0.43
3:C:179:ARG:O	3:C:180:ALA:C	2.60	0.43
7:G:95:ARG:HA	7:G:98:SER:OG	2.17	0.43
9:I:18:PHE:HD2	9:I:62:TYR:HD2	1.64	0.43
11:K:38:ASN:HA	11:K:39:PRO:HD3	1.62	0.43
11:K:43:SER:HB3	11:K:68:ALA:HB2	2.00	0.43
11:K:78:GLN:O	11:K:104:GLN:N	2.39	0.43
1:A:99:U:O2'	1:A:100:C:H5'	2.18	0.43
1:A:128:G:O2'	17:Q:3:LYS:HE3	2.18	0.43
1:A:380:G:C2	1:A:384:G:C6	3.06	0.43
1:A:716:A:N3	11:K:117:ASN:O	2.52	0.43
1:A:933:G:OP1	7:G:4:ARG:HB2	2.19	0.43
1:A:1460:A:H2'	1:A:1461:G:O4'	2.18	0.43
2:B:86:GLU:C	2:B:88:ALA:H	2.25	0.43
2:B:118:LEU:HD12	2:B:142:LEU:CG	2.48	0.43
2:B:137:ARG:O	2:B:141:GLU:HB2	2.18	0.43
2:B:222:ILE:HG22	2:B:226:ARG:NH2	2.33	0.43
3:C:39:ILE:HG21	3:C:57:ILE:HD11	2.00	0.43
3:C:101:LEU:C	3:C:101:LEU:CD2	2.91	0.43
3:C:115:LEU:O	3:C:117:ALA:N	2.51	0.43
6:F:94:GLN:NE2	18:R:32:ARG:CZ	2.81	0.43
9:I:16:ARG:HD2	9:I:18:PHE:CZ	2.53	0.43
10:J:34:VAL:H	10:J:75:ILE:HG22	1.83	0.43
11:K:120:ARG:HG3	11:K:120:ARG:NH1	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:82:VAL:HG23	12:L:105:TYR:HB3	1.99	0.43
13:M:39:ILE:O	13:M:40:ASN:C	2.61	0.43
14:N:25:VAL:CG1	14:N:26:ARG:N	2.81	0.43
18:R:23:LYS:HG2	18:R:23:LYS:O	2.19	0.43
20:T:10:LEU:O	20:T:10:LEU:HD13	2.18	0.43
20:T:103:GLY:O	20:T:104:LEU:HG	2.17	0.43
1:A:167:G:O2'	1:A:168:G:H5'	2.17	0.43
1:A:196:A:C3'	1:A:197:A:H5''	2.49	0.43
1:A:682:G:C6	1:A:709:G:C6	3.06	0.43
1:A:839:U:O2	1:A:839:U:C2'	2.65	0.43
1:A:1014:A:H2	1:A:1219:U:H1'	1.78	0.43
2:B:233:SER:C	2:B:235:SER:H	2.26	0.43
3:C:175:LEU:HD23	3:C:175:LEU:N	2.33	0.43
4:D:3:ARG:NE	4:D:71:SER:N	2.66	0.43
4:D:115:ARG:NH1	4:D:115:ARG:HG2	2.33	0.43
5:E:26:PHE:O	5:E:27:ARG:HB2	2.17	0.43
9:I:63:ILE:HD11	9:I:81:ILE:CD1	2.47	0.43
10:J:76:ASN:HB2	10:J:78:ASN:ND2	2.32	0.43
12:L:55:VAL:O	12:L:56:ALA:HB2	2.18	0.43
14:N:26:ARG:CG	14:N:27:CYS:N	2.79	0.43
16:P:75:ARG:C	16:P:77:ALA:N	2.75	0.43
19:S:25:LYS:O	19:S:26:GLY:C	2.61	0.43
1:A:329:A:H2'	1:A:332:G:N7	2.34	0.43
1:A:457:C:H2'	1:A:458:C:H6	1.82	0.43
1:A:802:A:H2'	1:A:803:G:H5'	2.00	0.43
1:A:940:C:H2'	1:A:941:G:H8	1.84	0.43
1:A:1043:C:H2'	1:A:1044:A:C8	2.53	0.43
1:A:1347:G:N7	9:I:10:ARG:NH2	2.64	0.43
5:E:107:ARG:O	5:E:108:ALA:C	2.61	0.43
12:L:9:GLN:O	12:L:13:LYS:N	2.36	0.43
20:T:74:LYS:HE2	20:T:74:LYS:HB3	1.73	0.43
1:A:499:A:N1	1:A:546:G:O2'	2.43	0.43
1:A:684:A:O4'	11:K:38:ASN:ND2	2.52	0.43
1:A:1030:C:C2	1:A:1032:G:N1	2.85	0.43
1:A:1418:A:C2'	1:A:1419:G:H5'	2.48	0.43
2:B:204:ASN:C	2:B:206:ASP:N	2.76	0.43
9:I:33:PHE:C	9:I:35:GLU:H	2.26	0.43
10:J:51:ARG:O	14:N:45:ARG:CZ	2.67	0.43
11:K:104:GLN:HE21	11:K:104:GLN:HB3	1.61	0.43
16:P:74:LEU:HB3	16:P:79:VAL:HG21	1.99	0.43
17:Q:95:TYR:O	17:Q:96:GLN:C	2.61	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:100:ILE:O	20:T:102:GLY:N	2.46	0.43
1:A:153:C:O2'	1:A:154:C:H5'	2.18	0.43
1:A:253:U:H2'	1:A:254:G:C8	2.53	0.43
1:A:1107:C:C4	1:A:1108:G:C8	3.06	0.43
2:B:61:LEU:HD22	2:B:61:LEU:N	2.33	0.43
3:C:5:ILE:H	3:C:5:ILE:HD13	1.82	0.43
3:C:31:HIS:O	3:C:33:LEU:N	2.51	0.43
4:D:100:ARG:HB3	4:D:102:ASP:OD1	2.19	0.43
4:D:150:GLU:CG	4:D:153:ARG:HH21	2.28	0.43
4:D:175:SER:OG	4:D:186:LEU:HD21	2.19	0.43
5:E:57:LYS:O	5:E:61:TYR:CD2	2.71	0.43
5:E:63:ARG:HG2	5:E:63:ARG:NH1	2.33	0.43
6:F:67:MET:HB2	6:F:68:PRO:HD2	2.01	0.43
8:H:63:LEU:N	8:H:63:LEU:HD23	2.32	0.43
10:J:20:ALA:HB1	10:J:72:VAL:HG21	1.99	0.43
10:J:45:ARG:HD3	10:J:47:PHE:CZ	2.53	0.43
10:J:76:ASN:O	10:J:78:ASN:N	2.45	0.43
13:M:21:TYR:HD1	13:M:21:TYR:H	1.67	0.43
13:M:23:TYR:HB3	13:M:67:GLU:H	1.84	0.43
13:M:30:ALA:C	13:M:32:GLU:N	2.76	0.43
19:S:78:ARG:H	19:S:78:ARG:HG3	1.65	0.43
20:T:58:LYS:O	20:T:58:LYS:HG2	2.18	0.43
23:Z:30:G:N1	23:Z:41:C:N4	2.65	0.43
23:Z:37:A:H3'	23:Z:38:A:H8	1.82	0.43
1:A:494:U:C2'	1:A:495:A:H5'	2.48	0.43
1:A:1032:G:H2'	1:A:1033:G:H8	1.83	0.43
1:A:1210:C:H2'	1:A:1211:U:O4'	2.18	0.43
2:B:64:ARG:NH1	2:B:64:ARG:HB2	2.34	0.43
2:B:98:LEU:HD23	2:B:98:LEU:N	2.16	0.43
2:B:157:ARG:HB2	2:B:157:ARG:HH11	1.83	0.43
3:C:119:ARG:O	3:C:122:GLU:HB3	2.18	0.43
4:D:77:ASN:HD22	4:D:77:ASN:N	2.15	0.43
4:D:187:ARG:NE	4:D:187:ARG:HA	2.34	0.43
6:F:11:ASN:HD21	6:F:13:ASN:HB2	1.84	0.43
7:G:140:ASP:O	7:G:144:MET:HB2	2.18	0.43
8:H:11:THR:C	8:H:13:ILE:N	2.75	0.43
11:K:111:ASP:OD1	18:R:84:LYS:HE3	2.18	0.43
12:L:53:ARG:HG2	12:L:53:ARG:NH1	2.33	0.43
13:M:23:TYR:HB2	13:M:67:GLU:CD	2.43	0.43
13:M:84:ILE:C	13:M:86:CYS:H	2.26	0.43
19:S:28:LYS:C	19:S:29:ARG:HG3	2.44	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:39:THR:CG2	19:S:40:ILE:N	2.63	0.43
19:S:51:VAL:O	19:S:57:HIS:HA	2.19	0.43
21:V:6:ARG:HB3	21:V:15:ARG:NH1	2.33	0.43
1:A:39:G:O2'	1:A:40:C:H5'	2.19	0.43
1:A:390:C:H2'	1:A:391:G:C8	2.54	0.43
1:A:792:A:H4'	1:A:793:U:C5'	2.48	0.43
1:A:1126:U:H3	1:A:1127:G:N2	2.17	0.43
1:A:1492:A:OP1	12:L:47:LYS:N	2.51	0.43
2:B:58:ILE:O	2:B:62:ALA:N	2.52	0.43
2:B:148:TYR:O	2:B:149:LEU:HD23	2.19	0.43
3:C:19:GLU:CB	3:C:40:ARG:HH22	2.30	0.43
3:C:22:TRP:CE3	3:C:22:TRP:O	2.71	0.43
3:C:46:GLU:C	3:C:48:TYR:N	2.73	0.43
5:E:82:VAL:HG12	5:E:89:ILE:CG2	2.48	0.43
8:H:25:ASP:C	8:H:26:VAL:HG12	2.44	0.43
10:J:45:ARG:HH11	10:J:45:ARG:CB	2.32	0.43
13:M:96:LEU:O	13:M:97:PRO:C	2.61	0.43
14:N:4:LYS:O	14:N:7:ILE:HG13	2.19	0.43
1:A:13:U:O4'	1:A:914:A:H5''	2.19	0.43
1:A:187:C:H5''	20:T:86:ARG:NH1	2.34	0.43
1:A:294:U:H2'	1:A:295:C:H6	1.83	0.43
1:A:581:G:O6	1:A:758:G:C8	2.72	0.43
1:A:969:A:C2'	1:A:970:C:H5'	2.48	0.43
1:A:1175:G:O2'	1:A:1176:A:H5'	2.19	0.43
1:A:1266:G:N2	1:A:1270:C:N3	2.66	0.43
2:B:18:GLY:HA2	2:B:42:ILE:H	1.84	0.43
3:C:113:ALA:C	3:C:115:LEU:N	2.76	0.43
3:C:173:VAL:HG12	3:C:175:LEU:HD21	2.00	0.43
4:D:31:CYS:O	4:D:32:ALA:CB	2.67	0.43
4:D:158:ILE:CG2	4:D:162:LEU:HD12	2.48	0.43
5:E:88:LYS:HB3	5:E:123:LEU:HB2	2.01	0.43
5:E:137:GLU:OE2	5:E:140:ARG:HD2	2.18	0.43
10:J:28:ARG:HG2	10:J:28:ARG:NH1	2.33	0.43
10:J:35:SER:HB3	10:J:72:VAL:O	2.19	0.43
10:J:44:VAL:HG22	10:J:66:ARG:HB3	2.00	0.43
10:J:72:VAL:HG12	10:J:73:ASP:N	2.33	0.43
16:P:26:ARG:CD	16:P:31:LYS:O	2.65	0.43
20:T:100:ILE:HD13	20:T:100:ILE:N	2.33	0.43
23:Z:38:A:C5	23:Z:39:U:H1'	2.54	0.43
1:A:1158:C:O2	1:A:1158:C:C4'	2.67	0.43
1:A:1249:C:O2'	9:I:73:GLN:NE2	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1405:G:O4'	1:A:1519:A:H4'	2.19	0.43
26:A:3005:AM2:HC6	26:A:3005:AM2:HA1	1.89	0.43
2:B:64:ARG:HH11	2:B:64:ARG:HB3	1.84	0.43
2:B:83:MET:HB3	2:B:235:SER:OG	2.19	0.43
3:C:77:ILE:O	3:C:83:ARG:N	2.52	0.43
4:D:11:LEU:O	4:D:12:CYS:C	2.61	0.43
4:D:58:LEU:O	4:D:62:GLN:HG2	2.19	0.43
4:D:150:GLU:CB	4:D:153:ARG:HH21	2.32	0.43
6:F:25:ILE:O	6:F:28:ARG:HB3	2.18	0.43
6:F:48:LEU:C	6:F:50:TYR:H	2.27	0.43
7:G:108:ALA:C	7:G:110:GLN:H	2.27	0.43
7:G:138:LYS:HG2	7:G:139:GLU:N	2.34	0.43
8:H:11:THR:HG23	8:H:14:ARG:HH12	1.84	0.43
10:J:21:GLN:HA	10:J:24:VAL:HG12	2.01	0.43
11:K:111:ASP:O	11:K:112:THR:C	2.61	0.43
12:L:58:VAL:O	12:L:65:GLU:HA	2.19	0.43
14:N:56:VAL:HG12	14:N:57:ARG:N	2.33	0.43
16:P:56:ALA:O	16:P:58:TYR:N	2.52	0.43
16:P:60:LEU:HD23	16:P:60:LEU:HA	1.88	0.43
17:Q:97:SER:CB	17:Q:103:GLY:HA3	2.48	0.43
19:S:29:ARG:HG3	19:S:29:ARG:HH11	1.84	0.43
20:T:50:GLU:O	20:T:100:ILE:CG1	2.59	0.43
20:T:51:GLU:HA	20:T:54:LYS:HB3	2.01	0.43
1:A:162:A:H2'	1:A:163:C:C5'	2.48	0.42
1:A:263:A:P	20:T:79:ARG:HH12	2.42	0.42
1:A:479:C:C5'	1:A:479:C:C6	2.91	0.42
1:A:969:A:H61	13:M:126:LYS:HB2	1.84	0.42
1:A:1030(A):G:H22	1:A:1030(C):G:H3'	1.83	0.42
1:A:1114:C:N3	1:A:1115:C:H5	2.16	0.42
2:B:132:LYS:CA	2:B:135:GLN:HB2	2.46	0.42
4:D:18:LYS:HE3	4:D:20:TYR:CZ	2.54	0.42
5:E:82:VAL:HG12	5:E:89:ILE:HG22	2.02	0.42
6:F:7:ASN:O	6:F:88:VAL:HA	2.17	0.42
7:G:72:ARG:HG3	7:G:72:ARG:HH11	1.84	0.42
7:G:80:VAL:HG12	7:G:81:GLY:N	2.34	0.42
8:H:41:ARG:HG2	8:H:41:ARG:O	2.18	0.42
9:I:3:GLN:HE21	9:I:3:GLN:CA	2.09	0.42
9:I:91:ASP:C	9:I:93:ARG:N	2.76	0.42
10:J:64:GLU:N	14:N:59:ALA:HB2	2.34	0.42
12:L:117:ARG:CG	12:L:122:THR:HB	2.47	0.42
18:R:47:THR:HG22	18:R:48:GLY:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:17:U:H2'	1:A:18:C:C6	2.54	0.42
1:A:429:U:H4'	1:A:430:A:O5'	2.19	0.42
1:A:1093:A:C5	1:A:1095:U:O4'	2.72	0.42
1:A:1479:C:O2'	1:A:1480:G:H5'	2.19	0.42
2:B:204:ASN:C	2:B:206:ASP:H	2.25	0.42
2:B:204:ASN:HB3	2:B:206:ASP:O	2.19	0.42
3:C:5:ILE:HD13	3:C:5:ILE:O	2.19	0.42
3:C:29:TYR:O	3:C:29:TYR:HD1	2.02	0.42
5:E:102:ALA:CB	5:E:120:THR:HB	2.45	0.42
7:G:78:ARG:HD3	7:G:156:TRP:CE3	2.54	0.42
8:H:114:THR:HG21	8:H:129:VAL:HG23	2.01	0.42
13:M:98:VAL:O	13:M:98:VAL:HG13	2.19	0.42
17:Q:48:GLU:O	17:Q:50:LYS:N	2.51	0.42
17:Q:93:GLN:HE21	17:Q:93:GLN:HB3	1.49	0.42
1:A:219:C:C4	1:A:220:G:C8	3.07	0.42
1:A:335:C:H2'	1:A:336:C:C6	2.54	0.42
1:A:620:C:C1'	4:D:135:LEU:HD13	2.50	0.42
1:A:1055:A:C8	1:A:1206:G:C2	3.08	0.42
1:A:1191:A:OP1	3:C:3:ASN:ND2	2.52	0.42
1:A:1309:G:C6	1:A:1329:A:C2	3.06	0.42
1:A:1347:G:C8	9:I:107:ARG:HB3	2.54	0.42
2:B:69:LEU:C	2:B:69:LEU:CD2	2.93	0.42
2:B:178:ARG:NH1	8:H:71:GLY:O	2.51	0.42
4:D:3:ARG:HH22	4:D:70:ILE:HG13	1.83	0.42
4:D:133:VAL:HG11	4:D:138:TYR:HD2	1.84	0.42
5:E:41:VAL:CG1	5:E:113:ALA:HA	2.48	0.42
6:F:26:ILE:HG21	6:F:63:TYR:HE2	1.78	0.42
6:F:48:LEU:CD1	6:F:52:ILE:HD12	2.47	0.42
6:F:95:GLU:O	6:F:97:PHE:N	2.52	0.42
7:G:31:MET:CG	7:G:32:ARG:N	2.81	0.42
7:G:88:PRO:CB	7:G:145:ALA:HB1	2.49	0.42
9:I:58:ARG:NH1	9:I:58:ARG:CB	2.82	0.42
12:L:15:ARG:HG3	12:L:15:ARG:NH1	2.34	0.42
12:L:117:ARG:HG2	12:L:122:THR:O	2.20	0.42
13:M:62:ASN:HD22	13:M:62:ASN:HA	1.71	0.42
18:R:51:LEU:HA	18:R:52:PRO:HD3	1.91	0.42
19:S:7:LYS:HE2	19:S:7:LYS:HB3	1.94	0.42
19:S:16:LEU:O	19:S:19:VAL:HG12	2.19	0.42
20:T:11:SER:N	20:T:13:LEU:CD1	2.83	0.42
23:Z:30:G:N2	23:Z:41:C:C5	2.87	0.42
23:Z:37:A:H3'	23:Z:38:A:C8	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:100:C:H2'	1:A:101:A:C8	2.54	0.42
1:A:1169:A:H2'	1:A:1170:A:C8	2.54	0.42
1:A:1368:G:H5''	9:I:112:LYS:CG	2.49	0.42
2:B:142:LEU:CD2	2:B:146:GLN:HE22	2.30	0.42
2:B:206:ASP:CG	2:B:207:ALA:N	2.77	0.42
3:C:13:GLY:HA3	14:N:57:ARG:HH21	1.85	0.42
4:D:9:CYS:SG	4:D:31:CYS:O	2.78	0.42
5:E:76:ILE:HG23	5:E:142:LEU:CD1	2.49	0.42
7:G:31:MET:HA	7:G:39:ALA:HB2	2.02	0.42
13:M:59:TYR:O	13:M:59:TYR:CG	2.71	0.42
14:N:27:CYS:SG	14:N:29:ARG:HB2	2.59	0.42
1:A:976:G:C8	1:A:1358:U:H2'	2.55	0.42
1:A:993:G:H2'	1:A:993:G:N3	2.34	0.42
1:A:1201:A:H4'	1:A:1202:G:H5''	2.01	0.42
1:A:1202:G:H2'	1:A:1203:C:C5'	2.49	0.42
1:A:1404:C:O4'	1:A:1499:A:C2	2.72	0.42
2:B:23:ARG:CZ	2:B:23:ARG:O	2.67	0.42
4:D:60:GLU:HG2	4:D:202:LEU:HD12	2.00	0.42
12:L:70:ILE:HD13	12:L:77:LEU:HD12	2.01	0.42
16:P:21:VAL:C	16:P:22:THR:HG22	2.45	0.42
17:Q:5:VAL:O	17:Q:6:LEU:HD23	2.20	0.42
1:A:175:C:O2'	1:A:176:C:H5'	2.19	0.42
1:A:1223:C:H3'	1:A:1224:G:H5''	2.02	0.42
1:A:1225:A:H2'	1:A:1225:A:N3	2.34	0.42
1:A:1237:C:C4'	1:A:1334:G:H21	2.33	0.42
1:A:1314:C:OP2	19:S:6:LYS:CD	2.52	0.42
1:A:1442(A):G:C3'	1:A:1442(B):A:H5'	2.50	0.42
2:B:23:ARG:NH1	2:B:24:TRP:O	2.53	0.42
3:C:131:ARG:HD3	5:E:50:GLU:OE2	2.20	0.42
6:F:33:TYR:HD2	6:F:75:LEU:CD2	2.32	0.42
8:H:89:PRO:HA	8:H:92:ARG:HH11	1.83	0.42
9:I:93:ARG:C	9:I:95:LYS:H	2.27	0.42
10:J:54:PHE:O	10:J:55:LYS:HG2	2.20	0.42
19:S:4:SER:O	19:S:5:LEU:HD12	2.19	0.42
1:A:603:U:H2'	1:A:604:G:H8	1.85	0.42
1:A:1050:G:N2	1:A:1209:C:H1'	2.35	0.42
1:A:1190:G:H5'	3:C:176:HIS:NE2	2.34	0.42
1:A:1356:G:H2'	1:A:1357:A:H8	1.82	0.42
2:B:50:GLU:O	2:B:51:LEU:C	2.61	0.42
2:B:178:ARG:HD3	2:B:184:VAL:HG21	2.02	0.42
3:C:22:TRP:CZ3	3:C:32:LEU:HB3	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:28:GLN:O	3:C:30:ARG:N	2.53	0.42
3:C:43:LEU:O	3:C:47:LEU:HD13	2.20	0.42
3:C:132:ARG:O	3:C:133:ALA:C	2.63	0.42
4:D:109:GLY:C	4:D:111:ALA:N	2.77	0.42
5:E:75:THR:HG23	5:E:76:ILE:N	2.35	0.42
5:E:80:ILE:CD1	5:E:138:ALA:HB1	2.50	0.42
6:F:75:LEU:HD13	6:F:75:LEU:O	2.19	0.42
7:G:155:ARG:O	7:G:156:TRP:HB3	2.20	0.42
11:K:82:VAL:HG12	11:K:83:ILE:N	2.35	0.42
11:K:101:SER:O	11:K:103:LEU:N	2.53	0.42
17:Q:60:ILE:HG12	17:Q:61:GLU:N	2.34	0.42
18:R:39:VAL:CG1	18:R:40:LEU:N	2.83	0.42
1:A:646:U:O2'	1:A:647:C:H5'	2.19	0.42
1:A:718:G:C4'	11:K:117:ASN:HD22	2.33	0.42
1:A:797:C:OP1	11:K:124:LYS:HD2	2.19	0.42
1:A:948:C:OP1	13:M:109:THR:N	2.52	0.42
1:A:1023:G:H2'	1:A:1024:G:H5'	2.01	0.42
1:A:1140:C:H6	1:A:1140:C:H5'	1.85	0.42
1:A:1230:C:H1'	13:M:126:LYS:HA	2.02	0.42
1:A:1459:C:O2'	1:A:1460:A:H5'	2.19	0.42
4:D:3:ARG:NH1	4:D:70:ILE:HA	2.35	0.42
4:D:4:TYR:CG	4:D:5:ILE:N	2.88	0.42
4:D:134:ASP:O	4:D:136:PRO:HD3	2.20	0.42
6:F:21:LEU:HD12	6:F:24:GLU:OE1	2.19	0.42
6:F:62:TRP:HB2	18:R:35:ARG:NH1	2.34	0.42
7:G:16:LEU:HD21	9:I:42:ARG:HG3	2.02	0.42
7:G:54:THR:CG2	7:G:56:GLN:HB2	2.50	0.42
10:J:76:ASN:CB	10:J:78:ASN:ND2	2.83	0.42
13:M:14:ARG:HE	13:M:42:ALA:HA	1.84	0.42
13:M:123:ALA:O	13:M:124:PRO:C	2.63	0.42
15:O:15:PHE:O	15:O:16:ALA:C	2.62	0.42
15:O:55:GLY:HA2	15:O:58:MET:CE	2.50	0.42
16:P:67:THR:HG23	16:P:70:ALA:CB	2.50	0.42
18:R:23:LYS:HD2	18:R:58:LEU:HD23	2.01	0.42
18:R:37:VAL:O	18:R:41:LYS:HG2	2.20	0.42
18:R:44:LEU:HD12	18:R:44:LEU:N	2.35	0.42
19:S:22:LEU:O	19:S:27:GLU:HA	2.19	0.42
20:T:49:ALA:O	20:T:100:ILE:HG12	2.20	0.42
1:A:30:U:O2	1:A:30:U:H2'	2.20	0.42
1:A:77:G:O2'	1:A:78:G:H5'	2.20	0.42
1:A:321:A:C2	1:A:333:G:C2	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:386:C:H2'	1:A:387:U:C5'	2.50	0.42
1:A:389:A:H2'	1:A:390:C:C5'	2.47	0.42
1:A:618:C:H5''	1:A:619:U:H5''	2.02	0.42
1:A:1054:C:O5'	1:A:1197:G:OP2	2.37	0.42
1:A:1197:G:O5'	1:A:1198:G:OP2	2.38	0.42
1:A:1272:G:O2'	1:A:1273:G:H5'	2.20	0.42
2:B:140:HIS:CA	2:B:143:GLU:HG2	2.42	0.42
2:B:157:ARG:O	2:B:158:LEU:C	2.62	0.42
3:C:103:VAL:CG1	3:C:104:GLN:H	2.32	0.42
3:C:103:VAL:CG1	3:C:104:GLN:N	2.81	0.42
6:F:8:ILE:HD13	6:F:26:ILE:HD12	2.01	0.42
7:G:143:ARG:CB	7:G:143:ARG:HH11	2.33	0.42
9:I:65:VAL:CG2	9:I:73:GLN:HB3	2.46	0.42
10:J:12:ASP:OD1	10:J:13:HIS:N	2.53	0.42
11:K:88:GLY:C	11:K:90:GLY:H	2.28	0.42
12:L:25:PRO:C	12:L:27:LEU:N	2.71	0.42
13:M:49:THR:O	13:M:50:GLU:C	2.59	0.42
14:N:23:ARG:CZ	14:N:30:ALA:HB2	2.50	0.42
17:Q:9:VAL:O	17:Q:11:VAL:HG13	2.20	0.42
17:Q:27:PHE:CE1	17:Q:36:ILE:HD11	2.55	0.42
17:Q:27:PHE:HD1	17:Q:28:PRO:O	2.02	0.42
1:A:455:C:H42	1:A:476:G:H1	1.67	0.42
1:A:802:A:C2'	1:A:803:G:H5'	2.50	0.42
1:A:949:A:C2	1:A:1233:G:N3	2.88	0.42
1:A:1051:C:H2'	1:A:1052:U:C6	2.49	0.42
1:A:1095:U:H2'	1:A:1096:C:C6	2.54	0.42
1:A:1158:C:C6	1:A:1160:G:C8	3.08	0.42
1:A:1311:G:O6	19:S:2:PRO:HB3	2.20	0.42
1:A:1360:A:H8	1:A:1360:A:O5'	2.02	0.42
2:B:28:PHE:CD2	2:B:190:THR:HA	2.55	0.42
2:B:211:ILE:H	2:B:211:ILE:CD1	2.32	0.42
3:C:79:ARG:O	3:C:81:GLY:N	2.52	0.42
3:C:83:ARG:CA	3:C:86:VAL:HG23	2.33	0.42
6:F:86:ARG:HG3	6:F:86:ARG:NH1	2.35	0.42
8:H:44:PHE:O	8:H:80:ILE:HD11	2.19	0.42
13:M:23:TYR:O	13:M:25:ILE:N	2.53	0.42
13:M:81:LEU:C	13:M:81:LEU:HD12	2.45	0.42
16:P:71:ARG:NH1	16:P:71:ARG:HB2	2.35	0.42
18:R:40:LEU:C	18:R:42:ARG:H	2.28	0.42
20:T:86:ARG:O	20:T:90:GLN:HG2	2.19	0.42
1:A:89:C:H2'	1:A:90:U:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:947:G:P	13:M:108:ARG:HG2	2.60	0.41
1:A:1051:C:N3	1:A:1052:U:C5	2.88	0.41
1:A:1103:C:H2'	1:A:1104:G:O4'	2.20	0.41
2:B:23:ARG:HH11	2:B:24:TRP:HA	1.85	0.41
2:B:219:VAL:HA	2:B:222:ILE:CG1	2.50	0.41
4:D:18:LYS:HD2	4:D:31:CYS:CB	2.50	0.41
4:D:47:ARG:HH12	4:D:49:ARG:HG2	1.85	0.41
4:D:107:ARG:HH12	4:D:114:ARG:HH22	1.68	0.41
7:G:141:VAL:HA	7:G:144:MET:HB2	2.02	0.41
8:H:90:GLY:O	8:H:91:ARG:HB2	2.19	0.41
12:L:43:VAL:HG12	12:L:44:THR:H	1.83	0.41
18:R:40:LEU:O	18:R:43:PHE:N	2.31	0.41
20:T:33:ILE:HD13	20:T:63:ILE:HA	2.02	0.41
20:T:49:ALA:HB3	20:T:99:LEU:HG	2.02	0.41
1:A:439:A:H2'	1:A:441:A:H5'	2.02	0.41
1:A:519:C:O2'	1:A:520:A:H5'	2.21	0.41
1:A:601:C:H2'	1:A:602:A:C8	2.56	0.41
1:A:667:G:H2'	1:A:668:G:C8	2.54	0.41
1:A:909:A:H2'	1:A:910:C:O4'	2.20	0.41
1:A:959:A:H5''	1:A:960:U:OP2	2.20	0.41
1:A:1172:C:H2'	1:A:1173:G:H8	1.84	0.41
1:A:1203:C:O2'	1:A:1204:A:H5'	2.21	0.41
1:A:1227:A:H8	1:A:1227:A:H3'	1.85	0.41
1:A:1297:C:HO2'	1:A:1298:C:H6	1.64	0.41
2:B:84:GLU:HG3	2:B:216:SER:HA	2.02	0.41
2:B:194:PRO:C	2:B:196:LEU:H	2.28	0.41
3:C:85:ARG:HH11	3:C:85:ARG:HG3	1.85	0.41
3:C:191:THR:OG1	3:C:192:THR:N	2.51	0.41
4:D:119:GLN:CG	4:D:123:HIS:HD2	2.33	0.41
6:F:23:LYS:NZ	6:F:42:GLU:OE1	2.53	0.41
8:H:51:VAL:HG21	8:H:60:ARG:CZ	2.49	0.41
10:J:56:HIS:C	10:J:58:ASP:N	2.72	0.41
11:K:120:ARG:HG3	11:K:120:ARG:HH11	1.86	0.41
12:L:104:VAL:O	12:L:105:TYR:HB2	2.20	0.41
17:Q:86:GLU:O	17:Q:87:LYS:C	2.61	0.41
3:C:44:GLU:HG2	3:C:52:LEU:CD2	2.50	0.41
3:C:135:LYS:NZ	5:E:52:PRO:HG3	2.35	0.41
6:F:5:GLU:O	6:F:6:VAL:C	2.61	0.41
8:H:109:ILE:HG12	8:H:137:VAL:HB	2.01	0.41
10:J:45:ARG:HB2	10:J:45:ARG:NH1	2.34	0.41
12:L:93:LEU:HD12	12:L:96:VAL:HG21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:66:LEU:O	13:M:67:GLU:O	2.38	0.41
15:O:17:ARG:HG3	15:O:17:ARG:NH1	2.31	0.41
16:P:8:ARG:HH11	16:P:8:ARG:HG3	1.85	0.41
1:A:52:G:H2'	1:A:53:A:H8	1.85	0.41
1:A:189(G):G:H4'	1:A:189(H):G:OP2	2.21	0.41
1:A:485:G:H2'	1:A:486:U:OP2	2.21	0.41
1:A:515:G:H8	1:A:515:G:O5'	2.03	0.41
1:A:662:G:O2'	1:A:836:G:C5'	2.68	0.41
1:A:721:G:H8	1:A:721:G:OP1	2.03	0.41
1:A:999:C:OP1	1:A:999:C:H4'	2.20	0.41
1:A:1288:A:H1'	1:A:1352:C:O2'	2.19	0.41
1:A:1385:G:C2'	1:A:1386:G:H5''	2.47	0.41
1:A:1466:C:H2'	1:A:1467:G:O4'	2.20	0.41
2:B:231:GLU:H	2:B:231:GLU:CD	2.27	0.41
3:C:52:LEU:HA	3:C:70:VAL:HG12	2.02	0.41
4:D:4:TYR:O	4:D:5:ILE:CB	2.66	0.41
4:D:35:ARG:O	4:D:36:ARG:CB	2.67	0.41
6:F:23:LYS:HB3	6:F:23:LYS:HE2	1.89	0.41
6:F:44:GLY:HA3	6:F:59:TYR:CE1	2.54	0.41
7:G:136:LYS:C	7:G:138:LYS:N	2.78	0.41
11:K:70:LYS:HE3	11:K:70:LYS:HB2	1.64	0.41
12:L:75:HIS:HD2	12:L:77:LEU:H	1.67	0.41
13:M:52:GLU:C	13:M:54:VAL:N	2.75	0.41
13:M:87:TYR:O	13:M:90:LEU:N	2.53	0.41
14:N:23:ARG:HH11	14:N:23:ARG:HB3	1.85	0.41
15:O:45:VAL:O	15:O:47:LYS:N	2.54	0.41
19:S:60:VAL:HG21	19:S:74:PHE:CB	2.48	0.41
20:T:44:ALA:C	20:T:46:GLU:H	2.28	0.41
20:T:65:LYS:O	20:T:68:LYS:HB2	2.21	0.41
1:A:596:C:O2'	1:A:597:G:H5'	2.20	0.41
1:A:840:C:O2	1:A:840:C:C2'	2.67	0.41
1:A:930:C:O2'	1:A:931:C:H5'	2.19	0.41
1:A:950:U:C5	13:M:102:ARG:CZ	3.04	0.41
1:A:1075:C:O2'	1:A:1076:C:H5'	2.20	0.41
1:A:1247:U:H2'	1:A:1248:A:C5'	2.38	0.41
1:A:1266:G:H5'	1:A:1267:C:OP2	2.21	0.41
1:A:1376:U:P	7:G:94:ARG:HH22	2.43	0.41
1:A:1442:G:N3	1:A:1442:G:H3'	2.36	0.41
2:B:54:THR:O	2:B:57:PHE:HB3	2.21	0.41
2:B:195:ASP:O	8:H:74:PRO:HG3	2.20	0.41
3:C:115:LEU:C	3:C:117:ALA:N	2.76	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:158:GLY:C	3:C:160:ALA:N	2.75	0.41
4:D:132:ARG:NH1	4:D:132:ARG:HB2	2.35	0.41
4:D:158:ILE:O	4:D:162:LEU:HB2	2.19	0.41
5:E:29:GLY:HA2	5:E:47:LYS:HB3	2.01	0.41
7:G:80:VAL:O	7:G:82:GLY:N	2.46	0.41
8:H:54:ASP:O	8:H:54:ASP:CG	2.63	0.41
8:H:117:GLY:C	8:H:119:LEU:HD23	2.45	0.41
10:J:99:LYS:O	10:J:100:THR:HB	2.20	0.41
12:L:28:LYS:HE2	12:L:33:ARG:HH22	1.85	0.41
13:M:108:ARG:HH11	13:M:114:ARG:NH1	2.17	0.41
17:Q:18:THR:HG23	17:Q:69:LYS:HE3	2.01	0.41
17:Q:93:GLN:O	17:Q:96:GLN:HB2	2.21	0.41
19:S:3:ARG:H	19:S:3:ARG:HD2	1.86	0.41
1:A:6:G:O2'	1:A:7:G:H5'	2.21	0.41
1:A:90:U:H2'	1:A:91:C:C6	2.55	0.41
1:A:129:U:O3'	1:A:129(A):G:H4'	2.20	0.41
1:A:1152:A:O3'	10:J:13:HIS:CD2	2.73	0.41
1:A:1372:U:O2'	1:A:1373:G:H5'	2.21	0.41
1:A:1477:C:H2'	1:A:1478:C:H6	1.86	0.41
2:B:187:LEU:O	2:B:187:LEU:HD13	2.21	0.41
2:B:231:GLU:CB	2:B:232:PRO:CD	2.99	0.41
5:E:147:ASP:OD1	5:E:147:ASP:N	2.53	0.41
8:H:83:ILE:O	8:H:83:ILE:HG23	2.20	0.41
9:I:80:GLY:C	9:I:82:ALA:N	2.79	0.41
10:J:29:ARG:HD3	10:J:29:ARG:N	2.36	0.41
11:K:59:TYR:CE2	11:K:63:LEU:HD11	2.55	0.41
14:N:56:VAL:O	14:N:57:ARG:HB2	2.20	0.41
17:Q:50:LYS:HD2	17:Q:51:TYR:CE1	2.56	0.41
18:R:37:VAL:O	18:R:39:VAL:N	2.53	0.41
23:Z:37:A:H2'	23:Z:38:A:O4'	2.20	0.41
1:A:76:C:O2'	1:A:77:G:H5'	2.20	0.41
1:A:162:A:H2'	1:A:163:C:C4'	2.50	0.41
1:A:749:C:HO2'	1:A:750:G:H8	1.68	0.41
1:A:1194:U:H2'	1:A:1195:C:H6	1.86	0.41
1:A:1196:U:C5	3:C:162:GLN:NE2	2.89	0.41
1:A:1370:G:C2	1:A:1371:G:C8	3.09	0.41
2:B:136:VAL:O	2:B:140:HIS:CB	2.61	0.41
5:E:76:ILE:HG23	5:E:142:LEU:HD13	2.02	0.41
7:G:129:GLU:HG3	7:G:131:LYS:NZ	2.35	0.41
8:H:84:ARG:HG3	8:H:84:ARG:NH1	2.31	0.41
10:J:79:ARG:NH1	10:J:82:ILE:HD12	2.33	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:53:VAL:HG12	13:M:57:ARG:HH21	1.85	0.41
13:M:96:LEU:O	13:M:97:PRO:O	2.39	0.41
14:N:14:PRO:O	14:N:15:LYS:CB	2.65	0.41
17:Q:95:TYR:HD1	17:Q:95:TYR:H	1.68	0.41
1:A:198:G:H2'	1:A:199:G:H8	1.85	0.41
1:A:229:U:H4'	16:P:33:ILE:CD1	2.51	0.41
1:A:552:U:O2	12:L:31:PRO:HB3	2.21	0.41
1:A:629:G:H8	1:A:629:G:O5'	2.03	0.41
1:A:760:G:H1	17:Q:105:ALA:HA	1.86	0.41
1:A:1051:C:C2	1:A:1052:U:C6	3.08	0.41
1:A:1173:G:H2'	1:A:1174:G:O4'	2.21	0.41
1:A:1397:C:C2	22:W:6:A:C2	3.09	0.41
2:B:64:ARG:CB	2:B:64:ARG:HH11	2.34	0.41
2:B:221:LEU:O	2:B:221:LEU:HD13	2.20	0.41
3:C:120:VAL:HG11	3:C:198:VAL:HG11	2.02	0.41
4:D:91:SER:O	4:D:94:LEU:N	2.54	0.41
4:D:200:GLU:HG2	4:D:201:GLN:N	2.35	0.41
5:E:127:ASN:HD22	5:E:130:ASN:HD22	1.61	0.41
6:F:48:LEU:C	6:F:50:TYR:N	2.79	0.41
7:G:72:ARG:CZ	7:G:142:GLU:OE2	2.69	0.41
7:G:126:ASP:O	7:G:129:GLU:HB2	2.21	0.41
8:H:11:THR:HG22	8:H:15:ASN:HD21	1.84	0.41
9:I:33:PHE:CE1	9:I:37:PHE:CD2	3.09	0.41
10:J:30:SER:CB	10:J:81:THR:HA	2.50	0.41
10:J:48:THR:HG1	10:J:62:HIS:CD2	2.39	0.41
10:J:90:LEU:HB2	10:J:91:PRO:CD	2.51	0.41
12:L:59:ARG:HG2	12:L:59:ARG:NH1	2.36	0.41
13:M:73:GLU:O	13:M:77:ASN:HB2	2.20	0.41
19:S:67:VAL:O	19:S:67:VAL:HG23	2.20	0.41
1:A:342:C:H2'	1:A:343:U:H5''	2.03	0.41
1:A:410:G:OP2	4:D:25:ARG:HD2	2.21	0.41
1:A:456:C:H2'	1:A:457:C:C6	2.56	0.41
1:A:818:G:C6	26:A:3002:AM2:HB61	2.56	0.41
1:A:973:G:C6	1:A:974:A:N6	2.89	0.41
1:A:1048:G:C8	1:A:1048:G:H3'	2.56	0.41
1:A:1095:U:H2'	1:A:1096:C:O4'	2.20	0.41
1:A:1190:G:H5''	3:C:176:HIS:NE2	2.36	0.41
1:A:1227:A:H3'	1:A:1227:A:C8	2.55	0.41
1:A:1406:U:C2'	1:A:1407:C:H5'	2.51	0.41
1:A:1482:G:HO2'	1:A:1483:A:H8	1.65	0.41
4:D:175:SER:HB3	4:D:186:LEU:HD11	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:150:ARG:HB3	5:E:150:ARG:NH1	2.28	0.41
6:F:2:ARG:CZ	6:F:69:GLU:HG2	2.51	0.41
6:F:27:GLN:H	6:F:27:GLN:HG2	1.59	0.41
6:F:67:MET:HB2	6:F:68:PRO:CD	2.51	0.41
7:G:94:ARG:HH12	7:G:98:SER:HB3	1.86	0.41
8:H:2:LEU:HD23	8:H:2:LEU:C	2.46	0.41
8:H:68:ARG:HG2	8:H:68:ARG:NH1	2.34	0.41
9:I:8:GLY:HA3	9:I:79:LEU:HB3	2.03	0.41
9:I:88:TYR:O	9:I:88:TYR:CG	2.73	0.41
10:J:4:ILE:O	10:J:73:ASP:OD1	2.39	0.41
11:K:105:VAL:HG11	11:K:108:ILE:CD1	2.50	0.41
11:K:109:VAL:CG2	18:R:86:VAL:HA	2.51	0.41
12:L:27:LEU:HB2	12:L:62:SER:HB2	2.02	0.41
13:M:15:VAL:HG11	13:M:34:LEU:HD21	2.02	0.41
13:M:23:TYR:C	13:M:25:ILE:H	2.28	0.41
16:P:38:TYR:CD1	16:P:38:TYR:O	2.74	0.41
18:R:50:ILE:HD12	18:R:70:ILE:HD12	2.03	0.41
18:R:86:VAL:O	18:R:87:ARG:HB2	2.21	0.41
20:T:22:ARG:C	20:T:24:LEU:N	2.77	0.41
20:T:92:LEU:HD23	20:T:92:LEU:HA	1.94	0.41
23:Z:38:A:H2'	23:Z:39:U:C4'	2.51	0.41
1:A:198:G:H2'	1:A:199:G:C8	2.56	0.41
1:A:382:A:H2'	1:A:383:A:C8	2.55	0.41
1:A:401:C:O2'	1:A:621:A:N3	2.45	0.41
1:A:520:A:N6	1:A:529:G:H1'	2.36	0.41
1:A:536:C:H2'	1:A:537:G:C8	2.56	0.41
1:A:1358:U:OP2	1:A:1359:C:H5	2.04	0.41
1:A:1429:C:O2'	1:A:1430:C:H5'	2.20	0.41
1:A:1502:A:H5'	1:A:1504:G:N7	2.35	0.41
2:B:97:TRP:CH2	2:B:176:GLU:HG3	2.56	0.41
2:B:184:VAL:N	2:B:198:ASP:OD2	2.45	0.41
3:C:151:VAL:HG12	3:C:152:ILE:N	2.36	0.41
5:E:122:GLU:O	5:E:123:LEU:HD23	2.21	0.41
9:I:10:ARG:O	9:I:11:LYS:C	2.63	0.41
10:J:89:ASP:CG	10:J:90:LEU:N	2.78	0.41
13:M:79:LYS:HA	13:M:82:MET:HG2	2.03	0.41
20:T:57:ARG:HH22	20:T:100:ILE:CG2	2.32	0.41
1:A:325:A:N6	1:A:326:G:N1	2.69	0.40
1:A:573:A:H3'	1:A:573:A:OP2	2.21	0.40
1:A:739:C:O2'	15:O:42:HIS:ND1	2.52	0.40
1:A:840:C:OP1	1:A:840:C:C4'	2.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1008:C:O2'	1:A:1009:G:H5'	2.21	0.40
1:A:1158:C:O2	1:A:1158:C:H5''	2.20	0.40
1:A:1226:C:N4	13:M:104:ARG:HB2	2.37	0.40
1:A:1281:U:H3'	1:A:1281:U:C6	2.55	0.40
1:A:1298:C:H4'	1:A:1299:A:O4'	2.21	0.40
2:B:100:GLY:O	2:B:108:ILE:HG13	2.21	0.40
4:D:59:ARG:C	4:D:61:LYS:N	2.79	0.40
6:F:34:GLY:O	6:F:67:MET:HB3	2.21	0.40
6:F:43:LEU:H	6:F:43:LEU:CD2	2.34	0.40
7:G:70:LYS:HA	7:G:71:PRO:HD2	1.97	0.40
9:I:55:ALA:O	9:I:56:LEU:CB	2.68	0.40
9:I:114:TYR:HE2	10:J:60:ARG:O	2.03	0.40
9:I:118:LYS:HG3	9:I:121:ARG:HB3	2.02	0.40
10:J:50:ILE:O	10:J:52:GLY:N	2.54	0.40
12:L:92:ASP:O	12:L:93:LEU:C	2.65	0.40
14:N:35:ARG:C	14:N:37:PHE:H	2.29	0.40
15:O:10:LYS:O	15:O:14:GLU:HB2	2.21	0.40
18:R:40:LEU:O	18:R:42:ARG:N	2.54	0.40
1:A:404:U:H2'	1:A:405:U:H6	1.86	0.40
1:A:541:G:H2'	1:A:542:G:H8	1.86	0.40
1:A:620:C:C6	4:D:135:LEU:CD1	3.05	0.40
1:A:937:A:C2	1:A:1379:G:C6	3.09	0.40
1:A:1058:G:C6	1:A:1059:C:N3	2.90	0.40
1:A:1115:C:O2	1:A:1115:C:C2'	2.70	0.40
1:A:1158:C:C4	1:A:1160:G:N7	2.89	0.40
2:B:239:VAL:O	2:B:239:VAL:HG12	2.21	0.40
3:C:120:VAL:O	3:C:124:ILE:HG12	2.21	0.40
3:C:167:TRP:O	3:C:168:ALA:CB	2.69	0.40
4:D:29:PRO:O	4:D:30:LYS:CB	2.68	0.40
4:D:119:GLN:HG2	4:D:123:HIS:HD2	1.86	0.40
4:D:153:ARG:HD3	4:D:180:GLY:O	2.21	0.40
5:E:12:LEU:CD1	5:E:12:LEU:C	2.94	0.40
6:F:62:TRP:CG	18:R:35:ARG:HH12	2.37	0.40
7:G:65:ALA:HB2	7:G:124:LEU:O	2.21	0.40
7:G:145:ALA:C	7:G:147:ALA:N	2.78	0.40
8:H:39:LEU:HD22	8:H:111:ILE:HD11	2.03	0.40
11:K:34:ASP:HB2	11:K:35:PRO:HD2	2.02	0.40
15:O:82:ILE:HG22	15:O:83:GLU:N	2.35	0.40
18:R:66:LEU:O	18:R:69:THR:HB	2.21	0.40
19:S:52:TYR:CD1	19:S:56:GLN:O	2.74	0.40
1:A:342:C:C2'	1:A:343:U:H5''	2.51	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:662:G:O2'	1:A:836:G:H5''	2.22	0.40
1:A:888:G:C3'	1:A:889:A:H5''	2.43	0.40
1:A:946:A:O2'	1:A:1333:A:N3	2.49	0.40
1:A:998:G:H2'	1:A:999:C:C4'	2.52	0.40
1:A:1350:A:C6	1:A:1351:U:N3	2.89	0.40
2:B:203:GLY:O	2:B:204:ASN:C	2.65	0.40
3:C:6:HIS:CD2	3:C:6:HIS:C	2.98	0.40
3:C:173:VAL:O	3:C:173:VAL:HG12	2.21	0.40
5:E:12:LEU:HD12	5:E:12:LEU:C	2.46	0.40
5:E:44:GLY:HA3	5:E:62:ALA:HB2	2.03	0.40
6:F:27:GLN:HE21	6:F:27:GLN:HB3	1.66	0.40
9:I:58:ARG:CB	9:I:58:ARG:HH11	2.34	0.40
9:I:102:LEU:N	9:I:102:LEU:CD1	2.73	0.40
10:J:17:ASP:O	10:J:21:GLN:CB	2.68	0.40
11:K:80:VAL:HG12	11:K:104:GLN:O	2.21	0.40
11:K:122:LYS:HB2	11:K:122:LYS:NZ	2.36	0.40
12:L:101:VAL:HG12	12:L:104:VAL:HG23	2.03	0.40
13:M:67:GLU:O	13:M:68:GLY:C	2.63	0.40
16:P:20:VAL:HG12	16:P:35:LYS:HA	2.03	0.40
19:S:12:ASP:H	19:S:38:SER:CB	2.29	0.40
20:T:57:ARG:NH1	20:T:102:GLY:HA3	2.37	0.40
1:A:59:A:H3'	1:A:331:G:H22	1.87	0.40
1:A:116:A:O2'	1:A:117:G:H5'	2.22	0.40
1:A:229:U:C5'	16:P:33:ILE:HD13	2.48	0.40
1:A:233:C:H2'	1:A:234:C:H6	1.85	0.40
1:A:404:U:O2'	1:A:405:U:H5'	2.21	0.40
1:A:658:G:C2	1:A:749:C:N3	2.89	0.40
1:A:716:A:O2'	1:A:717:C:H5'	2.21	0.40
1:A:726:C:O2'	1:A:727:G:H5'	2.21	0.40
1:A:1120:G:C2	1:A:1154:G:C2	3.09	0.40
1:A:1129:C:N4	1:A:1135:U:H3	2.20	0.40
1:A:1238:A:C8	1:A:1303:C:H1'	2.56	0.40
1:A:1281:U:H4'	1:A:1282:C:OP2	2.22	0.40
1:A:1371:G:OP1	9:I:11:LYS:O	2.39	0.40
2:B:19:HIS:CB	2:B:204:ASN:HA	2.51	0.40
2:B:22:LYS:HA	2:B:40:HIS:CE1	2.53	0.40
2:B:59:GLU:CB	2:B:221:LEU:HD11	2.46	0.40
2:B:142:LEU:CB	2:B:146:GLN:HE22	2.34	0.40
3:C:91:LEU:CD2	3:C:92:ALA:N	2.84	0.40
4:D:132:ARG:CZ	4:D:132:ARG:CB	3.00	0.40
5:E:17:ALA:HB2	5:E:26:PHE:CD1	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:24:ARG:NH2	22:W:6:A:N7	2.69	0.40
7:G:94:ARG:NH1	7:G:98:SER:HB3	2.36	0.40
7:G:111:ARG:NH2	7:G:122:HIS:HB3	2.36	0.40
10:J:83:GLU:C	10:J:85:LEU:N	2.80	0.40
11:K:88:GLY:C	11:K:90:GLY:N	2.79	0.40
13:M:13:LYS:O	13:M:45:VAL:HG12	2.21	0.40
20:T:101:GLY:O	20:T:102:GLY:O	2.39	0.40
1:A:803:G:C5	1:A:804:U:C4	3.09	0.40
1:A:878:G:OP1	8:H:89:PRO:O	2.39	0.40
3:C:37:GLN:C	3:C:39:ILE:N	2.75	0.40
3:C:118:GLN:H	3:C:118:GLN:HG2	1.72	0.40
4:D:88:VAL:O	4:D:92:VAL:HG23	2.22	0.40
4:D:157:LEU:C	4:D:157:LEU:CD2	2.94	0.40
6:F:14:LEU:HD21	6:F:84:ASN:OD1	2.22	0.40
7:G:50:ILE:HG13	7:G:125:MET:HE3	2.04	0.40
8:H:19:VAL:CG2	8:H:21:LYS:HD3	2.52	0.40
10:J:71:LEU:O	10:J:72:VAL:HB	2.22	0.40
10:J:91:PRO:HB2	10:J:94:VAL:CG2	2.51	0.40
11:K:91:ARG:HH11	18:R:88:LYS:HZ3	1.69	0.40
12:L:90:VAL:HG11	12:L:93:LEU:HD21	2.04	0.40
19:S:64:GLU:C	19:S:66:MET:H	2.30	0.40
20:T:97:ALA:O	20:T:99:LEU:N	2.55	0.40
23:Z:38:A:C8	23:Z:38:A:OP2	2.75	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
2	B	232/256 (91%)	150 (65%)	50 (22%)	32 (14%)	0 3
3	C	204/239 (85%)	123 (60%)	48 (24%)	33 (16%)	0 2

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	D	206/208 (99%)	140 (68%)	45 (22%)	21 (10%)	0	6
5	E	148/161 (92%)	115 (78%)	30 (20%)	3 (2%)	6	32
6	F	99/101 (98%)	74 (75%)	21 (21%)	4 (4%)	2	19
7	G	153/155 (99%)	116 (76%)	28 (18%)	9 (6%)	1	12
8	H	136/138 (99%)	100 (74%)	27 (20%)	9 (7%)	1	11
9	I	125/128 (98%)	94 (75%)	18 (14%)	13 (10%)	0	5
10	J	96/104 (92%)	61 (64%)	19 (20%)	16 (17%)	0	2
11	K	117/129 (91%)	84 (72%)	25 (21%)	8 (7%)	1	10
12	L	123/135 (91%)	88 (72%)	23 (19%)	12 (10%)	0	6
13	M	123/126 (98%)	79 (64%)	26 (21%)	18 (15%)	0	3
14	N	58/60 (97%)	33 (57%)	14 (24%)	11 (19%)	0	1
15	O	86/88 (98%)	72 (84%)	11 (13%)	3 (4%)	3	23
16	P	81/88 (92%)	60 (74%)	18 (22%)	3 (4%)	2	21
17	Q	102/104 (98%)	82 (80%)	14 (14%)	6 (6%)	1	12
18	R	71/88 (81%)	56 (79%)	9 (13%)	6 (8%)	0	7
19	S	78/92 (85%)	47 (60%)	22 (28%)	9 (12%)	0	5
20	T	97/106 (92%)	71 (73%)	16 (16%)	10 (10%)	0	5
21	V	22/26 (85%)	17 (77%)	3 (14%)	2 (9%)	0	7
All	All	2357/2532 (93%)	1662 (70%)	467 (20%)	228 (10%)	0	6

All (228) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	17	PHE
2	B	24	TRP
2	B	38	GLY
2	B	225	ALA
2	B	232	PRO
3	C	15	THR
3	C	47	LEU
3	C	60	ALA
3	C	61	ALA
3	C	100	ALA
3	C	101	LEU
3	C	108	ASN
3	C	154	SER

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Mol	Chain	Res	Type
3	C	157	ILE
3	C	179	ARG
3	C	180	ALA
3	C	188	LEU
3	C	189	ALA
4	D	29	PRO
4	D	30	LYS
4	D	36	ARG
4	D	88	VAL
4	D	131	ARG
4	D	179	GLU
5	E	26	PHE
7	G	7	ALA
7	G	17	VAL
7	G	53	LYS
7	G	155	ARG
8	H	3	THR
8	H	24	THR
8	H	91	ARG
9	I	31	GLN
9	I	127	LYS
10	J	32	ALA
10	J	54	PHE
10	J	57	LYS
10	J	60	ARG
10	J	82	ILE
10	J	86	MET
11	K	35	PRO
11	K	127	LYS
12	L	28	LYS
12	L	51	ALA
12	L	91	LYS
12	L	92	ASP
12	L	127	GLU
13	M	11	ARG
13	M	67	GLU
13	M	106	ASN
14	N	4	LYS
14	N	33	VAL
14	N	35	ARG
15	O	73	GLU
16	P	64	ALA

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Mol	Chain	Res	Type
17	Q	69	LYS
18	R	26	LEU
19	S	6	LYS
19	S	9	VAL
19	S	30	LEU
20	T	11	SER
20	T	73	HIS
2	B	74	LYS
2	B	76	GLN
2	B	95	GLN
2	B	131	PRO
2	B	168	THR
2	B	204	ASN
2	B	207	ALA
2	B	208	ILE
2	B	238	LEU
3	C	4	LYS
3	C	29	TYR
3	C	54	ARG
3	C	55	VAL
3	C	66	VAL
3	C	84	ILE
3	C	156	ARG
3	C	158	GLY
3	C	159	GLY
3	C	181	ASN
4	D	5	ILE
4	D	96	LEU
4	D	138	TYR
4	D	166	LYS
4	D	177	ASP
8	H	111	ILE
8	H	134	ILE
9	I	94	ALA
9	I	101	PHE
9	I	118	LYS
10	J	34	VAL
10	J	35	SER
10	J	36	GLY
10	J	51	ARG
10	J	72	VAL
10	J	84	GLN

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Mol	Chain	Res	Type
11	K	27	ASN
11	K	76	GLY
12	L	27	LEU
12	L	79	GLU
12	L	87	GLY
12	L	106	ASP
13	M	4	ILE
13	M	7	VAL
13	M	23	TYR
13	M	63	THR
13	M	124	PRO
14	N	50	LYS
15	O	88	ARG
16	P	76	GLN
17	Q	49	GLU
17	Q	80	GLY
18	R	38	GLU
18	R	54	ARG
20	T	50	GLU
20	T	96	GLY
20	T	102	GLY
20	T	103	GLY
21	V	3	LYS
2	B	20	GLU
2	B	52	GLU
2	B	123	ALA
2	B	155	LEU
2	B	191	ASP
2	B	195	ASP
2	B	227	GLY
3	C	16	ARG
3	C	32	LEU
3	C	168	ALA
4	D	25	ARG
4	D	99	SER
4	D	151	LYS
6	F	39	LYS
6	F	44	GLY
7	G	31	MET
7	G	149	ARG
9	I	55	ALA
9	I	119	ALA

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Mol	Chain	Res	Type
10	J	78	ASN
10	J	90	LEU
11	K	13	GLN
11	K	78	GLN
12	L	115	LYS
13	M	24	GLY
13	M	68	GLY
13	M	97	PRO
13	M	116	THR
14	N	10	ALA
14	N	34	TYR
18	R	19	LYS
18	R	87	ARG
19	S	14	HIS
20	T	94	ALA
21	V	6	ARG
2	B	11	LEU
2	B	15	VAL
2	B	21	ARG
3	C	38	ARG
3	C	98	ASN
3	C	206	GLU
4	D	85	LYS
4	D	159	ARG
5	E	27	ARG
6	F	96	PRO
7	G	42	ILE
8	H	82	HIS
9	I	24	GLY
9	I	81	ILE
9	I	121	ARG
10	J	27	ALA
10	J	76	ASN
11	K	15	ALA
12	L	56	ALA
13	M	38	GLY
13	M	118	ALA
13	M	125	ARG
14	N	32	SER
14	N	36	PHE
14	N	38	GLY
16	P	57	ARG

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Mol	Chain	Res	Type
17	Q	34	LYS
17	Q	98	LEU
19	S	39	THR
19	S	69	HIS
20	T	98	PRO
2	B	75	LYS
2	B	113	HIS
2	B	116	GLU
2	B	151	GLY
2	B	181	PHE
2	B	183	PRO
3	C	116	VAL
3	C	146	ALA
4	D	3	ARG
4	D	171	GLY
5	E	107	ARG
9	I	34	ASN
9	I	78	LYS
12	L	116	SER
13	M	21	TYR
15	O	46	HIS
19	S	53	ASN
2	B	228	GLY
4	D	16	GLY
4	D	40	PRO
6	F	98	LEU
17	Q	97	SER
18	R	63	GLN
19	S	31	ILE
20	T	9	ASN
20	T	97	ALA
7	G	81	GLY
8	H	83	ILE
13	M	123	ALA
14	N	51	GLY
2	B	91	PRO
9	I	89	ASN
13	M	6	GLY
3	C	7	PRO
3	C	195	VAL
4	D	178	VAL
8	H	67	PRO

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Mol	Chain	Res	Type
8	H	73	ASP
7	G	9	VAL
11	K	90	GLY
14	N	56	VAL
19	S	59	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	202/220 (92%)	175 (87%)	27 (13%)	4	20
3	C	160/188 (85%)	138 (86%)	22 (14%)	3	19
4	D	180/180 (100%)	154 (86%)	26 (14%)	3	18
5	E	115/122 (94%)	98 (85%)	17 (15%)	3	17
6	F	90/90 (100%)	81 (90%)	9 (10%)	7	28
7	G	126/126 (100%)	113 (90%)	13 (10%)	7	28
8	H	119/119 (100%)	102 (86%)	17 (14%)	3	18
9	I	98/99 (99%)	90 (92%)	8 (8%)	10	34
10	J	88/91 (97%)	76 (86%)	12 (14%)	3	19
11	K	90/99 (91%)	81 (90%)	9 (10%)	7	28
12	L	104/111 (94%)	92 (88%)	12 (12%)	5	24
13	M	100/101 (99%)	93 (93%)	7 (7%)	14	39
14	N	49/49 (100%)	44 (90%)	5 (10%)	7	28
15	O	79/79 (100%)	72 (91%)	7 (9%)	9	32
16	P	72/74 (97%)	62 (86%)	10 (14%)	3	19
17	Q	96/96 (100%)	83 (86%)	13 (14%)	4	20
18	R	64/77 (83%)	58 (91%)	6 (9%)	8	31
19	S	71/79 (90%)	64 (90%)	7 (10%)	7	29
20	T	76/82 (93%)	69 (91%)	7 (9%)	8	32
21	V	19/21 (90%)	18 (95%)	1 (5%)	20	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1998/2103 (95%)	1763 (88%)	235 (12%)	5 23

All (235) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	8	LYS
2	B	15	VAL
2	B	23	ARG
2	B	25	ASN
2	B	49	GLU
2	B	52	GLU
2	B	58	ILE
2	B	71	VAL
2	B	76	GLN
2	B	84	GLU
2	B	90	MET
2	B	92	TYR
2	B	98	LEU
2	B	117	GLU
2	B	118	LEU
2	B	143	GLU
2	B	144	ARG
2	B	145	LEU
2	B	154	LEU
2	B	176	GLU
2	B	178	ARG
2	B	185	ILE
2	B	187	LEU
2	B	215	LEU
2	B	223	ILE
2	B	231	GLU
2	B	232	PRO
3	C	3	ASN
3	C	5	ILE
3	C	17	ASP
3	C	26	LYS
3	C	39	ILE
3	C	52	LEU
3	C	75	VAL
3	C	79	ARG
3	C	86	VAL
3	C	93	LYS

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Mol	Chain	Res	Type
3	C	95	THR
3	C	101	LEU
3	C	102	ASN
3	C	139	GLN
3	C	162	GLN
3	C	165	THR
3	C	167	TRP
3	C	175	LEU
3	C	179	ARG
3	C	191	THR
3	C	195	VAL
3	C	204	LEU
4	D	9	CYS
4	D	10	ARG
4	D	11	LEU
4	D	12	CYS
4	D	15	GLU
4	D	26	CYS
4	D	27	TYR
4	D	29	PRO
4	D	50	ARG
4	D	58	LEU
4	D	62	GLN
4	D	67	ILE
4	D	70	ILE
4	D	74	GLN
4	D	80	GLU
4	D	105	VAL
4	D	106	TYR
4	D	110	PHE
4	D	112	VAL
4	D	122	ARG
4	D	127	THR
4	D	155	LEU
4	D	157	LEU
4	D	178	VAL
4	D	199	ASN
4	D	201	GLN
5	E	12	LEU
5	E	31	LEU
5	E	41	VAL
5	E	43	LEU

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Mol	Chain	Res	Type
5	E	47	LYS
5	E	51	VAL
5	E	64	ARG
5	E	79	GLU
5	E	98	THR
5	E	100	VAL
5	E	101	ILE
5	E	116	THR
5	E	120	THR
5	E	126	ARG
5	E	137	GLU
5	E	147	ASP
5	E	150	ARG
6	F	1	MET
6	F	6	VAL
6	F	10	LEU
6	F	24	GLU
6	F	28	ARG
6	F	30	LEU
6	F	69	GLU
6	F	74	ASP
6	F	100	ASN
7	G	8	GLU
7	G	11	GLN
7	G	50	ILE
7	G	75	VAL
7	G	113	GLU
7	G	114	ARG
7	G	126	ASP
7	G	136	LYS
7	G	140	ASP
7	G	142	GLU
7	G	144	MET
7	G	146	GLU
7	G	149	ARG
8	H	19	VAL
8	H	25	ASP
8	H	26	VAL
8	H	63	LEU
8	H	64	LYS
8	H	67	PRO
8	H	80	ILE

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Mol	Chain	Res	Type
8	H	81	HIS
8	H	83	ILE
8	H	84	ARG
8	H	85	ARG
8	H	88	LYS
8	H	91	ARG
8	H	105	ARG
8	H	107	LEU
8	H	119	LEU
8	H	127	LEU
9	I	3	GLN
9	I	38	GLN
9	I	65	VAL
9	I	79	LEU
9	I	102	LEU
9	I	113	LYS
9	I	114	TYR
9	I	127	LYS
10	J	4	ILE
10	J	6	ILE
10	J	21	GLN
10	J	29	ARG
10	J	40	LEU
10	J	45	ARG
10	J	50	ILE
10	J	65	LEU
10	J	68	HIS
10	J	71	LEU
10	J	79	ARG
10	J	86	MET
11	K	29	ILE
11	K	31	THR
11	K	35	PRO
11	K	47	VAL
11	K	54	ARG
11	K	84	VAL
11	K	93	GLN
11	K	109	VAL
11	K	122	LYS
12	L	15	ARG
12	L	23	LYS
12	L	27	LEU

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Mol	Chain	Res	Type
12	L	41	ARG
12	L	60	LEU
12	L	66	VAL
12	L	80	HIS
12	L	81	SER
12	L	89	ARG
12	L	93	LEU
12	L	122	THR
12	L	126	LYS
13	M	12	ASN
13	M	65	LYS
13	M	80	ARG
13	M	97	PRO
13	M	98	VAL
13	M	110	ARG
13	M	124	PRO
14	N	3	ARG
14	N	12	ARG
14	N	16	PHE
14	N	23	ARG
14	N	44	LEU
15	O	6	GLU
15	O	10	LYS
15	O	14	GLU
15	O	26	GLU
15	O	31	LEU
15	O	45	VAL
15	O	65	ARG
16	P	2	VAL
16	P	8	ARG
16	P	20	VAL
16	P	22	THR
16	P	45	THR
16	P	51	VAL
16	P	53	VAL
16	P	62	VAL
16	P	67	THR
16	P	81	ARG
17	Q	25	ARG
17	Q	26	GLN
17	Q	34	LYS
17	Q	36	ILE

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Mol	Chain	Res	Type
17	Q	38	ARG
17	Q	48	GLU
17	Q	68	ARG
17	Q	70	ARG
17	Q	77	VAL
17	Q	78	GLU
17	Q	93	GLN
17	Q	98	LEU
17	Q	101	ARG
18	R	26	LEU
18	R	28	GLU
18	R	38	GLU
18	R	54	ARG
18	R	61	LYS
18	R	69	THR
19	S	7	LYS
19	S	15	LEU
19	S	17	GLU
19	S	20	LEU
19	S	43	GLU
19	S	65	ASN
19	S	78	ARG
20	T	10	LEU
20	T	25	ARG
20	T	62	LEU
20	T	68	LYS
20	T	73	HIS
20	T	91	LEU
20	T	100	ILE
21	V	8	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (73) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	16	HIS
2	B	25	ASN
2	B	37	ASN
2	B	78	GLN
2	B	95	GLN
2	B	113	HIS
2	B	135	GLN
2	B	140	HIS

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Mol	Chain	Res	Type
2	B	224	GLN
2	B	240	GLN
3	C	69	HIS
3	C	102	ASN
3	C	107	GLN
3	C	110	ASN
3	C	123	GLN
3	C	139	GLN
3	C	162	GLN
3	C	170	GLN
4	D	62	GLN
4	D	74	GLN
4	D	77	ASN
4	D	123	HIS
4	D	199	ASN
5	E	20	GLN
5	E	65	ASN
5	E	130	ASN
6	F	13	ASN
6	F	18	GLN
6	F	27	GLN
6	F	32	ASN
6	F	57	GLN
6	F	94	GLN
7	G	13	GLN
7	G	28	ASN
7	G	37	ASN
7	G	56	GLN
7	G	64	GLN
7	G	96	GLN
7	G	106	GLN
7	G	148	ASN
9	I	3	GLN
9	I	23	ASN
9	I	73	GLN
10	J	13	HIS
10	J	56	HIS
10	J	76	ASN
10	J	78	ASN
11	K	62	GLN
11	K	93	GLN
11	K	99	GLN

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Mol	Chain	Res	Type
11	K	104	GLN
11	K	117	ASN
12	L	49	ASN
12	L	75	HIS
13	M	12	ASN
13	M	40	ASN
13	M	62	ASN
13	M	77	ASN
14	N	49	HIS
15	O	13	GLN
15	O	37	ASN
16	P	14	ASN
16	P	76	GLN
16	P	82	GLN
17	Q	16	GLN
17	Q	93	GLN
17	Q	94	ASN
19	S	14	HIS
19	S	23	ASN
19	S	65	ASN
19	S	69	HIS
20	T	73	HIS
20	T	75	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1508/1522 (99%)	251 (16%)	30 (1%)
22	W	5/6 (83%)	1 (20%)	0
23	Z	14/15 (93%)	10 (71%)	3 (21%)
All	All	1527/1543 (98%)	262 (17%)	33 (2%)

All (262) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	6	G
1	A	7	G
1	A	9	G
1	A	30	U
1	A	31	G
1	A	32	A

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Mol	Chain	Res	Type
1	A	39	G
1	A	47	C
1	A	48	C
1	A	51	A
1	A	52	G
1	A	55	A
1	A	60	A
1	A	61	G
1	A	62	U
1	A	65	U
1	A	66	G
1	A	81	U
1	A	109	A
1	A	119	A
1	A	120	A
1	A	121	C
1	A	129(A)	G
1	A	130	A
1	A	131	C
1	A	156	G
1	A	164	U
1	A	189(F)	U
1	A	195	A
1	A	197	A
1	A	198	G
1	A	202	U
1	A	203	U
1	A	204	U
1	A	216	G
1	A	224	C
1	A	232	G
1	A	244	U
1	A	245	C
1	A	247	G
1	A	250	A
1	A	251	G
1	A	266	G
1	A	267	C
1	A	274	A
1	A	275	G
1	A	280	C
1	A	289	G

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Mol	Chain	Res	Type
1	A	306	G
1	A	321	A
1	A	328	C
1	A	329	A
1	A	343	U
1	A	345	C
1	A	346	G
1	A	347	G
1	A	351	G
1	A	352	C
1	A	354	G
1	A	367	U
1	A	369	C
1	A	372	C
1	A	373	A
1	A	390	C
1	A	397	A
1	A	406	G
1	A	410	G
1	A	411	A
1	A	412	A
1	A	414	A
1	A	418	C
1	A	419	C
1	A	421	U
1	A	422	C
1	A	428	G
1	A	429	U
1	A	430	A
1	A	448	A
1	A	452	A
1	A	470	C
1	A	479	C
1	A	485	G
1	A	486	U
1	A	498	U
1	A	500	G
1	A	510	A
1	A	511	C
1	A	512	U
1	A	518	C
1	A	527	G

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Mol	Chain	Res	Type
1	A	532	A
1	A	533	A
1	A	547	A
1	A	548	G
1	A	559	A
1	A	567	G
1	A	568	G
1	A	572	A
1	A	573	A
1	A	576	G
1	A	588	G
1	A	620	C
1	A	653	A
1	A	665	A
1	A	686	U
1	A	688	G
1	A	721	G
1	A	722	A
1	A	733	A
1	A	749	C
1	A	750	G
1	A	755	G
1	A	777	A
1	A	794	A
1	A	817	C
1	A	839	U
1	A	840	C
1	A	841	U
1	A	859	A
1	A	871	U
1	A	872	A
1	A	885	G
1	A	889	A
1	A	890	G
1	A	914	A
1	A	926	G
1	A	927	G
1	A	934	C
1	A	935	A
1	A	960	U
1	A	966	G
1	A	969	A

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Mol	Chain	Res	Type
1	A	971	G
1	A	974	A
1	A	975	A
1	A	976	G
1	A	977	A
1	A	982	U
1	A	992	U
1	A	993	G
1	A	994	A
1	A	997	U
1	A	998	G
1	A	999	C
1	A	1001	A
1	A	1001(A)	G
1	A	1003	G
1	A	1004	A
1	A	1027	C
1	A	1029	C
1	A	1030	C
1	A	1030(A)	G
1	A	1034	G
1	A	1048	G
1	A	1054	C
1	A	1068	G
1	A	1081	G
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	1102	A
1	A	1104	G
1	A	1114	C
1	A	1118	C
1	A	1119	C
1	A	1122	U
1	A	1125	U
1	A	1126	U
1	A	1129	C
1	A	1130	A
1	A	1131	G
1	A	1136	U
1	A	1137	C
1	A	1139	G

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Mol	Chain	Res	Type
1	A	1146	A
1	A	1148	U
1	A	1156	G
1	A	1157	A
1	A	1158	C
1	A	1159	U
1	A	1181	G
1	A	1182	G
1	A	1183	A
1	A	1184	G
1	A	1196	U
1	A	1197	G
1	A	1198	G
1	A	1202	G
1	A	1209	C
1	A	1211	U
1	A	1212	U
1	A	1213	A
1	A	1214	C
1	A	1215	G
1	A	1225	A
1	A	1227	A
1	A	1238	A
1	A	1241	G
1	A	1245	A
1	A	1248	A
1	A	1250	A
1	A	1256	A
1	A	1257	U
1	A	1267	C
1	A	1272	G
1	A	1278	U
1	A	1279	A
1	A	1280	A
1	A	1281	U
1	A	1282	C
1	A	1287	A
1	A	1297	C
1	A	1298	C
1	A	1300	G
1	A	1301	U
1	A	1302	U

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Mol	Chain	Res	Type
1	A	1305	G
1	A	1306	A
1	A	1311	G
1	A	1320	C
1	A	1323	G
1	A	1336	C
1	A	1338	G
1	A	1346	A
1	A	1363	C
1	A	1363(A)	A
1	A	1364	U
1	A	1379	G
1	A	1381	U
1	A	1386	G
1	A	1401	G
1	A	1442	G
1	A	1442(A)	G
1	A	1442(B)	A
1	A	1452	C
1	A	1456	G
1	A	1474	G
1	A	1475	G
1	A	1485	U
1	A	1492	A
1	A	1494	G
1	A	1497	G
1	A	1499	A
1	A	1503	A
1	A	1506	U
1	A	1517	G
1	A	1520	G
1	A	1525	G
1	A	1529	G
1	A	1530	G
1	A	1542	U
22	W	5	A
23	Z	29	G
23	Z	30	G
23	Z	31	A
23	Z	32	U
23	Z	34	G
23	Z	38	A

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Mol	Chain	Res	Type
23	Z	39	U
23	Z	40	C
23	Z	41	C
23	Z	42	C

All (33) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	30	U
1	A	51	A
1	A	119	A
1	A	197	A
1	A	243	A
1	A	250	A
1	A	279	A
1	A	372	C
1	A	410	G
1	A	428	G
1	A	429	U
1	A	485	G
1	A	496	A
1	A	793	U
1	A	871	U
1	A	974	A
1	A	975	A
1	A	992	U
1	A	1001	A
1	A	1101	A
1	A	1145	C
1	A	1181	G
1	A	1182	G
1	A	1196	U
1	A	1201	A
1	A	1281	U
1	A	1305	G
1	A	1363(A)	A
1	A	1447	A
1	A	1452	C
23	Z	30	G
23	Z	39	U
23	Z	40	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 225 ligands modelled in this entry, 220 are monoatomic - leaving 5 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
26	AM2	A	3002	-	40,40,40	0.97	2 (5%)	53,60,60	0.94	1 (1%)
26	AM2	A	3004	-	40,40,40	0.88	0	53,60,60	0.94	1 (1%)
26	AM2	A	3005	-	40,40,40	0.91	1 (2%)	53,60,60	0.87	1 (1%)
26	AM2	A	3003	-	40,40,40	0.91	1 (2%)	53,60,60	0.99	1 (1%)
26	AM2	A	3001	-	40,40,40	0.86	1 (2%)	53,60,60	1.28	3 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
26	AM2	A	3002	-	-	3/12/84/84	0/4/4/4
26	AM2	A	3004	-	-	2/12/84/84	0/4/4/4
26	AM2	A	3005	-	-	4/12/84/84	0/4/4/4
26	AM2	A	3003	-	-	1/12/84/84	0/4/4/4
26	AM2	A	3001	-	-	2/12/84/84	0/4/4/4

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	A	3002	AM2	OB1-CB1	2.45	1.48	1.41
26	A	3003	AM2	CB5-CB4	2.14	1.56	1.52
26	A	3001	AM2	OB1-CB1	2.05	1.47	1.41
26	A	3005	AM2	OB1-CB1	2.03	1.47	1.41
26	A	3002	AM2	OA4-CA1	2.01	1.47	1.41

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	A	3001	AM2	CA9-NA7-CA7	7.68	124.14	114.23
26	A	3003	AM2	CA9-NA7-CA7	5.98	121.94	114.23
26	A	3004	AM2	CA9-NA7-CA7	5.48	121.30	114.23
26	A	3005	AM2	CA9-NA7-CA7	4.83	120.46	114.23
26	A	3002	AM2	CA9-NA7-CA7	4.68	120.26	114.23
26	A	3001	AM2	CA1-OA1-CC1	-2.54	111.96	117.98
26	A	3001	AM2	OA1-CA1-CA2	2.15	111.54	108.10

There are no chirality outliers.

All (12) torsion outliers are listed below:

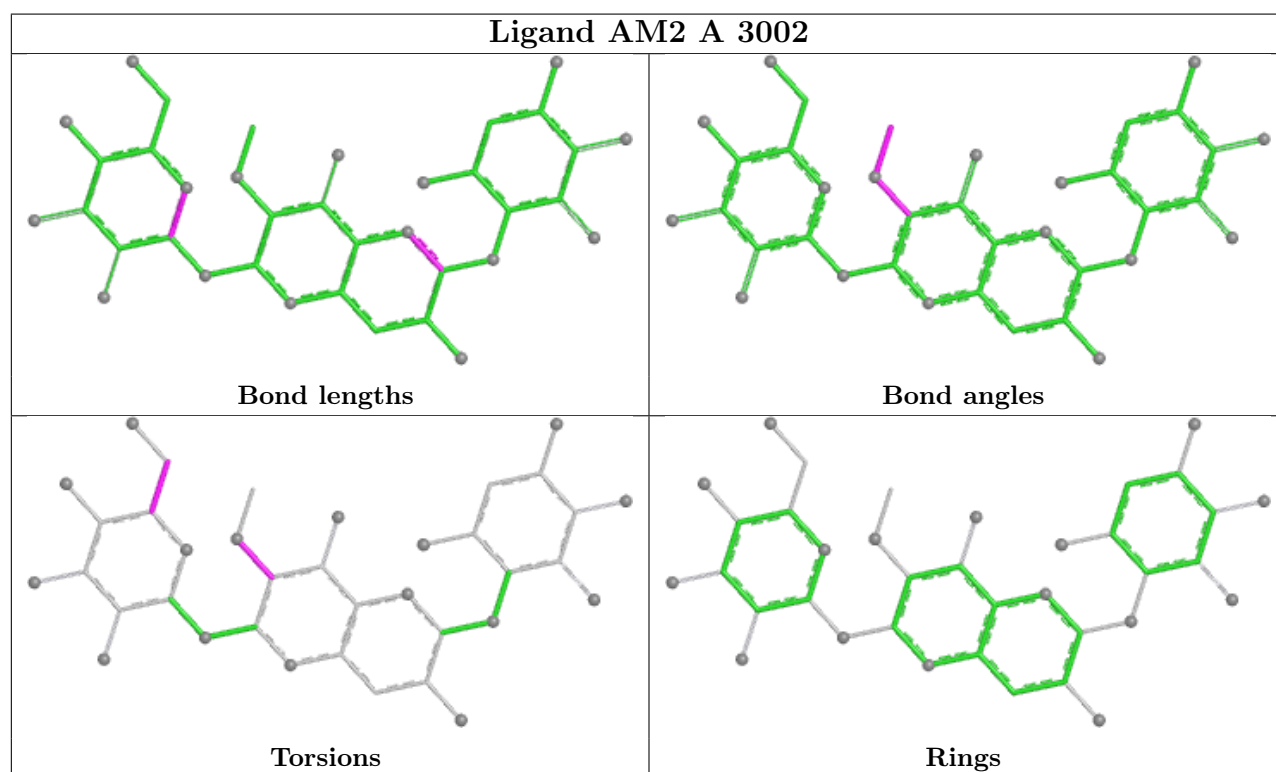
Mol	Chain	Res	Type	Atoms
26	A	3001	AM2	CA8-CA7-NA7-CA9
26	A	3005	AM2	CC6-CC1-OA1-CA1
26	A	3002	AM2	OB1-CB5-CB6-OB6
26	A	3004	AM2	OB1-CB5-CB6-OB6
26	A	3003	AM2	OB1-CB5-CB6-OB6
26	A	3001	AM2	OB1-CB5-CB6-OB6
26	A	3005	AM2	OB1-CB5-CB6-OB6
26	A	3002	AM2	CA8-CA7-NA7-CA9
26	A	3004	AM2	CA8-CA7-NA7-CA9
26	A	3005	AM2	CA8-CA7-NA7-CA9
26	A	3002	AM2	CA6-CA7-NA7-CA9
26	A	3005	AM2	CA2-CA1-OA1-CC1

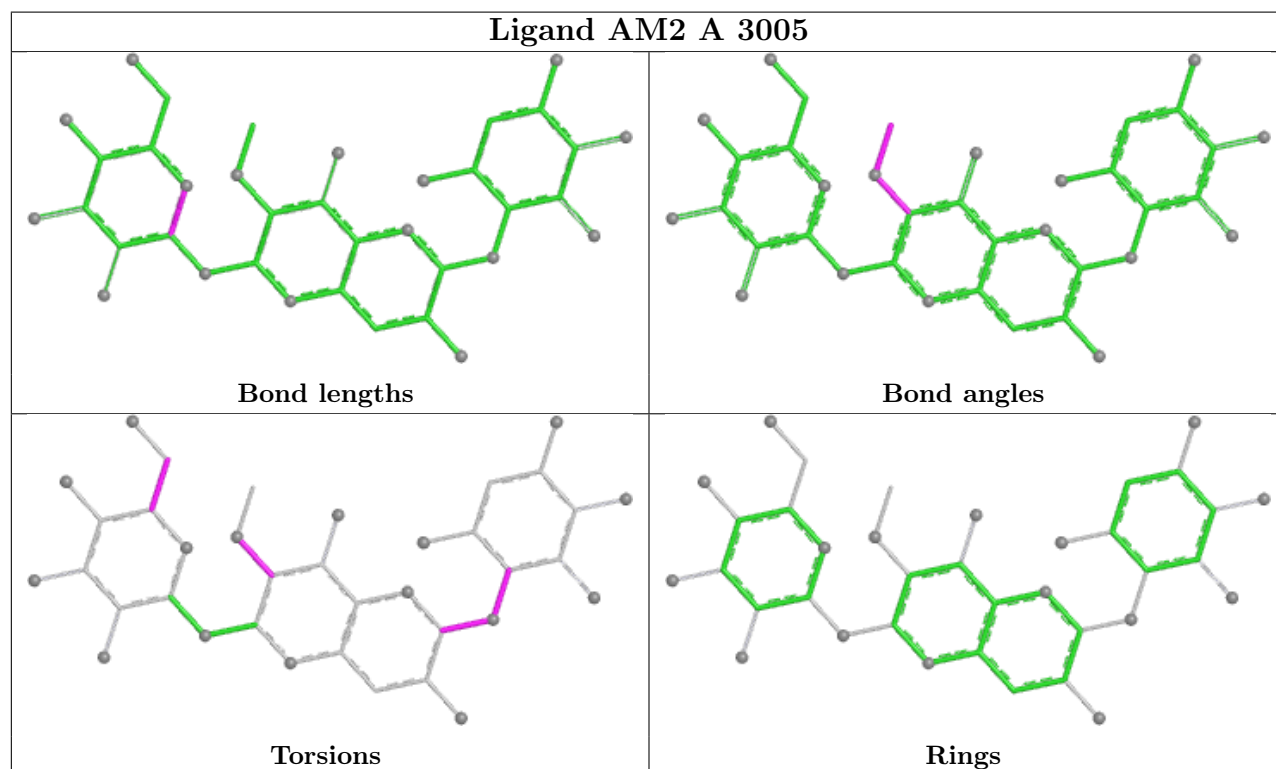
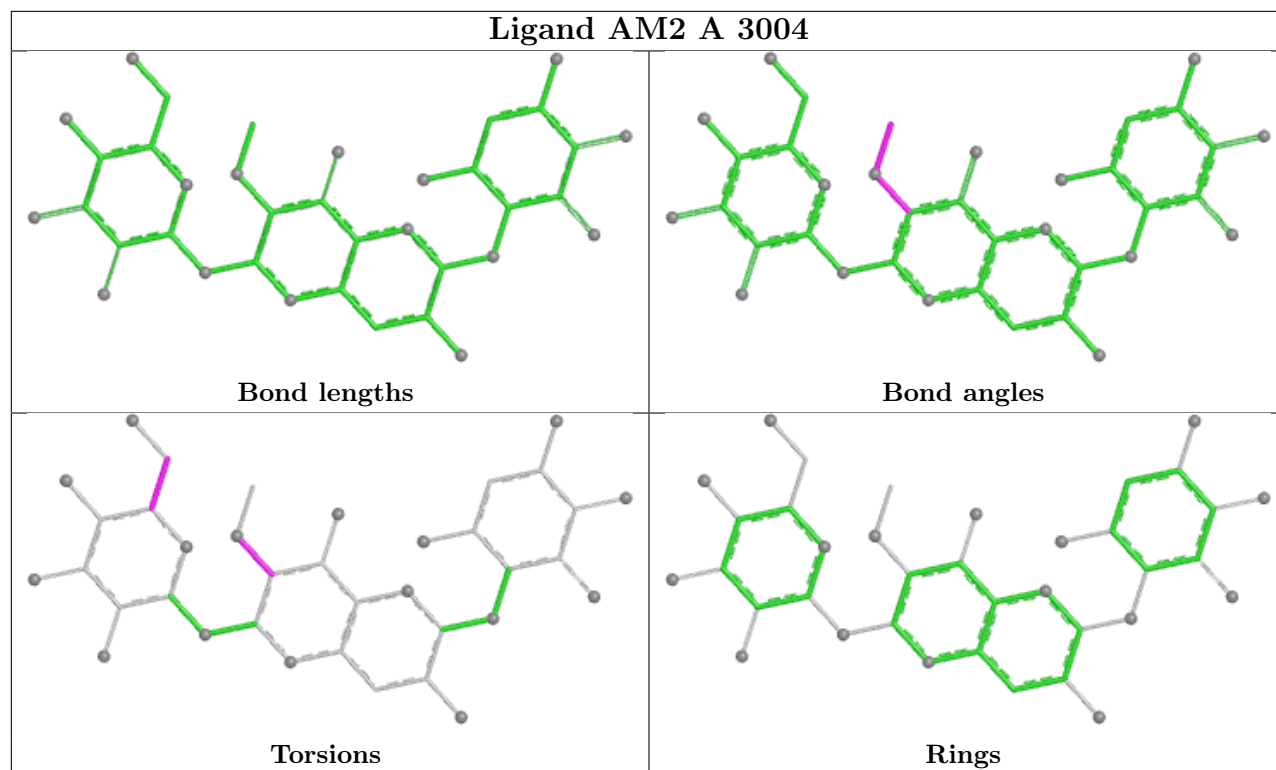
There are no ring outliers.

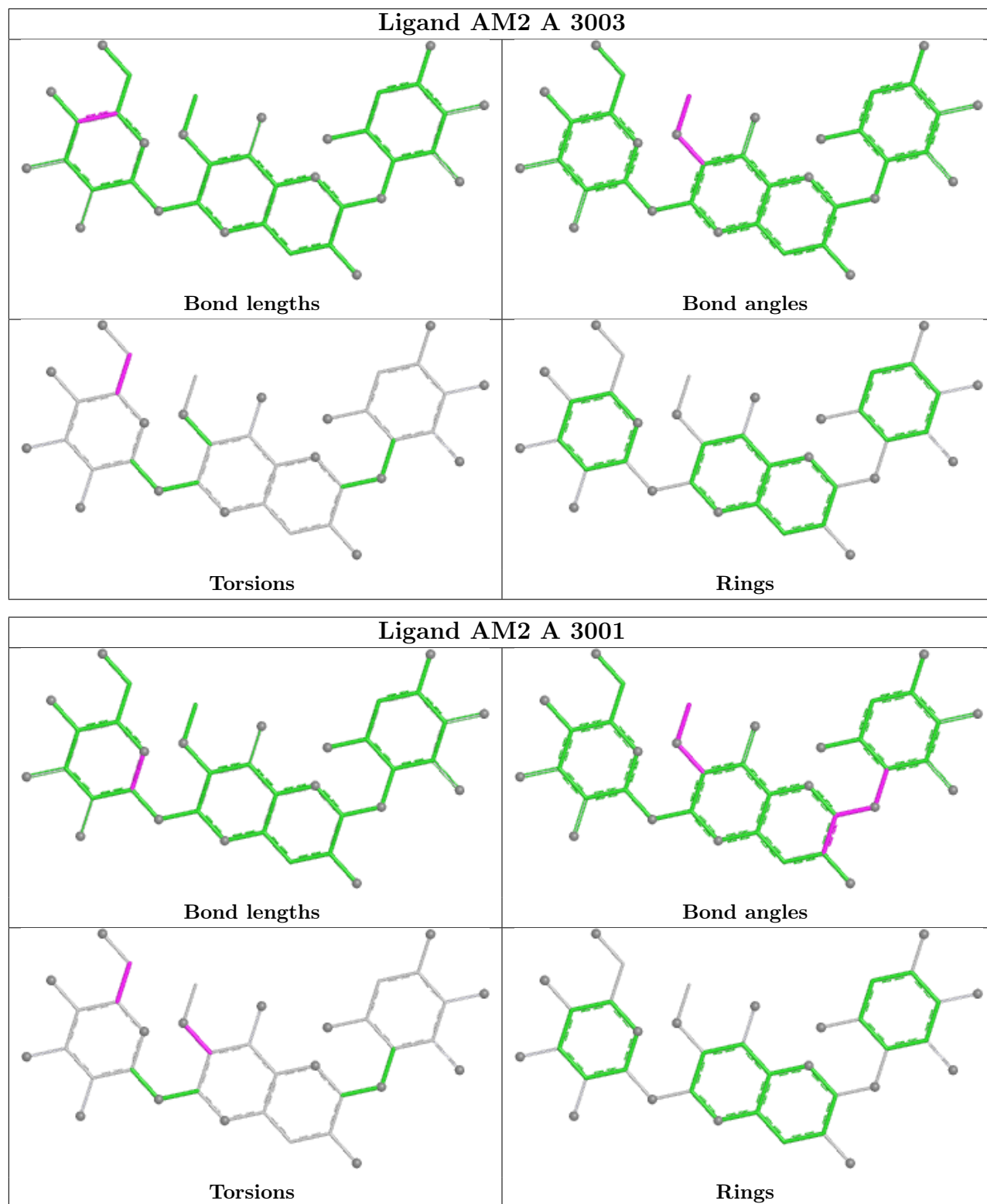
3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
26	A	3002	AM2	2	0
26	A	3005	AM2	3	0
26	A	3001	AM2	2	0

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







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	1510/1522 (99%)	0.10	28 (1%) 66 41	82, 115, 181, 202	0
2	B	234/256 (91%)	0.15	4 (1%) 69 43	84, 153, 190, 202	0
3	C	206/239 (86%)	0.12	6 (2%) 53 31	86, 139, 185, 202	0
4	D	208/208 (100%)	0.21	10 (4%) 35 19	90, 133, 184, 202	0
5	E	150/161 (93%)	-0.04	2 (1%) 75 50	83, 108, 153, 196	0
6	F	101/101 (100%)	-0.12	2 (1%) 65 39	104, 143, 177, 186	0
7	G	155/155 (100%)	0.01	2 (1%) 75 50	89, 131, 186, 202	0
8	H	138/138 (100%)	-0.23	0 100 100	76, 105, 141, 163	0
9	I	127/128 (99%)	0.40	8 (6%) 26 15	89, 144, 178, 202	0
10	J	98/104 (94%)	0.80	7 (7%) 22 14	97, 168, 202, 202	0
11	K	119/129 (92%)	0.11	7 (5%) 28 16	79, 113, 161, 197	0
12	L	125/135 (92%)	0.14	6 (4%) 35 19	74, 108, 155, 202	0
13	M	125/126 (99%)	0.50	9 (7%) 21 14	100, 133, 171, 200	0
14	N	60/60 (100%)	0.77	7 (11%) 9 6	93, 136, 178, 198	0
15	O	88/88 (100%)	0.02	1 (1%) 78 54	78, 123, 166, 192	0
16	P	83/88 (94%)	0.12	0 100 100	79, 105, 138, 196	0
17	Q	104/104 (100%)	0.16	5 (4%) 35 19	78, 106, 161, 202	0
18	R	73/88 (82%)	-0.14	1 (1%) 73 48	93, 130, 184, 196	0
19	S	80/92 (86%)	0.38	5 (6%) 26 15	103, 152, 188, 202	0
20	T	99/106 (93%)	0.28	6 (6%) 27 16	80, 112, 164, 200	0
21	V	24/26 (92%)	1.14	4 (16%) 4 4	82, 126, 160, 173	0
22	W	6/6 (100%)	0.24	0 100 100	112, 125, 180, 197	0
23	Z	15/15 (100%)	0.85	2 (13%) 7 6	97, 137, 200, 202	0
All	All	3928/4075 (96%)	0.15	122 (3%) 51 29	74, 123, 184, 202	0

All (122) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
13	M	123	ALA	11.9
13	M	124	PRO	11.2
13	M	126	LYS	9.5
19	S	3	ARG	8.0
12	L	19	ARG	6.7
1	A	1001(A)	G	6.5
9	I	128	ARG	5.8
13	M	120	LYS	5.7
19	S	37	ARG	5.7
3	C	161	GLU	5.3
7	G	5	ARG	5.1
21	V	25	LYS	5.1
1	A	1541	U	4.9
2	B	136	VAL	4.7
20	T	103	GLY	4.5
10	J	20	ALA	4.4
17	Q	105	ALA	4.4
1	A	1115	C	4.3
5	E	154	GLY	4.3
11	K	111	ASP	4.1
13	M	125	ARG	4.1
1	A	1003	G	4.1
1	A	202	U	4.0
10	J	34	VAL	3.9
11	K	89	ALA	3.9
13	M	122	LYS	3.8
4	D	3	ARG	3.7
19	S	2	PRO	3.7
1	A	1126	U	3.6
20	T	9	ASN	3.5
17	Q	24	GLU	3.4
11	K	127	LYS	3.4
5	E	20	GLN	3.3
1	A	1113	C	3.2
13	M	121	LYS	3.2
10	J	33	GLN	3.1
20	T	12	ALA	3.1
19	S	32	LYS	3.1
9	I	127	LYS	3.1
1	A	1112	C	3.1
1	A	982	U	3.0
10	J	10	GLY	3.0

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Mol	Chain	Res	Type	RSRZ
14	N	6	LEU	3.0
4	D	42	GLN	3.0
21	V	24	ARG	3.0
1	A	329	A	2.9
21	V	5	ASP	2.8
14	N	3	ARG	2.8
1	A	373	A	2.8
17	Q	87	LYS	2.8
9	I	75	ASP	2.7
23	Z	30	G	2.7
10	J	93	GLY	2.7
4	D	73	ARG	2.7
1	A	1196	U	2.7
1	A	977	A	2.7
9	I	105	ASP	2.7
11	K	129	SER	2.7
2	B	131	PRO	2.6
20	T	68	LYS	2.6
1	A	1038	C	2.6
1	A	991	U	2.6
19	S	34	TRP	2.6
6	F	88	VAL	2.6
18	R	48	GLY	2.6
1	A	1002	G	2.6
4	D	46	LYS	2.5
9	I	66	ARG	2.5
1	A	470	C	2.5
11	K	128	ALA	2.4
3	C	84	ILE	2.4
13	M	8	GLU	2.4
10	J	9	ARG	2.4
4	D	39	PRO	2.4
1	A	1129	C	2.3
11	K	12	ARG	2.3
1	A	1125	U	2.3
1	A	1281	U	2.3
1	A	1183	A	2.3
1	A	1362	C	2.3
14	N	2	ALA	2.3
7	G	7	ALA	2.3
14	N	51	GLY	2.3
3	C	184	TYR	2.3

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Mol	Chain	Res	Type	RSRZ
3	C	159	GLY	2.3
4	D	10	ARG	2.3
11	K	38	ASN	2.3
1	A	1181	G	2.3
20	T	106	ALA	2.3
20	T	74	LYS	2.2
1	A	1127	G	2.2
12	L	89	ARG	2.2
14	N	57	ARG	2.2
1	A	924	C	2.2
9	I	110	GLU	2.2
10	J	73	ASP	2.2
14	N	8	GLU	2.2
4	D	134	ASP	2.2
12	L	92	ASP	2.2
3	C	174	PRO	2.2
3	C	190	ARG	2.2
9	I	125	TYR	2.2
23	Z	42	C	2.2
12	L	20	LYS	2.2
12	L	27	LEU	2.2
14	N	35	ARG	2.1
12	L	17	LYS	2.1
4	D	77	ASN	2.1
1	A	1119	C	2.1
13	M	2	ALA	2.1
6	F	94	GLN	2.1
2	B	133	LYS	2.1
4	D	141	ARG	2.1
17	Q	40	LYS	2.1
15	O	2	PRO	2.1
4	D	147	ALA	2.1
21	V	20	LYS	2.0
17	Q	39	SER	2.0
2	B	188	ALA	2.0
1	A	1014	A	2.0
9	I	64	THR	2.0
1	A	1030	C	2.0

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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
24	MG	A	2721	1/1	0.30	1.30	174,174,174,174	1
24	MG	A	2661	1/1	0.31	0.28	107,107,107,107	0
24	MG	A	2550	1/1	0.39	0.40	105,105,105,105	0
24	MG	A	2549	1/1	0.42	0.29	103,103,103,103	0
24	MG	A	2596	1/1	0.42	0.18	105,105,105,105	0
24	MG	A	2587	1/1	0.46	0.64	129,129,129,129	0
24	MG	A	2601	1/1	0.47	0.23	105,105,105,105	0
25	K	A	2680	1/1	0.51	0.21	180,180,180,180	0
24	MG	A	2618	1/1	0.55	0.42	97,97,97,97	0
24	MG	A	2548	1/1	0.56	0.57	114,114,114,114	0
24	MG	A	2554	1/1	0.57	0.47	134,134,134,134	0
24	MG	A	2584	1/1	0.58	0.24	108,108,108,108	0
24	MG	A	2743	1/1	0.60	0.50	121,121,121,121	0
24	MG	A	2696	1/1	0.61	0.34	92,92,92,92	0
24	MG	A	2698	1/1	0.62	0.31	115,115,115,115	0
24	MG	A	2741	1/1	0.62	0.30	105,105,105,105	0
24	MG	A	2626	1/1	0.63	0.61	102,102,102,102	0
24	MG	A	2687	1/1	0.63	0.51	114,114,114,114	0
24	MG	A	2593	1/1	0.64	0.17	112,112,112,112	0
24	MG	A	2594	1/1	0.65	0.25	100,100,100,100	0
24	MG	A	2715	1/1	0.65	0.29	113,113,113,113	0
24	MG	W	1008	1/1	0.66	0.22	157,157,157,157	1
24	MG	A	2621	1/1	0.66	0.29	105,105,105,105	0
24	MG	S	1143	1/1	0.67	0.55	115,115,115,115	0
24	MG	A	2716	1/1	0.67	0.35	122,122,122,122	0
24	MG	A	2703	1/1	0.67	0.34	101,101,101,101	0
25	K	A	2676	1/1	0.68	0.23	142,142,142,142	0
24	MG	A	2631	1/1	0.69	0.36	96,96,96,96	0
24	MG	A	2688	1/1	0.69	0.52	109,109,109,109	0
24	MG	A	2745	1/1	0.70	0.43	101,101,101,101	0
25	K	A	2681	1/1	0.70	0.19	140,140,140,140	0
24	MG	A	2683	1/1	0.71	0.54	116,116,116,116	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
24	MG	A	2624	1/1	0.72	0.19	89,89,89,89	0
24	MG	A	2708	1/1	0.72	0.36	105,105,105,105	0
24	MG	A	2611	1/1	0.72	0.31	98,98,98,98	0
24	MG	A	2603	1/1	0.72	0.63	135,135,135,135	0
24	MG	A	2660	1/1	0.72	0.24	128,128,128,128	0
24	MG	A	2729	1/1	0.72	0.52	96,96,96,96	1
24	MG	A	2606	1/1	0.72	0.27	83,83,83,83	0
24	MG	A	2576	1/1	0.73	0.14	83,83,83,83	0
25	K	A	2678	1/1	0.73	0.12	131,131,131,131	0
24	MG	A	2695	1/1	0.73	0.15	98,98,98,98	0
24	MG	A	2595	1/1	0.73	0.37	112,112,112,112	0
24	MG	A	2545	1/1	0.75	0.27	122,122,122,122	0
24	MG	A	2625	1/1	0.75	0.30	81,81,81,81	0
24	MG	A	2739	1/1	0.75	0.23	101,101,101,101	0
24	MG	A	2742	1/1	0.76	0.37	106,106,106,106	0
24	MG	A	2552	1/1	0.76	0.15	84,84,84,84	0
24	MG	A	2738	1/1	0.76	0.36	94,94,94,94	0
24	MG	A	2579	1/1	0.77	0.27	94,94,94,94	0
24	MG	F	1102	1/1	0.77	0.10	128,128,128,128	0
24	MG	A	2633	1/1	0.77	0.14	87,87,87,87	0
24	MG	A	2555	1/1	0.77	0.34	129,129,129,129	0
24	MG	A	2546	1/1	0.78	0.16	100,100,100,100	0
24	MG	A	2609	1/1	0.78	0.40	94,94,94,94	0
24	MG	A	2734	1/1	0.78	0.71	113,113,113,113	0
24	MG	A	2646	1/1	0.78	0.23	96,96,96,96	0
24	MG	A	2747	1/1	0.78	0.20	104,104,104,104	0
24	MG	A	2720	1/1	0.78	0.59	128,128,128,128	0
24	MG	A	2712	1/1	0.79	0.26	99,99,99,99	0
24	MG	A	2691	1/1	0.79	0.28	94,94,94,94	0
24	MG	A	2590	1/1	0.79	0.44	76,76,76,76	0
24	MG	A	2575	1/1	0.79	0.15	108,108,108,108	0
24	MG	A	2684	1/1	0.79	0.24	88,88,88,88	0
24	MG	A	2580	1/1	0.79	0.39	76,76,76,76	0
24	MG	A	2627	1/1	0.79	0.31	75,75,75,75	0
24	MG	A	2612	1/1	0.80	0.43	92,92,92,92	0
24	MG	A	2701	1/1	0.80	0.39	85,85,85,85	0
24	MG	A	2641	1/1	0.80	0.21	98,98,98,98	0
24	MG	A	2613	1/1	0.80	0.33	89,89,89,89	0
24	MG	A	2563	1/1	0.80	0.55	87,87,87,87	0
24	MG	A	2572	1/1	0.81	0.26	89,89,89,89	0
24	MG	A	2704	1/1	0.81	0.24	94,94,94,94	0
24	MG	A	2644	1/1	0.81	0.57	121,121,121,121	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
24	MG	A	2581	1/1	0.81	0.25	69,69,69,69	0
24	MG	A	2697	1/1	0.81	0.21	92,92,92,92	0
24	MG	A	2648	1/1	0.81	0.16	89,89,89,89	0
25	K	A	2679	1/1	0.81	0.15	126,126,126,126	0
24	MG	A	2700	1/1	0.81	0.39	115,115,115,115	0
24	MG	A	2636	1/1	0.81	0.15	92,92,92,92	0
24	MG	A	2591	1/1	0.82	0.25	74,74,74,74	0
24	MG	A	2664	1/1	0.82	0.18	97,97,97,97	0
24	MG	A	2551	1/1	0.82	0.15	121,121,121,121	0
25	K	A	2674	1/1	0.82	0.14	133,133,133,133	0
25	K	A	2675	1/1	0.82	0.33	143,143,143,143	0
24	MG	A	2725	1/1	0.83	0.38	101,101,101,101	0
24	MG	A	2717	1/1	0.83	0.14	99,99,99,99	0
24	MG	A	2653	1/1	0.83	0.22	98,98,98,98	0
24	MG	A	2663	1/1	0.83	0.17	88,88,88,88	0
24	MG	A	2709	1/1	0.84	0.13	79,79,79,79	0
24	MG	A	2710	1/1	0.84	0.28	99,99,99,99	0
24	MG	A	2735	1/1	0.84	0.31	98,98,98,98	1
25	K	A	2672	1/1	0.84	0.17	159,159,159,159	0
24	MG	A	2557	1/1	0.84	0.15	110,110,110,110	0
24	MG	A	2689	1/1	0.84	0.39	101,101,101,101	0
24	MG	A	2566	1/1	0.84	0.21	91,91,91,91	0
24	MG	A	2600	1/1	0.84	0.38	93,93,93,93	0
24	MG	A	2568	1/1	0.84	0.26	91,91,91,91	0
24	MG	A	2705	1/1	0.84	0.09	104,104,104,104	0
24	MG	A	2629	1/1	0.84	0.27	78,78,78,78	0
24	MG	A	2694	1/1	0.85	0.16	88,88,88,88	0
24	MG	A	2722	1/1	0.85	0.58	93,93,93,93	0
24	MG	A	2724	1/1	0.85	0.33	95,95,95,95	0
24	MG	A	2628	1/1	0.85	0.13	95,95,95,95	0
24	MG	A	2744	1/1	0.85	0.37	90,90,90,90	0
24	MG	A	2559	1/1	0.85	0.21	81,81,81,81	0
24	MG	A	2630	1/1	0.85	0.18	99,99,99,99	0
24	MG	A	2692	1/1	0.85	0.12	69,69,69,69	0
24	MG	A	2693	1/1	0.85	0.17	89,89,89,89	0
24	MG	A	2588	1/1	0.86	0.19	71,71,71,71	0
24	MG	A	2562	1/1	0.86	0.23	108,108,108,108	0
24	MG	A	2561	1/1	0.86	0.26	66,66,66,66	0
24	MG	A	2731	1/1	0.86	0.72	88,88,88,88	0
24	MG	A	2667	1/1	0.86	0.24	92,92,92,92	0
25	K	A	2800	1/1	0.86	0.20	153,153,153,153	1
24	MG	A	2615	1/1	0.87	0.38	91,91,91,91	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
24	MG	H	1139	1/1	0.87	0.17	100,100,100,100	0
24	MG	A	2565	1/1	0.87	0.30	77,77,77,77	0
24	MG	A	2686	1/1	0.87	0.14	140,140,140,140	0
24	MG	A	2655	1/1	0.87	0.14	76,76,76,76	0
25	K	A	2673	1/1	0.87	0.13	126,126,126,126	0
24	MG	A	2634	1/1	0.87	0.16	86,86,86,86	0
24	MG	A	2619	1/1	0.87	0.39	82,82,82,82	0
24	MG	A	2598	1/1	0.87	0.24	60,60,60,60	0
24	MG	A	2623	1/1	0.87	0.40	56,56,56,56	0
24	MG	A	2666	1/1	0.87	0.14	87,87,87,87	0
24	MG	A	2706	1/1	0.87	0.29	87,87,87,87	0
24	MG	A	2602	1/1	0.87	0.38	81,81,81,81	0
24	MG	A	2728	1/1	0.87	0.91	108,108,108,108	0
25	K	A	2670	1/1	0.88	0.17	147,147,147,147	0
25	K	A	2671	1/1	0.88	0.18	117,117,117,117	0
24	MG	A	2585	1/1	0.88	0.28	78,78,78,78	0
24	MG	A	2578	1/1	0.88	0.26	66,66,66,66	0
24	MG	A	2658	1/1	0.89	0.06	121,121,121,121	0
24	MG	A	2732	1/1	0.89	0.15	88,88,88,88	1
24	MG	A	2733	1/1	0.89	0.42	93,93,93,93	0
24	MG	A	2702	1/1	0.89	0.18	94,94,94,94	0
24	MG	A	2608	1/1	0.89	0.18	106,106,106,106	0
24	MG	A	2736	1/1	0.89	0.37	103,103,103,103	0
24	MG	A	2719	1/1	0.89	0.67	96,96,96,96	0
24	MG	A	2553	1/1	0.89	0.16	69,69,69,69	0
24	MG	A	2662	1/1	0.89	0.43	109,109,109,109	0
24	MG	A	2614	1/1	0.89	0.09	83,83,83,83	0
24	MG	A	2639	1/1	0.89	0.45	129,129,129,129	0
24	MG	A	2665	1/1	0.89	0.14	89,89,89,89	0
24	MG	A	2726	1/1	0.89	0.62	106,106,106,106	0
24	MG	A	2699	1/1	0.89	0.21	88,88,88,88	0
24	MG	A	2558	1/1	0.89	0.46	74,74,74,74	0
24	MG	A	2564	1/1	0.90	0.30	57,57,57,57	0
24	MG	A	2583	1/1	0.90	0.27	83,83,83,83	0
24	MG	A	2622	1/1	0.90	0.07	73,73,73,73	0
24	MG	A	2645	1/1	0.90	0.23	78,78,78,78	0
24	MG	A	2711	1/1	0.90	0.21	103,103,103,103	0
24	MG	A	2604	1/1	0.90	0.24	89,89,89,89	0
25	K	A	2677	1/1	0.90	0.21	117,117,117,117	0
24	MG	A	2570	1/1	0.90	0.24	97,97,97,97	0
24	MG	A	2651	1/1	0.90	0.18	78,78,78,78	0
24	MG	W	1007	1/1	0.90	0.21	81,81,81,81	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
24	MG	A	2740	1/1	0.90	0.43	92,92,92,92	0
24	MG	A	2652	1/1	0.90	0.14	70,70,70,70	0
26	AM2	A	3005	37/37	0.90	0.16	126,131,135,136	0
24	MG	A	2727	1/1	0.91	0.71	107,107,107,107	0
24	MG	A	2713	1/1	0.91	0.17	104,104,104,104	0
24	MG	A	2714	1/1	0.91	0.29	92,92,92,92	0
24	MG	A	2635	1/1	0.91	0.13	95,95,95,95	0
24	MG	A	2610	1/1	0.91	0.29	75,75,75,75	0
24	MG	G	1157	1/1	0.91	0.37	134,134,134,134	1
24	MG	A	2605	1/1	0.91	0.10	79,79,79,79	0
25	K	V	1026	1/1	0.91	0.08	132,132,132,132	0
24	MG	A	2582	1/1	0.91	0.34	85,85,85,85	0
24	MG	A	2637	1/1	0.92	0.11	110,110,110,110	0
24	MG	M	1127	1/1	0.92	0.12	104,104,104,104	0
24	MG	A	2638	1/1	0.92	0.07	79,79,79,79	0
24	MG	A	2649	1/1	0.92	0.17	65,65,65,65	0
24	MG	A	2573	1/1	0.93	0.06	72,72,72,72	0
24	MG	A	2746	1/1	0.93	0.16	85,85,85,85	0
24	MG	A	2654	1/1	0.93	0.23	112,112,112,112	1
24	MG	A	2597	1/1	0.93	0.12	80,80,80,80	0
24	MG	A	2656	1/1	0.93	0.21	90,90,90,90	0
24	MG	A	2586	1/1	0.94	0.16	58,58,58,58	0
24	MG	L	1129	1/1	0.94	0.27	59,59,59,59	0
24	MG	A	2643	1/1	0.94	0.20	92,92,92,92	0
24	MG	A	2560	1/1	0.94	0.27	46,46,46,46	0
25	K	A	2682	1/1	0.94	0.10	147,147,147,147	0
24	MG	A	2616	1/1	0.94	0.15	57,57,57,57	0
24	MG	A	2617	1/1	0.94	0.52	72,72,72,72	0
26	AM2	A	3002	37/37	0.94	0.18	116,119,127,128	0
24	MG	A	2737	1/1	0.94	0.44	61,61,61,61	0
24	MG	A	2707	1/1	0.95	0.12	78,78,78,78	0
24	MG	A	2620	1/1	0.95	0.05	89,89,89,89	1
24	MG	A	2659	1/1	0.95	0.12	80,80,80,80	0
24	MG	A	2577	1/1	0.95	0.35	94,94,94,94	0
24	MG	A	2567	1/1	0.95	0.11	69,69,69,69	0
24	MG	A	2592	1/1	0.95	0.12	78,78,78,78	0
24	MG	A	2571	1/1	0.95	0.20	49,49,49,49	0
26	AM2	A	3001	37/37	0.95	0.14	103,105,119,121	0
24	MG	A	2642	1/1	0.95	0.22	101,101,101,101	0
26	AM2	A	3003	37/37	0.95	0.17	110,114,122,124	0
26	AM2	A	3004	37/37	0.95	0.14	130,133,141,143	0
24	MG	A	2657	1/1	0.95	0.04	132,132,132,132	0

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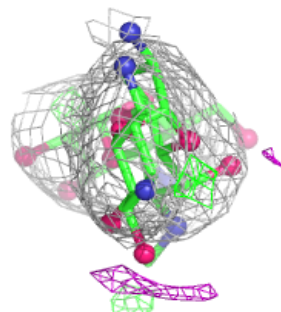
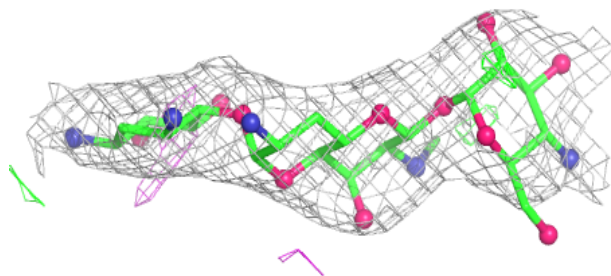
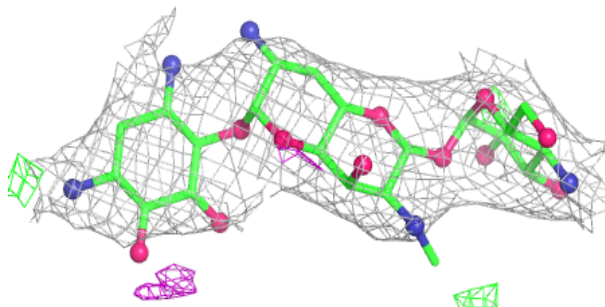
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
24	MG	A	2589	1/1	0.96	0.05	93,93,93,93	0
24	MG	A	2599	1/1	0.96	0.13	58,58,58,58	0
24	MG	A	2723	1/1	0.96	0.34	79,79,79,79	0
24	MG	G	1158	1/1	0.96	0.12	112,112,112,112	1
24	MG	A	2690	1/1	0.96	0.10	56,56,56,56	0
24	MG	A	2650	1/1	0.96	0.08	72,72,72,72	0
24	MG	A	2607	1/1	0.97	0.10	69,69,69,69	0
24	MG	A	2730	1/1	0.97	0.30	70,70,70,70	0
24	MG	J	1101	1/1	0.97	0.07	68,68,68,68	0
24	MG	K	1130	1/1	0.97	0.05	69,69,69,69	0
24	MG	A	2632	1/1	0.97	0.07	89,89,89,89	0
24	MG	A	2668	1/1	0.97	0.10	97,97,97,97	0
24	MG	A	2569	1/1	0.97	0.35	83,83,83,83	0
24	MG	A	2640	1/1	0.97	0.09	74,74,74,74	0
24	MG	A	2685	1/1	0.97	0.15	23,23,23,23	0
24	MG	Z	1043	1/1	0.97	0.05	123,123,123,123	0
24	MG	A	2556	1/1	0.98	0.22	114,114,114,114	1
24	MG	A	2669	1/1	0.98	0.06	114,114,114,114	0
24	MG	A	2547	1/1	0.98	0.10	125,125,125,125	0
24	MG	D	1211	1/1	0.98	0.08	82,82,82,82	0
24	MG	A	2718	1/1	0.99	0.33	60,60,60,60	0
24	MG	A	2647	1/1	0.99	0.09	60,60,60,60	0
24	MG	A	2574	1/1	0.99	0.08	2,2,2,2	0
27	ZN	D	1210	1/1	0.99	0.11	138,138,138,138	0
27	ZN	N	1062	1/1	0.99	0.06	172,172,172,172	0

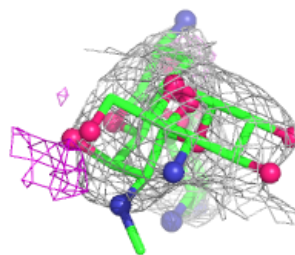
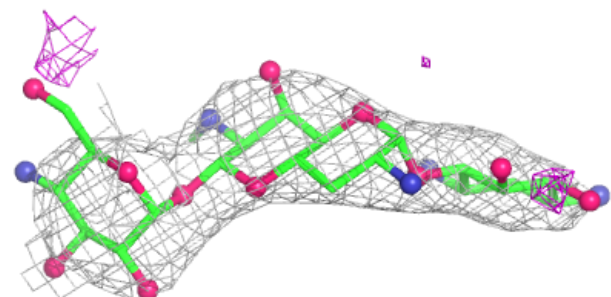
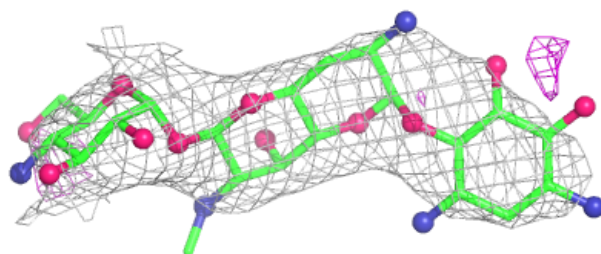
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around AM2 A 3005:

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

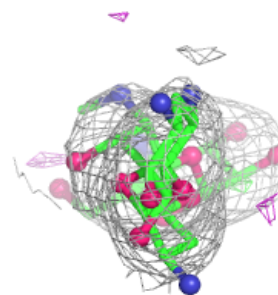
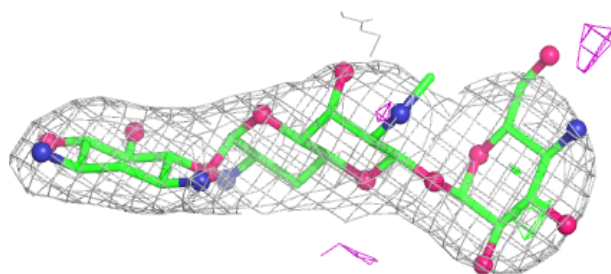
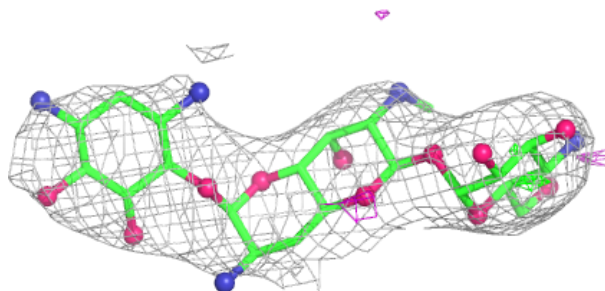
**Electron density around AM2 A 3002:**

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

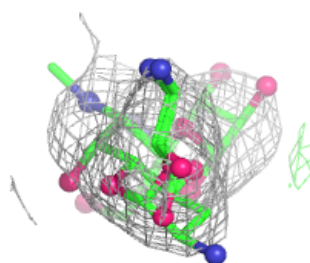
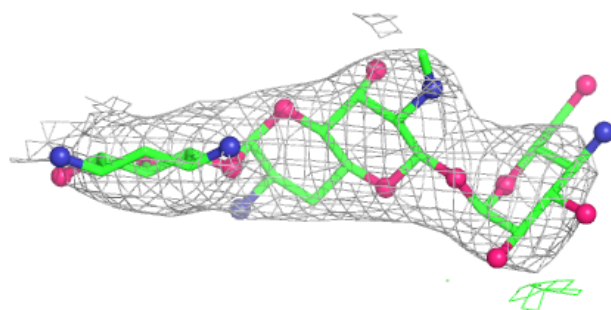
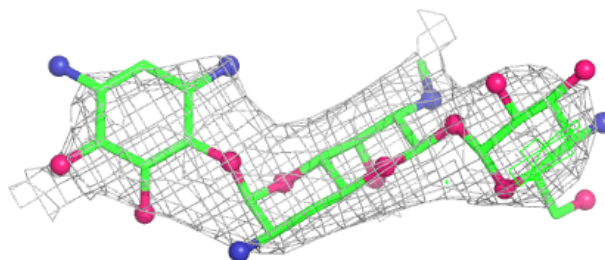


Electron density around AM2 A 3001:

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

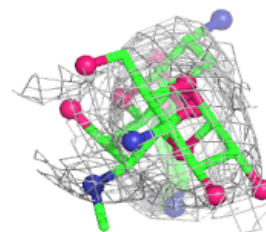
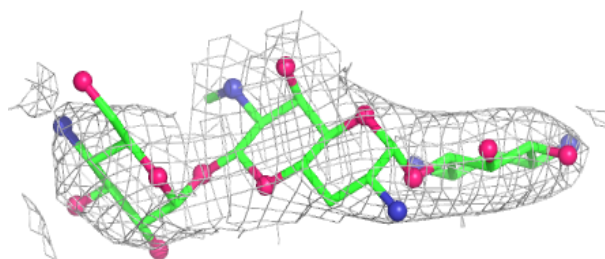
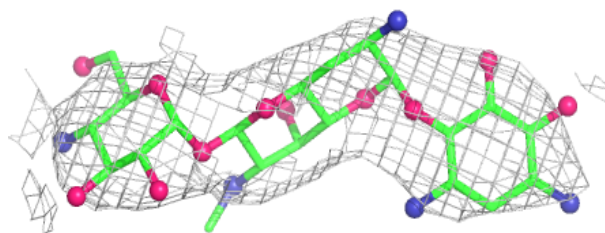
**Electron density around AM2 A 3003:**

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



Electron density around AM2 A 3004:

$2mF_o - DF_c$ (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.