



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2026 – 10:51 PM UTC

PDB ID : 4B3S / pdb_00004b3s
Title : Crystal structure of the 30S ribosome in complex with compound 37
Authors : Ng, C.L.; Lang, K.; Shcherbakov, D.; Matt, T.; Perez-Fernandez, D.; Patak, R.; Meyer, M.; Duscha, S.; Akbergenov, R.; Boukari, H.; Freihofer, P.; Kudyba, I.; Reddy, M.S.K.; Nandurikar, R.S.; Ramakrishnan, V.; Vasella, A.; Bottger, E.C.
Deposited on : 2012-07-26
Resolution : 3.15 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](#) ①) were used in the production of this report:

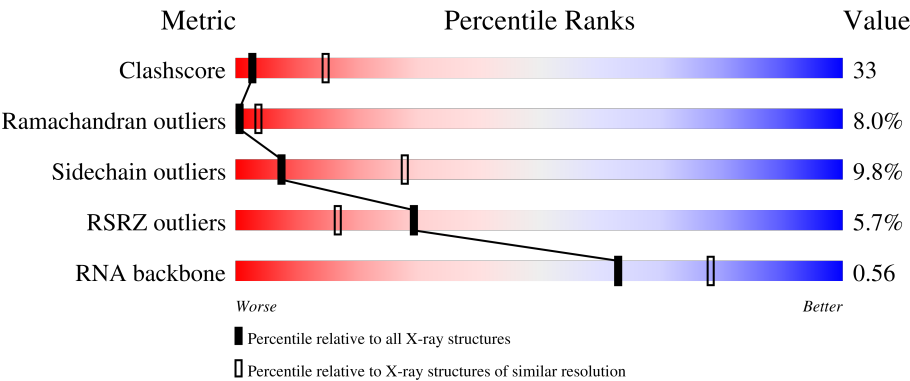
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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 3.15 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	2486 (3.20-3.12)
Ramachandran outliers	187476	2405 (3.20-3.12)
Sidechain outliers	187428	2404 (3.20-3.12)
RSRZ outliers	180081	2361 (3.20-3.12)
RNA backbone	3983	1113 (3.42-2.90)

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	1521	3% 34%52%11%
2	B	256	9% 21%55%14%8%
3	C	239	4% 20%50%15%13%
4	D	208	10% 31%56%11%
5	E	161	2% 34%48%11%6%

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

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
24	MG	A	2592	-	-	-	X
24	MG	A	2608	-	-	-	X
24	MG	A	2619	-	-	-	X
24	MG	A	2645	-	-	-	X
25	K	A	2676	-	-	-	X

2 Entry composition [i](#)

There are 27 unique types of molecules in this entry. The entry contains 52313 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	235	Total	C	N	O	S	0	0	1
			1901	1213	342	341	5			

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

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

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

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

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

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

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

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

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

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

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

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

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

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

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

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

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

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

- 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
			997	617	207	171	2			

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

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

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

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

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

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

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

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

There is a discrepancy between the modelled and reference sequences:

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	S	81	Total	C	N	O	S	0	0	1
			648	414	120	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
			762	469	162	129	2			

There is a discrepancy between the modelled and reference sequences:

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

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	V	25	Total	C	N	O	0	0	1
			209	128	51	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	4	Total	C	N	O	P	0	0	0
			79	37	12	27	3			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
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	156	Total	Mg	0	0
			156	156		
24	B	1	Total	Mg	0	0
			1	1		

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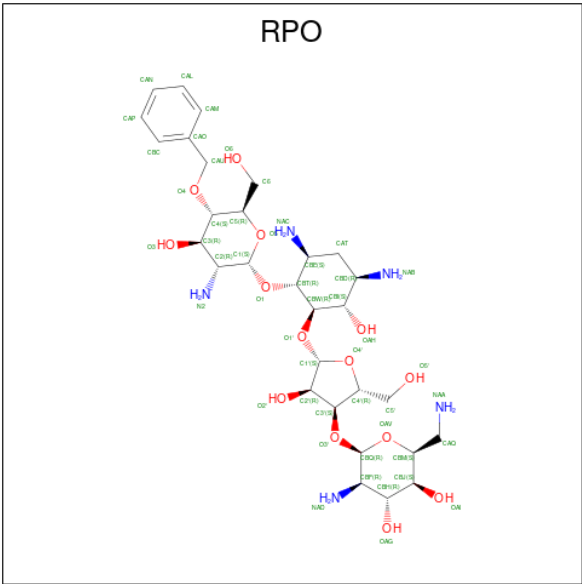
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
24	E	1	Total Mg 1 1	0	0
24	F	1	Total Mg 1 1	0	0
24	H	1	Total Mg 1 1	0	0
24	K	2	Total Mg 2 2	0	0
24	L	2	Total Mg 2 2	0	0
24	M	1	Total Mg 1 1	0	0
24	T	1	Total Mg 1 1	0	0

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

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
25	A	13	Total K 13 13	0	0

- Molecule 26 is (1R,2R,3S,4R,6S)-4,6-diamino-2-{[3-O-(2,6-diamino-2,6-dideoxy-beta-L-idop
yranosyl)-beta-D-ribofuranosyl]oxy}-3-hydroxycyclohexyl 2-amino-4-O-benzyl-2-deoxy-alpha
a-D-glucopyranoside (CCD ID: RPO) (formula: C₃₀H₅₁N₅O₁₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
26	A	1	Total	C	N	O	0	0
			49	30	5	14		

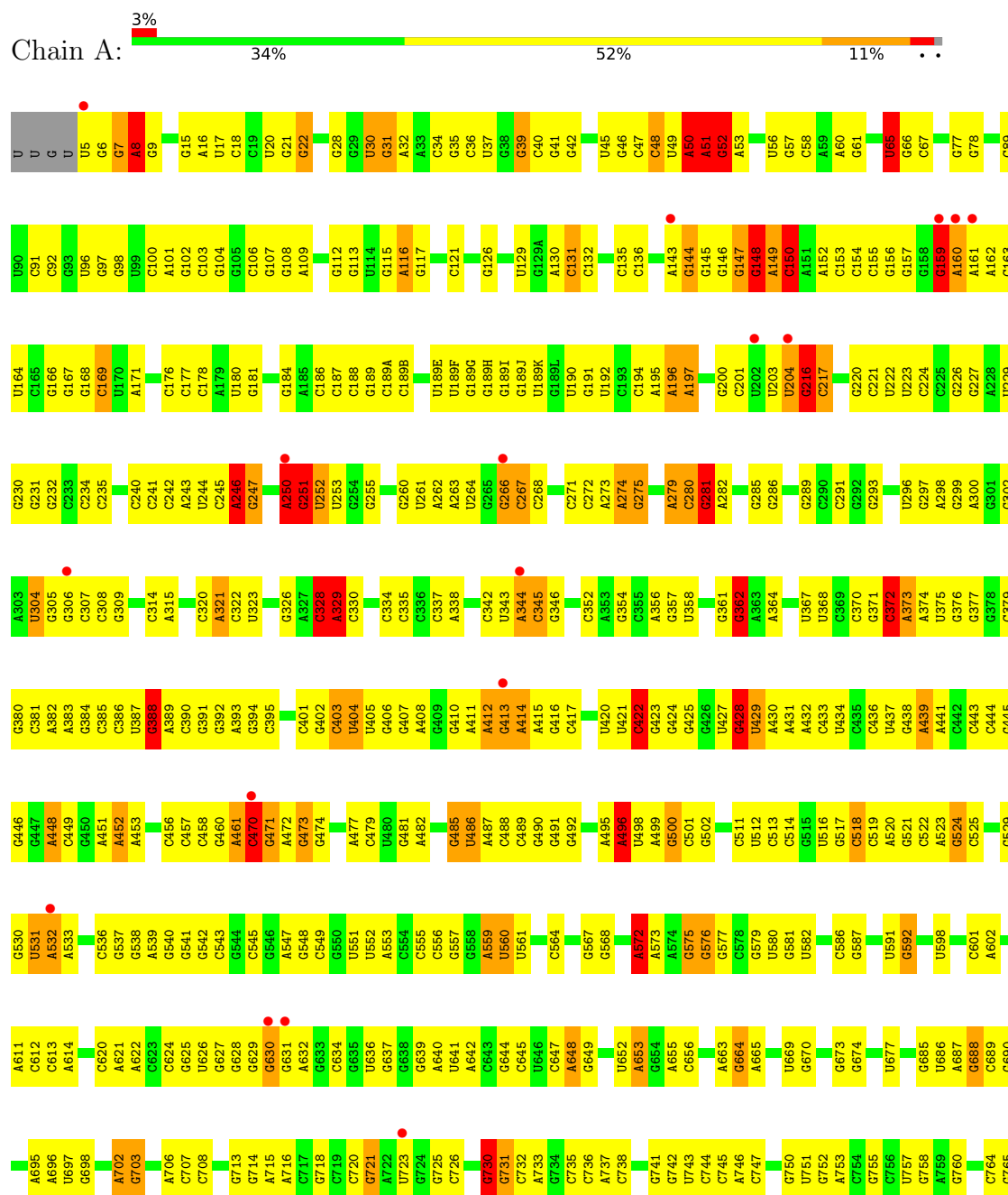
- Molecule 27 is ZINC ION (CCD ID: ZN) (formula: Zn).

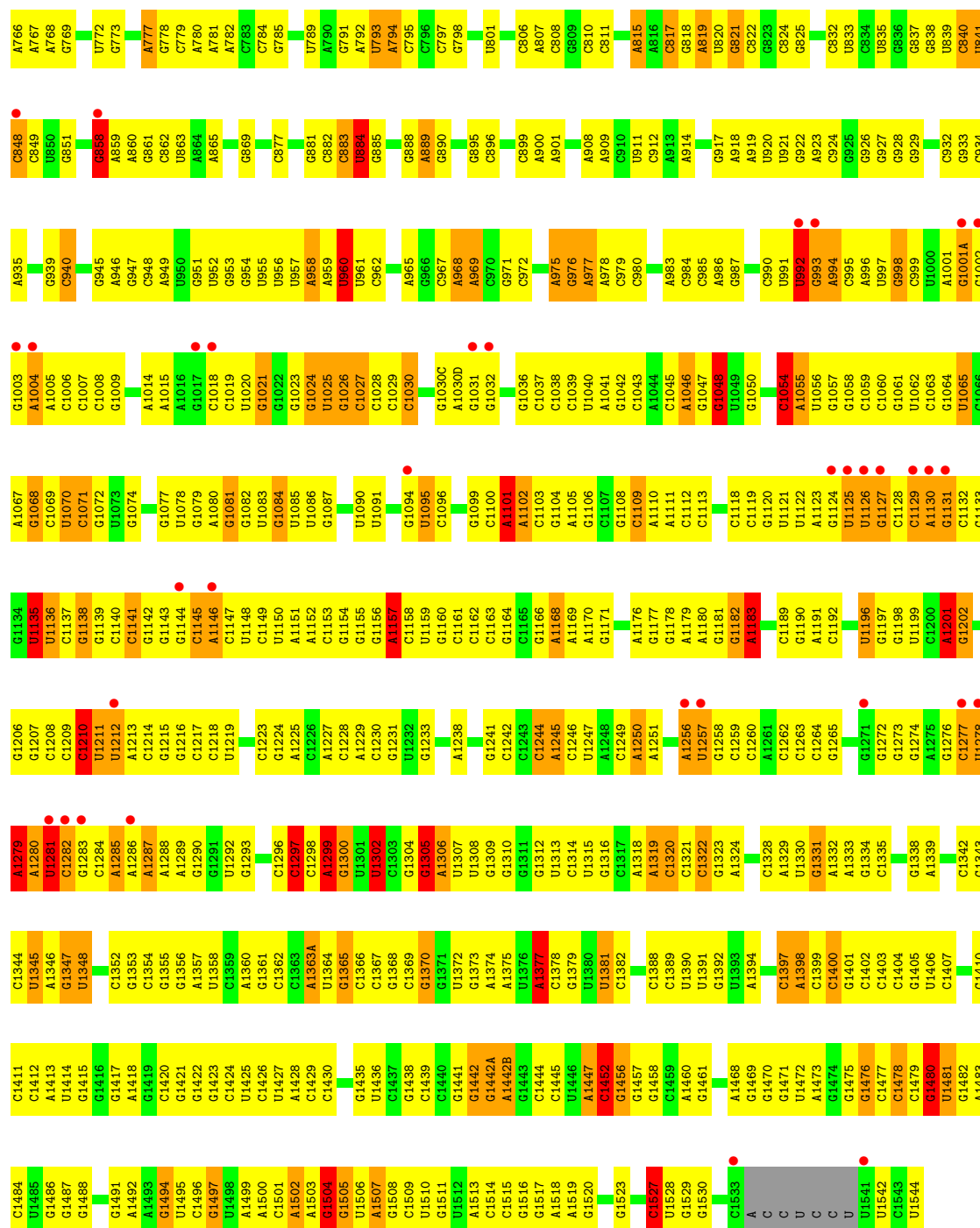
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
27	D	1	Total	Zn	0	0
			1	1		
27	N	1	Total	Zn	0	0
			1	1		

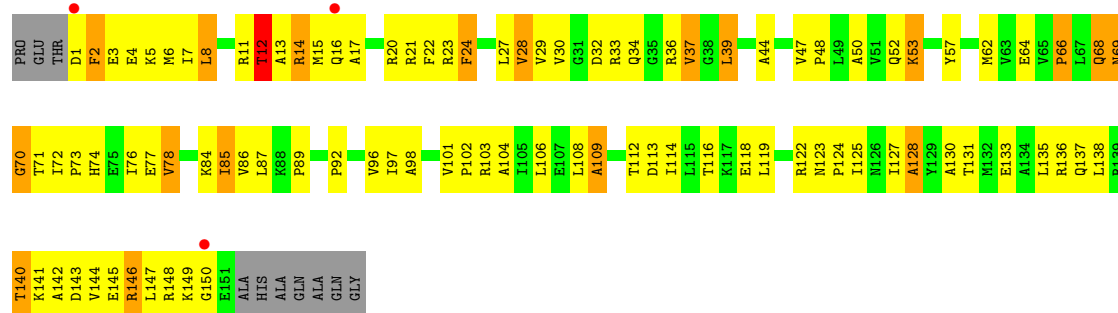
3 Residue-property plots

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

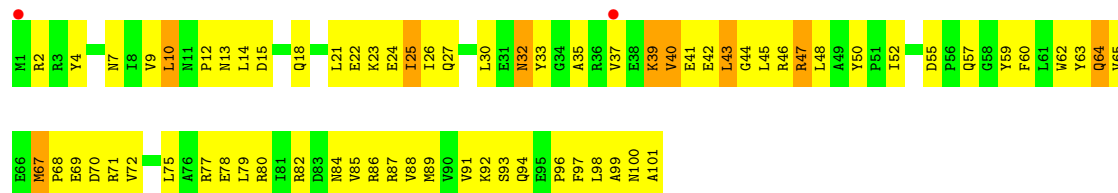
• Molecule 1: 16S RIBOSOMAL RNA







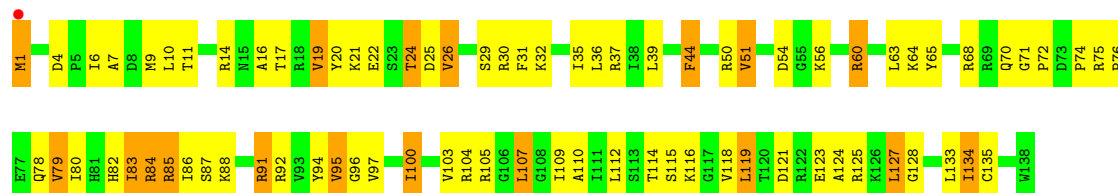
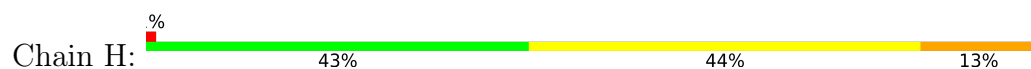
• Molecule 6: 30S RIBOSOMAL PROTEIN S6



• Molecule 7: 30S RIBOSOMAL PROTEIN S7

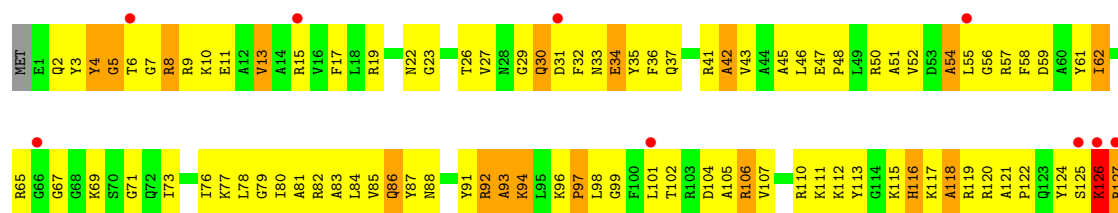


• Molecule 8: 30S RIBOSOMAL PROTEIN S8

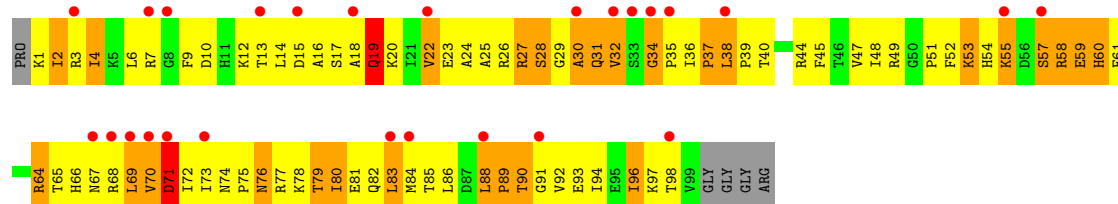
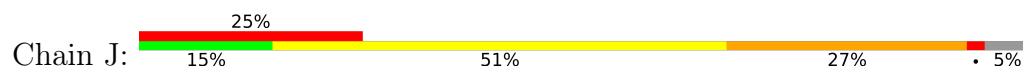


• Molecule 9: 30S RIBOSOMAL PROTEIN S9

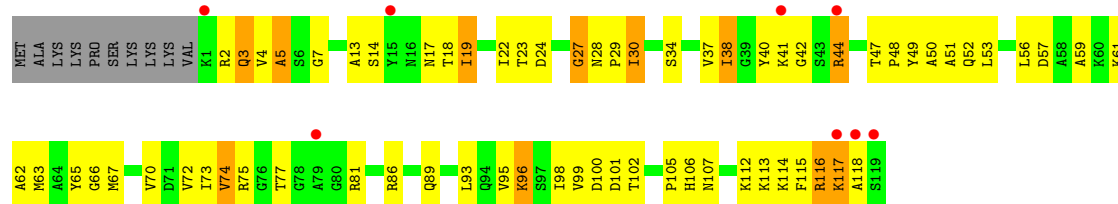




• Molecule 10: 30S RIBOSOMAL PROTEIN S10



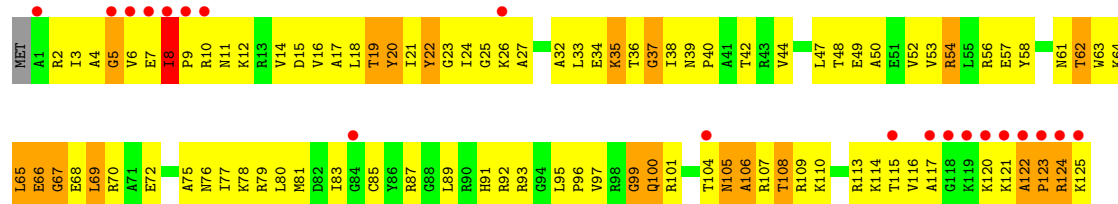
• Molecule 11: 30S RIBOSOMAL PROTEIN S11



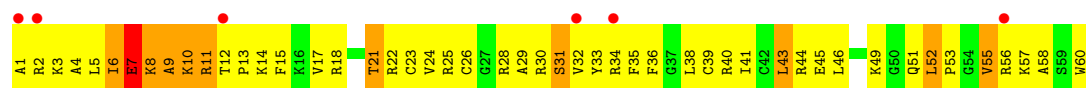
• Molecule 12: 30S RIBOSOMAL PROTEIN S12



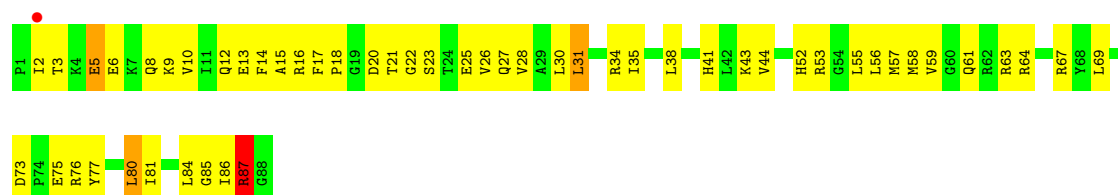
• Molecule 13: 30S RIBOSOMAL PROTEIN S13



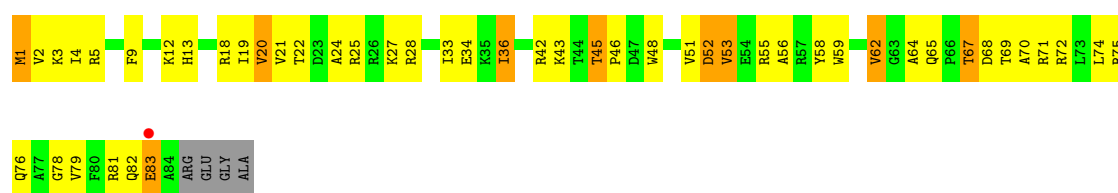
● Molecule 14: 30S RIBOSOMAL PROTEIN S14 TYPE Z



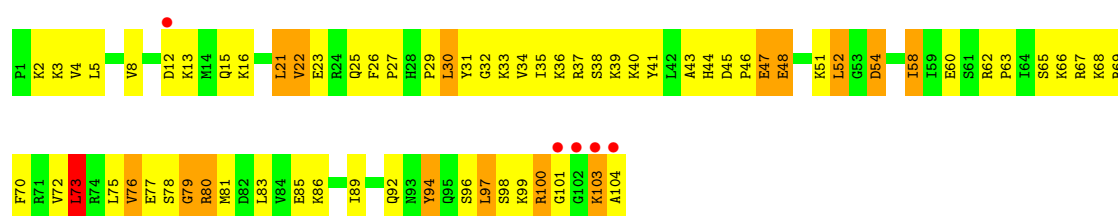
● Molecule 15: 30S RIBOSOMAL PROTEIN S15



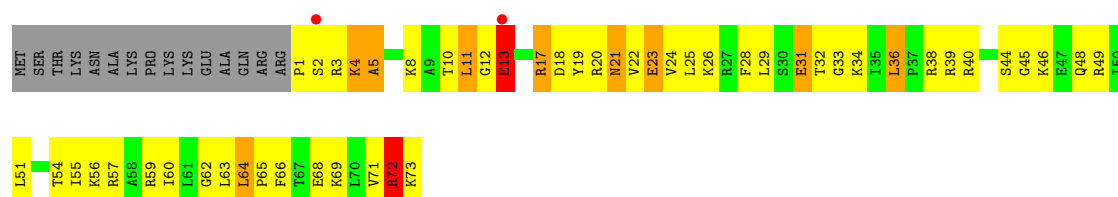
● Molecule 16: 30S RIBOSOMAL PROTEIN S16



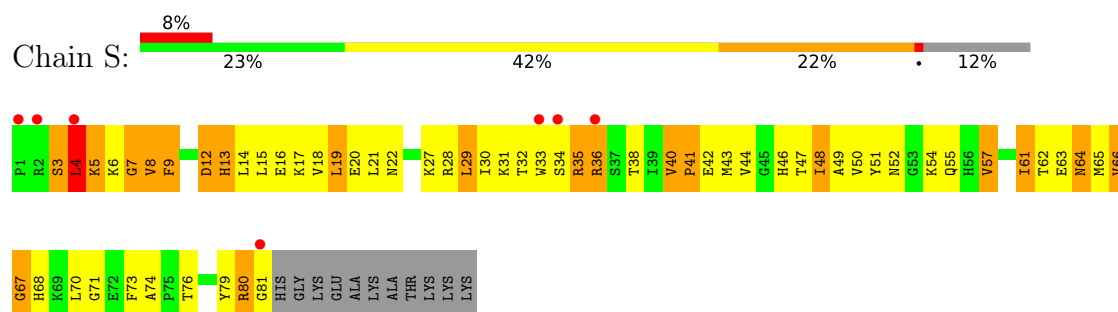
● Molecule 17: 30S RIBOSOMAL PROTEIN S17



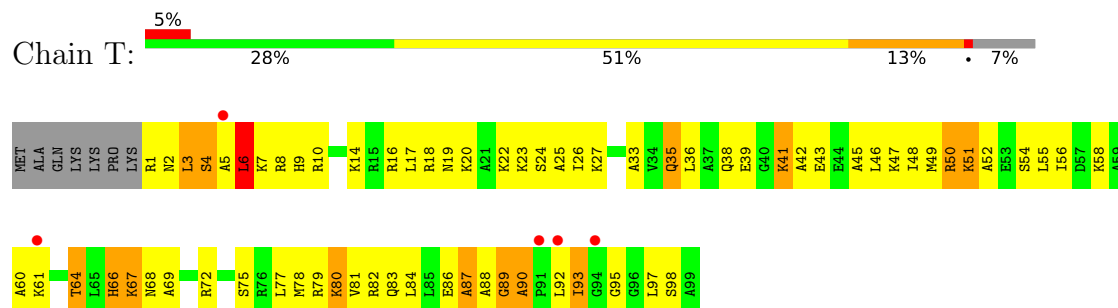
● Molecule 18: 30S RIBOSOMAL PROTEIN S18



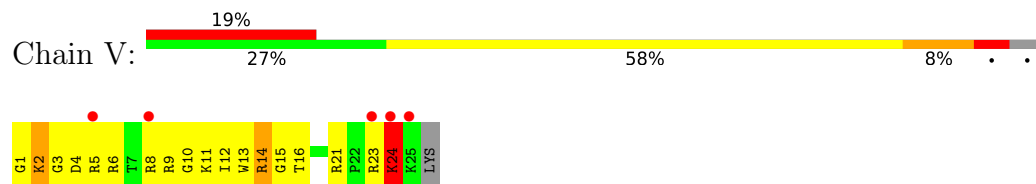
● Molecule 19: 30S RIBOSOMAL PROTEIN S19



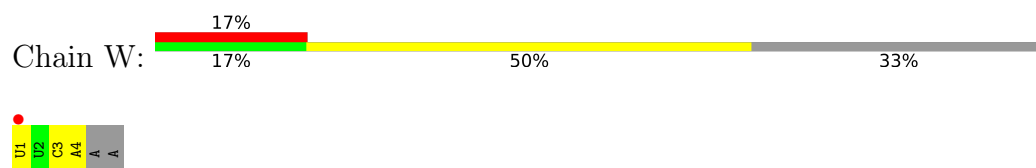
- Molecule 20: 30S RIBOSOMAL PROTEIN S20



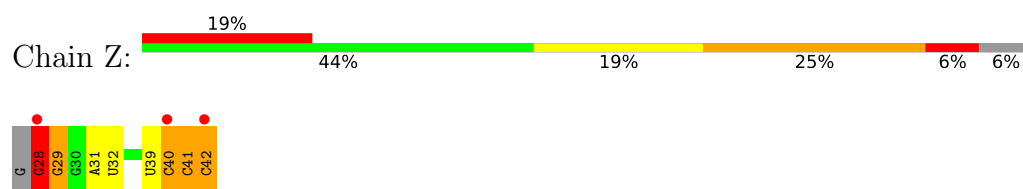
- Molecule 21: 30S RIBOSOMAL PROTEIN THX



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



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	401.15Å 401.15Å 173.64Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 3.15 40.00 – 3.15	Depositor EDS
% Data completeness (in resolution range)	99.3 (40.00-3.15) 99.2 (40.00-3.15)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.26 (at 3.12Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.210 , 0.247 0.213 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	75.6	Xtriage
Anisotropy	0.084	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 80.5	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	0.93	EDS
Total number of atoms	52313	wwPDB-VP
Average B, all atoms (Å ²)	81.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.60% 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, ZN, RPO, 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	0.43	0/36318	0.73	88/56682 (0.2%)
2	B	0.45	1/1936 (0.1%)	1.05	9/2611 (0.3%)
3	C	0.50	1/1637 (0.1%)	0.98	8/2207 (0.4%)
4	D	0.46	0/1733	1.00	10/2318 (0.4%)
5	E	0.60	1/1163 (0.1%)	1.06	4/1566 (0.3%)
6	F	0.43	0/856	0.96	1/1154 (0.1%)
7	G	0.43	0/1276	0.94	2/1709 (0.1%)
8	H	0.57	0/1136	1.22	14/1527 (0.9%)
9	I	0.43	0/1029	1.04	8/1378 (0.6%)
10	J	0.51	1/808 (0.1%)	1.06	6/1087 (0.6%)
11	K	0.52	0/900	1.11	6/1213 (0.5%)
12	L	0.57	1/987 (0.1%)	1.19	5/1322 (0.4%)
13	M	0.47	0/1008	1.02	5/1347 (0.4%)
14	N	0.50	0/501	1.08	4/664 (0.6%)
15	O	0.45	0/745	0.98	3/992 (0.3%)
16	P	0.56	1/717 (0.1%)	1.16	6/965 (0.6%)
17	Q	0.50	0/870	1.06	2/1159 (0.2%)
18	R	0.43	0/603	1.11	7/799 (0.9%)
19	S	0.53	0/662	1.05	5/892 (0.6%)
20	T	0.53	0/764	1.09	5/1006 (0.5%)
21	V	0.59	1/213 (0.5%)	0.90	1/279 (0.4%)
22	W	0.49	0/87	1.02	1/133 (0.8%)
23	Z	0.45	0/357	0.78	2/555 (0.4%)
All	All	0.45	7/56306 (0.0%)	0.85	202/83565 (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	36	29
23	Z	1	0
All	All	37	29

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	206	VAL	C-N	-5.68	1.25	1.33
5	E	150	GLY	C-N	-5.66	1.25	1.33
16	P	83	GLU	C-N	-5.60	1.25	1.33
21	V	24	LYS	C-N	-5.59	1.25	1.33
2	B	234	GLN	C-N	-5.51	1.25	1.33
10	J	98	THR	C-N	-5.48	1.25	1.33
12	L	124	ALA	C-N	-5.44	1.25	1.33

All (202) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	884	U	C2'-C3'-O3'	14.47	131.21	109.50
1	A	281	G	C2'-C3'-O3'	13.94	130.41	109.50
1	A	65	U	C2'-C3'-O3'	13.69	130.03	109.50
1	A	1452	C	C2'-C3'-O3'	13.04	129.06	109.50
12	L	22	ALA	N-CA-C	-12.06	95.84	112.25
20	T	6	LEU	N-CA-C	-11.76	99.04	113.50
1	A	246	A	C2'-C3'-O3'	10.90	125.85	109.50
1	A	1480	G	C2'-C3'-O3'	10.55	125.33	109.50
1	A	1054	C	C2'-C3'-O3'	10.46	125.19	109.50
1	A	159	G	C2'-C3'-O3'	10.33	125.00	109.50
1	A	372	C	C2'-C3'-O3'	10.33	124.99	109.50
1	A	1210	C	C2'-C3'-O3'	10.30	124.94	109.50
1	A	1101	A	C2'-C3'-O3'	10.23	124.85	109.50
1	A	246	A	C4'-C3'-O3'	10.14	124.61	109.40
11	K	27	GLY	N-CA-C	10.05	127.04	115.08
1	A	992	U	C5'-C4'-C3'	10.02	131.03	116.00
1	A	968	A	C2'-C3'-O3'	9.51	123.77	109.50
1	A	250	A	C5'-C4'-C3'	9.45	129.38	115.20
16	P	27	LYS	N-CA-C	-9.27	99.01	110.41
4	D	10	LEU	N-CA-C	-9.20	101.33	111.36
8	H	96	GLY	N-CA-C	-9.11	100.24	112.82
1	A	428	G	C2'-C3'-O3'	9.01	123.02	109.50
15	O	44	VAL	N-CA-C	-8.97	95.29	109.20
1	A	1452	C	C4'-C3'-O3'	8.96	122.84	109.40
8	H	134	ILE	N-CA-C	8.95	119.01	110.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
14	N	30	ARG	N-CA-C	8.95	123.92	112.92
1	A	1504	G	C2'-C3'-O3'	8.85	122.77	109.50
1	A	281	G	C4'-C3'-O3'	8.84	122.66	109.40
1	A	251	G	C2'-C3'-O3'	8.83	122.75	109.50
5	E	44	ALA	N-CA-C	8.77	115.87	108.07
1	A	1480	G	N9-C1'-C2'	8.66	127.00	114.00
23	Z	28	G	N9-C1'-C2'	8.59	124.89	112.00
1	A	730	G	C2'-C3'-O3'	8.53	126.49	113.70
6	F	43	LEU	N-CA-C	-8.42	103.01	113.28
15	O	43	LYS	N-CA-C	-8.41	102.46	112.89
1	A	559	A	C2'-C3'-O3'	8.25	121.87	109.50
1	A	884	U	C4'-C3'-O3'	8.24	121.77	109.40
1	A	250	A	C5'-C4'-O4'	7.99	121.08	109.10
11	K	106	HIS	N-CA-C	-7.93	101.94	112.72
12	L	113	ARG	N-CA-C	7.90	119.89	111.28
1	A	1297	C	C2'-C3'-O3'	7.86	125.49	113.70
1	A	50	A	N9-C1'-C2'	7.86	123.79	112.00
5	E	109	ALA	N-CA-C	-7.85	103.42	113.16
1	A	1305	G	N9-C1'-C2'	7.81	123.71	112.00
12	L	115	LYS	N-CA-C	-7.71	97.75	110.17
7	G	146	ALA	N-CA-C	-7.67	104.02	113.15
18	R	36	LEU	CA-C-N	7.67	127.59	119.85
18	R	36	LEU	C-N-CA	7.67	127.59	119.85
13	M	106	ALA	N-CA-C	-7.54	101.15	112.54
1	A	216	G	C2'-C3'-O3'	7.54	120.80	109.50
2	B	113	GLU	N-CA-C	-7.53	103.66	114.12
1	A	304	U	C2'-C3'-O3'	7.48	124.92	113.70
1	A	196	A	C2'-C3'-O3'	7.47	124.91	113.70
1	A	1377	A	C2'-C3'-O3'	7.46	124.89	113.70
1	A	1210	C	N1-C1'-C2'	7.45	125.17	114.00
1	A	572	A	C2'-C3'-O3'	7.41	124.82	113.70
1	A	992	U	N1-C1'-C2'	7.40	123.09	112.00
1	A	1527	C	C5'-C4'-C3'	-7.36	104.96	116.00
19	S	3	SER	N-CA-C	7.36	119.32	108.14
1	A	329	A	N9-C1'-C2'	7.28	124.91	114.00
16	P	25	ARG	N-CA-C	7.26	122.31	113.38
8	H	75	ARG	CA-C-N	7.21	127.20	119.78
8	H	75	ARG	C-N-CA	7.21	127.20	119.78
1	A	30	U	C2'-C3'-O3'	-7.10	103.05	113.70
1	A	1084	G	C2'-C3'-O3'	6.99	124.19	113.70
1	A	148	G	C2'-C3'-O3'	6.96	124.14	113.70
1	A	8	A	C4'-C3'-O3'	6.96	119.84	109.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1157	A	C2'-C3'-O3'	6.93	119.90	109.50
18	R	64	LEU	CA-C-N	6.92	127.09	120.31
18	R	64	LEU	C-N-CA	6.92	127.09	120.31
1	A	1299	A	N9-C1'-C2'	6.88	122.33	112.00
17	Q	30	LEU	N-CA-C	6.86	118.83	111.36
4	D	9	ARG	N-CA-C	-6.85	106.81	114.62
11	K	30	ILE	N-CA-C	-6.73	105.77	111.56
1	A	496	A	C2'-C3'-O3'	6.73	119.60	109.50
1	A	1504	G	C4'-C3'-O3'	6.73	119.50	109.40
8	H	100	ILE	CA-C-N	6.71	126.63	119.85
8	H	100	ILE	C-N-CA	6.71	126.63	119.85
2	B	127	LYS	N-CA-C	-6.71	104.04	111.82
1	A	1480	G	C4'-C3'-O3'	6.70	119.45	109.40
9	I	94	LYS	N-CA-C	-6.67	105.78	114.04
1	A	251	G	C4'-C3'-O3'	6.65	119.38	109.40
1	A	1305	G	C2'-C3'-O3'	6.49	123.44	113.70
1	A	65	U	C4'-C3'-O3'	6.48	119.11	109.40
1	A	1157	A	C4'-C3'-O3'	6.47	119.11	109.40
1	A	159	G	N9-C1'-C2'	6.45	123.67	114.00
20	T	51	LYS	N-CA-C	-6.44	103.95	110.97
5	E	24	PHE	N-CA-C	6.41	120.33	110.20
8	H	79	VAL	N-CA-C	-6.41	104.79	111.58
18	R	66	PHE	N-CA-C	-6.40	105.61	113.41
1	A	250	A	N9-C1'-C2'	6.39	123.58	114.00
1	A	1157	A	N9-C1'-C2'	6.38	123.57	114.00
14	N	52	LEU	CA-C-N	6.37	126.75	119.93
14	N	52	LEU	C-N-CA	6.37	126.75	119.93
1	A	1210	C	C5'-C4'-C3'	6.33	124.69	115.20
3	C	87	ARG	N-CA-C	-6.31	104.40	111.28
3	C	172	VAL	CA-C-N	6.30	127.71	119.84
3	C	172	VAL	C-N-CA	6.30	127.71	119.84
1	A	1502	A	N9-C1'-C2'	6.24	123.35	114.00
9	I	58	PHE	N-CA-C	6.23	118.02	109.18
7	G	49	ILE	N-CA-C	-6.21	103.86	112.50
1	A	992	U	C5'-C4'-O4'	6.21	119.11	109.80
21	V	6	ARG	N-CA-C	6.11	118.34	110.65
1	A	388	G	C4'-C3'-O3'	-6.09	103.86	113.00
1	A	422	C	N1-C1'-C2'	6.06	121.08	112.00
18	R	4	LYS	N-CA-C	-6.02	105.76	112.57
16	P	67	THR	N-CA-C	-6.01	102.58	110.33
1	A	470	C	C2'-C3'-O3'	6.00	118.50	109.50
1	A	52	G	C5'-C4'-C3'	5.97	124.96	116.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	27	SER	CA-C-N	5.97	127.30	119.84
4	D	27	SER	C-N-CA	5.97	127.30	119.84
8	H	7	ALA	N-CA-C	-5.96	104.79	111.28
4	D	203	ILE	N-CA-C	-5.93	104.96	110.53
19	S	9	PHE	N-CA-C	5.89	118.54	110.24
10	J	19	GLN	N-CA-C	-5.89	105.59	112.89
14	N	7	GLU	N-CA-C	-5.88	105.76	113.17
1	A	8	A	C2'-C3'-O3'	5.82	118.22	109.50
1	A	1480	G	C5'-C4'-C3'	5.81	123.92	115.20
2	B	180	ALA	N-CA-C	5.81	117.23	108.46
9	I	34	GLU	N-CA-C	-5.78	106.15	113.43
10	J	69	LEU	N-CA-C	5.75	120.08	112.72
2	B	214	ASP	N-CA-C	-5.75	105.01	111.28
1	A	329	A	C5'-C4'-O4'	5.75	117.72	109.10
5	E	128	ALA	N-CA-C	-5.74	104.93	111.07
22	W	4	A	C2'-C3'-O3'	5.73	122.29	113.70
10	J	22	VAL	N-CA-C	5.72	116.46	110.62
1	A	388	G	N9-C1'-C2'	5.71	120.56	112.00
2	B	219	ALA	N-CA-C	-5.69	106.68	113.97
13	M	8	ILE	CA-C-N	-5.69	113.92	119.78
13	M	8	ILE	C-N-CA	-5.69	113.92	119.78
3	C	182	ASP	N-CA-C	-5.67	102.50	110.50
10	J	83	LEU	N-CA-C	5.66	118.13	110.88
1	A	1084	G	C4'-C3'-O3'	5.63	121.44	113.00
11	K	117	LYS	N-CA-C	-5.60	101.89	113.31
12	L	45	ASN	N-CA-C	5.60	117.92	110.53
1	A	150	C	C5'-C4'-C3'	-5.54	107.68	116.00
18	R	31	GLU	N-CA-C	-5.52	104.65	111.33
8	H	84	ARG	N-CA-C	5.52	118.45	108.69
13	M	54	ARG	N-CA-C	-5.51	105.38	111.71
1	A	1297	C	N1-C1'-C2'	5.50	120.26	112.00
8	H	87	SER	N-CA-C	-5.50	102.75	110.50
20	T	25	ALA	N-CA-C	-5.50	104.98	110.97
1	A	1135	U	C2'-C3'-O3'	5.49	117.73	109.50
1	A	1201	A	C2'-C3'-O3'	5.47	117.70	109.50
1	A	159	G	C4'-C3'-O3'	5.47	117.60	109.40
1	A	328	C	N1-C1'-C2'	5.47	122.20	114.00
23	Z	42	C	C2'-C3'-O3'	-5.45	101.33	109.50
1	A	858	G	O4'-C1'-C2'	-5.44	102.16	107.60
1	A	1281	U	N1-C1'-C2'	5.43	120.14	112.00
20	T	14	LYS	N-CA-C	-5.42	105.28	111.07
15	O	10	VAL	N-CA-C	5.41	116.18	110.72

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	51	A	C2'-C3'-O3'	5.41	117.61	109.50
4	D	32	MET	N-CA-C	-5.40	106.39	112.87
1	A	196	A	C4'-C3'-O3'	5.40	121.09	113.00
9	I	62	ILE	N-CA-C	5.39	115.65	108.11
1	A	1183	A	C4'-C3'-O3'	-5.38	104.92	113.00
9	I	86	GLN	N-CA-C	-5.38	102.54	111.37
2	B	128	GLU	N-CA-C	-5.36	106.87	113.41
20	T	42	ALA	N-CA-C	5.35	116.97	111.03
3	C	84	ARG	N-CA-C	-5.34	106.70	113.43
1	A	992	U	O4'-C4'-C3'	5.33	109.33	104.00
4	D	195	LEU	CA-C-N	5.31	126.48	119.84
4	D	195	LEU	C-N-CA	5.31	126.48	119.84
19	S	40	VAL	CA-C-N	5.29	126.45	119.84
19	S	40	VAL	C-N-CA	5.29	126.45	119.84
8	H	44	PHE	N-CA-C	-5.28	107.38	113.88
3	C	98	VAL	N-CA-C	5.28	116.57	108.71
9	I	5	GLY	N-CA-C	-5.26	101.92	110.55
1	A	473	G	C5'-C4'-C3'	-5.23	108.16	116.00
10	J	60	HIS	N-CA-C	5.23	118.33	109.76
3	C	155	ARG	N-CA-C	-5.22	99.67	110.80
4	D	195	LEU	N-CA-C	5.22	117.79	109.64
11	K	41	LYS	N-CA-C	5.19	120.09	113.55
1	A	1071	C	C5'-C4'-C3'	-5.19	108.22	116.00
3	C	152	VAL	N-CA-C	-5.19	102.24	109.45
11	K	72	VAL	N-CA-C	5.18	116.03	108.53
17	Q	78	SER	N-CA-C	5.17	116.16	108.60
1	A	1456	G	C4'-C3'-O3'	-5.17	105.24	113.00
8	H	60	ARG	N-CA-C	-5.13	102.79	110.23
13	M	100	GLN	N-CA-C	5.13	116.60	108.96
2	B	106	VAL	N-CA-C	-5.11	105.72	110.53
16	P	20	VAL	N-CA-C	5.11	116.26	108.80
9	I	93	ALA	N-CA-C	-5.11	107.72	114.31
1	A	960	U	N1-C1'-C2'	5.11	121.66	114.00
8	H	19	VAL	N-CA-C	-5.10	107.78	112.83
1	A	329	A	C2'-C3'-O3'	5.10	117.15	109.50
12	L	88	ASP	N-CA-C	5.10	119.37	113.20
2	B	86	TYR	N-CA-C	5.09	116.55	108.96
10	J	64	ARG	N-CA-C	5.09	117.85	109.76
1	A	51	A	N9-C1'-C2'	5.08	121.63	114.00
1	A	362	G	C5'-C4'-O4'	-5.08	102.17	109.80
2	B	162	THR	N-CA-C	-5.08	105.75	111.28
16	P	36	ILE	CB-CA-C	-5.07	105.69	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	126	THR	N-CA-C	5.06	116.56	107.80
16	P	56	ALA	N-CA-C	-5.06	104.85	111.02
19	S	57	VAL	N-CA-C	5.05	113.49	107.73
8	H	51	VAL	CB-CA-C	-5.04	107.00	111.74
1	A	22	G	C5'-C4'-C3'	-5.03	108.45	116.00
9	I	4	TYR	N-CA-C	5.03	117.31	109.52
1	A	329	A	C5'-C4'-C3'	5.01	122.72	115.20
1	A	777	A	C5'-C4'-C3'	5.01	123.51	116.00
1	A	996	A	C5'-C4'-C3'	-5.00	108.49	116.00

All (37) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	50	A	C4'
1	A	65	U	C3'
1	A	159	G	C1',C3',C4'
1	A	196	A	C3'
1	A	246	A	C3'
1	A	250	A	C4',C1'
1	A	251	G	C1',C3',C4'
1	A	281	G	C3'
1	A	304	U	C3'
1	A	329	A	C1',C3',C4'
1	A	730	G	C3'
1	A	884	U	C3'
1	A	992	U	C4'
1	A	1084	G	C3'
1	A	1157	A	C1',C3',C4'
1	A	1210	C	C1',C3',C4'
1	A	1297	C	C3',C4'
1	A	1305	G	C3',C4'
1	A	1377	A	C3'
1	A	1452	C	C3'
1	A	1480	G	C1',C3',C4'
23	Z	28	G	C1'

All (29) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1048	G	Sidechain
1	A	1077	G	Sidechain
1	A	1081	G	Sidechain

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Mol	Chain	Res	Type	Group
1	A	1210	C	Sidechain
1	A	1244	C	Sidechain
1	A	1279	A	Sidechain
1	A	1299	A	Sidechain
1	A	1302	U	Sidechain
1	A	1331	G	Sidechain
1	A	1339	A	Sidechain
1	A	1345	U	Sidechain
1	A	1401	G	Sidechain
1	A	1528	U	Sidechain
1	A	159	G	Sidechain
1	A	253	U	Sidechain
1	A	291	C	Sidechain
1	A	297	G	Sidechain
1	A	380	G	Sidechain
1	A	404	U	Sidechain
1	A	51	A	Sidechain
1	A	529	G	Sidechain
1	A	560	U	Sidechain
1	A	561	U	Sidechain
1	A	592	G	Sidechain
1	A	611	A	Sidechain
1	A	664	G	Sidechain
1	A	858	G	Sidechain
1	A	883	C	Sidechain
1	A	940	C	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	16381	1030	0
2	B	1901	0	1954	246	0
3	C	1613	0	1680	217	0
4	D	1703	0	1766	176	0
5	E	1147	0	1210	118	0
6	F	843	0	857	89	0
7	G	1257	0	1299	83	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	H	1116	0	1177	102	0
9	I	1011	0	1046	118	0
10	J	795	0	843	154	0
11	K	885	0	907	91	0
12	L	971	0	1059	107	0
13	M	997	0	1075	125	0
14	N	492	0	532	80	0
15	O	734	0	773	53	0
16	P	701	0	720	50	0
17	Q	857	0	932	80	0
18	R	597	0	670	88	0
19	S	648	0	675	90	0
20	T	762	0	862	85	0
21	V	209	0	224	33	0
22	W	79	0	44	2	0
23	Z	319	0	164	10	0
24	A	156	0	0	0	0
24	B	1	0	0	0	0
24	E	1	0	0	0	0
24	F	1	0	0	0	0
24	H	1	0	0	0	0
24	K	2	0	0	0	0
24	L	2	0	0	0	0
24	M	1	0	0	0	0
24	T	1	0	0	0	0
25	A	13	0	0	0	0
26	A	49	0	51	6	0
27	D	1	0	0	0	0
27	N	1	0	0	0	0
All	All	52313	0	36901	2958	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 33.

All (2958) 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:361:G:H2'	1:A:362:G:H5''	1.27	1.12
3:C:25:LYS:H	3:C:25:LYS:HD3	1.09	1.12
12:L:43:LYS:HB3	12:L:44:PRO:HD3	1.30	1.11
1:A:402:G:H2'	1:A:403:C:H5''	1.26	1.11

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:190:THR:HG22	3:C:191:THR:H	1.11	1.10
1:A:1029:C:H2'	1:A:1030:C:H5''	1.31	1.10
8:H:86:ILE:HG21	8:H:133:LEU:HD23	1.32	1.09
4:D:82:SER:HA	4:D:88:THR:HG21	1.12	1.08
7:G:53:THR:HG22	7:G:55:GLN:H	1.13	1.08
16:P:74:LEU:HG	16:P:79:VAL:HG21	1.36	1.07
1:A:1130:A:H5'	1:A:1131:G:C5'	1.84	1.07
19:S:32:THR:HG22	19:S:34:SER:H	1.20	1.07
2:B:9:VAL:HG13	2:B:203:ARG:HG3	1.36	1.06
12:L:83:GLY:HA2	12:L:94:TYR:HA	1.36	1.06
2:B:78:GLU:HB3	2:B:213:VAL:HG21	1.39	1.05
10:J:25:ALA:HB2	10:J:83:LEU:HD11	1.37	1.04
11:K:96:LYS:HE2	11:K:96:LYS:HA	1.34	1.04
10:J:36:ILE:HD12	10:J:69:LEU:HD23	1.38	1.04
19:S:21:LEU:HD13	19:S:27:LYS:HD2	1.39	1.03
1:A:146:G:H2'	1:A:147:G:H5''	1.41	1.03
1:A:1130:A:C5'	1:A:1131:G:H5''	1.88	1.02
12:L:37:ARG:HG2	12:L:38:THR:H	1.23	1.02
12:L:79:VAL:HG21	12:L:96:ILE:HG23	1.42	1.01
1:A:647:C:H2'	1:A:648:A:H5''	1.36	1.00
1:A:839:U:H3'	1:A:840:C:H5''	1.42	1.00
1:A:1479:C:H2'	1:A:1480:G:H5''	1.43	1.00
3:C:90:LEU:HD12	3:C:91:ALA:N	1.75	1.00
12:L:43:LYS:HB3	12:L:44:PRO:CD	1.90	1.00
1:A:1086:U:H3	1:A:1099:G:H22	1.09	1.00
1:A:1130:A:H5'	1:A:1131:G:H5''	1.00	1.00
3:C:63:VAL:HB	3:C:98:VAL:HB	1.44	1.00
6:F:10:LEU:HD12	6:F:59:TYR:HB3	1.44	0.99
13:M:9:PRO:HB2	13:M:17:ALA:HB1	1.41	0.99
1:A:522:C:H41	12:L:49:ARG:HH22	1.10	0.99
1:A:647:C:C2'	1:A:648:A:H5''	1.93	0.98
2:B:71:ALA:HB2	2:B:205:ILE:HD13	1.46	0.98
4:D:82:SER:HA	4:D:88:THR:CG2	1.92	0.98
1:A:135:C:O2	16:P:1:MET:HB2	1.63	0.98
1:A:1276:G:H3'	1:A:1277:C:H5''	1.44	0.97
2:B:1:VAL:HG21	2:B:215:LEU:HD23	1.45	0.97
10:J:29:GLY:HA2	10:J:76:ASN:ND2	1.79	0.96
1:A:146:G:C2'	1:A:147:G:H5''	1.95	0.96
1:A:1502:A:H2	1:A:1505:G:H1	1.10	0.96
12:L:85:ARG:HH21	12:L:93:ARG:HE	1.14	0.95
3:C:27:GLN:HA	3:C:30:HIS:HD2	1.29	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:76:ILE:HA	3:C:83:ILE:HB	1.47	0.95
1:A:361:G:C2'	1:A:362:G:H5''	1.96	0.94
5:E:87:LEU:HD23	5:E:116:THR:HG22	1.47	0.94
11:K:114:LYS:HE3	11:K:115:PHE:HE1	1.31	0.94
1:A:1020:U:H2'	1:A:1021:G:H5''	1.49	0.94
1:A:1045:C:H2'	1:A:1046:A:H5''	1.48	0.94
11:K:44:ARG:O	11:K:47:THR:HG22	1.66	0.94
1:A:460:G:H3'	1:A:461:A:C5'	1.99	0.93
1:A:953:G:H1'	13:M:124:ARG:HA	1.49	0.93
3:C:13:ILE:HG22	3:C:14:THR:H	1.31	0.93
1:A:402:G:C2'	1:A:403:C:H5''	1.98	0.93
1:A:922:G:H4'	5:E:16:GLN:HA	1.50	0.92
5:E:78:VAL:HG12	5:E:85:ILE:HG22	1.48	0.92
1:A:371:G:O2'	1:A:372:C:H5'	1.69	0.92
10:J:30:ALA:HB2	10:J:74:ASN:ND2	1.85	0.91
4:D:104:VAL:HG21	4:D:125:ILE:HD13	1.51	0.91
3:C:190:THR:HG22	3:C:191:THR:N	1.85	0.91
12:L:71:HIS:HD2	12:L:73:LEU:H	1.16	0.90
1:A:1029:C:C2'	1:A:1030:C:H5''	2.01	0.90
11:K:77:THR:HG23	11:K:81:ARG:HH21	1.35	0.90
13:M:14:VAL:HG21	13:M:47:LEU:HD21	1.53	0.90
3:C:173:PRO:HB2	3:C:176:THR:HG23	1.54	0.90
13:M:36:THR:HG22	13:M:38:ILE:HD11	1.54	0.90
12:L:41:PRO:HG3	12:L:49:ARG:HD3	1.54	0.90
1:A:1182:G:H4'	1:A:1183:A:H5'	1.53	0.89
9:I:43:VAL:HG12	9:I:50:ARG:HH12	1.34	0.89
12:L:23:LEU:O	12:L:25:GLY:N	2.06	0.88
17:Q:94:TYR:HA	17:Q:97:LEU:HD11	1.55	0.88
13:M:48:THR:HG22	13:M:50:ALA:H	1.38	0.88
5:E:70:GLY:HA3	5:E:112:THR:HG22	1.55	0.88
10:J:30:ALA:HB2	10:J:74:ASN:HD22	1.38	0.88
15:O:25:GLU:OE2	15:O:76:ARG:HD2	1.72	0.88
14:N:56:ARG:HG2	14:N:57:LYS:H	1.35	0.88
1:A:939:G:H5''	7:G:101:ARG:NH2	1.89	0.88
3:C:31:LEU:O	3:C:35:ASP:HB2	1.74	0.88
4:D:37:TYR:HD1	4:D:37:TYR:H	1.17	0.88
9:I:105:ALA:O	9:I:107:VAL:HG23	1.73	0.87
10:J:17:SER:HA	10:J:20:LYS:HE2	1.55	0.87
1:A:251:G:H2'	1:A:252:U:H5''	1.57	0.87
12:L:37:ARG:HH22	12:L:53:LYS:HZ3	1.20	0.87
12:L:71:HIS:HA	12:L:98:ARG:HH22	1.39	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:451:A:H61	1:A:481:G:H5'	1.38	0.86
3:C:107:ASN:HD22	3:C:110:LEU:HG	1.39	0.86
11:K:99:VAL:HG22	18:R:71:VAL:HA	1.57	0.86
4:D:61:GLN:HE22	4:D:64:ARG:HH12	1.21	0.86
1:A:1060:C:C5	3:C:1:GLY:HA3	2.10	0.86
1:A:1128:C:O2'	1:A:1129:C:H5''	1.75	0.86
14:N:26:CYS:SG	14:N:28:ARG:HB2	2.16	0.86
1:A:1284:C:H3'	1:A:1285:A:H5''	1.58	0.85
4:D:208:ARG:HB3	4:D:208:ARG:NH1	1.91	0.85
4:D:61:GLN:HE22	4:D:64:ARG:NH1	1.74	0.85
12:L:51:VAL:HG12	12:L:52:ALA:H	1.41	0.85
6:F:25:ILE:H	6:F:25:ILE:HD12	1.40	0.85
10:J:6:LEU:CD1	10:J:18:ALA:HB2	2.06	0.85
1:A:1399:C:H4'	1:A:1400:C:H5''	1.56	0.84
6:F:101:ALA:HA	18:R:13:GLU:OE1	1.76	0.84
1:A:1108:G:H2'	1:A:1109:C:H5''	1.58	0.84
1:A:1190:G:OP1	3:C:3:LYS:HA	1.77	0.84
10:J:27:ARG:HB2	10:J:27:ARG:HH11	1.41	0.84
1:A:168:G:H2'	1:A:169:C:H5''	1.58	0.84
1:A:1366:C:H2'	1:A:1367:C:C6	2.13	0.84
2:B:160:ASP:HB2	2:B:199:ASP:HB2	1.60	0.84
11:K:17:ASN:HD22	11:K:18:THR:N	1.75	0.84
1:A:1038:C:H2'	1:A:1039:C:H6	1.43	0.84
12:L:30:ARG:O	12:L:57:THR:HG23	1.77	0.84
5:E:39:LEU:HD11	5:E:128:ALA:HB1	1.60	0.83
8:H:24:THR:HG22	8:H:63:LEU:HD21	1.60	0.83
11:K:114:LYS:HE3	11:K:115:PHE:CE1	2.14	0.83
13:M:116:VAL:HG12	13:M:117:ALA:H	1.43	0.83
19:S:36:ARG:H	19:S:36:ARG:HD2	1.41	0.83
1:A:1502:A:H2	1:A:1505:G:N1	1.76	0.83
9:I:7:GLY:HA2	9:I:78:LEU:HD12	1.58	0.83
1:A:168:G:C2'	1:A:169:C:H5''	2.08	0.83
2:B:65:VAL:HB	2:B:158:VAL:HG12	1.59	0.83
1:A:1321:C:H3'	1:A:1322:C:H5''	1.60	0.82
10:J:10:ASP:O	10:J:13:THR:HG22	1.79	0.82
11:K:17:ASN:HD22	11:K:18:THR:H	1.23	0.82
6:F:47:ARG:HE	6:F:47:ARG:N	1.77	0.82
3:C:69:VAL:HG12	3:C:71:LYS:H	1.43	0.82
1:A:647:C:H2'	1:A:648:A:C5'	2.09	0.82
11:K:81:ARG:CZ	18:R:73:LYS:HE2	2.09	0.82
1:A:180:U:H2'	1:A:181:G:H5'	1.62	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:24:LYS:C	12:L:26:ALA:H	1.84	0.82
5:E:123:ASN:HD22	5:E:124:PRO:HD2	1.44	0.81
13:M:14:VAL:HG23	13:M:42:THR:O	1.80	0.81
17:Q:3:LYS:HD2	17:Q:5:LEU:HD21	1.61	0.81
1:A:858:G:C5'	1:A:858:G:H8	1.93	0.81
1:A:969:A:H61	13:M:125:LYS:HG3	1.44	0.81
2:B:207:LEU:HD22	2:B:208:ILE:HD13	1.62	0.81
1:A:858:G:C6	1:A:869:G:N7	2.48	0.81
12:L:37:ARG:HH22	12:L:53:LYS:NZ	1.78	0.81
18:R:31:GLU:CD	18:R:31:GLU:H	1.89	0.81
3:C:25:LYS:HD3	3:C:25:LYS:N	1.94	0.81
10:J:1:LYS:HG2	10:J:73:ILE:HG23	1.62	0.81
15:O:52:HIS:CE1	15:O:56:LEU:HD13	2.16	0.81
3:C:190:THR:CG2	3:C:191:THR:H	1.91	0.80
2:B:124:ARG:HH22	3:C:178:ARG:HH12	1.28	0.80
13:M:39:ASN:O	13:M:42:THR:HG23	1.81	0.80
15:O:52:HIS:HE1	15:O:56:LEU:HD13	1.44	0.80
1:A:1472:U:H2'	1:A:1473:A:O4'	1.81	0.80
12:L:43:LYS:CB	12:L:44:PRO:HD3	2.10	0.80
15:O:86:ILE:O	15:O:87:ARG:HB2	1.81	0.80
5:E:106:LEU:HD13	5:E:114:ILE:HG21	1.63	0.80
2:B:53:GLU:HB3	2:B:215:LEU:HD11	1.63	0.80
1:A:1020:U:C2'	1:A:1021:G:H5''	2.12	0.80
2:B:4:LEU:HD23	2:B:42:MET:HE2	1.63	0.80
1:A:1024:G:O2'	1:A:1025:U:H5'	1.80	0.80
8:H:56:LYS:H	8:H:56:LYS:HD2	1.46	0.80
1:A:718:G:H5'	11:K:107:ASN:HD22	1.47	0.80
1:A:1201:A:H4'	1:A:1202:G:O5'	1.82	0.80
11:K:59:ALA:HB1	11:K:93:LEU:HD12	1.62	0.80
1:A:613:C:O2'	1:A:614:A:H5'	1.83	0.79
2:B:126:LYS:HA	2:B:129:GLN:HB2	1.63	0.79
7:G:68:VAL:HG11	7:G:133:ALA:HB1	1.61	0.79
1:A:580:U:H2'	1:A:581:G:O4'	1.82	0.79
17:Q:77:GLU:CD	17:Q:80:ARG:HD2	2.07	0.79
4:D:150:LYS:H	4:D:150:LYS:HD2	1.47	0.79
14:N:43:LEU:C	14:N:43:LEU:HD12	2.07	0.79
1:A:357:G:O2'	1:A:358:U:H5'	1.83	0.79
1:A:489:C:H2'	1:A:490:G:H8	1.48	0.79
1:A:1282:C:C6	1:A:1282:C:H5'	2.17	0.79
4:D:35:ARG:HA	4:D:37:TYR:HE1	1.47	0.78
4:D:161:LEU:HD13	4:D:180:MET:HG2	1.65	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:173:LEU:O	4:D:185:LEU:HG	1.83	0.78
12:L:51:VAL:HG12	12:L:52:ALA:N	1.94	0.78
5:E:101:VAL:HB	5:E:102:PRO:HD3	1.64	0.78
7:G:112:GLU:HG2	7:G:118:ARG:HG2	1.64	0.78
13:M:49:GLU:O	13:M:53:VAL:HG23	1.83	0.78
1:A:1367:C:H5'	10:J:58:ARG:HH21	1.47	0.78
17:Q:52:LEU:H	17:Q:52:LEU:HD12	1.48	0.78
6:F:100:ASN:HD22	18:R:8:LYS:HG2	1.47	0.78
1:A:386:C:C2'	1:A:387:U:H5'	2.12	0.78
1:A:1435:G:H2'	1:A:1436:U:C6	2.18	0.78
3:C:57:GLU:H	3:C:64:ALA:HB3	1.47	0.78
20:T:38:GLN:HB2	20:T:84:LEU:HD13	1.65	0.78
3:C:18:GLU:HG2	3:C:53:ARG:HD2	1.66	0.78
2:B:108:ARG:HH21	2:B:112:LEU:HG	1.49	0.78
20:T:78:MET:HE2	20:T:97:LEU:HD23	1.63	0.78
1:A:362:G:H5'	1:A:362:G:H8	1.49	0.78
1:A:1425:U:H2'	1:A:1426:C:H6	1.49	0.78
8:H:116:LYS:HD3	8:H:127:LEU:HD12	1.64	0.78
2:B:10:HIS:HB2	2:B:198:ASN:OD1	1.83	0.78
19:S:64:ASN:HD22	19:S:65:MET:N	1.82	0.78
1:A:1391:U:H2'	1:A:1392:G:C8	2.19	0.77
1:A:1038:C:H2'	1:A:1039:C:C6	2.19	0.77
3:C:130:ARG:NH1	3:C:130:ARG:HB2	1.99	0.77
10:J:85:THR:O	10:J:86:LEU:HD23	1.85	0.77
1:A:1144:G:H21	1:A:1146:A:H62	1.28	0.77
19:S:4:LEU:O	19:S:5:LYS:HB2	1.82	0.77
2:B:215:LEU:O	2:B:219:ALA:HB2	1.84	0.77
7:G:58:LEU:O	7:G:62:LYS:HG2	1.85	0.77
2:B:10:HIS:ND1	2:B:11:PHE:N	2.31	0.77
1:A:957:U:H3	1:A:960:U:H5''	1.47	0.77
2:B:71:ALA:HB2	2:B:205:ILE:CD1	2.15	0.77
6:F:48:LEU:HG	6:F:57:GLN:HA	1.65	0.77
12:L:42:LYS:HE3	12:L:43:LYS:HB2	1.67	0.77
10:J:47:VAL:HG13	14:N:40:ARG:HD2	1.66	0.77
10:J:82:GLN:O	10:J:86:LEU:HD12	1.84	0.77
5:E:11:ARG:HD3	5:E:22:PHE:HD2	1.49	0.77
5:E:11:ARG:HD3	5:E:22:PHE:CD2	2.19	0.76
18:R:21:ASN:C	18:R:21:ASN:HD22	1.91	0.76
1:A:706:A:O4'	11:K:19:ILE:HD11	1.86	0.76
5:E:14:ARG:HD3	5:E:21:ARG:HB2	1.67	0.76
13:M:61:ASN:O	13:M:62:THR:HB	1.84	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:V:5:ARG:HE	21:V:14:ARG:HH12	1.30	0.76
1:A:362:G:H5'	1:A:362:G:C8	2.20	0.76
1:A:939:G:H5''	7:G:101:ARG:HH22	1.50	0.76
5:E:123:ASN:HD22	5:E:124:PRO:CD	1.98	0.76
16:P:9:PHE:CD2	16:P:18:ARG:HG3	2.20	0.76
1:A:1060:C:H5	3:C:1:GLY:HA3	1.51	0.76
1:A:1425:U:H2'	1:A:1426:C:C6	2.21	0.76
8:H:56:LYS:HD2	8:H:56:LYS:N	2.00	0.76
1:A:371:G:C2'	1:A:372:C:H5'	2.16	0.76
3:C:90:LEU:HD12	3:C:91:ALA:H	1.48	0.76
4:D:82:SER:CA	4:D:88:THR:HG21	2.06	0.76
10:J:1:LYS:HA	10:J:73:ILE:HA	1.66	0.76
4:D:173:LEU:O	4:D:174:SER:HB3	1.85	0.76
19:S:63:GLU:O	19:S:66:VAL:HG23	1.84	0.76
10:J:55:LYS:HG2	10:J:58:ARG:HH12	1.47	0.76
17:Q:94:TYR:HA	17:Q:97:LEU:CD1	2.14	0.76
1:A:653:A:H5'	8:H:56:LYS:HE3	1.67	0.76
2:B:2:LYS:O	2:B:3:GLU:HB2	1.85	0.76
4:D:2:ARG:HA	4:D:2:ARG:HE	1.50	0.76
2:B:118:SER:O	2:B:121:ILE:HG13	1.86	0.75
4:D:111:VAL:HG23	4:D:160:ASN:HD21	1.50	0.75
21:V:5:ARG:HG2	21:V:14:ARG:NH1	2.01	0.75
3:C:51:LEU:HD23	3:C:51:LEU:H	1.49	0.75
6:F:21:LEU:O	6:F:24:GLU:HB3	1.85	0.75
1:A:1427:U:H3	1:A:1473:A:N6	1.84	0.75
20:T:67:LYS:HG3	20:T:68:ASN:H	1.52	0.75
8:H:9:MET:HG3	8:H:26:VAL:HG21	1.67	0.75
1:A:888:G:H3'	1:A:889:A:H5''	1.69	0.75
1:A:1343:G:H2'	1:A:1344:C:C6	2.22	0.75
1:A:1412:C:H2'	1:A:1413:A:C8	2.20	0.75
2:B:50:ARG:HB2	2:B:50:ARG:HH11	1.50	0.75
4:D:154:LEU:HB3	4:D:157:ILE:HD13	1.68	0.75
1:A:946:A:H2'	1:A:947:G:C8	2.22	0.75
2:B:149:LEU:HD21	2:B:153:PRO:HD3	1.69	0.75
1:A:1210:C:H4'	1:A:1211:U:OP2	1.87	0.74
1:A:1330:U:H2'	1:A:1331:G:H5'	1.66	0.74
4:D:25:CYS:HA	4:D:30:CYS:HB2	1.69	0.74
1:A:146:G:C3'	1:A:147:G:H5''	2.17	0.74
1:A:948:C:OP1	13:M:108:THR:HG22	1.87	0.74
1:A:993:G:H4'	1:A:994:A:OP2	1.85	0.74
1:A:1305:G:H5''	21:V:3:GLY:HA3	1.67	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:79:VAL:CG2	12:L:96:ILE:HG23	2.16	0.74
18:R:71:VAL:O	18:R:72:ARG:HB2	1.85	0.74
1:A:279:A:H5'	1:A:279:A:H8	1.50	0.74
1:A:738:C:H5''	6:F:69:GLU:HB3	1.68	0.74
12:L:51:VAL:HG11	12:L:63:THR:HG22	1.69	0.74
4:D:156:LEU:HD23	4:D:156:LEU:O	1.87	0.74
13:M:36:THR:CG2	13:M:38:ILE:HD11	2.17	0.74
16:P:67:THR:HG22	16:P:69:THR:H	1.51	0.74
13:M:8:ILE:HD12	13:M:8:ILE:N	2.01	0.74
13:M:15:ASP:HB3	13:M:40:PRO:HB3	1.68	0.74
1:A:1163:C:H2'	1:A:1164:G:H8	1.53	0.74
11:K:4:VAL:HG21	11:K:30:ILE:CD1	2.17	0.74
1:A:116:A:H5'	1:A:116:A:H8	1.51	0.74
2:B:63:LEU:HD12	2:B:149:LEU:HD22	1.69	0.74
18:R:71:VAL:O	18:R:72:ARG:HD3	1.88	0.74
11:K:38:ILE:HD12	11:K:53:LEU:HB3	1.69	0.74
1:A:255:G:H1'	17:Q:15:GLN:NE2	2.03	0.73
3:C:111:SER:HB3	3:C:114:LEU:HD12	1.70	0.73
5:E:15:MET:HE1	5:E:20:ARG:NH1	2.02	0.73
1:A:958:A:H5'	1:A:959:A:OP2	1.88	0.73
1:A:1189:C:P	10:J:49:ARG:HH22	2.10	0.73
3:C:78:ARG:HE	3:C:81:GLU:CB	2.00	0.73
16:P:81:ARG:HG2	16:P:83:GLU:HG2	1.68	0.73
3:C:37:ARG:HH11	3:C:37:ARG:HG3	1.53	0.73
11:K:81:ARG:HD3	18:R:73:LYS:HZ3	1.54	0.73
1:A:1141:C:O2'	1:A:1142:G:H5'	1.88	0.73
11:K:3:GLN:HA	11:K:65:TYR:O	1.87	0.73
12:L:67:PRO:O	12:L:98:ARG:HD2	1.88	0.73
19:S:43:MET:HA	19:S:46:HIS:HD2	1.52	0.73
18:R:23:GLU:H	18:R:23:GLU:CD	1.97	0.73
3:C:100:LEU:HD23	3:C:101:ASN:N	2.04	0.73
9:I:46:LEU:HB2	9:I:50:ARG:HH21	1.53	0.73
12:L:51:VAL:CG1	12:L:63:THR:HG22	2.18	0.73
1:A:189(I):G:O2'	1:A:189(J):G:H5'	1.88	0.73
1:A:49:U:C3'	1:A:50:A:H5''	2.19	0.73
2:B:194:ILE:HG22	2:B:195:ILE:N	2.04	0.73
12:L:71:HIS:CD2	12:L:73:LEU:H	2.05	0.73
1:A:1282:C:H5'	1:A:1282:C:H6	1.52	0.73
5:E:140:THR:O	5:E:144:VAL:HG23	1.89	0.73
5:E:146:ARG:CB	5:E:146:ARG:HH11	2.02	0.72
10:J:6:LEU:HD12	10:J:18:ALA:HB2	1.70	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1126:U:O2	1:A:1126:U:H2'	1.87	0.72
9:I:96:LYS:HB3	9:I:97:PRO:HD3	1.70	0.72
1:A:1477:C:H2'	1:A:1478:C:C6	2.25	0.72
3:C:25:LYS:H	3:C:25:LYS:CD	1.91	0.72
3:C:59:ALA:HB3	3:C:62:ASN:HD22	1.55	0.72
21:V:5:ARG:HE	21:V:14:ARG:HH22	1.37	0.72
1:A:1161:C:H2'	1:A:1162:C:C6	2.25	0.72
4:D:35:ARG:HA	4:D:37:TYR:CE1	2.25	0.72
10:J:47:VAL:O	10:J:58:ARG:HA	1.88	0.72
12:L:87:LYS:HA	12:L:87:LYS:HE3	1.70	0.72
15:O:61:GLN:HE22	15:O:64:ARG:NH2	1.88	0.72
18:R:21:ASN:O	18:R:25:LEU:HG	1.88	0.72
1:A:1230:C:H1'	13:M:125:LYS:HA	1.71	0.72
12:L:37:ARG:HG2	12:L:38:THR:N	2.03	0.72
4:D:208:ARG:HB3	4:D:208:ARG:HH11	1.55	0.72
7:G:17:TYR:CD2	7:G:58:LEU:HB2	2.25	0.72
19:S:15:LEU:O	19:S:18:VAL:HG12	1.90	0.72
19:S:18:VAL:O	19:S:22:ASN:HB2	1.89	0.72
13:M:3:ILE:HG23	13:M:56:ARG:HA	1.70	0.72
21:V:5:ARG:HE	21:V:14:ARG:NH1	1.88	0.72
1:A:620:C:N1	4:D:134:LEU:HD13	2.05	0.72
1:A:1125:U:O2	1:A:1125:U:H2'	1.88	0.72
19:S:50:VAL:O	19:S:57:VAL:HG22	1.89	0.72
3:C:78:ARG:HE	3:C:81:GLU:HG2	1.55	0.71
3:C:78:ARG:HD2	3:C:78:ARG:O	1.89	0.71
9:I:46:LEU:HB2	9:I:50:ARG:NH2	2.05	0.71
15:O:69:LEU:HD12	15:O:77:TYR:HB2	1.70	0.71
15:O:86:ILE:HG22	15:O:87:ARG:N	2.05	0.71
2:B:92:LEU:HG	2:B:95:MET:HE3	1.72	0.71
4:D:34:ARG:O	4:D:35:ARG:HB2	1.89	0.71
6:F:15:ASP:H	6:F:18:GLN:NE2	1.88	0.71
13:M:95:LEU:HB3	13:M:96:PRO:HD2	1.73	0.71
1:A:275:G:H5''	17:Q:13:LYS:HB3	1.70	0.71
3:C:33:LEU:HD13	14:N:24:VAL:HG21	1.71	0.71
4:D:17:LYS:HD2	4:D:19:TYR:HE1	1.54	0.71
4:D:28:PRO:O	4:D:29:LYS:HG3	1.91	0.71
15:O:16:ARG:HH11	15:O:16:ARG:HG3	1.55	0.71
2:B:181:LEU:HD23	2:B:195:ILE:O	1.91	0.71
1:A:235:C:H5'	17:Q:69:ARG:HG2	1.73	0.71
7:G:44:ASP:O	7:G:48:ILE:HG13	1.91	0.71
7:G:84:TYR:HD2	7:G:153:TYR:HE2	1.37	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:91:TRP:CH2	2:B:167:ALA:HA	2.26	0.71
2:B:172:ARG:HH22	8:H:74:PRO:HB3	1.55	0.71
12:L:122:LYS:N	12:L:122:LYS:HZ2	1.89	0.71
1:A:1208:C:H2'	1:A:1209:C:C6	2.26	0.71
12:L:79:VAL:HG21	12:L:96:ILE:CG2	2.19	0.71
21:V:5:ARG:NE	21:V:14:ARG:HH12	1.88	0.71
1:A:743:U:H2'	1:A:744:C:C6	2.26	0.70
1:A:1405:G:O2'	1:A:1406:U:H5'	1.89	0.70
2:B:94:GLY:O	2:B:102:ILE:HG13	1.91	0.70
3:C:107:ASN:ND2	3:C:110:LEU:HG	2.06	0.70
10:J:32:VAL:HA	10:J:72:ILE:HG22	1.72	0.70
11:K:44:ARG:NH1	11:K:44:ARG:HB3	2.06	0.70
5:E:68:GLN:O	5:E:69:ASN:HB3	1.91	0.70
10:J:76:ASN:HB2	10:J:79:THR:HG23	1.73	0.70
1:A:1427:U:H3	1:A:1473:A:H61	1.39	0.70
1:A:491:G:O2'	1:A:492:G:H5'	1.91	0.70
3:C:129:VAL:O	3:C:133:ILE:HG12	1.91	0.70
3:C:130:ARG:HG2	3:C:134:LYS:HE2	1.74	0.70
1:A:361:G:H2'	1:A:362:G:C5'	2.14	0.70
10:J:30:ALA:C	10:J:32:VAL:H	1.96	0.70
1:A:1263:C:H2'	1:A:1264:C:H6	1.57	0.70
11:K:96:LYS:HA	11:K:96:LYS:CE	2.18	0.70
20:T:50:ARG:HE	20:T:93:ILE:HG21	1.55	0.70
1:A:718:G:H5'	11:K:107:ASN:ND2	2.07	0.70
1:A:343:U:H2'	1:A:345:C:N4	2.07	0.69
7:G:53:THR:HG22	7:G:55:GLN:N	1.97	0.69
6:F:7:ASN:HB2	6:F:89:MET:HB3	1.73	0.69
1:A:279:A:H5'	1:A:279:A:C8	2.27	0.69
1:A:1064:G:H4'	1:A:1065:U:OP1	1.91	0.69
3:C:63:VAL:HG12	3:C:65:VAL:HG23	1.74	0.69
8:H:60:ARG:HH11	8:H:60:ARG:HG3	1.57	0.69
1:A:1369:C:H2'	1:A:1370:G:C8	2.27	0.69
2:B:92:LEU:N	2:B:92:LEU:HD23	2.07	0.69
13:M:7:GLU:OE2	13:M:21:ILE:HA	1.92	0.69
1:A:1314:C:H5''	19:S:5:LYS:NZ	2.07	0.69
2:B:50:ARG:HB2	2:B:50:ARG:NH1	2.07	0.69
10:J:59:GLU:OE1	14:N:44:ARG:NH1	2.21	0.69
4:D:61:GLN:HA	4:D:61:GLN:HE21	1.56	0.69
1:A:601:C:O2'	1:A:602:A:H5'	1.92	0.69
2:B:71:ALA:CB	2:B:205:ILE:HD13	2.22	0.69
2:B:78:GLU:OE1	2:B:210:SER:HA	1.92	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:13:ILE:O	3:C:15:ARG:N	2.25	0.69
4:D:69:ILE:HD11	4:D:99:ARG:NE	2.08	0.69
5:E:72:ILE:HG23	5:E:138:LEU:HD13	1.73	0.69
8:H:64:LYS:HG2	8:H:79:VAL:HG21	1.73	0.69
9:I:46:LEU:C	9:I:48:PRO:HD2	2.17	0.69
14:N:22:ARG:NH1	14:N:29:ALA:HB2	2.07	0.69
17:Q:39:LYS:HD2	17:Q:41:TYR:CZ	2.28	0.69
2:B:95:MET:HA	2:B:102:ILE:HG21	1.75	0.69
12:L:29:ARG:HD3	12:L:58:SER:HB3	1.75	0.69
13:M:80:LEU:HD23	13:M:80:LEU:H	1.57	0.69
3:C:99:ALA:O	3:C:100:LEU:HB2	1.92	0.69
14:N:56:ARG:CG	14:N:57:LYS:H	2.05	0.69
20:T:41:LYS:NZ	20:T:41:LYS:HB2	2.08	0.69
1:A:702:A:H4'	1:A:703:G:OP2	1.92	0.68
1:A:858:G:H8	1:A:858:G:H5''	1.59	0.68
1:A:386:C:H2'	1:A:387:U:H5'	1.75	0.68
3:C:7:ILE:HG23	3:C:15:ARG:HG2	1.75	0.68
6:F:26:ILE:O	6:F:30:LEU:HG	1.93	0.68
17:Q:103:LYS:NZ	17:Q:103:LYS:HB3	2.08	0.68
1:A:954:G:H2'	1:A:955:U:C6	2.28	0.68
1:A:1045:C:H2'	1:A:1046:A:C5'	2.23	0.68
1:A:1228:C:H4'	13:M:115:THR:HA	1.75	0.68
6:F:2:ARG:NE	6:F:69:GLU:HG2	2.07	0.68
3:C:12:GLY:HA3	14:N:56:ARG:CZ	2.24	0.68
9:I:4:TYR:O	9:I:83:ALA:HA	1.92	0.68
10:J:78:LYS:HD2	10:J:81:GLU:OE1	1.93	0.68
1:A:718:G:C5'	11:K:107:ASN:HD22	2.06	0.68
1:A:1251:A:H4'	9:I:11:GLU:OE2	1.93	0.68
13:M:2:ARG:HA	13:M:7:GLU:O	1.94	0.68
13:M:22:TYR:O	13:M:24:ILE:N	2.26	0.68
1:A:1060:C:O2'	1:A:1061:G:H5'	1.93	0.68
12:L:85:ARG:HE	12:L:93:ARG:HB3	1.59	0.68
20:T:22:LYS:O	20:T:26:ILE:HG13	1.94	0.68
5:E:78:VAL:HG11	5:E:130:ALA:O	1.94	0.68
11:K:4:VAL:HG21	11:K:30:ILE:HD11	1.75	0.68
12:L:24:LYS:O	12:L:26:ALA:N	2.27	0.68
12:L:122:LYS:HZ2	12:L:122:LYS:H	1.39	0.68
19:S:64:ASN:HD22	19:S:65:MET:H	1.40	0.68
1:A:1366:C:H2'	1:A:1367:C:H6	1.58	0.68
2:B:136:LEU:O	2:B:136:LEU:HD13	1.93	0.68
1:A:386:C:O2'	1:A:387:U:H5'	1.94	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1241:G:H2'	1:A:1242:C:C6	2.28	0.68
9:I:117:LYS:O	9:I:118:ALA:HB3	1.94	0.68
14:N:44:ARG:HH11	14:N:44:ARG:HG3	1.58	0.68
17:Q:39:LYS:HD2	17:Q:41:TYR:CE1	2.29	0.68
1:A:457:C:H2'	1:A:458:C:H6	1.59	0.67
8:H:118:VAL:C	8:H:119:LEU:HD23	2.18	0.67
16:P:59:TRP:HA	16:P:62:VAL:HG23	1.76	0.67
2:B:175:PHE:CD2	8:H:70:GLN:HB3	2.29	0.67
4:D:35:ARG:H	4:D:36:PRO:HD3	1.59	0.67
5:E:123:ASN:ND2	5:E:124:PRO:HD2	2.09	0.67
1:A:835:U:OP1	18:R:49:ARG:NH2	2.27	0.67
3:C:155:ARG:HH21	3:C:160:GLU:HA	1.59	0.67
1:A:1363(A):A:H1'	1:A:1365:G:N7	2.09	0.67
2:B:112:LEU:HB3	2:B:136:LEU:HD23	1.77	0.67
5:E:48:PRO:O	5:E:52:GLN:HG2	1.94	0.67
4:D:29:LYS:C	4:D:31:ALA:H	2.01	0.67
4:D:88:THR:HG22	4:D:88:THR:O	1.94	0.67
12:L:51:VAL:CG1	12:L:52:ALA:H	2.08	0.67
19:S:48:ILE:N	19:S:48:ILE:HD12	2.09	0.67
1:A:1027:C:H6	1:A:1027:C:H5'	1.60	0.67
3:C:126:ARG:HG2	3:C:126:ARG:HH11	1.59	0.67
4:D:24:ARG:C	4:D:26:TYR:H	2.01	0.67
12:L:122:LYS:N	12:L:122:LYS:NZ	2.41	0.67
1:A:203:U:H5''	1:A:204:U:OP1	1.94	0.67
1:A:262:A:H5'	20:T:67:LYS:HG2	1.77	0.67
1:A:302:G:H5''	12:L:13:LYS:HZ1	1.58	0.67
2:B:134:HIS:HA	2:B:137:GLU:HG2	1.76	0.67
4:D:35:ARG:H	4:D:36:PRO:CD	2.07	0.67
1:A:152:A:H5'	1:A:153:C:OP2	1.95	0.67
3:C:81:GLU:O	3:C:85:VAL:HG23	1.95	0.67
4:D:60:LYS:HD2	4:D:206:TYR:OH	1.95	0.67
2:B:217:ILE:C	2:B:219:ALA:H	2.02	0.66
6:F:100:ASN:HD22	18:R:8:LYS:CG	2.07	0.66
19:S:61:ILE:C	19:S:61:ILE:HD13	2.20	0.66
21:V:5:ARG:HE	21:V:14:ARG:NH2	1.93	0.66
13:M:33:LEU:HD13	13:M:40:PRO:HA	1.77	0.66
1:A:21:G:H2'	1:A:22:G:C8	2.30	0.66
3:C:178:ARG:HH11	3:C:206:VAL:HG22	1.59	0.66
14:N:49:LYS:HB2	14:N:51:GLN:HG3	1.78	0.66
1:A:664:G:H22	1:A:741:G:H1	1.42	0.66
1:A:1189:C:OP1	10:J:49:ARG:NH2	2.26	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:215:LEU:O	2:B:215:LEU:HD13	1.95	0.66
8:H:127:LEU:HD23	8:H:127:LEU:H	1.60	0.66
4:D:146:ALA:HA	4:D:181:LYS:HA	1.77	0.66
13:M:34:GLU:C	13:M:36:THR:H	2.02	0.66
19:S:79:TYR:CE2	19:S:80:ARG:HB2	2.30	0.66
1:A:639:G:O2'	1:A:640:A:H5'	1.96	0.66
12:L:23:LEU:C	12:L:25:GLY:H	2.03	0.66
14:N:23:CYS:HB2	14:N:39:CYS:HB3	1.76	0.66
1:A:489:C:H2'	1:A:490:G:C8	2.29	0.66
1:A:522:C:H41	12:L:49:ARG:NH2	1.88	0.66
3:C:133:ILE:HG22	3:C:167:ALA:HB3	1.78	0.66
9:I:9:ARG:HD3	9:I:104:ASP:HB3	1.76	0.66
12:L:32:VAL:HG22	12:L:78:VAL:HG22	1.76	0.66
19:S:44:VAL:HA	19:S:61:ILE:HD12	1.78	0.66
1:A:1169:A:H2'	1:A:1170:A:C8	2.31	0.66
2:B:172:ARG:HH11	2:B:172:ARG:HG3	1.61	0.66
6:F:101:ALA:HB1	18:R:13:GLU:HG3	1.78	0.66
11:K:40:TYR:HB3	11:K:44:ARG:HB2	1.75	0.66
16:P:59:TRP:HB3	16:P:64:ALA:HB2	1.76	0.66
1:A:975:A:H5''	1:A:976:G:O5'	1.96	0.65
10:J:6:LEU:CD2	10:J:94:ILE:HG12	2.26	0.65
15:O:63:ARG:HG3	15:O:63:ARG:HH11	1.61	0.65
2:B:63:LEU:HD23	2:B:64:PHE:N	2.12	0.65
2:B:17:ARG:NH1	2:B:18:TRP:HA	2.11	0.65
8:H:4:ASP:CG	8:H:85:ARG:HH11	2.04	0.65
2:B:175:PHE:HD2	8:H:70:GLN:HB3	1.61	0.65
12:L:20:VAL:HG12	12:L:20:VAL:O	1.97	0.65
1:A:820:U:H4'	1:A:821:G:OP2	1.97	0.65
1:A:954:G:H2'	1:A:955:U:H6	1.62	0.65
1:A:957:U:C3'	1:A:958:A:H5''	2.27	0.65
1:A:1130:A:N3	1:A:1130:A:H2'	2.12	0.65
1:A:1491:G:C6	26:A:2800:RPO:H2	2.31	0.65
4:D:69:ILE:HD11	4:D:99:ARG:CZ	2.26	0.65
9:I:91:TYR:C	9:I:93:ALA:H	2.04	0.65
1:A:1399:C:H4'	1:A:1400:C:C5'	2.23	0.65
8:H:65:TYR:HA	8:H:79:VAL:HG23	1.79	0.65
21:V:12:ILE:HD13	21:V:21:ARG:NE	2.12	0.65
4:D:148:ALA:HB3	4:D:151:SER:HB2	1.79	0.65
1:A:1244:C:HO2'	1:A:1245:A:H8	1.43	0.65
3:C:173:PRO:HB2	3:C:176:THR:CG2	2.26	0.65
1:A:159:G:H21	1:A:161:A:H3'	1.62	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:104:THR:HG22	13:M:105:ASN:H	1.61	0.65
1:A:1218:C:H2'	1:A:1219:U:C6	2.32	0.65
2:B:10:HIS:HB3	2:B:204:SER:HB2	1.79	0.65
5:E:85:ILE:HG13	5:E:131:THR:HG22	1.78	0.65
3:C:189:ARG:HB3	3:C:189:ARG:HH11	1.61	0.64
6:F:46:ARG:O	6:F:57:GLN:HB2	1.97	0.64
12:L:71:HIS:HA	12:L:98:ARG:NH2	2.10	0.64
14:N:22:ARG:O	14:N:23:CYS:C	2.39	0.64
1:A:180:U:C2'	1:A:181:G:H5'	2.26	0.64
1:A:390:C:H2'	1:A:391:G:C8	2.32	0.64
1:A:1323:G:H2'	1:A:1324:A:C8	2.33	0.64
8:H:63:LEU:HD22	8:H:63:LEU:H	1.61	0.64
2:B:10:HIS:CG	2:B:11:PHE:H	2.14	0.64
3:C:78:ARG:HE	3:C:81:GLU:CG	2.09	0.64
6:F:101:ALA:CB	18:R:13:GLU:HG3	2.27	0.64
8:H:86:ILE:CG2	8:H:133:LEU:HD23	2.20	0.64
1:A:797:C:O2'	1:A:798:G:H5'	1.96	0.64
1:A:957:U:H2'	1:A:958:A:H5''	1.79	0.64
10:J:20:LYS:NZ	10:J:88:LEU:H	1.95	0.64
10:J:60:HIS:HB3	14:N:58:ALA:HB3	1.78	0.64
12:L:37:ARG:NH1	12:L:37:ARG:HB3	2.12	0.64
8:H:9:MET:SD	8:H:32:LYS:HG2	2.37	0.64
10:J:4:ILE:HG23	10:J:96:ILE:HG23	1.79	0.64
1:A:1306:A:O2'	13:M:108:THR:HG21	1.98	0.64
3:C:36:GLN:NE2	14:N:46:LEU:HD13	2.12	0.64
1:A:159:G:H8	1:A:159:G:H5''	1.63	0.64
1:A:824:C:H2'	1:A:825:G:H8	1.63	0.64
1:A:865:A:H5'	1:A:1078:U:O4	1.97	0.64
3:C:190:THR:HG21	3:C:192:TYR:CZ	2.33	0.64
5:E:5:LYS:HB2	5:E:108:LEU:HD11	1.79	0.64
12:L:83:GLY:HA2	12:L:94:TYR:CA	2.22	0.64
18:R:72:ARG:O	18:R:73:LYS:HB3	1.97	0.64
1:A:1007:C:H2'	1:A:1008:C:C6	2.32	0.64
1:A:1352:C:H2'	1:A:1353:G:C8	2.33	0.64
4:D:2:ARG:HD2	4:D:117:ARG:CZ	2.27	0.64
1:A:52:G:O2'	1:A:53:A:H5'	1.98	0.64
2:B:50:ARG:HH11	2:B:50:ARG:CB	2.10	0.64
4:D:154:LEU:HD23	4:D:155:GLU:H	1.62	0.64
5:E:145:GLU:O	5:E:149:LYS:HG3	1.98	0.64
12:L:21:PRO:C	12:L:23:LEU:H	2.05	0.64
14:N:5:LEU:C	14:N:7:GLU:H	2.05	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:51:LYS:O	17:Q:54:ASP:HB2	1.98	0.64
1:A:166:G:O2'	1:A:167:G:H5'	1.98	0.64
1:A:556:C:O2'	1:A:557:G:H5'	1.98	0.64
1:A:718:G:C5'	11:K:107:ASN:ND2	2.60	0.64
1:A:743:U:H2'	1:A:744:C:H6	1.61	0.64
2:B:19:ASN:C	2:B:19:ASN:HD22	2.06	0.64
10:J:29:GLY:HA2	10:J:76:ASN:HD21	1.60	0.64
16:P:43:LYS:HB3	16:P:48:TRP:CD1	2.32	0.64
3:C:82:ARG:C	3:C:84:ARG:H	2.06	0.63
13:M:76:ASN:O	13:M:80:LEU:HD23	1.99	0.63
4:D:6:PRO:HB2	4:D:9:ARG:HD2	1.79	0.63
10:J:44:ARG:HH11	10:J:44:ARG:HG2	1.64	0.63
13:M:64:LYS:NZ	13:M:68:GLU:HG2	2.13	0.63
2:B:94:GLY:C	2:B:102:ILE:HG13	2.24	0.63
3:C:179:ALA:O	3:C:180:ASN:C	2.41	0.63
7:G:45:ALA:O	7:G:49:ILE:HG13	1.98	0.63
10:J:49:ARG:HG2	10:J:58:ARG:O	1.99	0.63
14:N:7:GLU:C	14:N:7:GLU:OE1	2.41	0.63
1:A:1346:A:N1	1:A:1374:A:H5''	2.13	0.63
2:B:181:LEU:HA	2:B:195:ILE:HB	1.79	0.63
3:C:100:LEU:HD23	3:C:100:LEU:C	2.23	0.63
3:C:133:ILE:CG2	3:C:167:ALA:HB3	2.28	0.63
4:D:11:CYS:HA	4:D:18:LEU:HD12	1.80	0.63
5:E:8:LEU:CD1	5:E:27:LEU:HB2	2.28	0.63
7:G:148:ARG:HD2	11:K:49:TYR:CE1	2.33	0.63
13:M:35:LYS:NZ	13:M:35:LYS:HB3	2.13	0.63
20:T:41:LYS:HB2	20:T:41:LYS:HZ3	1.62	0.63
1:A:190:U:O2	20:T:98:SER:HB2	1.97	0.63
1:A:1423:G:H2'	1:A:1424:C:C6	2.33	0.63
6:F:94:GLN:HE21	18:R:17:ARG:HE	1.47	0.63
11:K:115:PHE:O	11:K:116:ARG:HB3	1.98	0.63
17:Q:100:ARG:HA	17:Q:100:ARG:HE	1.64	0.63
17:Q:100:ARG:HA	17:Q:100:ARG:NE	2.14	0.63
3:C:57:GLU:HB2	3:C:64:ALA:HB2	1.80	0.63
1:A:720:C:H3'	1:A:721:G:H5''	1.80	0.63
1:A:731:G:OP1	1:A:766:A:H1'	1.98	0.63
1:A:953:G:H5'	1:A:965:A:H61	1.64	0.63
10:J:23:GLU:C	10:J:25:ALA:H	2.06	0.63
19:S:32:THR:HG22	19:S:33:TRP:H	1.64	0.63
20:T:60:ALA:O	20:T:66:HIS:ND1	2.32	0.63
11:K:81:ARG:NH1	18:R:73:LYS:HE2	2.14	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:19:LEU:HD12	19:S:20:GLU:N	2.13	0.63
1:A:1250:A:H4'	9:I:67:GLY:O	1.98	0.63
2:B:13:HIS:O	2:B:14:GLU:O	2.16	0.63
7:G:93:ARG:HH11	7:G:93:ARG:HG3	1.64	0.63
7:G:135:LYS:HE3	7:G:139:ASP:OD1	1.99	0.63
11:K:100:ASP:HB2	18:R:73:LYS:HD2	1.79	0.63
17:Q:44:HIS:CD2	17:Q:46:PRO:HG3	2.34	0.63
18:R:29:LEU:HD11	18:R:64:LEU:HD13	1.81	0.63
1:A:437:U:C2'	1:A:438:G:H5'	2.29	0.62
6:F:22:GLU:O	6:F:26:ILE:HG12	1.98	0.62
7:G:75:ARG:HD2	7:G:88:MET:SD	2.39	0.62
12:L:24:LYS:C	12:L:26:ALA:N	2.54	0.62
21:V:11:LYS:HB3	21:V:21:ARG:HD2	1.81	0.62
1:A:384:G:H2'	1:A:385:C:C6	2.33	0.62
1:A:627:G:O2'	1:A:628:G:H5'	2.00	0.62
16:P:67:THR:HG22	16:P:69:THR:N	2.14	0.62
19:S:62:THR:HG22	19:S:63:GLU:N	2.13	0.62
1:A:56:U:H2'	1:A:57:G:C8	2.35	0.62
1:A:477:A:O2'	1:A:479:C:H5'	2.00	0.62
1:A:1019:C:C2'	1:A:1020:U:H5'	2.29	0.62
1:A:1132:C:H2'	1:A:1133:G:H8	1.63	0.62
3:C:21:TRP:HB3	3:C:58:ARG:HB2	1.81	0.62
3:C:32:LEU:HD21	14:N:52:LEU:HD23	1.81	0.62
9:I:96:LYS:O	9:I:99:GLY:N	2.28	0.62
9:I:111:LYS:HG3	9:I:117:LYS:HA	1.82	0.62
1:A:522:C:N4	12:L:49:ARG:HH22	1.89	0.62
2:B:133:LYS:O	2:B:137:GLU:HG2	1.99	0.62
18:R:10:THR:O	18:R:11:LEU:HB2	1.98	0.62
1:A:443:C:H2'	1:A:444:C:H6	1.64	0.62
1:A:877:C:H5''	8:H:88:LYS:HD3	1.80	0.62
2:B:205:ILE:O	2:B:209:LEU:HB2	1.99	0.62
4:D:161:LEU:HD13	4:D:180:MET:CG	2.30	0.62
1:A:750:G:N3	15:O:22:GLY:HA3	2.15	0.62
1:A:1020:U:C3'	1:A:1021:G:H5''	2.29	0.62
1:A:1208:C:H2'	1:A:1209:C:H6	1.63	0.62
1:A:1353:G:H2'	1:A:1354:C:C6	2.35	0.62
2:B:112:LEU:HD11	2:B:135:GLU:OE1	1.99	0.62
13:M:77:ILE:HA	13:M:80:LEU:HD21	1.80	0.62
1:A:1054:C:H4'	1:A:1055:A:H5'	1.82	0.62
1:A:1140:C:H2'	1:A:1141:C:H5''	1.82	0.62
1:A:1166:G:C3'	1:A:1168:A:H5''	2.28	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:15:MET:HE1	5:E:20:ARG:HH12	1.63	0.62
11:K:105:PRO:C	11:K:107:ASN:H	2.04	0.62
1:A:302:G:H5''	12:L:13:LYS:NZ	2.15	0.62
1:A:542:G:O2'	1:A:543:C:H5'	1.99	0.62
10:J:47:VAL:HG22	14:N:40:ARG:HB2	1.81	0.62
1:A:17:U:H2'	1:A:18:C:C6	2.34	0.62
7:G:64:ALA:O	7:G:68:VAL:HG23	2.00	0.62
13:M:7:GLU:HG3	13:M:21:ILE:HG23	1.82	0.62
14:N:2:ARG:O	14:N:4:ALA:N	2.32	0.62
20:T:89:GLY:O	20:T:90:ALA:HB3	2.00	0.62
1:A:839:U:H3'	1:A:840:C:C5'	2.25	0.62
1:A:1427:U:H2'	1:A:1428:A:C8	2.35	0.62
2:B:6:GLU:HG3	2:B:207:LEU:HD11	1.82	0.62
3:C:37:ARG:HG3	3:C:37:ARG:NH1	2.11	0.62
20:T:3:LEU:O	20:T:5:ALA:N	2.32	0.62
1:A:166:G:H2'	1:A:167:G:H8	1.65	0.61
1:A:673:G:H2'	1:A:674:G:C8	2.35	0.61
7:G:138:GLU:O	7:G:142:ARG:HG3	2.00	0.61
10:J:73:ILE:O	10:J:74:ASN:HB2	2.00	0.61
20:T:50:ARG:NH1	20:T:50:ARG:HG2	2.14	0.61
1:A:1026:G:H2'	1:A:1027:C:H5''	1.81	0.61
2:B:11:PHE:CD1	2:B:35:ILE:HG23	2.35	0.61
4:D:149:GLU:HA	4:D:152:ARG:NH2	2.14	0.61
10:J:1:LYS:N	10:J:75:PRO:HD3	2.14	0.61
15:O:5:GLU:H	15:O:5:GLU:CD	2.06	0.61
1:A:384:G:H2'	1:A:385:C:H6	1.66	0.61
1:A:412:A:H61	4:D:34:ARG:HB3	1.65	0.61
15:O:34:ARG:NH2	15:O:58:MET:HE2	2.15	0.61
17:Q:79:GLY:O	17:Q:81:MET:HG2	1.99	0.61
18:R:28:PHE:HA	18:R:36:LEU:HD12	1.82	0.61
18:R:39:ARG:NH2	18:R:40:ARG:HG3	2.15	0.61
19:S:32:THR:HG22	19:S:33:TRP:N	2.14	0.61
21:V:5:ARG:NE	21:V:14:ARG:HH22	1.97	0.61
1:A:1001(A):G:H2'	1:A:1002:G:O4'	2.00	0.61
2:B:233:VAL:O	2:B:233:VAL:HG12	2.00	0.61
10:J:25:ALA:C	10:J:27:ARG:H	2.09	0.61
19:S:27:LYS:CG	19:S:28:ARG:H	2.12	0.61
19:S:61:ILE:HD13	19:S:62:THR:N	2.14	0.61
1:A:307:C:H5'	1:A:308:C:OP2	2.01	0.61
6:F:43:LEU:HD22	6:F:43:LEU:N	2.15	0.61
16:P:18:ARG:O	16:P:20:VAL:HG13	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1302:U:C5	13:M:16:VAL:HG21	2.35	0.61
13:M:22:TYR:HB2	13:M:66:GLU:OE2	2.00	0.61
19:S:4:LEU:O	19:S:5:LYS:CB	2.48	0.61
1:A:1342:C:O2'	1:A:1343:G:H5'	2.00	0.61
2:B:27:TYR:HB3	2:B:35:ILE:O	2.00	0.61
3:C:14:THR:O	3:C:15:ARG:HB2	2.00	0.61
4:D:10:LEU:O	4:D:14:GLU:HG2	2.01	0.61
12:L:23:LEU:C	12:L:25:GLY:N	2.59	0.61
17:Q:26:PHE:CZ	17:Q:35:ILE:HD11	2.36	0.61
17:Q:39:LYS:HG2	17:Q:40:LYS:N	2.15	0.61
1:A:1263:C:H2'	1:A:1264:C:C6	2.35	0.61
1:A:1347:G:N2	1:A:1373:G:H2'	2.15	0.61
1:A:251:G:C2'	1:A:252:U:H5''	2.28	0.61
3:C:174:LEU:HD21	3:C:200:TYR:CE2	2.36	0.61
10:J:80:ILE:O	10:J:84:MET:HB2	2.01	0.61
1:A:957:U:C2'	1:A:958:A:H5''	2.30	0.61
9:I:92:ARG:HG3	9:I:92:ARG:HH11	1.66	0.61
9:I:124:TYR:HD2	9:I:127:ARG:HG2	1.64	0.61
1:A:345:C:H4'	1:A:346:G:O5'	2.01	0.60
3:C:27:GLN:HA	3:C:30:HIS:CD2	2.22	0.60
20:T:43:GLU:O	20:T:93:ILE:HG13	2.01	0.60
2:B:91:TRP:HH2	2:B:170:GLU:CD	2.09	0.60
2:B:109:LEU:HD22	2:B:147:ARG:NH2	2.16	0.60
8:H:119:LEU:HD12	8:H:124:ALA:HA	1.83	0.60
10:J:15:ASP:O	10:J:19:GLN:HB2	2.01	0.60
15:O:23:SER:OG	15:O:26:VAL:HG23	2.01	0.60
20:T:67:LYS:HB2	20:T:67:LYS:NZ	2.16	0.60
21:V:4:ASP:O	21:V:10:GLY:HA3	2.00	0.60
2:B:79:ALA:HB3	2:B:86:TYR:HD2	1.65	0.60
1:A:131:C:H2'	1:A:132:C:C6	2.37	0.60
1:A:390:C:O3'	16:P:28:ARG:NH2	2.34	0.60
1:A:1030(C):G:H2'	1:A:1030(D):A:C8	2.36	0.60
1:A:1135:U:H4'	1:A:1136:U:OP1	2.01	0.60
3:C:118:ARG:NH1	3:C:139:ARG:HH12	1.99	0.60
9:I:41:ARG:HG2	9:I:41:ARG:HH11	1.65	0.60
9:I:126:LYS:HB3	13:M:125:LYS:NZ	2.16	0.60
10:J:3:ARG:HA	10:J:71:ASP:OD1	2.02	0.60
4:D:17:LYS:HD2	4:D:19:TYR:CE1	2.36	0.60
6:F:47:ARG:HE	6:F:47:ARG:H	1.49	0.60
13:M:61:ASN:O	13:M:62:THR:CB	2.49	0.60
13:M:64:LYS:HZ1	13:M:68:GLU:HG2	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:21:ASN:HD21	18:R:23:GLU:HG2	1.67	0.60
1:A:530:G:O6	22:W:3:C:H1'	2.02	0.60
1:A:1330:U:C2'	1:A:1331:G:H5'	2.30	0.60
13:M:49:GLU:OE1	13:M:49:GLU:HA	2.02	0.60
18:R:21:ASN:ND2	18:R:23:GLU:HG2	2.16	0.60
19:S:41:PRO:O	19:S:44:VAL:HG23	2.02	0.60
1:A:67:C:O2'	1:A:171:A:H1'	2.01	0.60
1:A:344:A:H5''	1:A:345:C:H5	1.67	0.60
5:E:146:ARG:HH11	5:E:146:ARG:HB3	1.66	0.60
10:J:55:LYS:O	10:J:58:ARG:NH1	2.35	0.60
12:L:2:THR:OG1	12:L:5:GLN:HG3	2.02	0.60
14:N:1:ALA:HB1	14:N:6:ILE:HD11	1.82	0.60
14:N:28:ARG:HG2	14:N:28:ARG:HH11	1.67	0.60
20:T:46:LEU:HD12	20:T:93:ILE:HB	1.84	0.60
1:A:858:G:C5'	1:A:858:G:C8	2.82	0.60
1:A:1045:C:C2'	1:A:1046:A:H5''	2.29	0.60
1:A:1048:G:H5'	1:A:1048:G:H8	1.65	0.60
1:A:1305:G:P	21:V:1:GLY:N	2.75	0.60
2:B:109:LEU:HD21	2:B:140:GLN:HE22	1.65	0.60
7:G:144:ALA:C	7:G:146:ALA:H	2.08	0.60
9:I:2:GLN:HB3	9:I:19:ARG:HG2	1.83	0.60
9:I:27:VAL:HA	9:I:62:ILE:O	2.00	0.60
9:I:45:ALA:HB1	9:I:76:ILE:CG2	2.31	0.60
13:M:16:VAL:O	13:M:19:THR:HB	2.02	0.60
19:S:15:LEU:O	19:S:19:LEU:HG	2.01	0.60
1:A:501:C:O2'	1:A:502:G:H5'	2.02	0.60
1:A:818:G:C3'	1:A:819:A:H5''	2.31	0.60
2:B:133:LYS:HG2	2:B:137:GLU:OE2	2.02	0.60
3:C:87:ARG:HA	3:C:90:LEU:HG	1.84	0.60
7:G:14:ASP:OD1	7:G:43:TYR:OH	2.19	0.60
8:H:10:LEU:HD22	8:H:83:ILE:HD11	1.84	0.60
10:J:61:PHE:CE1	14:N:57:LYS:HG2	2.36	0.60
11:K:77:THR:O	11:K:77:THR:HG22	2.02	0.60
20:T:86:GLU:HA	20:T:86:GLU:OE1	2.00	0.60
1:A:8:A:H5''	5:E:97:ILE:CG2	2.32	0.60
1:A:35:G:H2'	1:A:36:C:C6	2.37	0.60
1:A:1136:U:H5''	1:A:1137:C:OP2	2.01	0.60
1:A:1163:C:H2'	1:A:1164:G:C8	2.35	0.60
1:A:1330:U:OP1	13:M:22:TYR:O	2.20	0.60
2:B:135:GLU:O	2:B:139:LEU:HG	2.01	0.60
9:I:5:GLY:HA3	9:I:82:ARG:HG3	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:37:PRO:O	10:J:38:LEU:HB2	2.01	0.60
10:J:80:ILE:HD12	10:J:80:ILE:H	1.66	0.60
1:A:445:G:H2'	1:A:446:G:H8	1.66	0.59
1:A:718:G:C4'	11:K:107:ASN:HD22	2.15	0.59
3:C:2:ASN:O	3:C:3:LYS:HG2	2.02	0.59
7:G:14:ASP:HB3	7:G:18:GLY:N	2.17	0.59
10:J:59:GLU:OE2	14:N:57:LYS:HE3	2.01	0.59
11:K:44:ARG:HB3	11:K:44:ARG:HH11	1.66	0.59
20:T:93:ILE:C	20:T:95:GLY:H	2.10	0.59
1:A:101:A:O2'	1:A:102:G:H5'	2.01	0.59
4:D:86:GLY:O	4:D:88:THR:N	2.35	0.59
7:G:107:ALA:HA	7:G:110:ARG:HD2	1.84	0.59
11:K:96:LYS:HE2	11:K:96:LYS:CA	2.21	0.59
15:O:15:ALA:HB1	15:O:20:ASP:HB3	1.82	0.59
17:Q:80:ARG:HG3	17:Q:80:ARG:O	2.01	0.59
1:A:460:G:H3'	1:A:461:A:H5''	1.80	0.59
1:A:501:C:H2'	1:A:502:G:H8	1.67	0.59
6:F:33:TYR:HE2	6:F:78:GLU:HG2	1.67	0.59
3:C:146:LYS:HE2	3:C:204:GLY:H	1.67	0.59
6:F:30:LEU:HB3	6:F:35:ALA:HB3	1.83	0.59
8:H:56:LYS:H	8:H:56:LYS:CD	2.16	0.59
10:J:48:ILE:HD12	10:J:48:ILE:N	2.18	0.59
15:O:2:ILE:N	15:O:2:ILE:HD12	2.16	0.59
1:A:192:U:H5'	20:T:95:GLY:HA2	1.84	0.59
3:C:206:VAL:HG12	3:C:207:ILE:N	2.17	0.59
13:M:25:GLY:O	13:M:27:ALA:N	2.35	0.59
16:P:52:ASP:OD2	16:P:55:ARG:HG3	2.03	0.59
18:R:32:THR:HA	18:R:68:GLU:HB2	1.84	0.59
20:T:58:LYS:O	20:T:61:LYS:HB2	2.03	0.59
1:A:997:U:C3'	1:A:998:G:H5''	2.33	0.59
3:C:187:LEU:O	3:C:188:ALA:HB2	2.02	0.59
7:G:14:ASP:HB3	7:G:18:GLY:H	1.67	0.59
1:A:976:G:H5''	1:A:1358:U:O2'	2.03	0.59
1:A:1156:G:H2'	1:A:1157:A:H5''	1.85	0.59
8:H:24:THR:CG2	8:H:63:LEU:HD21	2.33	0.59
8:H:103:VAL:HG21	8:H:109:ILE:O	2.03	0.59
10:J:28:SER:HB3	10:J:82:GLN:HE21	1.68	0.59
12:L:28:PHE:HB3	12:L:81:ILE:O	2.02	0.59
14:N:22:ARG:HG2	14:N:22:ARG:HH11	1.66	0.59
1:A:677:U:H3	1:A:713:G:H22	1.49	0.59
1:A:994:A:H2'	1:A:994:A:N3	2.17	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1148:U:H2'	1:A:1149:C:O4'	2.03	0.59
1:A:1176:A:H2'	1:A:1177:G:C8	2.38	0.59
2:B:172:ARG:HG3	2:B:172:ARG:NH1	2.18	0.59
3:C:22:TYR:C	3:C:22:TYR:CD1	2.80	0.59
5:E:76:ILE:HG22	5:E:87:LEU:HB2	1.85	0.59
12:L:37:ARG:NH2	12:L:53:LYS:NZ	2.49	0.59
15:O:86:ILE:HG22	15:O:87:ARG:H	1.67	0.59
1:A:1144:G:N2	1:A:1146:A:H62	1.97	0.59
2:B:16:LYS:HD2	2:B:29:GLU:OE2	2.02	0.59
2:B:91:TRP:HZ3	2:B:166:ILE:HG22	1.68	0.59
5:E:84:LYS:HB3	5:E:119:LEU:HB2	1.83	0.59
10:J:74:ASN:O	10:J:76:ASN:N	2.31	0.59
17:Q:47:GLU:O	17:Q:48:GLU:C	2.46	0.59
20:T:49:MET:HE1	20:T:97:LEU:HD21	1.84	0.59
1:A:636:U:O2'	1:A:637:G:H5'	2.03	0.59
1:A:1480:G:H4'	1:A:1481:U:OP2	2.02	0.59
2:B:49:PHE:O	2:B:52:ILE:HB	2.03	0.59
2:B:79:ALA:HB3	2:B:86:TYR:CD2	2.37	0.59
2:B:136:LEU:HD13	2:B:140:GLN:OE1	2.02	0.59
4:D:50:PRO:HB2	4:D:55:VAL:HG23	1.83	0.59
5:E:8:LEU:HD13	5:E:27:LEU:HB2	1.84	0.59
5:E:70:GLY:CA	5:E:112:THR:HG22	2.30	0.59
5:E:147:LEU:CD2	8:H:79:VAL:HG22	2.33	0.59
9:I:47:GLU:N	9:I:48:PRO:HD2	2.17	0.59
18:R:21:ASN:C	18:R:21:ASN:ND2	2.59	0.59
1:A:116:A:H2'	1:A:117:G:O4'	2.02	0.58
1:A:648:A:H5'	1:A:648:A:H8	1.68	0.58
2:B:22:PHE:CZ	2:B:183:ASP:HA	2.38	0.58
7:G:91:SER:HB2	7:G:92:PRO:HD2	1.85	0.58
10:J:25:ALA:CB	10:J:83:LEU:HD11	2.24	0.58
2:B:194:ILE:CG2	2:B:195:ILE:N	2.66	0.58
1:A:841:U:H5''	1:A:848:C:C2	2.38	0.58
1:A:1262:C:H2'	1:A:1263:C:C6	2.38	0.58
4:D:87:VAL:O	4:D:89:GLY:N	2.32	0.58
5:E:72:ILE:HG23	5:E:138:LEU:CD1	2.34	0.58
6:F:99:ALA:C	6:F:101:ALA:H	2.10	0.58
7:G:77:ARG:HB2	7:G:155:TRP:CZ3	2.38	0.58
10:J:73:ILE:HG22	10:J:74:ASN:H	1.67	0.58
12:L:29:ARG:CD	12:L:58:SER:HB3	2.34	0.58
2:B:11:PHE:HD1	2:B:35:ILE:HG23	1.69	0.58
3:C:154:GLY:O	3:C:155:ARG:HB2	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:37:TYR:N	4:D:37:TYR:CD1	2.68	0.58
13:M:32:ALA:O	13:M:36:THR:HB	2.03	0.58
2:B:222:GLY:O	2:B:224:VAL:HG23	2.03	0.58
4:D:37:TYR:CE2	4:D:44:GLN:HG2	2.38	0.58
4:D:153:ASN:HA	4:D:158:ARG:NH2	2.18	0.58
8:H:6:ILE:O	8:H:10:LEU:HG	2.04	0.58
10:J:6:LEU:HD11	10:J:18:ALA:HB2	1.85	0.58
10:J:55:LYS:HG2	10:J:55:LYS:O	2.03	0.58
1:A:424:G:O2'	1:A:425:G:H5'	2.03	0.58
1:A:923:A:OP1	5:E:17:ALA:HB2	2.03	0.58
4:D:31:ALA:C	4:D:33:GLU:H	2.11	0.58
4:D:31:ALA:C	4:D:33:GLU:N	2.60	0.58
4:D:60:LYS:HA	4:D:202:VAL:HG22	1.85	0.58
3:C:68:HIS:HA	3:C:103:GLN:HB2	1.85	0.58
3:C:69:VAL:HG12	3:C:70:ALA:N	2.17	0.58
6:F:33:TYR:HA	6:F:71:ARG:NH2	2.19	0.58
8:H:11:THR:HA	8:H:14:ARG:NH1	2.18	0.58
18:R:4:LYS:N	18:R:4:LYS:HD2	2.18	0.58
18:R:72:ARG:O	18:R:73:LYS:CB	2.52	0.58
3:C:118:ARG:NH1	3:C:139:ARG:NH1	2.52	0.58
6:F:33:TYR:CD2	6:F:75:LEU:HD23	2.39	0.58
10:J:80:ILE:HD12	10:J:80:ILE:N	2.18	0.58
12:L:57:THR:C	12:L:59:GLY:H	2.12	0.58
14:N:56:ARG:HG2	14:N:57:LYS:N	2.13	0.58
20:T:36:LEU:HD12	20:T:45:ALA:HA	1.84	0.58
1:A:1249:C:H4'	9:I:35:TYR:OH	2.04	0.58
1:A:1475:G:H2'	1:A:1476:G:O4'	2.03	0.58
2:B:16:LYS:HG3	2:B:34:HIS:HE1	1.69	0.58
20:T:1:ARG:O	20:T:2:ASN:HB2	2.02	0.58
1:A:49:U:C2'	1:A:50:A:H5''	2.33	0.58
1:A:460:G:C3'	1:A:461:A:H5''	2.34	0.58
1:A:1201:A:H4'	1:A:1202:G:C5'	2.34	0.58
1:A:1447:A:O2'	1:A:1452:C:OP1	2.20	0.58
3:C:38:ILE:HG22	3:C:39:ARG:N	2.18	0.58
10:J:96:ILE:HD12	10:J:96:ILE:N	2.19	0.58
12:L:123:GLU:HG3	12:L:123:GLU:O	2.02	0.58
20:T:49:MET:HG3	20:T:77:LEU:CD1	2.33	0.58
1:A:472:A:H2'	1:A:473:G:O4'	2.04	0.57
2:B:45:LEU:HD22	2:B:49:PHE:HE1	1.67	0.57
3:C:130:ARG:O	3:C:134:LYS:HG3	2.04	0.57
1:A:143:A:H2	1:A:220:G:H1	1.52	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:838:G:H1	1:A:848:C:H42	1.51	0.57
4:D:111:VAL:HG23	4:D:160:ASN:ND2	2.16	0.57
10:J:73:ILE:HG22	10:J:74:ASN:N	2.19	0.57
1:A:513:C:O2'	1:A:514:C:H5'	2.04	0.57
1:A:1145:C:H4'	1:A:1146:A:H5'	1.85	0.57
1:A:1230:C:O2'	1:A:1231:G:H5'	2.04	0.57
1:A:1481:U:O2'	1:A:1482:G:H5'	2.04	0.57
2:B:209:LEU:O	2:B:213:VAL:HG23	2.04	0.57
3:C:21:TRP:CZ3	3:C:31:LEU:HB2	2.40	0.57
4:D:30:CYS:C	4:D:32:MET:H	2.12	0.57
7:G:56:GLU:O	7:G:60:VAL:HG23	2.03	0.57
20:T:50:ARG:HH11	20:T:50:ARG:CG	2.16	0.57
1:A:922:G:H2'	1:A:923:A:C8	2.38	0.57
1:A:1144:G:H21	1:A:1146:A:N6	2.01	0.57
1:A:1182:G:C4'	1:A:1183:A:H5'	2.30	0.57
1:A:1368:G:O2'	1:A:1369:C:H5'	2.05	0.57
4:D:2:ARG:HE	4:D:2:ARG:CA	2.17	0.57
4:D:82:SER:CA	4:D:88:THR:CG2	2.77	0.57
5:E:87:LEU:HD23	5:E:116:THR:CG2	2.28	0.57
9:I:78:LEU:O	9:I:81:ALA:HB3	2.04	0.57
10:J:19:GLN:C	10:J:22:VAL:HG12	2.30	0.57
13:M:48:THR:HG22	13:M:50:ALA:N	2.15	0.57
16:P:12:LYS:O	16:P:13:HIS:HB2	2.05	0.57
18:R:32:THR:HG23	18:R:68:GLU:H	1.69	0.57
1:A:153:C:O2'	1:A:154:C:H5'	2.04	0.57
1:A:1004:A:H2'	1:A:1005:A:O4'	2.04	0.57
1:A:1318:A:H2'	1:A:1319:A:H5'	1.86	0.57
3:C:54:VAL:O	3:C:54:VAL:HG12	2.04	0.57
4:D:31:ALA:O	4:D:35:ARG:HB3	2.03	0.57
8:H:91:ARG:O	8:H:91:ARG:HG3	2.04	0.57
2:B:13:HIS:ND1	2:B:198:ASN:ND2	2.52	0.57
2:B:48:THR:O	2:B:52:ILE:HG12	2.03	0.57
3:C:21:TRP:CH2	3:C:31:LEU:HB2	2.39	0.57
4:D:198:ASN:HD22	4:D:198:ASN:C	2.13	0.57
5:E:53:LYS:HG2	5:E:57:TYR:CE2	2.40	0.57
6:F:10:LEU:CD1	6:F:59:TYR:HB3	2.29	0.57
8:H:63:LEU:HD22	8:H:63:LEU:N	2.19	0.57
12:L:22:ALA:O	12:L:23:LEU:O	2.23	0.57
1:A:664:G:OP1	18:R:49:ARG:HD2	2.04	0.57
1:A:838:G:H1	1:A:848:C:N4	2.03	0.57
2:B:21:LYS:HD3	2:B:189:ASP:OD2	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:126:LYS:CA	9:I:126:LYS:HE3	2.34	0.57
14:N:21:THR:OG1	14:N:32:VAL:HG21	2.04	0.57
17:Q:94:TYR:N	17:Q:94:TYR:CD1	2.72	0.57
17:Q:94:TYR:N	17:Q:94:TYR:HD1	2.02	0.57
1:A:1442:G:H2'	1:A:1442(B):A:N7	2.18	0.57
3:C:51:LEU:H	3:C:51:LEU:CD2	2.17	0.57
4:D:57:LEU:HD23	4:D:205:PHE:CZ	2.40	0.57
4:D:173:LEU:O	4:D:174:SER:CB	2.52	0.57
10:J:30:ALA:C	10:J:32:VAL:N	2.62	0.57
20:T:50:ARG:HG2	20:T:50:ARG:HH11	1.70	0.57
1:A:8:A:H5''	5:E:97:ILE:HG22	1.87	0.57
2:B:3:GLU:CD	2:B:4:LEU:H	2.12	0.57
3:C:22:TYR:CD1	3:C:23:ALA:N	2.73	0.57
5:E:89:PRO:HD2	8:H:105:ARG:HH21	1.69	0.57
12:L:85:ARG:HH21	12:L:93:ARG:NE	1.94	0.57
13:M:58:TYR:O	13:M:62:THR:HG21	2.05	0.57
1:A:422:C:O2	1:A:422:C:H2'	2.04	0.57
1:A:706:A:C4'	11:K:19:ILE:HD11	2.35	0.57
1:A:1157:A:H2'	1:A:1181:G:H22	1.69	0.57
2:B:96:LEU:N	2:B:96:LEU:HD12	2.18	0.57
4:D:61:GLN:HA	4:D:61:GLN:NE2	2.19	0.57
5:E:27:LEU:HD22	5:E:39:LEU:CD2	2.35	0.57
5:E:123:ASN:HD22	5:E:124:PRO:N	2.01	0.57
9:I:36:PHE:HB3	9:I:42:ALA:HB2	1.86	0.57
10:J:28:SER:HB3	10:J:82:GLN:NE2	2.20	0.57
11:K:57:ASP:OD1	11:K:61:LYS:HE3	2.05	0.57
12:L:107:LYS:O	12:L:108:ASP:HB2	2.04	0.57
18:R:4:LYS:HD2	18:R:4:LYS:H	1.70	0.57
20:T:35:GLN:OE1	20:T:35:GLN:HA	2.05	0.57
1:A:189:G:O2'	1:A:189(A):C:H5'	2.04	0.56
1:A:410:G:H2'	1:A:429:U:C5	2.40	0.56
1:A:461:A:O2'	1:A:470:C:H5'	2.04	0.56
1:A:742:G:O2'	1:A:743:U:H5'	2.05	0.56
1:A:972:C:OP2	10:J:55:LYS:HD2	2.05	0.56
1:A:997:U:H3'	1:A:998:G:H5''	1.86	0.56
1:A:1329:A:P	13:M:27:ALA:HB3	2.44	0.56
4:D:61:GLN:NE2	4:D:64:ARG:NH1	2.49	0.56
10:J:16:ALA:O	10:J:20:LYS:HG3	2.04	0.56
16:P:12:LYS:HG2	16:P:13:HIS:CD2	2.40	0.56
20:T:75:SER:O	20:T:79:ARG:HG3	2.05	0.56
1:A:344:A:C5'	1:A:345:C:H5	2.18	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:119:VAL:O	3:C:123:ILE:HD13	2.05	0.56
4:D:67:TYR:CE2	4:D:96:LEU:HB3	2.39	0.56
4:D:101:ASP:HB3	4:D:135:PRO:CB	2.35	0.56
13:M:20:TYR:HD1	13:M:20:TYR:H	1.53	0.56
1:A:420:U:H2'	1:A:422:C:H6	1.71	0.56
1:A:537:G:OP1	12:L:109:ARG:NH2	2.39	0.56
3:C:128:ALA:O	3:C:131:ARG:HB3	2.05	0.56
4:D:69:ILE:HG23	4:D:73:GLN:HB2	1.87	0.56
5:E:12:THR:HG23	5:E:23:ARG:O	2.05	0.56
6:F:22:GLU:OE1	6:F:22:GLU:HA	2.05	0.56
9:I:8:ARG:HG3	9:I:13:VAL:HG22	1.86	0.56
9:I:125:SER:C	9:I:127:ARG:H	2.12	0.56
10:J:96:ILE:HD12	10:J:96:ILE:H	1.70	0.56
13:M:34:GLU:C	13:M:36:THR:N	2.63	0.56
16:P:34:GLU:OE2	16:P:55:ARG:HD3	2.05	0.56
17:Q:67:ARG:HH11	17:Q:67:ARG:HG3	1.71	0.56
23:Z:39:U:H2'	23:Z:40:C:C6	2.41	0.56
1:A:153:C:H42	1:A:168:G:H1	1.53	0.56
1:A:471:G:H21	16:P:82:GLN:NE2	2.03	0.56
2:B:160:ASP:CB	2:B:199:ASP:HB2	2.33	0.56
2:B:181:LEU:C	2:B:181:LEU:HD22	2.30	0.56
1:A:56:U:H2'	1:A:57:G:H8	1.70	0.56
1:A:542:G:OP1	4:D:9:ARG:NH2	2.35	0.56
1:A:1047:G:H2'	1:A:1048:G:H5''	1.88	0.56
1:A:1417:G:H2'	1:A:1482:G:N2	2.20	0.56
2:B:17:ARG:HH12	2:B:185:ASP:HA	1.70	0.56
2:B:211:ARG:HA	2:B:214:ASP:OD2	2.06	0.56
20:T:3:LEU:HD12	20:T:5:ALA:HB3	1.87	0.56
1:A:131:C:H2'	1:A:132:C:H6	1.71	0.56
1:A:1001(A):G:H3'	1:A:1002:G:H8	1.71	0.56
1:A:1241:G:H2'	1:A:1242:C:H6	1.70	0.56
1:A:1276:G:C3'	1:A:1277:C:H5''	2.27	0.56
1:A:1347:G:O2'	1:A:1348:U:P	2.64	0.56
4:D:120:VAL:HG22	4:D:125:ILE:HD12	1.87	0.56
4:D:195:LEU:C	4:D:197:VAL:H	2.14	0.56
8:H:4:ASP:OD2	8:H:85:ARG:NH1	2.37	0.56
1:A:1508:G:O2'	1:A:1509:C:H5'	2.06	0.56
7:G:119:ILE:HD12	7:G:119:ILE:H	1.70	0.56
18:R:24:VAL:HG13	18:R:25:LEU:HD23	1.87	0.56
20:T:93:ILE:O	20:T:95:GLY:N	2.35	0.56
21:V:23:ARG:O	21:V:24:LYS:HG2	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:337:C:H2'	1:A:338:A:H8	1.71	0.56
2:B:80:GLU:HG3	2:B:86:TYR:HE2	1.71	0.56
5:E:11:ARG:CD	5:E:22:PHE:HD2	2.17	0.56
6:F:101:ALA:HA	18:R:13:GLU:CD	2.30	0.56
8:H:84:ARG:HH21	8:H:86:ILE:HD11	1.71	0.56
9:I:48:PRO:O	9:I:51:ALA:HB3	2.05	0.56
12:L:54:VAL:O	12:L:61:GLU:HA	2.05	0.56
12:L:122:LYS:HD2	12:L:122:LYS:O	2.06	0.56
15:O:3:THR:HB	15:O:5:GLU:OE2	2.05	0.56
1:A:437:U:H5''	4:D:154:LEU:HD11	1.87	0.56
1:A:861:G:O2'	1:A:862:C:H5'	2.05	0.56
2:B:73:ASP:O	2:B:76:ARG:HG3	2.05	0.56
5:E:122:ARG:HH11	5:E:122:ARG:HG3	1.71	0.56
16:P:4:ILE:HG13	16:P:64:ALA:HB1	1.88	0.56
17:Q:62:ARG:HG2	17:Q:63:PRO:HD2	1.87	0.56
1:A:103:C:H2'	1:A:104:G:H5'	1.88	0.56
1:A:337:C:H2'	1:A:338:A:C8	2.41	0.56
1:A:718:G:H4'	11:K:107:ASN:ND2	2.21	0.56
12:L:23:LEU:HB2	12:L:58:SER:HB2	1.87	0.56
12:L:24:LYS:HD3	12:L:29:ARG:HH12	1.71	0.56
17:Q:63:PRO:HB3	17:Q:69:ARG:NH1	2.21	0.56
21:V:5:ARG:HE	21:V:14:ARG:CZ	2.18	0.56
23:Z:41:C:H2'	23:Z:42:C:H5''	1.87	0.56
1:A:991:U:C4	1:A:1212:U:H1'	2.41	0.55
1:A:1314:C:O5'	19:S:5:LYS:HD3	2.05	0.55
4:D:29:LYS:C	4:D:31:ALA:N	2.64	0.55
5:E:140:THR:HB	5:E:143:ASP:OD1	2.06	0.55
15:O:63:ARG:HH12	15:O:67:ARG:NH2	2.05	0.55
16:P:3:LYS:HD2	16:P:65:GLN:O	2.05	0.55
1:A:586:C:O2'	1:A:587:G:H5'	2.05	0.55
19:S:36:ARG:HD2	19:S:36:ARG:N	2.16	0.55
1:A:437:U:O2'	1:A:438:G:H5'	2.05	0.55
1:A:735:C:O2'	1:A:736:C:H5'	2.06	0.55
1:A:1481:U:H2'	1:A:1482:G:C8	2.41	0.55
4:D:7:VAL:C	4:D:9:ARG:H	2.14	0.55
9:I:117:LYS:O	9:I:118:ALA:CB	2.55	0.55
10:J:32:VAL:HG13	10:J:72:ILE:CG2	2.37	0.55
12:L:86:VAL:HG11	12:L:89:LEU:HD12	1.89	0.55
13:M:99:GLY:C	13:M:100:GLN:HG3	2.31	0.55
19:S:16:GLU:HA	19:S:19:LEU:HD11	1.89	0.55
1:A:186:C:H2'	1:A:187:C:C6	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:413:G:H2'	1:A:428:G:N2	2.21	0.55
1:A:451:A:N6	1:A:481:G:H5'	2.14	0.55
1:A:524:G:H5'	1:A:525:C:OP2	2.07	0.55
1:A:1126:U:H6	1:A:1280:A:N7	2.05	0.55
5:E:1:ASP:CG	5:E:2:PHE:H	2.15	0.55
8:H:82:HIS:HD2	8:H:83:ILE:N	2.04	0.55
9:I:126:LYS:HB3	13:M:125:LYS:HZ3	1.70	0.55
12:L:41:PRO:HB3	12:L:88:ASP:HB3	1.88	0.55
1:A:1245:A:H61	1:A:1292:U:H3	1.54	0.55
1:A:1402:C:O2	1:A:1500:A:N1	2.40	0.55
3:C:18:GLU:O	3:C:39:ARG:NH2	2.39	0.55
12:L:39:VAL:HG12	12:L:40:THR:H	1.71	0.55
13:M:7:GLU:OE1	13:M:7:GLU:HA	2.06	0.55
14:N:43:LEU:C	14:N:43:LEU:CD1	2.79	0.55
15:O:86:ILE:C	15:O:87:ARG:HD2	2.31	0.55
16:P:67:THR:HG22	16:P:68:ASP:N	2.21	0.55
1:A:115:G:H1'	1:A:116:A:N7	2.22	0.55
1:A:523:A:H61	12:L:88:ASP:HB2	1.71	0.55
1:A:629:G:H2'	1:A:630:G:C4'	2.37	0.55
3:C:155:ARG:O	3:C:155:ARG:HD3	2.07	0.55
4:D:193:LEU:N	4:D:193:LEU:HD22	2.21	0.55
14:N:13:PRO:O	14:N:14:LYS:HB2	2.05	0.55
19:S:66:VAL:HG12	19:S:67:GLY:N	2.21	0.55
1:A:718:G:C4'	11:K:107:ASN:ND2	2.69	0.55
1:A:1029:C:C3'	1:A:1030:C:H5''	2.37	0.55
3:C:133:ILE:HD11	3:C:152:VAL:CG2	2.36	0.55
5:E:122:ARG:HG3	5:E:122:ARG:NH1	2.22	0.55
1:A:275:G:H5''	17:Q:13:LYS:CB	2.36	0.55
1:A:824:C:H2'	1:A:825:G:C8	2.41	0.55
1:A:1244:C:O2'	1:A:1245:A:H8	1.89	0.55
1:A:1381:U:O2'	1:A:1382:C:H5'	2.07	0.55
10:J:69:LEU:O	10:J:70:VAL:HB	2.07	0.55
17:Q:4:VAL:HA	17:Q:58:ILE:O	2.05	0.55
1:A:1118:C:H2'	1:A:1119:C:H6	1.70	0.55
14:N:23:CYS:H	14:N:32:VAL:HG12	1.72	0.55
15:O:86:ILE:CG2	15:O:87:ARG:N	2.70	0.55
17:Q:58:ILE:CD1	17:Q:72:VAL:HA	2.36	0.55
1:A:299:G:H2'	1:A:300:A:C8	2.42	0.55
1:A:343:U:H2'	1:A:345:C:C4	2.42	0.55
1:A:564:C:C6	17:Q:30:LEU:HD11	2.42	0.55
1:A:1019:C:H2'	1:A:1020:U:H5'	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1366:C:O2'	10:J:58:ARG:NH2	2.39	0.55
5:E:92:PRO:HA	5:E:113:ASP:OD2	2.07	0.55
5:E:135:LEU:C	5:E:137:GLN:H	2.14	0.55
9:I:126:LYS:HE3	9:I:126:LYS:HA	1.88	0.55
13:M:22:TYR:HB3	13:M:66:GLU:H	1.71	0.55
15:O:86:ILE:O	15:O:87:ARG:CB	2.55	0.55
18:R:31:GLU:CD	18:R:31:GLU:N	2.58	0.55
1:A:376:G:H5''	16:P:5:ARG:HB2	1.89	0.54
1:A:1014:A:H2'	1:A:1015:A:C8	2.41	0.54
1:A:1299:A:H5'	1:A:1300:G:OP2	2.06	0.54
1:A:1510:U:H2'	1:A:1511:G:C8	2.42	0.54
2:B:200:ASP:O	2:B:201:ALA:HB3	2.07	0.54
6:F:100:ASN:ND2	18:R:8:LYS:HG2	2.19	0.54
10:J:92:VAL:HG12	10:J:93:GLU:N	2.21	0.54
17:Q:75:LEU:C	17:Q:75:LEU:HD23	2.32	0.54
1:A:5:U:H5''	1:A:5:U:O2	2.07	0.54
1:A:30:U:H5'	1:A:31:G:OP2	2.07	0.54
1:A:159:G:H5''	1:A:159:G:C8	2.42	0.54
1:A:629:G:H2'	1:A:630:G:O4'	2.08	0.54
1:A:1031:G:O2'	1:A:1032:G:H5'	2.07	0.54
1:A:1305:G:P	21:V:1:GLY:H3	2.30	0.54
4:D:126:THR:HG23	4:D:146:ALA:HB3	1.88	0.54
8:H:94:TYR:O	8:H:95:VAL:HG13	2.07	0.54
13:M:10:ARG:CG	13:M:11:ASN:N	2.70	0.54
13:M:89:LEU:HD23	13:M:92:ARG:HD2	1.89	0.54
14:N:23:CYS:H	14:N:32:VAL:CG1	2.21	0.54
20:T:52:ALA:O	20:T:56:ILE:HG13	2.06	0.54
1:A:1316:G:N2	1:A:1318:A:H3'	2.23	0.54
2:B:85:PRO:HG3	2:B:149:LEU:HD13	1.88	0.54
2:B:160:ASP:HB3	2:B:163:LYS:HB2	1.88	0.54
4:D:151:SER:O	4:D:154:LEU:HB2	2.08	0.54
6:F:48:LEU:HD13	6:F:52:ILE:HG13	1.89	0.54
1:A:49:U:H3'	1:A:50:A:H5''	1.88	0.54
1:A:1030(D):A:H2'	1:A:1031:G:O4'	2.08	0.54
1:A:1286:A:H2'	1:A:1287:A:H4'	1.88	0.54
2:B:90:ARG:O	2:B:92:LEU:HD23	2.08	0.54
9:I:8:ARG:CG	9:I:13:VAL:HG22	2.37	0.54
14:N:10:LYS:C	14:N:12:THR:H	2.14	0.54
1:A:746:A:O2'	1:A:747:C:H5'	2.08	0.54
2:B:10:HIS:HB2	2:B:198:ASN:CG	2.33	0.54
2:B:38:LEU:HA	2:B:41:THR:OG1	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:77:GLU:OE2	17:Q:80:ARG:HD2	2.07	0.54
1:A:100:C:H2'	1:A:101:A:C8	2.43	0.54
1:A:267:C:H2'	1:A:268:C:C6	2.43	0.54
1:A:1152:A:OP1	10:J:66:HIS:ND1	2.41	0.54
1:A:1157:A:H2'	1:A:1181:G:N2	2.23	0.54
1:A:1406:U:O2'	1:A:1407:C:H5'	2.08	0.54
3:C:36:GLN:HE21	14:N:46:LEU:HD13	1.72	0.54
8:H:127:LEU:HD23	8:H:127:LEU:N	2.22	0.54
1:A:1024:G:HO2'	1:A:1025:U:H5'	1.73	0.54
1:A:1145:C:O2'	1:A:1146:A:H5'	2.07	0.54
1:A:1198:G:H2'	1:A:1199:U:C6	2.43	0.54
2:B:45:LEU:HD22	2:B:49:PHE:CE1	2.42	0.54
3:C:69:VAL:C	3:C:105:VAL:HG23	2.33	0.54
6:F:75:LEU:O	6:F:79:LEU:HG	2.08	0.54
8:H:119:LEU:HD12	8:H:124:ALA:CA	2.38	0.54
1:A:647:C:O2'	1:A:648:A:H5''	2.08	0.54
2:B:91:TRP:HZ2	2:B:96:LEU:HD13	1.73	0.54
6:F:13:ASN:O	6:F:14:LEU:HD23	2.08	0.54
7:G:144:ALA:O	7:G:146:ALA:N	2.39	0.54
9:I:126:LYS:HE3	9:I:126:LYS:H	1.72	0.54
11:K:4:VAL:HG21	11:K:30:ILE:HD13	1.89	0.54
13:M:115:THR:HG22	13:M:116:VAL:N	2.22	0.54
14:N:23:CYS:N	14:N:32:VAL:HG12	2.23	0.54
1:A:858:G:H22	1:A:869:G:H3'	1.72	0.54
1:A:979:C:H2'	1:A:980:C:H5'	1.90	0.54
1:A:1178:G:N2	1:A:1180:A:H3'	2.22	0.54
4:D:4:ILE:H	4:D:114:ARG:NH2	2.06	0.54
5:E:123:ASN:HD22	5:E:123:ASN:C	2.15	0.54
10:J:47:VAL:HG13	14:N:40:ARG:HB2	1.90	0.54
11:K:7:GLY:O	11:K:70:VAL:HG23	2.07	0.54
20:T:38:GLN:HA	20:T:84:LEU:HD22	1.89	0.54
1:A:77:G:O2'	1:A:78:G:H5'	2.08	0.54
1:A:382:A:H2'	1:A:383:A:C8	2.43	0.54
1:A:778:G:O2'	1:A:779:C:H5'	2.08	0.54
1:A:806:C:O2'	1:A:807:A:H5'	2.06	0.54
1:A:1216:G:H5''	14:N:4:ALA:CB	2.38	0.54
1:A:1276:G:H3'	1:A:1277:C:C5'	2.28	0.54
1:A:1429:C:H2'	1:A:1430:C:H6	1.72	0.54
2:B:212:ALA:O	2:B:216:ILE:HG12	2.08	0.54
3:C:16:ASP:HB3	3:C:20:ARG:HH12	1.73	0.54
4:D:200:GLN:OE1	4:D:200:GLN:HA	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:4:TYR:CE1	6:F:92:LYS:HG2	2.43	0.54
6:F:101:ALA:HB2	18:R:13:GLU:HA	1.90	0.54
11:K:17:ASN:ND2	11:K:18:THR:N	2.53	0.54
15:O:16:ARG:HG3	15:O:16:ARG:NH1	2.20	0.54
18:R:23:GLU:HA	18:R:26:LYS:HE2	1.90	0.54
1:A:36:C:C2'	1:A:37:U:H5'	2.38	0.53
1:A:697:U:H2'	1:A:698:G:H5'	1.89	0.53
1:A:753:A:H2	8:H:1:MET:HE2	1.73	0.53
1:A:818:G:C2'	1:A:819:A:H5''	2.38	0.53
1:A:1048:G:C6	1:A:1210:C:N4	2.76	0.53
2:B:80:GLU:C	2:B:82:ALA:H	2.16	0.53
6:F:40:VAL:O	6:F:41:GLU:HG3	2.08	0.53
7:G:19:ASP:HB3	7:G:22:VAL:HG23	1.89	0.53
8:H:80:ILE:O	8:H:80:ILE:HG22	2.07	0.53
10:J:14:LEU:C	10:J:16:ALA:N	2.65	0.53
16:P:74:LEU:O	16:P:79:VAL:HG23	2.08	0.53
19:S:12:ASP:O	19:S:13:HIS:C	2.51	0.53
1:A:629:G:H3'	1:A:630:G:H5''	1.90	0.53
1:A:862:C:O2'	1:A:863:U:H5'	2.08	0.53
1:A:1126:U:O2	1:A:1126:U:C2'	2.56	0.53
1:A:1145:C:H4'	1:A:1146:A:C5'	2.38	0.53
1:A:1314:C:H5''	19:S:5:LYS:HZ3	1.73	0.53
1:A:1375:A:H4'	7:G:28:LYS:HE3	1.91	0.53
2:B:96:LEU:N	2:B:96:LEU:CD1	2.71	0.53
9:I:124:TYR:CD2	9:I:127:ARG:HG2	2.43	0.53
10:J:80:ILE:H	10:J:80:ILE:CD1	2.21	0.53
1:A:376:G:H2'	1:A:377:G:H8	1.73	0.53
1:A:404:U:H2'	1:A:405:U:H6	1.74	0.53
2:B:151:ARG:O	2:B:152:LEU:C	2.51	0.53
4:D:17:LYS:HA	4:D:32:MET:HG3	1.89	0.53
6:F:100:ASN:OD1	18:R:12:GLY:HA2	2.09	0.53
10:J:32:VAL:C	10:J:34:GLY:H	2.16	0.53
11:K:116:ARG:O	11:K:117:LYS:HB2	2.07	0.53
13:M:65:LEU:N	13:M:65:LEU:HD12	2.23	0.53
1:A:411:A:C4	1:A:413:G:H1'	2.43	0.53
1:A:1121:U:H2'	1:A:1122:U:C6	2.44	0.53
2:B:2:LYS:HD2	2:B:2:LYS:C	2.34	0.53
2:B:31:ASN:O	2:B:33:ILE:HG13	2.08	0.53
2:B:108:ARG:NH2	2:B:112:LEU:HG	2.20	0.53
4:D:63:LEU:HD12	4:D:74:PHE:HZ	1.73	0.53
11:K:34:SER:H	11:K:37:VAL:HG22	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:105:GLY:HA3	12:L:117:GLY:O	2.09	0.53
13:M:72:GLU:O	13:M:75:ALA:HB3	2.09	0.53
16:P:22:THR:HA	16:P:33:ILE:HG13	1.90	0.53
19:S:14:LEU:HD23	19:S:14:LEU:H	1.74	0.53
20:T:58:LYS:HA	20:T:61:LYS:HG2	1.90	0.53
1:A:404:U:H2'	1:A:405:U:C6	2.44	0.53
1:A:437:U:H2'	1:A:438:G:H5'	1.90	0.53
1:A:470:C:O2'	1:A:471:G:OP1	2.27	0.53
1:A:877:C:OP1	8:H:88:LYS:HE2	2.08	0.53
2:B:11:PHE:HB3	2:B:38:LEU:HD11	1.91	0.53
2:B:123:GLU:O	2:B:124:ARG:HB2	2.08	0.53
1:A:997:U:H2'	1:A:998:G:H5''	1.90	0.53
1:A:1124:G:O2'	1:A:1145:C:N4	2.42	0.53
2:B:62:ILE:HG12	2:B:155:ALA:HB3	1.90	0.53
3:C:133:ILE:O	3:C:137:VAL:HG23	2.09	0.53
10:J:84:MET:O	10:J:84:MET:HE3	2.09	0.53
13:M:4:ALA:O	13:M:5:GLY:C	2.52	0.53
13:M:7:GLU:C	13:M:8:ILE:HD12	2.34	0.53
13:M:10:ARG:HG3	13:M:11:ASN:N	2.24	0.53
15:O:69:LEU:HD12	15:O:77:TYR:CB	2.38	0.53
1:A:620:C:C2	4:D:134:LEU:HD13	2.43	0.53
2:B:65:VAL:HG12	2:B:164:GLU:HG2	1.90	0.53
7:G:135:LYS:O	7:G:139:ASP:HB2	2.09	0.53
9:I:88:ASN:HB3	9:I:91:TYR:CD2	2.44	0.53
17:Q:12:ASP:OD2	17:Q:51:LYS:HG2	2.09	0.53
1:A:163:C:O2'	1:A:164:U:H5'	2.09	0.53
1:A:1264:C:H2'	1:A:1265:G:H8	1.73	0.53
1:A:1347:G:O2'	1:A:1348:U:OP2	2.24	0.53
1:A:1438:G:H2'	1:A:1439:C:C6	2.44	0.53
2:B:87:VAL:HG11	2:B:91:TRP:HD1	1.74	0.53
3:C:130:ARG:HB2	3:C:130:ARG:HH11	1.70	0.53
7:G:153:TYR:O	7:G:155:TRP:N	2.41	0.53
8:H:118:VAL:O	8:H:119:LEU:HD23	2.08	0.53
10:J:6:LEU:HB2	10:J:68:ARG:HB2	1.91	0.53
13:M:104:THR:O	13:M:105:ASN:C	2.51	0.53
15:O:84:LEU:HD13	15:O:86:ILE:HD11	1.91	0.53
18:R:32:THR:C	18:R:34:LYS:H	2.17	0.53
1:A:818:G:H3'	1:A:819:A:C5'	2.39	0.53
2:B:198:ASN:HB3	2:B:200:ASP:O	2.09	0.53
3:C:130:ARG:HH11	3:C:130:ARG:CB	2.22	0.53
6:F:46:ARG:HB2	6:F:60:PHE:CE1	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:122:LYS:H	12:L:122:LYS:NZ	2.06	0.53
19:S:62:THR:CG2	19:S:63:GLU:N	2.72	0.53
20:T:19:ASN:O	20:T:20:LYS:C	2.52	0.53
3:C:39:ARG:O	3:C:43:GLU:HG3	2.10	0.52
3:C:57:GLU:HB2	3:C:64:ALA:CB	2.39	0.52
6:F:30:LEU:HD23	6:F:75:LEU:HD21	1.92	0.52
8:H:25:ASP:OD1	8:H:60:ARG:NE	2.42	0.52
10:J:88:LEU:N	10:J:89:PRO:CD	2.72	0.52
14:N:10:LYS:C	14:N:12:THR:N	2.66	0.52
16:P:75:ARG:O	16:P:78:GLY:N	2.42	0.52
17:Q:3:LYS:HD2	17:Q:5:LEU:CD2	2.37	0.52
1:A:129:U:O2'	1:A:130:A:H2'	2.09	0.52
1:A:445:G:H2'	1:A:446:G:C8	2.45	0.52
1:A:652:U:O4	1:A:752:G:O2'	2.23	0.52
5:E:2:PHE:CZ	5:E:62:MET:HE2	2.44	0.52
6:F:99:ALA:C	6:F:101:ALA:N	2.64	0.52
10:J:4:ILE:CG2	10:J:96:ILE:HG23	2.39	0.52
1:A:460:G:C3'	1:A:461:A:C5'	2.79	0.52
1:A:730:G:C5	1:A:731:G:H1'	2.44	0.52
1:A:1284:C:C3'	1:A:1285:A:H5''	2.36	0.52
2:B:53:GLU:HB3	2:B:215:LEU:CD1	2.35	0.52
3:C:34:GLU:O	3:C:37:ARG:HB2	2.10	0.52
3:C:153:SER:OG	3:C:154:GLY:N	2.39	0.52
8:H:119:LEU:HB3	8:H:123:GLU:HB3	1.92	0.52
18:R:18:ASP:OD2	18:R:21:ASN:HB2	2.08	0.52
1:A:909:A:OP1	12:L:17:LYS:HD3	2.10	0.52
1:A:1356:G:H2'	1:A:1357:A:C8	2.44	0.52
2:B:129:GLN:O	2:B:133:LYS:HB2	2.09	0.52
5:E:27:LEU:HD22	5:E:39:LEU:HD22	1.91	0.52
7:G:5:ARG:O	7:G:6:ALA:C	2.52	0.52
7:G:120:ALA:O	7:G:124:MET:HG3	2.09	0.52
11:K:22:ILE:HD12	11:K:62:ALA:HB2	1.92	0.52
11:K:44:ARG:HH11	11:K:44:ARG:CB	2.22	0.52
12:L:115:LYS:O	12:L:116:TYR:HB2	2.10	0.52
1:A:1047:G:C2'	1:A:1048:G:H5''	2.39	0.52
2:B:148:LEU:HD23	2:B:148:LEU:N	2.25	0.52
2:B:161:PRO:O	2:B:165:ALA:N	2.43	0.52
5:E:47:VAL:O	5:E:50:ALA:HB3	2.09	0.52
6:F:67:MET:HB2	6:F:68:PRO:CD	2.40	0.52
7:G:77:ARG:HB2	7:G:155:TRP:HZ3	1.75	0.52
13:M:53:VAL:O	13:M:57:GLU:HB2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:17:U:H1'	1:A:1080:A:N3	2.24	0.52
3:C:26:LYS:HA	3:C:29:ARG:HH22	1.74	0.52
7:G:47:LYS:O	7:G:50:GLN:HB3	2.09	0.52
12:L:109:ARG:NH1	12:L:112:SER:H	2.08	0.52
13:M:10:ARG:HG3	13:M:11:ASN:H	1.74	0.52
13:M:35:LYS:HB3	13:M:35:LYS:HZ3	1.75	0.52
14:N:8:LYS:HD3	14:N:9:ALA:N	2.25	0.52
16:P:28:ARG:HH11	16:P:28:ARG:HG3	1.75	0.52
16:P:42:ARG:C	16:P:43:LYS:HG3	2.35	0.52
16:P:67:THR:CG2	16:P:68:ASP:N	2.72	0.52
17:Q:43:ALA:HA	17:Q:70:PHE:O	2.10	0.52
1:A:36:C:OP1	12:L:119:LYS:HE3	2.10	0.52
1:A:858:G:H5''	1:A:858:G:C8	2.40	0.52
1:A:977:A:H2'	1:A:978:A:H5''	1.90	0.52
1:A:1309:G:O2'	1:A:1310:G:H5'	2.10	0.52
4:D:121:ARG:NH2	4:D:133:ASP:OD2	2.43	0.52
9:I:45:ALA:HB2	9:I:73:ILE:HG23	1.92	0.52
10:J:31:GLN:HG2	10:J:31:GLN:O	2.08	0.52
12:L:46:SER:O	12:L:47:ALA:HB2	2.09	0.52
21:V:13:TRP:C	21:V:15:GLY:H	2.18	0.52
1:A:108:G:H5'	1:A:109:A:H5''	1.92	0.52
1:A:1125:U:O4	10:J:3:ARG:NH2	2.43	0.52
1:A:1312:G:O2'	1:A:1313:U:H5'	2.09	0.52
4:D:154:LEU:HD23	4:D:155:GLU:N	2.24	0.52
10:J:3:ARG:HD2	10:J:97:LYS:HB2	1.90	0.52
13:M:93:ARG:HH11	13:M:93:ARG:HG3	1.75	0.52
14:N:22:ARG:NH1	14:N:22:ARG:HG2	2.25	0.52
15:O:13:GLU:HG3	15:O:14:PHE:CE1	2.44	0.52
21:V:8:ARG:O	21:V:12:ILE:HG12	2.10	0.52
1:A:858:G:C6	1:A:869:G:C8	2.98	0.52
1:A:1112:C:O2	3:C:178:ARG:HG2	2.10	0.52
1:A:1132:C:H2'	1:A:1133:G:C8	2.45	0.52
1:A:1442(A):G:H4'	1:A:1442(B):A:O5'	2.10	0.52
2:B:159:VAL:O	2:B:181:LEU:O	2.28	0.52
5:E:146:ARG:HB2	5:E:146:ARG:NH1	2.25	0.52
7:G:34:LYS:HD3	7:G:37:LEU:HD23	1.92	0.52
14:N:35:PHE:C	14:N:35:PHE:CD1	2.88	0.52
1:A:251:G:O2'	1:A:252:U:H6	1.94	0.52
3:C:10:ARG:O	3:C:13:ILE:O	2.28	0.52
3:C:185:PHE:HD1	3:C:198:LYS:HG2	1.75	0.52
4:D:37:TYR:CD2	4:D:44:GLN:HG2	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:77:ARG:HA	6:F:80:ARG:HD2	1.92	0.52
17:Q:8:VAL:HG21	17:Q:83:LEU:HD12	1.92	0.52
17:Q:86:LYS:HA	17:Q:89:ILE:HD12	1.92	0.52
1:A:760:G:H1	17:Q:104:ALA:HB2	1.76	0.51
1:A:1166:G:H5'	1:A:1168:A:OP2	2.10	0.51
1:A:1347:G:C2'	1:A:1348:U:OP2	2.58	0.51
1:A:1470:G:O2'	1:A:1471:G:H5'	2.10	0.51
1:A:1472:U:H2'	1:A:1473:A:C1'	2.40	0.51
5:E:72:ILE:HG12	5:E:114:ILE:HD12	1.92	0.51
5:E:96:VAL:O	5:E:103:ARG:NH2	2.41	0.51
15:O:86:ILE:CG2	15:O:87:ARG:H	2.23	0.51
19:S:14:LEU:HA	19:S:17:LYS:HE2	1.93	0.51
19:S:20:GLU:C	19:S:22:ASN:H	2.16	0.51
1:A:116:A:H5'	1:A:116:A:C8	2.39	0.51
1:A:242:C:H2'	1:A:243:A:H5'	1.92	0.51
1:A:436:C:H2'	1:A:437:U:H6	1.75	0.51
1:A:990:C:O2'	1:A:991:U:H5'	2.10	0.51
5:E:146:ARG:CB	5:E:146:ARG:NH1	2.71	0.51
6:F:32:ASN:N	6:F:32:ASN:ND2	2.58	0.51
7:G:23:THR:O	7:G:27:ASN:ND2	2.43	0.51
8:H:119:LEU:HD12	8:H:124:ALA:CB	2.40	0.51
18:R:44:SER:O	18:R:45:GLY:C	2.53	0.51
1:A:220:G:O2'	1:A:221:C:H5'	2.10	0.51
1:A:848:C:O2'	1:A:849:C:H5'	2.09	0.51
1:A:1279:A:H2'	1:A:1282:C:N4	2.26	0.51
4:D:56:ARG:HD2	4:D:204:GLU:HB2	1.92	0.51
6:F:10:LEU:HB3	6:F:84:ASN:O	2.10	0.51
11:K:99:VAL:HG11	18:R:69:LYS:HD3	1.91	0.51
13:M:58:TYR:O	13:M:58:TYR:CG	2.62	0.51
14:N:25:ARG:NH2	14:N:46:LEU:HD21	2.26	0.51
15:O:38:LEU:O	15:O:41:HIS:HB3	2.10	0.51
19:S:13:HIS:H	19:S:13:HIS:CD2	2.28	0.51
19:S:62:THR:H	19:S:65:MET:CG	2.24	0.51
1:A:653:A:H5'	8:H:56:LYS:CE	2.39	0.51
1:A:757:U:H2'	1:A:758:G:O4'	2.10	0.51
1:A:967:C:H5'	9:I:127:ARG:HB2	1.93	0.51
2:B:9:VAL:HG21	2:B:207:LEU:HD12	1.92	0.51
3:C:126:ARG:HG2	3:C:126:ARG:NH1	2.24	0.51
3:C:166:TRP:O	3:C:167:ALA:HB3	2.10	0.51
4:D:24:ARG:C	4:D:26:TYR:N	2.69	0.51
14:N:32:VAL:HG23	14:N:32:VAL:O	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:V:2:LYS:HB3	21:V:13:TRP:CG	2.45	0.51
23:Z:40:C:H2'	23:Z:41:C:OP1	2.11	0.51
1:A:57:G:H2'	1:A:58:C:C6	2.46	0.51
1:A:992:U:O2	1:A:992:U:H2'	2.09	0.51
1:A:1057:G:H2'	1:A:1058:G:O4'	2.11	0.51
1:A:1397:C:H4'	1:A:1398:A:OP2	2.10	0.51
2:B:13:HIS:HD2	2:B:14:GLU:HG2	1.75	0.51
2:B:172:ARG:NH1	8:H:71:GLY:O	2.44	0.51
3:C:133:ILE:HD11	3:C:152:VAL:HG21	1.92	0.51
4:D:121:ARG:C	4:D:123:GLY:H	2.19	0.51
9:I:116:HIS:CD2	9:I:122:PRO:HA	2.46	0.51
10:J:85:THR:C	10:J:86:LEU:HD23	2.34	0.51
11:K:89:GLN:HG2	11:K:95:VAL:HG21	1.93	0.51
12:L:42:LYS:O	12:L:44:PRO:HD2	2.10	0.51
1:A:1202:G:H1'	14:N:28:ARG:HD3	1.93	0.51
1:A:1392:G:N2	1:A:1502:A:H8	2.09	0.51
2:B:174:LEU:C	2:B:176:ILE:H	2.18	0.51
4:D:18:LEU:HB3	4:D:20:LEU:HG	1.93	0.51
5:E:135:LEU:C	5:E:137:GLN:N	2.67	0.51
6:F:69:GLU:HA	6:F:72:VAL:HG23	1.91	0.51
7:G:42:PHE:O	7:G:45:ALA:HB3	2.10	0.51
8:H:24:THR:HG23	8:H:24:THR:O	2.10	0.51
12:L:79:VAL:HG22	12:L:80:LEU:N	2.25	0.51
19:S:35:ARG:HH21	19:S:74:ALA:HB3	1.74	0.51
1:A:229:U:H5''	16:P:33:ILE:HD13	1.92	0.51
1:A:461:A:H8	1:A:461:A:OP1	1.93	0.51
1:A:1123:A:O3'	10:J:34:GLY:HA3	2.10	0.51
1:A:1346:A:C5	7:G:9:ARG:NH1	2.78	0.51
3:C:107:ASN:ND2	3:C:143:SER:HB3	2.25	0.51
4:D:153:ASN:HA	4:D:158:ARG:HH21	1.75	0.51
4:D:195:LEU:CD2	4:D:196:PRO:HD2	2.41	0.51
5:E:86:VAL:O	5:E:116:THR:HA	2.11	0.51
13:M:107:ARG:O	13:M:110:LYS:N	2.44	0.51
15:O:25:GLU:HG3	15:O:80:LEU:HG	1.92	0.51
17:Q:73:LEU:C	17:Q:73:LEU:CD2	2.84	0.51
1:A:106:C:C2'	1:A:107:G:H5'	2.41	0.51
1:A:144:G:O2'	1:A:145:G:H5'	2.10	0.51
1:A:485:G:C2'	1:A:486:U:OP2	2.58	0.51
1:A:1129:C:H4'	1:A:1130:A:H8	1.76	0.51
1:A:1296:C:H4'	1:A:1302:U:C4	2.46	0.51
1:A:1353:G:H2'	1:A:1354:C:H6	1.73	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1372:U:O2'	1:A:1373:G:H5'	2.10	0.51
2:B:108:ARG:HH21	2:B:112:LEU:CG	2.21	0.51
3:C:34:GLU:OE2	3:C:58:ARG:NH1	2.43	0.51
4:D:35:ARG:N	4:D:36:PRO:CD	2.74	0.51
9:I:26:THR:OG1	9:I:61:TYR:HA	2.10	0.51
10:J:74:ASN:C	10:J:76:ASN:H	2.18	0.51
12:L:79:VAL:CG2	12:L:80:LEU:N	2.74	0.51
20:T:3:LEU:O	20:T:6:LEU:HD12	2.11	0.51
1:A:1113:C:O5'	1:A:1113:C:H6	1.94	0.51
1:A:1391:U:H2'	1:A:1392:G:H8	1.70	0.51
1:A:1394:A:C5	1:A:1501:C:H4'	2.46	0.51
2:B:217:ILE:HG21	2:B:224:VAL:CG2	2.41	0.51
4:D:144:GLU:OE2	4:D:183:LYS:HE3	2.10	0.51
5:E:124:PRO:O	5:E:125:ILE:C	2.54	0.51
11:K:5:ALA:HA	11:K:67:MET:HA	1.93	0.51
11:K:48:PRO:O	11:K:51:ALA:HB3	2.11	0.51
11:K:73:ILE:HD12	11:K:73:ILE:N	2.25	0.51
12:L:66:ILE:HD13	12:L:73:LEU:HD12	1.91	0.51
13:M:22:TYR:CE2	13:M:69:LEU:HB3	2.46	0.51
13:M:34:GLU:O	13:M:36:THR:N	2.44	0.51
18:R:11:LEU:HD21	18:R:24:VAL:CG2	2.41	0.51
18:R:24:VAL:CG1	18:R:25:LEU:N	2.73	0.51
1:A:103:C:C2'	1:A:104:G:H5'	2.41	0.51
1:A:1109:C:H2'	1:A:1110:A:O4'	2.10	0.51
1:A:1273:G:H2'	1:A:1274:G:O4'	2.11	0.51
4:D:5:GLY:O	4:D:7:VAL:HG23	2.11	0.51
4:D:130:ARG:HD2	4:D:130:ARG:N	2.26	0.51
7:G:51:GLU:O	7:G:52:LYS:C	2.54	0.51
9:I:6:THR:H	9:I:82:ARG:CD	2.24	0.51
9:I:15:ARG:HD3	9:I:17:PHE:CZ	2.46	0.51
1:A:412:A:N6	4:D:34:ARG:HB3	2.24	0.50
1:A:448:A:C4	1:A:487:A:C2	2.99	0.50
1:A:648:A:O2'	1:A:649:G:H5'	2.11	0.50
1:A:1056:U:H5'	3:C:162:ALA:CB	2.41	0.50
1:A:1428:A:H2'	1:A:1429:C:C6	2.47	0.50
2:B:91:TRP:CH2	2:B:170:GLU:CD	2.89	0.50
7:G:147:ASN:C	7:G:149:ALA:H	2.18	0.50
9:I:4:TYR:HE2	9:I:15:ARG:HG2	1.75	0.50
10:J:26:ARG:O	10:J:27:ARG:HG3	2.11	0.50
10:J:36:ILE:HB	10:J:69:LEU:HB3	1.92	0.50
20:T:33:ALA:HB2	20:T:48:ILE:HG22	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:V:16:THR:O	21:V:21:ARG:HD3	2.11	0.50
1:A:149:A:H2'	1:A:150:C:C6	2.46	0.50
1:A:1040:U:H2'	1:A:1041:A:H8	1.75	0.50
1:A:1166:G:H3'	1:A:1168:A:H5''	1.93	0.50
1:A:1426:C:O2'	1:A:1427:U:H5'	2.10	0.50
2:B:86:TYR:CD1	2:B:145:GLY:HA3	2.46	0.50
2:B:128:GLU:HG2	2:B:132:LEU:CD1	2.42	0.50
3:C:78:ARG:HH21	3:C:81:GLU:HG2	1.76	0.50
3:C:107:ASN:HD21	3:C:143:SER:CB	2.24	0.50
7:G:115:ALA:O	7:G:119:ILE:HD12	2.10	0.50
10:J:77:ARG:C	10:J:79:THR:H	2.19	0.50
17:Q:103:LYS:HB3	17:Q:103:LYS:HZ3	1.76	0.50
18:R:21:ASN:O	18:R:24:VAL:HG12	2.11	0.50
20:T:43:GLU:H	20:T:92:LEU:HD12	1.76	0.50
1:A:321:A:O2'	1:A:322:C:H5'	2.10	0.50
1:A:411:A:N3	1:A:413:G:H1'	2.26	0.50
1:A:501:C:H2'	1:A:502:G:C8	2.45	0.50
1:A:1123:A:H4'	10:J:35:PRO:HD2	1.94	0.50
1:A:1475:G:H3'	1:A:1476:G:H5''	1.92	0.50
2:B:105:ARG:HB3	2:B:143:LEU:HD11	1.92	0.50
4:D:157:ILE:N	4:D:157:ILE:HD12	2.25	0.50
8:H:10:LEU:CD2	8:H:83:ILE:HD11	2.41	0.50
11:K:14:SER:HB3	11:K:17:ASN:O	2.11	0.50
12:L:36:VAL:O	12:L:36:VAL:HG12	2.11	0.50
13:M:106:ALA:O	13:M:110:LYS:HG3	2.12	0.50
15:O:17:PHE:HB2	15:O:18:PRO:HD2	1.93	0.50
18:R:2:SER:O	18:R:3:ARG:HD3	2.10	0.50
1:A:640:A:O2'	1:A:641:U:H5'	2.11	0.50
1:A:818:G:O2'	1:A:819:A:H5''	2.12	0.50
1:A:1138:G:C8	1:A:1140:C:H1'	2.46	0.50
1:A:1374:A:OP1	7:G:35:LYS:HE3	2.12	0.50
1:A:1394:A:C6	1:A:1501:C:H4'	2.46	0.50
26:A:2800:RPO:HAU	26:A:2800:RPO:H6	1.93	0.50
2:B:143:LEU:O	2:B:147:ARG:HB2	2.11	0.50
3:C:76:ILE:O	3:C:82:ARG:HB3	2.11	0.50
8:H:20:TYR:CE1	8:H:76:PRO:HG2	2.46	0.50
8:H:103:VAL:CG2	8:H:110:ALA:HB2	2.42	0.50
12:L:82:ARG:HG3	12:L:82:ARG:HH11	1.76	0.50
1:A:714:G:H2'	1:A:715:A:C8	2.46	0.50
1:A:1106:G:OP1	3:C:171:ARG:HD3	2.11	0.50
6:F:100:ASN:ND2	18:R:8:LYS:O	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:10:ARG:HA	13:M:44:VAL:HB	1.93	0.50
13:M:121:LYS:O	13:M:122:ALA:HB2	2.11	0.50
3:C:13:ILE:HG22	3:C:14:THR:N	2.11	0.50
3:C:155:ARG:N	3:C:162:ALA:HA	2.25	0.50
3:C:171:ARG:HH12	3:C:173:PRO:HG3	1.76	0.50
4:D:198:ASN:C	4:D:198:ASN:ND2	2.69	0.50
5:E:118:GLU:O	5:E:119:LEU:HD23	2.11	0.50
9:I:85:VAL:O	9:I:86:GLN:C	2.53	0.50
9:I:126:LYS:HE3	9:I:126:LYS:N	2.26	0.50
12:L:24:LYS:HD3	12:L:29:ARG:HH22	1.75	0.50
17:Q:73:LEU:C	17:Q:73:LEU:HD23	2.37	0.50
1:A:159:G:H4'	1:A:160:A:OP2	2.11	0.50
1:A:460:G:H3'	1:A:461:A:H5'	1.88	0.50
1:A:858:G:N2	1:A:869:G:H3'	2.27	0.50
1:A:953:G:H1'	13:M:124:ARG:CA	2.33	0.50
1:A:1042:G:O2'	1:A:1043:C:H5'	2.12	0.50
2:B:76:ARG:HG2	2:B:76:ARG:HH11	1.76	0.50
2:B:217:ILE:O	2:B:219:ALA:N	2.45	0.50
3:C:59:ALA:O	3:C:61:ASP:N	2.45	0.50
4:D:104:VAL:CG2	4:D:125:ILE:HD13	2.34	0.50
5:E:78:VAL:HG21	5:E:133:GLU:HB3	1.94	0.50
6:F:93:SER:C	6:F:94:GLN:HG3	2.36	0.50
9:I:19:ARG:O	9:I:59:ASP:N	2.45	0.50
9:I:57:ARG:HG2	9:I:57:ARG:O	2.12	0.50
9:I:126:LYS:O	13:M:125:LYS:NZ	2.45	0.50
10:J:75:PRO:O	10:J:76:ASN:O	2.30	0.50
13:M:76:ASN:O	13:M:79:ARG:N	2.45	0.50
18:R:1:PRO:O	18:R:3:ARG:HG2	2.12	0.50
1:A:154:C:H2'	1:A:155:C:H6	1.76	0.50
1:A:443:C:H2'	1:A:444:C:C6	2.47	0.50
1:A:807:A:H2'	1:A:808:C:C6	2.47	0.50
1:A:841:U:H3'	1:A:848:C:O4'	2.12	0.50
1:A:1258:G:H2'	1:A:1259:C:C6	2.47	0.50
1:A:1308:U:OP1	13:M:97:VAL:N	2.33	0.50
3:C:27:GLN:OE1	3:C:27:GLN:N	2.45	0.50
3:C:127:PHE:HB3	3:C:131:ARG:NH1	2.27	0.50
4:D:21:LYS:O	4:D:112:SER:HB3	2.12	0.50
5:E:4:GLU:HA	5:E:29:VAL:O	2.11	0.50
19:S:21:LEU:HB3	19:S:27:LYS:HB2	1.93	0.50
1:A:420:U:H2'	1:A:422:C:C6	2.47	0.50
1:A:647:C:C2'	1:A:648:A:C5'	2.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:752:G:H8	1:A:752:G:OP2	1.93	0.50
4:D:42:HIS:O	4:D:44:GLN:N	2.45	0.50
7:G:56:GLU:OE1	7:G:57:PRO:HD2	2.11	0.50
7:G:115:ALA:HA	7:G:118:ARG:CZ	2.41	0.50
8:H:119:LEU:HD12	8:H:124:ALA:HB2	1.93	0.50
9:I:125:SER:C	9:I:127:ARG:N	2.68	0.50
13:M:21:ILE:O	13:M:22:TYR:O	2.29	0.50
15:O:28:VAL:HG12	15:O:84:LEU:CD1	2.41	0.50
1:A:629:G:C3'	1:A:630:G:H5''	2.42	0.49
1:A:1149:C:OP1	9:I:13:VAL:HG21	2.11	0.49
2:B:18:TRP:CD1	2:B:18:TRP:N	2.78	0.49
2:B:172:ARG:O	8:H:71:GLY:HA2	2.12	0.49
3:C:99:ALA:O	3:C:100:LEU:CB	2.57	0.49
12:L:64:ALA:CB	12:L:81:ILE:HD11	2.41	0.49
13:M:93:ARG:HG3	13:M:93:ARG:NH1	2.27	0.49
18:R:2:SER:H	18:R:4:LYS:HZ2	1.59	0.49
19:S:15:LEU:C	19:S:17:LYS:H	2.20	0.49
1:A:184:G:O4'	1:A:224:C:H4'	2.12	0.49
2:B:109:LEU:HD22	2:B:147:ARG:HH21	1.77	0.49
2:B:159:VAL:O	2:B:161:PRO:HD3	2.12	0.49
3:C:50:GLY:O	3:C:69:VAL:HG13	2.13	0.49
5:E:64:GLU:O	5:E:66:PRO:HD3	2.12	0.49
5:E:135:LEU:O	5:E:137:GLN:N	2.45	0.49
5:E:140:THR:HG23	5:E:141:LYS:N	2.27	0.49
6:F:69:GLU:HA	6:F:72:VAL:CG2	2.41	0.49
9:I:45:ALA:HB1	9:I:76:ILE:HG22	1.94	0.49
10:J:32:VAL:HG22	10:J:72:ILE:HG21	1.94	0.49
1:A:91:C:H2'	1:A:92:C:H6	1.78	0.49
1:A:106:C:O2'	1:A:107:G:H5'	2.12	0.49
1:A:364:A:N6	12:L:24:LYS:HZ1	2.10	0.49
1:A:428:G:OP2	4:D:6:PRO:HG2	2.12	0.49
1:A:1346:A:C6	7:G:9:ARG:NH1	2.81	0.49
1:A:1441:G:H4'	1:A:1442:G:C5	2.47	0.49
6:F:23:LYS:NZ	6:F:42:GLU:OE1	2.42	0.49
10:J:89:PRO:HB2	10:J:92:VAL:HB	1.93	0.49
18:R:38:ARG:HA	18:R:48:GLN:OE1	2.12	0.49
19:S:29:LEU:O	19:S:30:ILE:HD13	2.12	0.49
20:T:80:LYS:HB2	20:T:80:LYS:NZ	2.28	0.49
23:Z:28:G:H4'	23:Z:29:G:O5'	2.12	0.49
3:C:106:GLN:NE2	3:C:106:GLN:H	2.10	0.49
4:D:80:GLU:O	4:D:84:LYS:HG3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:98:LEU:HD13	6:F:101:ALA:CB	2.42	0.49
9:I:117:LYS:HG2	9:I:120:ARG:HB3	1.94	0.49
12:L:6:LEU:O	12:L:10:GLY:N	2.45	0.49
13:M:64:LYS:HZ2	13:M:72:GLU:HB2	1.77	0.49
14:N:55:VAL:O	14:N:55:VAL:HG12	2.12	0.49
17:Q:27:PRO:HA	17:Q:34:VAL:HA	1.93	0.49
19:S:27:LYS:C	19:S:28:ARG:HG3	2.38	0.49
1:A:216:G:O2'	1:A:217:C:P	2.70	0.49
1:A:1347:G:HO2'	1:A:1348:U:P	2.35	0.49
2:B:19:ASN:C	2:B:19:ASN:ND2	2.70	0.49
5:E:72:ILE:HG23	5:E:73:PRO:HD2	1.93	0.49
1:A:625:G:H2'	1:A:626:U:C6	2.48	0.49
1:A:895:G:H2'	1:A:896:C:C6	2.47	0.49
1:A:918:A:H2'	1:A:919:A:C8	2.48	0.49
1:A:1486:G:H2'	1:A:1487:G:O4'	2.13	0.49
2:B:7:ALA:HA	2:B:11:PHE:HD2	1.77	0.49
2:B:92:LEU:N	2:B:92:LEU:CD2	2.74	0.49
1:A:34:C:H1'	12:L:28:PHE:CZ	2.48	0.49
1:A:320:C:H2'	1:A:321:A:C8	2.48	0.49
1:A:953:G:C1'	13:M:124:ARG:HA	2.32	0.49
1:A:1072:G:O6	1:A:1102:A:N6	2.46	0.49
6:F:80:ARG:NH1	6:F:88:VAL:HB	2.28	0.49
9:I:47:GLU:OE1	9:I:50:ARG:HD2	2.13	0.49
11:K:47:THR:HG23	11:K:50:ALA:H	1.78	0.49
11:K:113:LYS:O	11:K:116:ARG:HG2	2.13	0.49
12:L:106:VAL:HG23	12:L:116:TYR:HB3	1.95	0.49
13:M:50:ALA:O	13:M:54:ARG:HG3	2.13	0.49
16:P:45:THR:OG1	16:P:46:PRO:HD2	2.12	0.49
1:A:1142:G:H2'	1:A:1143:G:O4'	2.13	0.49
1:A:1216:G:O2'	1:A:1217:C:H5'	2.13	0.49
3:C:171:ARG:HB3	3:C:171:ARG:HH11	1.77	0.49
7:G:145:GLU:C	7:G:147:ASN:H	2.19	0.49
9:I:65:ARG:HH11	9:I:65:ARG:HG3	1.77	0.49
12:L:57:THR:C	12:L:59:GLY:N	2.70	0.49
1:A:8:A:C6	4:D:208:ARG:HA	2.47	0.49
1:A:837:G:H1	1:A:849:C:H42	1.60	0.49
1:A:1119:C:O2'	1:A:1120:G:H5'	2.13	0.49
3:C:21:TRP:CB	3:C:58:ARG:HB2	2.42	0.49
3:C:82:ARG:C	3:C:84:ARG:N	2.71	0.49
3:C:107:ASN:HD21	3:C:143:SER:HB3	1.77	0.49
6:F:7:ASN:HD21	18:R:19:TYR:HE2	1.61	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:36:ILE:HB	10:J:69:LEU:CB	2.43	0.49
19:S:27:LYS:HG2	19:S:28:ARG:H	1.77	0.49
20:T:67:LYS:HB2	20:T:67:LYS:HZ3	1.78	0.49
1:A:401:C:H1'	1:A:622:A:H1'	1.94	0.49
1:A:1121:U:H2'	1:A:1122:U:H6	1.77	0.49
1:A:1170:A:H2'	1:A:1171:G:O4'	2.13	0.49
3:C:96:LYS:O	3:C:97:ASN:C	2.55	0.49
4:D:51:SER:O	4:D:52:ASP:C	2.56	0.49
17:Q:89:ILE:O	17:Q:92:GLN:HB3	2.13	0.49
21:V:9:ARG:CZ	21:V:9:ARG:HB2	2.43	0.49
1:A:328:C:O2	1:A:328:C:C2'	2.60	0.48
1:A:389:A:H2'	1:A:389:A:N3	2.28	0.48
1:A:449:C:O2	16:P:42:ARG:HG2	2.12	0.48
1:A:939:G:H2'	1:A:940:C:C6	2.47	0.48
1:A:1105:A:H2'	1:A:1106:G:C8	2.48	0.48
2:B:75:VAL:HG22	2:B:209:LEU:HD11	1.94	0.48
2:B:77:MET:HE3	2:B:228:PRO:HG2	1.95	0.48
2:B:207:LEU:HD23	2:B:207:LEU:C	2.38	0.48
3:C:125:ARG:HB3	3:C:127:PHE:CE1	2.47	0.48
5:E:14:ARG:HD3	5:E:21:ARG:O	2.12	0.48
6:F:44:GLY:HA3	6:F:59:TYR:CE1	2.49	0.48
7:G:92:PRO:HG2	7:G:93:ARG:H	1.78	0.48
10:J:27:ARG:HH11	10:J:27:ARG:CB	2.20	0.48
10:J:72:ILE:O	10:J:72:ILE:HG13	2.13	0.48
13:M:18:LEU:O	13:M:21:ILE:HG13	2.13	0.48
13:M:20:TYR:N	13:M:20:TYR:CD1	2.81	0.48
13:M:97:VAL:HG23	13:M:109:ARG:NH1	2.27	0.48
14:N:11:ARG:C	14:N:13:PRO:HD3	2.38	0.48
15:O:69:LEU:HD12	15:O:77:TYR:CA	2.43	0.48
1:A:382:A:C2	1:A:383:A:C4	3.01	0.48
1:A:572:A:H5''	1:A:917:G:H4'	1.94	0.48
1:A:781:A:H5'	1:A:782:A:OP2	2.13	0.48
1:A:969:A:N1	13:M:125:LYS:OXT	2.46	0.48
1:A:1288:A:H2'	1:A:1289:A:C8	2.48	0.48
1:A:1390:U:H2'	1:A:1391:U:C6	2.48	0.48
1:A:1479:C:C2'	1:A:1480:G:H5''	2.29	0.48
2:B:17:ARG:HH12	2:B:185:ASP:CA	2.26	0.48
3:C:154:GLY:O	3:C:155:ARG:CB	2.61	0.48
4:D:11:CYS:SG	4:D:18:LEU:HB2	2.53	0.48
10:J:13:THR:HG23	10:J:92:VAL:HG22	1.95	0.48
10:J:23:GLU:C	10:J:25:ALA:N	2.71	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:50:LYS:HD2	12:L:50:LYS:N	2.29	0.48
19:S:29:LEU:HD23	19:S:47:THR:HG22	1.94	0.48
19:S:64:ASN:ND2	19:S:65:MET:N	2.58	0.48
19:S:79:TYR:O	19:S:81:GLY:N	2.46	0.48
1:A:539:A:H2'	1:A:540:G:C8	2.48	0.48
1:A:1140:C:H2'	1:A:1140:C:O2	2.12	0.48
2:B:38:LEU:O	2:B:39:GLN:C	2.55	0.48
3:C:5:HIS:CD2	3:C:7:ILE:H	2.32	0.48
3:C:5:HIS:CD2	3:C:7:ILE:HB	2.47	0.48
3:C:190:THR:HG21	3:C:192:TYR:CE1	2.48	0.48
6:F:48:LEU:HD13	6:F:52:ILE:CG1	2.44	0.48
9:I:7:GLY:CA	9:I:78:LEU:HD12	2.39	0.48
9:I:91:TYR:C	9:I:93:ALA:N	2.71	0.48
10:J:80:ILE:O	10:J:80:ILE:HG22	2.13	0.48
19:S:51:TYR:HA	19:S:55:GLN:O	2.13	0.48
1:A:97:G:O2'	1:A:98:G:H5'	2.13	0.48
1:A:271:C:O2'	1:A:272:C:H5'	2.13	0.48
1:A:818:G:C3'	1:A:819:A:C5'	2.91	0.48
1:A:1207:G:O2'	1:A:1208:C:H5'	2.13	0.48
1:A:1289:A:H5'	1:A:1290:G:OP2	2.12	0.48
2:B:11:PHE:CD1	2:B:11:PHE:C	2.91	0.48
2:B:72:GLN:O	2:B:88:ASN:ND2	2.47	0.48
3:C:35:ASP:OD1	3:C:56:ILE:HD12	2.12	0.48
3:C:46:LEU:N	3:C:46:LEU:HD12	2.28	0.48
3:C:173:PRO:O	3:C:175:HIS:N	2.46	0.48
4:D:123:GLY:HA3	4:D:131:ARG:HD2	1.94	0.48
5:E:148:ARG:NH2	8:H:107:LEU:O	2.47	0.48
6:F:50:TYR:CE1	18:R:62:GLY:HA2	2.48	0.48
17:Q:23:GLU:CD	17:Q:36:LYS:HD3	2.38	0.48
17:Q:77:GLU:OE1	17:Q:80:ARG:HD2	2.13	0.48
19:S:71:GLY:C	19:S:73:PHE:H	2.20	0.48
20:T:4:SER:HA	20:T:6:LEU:CD1	2.44	0.48
1:A:8:A:H3'	1:A:8:A:OP1	2.13	0.48
3:C:46:LEU:H	3:C:46:LEU:CD1	2.27	0.48
3:C:149:LYS:HG2	3:C:150:VAL:N	2.27	0.48
4:D:30:CYS:SG	4:D:30:CYS:O	2.71	0.48
8:H:60:ARG:NH1	8:H:60:ARG:CG	2.76	0.48
9:I:105:ALA:O	9:I:106:ARG:C	2.56	0.48
14:N:44:ARG:NH1	14:N:44:ARG:HG3	2.27	0.48
1:A:49:U:O2'	1:A:50:A:H5''	2.13	0.48
1:A:488:C:O2'	1:A:489:C:H5'	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:521:G:OP2	12:L:50:LYS:HE2	2.14	0.48
1:A:644:G:O2'	1:A:645:C:H5'	2.13	0.48
5:E:68:GLN:O	5:E:69:ASN:CB	2.61	0.48
7:G:16:VAL:HG12	7:G:17:TYR:CD1	2.48	0.48
1:A:946:A:H2'	1:A:947:G:H8	1.72	0.48
1:A:986:A:H2'	1:A:987:G:C8	2.49	0.48
1:A:1056:U:H5'	3:C:162:ALA:HB2	1.96	0.48
1:A:1277:C:H3'	1:A:1277:C:H6	1.77	0.48
4:D:2:ARG:HA	4:D:2:ARG:NE	2.25	0.48
7:G:41:ILE:HD12	7:G:115:ALA:HB3	1.96	0.48
9:I:3:TYR:HB3	9:I:86:GLN:HB2	1.96	0.48
9:I:6:THR:H	9:I:82:ARG:HD2	1.79	0.48
10:J:64:ARG:HD3	10:J:66:HIS:CE1	2.48	0.48
13:M:115:THR:CG2	13:M:116:VAL:N	2.77	0.48
16:P:1:MET:O	16:P:24:ALA:HB2	2.14	0.48
1:A:275:G:C5'	17:Q:13:LYS:HB3	2.41	0.48
1:A:280:C:H4'	1:A:281:G:OP2	2.13	0.48
1:A:628:G:H2'	1:A:629:G:C8	2.48	0.48
1:A:818:G:H3'	1:A:819:A:H5''	1.96	0.48
1:A:945:G:H2'	1:A:945:G:N3	2.29	0.48
1:A:1090:U:H2'	1:A:1091:U:H6	1.78	0.48
1:A:1420:C:H2'	1:A:1421:G:C8	2.48	0.48
2:B:82:ALA:C	2:B:84:MET:H	2.22	0.48
2:B:200:ASP:O	2:B:201:ALA:CB	2.62	0.48
4:D:7:VAL:HG13	4:D:20:LEU:HD13	1.96	0.48
8:H:134:ILE:HG22	8:H:135:CYS:SG	2.52	0.48
9:I:55:LEU:O	9:I:55:LEU:HD23	2.13	0.48
9:I:92:ARG:HG3	9:I:92:ARG:NH1	2.29	0.48
9:I:112:LYS:HD3	9:I:118:ALA:HA	1.96	0.48
13:M:83:ILE:C	13:M:85:CYS:H	2.22	0.48
14:N:53:PRO:C	14:N:55:VAL:H	2.21	0.48
19:S:62:THR:HB	19:S:64:ASN:HD21	1.78	0.48
1:A:148:G:H5''	1:A:148:G:C8	2.49	0.48
1:A:815:A:O2'	1:A:1527:C:H1'	2.14	0.48
1:A:994:A:N7	1:A:1216:G:H4'	2.29	0.48
1:A:1020:U:H2'	1:A:1021:G:C5'	2.32	0.48
1:A:1118:C:H2'	1:A:1119:C:C6	2.49	0.48
1:A:1126:U:C6	1:A:1280:A:N7	2.81	0.48
2:B:134:HIS:CA	2:B:137:GLU:HG2	2.42	0.48
3:C:133:ILE:CD1	3:C:152:VAL:HG23	2.44	0.48
4:D:63:LEU:HD12	4:D:74:PHE:CZ	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:67:GLY:HA2	13:M:70:ARG:HD2	1.96	0.48
16:P:55:ARG:O	16:P:58:TYR:HB3	2.14	0.48
18:R:24:VAL:HG13	18:R:25:LEU:N	2.28	0.48
1:A:407:G:O2'	4:D:115:GLN:HG3	2.14	0.48
1:A:1002:G:H2'	1:A:1003:G:C8	2.48	0.48
6:F:35:ALA:HA	6:F:67:MET:HB3	1.94	0.48
17:Q:25:GLN:O	17:Q:26:PHE:HB3	2.13	0.48
20:T:23:LYS:HE3	20:T:64:THR:HG22	1.96	0.48
1:A:245:C:O2'	1:A:246:A:H5''	2.14	0.47
1:A:334:C:H2'	1:A:335:C:C6	2.49	0.47
1:A:456:C:H2'	1:A:457:C:C6	2.49	0.47
1:A:984:C:H2'	1:A:985:C:H6	1.78	0.47
1:A:1105:A:H2'	1:A:1106:G:H8	1.79	0.47
1:A:1468:A:H2'	1:A:1469:G:O4'	2.14	0.47
2:B:37:ASP:OD1	2:B:39:GLN:HB2	2.14	0.47
2:B:47:ARG:HH12	2:B:193:TYR:HA	1.78	0.47
2:B:79:ALA:CB	2:B:86:TYR:HD2	2.26	0.47
2:B:126:LYS:O	2:B:130:VAL:HG23	2.14	0.47
2:B:156:ILE:HG22	2:B:158:VAL:HG13	1.95	0.47
3:C:21:TRP:O	3:C:21:TRP:CE3	2.67	0.47
6:F:62:TRP:CG	18:R:20:ARG:NH1	2.82	0.47
17:Q:44:HIS:ND1	17:Q:68:LYS:NZ	2.42	0.47
20:T:66:HIS:O	20:T:67:LYS:HB3	2.13	0.47
21:V:13:TRP:C	21:V:15:GLY:N	2.71	0.47
1:A:189(E):U:O2'	1:A:189(F):U:H5'	2.14	0.47
1:A:1087:G:N2	1:A:1099:G:H1'	2.29	0.47
1:A:1131:G:H2'	1:A:1132:C:C6	2.48	0.47
1:A:1168:A:H3'	1:A:1169:A:C8	2.49	0.47
2:B:53:GLU:HA	2:B:56:ALA:HB3	1.96	0.47
3:C:42:LEU:HD13	3:C:67:VAL:HG21	1.95	0.47
5:E:6:MET:HA	5:E:28:VAL:HG23	1.96	0.47
6:F:41:GLU:HB2	6:F:62:TRP:HB3	1.96	0.47
7:G:94:ARG:CZ	7:G:98:LEU:HD11	2.44	0.47
10:J:88:LEU:H	10:J:89:PRO:CD	2.26	0.47
17:Q:65:SER:OG	17:Q:68:LYS:HB2	2.14	0.47
1:A:1189:C:P	10:J:49:ARG:NH2	2.85	0.47
2:B:128:GLU:HG2	2:B:132:LEU:HD11	1.96	0.47
5:E:69:ASN:C	5:E:71:THR:H	2.22	0.47
5:E:72:ILE:HD12	5:E:138:LEU:CD1	2.44	0.47
11:K:100:ASP:OD2	18:R:73:LYS:HE3	2.13	0.47
11:K:101:ASP:CG	11:K:101:ASP:O	2.57	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:116:VAL:HG12	13:M:117:ALA:N	2.21	0.47
20:T:17:LEU:HD12	20:T:17:LEU:O	2.14	0.47
20:T:77:LEU:O	20:T:81:VAL:HG23	2.13	0.47
20:T:79:ARG:HG2	20:T:79:ARG:HH11	1.79	0.47
1:A:36:C:H2'	1:A:37:U:H5'	1.97	0.47
1:A:89:C:O5'	1:A:89:C:H6	1.96	0.47
1:A:184:G:C4'	1:A:224:C:H4'	2.44	0.47
1:A:663:A:H5''	18:R:46:LYS:HE3	1.96	0.47
2:B:84:MET:HA	2:B:84:MET:HE2	1.97	0.47
2:B:173:LYS:HA	8:H:72:PRO:HD3	1.97	0.47
4:D:148:ALA:O	4:D:149:GLU:C	2.57	0.47
7:G:17:TYR:CE2	7:G:58:LEU:HB2	2.49	0.47
7:G:137:LYS:HD2	7:G:137:LYS:C	2.39	0.47
11:K:86:ARG:HG2	11:K:86:ARG:HH11	1.78	0.47
17:Q:2:LYS:HB3	17:Q:60:GLU:HB3	1.96	0.47
1:A:519:C:H2'	1:A:520:A:C8	2.50	0.47
1:A:707:C:OP1	11:K:75:ARG:HD2	2.15	0.47
1:A:721:G:H8	1:A:721:G:OP1	1.96	0.47
1:A:858:G:C5	1:A:869:G:N7	2.82	0.47
1:A:983:A:H5'	1:A:984:C:OP2	2.13	0.47
1:A:1014:A:C2	1:A:1219:U:H1'	2.49	0.47
1:A:1392:G:H21	1:A:1502:A:H8	1.61	0.47
2:B:17:ARG:O	2:B:18:TRP:O	2.32	0.47
4:D:81:ALA:C	4:D:88:THR:HG23	2.40	0.47
6:F:78:GLU:OE1	6:F:78:GLU:HA	2.15	0.47
10:J:47:VAL:HG11	14:N:40:ARG:O	2.15	0.47
11:K:22:ILE:CD1	11:K:62:ALA:HB2	2.45	0.47
19:S:7:GLY:O	19:S:9:PHE:N	2.47	0.47
19:S:43:MET:O	19:S:44:VAL:C	2.58	0.47
20:T:46:LEU:O	20:T:49:MET:HB3	2.14	0.47
1:A:501:C:H1'	1:A:549:C:H1'	1.95	0.47
1:A:541:G:O2'	1:A:542:G:H5'	2.15	0.47
1:A:1544:U:H4'	22:W:1:U:O5'	2.14	0.47
8:H:50:ARG:O	8:H:51:VAL:HG13	2.14	0.47
8:H:82:HIS:C	8:H:82:HIS:CD2	2.91	0.47
8:H:112:LEU:HD11	8:H:114:THR:HG22	1.95	0.47
15:O:61:GLN:HA	15:O:61:GLN:HE21	1.79	0.47
19:S:31:LYS:HA	19:S:49:ALA:HB3	1.96	0.47
1:A:168:G:C2	1:A:169:C:C5	3.03	0.47
1:A:402:G:C3'	1:A:403:C:H5''	2.45	0.47
1:A:745:C:H5''	1:A:851:G:O2'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1060:C:H5''	10:J:49:ARG:HB3	1.97	0.47
1:A:1402:C:H2'	1:A:1403:C:O4'	2.14	0.47
1:A:1418:A:N6	1:A:1482:G:O2'	2.47	0.47
3:C:98:VAL:HG23	3:C:99:ALA:O	2.15	0.47
3:C:172:VAL:O	3:C:174:LEU:N	2.37	0.47
4:D:157:ILE:N	4:D:157:ILE:CD1	2.78	0.47
7:G:109:GLN:HA	7:G:109:GLN:OE1	2.14	0.47
9:I:42:ALA:HA	9:I:73:ILE:HD13	1.97	0.47
9:I:79:GLY:C	9:I:81:ALA:H	2.22	0.47
10:J:14:LEU:C	10:J:16:ALA:H	2.22	0.47
16:P:71:ARG:HD3	16:P:75:ARG:NH2	2.30	0.47
20:T:23:LYS:O	20:T:27:LYS:HG3	2.15	0.47
1:A:96:U:O2'	1:A:97:G:H5'	2.15	0.47
1:A:414:A:H2'	1:A:415:A:H8	1.80	0.47
1:A:495:A:H4'	1:A:496:A:OP1	2.14	0.47
1:A:715:A:H2'	1:A:716:A:H8	1.80	0.47
1:A:1118:C:H1'	1:A:1179:A:C4	2.49	0.47
1:A:1314:C:H5''	19:S:5:LYS:HZ2	1.80	0.47
1:A:1491:G:O2'	26:A:2800:RPO:HAM	2.14	0.47
6:F:47:ARG:N	6:F:47:ARG:NE	2.57	0.47
9:I:9:ARG:O	9:I:10:LYS:C	2.57	0.47
9:I:69:LYS:O	9:I:73:ILE:HG13	2.14	0.47
11:K:49:TYR:CE2	11:K:53:LEU:HD11	2.50	0.47
19:S:8:VAL:CG1	19:S:38:THR:HG21	2.45	0.47
1:A:390:C:H2'	1:A:391:G:H8	1.78	0.47
1:A:591:U:H2'	1:A:592:G:H8	1.80	0.47
1:A:932:C:C6	7:G:2:ARG:HD3	2.50	0.47
1:A:958:A:C5'	1:A:959:A:OP2	2.61	0.47
1:A:1004:A:H8	1:A:1036:G:H22	1.62	0.47
1:A:1014:A:H2	1:A:1219:U:O2	1.97	0.47
1:A:1106:G:H5''	3:C:171:ARG:HG2	1.97	0.47
1:A:1245:A:N6	1:A:1292:U:H3	2.13	0.47
1:A:1245:A:H2'	1:A:1246:C:C6	2.50	0.47
1:A:1264:C:H2'	1:A:1265:G:C8	2.50	0.47
3:C:178:ARG:NH1	3:C:206:VAL:HG22	2.30	0.47
4:D:16:VAL:C	4:D:32:MET:HE2	2.38	0.47
10:J:4:ILE:HD11	10:J:70:VAL:HG11	1.96	0.47
10:J:20:LYS:NZ	10:J:88:LEU:N	2.61	0.47
12:L:115:LYS:O	12:L:116:TYR:CB	2.62	0.47
15:O:8:GLN:O	15:O:9:LYS:C	2.58	0.47
1:A:130:A:O2'	1:A:131:C:H5''	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:345:C:H4'	1:A:346:G:C5'	2.45	0.47
1:A:586:C:C2'	1:A:587:G:H5'	2.45	0.47
1:A:921:U:O2'	5:E:15:MET:O	2.24	0.47
1:A:1095:U:H2'	1:A:1096:C:C6	2.49	0.47
1:A:1191:A:P	3:C:2:ASN:HD22	2.38	0.47
2:B:213:VAL:O	2:B:216:ILE:HB	2.14	0.47
3:C:24:GLY:C	3:C:26:LYS:H	2.23	0.47
3:C:66:THR:HG23	3:C:101:ASN:HB2	1.96	0.47
5:E:37:VAL:HG21	5:E:109:ALA:HB2	1.97	0.47
6:F:30:LEU:HB3	6:F:35:ALA:CB	2.45	0.47
6:F:39:LYS:HB2	6:F:39:LYS:NZ	2.29	0.47
8:H:103:VAL:HG21	8:H:109:ILE:C	2.39	0.47
9:I:112:LYS:H	9:I:118:ALA:HA	1.80	0.47
13:M:81:MET:CE	13:M:91:HIS:HB3	2.45	0.47
1:A:146:G:H2'	1:A:147:G:C5'	2.30	0.46
1:A:538:G:OP2	12:L:111:LYS:HD2	2.15	0.46
1:A:1292:U:H2'	1:A:1293:G:C8	2.50	0.46
2:B:215:LEU:HD13	2:B:215:LEU:C	2.40	0.46
5:E:140:THR:CG2	5:E:141:LYS:N	2.77	0.46
10:J:48:ILE:N	10:J:48:ILE:CD1	2.78	0.46
10:J:92:VAL:CG1	10:J:93:GLU:N	2.78	0.46
13:M:22:TYR:CE2	13:M:69:LEU:HD13	2.50	0.46
13:M:95:LEU:O	13:M:109:ARG:NH1	2.48	0.46
13:M:96:PRO:HB2	13:M:100:GLN:OE1	2.14	0.46
20:T:9:HIS:O	20:T:10:ARG:C	2.58	0.46
20:T:89:GLY:O	20:T:90:ALA:CB	2.63	0.46
21:V:1:GLY:C	21:V:3:GLY:N	2.73	0.46
23:Z:41:C:H2'	23:Z:42:C:C5'	2.45	0.46
1:A:251:G:HO2'	1:A:252:U:H6	1.63	0.46
1:A:688:G:H5'	11:K:37:VAL:HG12	1.97	0.46
1:A:707:C:O2'	1:A:708:C:H5'	2.15	0.46
1:A:997:U:C2'	1:A:998:G:H5''	2.45	0.46
2:B:76:ARG:HB3	2:B:88:ASN:ND2	2.31	0.46
9:I:79:GLY:C	9:I:81:ALA:N	2.72	0.46
9:I:110:ARG:HD2	14:N:60:TRP:O	2.15	0.46
9:I:125:SER:O	9:I:127:ARG:N	2.48	0.46
16:P:19:ILE:HG22	16:P:36:ILE:HG13	1.97	0.46
17:Q:58:ILE:HD13	17:Q:72:VAL:HA	1.96	0.46
19:S:14:LEU:H	19:S:14:LEU:CD2	2.28	0.46
19:S:29:LEU:HA	19:S:47:THR:O	2.15	0.46
20:T:16:ARG:HG2	20:T:16:ARG:HH11	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:80:LYS:O	20:T:84:LEU:HB2	2.16	0.46
1:A:1249:C:H2'	1:A:1250:A:H5''	1.96	0.46
1:A:1483:A:H2'	1:A:1484:C:O4'	2.15	0.46
3:C:136:ALA:O	3:C:139:ARG:HG2	2.16	0.46
4:D:189:ASP:O	4:D:190:ARG:C	2.59	0.46
5:E:11:ARG:CD	5:E:22:PHE:CD2	2.94	0.46
5:E:16:GLN:O	5:E:17:ALA:C	2.56	0.46
5:E:47:VAL:HB	5:E:48:PRO:CD	2.45	0.46
5:E:74:HIS:CE1	5:E:138:LEU:HD23	2.50	0.46
8:H:107:LEU:HD23	8:H:107:LEU:N	2.29	0.46
1:A:106:C:O2	1:A:379:C:H4'	2.15	0.46
1:A:189:G:H1	1:A:189(K):U:H3	1.63	0.46
1:A:361:G:C3'	1:A:362:G:H5''	2.43	0.46
1:A:422:C:O2	1:A:422:C:C2'	2.64	0.46
1:A:436:C:H2'	1:A:437:U:C6	2.50	0.46
1:A:715:A:H2'	1:A:716:A:C8	2.50	0.46
1:A:899:C:H2'	1:A:900:A:C8	2.50	0.46
1:A:1062:U:H2'	1:A:1063:C:C6	2.51	0.46
1:A:1124:G:N2	1:A:1127:G:N2	2.64	0.46
1:A:1329:A:O2'	1:A:1330:U:H5'	2.15	0.46
3:C:69:VAL:HG12	3:C:71:LYS:N	2.21	0.46
4:D:30:CYS:O	4:D:31:ALA:HB3	2.16	0.46
4:D:172:TRP:O	4:D:185:LEU:HB2	2.14	0.46
5:E:3:GLU:O	5:E:30:VAL:HA	2.15	0.46
5:E:13:ALA:HB2	5:E:22:PHE:CD2	2.51	0.46
7:G:144:ALA:C	7:G:146:ALA:N	2.72	0.46
10:J:67:ASN:O	10:J:68:ARG:HD3	2.15	0.46
12:L:37:ARG:HB3	12:L:37:ARG:HH11	1.78	0.46
14:N:23:CYS:N	14:N:32:VAL:CG1	2.78	0.46
19:S:5:LYS:C	19:S:6:LYS:HG3	2.40	0.46
20:T:4:SER:HA	20:T:6:LEU:HD12	1.97	0.46
20:T:38:GLN:O	20:T:38:GLN:CD	2.59	0.46
1:A:17:U:O2'	1:A:1079:G:H1'	2.15	0.46
1:A:952:U:O2'	1:A:953:G:H5'	2.15	0.46
1:A:1030:C:H6	1:A:1030:C:H5'	1.81	0.46
2:B:155:ALA:HB1	2:B:179:ILE:HD11	1.98	0.46
2:B:172:ARG:NH2	8:H:74:PRO:HG3	2.31	0.46
3:C:67:VAL:HG12	3:C:69:VAL:HG23	1.97	0.46
4:D:7:VAL:C	4:D:9:ARG:N	2.73	0.46
4:D:175:LEU:HA	4:D:182:GLY:HA2	1.98	0.46
5:E:148:ARG:CZ	8:H:44:PHE:CZ	2.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:57:SER:O	10:J:58:ARG:HB2	2.15	0.46
13:M:24:ILE:HG13	13:M:65:LEU:HD23	1.97	0.46
15:O:61:GLN:HA	15:O:61:GLN:NE2	2.31	0.46
17:Q:8:VAL:HG21	17:Q:83:LEU:CD1	2.45	0.46
18:R:28:PHE:O	18:R:36:LEU:HG	2.15	0.46
19:S:27:LYS:HD3	19:S:28:ARG:H	1.80	0.46
1:A:933:G:OP2	7:G:2:ARG:HB3	2.14	0.46
1:A:1140:C:C2'	1:A:1141:C:H5''	2.45	0.46
1:A:1251:A:H4'	9:I:11:GLU:CD	2.40	0.46
1:A:1288:A:H2'	1:A:1289:A:H8	1.81	0.46
1:A:1472:U:C2'	1:A:1473:A:O4'	2.60	0.46
2:B:92:LEU:O	2:B:95:MET:HG3	2.16	0.46
3:C:27:GLN:O	3:C:31:LEU:HG	2.16	0.46
4:D:127:VAL:O	4:D:129:GLY:N	2.49	0.46
9:I:8:ARG:HD3	9:I:13:VAL:HG22	1.98	0.46
9:I:80:ILE:HG22	9:I:80:ILE:O	2.16	0.46
12:L:6:LEU:HD23	12:L:6:LEU:HA	1.78	0.46
12:L:49:ARG:N	12:L:49:ARG:HD2	2.30	0.46
13:M:12:LYS:HE3	13:M:20:TYR:OH	2.15	0.46
17:Q:89:ILE:H	17:Q:89:ILE:HG13	1.55	0.46
17:Q:94:TYR:HD1	17:Q:94:TYR:H	1.59	0.46
18:R:68:GLU:HA	18:R:68:GLU:OE1	2.15	0.46
20:T:6:LEU:HD12	20:T:6:LEU:H	1.81	0.46
1:A:408:A:H5'	4:D:115:GLN:HB2	1.98	0.46
1:A:992:U:O4'	1:A:992:U:OP2	2.33	0.46
1:A:1333:A:H2'	1:A:1334:G:O4'	2.16	0.46
1:A:1475:G:C3'	1:A:1476:G:H5''	2.45	0.46
2:B:22:PHE:HD2	2:B:26:ILE:HD11	1.81	0.46
11:K:116:ARG:C	11:K:118:ALA:H	2.22	0.46
12:L:19:LYS:C	12:L:20:VAL:HG23	2.41	0.46
13:M:99:GLY:O	13:M:100:GLN:HG3	2.15	0.46
19:S:66:VAL:O	19:S:68:HIS:N	2.48	0.46
20:T:93:ILE:C	20:T:95:GLY:N	2.70	0.46
1:A:362:G:C8	1:A:362:G:H3'	2.51	0.46
1:A:689:C:H2'	1:A:690:G:O4'	2.15	0.46
1:A:769:G:H4'	1:A:1513:A:H4'	1.98	0.46
1:A:976:G:C8	1:A:1358:U:C2	3.04	0.46
1:A:1314:C:C5	19:S:5:LYS:HE2	2.51	0.46
1:A:1444:C:H2'	1:A:1445:C:H6	1.81	0.46
2:B:13:HIS:O	2:B:33:ILE:HG23	2.15	0.46
10:J:47:VAL:O	10:J:58:ARG:C	2.59	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:86:ARG:HG2	11:K:86:ARG:NH1	2.31	0.46
12:L:39:VAL:HG12	12:L:40:THR:N	2.30	0.46
17:Q:58:ILE:CG2	17:Q:70:PHE:CD1	2.99	0.46
18:R:59:ARG:HA	18:R:64:LEU:O	2.16	0.46
1:A:130:A:C8	17:Q:62:ARG:HG3	2.50	0.46
1:A:433:C:H2'	1:A:434:U:C6	2.51	0.46
1:A:1154:G:O2'	1:A:1155:G:H5'	2.15	0.46
1:A:1315:U:H2'	1:A:1316:G:O4'	2.16	0.46
1:A:1328:C:O2'	1:A:1329:A:H5'	2.16	0.46
1:A:1516:G:H2'	1:A:1518:A:OP2	2.15	0.46
2:B:125:PRO:C	2:B:127:LYS:H	2.22	0.46
2:B:194:ILE:CG2	2:B:195:ILE:H	2.29	0.46
5:E:133:GLU:O	5:E:137:GLN:HB2	2.16	0.46
9:I:78:LEU:HD13	9:I:78:LEU:C	2.40	0.46
10:J:17:SER:OG	10:J:89:PRO:HB3	2.15	0.46
11:K:105:PRO:C	11:K:107:ASN:N	2.74	0.46
12:L:22:ALA:C	12:L:23:LEU:O	2.59	0.46
20:T:46:LEU:O	20:T:50:ARG:HD2	2.15	0.46
1:A:106:C:HO2'	1:A:107:G:H5'	1.81	0.46
1:A:753:A:C2	8:H:1:MET:HE2	2.51	0.46
1:A:1001:A:N1	1:A:1002:G:O6	2.49	0.46
1:A:1111:A:H2'	1:A:1112:C:H6	1.80	0.46
2:B:22:PHE:HD1	2:B:188:PRO:HG3	1.81	0.46
9:I:7:GLY:HA2	9:I:78:LEU:HB3	1.97	0.46
10:J:61:PHE:HE1	14:N:57:LYS:HG2	1.79	0.46
12:L:100:VAL:O	12:L:101:TYR:HB2	2.16	0.46
19:S:19:LEU:HD12	19:S:20:GLU:HG2	1.96	0.46
19:S:20:GLU:C	19:S:22:ASN:N	2.74	0.46
1:A:20:U:C2'	1:A:21:G:H5'	2.47	0.45
1:A:65:U:H6	1:A:65:U:H5''	1.82	0.45
1:A:262:A:C6	1:A:263:A:C6	3.03	0.45
1:A:393:A:O2'	1:A:394:G:H5'	2.16	0.45
1:A:582:U:OP1	15:O:63:ARG:NH1	2.49	0.45
1:A:720:C:H2'	1:A:721:G:C8	2.51	0.45
1:A:731:G:O2'	1:A:732:C:H5'	2.16	0.45
1:A:1014:A:N3	1:A:1219:U:H1'	2.31	0.45
1:A:1054:C:N4	1:A:1196:U:H5	2.15	0.45
1:A:1057:G:O2'	1:A:1058:G:H5'	2.17	0.45
26:A:2800:RPO:O1'	26:A:2800:RPO:H1	2.16	0.45
2:B:102:ILE:HG22	2:B:102:ILE:O	2.15	0.45
2:B:108:ARG:NH2	2:B:112:LEU:CG	2.79	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:133:ILE:HG21	3:C:166:TRP:O	2.16	0.45
4:D:103:VAL:HG11	4:D:145:ILE:CD1	2.45	0.45
9:I:94:LYS:C	9:I:97:PRO:HD2	2.41	0.45
11:K:81:ARG:CD	18:R:73:LYS:HZ3	2.25	0.45
13:M:34:GLU:O	13:M:37:GLY:N	2.45	0.45
13:M:66:GLU:O	13:M:68:GLU:N	2.48	0.45
13:M:107:ARG:HD3	13:M:113:ARG:NH1	2.31	0.45
1:A:955:U:O2'	1:A:956:U:H5'	2.16	0.45
1:A:1041:A:H2'	1:A:1042:G:H8	1.81	0.45
1:A:1476:G:H2'	1:A:1477:C:H5'	1.99	0.45
1:A:1494:G:O2'	1:A:1495:U:H5'	2.16	0.45
2:B:128:GLU:C	2:B:130:VAL:H	2.24	0.45
3:C:5:HIS:HD2	3:C:7:ILE:H	1.64	0.45
6:F:37:VAL:HA	6:F:65:VAL:HG12	1.98	0.45
7:G:91:SER:O	7:G:95:GLN:HG2	2.16	0.45
7:G:107:ALA:O	7:G:110:ARG:HB2	2.16	0.45
17:Q:23:GLU:OE2	17:Q:36:LYS:HD3	2.15	0.45
21:V:5:ARG:HG2	21:V:14:ARG:HH12	1.76	0.45
1:A:356:A:H1'	1:A:368:U:O2'	2.16	0.45
1:A:458:C:H2'	1:A:460:G:O4'	2.17	0.45
1:A:1166:G:H3'	1:A:1168:A:C5'	2.46	0.45
1:A:1404:C:H2'	1:A:1405:G:C8	2.51	0.45
2:B:10:HIS:C	2:B:12:GLY:H	2.23	0.45
2:B:109:LEU:C	2:B:109:LEU:HD23	2.41	0.45
2:B:120:GLU:HA	2:B:123:GLU:HB3	1.98	0.45
4:D:50:PRO:HB2	4:D:55:VAL:CG2	2.46	0.45
8:H:31:PHE:O	8:H:35:ILE:HG12	2.16	0.45
10:J:37:PRO:O	10:J:67:ASN:O	2.33	0.45
11:K:23:THR:HG22	11:K:29:PRO:HA	1.98	0.45
11:K:63:MET:O	11:K:66:GLY:N	2.49	0.45
19:S:52:ASN:HD21	19:S:55:GLN:HB2	1.80	0.45
20:T:3:LEU:C	20:T:5:ALA:H	2.24	0.45
1:A:200:G:H2'	1:A:201:C:O4'	2.16	0.45
1:A:1023:G:H2'	1:A:1023:G:N3	2.31	0.45
3:C:73:GLY:O	3:C:75:VAL:N	2.49	0.45
5:E:98:ALA:HB2	5:E:116:THR:OG1	2.17	0.45
6:F:15:ASP:H	6:F:18:GLN:HE21	1.64	0.45
7:G:5:ARG:O	7:G:6:ALA:O	2.35	0.45
7:G:147:ASN:C	7:G:149:ALA:N	2.71	0.45
9:I:88:ASN:O	9:I:91:TYR:HB2	2.17	0.45
11:K:13:ALA:CB	11:K:81:ARG:HB2	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:41:PRO:C	19:S:43:MET:H	2.25	0.45
1:A:328:C:O2	1:A:328:C:H2'	2.16	0.45
1:A:485:G:O2'	1:A:486:U:P	2.74	0.45
1:A:928:G:O2'	1:A:929:G:H5'	2.16	0.45
1:A:1442(A):G:H5''	1:A:1442(B):A:O5'	2.17	0.45
2:B:17:ARG:HD3	2:B:18:TRP:N	2.31	0.45
2:B:157:PHE:HD1	2:B:179:ILE:HB	1.81	0.45
3:C:75:VAL:HG11	3:C:102:VAL:CG2	2.47	0.45
3:C:76:ILE:C	3:C:82:ARG:HB3	2.41	0.45
3:C:147:GLY:HA2	3:C:170:GLY:HA3	1.98	0.45
3:C:171:ARG:HB3	3:C:171:ARG:NH1	2.31	0.45
4:D:69:ILE:HD11	4:D:99:ARG:CD	2.46	0.45
4:D:208:ARG:HB3	4:D:208:ARG:CZ	2.44	0.45
5:E:147:LEU:HD23	8:H:79:VAL:HG22	1.96	0.45
6:F:82:ARG:HB2	6:F:85:VAL:CG2	2.47	0.45
8:H:86:ILE:HG21	8:H:133:LEU:CD2	2.23	0.45
12:L:23:LEU:HG	12:L:24:LYS:H	1.81	0.45
13:M:122:ALA:O	13:M:123:PRO:C	2.60	0.45
15:O:81:ILE:O	15:O:85:GLY:N	2.46	0.45
1:A:431:A:O2'	1:A:432:A:H5'	2.16	0.45
1:A:1090:U:H2'	1:A:1091:U:C6	2.51	0.45
14:N:7:GLU:O	14:N:8:LYS:C	2.60	0.45
14:N:43:LEU:HD12	14:N:43:LEU:O	2.16	0.45
20:T:83:GLN:O	20:T:86:GLU:HG2	2.16	0.45
21:V:5:ARG:CG	21:V:14:ARG:NH1	2.76	0.45
1:A:194:C:O2'	20:T:61:LYS:HD3	2.17	0.45
1:A:394:G:H2'	1:A:395:C:C6	2.52	0.45
1:A:403:C:H6	1:A:403:C:H5'	1.82	0.45
1:A:579:G:O2'	15:O:53:ARG:NE	2.48	0.45
1:A:811:C:O2'	1:A:901:A:N1	2.46	0.45
3:C:24:GLY:O	3:C:26:LYS:N	2.49	0.45
3:C:78:ARG:HE	3:C:81:GLU:HB3	1.79	0.45
8:H:82:HIS:CD2	8:H:83:ILE:N	2.85	0.45
9:I:99:GLY:C	9:I:101:LEU:H	2.24	0.45
17:Q:32:GLY:O	17:Q:33:LYS:C	2.59	0.45
19:S:50:VAL:CG2	19:S:70:LEU:HD22	2.47	0.45
1:A:50:A:H3'	1:A:52:G:C8	2.52	0.45
1:A:403:C:H2'	1:A:404:U:H6	1.82	0.45
1:A:520:A:N1	1:A:536:C:H1'	2.32	0.45
1:A:738:C:OP2	6:F:92:LYS:NZ	2.43	0.45
1:A:858:G:C8	1:A:858:G:C4'	3.00	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:957:U:C3'	1:A:958:A:C5'	2.95	0.45
1:A:957:U:N3	1:A:960:U:H5''	2.25	0.45
1:A:967:C:H4'	9:I:127:ARG:NE	2.31	0.45
1:A:972:C:P	10:J:55:LYS:HD3	2.56	0.45
1:A:1056:U:O2'	1:A:1057:G:H5'	2.16	0.45
1:A:1360:A:O2'	1:A:1361:G:H5'	2.17	0.45
2:B:126:LYS:HA	2:B:129:GLN:CB	2.41	0.45
4:D:125:ILE:HG22	4:D:126:THR:N	2.30	0.45
5:E:74:HIS:HD2	8:H:107:LEU:HD12	1.80	0.45
6:F:91:VAL:CG1	18:R:57:ARG:NH2	2.80	0.45
13:M:47:LEU:HB3	13:M:52:VAL:HG23	1.98	0.45
20:T:16:ARG:HG2	20:T:16:ARG:NH1	2.31	0.45
20:T:48:ILE:HD13	20:T:51:LYS:HD2	1.99	0.45
1:A:234:C:H2'	1:A:235:C:H6	1.82	0.45
1:A:261:U:O2	1:A:263:A:C8	2.70	0.45
1:A:567:G:H2'	1:A:568:G:O4'	2.17	0.45
1:A:778:G:C2'	1:A:779:C:H5'	2.46	0.45
1:A:1111:A:N1	3:C:176:THR:HG22	2.32	0.45
1:A:1278:U:O2'	1:A:1279:A:OP1	2.34	0.45
1:A:1287:A:H2'	1:A:1288:A:C8	2.52	0.45
1:A:1479:C:H2'	1:A:1480:G:C5'	2.32	0.45
2:B:21:LYS:HB3	2:B:188:PRO:HD2	1.98	0.45
2:B:21:LYS:HD2	2:B:187:ASP:OD2	2.17	0.45
2:B:94:GLY:O	2:B:95:MET:C	2.60	0.45
2:B:122:GLU:H	2:B:122:GLU:CD	2.24	0.45
2:B:158:VAL:HG22	2:B:180:ALA:HB2	1.99	0.45
2:B:172:ARG:NH2	8:H:68:ARG:HH22	2.13	0.45
2:B:213:VAL:HA	2:B:216:ILE:HG12	1.99	0.45
3:C:83:ILE:O	3:C:83:ILE:HG12	2.16	0.45
4:D:29:LYS:O	4:D:31:ALA:N	2.50	0.45
4:D:181:LYS:NZ	4:D:181:LYS:HB3	2.32	0.45
11:K:23:THR:HB	11:K:27:GLY:C	2.42	0.45
11:K:42:GLY:C	11:K:44:ARG:H	2.25	0.45
1:A:135:C:C2	16:P:1:MET:HB2	2.45	0.45
1:A:555:C:H2'	1:A:556:C:C6	2.52	0.45
1:A:780:A:C2	1:A:801:U:C5	3.05	0.45
1:A:883:C:O2'	1:A:884:U:H5'	2.17	0.45
1:A:1414:U:H2'	1:A:1415:G:H8	1.81	0.45
8:H:65:TYR:N	8:H:65:TYR:CD1	2.85	0.45
8:H:104:ARG:O	8:H:105:ARG:C	2.60	0.45
9:I:41:ARG:O	9:I:42:ALA:C	2.59	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:51:PRO:HA	14:N:41:ILE:CD1	2.47	0.45
15:O:5:GLU:HG2	15:O:6:GLU:H	1.81	0.45
15:O:69:LEU:HD13	15:O:69:LEU:C	2.42	0.45
19:S:79:TYR:O	19:S:80:ARG:C	2.60	0.45
1:A:147:G:H5'	1:A:147:G:H8	1.82	0.44
1:A:598:U:H4'	8:H:94:TYR:CG	2.52	0.44
1:A:1230:C:H2'	1:A:1231:G:H8	1.82	0.44
2:B:76:ARG:CZ	2:B:76:ARG:HB2	2.47	0.44
3:C:46:LEU:HD12	3:C:46:LEU:H	1.82	0.44
4:D:27:SER:O	4:D:29:LYS:N	2.50	0.44
6:F:21:LEU:O	6:F:25:ILE:HD12	2.17	0.44
8:H:91:ARG:HH11	17:Q:32:GLY:HA3	1.82	0.44
17:Q:21:LEU:HD11	17:Q:38:SER:HB2	1.99	0.44
19:S:14:LEU:O	19:S:18:VAL:N	2.50	0.44
19:S:62:THR:HB	19:S:65:MET:HE3	1.99	0.44
1:A:433:C:O5'	1:A:433:C:H6	1.99	0.44
1:A:437:U:C5'	4:D:154:LEU:HD21	2.47	0.44
1:A:702:A:O2'	1:A:703:G:OP1	2.35	0.44
2:B:3:GLU:OE1	2:B:4:LEU:N	2.46	0.44
2:B:4:LEU:CD2	2:B:42:MET:HE2	2.42	0.44
2:B:49:PHE:CE2	2:B:212:ALA:HA	2.51	0.44
3:C:118:ARG:HG2	3:C:139:ARG:HH12	1.83	0.44
4:D:156:LEU:HD23	4:D:156:LEU:C	2.41	0.44
6:F:100:ASN:OD1	6:F:100:ASN:O	2.35	0.44
10:J:73:ILE:O	10:J:74:ASN:CB	2.63	0.44
11:K:115:PHE:O	11:K:116:ARG:CB	2.65	0.44
18:R:22:VAL:HG22	18:R:63:LEU:HB3	1.99	0.44
18:R:54:THR:O	18:R:55:ILE:C	2.60	0.44
19:S:44:VAL:HA	19:S:61:ILE:CD1	2.46	0.44
20:T:67:LYS:CG	20:T:68:ASN:H	2.26	0.44
20:T:82:ARG:HB2	20:T:97:LEU:HD13	1.99	0.44
1:A:263:A:OP2	20:T:72:ARG:NH1	2.51	0.44
1:A:620:C:H2'	1:A:621:A:O4'	2.16	0.44
1:A:865:A:H1'	1:A:918:A:O2'	2.17	0.44
1:A:997:U:H2'	1:A:998:G:O4'	2.18	0.44
1:A:1040:U:H2'	1:A:1041:A:C8	2.52	0.44
1:A:1055:A:N6	1:A:1206:G:C5	2.85	0.44
1:A:1058:G:C6	1:A:1059:C:N3	2.85	0.44
1:A:1256:A:O3'	1:A:1257:U:C4'	2.66	0.44
1:A:1347:G:H22	1:A:1373:G:H2'	1.82	0.44
1:A:1372:U:H2'	1:A:1373:G:O4'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:130:VAL:HA	2:B:133:LYS:HE2	1.99	0.44
3:C:135:GLN:O	3:C:136:ALA:C	2.60	0.44
3:C:166:TRP:HB3	3:C:167:ALA:H	1.41	0.44
4:D:61:GLN:HE21	4:D:61:GLN:CA	2.22	0.44
4:D:195:LEU:HD23	4:D:196:PRO:HD2	1.99	0.44
5:E:11:ARG:HD2	5:E:11:ARG:C	2.43	0.44
5:E:77:GLU:HG2	5:E:86:VAL:HG13	1.99	0.44
6:F:91:VAL:HG13	18:R:57:ARG:NH2	2.32	0.44
7:G:13:PRO:HB2	7:G:18:GLY:C	2.43	0.44
8:H:121:ASP:HB2	8:H:125:ARG:HH21	1.83	0.44
9:I:2:GLN:C	9:I:3:TYR:CD1	2.94	0.44
11:K:42:GLY:C	11:K:44:ARG:N	2.76	0.44
11:K:63:MET:C	11:K:65:TYR:N	2.75	0.44
13:M:97:VAL:O	13:M:97:VAL:HG12	2.17	0.44
15:O:16:ARG:NH1	15:O:76:ARG:NH1	2.65	0.44
17:Q:5:LEU:N	17:Q:58:ILE:O	2.47	0.44
20:T:87:ALA:O	20:T:88:ALA:HB3	2.18	0.44
21:V:12:ILE:HD13	21:V:21:ARG:CZ	2.47	0.44
1:A:167:G:H2'	1:A:168:G:H8	1.82	0.44
1:A:247:G:OP2	17:Q:99:LYS:HG3	2.18	0.44
1:A:591:U:H2'	1:A:592:G:C8	2.52	0.44
1:A:1258:G:O2'	1:A:1259:C:H5'	2.17	0.44
4:D:35:ARG:HD2	4:D:37:TYR:CE1	2.52	0.44
4:D:99:ARG:NH1	4:D:136:SER:HA	2.32	0.44
5:E:24:PHE:CD1	5:E:24:PHE:N	2.84	0.44
7:G:19:ASP:OD2	7:G:21:LEU:HB3	2.17	0.44
9:I:99:GLY:C	9:I:101:LEU:N	2.73	0.44
10:J:23:GLU:O	10:J:25:ALA:N	2.50	0.44
11:K:4:VAL:O	11:K:5:ALA:HB3	2.18	0.44
15:O:53:ARG:O	15:O:57:MET:HG3	2.17	0.44
1:A:109:A:H2'	1:A:326:G:N2	2.33	0.44
1:A:126:G:H4'	1:A:634:C:O2	2.16	0.44
1:A:370:C:H2'	1:A:371:G:H8	1.82	0.44
1:A:427:U:C4	1:A:428:G:C6	3.05	0.44
1:A:1036:G:O2'	1:A:1037:C:H5'	2.17	0.44
1:A:1102:A:C6	1:A:1103:C:N4	2.85	0.44
1:A:1460:A:H2'	1:A:1461:G:O4'	2.17	0.44
1:A:1494:G:O6	26:A:2800:RPO:HBT	2.17	0.44
2:B:63:LEU:HD23	2:B:63:LEU:C	2.42	0.44
3:C:90:LEU:HD13	3:C:98:VAL:CG1	2.47	0.44
3:C:194:VAL:O	3:C:195:LEU:HD22	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:12:ARG:NH1	4:D:37:TYR:O	2.51	0.44
4:D:148:ALA:HB3	4:D:151:SER:CB	2.45	0.44
5:E:11:ARG:O	5:E:12:THR:O	2.35	0.44
9:I:29:GLY:O	9:I:30:GLN:C	2.61	0.44
9:I:32:PHE:C	9:I:34:GLU:H	2.25	0.44
10:J:1:LYS:CG	10:J:73:ILE:HG23	2.41	0.44
10:J:6:LEU:HB3	10:J:14:LEU:HD22	1.98	0.44
11:K:116:ARG:C	11:K:118:ALA:N	2.74	0.44
16:P:76:GLN:C	16:P:78:GLY:H	2.25	0.44
18:R:23:GLU:CD	18:R:23:GLU:N	2.72	0.44
1:A:159:G:N2	1:A:161:A:H3'	2.28	0.44
1:A:191:G:H1'	20:T:98:SER:HA	2.00	0.44
1:A:1018:C:O5'	1:A:1018:C:H6	2.00	0.44
1:A:1360:A:H8	1:A:1360:A:OP1	2.00	0.44
2:B:101:THR:C	2:B:103:SER:H	2.26	0.44
2:B:213:VAL:HA	2:B:216:ILE:CG1	2.47	0.44
4:D:152:ARG:HG2	4:D:180:MET:CE	2.48	0.44
5:E:85:ILE:HD13	5:E:86:VAL:H	1.82	0.44
6:F:33:TYR:HD2	6:F:75:LEU:HD23	1.81	0.44
7:G:15:LEU:HD22	7:G:15:LEU:N	2.33	0.44
9:I:113:TYR:CE2	10:J:57:SER:O	2.70	0.44
11:K:24:ASP:C	11:K:24:ASP:OD1	2.60	0.44
13:M:9:PRO:O	13:M:10:ARG:HB2	2.17	0.44
21:V:23:ARG:O	21:V:24:LYS:CB	2.65	0.44
1:A:191:G:C4	20:T:98:SER:HB3	2.52	0.44
1:A:810:C:O2'	1:A:811:C:H5'	2.17	0.44
1:A:860:A:H2'	1:A:861:G:O4'	2.18	0.44
1:A:881:G:P	12:L:8:ARG:NH2	2.90	0.44
1:A:1067:A:H4'	1:A:1068:G:OP1	2.18	0.44
1:A:1176:A:H2'	1:A:1177:G:O4'	2.18	0.44
1:A:1354:C:O2'	1:A:1355:G:H5'	2.17	0.44
1:A:1496:C:H2'	1:A:1497:G:O4'	2.18	0.44
1:A:1514:C:H2'	1:A:1515:C:H6	1.81	0.44
2:B:92:LEU:HD23	2:B:92:LEU:H	1.83	0.44
2:B:174:LEU:C	2:B:176:ILE:N	2.76	0.44
7:G:74:VAL:HB	7:G:85:GLN:HB3	2.00	0.44
7:G:76:SER:HA	7:G:84:TYR:O	2.18	0.44
10:J:12:LYS:NZ	10:J:12:LYS:HB3	2.32	0.44
10:J:19:GLN:O	10:J:22:VAL:HG12	2.18	0.44
17:Q:26:PHE:CE1	17:Q:35:ILE:HD11	2.52	0.44
1:A:186:C:H2'	1:A:187:C:H6	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:342:C:H5'	1:A:343:U:OP2	2.18	0.44
1:A:362:G:C8	1:A:362:G:C3'	3.01	0.44
1:A:575:G:H4'	1:A:576:G:C5'	2.47	0.44
1:A:721:G:OP2	18:R:48:GLN:HG2	2.18	0.44
1:A:1315:U:O2'	1:A:1360:A:N3	2.50	0.44
1:A:1405:G:O4'	1:A:1519:A:H4'	2.17	0.44
1:A:1504:G:OP1	1:A:1507:A:H4'	2.17	0.44
2:B:17:ARG:HH12	2:B:185:ASP:CB	2.30	0.44
2:B:49:PHE:O	2:B:50:ARG:C	2.61	0.44
2:B:98:ASN:O	2:B:102:ILE:HG12	2.18	0.44
3:C:78:ARG:NE	3:C:81:GLU:CB	2.75	0.44
3:C:127:PHE:N	3:C:127:PHE:CD1	2.85	0.44
5:E:14:ARG:HH11	5:E:21:ARG:HB2	1.83	0.44
5:E:147:LEU:CD2	8:H:79:VAL:HA	2.46	0.44
6:F:46:ARG:HB2	6:F:60:PHE:HE1	1.83	0.44
9:I:115:LYS:HE3	9:I:121:ALA:HB2	1.99	0.44
10:J:4:ILE:HG22	10:J:96:ILE:HA	2.00	0.44
13:M:9:PRO:HB3	13:M:17:ALA:O	2.18	0.44
16:P:59:TRP:HB3	16:P:64:ALA:CB	2.44	0.44
17:Q:44:HIS:NE2	17:Q:46:PRO:HG3	2.33	0.44
20:T:36:LEU:O	20:T:39:GLU:HB2	2.18	0.44
1:A:36:C:O2'	1:A:37:U:H5'	2.17	0.44
1:A:153:C:C2'	1:A:154:C:H5'	2.48	0.44
1:A:264:U:O2'	17:Q:63:PRO:HB2	2.17	0.44
1:A:767:A:H2'	1:A:768:A:O4'	2.18	0.44
1:A:1069:C:O2'	1:A:1192:C:H1'	2.18	0.44
5:E:85:ILE:HG13	5:E:131:THR:CG2	2.45	0.44
5:E:97:ILE:HG22	5:E:97:ILE:O	2.17	0.44
8:H:116:LYS:CD	8:H:127:LEU:HD12	2.41	0.44
9:I:42:ALA:O	9:I:43:VAL:C	2.61	0.44
11:K:59:ALA:CB	11:K:93:LEU:HD12	2.41	0.44
1:A:255:G:O6	1:A:266:G:O6	2.35	0.43
1:A:344:A:H5''	1:A:345:C:C5	2.49	0.43
1:A:370:C:O2'	1:A:371:G:H5'	2.18	0.43
1:A:386:C:H2'	1:A:387:U:C5'	2.47	0.43
1:A:457:C:H42	1:A:474:G:H1	1.64	0.43
1:A:552:U:O2'	1:A:553:A:H5'	2.18	0.43
1:A:631:G:H2'	1:A:632:A:C8	2.53	0.43
1:A:746:A:C2'	1:A:747:C:H5'	2.48	0.43
1:A:895:G:H2'	1:A:896:C:H6	1.82	0.43
1:A:961:U:C2'	1:A:962:C:H5'	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1014:A:H4'	19:S:13:HIS:ND1	2.33	0.43
1:A:1305:G:H4'	21:V:3:GLY:O	2.16	0.43
2:B:73:ASP:HA	2:B:76:ARG:HG3	1.99	0.43
4:D:3:TYR:CE2	4:D:10:LEU:HD11	2.53	0.43
4:D:37:TYR:HE2	4:D:44:GLN:CD	2.26	0.43
4:D:87:VAL:O	4:D:87:VAL:HG12	2.17	0.43
7:G:119:ILE:HD12	7:G:119:ILE:N	2.32	0.43
8:H:17:THR:HB	8:H:78:GLN:OE1	2.18	0.43
9:I:52:VAL:HG21	9:I:84:LEU:HD21	1.99	0.43
13:M:76:ASN:O	13:M:79:ARG:HB3	2.17	0.43
15:O:13:GLU:HG3	15:O:14:PHE:CD1	2.54	0.43
16:P:51:VAL:O	16:P:53:VAL:N	2.50	0.43
1:A:16:A:C2	1:A:920:U:O2	2.71	0.43
1:A:166:G:H2'	1:A:167:G:C8	2.51	0.43
1:A:251:G:O2'	1:A:252:U:C6	2.71	0.43
1:A:428:G:H5''	4:D:6:PRO:HB3	2.01	0.43
1:A:433:C:O2'	1:A:434:U:H5'	2.18	0.43
1:A:620:C:C6	4:D:134:LEU:HD13	2.52	0.43
1:A:655:A:H2'	1:A:656:C:C6	2.52	0.43
1:A:815:A:H4'	1:A:817:C:C4	2.53	0.43
1:A:1152:A:H2'	1:A:1153:C:O4'	2.18	0.43
1:A:1305:G:O2'	1:A:1332:A:N6	2.50	0.43
1:A:1362:C:H6	1:A:1362:C:H5''	1.83	0.43
2:B:194:ILE:HG22	2:B:195:ILE:H	1.83	0.43
3:C:110:LEU:HD21	3:C:143:SER:O	2.17	0.43
3:C:142:GLU:O	3:C:144:GLY:N	2.47	0.43
3:C:153:SER:HB3	3:C:196:GLY:H	1.82	0.43
4:D:157:ILE:O	4:D:161:LEU:HB2	2.18	0.43
13:M:87:ARG:HG2	13:M:97:VAL:CG1	2.48	0.43
15:O:63:ARG:HG3	15:O:63:ARG:NH1	2.30	0.43
16:P:34:GLU:OE1	16:P:55:ARG:NH1	2.50	0.43
19:S:79:TYR:CZ	19:S:80:ARG:HB2	2.53	0.43
20:T:46:LEU:HB2	20:T:93:ILE:HB	1.99	0.43
1:A:156:G:O2'	1:A:157:G:H5'	2.19	0.43
1:A:437:U:H5'	4:D:154:LEU:HD21	2.00	0.43
1:A:640:A:C2'	1:A:641:U:H5'	2.48	0.43
1:A:1109:C:H6	1:A:1109:C:H5'	1.82	0.43
1:A:1297:C:O2	1:A:1297:C:H2'	2.18	0.43
1:A:1307:U:H2'	1:A:1308:U:C6	2.54	0.43
2:B:134:HIS:O	2:B:137:GLU:N	2.51	0.43
2:B:217:ILE:HG21	2:B:224:VAL:HG21	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:32:ASN:N	6:F:32:ASN:HD22	2.14	0.43
6:F:43:LEU:N	6:F:43:LEU:CD2	2.82	0.43
8:H:110:ALA:HB3	8:H:121:ASP:HB3	2.00	0.43
10:J:20:LYS:HZ1	10:J:88:LEU:H	1.63	0.43
17:Q:85:GLU:O	17:Q:89:ILE:HG13	2.17	0.43
20:T:22:LYS:HE3	20:T:22:LYS:HB2	1.81	0.43
1:A:197:A:N1	1:A:220:G:O2'	2.46	0.43
1:A:457:C:H2'	1:A:458:C:C6	2.47	0.43
1:A:832:C:O2'	1:A:833:U:H5'	2.19	0.43
1:A:1038:C:C6	1:A:1039:C:H5	2.36	0.43
1:A:1179:A:O3'	9:I:102:THR:HG23	2.18	0.43
1:A:1304:G:H2'	1:A:1305:G:H1'	2.00	0.43
1:A:1347:G:C8	9:I:106:ARG:HB3	2.54	0.43
1:A:1447:A:HO2'	1:A:1452:C:P	2.40	0.43
1:A:1457:G:O2'	1:A:1458:G:H5'	2.17	0.43
2:B:49:PHE:HA	2:B:52:ILE:CG1	2.49	0.43
6:F:23:LYS:NZ	6:F:42:GLU:CD	2.77	0.43
7:G:144:ALA:O	7:G:145:GLU:HB3	2.19	0.43
9:I:31:ASP:O	9:I:34:GLU:HB3	2.18	0.43
10:J:79:THR:C	10:J:81:GLU:N	2.76	0.43
10:J:79:THR:C	10:J:81:GLU:H	2.26	0.43
10:J:90:THR:HG23	10:J:91:GLY:N	2.33	0.43
11:K:98:ILE:O	18:R:72:ARG:N	2.51	0.43
13:M:22:TYR:CD2	13:M:69:LEU:HD13	2.53	0.43
13:M:124:ARG:HD2	13:M:125:LYS:N	2.33	0.43
18:R:64:LEU:HD22	18:R:65:PRO:HD2	2.01	0.43
23:Z:40:C:C2'	23:Z:41:C:OP1	2.67	0.43
1:A:189(G):G:H4'	1:A:189(H):G:OP2	2.18	0.43
1:A:190:U:O2'	1:A:191:G:H5'	2.18	0.43
1:A:404:U:C2	1:A:405:U:C5	3.07	0.43
1:A:764:C:H2'	1:A:765:G:O4'	2.19	0.43
1:A:1102:A:H2'	1:A:1103:C:C6	2.54	0.43
2:B:11:PHE:CB	2:B:38:LEU:HD21	2.48	0.43
3:C:12:GLY:O	3:C:13:ILE:HD13	2.18	0.43
4:D:7:VAL:HG21	4:D:114:ARG:NH1	2.33	0.43
4:D:207:SER:O	4:D:208:ARG:C	2.61	0.43
5:E:47:VAL:N	5:E:48:PRO:HD2	2.33	0.43
8:H:103:VAL:HG21	8:H:110:ALA:HB2	2.01	0.43
9:I:31:ASP:O	9:I:32:PHE:C	2.61	0.43
13:M:52:VAL:O	13:M:52:VAL:HG12	2.16	0.43
15:O:55:LEU:O	15:O:59:VAL:HG23	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:407:G:H2'	1:A:408:A:H8	1.84	0.43
1:A:413:G:H2'	1:A:428:G:H22	1.81	0.43
1:A:716:A:N3	11:K:107:ASN:O	2.51	0.43
1:A:789:U:H2'	1:A:791:G:OP2	2.19	0.43
1:A:999:C:H42	1:A:1042:G:H1	1.67	0.43
1:A:1019:C:O2'	1:A:1020:U:H5'	2.19	0.43
1:A:1061:G:H1'	10:J:54:HIS:CE1	2.53	0.43
1:A:1099:G:C6	1:A:1100:C:N3	2.87	0.43
1:A:1230:C:O2'	13:M:125:LYS:HB3	2.19	0.43
1:A:1321:C:C3'	1:A:1322:C:H5''	2.36	0.43
2:B:72:GLN:O	2:B:88:ASN:OD1	2.37	0.43
2:B:99:PHE:O	2:B:100:LYS:C	2.61	0.43
2:B:101:THR:O	2:B:103:SER:N	2.52	0.43
2:B:225:GLU:CD	2:B:225:GLU:H	2.25	0.43
3:C:32:LEU:O	3:C:33:LEU:C	2.60	0.43
3:C:42:LEU:HD13	3:C:67:VAL:CG2	2.49	0.43
4:D:95:LEU:O	4:D:98:SER:HB2	2.19	0.43
7:G:22:VAL:HG13	7:G:42:PHE:CE2	2.54	0.43
8:H:60:ARG:HG3	8:H:60:ARG:NH1	2.30	0.43
10:J:28:SER:HB2	10:J:78:LYS:C	2.44	0.43
16:P:82:GLN:O	16:P:83:GLU:C	2.60	0.43
18:R:10:THR:O	18:R:11:LEU:CB	2.67	0.43
19:S:3:SER:OG	19:S:4:LEU:N	2.52	0.43
1:A:35:G:H2'	1:A:36:C:H6	1.82	0.43
1:A:65:U:C5	1:A:381:C:C4	3.07	0.43
1:A:190:U:C2	20:T:98:SER:HB2	2.53	0.43
1:A:374:A:C6	1:A:375:U:C4	3.06	0.43
1:A:564:C:OP1	12:L:11:ARG:NE	2.51	0.43
1:A:1027:C:H5'	1:A:1027:C:C6	2.48	0.43
1:A:1141:C:HO2'	1:A:1142:G:H5'	1.82	0.43
1:A:1145:C:C4'	1:A:1146:A:H5'	2.48	0.43
1:A:1429:C:H2'	1:A:1430:C:C6	2.52	0.43
2:B:187:ASP:HB3	2:B:190:LEU:HD12	2.01	0.43
4:D:186:ARG:HG3	4:D:187:LEU:H	1.83	0.43
7:G:114:ARG:HB2	7:G:117:VAL:HG23	2.00	0.43
10:J:23:GLU:C	10:J:27:ARG:HH22	2.27	0.43
14:N:5:LEU:C	14:N:7:GLU:N	2.72	0.43
15:O:30:LEU:HD12	15:O:30:LEU:N	2.34	0.43
15:O:52:HIS:O	15:O:55:LEU:HB3	2.18	0.43
1:A:285:G:O2'	1:A:286:G:H5'	2.18	0.43
1:A:416:G:H2'	1:A:417:C:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1168:A:H3'	1:A:1169:A:H8	1.83	0.43
1:A:1281:U:H5''	1:A:1282:C:H5	1.84	0.43
1:A:1372:U:OP1	9:I:71:GLY:N	2.48	0.43
3:C:6:PRO:HG2	3:C:183:TYR:CD1	2.54	0.43
3:C:28:TYR:OH	14:N:53:PRO:HD2	2.19	0.43
3:C:124:GLU:HG2	3:C:189:ARG:O	2.18	0.43
8:H:60:ARG:HH11	8:H:60:ARG:CG	2.21	0.43
12:L:25:GLY:O	12:L:26:ALA:O	2.35	0.43
12:L:81:ILE:HD12	12:L:81:ILE:HA	1.85	0.43
15:O:21:THR:O	15:O:26:VAL:HG11	2.18	0.43
1:A:243:A:H4'	1:A:244:U:H5''	2.01	0.43
1:A:308:C:H2'	1:A:309:G:H8	1.84	0.43
1:A:410:G:OP2	4:D:24:ARG:HD2	2.18	0.43
1:A:1314:C:OP2	19:S:5:LYS:CD	2.67	0.43
1:A:1320:C:N3	19:S:35:ARG:HD3	2.33	0.43
1:A:1345:U:C2	1:A:1377:A:C2	3.07	0.43
1:A:1365:G:C6	1:A:1366:C:C4	3.07	0.43
1:A:1367:C:H5'	10:J:58:ARG:NH2	2.23	0.43
2:B:10:HIS:O	2:B:11:PHE:CG	2.72	0.43
2:B:14:GLU:HB2	2:B:184:THR:HB	2.00	0.43
2:B:186:SER:O	2:B:188:PRO:HD3	2.18	0.43
3:C:86:LEU:O	3:C:89:GLU:HB3	2.19	0.43
4:D:30:CYS:C	4:D:32:MET:N	2.76	0.43
4:D:106:ARG:HB3	4:D:173:LEU:HD11	2.01	0.43
4:D:152:ARG:HG3	4:D:180:MET:SD	2.59	0.43
9:I:32:PHE:CE2	9:I:46:LEU:HD11	2.54	0.43
9:I:78:LEU:HD11	9:I:82:ARG:NE	2.34	0.43
10:J:45:PHE:CE2	14:N:36:PHE:HE2	2.36	0.43
14:N:24:VAL:HG13	14:N:25:ARG:N	2.33	0.43
14:N:39:CYS:O	14:N:43:LEU:HB3	2.19	0.43
19:S:28:ARG:HG3	19:S:28:ARG:HH11	1.83	0.43
19:S:40:VAL:HB	19:S:41:PRO:HD2	2.00	0.43
19:S:48:ILE:N	19:S:48:ILE:CD1	2.77	0.43
20:T:69:ALA:HA	20:T:72:ARG:NH1	2.34	0.43
1:A:388:G:H8	1:A:388:G:OP1	2.02	0.43
1:A:556:C:C2'	1:A:557:G:H5'	2.49	0.43
1:A:1151:A:O2'	1:A:1152:A:H5''	2.19	0.43
1:A:1360:A:H2'	1:A:1361:G:O4'	2.19	0.43
2:B:134:HIS:HA	2:B:137:GLU:CG	2.46	0.43
3:C:63:VAL:HG12	3:C:65:VAL:CG2	2.45	0.43
3:C:78:ARG:O	3:C:78:ARG:CD	2.63	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:112:ALA:HB3	3:C:113:PRO:HD3	2.01	0.43
6:F:44:GLY:O	6:F:59:TYR:HA	2.19	0.43
6:F:62:TRP:CG	6:F:63:TYR:N	2.87	0.43
9:I:4:TYR:CG	9:I:5:GLY:N	2.87	0.43
10:J:74:ASN:O	10:J:76:ASN:ND2	2.52	0.43
13:M:25:GLY:C	13:M:27:ALA:N	2.77	0.43
13:M:78:LYS:C	13:M:78:LYS:HD3	2.44	0.43
13:M:83:ILE:HG13	13:M:85:CYS:H	1.84	0.43
20:T:3:LEU:O	20:T:6:LEU:CD1	2.67	0.43
1:A:411:A:C5	1:A:429:U:C5	3.07	0.42
1:A:1074:G:O3'	2:B:97:THR:HG22	2.18	0.42
1:A:1140:C:H2'	1:A:1141:C:C5'	2.47	0.42
1:A:1457:G:H2'	1:A:1458:G:H8	1.82	0.42
2:B:45:LEU:O	2:B:49:PHE:HD1	2.01	0.42
2:B:86:TYR:CD1	2:B:86:TYR:C	2.97	0.42
3:C:72:PRO:O	3:C:75:VAL:HB	2.19	0.42
4:D:7:VAL:HG11	4:D:20:LEU:HB3	2.00	0.42
5:E:72:ILE:HD12	5:E:138:LEU:HD11	1.99	0.42
10:J:2:ILE:HD13	10:J:2:ILE:HA	1.91	0.42
10:J:10:ASP:OD1	10:J:12:LYS:N	2.45	0.42
18:R:19:TYR:HA	18:R:54:THR:HG23	2.00	0.42
18:R:39:ARG:HH21	18:R:40:ARG:HG3	1.83	0.42
20:T:50:ARG:HE	20:T:93:ILE:CG2	2.25	0.42
1:A:232:G:H1'	1:A:262:A:N1	2.34	0.42
1:A:298:A:H2'	1:A:299:G:O4'	2.19	0.42
2:B:91:TRP:CH2	2:B:170:GLU:OE2	2.72	0.42
2:B:101:THR:C	2:B:103:SER:N	2.77	0.42
2:B:108:ARG:NH2	2:B:112:LEU:HD21	2.33	0.42
3:C:69:VAL:CG1	3:C:70:ALA:N	2.81	0.42
3:C:194:VAL:HG12	3:C:195:LEU:N	2.34	0.42
3:C:206:VAL:CG1	3:C:207:ILE:N	2.80	0.42
5:E:140:THR:HG22	5:E:142:ALA:N	2.34	0.42
8:H:10:LEU:HD12	8:H:85:ARG:CG	2.49	0.42
10:J:32:VAL:HG22	10:J:72:ILE:CG2	2.49	0.42
10:J:70:VAL:HG12	10:J:71:ASP:N	2.33	0.42
13:M:58:TYR:O	13:M:62:THR:CG2	2.67	0.42
15:O:26:VAL:O	15:O:30:LEU:HD13	2.19	0.42
18:R:51:LEU:O	18:R:55:ILE:HG12	2.19	0.42
20:T:66:HIS:O	20:T:67:LYS:CB	2.67	0.42
23:Z:31:A:H2'	23:Z:32:U:C6	2.53	0.42
1:A:31:G:O2'	1:A:48:C:N4	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:104:G:N7	20:T:7:LYS:NZ	2.57	0.42
1:A:176:C:O2'	1:A:177:C:H5'	2.19	0.42
1:A:614:A:C2	1:A:627:G:C2	3.08	0.42
1:A:858:G:H8	1:A:858:G:O5'	2.02	0.42
1:A:1008:C:O2'	1:A:1009:G:H5'	2.19	0.42
1:A:1069:C:H2'	1:A:1070:U:H5''	2.02	0.42
1:A:1422:G:O2'	1:A:1423:G:H5'	2.18	0.42
2:B:45:LEU:CD2	2:B:49:PHE:HE1	2.30	0.42
2:B:189:ASP:O	8:H:68:ARG:NH2	2.52	0.42
3:C:28:TYR:HE2	10:J:9:PHE:HE2	1.66	0.42
4:D:62:LYS:O	4:D:66:ILE:HG13	2.19	0.42
6:F:39:LYS:NZ	6:F:64:GLN:HE21	2.17	0.42
6:F:67:MET:HB2	6:F:68:PRO:HD2	2.02	0.42
7:G:14:ASP:OD1	7:G:15:LEU:N	2.51	0.42
7:G:40:ARG:O	7:G:41:ILE:C	2.62	0.42
8:H:11:THR:HA	8:H:14:ARG:HH12	1.84	0.42
8:H:54:ASP:O	8:H:54:ASP:CG	2.61	0.42
16:P:4:ILE:HG23	16:P:36:ILE:HD11	2.01	0.42
16:P:4:ILE:HA	16:P:20:VAL:O	2.19	0.42
1:A:189(I):G:C2'	1:A:189(J):G:H5'	2.48	0.42
1:A:314:C:O2'	1:A:315:A:H5'	2.19	0.42
1:A:370:C:H2'	1:A:371:G:C8	2.53	0.42
1:A:737:A:H2'	1:A:738:C:C6	2.55	0.42
1:A:858:G:N1	1:A:869:G:C8	2.87	0.42
1:A:1355:G:O2'	1:A:1356:G:H5'	2.19	0.42
2:B:46:GLU:CD	2:B:50:ARG:HH12	2.28	0.42
2:B:176:ILE:O	2:B:177:PRO:C	2.62	0.42
2:B:181:LEU:C	2:B:181:LEU:CD2	2.93	0.42
3:C:69:VAL:O	3:C:105:VAL:HG23	2.19	0.42
3:C:100:LEU:C	3:C:100:LEU:CD2	2.92	0.42
3:C:130:ARG:HB2	3:C:130:ARG:CZ	2.48	0.42
4:D:93:LEU:O	4:D:94:GLY:C	2.61	0.42
8:H:10:LEU:HD12	8:H:85:ARG:HG2	2.01	0.42
14:N:21:THR:CB	14:N:32:VAL:HG21	2.50	0.42
21:V:23:ARG:O	21:V:24:LYS:CG	2.67	0.42
1:A:28:G:O2'	1:A:296:U:OP1	2.37	0.42
1:A:159:G:H1	1:A:163:C:N4	2.17	0.42
1:A:189(A):C:H2'	1:A:189(B):C:H6	1.85	0.42
1:A:427:U:OP1	4:D:12:ARG:NH2	2.51	0.42
1:A:458:C:H2'	1:A:460:G:C8	2.53	0.42
1:A:725:G:O2'	1:A:726:C:H5'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:750:G:O2'	1:A:751:U:H5'	2.19	0.42
1:A:772:U:O2'	1:A:773:G:H5'	2.19	0.42
1:A:889:A:H8	1:A:889:A:OP1	2.03	0.42
1:A:949:A:C2	1:A:1233:G:N3	2.88	0.42
1:A:1055:A:H2'	1:A:1055:A:N3	2.34	0.42
3:C:65:VAL:O	3:C:65:VAL:HG12	2.19	0.42
3:C:133:ILE:HD11	3:C:152:VAL:HG23	2.02	0.42
4:D:23:GLU:OE1	4:D:23:GLU:HA	2.18	0.42
6:F:94:GLN:HE21	18:R:17:ARG:NE	2.15	0.42
8:H:16:ALA:O	8:H:19:VAL:HG22	2.19	0.42
9:I:10:LYS:O	9:I:11:GLU:HB3	2.20	0.42
9:I:54:ALA:O	9:I:55:LEU:HB3	2.18	0.42
10:J:1:LYS:CA	10:J:73:ILE:HA	2.43	0.42
10:J:27:ARG:C	10:J:82:GLN:HE22	2.27	0.42
12:L:43:LYS:CB	12:L:44:PRO:CD	2.70	0.42
15:O:73:ASP:C	15:O:75:GLU:N	2.77	0.42
17:Q:67:ARG:HG3	17:Q:67:ARG:NH1	2.33	0.42
18:R:12:GLY:O	18:R:13:GLU:C	2.61	0.42
19:S:43:MET:HA	19:S:46:HIS:CD2	2.41	0.42
19:S:71:GLY:C	19:S:73:PHE:N	2.77	0.42
21:V:1:GLY:O	21:V:3:GLY:N	2.52	0.42
1:A:695:A:H2'	1:A:696:A:C8	2.54	0.42
1:A:908:A:O2'	1:A:909:A:H5'	2.20	0.42
1:A:911:U:H2'	1:A:912:C:C6	2.54	0.42
2:B:13:HIS:HE2	2:B:200:ASP:CG	2.27	0.42
2:B:68:LYS:HE3	2:B:68:LYS:HB2	1.86	0.42
2:B:172:ARG:NH2	8:H:68:ARG:NH2	2.68	0.42
3:C:73:GLY:C	3:C:75:VAL:N	2.76	0.42
3:C:106:GLN:O	3:C:107:ASN:HB3	2.20	0.42
4:D:37:TYR:HE2	4:D:44:GLN:HG2	1.84	0.42
4:D:139:VAL:HG11	4:D:145:ILE:HD11	2.01	0.42
5:E:53:LYS:O	5:E:57:TYR:CD2	2.73	0.42
5:E:69:ASN:O	5:E:71:THR:N	2.53	0.42
6:F:12:PRO:HG3	6:F:57:GLN:O	2.18	0.42
9:I:45:ALA:HB1	9:I:76:ILE:HG21	2.00	0.42
10:J:19:GLN:O	10:J:19:GLN:OE1	2.37	0.42
10:J:44:ARG:HG2	10:J:44:ARG:NH1	2.31	0.42
10:J:52:PHE:O	10:J:53:LYS:C	2.62	0.42
12:L:45:ASN:OD1	12:L:88:ASP:OD2	2.38	0.42
13:M:22:TYR:HE2	13:M:69:LEU:HB3	1.85	0.42
14:N:33:TYR:N	14:N:38:LEU:O	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:4:LYS:O	18:R:5:ALA:HB3	2.20	0.42
19:S:27:LYS:CD	19:S:28:ARG:H	2.33	0.42
19:S:61:ILE:C	19:S:61:ILE:CD1	2.91	0.42
20:T:43:GLU:HG3	20:T:93:ILE:HG12	2.00	0.42
1:A:7:G:H5''	1:A:298:A:O4'	2.20	0.42
1:A:460:G:H2'	1:A:461:A:H5''	2.01	0.42
1:A:499:A:H4'	1:A:500:G:O5'	2.19	0.42
1:A:598:U:H4'	8:H:94:TYR:CD2	2.55	0.42
1:A:642:A:C5	8:H:115:SER:HA	2.54	0.42
1:A:644:G:C5	1:A:645:C:C5	3.07	0.42
1:A:1041:A:H2'	1:A:1042:G:C8	2.54	0.42
1:A:1260:C:H4'	1:A:1283:G:O2'	2.19	0.42
1:A:1297:C:O2	1:A:1297:C:C2'	2.66	0.42
1:A:1491:G:C5	26:A:2800:RPO:H2	2.55	0.42
2:B:207:LEU:C	2:B:207:LEU:CD2	2.93	0.42
3:C:45:GLU:C	3:C:47:TYR:H	2.28	0.42
3:C:163:ARG:NH2	3:C:165:GLU:OE1	2.51	0.42
7:G:117:VAL:O	7:G:118:ARG:C	2.63	0.42
9:I:47:GLU:N	9:I:48:PRO:CD	2.83	0.42
9:I:115:LYS:HE2	9:I:119:ARG:O	2.20	0.42
10:J:2:ILE:O	10:J:71:ASP:HA	2.20	0.42
10:J:30:ALA:O	10:J:32:VAL:N	2.52	0.42
10:J:77:ARG:C	10:J:79:THR:N	2.78	0.42
13:M:18:LEU:HD11	13:M:33:LEU:HD21	2.01	0.42
13:M:87:ARG:HG2	13:M:97:VAL:HG12	2.01	0.42
1:A:112:G:O2'	1:A:113:G:H5'	2.19	0.42
1:A:189(B):C:H42	1:A:189(I):G:H1	1.65	0.42
1:A:300:A:H8	1:A:300:A:O5'	2.03	0.42
1:A:429:U:H4'	1:A:430:A:O5'	2.20	0.42
1:A:518:C:H2'	1:A:530:G:N3	2.34	0.42
1:A:781:A:OP1	1:A:1523:G:H5'	2.20	0.42
1:A:975:A:C5'	1:A:976:G:O5'	2.66	0.42
1:A:975:A:N6	1:A:1367:C:O4'	2.52	0.42
1:A:1082:G:O2'	1:A:1083:U:H5'	2.19	0.42
1:A:1152:A:O2'	1:A:1153:C:H5'	2.19	0.42
1:A:1246:C:O2'	1:A:1247:U:H5'	2.20	0.42
1:A:1259:C:O5'	1:A:1259:C:H6	2.03	0.42
1:A:1379:G:N7	7:G:1:ALA:HB3	2.35	0.42
1:A:1487:G:O2'	1:A:1488:G:H5'	2.19	0.42
2:B:223:VAL:HG23	2:B:223:VAL:O	2.19	0.42
4:D:88:THR:CG2	4:D:88:THR:O	2.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:32:ASP:OD2	5:E:36:ARG:HB2	2.19	0.42
7:G:4:ARG:HB3	7:G:5:ARG:H	1.67	0.42
8:H:29:SER:OG	8:H:32:LYS:HB2	2.20	0.42
12:L:6:LEU:HB3	17:Q:31:TYR:CE2	2.55	0.42
16:P:3:LYS:O	16:P:21:VAL:HA	2.19	0.42
16:P:43:LYS:HA	16:P:48:TRP:HB3	2.00	0.42
17:Q:26:PHE:CD1	17:Q:26:PHE:C	2.97	0.42
19:S:44:VAL:CA	19:S:61:ILE:HD12	2.47	0.42
19:S:49:ALA:HA	19:S:57:VAL:O	2.20	0.42
23:Z:41:C:OP1	23:Z:41:C:C6	2.72	0.42
1:A:136:C:O4'	16:P:1:MET:HG2	2.20	0.42
1:A:242:C:C2'	1:A:243:A:H5'	2.49	0.42
1:A:262:A:C5'	20:T:67:LYS:HG2	2.48	0.42
1:A:1103:C:H5''	2:B:92:LEU:HD13	2.02	0.42
1:A:1272:G:O2'	1:A:1273:G:H5'	2.20	0.42
1:A:1390:U:H2'	1:A:1391:U:H6	1.83	0.42
1:A:1476:G:C2'	1:A:1477:C:H5'	2.50	0.42
2:B:41:THR:HG23	2:B:196:PRO:HG2	2.02	0.42
2:B:68:LYS:NZ	2:B:160:ASP:HB2	2.35	0.42
4:D:59:GLU:OE1	4:D:62:LYS:HD2	2.20	0.42
4:D:161:LEU:HD13	4:D:180:MET:SD	2.60	0.42
5:E:101:VAL:HB	5:E:102:PRO:CD	2.42	0.42
10:J:6:LEU:HD21	10:J:94:ILE:HG12	1.99	0.42
14:N:28:ARG:HB3	14:N:39:CYS:HB3	2.01	0.42
1:A:260:G:H2'	1:A:261:U:C6	2.55	0.42
1:A:439:A:H2'	1:A:441:A:H5'	2.02	0.42
1:A:1056:U:C5'	3:C:162:ALA:HB2	2.49	0.42
1:A:1229:A:H2'	1:A:1230:C:C6	2.55	0.42
1:A:1277:C:H3'	1:A:1277:C:C6	2.54	0.42
1:A:1442(A):G:C4'	1:A:1442(B):A:O5'	2.67	0.42
2:B:74:ILE:HG13	2:B:202:ILE:HG23	2.02	0.42
2:B:125:PRO:C	2:B:127:LYS:N	2.78	0.42
3:C:69:VAL:O	3:C:104:GLU:HA	2.19	0.42
3:C:142:GLU:C	3:C:144:GLY:H	2.26	0.42
5:E:11:ARG:HD3	5:E:22:PHE:HB3	2.02	0.42
7:G:140:VAL:O	7:G:143:MET:HB3	2.19	0.42
7:G:154:ARG:HA	7:G:154:ARG:HD3	1.71	0.42
8:H:36:LEU:O	8:H:37:ARG:C	2.62	0.42
9:I:32:PHE:CE1	9:I:36:PHE:HD2	2.38	0.42
9:I:54:ALA:C	9:I:56:GLY:H	2.28	0.42
10:J:23:GLU:O	10:J:27:ARG:NH1	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:53:LYS:HG3	10:J:54:HIS:N	2.35	0.42
11:K:49:TYR:O	11:K:50:ALA:C	2.63	0.42
14:N:44:ARG:NH1	14:N:44:ARG:CG	2.83	0.42
16:P:74:LEU:HG	16:P:79:VAL:CG2	2.27	0.42
18:R:71:VAL:O	18:R:72:ARG:CB	2.59	0.42
1:A:45:U:H2'	1:A:46:G:C8	2.55	0.41
1:A:188:C:O2'	1:A:189:G:H5'	2.20	0.41
1:A:255:G:H1'	17:Q:15:GLN:HE22	1.81	0.41
1:A:373:A:C2	1:A:482:A:C6	3.08	0.41
1:A:824:C:H4'	8:H:1:MET:N	2.35	0.41
1:A:983:A:H3'	1:A:983:A:N3	2.35	0.41
1:A:1149:C:H2'	1:A:1150:U:C6	2.55	0.41
1:A:1179:A:H2'	1:A:1180:A:O4'	2.20	0.41
1:A:1202:G:N1	14:N:41:ILE:HG21	2.35	0.41
1:A:1410:G:H2'	1:A:1411:C:C6	2.55	0.41
4:D:120:VAL:O	4:D:133:ASP:HA	2.20	0.41
11:K:59:ALA:HB1	11:K:93:LEU:CD1	2.44	0.41
11:K:101:ASP:O	11:K:102:THR:C	2.61	0.41
16:P:67:THR:HB	16:P:70:ALA:CB	2.50	0.41
17:Q:79:GLY:O	17:Q:81:MET:N	2.53	0.41
18:R:39:ARG:CZ	18:R:40:ARG:HG3	2.50	0.41
20:T:36:LEU:HB2	20:T:45:ALA:HB2	2.01	0.41
1:A:8:A:H5''	5:E:97:ILE:HG23	2.01	0.41
1:A:40:C:H2'	1:A:41:G:C8	2.55	0.41
1:A:91:C:H2'	1:A:92:C:C6	2.55	0.41
1:A:551:U:H2'	1:A:552:U:C6	2.54	0.41
1:A:612:C:O5'	1:A:612:C:H6	2.03	0.41
1:A:750:G:O2'	15:O:20:ASP:OD1	2.39	0.41
1:A:961:U:H2'	1:A:962:C:H5'	2.02	0.41
1:A:986:A:O2'	19:S:54:LYS:HA	2.20	0.41
1:A:987:G:H1	1:A:1218:C:H42	1.66	0.41
1:A:1101:A:H4'	1:A:1102:A:O5'	2.21	0.41
1:A:1129:C:H4'	1:A:1130:A:C8	2.53	0.41
1:A:1180:A:P	9:I:102:THR:HG23	2.60	0.41
3:C:154:GLY:HA3	3:C:163:ARG:O	2.20	0.41
4:D:208:ARG:HH11	4:D:208:ARG:CB	2.26	0.41
5:E:32:ASP:OD1	5:E:34:GLN:N	2.38	0.41
5:E:143:ASP:O	5:E:144:VAL:C	2.62	0.41
9:I:96:LYS:O	9:I:98:LEU:N	2.53	0.41
10:J:47:VAL:O	10:J:58:ARG:CA	2.64	0.41
10:J:74:ASN:C	10:J:76:ASN:N	2.76	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:23:CYS:N	14:N:28:ARG:O	2.52	0.41
18:R:2:SER:H	18:R:4:LYS:NZ	2.17	0.41
20:T:61:LYS:HD2	20:T:61:LYS:HA	1.95	0.41
1:A:437:U:H2'	1:A:438:G:C5'	2.50	0.41
1:A:697:U:C2'	1:A:698:G:H5'	2.50	0.41
1:A:1182:G:O2'	1:A:1183:A:P	2.79	0.41
1:A:1229:A:C2	1:A:1230:C:C4	3.08	0.41
2:B:69:LYS:C	2:B:71:ALA:H	2.27	0.41
2:B:96:LEU:O	2:B:99:PHE:HB2	2.19	0.41
3:C:31:LEU:O	3:C:35:ASP:CB	2.59	0.41
3:C:127:PHE:N	3:C:127:PHE:HD1	2.18	0.41
3:C:128:ALA:H	3:C:131:ARG:NH2	2.19	0.41
3:C:153:SER:CB	3:C:196:GLY:H	2.33	0.41
6:F:63:TYR:HB3	6:F:64:GLN:H	1.71	0.41
8:H:97:VAL:HA	8:H:100:ILE:HG13	2.01	0.41
13:M:48:THR:HG22	13:M:49:GLU:N	2.35	0.41
16:P:28:ARG:HH11	16:P:28:ARG:CG	2.31	0.41
19:S:36:ARG:HH11	19:S:36:ARG:HG2	1.84	0.41
23:Z:41:C:O2'	23:Z:42:C:H4'	2.21	0.41
1:A:627:G:H2'	1:A:628:G:H8	1.86	0.41
1:A:653:A:OP1	8:H:56:LYS:NZ	2.44	0.41
1:A:674:G:OP1	6:F:87:ARG:NH2	2.51	0.41
1:A:1005:A:C5	1:A:1006:C:H1'	2.56	0.41
1:A:1122:U:O2'	1:A:1123:A:H5'	2.20	0.41
1:A:1223:C:H3'	1:A:1224:G:H5''	2.03	0.41
1:A:1499:A:H2'	1:A:1500:A:H8	1.85	0.41
2:B:51:PHE:O	2:B:55:LEU:HD23	2.20	0.41
2:B:71:ALA:HB1	2:B:205:ILE:HG21	2.02	0.41
3:C:189:ARG:HH11	3:C:189:ARG:CB	2.31	0.41
7:G:125:ASP:OD1	7:G:130:LYS:HE2	2.20	0.41
13:M:66:GLU:O	13:M:67:GLY:C	2.64	0.41
21:V:9:ARG:HB2	21:V:9:ARG:NH1	2.36	0.41
1:A:162:A:O5'	1:A:162:A:H8	2.03	0.41
1:A:177:C:O2'	1:A:178:C:H5'	2.21	0.41
1:A:194:C:OP1	20:T:54:SER:OG	2.37	0.41
1:A:226:G:O2'	1:A:227:G:H5'	2.19	0.41
1:A:267:C:H2'	1:A:268:C:H6	1.85	0.41
1:A:322:C:H2'	1:A:323:U:C6	2.55	0.41
1:A:392:G:C2	1:A:393:A:C4	3.08	0.41
1:A:485:G:H2'	1:A:486:U:OP2	2.20	0.41
1:A:669:U:O2'	1:A:670:G:H5'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:794:A:H2'	1:A:795:C:C6	2.55	0.41
1:A:949:A:H1'	1:A:1364:U:H3	1.85	0.41
1:A:951:G:OP2	13:M:101:ARG:NH2	2.50	0.41
1:A:1019:C:H2'	1:A:1020:U:C5'	2.49	0.41
1:A:1027:C:H2'	1:A:1028:C:C6	2.55	0.41
1:A:1071:C:H42	1:A:1104:G:H1	1.69	0.41
1:A:1103:C:H2'	1:A:1104:G:O4'	2.19	0.41
1:A:1178:G:P	9:I:92:ARG:HH22	2.44	0.41
1:A:1279:A:H5'	1:A:1280:A:OP1	2.20	0.41
1:A:1365:G:C5	1:A:1366:C:C5	3.08	0.41
2:B:13:HIS:CD2	2:B:199:ASP:OD1	2.73	0.41
3:C:28:TYR:HE2	10:J:9:PHE:CE2	2.38	0.41
3:C:172:VAL:N	3:C:173:PRO:CD	2.84	0.41
3:C:187:LEU:O	3:C:188:ALA:CB	2.68	0.41
4:D:3:TYR:CD2	4:D:114:ARG:NH2	2.88	0.41
4:D:37:TYR:HD1	4:D:37:TYR:N	1.98	0.41
5:E:7:ILE:HD11	5:E:29:VAL:HG22	2.02	0.41
6:F:47:ARG:H	6:F:47:ARG:NE	2.16	0.41
10:J:7:ARG:HG2	10:J:7:ARG:HH11	1.85	0.41
10:J:88:LEU:H	10:J:89:PRO:HD3	1.85	0.41
11:K:74:VAL:HG11	11:K:81:ARG:HD3	2.03	0.41
11:K:112:LYS:O	11:K:113:LYS:C	2.62	0.41
13:M:62:THR:HG23	13:M:63:TRP:CD2	2.55	0.41
14:N:40:ARG:HG3	14:N:41:ILE:N	2.35	0.41
17:Q:52:LEU:C	17:Q:54:ASP:H	2.28	0.41
17:Q:62:ARG:HG2	17:Q:63:PRO:CD	2.50	0.41
18:R:21:ASN:O	18:R:21:ASN:ND2	2.53	0.41
18:R:56:LYS:O	18:R:60:ILE:HG12	2.20	0.41
21:V:1:GLY:C	21:V:3:GLY:H	2.27	0.41
1:A:452:A:O3'	16:P:72:ARG:HD2	2.20	0.41
1:A:531:U:H4'	1:A:532:A:O5'	2.19	0.41
1:A:784:C:H2'	1:A:785:G:O5'	2.20	0.41
1:A:924:C:H5'	1:A:1399:C:OP2	2.21	0.41
1:A:1182:G:O2'	1:A:1183:A:OP2	2.30	0.41
1:A:1281:U:H5''	1:A:1282:C:C5	2.56	0.41
3:C:130:ARG:NH1	3:C:130:ARG:CB	2.75	0.41
4:D:48:ARG:O	4:D:49:ARG:C	2.64	0.41
5:E:14:ARG:NH1	5:E:21:ARG:HB2	2.36	0.41
9:I:8:ARG:HG3	9:I:13:VAL:HG13	2.01	0.41
11:K:100:ASP:OD1	11:K:100:ASP:C	2.63	0.41
14:N:11:ARG:O	14:N:13:PRO:HD3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:100:ARG:HB3	17:Q:101:GLY:H	1.51	0.41
18:R:28:PHE:C	18:R:36:LEU:HD12	2.46	0.41
19:S:27:LYS:CG	19:S:28:ARG:N	2.82	0.41
21:V:14:ARG:NH1	21:V:14:ARG:HG2	2.35	0.41
23:Z:40:C:O5'	23:Z:40:C:H6	2.02	0.41
1:A:1001(A):G:H3'	1:A:1002:G:C8	2.52	0.41
1:A:1202:G:C6	14:N:41:ILE:HG21	2.56	0.41
2:B:6:GLU:OE1	2:B:9:VAL:CG2	2.69	0.41
2:B:21:LYS:HD2	2:B:187:ASP:CG	2.46	0.41
4:D:77:LEU:HB3	4:D:92:PHE:HE1	1.84	0.41
4:D:150:LYS:H	4:D:150:LYS:CD	2.24	0.41
6:F:82:ARG:HB2	6:F:85:VAL:HG23	2.03	0.41
6:F:97:PHE:HB2	18:R:17:ARG:HH11	1.86	0.41
7:G:24:ALA:HA	7:G:27:ASN:HD22	1.84	0.41
8:H:68:ARG:HG2	8:H:68:ARG:HH11	1.84	0.41
10:J:40:THR:HG23	10:J:65:THR:O	2.21	0.41
11:K:77:THR:CG2	11:K:81:ARG:HH21	2.19	0.41
11:K:100:ASP:OD2	18:R:73:LYS:CE	2.68	0.41
13:M:35:LYS:NZ	13:M:35:LYS:CB	2.82	0.41
14:N:13:PRO:C	14:N:15:PHE:H	2.28	0.41
14:N:33:TYR:O	14:N:34:ARG:C	2.63	0.41
15:O:73:ASP:C	15:O:75:GLU:H	2.28	0.41
17:Q:5:LEU:HB3	17:Q:22:VAL:HG11	2.02	0.41
19:S:28:ARG:HG3	19:S:28:ARG:NH1	2.35	0.41
1:A:222:U:H2'	1:A:223:U:C6	2.56	0.41
1:A:230:G:H2'	1:A:231:G:O4'	2.21	0.41
1:A:791:G:C6	1:A:792:A:N7	2.88	0.41
1:A:1058:G:OP1	3:C:198:LYS:HE3	2.21	0.41
1:A:1217:C:H2'	1:A:1218:C:O4'	2.20	0.41
2:B:172:ARG:NH2	8:H:74:PRO:HB3	2.29	0.41
3:C:90:LEU:CD1	3:C:98:VAL:HG22	2.51	0.41
3:C:111:SER:OG	3:C:114:LEU:HG	2.20	0.41
3:C:205:GLU:O	3:C:206:VAL:O	2.37	0.41
4:D:86:GLY:O	4:D:87:VAL:C	2.64	0.41
5:E:27:LEU:HD22	5:E:39:LEU:HD21	2.02	0.41
14:N:25:ARG:HH21	14:N:46:LEU:HD21	1.86	0.41
14:N:36:PHE:C	14:N:38:LEU:N	2.78	0.41
14:N:41:ILE:O	14:N:45:GLU:HG3	2.21	0.41
15:O:58:MET:O	15:O:59:VAL:C	2.64	0.41
1:A:39:G:H2'	1:A:40:C:H6	1.85	0.41
1:A:41:G:H2'	1:A:42:G:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:163:C:H2'	1:A:164:U:H6	1.85	0.41
1:A:240:C:H2'	1:A:241:C:C6	2.56	0.41
1:A:431:A:C2'	1:A:432:A:H5'	2.51	0.41
1:A:496:A:N3	1:A:496:A:H2'	2.36	0.41
1:A:685:G:C2	1:A:686:U:C4	3.09	0.41
1:A:757:U:H5''	1:A:822:C:O2	2.21	0.41
1:A:1307:U:H5'	13:M:108:THR:HG21	2.01	0.41
1:A:1361:G:H2'	1:A:1362:C:O4'	2.21	0.41
1:A:1388:C:H2'	1:A:1389:C:C6	2.56	0.41
2:B:67:THR:CG2	2:B:90:ARG:NH1	2.84	0.41
3:C:12:GLY:HA3	14:N:56:ARG:NH2	2.36	0.41
3:C:133:ILE:HG21	3:C:167:ALA:HB3	2.02	0.41
4:D:69:ILE:HG22	4:D:70:SER:O	2.20	0.41
8:H:84:ARG:HH21	8:H:86:ILE:CD1	2.34	0.41
8:H:112:LEU:HD12	8:H:112:LEU:C	2.46	0.41
9:I:29:GLY:O	9:I:30:GLN:O	2.38	0.41
9:I:85:VAL:CG2	9:I:92:ARG:HB3	2.51	0.41
11:K:28:ASN:HA	11:K:29:PRO:HD3	1.82	0.41
13:M:76:ASN:O	13:M:77:ILE:C	2.64	0.41
14:N:36:PHE:C	14:N:38:LEU:H	2.29	0.41
17:Q:103:LYS:HB3	17:Q:103:LYS:HZ2	1.83	0.41
18:R:32:THR:HG22	18:R:33:GLY:N	2.36	0.41
19:S:79:TYR:OH	19:S:80:ARG:HD3	2.21	0.41
20:T:8:ARG:O	20:T:9:HIS:C	2.63	0.41
1:A:160:A:H1'	1:A:344:A:C5	2.56	0.41
1:A:738:C:P	6:F:92:LYS:HZ2	2.44	0.41
1:A:918:A:H2'	1:A:919:A:O4'	2.21	0.41
1:A:1201:A:H4'	1:A:1202:G:H5''	2.01	0.41
1:A:1305:G:H5''	21:V:3:GLY:CA	2.44	0.41
2:B:38:LEU:HA	2:B:38:LEU:HD23	1.91	0.41
6:F:40:VAL:HG22	6:F:41:GLU:H	1.86	0.41
8:H:29:SER:O	8:H:30:ARG:C	2.64	0.41
8:H:30:ARG:HG2	8:H:30:ARG:HH11	1.85	0.41
9:I:83:ALA:C	9:I:85:VAL:N	2.79	0.41
14:N:17:VAL:HG23	14:N:18:ARG:H	1.86	0.41
18:R:73:LYS:HD3	18:R:73:LYS:OXT	2.21	0.41
1:A:15:G:H21	5:E:14:ARG:HA	1.85	0.40
1:A:273:A:H1'	17:Q:15:GLN:OE1	2.21	0.40
1:A:413:G:C2'	1:A:428:G:N2	2.85	0.40
1:A:471:G:H21	16:P:82:GLN:HE21	1.68	0.40
1:A:959:A:O3'	1:A:960:U:H4'	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1469:G:O2'	1:A:1470:G:H5'	2.22	0.40
2:B:7:ALA:HA	2:B:11:PHE:CD2	2.56	0.40
2:B:105:ARG:NE	2:B:105:ARG:HA	2.36	0.40
2:B:122:GLU:CD	2:B:122:GLU:N	2.80	0.40
3:C:41:LEU:HD23	3:C:41:LEU:HA	1.90	0.40
5:E:11:ARG:HG3	5:E:11:ARG:NH1	2.36	0.40
5:E:32:ASP:O	5:E:33:ARG:HB2	2.20	0.40
6:F:62:TRP:CG	6:F:63:TYR:H	2.39	0.40
7:G:49:ILE:O	7:G:53:THR:HB	2.21	0.40
7:G:68:VAL:O	7:G:68:VAL:HG12	2.21	0.40
9:I:43:VAL:CG1	9:I:50:ARG:HH12	2.18	0.40
9:I:92:ARG:HB2	9:I:101:LEU:HD11	2.03	0.40
11:K:7:GLY:C	11:K:70:VAL:HG23	2.47	0.40
12:L:31:GLY:HA3	12:L:55:ARG:O	2.21	0.40
13:M:120:LYS:N	13:M:120:LYS:HD2	2.35	0.40
15:O:27:GLN:O	15:O:31:LEU:HB2	2.20	0.40
16:P:43:LYS:HD3	16:P:48:TRP:CE2	2.56	0.40
18:R:23:GLU:O	18:R:26:LYS:HE2	2.21	0.40
1:A:274:A:O2'	1:A:275:G:C8	2.74	0.40
1:A:334:C:H2'	1:A:335:C:H6	1.85	0.40
1:A:413:G:C2'	1:A:428:G:H22	2.34	0.40
1:A:537:G:H2'	1:A:538:G:H8	1.86	0.40
1:A:624:C:H2'	1:A:625:G:C8	2.57	0.40
1:A:882:C:O2'	1:A:883:C:H5'	2.21	0.40
1:A:1202:G:C2	14:N:41:ILE:HG21	2.56	0.40
1:A:1442:G:H2'	1:A:1442(B):A:C8	2.56	0.40
2:B:126:LYS:HD2	2:B:126:LYS:H	1.85	0.40
3:C:106:GLN:O	3:C:107:ASN:CB	2.68	0.40
3:C:174:LEU:HD21	3:C:200:TYR:HE2	1.84	0.40
5:E:15:MET:HG3	5:E:16:GLN:H	1.85	0.40
6:F:68:PRO:HB3	6:F:70:ASP:OD1	2.21	0.40
7:G:36:ASN:O	7:G:37:LEU:C	2.63	0.40
9:I:2:GLN:C	9:I:3:TYR:CG	2.99	0.40
9:I:117:LYS:CG	9:I:120:ARG:HB3	2.51	0.40
11:K:52:GLN:O	11:K:56:LEU:HG	2.22	0.40
13:M:121:LYS:O	13:M:122:ALA:CB	2.68	0.40
14:N:28:ARG:HG2	14:N:28:ARG:NH1	2.33	0.40
17:Q:96:SER:HA	17:Q:101:GLY:C	2.46	0.40
1:A:240:C:H2'	1:A:241:C:H6	1.86	0.40
1:A:1048:G:N1	1:A:1210:C:N4	2.68	0.40
1:A:1277:C:C6	1:A:1277:C:C3'	3.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:87:VAL:HG11	2:B:91:TRP:CD1	2.55	0.40
4:D:69:ILE:CG2	4:D:73:GLN:HB2	2.51	0.40
5:E:98:ALA:HB1	5:E:102:PRO:HB2	2.03	0.40
10:J:23:GLU:O	10:J:27:ARG:NH2	2.54	0.40
10:J:40:THR:HG23	10:J:65:THR:C	2.46	0.40
11:K:38:ILE:CD1	11:K:53:LEU:HB3	2.43	0.40
11:K:59:ALA:O	11:K:62:ALA:HB3	2.20	0.40
11:K:99:VAL:HA	18:R:72:ARG:H	1.86	0.40
12:L:113:ARG:O	12:L:115:LYS:O	2.39	0.40
19:S:4:LEU:O	19:S:5:LYS:HE3	2.22	0.40
19:S:36:ARG:HH11	19:S:36:ARG:CG	2.34	0.40
20:T:49:MET:HE3	20:T:81:VAL:HG11	2.04	0.40
20:T:87:ALA:C	20:T:89:GLY:H	2.30	0.40
1:A:407:G:H2'	1:A:408:A:C8	2.56	0.40
1:A:953:G:C5'	1:A:965:A:H61	2.30	0.40
1:A:993:G:C4'	1:A:994:A:OP2	2.65	0.40
1:A:1147:C:O2'	9:I:15:ARG:HG3	2.21	0.40
2:B:95:MET:O	2:B:99:PHE:HA	2.22	0.40
2:B:198:ASN:O	2:B:199:ASP:C	2.64	0.40
3:C:12:GLY:CA	14:N:56:ARG:CZ	2.98	0.40
4:D:87:VAL:O	4:D:91:VAL:HG23	2.22	0.40
5:E:2:PHE:HD1	5:E:2:PHE:HA	1.76	0.40
5:E:74:HIS:C	5:E:74:HIS:HD1	2.29	0.40
5:E:103:ARG:O	5:E:104:ALA:C	2.63	0.40
9:I:78:LEU:HD11	9:I:82:ARG:CZ	2.52	0.40
10:J:3:ARG:HH11	10:J:97:LYS:HD3	1.86	0.40
12:L:82:ARG:HB3	12:L:97:VAL:CG2	2.52	0.40
17:Q:16:LYS:HA	17:Q:45:ASP:O	2.21	0.40
1:A:18:C:H6	1:A:18:C:O5'	2.04	0.40
1:A:564:C:C5	17:Q:30:LEU:HD11	2.57	0.40
1:A:792:A:H4'	1:A:793:U:O5'	2.21	0.40
1:A:1126:U:H6	1:A:1280:A:C5	2.39	0.40
1:A:1201:A:O2'	1:A:1202:G:OP2	2.33	0.40
2:B:17:ARG:C	2:B:18:TRP:HD1	2.29	0.40
3:C:29:ARG:HG2	3:C:29:ARG:NH1	2.36	0.40
4:D:7:VAL:O	4:D:9:ARG:N	2.46	0.40
4:D:35:ARG:HD2	4:D:37:TYR:HE1	1.87	0.40
5:E:29:VAL:HG12	5:E:30:VAL:N	2.37	0.40
7:G:114:ARG:HB2	7:G:117:VAL:CG2	2.51	0.40
11:K:116:ARG:O	11:K:117:LYS:CB	2.70	0.40
14:N:17:VAL:HG23	14:N:18:ARG:N	2.35	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:65:SER:O	17:Q:66:LYS:C	2.63	0.40
20:T:46:LEU:O	20:T:47:LYS:C	2.63	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	233/256 (91%)	168 (72%)	43 (18%)	22 (9%)	0	2
3	C	205/239 (86%)	138 (67%)	37 (18%)	30 (15%)	0	1
4	D	206/208 (99%)	162 (79%)	31 (15%)	13 (6%)	1	7
5	E	149/161 (92%)	129 (87%)	15 (10%)	5 (3%)	3	16
6	F	99/101 (98%)	78 (79%)	19 (19%)	2 (2%)	6	27
7	G	153/155 (99%)	113 (74%)	31 (20%)	9 (6%)	1	8
8	H	136/138 (99%)	111 (82%)	21 (15%)	4 (3%)	3	20
9	I	125/128 (98%)	93 (74%)	19 (15%)	13 (10%)	0	2
10	J	97/104 (93%)	62 (64%)	15 (16%)	20 (21%)	0	0
11	K	117/129 (91%)	95 (81%)	18 (15%)	4 (3%)	3	16
12	L	123/132 (93%)	96 (78%)	17 (14%)	10 (8%)	1	3
13	M	123/126 (98%)	85 (69%)	22 (18%)	16 (13%)	0	1
14	N	58/60 (97%)	36 (62%)	16 (28%)	6 (10%)	0	2
15	O	86/88 (98%)	70 (81%)	14 (16%)	2 (2%)	5	24
16	P	82/88 (93%)	72 (88%)	9 (11%)	1 (1%)	10	37
17	Q	102/104 (98%)	79 (78%)	13 (13%)	10 (10%)	0	2
18	R	71/88 (81%)	57 (80%)	10 (14%)	4 (6%)	1	9
19	S	79/92 (86%)	50 (63%)	19 (24%)	10 (13%)	0	1

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	T	97/106 (92%)	67 (69%)	25 (26%)	5 (5%)	1	10
21	V	23/26 (88%)	16 (70%)	5 (22%)	2 (9%)	0	3
All	All	2364/2529 (94%)	1777 (75%)	399 (17%)	188 (8%)	1	4

All (188) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	3	GLU
2	B	14	GLU
2	B	17	ARG
2	B	18	TRP
2	B	226	PRO
3	C	3	LYS
3	C	14	THR
3	C	25	LYS
3	C	46	LEU
3	C	49	ALA
3	C	100	LEU
3	C	145	ALA
3	C	174	LEU
3	C	188	ALA
3	C	206	VAL
4	D	28	PRO
4	D	35	ARG
4	D	43	GLY
4	D	87	VAL
4	D	128	ASN
4	D	174	SER
5	E	12	THR
6	F	64	GLN
7	G	6	ALA
7	G	154	ARG
8	H	91	ARG
9	I	30	GLN
9	I	42	ALA
9	I	54	ALA
9	I	87	TYR
9	I	116	HIS
10	J	53	LYS
10	J	76	ASN
11	K	116	ARG

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Mol	Chain	Res	Type
12	L	23	LEU
12	L	24	LYS
12	L	26	ALA
12	L	43	LYS
13	M	22	TYR
13	M	26	LYS
13	M	66	GLU
13	M	122	ALA
14	N	3	LYS
14	N	10	LYS
15	O	87	ARG
17	Q	52	LEU
17	Q	98	SER
18	R	72	ARG
19	S	5	LYS
19	S	8	VAL
19	S	80	ARG
20	T	4	SER
20	T	87	ALA
21	V	24	LYS
2	B	15	ARG
2	B	71	ALA
2	B	117	ALA
2	B	159	VAL
2	B	201	ALA
2	B	218	GLN
2	B	222	GLY
3	C	15	ARG
3	C	60	ALA
3	C	75	VAL
3	C	99	ALA
3	C	155	ARG
3	C	180	ASN
4	D	3	TYR
4	D	88	THR
4	D	89	GLY
7	G	80	GLY
8	H	24	THR
8	H	128	GLY
9	I	118	ALA
9	I	126	LYS
10	J	24	ALA

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Mol	Chain	Res	Type
10	J	32	VAL
10	J	34	GLY
10	J	55	LYS
10	J	59	GLU
10	J	70	VAL
10	J	71	ASP
11	K	2	ARG
12	L	44	PRO
13	M	23	GLY
13	M	37	GLY
13	M	62	THR
13	M	67	GLY
13	M	99	GLY
13	M	105	ASN
13	M	123	PRO
14	N	31	SER
16	P	52	ASP
17	Q	79	GLY
18	R	13	GLU
19	S	4	LEU
19	S	13	HIS
19	S	42	GLU
19	S	66	VAL
19	S	67	GLY
20	T	89	GLY
2	B	70	GLN
2	B	143	LEU
2	B	207	LEU
5	E	70	GLY
8	H	22	GLU
9	I	106	ARG
10	J	39	PRO
10	J	90	THR
11	K	3	GLN
12	L	47	ALA
12	L	117	GLY
13	M	20	TYR
13	M	35	LYS
13	M	108	THR
14	N	6	ILE
14	N	9	ALA
14	N	55	VAL

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Mol	Chain	Res	Type
17	Q	29	PRO
17	Q	48	GLU
18	R	11	LEU
19	S	29	LEU
2	B	10	HIS
2	B	124	ARG
2	B	189	ASP
3	C	73	GLY
3	C	80	GLY
3	C	83	ILE
3	C	107	ASN
3	C	143	SER
3	C	167	ALA
3	C	173	PRO
3	C	187	LEU
4	D	25	CYS
4	D	29	LYS
5	E	69	ASN
5	E	136	ARG
7	G	32	ASP
7	G	38	ALA
7	G	111	PRO
9	I	22	ASN
9	I	33	ASN
9	I	92	ARG
10	J	28	SER
10	J	38	LEU
10	J	58	ARG
10	J	88	LEU
11	K	5	ALA
17	Q	73	LEU
20	T	64	THR
20	T	90	ALA
2	B	102	ILE
3	C	74	VAL
3	C	97	ASN
3	C	153	SER
3	C	178	ARG
4	D	170	GLY
5	E	66	PRO
7	G	51	GLU
9	I	23	GLY

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Mol	Chain	Res	Type
9	I	97	PRO
10	J	31	GLN
10	J	37	PRO
12	L	101	TYR
17	Q	80	ARG
17	Q	94	TYR
18	R	5	ALA
21	V	2	LYS
2	B	11	PHE
4	D	4	ILE
7	G	129	GLY
10	J	30	ALA
10	J	79	THR
12	L	83	GLY
17	Q	103	LYS
6	F	96	PRO
19	S	7	GLY
7	G	68	VAL
13	M	5	GLY
10	J	89	PRO
15	O	35	ILE
2	B	121	ILE
3	C	50	GLY
13	M	6	VAL
17	Q	76	VAL
2	B	9	VAL
3	C	204	GLY
12	L	25	GLY

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%)	179 (89%)	23 (11%)	5	21
3	C	160/188 (85%)	141 (88%)	19 (12%)	5	20
4	D	180/180 (100%)	163 (91%)	17 (9%)	8	29

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	E	115/122 (94%)	101 (88%)	14 (12%)	5	19
6	F	90/90 (100%)	78 (87%)	12 (13%)	4	17
7	G	126/126 (100%)	118 (94%)	8 (6%)	16	44
8	H	119/119 (100%)	108 (91%)	11 (9%)	8	30
9	I	98/99 (99%)	92 (94%)	6 (6%)	17	45
10	J	88/91 (97%)	80 (91%)	8 (9%)	9	30
11	K	90/99 (91%)	85 (94%)	5 (6%)	19	47
12	L	104/109 (95%)	92 (88%)	12 (12%)	5	21
13	M	100/101 (99%)	94 (94%)	6 (6%)	17	45
14	N	49/49 (100%)	43 (88%)	6 (12%)	5	19
15	O	79/79 (100%)	74 (94%)	5 (6%)	16	44
16	P	72/74 (97%)	67 (93%)	5 (7%)	14	40
17	Q	96/96 (100%)	86 (90%)	10 (10%)	7	24
18	R	64/77 (83%)	59 (92%)	5 (8%)	11	36
19	S	71/79 (90%)	61 (86%)	10 (14%)	3	15
20	T	76/82 (93%)	64 (84%)	12 (16%)	2	11
21	V	19/21 (90%)	18 (95%)	1 (5%)	20	49
All	All	1998/2101 (95%)	1803 (90%)	195 (10%)	7	28

All (195) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	3	GLU
2	B	17	ARG
2	B	19	ASN
2	B	37	ASP
2	B	50	ARG
2	B	61	THR
2	B	76	ARG
2	B	92	LEU
2	B	95	MET
2	B	108	ARG
2	B	111	GLU
2	B	140	GLN
2	B	148	LEU
2	B	159	VAL

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Mol	Chain	Res	Type
2	B	163	LYS
2	B	164	GLU
2	B	172	ARG
2	B	181	LEU
2	B	202	ILE
2	B	207	LEU
2	B	209	LEU
2	B	218	GLN
2	B	225	GLU
3	C	2	ASN
3	C	3	LYS
3	C	4	ILE
3	C	25	LYS
3	C	27	GLN
3	C	32	LEU
3	C	36	GLN
3	C	74	VAL
3	C	78	ARG
3	C	94	THR
3	C	98	VAL
3	C	155	ARG
3	C	165	GLU
3	C	166	TRP
3	C	174	LEU
3	C	176	THR
3	C	189	ARG
3	C	191	THR
3	C	203	LEU
4	D	2	ARG
4	D	8	CYS
4	D	9	ARG
4	D	28	PRO
4	D	37	TYR
4	D	63	LEU
4	D	79	GLU
4	D	85	LYS
4	D	95	LEU
4	D	113	ARG
4	D	126	THR
4	D	154	LEU
4	D	155	GLU
4	D	161	LEU

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Mol	Chain	Res	Type
4	D	181	LYS
4	D	193	LEU
4	D	198	ASN
5	E	2	PHE
5	E	8	LEU
5	E	12	THR
5	E	14	ARG
5	E	28	VAL
5	E	37	VAL
5	E	39	LEU
5	E	53	LYS
5	E	68	GLN
5	E	78	VAL
5	E	85	ILE
5	E	127	ILE
5	E	140	THR
5	E	146	ARG
6	F	9	VAL
6	F	10	LEU
6	F	25	ILE
6	F	27	GLN
6	F	32	ASN
6	F	39	LYS
6	F	40	VAL
6	F	45	LEU
6	F	47	ARG
6	F	55	ASP
6	F	67	MET
6	F	86	ARG
7	G	7	GLU
7	G	11	LEU
7	G	12	GLN
7	G	68	VAL
7	G	109	GLN
7	G	112	GLU
7	G	135	LYS
7	G	139	ASP
8	H	1	MET
8	H	21	LYS
8	H	26	VAL
8	H	39	LEU
8	H	83	ILE

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Mol	Chain	Res	Type
8	H	85	ARG
8	H	92	ARG
8	H	95	VAL
8	H	107	LEU
8	H	119	LEU
8	H	127	LEU
9	I	8	ARG
9	I	13	VAL
9	I	37	GLN
9	I	77	LYS
9	I	126	LYS
9	I	127	ARG
10	J	2	ILE
10	J	4	ILE
10	J	19	GLN
10	J	27	ARG
10	J	57	SER
10	J	71	ASP
10	J	80	ILE
10	J	96	ILE
11	K	19	ILE
11	K	38	ILE
11	K	44	ARG
11	K	74	VAL
11	K	96	LYS
12	L	3	ILE
12	L	8	ARG
12	L	29	ARG
12	L	39	VAL
12	L	44	PRO
12	L	55	ARG
12	L	56	LEU
12	L	63	THR
12	L	81	ILE
12	L	87	LYS
12	L	119	LYS
12	L	122	LYS
13	M	8	ILE
13	M	19	THR
13	M	65	LEU
13	M	69	LEU
13	M	114	LYS

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Mol	Chain	Res	Type
13	M	124	ARG
14	N	7	GLU
14	N	8	LYS
14	N	11	ARG
14	N	21	THR
14	N	31	SER
14	N	43	LEU
15	O	5	GLU
15	O	12	GLN
15	O	31	LEU
15	O	80	LEU
15	O	87	ARG
16	P	1	MET
16	P	2	VAL
16	P	45	THR
16	P	53	VAL
16	P	62	VAL
17	Q	21	LEU
17	Q	22	VAL
17	Q	37	ARG
17	Q	47	GLU
17	Q	54	ASP
17	Q	58	ILE
17	Q	73	LEU
17	Q	76	VAL
17	Q	97	LEU
17	Q	100	ARG
18	R	13	GLU
18	R	17	ARG
18	R	21	ASN
18	R	23	GLU
18	R	72	ARG
19	S	4	LEU
19	S	12	ASP
19	S	19	LEU
19	S	35	ARG
19	S	36	ARG
19	S	41	PRO
19	S	48	ILE
19	S	61	ILE
19	S	64	ASN
19	S	76	THR

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Mol	Chain	Res	Type
20	T	3	LEU
20	T	6	LEU
20	T	18	ARG
20	T	24	SER
20	T	35	GLN
20	T	41	LYS
20	T	50	ARG
20	T	55	LEU
20	T	66	HIS
20	T	67	LYS
20	T	80	LYS
20	T	93	ILE
21	V	14	ARG

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

Mol	Chain	Res	Type
2	B	19	ASN
2	B	34	HIS
2	B	140	GLN
2	B	198	ASN
2	B	206	GLN
2	B	218	GLN
2	B	234	GLN
3	C	5	HIS
3	C	30	HIS
3	C	62	ASN
3	C	97	ASN
3	C	106	GLN
3	C	107	ASN
3	C	117	GLN
3	C	135	GLN
3	C	161	GLN
3	C	180	ASN
4	D	61	GLN
4	D	73	GLN
4	D	198	ASN
5	E	68	GLN
5	E	69	ASN
5	E	123	ASN
6	F	18	GLN
6	F	27	GLN

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Mol	Chain	Res	Type
6	F	32	ASN
6	F	57	GLN
6	F	64	GLN
6	F	94	GLN
6	F	100	ASN
7	G	10	GLN
9	I	28	ASN
10	J	54	HIS
10	J	60	HIS
10	J	74	ASN
10	J	76	ASN
11	K	12	HIS
11	K	17	ASN
11	K	52	GLN
11	K	83	GLN
11	K	89	GLN
11	K	94	GLN
11	K	107	ASN
12	L	71	HIS
13	M	11	ASN
15	O	52	HIS
15	O	61	GLN
16	P	13	HIS
16	P	76	GLN
16	P	82	GLN
17	Q	15	GLN
17	Q	95	GLN
18	R	21	ASN
19	S	46	HIS
19	S	56	HIS
19	S	64	ASN
20	T	38	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1508/1521 (99%)	248 (16%)	57 (3%)
22	W	3/6 (50%)	0	0
23	Z	15/16 (93%)	2 (13%)	2 (13%)
All	All	1526/1543 (98%)	250 (16%)	59 (3%)

All (250) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	6	G
1	A	7	G
1	A	8	A
1	A	9	G
1	A	31	G
1	A	32	A
1	A	39	G
1	A	47	C
1	A	48	C
1	A	50	A
1	A	51	A
1	A	52	G
1	A	60	A
1	A	61	G
1	A	65	U
1	A	66	G
1	A	116	A
1	A	121	C
1	A	131	C
1	A	144	G
1	A	147	G
1	A	149	A
1	A	150	C
1	A	159	G
1	A	160	A
1	A	169	C
1	A	195	A
1	A	196	A
1	A	197	A
1	A	204	U
1	A	217	C
1	A	246	A
1	A	247	G
1	A	250	A
1	A	251	G
1	A	252	U
1	A	266	G
1	A	267	C
1	A	274	A
1	A	275	G
1	A	279	A
1	A	281	G
1	A	282	A

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Mol	Chain	Res	Type
1	A	289	G
1	A	293	G
1	A	304	U
1	A	305	G
1	A	306	G
1	A	321	A
1	A	328	C
1	A	329	A
1	A	330	C
1	A	345	C
1	A	352	C
1	A	354	G
1	A	362	G
1	A	367	U
1	A	373	A
1	A	388	G
1	A	403	C
1	A	406	G
1	A	412	A
1	A	414	A
1	A	421	U
1	A	422	C
1	A	423	G
1	A	428	G
1	A	429	U
1	A	439	A
1	A	448	A
1	A	452	A
1	A	453	A
1	A	461	A
1	A	471	G
1	A	485	G
1	A	486	U
1	A	498	U
1	A	500	G
1	A	511	C
1	A	512	U
1	A	516	U
1	A	517	G
1	A	518	C
1	A	524	G
1	A	531	U

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Mol	Chain	Res	Type
1	A	532	A
1	A	533	A
1	A	545	C
1	A	547	A
1	A	548	G
1	A	559	A
1	A	560	U
1	A	572	A
1	A	573	A
1	A	576	G
1	A	577	G
1	A	630	G
1	A	648	A
1	A	653	A
1	A	665	A
1	A	687	A
1	A	688	G
1	A	703	G
1	A	721	G
1	A	723	U
1	A	730	G
1	A	731	G
1	A	733	A
1	A	755	G
1	A	777	A
1	A	793	U
1	A	794	A
1	A	815	A
1	A	817	C
1	A	819	A
1	A	821	G
1	A	840	C
1	A	841	U
1	A	848	C
1	A	859	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

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Mol	Chain	Res	Type
1	A	935	A
1	A	958	A
1	A	960	U
1	A	968	A
1	A	969	A
1	A	971	G
1	A	976	G
1	A	977	A
1	A	992	U
1	A	993	G
1	A	994	A
1	A	995	C
1	A	998	G
1	A	1001(A)	G
1	A	1004	A
1	A	1021	G
1	A	1024	G
1	A	1025	U
1	A	1026	G
1	A	1027	C
1	A	1030	C
1	A	1046	A
1	A	1048	G
1	A	1050	G
1	A	1054	C
1	A	1055	A
1	A	1065	U
1	A	1068	G
1	A	1070	U
1	A	1081	G
1	A	1084	G
1	A	1085	U
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	1102	A
1	A	1109	C
1	A	1125	U
1	A	1126	U
1	A	1127	G
1	A	1129	C
1	A	1130	A

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Mol	Chain	Res	Type
1	A	1131	G
1	A	1136	U
1	A	1138	G
1	A	1139	G
1	A	1141	C
1	A	1146	A
1	A	1157	A
1	A	1158	C
1	A	1159	U
1	A	1160	G
1	A	1168	A
1	A	1183	A
1	A	1196	U
1	A	1197	G
1	A	1202	G
1	A	1210	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	1245	A
1	A	1250	A
1	A	1256	A
1	A	1257	U
1	A	1277	C
1	A	1278	U
1	A	1279	A
1	A	1280	A
1	A	1281	U
1	A	1282	C
1	A	1285	A
1	A	1287	A
1	A	1297	C
1	A	1298	C
1	A	1299	A
1	A	1300	G
1	A	1302	U
1	A	1305	G

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Mol	Chain	Res	Type
1	A	1306	A
1	A	1319	A
1	A	1320	C
1	A	1322	C
1	A	1338	G
1	A	1347	G
1	A	1348	U
1	A	1363(A)	A
1	A	1365	G
1	A	1370	G
1	A	1377	A
1	A	1378	C
1	A	1381	U
1	A	1398	A
1	A	1400	C
1	A	1442	G
1	A	1442(B)	A
1	A	1452	C
1	A	1456	G
1	A	1476	G
1	A	1478	C
1	A	1480	G
1	A	1481	U
1	A	1492	A
1	A	1494	G
1	A	1497	G
1	A	1503	A
1	A	1504	G
1	A	1505	G
1	A	1506	U
1	A	1507	A
1	A	1517	G
1	A	1520	G
1	A	1527	C
1	A	1529	G
1	A	1530	G
1	A	1542	U
23	Z	29	G
23	Z	41	C

All (59) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	8	A
1	A	50	A
1	A	51	A
1	A	65	U
1	A	148	G
1	A	159	G
1	A	196	A
1	A	216	G
1	A	246	A
1	A	250	A
1	A	251	G
1	A	280	C
1	A	281	G
1	A	304	U
1	A	329	A
1	A	344	A
1	A	372	C
1	A	413	G
1	A	428	G
1	A	470	C
1	A	485	G
1	A	496	A
1	A	531	U
1	A	559	A
1	A	572	A
1	A	575	G
1	A	702	A
1	A	730	G
1	A	819	A
1	A	884	U
1	A	968	A
1	A	975	A
1	A	992	U
1	A	993	G
1	A	1054	C
1	A	1084	G
1	A	1101	A
1	A	1135	U
1	A	1145	C
1	A	1157	A
1	A	1182	G
1	A	1201	A
1	A	1210	C

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Mol	Chain	Res	Type
1	A	1214	C
1	A	1282	C
1	A	1297	C
1	A	1305	G
1	A	1319	A
1	A	1335	C
1	A	1347	G
1	A	1377	A
1	A	1397	C
1	A	1442(A)	G
1	A	1447	A
1	A	1452	C
1	A	1480	G
1	A	1504	G
23	Z	28	G
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 182 ligands modelled in this entry, 181 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
26	RPO	A	2800	24	52,53,53	1.46	9 (17%)	72,77,77	1.14	6 (8%)

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	RPO	A	2800	24	-	9/23/99/99	0/5/5/5

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	A	2800	RPO	CAU-CAO	-4.73	1.39	1.50
26	A	2800	RPO	CBI-CBW	3.29	1.61	1.52
26	A	2800	RPO	OAV-CBQ	2.65	1.48	1.41
26	A	2800	RPO	CAN-CAL	2.45	1.43	1.38
26	A	2800	RPO	CAL-CAM	2.41	1.43	1.38
26	A	2800	RPO	CAP-CAN	2.39	1.43	1.38
26	A	2800	RPO	CBC-CAO	2.30	1.43	1.38
26	A	2800	RPO	CAP-CBC	2.18	1.42	1.38
26	A	2800	RPO	CAM-CAO	2.18	1.43	1.38

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	A	2800	RPO	O1'-C1'-O4'	-4.92	106.35	111.37
26	A	2800	RPO	O4-CAU-CAO	2.98	116.73	109.91
26	A	2800	RPO	OAV-CBM-CAQ	2.76	111.37	106.07
26	A	2800	RPO	O1'-CBW-CBI	2.45	113.47	107.23
26	A	2800	RPO	CBI-CBW-CBT	-2.10	106.99	111.72
26	A	2800	RPO	OAH-CBI-CBD	-2.01	106.15	109.90

There are no chirality outliers.

All (9) torsion outliers are listed below:

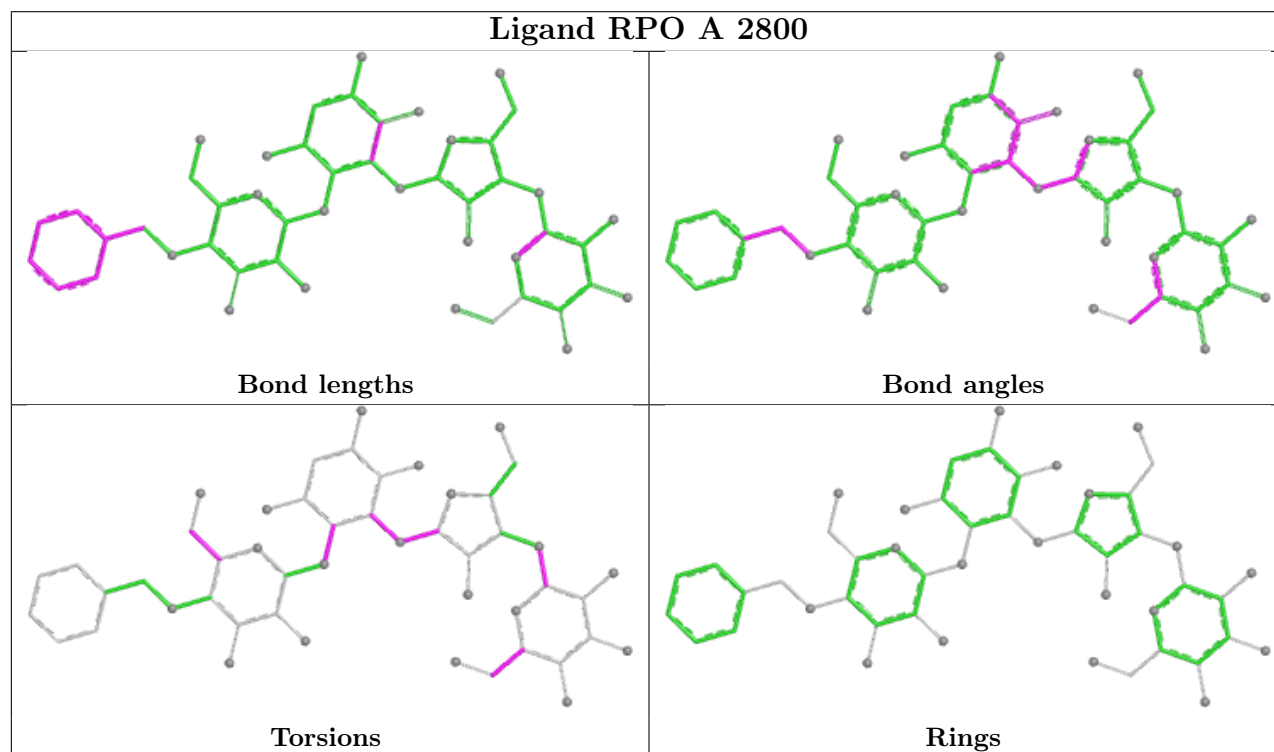
Mol	Chain	Res	Type	Atoms
26	A	2800	RPO	NAA-CAQ-CBM-OAV
26	A	2800	RPO	O5-C5-C6-O6
26	A	2800	RPO	C4-C5-C6-O6
26	A	2800	RPO	CBT-CBW-O1'-C1'
26	A	2800	RPO	CBI-CBW-O1'-C1'
26	A	2800	RPO	OAV-CBQ-O3'-C3'
26	A	2800	RPO	O4'-C1'-O1'-CBW
26	A	2800	RPO	C2'-C1'-O1'-CBW
26	A	2800	RPO	CBW-CBT-O1-C1

There are no ring outliers.

1 monomer is involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
26	A	2800	RPO	6	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 ⓘ

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	1510/1521 (99%)	0.25	51 (3%) 48 28	42, 70, 136, 190	0
2	B	235/256 (91%)	0.72	24 (10%) 12 7	50, 100, 157, 197	0
3	C	207/239 (86%)	0.70	10 (4%) 35 20	50, 90, 137, 169	0
4	D	208/208 (100%)	0.59	20 (9%) 13 8	49, 83, 134, 196	0
5	E	151/161 (93%)	0.04	3 (1%) 65 44	38, 62, 102, 160	0
6	F	101/101 (100%)	0.44	2 (1%) 65 44	61, 96, 126, 150	0
7	G	155/155 (100%)	0.43	9 (5%) 29 16	51, 89, 149, 183	0
8	H	138/138 (100%)	-0.12	1 (0%) 84 69	36, 60, 90, 112	0
9	I	127/128 (99%)	0.84	9 (7%) 22 12	42, 102, 138, 201	0
10	J	99/104 (95%)	1.44	26 (26%) 1 1	51, 118, 178, 201	0
11	K	119/129 (92%)	0.33	8 (6%) 24 13	44, 72, 122, 182	0
12	L	125/132 (94%)	0.35	5 (4%) 42 24	37, 67, 122, 184	0
13	M	125/126 (99%)	0.87	20 (16%) 5 3	52, 86, 152, 201	0
14	N	60/60 (100%)	0.78	6 (10%) 12 7	46, 82, 104, 173	0
15	O	88/88 (100%)	0.13	1 (1%) 78 60	43, 75, 115, 170	0
16	P	84/88 (95%)	0.09	1 (1%) 76 57	45, 64, 94, 172	0
17	Q	104/104 (100%)	0.30	5 (4%) 35 20	37, 68, 136, 201	0
18	R	73/88 (82%)	0.20	2 (2%) 56 35	55, 82, 145, 179	0
19	S	81/92 (88%)	1.02	7 (8%) 16 9	67, 100, 150, 166	0
20	T	99/106 (93%)	0.33	5 (5%) 33 19	40, 68, 116, 176	0
21	V	25/26 (96%)	0.94	5 (20%) 3 2	51, 73, 121, 144	0
22	W	4/6 (66%)	1.28	1 (25%) 2 1	86, 89, 91, 91	0
23	Z	15/16 (93%)	1.08	3 (20%) 3 2	74, 107, 185, 189	0
All	All	3933/4072 (96%)	0.41	224 (5%) 29 17	36, 76, 142, 201	0

All (224) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
19	S	2	ARG	9.3
13	M	122	ALA	8.3
13	M	123	PRO	7.8
1	A	1129	C	7.2
19	S	1	PRO	7.1
4	D	22	GLY	6.9
17	Q	104	ALA	6.2
19	S	4	LEU	5.6
1	A	1126	U	5.4
1	A	630	G	5.4
13	M	124	ARG	5.4
17	Q	102	GLY	5.3
14	N	1	ALA	5.3
13	M	6	VAL	5.2
7	G	4	ARG	5.0
13	M	7	GLU	4.8
13	M	119	LYS	4.8
4	D	2	ARG	4.7
1	A	1541	U	4.6
10	J	15	ASP	4.6
19	S	81	GLY	4.5
13	M	120	LYS	4.3
10	J	91	GLY	4.3
4	D	36	PRO	4.3
1	A	1125	U	4.3
13	M	125	LYS	4.2
4	D	8	CYS	4.2
12	L	43	LYS	4.2
2	B	134	HIS	4.2
9	I	127	ARG	4.1
10	J	8	GLY	4.0
21	V	24	LYS	4.0
1	A	1533	C	3.9
2	B	83	GLY	3.9
1	A	723	U	3.9
4	D	34	ARG	3.8
1	A	1281	U	3.8
12	L	111	LYS	3.8
21	V	25	LYS	3.8
4	D	3	TYR	3.8
12	L	24	LYS	3.8
4	D	25	CYS	3.8

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Mol	Chain	Res	Type	RSRZ
10	J	35	PRO	3.7
4	D	30	CYS	3.7
1	A	1003	G	3.7
1	A	532	A	3.6
9	I	126	LYS	3.6
13	M	121	LYS	3.6
2	B	70	GLN	3.6
19	S	36	ARG	3.5
23	Z	42	C	3.5
19	S	34	SER	3.5
13	M	10	ARG	3.4
1	A	1277	C	3.4
1	A	1131	G	3.4
21	V	8	ARG	3.3
12	L	85	ARG	3.3
13	M	26	LYS	3.3
11	K	15	TYR	3.2
13	M	1	ALA	3.2
13	M	8	ILE	3.2
3	C	166	TRP	3.1
10	J	83	LEU	3.1
1	A	159	G	3.1
9	I	101	LEU	3.1
10	J	71	ASP	3.1
11	K	117	LYS	3.0
2	B	127	LYS	3.0
1	A	1256	A	3.0
1	A	1282	C	3.0
11	K	1	LYS	3.0
17	Q	101	GLY	3.0
10	J	13	THR	2.9
7	G	6	ALA	2.9
2	B	223	VAL	2.9
1	A	1127	G	2.9
13	M	5	GLY	2.9
11	K	41	LYS	2.9
10	J	68	ARG	2.9
17	Q	103	LYS	2.9
10	J	22	VAL	2.8
20	T	61	LYS	2.8
1	A	161	A	2.8
20	T	94	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
8	H	1	MET	2.8
4	D	29	LYS	2.8
14	N	2	ARG	2.8
10	J	73	ILE	2.8
1	A	1017	G	2.8
2	B	16	LYS	2.7
1	A	160	A	2.7
1	A	202	U	2.7
1	A	1278	U	2.7
2	B	224	VAL	2.7
4	D	41	GLN	2.7
4	D	18	LEU	2.7
10	J	55	LYS	2.7
1	A	306	G	2.7
21	V	23	ARG	2.7
1	A	5	U	2.7
19	S	33	TRP	2.7
10	J	34	GLY	2.7
1	A	992	U	2.7
7	G	84	TYR	2.7
1	A	631	G	2.6
3	C	121	GLU	2.6
1	A	204	U	2.6
1	A	1004	A	2.6
14	N	34	ARG	2.6
14	N	56	ARG	2.6
1	A	1018	C	2.6
17	Q	12	ASP	2.5
13	M	117	ALA	2.5
9	I	66	GLY	2.5
11	K	119	SER	2.5
10	J	18	ALA	2.5
7	G	25	PHE	2.5
3	C	144	GLY	2.5
10	J	7	ARG	2.5
3	C	74	VAL	2.5
1	A	858	G	2.5
1	A	1283	G	2.5
5	E	1	ASP	2.5
13	M	84	GLY	2.5
10	J	32	VAL	2.4
4	D	48	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
9	I	15	ARG	2.4
20	T	5	ALA	2.4
1	A	1146	A	2.4
2	B	202	ILE	2.4
2	B	138	ARG	2.4
4	D	114	ARG	2.4
2	B	142	TYR	2.4
7	G	77	ARG	2.4
10	J	3	ARG	2.4
5	E	16	GLN	2.4
7	G	15	LEU	2.4
10	J	69	LEU	2.4
1	A	1286	A	2.4
1	A	1001(A)	G	2.3
16	P	83	GLU	2.3
3	C	105	VAL	2.3
1	A	250	A	2.3
5	E	150	GLY	2.3
14	N	12	THR	2.3
1	A	1271	G	2.3
3	C	98	VAL	2.3
10	J	70	VAL	2.3
23	Z	28	G	2.3
10	J	38	LEU	2.3
1	A	1130	A	2.3
2	B	104	GLN	2.3
2	B	125	PRO	2.3
3	C	153	SER	2.3
9	I	125	SER	2.3
10	J	88	LEU	2.3
20	T	92	LEU	2.3
10	J	67	ASN	2.3
2	B	220	ARG	2.3
2	B	160	ASP	2.3
6	F	1	MET	2.2
13	M	115	THR	2.2
18	R	2	SER	2.2
9	I	31	ASP	2.2
4	D	1	GLY	2.2
1	A	1124	G	2.2
9	I	6	THR	2.2
1	A	1212	U	2.2

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Mol	Chain	Res	Type	RSRZ
21	V	5	ARG	2.2
10	J	33	SER	2.2
7	G	79	VAL	2.2
2	B	226	PRO	2.2
4	D	32	MET	2.2
11	K	118	ALA	2.2
11	K	44	ARG	2.2
10	J	98	THR	2.2
4	D	44	GLN	2.2
1	A	266	G	2.2
1	A	413	G	2.2
1	A	993	G	2.2
1	A	1094	G	2.2
12	L	123	GLU	2.2
13	M	9	PRO	2.2
2	B	90	ARG	2.2
2	B	116	PHE	2.2
7	G	145	GLU	2.2
2	B	221	GLY	2.2
20	T	91	PRO	2.2
3	C	22	TYR	2.1
13	M	118	GLY	2.1
2	B	159	VAL	2.1
1	A	1032	G	2.1
4	D	31	ALA	2.1
2	B	6	GLU	2.1
6	F	37	VAL	2.1
14	N	32	VAL	2.1
1	A	1257	U	2.1
10	J	57	SER	2.1
1	A	1002	G	2.1
1	A	1031	G	2.1
4	D	186	ARG	2.1
4	D	26	TYR	2.1
11	K	79	ALA	2.1
2	B	222	GLY	2.1
4	D	144	GLU	2.1
18	R	13	GLU	2.1
9	I	55	LEU	2.1
2	B	57	MET	2.1
10	J	84	MET	2.1
1	A	848	C	2.1

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Mol	Chain	Res	Type	RSRZ
23	Z	40	C	2.1
22	W	1	U	2.0
2	B	55	LEU	2.0
13	M	104	THR	2.0
1	A	1144	G	2.0
3	C	207	ILE	2.0
15	O	2	ILE	2.0
7	G	155	TRP	2.0
10	J	30	ALA	2.0
2	B	60	GLY	2.0
1	A	143	A	2.0
1	A	344	A	2.0
3	C	20	ARG	2.0
1	A	470	C	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
24	MG	A	2636	1/1	0.54	0.28	68,68,68,68	0
24	MG	L	1125	1/1	0.55	0.31	84,84,84,84	0
24	MG	A	2608	1/1	0.56	0.57	82,82,82,82	0
24	MG	A	2619	1/1	0.60	0.53	83,83,83,83	0
25	K	A	2676	1/1	0.60	0.41	111,111,111,111	0
24	MG	A	2551	1/1	0.69	0.24	81,81,81,81	0
24	MG	A	2621	1/1	0.70	0.19	70,70,70,70	0
24	MG	A	2661	1/1	0.72	0.23	67,67,67,67	0
24	MG	A	2596	1/1	0.73	0.25	90,90,90,90	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
24	MG	A	2550	1/1	0.74	0.13	50,50,50,50	0
24	MG	A	2700	1/1	0.74	0.29	69,69,69,69	0
24	MG	A	2645	1/1	0.75	0.67	76,76,76,76	0
24	MG	A	2592	1/1	0.76	0.57	81,81,81,81	0
24	MG	A	2629	1/1	0.76	0.19	58,58,58,58	0
24	MG	A	2611	1/1	0.77	0.30	38,38,38,38	0
24	MG	A	2662	1/1	0.77	0.35	89,89,89,89	0
24	MG	A	2666	1/1	0.77	0.30	68,68,68,68	0
25	K	A	2683	1/1	0.77	0.22	110,110,110,110	0
24	MG	A	2667	1/1	0.78	0.22	57,57,57,57	0
24	MG	A	2618	1/1	0.80	0.26	61,61,61,61	0
24	MG	A	2584	1/1	0.81	0.23	56,56,56,56	0
24	MG	A	2656	1/1	0.81	0.25	77,77,77,77	0
24	MG	A	2663	1/1	0.81	0.12	58,58,58,58	0
24	MG	A	2554	1/1	0.82	0.20	82,82,82,82	0
24	MG	A	2652	1/1	0.83	0.20	61,61,61,61	0
24	MG	A	2560	1/1	0.84	0.34	45,45,45,45	0
24	MG	A	2703	1/1	0.84	0.41	59,59,59,59	0
24	MG	A	2627	1/1	0.84	0.15	56,56,56,56	0
24	MG	A	2599	1/1	0.84	0.28	75,75,75,75	0
24	MG	A	2689	1/1	0.84	0.28	49,49,49,49	0
24	MG	A	2690	1/1	0.85	0.29	80,80,80,80	0
24	MG	A	2606	1/1	0.85	0.34	69,69,69,69	0
24	MG	A	2632	1/1	0.85	0.09	75,75,75,75	0
24	MG	A	2622	1/1	0.85	0.09	50,50,50,50	0
24	MG	M	1126	1/1	0.85	0.12	57,57,57,57	0
24	MG	A	2687	1/1	0.85	0.21	65,65,65,65	0
24	MG	A	2616	1/1	0.85	0.34	54,54,54,54	0
24	MG	A	2568	1/1	0.86	0.35	66,66,66,66	0
24	MG	A	2594	1/1	0.86	0.23	39,39,39,39	0
24	MG	A	2670	1/1	0.86	0.17	57,57,57,57	0
25	K	A	2672	1/1	0.86	0.15	100,100,100,100	0
25	K	A	2675	1/1	0.86	0.22	97,97,97,97	0
24	MG	A	2686	1/1	0.86	0.40	75,75,75,75	0
24	MG	A	2701	1/1	0.86	0.46	65,65,65,65	0
24	MG	A	2626	1/1	0.87	0.45	61,61,61,61	0
24	MG	A	2706	1/1	0.87	0.35	57,57,57,57	0
24	MG	B	1235	1/1	0.87	0.22	66,66,66,66	0
24	MG	A	2638	1/1	0.87	0.16	64,64,64,64	0
24	MG	A	2640	1/1	0.87	0.12	55,55,55,55	0
24	MG	T	1100	1/1	0.87	0.21	51,51,51,51	0
24	MG	A	2581	1/1	0.87	0.10	67,67,67,67	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
24	MG	A	2695	1/1	0.87	0.40	66,66,66,66	0
24	MG	A	2607	1/1	0.87	0.39	56,56,56,56	0
24	MG	A	2555	1/1	0.87	0.28	32,32,32,32	0
24	MG	A	2545	1/1	0.88	0.11	58,58,58,58	0
24	MG	A	2591	1/1	0.88	0.24	53,53,53,53	0
24	MG	A	2617	1/1	0.88	0.13	47,47,47,47	0
24	MG	A	2634	1/1	0.88	0.11	45,45,45,45	0
24	MG	A	2601	1/1	0.88	0.21	36,36,36,36	0
24	MG	A	2669	1/1	0.88	0.22	70,70,70,70	0
24	MG	A	2620	1/1	0.89	0.19	56,56,56,56	0
24	MG	A	2664	1/1	0.89	0.08	47,47,47,47	0
24	MG	A	2566	1/1	0.89	0.23	55,55,55,55	0
24	MG	A	2595	1/1	0.89	0.22	55,55,55,55	0
24	MG	A	2668	1/1	0.89	0.15	60,60,60,60	0
24	MG	A	2556	1/1	0.89	0.30	49,49,49,49	0
24	MG	A	2650	1/1	0.89	0.15	32,32,32,32	0
24	MG	A	2685	1/1	0.89	0.09	45,45,45,45	0
24	MG	A	2598	1/1	0.89	0.24	38,38,38,38	0
24	MG	A	2587	1/1	0.89	0.30	40,40,40,40	0
25	K	A	2673	1/1	0.89	0.15	105,105,105,105	0
24	MG	A	2570	1/1	0.89	0.12	89,89,89,89	0
24	MG	A	2580	1/1	0.89	0.17	37,37,37,37	0
24	MG	A	2694	1/1	0.89	0.44	68,68,68,68	0
24	MG	A	2649	1/1	0.90	0.10	48,48,48,48	0
24	MG	A	2635	1/1	0.90	0.16	57,57,57,57	0
24	MG	F	1102	1/1	0.90	0.12	61,61,61,61	0
24	MG	A	2600	1/1	0.90	0.30	53,53,53,53	0
24	MG	A	2653	1/1	0.90	0.21	57,57,57,57	0
24	MG	A	2552	1/1	0.90	0.47	58,58,58,58	0
24	MG	A	2697	1/1	0.90	0.18	86,86,86,86	0
24	MG	A	2698	1/1	0.90	0.34	56,56,56,56	0
24	MG	A	2633	1/1	0.90	0.10	51,51,51,51	0
24	MG	A	2585	1/1	0.90	0.42	73,73,73,73	0
25	K	A	2678	1/1	0.90	0.12	108,108,108,108	0
24	MG	A	2646	1/1	0.90	0.12	46,46,46,46	0
24	MG	A	2561	1/1	0.91	0.30	44,44,44,44	0
24	MG	A	2704	1/1	0.91	0.39	63,63,63,63	0
24	MG	A	2684	1/1	0.91	0.55	65,65,65,65	0
24	MG	A	2655	1/1	0.91	0.17	56,56,56,56	0
24	MG	A	2574	1/1	0.91	0.29	42,42,42,42	0
24	MG	A	2660	1/1	0.91	0.08	49,49,49,49	0
24	MG	A	2614	1/1	0.91	0.16	46,46,46,46	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
24	MG	A	2590	1/1	0.91	0.43	56,56,56,56	0
24	MG	A	2628	1/1	0.91	0.15	42,42,42,42	0
24	MG	A	2575	1/1	0.91	0.17	40,40,40,40	0
24	MG	A	2564	1/1	0.91	0.22	41,41,41,41	0
24	MG	A	2548	1/1	0.91	0.57	70,70,70,70	0
24	MG	A	2651	1/1	0.91	0.07	58,58,58,58	0
25	K	A	2682	1/1	0.91	0.19	107,107,107,107	0
24	MG	A	2547	1/1	0.91	0.19	14,14,14,14	0
24	MG	L	1126	1/1	0.92	0.12	47,47,47,47	0
24	MG	A	2658	1/1	0.92	0.10	72,72,72,72	0
24	MG	A	2688	1/1	0.92	0.12	44,44,44,44	0
24	MG	A	2612	1/1	0.92	0.13	40,40,40,40	0
24	MG	A	2613	1/1	0.92	0.27	50,50,50,50	0
24	MG	A	2577	1/1	0.92	0.31	50,50,50,50	0
24	MG	A	2709	1/1	0.92	0.30	95,95,95,95	0
24	MG	A	2572	1/1	0.92	0.10	32,32,32,32	0
25	K	A	2681	1/1	0.92	0.10	87,87,87,87	0
24	MG	A	2553	1/1	0.92	0.21	58,58,58,58	0
24	MG	A	2567	1/1	0.92	0.25	38,38,38,38	0
24	MG	A	2602	1/1	0.93	0.43	60,60,60,60	0
24	MG	A	2604	1/1	0.93	0.34	51,51,51,51	0
24	MG	A	2579	1/1	0.93	0.20	38,38,38,38	0
25	K	A	2671	1/1	0.93	0.07	93,93,93,93	0
24	MG	A	2583	1/1	0.93	0.17	52,52,52,52	0
24	MG	A	2693	1/1	0.93	0.24	64,64,64,64	0
24	MG	A	2615	1/1	0.93	0.08	37,37,37,37	0
24	MG	A	2710	1/1	0.93	0.50	81,81,81,81	0
24	MG	A	2714	1/1	0.93	0.35	64,64,64,64	0
25	K	A	2680	1/1	0.93	0.25	114,114,114,114	0
24	MG	A	2642	1/1	0.93	0.10	47,47,47,47	0
24	MG	A	2569	1/1	0.93	0.09	48,48,48,48	0
24	MG	A	2665	1/1	0.93	0.21	52,52,52,52	0
26	RPO	A	2800	49/49	0.93	0.13	51,58,75,76	0
27	ZN	D	1209	1/1	0.93	0.13	107,107,107,107	0
24	MG	A	2593	1/1	0.94	0.12	31,31,31,31	0
24	MG	A	2639	1/1	0.94	0.10	48,48,48,48	0
24	MG	A	2657	1/1	0.94	0.08	55,55,55,55	0
24	MG	A	2589	1/1	0.94	0.20	38,38,38,38	0
24	MG	A	2610	1/1	0.94	0.16	42,42,42,42	0
24	MG	A	2630	1/1	0.94	0.08	39,39,39,39	0
24	MG	A	2631	1/1	0.94	0.12	64,64,64,64	0
24	MG	A	2705	1/1	0.94	0.09	59,59,59,59	0

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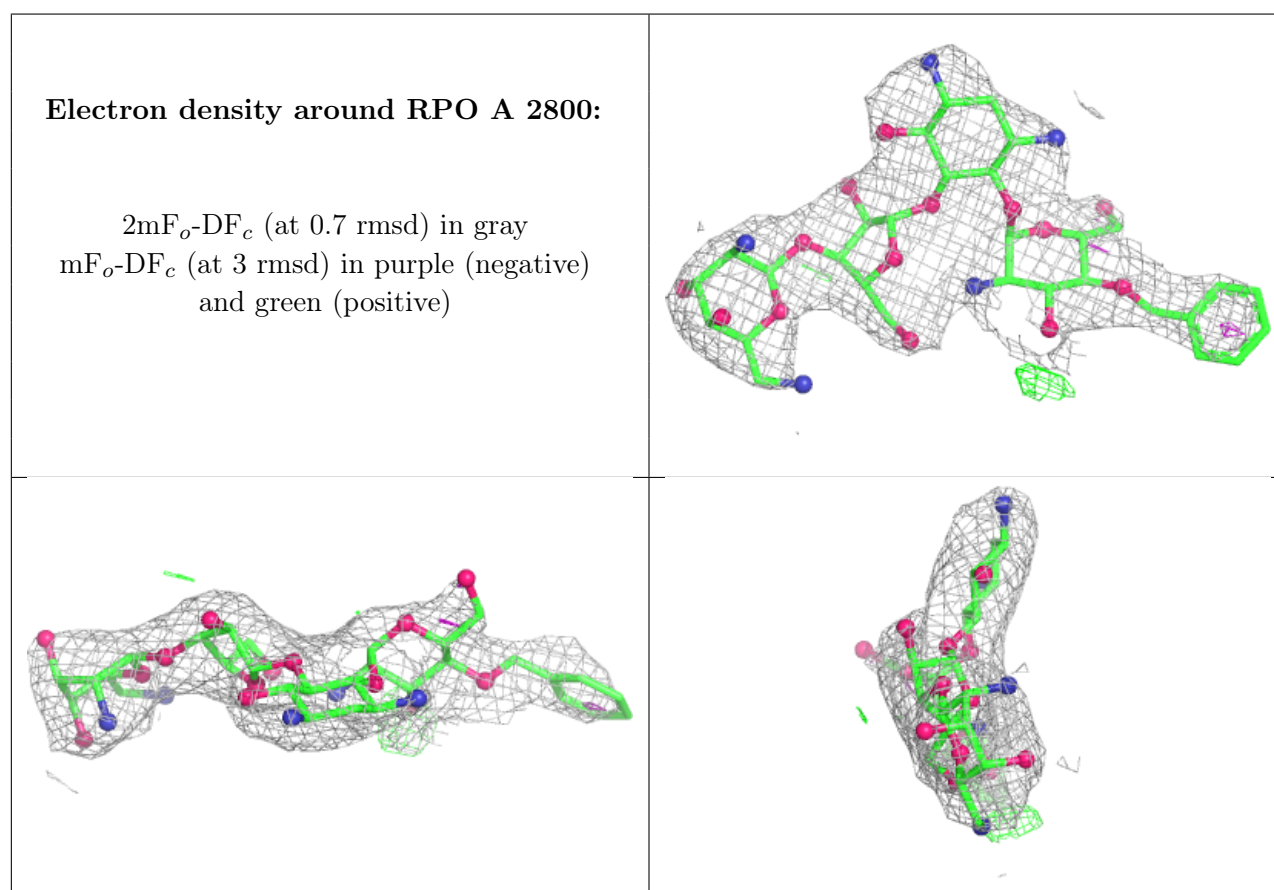
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
24	MG	A	2573	1/1	0.94	0.35	51,51,51,51	0
24	MG	A	2708	1/1	0.94	0.18	57,57,57,57	0
25	K	A	2677	1/1	0.94	0.14	98,98,98,98	0
24	MG	A	2586	1/1	0.94	0.22	46,46,46,46	0
25	K	A	2679	1/1	0.94	0.21	85,85,85,85	0
24	MG	A	2597	1/1	0.94	0.48	62,62,62,62	0
24	MG	A	2712	1/1	0.94	0.44	49,49,49,49	0
24	MG	A	2713	1/1	0.94	0.29	75,75,75,75	0
24	MG	A	2605	1/1	0.94	0.42	50,50,50,50	0
24	MG	A	2576	1/1	0.94	0.18	37,37,37,37	0
24	MG	E	1151	1/1	0.94	0.30	55,55,55,55	0
24	MG	A	2588	1/1	0.95	0.18	36,36,36,36	0
24	MG	A	2578	1/1	0.95	0.12	43,43,43,43	0
24	MG	A	2654	1/1	0.95	0.15	95,95,95,95	0
24	MG	A	2546	1/1	0.95	0.27	29,29,29,29	0
24	MG	A	2641	1/1	0.95	0.16	35,35,35,35	0
24	MG	A	2623	1/1	0.95	0.08	48,48,48,48	0
24	MG	A	2625	1/1	0.95	0.09	42,42,42,42	0
24	MG	A	2559	1/1	0.95	0.34	51,51,51,51	0
24	MG	A	2702	1/1	0.95	0.28	46,46,46,46	0
24	MG	K	1121	1/1	0.95	0.09	43,43,43,43	0
24	MG	A	2647	1/1	0.95	0.13	45,45,45,45	0
24	MG	A	2562	1/1	0.95	0.31	44,44,44,44	0
24	MG	A	2582	1/1	0.95	0.38	39,39,39,39	0
24	MG	A	2637	1/1	0.95	0.18	78,78,78,78	0
24	MG	A	2603	1/1	0.96	0.12	18,18,18,18	0
24	MG	H	1139	1/1	0.96	0.07	56,56,56,56	0
24	MG	K	1120	1/1	0.96	0.07	46,46,46,46	0
24	MG	A	2648	1/1	0.96	0.21	35,35,35,35	0
24	MG	A	2609	1/1	0.96	0.38	57,57,57,57	0
24	MG	A	2557	1/1	0.96	0.15	118,118,118,118	0
24	MG	A	2563	1/1	0.96	0.14	37,37,37,37	0
24	MG	A	2644	1/1	0.96	0.06	35,35,35,35	0
24	MG	A	2691	1/1	0.96	0.11	57,57,57,57	0
24	MG	A	2549	1/1	0.96	0.08	55,55,55,55	0
24	MG	A	2565	1/1	0.96	0.26	37,37,37,37	0
25	K	A	2674	1/1	0.97	0.16	91,91,91,91	0
24	MG	A	2707	1/1	0.97	0.22	51,51,51,51	0
24	MG	A	2643	1/1	0.97	0.07	32,32,32,32	0
24	MG	A	2571	1/1	0.97	0.35	53,53,53,53	0
24	MG	A	2696	1/1	0.97	0.05	43,43,43,43	0
24	MG	A	2624	1/1	0.97	0.07	40,40,40,40	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
24	MG	A	2692	1/1	0.98	0.47	55,55,55,55	0
24	MG	A	2659	1/1	0.98	0.09	31,31,31,31	0
24	MG	A	2558	1/1	0.98	0.33	69,69,69,69	0
24	MG	A	2711	1/1	0.98	0.31	50,50,50,50	0
27	ZN	N	1061	1/1	0.99	0.04	160,160,160,160	0

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



6.5 Other polymers ⓘ

There are no such residues in this entry.