



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 25, 2026 – 06:36 AM UTC

PDB ID : 1IBL / pdb_00001ibl
Title : STRUCTURE OF THE THERMUS THERMOPHILUS 30S RIBOSOMAL SUBUNIT IN COMPLEX WITH A MESSENGER RNA FRAGMENT AND COGNATE TRANSFER RNA ANTICODON STEM-LOOP BOUND AT THE A SITE AND WITH THE ANTIBIOTIC PAROMOMYCIN
Authors : Ogle, J.M.; Brodersen, D.E.; Clemons Jr., W.M.; Tarry, M.J.; Carter, A.P.; Ramakrishnan, V.
Deposited on : 2001-03-28
Resolution : 3.11 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

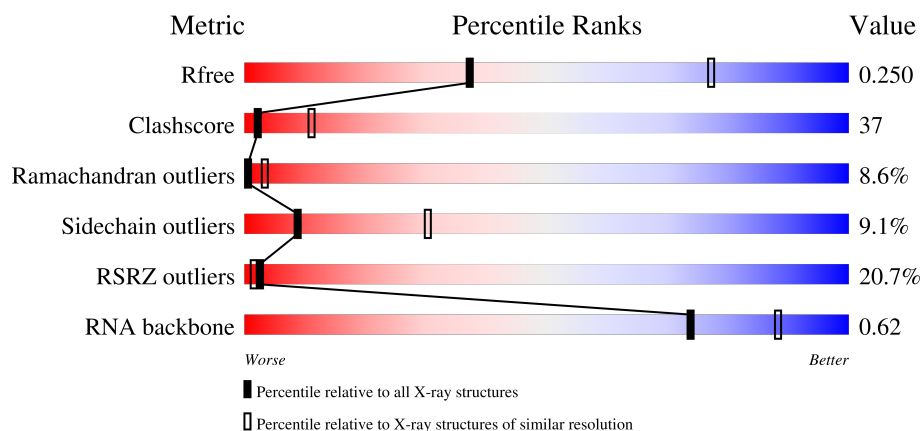
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.11 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1816 (3.14-3.10)
Clashscore	190562	1906 (3.14-3.10)
Ramachandran outliers	187476	1802 (3.14-3.10)
Sidechain outliers	187428	1802 (3.14-3.10)
RSRZ outliers	180081	1816 (3.14-3.10)
RNA backbone	3983	1017 (3.34-2.90)

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	1522	
2	X	6	

Continued on next page...

Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

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Mol	Chain	Length	Quality of chain
3	Y	15	
4	Z	4	
5	B	256	
6	C	239	
7	D	209	
8	E	162	
9	F	101	
10	G	156	
11	H	138	
12	I	128	
13	J	105	
14	K	129	
15	L	135	
16	M	126	
17	N	61	
18	O	89	
19	P	88	
20	Q	105	
21	R	88	
22	S	93	
23	T	106	
24	V	26	

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
26	MG	A	1589	-	-	-	X
26	MG	A	1616	-	-	-	X
26	MG	A	1628	-	-	-	X
26	MG	A	1633	-	-	-	X
26	MG	A	1640	-	-	-	X
26	MG	A	1642	-	-	-	X
26	MG	A	1645	-	-	-	X
26	MG	A	441	-	-	-	X

2 Entry composition

There are 27 unique types of molecules in this entry. The entry contains 52270 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	1507	Total	C	N	O	P	0	0	0
			32391	14418	6002	10465	1506			

- Molecule 2 is a RNA chain called P-SITE MESSENGER RNA FRAGMENT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	X	6	Total	C	N	O	P	0	0	0
			117	54	14	44	5			

- Molecule 3 is a RNA chain called ANTICODON STEM-LOOP OF PHENYLALANINE TRANSFER RNA.

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

- Molecule 4 is a RNA chain called A-SITE MESSENGER RNA FRAGMENT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	Z	4	Total	C	N	O	P	0	0	0
			77	36	8	30	3			

- Molecule 5 is a protein called 30S RIBOSOMAL PROTEIN S2.

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

- Molecule 6 is a protein called 30S RIBOSOMAL PROTEIN S3.

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

- Molecule 7 is a protein called 30S RIBOSOMAL PROTEIN S4.

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

- Molecule 8 is a protein called 30S RIBOSOMAL PROTEIN S5.

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

- Molecule 9 is a protein called 30S RIBOSOMAL PROTEIN S6.

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

- Molecule 10 is a protein called 30S RIBOSOMAL PROTEIN S7.

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

- Molecule 11 is a protein called 30S RIBOSOMAL PROTEIN S8.

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

- Molecule 12 is a protein called 30S RIBOSOMAL PROTEIN S9.

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

- Molecule 13 is a protein called 30S RIBOSOMAL PROTEIN S10.

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

- Molecule 14 is a protein called 30S RIBOSOMAL PROTEIN S11.

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

- Molecule 15 is a protein called 30S RIBOSOMAL PROTEIN S12.

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

- Molecule 16 is a protein called 30S RIBOSOMAL PROTEIN S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	M	118	Total	C	N	O	S	0	0	0
			937	579	193	163	2			

- Molecule 17 is a protein called 30S RIBOSOMAL PROTEIN S14.

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

- Molecule 18 is a protein called 30S RIBOSOMAL PROTEIN S15.

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

- Molecule 19 is a protein called 30S RIBOSOMAL PROTEIN S16.

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

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	?	-	PHE	conflict	GB 12056104
P	?	-	HIS	conflict	GB 12056104
P	?	-	TYR	conflict	GB 12056104

- Molecule 20 is a protein called 30S RIBOSOMAL PROTEIN S17.

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

- Molecule 21 is a protein called 30S RIBOSOMAL PROTEIN S18.

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

- Molecule 22 is a protein called 30S RIBOSOMAL PROTEIN S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	S	84	Total	C	N	O	S	0	0	0
			674	430	126	116	2			

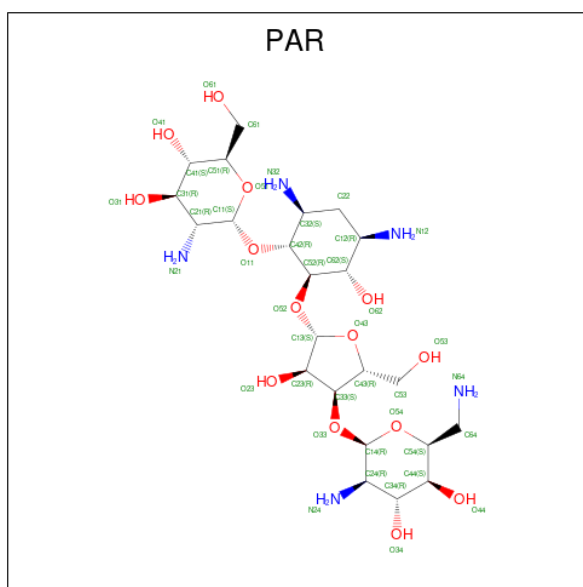
- Molecule 23 is a protein called 30S RIBOSOMAL PROTEIN S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	T	99	Total	C	N	O	S	0	0	0
			763	470	162	129	2			

- Molecule 24 is a protein called 30S RIBOSOMAL PROTEIN THX.

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

- Molecule 25 is PAROMOMYCIN (CCD ID: PAR) (formula: C₂₃H₄₅N₅O₁₄).



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

- Molecule 26 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
26	A	120	Total	Mg	0	0
			120	120		
26	Y	1	Total	Mg	0	0
			1	1		
26	D	2	Total	Mg	0	0
			2	2		
26	J	2	Total	Mg	0	0
			2	2		

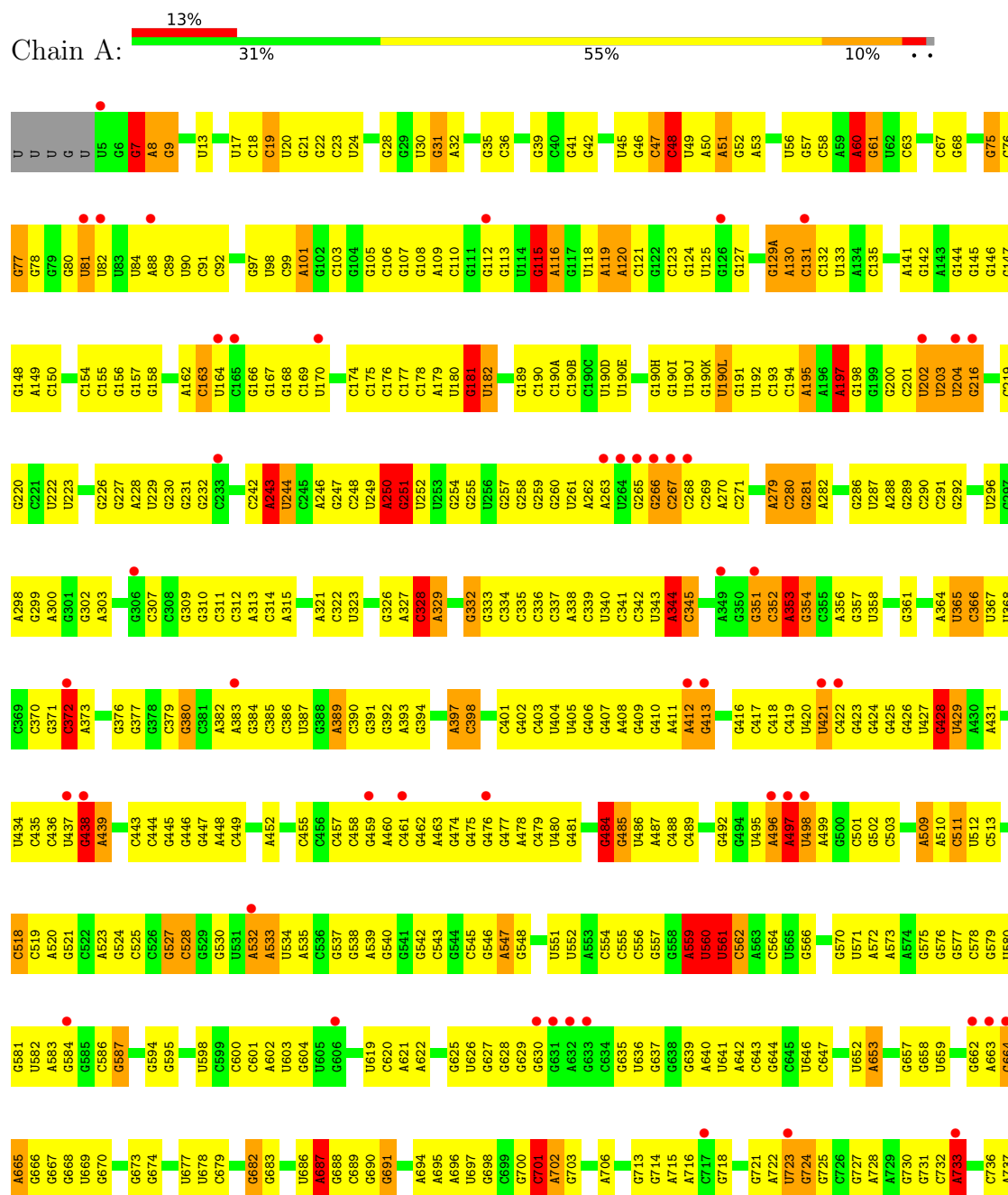
- Molecule 27 is ZINC ION (CCD ID: ZN) (formula: Zn).

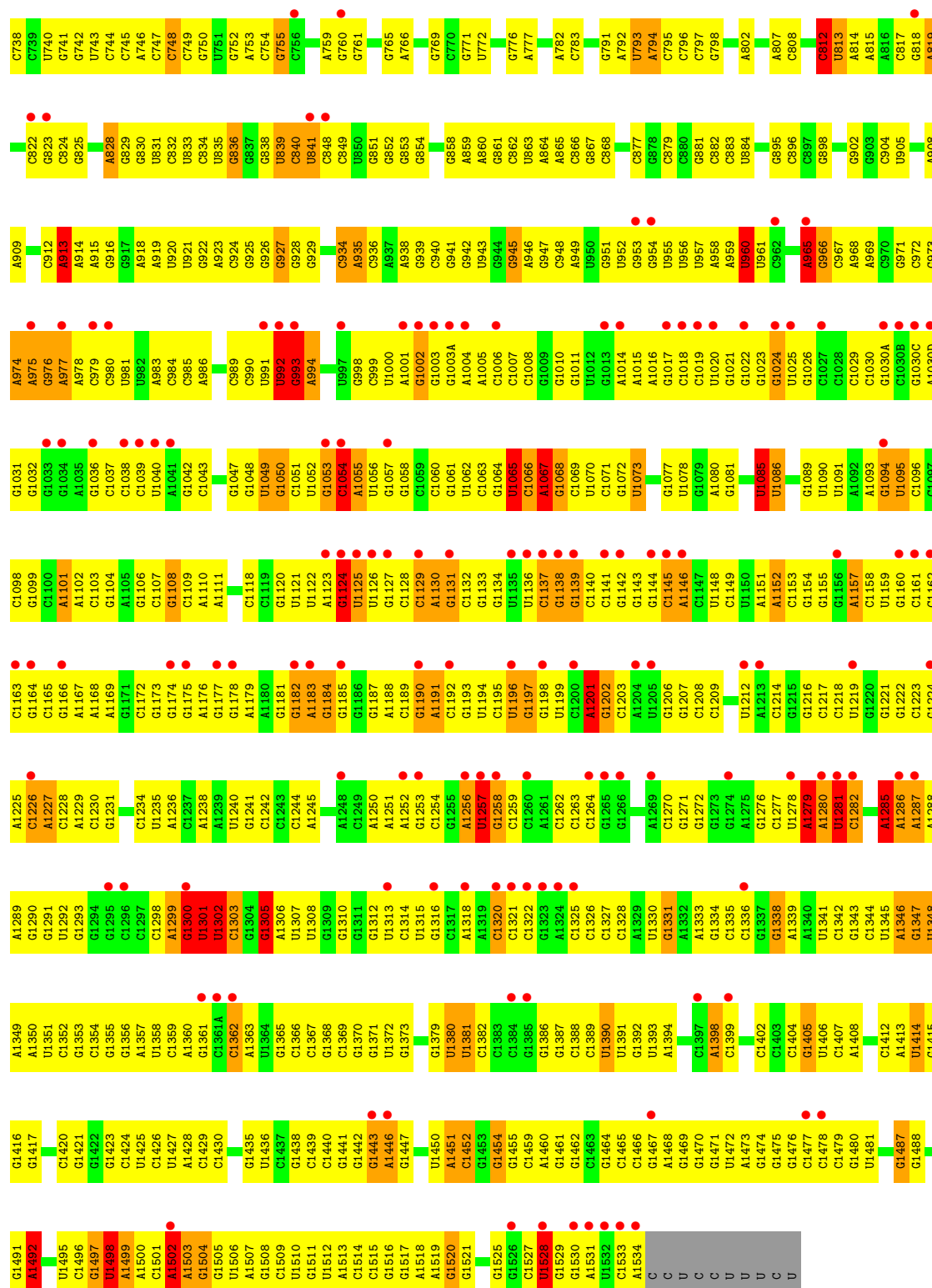
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
27	D	1	Total	Zn	0	0
			1	1		
27	N	1	Total	Zn	0	0
			1	1		

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.

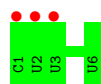
• Molecule 1: 16S RIBOSOMAL RNA





• Molecule 2: P-SITE MESSENGER RNA FRAGMENT





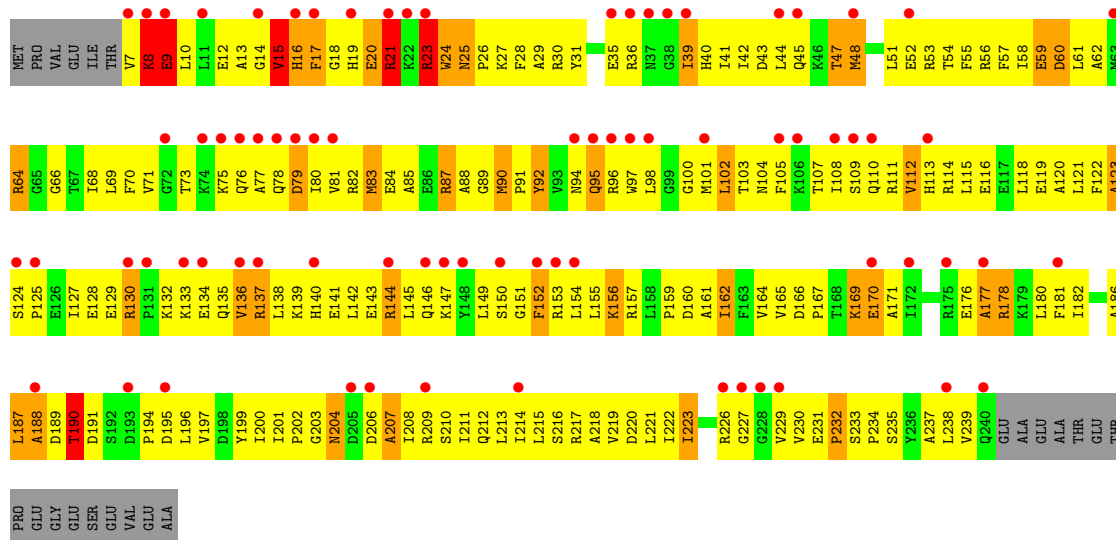
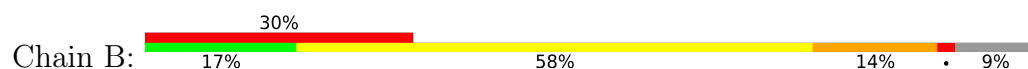
• Molecule 3: ANTICODON STEM-LOOP OF PHENYLALANINE TRANSFER RNA



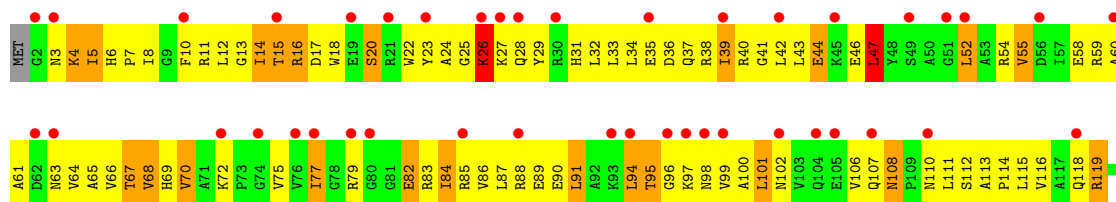
• Molecule 4: A-SITE MESSENGER RNA FRAGMENT

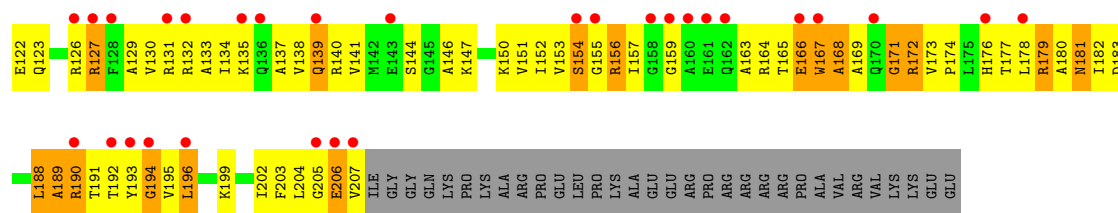


• Molecule 5: 30S RIBOSOMAL PROTEIN S2

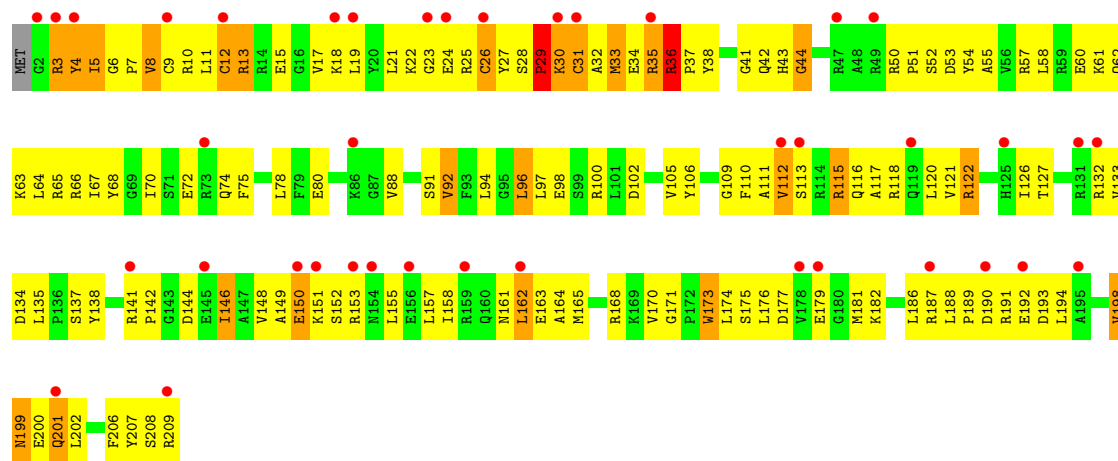


• Molecule 6: 30S RIBOSOMAL PROTEIN S3

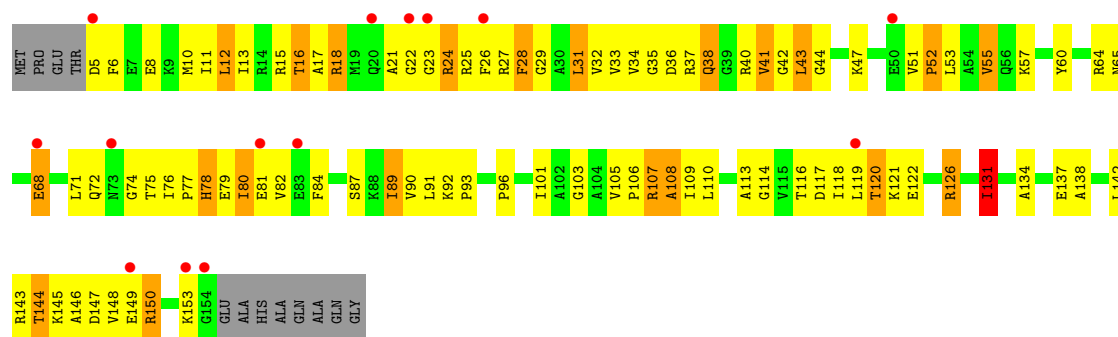




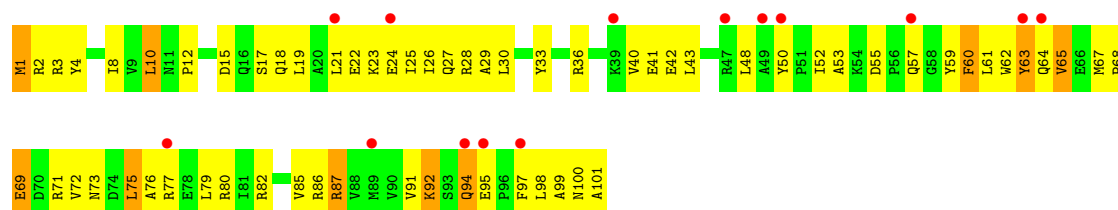
• Molecule 7: 30S RIBOSOMAL PROTEIN S4



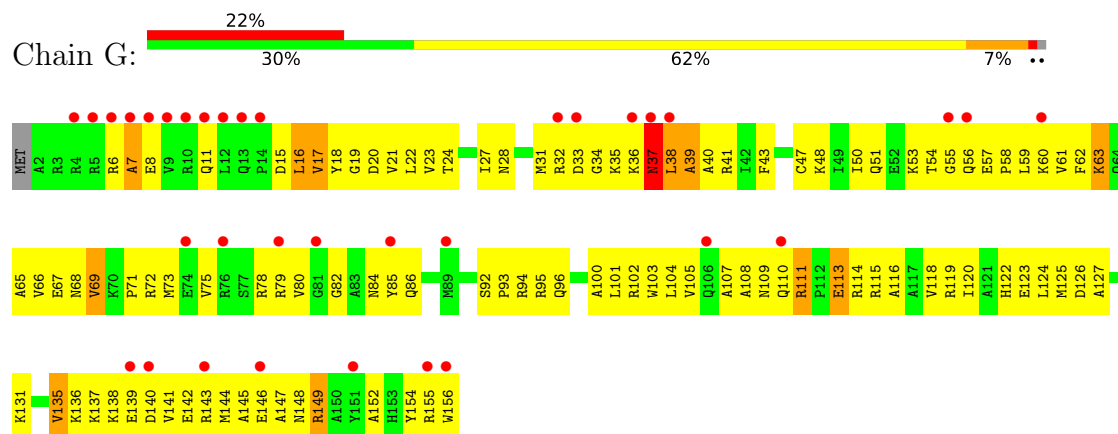
• Molecule 8: 30S RIBOSOMAL PROTEIN S5



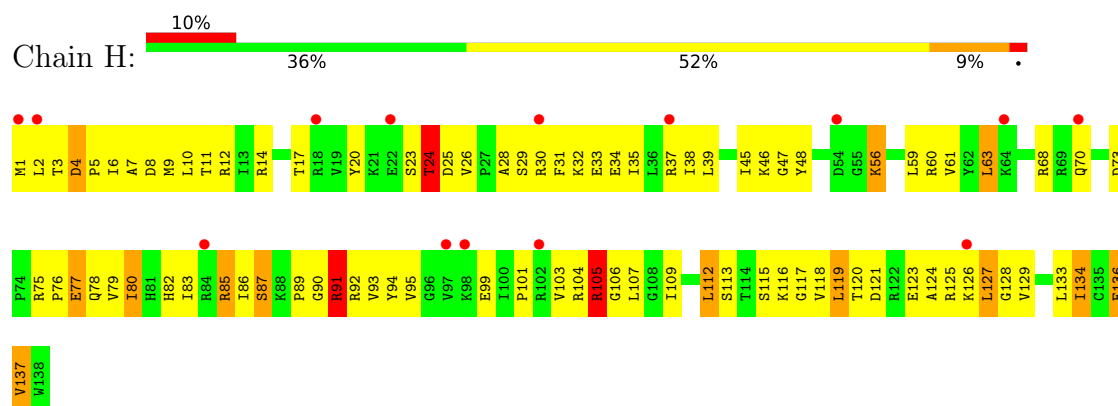
• Molecule 9: 30S RIBOSOMAL PROTEIN S6



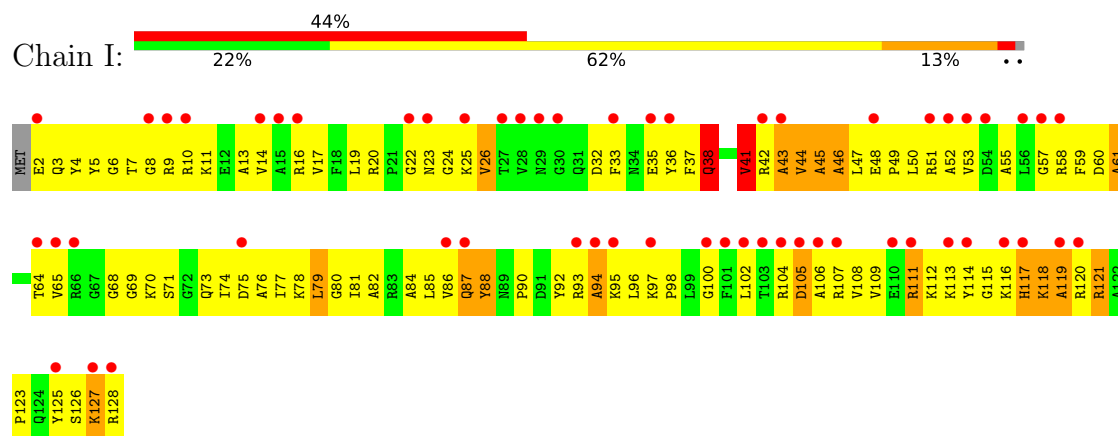
- Molecule 10: 30S RIBOSOMAL PROTEIN S7



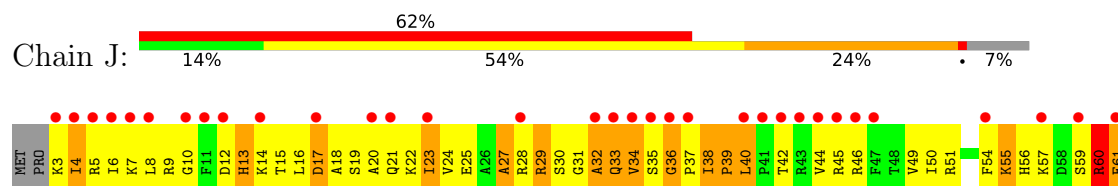
- Molecule 11: 30S RIBOSOMAL PROTEIN S8

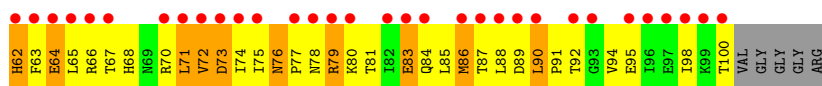


- Molecule 12: 30S RIBOSOMAL PROTEIN S9

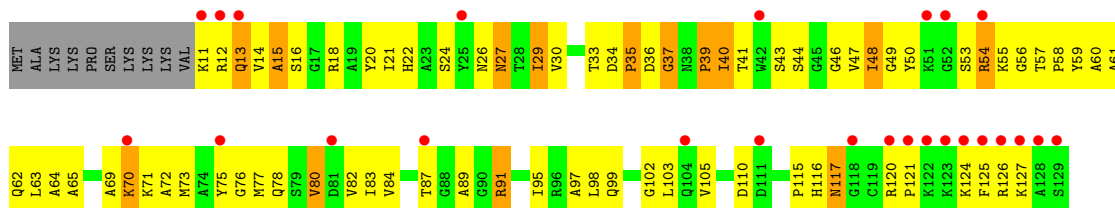


- Molecule 13: 30S RIBOSOMAL PROTEIN S10

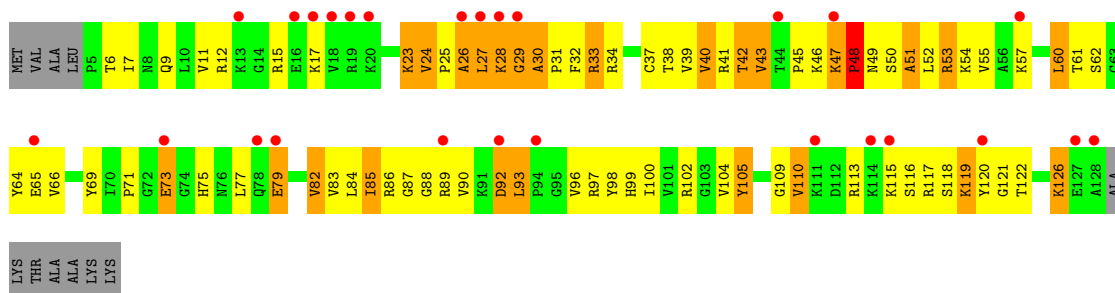




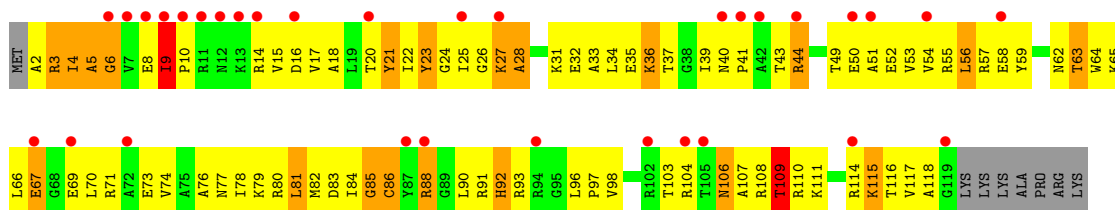
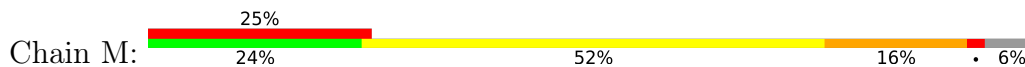
• Molecule 14: 30S RIBOSOMAL PROTEIN S11



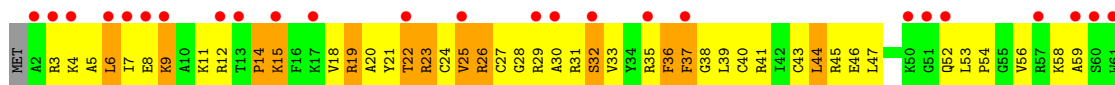
• Molecule 15: 30S RIBOSOMAL PROTEIN S12



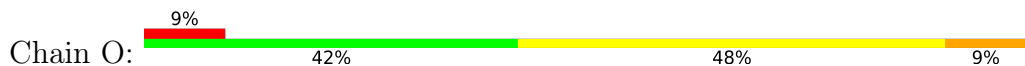
• Molecule 16: 30S RIBOSOMAL PROTEIN S13

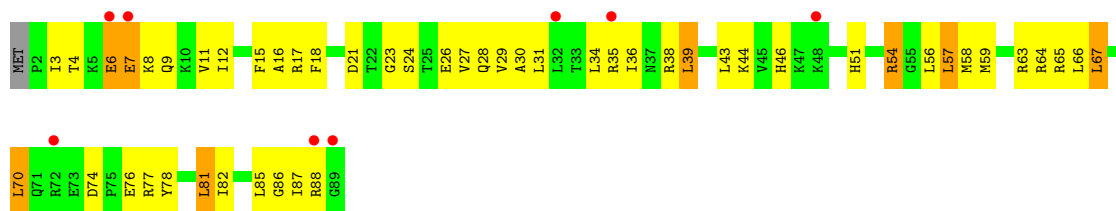


• Molecule 17: 30S RIBOSOMAL PROTEIN S14

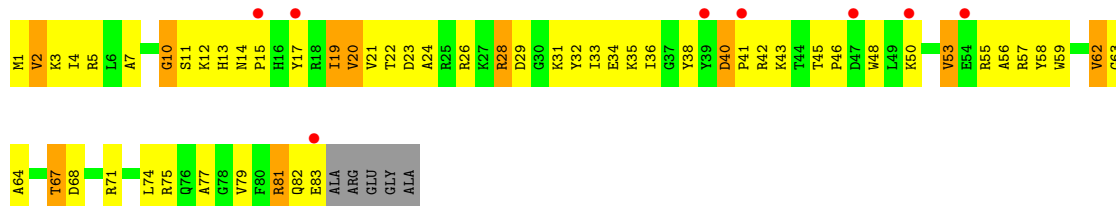


• Molecule 18: 30S RIBOSOMAL PROTEIN S15

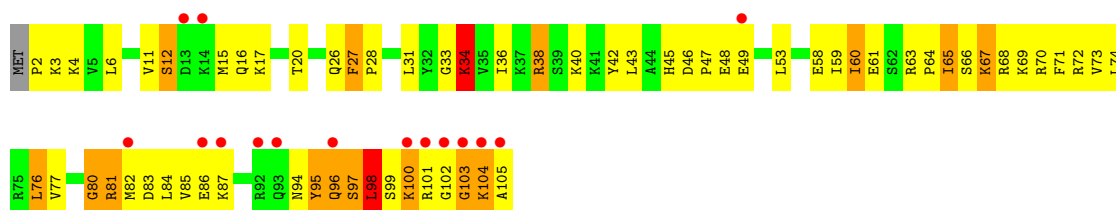




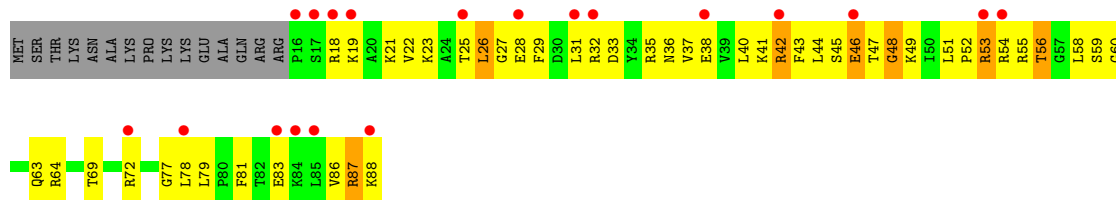
• Molecule 19: 30S RIBOSOMAL PROTEIN S16



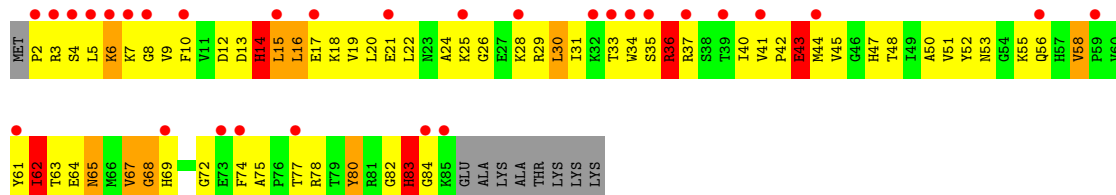
• Molecule 20: 30S RIBOSOMAL PROTEIN S17



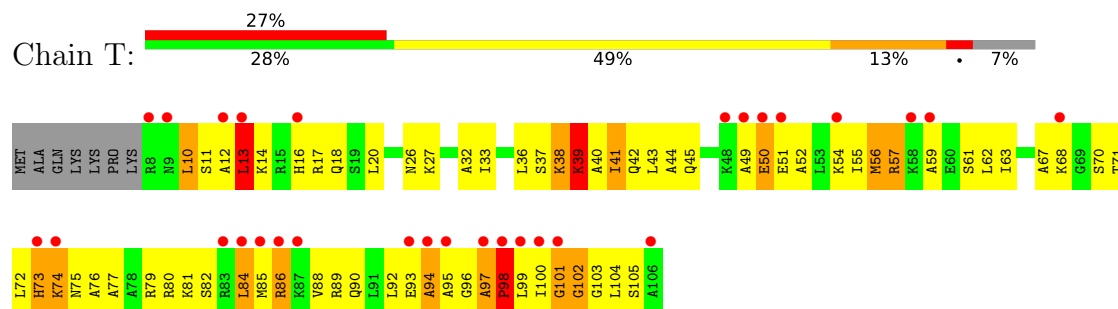
• Molecule 21: 30S RIBOSOMAL PROTEIN S18



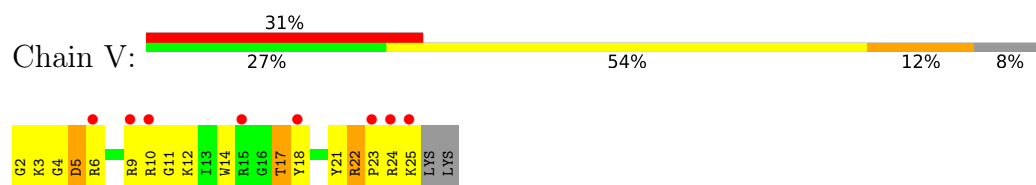
• Molecule 22: 30S RIBOSOMAL PROTEIN S19



● Molecule 23: 30S RIBOSOMAL PROTEIN S20



● Molecule 24: 30S RIBOSOMAL PROTEIN THX



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	400.80Å 400.80Å 175.88Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	316.23 – 3.11 283.41 – 3.11	Depositor EDS
% Data completeness (in resolution range)	89.9 (316.23-3.11) 89.8 (283.41-3.11)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.36 (at 3.13Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.232 , 0.275 0.211 , 0.250	Depositor DCC
R_{free} test set	11493 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	72.7	Xtriage
Anisotropy	0.163	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 548.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	52270	wwPDB-VP
Average B, all atoms (Å ²)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.48% 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: ZN, PAR, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.44	0/36259	0.72	73/56593 (0.1%)
2	X	0.44	0/128	0.64	0/196
3	Y	0.41	0/357	0.63	0/555
4	Z	0.40	0/84	0.85	0/128
5	B	0.39	0/1935	0.97	5/2609 (0.2%)
6	C	0.45	0/1636	0.93	2/2205 (0.1%)
7	D	0.65	2/1733 (0.1%)	1.07	14/2318 (0.6%)
8	E	0.59	0/1162	1.03	4/1564 (0.3%)
9	F	0.38	0/856	0.97	1/1154 (0.1%)
10	G	0.45	0/1276	0.94	5/1709 (0.3%)
11	H	0.60	0/1136	1.22	14/1527 (0.9%)
12	I	0.42	0/1029	0.97	3/1378 (0.2%)
13	J	0.43	0/805	0.97	2/1082 (0.2%)
14	K	0.53	0/900	1.05	4/1213 (0.3%)
15	L	0.58	0/986	1.25	11/1320 (0.8%)
16	M	0.44	0/947	0.96	2/1270 (0.2%)
17	N	0.47	0/501	1.10	3/664 (0.5%)
18	O	0.52	0/745	0.91	2/992 (0.2%)
19	P	0.60	0/716	1.12	6/963 (0.6%)
20	Q	0.60	0/870	1.11	5/1159 (0.4%)
21	R	0.44	0/603	0.96	4/799 (0.5%)
22	S	0.39	0/689	1.06	5/926 (0.5%)
23	T	0.64	1/765 (0.1%)	1.20	7/1007 (0.7%)
24	V	0.47	0/212	1.00	2/277 (0.7%)
All	All	0.47	3/56330 (0.0%)	0.83	174/83608 (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	3	34

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	D	198	VAL	C-N	-13.35	1.15	1.33
7	D	200	GLU	C-N	10.25	1.47	1.33
23	T	40	ALA	C-N	-7.72	1.24	1.33

All (174) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1498	U	C2'-C3'-O3'	14.77	131.65	109.50
15	L	26	ALA	N-CA-C	-14.09	96.42	113.19
1	A	243	A	C2'-C3'-O3'	13.91	130.37	109.50
1	A	281	G	C2'-C3'-O3'	13.70	130.05	109.50
23	T	13	LEU	N-CA-C	-13.35	97.12	113.41
1	A	484	G	C2'-C3'-O3'	12.88	128.82	109.50
1	A	1302	U	C2'-C3'-O3'	12.68	128.53	109.50
1	A	366	C	C2'-C3'-O3'	12.34	128.01	109.50
1	A	687	A	C2'-C3'-O3'	12.32	127.98	109.50
1	A	1528	U	C2'-C3'-O3'	11.85	127.28	109.50
1	A	965	A	C2'-C3'-O3'	10.98	125.97	109.50
1	A	181	G	C2'-C3'-O3'	10.94	125.91	109.50
1	A	1528	U	C4'-C3'-O3'	10.91	125.77	109.40
7	D	33	MET	N-CA-C	-10.86	99.22	111.71
1	A	328	C	C2'-C3'-O3'	10.80	125.71	109.50
1	A	372	C	C2'-C3'-O3'	10.70	125.55	109.50
1	A	1346	A	C2'-C3'-O3'	10.48	125.22	109.50
1	A	48	C	C2'-C3'-O3'	10.35	125.02	109.50
1	A	129(A)	G	C2'-C3'-O3'	9.98	124.47	109.50
1	A	60	A	C2'-C3'-O3'	9.82	124.23	109.50
1	A	197	A	C2'-C3'-O3'	9.71	124.07	109.50
1	A	559	A	C2'-C3'-O3'	9.51	123.76	109.50
1	A	913	A	C2'-C3'-O3'	9.49	123.74	109.50
1	A	281	G	C4'-C3'-O3'	9.06	122.99	109.40
1	A	1380	U	C2'-C3'-O3'	8.74	122.61	109.50
1	A	366	C	C4'-C3'-O3'	8.70	122.45	109.40
17	N	22	THR	N-CA-C	8.69	120.68	111.03
1	A	115	G	C2'-C3'-O3'	8.59	122.39	109.50
1	A	243	A	C4'-C3'-O3'	8.50	122.15	109.40
15	L	119	LYS	N-CA-C	-8.32	98.20	110.52
1	A	748	C	C2'-C3'-O3'	8.19	121.79	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	7	G	C2'-C3'-O3'	8.15	121.72	109.50
1	A	1301	U	C2'-C3'-O3'	8.08	121.62	109.50
1	A	1335	C	C4'-C3'-O3'	-8.03	100.95	113.00
21	R	46	GLU	N-CA-C	-7.96	103.32	112.87
10	G	111	ARG	CA-C-N	7.93	127.65	119.64
10	G	111	ARG	C-N-CA	7.93	127.65	119.64
7	D	28	SER	CA-C-N	7.86	129.66	119.84
7	D	28	SER	C-N-CA	7.86	129.66	119.84
15	L	24	VAL	CA-C-N	-7.54	110.42	119.84
15	L	24	VAL	C-N-CA	-7.54	110.42	119.84
1	A	129(A)	G	C4'-C3'-O3'	7.52	120.68	109.40
23	T	41	ILE	O-C-N	7.51	129.27	121.91
15	L	42	THR	N-CA-C	-7.50	98.34	109.81
20	Q	67	LYS	N-CA-C	-7.47	99.96	110.50
11	H	134	ILE	N-CA-C	7.45	118.05	110.82
11	H	77	GLU	N-CA-C	-7.44	100.93	110.53
1	A	484	G	C4'-C3'-O3'	7.37	120.46	109.40
7	D	12	CYS	N-CA-C	-7.37	102.27	111.11
1	A	1067	A	C2'-C3'-O3'	7.30	120.45	109.50
7	D	8	VAL	N-CA-C	7.09	117.65	111.90
23	T	94	ALA	N-CA-C	-7.05	102.79	112.03
11	H	56	LYS	CA-C-N	7.02	128.62	119.84
11	H	56	LYS	C-N-CA	7.02	128.62	119.84
7	D	11	LEU	N-CA-C	-6.98	103.11	111.69
13	J	60	ARG	N-CA-C	6.95	125.60	110.80
17	N	8	GLU	N-CA-C	-6.95	104.68	113.02
15	L	38	THR	N-CA-C	-6.92	105.36	113.88
21	R	56	THR	N-CA-C	-6.92	104.83	113.28
7	D	26	CYS	N-CA-C	-6.90	103.85	113.37
1	A	687	A	C4'-C3'-O3'	6.89	119.74	109.40
1	A	533	A	C2'-C3'-O3'	6.88	119.82	109.50
5	B	160	ASP	N-CA-C	-6.86	104.94	113.38
1	A	60	A	C4'-C3'-O3'	6.84	119.66	109.40
11	H	7	ALA	N-CA-C	-6.79	103.81	111.07
19	P	19	ILE	N-CA-C	-6.77	100.23	109.37
18	O	54	ARG	N-CA-C	-6.77	103.97	111.82
12	I	87	GLN	N-CA-C	-6.76	103.91	111.28
20	Q	27	PHE	CA-C-N	6.75	127.28	119.99
20	Q	27	PHE	C-N-CA	6.75	127.28	119.99
1	A	960	U	C2'-C3'-O3'	6.73	119.60	109.50
1	A	460	A	N9-C1'-C2'	6.72	122.07	112.00
1	A	1065	U	C2'-C3'-O3'	6.70	119.55	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	H	79	VAL	N-CA-C	-6.67	104.26	110.53
1	A	481	G	C5'-C4'-C3'	-6.62	105.26	115.20
1	A	1299	A	N9-C1'-C2'	6.61	121.92	112.00
13	J	62	HIS	N-CA-C	6.59	120.42	109.95
19	P	35	LYS	N-CA-C	-6.53	99.05	109.76
14	K	40	ILE	N-CA-C	-6.53	105.38	111.45
1	A	1285	A	C2'-C3'-O3'	6.53	119.29	109.50
1	A	1305	G	N9-C1'-C2'	6.43	121.65	112.00
15	L	60	LEU	N-CA-C	6.38	118.95	110.53
1	A	1225	A	N9-C1'-C2'	6.36	121.53	112.00
7	D	13	ARG	N-CA-C	6.34	117.86	111.07
21	R	81	PHE	N-CA-C	-6.33	105.69	113.41
1	A	1498	U	C4'-C3'-O3'	6.30	118.86	109.40
11	H	136	GLU	N-CA-C	-6.29	100.67	110.17
23	T	44	ALA	N-CA-C	-6.26	104.56	111.82
1	A	1502	A	N9-C1'-C2'	6.21	123.32	114.00
8	E	131	ILE	N-CA-C	-6.21	104.79	110.82
22	S	36	ARG	N-CA-C	-6.20	105.36	113.17
5	B	152	PHE	N-CA-C	-6.18	105.83	113.19
1	A	250	A	C2'-C3'-O3'	6.13	118.69	109.50
1	A	1257	U	C2'-C3'-O3'	6.09	118.64	109.50
5	B	47	THR	N-CA-C	-6.09	104.56	111.07
20	Q	65	ILE	N-CA-C	-6.05	104.50	113.39
22	S	62	ILE	N-CA-C	6.00	116.50	107.80
21	R	53	ARG	N-CA-C	-5.95	104.87	111.71
6	C	77	ILE	N-CA-C	5.92	116.13	110.74
1	A	353	A	C5'-C4'-O4'	-5.85	101.02	109.80
1	A	63	C	C5'-C4'-C3'	-5.84	107.24	116.00
1	A	992	U	C2'-C3'-O3'	5.84	118.25	109.50
23	T	45	GLN	N-CA-C	-5.80	104.65	110.97
15	L	88	GLY	N-CA-C	-5.77	99.50	113.18
19	P	20	VAL	N-CA-C	5.76	116.97	108.45
23	T	103	GLY	N-CA-C	5.73	119.42	112.49
1	A	812	C	C2'-C3'-O3'	5.70	118.05	109.50
17	N	9	LYS	N-CA-C	-5.70	105.15	111.36
24	V	17	THR	N-CA-C	5.70	118.32	109.60
7	D	36	ARG	CA-C-N	5.68	126.42	120.12
7	D	36	ARG	C-N-CA	5.68	126.42	120.12
15	L	23	LYS	N-CA-C	-5.67	104.77	112.26
1	A	344	A	C2'-C3'-O3'	5.64	117.97	109.50
1	A	701	C	C2'-C3'-O3'	5.64	117.96	109.50
7	D	173	TRP	N-CA-C	-5.64	104.99	112.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	389	A	C2'-C3'-O3'	-5.61	105.28	113.70
11	H	80	ILE	CB-CA-C	-5.59	106.96	113.22
22	S	4	SER	N-CA-C	5.58	117.56	109.07
1	A	365	U	C4'-C3'-O3'	-5.57	104.65	113.00
14	K	37	GLY	N-CA-C	5.55	122.50	114.67
8	E	38	GLN	N-CA-C	-5.55	104.04	111.87
15	L	28	LYS	N-CA-C	-5.52	106.92	113.38
9	F	60	PHE	N-CA-C	5.48	119.03	110.32
20	Q	100	LYS	N-CA-C	-5.48	106.96	113.97
1	A	1201	A	C2'-C3'-O3'	5.44	117.66	109.50
1	A	438	G	C4'-C3'-O3'	5.44	117.55	109.40
1	A	428	G	C2'-C3'-O3'	5.43	117.65	109.50
19	P	67	THR	N-CA-C	-5.43	103.32	110.43
7	D	112	VAL	N-CA-C	5.42	115.62	110.42
1	A	509	A	C2'-C3'-O3'	5.36	121.73	113.70
1	A	1124	G	N9-C1'-C2'	5.34	120.02	112.00
6	C	194	GLY	N-CA-C	5.34	117.32	110.96
1	A	1279	A	N9-C1'-C2'	5.34	120.01	112.00
16	M	106	ASN	CB-CA-C	-5.31	109.47	115.79
10	G	17	VAL	N-CA-C	5.30	115.81	111.62
11	H	4	ASP	CA-C-N	5.29	125.35	119.32
11	H	4	ASP	C-N-CA	5.29	125.35	119.32
1	A	1281	U	C4'-C3'-O3'	-5.28	105.08	113.00
1	A	1331	G	C4'-C3'-O3'	-5.28	105.08	113.00
1	A	75	G	C5'-C4'-C3'	5.27	123.91	116.00
15	L	92	ASP	N-CA-C	5.27	119.76	113.23
1	A	836	G	C5'-C4'-C3'	5.27	123.90	116.00
1	A	560	U	C2'-C3'-O3'	5.26	121.59	113.70
16	M	92	HIS	N-CA-C	-5.26	105.72	111.82
19	P	40	ASP	CA-C-N	5.25	125.30	119.32
19	P	40	ASP	C-N-CA	5.25	125.30	119.32
7	D	115	ARG	N-CA-C	-5.24	105.57	111.28
23	T	56	MET	N-CA-C	-5.24	104.99	111.33
1	A	1331	G	N9-C1'-C2'	5.22	119.83	112.00
11	H	73	ASP	CA-C-N	5.20	126.22	120.45
11	H	73	ASP	C-N-CA	5.20	126.22	120.45
18	O	44	LYS	N-CA-C	-5.20	105.79	111.82
1	A	1335	C	N1-C1'-C2'	5.19	119.79	112.00
1	A	1108	G	C5'-C4'-C3'	5.17	123.76	116.00
10	G	55	GLY	N-CA-C	-5.17	107.22	115.66
12	I	22	GLY	N-CA-C	5.17	117.00	110.38
1	A	993	G	C2'-C3'-O3'	5.17	117.25	109.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	S	25	LYS	N-CA-C	-5.16	107.28	113.21
8	E	32	VAL	N-CA-C	5.15	115.54	108.12
22	S	58	VAL	N-CA-C	5.14	114.11	108.05
7	D	44	GLY	N-CA-C	5.14	120.10	113.27
12	I	61	ALA	N-CA-C	5.13	117.53	108.75
11	H	46	LYS	N-CA-C	-5.13	106.71	112.87
1	A	497	A	C2'-C3'-O3'	5.12	117.18	109.50
8	E	28	PHE	N-CA-C	5.12	117.75	109.40
11	H	87	SER	N-CA-C	-5.10	103.41	110.35
1	A	1054	C	N1-C1'-C2'	5.09	119.64	112.00
5	B	64	ARG	N-CA-C	-5.06	105.16	113.50
5	B	137	ARG	N-CA-C	-5.05	106.22	112.38
1	A	1085	U	C2'-C3'-O3'	5.05	117.07	109.50
14	K	39	PRO	N-CA-C	5.04	118.80	111.03
10	G	39	ALA	N-CA-C	-5.03	105.49	110.97
14	K	55	LYS	N-CA-C	-5.02	105.94	111.71
24	V	5	ASP	N-CA-C	5.01	116.44	108.67

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	243	A	C3'
1	A	281	G	C3'
1	A	1528	U	C3'

All (34) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1073	U	Sidechain
1	A	1077	G	Sidechain
1	A	1185	G	Sidechain
1	A	1300	G	Sidechain
1	A	1341	U	Sidechain
1	A	1390	U	Sidechain
1	A	1405	G	Sidechain
1	A	1414	U	Sidechain
1	A	1454	G	Sidechain
1	A	1492	A	Sidechain
1	A	1519	A	Sidechain
1	A	19	C	Sidechain
1	A	190(L)	U	Sidechain
1	A	197	A	Sidechain

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Mol	Chain	Res	Type	Group
1	A	250	A	Sidechain
1	A	251	G	Sidechain
1	A	290	C	Sidechain
1	A	368	U	Sidechain
1	A	380	G	Sidechain
1	A	387	U	Sidechain
1	A	495	U	Sidechain
1	A	528	C	Sidechain
1	A	561	U	Sidechain
1	A	587	G	Sidechain
1	A	664	G	Sidechain
1	A	682	G	Sidechain
1	A	691	G	Sidechain
1	A	724	G	Sidechain
1	A	727	G	Sidechain
1	A	733	A	Sidechain
1	A	759	A	Sidechain
1	A	77	G	Sidechain
1	A	879	C	Sidechain
1	A	898	G	Sidechain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of 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	32391	0	16349	1160	0
2	X	117	0	64	0	0
3	Y	319	0	164	12	0
4	Z	77	0	42	6	0
5	B	1900	0	1951	305	0
6	C	1612	0	1677	256	0
7	D	1703	0	1764	164	0
8	E	1146	0	1207	115	0
9	F	843	0	857	91	0
10	G	1257	0	1296	109	0
11	H	1116	0	1177	113	0
12	I	1011	0	1043	143	0
13	J	792	0	835	154	1

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
14	K	885	0	904	91	0
15	L	970	0	1057	130	0
16	M	937	0	995	136	0
17	N	492	0	529	81	0
18	O	734	0	771	56	0
19	P	700	0	720	62	0
20	Q	857	0	930	98	0
21	R	597	0	668	79	0
22	S	674	0	699	95	0
23	T	763	0	861	92	0
24	V	208	0	221	21	0
25	A	42	0	45	2	0
26	A	120	0	0	0	0
26	D	2	0	0	0	0
26	J	2	0	0	0	0
26	Y	1	0	0	0	0
27	D	1	0	0	0	0
27	N	1	0	0	0	0
All	All	52270	0	36826	3272	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 37.

All (3272) 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)
5:B:132:LYS:HA	5:B:135:GLN:HB3	1.20	1.14
7:D:36:ARG:H	7:D:37:PRO:HD3	1.09	1.13
1:A:975:A:H4'	1:A:976:G:H5''	1.25	1.12
1:A:1286:A:H3'	1:A:1287:A:H5''	1.28	1.12
8:E:80:ILE:HD11	8:E:91:LEU:HB2	1.31	1.11
5:B:84:GLU:HB3	5:B:219:VAL:HG21	1.24	1.11
1:A:1443:G:H5''	1:A:1446:A:H5'	1.20	1.10
8:E:80:ILE:CD1	8:E:91:LEU:HB2	1.81	1.09
14:K:48:ILE:HG22	14:K:49:GLY:H	0.99	1.08
6:C:33:LEU:HD11	17:N:53:LEU:HD22	1.33	1.08
17:N:26:ARG:HH12	17:N:47:LEU:HD21	1.15	1.06
5:B:21:ARG:HD3	5:B:21:ARG:H	1.17	1.05
7:D:151:LYS:H	7:D:151:LYS:HD2	1.16	1.04
15:L:47:LYS:HB3	15:L:48:PRO:HD3	1.37	1.04
22:S:33:THR:HG22	22:S:35:SER:H	1.18	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:77:ALA:HB2	5:B:211:ILE:HD13	1.40	1.04
1:A:1250:A:H4'	12:I:68:GLY:H	1.19	1.03
1:A:877:C:O2	11:H:3:THR:HG21	1.60	1.02
1:A:1286:A:C3'	1:A:1287:A:H5''	1.88	1.02
15:L:27:LEU:HD23	15:L:62:SER:HB2	1.43	1.00
22:S:28:LYS:HG2	22:S:29:ARG:H	1.22	1.00
1:A:1190:G:H3'	6:C:3:ASN:HD22	1.27	1.00
11:H:86:ILE:HD11	11:H:136:GLU:HG3	1.42	0.99
5:B:80:ILE:HD12	5:B:80:ILE:H	1.27	0.99
13:J:32:ALA:HB2	13:J:76:ASN:HD22	1.27	0.98
1:A:371:G:O2'	1:A:372:C:H5'	1.63	0.98
14:K:91:ARG:HH11	21:R:88:LYS:HZ1	1.09	0.97
8:E:81:GLU:HG2	8:E:90:VAL:HG22	1.44	0.97
6:C:108:ASN:HD22	6:C:111:LEU:HG	1.30	0.96
10:G:50:ILE:HG21	10:G:61:VAL:HG21	1.47	0.96
1:A:1056:U:H5'	6:C:163:ALA:HB2	1.48	0.95
10:G:75:VAL:HG21	10:G:86:GLN:HB3	1.45	0.95
14:K:54:ARG:O	14:K:57:THR:HG22	1.65	0.95
16:M:10:PRO:HB2	16:M:18:ALA:HB1	1.47	0.95
1:A:243:A:H4'	1:A:244:U:H5'	1.48	0.95
6:C:14:ILE:HG22	6:C:15:THR:H	1.28	0.94
1:A:1086:U:H3	1:A:1099:G:H22	1.07	0.94
14:K:48:ILE:HG22	14:K:49:GLY:N	1.81	0.94
15:L:28:LYS:C	15:L:30:ALA:H	1.76	0.94
20:Q:67:LYS:HA	20:Q:70:ARG:HH12	1.31	0.94
1:A:737:A:H1'	9:F:73:ASN:HD21	1.31	0.94
15:L:25:PRO:C	15:L:27:LEU:H	1.67	0.92
1:A:1057:G:H5''	6:C:154:SER:HB2	1.52	0.92
9:F:100:ASN:HD22	21:R:23:LYS:HG2	1.35	0.92
1:A:1502:A:H2	1:A:1505:G:H1	1.03	0.91
1:A:1305:G:O2'	1:A:1306:A:H8	1.52	0.91
1:A:1190:G:H3'	6:C:3:ASN:ND2	1.85	0.91
8:E:11:ILE:HB	8:E:31:LEU:HB3	1.53	0.91
5:B:77:ALA:HA	5:B:80:ILE:HD13	1.52	0.90
1:A:975:A:H5'	1:A:975:A:H8	1.34	0.90
1:A:579:G:H5'	1:A:728:A:H1'	1.53	0.90
1:A:975:A:H4'	1:A:976:G:C5'	2.00	0.90
5:B:59:GLU:HG2	5:B:221:LEU:HD11	1.53	0.90
6:C:58:GLU:HB3	13:J:92:THR:HG21	1.52	0.90
7:D:162:LEU:HG	7:D:181:MET:HE2	1.54	0.90
10:G:16:LEU:H	10:G:16:LEU:HD22	1.36	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:E:76:ILE:HG13	8:E:77:PRO:HD2	1.55	0.89
18:O:70:LEU:HD13	18:O:78:TYR:HA	1.55	0.89
9:F:2:ARG:HE	9:F:69:GLU:HG2	1.38	0.89
1:A:1190:G:OP1	6:C:4:LYS:HA	1.71	0.89
6:C:174:PRO:HB2	6:C:177:THR:HG22	1.55	0.89
18:O:16:ALA:HB1	18:O:21:ASP:HB3	1.52	0.88
1:A:390:C:H2'	1:A:391:G:H8	1.36	0.88
5:B:219:VAL:O	5:B:223:ILE:HG12	1.73	0.87
1:A:664:G:H22	1:A:741:G:H1	1.22	0.87
1:A:1504:G:OP1	1:A:1507:A:H4'	1.74	0.87
15:L:24:VAL:O	15:L:24:VAL:HG12	1.74	0.87
1:A:390:C:H2'	1:A:391:G:C8	2.10	0.87
6:C:191:THR:HG21	6:C:193:TYR:CZ	2.10	0.87
7:D:62:GLN:HE22	7:D:65:ARG:HH12	1.22	0.87
13:J:8:LEU:HD22	13:J:20:ALA:HB2	1.54	0.87
1:A:1250:A:H4'	12:I:68:GLY:N	1.90	0.87
5:B:71:VAL:HG23	5:B:164:VAL:HA	1.54	0.87
15:L:47:LYS:HB3	15:L:48:PRO:CD	2.04	0.86
6:C:34:LEU:HD23	6:C:34:LEU:C	2.00	0.86
9:F:28:ARG:NH1	9:F:28:ARG:HB2	1.91	0.86
12:I:93:ARG:HD3	12:I:97:LYS:HZ1	1.40	0.86
14:K:48:ILE:CG2	14:K:49:GLY:H	1.85	0.85
17:N:27:CYS:SG	17:N:29:ARG:HB2	2.15	0.85
1:A:1256:A:H4'	1:A:1257:U:H5'	1.57	0.85
21:R:47:THR:HG23	21:R:83:GLU:H	1.40	0.85
6:C:26:LYS:H	6:C:26:LYS:HD3	1.40	0.85
15:L:60:LEU:HD21	15:L:66:VAL:HG22	1.58	0.85
5:B:69:LEU:HD23	5:B:70:PHE:N	1.91	0.85
14:K:40:ILE:HG22	14:K:41:THR:HG23	1.59	0.85
15:L:25:PRO:C	15:L:27:LEU:N	2.32	0.85
10:G:51:GLN:HE21	10:G:58:PRO:HD3	1.42	0.85
1:A:250:A:H4'	1:A:251:G:O5'	1.77	0.85
23:T:43:LEU:HD13	23:T:51:GLU:HG3	1.59	0.85
6:C:119:ARG:HG2	6:C:140:ARG:NH1	1.92	0.84
13:J:34:VAL:HA	13:J:74:ILE:HG22	1.59	0.84
7:D:36:ARG:N	7:D:37:PRO:HD3	1.88	0.84
8:E:76:ILE:HD11	8:E:142:LEU:HD13	1.59	0.84
1:A:1286:A:H3'	1:A:1287:A:C5'	2.06	0.84
8:E:79:GLU:HG3	8:E:93:PRO:HD2	1.59	0.84
17:N:6:LEU:HD22	17:N:23:ARG:NH2	1.92	0.84
13:J:23:ILE:HD12	13:J:23:ILE:H	1.43	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:K:91:ARG:HH11	21:R:88:LYS:NZ	1.76	0.84
5:B:144:ARG:HD2	5:B:145:LEU:HD23	1.60	0.84
15:L:28:LYS:O	15:L:30:ALA:N	2.09	0.84
15:L:47:LYS:CB	15:L:48:PRO:HD3	2.08	0.83
15:L:126:LYS:H	15:L:126:LYS:HD2	1.43	0.83
21:R:47:THR:HA	21:R:83:GLU:HB2	1.60	0.83
1:A:1226:C:H4'	1:A:1227:A:OP1	1.77	0.83
22:S:20:LEU:HD12	22:S:21:GLU:N	1.94	0.83
13:J:6:ILE:HG22	13:J:98:ILE:HG12	1.61	0.82
1:A:1015:A:H2'	1:A:1016:A:C8	2.14	0.82
1:A:254:G:H21	20:Q:16:GLN:HE21	1.24	0.82
1:A:1168:A:H2'	1:A:1169:A:C8	2.14	0.82
5:B:80:ILE:HG12	5:B:208:ILE:HG23	1.60	0.82
8:E:74:GLY:HA3	8:E:116:THR:HG22	1.62	0.82
16:M:14:ARG:N	16:M:44:ARG:HH21	1.77	0.82
5:B:139:LYS:O	5:B:143:GLU:HG2	1.80	0.82
23:T:56:MET:HE1	23:T:104:LEU:HD21	1.62	0.81
1:A:1152:A:H2'	1:A:1153:C:C6	2.14	0.81
5:B:88:ALA:HB2	5:B:219:VAL:HG13	1.62	0.81
11:H:120:THR:OG1	11:H:123:GLU:HG3	1.80	0.81
10:G:15:ASP:HB3	10:G:19:GLY:N	1.95	0.81
16:M:14:ARG:H	16:M:44:ARG:HH21	1.28	0.81
1:A:1279:A:H5''	1:A:1280:A:OP1	1.81	0.80
1:A:1502:A:H2	1:A:1505:G:N1	1.78	0.80
5:B:116:GLU:HG2	5:B:153:ARG:NH2	1.97	0.80
6:C:190:ARG:HB3	6:C:190:ARG:HH11	1.47	0.80
13:J:49:VAL:O	13:J:60:ARG:HA	1.82	0.80
1:A:1250:A:C4'	12:I:68:GLY:H	1.93	0.80
9:F:33:TYR:HA	9:F:71:ARG:NH2	1.95	0.80
12:I:46:ALA:HB2	12:I:74:ILE:HG23	1.63	0.80
6:C:64:VAL:HB	6:C:99:VAL:HB	1.64	0.80
9:F:4:TYR:CZ	9:F:72:VAL:HG21	2.16	0.80
1:A:524:G:H2'	1:A:525:C:C6	2.17	0.80
6:C:180:ALA:O	6:C:181:ASN:HB3	1.82	0.80
5:B:71:VAL:HG21	5:B:164:VAL:HG22	1.64	0.80
14:K:18:ARG:HB2	14:K:33:THR:CG2	2.12	0.80
18:O:17:ARG:HG3	18:O:17:ARG:HH11	1.46	0.79
1:A:1443:G:H5''	1:A:1446:A:C5'	2.09	0.79
1:A:972:C:H4'	13:J:57:LYS:HG2	1.63	0.79
5:B:218:ALA:O	5:B:222:ILE:HG13	1.82	0.79
1:A:1003(A):G:H2'	1:A:1004:A:H4'	1.63	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:I:81:ILE:O	12:I:85:LEU:HB2	1.82	0.79
8:E:80:ILE:HD12	8:E:80:ILE:H	1.46	0.79
12:I:8:GLY:HA2	12:I:79:LEU:HD13	1.64	0.79
14:K:91:ARG:NH1	21:R:88:LYS:HZ1	1.81	0.79
18:O:3:ILE:HD11	18:O:38:ARG:HG3	1.65	0.79
17:N:26:ARG:NH1	17:N:47:LEU:HD21	1.96	0.79
18:O:29:VAL:HG11	18:O:67:LEU:HD21	1.63	0.79
1:A:80:G:H3'	1:A:81:U:H5''	1.65	0.79
13:J:20:ALA:HA	13:J:23:ILE:HD13	1.63	0.79
16:M:78:ILE:HA	16:M:81:LEU:HD21	1.65	0.79
13:J:31:GLY:HA2	13:J:78:ASN:ND2	1.98	0.78
5:B:91:PRO:HB3	5:B:154:LEU:HB2	1.64	0.78
1:A:975:A:H5'	1:A:975:A:C8	2.17	0.78
5:B:118:LEU:HB3	5:B:142:LEU:HD12	1.64	0.78
6:C:14:ILE:O	6:C:16:ARG:N	2.16	0.78
12:I:26:VAL:HB	12:I:33:PHE:HB2	1.65	0.78
12:I:86:VAL:HG13	12:I:90:PRO:HA	1.66	0.78
12:I:106:ALA:O	12:I:108:VAL:HG23	1.83	0.78
5:B:57:PHE:CE2	5:B:61:LEU:HD11	2.17	0.78
1:A:853:G:O2'	1:A:854:G:H5'	1.83	0.78
1:A:1124:G:H5'	13:J:35:SER:O	1.83	0.78
23:T:85:MET:HE2	23:T:104:LEU:HD23	1.65	0.78
1:A:1305:G:HO2'	1:A:1306:A:H8	1.19	0.78
9:F:28:ARG:HB2	9:F:28:ARG:HH11	1.49	0.78
1:A:1226:C:H1'	22:S:83:HIS:HE1	1.49	0.78
6:C:108:ASN:HD21	6:C:110:ASN:HB2	1.47	0.78
5:B:57:PHE:O	5:B:61:LEU:HG	1.84	0.77
13:J:18:ALA:O	13:J:21:GLN:HB3	1.83	0.77
16:M:8:GLU:O	16:M:9:ILE:HG23	1.83	0.77
1:A:1201:A:H4'	1:A:1202:G:O5'	1.84	0.77
1:A:838:G:H2'	1:A:839:U:H5''	1.65	0.77
5:B:142:LEU:HD21	5:B:146:GLN:HE21	1.49	0.77
1:A:1238:A:H5'	1:A:1336:C:H41	1.48	0.77
5:B:68:ILE:HB	5:B:90:MET:HE3	1.66	0.77
15:L:34:ARG:O	15:L:61:THR:HG23	1.83	0.77
1:A:1038:C:H2'	1:A:1039:C:C6	2.19	0.77
1:A:1369:C:H2'	1:A:1370:G:C8	2.19	0.77
7:D:7:PRO:HB2	7:D:10:ARG:HD2	1.67	0.77
1:A:443:C:H2'	1:A:444:C:H6	1.50	0.77
1:A:1196:U:H5''	1:A:1197:G:H5'	1.67	0.77
16:M:62:ASN:O	16:M:63:THR:HB	1.82	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1286:A:C2'	1:A:1287:A:H5''	2.14	0.77
6:C:35:GLU:CD	6:C:59:ARG:HH22	1.93	0.77
13:J:8:LEU:HB2	13:J:70:ARG:HB2	1.67	0.77
13:J:31:GLY:HA2	13:J:78:ASN:HD22	1.50	0.77
1:A:1003(A):G:H2'	1:A:1004:A:C4'	2.15	0.76
15:L:41:ARG:HH12	15:L:57:LYS:HZ3	1.33	0.76
23:T:13:LEU:H	23:T:13:LEU:HD12	1.51	0.76
1:A:328:C:O2	1:A:328:C:H2'	1.83	0.76
9:F:2:ARG:HE	9:F:69:GLU:CG	1.98	0.76
1:A:371:G:C2'	1:A:372:C:H5'	2.14	0.76
1:A:1137:C:H4'	1:A:1138:G:C2	2.20	0.76
5:B:123:ALA:N	5:B:127:ILE:HD11	2.01	0.76
5:B:124:SER:HB2	5:B:125:PRO:HD2	1.66	0.76
1:A:839:U:H5'	1:A:840:C:H5	1.49	0.76
1:A:1443:G:C5'	1:A:1446:A:H5'	2.10	0.76
8:E:51:VAL:HB	8:E:52:PRO:HD3	1.65	0.76
16:M:49:THR:HB	16:M:52:GLU:HG3	1.65	0.76
1:A:8:A:H62	7:D:208:SER:HB2	1.51	0.76
1:A:127:G:HO2'	20:Q:2:PRO:N	1.83	0.76
1:A:1278:U:H4'	1:A:1279:A:C5'	2.16	0.76
5:B:15:VAL:HG11	5:B:209:ARG:HB3	1.68	0.76
16:M:33:ALA:HA	16:M:59:TYR:CE2	2.20	0.76
20:Q:101:ARG:HA	20:Q:101:ARG:HE	1.51	0.76
23:T:56:MET:HE2	23:T:85:MET:HA	1.67	0.76
16:M:108:ARG:HD3	16:M:114:ARG:NH1	2.00	0.76
18:O:39:LEU:HD13	18:O:56:LEU:HB2	1.68	0.76
11:H:24:THR:HG22	11:H:63:LEU:HD21	1.65	0.76
1:A:1352:C:H2'	1:A:1353:G:C8	2.21	0.75
6:C:112:SER:HB3	6:C:115:LEU:HD12	1.69	0.75
11:H:86:ILE:HG21	11:H:133:LEU:HD22	1.68	0.75
16:M:4:ILE:HG22	16:M:5:ALA:N	1.99	0.75
1:A:1425:U:H2'	1:A:1426:C:C6	2.21	0.75
13:J:30:SER:HB3	13:J:84:GLN:NE2	2.00	0.75
15:L:89:ARG:HG2	15:L:97:ARG:HA	1.67	0.75
1:A:254:G:OP1	20:Q:67:LYS:O	2.04	0.75
10:G:15:ASP:HB3	10:G:19:GLY:H	1.51	0.75
12:I:65:VAL:HG21	12:I:73:GLN:HB3	1.68	0.75
1:A:946:A:H2'	1:A:947:G:C8	2.22	0.75
5:B:21:ARG:HD3	5:B:21:ARG:N	2.00	0.75
5:B:25:ASN:ND2	5:B:27:LYS:H	1.83	0.75
6:C:15:THR:HB	6:C:181:ASN:HB2	1.69	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:191:THR:HG22	6:C:192:THR:N	2.01	0.75
7:D:111:ALA:HA	7:D:161:ASN:ND2	2.01	0.75
14:K:99:GLN:HG2	14:K:105:VAL:HG21	1.67	0.74
19:P:22:THR:HA	19:P:33:ILE:HG13	1.69	0.74
22:S:64:GLU:O	22:S:67:VAL:HG23	1.87	0.74
23:T:50:GLU:O	23:T:100:ILE:HD12	1.87	0.74
1:A:722:A:H4'	1:A:723:U:C5	2.21	0.74
1:A:1133:G:H2'	1:A:1134:G:H8	1.52	0.74
11:H:127:LEU:N	11:H:127:LEU:HD23	2.01	0.74
15:L:89:ARG:NH2	15:L:97:ARG:HE	1.85	0.74
16:M:33:ALA:HA	16:M:59:TYR:HE2	1.53	0.74
1:A:112:G:H21	1:A:354:G:H5'	1.52	0.74
1:A:975:A:C4'	1:A:976:G:H5''	2.13	0.74
14:K:18:ARG:HB2	14:K:33:THR:HG22	1.69	0.74
21:R:55:ARG:NH1	21:R:55:ARG:HB3	2.02	0.74
5:B:197:VAL:HB	5:B:200:ILE:HG12	1.70	0.74
9:F:2:ARG:NE	9:F:69:GLU:HG2	2.02	0.74
1:A:954:G:H2'	1:A:955:U:C6	2.23	0.74
1:A:1127:G:H21	1:A:1146:A:H62	1.33	0.74
1:A:761:G:H5''	20:Q:102:GLY:HA3	1.69	0.74
1:A:1355:G:H2'	1:A:1356:G:C8	2.23	0.74
8:E:105:VAL:HB	8:E:106:PRO:HD3	1.70	0.74
11:H:103:VAL:HG21	11:H:109:ILE:O	1.88	0.74
1:A:1191:A:P	6:C:3:ASN:HD21	2.10	0.74
5:B:16:HIS:HA	5:B:204:ASN:CB	2.18	0.74
18:O:78:TYR:CZ	18:O:82:ILE:HD11	2.22	0.74
1:A:1056:U:H5'	6:C:163:ALA:CB	2.17	0.73
1:A:1435:G:H2'	1:A:1436:U:C6	2.22	0.73
9:F:10:LEU:HD12	9:F:59:TYR:HB3	1.68	0.73
17:N:6:LEU:HD22	17:N:23:ARG:HH21	1.52	0.73
18:O:6:GLU:H	18:O:6:GLU:CD	1.95	0.73
18:O:29:VAL:HG21	18:O:67:LEU:HD23	1.70	0.73
9:F:36:ARG:O	9:F:65:VAL:HB	1.88	0.73
12:I:49:PRO:O	12:I:52:ALA:HB3	1.88	0.73
16:M:36:LYS:HD3	16:M:59:TYR:OH	1.89	0.73
22:S:45:VAL:HA	22:S:62:ILE:HG13	1.70	0.73
1:A:1132:C:H2'	1:A:1133:G:H8	1.52	0.73
5:B:84:GLU:OE1	5:B:216:SER:HA	1.87	0.73
8:E:144:THR:HB	8:E:147:ASP:OD2	1.88	0.73
6:C:10:PHE:CE2	6:C:178:LEU:HD13	2.23	0.73
17:N:22:THR:HB	17:N:33:VAL:HG21	1.69	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:E:16:THR:HG22	8:E:27:ARG:HB3	1.70	0.73
20:Q:27:PHE:HB2	20:Q:28:PRO:HD2	1.69	0.73
1:A:750:G:N3	18:O:23:GLY:HA3	2.04	0.72
8:E:11:ILE:HG22	8:E:12:LEU:HD12	1.70	0.72
5:B:84:GLU:HB3	5:B:219:VAL:CG2	2.13	0.72
11:H:60:ARG:HH11	11:H:60:ARG:HG3	1.53	0.72
1:A:1125:U:H5''	1:A:1126:U:H5	1.53	0.72
1:A:840:C:H5''	1:A:841:U:OP1	1.89	0.72
1:A:677:U:H3	1:A:713:G:H22	1.37	0.72
5:B:92:TYR:CE2	5:B:151:GLY:HA3	2.24	0.72
11:H:82:HIS:HD2	11:H:83:ILE:N	1.88	0.72
1:A:1054:C:O2	1:A:1054:C:H3'	1.88	0.72
5:B:25:ASN:HD22	5:B:25:ASN:C	1.96	0.72
1:A:438:G:H4'	1:A:439:A:OP1	1.88	0.72
5:B:71:VAL:O	5:B:165:VAL:HG23	1.89	0.72
21:R:86:VAL:HG12	21:R:87:ARG:H	1.54	0.72
5:B:141:GLU:O	5:B:145:LEU:HG	1.89	0.71
10:G:50:ILE:CG2	10:G:61:VAL:HG21	2.19	0.71
1:A:1086:U:H3	1:A:1099:G:N2	1.86	0.71
5:B:25:ASN:HD22	5:B:27:LYS:H	1.37	0.71
1:A:35:G:H2'	1:A:36:C:C6	2.25	0.71
1:A:1355:G:H2'	1:A:1356:G:H8	1.54	0.71
6:C:52:LEU:HD23	6:C:52:LEU:H	1.54	0.71
1:A:989:C:O2'	1:A:990:C:H5'	1.90	0.71
7:D:98:GLU:HG2	7:D:189:PRO:HG3	1.72	0.71
12:I:6:GLY:N	12:I:84:ALA:HB2	2.04	0.71
1:A:501:C:H2'	1:A:502:G:H8	1.55	0.71
6:C:115:LEU:HD23	6:C:118:GLN:OE1	1.91	0.71
16:M:34:LEU:HD13	16:M:41:PRO:HA	1.72	0.71
1:A:113:G:H1'	1:A:354:G:H5'	1.73	0.71
1:A:115:G:H1'	1:A:116:A:N7	2.05	0.71
1:A:839:U:H5'	1:A:840:C:C5	2.26	0.71
1:A:1057:G:H5''	6:C:154:SER:CB	2.21	0.71
1:A:1190:G:C3'	6:C:3:ASN:ND2	2.53	0.71
7:D:36:ARG:H	7:D:37:PRO:CD	1.98	0.71
1:A:1370:G:O2'	1:A:1371:G:H5'	1.91	0.71
6:C:171:GLY:O	6:C:173:VAL:HG23	1.91	0.71
7:D:57:ARG:HH11	7:D:57:ARG:HG3	1.55	0.71
7:D:62:GLN:HE22	7:D:65:ARG:NH1	1.89	0.71
14:K:54:ARG:H	14:K:54:ARG:HD3	1.54	0.71
19:P:58:TYR:O	19:P:62:VAL:HG23	1.90	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1125:U:H3	13:J:5:ARG:HH21	1.38	0.71
1:A:1441:G:H4'	1:A:1442:G:C5	2.26	0.71
6:C:6:HIS:HD2	6:C:8:ILE:H	1.36	0.71
1:A:673:G:H2'	1:A:674:G:C8	2.26	0.71
1:A:1039:C:H2'	1:A:1040:U:C6	2.26	0.71
1:A:1139:G:H4'	1:A:1140:C:H5'	1.72	0.71
5:B:69:LEU:HD12	5:B:155:LEU:HD11	1.73	0.71
13:J:34:VAL:HG12	13:J:35:SER:H	1.56	0.71
17:N:27:CYS:SG	17:N:29:ARG:CB	2.79	0.71
17:N:36:PHE:O	17:N:36:PHE:HD1	1.74	0.71
1:A:265:G:H2'	1:A:267:C:H5	1.55	0.70
6:C:119:ARG:HG2	6:C:140:ARG:HH12	1.56	0.70
22:S:41:VAL:HG22	22:S:44:MET:HE3	1.72	0.70
12:I:93:ARG:HD3	12:I:97:LYS:NZ	2.06	0.70
13:J:35:SER:HB2	13:J:72:VAL:O	1.90	0.70
1:A:112:G:N2	1:A:354:G:H5'	2.07	0.70
1:A:1250:A:H5''	12:I:68:GLY:N	2.06	0.70
5:B:95:GLN:O	5:B:96:ARG:HD2	1.90	0.70
8:E:41:VAL:HG13	8:E:113:ALA:HA	1.73	0.70
8:E:76:ILE:HD11	8:E:142:LEU:CD1	2.22	0.70
12:I:47:LEU:C	12:I:49:PRO:HD2	2.16	0.70
12:I:118:LYS:HB2	12:I:118:LYS:HZ2	1.55	0.70
22:S:28:LYS:HG2	22:S:29:ARG:N	2.03	0.70
1:A:1128:C:H4'	12:I:16:ARG:HH12	1.57	0.70
13:J:22:LYS:C	13:J:24:VAL:H	2.00	0.70
1:A:328:C:H4'	1:A:329:A:H5'	1.74	0.70
6:C:14:ILE:HG22	6:C:15:THR:N	2.07	0.70
1:A:382:A:H2'	1:A:383:A:C8	2.26	0.70
5:B:82:ARG:HA	5:B:92:TYR:CD1	2.27	0.70
5:B:133:LYS:O	5:B:137:ARG:HG3	1.92	0.70
1:A:384:G:H2'	1:A:385:C:H6	1.56	0.69
1:A:420:U:H2'	1:A:422:C:C5	2.27	0.69
5:B:55:PHE:HA	5:B:58:ILE:HD12	1.74	0.69
7:D:8:VAL:HG21	7:D:115:ARG:NH1	2.07	0.69
1:A:202:U:H5''	1:A:203:U:OP2	1.92	0.69
1:A:530:G:O6	4:Z:3:U:H1'	1.92	0.69
1:A:912:C:O2'	1:A:913:A:H5'	1.92	0.69
1:A:1038:C:H2'	1:A:1039:C:H6	1.57	0.69
1:A:1226:C:H1'	22:S:83:HIS:CE1	2.27	0.69
1:A:1372:U:O2'	1:A:1373:G:H5'	1.92	0.69
10:G:23:VAL:O	10:G:27:ILE:HG13	1.92	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:H:133:LEU:C	11:H:133:LEU:HD23	2.16	0.69
13:J:19:SER:HA	13:J:22:LYS:NZ	2.07	0.69
13:J:25:GLU:HA	13:J:28:ARG:HB2	1.74	0.69
1:A:1356:G:H2'	1:A:1357:A:C8	2.28	0.69
6:C:6:HIS:CD2	6:C:8:ILE:H	2.08	0.69
17:N:9:LYS:HD3	17:N:9:LYS:C	2.17	0.69
1:A:706:A:O4'	14:K:29:ILE:HD11	1.92	0.69
5:B:12:GLU:C	5:B:14:GLY:H	1.99	0.69
8:E:80:ILE:HD12	8:E:80:ILE:N	2.07	0.69
16:M:50:GLU:O	16:M:54:VAL:HG23	1.92	0.69
23:T:54:LYS:HE3	23:T:100:ILE:CD1	2.21	0.69
1:A:1222:G:OP1	22:S:77:THR:HG21	1.93	0.69
5:B:219:VAL:HA	5:B:222:ILE:HD12	1.73	0.69
14:K:44:SER:H	14:K:47:VAL:HB	1.58	0.69
15:L:27:LEU:HD12	15:L:28:LYS:H	1.58	0.69
17:N:24:CYS:HB3	17:N:28:GLY:H	1.56	0.69
21:R:86:VAL:HG12	21:R:87:ARG:N	2.08	0.69
1:A:1052:U:H2'	1:A:1055:A:OP1	1.93	0.69
1:A:1108:G:H5'	1:A:1191:A:H4'	1.75	0.69
1:A:1152:A:H5''	13:J:13:HIS:CD2	2.27	0.69
1:A:1287:A:H2'	1:A:1288:A:C8	2.28	0.69
1:A:1330:U:OP1	16:M:23:TYR:O	2.11	0.69
14:K:48:ILE:HD13	14:K:63:LEU:HB3	1.74	0.69
14:K:84:VAL:HG11	14:K:91:ARG:HD3	1.74	0.69
21:R:37:VAL:O	21:R:41:LYS:HG3	1.93	0.69
1:A:434:U:H2'	1:A:435:C:C6	2.28	0.69
1:A:478:A:O2'	1:A:479:C:H5'	1.92	0.69
7:D:111:ALA:HB1	7:D:116:GLN:OE1	1.92	0.69
1:A:881:G:P	15:L:12:ARG:HH22	2.15	0.68
1:A:1251:A:H2'	1:A:1252:A:C8	2.28	0.68
5:B:92:TYR:CD2	5:B:151:GLY:HA3	2.28	0.68
13:J:30:SER:OG	13:J:81:THR:HA	1.94	0.68
1:A:952:U:O4	16:M:104:ARG:HD3	1.94	0.68
21:R:55:ARG:HB3	21:R:55:ARG:HH11	1.58	0.68
5:B:114:ARG:HH11	5:B:118:LEU:HG	1.58	0.68
7:D:29:PRO:HA	7:D:34:GLU:HG2	1.73	0.68
1:A:1262:C:O2'	1:A:1263:C:H5'	1.94	0.68
1:A:1343:G:H2'	1:A:1344:C:C6	2.29	0.68
6:C:20:SER:O	17:N:54:PRO:HB3	1.92	0.68
13:J:30:SER:HB3	13:J:84:GLN:CD	2.18	0.68
1:A:794:A:H2'	1:A:795:C:C6	2.28	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:967:C:H4'	12:I:128:ARG:HG3	1.73	0.68
7:D:100:ARG:HB3	7:D:102:ASP:OD1	1.94	0.68
11:H:90:GLY:O	11:H:91:ARG:HB2	1.92	0.68
11:H:95:VAL:HB	11:H:99:GLU:HB2	1.75	0.68
14:K:115:PRO:C	14:K:117:ASN:H	2.01	0.68
17:N:35:ARG:C	17:N:37:PHE:H	2.01	0.68
1:A:384:G:H2'	1:A:385:C:C6	2.28	0.68
1:A:523:A:H61	15:L:92:ASP:HB2	1.57	0.68
1:A:539:A:H2'	1:A:540:G:C8	2.28	0.68
1:A:979:C:H2'	1:A:980:C:H5'	1.76	0.68
1:A:1257:U:H4'	1:A:1258:G:O5'	1.94	0.68
1:A:1259:C:H42	1:A:1276:G:H1	1.41	0.68
1:A:1333:A:H2'	1:A:1334:G:O4'	1.94	0.68
10:G:113:GLU:HG2	10:G:119:ARG:HG2	1.76	0.68
17:N:36:PHE:O	17:N:36:PHE:CD1	2.47	0.68
1:A:190(L):U:O2	23:T:105:SER:HB2	1.94	0.68
11:H:63:LEU:HD22	11:H:63:LEU:H	1.59	0.68
6:C:33:LEU:HD11	17:N:53:LEU:CD2	2.17	0.68
22:S:22:LEU:HD22	22:S:28:LYS:HD2	1.76	0.68
1:A:393:A:O2'	1:A:394:G:H5'	1.94	0.68
1:A:627:G:O2'	1:A:628:G:H5'	1.92	0.68
1:A:939:G:H5''	10:G:102:ARG:NH2	2.08	0.68
9:F:94:GLN:HB3	21:R:32:ARG:HH11	1.58	0.68
11:H:63:LEU:HD22	11:H:63:LEU:N	2.09	0.68
13:J:78:ASN:O	13:J:80:LYS:N	2.27	0.68
1:A:195:A:H4'	23:T:68:LYS:HE2	1.76	0.67
1:A:1305:G:O2'	1:A:1306:A:C8	2.39	0.67
6:C:188:LEU:HD13	6:C:189:ALA:H	1.58	0.67
8:E:126:ARG:NH1	8:E:126:ARG:HG3	2.09	0.67
16:M:14:ARG:HG3	16:M:44:ARG:NH2	2.09	0.67
16:M:54:VAL:O	16:M:58:GLU:HG2	1.94	0.67
1:A:1095:U:H2'	1:A:1096:C:C6	2.29	0.67
1:A:1127:G:N2	1:A:1146:A:H62	1.92	0.67
1:A:1320:C:N3	22:S:36:ARG:HG3	2.10	0.67
5:B:19:HIS:CD2	5:B:20:GLU:HG2	2.29	0.67
5:B:137:ARG:O	5:B:141:GLU:HB2	1.95	0.67
9:F:19:LEU:C	9:F:19:LEU:HD23	2.20	0.67
12:I:118:LYS:O	12:I:119:ALA:HB3	1.93	0.67
13:J:3:LYS:HA	13:J:75:ILE:HG12	1.75	0.67
15:L:28:LYS:C	15:L:30:ALA:N	2.45	0.67
20:Q:97:SER:HB3	20:Q:103:GLY:C	2.19	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:M:84:ILE:O	16:M:85:GLY:C	2.37	0.67
1:A:357:G:O2'	1:A:358:U:H5'	1.94	0.67
8:E:76:ILE:CG1	8:E:77:PRO:HD2	2.24	0.67
1:A:351:G:H4'	1:A:352:C:OP1	1.93	0.67
1:A:974:A:C8	17:N:31:ARG:HD3	2.30	0.67
1:A:984:C:H2'	1:A:985:C:H6	1.60	0.67
6:C:47:LEU:H	6:C:47:LEU:HD12	1.59	0.67
6:C:191:THR:HG21	6:C:193:TYR:CE1	2.29	0.67
1:A:180:U:H2'	1:A:181:G:H5'	1.76	0.67
6:C:8:ILE:HG23	6:C:16:ARG:HG2	1.77	0.67
15:L:41:ARG:HG2	15:L:42:THR:H	1.59	0.67
16:M:4:ILE:HD11	16:M:56:LEU:HD13	1.77	0.67
1:A:1141:C:O2'	1:A:1142:G:H5'	1.95	0.67
1:A:1366:C:H2'	1:A:1367:C:C6	2.30	0.67
5:B:97:TRP:HZ2	5:B:102:LEU:HD13	1.59	0.67
6:C:33:LEU:CD1	17:N:53:LEU:HD22	2.16	0.67
1:A:954:G:H2'	1:A:955:U:H6	1.59	0.67
11:H:80:ILE:O	11:H:80:ILE:HG22	1.94	0.67
12:I:50:LEU:HA	12:I:55:ALA:HB3	1.75	0.67
7:D:162:LEU:CG	7:D:181:MET:HE2	2.24	0.66
10:G:145:ALA:O	10:G:147:ALA:N	2.25	0.66
11:H:91:ARG:HG3	15:L:7:ILE:HG13	1.76	0.66
1:A:838:G:C2'	1:A:839:U:H5''	2.24	0.66
7:D:70:ILE:HD11	7:D:100:ARG:CD	2.25	0.66
13:J:22:LYS:HE2	13:J:90:LEU:HD12	1.77	0.66
6:C:174:PRO:HB2	6:C:177:THR:CG2	2.24	0.66
13:J:23:ILE:HD12	13:J:23:ILE:N	2.10	0.66
13:J:65:LEU:HD23	13:J:65:LEU:O	1.94	0.66
24:V:5:ASP:O	24:V:11:GLY:HA3	1.95	0.66
11:H:89:PRO:HA	11:H:92:ARG:NH1	2.10	0.66
17:N:33:VAL:HA	17:N:40:CYS:HA	1.78	0.66
18:O:36:ILE:HG12	18:O:59:MET:HE3	1.78	0.66
1:A:761:G:H1'	20:Q:104:LYS:O	1.96	0.66
1:A:1128:C:O2'	1:A:1130:A:C8	2.47	0.66
1:A:1196:U:H5''	1:A:1197:G:C5'	2.26	0.66
9:F:8:ILE:HD11	9:F:79:LEU:HD13	1.78	0.66
19:P:45:THR:HB	19:P:46:PRO:HD2	1.77	0.66
23:T:70:SER:HA	23:T:73:HIS:CD2	2.30	0.66
1:A:1031:G:H2'	1:A:1032:G:H8	1.61	0.66
1:A:1241:G:H2'	1:A:1242:C:C6	2.30	0.66
7:D:151:LYS:H	7:D:151:LYS:CD	1.94	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:M:88:ARG:HG2	16:M:88:ARG:HH11	1.59	0.66
23:T:51:GLU:HA	23:T:54:LYS:HB2	1.76	0.66
1:A:8:A:N6	7:D:209:ARG:H	1.94	0.66
14:K:121:PRO:HG2	14:K:126:ARG:HG2	1.78	0.66
23:T:10:LEU:HD12	23:T:12:ALA:HB3	1.78	0.66
23:T:97:ALA:O	23:T:99:LEU:N	2.28	0.66
1:A:538:G:OP2	15:L:115:LYS:HG3	1.95	0.66
7:D:158:ILE:HG22	7:D:181:MET:HE1	1.78	0.66
12:I:33:PHE:CE1	12:I:47:LEU:HD21	2.30	0.66
15:L:41:ARG:HG2	15:L:42:THR:O	1.96	0.66
15:L:50:SER:O	15:L:51:ALA:HB2	1.95	0.66
16:M:4:ILE:CD1	16:M:56:LEU:HD13	2.25	0.66
1:A:1081:G:OP1	8:E:16:THR:HG23	1.96	0.66
5:B:118:LEU:HD13	5:B:142:LEU:HB2	1.76	0.66
7:D:64:LEU:HD12	7:D:75:PHE:CZ	2.31	0.66
10:G:75:VAL:CG2	10:G:86:GLN:HB3	2.25	0.66
11:H:105:ARG:HG3	11:H:105:ARG:HH11	1.61	0.66
22:S:5:LEU:O	22:S:6:LYS:HB2	1.94	0.66
5:B:101:MET:HA	5:B:108:ILE:HD12	1.78	0.66
7:D:165:MET:SD	7:D:168:ARG:HD3	2.35	0.66
13:J:94:VAL:HG12	13:J:95:GLU:N	2.10	0.65
1:A:149:A:H2'	1:A:150:C:C6	2.32	0.65
1:A:353:A:H5'	1:A:353:A:H8	1.60	0.65
1:A:443:C:H2'	1:A:444:C:C6	2.29	0.65
6:C:83:ARG:C	6:C:85:ARG:H	2.04	0.65
17:N:18:VAL:HG23	17:N:19:ARG:H	1.60	0.65
20:Q:59:ILE:HG22	20:Q:71:PHE:CD1	2.31	0.65
1:A:243:A:C4'	1:A:244:U:H5'	2.23	0.65
6:C:64:VAL:HG12	6:C:65:ALA:N	2.11	0.65
13:J:34:VAL:HG12	13:J:35:SER:N	2.11	0.65
15:L:75:HIS:HD2	15:L:77:LEU:H	1.45	0.65
1:A:689:C:P	14:K:46:GLY:HA3	2.36	0.65
1:A:1363:A:H1'	1:A:1365:G:N7	2.11	0.65
6:C:195:VAL:HG12	6:C:196:LEU:N	2.10	0.65
7:D:175:SER:HB3	7:D:186:LEU:HD11	1.78	0.65
7:D:177:ASP:OD1	7:D:179:GLU:HG2	1.97	0.65
8:E:16:THR:CG2	8:E:27:ARG:HB3	2.26	0.65
12:I:48:GLU:N	12:I:49:PRO:HD2	2.11	0.65
23:T:49:ALA:HB3	23:T:99:LEU:HG	1.78	0.65
1:A:168:G:O2'	1:A:169:C:H5'	1.96	0.65
1:A:992:U:H4'	1:A:993:G:O5'	1.96	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:52:LEU:H	6:C:52:LEU:CD2	2.08	0.65
8:E:144:THR:O	8:E:148:VAL:HG23	1.97	0.65
15:L:24:VAL:O	15:L:24:VAL:CG1	2.42	0.65
22:S:77:THR:HG22	22:S:78:ARG:N	2.11	0.65
17:N:24:CYS:HB3	17:N:28:GLY:N	2.11	0.65
1:A:1053:G:C4'	1:A:1054:C:H5'	2.27	0.65
1:A:1222:G:P	22:S:77:THR:HG21	2.37	0.65
12:I:69:GLY:O	12:I:73:GLN:HG3	1.97	0.65
5:B:16:HIS:HA	5:B:204:ASN:HB2	1.78	0.65
5:B:102:LEU:HD21	5:B:162:ILE:HD12	1.78	0.65
8:E:77:PRO:O	8:E:78:HIS:HB3	1.95	0.65
1:A:1053:G:C3'	1:A:1054:C:H5'	2.27	0.64
1:A:1281:U:H5'	1:A:1282:C:H5	1.61	0.64
5:B:71:VAL:CG2	5:B:164:VAL:HG22	2.26	0.64
5:B:142:LEU:CD2	5:B:146:GLN:HE21	2.10	0.64
17:N:18:VAL:HG23	17:N:19:ARG:N	2.11	0.64
1:A:424:G:O2'	1:A:425:G:H5'	1.97	0.64
1:A:807:A:H2'	1:A:808:C:C6	2.32	0.64
16:M:26:GLY:O	16:M:28:ALA:N	2.31	0.64
1:A:176:C:H2'	1:A:177:C:H6	1.62	0.64
1:A:254:G:H21	20:Q:16:GLN:NE2	1.96	0.64
1:A:1292:U:P	10:G:41:ARG:HH22	2.20	0.64
1:A:1305:G:N2	1:A:1331:G:O2'	2.30	0.64
1:A:1347:G:H2'	1:A:1373:G:H1	1.60	0.64
5:B:16:HIS:O	5:B:18:GLY:N	2.30	0.64
22:S:30:LEU:O	22:S:31:ILE:HD13	1.96	0.64
1:A:344:A:H4'	1:A:345:C:OP2	1.96	0.64
1:A:1176:A:H2'	1:A:1177:G:C8	2.32	0.64
1:A:1368:G:O2'	1:A:1369:C:H5'	1.96	0.64
5:B:135:GLN:HG2	5:B:139:LYS:HE2	1.79	0.64
8:E:92:LYS:HB3	8:E:119:LEU:HB2	1.78	0.64
13:J:16:LEU:O	13:J:19:SER:N	2.30	0.64
1:A:1298:C:H4'	1:A:1299:A:O4'	1.97	0.64
6:C:34:LEU:HD23	6:C:34:LEU:O	1.96	0.64
10:G:135:VAL:O	10:G:139:GLU:HG3	1.98	0.64
18:O:24:SER:OG	18:O:27:VAL:HG23	1.98	0.64
1:A:1004:A:H5''	1:A:1025:U:O4	1.98	0.64
1:A:1054:C:H42	3:Y:34:G:C1'	2.10	0.64
11:H:101:PRO:HG3	11:H:133:LEU:HD11	1.78	0.64
13:J:49:VAL:O	13:J:60:ARG:O	2.15	0.64
1:A:1194:U:H4'	8:E:22:GLY:CA	2.28	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:E:145:LYS:O	8:E:149:GLU:HG3	1.97	0.64
15:L:87:GLY:HA2	15:L:98:TYR:HA	1.79	0.64
5:B:112:VAL:C	5:B:114:ARG:H	2.05	0.64
7:D:187:ARG:HG3	7:D:188:LEU:N	2.13	0.64
8:E:72:GLN:C	8:E:74:GLY:H	2.04	0.64
9:F:92:LYS:HB2	9:F:92:LYS:NZ	2.13	0.64
1:A:1194:U:H4'	8:E:22:GLY:HA3	1.78	0.64
1:A:1427:U:H2'	1:A:1428:A:C8	2.32	0.64
11:H:119:LEU:HB2	11:H:123:GLU:HB2	1.80	0.64
1:A:662:G:H2'	1:A:663:A:C8	2.33	0.64
1:A:1454:G:H2'	1:A:1455:G:H8	1.63	0.64
5:B:178:ARG:HH11	5:B:178:ARG:HG3	1.62	0.64
7:D:29:PRO:O	7:D:30:LYS:HG3	1.98	0.64
13:J:4:ILE:HB	13:J:74:ILE:HG13	1.80	0.64
1:A:1241:G:H2'	1:A:1242:C:H6	1.63	0.63
7:D:3:ARG:NH1	7:D:118:ARG:HH12	1.96	0.63
14:K:126:ARG:HB3	14:K:126:ARG:NH1	2.13	0.63
1:A:1065:U:H4'	1:A:1066:C:O5'	1.98	0.63
9:F:22:GLU:OE1	9:F:22:GLU:HA	1.99	0.63
16:M:35:GLU:C	16:M:37:THR:H	2.07	0.63
18:O:21:ASP:OD2	18:O:24:SER:HB3	1.98	0.63
23:T:67:ALA:HA	23:T:73:HIS:H	1.63	0.63
1:A:620:C:N1	7:D:135:LEU:HD13	2.12	0.63
1:A:760:G:N2	20:Q:104:LYS:H	1.95	0.63
1:A:1351:U:H4'	10:G:33:ASP:OD2	1.98	0.63
6:C:15:THR:O	6:C:16:ARG:HB2	1.97	0.63
6:C:43:LEU:HD13	6:C:68:VAL:HG23	1.81	0.63
1:A:496:A:H4'	1:A:497:A:OP1	1.97	0.63
5:B:15:VAL:O	5:B:17:PHE:N	2.31	0.63
1:A:1125:U:H5''	1:A:1126:U:C5	2.34	0.63
1:A:1152:A:H2'	1:A:1153:C:H6	1.61	0.63
9:F:10:LEU:CD1	9:F:59:TYR:HB3	2.27	0.63
10:G:146:GLU:HA	10:G:149:ARG:HG2	1.81	0.63
21:R:47:THR:CG2	21:R:83:GLU:H	2.10	0.63
1:A:258:G:H2'	1:A:259:G:H8	1.62	0.63
1:A:352:C:H4'	1:A:354:G:OP1	1.97	0.63
1:A:1352:C:H2'	1:A:1353:G:H8	1.63	0.63
20:Q:67:LYS:CA	20:Q:70:ARG:HH12	2.07	0.63
20:Q:76:LEU:C	20:Q:76:LEU:HD23	2.23	0.63
23:T:76:ALA:O	23:T:80:ARG:HG3	1.97	0.63
1:A:112:G:H21	1:A:354:G:C5'	2.12	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1258:G:H1	1:A:1277:C:H42	1.44	0.63
5:B:17:PHE:CG	5:B:18:GLY:N	2.66	0.63
5:B:156:LYS:HZ3	5:B:156:LYS:HA	1.62	0.63
6:C:13:GLY:O	6:C:14:ILE:HD13	1.99	0.63
7:D:25:ARG:C	7:D:27:TYR:H	2.05	0.63
12:I:95:LYS:C	12:I:98:PRO:HD2	2.23	0.63
15:L:110:VAL:O	15:L:122:THR:HG21	1.98	0.63
23:T:57:ARG:CB	23:T:57:ARG:HH11	2.11	0.63
1:A:1510:U:H2'	1:A:1511:G:C8	2.34	0.63
5:B:17:PHE:HA	5:B:44:LEU:HD21	1.80	0.63
5:B:111:ARG:HB3	5:B:149:LEU:HD11	1.79	0.63
5:B:206:ASP:O	5:B:207:ALA:HB3	1.99	0.63
1:A:528:C:H5'	1:A:535:A:C6	2.34	0.63
1:A:1305:G:H5''	24:V:4:GLY:C	2.23	0.63
13:J:19:SER:HA	13:J:22:LYS:HZ2	1.64	0.63
15:L:54:LYS:N	15:L:54:LYS:HD2	2.14	0.63
18:O:70:LEU:HD13	18:O:78:TYR:CA	2.28	0.63
1:A:328:C:O2	1:A:328:C:C2'	2.47	0.62
1:A:407:G:O2'	7:D:116:GLN:HG3	1.99	0.62
1:A:713:G:H2'	1:A:714:G:C8	2.34	0.62
6:C:179:ARG:HD3	6:C:207:VAL:HA	1.80	0.62
11:H:121:ASP:HB2	11:H:125:ARG:HH22	1.64	0.62
1:A:1030(C):G:H2'	1:A:1030(D):A:C8	2.34	0.62
15:L:53:ARG:HG2	15:L:69:TYR:HE1	1.62	0.62
5:B:57:PHE:CZ	5:B:61:LEU:HD11	2.34	0.62
16:M:17:VAL:O	16:M:20:THR:HB	1.98	0.62
1:A:67:C:H2'	1:A:68:G:C8	2.35	0.62
1:A:959:A:H3'	1:A:960:U:H5''	1.81	0.62
6:C:34:LEU:C	6:C:34:LEU:CD2	2.72	0.62
11:H:92:ARG:HG2	11:H:92:ARG:HH11	1.65	0.62
11:H:118:VAL:C	11:H:119:LEU:HD23	2.25	0.62
20:Q:101:ARG:HA	20:Q:101:ARG:NE	2.14	0.62
1:A:31:G:N1	1:A:48:C:H5''	2.13	0.62
1:A:1060:C:O2'	1:A:1061:G:H5'	1.99	0.62
8:E:82:VAL:HG21	8:E:138:ALA:HA	1.81	0.62
15:L:28:LYS:HD3	15:L:33:ARG:HH22	1.63	0.62
1:A:1391:U:H2'	1:A:1392:G:C8	2.35	0.62
7:D:4:TYR:O	7:D:5:ILE:HB	1.99	0.62
11:H:10:LEU:HD22	11:H:83:ILE:HD11	1.81	0.62
22:S:16:LEU:O	22:S:19:VAL:HG12	2.00	0.62
1:A:941:G:O2'	1:A:942:G:H5'	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1016:A:H2'	1:A:1017:G:O4'	1.99	0.62
1:A:1427:U:H2'	1:A:1428:A:H8	1.65	0.62
8:E:60:TYR:O	8:E:64:ARG:HG2	2.00	0.62
11:H:112:LEU:N	11:H:112:LEU:HD23	2.15	0.62
13:J:32:ALA:HB2	13:J:76:ASN:ND2	2.07	0.62
23:T:50:GLU:H	23:T:99:LEU:HD12	1.64	0.62
1:A:1129:C:H1'	1:A:1132:C:H5	1.64	0.62
1:A:1305:G:C5'	24:V:4:GLY:HA3	2.30	0.62
1:A:1314:C:C5	22:S:6:LYS:HE3	2.35	0.62
9:F:33:TYR:HB2	9:F:75:LEU:HD23	1.82	0.62
13:J:51:ARG:CZ	13:J:61:GLU:HB2	2.29	0.62
1:A:254:G:OP1	20:Q:68:ARG:HB3	2.00	0.62
5:B:16:HIS:HA	5:B:204:ASN:HB3	1.82	0.62
15:L:27:LEU:CD2	15:L:62:SER:HB2	2.26	0.62
24:V:3:LYS:HB3	24:V:14:TRP:CG	2.34	0.62
3:Y:36:A:H2'	3:Y:37:A:H8	1.64	0.62
5:B:143:GLU:O	5:B:147:LYS:HG3	2.00	0.62
6:C:64:VAL:HB	6:C:99:VAL:CB	2.29	0.62
10:G:38:LEU:HD12	10:G:38:LEU:O	2.00	0.62
17:N:12:ARG:O	17:N:14:PRO:HD3	2.00	0.62
22:S:19:VAL:HG13	22:S:20:LEU:N	2.14	0.62
1:A:851:G:H2'	1:A:852:G:H8	1.64	0.61
1:A:1286:A:H2'	1:A:1287:A:H5''	1.81	0.61
5:B:121:LEU:HD23	5:B:121:LEU:C	2.25	0.61
6:C:191:THR:CG2	6:C:192:THR:N	2.63	0.61
1:A:547:A:H4'	1:A:548:G:O5'	2.00	0.61
5:B:82:ARG:HA	5:B:92:TYR:CE1	2.35	0.61
6:C:119:ARG:O	6:C:122:GLU:HB2	2.00	0.61
1:A:1347:G:O2'	1:A:1348:U:P	2.57	0.61
1:A:382:A:H2'	1:A:383:A:H8	1.64	0.61
7:D:70:ILE:HD11	7:D:100:ARG:NE	2.14	0.61
7:D:106:TYR:CE1	7:D:113:SER:HA	2.35	0.61
9:F:62:TRP:CH2	9:F:64:GLN:HB2	2.35	0.61
9:F:100:ASN:HD22	21:R:23:LYS:CG	2.12	0.61
15:L:120:TYR:O	15:L:122:THR:HG23	1.99	0.61
23:T:54:LYS:HE3	23:T:100:ILE:HD13	1.81	0.61
1:A:984:C:H2'	1:A:985:C:C6	2.35	0.61
1:A:1004:A:H5''	1:A:1025:U:C4	2.35	0.61
3:Y:29:G:H2'	3:Y:30:G:H8	1.65	0.61
5:B:23:ARG:HH11	5:B:24:TRP:HA	1.65	0.61
5:B:144:ARG:CD	5:B:145:LEU:HD23	2.30	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:108:ASN:ND2	6:C:110:ASN:HB2	2.16	0.61
6:C:181:ASN:C	6:C:182:ILE:HD12	2.26	0.61
8:E:18:ARG:HG2	8:E:25:ARG:HB2	1.82	0.61
5:B:68:ILE:O	5:B:90:MET:HB3	2.01	0.61
6:C:23:TYR:C	6:C:23:TYR:CD2	2.78	0.61
13:J:49:VAL:HG13	17:N:41:ARG:HB2	1.83	0.61
16:M:106:ASN:O	16:M:107:ALA:HB3	2.00	0.61
22:S:15:LEU:O	22:S:19:VAL:N	2.31	0.61
1:A:1132:C:H2'	1:A:1133:G:C8	2.34	0.61
5:B:68:ILE:CB	5:B:90:MET:HE3	2.31	0.61
15:L:41:ARG:NH1	15:L:57:LYS:HZ3	1.99	0.61
17:N:35:ARG:O	17:N:37:PHE:N	2.33	0.61
1:A:404:U:H2'	1:A:405:U:C6	2.35	0.61
1:A:488:C:H2'	1:A:489:C:H6	1.64	0.61
1:A:580:U:H2'	1:A:581:G:O4'	2.01	0.61
1:A:1193:G:O2'	1:A:1194:U:H5'	2.01	0.61
5:B:59:GLU:CG	5:B:221:LEU:HD11	2.30	0.61
5:B:155:LEU:HD22	5:B:157:ARG:O	2.01	0.61
8:E:144:THR:HG22	8:E:147:ASP:H	1.65	0.61
11:H:86:ILE:HD12	11:H:133:LEU:HD21	1.82	0.61
15:L:51:ALA:O	15:L:52:LEU:HD23	2.01	0.61
19:P:19:ILE:HG22	19:P:36:ILE:HG13	1.81	0.61
23:T:96:GLY:O	23:T:97:ALA:HB3	2.00	0.61
1:A:265:G:H2'	1:A:267:C:C5	2.35	0.61
1:A:1198:G:H2'	1:A:1199:U:C6	2.36	0.61
6:C:28:GLN:HA	6:C:31:HIS:HD2	1.64	0.61
10:G:146:GLU:C	10:G:148:ASN:H	2.07	0.61
12:I:32:ASP:HB3	12:I:35:GLU:HB2	1.83	0.61
13:J:38:ILE:HG13	13:J:71:LEU:HB3	1.82	0.61
13:J:87:THR:O	13:J:88:LEU:HD23	2.01	0.61
1:A:1314:C:C6	22:S:6:LYS:HE3	2.36	0.61
5:B:12:GLU:C	5:B:14:GLY:N	2.59	0.61
6:C:84:ILE:O	6:C:84:ILE:HG12	2.01	0.61
1:A:955:U:O2'	1:A:956:U:H5'	2.01	0.60
7:D:151:LYS:HD2	7:D:151:LYS:N	2.01	0.60
11:H:31:PHE:O	11:H:35:ILE:HG13	2.01	0.60
12:I:118:LYS:NZ	12:I:118:LYS:CB	2.63	0.60
1:A:639:G:O2'	1:A:640:A:H5'	2.02	0.60
1:A:1003:G:H2'	1:A:1003(A):G:C8	2.35	0.60
7:D:150:GLU:HG3	7:D:153:ARG:NH2	2.16	0.60
9:F:50:TYR:CE1	21:R:77:GLY:HA2	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:H:11:THR:HA	11:H:14:ARG:NH1	2.16	0.60
12:I:44:VAL:HG13	12:I:51:ARG:NH2	2.16	0.60
13:J:86:MET:HA	13:J:86:MET:HE3	1.83	0.60
15:L:42:THR:O	15:L:43:VAL:HG23	2.01	0.60
23:T:38:LYS:O	23:T:39:LYS:C	2.44	0.60
1:A:178:C:O2'	1:A:179:A:H5'	2.01	0.60
1:A:521:G:OP1	15:L:73:GLU:O	2.18	0.60
1:A:564:C:C2	20:Q:31:LEU:HD11	2.36	0.60
1:A:981:U:H5'	17:N:21:TYR:CE1	2.35	0.60
5:B:16:HIS:NE2	5:B:214:ILE:HG12	2.15	0.60
5:B:48:MET:HA	5:B:51:LEU:HD12	1.84	0.60
5:B:213:LEU:HD23	5:B:213:LEU:C	2.26	0.60
7:D:146:ILE:N	7:D:146:ILE:HD12	2.15	0.60
8:E:6:PHE:CE2	8:E:36:ASP:HB3	2.36	0.60
12:I:113:LYS:H	12:I:119:ALA:HA	1.66	0.60
23:T:11:SER:C	23:T:13:LEU:HD12	2.26	0.60
15:L:53:ARG:HG2	15:L:69:TYR:CE1	2.36	0.60
20:Q:98:LEU:H	20:Q:103:GLY:HA2	1.67	0.60
23:T:100:ILE:O	23:T:102:GLY:N	2.33	0.60
1:A:1104:G:OP1	5:B:111:ARG:HD2	2.00	0.60
1:A:1285:A:H4'	1:A:1286:A:O5'	2.01	0.60
7:D:162:LEU:HD12	7:D:181:MET:HG2	1.83	0.60
10:G:57:GLU:O	10:G:61:VAL:HG23	2.00	0.60
16:M:15:VAL:HG23	16:M:43:THR:O	2.00	0.60
23:T:56:MET:HE3	23:T:88:VAL:HG11	1.83	0.60
1:A:1182:G:O2'	1:A:1183:A:OP2	2.14	0.60
11:H:127:LEU:HD23	11:H:127:LEU:H	1.65	0.60
12:I:70:LYS:O	12:I:74:ILE:HG13	2.01	0.60
21:R:46:GLU:H	21:R:46:GLU:CD	2.09	0.60
1:A:1152:A:H5''	13:J:13:HIS:CG	2.36	0.60
5:B:69:LEU:HD23	5:B:69:LEU:C	2.27	0.60
6:C:155:GLY:O	6:C:156:ARG:HB2	2.01	0.60
9:F:22:GLU:OE1	9:F:25:ILE:HD12	2.01	0.60
10:G:145:ALA:O	10:G:146:GLU:HB2	2.01	0.60
14:K:126:ARG:O	14:K:127:LYS:HB2	2.00	0.60
16:M:63:THR:HG23	16:M:64:TRP:CD2	2.37	0.60
19:P:20:VAL:HG11	19:P:32:TYR:CB	2.31	0.60
1:A:657:G:H4'	18:O:28:GLN:HG2	1.84	0.60
1:A:1064:G:H4'	1:A:1065:U:H5''	1.84	0.60
1:A:1208:C:H2'	1:A:1209:C:C6	2.37	0.60
5:B:187:LEU:HA	5:B:201:ILE:HB	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:72:LYS:O	6:C:75:VAL:HG23	2.01	0.60
13:J:51:ARG:HB2	13:J:59:SER:HB2	1.84	0.60
14:K:34:ASP:O	14:K:36:ASP:N	2.34	0.60
15:L:41:ARG:NH1	15:L:57:LYS:NZ	2.49	0.60
17:N:29:ARG:HG2	17:N:29:ARG:HH11	1.67	0.60
1:A:835:U:OP1	21:R:64:ARG:NH2	2.29	0.60
14:K:57:THR:HG23	14:K:60:ALA:H	1.67	0.60
15:L:126:LYS:H	15:L:126:LYS:CD	2.10	0.60
19:P:34:GLU:OE2	19:P:55:ARG:HD3	2.01	0.60
20:Q:97:SER:HB2	20:Q:103:GLY:HA2	1.82	0.60
1:A:560:U:H5'	1:A:566:G:N2	2.17	0.60
6:C:11:ARG:O	6:C:14:ILE:O	2.20	0.60
9:F:3:ARG:HH11	9:F:3:ARG:HG3	1.66	0.60
11:H:82:HIS:CD2	11:H:83:ILE:N	2.70	0.60
1:A:353:A:H5'	1:A:353:A:C8	2.37	0.59
1:A:1300:G:O2'	1:A:1301:U:H6	1.84	0.59
5:B:28:PHE:CD2	5:B:190:THR:HA	2.37	0.59
6:C:44:GLU:C	6:C:46:GLU:H	2.09	0.59
8:E:8:GLU:HG2	8:E:34:VAL:HG22	1.82	0.59
20:Q:63:ARG:HG2	20:Q:64:PRO:HD2	1.83	0.59
1:A:501:C:H2'	1:A:502:G:C8	2.37	0.59
1:A:1108:G:H4'	1:A:1191:A:O4'	2.02	0.59
6:C:182:ILE:O	6:C:183:ASP:C	2.43	0.59
8:E:89:ILE:HD13	8:E:90:VAL:H	1.66	0.59
14:K:91:ARG:NH1	21:R:88:LYS:NZ	2.44	0.59
17:N:14:PRO:O	17:N:15:LYS:HB2	2.02	0.59
1:A:60:A:H4'	1:A:61:G:O5'	2.03	0.59
1:A:1128:C:H4'	12:I:16:ARG:NH1	2.16	0.59
6:C:35:GLU:CG	6:C:59:ARG:HH22	2.16	0.59
14:K:30:VAL:HG21	14:K:65:ALA:HA	1.84	0.59
19:P:74:LEU:O	19:P:79:VAL:HG23	2.01	0.59
20:Q:58:GLU:O	20:Q:59:ILE:HD13	2.02	0.59
1:A:818:G:C3'	1:A:819:A:H5''	2.33	0.59
1:A:1121:U:H2'	1:A:1122:U:H6	1.68	0.59
5:B:79:ASP:HB3	5:B:238:LEU:HD13	1.83	0.59
5:B:102:LEU:N	5:B:102:LEU:CD1	2.65	0.59
5:B:140:HIS:HA	5:B:143:GLU:HG2	1.84	0.59
6:C:151:VAL:C	6:C:152:ILE:HD12	2.27	0.59
7:D:7:PRO:CB	7:D:10:ARG:HD2	2.32	0.59
15:L:39:VAL:HG12	15:L:40:VAL:N	2.17	0.59
15:L:82:VAL:HG12	15:L:105:TYR:HB3	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:M:88:ARG:HG2	16:M:88:ARG:NH1	2.18	0.59
18:O:17:ARG:HG3	18:O:17:ARG:NH1	2.17	0.59
1:A:812:C:O2'	1:A:813:U:P	2.59	0.59
5:B:10:LEU:HG	5:B:48:MET:HE2	1.85	0.59
15:L:93:LEU:HB2	15:L:96:VAL:CG2	2.33	0.59
20:Q:97:SER:HB3	20:Q:102:GLY:O	2.01	0.59
1:A:163:C:O2'	1:A:164:U:H5'	2.03	0.59
1:A:1154:G:H2'	1:A:1155:G:H8	1.68	0.59
1:A:1316:G:N2	1:A:1318:A:H3'	2.18	0.59
5:B:95:GLN:C	5:B:96:ARG:HD2	2.27	0.59
15:L:60:LEU:CD2	15:L:66:VAL:HG22	2.32	0.59
1:A:1231:G:H4'	12:I:126:SER:OG	2.03	0.59
9:F:100:ASN:ND2	21:R:23:LYS:HG2	2.12	0.59
21:R:19:LYS:HD2	21:R:19:LYS:N	2.17	0.59
22:S:82:GLY:O	22:S:83:HIS:HB2	2.03	0.59
1:A:1366:C:H2'	1:A:1367:C:H6	1.67	0.59
1:A:1425:U:H3	1:A:1475:G:H1	1.49	0.59
5:B:102:LEU:N	5:B:102:LEU:HD12	2.17	0.59
5:B:201:ILE:HG21	5:B:214:ILE:HG21	1.84	0.59
7:D:23:GLY:HA3	7:D:112:VAL:HG12	1.85	0.59
8:E:149:GLU:O	8:E:153:LYS:HG3	2.03	0.59
11:H:119:LEU:HD12	11:H:124:ALA:HA	1.85	0.59
13:J:4:ILE:HD12	13:J:74:ILE:HG13	1.84	0.59
16:M:40:ASN:HD22	16:M:41:PRO:HD2	1.68	0.59
21:R:18:ARG:C	21:R:19:LYS:HD2	2.27	0.59
21:R:45:SER:C	21:R:47:THR:N	2.56	0.59
1:A:130:A:C8	20:Q:63:ARG:HG3	2.38	0.59
1:A:404:U:O2'	1:A:405:U:H5'	2.03	0.59
1:A:861:G:O2'	1:A:862:C:H5'	2.03	0.59
1:A:1404:C:H2'	1:A:1405:G:C8	2.37	0.59
11:H:86:ILE:HD11	11:H:136:GLU:CG	2.27	0.59
20:Q:59:ILE:HG23	20:Q:71:PHE:HB3	1.85	0.59
20:Q:66:SER:O	20:Q:70:ARG:NH1	2.35	0.59
22:S:55:LYS:HG2	22:S:56:GLN:HE21	1.68	0.59
1:A:1497:G:C2'	1:A:1498:U:H5'	2.33	0.58
9:F:2:ARG:HH21	9:F:69:GLU:CB	2.16	0.58
10:G:51:GLN:NE2	10:G:56:GLN:O	2.36	0.58
13:J:90:LEU:H	13:J:91:PRO:HD2	1.67	0.58
19:P:81:ARG:HH11	19:P:81:ARG:HB2	1.68	0.58
23:T:86:ARG:HG3	23:T:90:GLN:NE2	2.18	0.58
1:A:701:C:H5''	1:A:703:G:O4'	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1091:U:O2	1:A:1093:A:C8	2.57	0.58
14:K:43:SER:HA	14:K:47:VAL:HG21	1.83	0.58
1:A:413:G:H2'	1:A:428:G:N2	2.18	0.58
1:A:706:A:C4'	14:K:29:ILE:HD11	2.33	0.58
1:A:1381:U:H2'	1:A:1382:C:H6	1.68	0.58
6:C:82:GLU:O	6:C:85:ARG:HB3	2.03	0.58
12:I:107:ARG:HB3	12:I:107:ARG:HH11	1.69	0.58
1:A:537:G:OP1	15:L:113:ARG:NH2	2.36	0.58
1:A:1125:U:H3	13:J:5:ARG:NH2	2.01	0.58
5:B:136:VAL:HA	5:B:139:LYS:HB2	1.84	0.58
6:C:88:ARG:HA	6:C:101:LEU:HD12	1.85	0.58
6:C:172:ARG:HB3	6:C:172:ARG:HH11	1.66	0.58
12:I:8:GLY:HA3	12:I:79:LEU:HB3	1.83	0.58
15:L:41:ARG:HG2	15:L:42:THR:N	2.18	0.58
16:M:79:LYS:HG2	16:M:83:ASP:OD2	2.04	0.58
1:A:948:C:OP1	16:M:109:THR:HG22	2.03	0.58
1:A:1125:U:H3	13:J:5:ARG:HE	1.50	0.58
1:A:1278:U:H4'	1:A:1279:A:H5'	1.85	0.58
1:A:1372:U:OP1	12:I:71:SER:HB3	2.02	0.58
5:B:15:VAL:CG2	5:B:209:ARG:HG3	2.33	0.58
5:B:35:GLU:HG2	5:B:40:HIS:HA	1.84	0.58
5:B:213:LEU:O	5:B:217:ARG:HG2	2.04	0.58
10:G:78:ARG:HB2	10:G:156:TRP:HZ3	1.68	0.58
11:H:77:GLU:HG3	11:H:78:GLN:H	1.68	0.58
13:J:49:VAL:HG13	17:N:41:ARG:HD2	1.85	0.58
20:Q:104:LYS:O	20:Q:105:ALA:CB	2.50	0.58
1:A:413:G:H2'	1:A:428:G:H21	1.67	0.58
1:A:730:G:N2	1:A:765:G:H5''	2.19	0.58
1:A:1015:A:H2'	1:A:1016:A:H8	1.67	0.58
1:A:1195:C:H3'	1:A:1196:U:C5'	2.33	0.58
1:A:1412:C:H2'	1:A:1413:A:C8	2.38	0.58
3:Y:34:G:H2'	3:Y:35:A:H8	1.69	0.58
5:B:55:PHE:O	5:B:58:ILE:HB	2.04	0.58
5:B:78:GLN:HG2	5:B:94:ASN:ND2	2.18	0.58
5:B:97:TRP:CZ2	5:B:102:LEU:HD13	2.37	0.58
7:D:150:GLU:CD	7:D:153:ARG:HH12	2.12	0.58
8:E:126:ARG:HG3	8:E:126:ARG:HH11	1.68	0.58
10:G:138:LYS:HE2	10:G:142:GLU:OE1	2.03	0.58
13:J:23:ILE:H	13:J:23:ILE:CD1	2.15	0.58
1:A:824:C:H2'	1:A:825:G:H8	1.68	0.58
6:C:22:TRP:CE3	6:C:22:TRP:O	2.56	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:152:SER:O	7:D:155:LEU:HD12	2.02	0.58
8:E:74:GLY:CA	8:E:116:THR:HG22	2.32	0.58
14:K:77:MET:HE3	14:K:103:LEU:HD22	1.84	0.58
16:M:8:GLU:C	16:M:9:ILE:HG13	2.27	0.58
16:M:91:ARG:HB2	16:M:98:VAL:HG12	1.86	0.58
21:R:87:ARG:O	21:R:88:LYS:HB3	2.03	0.58
23:T:39:LYS:HD2	23:T:55:ILE:CD1	2.33	0.58
1:A:951:G:O2'	1:A:952:U:H5'	2.04	0.58
5:B:15:VAL:HG21	5:B:209:ARG:HG3	1.84	0.58
5:B:140:HIS:HA	5:B:143:GLU:CG	2.33	0.58
5:B:167:PRO:HG3	5:B:188:ALA:HB2	1.86	0.58
20:Q:60:ILE:HD13	20:Q:61:GLU:N	2.19	0.58
1:A:862:C:H2'	1:A:863:U:H6	1.68	0.58
6:C:113:ALA:HB3	6:C:114:PRO:HD3	1.86	0.58
7:D:63:LYS:HD2	7:D:198:VAL:HG22	1.84	0.58
21:R:37:VAL:HG22	21:R:78:LEU:HB3	1.85	0.58
1:A:1054:C:OP1	1:A:1197:G:OP1	2.20	0.58
5:B:77:ALA:HB2	5:B:211:ILE:CD1	2.26	0.58
5:B:98:LEU:O	5:B:101:MET:HG3	2.03	0.58
8:E:12:LEU:HD13	8:E:31:LEU:HB2	1.84	0.58
13:J:46:ARG:HH11	13:J:64:GLU:CB	2.17	0.58
22:S:30:LEU:HD23	22:S:31:ILE:N	2.19	0.58
1:A:948:C:O2'	1:A:949:A:H5'	2.04	0.57
6:C:134:ILE:O	6:C:138:VAL:HG23	2.04	0.57
16:M:4:ILE:HG22	16:M:5:ALA:H	1.69	0.57
1:A:190:C:H2'	1:A:190(A):C:H6	1.69	0.57
1:A:539:A:H2'	1:A:540:G:H8	1.68	0.57
5:B:23:ARG:HD3	5:B:24:TRP:N	2.19	0.57
6:C:35:GLU:HB3	6:C:59:ARG:NH2	2.19	0.57
7:D:60:GLU:OE1	7:D:60:GLU:HA	2.04	0.57
1:A:340:U:H2'	1:A:341:C:C6	2.39	0.57
1:A:1347:G:N2	1:A:1373:G:H2'	2.18	0.57
3:Y:34:G:H2'	3:Y:35:A:C8	2.39	0.57
6:C:6:HIS:NE2	6:C:8:ILE:HD12	2.19	0.57
6:C:47:LEU:H	6:C:47:LEU:CD1	2.17	0.57
12:I:75:ASP:O	12:I:78:LYS:HB3	2.05	0.57
21:R:86:VAL:O	21:R:87:ARG:HB2	2.03	0.57
1:A:927:G:H4'	1:A:1503:A:N7	2.19	0.57
1:A:1271:G:H2'	1:A:1272:G:C8	2.39	0.57
1:A:1286:A:C3'	1:A:1287:A:C5'	2.73	0.57
1:A:1349:A:H2'	1:A:1350:A:H8	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:87:ARG:HD2	5:B:87:ARG:C	2.29	0.57
6:C:34:LEU:HD12	17:N:25:VAL:HG21	1.86	0.57
9:F:10:LEU:HD11	9:F:59:TYR:HD2	1.69	0.57
13:J:32:ALA:CB	13:J:76:ASN:HD22	2.10	0.57
19:P:4:ILE:HG23	19:P:36:ILE:HD11	1.86	0.57
1:A:1314:C:OP2	22:S:6:LYS:HG2	2.03	0.57
9:F:92:LYS:HB2	9:F:92:LYS:HZ2	1.67	0.57
11:H:86:ILE:CG2	11:H:133:LEU:HD22	2.32	0.57
14:K:116:HIS:O	14:K:117:ASN:HB2	2.04	0.57
1:A:1314:C:H3'	22:S:6:LYS:NZ	2.19	0.57
10:G:16:LEU:HD22	10:G:16:LEU:N	2.15	0.57
10:G:115:ARG:HB2	10:G:118:VAL:HG23	1.86	0.57
11:H:119:LEU:HD23	11:H:119:LEU:N	2.20	0.57
19:P:28:ARG:HG3	19:P:29:ASP:OD2	2.03	0.57
19:P:38:TYR:CE2	19:P:50:LYS:HD3	2.39	0.57
1:A:76:C:O2'	1:A:77:G:H5'	2.04	0.57
6:C:15:THR:HG21	6:C:179:ARG:O	2.04	0.57
11:H:10:LEU:CD2	11:H:83:ILE:HD11	2.34	0.57
16:M:49:THR:HG22	16:M:51:ALA:H	1.68	0.57
16:M:84:ILE:CG2	22:S:65:ASN:HD22	2.18	0.57
17:N:24:CYS:SG	17:N:40:CYS:HB3	2.44	0.57
1:A:109:A:H2'	1:A:326:G:N2	2.19	0.57
1:A:123:C:OP1	1:A:312:C:H5'	2.04	0.57
5:B:12:GLU:OE2	5:B:213:LEU:HD11	2.04	0.57
6:C:137:ALA:HA	6:C:140:ARG:HD2	1.86	0.57
7:D:62:GLN:NE2	7:D:65:ARG:NH1	2.53	0.57
13:J:25:GLU:C	13:J:27:ALA:H	2.11	0.57
13:J:51:ARG:NE	13:J:61:GLU:HB2	2.19	0.57
19:P:42:ARG:O	19:P:43:LYS:C	2.48	0.57
1:A:1306:A:N6	1:A:1331:G:H1'	2.20	0.57
1:A:1306:A:O2'	16:M:109:THR:HG21	2.05	0.57
5:B:97:TRP:HH2	5:B:176:GLU:CD	2.13	0.57
5:B:159:PRO:HB2	5:B:161:ALA:O	2.05	0.57
6:C:64:VAL:CG2	6:C:99:VAL:HG11	2.34	0.57
10:G:85:TYR:CD1	10:G:154:TYR:HE1	2.23	0.57
12:I:10:ARG:HD2	12:I:11:LYS:N	2.20	0.57
13:J:38:ILE:HD12	13:J:71:LEU:HD12	1.87	0.57
13:J:46:ARG:HH11	13:J:64:GLU:HB3	1.69	0.57
13:J:59:SER:O	13:J:60:ARG:HB2	2.05	0.57
14:K:48:ILE:CG2	14:K:49:GLY:N	2.54	0.57
16:M:90:LEU:O	16:M:93:ARG:HB2	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:R:51:LEU:HB2	21:R:56:THR:HG22	1.87	0.57
1:A:1061:G:O2'	1:A:1062:U:H5'	2.05	0.57
1:A:1148:U:H2'	1:A:1149:C:O4'	2.05	0.57
1:A:1250:A:H2'	1:A:1251:A:C8	2.40	0.57
9:F:43:LEU:HD22	9:F:43:LEU:N	2.20	0.57
9:F:61:LEU:HB3	9:F:63:TYR:HE2	1.70	0.57
12:I:93:ARG:HB3	12:I:97:LYS:HE3	1.85	0.57
13:J:38:ILE:HG22	13:J:39:PRO:HD2	1.86	0.57
13:J:75:ILE:O	13:J:76:ASN:HB2	2.03	0.57
18:O:63:ARG:O	18:O:66:LEU:N	2.38	0.57
23:T:49:ALA:HB3	23:T:99:LEU:CD1	2.34	0.57
1:A:812:C:O2'	1:A:813:U:OP2	2.23	0.56
1:A:939:G:H5''	10:G:102:ARG:CZ	2.35	0.56
1:A:960:U:H1'	1:A:1223:C:H5'	1.86	0.56
1:A:1454:G:O2'	1:A:1455:G:H5'	2.04	0.56
5:B:87:ARG:NH2	5:B:233:SER:HB2	2.20	0.56
6:C:47:LEU:HD12	6:C:47:LEU:N	2.19	0.56
6:C:64:VAL:HG12	6:C:66:VAL:HG23	1.87	0.56
6:C:108:ASN:HD22	6:C:111:LEU:CG	2.13	0.56
14:K:69:ALA:O	14:K:70:LYS:C	2.48	0.56
18:O:74:ASP:CG	18:O:77:ARG:HG3	2.29	0.56
20:Q:67:LYS:HA	20:Q:70:ARG:NH1	2.12	0.56
21:R:45:SER:C	21:R:47:THR:H	2.11	0.56
22:S:18:LYS:O	22:S:22:LEU:HG	2.04	0.56
23:T:14:LYS:O	23:T:18:GLN:HG3	2.05	0.56
1:A:967:C:O2'	12:I:128:ARG:HD3	2.05	0.56
1:A:972:C:OP1	13:J:57:LYS:HE2	2.05	0.56
1:A:1271:G:H2'	1:A:1272:G:H8	1.69	0.56
15:L:29:GLY:O	15:L:30:ALA:O	2.23	0.56
16:M:107:ALA:O	16:M:111:LYS:HG3	2.05	0.56
1:A:248:C:O2'	1:A:249:U:H5'	2.06	0.56
1:A:270:A:H2'	1:A:271:C:C6	2.40	0.56
1:A:404:U:H2'	1:A:405:U:H6	1.69	0.56
1:A:1007:C:H42	1:A:1022:G:H1	1.53	0.56
1:A:1054:C:O2	1:A:1054:C:C3'	2.53	0.56
1:A:1101:A:H4'	1:A:1102:A:O5'	2.04	0.56
5:B:162:ILE:HG23	5:B:164:VAL:HG23	1.86	0.56
5:B:204:ASN:ND2	5:B:206:ASP:H	2.03	0.56
6:C:29:TYR:HE2	6:C:33:LEU:HD12	1.69	0.56
6:C:83:ARG:O	6:C:85:ARG:N	2.31	0.56
7:D:100:ARG:HH12	7:D:137:SER:HB3	1.68	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:150:GLU:HG3	7:D:153:ARG:HH22	1.70	0.56
10:G:78:ARG:HB2	10:G:156:TRP:CZ3	2.40	0.56
11:H:68:ARG:HG2	11:H:68:ARG:HH11	1.70	0.56
12:I:17:VAL:HG11	12:I:81:ILE:HG12	1.87	0.56
13:J:44:VAL:HG21	13:J:66:ARG:HH21	1.70	0.56
13:J:45:ARG:O	13:J:64:GLU:HA	2.05	0.56
16:M:62:ASN:O	16:M:63:THR:CB	2.50	0.56
18:O:26:GLU:OE1	18:O:77:ARG:HD2	2.06	0.56
19:P:1:MET:HE3	19:P:3:LYS:HD2	1.88	0.56
1:A:287:U:O2'	1:A:288:A:H5'	2.05	0.56
1:A:1004:A:H5''	1:A:1025:U:C5	2.40	0.56
1:A:1347:G:H2'	1:A:1373:G:N1	2.21	0.56
1:A:1347:G:C8	12:I:107:ARG:NH1	2.73	0.56
5:B:21:ARG:HA	5:B:39:ILE:HA	1.87	0.56
6:C:55:VAL:O	6:C:55:VAL:HG12	2.04	0.56
13:J:30:SER:CB	13:J:81:THR:HA	2.34	0.56
16:M:40:ASN:HD22	16:M:41:PRO:CD	2.19	0.56
16:M:78:ILE:O	16:M:81:LEU:HD23	2.06	0.56
20:Q:95:TYR:O	20:Q:97:SER:N	2.37	0.56
22:S:28:LYS:HD3	22:S:31:ILE:HD11	1.86	0.56
22:S:42:PRO:O	22:S:45:VAL:HG23	2.06	0.56
1:A:8:A:H5'	8:E:101:ILE:HG22	1.86	0.56
1:A:1168:A:H2'	1:A:1169:A:H8	1.67	0.56
5:B:24:TRP:CG	5:B:25:ASN:N	2.70	0.56
5:B:223:ILE:HD12	5:B:230:VAL:HG11	1.87	0.56
7:D:110:PHE:CD1	7:D:162:LEU:HD21	2.41	0.56
8:E:87:SER:HB3	8:E:131:ILE:HD13	1.87	0.56
10:G:114:ARG:HG2	10:G:114:ARG:HH11	1.71	0.56
13:J:16:LEU:O	13:J:17:ASP:C	2.48	0.56
15:L:23:LYS:O	15:L:24:VAL:HG23	2.06	0.56
16:M:14:ARG:H	16:M:44:ARG:NH2	1.99	0.56
19:P:20:VAL:CG1	19:P:32:TYR:HB2	2.34	0.56
1:A:405:U:H3'	1:A:406:G:H5'	1.88	0.56
1:A:586:C:O2'	1:A:587:G:H5'	2.05	0.56
1:A:792:A:H4'	1:A:793:U:H5''	1.88	0.56
1:A:1094:G:OP2	1:A:1095:U:H5	1.89	0.56
7:D:142:PRO:HG2	7:D:187:ARG:HH21	1.71	0.56
11:H:104:ARG:O	11:H:106:GLY:N	2.39	0.56
15:L:31:PRO:HB2	15:L:32:PHE:CD2	2.41	0.56
1:A:714:G:H2'	1:A:715:A:C8	2.41	0.56
1:A:1343:G:H2'	1:A:1344:C:H6	1.69	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:123:GLN:NE2	6:C:140:ARG:HH22	2.04	0.56
8:E:116:THR:HG23	8:E:117:ASP:OD2	2.06	0.56
11:H:34:GLU:O	11:H:37:ARG:HB2	2.04	0.56
15:L:62:SER:O	15:L:64:TYR:HD1	1.89	0.56
19:P:5:ARG:HH12	19:P:24:ALA:HA	1.71	0.56
19:P:67:THR:HG22	19:P:68:ASP:N	2.20	0.56
1:A:455:C:H42	1:A:477:G:H1	1.53	0.56
1:A:1314:C:O5'	22:S:6:LYS:HE2	2.06	0.56
5:B:30:ARG:HG3	5:B:31:TYR:N	2.20	0.56
10:G:37:ASN:ND2	12:I:41:VAL:HG23	2.21	0.56
13:J:10:GLY:N	13:J:16:LEU:HD11	2.21	0.56
1:A:135:C:O2	19:P:1:MET:HB2	2.06	0.56
1:A:416:G:H2'	1:A:417:C:C6	2.41	0.56
5:B:71:VAL:CG2	5:B:164:VAL:HA	2.30	0.56
5:B:80:ILE:H	5:B:80:ILE:CD1	2.04	0.56
6:C:61:ALA:C	6:C:63:ASN:H	2.12	0.56
9:F:55:ASP:HB3	9:F:86:ARG:HH12	1.71	0.56
10:G:124:LEU:O	10:G:127:ALA:HB3	2.06	0.56
11:H:86:ILE:CD1	11:H:133:LEU:HD21	2.35	0.56
1:A:89:C:H2'	1:A:90:U:O4'	2.06	0.56
1:A:428:G:H4'	1:A:429:U:O5'	2.06	0.56
1:A:851:G:H2'	1:A:852:G:C8	2.41	0.56
1:A:967:C:C4'	12:I:128:ARG:HG3	2.35	0.56
1:A:1353:G:O2'	1:A:1354:C:H5'	2.06	0.56
1:A:1468:A:H2'	1:A:1469:G:O4'	2.07	0.56
1:A:1515:C:O2'	1:A:1516:G:H5'	2.06	0.56
5:B:14:GLY:C	5:B:15:VAL:HG22	2.31	0.56
5:B:217:ARG:HA	5:B:220:ASP:OD2	2.06	0.56
6:C:66:VAL:O	6:C:66:VAL:HG12	2.06	0.56
7:D:61:LYS:CE	7:D:62:GLN:HE21	2.18	0.56
8:E:21:ALA:O	8:E:23:GLY:N	2.36	0.56
12:I:33:PHE:HZ	12:I:46:ALA:HB3	1.71	0.56
15:L:46:LYS:CG	15:L:47:LYS:N	2.69	0.56
17:N:31:ARG:O	17:N:32:SER:CB	2.53	0.56
1:A:691:G:O2'	1:A:797:C:H4'	2.06	0.55
1:A:1133:G:H2'	1:A:1134:G:C8	2.39	0.55
11:H:136:GLU:O	11:H:137:VAL:HG23	2.07	0.55
1:A:174:C:H2'	1:A:175:C:H6	1.69	0.55
1:A:397:A:H5'	1:A:398:C:OP1	2.05	0.55
1:A:421:U:H5'	1:A:422:C:H5	1.70	0.55
1:A:528:C:H41	15:L:49:ASN:ND2	2.04	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:560:U:O2'	1:A:561:U:OP2	2.21	0.55
1:A:840:C:OP2	1:A:840:C:H3'	2.05	0.55
1:A:895:G:H2'	1:A:896:C:C6	2.41	0.55
7:D:64:LEU:C	7:D:64:LEU:HD13	2.31	0.55
13:J:55:LYS:O	13:J:56:HIS:HB2	2.06	0.55
17:N:4:LYS:HA	17:N:7:ILE:HG12	1.88	0.55
19:P:10:GLY:HA3	19:P:14:ASN:O	2.05	0.55
19:P:21:VAL:HG21	19:P:59:TRP:CD1	2.41	0.55
1:A:154:C:H2'	1:A:155:C:H6	1.72	0.55
1:A:1286:A:H8	1:A:1287:A:H5''	1.71	0.55
1:A:1300:G:HO2'	1:A:1301:U:H6	1.51	0.55
8:E:96:PRO:HA	8:E:117:ASP:OD2	2.06	0.55
11:H:87:SER:HA	11:H:93:VAL:HG23	1.86	0.55
12:I:50:LEU:CA	12:I:55:ALA:HB3	2.36	0.55
13:J:38:ILE:CG1	13:J:71:LEU:HB3	2.36	0.55
1:A:448:A:OP2	1:A:485:G:N2	2.34	0.55
5:B:24:TRP:HB3	5:B:40:HIS:CE1	2.42	0.55
12:I:84:ALA:O	12:I:87:GLN:HB2	2.07	0.55
15:L:46:LYS:HD2	15:L:47:LYS:H	1.70	0.55
19:P:11:SER:OG	19:P:14:ASN:HB3	2.06	0.55
20:Q:45:HIS:CD2	20:Q:47:PRO:HG3	2.40	0.55
1:A:1051:C:H2'	1:A:1052:U:H6	1.70	0.55
1:A:1055:A:C2	1:A:1056:U:H1'	2.42	0.55
7:D:70:ILE:HD11	7:D:100:ARG:HD2	1.88	0.55
10:G:107:ALA:O	10:G:110:GLN:HB2	2.06	0.55
10:G:111:ARG:HB3	10:G:113:GLU:OE2	2.06	0.55
10:G:115:ARG:HB2	10:G:118:VAL:CG2	2.37	0.55
22:S:5:LEU:O	22:S:6:LYS:CB	2.54	0.55
6:C:33:LEU:HD23	6:C:33:LEU:C	2.32	0.55
6:C:54:ARG:HG2	6:C:55:VAL:H	1.71	0.55
8:E:6:PHE:HE2	8:E:36:ASP:HB3	1.71	0.55
9:F:12:PRO:HG3	9:F:57:GLN:O	2.06	0.55
9:F:55:ASP:CB	9:F:86:ARG:HH12	2.20	0.55
11:H:119:LEU:HD12	11:H:124:ALA:CA	2.37	0.55
13:J:4:ILE:HA	13:J:100:THR:CB	2.36	0.55
17:N:3:ARG:CZ	17:N:6:LEU:HD12	2.37	0.55
17:N:26:ARG:NH1	17:N:47:LEU:HD11	2.22	0.55
19:P:19:ILE:HD12	19:P:19:ILE:N	2.21	0.55
23:T:85:MET:CE	23:T:104:LEU:HD23	2.37	0.55
23:T:100:ILE:O	23:T:100:ILE:HG22	2.06	0.55
1:A:190(L):U:C2	23:T:105:SER:HB2	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:10:LEU:HD23	5:B:10:LEU:C	2.32	0.55
6:C:58:GLU:O	6:C:64:VAL:HA	2.07	0.55
6:C:134:ILE:HG22	6:C:168:ALA:HB3	1.86	0.55
11:H:24:THR:CG2	11:H:63:LEU:HD21	2.35	0.55
1:A:864:A:H2'	1:A:865:A:C8	2.42	0.55
5:B:134:GLU:HG2	5:B:137:ARG:NH2	2.21	0.55
5:B:151:GLY:C	5:B:153:ARG:H	2.14	0.55
6:C:54:ARG:HG2	6:C:55:VAL:N	2.22	0.55
6:C:130:VAL:O	6:C:134:ILE:HG13	2.05	0.55
6:C:139:GLN:CA	6:C:139:GLN:HE21	2.18	0.55
15:L:75:HIS:CD2	15:L:77:LEU:H	2.25	0.55
16:M:77:ASN:O	16:M:80:ARG:HB3	2.06	0.55
20:Q:104:LYS:O	20:Q:105:ALA:HB2	2.07	0.55
22:S:82:GLY:O	22:S:83:HIS:CB	2.55	0.55
1:A:1121:U:H2'	1:A:1122:U:C6	2.41	0.55
11:H:127:LEU:N	11:H:127:LEU:CD2	2.70	0.55
13:J:39:PRO:O	13:J:40:LEU:HB2	2.05	0.55
13:J:80:LYS:HA	13:J:83:GLU:HB2	1.88	0.55
1:A:1053:G:H4'	1:A:1054:C:H4'	1.88	0.55
1:A:1118:C:O4'	1:A:1179:A:H1'	2.07	0.55
1:A:1278:U:H4'	1:A:1279:A:O4'	2.07	0.55
9:F:63:TYR:HD2	9:F:63:TYR:N	2.05	0.55
12:I:23:ASN:HD22	12:I:23:ASN:C	2.14	0.55
13:J:4:ILE:HD11	13:J:77:PRO:HB3	1.89	0.55
13:J:14:LYS:C	13:J:16:LEU:H	2.14	0.55
13:J:27:ALA:HA	13:J:30:SER:OG	2.06	0.55
13:J:38:ILE:H	13:J:72:VAL:H	1.55	0.55
15:L:40:VAL:O	15:L:40:VAL:HG12	2.06	0.55
1:A:427:U:OP1	7:D:13:ARG:NH2	2.39	0.54
1:A:458:C:H2'	1:A:459:G:H8	1.71	0.54
1:A:1234:C:O2'	1:A:1235:U:H5'	2.07	0.54
6:C:191:THR:HG21	6:C:193:TYR:CE2	2.41	0.54
7:D:100:ARG:NH1	7:D:137:SER:HA	2.22	0.54
8:E:120:THR:HG23	8:E:121:LYS:N	2.21	0.54
11:H:120:THR:HG23	11:H:123:GLU:OE2	2.07	0.54
12:I:93:ARG:O	12:I:95:LYS:N	2.39	0.54
1:A:947:G:O3'	16:M:109:THR:HB	2.07	0.54
1:A:1128:C:H1'	1:A:1146:A:H61	1.71	0.54
1:A:1197:G:OP1	1:A:1197:G:H3'	2.07	0.54
1:A:1250:A:C5'	12:I:68:GLY:N	2.69	0.54
1:A:1250:A:C5'	12:I:68:GLY:H	2.20	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:127:ILE:HB	5:B:128:GLU:OE2	2.07	0.54
6:C:150:LYS:HE2	6:C:152:ILE:HD11	1.88	0.54
9:F:91:VAL:HG12	9:F:92:LYS:O	2.06	0.54
11:H:77:GLU:HG3	11:H:78:GLN:N	2.22	0.54
12:I:117:HIS:CD2	12:I:123:PRO:HA	2.42	0.54
15:L:53:ARG:CD	15:L:93:LEU:HD21	2.37	0.54
15:L:53:ARG:HD2	15:L:93:LEU:HD21	1.89	0.54
23:T:13:LEU:HD12	23:T:13:LEU:N	2.21	0.54
1:A:56:U:H2'	1:A:57:G:C8	2.42	0.54
1:A:408:A:O2'	1:A:409:G:H5'	2.07	0.54
1:A:1137:C:H4'	1:A:1138:G:N1	2.22	0.54
1:A:1347:G:C2'	1:A:1348:U:OP2	2.55	0.54
7:D:190:ASP:HB3	7:D:193:ASP:OD2	2.08	0.54
8:E:51:VAL:O	8:E:55:VAL:HG23	2.07	0.54
9:F:87:ARG:HG2	9:F:87:ARG:HH11	1.71	0.54
13:J:55:LYS:HG3	13:J:56:HIS:N	2.22	0.54
18:O:87:ILE:HG22	18:O:88:ARG:HG2	1.88	0.54
20:Q:81:ARG:HG3	20:Q:81:ARG:O	2.07	0.54
1:A:994:A:H2'	1:A:994:A:N3	2.22	0.54
1:A:1109:C:OP2	6:C:176:HIS:CD2	2.60	0.54
1:A:1423:G:O2'	1:A:1424:C:H5'	2.06	0.54
5:B:129:GLU:O	5:B:130:ARG:HB2	2.06	0.54
6:C:47:LEU:CD2	6:C:68:VAL:HG11	2.37	0.54
10:G:123:GLU:HA	10:G:123:GLU:OE2	2.08	0.54
18:O:87:ILE:HG22	18:O:88:ARG:N	2.21	0.54
1:A:191:G:C4	23:T:105:SER:HB3	2.43	0.54
1:A:243:A:H4'	1:A:244:U:C5'	2.29	0.54
1:A:993:G:H4'	1:A:994:A:OP2	2.07	0.54
1:A:1441:G:H4'	1:A:1442:G:C4	2.41	0.54
7:D:52:SER:O	7:D:53:ASP:C	2.51	0.54
17:N:35:ARG:C	17:N:37:PHE:N	2.66	0.54
19:P:20:VAL:HG11	19:P:32:TYR:HB3	1.90	0.54
22:S:67:VAL:HG12	22:S:68:GLY:N	2.23	0.54
1:A:695:A:P	14:K:53:SER:HB2	2.47	0.54
1:A:1001:A:H2	1:A:1040:U:H3	1.54	0.54
1:A:1014:A:C2	1:A:1219:U:H1'	2.41	0.54
5:B:123:ALA:CA	5:B:127:ILE:HD11	2.37	0.54
6:C:52:LEU:HD23	6:C:52:LEU:N	2.21	0.54
15:L:46:LYS:HE3	15:L:47:LYS:HB2	1.88	0.54
1:A:1064:G:H4'	1:A:1065:U:C5'	2.37	0.54
1:A:1320:C:O2	22:S:72:GLY:HA3	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1381:U:O2'	1:A:1382:C:H5'	2.07	0.54
15:L:41:ARG:HB3	15:L:41:ARG:HH11	1.73	0.54
19:P:21:VAL:HG21	19:P:59:TRP:CG	2.43	0.54
20:Q:76:LEU:HD23	20:Q:77:VAL:N	2.22	0.54
1:A:99:C:H2'	1:A:101:A:O4'	2.08	0.54
1:A:229:U:O2'	1:A:230:G:H5'	2.08	0.54
1:A:338:A:H2	1:A:351:G:H22	1.55	0.54
1:A:977:A:H2'	1:A:978:A:H5''	1.90	0.54
1:A:1128:C:C4'	12:I:16:ARG:HH12	2.20	0.54
1:A:1290:G:H21	12:I:70:LYS:HZ1	1.55	0.54
5:B:69:LEU:HD12	5:B:155:LEU:CD1	2.38	0.54
6:C:150:LYS:HB2	6:C:169:ALA:CB	2.38	0.54
9:F:101:ALA:HB2	21:R:28:GLU:CB	2.38	0.54
18:O:26:GLU:HA	18:O:81:LEU:HD11	1.88	0.54
19:P:4:ILE:HG13	19:P:64:ALA:HB1	1.89	0.54
1:A:376:G:OP2	19:P:67:THR:HG21	2.08	0.54
1:A:760:G:N2	20:Q:104:LYS:N	2.56	0.54
1:A:1066:C:C5	1:A:1067:A:N6	2.76	0.54
9:F:82:ARG:HB2	9:F:85:VAL:CG2	2.38	0.54
10:G:16:LEU:H	10:G:16:LEU:CD2	2.13	0.54
13:J:3:LYS:N	13:J:75:ILE:HG23	2.23	0.54
13:J:23:ILE:O	13:J:23:ILE:HG22	2.08	0.54
15:L:83:VAL:CG2	15:L:100:ILE:HG23	2.37	0.54
20:Q:27:PHE:CE1	20:Q:36:ILE:HD11	2.43	0.54
20:Q:76:LEU:C	20:Q:76:LEU:CD2	2.81	0.54
20:Q:97:SER:CB	20:Q:103:GLY:HA2	2.38	0.54
1:A:204:U:H5'	1:A:216:G:O5'	2.08	0.54
1:A:960:U:H5'	1:A:960:U:O2	2.08	0.54
1:A:1320:C:C2	22:S:72:GLY:HA3	2.43	0.54
6:C:95:THR:O	6:C:97:LYS:N	2.39	0.54
8:E:24:ARG:HG2	8:E:24:ARG:HH11	1.72	0.54
10:G:116:ALA:HA	10:G:119:ARG:NH2	2.22	0.54
12:I:125:TYR:CE1	12:I:128:ARG:HD2	2.42	0.54
13:J:38:ILE:CD1	13:J:71:LEU:HD12	2.38	0.54
14:K:69:ALA:O	14:K:72:ALA:N	2.41	0.54
19:P:58:TYR:CZ	19:P:62:VAL:HG21	2.43	0.54
20:Q:2:PRO:O	20:Q:3:LYS:C	2.51	0.54
1:A:407:G:H2'	1:A:408:A:C8	2.44	0.53
1:A:940:C:H2'	1:A:941:G:H8	1.72	0.53
1:A:1005:A:H2'	1:A:1006:C:H5'	1.89	0.53
1:A:1499:A:O2'	1:A:1500:A:H5'	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:29:TYR:CE1	13:J:65:LEU:HD11	2.42	0.53
7:D:189:PRO:HB2	7:D:194:LEU:HD21	1.89	0.53
8:E:103:GLY:O	8:E:106:PRO:HD2	2.07	0.53
9:F:1:MET:HG2	9:F:68:PRO:HA	1.88	0.53
10:G:51:GLN:NE2	10:G:58:PRO:HD3	2.20	0.53
13:J:3:LYS:C	13:J:4:ILE:HG13	2.32	0.53
20:Q:45:HIS:NE2	20:Q:47:PRO:HG3	2.23	0.53
21:R:59:SER:O	21:R:60:GLY:C	2.51	0.53
1:A:527:G:O2'	1:A:535:A:N1	2.37	0.53
1:A:642:A:N7	11:H:115:SER:HA	2.23	0.53
1:A:975:A:O2'	1:A:976:G:OP2	2.25	0.53
1:A:1286:A:C2	24:V:18:TYR:OH	2.62	0.53
5:B:134:GLU:O	5:B:138:LEU:HG	2.07	0.53
5:B:189:ASP:HB3	5:B:203:GLY:O	2.07	0.53
9:F:1:MET:SD	9:F:1:MET:N	2.80	0.53
11:H:60:ARG:HH11	11:H:60:ARG:CG	2.21	0.53
12:I:42:ARG:O	12:I:43:ALA:C	2.51	0.53
23:T:49:ALA:HB3	23:T:99:LEU:CG	2.39	0.53
1:A:1218:C:H2'	1:A:1219:U:C6	2.43	0.53
5:B:204:ASN:HD22	5:B:206:ASP:H	1.56	0.53
10:G:6:ARG:O	10:G:7:ALA:C	2.51	0.53
19:P:81:ARG:HG3	19:P:83:GLU:HG2	1.90	0.53
23:T:36:LEU:O	23:T:37:SER:C	2.51	0.53
1:A:448:A:H2'	1:A:449:C:C6	2.43	0.53
1:A:952:U:O2'	1:A:953:G:H5'	2.08	0.53
1:A:1031:G:H2'	1:A:1032:G:C8	2.43	0.53
1:A:1123:A:O3'	13:J:36:GLY:HA3	2.09	0.53
5:B:30:ARG:HD2	5:B:31:TYR:CE2	2.43	0.53
6:C:28:GLN:O	6:C:31:HIS:N	2.37	0.53
7:D:121:VAL:O	7:D:134:ASP:HA	2.09	0.53
8:E:37:ARG:HG2	8:E:37:ARG:HH11	1.74	0.53
9:F:99:ALA:HB2	21:R:31:LEU:CD1	2.39	0.53
10:G:92:SER:O	10:G:96:GLN:HG3	2.08	0.53
10:G:143:ARG:O	10:G:145:ALA:O	2.27	0.53
12:I:11:LYS:O	12:I:11:LYS:HG2	2.08	0.53
21:R:53:ARG:HD3	21:R:59:SER:HA	1.89	0.53
1:A:406:G:H2'	1:A:407:G:H8	1.74	0.53
1:A:458:C:H2'	1:A:459:G:C8	2.44	0.53
1:A:1002:G:O2'	1:A:1003:G:H5'	2.09	0.53
1:A:1208:C:H2'	1:A:1209:C:H6	1.73	0.53
1:A:1479:C:H2'	1:A:1480:G:C8	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:111:LEU:HD21	6:C:144:SER:O	2.08	0.53
9:F:18:GLN:O	9:F:21:LEU:HB3	2.08	0.53
13:J:8:LEU:CD2	13:J:20:ALA:HB2	2.35	0.53
15:L:93:LEU:HB2	15:L:96:VAL:HG21	1.89	0.53
1:A:269:C:H2'	1:A:270:A:C8	2.43	0.53
1:A:695:A:OP2	14:K:53:SER:HB2	2.08	0.53
1:A:791:G:C6	1:A:792:A:N7	2.76	0.53
9:F:22:GLU:O	9:F:26:ILE:HG13	2.09	0.53
11:H:83:ILE:HG23	11:H:83:ILE:O	2.09	0.53
12:I:43:ALA:O	12:I:44:VAL:C	2.52	0.53
13:J:42:THR:HG23	13:J:68:HIS:HA	1.89	0.53
16:M:23:TYR:O	16:M:25:ILE:N	2.40	0.53
1:A:190(D):U:O2'	1:A:190(E):U:H5'	2.09	0.53
1:A:370:C:HO2'	1:A:371:G:H5'	1.73	0.53
1:A:919:A:O2'	1:A:920:U:H5'	2.09	0.53
1:A:1067:A:N3	1:A:1068:G:H1'	2.23	0.53
1:A:1118:C:H1'	1:A:1179:A:C4	2.44	0.53
1:A:1196:U:H4'	1:A:1197:G:OP2	2.07	0.53
1:A:1349:A:H2'	1:A:1350:A:C8	2.43	0.53
5:B:144:ARG:HG3	5:B:145:LEU:H	1.72	0.53
7:D:106:TYR:HE1	7:D:113:SER:HA	1.71	0.53
8:E:52:PRO:O	8:E:53:LEU:C	2.52	0.53
9:F:63:TYR:N	9:F:63:TYR:CD2	2.76	0.53
9:F:76:ALA:O	9:F:77:ARG:C	2.50	0.53
13:J:44:VAL:HG22	13:J:66:ARG:HB3	1.91	0.53
14:K:73:MET:SD	14:K:102:GLY:HA3	2.49	0.53
16:M:22:ILE:HG21	16:M:25:ILE:HD12	1.91	0.53
1:A:133:U:OP1	23:T:74:LYS:HE2	2.09	0.53
1:A:1163:C:O2'	1:A:1164:G:H5'	2.08	0.53
1:A:1286:A:H8	1:A:1287:A:C5'	2.22	0.53
1:A:1373:G:H5''	10:G:36:LYS:HB2	1.90	0.53
5:B:77:ALA:HA	5:B:80:ILE:CD1	2.34	0.53
5:B:101:MET:CA	5:B:108:ILE:HD12	2.38	0.53
6:C:157:ILE:HG21	6:C:164:ARG:NH2	2.24	0.53
13:J:6:ILE:O	13:J:71:LEU:O	2.27	0.53
15:L:33:ARG:HD2	15:L:62:SER:HB3	1.91	0.53
16:M:5:ALA:O	16:M:6:GLY:C	2.50	0.53
16:M:78:ILE:HA	16:M:81:LEU:CD2	2.37	0.53
23:T:59:ALA:O	23:T:63:ILE:HG13	2.09	0.53
1:A:105:G:H2'	1:A:106:C:C6	2.44	0.53
1:A:370:C:O2'	1:A:371:G:H5'	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:881:G:OP2	15:L:12:ARG:NH2	2.42	0.53
3:Y:36:A:H2'	3:Y:37:A:C8	2.43	0.53
9:F:48:LEU:HD13	9:F:52:ILE:HG13	1.91	0.53
9:F:95:GLU:CD	9:F:95:GLU:H	2.17	0.53
12:I:32:ASP:O	12:I:35:GLU:N	2.42	0.53
13:J:24:VAL:O	13:J:28:ARG:HG3	2.09	0.53
15:L:47:LYS:CB	15:L:48:PRO:CD	2.77	0.53
19:P:38:TYR:HE2	19:P:50:LYS:HD3	1.74	0.53
1:A:598:U:H4'	11:H:94:TYR:CD1	2.44	0.53
1:A:653:A:C8	11:H:56:LYS:HG2	2.44	0.53
1:A:1315:U:H2'	1:A:1316:G:O4'	2.08	0.53
6:C:91:LEU:HD23	6:C:91:LEU:C	2.34	0.53
13:J:6:ILE:HG22	13:J:98:ILE:HG23	1.90	0.53
15:L:24:VAL:O	15:L:26:ALA:N	2.35	0.53
17:N:14:PRO:O	17:N:15:LYS:CB	2.57	0.53
21:R:47:THR:O	21:R:49:LYS:N	2.43	0.53
22:S:15:LEU:O	22:S:19:VAL:HG12	2.09	0.53
24:V:12:LYS:HB3	24:V:22:ARG:HD2	1.91	0.53
1:A:80:G:H3'	1:A:81:U:C5'	2.37	0.52
1:A:262:A:H5'	23:T:74:LYS:HG3	1.91	0.52
1:A:502:G:OP1	15:L:118:SER:CB	2.57	0.52
1:A:542:G:H2'	1:A:543:C:H6	1.74	0.52
1:A:966:G:H2'	1:A:967:C:C6	2.44	0.52
1:A:1053:G:C3'	1:A:1054:C:C5'	2.88	0.52
1:A:1228:C:H2'	1:A:1229:A:H8	1.74	0.52
7:D:17:VAL:HG12	7:D:18:LYS:N	2.24	0.52
10:G:111:ARG:NH2	10:G:122:HIS:HB3	2.23	0.52
13:J:12:ASP:HB3	13:J:15:THR:CG2	2.40	0.52
22:S:36:ARG:NH2	22:S:75:ALA:O	2.38	0.52
1:A:421:U:H5'	1:A:422:C:C5	2.44	0.52
1:A:498:U:O2'	1:A:499:A:H5'	2.09	0.52
1:A:1048:G:H5''	17:N:3:ARG:HG2	1.92	0.52
1:A:1095:U:H2'	1:A:1096:C:H6	1.74	0.52
1:A:1202:G:O2'	1:A:1203:C:H5'	2.09	0.52
6:C:191:THR:HG22	6:C:193:TYR:H	1.74	0.52
7:D:6:GLY:O	7:D:8:VAL:HG23	2.08	0.52
8:E:89:ILE:HD13	8:E:90:VAL:N	2.24	0.52
8:E:107:ARG:O	8:E:109:ILE:N	2.43	0.52
14:K:59:TYR:O	14:K:62:GLN:N	2.43	0.52
19:P:26:ARG:HD2	19:P:31:LYS:O	2.08	0.52
22:S:13:ASP:O	22:S:14:HIS:C	2.51	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:556:C:O2'	1:A:557:G:H5'	2.08	0.52
1:A:730:G:H21	1:A:765:G:H5''	1.72	0.52
1:A:761:G:C5'	20:Q:102:GLY:HA3	2.38	0.52
1:A:1129:C:O5'	1:A:1130:A:H5'	2.09	0.52
5:B:10:LEU:O	5:B:12:GLU:N	2.39	0.52
5:B:89:GLY:H	5:B:226:ARG:HH22	1.57	0.52
7:D:30:LYS:C	7:D:32:ALA:H	2.18	0.52
8:E:72:GLN:C	8:E:74:GLY:N	2.67	0.52
8:E:110:LEU:HD13	8:E:118:ILE:HG21	1.92	0.52
16:M:37:THR:HG23	16:M:55:ARG:HB3	1.92	0.52
16:M:82:MET:HE3	16:M:92:HIS:HB3	1.91	0.52
19:P:63:GLY:O	19:P:64:ALA:C	2.51	0.52
1:A:646:U:H2'	1:A:647:C:C6	2.43	0.52
1:A:1250:A:H4'	12:I:68:GLY:CA	2.39	0.52
6:C:147:LYS:HE3	6:C:203:PHE:CE2	2.44	0.52
6:C:190:ARG:HH11	6:C:190:ARG:CB	2.19	0.52
7:D:64:LEU:HD12	7:D:75:PHE:CE1	2.43	0.52
8:E:101:ILE:O	8:E:120:THR:HB	2.10	0.52
9:F:60:PHE:CE2	21:R:78:LEU:HD21	2.45	0.52
12:I:118:LYS:HZ2	12:I:118:LYS:CB	2.20	0.52
16:M:8:GLU:HG3	16:M:22:ILE:HG12	1.91	0.52
20:Q:12:SER:HB3	20:Q:20:THR:HB	1.90	0.52
22:S:44:MET:HA	22:S:47:HIS:HD2	1.74	0.52
23:T:72:LEU:O	23:T:73:HIS:C	2.52	0.52
23:T:79:ARG:O	23:T:82:SER:HB3	2.10	0.52
1:A:17:U:H2'	1:A:18:C:C6	2.44	0.52
1:A:502:G:OP1	15:L:118:SER:HB2	2.08	0.52
1:A:668:G:O2'	18:O:46:HIS:HD2	1.93	0.52
1:A:1178:G:P	12:I:97:LYS:HZ2	2.32	0.52
5:B:178:ARG:HG3	5:B:178:ARG:NH1	2.23	0.52
7:D:149:ALA:O	7:D:150:GLU:C	2.51	0.52
10:G:120:ILE:O	10:G:124:LEU:HG	2.09	0.52
13:J:3:LYS:N	13:J:75:ILE:HA	2.24	0.52
14:K:15:ALA:O	14:K:77:MET:HA	2.09	0.52
19:P:28:ARG:HG3	19:P:29:ASP:N	2.24	0.52
22:S:17:GLU:O	22:S:21:GLU:HG3	2.10	0.52
1:A:242:C:H2'	1:A:243:A:H5'	1.91	0.52
1:A:337:C:H2'	1:A:338:A:H8	1.75	0.52
1:A:795:C:H5''	1:A:796:C:OP2	2.09	0.52
1:A:1042:G:O2'	1:A:1043:C:H5'	2.09	0.52
6:C:157:ILE:HD13	6:C:166:GLU:OE1	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:G:23:VAL:HG13	10:G:43:PHE:CE2	2.43	0.52
17:N:30:ALA:O	17:N:33:VAL:HG22	2.10	0.52
1:A:107:G:C2'	1:A:108:G:H5'	2.39	0.52
1:A:1286:A:C8	1:A:1287:A:H5''	2.45	0.52
5:B:102:LEU:HD21	5:B:162:ILE:CD1	2.38	0.52
6:C:36:ASP:O	6:C:39:ILE:HB	2.09	0.52
10:G:146:GLU:C	10:G:148:ASN:N	2.67	0.52
22:S:21:GLU:O	22:S:24:ALA:N	2.42	0.52
23:T:16:HIS:CE1	23:T:20:LEU:HD11	2.44	0.52
24:V:24:ARG:O	24:V:25:LYS:HB3	2.09	0.52
1:A:21:G:H2'	1:A:22:G:C8	2.44	0.52
1:A:760:G:H21	20:Q:104:LYS:H	1.58	0.52
1:A:1207:G:O2'	1:A:1208:C:H5'	2.10	0.52
1:A:1263:C:H2'	1:A:1264:C:C6	2.45	0.52
5:B:78:GLN:HG3	5:B:94:ASN:O	2.10	0.52
5:B:135:GLN:O	5:B:139:LYS:HE2	2.10	0.52
6:C:64:VAL:HG12	6:C:65:ALA:H	1.74	0.52
6:C:150:LYS:CE	6:C:152:ILE:HD11	2.40	0.52
11:H:29:SER:O	11:H:30:ARG:C	2.53	0.52
21:R:87:ARG:HG3	21:R:87:ARG:HH11	1.75	0.52
22:S:62:ILE:HD12	22:S:63:THR:N	2.25	0.52
1:A:254:G:O2'	1:A:255:G:H5'	2.08	0.52
1:A:1049:U:H4'	1:A:1050:G:OP2	2.08	0.52
1:A:1057:G:O2'	1:A:1058:G:H5'	2.09	0.52
1:A:1351:U:O2'	1:A:1352:C:H5'	2.10	0.52
1:A:1394:A:C5	1:A:1501:C:H4'	2.44	0.52
5:B:80:ILE:HG12	5:B:208:ILE:CG2	2.37	0.52
13:J:71:LEU:HD13	13:J:73:ASP:HB2	1.92	0.52
14:K:95:ILE:O	14:K:99:GLN:HG3	2.09	0.52
15:L:119:LYS:O	15:L:120:TYR:HB2	2.10	0.52
16:M:14:ARG:N	16:M:44:ARG:NH2	2.53	0.52
20:Q:33:GLY:O	20:Q:34:LYS:C	2.52	0.52
22:S:67:VAL:O	22:S:69:HIS:N	2.43	0.52
1:A:41:G:H2'	1:A:42:G:C8	2.45	0.52
1:A:1228:C:H4'	16:M:116:THR:HA	1.92	0.52
5:B:44:LEU:HA	5:B:47:THR:OG1	2.09	0.52
11:H:9:MET:HE1	11:H:32:LYS:HA	1.91	0.52
13:J:14:LYS:C	13:J:16:LEU:N	2.67	0.52
13:J:22:LYS:C	13:J:24:VAL:N	2.68	0.52
14:K:18:ARG:CB	14:K:33:THR:HG22	2.39	0.52
16:M:8:GLU:HA	16:M:8:GLU:OE2	2.11	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:S:80:TYR:C	22:S:80:TYR:CD2	2.88	0.52
24:V:2:GLY:C	24:V:4:GLY:N	2.65	0.52
1:A:47:C:H5''	1:A:365:U:C6	2.44	0.51
1:A:761:G:H5'	20:Q:103:GLY:H	1.74	0.51
1:A:1161:C:H2'	1:A:1162:C:C6	2.44	0.51
1:A:1392:G:O2'	1:A:1502:A:H5''	2.10	0.51
6:C:43:LEU:HD13	6:C:68:VAL:CG2	2.39	0.51
11:H:125:ARG:HB2	11:H:125:ARG:NH1	2.25	0.51
14:K:26:ASN:O	14:K:27:ASN:HB2	2.11	0.51
16:M:63:THR:HG23	16:M:64:TRP:CG	2.44	0.51
23:T:57:ARG:HH11	23:T:57:ARG:HB3	1.73	0.51
1:A:232:G:H1'	1:A:262:A:N1	2.25	0.51
1:A:945:G:C2	1:A:946:A:C8	2.98	0.51
1:A:1165:C:O2'	1:A:1166:G:H5'	2.10	0.51
1:A:1257:U:O2'	1:A:1258:G:OP2	2.25	0.51
5:B:59:GLU:O	5:B:62:ALA:N	2.44	0.51
8:E:12:LEU:CD1	8:E:31:LEU:HB2	2.40	0.51
8:E:110:LEU:O	8:E:113:ALA:HB3	2.10	0.51
8:E:126:ARG:HH11	8:E:126:ARG:CG	2.23	0.51
14:K:40:ILE:HG23	14:K:75:TYR:CD2	2.46	0.51
23:T:94:ALA:O	23:T:95:ALA:HB3	2.09	0.51
1:A:190:C:H2'	1:A:190(A):C:C6	2.45	0.51
1:A:335:C:H2'	1:A:336:C:C6	2.45	0.51
1:A:1195:C:H3'	1:A:1196:U:H5'	1.91	0.51
7:D:8:VAL:CG1	7:D:21:LEU:HD13	2.40	0.51
12:I:44:VAL:O	12:I:45:ALA:C	2.53	0.51
12:I:93:ARG:O	12:I:94:ALA:C	2.53	0.51
12:I:114:TYR:CE1	13:J:59:SER:O	2.63	0.51
21:R:47:THR:C	21:R:49:LYS:H	2.18	0.51
1:A:1056:U:C5'	6:C:163:ALA:HB2	2.32	0.51
1:A:1321:C:N4	22:S:37:ARG:HH12	2.08	0.51
1:A:1496:C:H2'	1:A:1497:G:O4'	2.10	0.51
5:B:166:ASP:OD2	5:B:169:LYS:HB2	2.10	0.51
6:C:195:VAL:CG1	6:C:196:LEU:N	2.73	0.51
9:F:91:VAL:HG13	21:R:72:ARG:NH2	2.25	0.51
12:I:116:LYS:O	12:I:118:LYS:N	2.43	0.51
20:Q:65:ILE:HD12	20:Q:65:ILE:N	2.25	0.51
1:A:629:G:O2'	1:A:630:G:H5'	2.11	0.51
1:A:1029:C:H2'	1:A:1030:C:C6	2.45	0.51
1:A:1216:G:O2'	1:A:1217:C:H5'	2.10	0.51
1:A:1223:C:P	22:S:78:ARG:NH1	2.83	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1312:G:O2'	1:A:1313:U:H5'	2.11	0.51
7:D:23:GLY:HA3	7:D:112:VAL:CG1	2.40	0.51
11:H:104:ARG:O	11:H:105:ARG:C	2.54	0.51
14:K:87:THR:HG23	14:K:91:ARG:NH2	2.25	0.51
20:Q:104:LYS:CD	20:Q:105:ALA:H	2.24	0.51
21:R:42:ARG:HG3	21:R:42:ARG:HH11	1.74	0.51
22:S:15:LEU:HD12	22:S:16:LEU:H	1.74	0.51
23:T:57:ARG:HB3	23:T:57:ARG:NH1	2.25	0.51
1:A:190(L):U:O2'	1:A:191:G:H5'	2.11	0.51
1:A:669:U:H2'	1:A:670:G:C8	2.45	0.51
1:A:1392:G:O2'	1:A:1393:U:H5'	2.11	0.51
5:B:73:THR:HG23	5:B:95:GLN:O	2.11	0.51
6:C:177:THR:HG23	6:C:177:THR:O	2.11	0.51
7:D:199:ASN:ND2	7:D:199:ASN:C	2.65	0.51
9:F:40:VAL:HG22	9:F:41:GLU:N	2.24	0.51
17:N:37:PHE:CE2	17:N:53:LEU:HD13	2.46	0.51
22:S:28:LYS:CG	22:S:29:ARG:H	2.06	0.51
1:A:180:U:H2'	1:A:181:G:C5'	2.41	0.51
1:A:364:A:N6	15:L:28:LYS:NZ	2.58	0.51
1:A:792:A:H4'	1:A:793:U:C5'	2.41	0.51
1:A:895:G:H2'	1:A:896:C:H6	1.75	0.51
5:B:13:ALA:C	5:B:15:VAL:N	2.67	0.51
6:C:47:LEU:HD23	6:C:68:VAL:HG11	1.93	0.51
6:C:190:ARG:HB3	6:C:190:ARG:NH1	2.22	0.51
7:D:21:LEU:HD21	7:D:66:ARG:O	2.10	0.51
10:G:51:GLN:C	10:G:53:LYS:H	2.19	0.51
12:I:55:ALA:C	12:I:57:GLY:H	2.19	0.51
20:Q:104:LYS:HD2	20:Q:105:ALA:H	1.74	0.51
21:R:25:THR:O	21:R:26:LEU:HB2	2.11	0.51
1:A:620:C:C1'	7:D:135:LEU:HD13	2.41	0.51
1:A:973:G:H3'	1:A:974:A:H5''	1.93	0.51
1:A:1469:G:O2'	1:A:1470:G:H5'	2.11	0.51
5:B:208:ILE:HG22	5:B:212:GLN:HB2	1.93	0.51
8:E:24:ARG:HG2	8:E:24:ARG:NH1	2.26	0.51
12:I:111:ARG:HD3	12:I:112:LYS:N	2.25	0.51
20:Q:48:GLU:O	20:Q:49:GLU:C	2.54	0.51
20:Q:60:ILE:HD13	20:Q:61:GLU:H	1.75	0.51
20:Q:82:MET:O	20:Q:83:ASP:C	2.51	0.51
1:A:413:G:N2	1:A:428:G:O2'	2.44	0.51
1:A:722:A:H2'	1:A:724:G:H8	1.75	0.51
1:A:1129:C:H1'	1:A:1132:C:C5	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1227:A:H2'	1:A:1228:C:O5'	2.10	0.51
5:B:62:ALA:C	5:B:64:ARG:H	2.18	0.51
5:B:101:MET:HB3	5:B:152:PHE:CZ	2.45	0.51
8:E:75:THR:HG23	8:E:76:ILE:N	2.24	0.51
8:E:79:GLU:O	11:H:104:ARG:NH1	2.44	0.51
10:G:15:ASP:HB2	10:G:20:ASP:O	2.11	0.51
13:J:33:GLN:HG2	13:J:33:GLN:O	2.11	0.51
15:L:93:LEU:O	15:L:96:VAL:HG23	2.11	0.51
20:Q:95:TYR:O	20:Q:96:GLN:C	2.53	0.51
20:Q:95:TYR:C	20:Q:97:SER:N	2.69	0.51
22:S:41:VAL:HB	22:S:42:PRO:HD2	1.93	0.51
23:T:38:LYS:O	23:T:41:ILE:N	2.43	0.51
23:T:39:LYS:HD2	23:T:55:ILE:HD13	1.93	0.51
23:T:43:LEU:HD12	23:T:52:ALA:HA	1.92	0.51
1:A:411:A:N6	1:A:413:G:N2	2.59	0.51
1:A:457:C:H2'	1:A:458:C:H6	1.76	0.51
1:A:1148:U:H4'	12:I:14:VAL:HG11	1.93	0.51
1:A:1310:G:N7	22:S:2:PRO:HD3	2.26	0.51
5:B:134:GLU:C	5:B:136:VAL:H	2.18	0.51
5:B:146:GLN:O	5:B:150:SER:HB3	2.10	0.51
6:C:77:ILE:O	6:C:83:ARG:N	2.44	0.51
6:C:94:LEU:HD23	6:C:95:THR:N	2.25	0.51
10:G:140:ASP:HA	10:G:143:ARG:HD2	1.91	0.51
11:H:126:LYS:C	11:H:128:GLY:H	2.19	0.51
13:J:49:VAL:HG11	17:N:41:ARG:O	2.11	0.51
13:J:94:VAL:CG1	13:J:95:GLU:N	2.73	0.51
14:K:11:LYS:C	14:K:12:ARG:HG3	2.35	0.51
19:P:5:ARG:NH1	19:P:24:ALA:HA	2.25	0.51
1:A:740:U:O2'	1:A:741:G:H5'	2.11	0.50
1:A:1023:G:H2'	1:A:1024:G:H5'	1.92	0.50
1:A:1495:U:H2'	1:A:1496:C:H6	1.76	0.50
5:B:144:ARG:HD2	5:B:145:LEU:CD2	2.38	0.50
5:B:169:LYS:HD2	5:B:169:LYS:C	2.35	0.50
7:D:179:GLU:OE1	7:D:179:GLU:N	2.33	0.50
19:P:82:GLN:O	19:P:83:GLU:C	2.53	0.50
21:R:52:PRO:O	21:R:56:THR:HG23	2.10	0.50
1:A:393:A:C2'	1:A:394:G:H5'	2.41	0.50
1:A:722:A:H2'	1:A:724:G:C8	2.46	0.50
1:A:776:G:N2	1:A:802:A:OP2	2.41	0.50
1:A:877:C:H1'	11:H:3:THR:CG2	2.42	0.50
1:A:1187:G:OP1	12:I:113:LYS:HE2	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:21:ARG:H	5:B:21:ARG:CD	2.02	0.50
5:B:30:ARG:HD2	5:B:31:TYR:CZ	2.46	0.50
5:B:87:ARG:HH22	5:B:233:SER:HB2	1.76	0.50
12:I:107:ARG:HH11	12:I:107:ARG:CB	2.25	0.50
13:J:7:LYS:HE3	13:J:40:LEU:CD1	2.41	0.50
19:P:20:VAL:CG1	19:P:32:TYR:CB	2.89	0.50
23:T:67:ALA:O	23:T:73:HIS:ND1	2.44	0.50
1:A:157:G:O2'	1:A:158:G:H5'	2.11	0.50
1:A:761:G:H5'	20:Q:103:GLY:N	2.26	0.50
1:A:954:G:H21	1:A:1227:A:H62	1.60	0.50
1:A:1277:C:HO2'	1:A:1279:A:C1'	2.24	0.50
1:A:1388:C:H2'	1:A:1389:C:C6	2.47	0.50
1:A:1460:A:H2'	1:A:1461:G:O4'	2.11	0.50
1:A:1497:G:H2'	1:A:1498:U:H5'	1.93	0.50
5:B:209:ARG:NH2	5:B:239:VAL:HG11	2.26	0.50
9:F:80:ARG:HG2	9:F:80:ARG:HH11	1.76	0.50
16:M:117:VAL:HG12	16:M:118:ALA:N	2.27	0.50
17:N:36:PHE:O	17:N:37:PHE:CG	2.64	0.50
21:R:22:VAL:HG13	21:R:42:ARG:HD2	1.92	0.50
22:S:42:PRO:C	22:S:44:MET:H	2.20	0.50
1:A:279:A:H4'	1:A:280:C:OP2	2.09	0.50
1:A:502:G:H2'	1:A:503:C:C6	2.47	0.50
1:A:667:G:H4'	18:O:51:HIS:ND1	2.27	0.50
1:A:694:A:H2'	1:A:695:A:O5'	2.11	0.50
1:A:1314:C:P	22:S:6:LYS:HE2	2.52	0.50
1:A:1465:C:H2'	1:A:1466:C:O4'	2.12	0.50
5:B:18:GLY:CA	5:B:41:ILE:HA	2.41	0.50
5:B:66:GLY:O	5:B:90:MET:HE1	2.11	0.50
6:C:37:GLN:NE2	17:N:52:GLN:OE1	2.45	0.50
6:C:191:THR:HB	6:C:194:GLY:O	2.11	0.50
7:D:176:LEU:HG	7:D:177:ASP:N	2.27	0.50
8:E:40:ARG:HG2	8:E:68:GLU:OE2	2.12	0.50
12:I:10:ARG:HD3	12:I:105:ASP:HB3	1.92	0.50
1:A:9:G:H5'	8:E:122:GLU:OE2	2.11	0.50
1:A:103:C:P	23:T:17:ARG:HH11	2.34	0.50
1:A:519:C:H2'	1:A:520:A:C8	2.45	0.50
12:I:53:VAL:CG2	12:I:85:LEU:HD21	2.41	0.50
12:I:128:ARG:O	12:I:128:ARG:HG2	2.11	0.50
1:A:258:G:H2'	1:A:259:G:C8	2.44	0.50
1:A:392:G:H2'	1:A:393:A:C8	2.46	0.50
1:A:818:G:O2'	1:A:819:A:H5''	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1193:G:C2'	1:A:1194:U:H5'	2.41	0.50
1:A:1307:U:H5'	16:M:109:THR:HG21	1.94	0.50
4:Z:2:U:H6	4:Z:2:U:H5'	1.77	0.50
5:B:89:GLY:N	5:B:226:ARG:HH22	2.10	0.50
6:C:3:ASN:O	6:C:4:LYS:HB2	2.11	0.50
6:C:64:VAL:CG1	6:C:66:VAL:HG23	2.41	0.50
6:C:182:ILE:HD12	6:C:182:ILE:N	2.26	0.50
11:H:5:PRO:O	11:H:8:ASP:HB3	2.12	0.50
13:J:62:HIS:HB3	17:N:59:ALA:HB3	1.93	0.50
18:O:63:ARG:O	18:O:64:ARG:C	2.55	0.50
20:Q:11:VAL:O	20:Q:12:SER:HB2	2.11	0.50
1:A:1298:C:C4	10:G:114:ARG:HD3	2.47	0.50
1:A:1491:G:C5	25:A:1545:PAR:H21	2.46	0.50
5:B:23:ARG:HD3	5:B:23:ARG:C	2.36	0.50
5:B:43:ASP:OD1	5:B:45:GLN:HB2	2.12	0.50
6:C:83:ARG:C	6:C:85:ARG:N	2.69	0.50
6:C:151:VAL:HA	6:C:199:LYS:O	2.11	0.50
8:E:11:ILE:HG12	8:E:33:VAL:HG23	1.94	0.50
12:I:25:LYS:HG2	12:I:60:ASP:OD2	2.11	0.50
12:I:45:ALA:O	12:I:47:LEU:N	2.44	0.50
15:L:71:PRO:HG2	15:L:102:ARG:HG3	1.93	0.50
16:M:8:GLU:OE1	16:M:22:ILE:HA	2.10	0.50
19:P:26:ARG:HD3	19:P:31:LYS:N	2.27	0.50
20:Q:59:ILE:HD13	20:Q:73:VAL:HA	1.94	0.50
1:A:731:G:OP1	1:A:766:A:H1'	2.12	0.50
1:A:818:G:H3'	1:A:819:A:C5'	2.42	0.50
1:A:1094:G:OP2	1:A:1095:U:C5	2.64	0.50
1:A:1473:A:H2'	1:A:1474:G:C8	2.47	0.50
5:B:112:VAL:C	5:B:114:ARG:N	2.68	0.50
6:C:75:VAL:O	6:C:83:ARG:HD3	2.12	0.50
22:S:51:VAL:O	22:S:58:VAL:HG22	2.12	0.50
1:A:1201:A:O2'	1:A:1202:G:OP2	2.28	0.50
1:A:1278:U:H4'	1:A:1279:A:O5'	2.11	0.50
1:A:1466:C:H2'	1:A:1467:G:O4'	2.12	0.50
3:Y:29:G:H2'	3:Y:30:G:C8	2.46	0.50
6:C:108:ASN:ND2	6:C:111:LEU:HG	2.13	0.50
6:C:126:ARG:O	6:C:127:ARG:HB2	2.12	0.50
7:D:8:VAL:C	7:D:10:ARG:N	2.70	0.50
7:D:163:GLU:O	7:D:165:MET:N	2.45	0.50
11:H:48:TYR:HB2	11:H:60:ARG:O	2.12	0.50
16:M:14:ARG:HH12	16:M:16:ASP:CG	2.18	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:O:4:THR:OG1	18:O:7:GLU:HB2	2.12	0.50
21:R:36:ASN:HD22	21:R:36:ASN:C	2.19	0.50
23:T:100:ILE:C	23:T:102:GLY:N	2.69	0.50
1:A:438:G:C4'	1:A:439:A:OP1	2.57	0.49
1:A:640:A:O2'	1:A:641:U:H5'	2.12	0.49
1:A:818:G:C2'	1:A:819:A:H5''	2.42	0.49
1:A:918:A:H2'	1:A:919:A:O4'	2.12	0.49
1:A:1054:C:H5	1:A:1196:U:C6	2.29	0.49
1:A:1278:U:C5'	1:A:1279:A:H5'	2.42	0.49
6:C:173:VAL:O	6:C:173:VAL:HG12	2.11	0.49
7:D:32:ALA:C	7:D:34:GLU:N	2.63	0.49
7:D:61:LYS:HD2	7:D:207:TYR:OH	2.11	0.49
9:F:94:GLN:CB	21:R:32:ARG:HH11	2.24	0.49
10:G:108:ALA:C	10:G:110:GLN:H	2.20	0.49
12:I:4:TYR:HB2	12:I:19:LEU:HB2	1.94	0.49
13:J:89:ASP:O	13:J:90:LEU:HD23	2.12	0.49
15:L:29:GLY:O	15:L:30:ALA:C	2.53	0.49
16:M:34:LEU:HD13	16:M:41:PRO:CA	2.41	0.49
21:R:43:PHE:C	21:R:51:LEU:HD12	2.37	0.49
1:A:314:C:O2'	1:A:315:A:H5'	2.11	0.49
1:A:443:C:N3	1:A:492:G:C2	2.80	0.49
1:A:883:C:O2'	1:A:884:U:H5'	2.13	0.49
1:A:1054:C:N3	3:Y:34:G:O4'	2.45	0.49
1:A:1372:U:C2'	1:A:1373:G:H5'	2.43	0.49
1:A:1477:C:O2'	1:A:1478:C:H5'	2.12	0.49
5:B:130:ARG:HD2	5:B:134:GLU:OE1	2.12	0.49
6:C:151:VAL:HG12	6:C:152:ILE:N	2.27	0.49
7:D:64:LEU:HD12	7:D:75:PHE:HZ	1.74	0.49
9:F:33:TYR:CD1	9:F:75:LEU:HD22	2.47	0.49
9:F:101:ALA:HB2	21:R:28:GLU:HB2	1.94	0.49
11:H:9:MET:HE2	11:H:32:LYS:HG2	1.93	0.49
12:I:47:LEU:HB3	12:I:50:LEU:HD12	1.94	0.49
20:Q:53:LEU:HD12	20:Q:53:LEU:N	2.26	0.49
1:A:57:G:H2'	1:A:58:C:C6	2.47	0.49
1:A:737:A:H1'	9:F:73:ASN:ND2	2.14	0.49
1:A:939:G:C6	1:A:940:C:N4	2.80	0.49
1:A:1098:C:H2'	1:A:1099:G:O4'	2.12	0.49
1:A:1369:C:H2'	1:A:1370:G:H8	1.73	0.49
5:B:142:LEU:O	5:B:142:LEU:HD23	2.12	0.49
6:C:67:THR:HG23	6:C:102:ASN:HB2	1.93	0.49
6:C:137:ALA:O	6:C:141:VAL:HG23	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:I:7:THR:HG22	12:I:8:GLY:N	2.26	0.49
16:M:85:GLY:O	16:M:86:CYS:O	2.30	0.49
17:N:25:VAL:HG13	17:N:25:VAL:O	2.12	0.49
17:N:29:ARG:O	17:N:33:VAL:HG13	2.13	0.49
21:R:18:ARG:HA	21:R:18:ARG:HE	1.77	0.49
22:S:19:VAL:HG13	22:S:20:LEU:H	1.76	0.49
23:T:11:SER:HA	23:T:13:LEU:HD11	1.92	0.49
1:A:50:A:N6	1:A:361:G:H4'	2.27	0.49
1:A:403:C:O2'	1:A:404:U:H5'	2.12	0.49
1:A:484:G:H5'	1:A:486:U:O4'	2.12	0.49
1:A:942:G:H2'	1:A:943:U:H6	1.77	0.49
1:A:1057:G:H2'	1:A:1058:G:O4'	2.12	0.49
5:B:27:LYS:C	5:B:29:ALA:H	2.20	0.49
6:C:139:GLN:HA	6:C:139:GLN:NE2	2.27	0.49
10:G:17:VAL:HG12	10:G:18:TYR:CD1	2.48	0.49
14:K:21:ILE:HG12	14:K:30:VAL:HG12	1.93	0.49
14:K:115:PRO:C	14:K:117:ASN:N	2.70	0.49
15:L:45:PRO:HD3	15:L:51:ALA:O	2.12	0.49
22:S:33:THR:HG22	22:S:35:SER:N	2.03	0.49
1:A:31:G:H1	1:A:48:C:H5''	1.76	0.49
1:A:242:C:C2'	1:A:243:A:H5'	2.43	0.49
1:A:299:G:H2'	1:A:300:A:C8	2.47	0.49
1:A:570:G:H2'	1:A:571:U:C6	2.48	0.49
1:A:686:U:O4	1:A:703:G:H1'	2.12	0.49
1:A:1174:G:O2'	1:A:1175:G:H5'	2.12	0.49
1:A:1216:G:H5''	17:N:5:ALA:CB	2.43	0.49
1:A:1288:A:N1	1:A:1371:G:H1'	2.27	0.49
1:A:1305:G:H5'	24:V:4:GLY:HA3	1.93	0.49
5:B:36:ARG:HG3	5:B:41:ILE:HD12	1.94	0.49
5:B:144:ARG:HA	5:B:147:LYS:HD2	1.92	0.49
5:B:204:ASN:HD22	5:B:204:ASN:C	2.19	0.49
9:F:19:LEU:HD21	9:F:23:LYS:HD2	1.95	0.49
10:G:95:ARG:HG3	10:G:95:ARG:HH11	1.76	0.49
11:H:116:LYS:HD2	11:H:129:VAL:HG11	1.94	0.49
11:H:136:GLU:O	11:H:137:VAL:CG2	2.60	0.49
16:M:66:LEU:O	16:M:67:GLU:C	2.55	0.49
16:M:88:ARG:NH1	22:S:3:ARG:HH21	2.11	0.49
22:S:15:LEU:HD12	22:S:16:LEU:N	2.28	0.49
1:A:750:G:H1'	18:O:23:GLY:H	1.78	0.49
1:A:957:U:H3	1:A:960:U:C5'	2.25	0.49
1:A:1172:C:H2'	1:A:1173:G:H8	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1367:C:H5'	13:J:60:ARG:NH1	2.28	0.49
5:B:87:ARG:HD2	5:B:87:ARG:O	2.13	0.49
5:B:124:SER:O	5:B:127:ILE:HG13	2.12	0.49
5:B:156:LYS:HA	5:B:156:LYS:NZ	2.26	0.49
6:C:89:GLU:C	6:C:91:LEU:H	2.20	0.49
6:C:180:ALA:HB1	6:C:203:PHE:CE1	2.47	0.49
7:D:199:ASN:C	7:D:199:ASN:HD22	2.20	0.49
12:I:4:TYR:CE2	12:I:88:TYR:HA	2.47	0.49
19:P:7:ALA:O	19:P:17:TYR:HA	2.12	0.49
20:Q:26:GLN:O	20:Q:27:PHE:HB3	2.12	0.49
23:T:54:LYS:HA	23:T:57:ARG:HD3	1.95	0.49
1:A:382:A:C2	1:A:383:A:C4	3.00	0.49
1:A:976:G:H5'	1:A:1358:U:O2'	2.13	0.49
1:A:1048:G:H5''	17:N:3:ARG:CG	2.43	0.49
1:A:1072:G:H2'	1:A:1073:U:C6	2.47	0.49
1:A:1120:G:H2'	1:A:1121:U:C6	2.48	0.49
1:A:1250:A:H5''	12:I:68:GLY:H	1.76	0.49
5:B:53:ARG:NH1	5:B:199:TYR:CD2	2.81	0.49
5:B:75:LYS:HA	5:B:78:GLN:HB2	1.94	0.49
15:L:115:LYS:C	15:L:117:ARG:H	2.21	0.49
15:L:126:LYS:HD2	15:L:126:LYS:N	2.20	0.49
18:O:9:GLN:OE1	18:O:9:GLN:HA	2.11	0.49
22:S:16:LEU:C	22:S:18:LYS:H	2.19	0.49
23:T:93:GLU:HA	23:T:93:GLU:OE2	2.12	0.49
1:A:169:C:O2'	1:A:170:U:H5'	2.13	0.49
1:A:302:G:H5''	15:L:17:LYS:NZ	2.27	0.49
5:B:85:ALA:HB1	5:B:92:TYR:HB3	1.94	0.49
5:B:194:PRO:O	5:B:196:LEU:N	2.46	0.49
7:D:58:LEU:HD23	7:D:206:PHE:CZ	2.48	0.49
9:F:87:ARG:HH11	9:F:87:ARG:CG	2.24	0.49
13:J:27:ALA:HB2	13:J:85:LEU:HD21	1.94	0.49
14:K:89:ALA:C	14:K:91:ARG:H	2.21	0.49
15:L:46:LYS:O	15:L:47:LYS:C	2.55	0.49
16:M:109:THR:HG23	16:M:109:THR:O	2.13	0.49
18:O:78:TYR:CE1	18:O:82:ILE:HD11	2.48	0.49
21:R:47:THR:HG23	21:R:83:GLU:N	2.18	0.49
22:S:30:LEU:HA	22:S:48:THR:O	2.13	0.49
1:A:19:C:H2'	1:A:20:U:H6	1.77	0.49
1:A:1053:G:C5'	1:A:1054:C:H5'	2.43	0.49
1:A:1054:C:H2'	1:A:1055:A:H5''	1.94	0.49
1:A:1197:G:O2'	1:A:1198:G:H5'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1424:C:O2'	1:A:1425:U:H5'	2.12	0.49
7:D:36:ARG:N	7:D:37:PRO:CD	2.65	0.49
11:H:24:THR:HG23	11:H:61:VAL:HB	1.95	0.49
1:A:112:G:O2'	1:A:113:G:H5'	2.12	0.49
1:A:337:C:H2'	1:A:338:A:C8	2.48	0.49
1:A:1167:A:H2'	1:A:1168:A:C8	2.48	0.49
5:B:84:GLU:HA	5:B:87:ARG:HB3	1.95	0.49
8:E:51:VAL:CB	8:E:52:PRO:HD3	2.38	0.49
9:F:1:MET:H1	9:F:1:MET:HE3	1.77	0.49
10:G:62:PHE:O	10:G:65:ALA:HB3	2.12	0.49
15:L:109:GLY:O	15:L:110:VAL:C	2.56	0.49
23:T:26:ASN:OD1	23:T:71:THR:HG23	2.13	0.49
23:T:36:LEU:HD12	23:T:62:LEU:HD12	1.95	0.49
24:V:17:THR:O	24:V:22:ARG:NH1	2.41	0.49
1:A:334:C:H2'	1:A:335:C:C6	2.49	0.48
1:A:411:A:C2	1:A:431:A:N6	2.81	0.48
1:A:1038:C:H2'	1:A:1039:C:C5	2.48	0.48
1:A:1216:G:H5''	17:N:5:ALA:HB2	1.94	0.48
1:A:1302:U:C5	16:M:17:VAL:HG21	2.47	0.48
1:A:1429:C:H2'	1:A:1430:C:C6	2.48	0.48
7:D:9:CYS:O	7:D:12:CYS:HB2	2.13	0.48
10:G:51:GLN:C	10:G:53:LYS:N	2.71	0.48
11:H:91:ARG:NH1	20:Q:33:GLY:HA3	2.28	0.48
14:K:54:ARG:HH11	14:K:54:ARG:HG3	1.78	0.48
15:L:104:VAL:O	15:L:105:TYR:HB2	2.12	0.48
19:P:22:THR:OG1	19:P:23:ASP:N	2.46	0.48
1:A:190(L):U:H3	23:T:105:SER:CB	2.26	0.48
1:A:753:A:H4'	1:A:754:C:H5''	1.95	0.48
1:A:1143:G:H2'	1:A:1144:G:C8	2.48	0.48
1:A:1348:U:O2'	1:A:1349:A:H5'	2.13	0.48
1:A:1497:G:O2'	1:A:1498:U:H5'	2.13	0.48
1:A:1533:C:O2'	1:A:1534:A:H5'	2.14	0.48
5:B:83:MET:HE3	5:B:234:PRO:HG2	1.95	0.48
6:C:112:SER:OG	6:C:115:LEU:HG	2.14	0.48
7:D:190:ASP:O	7:D:193:ASP:HB2	2.13	0.48
12:I:53:VAL:HG21	12:I:85:LEU:HD21	1.94	0.48
14:K:82:VAL:HG23	14:K:105:VAL:HG13	1.95	0.48
22:S:40:ILE:HB	22:S:67:VAL:O	2.13	0.48
1:A:643:C:H2'	1:A:644:G:H8	1.78	0.48
1:A:687:A:H2	1:A:700:G:N3	2.11	0.48
5:B:144:ARG:HG3	5:B:145:LEU:N	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:188:LEU:O	6:C:189:ALA:HB2	2.13	0.48
7:D:122:ARG:NH2	7:D:134:ASP:OD2	2.46	0.48
13:J:42:THR:HG23	13:J:67:THR:C	2.38	0.48
14:K:33:THR:OG1	14:K:37:GLY:C	2.56	0.48
16:M:81:LEU:HD23	16:M:81:LEU:N	2.29	0.48
17:N:44:LEU:C	17:N:44:LEU:HD12	2.37	0.48
20:Q:94:ASN:O	20:Q:97:SER:HB2	2.13	0.48
23:T:90:GLN:O	23:T:93:GLU:HB2	2.14	0.48
1:A:502:G:H2'	1:A:503:C:H6	1.79	0.48
1:A:1048:G:OP1	17:N:3:ARG:HA	2.12	0.48
1:A:1125:U:H3	13:J:5:ARG:NE	2.11	0.48
1:A:1229:A:H2'	1:A:1230:C:H6	1.79	0.48
1:A:1451:A:O2'	1:A:1452:C:OP1	2.26	0.48
5:B:30:ARG:HG3	5:B:31:TYR:CD2	2.48	0.48
6:C:7:PRO:O	6:C:11:ARG:HD2	2.13	0.48
6:C:118:GLN:O	6:C:122:GLU:HG3	2.14	0.48
15:L:60:LEU:HD11	15:L:85:ILE:HD12	1.94	0.48
18:O:15:PHE:O	18:O:16:ALA:C	2.56	0.48
20:Q:97:SER:O	20:Q:99:SER:N	2.47	0.48
21:R:21:LYS:C	21:R:23:LYS:H	2.21	0.48
1:A:88:A:H2'	1:A:89:C:O4'	2.14	0.48
1:A:860:A:H2'	1:A:861:G:O4'	2.13	0.48
1:A:1003(A):G:C2'	1:A:1004:A:H4'	2.39	0.48
1:A:1053:G:H3'	1:A:1054:C:H5'	1.96	0.48
4:Z:1:U:H2'	4:Z:2:U:H5'	1.95	0.48
5:B:92:TYR:H	5:B:92:TYR:HD2	1.60	0.48
5:B:101:MET:HG2	5:B:108:ILE:HD13	1.95	0.48
6:C:139:GLN:HE21	6:C:139:GLN:HA	1.78	0.48
11:H:92:ARG:HH11	11:H:92:ARG:CG	2.23	0.48
14:K:15:ALA:HA	14:K:76:GLY:O	2.14	0.48
14:K:72:ALA:O	14:K:77:MET:HB2	2.14	0.48
16:M:2:ALA:O	16:M:3:ARG:C	2.56	0.48
16:M:88:ARG:HH11	22:S:3:ARG:HH21	1.62	0.48
21:R:29:PHE:HE1	21:R:31:LEU:HD23	1.79	0.48
1:A:545:C:O2'	1:A:546:G:H5'	2.13	0.48
1:A:562:C:H1'	15:L:15:ARG:HB3	1.95	0.48
1:A:867:G:O2'	1:A:868:C:H5'	2.13	0.48
1:A:1003(A):G:C4	1:A:1004:A:H1'	2.48	0.48
1:A:1060:C:H2'	1:A:1061:G:H8	1.78	0.48
12:I:97:LYS:HB3	12:I:98:PRO:HD3	1.95	0.48
13:J:46:ARG:HD3	13:J:64:GLU:HB3	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:L:50:SER:O	15:L:51:ALA:CB	2.61	0.48
16:M:80:ARG:C	16:M:82:MET:N	2.72	0.48
1:A:302:G:H5''	15:L:17:LYS:HZ1	1.79	0.48
1:A:377:G:OP1	19:P:3:LYS:NZ	2.43	0.48
1:A:423:G:H2'	1:A:424:G:O4'	2.13	0.48
1:A:920:U:H2'	1:A:921:U:C6	2.49	0.48
1:A:924:C:H5'	1:A:1399:C:OP2	2.13	0.48
1:A:1062:U:H2'	1:A:1063:C:C6	2.49	0.48
5:B:18:GLY:HA2	5:B:41:ILE:HA	1.95	0.48
5:B:151:GLY:C	5:B:153:ARG:N	2.71	0.48
8:E:144:THR:HG23	8:E:145:LYS:N	2.29	0.48
11:H:133:LEU:C	11:H:133:LEU:CD2	2.85	0.48
12:I:10:ARG:O	12:I:11:LYS:C	2.55	0.48
12:I:104:ARG:O	12:I:105:ASP:C	2.56	0.48
12:I:118:LYS:O	12:I:119:ALA:CB	2.59	0.48
20:Q:45:HIS:HB2	20:Q:69:LYS:HE2	1.95	0.48
22:S:17:GLU:HA	22:S:20:LEU:HD21	1.95	0.48
1:A:167:G:H2'	1:A:168:G:H8	1.78	0.48
1:A:176:C:H2'	1:A:177:C:C6	2.45	0.48
1:A:258:G:O2'	1:A:259:G:H5'	2.13	0.48
1:A:439:A:C4	1:A:497:A:C2	3.01	0.48
1:A:1160:G:O2'	1:A:1161:C:H5'	2.14	0.48
6:C:42:LEU:C	6:C:44:GLU:H	2.21	0.48
6:C:69:HIS:O	6:C:70:VAL:HG13	2.14	0.48
6:C:204:LEU:O	6:C:205:GLY:C	2.57	0.48
7:D:191:ARG:O	7:D:191:ARG:HD2	2.14	0.48
8:E:15:ARG:HD2	8:E:15:ARG:C	2.38	0.48
9:F:53:ALA:C	9:F:55:ASP:H	2.21	0.48
11:H:91:ARG:HH11	20:Q:33:GLY:HA3	1.79	0.48
12:I:19:LEU:HB3	12:I:59:PHE:CD2	2.47	0.48
15:L:33:ARG:CD	15:L:62:SER:HB3	2.43	0.48
15:L:41:ARG:HH12	15:L:57:LYS:NZ	2.03	0.48
15:L:46:LYS:CG	15:L:47:LYS:H	2.24	0.48
16:M:74:VAL:HA	16:M:77:ASN:HD22	1.78	0.48
22:S:50:ALA:HA	22:S:58:VAL:O	2.14	0.48
1:A:409:G:H2'	1:A:410:G:O4'	2.13	0.48
1:A:765:G:H1	1:A:812:C:H2'	1.78	0.48
1:A:1402:C:O2	1:A:1500:A:N1	2.47	0.48
5:B:42:ILE:HD12	5:B:203:GLY:HA2	1.95	0.48
6:C:112:SER:CB	6:C:115:LEU:HD12	2.42	0.48
6:C:188:LEU:HD13	6:C:195:VAL:HG13	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:E:77:PRO:O	8:E:78:HIS:CB	2.62	0.48
9:F:40:VAL:CG2	9:F:41:GLU:N	2.76	0.48
12:I:16:ARG:HB2	12:I:64:THR:HB	1.95	0.48
12:I:111:ARG:HD3	12:I:112:LYS:O	2.13	0.48
15:L:60:LEU:N	15:L:64:TYR:O	2.47	0.48
17:N:23:ARG:C	17:N:33:VAL:HG11	2.39	0.48
20:Q:45:HIS:HB3	20:Q:72:ARG:HG2	1.94	0.48
1:A:116:A:H61	1:A:313:A:H1'	1.79	0.48
1:A:411:A:N9	1:A:413:G:H1'	2.29	0.48
1:A:664:G:OP1	21:R:64:ARG:HD2	2.14	0.48
1:A:724:G:O2'	1:A:725:G:H5'	2.13	0.48
1:A:1128:C:H2'	1:A:1129:C:H5''	1.95	0.48
1:A:1291:G:H4'	12:I:38:GLN:O	2.13	0.48
5:B:16:HIS:NE2	5:B:214:ILE:CG1	2.77	0.48
5:B:23:ARG:HH12	5:B:191:ASP:HA	1.78	0.48
6:C:25:GLY:O	6:C:27:LYS:N	2.46	0.48
6:C:34:LEU:CD2	6:C:38:ARG:HG2	2.44	0.48
6:C:39:ILE:C	6:C:41:GLY:H	2.22	0.48
6:C:70:VAL:O	6:C:106:VAL:HG23	2.14	0.48
8:E:74:GLY:HA3	8:E:116:THR:CG2	2.38	0.48
14:K:99:GLN:CG	14:K:105:VAL:HG21	2.40	0.48
20:Q:15:MET:HE1	20:Q:43:LEU:HD22	1.96	0.48
1:A:22:G:H2'	1:A:23:C:C6	2.49	0.47
1:A:106:C:O2	1:A:379:C:H4'	2.14	0.47
1:A:578:C:O2'	1:A:728:A:N3	2.42	0.47
1:A:642:A:C8	11:H:115:SER:HA	2.49	0.47
1:A:730:G:N3	1:A:765:G:H4'	2.28	0.47
6:C:38:ARG:O	6:C:42:LEU:HG	2.14	0.47
6:C:191:THR:CG2	6:C:192:THR:H	2.26	0.47
7:D:170:VAL:HG22	7:D:171:GLY:N	2.29	0.47
24:V:2:GLY:O	24:V:4:GLY:N	2.47	0.47
1:A:673:G:H5''	9:F:87:ARG:NH1	2.29	0.47
1:A:1010:G:O2'	1:A:1011:G:H5'	2.14	0.47
1:A:1081:G:OP1	8:E:16:THR:CG2	2.61	0.47
1:A:1223:C:P	22:S:78:ARG:HH12	2.37	0.47
1:A:1495:U:O2'	1:A:1496:C:H5'	2.14	0.47
1:A:1525:G:P	14:K:120:ARG:HH22	2.37	0.47
6:C:15:THR:HG21	6:C:179:ARG:C	2.39	0.47
9:F:2:ARG:HH21	9:F:69:GLU:HB3	1.79	0.47
9:F:62:TRP:C	9:F:63:TYR:HD2	2.22	0.47
10:G:61:VAL:O	10:G:62:PHE:C	2.57	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:G:85:TYR:HD1	10:G:154:TYR:CE1	2.31	0.47
18:O:36:ILE:HA	18:O:59:MET:HE1	1.96	0.47
20:Q:80:GLY:O	20:Q:81:ARG:HB3	2.15	0.47
20:Q:97:SER:CB	20:Q:103:GLY:C	2.87	0.47
1:A:447:G:H2'	1:A:485:G:N2	2.29	0.47
1:A:662:G:O2'	1:A:836:G:H5'	2.14	0.47
1:A:766:A:C8	1:A:814:A:C6	3.02	0.47
1:A:1089:G:O2'	1:A:1090:U:H5'	2.14	0.47
1:A:1470:G:O2'	1:A:1471:G:H5'	2.14	0.47
5:B:68:ILE:O	5:B:91:PRO:HD2	2.13	0.47
6:C:43:LEU:HD11	6:C:66:VAL:CG1	2.44	0.47
6:C:159:GLY:HA2	6:C:193:TYR:CE2	2.49	0.47
11:H:10:LEU:HD12	11:H:85:ARG:HG2	1.96	0.47
13:J:12:ASP:HB3	13:J:15:THR:HG22	1.96	0.47
15:L:41:ARG:NH1	15:L:41:ARG:CB	2.77	0.47
16:M:14:ARG:NH1	16:M:16:ASP:OD1	2.47	0.47
16:M:23:TYR:HB2	16:M:67:GLU:OE2	2.13	0.47
18:O:7:GLU:O	18:O:11:VAL:HG23	2.14	0.47
24:V:24:ARG:O	24:V:25:LYS:CB	2.62	0.47
1:A:41:G:H2'	1:A:42:G:H8	1.78	0.47
1:A:537:G:H5''	15:L:113:ARG:NH2	2.28	0.47
1:A:652:U:O4	1:A:752:G:O2'	2.28	0.47
1:A:669:U:H2'	1:A:670:G:H8	1.79	0.47
1:A:771:G:H2'	1:A:772:U:C6	2.49	0.47
1:A:840:C:H5'	1:A:848:C:O2	2.13	0.47
1:A:1372:U:H2'	1:A:1373:G:O4'	2.14	0.47
5:B:56:ARG:O	5:B:57:PHE:C	2.57	0.47
6:C:79:ARG:N	6:C:82:GLU:HB3	2.29	0.47
6:C:167:TRP:O	6:C:168:ALA:HB3	2.13	0.47
7:D:57:ARG:HG3	7:D:57:ARG:NH1	2.25	0.47
7:D:173:TRP:CD1	7:D:174:LEU:HG	2.49	0.47
7:D:199:ASN:HD21	7:D:201:GLN:HB3	1.80	0.47
8:E:5:ASP:CG	8:E:6:PHE:H	2.22	0.47
12:I:23:ASN:C	12:I:23:ASN:ND2	2.71	0.47
12:I:108:VAL:HG12	12:I:109:VAL:N	2.29	0.47
12:I:120:ARG:O	12:I:121:ARG:C	2.57	0.47
13:J:30:SER:HB2	13:J:81:THR:HA	1.95	0.47
15:L:47:LYS:CG	15:L:48:PRO:HD3	2.44	0.47
15:L:71:PRO:O	15:L:102:ARG:HD2	2.14	0.47
21:R:21:LYS:C	21:R:23:LYS:N	2.70	0.47
23:T:50:GLU:HA	23:T:100:ILE:HG13	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:939:G:H2'	1:A:940:C:C6	2.50	0.47
1:A:1327:C:O2'	1:A:1328:C:H5'	2.15	0.47
5:B:181:PHE:HD2	11:H:70:GLN:HB3	1.78	0.47
6:C:8:ILE:O	6:C:11:ARG:N	2.42	0.47
7:D:111:ALA:HB2	7:D:120:LEU:CD1	2.45	0.47
7:D:146:ILE:N	7:D:146:ILE:CD1	2.77	0.47
9:F:27:GLN:HA	9:F:27:GLN:NE2	2.30	0.47
10:G:47:CYS:SG	10:G:58:PRO:HB2	2.54	0.47
13:J:6:ILE:HG13	13:J:72:VAL:HB	1.97	0.47
13:J:37:PRO:HA	13:J:72:VAL:HA	1.96	0.47
13:J:81:THR:C	13:J:83:GLU:N	2.72	0.47
16:M:55:ARG:O	16:M:56:LEU:C	2.57	0.47
21:R:53:ARG:HG3	21:R:63:GLN:HB2	1.96	0.47
23:T:26:ASN:O	23:T:27:LYS:C	2.57	0.47
23:T:76:ALA:HA	23:T:79:ARG:NH1	2.29	0.47
1:A:335:C:H2'	1:A:336:C:H6	1.79	0.47
1:A:392:G:H2'	1:A:393:A:H8	1.80	0.47
1:A:830:G:O2'	1:A:831:U:H5'	2.14	0.47
1:A:1107:C:H2'	1:A:1108:G:H5'	1.96	0.47
1:A:1286:A:C8	1:A:1287:A:H4'	2.50	0.47
5:B:92:TYR:CD2	5:B:92:TYR:N	2.82	0.47
6:C:35:GLU:O	6:C:36:ASP:C	2.58	0.47
6:C:94:LEU:HD23	6:C:94:LEU:C	2.39	0.47
7:D:24:GLU:HG2	7:D:25:ARG:N	2.29	0.47
8:E:107:ARG:O	8:E:108:ALA:C	2.57	0.47
10:G:72:ARG:HG2	10:G:142:GLU:OE1	2.15	0.47
16:M:93:ARG:HH11	16:M:93:ARG:HG3	1.79	0.47
19:P:71:ARG:HD3	19:P:75:ARG:HH21	1.79	0.47
23:T:67:ALA:HB2	23:T:77:ALA:HB2	1.96	0.47
1:A:18:C:O2'	1:A:19:C:H5'	2.14	0.47
1:A:179:A:H2'	1:A:180:U:C6	2.50	0.47
1:A:401:C:O2'	1:A:402:G:H5'	2.15	0.47
1:A:406:G:H2'	1:A:407:G:C8	2.49	0.47
1:A:407:G:HO2'	7:D:116:GLN:HG3	1.78	0.47
1:A:444:C:H2'	1:A:445:G:H8	1.79	0.47
1:A:636:U:H2'	1:A:637:G:H8	1.79	0.47
1:A:938:A:N6	1:A:939:G:C6	2.83	0.47
1:A:983:A:H2	1:A:984:C:C6	2.32	0.47
1:A:1157:A:H4'	1:A:1158:C:O5'	2.15	0.47
1:A:1348:U:H2'	1:A:1349:A:H8	1.80	0.47
1:A:1406:U:C2'	1:A:1407:C:H5'	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1487:G:O2'	1:A:1488:G:H5'	2.15	0.47
5:B:69:LEU:C	5:B:69:LEU:CD2	2.87	0.47
5:B:107:THR:C	5:B:109:SER:N	2.72	0.47
5:B:177:ALA:O	5:B:180:LEU:N	2.44	0.47
6:C:39:ILE:C	6:C:41:GLY:N	2.72	0.47
6:C:44:GLU:C	6:C:46:GLU:N	2.73	0.47
6:C:179:ARG:C	6:C:179:ARG:HD2	2.39	0.47
7:D:68:TYR:CE2	7:D:97:LEU:HB3	2.49	0.47
8:E:146:ALA:O	8:E:149:GLU:HB2	2.14	0.47
9:F:25:ILE:O	9:F:26:ILE:C	2.56	0.47
11:H:28:ALA:HB2	11:H:59:LEU:HG	1.96	0.47
11:H:48:TYR:CD1	11:H:48:TYR:C	2.92	0.47
11:H:60:ARG:HG3	11:H:60:ARG:NH1	2.24	0.47
11:H:82:HIS:CD2	11:H:82:HIS:C	2.92	0.47
13:J:5:ARG:HA	13:J:73:ASP:OD1	2.14	0.47
16:M:81:LEU:O	16:M:86:CYS:HB3	2.15	0.47
20:Q:97:SER:HB3	20:Q:103:GLY:CA	2.45	0.47
22:S:40:ILE:HG21	22:S:62:ILE:HD13	1.96	0.47
1:A:75:G:O2'	1:A:76:C:H5'	2.15	0.47
1:A:154:C:H2'	1:A:155:C:C6	2.50	0.47
1:A:222:U:H2'	1:A:223:U:C6	2.50	0.47
1:A:291:C:O2'	1:A:292:G:H5'	2.15	0.47
1:A:426:G:H2'	1:A:427:U:C6	2.50	0.47
1:A:918:A:H2'	1:A:919:A:C8	2.50	0.47
1:A:1070:U:O2'	1:A:1071:C:H5'	2.14	0.47
5:B:78:GLN:HE22	5:B:96:ARG:NH1	2.12	0.47
6:C:64:VAL:CG1	6:C:65:ALA:N	2.77	0.47
6:C:91:LEU:HD21	6:C:99:VAL:HG22	1.97	0.47
6:C:129:ALA:HB3	6:C:132:ARG:HB3	1.96	0.47
6:C:139:GLN:O	6:C:140:ARG:C	2.56	0.47
6:C:195:VAL:HG12	6:C:196:LEU:H	1.78	0.47
7:D:6:GLY:O	7:D:7:PRO:C	2.57	0.47
7:D:18:LYS:HA	7:D:33:MET:HG3	1.97	0.47
7:D:78:LEU:HD22	7:D:96:LEU:HB3	1.97	0.47
8:E:15:ARG:HD3	8:E:26:PHE:CD2	2.50	0.47
13:J:38:ILE:HB	13:J:71:LEU:CB	2.45	0.47
16:M:59:TYR:O	16:M:63:THR:CG2	2.62	0.47
18:O:36:ILE:HD12	18:O:63:ARG:NH1	2.30	0.47
19:P:81:ARG:HB2	19:P:81:ARG:NH1	2.30	0.47
22:S:44:MET:O	22:S:45:VAL:C	2.56	0.47
1:A:445:G:O2'	1:A:446:G:H5'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:992:U:O2'	1:A:993:G:OP2	2.29	0.47
1:A:1005:A:C2'	1:A:1006:C:H5'	2.45	0.47
1:A:1109:C:P	6:C:176:HIS:CD2	3.07	0.47
1:A:1222:G:O2'	1:A:1223:C:H5'	2.15	0.47
1:A:1450:U:HO2'	1:A:1451:A:H8	1.60	0.47
10:G:79:ARG:HA	10:G:84:ASN:HA	1.96	0.47
11:H:104:ARG:C	11:H:106:GLY:N	2.70	0.47
18:O:27:VAL:O	18:O:30:ALA:HB3	2.15	0.47
20:Q:67:LYS:CA	20:Q:70:ARG:NH1	2.74	0.47
1:A:407:G:H2'	1:A:408:A:H8	1.79	0.47
1:A:511:C:C2	1:A:512:U:C5	3.03	0.47
1:A:663:A:O2'	1:A:664:G:H5'	2.15	0.47
1:A:865:A:H5'	1:A:1078:U:O4	2.15	0.47
1:A:1206:G:H1'	6:C:193:TYR:O	2.14	0.47
1:A:1305:G:C8	1:A:1305:G:OP2	2.68	0.47
5:B:25:ASN:ND2	5:B:25:ASN:C	2.67	0.47
6:C:206:GLU:O	6:C:207:VAL:O	2.33	0.47
10:G:57:GLU:HB2	10:G:60:LYS:HB2	1.97	0.47
13:J:75:ILE:O	13:J:76:ASN:CB	2.64	0.47
15:L:32:PHE:HB3	15:L:85:ILE:O	2.14	0.47
15:L:39:VAL:HG12	15:L:40:VAL:H	1.80	0.47
15:L:60:LEU:HB2	15:L:64:TYR:HB2	1.97	0.47
17:N:44:LEU:HD12	17:N:44:LEU:O	2.15	0.47
21:R:86:VAL:CG1	21:R:87:ARG:H	2.25	0.47
21:R:88:LYS:OXT	21:R:88:LYS:HG2	2.15	0.47
1:A:402:G:O2'	1:A:403:C:H5'	2.16	0.46
1:A:1461:G:O2'	1:A:1462:G:H5'	2.15	0.46
5:B:91:PRO:HA	5:B:154:LEU:HD12	1.96	0.46
5:B:187:LEU:O	5:B:187:LEU:CD2	2.62	0.46
6:C:14:ILE:O	6:C:15:THR:C	2.57	0.46
6:C:173:VAL:N	6:C:174:PRO:CD	2.77	0.46
12:I:84:ALA:O	12:I:87:GLN:N	2.49	0.46
13:J:34:VAL:CA	13:J:74:ILE:HG22	2.38	0.46
16:M:108:ARG:C	16:M:110:ARG:H	2.24	0.46
18:O:6:GLU:O	18:O:7:GLU:C	2.58	0.46
20:Q:27:PHE:CZ	20:Q:36:ILE:HD11	2.50	0.46
1:A:664:G:N2	1:A:741:G:H1	2.03	0.46
1:A:865:A:H2'	1:A:866:C:C6	2.50	0.46
1:A:1195:C:H2'	1:A:1197:G:H5'	1.98	0.46
7:D:126:ILE:HG22	7:D:127:THR:N	2.29	0.46
7:D:194:LEU:HD22	7:D:194:LEU:N	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:E:43:LEU:HD22	8:E:44:GLY:N	2.31	0.46
8:E:60:TYR:CE1	8:E:64:ARG:CZ	2.98	0.46
10:G:15:ASP:CG	10:G:18:TYR:H	2.23	0.46
15:L:7:ILE:HG21	20:Q:34:LYS:HB3	1.96	0.46
16:M:49:THR:O	16:M:50:GLU:C	2.58	0.46
20:Q:98:LEU:CD1	20:Q:98:LEU:O	2.64	0.46
22:S:52:TYR:HA	22:S:56:GLN:O	2.15	0.46
22:S:63:THR:HG22	22:S:64:GLU:N	2.31	0.46
1:A:501:C:O3'	15:L:118:SER:HB2	2.16	0.46
1:A:792:A:H1'	1:A:794:A:N7	2.30	0.46
1:A:985:C:H2'	1:A:986:A:C8	2.51	0.46
1:A:1019:C:O2'	1:A:1020:U:H5'	2.15	0.46
1:A:1189:C:OP1	13:J:51:ARG:NH2	2.38	0.46
6:C:132:ARG:O	6:C:133:ALA:C	2.58	0.46
7:D:100:ARG:HH12	7:D:137:SER:CB	2.28	0.46
8:E:71:LEU:HD22	8:E:114:GLY:O	2.16	0.46
10:G:28:ASN:OD1	10:G:36:LYS:NZ	2.49	0.46
10:G:37:ASN:HD22	10:G:37:ASN:HA	1.60	0.46
14:K:77:MET:HB3	14:K:103:LEU:HD21	1.96	0.46
15:L:6:THR:OG1	15:L:9:GLN:HG3	2.16	0.46
15:L:41:ARG:NH1	15:L:41:ARG:HB3	2.30	0.46
15:L:89:ARG:NE	15:L:97:ARG:HG2	2.30	0.46
16:M:91:ARG:CB	16:M:98:VAL:HG12	2.44	0.46
18:O:17:ARG:HD3	18:O:26:GLU:CD	2.41	0.46
22:S:62:ILE:HG13	22:S:62:ILE:O	2.16	0.46
1:A:8:A:H62	7:D:209:ARG:H	1.62	0.46
1:A:46:G:O2'	1:A:365:U:H1'	2.16	0.46
1:A:427:U:OP2	7:D:36:ARG:NH2	2.47	0.46
1:A:665:A:N3	1:A:732:C:H2'	2.31	0.46
1:A:915:A:H2'	1:A:916:G:H5'	1.98	0.46
1:A:1021:G:H2'	1:A:1022:G:C8	2.50	0.46
5:B:12:GLU:CD	5:B:213:LEU:HD11	2.40	0.46
6:C:6:HIS:CD2	6:C:6:HIS:C	2.92	0.46
7:D:8:VAL:C	7:D:10:ARG:H	2.22	0.46
10:G:18:TYR:CD2	10:G:59:LEU:HD13	2.50	0.46
15:L:46:LYS:HG3	15:L:47:LYS:N	2.30	0.46
16:M:53:VAL:O	16:M:54:VAL:C	2.59	0.46
16:M:58:GLU:HA	16:M:58:GLU:OE2	2.16	0.46
23:T:50:GLU:CD	23:T:100:ILE:HD11	2.41	0.46
1:A:689:C:OP2	14:K:46:GLY:HA3	2.14	0.46
1:A:743:U:H2'	1:A:744:C:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:877:C:H1'	11:H:3:THR:HG23	1.98	0.46
1:A:1110:A:H8	1:A:1110:A:O5'	1.99	0.46
1:A:1227:A:C2'	1:A:1228:C:O5'	2.63	0.46
1:A:1407:C:O2'	1:A:1408:A:H5'	2.16	0.46
1:A:1531:A:O5'	1:A:1531:A:H8	1.99	0.46
5:B:16:HIS:O	5:B:17:PHE:C	2.58	0.46
5:B:177:ALA:O	5:B:178:ARG:C	2.59	0.46
6:C:153:VAL:CG1	6:C:196:LEU:HD23	2.45	0.46
7:D:25:ARG:C	7:D:27:TYR:N	2.68	0.46
10:G:139:GLU:O	10:G:143:ARG:HG3	2.16	0.46
12:I:8:GLY:HA2	12:I:79:LEU:CD1	2.41	0.46
12:I:53:VAL:HG23	12:I:55:ALA:HB2	1.97	0.46
14:K:70:LYS:O	14:K:71:LYS:C	2.59	0.46
15:L:11:VAL:HG21	20:Q:34:LYS:HG2	1.96	0.46
20:Q:3:LYS:HB3	20:Q:60:ILE:CD1	2.45	0.46
22:S:20:LEU:HD12	22:S:20:LEU:C	2.41	0.46
1:A:270:A:H2'	1:A:271:C:H6	1.80	0.46
1:A:600:C:H2'	1:A:601:C:C6	2.50	0.46
1:A:628:G:H2'	1:A:629:G:C8	2.51	0.46
1:A:927:G:H2'	1:A:928:G:H8	1.81	0.46
1:A:1051:C:H2'	1:A:1052:U:C6	2.49	0.46
5:B:89:GLY:HA3	5:B:226:ARG:HH12	1.81	0.46
5:B:103:THR:OG1	5:B:176:GLU:HG2	2.16	0.46
5:B:206:ASP:O	5:B:207:ALA:CB	2.61	0.46
6:C:10:PHE:CD2	6:C:178:LEU:HD13	2.50	0.46
6:C:61:ALA:C	6:C:63:ASN:N	2.74	0.46
7:D:24:GLU:O	7:D:25:ARG:HB3	2.16	0.46
7:D:31:CYS:O	7:D:32:ALA:HB3	2.14	0.46
7:D:179:GLU:H	7:D:179:GLU:CD	2.17	0.46
8:E:36:ASP:CG	8:E:40:ARG:HB2	2.41	0.46
14:K:56:GLY:O	14:K:57:THR:C	2.59	0.46
16:M:39:ILE:HD13	16:M:52:GLU:HB3	1.97	0.46
17:N:23:ARG:NH1	17:N:30:ALA:HB2	2.30	0.46
17:N:25:VAL:O	17:N:25:VAL:HG22	2.16	0.46
21:R:46:GLU:CD	21:R:46:GLU:N	2.73	0.46
24:V:2:GLY:C	24:V:4:GLY:H	2.24	0.46
1:A:113:G:C1'	1:A:354:G:H5'	2.45	0.46
1:A:327:A:O2'	1:A:328:C:O4'	2.33	0.46
1:A:1070:U:OP1	8:E:25:ARG:NH1	2.49	0.46
1:A:1226:C:N4	16:M:104:ARG:HB2	2.30	0.46
1:A:1256:A:H4'	1:A:1257:U:C5'	2.39	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1343:G:OP1	12:I:125:TYR:HE2	1.99	0.46
1:A:1347:G:H2'	1:A:1348:U:OP2	2.16	0.46
5:B:92:TYR:HD2	5:B:92:TYR:N	2.13	0.46
6:C:23:TYR:CD2	6:C:24:ALA:N	2.84	0.46
6:C:182:ILE:HG23	6:C:202:ILE:C	2.40	0.46
15:L:86:ARG:NH2	15:L:99:HIS:CD2	2.84	0.46
16:M:35:GLU:C	16:M:37:THR:N	2.73	0.46
23:T:49:ALA:HB3	23:T:99:LEU:HD12	1.98	0.46
1:A:689:C:H2'	1:A:690:G:O4'	2.16	0.46
1:A:818:G:C3'	1:A:819:A:C5'	2.94	0.46
1:A:828:A:H5''	1:A:859:A:C2	2.51	0.46
1:A:925:G:C6	1:A:927:G:N7	2.84	0.46
1:A:940:C:H2'	1:A:941:G:C8	2.51	0.46
1:A:1320:C:H41	22:S:37:ARG:CZ	2.28	0.46
1:A:1508:G:O2'	1:A:1509:C:H5'	2.16	0.46
5:B:79:ASP:HA	5:B:82:ARG:HG2	1.98	0.46
5:B:200:ILE:HG22	5:B:202:PRO:HD3	1.97	0.46
11:H:6:ILE:HD11	11:H:31:PHE:CD2	2.50	0.46
13:J:64:GLU:HG2	17:N:59:ALA:HB2	1.97	0.46
17:N:53:LEU:HB3	17:N:56:VAL:HG21	1.97	0.46
22:S:28:LYS:HD3	22:S:31:ILE:CD1	2.45	0.46
1:A:409:G:OP1	7:D:24:GLU:O	2.33	0.46
1:A:555:C:H2'	1:A:556:C:C6	2.51	0.46
1:A:665:A:C1'	1:A:733:A:H1'	2.45	0.46
1:A:1054:C:HO2'	1:A:1055:A:P	2.38	0.46
1:A:1183:A:O2'	1:A:1184:G:P	2.74	0.46
1:A:1292:U:H2'	1:A:1293:G:C8	2.51	0.46
1:A:1300:G:O2'	1:A:1301:U:P	2.73	0.46
6:C:43:LEU:HA	6:C:47:LEU:HD13	1.98	0.46
7:D:70:ILE:HG23	7:D:74:GLN:HB2	1.98	0.46
10:G:72:ARG:O	10:G:73:MET:HG2	2.16	0.46
10:G:75:VAL:HG13	10:G:75:VAL:O	2.16	0.46
10:G:85:TYR:HD1	10:G:154:TYR:HE1	1.63	0.46
12:I:115:GLY:O	12:I:116:LYS:HG3	2.16	0.46
13:J:13:HIS:CD2	13:J:13:HIS:C	2.94	0.46
15:L:27:LEU:C	15:L:29:GLY:N	2.74	0.46
22:S:43:GLU:H	22:S:43:GLU:CD	2.22	0.46
23:T:37:SER:O	23:T:38:LYS:C	2.58	0.46
1:A:200:G:H2'	1:A:201:C:O4'	2.16	0.46
1:A:1390:U:H2'	1:A:1391:U:C6	2.51	0.46
5:B:54:THR:HG23	5:B:199:TYR:HB3	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:208:ILE:CG2	5:B:212:GLN:HB2	2.46	0.46
7:D:52:SER:C	7:D:54:TYR:N	2.71	0.46
8:E:79:GLU:OE1	8:E:79:GLU:N	2.44	0.46
10:G:65:ALA:O	10:G:69:VAL:HG23	2.15	0.46
12:I:100:GLY:C	12:I:102:LEU:N	2.69	0.46
14:K:44:SER:H	14:K:47:VAL:CB	2.26	0.46
21:R:35:ARG:O	21:R:37:VAL:HG23	2.16	0.46
23:T:100:ILE:O	23:T:101:GLY:C	2.59	0.46
1:A:112:G:H4'	1:A:389:A:C5'	2.46	0.45
1:A:753:A:H4'	1:A:754:C:C5'	2.46	0.45
1:A:782:A:H2'	1:A:783:C:O4'	2.16	0.45
1:A:824:C:H2'	1:A:825:G:C8	2.48	0.45
1:A:1288:A:H2'	1:A:1289:A:C8	2.51	0.45
1:A:1392:G:N2	1:A:1502:A:C8	2.84	0.45
5:B:55:PHE:O	5:B:56:ARG:C	2.60	0.45
5:B:85:ALA:CB	5:B:92:TYR:HB3	2.46	0.45
6:C:23:TYR:HE1	13:J:67:THR:HG23	1.81	0.45
6:C:191:THR:HG22	6:C:192:THR:H	1.79	0.45
14:K:126:ARG:HB3	14:K:126:ARG:HH11	1.78	0.45
16:M:23:TYR:CB	16:M:67:GLU:HA	2.46	0.45
17:N:31:ARG:O	17:N:32:SER:OG	2.34	0.45
21:R:86:VAL:CG1	21:R:87:ARG:N	2.77	0.45
23:T:85:MET:HE2	23:T:104:LEU:CD2	2.42	0.45
1:A:742:G:P	18:O:35:ARG:HH22	2.38	0.45
1:A:882:C:O2'	1:A:883:C:H5'	2.16	0.45
1:A:975:A:H8	1:A:975:A:C5'	2.19	0.45
1:A:1182:G:H4'	1:A:1183:A:H5''	1.97	0.45
1:A:1196:U:OP1	1:A:1197:G:H5'	2.17	0.45
1:A:1307:U:H2'	1:A:1308:U:C6	2.52	0.45
1:A:1326:C:H5''	24:V:12:LYS:HZ2	1.82	0.45
5:B:53:ARG:HA	5:B:56:ARG:HE	1.80	0.45
6:C:72:LYS:HE2	6:C:75:VAL:HG21	1.96	0.45
6:C:86:VAL:O	6:C:90:GLU:HB2	2.16	0.45
8:E:143:ARG:NH1	11:H:77:GLU:OE2	2.43	0.45
9:F:19:LEU:C	9:F:19:LEU:CD2	2.89	0.45
10:G:69:VAL:O	10:G:138:LYS:HG3	2.15	0.45
11:H:105:ARG:HH11	11:H:105:ARG:CG	2.28	0.45
12:I:19:LEU:HD23	12:I:61:ALA:HB2	1.98	0.45
13:J:38:ILE:CG2	13:J:39:PRO:HD2	2.45	0.45
13:J:85:LEU:O	13:J:87:THR:N	2.50	0.45
14:K:44:SER:N	14:K:47:VAL:CG2	2.78	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:M:4:ILE:CG2	16:M:5:ALA:N	2.68	0.45
16:M:80:ARG:O	16:M:83:ASP:N	2.48	0.45
17:N:25:VAL:HG12	17:N:38:GLY:O	2.16	0.45
19:P:12:LYS:O	19:P:13:HIS:HB2	2.15	0.45
20:Q:63:ARG:HG2	20:Q:64:PRO:CD	2.46	0.45
21:R:37:VAL:CG2	21:R:78:LEU:HB3	2.46	0.45
1:A:109:A:H4'	1:A:110:C:OP2	2.16	0.45
1:A:265:G:O2'	1:A:266:G:H5'	2.17	0.45
1:A:286:G:O2'	1:A:287:U:H5'	2.17	0.45
1:A:302:G:N3	1:A:556:C:H4'	2.31	0.45
1:A:436:C:H2'	1:A:437:U:C6	2.52	0.45
1:A:1139:G:N2	1:A:1143:G:C6	2.84	0.45
1:A:1223:C:OP2	1:A:1224:G:H2'	2.16	0.45
1:A:1256:A:O2'	1:A:1257:U:P	2.75	0.45
1:A:1349:A:P	12:I:118:LYS:NZ	2.90	0.45
1:A:1365:G:O2'	1:A:1366:C:H5'	2.16	0.45
5:B:98:LEU:HG	5:B:101:MET:HE3	1.97	0.45
6:C:42:LEU:C	6:C:44:GLU:N	2.74	0.45
10:G:152:ALA:C	10:G:154:TYR:H	2.24	0.45
11:H:20:TYR:HE2	11:H:75:ARG:HD2	1.81	0.45
12:I:111:ARG:HD3	12:I:112:LYS:C	2.41	0.45
18:O:12:ILE:HG23	18:O:27:VAL:CG1	2.46	0.45
19:P:2:VAL:O	19:P:64:ALA:HA	2.15	0.45
20:Q:45:HIS:HA	20:Q:69:LYS:CE	2.47	0.45
22:S:74:PHE:CD1	22:S:74:PHE:N	2.83	0.45
23:T:49:ALA:O	23:T:50:GLU:C	2.59	0.45
23:T:56:MET:HE3	23:T:88:VAL:CG1	2.45	0.45
1:A:518:C:H2'	1:A:530:G:N3	2.31	0.45
1:A:1004:A:N7	1:A:1037:C:N3	2.64	0.45
5:B:12:GLU:O	5:B:14:GLY:N	2.50	0.45
5:B:23:ARG:NH1	5:B:24:TRP:HA	2.30	0.45
5:B:118:LEU:O	5:B:119:GLU:C	2.59	0.45
7:D:116:GLN:O	7:D:117:ALA:C	2.59	0.45
7:D:162:LEU:CB	7:D:181:MET:HE2	2.46	0.45
10:G:104:LEU:O	10:G:105:VAL:C	2.59	0.45
11:H:30:ARG:O	11:H:33:GLU:HB3	2.16	0.45
12:I:121:ARG:C	12:I:121:ARG:CD	2.90	0.45
15:L:90:VAL:HG11	15:L:93:LEU:CD1	2.47	0.45
16:M:4:ILE:HG23	16:M:57:ARG:HA	1.98	0.45
16:M:81:LEU:HD12	16:M:88:ARG:HB3	1.98	0.45
19:P:43:LYS:HB3	19:P:48:TRP:CD1	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:R:38:GLU:HA	21:R:41:LYS:HE2	1.97	0.45
24:V:10:ARG:O	24:V:11:GLY:C	2.59	0.45
1:A:19:C:H2'	1:A:20:U:C6	2.50	0.45
1:A:91:C:H2'	1:A:92:C:H6	1.82	0.45
1:A:112:G:C2'	1:A:113:G:H5'	2.46	0.45
1:A:380:G:N2	1:A:384:G:C5	2.85	0.45
1:A:389:A:N3	1:A:389:A:H2'	2.32	0.45
1:A:463:A:O4'	19:P:82:GLN:NE2	2.45	0.45
1:A:721:G:H4'	1:A:722:A:O4'	2.17	0.45
5:B:59:GLU:HG2	5:B:221:LEU:CD1	2.35	0.45
6:C:39:ILE:HG22	6:C:40:ARG:N	2.29	0.45
6:C:177:THR:CG2	6:C:180:ALA:HB2	2.46	0.45
6:C:177:THR:HG23	6:C:180:ALA:HB2	1.99	0.45
8:E:12:LEU:HD22	8:E:12:LEU:C	2.41	0.45
13:J:6:ILE:HD11	13:J:72:VAL:CG1	2.46	0.45
15:L:117:ARG:O	15:L:119:LYS:O	2.34	0.45
20:Q:98:LEU:O	20:Q:98:LEU:HD13	2.16	0.45
20:Q:98:LEU:HA	20:Q:102:GLY:C	2.41	0.45
22:S:33:THR:HG22	22:S:34:TRP:N	2.32	0.45
1:A:13:U:C5	1:A:916:G:O6	2.69	0.45
1:A:226:G:O2'	1:A:227:G:H5'	2.16	0.45
1:A:474:G:H2'	1:A:475:G:H8	1.80	0.45
1:A:665:A:H1'	1:A:733:A:H1'	1.99	0.45
1:A:745:C:H2'	1:A:746:A:H8	1.81	0.45
1:A:1108:G:C5'	1:A:1191:A:H4'	2.46	0.45
1:A:1165:C:C2'	1:A:1166:G:H5'	2.47	0.45
1:A:1478:C:O2'	1:A:1479:C:H5'	2.17	0.45
3:Y:37:A:C2	4:Z:1:U:N3	2.85	0.45
6:C:134:ILE:CG2	6:C:168:ALA:HB3	2.47	0.45
8:E:35:GLY:HA2	8:E:40:ARG:O	2.16	0.45
11:H:125:ARG:HB2	11:H:125:ARG:CZ	2.46	0.45
11:H:126:LYS:C	11:H:128:GLY:N	2.75	0.45
12:I:20:ARG:O	12:I:60:ASP:HB3	2.17	0.45
12:I:116:LYS:O	12:I:117:HIS:C	2.60	0.45
13:J:63:PHE:CE1	17:N:45:ARG:HG3	2.51	0.45
14:K:77:MET:HE3	14:K:103:LEU:CD2	2.47	0.45
15:L:49:ASN:OD1	15:L:92:ASP:OD2	2.35	0.45
17:N:18:VAL:C	17:N:20:ALA:H	2.25	0.45
20:Q:40:LYS:HE2	20:Q:42:TYR:CZ	2.51	0.45
21:R:26:LEU:HD12	21:R:27:GLY:H	1.82	0.45
22:S:53:ASN:HD21	22:S:56:GLN:HB2	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:377:G:P	19:P:3:LYS:HZ3	2.40	0.45
1:A:434:U:H2'	1:A:435:C:H6	1.77	0.45
1:A:1314:C:OP2	22:S:6:LYS:HE2	2.16	0.45
5:B:25:ASN:HD22	5:B:26:PRO:N	2.15	0.45
5:B:25:ASN:HD22	5:B:27:LYS:N	2.12	0.45
5:B:80:ILE:HG21	5:B:212:GLN:HA	1.99	0.45
6:C:115:LEU:O	6:C:118:GLN:N	2.49	0.45
6:C:188:LEU:CD1	6:C:195:VAL:HG13	2.47	0.45
7:D:72:GLU:OE2	7:D:72:GLU:HA	2.16	0.45
8:E:144:THR:H	8:E:147:ASP:HB2	1.82	0.45
10:G:85:TYR:CD1	10:G:154:TYR:CE1	3.05	0.45
13:J:12:ASP:OD1	13:J:14:LYS:N	2.47	0.45
16:M:20:THR:C	16:M:22:ILE:H	2.24	0.45
18:O:8:LYS:O	18:O:11:VAL:HB	2.16	0.45
18:O:21:ASP:CG	18:O:24:SER:HB3	2.42	0.45
18:O:36:ILE:CG1	18:O:59:MET:HE3	2.43	0.45
19:P:55:ARG:O	19:P:58:TYR:HB3	2.17	0.45
23:T:80:ARG:O	23:T:81:LYS:C	2.57	0.45
1:A:52:G:O2'	1:A:53:A:H5'	2.17	0.45
1:A:1055:A:C8	1:A:1206:G:C2	3.05	0.45
1:A:1111:A:H61	6:C:177:THR:HA	1.81	0.45
1:A:1371:G:OP2	12:I:11:LYS:HE3	2.17	0.45
6:C:34:LEU:HD21	6:C:38:ARG:HG2	1.99	0.45
6:C:66:VAL:HG11	6:C:91:LEU:HD11	1.97	0.45
6:C:87:LEU:C	6:C:89:GLU:N	2.74	0.45
6:C:87:LEU:O	6:C:91:LEU:N	2.50	0.45
9:F:26:ILE:O	9:F:30:LEU:HG	2.17	0.45
14:K:48:ILE:HD13	14:K:63:LEU:CB	2.45	0.45
16:M:21:TYR:HD1	16:M:21:TYR:H	1.63	0.45
16:M:51:ALA:O	16:M:54:VAL:HB	2.17	0.45
17:N:14:PRO:HG2	17:N:15:LYS:N	2.32	0.45
21:R:47:THR:HG22	21:R:48:GLY:N	2.30	0.45
1:A:107:G:O2'	1:A:108:G:H5'	2.17	0.45
1:A:204:U:H4'	1:A:216:G:H5''	1.97	0.45
1:A:479:C:O2'	1:A:480:U:H5'	2.16	0.45
1:A:620:C:C2	7:D:135:LEU:HD13	2.52	0.45
1:A:1072:G:O6	1:A:1102:A:N6	2.50	0.45
1:A:1190:G:P	6:C:5:ILE:HG13	2.57	0.45
1:A:1191:A:OP1	6:C:4:LYS:HE3	2.17	0.45
1:A:1342:C:O2'	1:A:1343:G:H5'	2.16	0.45
5:B:59:GLU:O	5:B:61:LEU:N	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:84:GLU:CD	5:B:216:SER:HA	2.42	0.45
5:B:144:ARG:O	5:B:147:LYS:HB2	2.17	0.45
6:C:171:GLY:O	6:C:172:ARG:C	2.60	0.45
8:E:28:PHE:O	8:E:47:LYS:HA	2.17	0.45
11:H:77:GLU:CG	11:H:78:GLN:N	2.80	0.45
19:P:67:THR:CG2	19:P:68:ASP:N	2.79	0.45
22:S:19:VAL:CG1	22:S:20:LEU:N	2.78	0.45
1:A:303:A:P	15:L:17:LYS:HE2	2.57	0.45
1:A:322:C:O2'	1:A:323:U:H5'	2.17	0.45
1:A:942:G:H2'	1:A:943:U:C6	2.52	0.45
1:A:1054:C:H5	1:A:1196:U:C5	2.34	0.45
1:A:1130:A:OP2	1:A:1131:G:OP2	2.34	0.45
1:A:1206:G:C6	1:A:1207:G:C5	3.04	0.45
12:I:85:LEU:O	12:I:92:TYR:HD1	2.00	0.45
12:I:97:LYS:O	12:I:100:GLY:N	2.42	0.45
12:I:100:GLY:C	12:I:102:LEU:H	2.24	0.45
14:K:48:ILE:HD11	14:K:64:ALA:HA	1.98	0.45
14:K:121:PRO:HG2	14:K:126:ARG:CG	2.44	0.45
23:T:89:ARG:O	23:T:93:GLU:HG2	2.17	0.45
1:A:77:G:O2'	1:A:78:G:H5'	2.17	0.44
1:A:255:G:O6	1:A:266:G:O6	2.34	0.44
1:A:1176:A:H2'	1:A:1177:G:H8	1.82	0.44
1:A:1333:A:O2'	1:A:1334:G:H5'	2.18	0.44
1:A:1477:C:H2'	1:A:1478:C:C6	2.52	0.44
6:C:167:TRP:HB3	6:C:168:ALA:H	1.30	0.44
9:F:3:ARG:HG3	9:F:3:ARG:NH1	2.31	0.44
9:F:87:ARG:CG	9:F:87:ARG:NH1	2.80	0.44
10:G:15:ASP:H	10:G:19:GLY:C	2.25	0.44
10:G:48:LYS:O	10:G:51:GLN:HB2	2.17	0.44
11:H:60:ARG:CG	11:H:60:ARG:NH1	2.75	0.44
12:I:107:ARG:NH1	12:I:107:ARG:CB	2.80	0.44
14:K:54:ARG:HG3	14:K:54:ARG:NH1	2.33	0.44
16:M:73:GLU:O	16:M:76:ALA:HB3	2.16	0.44
20:Q:59:ILE:CG2	20:Q:71:PHE:CD1	3.00	0.44
21:R:36:ASN:C	21:R:36:ASN:ND2	2.74	0.44
21:R:44:LEU:HD22	21:R:48:GLY:O	2.17	0.44
1:A:23:C:O2'	1:A:24:U:H5'	2.17	0.44
1:A:141:A:O2'	1:A:142:G:H5'	2.17	0.44
1:A:332:G:H2'	1:A:333:G:H8	1.82	0.44
1:A:694:A:C2'	1:A:695:A:O5'	2.64	0.44
1:A:818:G:H3'	1:A:819:A:H5''	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:947:G:H2'	1:A:948:C:O4'	2.18	0.44
1:A:1111:A:N6	6:C:177:THR:HA	2.31	0.44
1:A:1145:C:O2'	1:A:1146:A:O5'	2.35	0.44
5:B:24:TRP:CG	5:B:25:ASN:H	2.28	0.44
5:B:176:GLU:O	5:B:177:ALA:C	2.60	0.44
5:B:235:SER:C	5:B:237:ALA:H	2.25	0.44
7:D:150:GLU:HA	7:D:153:ARG:NH1	2.32	0.44
8:E:37:ARG:HG2	8:E:37:ARG:NH1	2.32	0.44
10:G:21:VAL:HG23	10:G:22:LEU:N	2.31	0.44
10:G:36:LYS:O	10:G:39:ALA:HB3	2.18	0.44
11:H:113:SER:HB2	11:H:134:ILE:HD11	1.98	0.44
20:Q:61:GLU:HA	20:Q:71:PHE:CE1	2.52	0.44
21:R:45:SER:OG	21:R:49:LYS:HB2	2.18	0.44
22:S:15:LEU:HA	22:S:18:LYS:HB3	1.98	0.44
23:T:84:LEU:C	23:T:86:ARG:N	2.72	0.44
1:A:132:C:O3'	23:T:74:LYS:HE2	2.17	0.44
1:A:411:A:O2'	1:A:412:A:H5'	2.17	0.44
1:A:822:C:O2'	1:A:823:G:H5'	2.18	0.44
1:A:1091:U:O2	1:A:1093:A:H8	1.99	0.44
1:A:1305:G:H2'	1:A:1331:G:N2	2.31	0.44
1:A:1439:C:H2'	1:A:1440:C:C6	2.52	0.44
5:B:77:ALA:HB1	5:B:211:ILE:HG21	1.99	0.44
5:B:79:ASP:C	5:B:81:VAL:N	2.73	0.44
6:C:89:GLU:C	6:C:91:LEU:N	2.73	0.44
7:D:182:LYS:NZ	7:D:182:LYS:HB3	2.33	0.44
9:F:98:LEU:HD23	21:R:29:PHE:C	2.42	0.44
10:G:78:ARG:HG2	10:G:80:VAL:HG23	1.98	0.44
10:G:100:ALA:O	10:G:101:LEU:C	2.60	0.44
14:K:33:THR:HA	14:K:39:PRO:HA	1.99	0.44
15:L:102:ARG:HE	15:L:102:ARG:HB3	1.62	0.44
18:O:87:ILE:CG2	18:O:88:ARG:N	2.80	0.44
20:Q:68:ARG:HG2	20:Q:68:ARG:HH11	1.82	0.44
1:A:162:A:H2'	1:A:163:C:O4'	2.17	0.44
1:A:280:C:O2	20:Q:38:ARG:HG3	2.17	0.44
1:A:528:C:H41	15:L:49:ASN:CG	2.25	0.44
1:A:769:G:H4'	1:A:1513:A:H4'	2.00	0.44
1:A:1270:C:O2'	1:A:1271:G:H5'	2.17	0.44
1:A:1420:C:H2'	1:A:1421:G:H8	1.83	0.44
5:B:87:ARG:CZ	5:B:233:SER:HB2	2.47	0.44
5:B:235:SER:C	5:B:237:ALA:N	2.75	0.44
6:C:94:LEU:CD2	6:C:95:THR:N	2.81	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:195:VAL:CG1	6:C:196:LEU:H	2.30	0.44
8:E:18:ARG:NH2	8:E:25:ARG:HB3	2.33	0.44
10:G:31:MET:SD	10:G:34:GLY:HA2	2.58	0.44
10:G:62:PHE:O	10:G:63:LYS:C	2.59	0.44
10:G:113:GLU:CD	10:G:113:GLU:H	2.24	0.44
10:G:145:ALA:C	10:G:147:ALA:N	2.74	0.44
11:H:17:THR:O	11:H:78:GLN:NE2	2.44	0.44
12:I:71:SER:HA	12:I:74:ILE:HD12	1.99	0.44
12:I:125:TYR:CE1	12:I:128:ARG:HB3	2.52	0.44
20:Q:27:PHE:C	20:Q:27:PHE:CD1	2.95	0.44
1:A:192:U:O2'	1:A:193:C:H5'	2.18	0.44
1:A:397:A:H5'	1:A:398:C:P	2.58	0.44
1:A:447:G:H1'	1:A:487:A:N6	2.32	0.44
1:A:601:C:O2'	1:A:602:A:H5'	2.17	0.44
1:A:922:G:O2'	1:A:1398:A:N1	2.45	0.44
1:A:976:G:C8	1:A:1358:U:O2	2.70	0.44
1:A:1172:C:H2'	1:A:1173:G:C8	2.53	0.44
1:A:1206:G:H2'	1:A:1207:G:H8	1.83	0.44
1:A:1240:U:O2'	10:G:32:ARG:HD2	2.18	0.44
1:A:1476:G:O2'	1:A:1477:C:H5'	2.18	0.44
1:A:1480:G:O2'	1:A:1481:U:H5'	2.17	0.44
5:B:15:VAL:HB	5:B:210:SER:OG	2.17	0.44
5:B:92:TYR:CE2	5:B:151:GLY:CA	2.99	0.44
6:C:60:ALA:O	6:C:61:ALA:HB3	2.17	0.44
6:C:96:GLY:C	6:C:97:LYS:HG3	2.42	0.44
7:D:105:VAL:HG13	7:D:110:PHE:HB2	2.00	0.44
8:E:76:ILE:HG23	8:E:78:HIS:H	1.83	0.44
8:E:120:THR:CG2	8:E:121:LYS:N	2.76	0.44
8:E:121:LYS:HD2	8:E:122:GLU:N	2.32	0.44
16:M:81:LEU:CD2	16:M:81:LEU:H	2.30	0.44
16:M:84:ILE:HG21	22:S:65:ASN:HD22	1.82	0.44
19:P:19:ILE:N	19:P:19:ILE:CD1	2.80	0.44
21:R:36:ASN:HD21	21:R:38:GLU:HB2	1.81	0.44
21:R:87:ARG:O	21:R:88:LYS:CB	2.65	0.44
1:A:475:G:O2'	1:A:476:G:H5'	2.18	0.44
1:A:477:G:O2'	1:A:478:A:H5'	2.18	0.44
1:A:554:C:H2'	1:A:555:C:C6	2.53	0.44
1:A:594:G:C2'	1:A:595:G:H5'	2.47	0.44
1:A:668:G:O2'	18:O:46:HIS:CD2	2.71	0.44
1:A:695:A:H2'	1:A:696:A:C8	2.53	0.44
1:A:1061:G:C2'	1:A:1062:U:H5'	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1151:A:O2'	1:A:1152:A:H8	2.01	0.44
1:A:1253:G:H2'	1:A:1254:C:C6	2.53	0.44
8:E:42:GLY:HA2	8:E:65:ASN:O	2.18	0.44
9:F:4:TYR:OH	9:F:72:VAL:HG21	2.18	0.44
12:I:32:ASP:O	12:I:33:PHE:C	2.59	0.44
13:J:19:SER:OG	13:J:91:PRO:HG3	2.18	0.44
16:M:20:THR:C	16:M:22:ILE:N	2.76	0.44
19:P:74:LEU:O	19:P:79:VAL:CG2	2.66	0.44
20:Q:45:HIS:HA	20:Q:69:LYS:HE3	1.99	0.44
1:A:31:G:C6	1:A:48:C:H5''	2.53	0.44
1:A:132:C:O2'	1:A:133:U:H5'	2.17	0.44
1:A:166:G:O2'	1:A:167:G:H5'	2.18	0.44
1:A:636:U:H2'	1:A:637:G:C8	2.52	0.44
1:A:908:A:H2'	1:A:909:A:C8	2.53	0.44
1:A:946:A:H2'	1:A:947:G:H8	1.76	0.44
1:A:1238:A:C2	1:A:1241:G:N3	2.85	0.44
5:B:77:ALA:CB	5:B:211:ILE:HG21	2.47	0.44
5:B:87:ARG:NH1	5:B:233:SER:CB	2.81	0.44
5:B:87:ARG:NH1	5:B:233:SER:HB2	2.33	0.44
5:B:135:GLN:HG2	5:B:135:GLN:O	2.18	0.44
6:C:134:ILE:HG22	6:C:168:ALA:CB	2.48	0.44
7:D:111:ALA:HB2	7:D:120:LEU:HD12	1.99	0.44
10:G:37:ASN:O	10:G:40:ALA:N	2.51	0.44
11:H:119:LEU:HD12	11:H:124:ALA:N	2.32	0.44
13:J:42:THR:HG23	13:J:67:THR:O	2.18	0.44
16:M:86:CYS:SG	16:M:88:ARG:HB3	2.58	0.44
17:N:18:VAL:O	17:N:20:ALA:N	2.51	0.44
22:S:62:ILE:HD12	22:S:62:ILE:C	2.43	0.44
1:A:862:C:O2'	1:A:863:U:H5'	2.18	0.44
1:A:1002:G:O6	1:A:1040:U:O2	2.35	0.44
1:A:1036:G:H2'	1:A:1037:C:C6	2.53	0.44
1:A:1318:A:H4'	22:S:10:PHE:CE1	2.51	0.44
9:F:95:GLU:CD	9:F:95:GLU:N	2.75	0.44
11:H:75:ARG:HA	11:H:76:PRO:HD3	1.77	0.44
14:K:20:TYR:CZ	14:K:83:ILE:HD12	2.53	0.44
15:L:34:ARG:HG2	15:L:61:THR:HG21	2.00	0.44
15:L:46:LYS:CD	15:L:47:LYS:H	2.31	0.44
16:M:34:LEU:CD1	16:M:41:PRO:HA	2.43	0.44
22:S:24:ALA:C	22:S:26:GLY:H	2.25	0.44
1:A:417:C:O2'	1:A:418:C:H5'	2.18	0.44
1:A:603:U:H2'	1:A:604:G:H8	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:682:G:O2'	1:A:683:G:H5'	2.18	0.44
1:A:745:C:H2'	1:A:746:A:C8	2.52	0.44
1:A:858:G:O2'	1:A:859:A:H5'	2.17	0.44
1:A:1102:A:H2'	1:A:1103:C:C6	2.53	0.44
5:B:9:GLU:OE2	5:B:12:GLU:HA	2.17	0.44
5:B:78:GLN:HG2	5:B:94:ASN:CG	2.43	0.44
5:B:164:VAL:O	5:B:186:ALA:HA	2.17	0.44
6:C:112:SER:O	6:C:115:LEU:HB2	2.18	0.44
6:C:179:ARG:HH11	6:C:179:ARG:HG3	1.82	0.44
10:G:66:VAL:C	10:G:68:ASN:N	2.76	0.44
10:G:110:GLN:OE1	10:G:110:GLN:HA	2.18	0.44
10:G:137:LYS:O	10:G:138:LYS:C	2.59	0.44
12:I:42:ARG:NH2	12:I:71:SER:OG	2.48	0.44
13:J:34:VAL:HG22	13:J:74:ILE:CG2	2.48	0.44
19:P:26:ARG:CD	19:P:31:LYS:O	2.64	0.44
19:P:58:TYR:CE2	19:P:62:VAL:HG21	2.53	0.44
20:Q:86:GLU:O	20:Q:87:LYS:C	2.61	0.44
20:Q:98:LEU:HA	20:Q:102:GLY:HA2	2.00	0.44
23:T:11:SER:HA	23:T:13:LEU:CD1	2.48	0.44
23:T:11:SER:O	23:T:13:LEU:HD12	2.17	0.44
23:T:70:SER:HA	23:T:73:HIS:HD2	1.82	0.44
1:A:457:C:H2'	1:A:458:C:C6	2.53	0.43
1:A:579:G:H2'	1:A:580:U:C6	2.53	0.43
1:A:583:A:H2'	1:A:584:G:O4'	2.18	0.43
1:A:1054:C:O2'	1:A:1055:A:O5'	2.32	0.43
1:A:1066:C:O2'	1:A:1067:A:H5'	2.18	0.43
1:A:1168:A:C6	1:A:1169:A:C6	3.05	0.43
5:B:108:ILE:O	5:B:111:ARG:HB2	2.17	0.43
6:C:22:TRP:HB3	6:C:59:ARG:H	1.84	0.43
8:E:101:ILE:HD12	8:E:119:LEU:HD23	1.99	0.43
12:I:92:TYR:O	12:I:93:ARG:C	2.61	0.43
13:J:22:LYS:O	13:J:24:VAL:N	2.49	0.43
16:M:37:THR:HG22	16:M:37:THR:O	2.18	0.43
19:P:56:ALA:O	19:P:57:ARG:C	2.61	0.43
20:Q:4:LYS:HD2	20:Q:6:LEU:HD21	1.99	0.43
1:A:192:U:H5'	23:T:102:GLY:O	2.17	0.43
1:A:243:A:C2	1:A:246:A:C8	3.06	0.43
1:A:528:C:H5'	1:A:535:A:N6	2.33	0.43
1:A:1142:G:H2'	1:A:1143:G:O4'	2.18	0.43
1:A:1256:A:O2'	1:A:1257:U:O4'	2.34	0.43
5:B:28:PHE:CD2	5:B:28:PHE:O	2.70	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:82:ARG:HB2	5:B:92:TYR:HE1	1.83	0.43
6:C:11:ARG:O	6:C:12:LEU:C	2.61	0.43
6:C:138:VAL:HG21	6:C:168:ALA:HB1	1.99	0.43
7:D:31:CYS:O	7:D:31:CYS:SG	2.77	0.43
7:D:35:ARG:O	7:D:36:ARG:CB	2.66	0.43
7:D:187:ARG:HA	7:D:187:ARG:HE	1.83	0.43
9:F:1:MET:SD	9:F:68:PRO:HG3	2.58	0.43
9:F:62:TRP:HE3	9:F:62:TRP:O	2.01	0.43
12:I:9:ARG:HG2	12:I:13:ALA:O	2.18	0.43
13:J:6:ILE:O	13:J:6:ILE:HG13	2.18	0.43
13:J:29:ARG:H	13:J:29:ARG:HD2	1.83	0.43
14:K:14:VAL:O	14:K:16:SER:N	2.51	0.43
15:L:65:GLU:CD	15:L:65:GLU:N	2.76	0.43
15:L:71:PRO:O	15:L:102:ARG:CD	2.66	0.43
15:L:119:LYS:O	15:L:120:TYR:CB	2.67	0.43
1:A:428:G:O2'	1:A:429:U:P	2.76	0.43
1:A:958:A:C6	1:A:959:A:N1	2.86	0.43
1:A:1090:U:O2'	1:A:1091:U:H5'	2.18	0.43
1:A:1153:C:C2	1:A:1154:G:C8	3.06	0.43
1:A:1244:C:O2'	1:A:1245:A:H5'	2.18	0.43
1:A:1450:U:H2'	1:A:1452:C:C5	2.53	0.43
5:B:24:TRP:N	5:B:24:TRP:CD1	2.84	0.43
5:B:77:ALA:C	5:B:79:ASP:H	2.26	0.43
8:E:41:VAL:HG13	8:E:113:ALA:CA	2.46	0.43
9:F:2:ARG:CZ	9:F:69:GLU:HG2	2.48	0.43
11:H:104:ARG:O	11:H:107:LEU:N	2.47	0.43
12:I:17:VAL:HG11	12:I:81:ILE:HA	2.01	0.43
12:I:20:ARG:O	12:I:60:ASP:N	2.51	0.43
12:I:93:ARG:O	12:I:96:LEU:N	2.51	0.43
16:M:26:GLY:O	16:M:27:LYS:C	2.62	0.43
16:M:81:LEU:HB2	16:M:86:CYS:SG	2.59	0.43
21:R:22:VAL:CG1	21:R:42:ARG:HB3	2.48	0.43
1:A:8:A:C6	7:D:209:ARG:HA	2.54	0.43
1:A:411:A:C6	1:A:429:U:C4	3.06	0.43
1:A:678:U:H2'	1:A:679:C:C6	2.54	0.43
1:A:746:A:O2'	1:A:747:C:H5'	2.19	0.43
1:A:1003(A):G:H2'	1:A:1004:A:O4'	2.18	0.43
1:A:1030:C:H2'	1:A:1030(A):G:O4'	2.19	0.43
1:A:1167:A:C6	1:A:1168:A:C6	3.07	0.43
1:A:1206:G:H2'	1:A:1207:G:C8	2.54	0.43
1:A:1441:G:H1'	1:A:1460:A:H61	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1455:G:O2'	1:A:1459:C:H5'	2.19	0.43
1:A:1459:C:O2'	1:A:1460:A:H5'	2.18	0.43
5:B:144:ARG:HA	5:B:147:LYS:CD	2.48	0.43
6:C:154:SER:OG	6:C:196:LEU:HA	2.18	0.43
7:D:162:LEU:HD22	7:D:162:LEU:HA	1.83	0.43
9:F:94:GLN:NE2	9:F:94:GLN:H	2.16	0.43
12:I:97:LYS:N	12:I:98:PRO:CD	2.81	0.43
14:K:59:TYR:O	14:K:60:ALA:C	2.62	0.43
16:M:37:THR:O	16:M:39:ILE:HG13	2.17	0.43
1:A:84:U:H2'	1:A:88:A:C8	2.54	0.43
1:A:190(A):C:O2'	1:A:190(B):C:H5'	2.18	0.43
1:A:559:A:O2'	1:A:560:U:OP2	2.31	0.43
1:A:1238:A:N7	1:A:1303:C:H1'	2.34	0.43
5:B:39:ILE:HG22	5:B:40:HIS:O	2.19	0.43
5:B:135:GLN:O	5:B:136:VAL:HG23	2.19	0.43
5:B:212:GLN:NE2	5:B:216:SER:HB3	2.34	0.43
6:C:34:LEU:HD21	6:C:38:ARG:CG	2.48	0.43
8:E:96:PRO:HA	8:E:117:ASP:CG	2.43	0.43
9:F:82:ARG:HB2	9:F:85:VAL:HG23	2.00	0.43
9:F:97:PHE:O	9:F:98:LEU:C	2.60	0.43
10:G:66:VAL:O	10:G:68:ASN:N	2.51	0.43
12:I:88:TYR:O	12:I:90:PRO:HD3	2.18	0.43
13:J:25:GLU:C	13:J:27:ALA:N	2.77	0.43
15:L:27:LEU:HD23	15:L:62:SER:CB	2.29	0.43
19:P:57:ARG:HG2	19:P:57:ARG:HH11	1.83	0.43
22:S:80:TYR:C	22:S:80:TYR:HD2	2.26	0.43
1:A:7:G:O2'	8:E:120:THR:O	2.36	0.43
1:A:149:A:H2'	1:A:150:C:H6	1.80	0.43
1:A:560:U:H4'	1:A:561:U:H5''	2.01	0.43
1:A:1118:C:H1'	1:A:1179:A:N9	2.33	0.43
1:A:1277:C:H2'	1:A:1278:U:C2	2.54	0.43
1:A:1514:C:O2'	1:A:1515:C:H5'	2.19	0.43
5:B:53:ARG:NH1	5:B:199:TYR:HD2	2.15	0.43
5:B:60:ASP:O	5:B:64:ARG:HB2	2.17	0.43
6:C:15:THR:HB	6:C:181:ASN:CB	2.45	0.43
6:C:29:TYR:OH	17:N:54:PRO:O	2.34	0.43
6:C:33:LEU:O	6:C:34:LEU:C	2.62	0.43
8:E:53:LEU:O	8:E:57:LYS:HB2	2.19	0.43
8:E:60:TYR:HE1	8:E:64:ARG:NH2	2.17	0.43
11:H:4:ASP:C	11:H:4:ASP:OD1	2.61	0.43
22:S:6:LYS:HB3	22:S:7:LYS:H	1.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:190(J):U:H2'	1:A:190(K):G:C8	2.53	0.43
1:A:512:U:H2'	1:A:513:C:C6	2.54	0.43
1:A:653:A:OP1	11:H:56:LYS:NZ	2.38	0.43
1:A:697:U:H2'	1:A:698:G:H5'	1.99	0.43
1:A:701:C:O2'	1:A:702:A:OP2	2.34	0.43
1:A:1039:C:H2'	1:A:1040:U:H6	1.80	0.43
1:A:1085:U:O3'	1:A:1086:U:C6	2.72	0.43
1:A:1278:U:C4'	1:A:1279:A:H5'	2.47	0.43
1:A:1298:C:H1'	1:A:1299:A:C2	2.53	0.43
1:A:1439:C:H2'	1:A:1440:C:H6	1.84	0.43
5:B:73:THR:HB	5:B:170:GLU:OE1	2.18	0.43
7:D:17:VAL:CA	7:D:33:MET:HE2	2.49	0.43
7:D:17:VAL:CG1	7:D:18:LYS:N	2.81	0.43
7:D:35:ARG:O	7:D:36:ARG:HB2	2.19	0.43
7:D:163:GLU:C	7:D:165:MET:N	2.73	0.43
8:E:109:ILE:O	8:E:110:LEU:C	2.62	0.43
9:F:1:MET:HB2	9:F:67:MET:O	2.18	0.43
9:F:62:TRP:CD1	21:R:35:ARG:CZ	3.02	0.43
10:G:111:ARG:HH21	10:G:122:HIS:HB3	1.84	0.43
11:H:31:PHE:HZ	11:H:134:ILE:CD1	2.32	0.43
11:H:68:ARG:HG2	11:H:68:ARG:NH1	2.34	0.43
15:L:89:ARG:HG2	15:L:97:ARG:CA	2.42	0.43
17:N:14:PRO:HG2	17:N:15:LYS:H	1.83	0.43
21:R:33:ASP:OD2	21:R:36:ASN:HB2	2.18	0.43
23:T:62:LEU:HD23	23:T:62:LEU:HA	1.84	0.43
1:A:113:G:H1'	1:A:354:G:C5'	2.46	0.43
1:A:229:U:H5''	19:P:33:ILE:HD13	2.01	0.43
1:A:231:G:O2'	1:A:232:G:H5'	2.19	0.43
1:A:332:G:O2'	1:A:333:G:H5'	2.19	0.43
1:A:383:A:H2'	1:A:384:G:H5'	2.01	0.43
1:A:935:A:C2	1:A:936:C:C2	3.07	0.43
1:A:1251:A:H2'	1:A:1252:A:H8	1.80	0.43
6:C:65:ALA:O	6:C:66:VAL:C	2.60	0.43
6:C:107:GLN:CD	6:C:107:GLN:N	2.77	0.43
12:I:8:GLY:CA	12:I:79:LEU:HB3	2.47	0.43
13:J:81:THR:C	13:J:83:GLU:H	2.25	0.43
14:K:97:ALA:O	14:K:98:LEU:C	2.62	0.43
15:L:98:TYR:N	15:L:98:TYR:CD1	2.86	0.43
16:M:35:GLU:O	16:M:37:THR:N	2.50	0.43
21:R:35:ARG:O	21:R:37:VAL:N	2.46	0.43
23:T:96:GLY:O	23:T:97:ALA:CB	2.65	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:118:U:O4	1:A:288:A:H2'	2.18	0.43
1:A:262:A:C6	1:A:263:A:C6	3.06	0.43
1:A:279:A:C6	20:Q:98:LEU:HD13	2.54	0.43
1:A:621:A:H2'	1:A:622:A:C8	2.54	0.43
1:A:662:G:H2'	1:A:663:A:H8	1.84	0.43
1:A:974:A:OP2	17:N:41:ARG:NH1	2.52	0.43
1:A:1189:C:H5''	6:C:5:ILE:HG12	2.01	0.43
1:A:1190:G:C2'	1:A:1191:A:OP2	2.67	0.43
1:A:1358:U:H2'	1:A:1359:C:O4'	2.18	0.43
1:A:1405:G:O2'	1:A:1406:U:H5'	2.19	0.43
1:A:1406:U:O2'	1:A:1407:C:H5'	2.19	0.43
5:B:178:ARG:NH2	11:H:68:ARG:HH22	2.17	0.43
6:C:17:ASP:OD1	6:C:18:TRP:N	2.52	0.43
6:C:43:LEU:HD22	6:C:68:VAL:HG21	2.01	0.43
6:C:139:GLN:CA	6:C:139:GLN:NE2	2.82	0.43
7:D:19:LEU:HD22	7:D:67:ILE:HG12	2.01	0.43
11:H:86:ILE:CD1	11:H:133:LEU:CD2	2.97	0.43
15:L:83:VAL:HG22	15:L:84:LEU:N	2.32	0.43
16:M:25:ILE:HG22	16:M:26:GLY:N	2.33	0.43
20:Q:99:SER:OG	20:Q:100:LYS:N	2.49	0.43
1:A:190(L):U:H3	23:T:105:SER:HB2	1.84	0.43
1:A:335:C:O2'	1:A:336:C:H5'	2.17	0.43
1:A:1229:A:C2	1:A:1230:C:C5	3.07	0.43
1:A:1392:G:H21	1:A:1502:A:H8	1.66	0.43
5:B:128:GLU:HA	5:B:135:GLN:NE2	2.34	0.43
7:D:31:CYS:C	7:D:33:MET:H	2.27	0.43
7:D:109:GLY:C	7:D:111:ALA:N	2.77	0.43
7:D:150:GLU:CD	7:D:153:ARG:HH22	2.26	0.43
9:F:22:GLU:OE1	9:F:82:ARG:HD3	2.19	0.43
9:F:62:TRP:O	9:F:62:TRP:CE3	2.72	0.43
11:H:45:ILE:C	11:H:47:GLY:N	2.76	0.43
11:H:117:GLY:C	11:H:119:LEU:HD23	2.44	0.43
13:J:61:GLU:OE1	17:N:45:ARG:NH1	2.41	0.43
14:K:124:LYS:HE2	14:K:125:PHE:CZ	2.53	0.43
16:M:103:THR:O	16:M:104:ARG:C	2.62	0.43
16:M:106:ASN:O	16:M:107:ALA:CB	2.65	0.43
18:O:12:ILE:HG23	18:O:27:VAL:HG11	2.01	0.43
21:R:22:VAL:HG13	21:R:42:ARG:HB3	2.01	0.43
22:S:16:LEU:C	22:S:18:LYS:N	2.76	0.43
1:A:97:G:H2'	1:A:98:U:O4'	2.19	0.42
1:A:228:A:H4'	19:P:62:VAL:HG11	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:761:G:H4'	20:Q:103:GLY:O	2.19	0.42
1:A:839:U:O2	1:A:839:U:H2'	2.19	0.42
1:A:975:A:C8	1:A:975:A:C5'	2.97	0.42
1:A:998:G:O2'	1:A:999:C:H5'	2.19	0.42
1:A:1091:U:C2	1:A:1093:A:OP2	2.71	0.42
1:A:1286:A:C8	1:A:1287:A:C5'	3.02	0.42
1:A:1338:G:H2'	1:A:1339:A:C8	2.54	0.42
6:C:28:GLN:O	6:C:29:TYR:C	2.61	0.42
7:D:50:ARG:NH1	7:D:51:PRO:O	2.52	0.42
10:G:145:ALA:O	10:G:146:GLU:CB	2.66	0.42
13:J:44:VAL:HG21	13:J:66:ARG:NH2	2.34	0.42
14:K:69:ALA:HA	14:K:103:LEU:HD11	2.01	0.42
17:N:3:ARG:O	17:N:4:LYS:C	2.62	0.42
21:R:22:VAL:O	21:R:22:VAL:HG12	2.18	0.42
23:T:10:LEU:CD1	23:T:12:ALA:H	2.32	0.42
24:V:22:ARG:N	24:V:23:PRO:HD3	2.34	0.42
1:A:219:C:H2'	1:A:220:G:O4'	2.19	0.42
1:A:380:G:C2	1:A:384:G:C6	3.07	0.42
1:A:635:G:O2'	1:A:636:U:H5'	2.19	0.42
1:A:938:A:C6	1:A:939:G:C5	3.07	0.42
1:A:960:U:O2	1:A:960:U:H2'	2.19	0.42
1:A:1229:A:H2'	1:A:1230:C:C6	2.54	0.42
1:A:1299:A:C8	1:A:1301:U:H1'	2.54	0.42
1:A:1347:G:H1'	1:A:1348:U:H5	1.84	0.42
5:B:78:GLN:NE2	5:B:96:ARG:NH1	2.67	0.42
7:D:13:ARG:HD2	7:D:38:TYR:O	2.20	0.42
7:D:30:LYS:C	7:D:32:ALA:N	2.77	0.42
7:D:141:ARG:N	7:D:144:ASP:OD2	2.52	0.42
7:D:173:TRP:HB2	7:D:187:ARG:O	2.19	0.42
11:H:11:THR:O	11:H:12:ARG:C	2.62	0.42
11:H:25:ASP:OD1	11:H:25:ASP:N	2.52	0.42
12:I:79:LEU:O	12:I:82:ALA:N	2.53	0.42
12:I:80:GLY:O	12:I:84:ALA:N	2.44	0.42
13:J:20:ALA:O	13:J:24:VAL:HG23	2.18	0.42
20:Q:81:ARG:HE	20:Q:81:ARG:HB2	1.27	0.42
23:T:97:ALA:O	23:T:98:PRO:C	2.62	0.42
1:A:530:G:O2'	3:Y:35:A:H4'	2.19	0.42
1:A:831:U:O2'	1:A:832:C:H5'	2.19	0.42
1:A:1072:G:H2'	1:A:1073:U:O4'	2.19	0.42
1:A:1176:A:O2'	1:A:1177:G:H5'	2.20	0.42
5:B:51:LEU:O	5:B:52:GLU:C	2.62	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:83:MET:O	5:B:84:GLU:C	2.61	0.42
5:B:209:ARG:O	5:B:213:LEU:HB2	2.19	0.42
6:C:127:ARG:HG2	6:C:127:ARG:HH11	1.84	0.42
7:D:150:GLU:CG	7:D:153:ARG:HH22	2.31	0.42
8:E:31:LEU:HA	8:E:31:LEU:HD23	1.76	0.42
8:E:101:ILE:HD12	8:E:119:LEU:CD2	2.49	0.42
10:G:79:ARG:HG2	10:G:79:ARG:HH11	1.84	0.42
11:H:38:ILE:N	11:H:38:ILE:HD12	2.35	0.42
12:I:76:ALA:O	12:I:79:LEU:N	2.52	0.42
23:T:86:ARG:HG3	23:T:90:GLN:HE21	1.83	0.42
1:A:28:G:O2'	1:A:296:U:OP1	2.37	0.42
1:A:130:A:H1'	1:A:263:A:O2'	2.19	0.42
5:B:23:ARG:NH1	5:B:191:ASP:HA	2.34	0.42
5:B:76:GLN:HG3	5:B:206:ASP:OD1	2.19	0.42
5:B:111:ARG:NE	5:B:111:ARG:HA	2.34	0.42
12:I:36:TYR:CD2	12:I:37:PHE:CE2	3.08	0.42
12:I:79:LEU:O	12:I:80:GLY:C	2.62	0.42
13:J:19:SER:HA	13:J:22:LYS:HZ3	1.80	0.42
16:M:21:TYR:CD1	16:M:21:TYR:N	2.87	0.42
19:P:40:ASP:OD2	19:P:40:ASP:C	2.62	0.42
20:Q:45:HIS:CB	20:Q:69:LYS:HE2	2.49	0.42
1:A:166:G:H2'	1:A:167:G:H8	1.84	0.42
1:A:686:U:O2'	1:A:687:A:H8	2.02	0.42
1:A:828:A:H2'	1:A:829:G:O4'	2.19	0.42
1:A:1188:A:H2'	1:A:1189:C:O4'	2.19	0.42
1:A:1250:A:H5'	12:I:68:GLY:O	2.19	0.42
3:Y:33:U:H5'	3:Y:34:G:OP2	2.19	0.42
4:Z:2:U:H2'	4:Z:3:U:C6	2.54	0.42
5:B:26:PRO:O	5:B:29:ALA:CB	2.67	0.42
5:B:59:GLU:O	5:B:60:ASP:C	2.62	0.42
5:B:100:GLY:O	5:B:104:ASN:N	2.47	0.42
6:C:131:ARG:O	6:C:135:LYS:HG3	2.19	0.42
7:D:3:ARG:NH2	7:D:74:GLN:OE1	2.52	0.42
7:D:91:SER:O	7:D:94:LEU:N	2.53	0.42
9:F:23:LYS:NZ	9:F:42:GLU:OE2	2.50	0.42
10:G:71:PRO:HG3	10:G:103:TRP:CH2	2.55	0.42
11:H:9:MET:O	11:H:10:LEU:C	2.62	0.42
12:I:50:LEU:C	12:I:52:ALA:N	2.76	0.42
14:K:91:ARG:HH11	21:R:88:LYS:CE	2.31	0.42
14:K:99:GLN:HG2	14:K:105:VAL:CG2	2.43	0.42
15:L:28:LYS:HD3	15:L:33:ARG:NH2	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:N:43:CYS:HA	17:N:46:GLU:HG3	2.02	0.42
18:O:39:LEU:O	18:O:43:LEU:HG	2.19	0.42
24:V:24:ARG:HG3	24:V:24:ARG:HH11	1.84	0.42
1:A:189:G:H2'	1:A:190:C:C6	2.54	0.42
1:A:190(H):G:O2'	1:A:190(I):G:H5'	2.20	0.42
1:A:193:C:H2'	1:A:194:C:C6	2.55	0.42
1:A:379:C:O2'	1:A:380:G:H5'	2.20	0.42
1:A:385:C:O2'	1:A:386:C:H5'	2.19	0.42
1:A:448:A:C4	1:A:487:A:C2	3.07	0.42
1:A:686:U:HO2'	1:A:687:A:H8	1.68	0.42
1:A:1010:G:N2	1:A:1020:U:H1'	2.34	0.42
1:A:1017:G:H2'	1:A:1018:C:C6	2.55	0.42
1:A:1322:C:OP1	22:S:78:ARG:NH2	2.52	0.42
1:A:1392:G:N2	1:A:1502:A:H8	2.17	0.42
1:A:1492:A:H1'	4:Z:2:U:O2'	2.19	0.42
5:B:14:GLY:C	5:B:15:VAL:CG2	2.92	0.42
6:C:10:PHE:O	6:C:178:LEU:HD11	2.19	0.42
6:C:59:ARG:HG2	6:C:64:VAL:HG22	2.01	0.42
7:D:60:GLU:HG2	7:D:202:LEU:HB2	2.00	0.42
8:E:144:THR:N	8:E:147:ASP:OD2	2.52	0.42
11:H:2:LEU:HD23	11:H:2:LEU:HA	1.87	0.42
11:H:20:TYR:CE2	11:H:75:ARG:HD2	2.54	0.42
11:H:63:LEU:N	11:H:63:LEU:CD2	2.82	0.42
12:I:42:ARG:O	12:I:45:ALA:N	2.53	0.42
13:J:57:LYS:HD2	13:J:57:LYS:C	2.45	0.42
16:M:49:THR:HB	16:M:52:GLU:CG	2.43	0.42
16:M:96:LEU:HB3	16:M:97:PRO:HD2	2.01	0.42
21:R:53:ARG:HB2	21:R:63:GLN:HG2	2.02	0.42
1:A:687:A:C2	1:A:700:G:N3	2.87	0.42
1:A:791:G:C5	1:A:792:A:N7	2.88	0.42
1:A:999:C:H2'	1:A:1000:U:C6	2.54	0.42
1:A:1007:C:O2'	1:A:1008:C:H5'	2.19	0.42
1:A:1520:G:O2'	1:A:1521:G:H5'	2.19	0.42
5:B:19:HIS:CE1	5:B:206:ASP:HB3	2.54	0.42
5:B:100:GLY:N	5:B:176:GLU:OE2	2.53	0.42
5:B:111:ARG:HB3	5:B:149:LEU:CD1	2.46	0.42
5:B:221:LEU:O	5:B:221:LEU:HD13	2.20	0.42
8:E:51:VAL:HB	8:E:52:PRO:CD	2.43	0.42
8:E:84:PHE:HB2	8:E:134:ALA:HB2	2.01	0.42
10:G:22:LEU:HD12	10:G:101:LEU:HD11	2.01	0.42
12:I:5:TYR:CD1	12:I:5:TYR:C	2.98	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:N:29:ARG:HG2	17:N:29:ARG:NH1	2.34	0.42
19:P:53:VAL:O	19:P:57:ARG:HG3	2.20	0.42
23:T:50:GLU:OE1	23:T:100:ILE:HD11	2.19	0.42
1:A:418:C:H2'	1:A:419:C:H6	1.85	0.42
1:A:736:C:H2'	1:A:737:A:C8	2.54	0.42
1:A:1533:C:O2	1:A:1533:C:H3'	2.20	0.42
5:B:51:LEU:O	5:B:55:PHE:HD1	2.03	0.42
5:B:80:ILE:HD12	5:B:80:ILE:N	2.11	0.42
5:B:118:LEU:C	5:B:120:ALA:N	2.77	0.42
6:C:119:ARG:CG	6:C:140:ARG:HH12	2.28	0.42
6:C:155:GLY:O	6:C:156:ARG:CB	2.68	0.42
6:C:157:ILE:CG2	6:C:164:ARG:NH2	2.83	0.42
7:D:54:TYR:O	7:D:55:ALA:C	2.63	0.42
8:E:16:THR:HG23	8:E:17:ALA:N	2.33	0.42
10:G:126:ASP:HB3	10:G:131:LYS:HG3	2.02	0.42
10:G:137:LYS:C	10:G:139:GLU:N	2.74	0.42
13:J:9:ARG:HG3	13:J:9:ARG:O	2.19	0.42
13:J:12:ASP:O	13:J:15:THR:HG22	2.20	0.42
13:J:34:VAL:HG13	13:J:74:ILE:HG23	2.00	0.42
13:J:74:ILE:CD1	13:J:85:LEU:HD11	2.49	0.42
16:M:33:ALA:HA	16:M:59:TYR:CD2	2.53	0.42
17:N:24:CYS:CB	17:N:27:CYS:SG	3.07	0.42
21:R:40:LEU:HB3	21:R:79:LEU:HD11	2.02	0.42
1:A:119:A:O2'	1:A:120:A:OP2	2.29	0.42
1:A:268:C:H2'	1:A:269:C:H6	1.84	0.42
1:A:342:C:O2'	1:A:343:U:H5'	2.20	0.42
1:A:344:A:H5''	1:A:345:C:H5	1.85	0.42
1:A:582:U:C2	1:A:760:G:C6	3.07	0.42
1:A:1207:G:H2'	1:A:1208:C:H6	1.85	0.42
1:A:1286:A:H2'	1:A:1287:A:C5'	2.50	0.42
5:B:211:ILE:O	5:B:215:LEU:HB2	2.19	0.42
6:C:8:ILE:C	6:C:10:PHE:N	2.77	0.42
6:C:107:GLN:CD	6:C:107:GLN:H	2.27	0.42
8:E:150:ARG:HG3	8:E:150:ARG:HH11	1.83	0.42
13:J:60:ARG:O	13:J:61:GLU:HB3	2.20	0.42
16:M:31:LYS:O	16:M:35:GLU:HB2	2.20	0.42
16:M:82:MET:HE3	16:M:92:HIS:CB	2.50	0.42
18:O:63:ARG:O	18:O:65:ARG:N	2.53	0.42
21:R:21:LYS:O	21:R:23:LYS:N	2.52	0.42
22:S:22:LEU:HD22	22:S:28:LYS:CD	2.48	0.42
22:S:61:TYR:HD2	22:S:62:ILE:N	2.17	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:145:G:O2'	1:A:146:G:H5'	2.20	0.42
1:A:371:G:C2'	1:A:372:C:C5'	2.94	0.42
1:A:502:G:P	15:L:118:SER:HB2	2.60	0.42
1:A:520:A:H2'	1:A:521:G:O4'	2.20	0.42
1:A:542:G:OP1	7:D:10:ARG:NH2	2.53	0.42
1:A:642:A:C5	11:H:115:SER:HA	2.55	0.42
1:A:928:G:O2'	1:A:929:G:H5'	2.20	0.42
1:A:1047:G:H5''	17:N:4:LYS:HD2	2.01	0.42
1:A:1157:A:H1'	1:A:1181:G:N2	2.35	0.42
1:A:1288:A:H2'	1:A:1289:A:O4'	2.20	0.42
1:A:1328:C:H41	24:V:6:ARG:HH22	1.68	0.42
1:A:1370:G:C2	1:A:1371:G:N7	2.88	0.42
1:A:1386:G:H2'	1:A:1387:G:H8	1.85	0.42
5:B:16:HIS:C	5:B:17:PHE:CD1	2.97	0.42
5:B:102:LEU:CD1	5:B:102:LEU:H	2.33	0.42
6:C:37:GLN:O	6:C:38:ARG:C	2.62	0.42
7:D:133:VAL:HG11	7:D:138:TYR:CD1	2.54	0.42
7:D:192:GLU:HA	7:D:192:GLU:OE1	2.20	0.42
8:E:24:ARG:O	8:E:25:ARG:HD3	2.20	0.42
10:G:20:ASP:OD2	10:G:63:LYS:NZ	2.53	0.42
10:G:54:THR:C	10:G:56:GLN:H	2.27	0.42
12:I:24:GLY:HA2	12:I:59:PHE:O	2.20	0.42
14:K:12:ARG:O	14:K:13:GLN:C	2.63	0.42
14:K:58:PRO:O	14:K:61:ALA:HB3	2.20	0.42
16:M:16:ASP:OD1	16:M:16:ASP:N	2.52	0.42
16:M:71:ARG:HG2	16:M:71:ARG:HH11	1.85	0.42
18:O:16:ALA:C	18:O:18:PHE:H	2.28	0.42
22:S:21:GLU:O	22:S:22:LEU:C	2.62	0.42
1:A:310:G:H2'	1:A:311:C:H6	1.85	0.41
1:A:934:C:C4	1:A:1345:U:C5	3.08	0.41
1:A:1328:C:OP1	24:V:21:TYR:OH	2.35	0.41
1:A:1438:G:C2	1:A:1464:G:N3	2.88	0.41
1:A:1516:G:H2'	1:A:1518:A:OP2	2.20	0.41
5:B:30:ARG:CG	5:B:31:TYR:N	2.84	0.41
5:B:91:PRO:HG3	5:B:155:LEU:HG	2.01	0.41
5:B:103:THR:N	5:B:176:GLU:OE1	2.33	0.41
5:B:112:VAL:O	5:B:114:ARG:N	2.53	0.41
6:C:38:ARG:HB3	6:C:94:LEU:HD11	2.02	0.41
6:C:113:ALA:N	6:C:114:PRO:CD	2.83	0.41
7:D:163:GLU:HA	7:D:163:GLU:OE2	2.18	0.41
8:E:21:ALA:C	8:E:23:GLY:H	2.25	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:G:78:ARG:NH1	10:G:154:TYR:HB3	2.35	0.41
12:I:77:ILE:O	12:I:78:LYS:C	2.63	0.41
13:J:27:ALA:HA	13:J:30:SER:HG	1.84	0.41
14:K:20:TYR:CE1	14:K:83:ILE:HD12	2.55	0.41
15:L:90:VAL:CG1	15:L:93:LEU:HG	2.50	0.41
18:O:17:ARG:NH1	18:O:77:ARG:NH1	2.68	0.41
1:A:193:C:O3'	23:T:61:SER:HB2	2.20	0.41
1:A:228:A:H2'	1:A:229:U:C6	2.55	0.41
1:A:411:A:N3	1:A:413:G:O2'	2.54	0.41
1:A:542:G:H5'	7:D:41:GLY:HA3	2.02	0.41
1:A:628:G:H2'	1:A:629:G:H8	1.84	0.41
1:A:640:A:C2'	1:A:641:U:H5'	2.50	0.41
1:A:1227:A:O3'	16:M:115:LYS:HE3	2.19	0.41
1:A:1315:U:OP2	22:S:6:LYS:NZ	2.53	0.41
1:A:1399:C:C2	1:A:1502:A:N6	2.88	0.41
1:A:1512:U:O2'	1:A:1513:A:H5'	2.19	0.41
5:B:52:GLU:O	5:B:56:ARG:HG3	2.20	0.41
5:B:101:MET:N	5:B:108:ILE:HD12	2.34	0.41
5:B:178:ARG:HH21	5:B:196:LEU:HA	1.85	0.41
11:H:112:LEU:HD23	11:H:112:LEU:H	1.83	0.41
12:I:76:ALA:O	12:I:77:ILE:C	2.61	0.41
13:J:38:ILE:CB	13:J:71:LEU:HB3	2.51	0.41
18:O:66:LEU:O	18:O:67:LEU:C	2.63	0.41
21:R:18:ARG:H	21:R:19:LYS:HD2	1.85	0.41
21:R:52:PRO:HB2	21:R:54:ARG:HB2	2.02	0.41
23:T:72:LEU:O	23:T:73:HIS:O	2.37	0.41
1:A:130:A:OP2	1:A:190(E):U:O2'	2.25	0.41
1:A:147:G:O2'	1:A:148:G:H5'	2.20	0.41
1:A:222:U:H2'	1:A:223:U:H6	1.85	0.41
1:A:298:A:H2'	1:A:299:G:O4'	2.21	0.41
1:A:425:G:O2'	1:A:426:G:H5'	2.20	0.41
1:A:1053:G:O3'	1:A:1054:C:H4'	2.20	0.41
1:A:1091:U:H2'	1:A:1093:A:OP2	2.19	0.41
1:A:1153:C:O2'	1:A:1154:G:H5'	2.20	0.41
1:A:1285:A:O2'	1:A:1286:A:OP2	2.38	0.41
7:D:61:LYS:HD3	7:D:206:PHE:CD2	2.55	0.41
7:D:170:VAL:HG22	7:D:171:GLY:H	1.86	0.41
8:E:34:VAL:O	8:E:42:GLY:N	2.51	0.41
9:F:1:MET:N	9:F:1:MET:HE3	2.34	0.41
10:G:93:PRO:HG2	10:G:94:ARG:H	1.85	0.41
14:K:14:VAL:O	14:K:14:VAL:HG12	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:L:7:ILE:O	15:L:11:VAL:HG23	2.20	0.41
16:M:20:THR:O	16:M:22:ILE:N	2.53	0.41
16:M:56:LEU:HD23	16:M:56:LEU:HA	1.87	0.41
16:M:59:TYR:O	16:M:63:THR:HG21	2.20	0.41
16:M:80:ARG:C	16:M:82:MET:H	2.27	0.41
16:M:81:LEU:HD12	16:M:88:ARG:HG2	2.02	0.41
16:M:96:LEU:O	16:M:110:ARG:NH1	2.54	0.41
18:O:16:ALA:CB	18:O:21:ASP:HB3	2.38	0.41
20:Q:96:GLN:C	20:Q:96:GLN:CD	2.88	0.41
22:S:30:LEU:C	22:S:31:ILE:HD13	2.44	0.41
1:A:17:U:H1'	1:A:1080:A:N3	2.35	0.41
1:A:182:U:O4	1:A:223:U:H1'	2.19	0.41
1:A:336:C:H2'	1:A:337:C:H6	1.85	0.41
1:A:339:C:H2'	1:A:340:U:C6	2.54	0.41
1:A:797:C:O2'	1:A:798:G:H5'	2.19	0.41
1:A:1285:A:H8	1:A:1285:A:OP1	2.03	0.41
1:A:1292:U:P	10:G:41:ARG:NH2	2.92	0.41
1:A:1362:C:H5'	1:A:1363:A:O5'	2.21	0.41
1:A:1414:U:H2'	1:A:1415:G:H8	1.85	0.41
5:B:16:HIS:C	5:B:17:PHE:HD1	2.27	0.41
5:B:19:HIS:CG	5:B:20:GLU:N	2.88	0.41
6:C:79:ARG:O	6:C:82:GLU:HB2	2.20	0.41
6:C:159:GLY:HA2	6:C:193:TYR:CD2	2.55	0.41
7:D:142:PRO:HG2	7:D:187:ARG:NH2	2.33	0.41
8:E:36:ASP:OD2	8:E:40:ARG:HB2	2.21	0.41
9:F:27:GLN:CA	9:F:27:GLN:HE21	2.32	0.41
9:F:69:GLU:OE1	9:F:69:GLU:N	2.54	0.41
10:G:122:HIS:HD2	10:G:125:MET:CE	2.33	0.41
13:J:49:VAL:HG12	13:J:50:ILE:N	2.34	0.41
14:K:87:THR:HG23	14:K:91:ARG:HH21	1.85	0.41
15:L:93:LEU:HB2	15:L:96:VAL:HG23	2.02	0.41
16:M:65:LYS:HD3	16:M:69:GLU:HG2	2.01	0.41
1:A:257:G:O2'	1:A:258:G:H5'	2.20	0.41
1:A:519:C:H2'	1:A:520:A:H8	1.85	0.41
1:A:519:C:O2'	1:A:520:A:H5'	2.21	0.41
1:A:1236:A:OP1	24:V:2:GLY:HA3	2.19	0.41
1:A:1416:G:H2'	1:A:1417:G:O4'	2.20	0.41
1:A:1429:C:H2'	1:A:1430:C:H6	1.85	0.41
1:A:1472:U:H2'	1:A:1473:A:C8	2.56	0.41
5:B:23:ARG:C	5:B:24:TRP:HD1	2.27	0.41
5:B:107:THR:O	5:B:110:GLN:N	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:B:121:LEU:HD23	5:B:121:LEU:O	2.21	0.41
6:C:11:ARG:O	6:C:14:ILE:N	2.53	0.41
6:C:64:VAL:CG1	6:C:65:ALA:H	2.34	0.41
7:D:8:VAL:HG11	7:D:21:LEU:CB	2.51	0.41
7:D:62:GLN:O	7:D:63:LYS:C	2.63	0.41
10:G:23:VAL:O	10:G:24:THR:C	2.63	0.41
12:I:3:GLN:O	12:I:4:TYR:CG	2.74	0.41
16:M:49:THR:HG22	16:M:51:ALA:N	2.34	0.41
18:O:17:ARG:O	18:O:18:PHE:HB3	2.20	0.41
18:O:54:ARG:O	18:O:58:MET:HG3	2.21	0.41
19:P:75:ARG:C	19:P:77:ALA:N	2.78	0.41
23:T:49:ALA:HA	23:T:92:LEU:HD21	2.03	0.41
1:A:131:C:H2'	1:A:132:C:H6	1.86	0.41
1:A:309:G:O2'	1:A:310:G:H5'	2.21	0.41
1:A:390:C:O2'	19:P:28:ARG:NH2	2.54	0.41
1:A:625:G:H2'	1:A:626:U:C6	2.55	0.41
1:A:738:C:OP1	9:F:92:LYS:HE3	2.20	0.41
1:A:807:A:H2'	1:A:808:C:H6	1.82	0.41
1:A:866:C:H2'	1:A:867:G:O4'	2.21	0.41
1:A:1054:C:C2'	1:A:1055:A:H5''	2.50	0.41
1:A:1069:C:O2'	1:A:1192:C:H1'	2.21	0.41
1:A:1145:C:HO2'	1:A:1146:A:H8	1.64	0.41
5:B:52:GLU:OE2	5:B:53:ARG:N	2.53	0.41
6:C:43:LEU:HD11	6:C:66:VAL:HG13	2.03	0.41
6:C:119:ARG:O	6:C:122:GLU:N	2.54	0.41
7:D:173:TRP:CD2	7:D:189:PRO:HB3	2.56	0.41
9:F:15:ASP:OD1	9:F:17:SER:HB2	2.21	0.41
10:G:138:LYS:O	10:G:142:GLU:HG3	2.20	0.41
12:I:9:ARG:HG2	12:I:14:VAL:HG22	2.02	0.41
12:I:17:VAL:CG1	12:I:81:ILE:HG12	2.50	0.41
14:K:12:ARG:O	14:K:13:GLN:O	2.38	0.41
14:K:26:ASN:O	14:K:27:ASN:CB	2.68	0.41
14:K:126:ARG:HH11	14:K:126:ARG:CB	2.33	0.41
16:M:27:LYS:HD3	16:M:27:LYS:HA	1.91	0.41
16:M:39:ILE:CD1	16:M:52:GLU:HB3	2.50	0.41
17:N:23:ARG:HA	17:N:30:ALA:HA	2.01	0.41
17:N:24:CYS:HB2	17:N:40:CYS:HB3	2.02	0.41
19:P:40:ASP:HA	19:P:41:PRO:HD3	1.90	0.41
1:A:35:G:O2'	15:L:118:SER:O	2.35	0.41
1:A:174:C:H2'	1:A:175:C:C6	2.51	0.41
1:A:356:A:O2'	1:A:357:G:H5'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:839:U:O2	1:A:839:U:C2'	2.68	0.41
1:A:904:C:H2'	1:A:905:U:O4'	2.21	0.41
1:A:965:A:O2'	1:A:966:G:OP2	2.31	0.41
1:A:1064:G:C8	1:A:1066:C:O2	2.74	0.41
1:A:1368:G:OP2	12:I:112:LYS:HD2	2.20	0.41
1:A:1527:C:O2'	1:A:1528:U:H5'	2.20	0.41
5:B:55:PHE:HA	5:B:58:ILE:CD1	2.46	0.41
5:B:105:PHE:C	5:B:107:THR:N	2.78	0.41
5:B:208:ILE:C	5:B:210:SER:N	2.78	0.41
7:D:7:PRO:HG2	7:D:10:ARG:HD2	2.02	0.41
7:D:12:CYS:HB3	7:D:33:MET:HG2	2.02	0.41
7:D:190:ASP:O	7:D:193:ASP:N	2.46	0.41
8:E:51:VAL:O	8:E:52:PRO:C	2.63	0.41
9:F:4:TYR:CE2	9:F:72:VAL:HG21	2.54	0.41
11:H:23:SER:C	11:H:24:THR:HG22	2.46	0.41
14:K:77:MET:HE1	14:K:80:VAL:HG13	2.03	0.41
17:N:3:ARG:NH1	17:N:6:LEU:HD12	2.35	0.41
18:O:57:LEU:HD12	18:O:57:LEU:HA	1.87	0.41
20:Q:97:SER:CB	20:Q:103:GLY:CA	2.99	0.41
1:A:124:G:C6	1:A:125:U:C4	3.08	0.41
1:A:463:A:C8	1:A:474:G:C8	3.08	0.41
1:A:497:A:O2'	1:A:498:U:OP1	2.28	0.41
1:A:532:A:N6	6:C:159:GLY:O	2.53	0.41
1:A:658:G:H2'	1:A:659:U:C6	2.55	0.41
1:A:1125:U:N3	13:J:5:ARG:NH2	2.66	0.41
1:A:1206:G:C6	1:A:1207:G:C6	3.09	0.41
1:A:1226:C:H6	16:M:103:THR:HG1	1.65	0.41
5:B:82:ARG:HG3	5:B:83:MET:N	2.35	0.41
5:B:115:LEU:O	5:B:119:GLU:HG3	2.21	0.41
5:B:178:ARG:NH2	11:H:68:ARG:NH2	2.69	0.41
6:C:5:ILE:O	6:C:5:ILE:HD12	2.21	0.41
7:D:7:PRO:CG	7:D:10:ARG:HD2	2.50	0.41
7:D:17:VAL:C	7:D:33:MET:HE2	2.45	0.41
8:E:76:ILE:HG13	8:E:77:PRO:CD	2.38	0.41
9:F:67:MET:HB2	9:F:68:PRO:CD	2.51	0.41
12:I:19:LEU:HB3	12:I:59:PHE:CE2	2.56	0.41
13:J:19:SER:C	13:J:21:GLN:N	2.77	0.41
13:J:50:ILE:HB	17:N:41:ARG:HE	1.86	0.41
16:M:32:GLU:OE1	16:M:64:TRP:HZ2	2.04	0.41
18:O:76:GLU:O	18:O:77:ARG:C	2.62	0.41
19:P:20:VAL:HG13	19:P:32:TYR:HB2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:S:41:VAL:HB	22:S:42:PRO:CD	2.51	0.41
23:T:50:GLU:N	23:T:99:LEU:HD12	2.34	0.41
1:A:260:G:H2'	1:A:261:U:C6	2.56	0.41
1:A:848:C:H2'	1:A:849:C:C6	2.56	0.41
1:A:848:C:O2'	1:A:849:C:H5'	2.21	0.41
1:A:926:G:H2'	1:A:1505:G:N3	2.36	0.41
1:A:1037:C:H2'	1:A:1038:C:O4'	2.20	0.41
1:A:1053:G:H5'	1:A:1054:C:H5'	2.03	0.41
1:A:1054:C:O2	1:A:1054:C:C2'	2.69	0.41
1:A:1106:G:OP1	6:C:172:ARG:HD3	2.21	0.41
1:A:1259:C:N4	1:A:1276:G:H1	2.15	0.41
1:A:1302:U:H5	16:M:17:VAL:HG21	1.85	0.41
1:A:1440:C:O2'	1:A:1441:G:H5'	2.21	0.41
5:B:27:LYS:C	5:B:29:ALA:N	2.79	0.41
6:C:29:TYR:HE1	13:J:65:LEU:HD11	1.85	0.41
7:D:148:VAL:HG23	7:D:181:MET:HB3	2.01	0.41
9:F:27:GLN:HA	9:F:27:GLN:HE21	1.86	0.41
9:F:28:ARG:O	9:F:29:ALA:C	2.64	0.41
10:G:149:ARG:HH11	10:G:149:ARG:HG3	1.86	0.41
11:H:119:LEU:CD1	11:H:124:ALA:HA	2.49	0.41
12:I:17:VAL:HG11	12:I:81:ILE:CG1	2.49	0.41
12:I:126:SER:O	12:I:127:LYS:C	2.64	0.41
13:J:4:ILE:HA	13:J:100:THR:HA	2.02	0.41
13:J:6:ILE:CG2	13:J:98:ILE:HG23	2.51	0.41
14:K:21:ILE:HA	14:K:30:VAL:HG12	2.03	0.41
14:K:82:VAL:HG12	14:K:83:ILE:N	2.35	0.41
15:L:27:LEU:C	15:L:29:GLY:H	2.27	0.41
15:L:37:CYS:O	15:L:79:GLU:O	2.39	0.41
16:M:8:GLU:O	16:M:9:ILE:CG2	2.63	0.41
17:N:4:LYS:O	17:N:7:ILE:HG12	2.21	0.41
17:N:37:PHE:C	17:N:39:LEU:H	2.27	0.41
18:O:17:ARG:NH1	18:O:17:ARG:CG	2.79	0.41
19:P:14:ASN:N	19:P:15:PRO:CD	2.83	0.41
20:Q:98:LEU:N	20:Q:103:GLY:HA2	2.35	0.41
23:T:56:MET:CE	23:T:88:VAL:HB	2.51	0.41
23:T:73:HIS:HB3	23:T:74:LYS:H	1.58	0.41
1:A:22:G:O2'	1:A:23:C:H5'	2.21	0.41
1:A:91:C:H2'	1:A:92:C:C6	2.56	0.41
1:A:190(L):U:N3	23:T:105:SER:HB2	2.36	0.41
1:A:556:C:C2'	1:A:557:G:H5'	2.51	0.41
1:A:983:A:H5'	1:A:984:C:OP2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1128:C:H42	1:A:1143:G:H1	1.68	0.41
1:A:1290:G:N2	12:I:70:LYS:HZ1	2.19	0.41
1:A:1406:U:OP2	25:A:1545:PAR:N24	2.54	0.41
5:B:122:PHE:HA	5:B:127:ILE:HG12	2.03	0.41
7:D:38:TYR:HB2	7:D:44:GLY:O	2.20	0.41
10:G:141:VAL:O	10:G:144:MET:N	2.53	0.41
14:K:20:TYR:O	14:K:30:VAL:HA	2.21	0.41
15:L:7:ILE:HD13	15:L:7:ILE:HA	1.95	0.41
23:T:51:GLU:HA	23:T:54:LYS:HD2	2.03	0.41
1:A:155:C:O2'	1:A:156:G:H5'	2.21	0.40
1:A:582:U:H2'	1:A:583:A:C8	2.56	0.40
1:A:716:A:N3	14:K:117:ASN:O	2.54	0.40
1:A:755:G:H1'	11:H:1:MET:HE3	2.02	0.40
1:A:1052:U:C2'	1:A:1055:A:OP1	2.65	0.40
1:A:1066:C:H5	1:A:1067:A:N6	2.19	0.40
1:A:1118:C:O5'	1:A:1118:C:H6	2.04	0.40
1:A:1193:G:N2	1:A:1194:U:C2	2.89	0.40
1:A:1258:G:O2'	1:A:1259:C:H5'	2.22	0.40
1:A:1325:C:O3'	24:V:17:THR:HG21	2.22	0.40
5:B:159:PRO:HG2	5:B:182:ILE:HG21	2.03	0.40
5:B:213:LEU:C	5:B:213:LEU:CD2	2.94	0.40
6:C:32:LEU:HD12	6:C:32:LEU:N	2.36	0.40
6:C:115:LEU:O	6:C:116:VAL:C	2.64	0.40
7:D:8:VAL:HG13	7:D:21:LEU:HD13	2.03	0.40
7:D:80:GLU:HA	7:D:80:GLU:OE2	2.21	0.40
10:G:31:MET:HG3	10:G:35:LYS:H	1.85	0.40
12:I:48:GLU:HA	12:I:51:ARG:HH11	1.85	0.40
17:N:18:VAL:CG2	17:N:19:ARG:N	2.79	0.40
1:A:619:U:H3	7:D:134:ASP:CG	2.30	0.40
1:A:664:G:H2'	1:A:666:G:OP1	2.21	0.40
1:A:833:U:H2'	1:A:834:C:C6	2.56	0.40
1:A:1053:G:H4'	1:A:1054:C:C4'	2.52	0.40
1:A:1221:G:O3'	22:S:77:THR:HG21	2.21	0.40
1:A:1372:U:H2'	1:A:1373:G:C5'	2.51	0.40
3:Y:39:U:H2'	3:Y:40:C:C6	2.56	0.40
7:D:30:LYS:O	7:D:32:ALA:N	2.54	0.40
7:D:41:GLY:O	7:D:43:HIS:N	2.54	0.40
13:J:38:ILE:O	13:J:71:LEU:N	2.54	0.40
13:J:66:ARG:HB3	13:J:66:ARG:HE	1.71	0.40
16:M:53:VAL:CG1	16:M:57:ARG:HH21	2.34	0.40
16:M:81:LEU:HD23	16:M:81:LEU:H	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:M:82:MET:CE	16:M:92:HIS:HB3	2.50	0.40
23:T:32:ALA:O	23:T:33:ILE:C	2.64	0.40
1:A:45:U:OP1	1:A:307:C:O2'	2.40	0.40
1:A:261:U:O2	1:A:263:A:C8	2.75	0.40
1:A:300:A:O5'	1:A:300:A:H8	2.04	0.40
1:A:551:U:H2'	1:A:552:U:C6	2.56	0.40
1:A:794:A:H2'	1:A:795:C:H6	1.84	0.40
1:A:922:G:N3	1:A:1398:A:H2	2.18	0.40
1:A:1310:G:OP1	16:M:80:ARG:NH2	2.54	0.40
1:A:1347:G:O2'	1:A:1348:U:C6	2.73	0.40
1:A:1388:C:H2'	1:A:1389:C:H6	1.86	0.40
5:B:145:LEU:C	5:B:147:LYS:N	2.80	0.40
5:B:212:GLN:O	5:B:213:LEU:C	2.64	0.40
6:C:101:LEU:O	6:C:101:LEU:CD2	2.70	0.40
7:D:61:LYS:HE2	7:D:62:GLN:HE21	1.84	0.40
8:E:144:THR:CG2	8:E:145:LYS:N	2.84	0.40
10:G:51:GLN:O	10:G:53:LYS:N	2.54	0.40
13:J:38:ILE:HB	13:J:71:LEU:HB3	2.03	0.40
13:J:71:LEU:CD1	13:J:73:ASP:HB2	2.51	0.40
14:K:22:HIS:HB3	14:K:29:ILE:HG12	2.03	0.40
15:L:97:ARG:HB2	15:L:98:TYR:CE1	2.55	0.40
16:M:23:TYR:C	16:M:25:ILE:H	2.27	0.40
20:Q:17:LYS:HA	20:Q:46:ASP:O	2.21	0.40
20:Q:84:LEU:O	20:Q:85:VAL:C	2.63	0.40
1:A:31:G:N2	1:A:48:C:OP1	2.42	0.40
1:A:51:A:H4'	1:A:52:G:C5'	2.51	0.40
1:A:109:A:H2'	1:A:326:G:H21	1.86	0.40
1:A:344:A:O2'	1:A:345:C:OP1	2.35	0.40
1:A:1161:C:H2'	1:A:1162:C:H6	1.83	0.40
1:A:1278:U:H5''	1:A:1279:A:H5'	2.03	0.40
1:A:1314:C:N3	1:A:1315:U:C4	2.89	0.40
1:A:1513:A:H2'	1:A:1514:C:C6	2.56	0.40
5:B:7:VAL:C	5:B:8:LYS:HG3	2.47	0.40
5:B:23:ARG:O	5:B:24:TRP:O	2.40	0.40
5:B:144:ARG:CG	5:B:145:LEU:N	2.84	0.40
6:C:29:TYR:CZ	17:N:54:PRO:HG2	2.56	0.40
7:D:91:SER:O	7:D:92:VAL:C	2.64	0.40
8:E:13:ILE:HA	8:E:29:GLY:O	2.20	0.40
13:J:64:GLU:HG2	17:N:59:ALA:CB	2.51	0.40
14:K:46:GLY:O	14:K:48:ILE:O	2.39	0.40
14:K:50:TYR:CD1	14:K:60:ALA:HB2	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:K:84:VAL:HB	14:K:110:ASP:HA	2.03	0.40
18:O:36:ILE:HA	18:O:59:MET:CE	2.51	0.40
20:Q:59:ILE:CD1	20:Q:73:VAL:HA	2.52	0.40
21:R:25:THR:O	21:R:26:LEU:CB	2.69	0.40
1:A:554:C:H2'	1:A:555:C:H6	1.85	0.40
1:A:922:G:H2'	1:A:923:A:O4'	2.22	0.40
1:A:977:A:C2'	1:A:978:A:H5''	2.52	0.40
1:A:1230:C:O2'	1:A:1231:G:H5'	2.22	0.40
1:A:1360:A:O2'	1:A:1361:G:H5'	2.22	0.40
5:B:15:VAL:HB	5:B:16:HIS:H	1.51	0.40
5:B:153:ARG:HH11	5:B:153:ARG:HG2	1.85	0.40
5:B:167:PRO:O	5:B:171:ALA:CA	2.70	0.40
8:E:11:ILE:HD13	8:E:11:ILE:HA	1.94	0.40
12:I:55:ALA:C	12:I:57:GLY:N	2.78	0.40
13:J:6:ILE:HD11	13:J:72:VAL:HG11	2.03	0.40
15:L:39:VAL:CG1	15:L:40:VAL:N	2.84	0.40
15:L:83:VAL:HG21	15:L:100:ILE:HG23	2.03	0.40
17:N:4:LYS:HA	17:N:7:ILE:CG1	2.51	0.40

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:J:79:ARG:CD	13:J:79:ARG:CD[8_665]	2.14	0.06

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
5	B	232/256 (91%)	145 (62%)	59 (25%)	28 (12%)	 
6	C	204/239 (85%)	126 (62%)	51 (25%)	27 (13%)	 

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	D	206/209 (99%)	160 (78%)	32 (16%)	14 (7%)	1	5
8	E	148/162 (91%)	132 (89%)	13 (9%)	3 (2%)	6	24
9	F	99/101 (98%)	82 (83%)	17 (17%)	0	100	100
10	G	153/156 (98%)	118 (77%)	28 (18%)	7 (5%)	2	11
11	H	136/138 (99%)	112 (82%)	20 (15%)	4 (3%)	3	18
12	I	125/128 (98%)	94 (75%)	18 (14%)	13 (10%)	0	2
13	J	96/105 (91%)	59 (62%)	17 (18%)	20 (21%)	0	0
14	K	117/129 (91%)	88 (75%)	20 (17%)	9 (8%)	1	4
15	L	122/135 (90%)	96 (79%)	13 (11%)	13 (11%)	0	2
16	M	116/126 (92%)	77 (66%)	23 (20%)	16 (14%)	0	1
17	N	58/61 (95%)	37 (64%)	11 (19%)	10 (17%)	0	0
18	O	86/89 (97%)	67 (78%)	17 (20%)	2 (2%)	5	21
19	P	81/88 (92%)	71 (88%)	9 (11%)	1 (1%)	10	34
20	Q	102/105 (97%)	78 (76%)	15 (15%)	9 (9%)	0	3
21	R	71/88 (81%)	59 (83%)	8 (11%)	4 (6%)	1	8
22	S	82/93 (88%)	53 (65%)	18 (22%)	11 (13%)	0	1
23	T	97/106 (92%)	61 (63%)	26 (27%)	10 (10%)	0	2
24	V	22/26 (85%)	15 (68%)	5 (23%)	2 (9%)	0	3
All	All	2353/2540 (93%)	1730 (74%)	420 (18%)	203 (9%)	0	3

All (203) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	B	8	LYS
5	B	15	VAL
5	B	16	HIS
5	B	17	PHE
5	B	23	ARG
5	B	24	TRP
5	B	95	GLN
5	B	188	ALA
6	C	15	THR
6	C	26	LYS
6	C	82	GLU
6	C	84	ILE
6	C	98	ASN

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Mol	Chain	Res	Type
6	C	100	ALA
6	C	179	ARG
7	D	29	PRO
7	D	36	ARG
7	D	88	VAL
11	H	91	ARG
12	I	41	VAL
12	I	88	TYR
12	I	94	ALA
12	I	117	HIS
13	J	32	ALA
13	J	34	VAL
13	J	54	PHE
13	J	86	MET
14	K	13	GLN
14	K	35	PRO
14	K	78	GLN
15	L	27	LEU
15	L	47	LYS
15	L	110	VAL
16	M	4	ILE
16	M	23	TYR
16	M	27	LYS
16	M	67	GLU
16	M	86	CYS
17	N	19	ARG
20	Q	80	GLY
20	Q	81	ARG
20	Q	98	LEU
21	R	58	LEU
22	S	6	LYS
22	S	14	HIS
22	S	67	VAL
23	T	98	PRO
5	B	20	GLU
5	B	39	ILE
5	B	60	ASP
5	B	83	MET
5	B	123	ALA
5	B	190	THR
5	B	195	ASP
5	B	227	GLY

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Mol	Chain	Res	Type
6	C	16	ARG
6	C	39	ILE
6	C	47	LEU
6	C	101	LEU
6	C	171	GLY
6	C	189	ALA
7	D	3	ARG
7	D	4	TYR
7	D	42	GLN
7	D	164	ALA
8	E	78	HIS
8	E	107	ARG
8	E	108	ALA
10	G	7	ALA
10	G	63	LYS
10	G	155	ARG
11	H	24	THR
11	H	105	ARG
12	I	38	GLN
12	I	46	ALA
12	I	58	ARG
12	I	127	LYS
13	J	23	ILE
13	J	33	GLN
13	J	36	GLY
13	J	60	ARG
13	J	72	VAL
13	J	79	ARG
14	K	15	ALA
14	K	91	ARG
15	L	29	GLY
15	L	30	ALA
15	L	48	PRO
15	L	51	ALA
15	L	73	GLU
15	L	79	GLU
15	L	121	GLY
16	M	3	ARG
16	M	6	GLY
16	M	28	ALA
16	M	63	THR
16	M	85	GLY

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Mol	Chain	Res	Type
17	N	15	LYS
17	N	32	SER
17	N	36	PHE
19	P	10	GLY
20	Q	96	GLN
20	Q	97	SER
21	R	26	LEU
21	R	48	GLY
22	S	8	GLY
22	S	43	GLU
22	S	68	GLY
22	S	83	HIS
22	S	84	GLY
23	T	50	GLU
23	T	73	HIS
23	T	74	LYS
23	T	86	ARG
23	T	101	GLY
23	T	102	GLY
24	V	9	ARG
5	B	9	GLU
5	B	21	ARG
5	B	136	VAL
5	B	204	ASN
6	C	20	SER
6	C	127	ARG
6	C	146	ALA
6	C	154	SER
6	C	156	ARG
6	C	206	GLU
7	D	5	ILE
7	D	30	LYS
7	D	150	GLU
10	G	67	GLU
12	I	43	ALA
13	J	27	ALA
13	J	55	LYS
13	J	61	GLU
13	J	90	LEU
14	K	27	ASN
14	K	117	ASN
15	L	105	TYR

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Mol	Chain	Res	Type
16	M	21	TYR
16	M	24	GLY
16	M	36	LYS
16	M	109	THR
17	N	11	LYS
17	N	14	PRO
17	N	23	ARG
17	N	37	PHE
21	R	87	ARG
22	S	9	VAL
23	T	39	LYS
5	B	113	HIS
5	B	177	ALA
6	C	67	THR
6	C	108	ASN
6	C	168	ALA
10	G	109	ASN
12	I	119	ALA
13	J	4	ILE
13	J	17	ASP
13	J	40	LEU
17	N	26	ARG
18	O	85	LEU
20	Q	12	SER
22	S	16	LEU
22	S	30	LEU
5	B	59	GLU
5	B	232	PRO
6	C	119	ARG
6	C	181	ASN
7	D	22	LYS
7	D	31	CYS
7	D	35	ARG
10	G	37	ASN
12	I	45	ALA
12	I	105	ASP
13	J	73	ASP
16	M	5	ALA
18	O	86	GLY
20	Q	95	TYR
20	Q	103	GLY
23	T	38	LYS

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Mol	Chain	Res	Type
5	B	48	MET
5	B	79	ASP
5	B	207	ALA
6	C	4	LYS
10	G	82	GLY
12	I	44	VAL
13	J	76	ASN
14	K	48	ILE
14	K	70	LYS
15	L	116	SER
16	M	9	ILE
20	Q	34	LYS
23	T	97	ALA
11	H	137	VAL
17	N	25	VAL
7	D	92	VAL
5	B	130	ARG
6	C	14	ILE
13	J	39	PRO
6	C	55	VAL
24	V	22	ARG
15	L	40	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	B	202/220 (92%)	179 (89%)	23 (11%)	5	22
6	C	160/188 (85%)	142 (89%)	18 (11%)	5	22
7	D	180/181 (99%)	169 (94%)	11 (6%)	17	44
8	E	115/123 (94%)	95 (83%)	20 (17%)	2	9
9	F	90/90 (100%)	80 (89%)	10 (11%)	6	22
10	G	126/127 (99%)	116 (92%)	10 (8%)	11	35
11	H	119/119 (100%)	109 (92%)	10 (8%)	10	33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	I	98/99 (99%)	90 (92%)	8 (8%)	10	34
13	J	87/92 (95%)	81 (93%)	6 (7%)	14	40
14	K	90/99 (91%)	85 (94%)	5 (6%)	19	47
15	L	104/111 (94%)	95 (91%)	9 (9%)	9	32
16	M	94/101 (93%)	86 (92%)	8 (8%)	10	33
17	N	49/50 (98%)	46 (94%)	3 (6%)	17	44
18	O	79/80 (99%)	70 (89%)	9 (11%)	5	22
19	P	72/74 (97%)	67 (93%)	5 (7%)	14	40
20	Q	96/97 (99%)	89 (93%)	7 (7%)	13	38
21	R	64/77 (83%)	62 (97%)	2 (3%)	35	62
22	S	73/80 (91%)	64 (88%)	9 (12%)	4	19
23	T	76/82 (93%)	68 (90%)	8 (10%)	6	25
24	V	19/21 (90%)	19 (100%)	0	100	100
All	All	1993/2111 (94%)	1812 (91%)	181 (9%)	9	30

All (181) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	B	8	LYS
5	B	9	GLU
5	B	15	VAL
5	B	21	ARG
5	B	23	ARG
5	B	25	ASN
5	B	87	ARG
5	B	90	MET
5	B	92	TYR
5	B	102	LEU
5	B	112	VAL
5	B	144	ARG
5	B	156	LYS
5	B	162	ILE
5	B	169	LYS
5	B	170	GLU
5	B	178	ARG
5	B	187	LEU
5	B	190	THR

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Mol	Chain	Res	Type
5	B	223	ILE
5	B	229	VAL
5	B	231	GLU
5	B	232	PRO
6	C	5	ILE
6	C	26	LYS
6	C	44	GLU
6	C	47	LEU
6	C	52	LEU
6	C	68	VAL
6	C	70	VAL
6	C	91	LEU
6	C	94	LEU
6	C	95	THR
6	C	139	GLN
6	C	165	THR
6	C	166	GLU
6	C	167	TRP
6	C	172	ARG
6	C	188	LEU
6	C	190	ARG
6	C	196	LEU
7	D	15	GLU
7	D	26	CYS
7	D	29	PRO
7	D	96	LEU
7	D	122	ARG
7	D	132	ARG
7	D	146	ILE
7	D	157	LEU
7	D	162	LEU
7	D	199	ASN
7	D	201	GLN
8	E	10	MET
8	E	12	LEU
8	E	16	THR
8	E	18	ARG
8	E	24	ARG
8	E	31	LEU
8	E	38	GLN
8	E	41	VAL
8	E	43	LEU

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Mol	Chain	Res	Type
8	E	52	PRO
8	E	55	VAL
8	E	68	GLU
8	E	80	ILE
8	E	89	ILE
8	E	120	THR
8	E	126	ARG
8	E	131	ILE
8	E	137	GLU
8	E	144	THR
8	E	150	ARG
9	F	1	MET
9	F	10	LEU
9	F	24	GLU
9	F	63	TYR
9	F	65	VAL
9	F	69	GLU
9	F	75	LEU
9	F	87	ARG
9	F	92	LYS
9	F	94	GLN
10	G	8	GLU
10	G	11	GLN
10	G	16	LEU
10	G	37	ASN
10	G	38	LEU
10	G	69	VAL
10	G	113	GLU
10	G	135	VAL
10	G	136	LYS
10	G	149	ARG
11	H	24	THR
11	H	26	VAL
11	H	39	LEU
11	H	63	LEU
11	H	85	ARG
11	H	91	ARG
11	H	105	ARG
11	H	112	LEU
11	H	119	LEU
11	H	127	LEU
12	I	2	GLU

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Mol	Chain	Res	Type
12	I	26	VAL
12	I	38	GLN
12	I	41	VAL
12	I	79	LEU
12	I	111	ARG
12	I	118	LYS
12	I	121	ARG
13	J	13	HIS
13	J	29	ARG
13	J	38	ILE
13	J	64	GLU
13	J	71	LEU
13	J	83	GLU
14	K	24	SER
14	K	29	ILE
14	K	35	PRO
14	K	54	ARG
14	K	80	VAL
15	L	33	ARG
15	L	43	VAL
15	L	48	PRO
15	L	53	ARG
15	L	55	VAL
15	L	82	VAL
15	L	85	ILE
15	L	93	LEU
15	L	126	LYS
16	M	9	ILE
16	M	44	ARG
16	M	56	LEU
16	M	70	LEU
16	M	81	LEU
16	M	88	ARG
16	M	109	THR
16	M	115	LYS
17	N	6	LEU
17	N	44	LEU
17	N	58	LYS
18	O	6	GLU
18	O	7	GLU
18	O	31	LEU
18	O	34	LEU

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Mol	Chain	Res	Type
18	O	39	LEU
18	O	57	LEU
18	O	67	LEU
18	O	70	LEU
18	O	81	LEU
19	P	2	VAL
19	P	28	ARG
19	P	53	VAL
19	P	62	VAL
19	P	81	ARG
20	Q	34	LYS
20	Q	38	ARG
20	Q	60	ILE
20	Q	74	LEU
20	Q	76	LEU
20	Q	98	LEU
20	Q	104	LYS
21	R	42	ARG
21	R	69	THR
22	S	12	ASP
22	S	14	HIS
22	S	15	LEU
22	S	36	ARG
22	S	43	GLU
22	S	62	ILE
22	S	65	ASN
22	S	80	TYR
22	S	83	HIS
23	T	10	LEU
23	T	13	LEU
23	T	39	LYS
23	T	42	GLN
23	T	57	ARG
23	T	75	ASN
23	T	84	LEU
23	T	98	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (59) such sidechains are listed below:

Mol	Chain	Res	Type
5	B	25	ASN
5	B	40	HIS

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Mol	Chain	Res	Type
5	B	146	GLN
5	B	204	ASN
6	C	3	ASN
6	C	31	HIS
6	C	37	GLN
6	C	108	ASN
6	C	110	ASN
6	C	123	GLN
6	C	139	GLN
6	C	176	HIS
7	D	42	GLN
7	D	62	GLN
7	D	161	ASN
7	D	199	ASN
8	E	65	ASN
8	E	73	ASN
9	F	7	ASN
9	F	18	GLN
9	F	27	GLN
9	F	32	ASN
9	F	73	ASN
9	F	94	GLN
9	F	100	ASN
10	G	37	ASN
10	G	51	GLN
10	G	106	GLN
10	G	122	HIS
12	I	23	ASN
12	I	31	GLN
12	I	73	GLN
13	J	56	HIS
13	J	76	ASN
13	J	78	ASN
14	K	38	ASN
14	K	62	GLN
14	K	116	HIS
14	K	117	ASN
15	L	49	ASN
15	L	75	HIS
16	M	12	ASN
16	M	40	ASN
16	M	77	ASN

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Mol	Chain	Res	Type
17	N	52	GLN
18	O	13	GLN
18	O	37	ASN
18	O	46	HIS
19	P	16	HIS
19	P	76	GLN
20	Q	16	GLN
20	Q	96	GLN
21	R	36	ASN
22	S	23	ASN
22	S	47	HIS
22	S	56	GLN
22	S	83	HIS
23	T	16	HIS
23	T	90	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1506/1522 (98%)	201 (13%)	67 (4%)
2	X	5/6 (83%)	0	0
3	Y	14/15 (93%)	1 (7%)	0
4	Z	3/4 (75%)	1 (33%)	0
All	All	1528/1547 (98%)	203 (13%)	67 (4%)

All (203) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	8	A
1	A	9	G
1	A	31	G
1	A	32	A
1	A	39	G
1	A	47	C
1	A	48	C
1	A	49	U
1	A	51	A
1	A	61	G
1	A	81	U
1	A	82	U
1	A	101	A

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Mol	Chain	Res	Type
1	A	116	A
1	A	120	A
1	A	121	C
1	A	129(A)	G
1	A	130	A
1	A	131	C
1	A	144	G
1	A	163	C
1	A	181	G
1	A	182	U
1	A	195	A
1	A	197	A
1	A	198	G
1	A	202	U
1	A	203	U
1	A	204	U
1	A	216	G
1	A	244	U
1	A	247	G
1	A	251	G
1	A	252	U
1	A	266	G
1	A	267	C
1	A	280	C
1	A	282	A
1	A	289	G
1	A	321	A
1	A	328	C
1	A	329	A
1	A	332	G
1	A	344	A
1	A	345	C
1	A	352	C
1	A	353	A
1	A	354	G
1	A	367	U
1	A	373	A
1	A	397	A
1	A	398	C
1	A	412	A
1	A	413	G
1	A	421	U

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Mol	Chain	Res	Type
1	A	428	G
1	A	429	U
1	A	439	A
1	A	452	A
1	A	461	C
1	A	462	G
1	A	484	G
1	A	485	G
1	A	497	A
1	A	498	U
1	A	509	A
1	A	510	A
1	A	511	C
1	A	518	C
1	A	527	G
1	A	532	A
1	A	533	A
1	A	534	U
1	A	547	A
1	A	559	A
1	A	560	U
1	A	561	U
1	A	562	C
1	A	572	A
1	A	573	A
1	A	576	G
1	A	577	G
1	A	653	A
1	A	665	A
1	A	688	G
1	A	701	C
1	A	702	A
1	A	718	G
1	A	723	U
1	A	733	A
1	A	749	C
1	A	755	G
1	A	777	A
1	A	793	U
1	A	794	A
1	A	813	U
1	A	815	A

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Mol	Chain	Res	Type
1	A	817	C
1	A	819	A
1	A	828	A
1	A	839	U
1	A	840	C
1	A	841	U
1	A	902	G
1	A	914	A
1	A	927	G
1	A	934	C
1	A	935	A
1	A	945	G
1	A	960	U
1	A	961	U
1	A	965	A
1	A	966	G
1	A	968	A
1	A	969	A
1	A	971	G
1	A	974	A
1	A	975	A
1	A	976	G
1	A	977	A
1	A	991	U
1	A	992	U
1	A	993	G
1	A	994	A
1	A	1002	G
1	A	1024	G
1	A	1026	G
1	A	1050	G
1	A	1053	G
1	A	1054	C
1	A	1055	A
1	A	1065	U
1	A	1066	C
1	A	1068	G
1	A	1085	U
1	A	1086	U
1	A	1094	G
1	A	1095	U
1	A	1101	A

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Mol	Chain	Res	Type
1	A	1124	G
1	A	1125	U
1	A	1129	C
1	A	1130	A
1	A	1131	G
1	A	1136	U
1	A	1137	C
1	A	1138	G
1	A	1139	G
1	A	1146	A
1	A	1152	A
1	A	1157	A
1	A	1159	U
1	A	1183	A
1	A	1184	G
1	A	1191	A
1	A	1196	U
1	A	1197	G
1	A	1202	G
1	A	1212	U
1	A	1214	C
1	A	1226	C
1	A	1227	A
1	A	1257	U
1	A	1258	G
1	A	1279	A
1	A	1280	A
1	A	1281	U
1	A	1282	C
1	A	1285	A
1	A	1286	A
1	A	1287	A
1	A	1300	G
1	A	1301	U
1	A	1302	U
1	A	1303	C
1	A	1305	G
1	A	1320	C
1	A	1338	G
1	A	1346	A
1	A	1347	G
1	A	1348	U

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Mol	Chain	Res	Type
1	A	1362	C
1	A	1379	G
1	A	1381	U
1	A	1398	A
1	A	1443	G
1	A	1446	A
1	A	1447	G
1	A	1452	C
1	A	1487	G
1	A	1492	A
1	A	1497	G
1	A	1499	A
1	A	1502	A
1	A	1503	A
1	A	1504	G
1	A	1506	U
1	A	1517	G
1	A	1520	G
1	A	1529	G
1	A	1530	G
3	Y	34	G
4	Z	2	U

All (67) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	7	G
1	A	30	U
1	A	48	C
1	A	60	A
1	A	115	G
1	A	119	A
1	A	129(A)	G
1	A	181	G
1	A	197	A
1	A	202	U
1	A	243	A
1	A	250	A
1	A	251	G
1	A	279	A
1	A	281	G
1	A	328	C

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Mol	Chain	Res	Type
1	A	344	A
1	A	351	G
1	A	353	A
1	A	366	C
1	A	372	C
1	A	428	G
1	A	438	G
1	A	484	G
1	A	496	A
1	A	497	A
1	A	509	A
1	A	533	A
1	A	559	A
1	A	560	U
1	A	575	G
1	A	687	A
1	A	701	C
1	A	748	C
1	A	793	U
1	A	812	C
1	A	819	A
1	A	913	A
1	A	960	U
1	A	965	A
1	A	975	A
1	A	992	U
1	A	993	G
1	A	1049	U
1	A	1065	U
1	A	1067	A
1	A	1085	U
1	A	1145	C
1	A	1182	G
1	A	1183	A
1	A	1190	G
1	A	1196	U
1	A	1201	A
1	A	1226	C
1	A	1256	A
1	A	1257	U
1	A	1281	U
1	A	1285	A

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Mol	Chain	Res	Type
1	A	1300	G
1	A	1301	U
1	A	1302	U
1	A	1346	A
1	A	1347	G
1	A	1380	U
1	A	1451	A
1	A	1498	U
1	A	1528	U

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 128 ligands modelled in this entry, 127 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
25	PAR	A	1545	-	44,45,45	1.32	6 (13%)	63,67,67	1.19	6 (9%)

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
25	PAR	A	1545	-	-	5/18/94/94	0/4/4/4

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	A	1545	PAR	O54-C14	3.10	1.49	1.41
25	A	1545	PAR	C11-C21	2.89	1.58	1.52
25	A	1545	PAR	C52-C42	2.41	1.57	1.52
25	A	1545	PAR	C31-C21	2.34	1.56	1.53
25	A	1545	PAR	O51-C11	2.19	1.47	1.41
25	A	1545	PAR	O33-C14	2.16	1.47	1.41

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	A	1545	PAR	O54-C54-C64	3.59	112.96	106.07
25	A	1545	PAR	O33-C14-C24	3.25	113.39	108.08
25	A	1545	PAR	O11-C11-C21	3.16	113.24	108.08
25	A	1545	PAR	C14-O54-C54	2.88	119.35	113.72
25	A	1545	PAR	O52-C13-O43	-2.38	108.93	111.37
25	A	1545	PAR	C22-C32-C42	2.19	114.87	109.50

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
25	A	1545	PAR	C44-C54-C64-N64
25	A	1545	PAR	O54-C54-C64-N64
25	A	1545	PAR	C33-C43-C53-O53
25	A	1545	PAR	O43-C43-C53-O53
25	A	1545	PAR	O51-C11-O11-C42

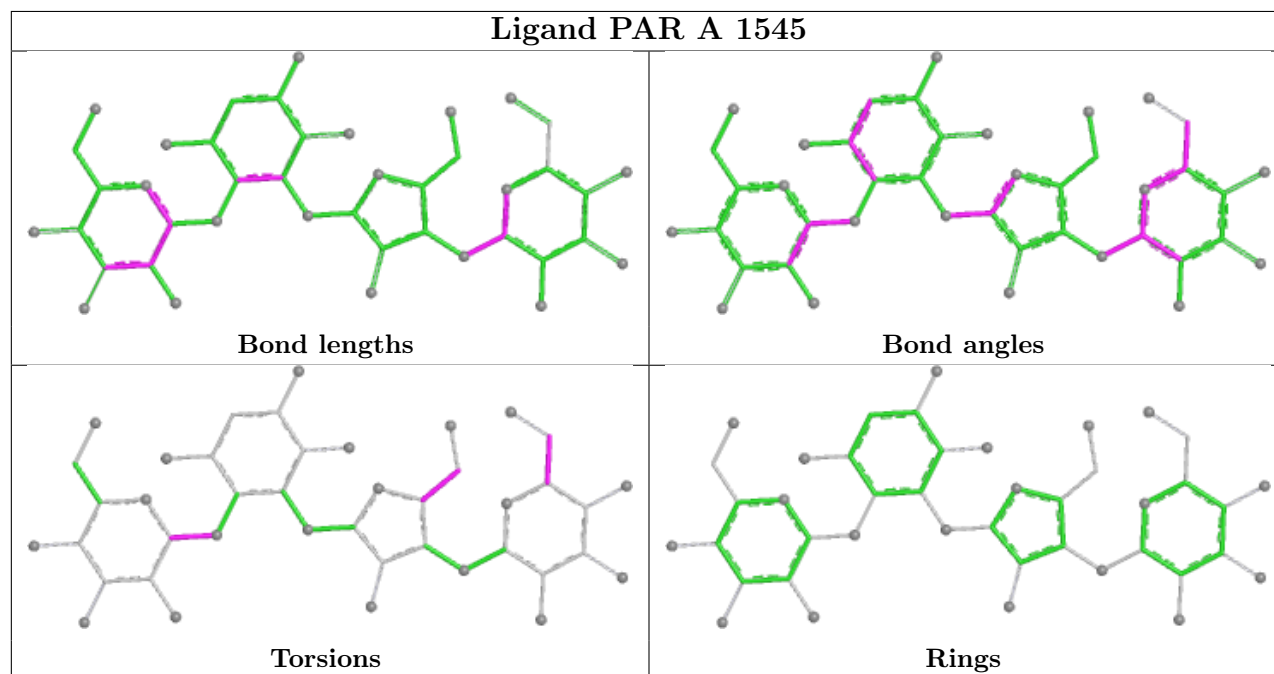
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
25	A	1545	PAR	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring

in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
7	D	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	D	198:VAL	C	199:ASN	N	1.15

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	1507/1522 (99%)	0.72	194 (12%) 7 4	22, 56, 140, 201	0
2	X	6/6 (100%)	2.47	3 (50%) 0 0	47, 59, 141, 164	0
3	Y	15/15 (100%)	1.17	4 (26%) 1 1	58, 100, 200, 201	0
4	Z	4/4 (100%)	1.98	2 (50%) 0 0	69, 71, 82, 141	0
5	B	234/256 (91%)	1.57	77 (32%) 1 1	30, 94, 172, 201	0
6	C	206/239 (86%)	1.65	71 (34%) 1 1	38, 81, 170, 192	0
7	D	208/209 (99%)	0.95	40 (19%) 3 2	25, 62, 145, 181	0
8	E	150/162 (92%)	0.56	14 (9%) 14 8	21, 47, 109, 164	0
9	F	101/101 (100%)	1.19	14 (13%) 6 3	45, 90, 145, 176	0
10	G	155/156 (99%)	1.36	34 (21%) 2 1	38, 73, 150, 191	0
11	H	138/138 (100%)	0.39	14 (10%) 12 6	17, 43, 103, 150	0
12	I	127/128 (99%)	1.91	56 (44%) 0 0	34, 89, 151, 180	0
13	J	98/105 (93%)	2.87	65 (66%) 0 0	36, 114, 185, 201	0
14	K	119/129 (92%)	1.44	25 (21%) 2 1	24, 60, 123, 201	0
15	L	124/135 (91%)	1.14	26 (20%) 2 1	16, 55, 125, 192	0
16	M	118/126 (93%)	1.26	32 (27%) 1 1	36, 74, 131, 165	0
17	N	60/61 (98%)	2.01	25 (41%) 0 0	44, 76, 139, 194	0
18	O	88/89 (98%)	0.73	8 (9%) 15 8	26, 56, 137, 199	0
19	P	83/88 (94%)	0.78	8 (9%) 13 7	22, 47, 77, 158	0
20	Q	104/105 (99%)	0.96	15 (14%) 6 3	13, 45, 137, 201	0
21	R	73/88 (82%)	1.18	19 (26%) 1 1	33, 71, 164, 201	0
22	S	84/93 (90%)	1.69	30 (35%) 1 1	54, 100, 165, 201	0
23	T	99/106 (93%)	1.53	29 (29%) 1 1	25, 56, 127, 198	0
24	V	24/26 (92%)	1.55	8 (33%) 1 1	42, 61, 113, 188	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
All	All	3925/4087 (96%)	1.08	813 (20%) 2 1	13, 63, 153, 201	0

All (813) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
14	K	128	ALA	22.1
14	K	129	SER	20.7
24	V	25	LYS	10.9
10	G	13	GLN	10.3
1	A	532	A	10.2
23	T	9	ASN	10.0
9	F	95	GLU	9.7
13	J	73	ASP	9.6
14	K	127	LYS	9.6
15	L	128	ALA	9.5
22	S	3	ARG	9.2
10	G	5	ARG	9.0
12	I	128	ARG	9.0
15	L	127	GLU	8.8
22	S	2	PRO	7.9
12	I	105	ASP	7.8
6	C	161	GLU	7.8
10	G	11	GLN	7.6
14	K	126	ARG	7.4
15	L	19	ARG	7.4
6	C	162	GLN	7.2
1	A	82	U	7.2
20	Q	101	ARG	6.9
20	Q	103	GLY	6.7
5	B	7	VAL	6.7
10	G	143	ARG	6.5
20	Q	105	ALA	6.4
12	I	125	TYR	6.4
1	A	202	U	6.4
13	J	100	THR	6.4
13	J	72	VAL	6.4
23	T	101	GLY	6.3
13	J	64	GLU	6.3
16	M	9	ILE	6.3
1	A	1397	C	6.2
22	S	4	SER	6.2
13	J	5	ARG	6.2

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Mol	Chain	Res	Type	RSRZ
17	N	17	LYS	6.2
7	D	31	CYS	6.2
5	B	17	PHE	5.9
20	Q	13	ASP	5.9
1	A	1129	C	5.9
13	J	7	LYS	5.9
13	J	99	LYS	5.9
10	G	8	GLU	5.9
20	Q	102	GLY	5.8
1	A	1002	G	5.7
10	G	60	LYS	5.7
16	M	7	VAL	5.7
10	G	156	TRP	5.7
10	G	14	PRO	5.6
20	Q	96	GLN	5.6
6	C	207	VAL	5.6
12	I	119	ALA	5.5
14	K	51	LYS	5.5
1	A	1281	U	5.5
13	J	10	GLY	5.4
18	O	89	GLY	5.4
1	A	461	C	5.4
5	B	148	TYR	5.4
10	G	140	ASP	5.4
1	A	631	G	5.4
20	Q	104	LYS	5.4
23	T	98	PRO	5.3
6	C	193	TYR	5.3
1	A	1531	A	5.3
14	K	11	LYS	5.3
8	E	5	ASP	5.2
15	L	17	LYS	5.2
1	A	1030(A)	G	5.2
9	F	47	ARG	5.2
13	J	93	GLY	5.2
17	N	22	THR	5.1
7	D	26	CYS	5.1
8	E	154	GLY	5.1
1	A	1125	U	5.1
7	D	141	ARG	5.1
6	C	15	THR	5.1
13	J	46	ARG	5.1

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Mol	Chain	Res	Type	RSRZ
6	C	45	LYS	5.0
13	J	65	LEU	5.0
1	A	1126	U	4.9
10	G	81	GLY	4.9
13	J	79	ARG	4.9
5	B	78	GLN	4.9
5	B	96	ARG	4.9
13	J	89	ASP	4.9
1	A	265	G	4.9
7	D	159	ARG	4.9
17	N	57	ARG	4.9
23	T	94	ALA	4.9
10	G	12	LEU	4.9
5	B	44	LEU	4.8
5	B	35	GLU	4.8
1	A	1278	U	4.8
16	M	87	TYR	4.8
6	C	167	TRP	4.8
13	J	59	SER	4.8
2	X	1	C	4.8
13	J	6	ILE	4.8
10	G	37	ASN	4.7
7	D	187	ARG	4.7
12	I	103	THR	4.7
17	N	12	ARG	4.7
8	E	22	GLY	4.7
7	D	201	GLN	4.7
1	A	1019	C	4.7
1	A	1533	C	4.7
1	A	264	U	4.6
8	E	50	GLU	4.6
22	S	84	GLY	4.6
13	J	34	VAL	4.6
15	L	18	VAL	4.6
5	B	16	HIS	4.6
9	F	94	GLN	4.6
13	J	88	LEU	4.6
16	M	11	ARG	4.5
13	J	45	ARG	4.5
1	A	953	G	4.5
6	C	28	GLN	4.5
11	H	102	ARG	4.5

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Mol	Chain	Res	Type	RSRZ
23	T	99	LEU	4.5
10	G	33	ASP	4.4
13	J	62	HIS	4.4
1	A	81	U	4.4
10	G	155	ARG	4.4
7	D	9	CYS	4.4
13	J	80	LYS	4.4
1	A	1124	G	4.4
7	D	19	LEU	4.4
13	J	3	LYS	4.4
23	T	73	HIS	4.4
16	M	50	GLU	4.4
6	C	205	GLY	4.4
23	T	74	LYS	4.4
13	J	74	ILE	4.4
17	N	61	TRP	4.4
4	Z	4	U	4.4
6	C	143	GLU	4.3
1	A	733	A	4.3
13	J	87	THR	4.3
12	I	100	GLY	4.3
23	T	12	ALA	4.3
16	M	42	ALA	4.3
23	T	84	LEU	4.3
1	A	1256	A	4.3
5	B	152	PHE	4.3
7	D	3	ARG	4.3
9	F	77	ARG	4.3
12	I	57	GLY	4.3
1	A	1321	C	4.2
6	C	178	LEU	4.2
12	I	106	ALA	4.2
20	Q	14	LYS	4.2
5	B	238	LEU	4.2
14	K	12	ARG	4.2
22	S	5	LEU	4.2
22	S	37	ARG	4.2
7	D	23	GLY	4.2
1	A	1024	G	4.2
12	I	65	VAL	4.2
23	T	16	HIS	4.2
13	J	35	SER	4.2

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Mol	Chain	Res	Type	RSRZ
6	C	27	LYS	4.2
6	C	192	THR	4.2
1	A	1257	U	4.1
1	A	1003(A)	G	4.1
1	A	1196	U	4.1
13	J	42	THR	4.1
1	A	1280	A	4.1
7	D	131	ARG	4.1
6	C	154	SER	4.1
11	H	98	LYS	4.1
7	D	151	LYS	4.0
1	A	1145	C	4.0
5	B	147	LYS	4.0
5	B	95	GLN	4.0
16	M	41	PRO	4.0
5	B	227	GLY	4.0
10	G	89	MET	4.0
5	B	14	GLY	4.0
21	R	46	GLU	4.0
1	A	630	G	4.0
16	M	104	ARG	4.0
1	A	204	U	3.9
6	C	190	ARG	3.9
1	A	980	C	3.9
12	I	16	ARG	3.9
5	B	11	LEU	3.9
16	M	40	ASN	3.9
13	J	75	ILE	3.9
13	J	82	ILE	3.9
13	J	4	ILE	3.9
15	L	20	LYS	3.9
22	S	34	TRP	3.9
17	N	2	ALA	3.9
16	M	8	GLU	3.9
1	A	965	A	3.8
1	A	1030(B)	C	3.8
1	A	1003	G	3.8
2	X	3	U	3.8
14	K	125	PHE	3.8
2	X	2	U	3.8
17	N	60	SER	3.8
20	Q	100	LYS	3.8

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Mol	Chain	Res	Type	RSRZ
1	A	412	A	3.8
5	B	214	ILE	3.8
23	T	83	ARG	3.8
1	A	267	C	3.7
13	J	12	ASP	3.7
14	K	52	GLY	3.7
22	S	8	GLY	3.7
15	L	26	ALA	3.7
15	L	47	LYS	3.7
13	J	86	MET	3.7
6	C	52	LEU	3.7
12	I	102	LEU	3.7
13	J	96	ILE	3.7
6	C	80	GLY	3.7
22	S	33	THR	3.7
22	S	69	HIS	3.7
10	G	79	ARG	3.6
23	T	86	ARG	3.6
6	C	2	GLY	3.6
21	R	16	PRO	3.6
5	B	137	ARG	3.6
6	C	127	ARG	3.6
12	I	42	ARG	3.6
11	H	1	MET	3.6
6	C	159	GLY	3.6
16	M	119	GLY	3.6
6	C	135	LYS	3.6
23	T	100	ILE	3.6
17	N	13	THR	3.6
10	G	110	GLN	3.5
1	A	1322	C	3.5
1	A	1020	U	3.5
10	G	4	ARG	3.5
8	E	20	GLN	3.5
10	G	106	GLN	3.5
23	T	54	LYS	3.5
1	A	263	A	3.5
8	E	119	LEU	3.5
5	B	72	GLY	3.5
5	B	106	LYS	3.5
22	S	28	LYS	3.5
13	J	97	GLU	3.5

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Mol	Chain	Res	Type	RSRZ
15	L	16	GLU	3.5
22	S	73	GLU	3.5
1	A	1163	C	3.5
22	S	25	LYS	3.5
5	B	150	SER	3.5
6	C	158	GLY	3.5
17	N	59	ALA	3.5
6	C	102	ASN	3.5
22	S	85	LYS	3.5
1	A	1178	G	3.5
1	A	1198	G	3.5
15	L	89	ARG	3.5
6	C	74	GLY	3.4
17	N	51	GLY	3.4
18	O	88	ARG	3.4
14	K	111	ASP	3.4
17	N	8	GLU	3.4
23	T	50	GLU	3.4
13	J	37	PRO	3.4
15	L	79	GLU	3.4
17	N	6	LEU	3.4
6	C	160	ALA	3.4
12	I	120	ARG	3.4
9	F	57	GLN	3.4
1	A	1258	G	3.4
10	G	146	GLU	3.4
21	R	78	LEU	3.4
12	I	66	ARG	3.4
5	B	133	LYS	3.4
22	S	6	LYS	3.4
12	I	14	VAL	3.4
1	A	954	G	3.4
23	T	95	ALA	3.4
10	G	36	LYS	3.4
1	A	663	A	3.3
1	A	1039	C	3.3
12	I	51	ARG	3.3
13	J	90	LEU	3.3
6	C	206	GLU	3.3
19	P	47	ASP	3.3
12	I	113	LYS	3.3
6	C	104	GLN	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	1057	G	3.3
6	C	131	ARG	3.3
1	A	1030(D)	A	3.3
21	R	72	ARG	3.3
13	J	57	LYS	3.3
14	K	124	LYS	3.3
5	B	48	MET	3.3
1	A	1446	A	3.3
1	A	164	U	3.3
1	A	1162	C	3.3
12	I	56	LEU	3.3
8	E	73	ASN	3.3
17	N	4	LYS	3.3
21	R	84	LYS	3.3
7	D	192	GLU	3.3
22	S	35	SER	3.3
1	A	1144	G	3.3
11	H	22	GLU	3.3
5	B	130	ARG	3.2
6	C	42	LEU	3.2
23	T	13	LEU	3.2
5	B	240	GLN	3.2
5	B	80	ILE	3.2
7	D	49	ARG	3.2
12	I	97	LYS	3.2
5	B	79	ASP	3.2
13	J	32	ALA	3.2
6	C	79	ARG	3.2
1	A	992	U	3.2
1	A	476	G	3.2
3	Y	42	C	3.2
6	C	60	ALA	3.2
17	N	29	ARG	3.2
9	F	24	GLU	3.2
11	H	2	LEU	3.2
13	J	66	ARG	3.2
15	L	92	ASP	3.2
23	T	106	ALA	3.2
13	J	54	PHE	3.2
7	D	24	GLU	3.1
1	A	1204	A	3.1
17	N	9	LYS	3.1

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Mol	Chain	Res	Type	RSRZ
7	D	190	ASP	3.1
5	B	9	GLU	3.1
7	D	150	GLU	3.1
16	M	10	PRO	3.1
1	A	1534	A	3.1
21	R	19	LYS	3.1
1	A	438	G	3.1
1	A	1323	G	3.1
16	M	16	ASP	3.1
12	I	111	ARG	3.1
13	J	47	PHE	3.1
16	M	88	ARG	3.1
17	N	52	GLN	3.1
5	B	98	LEU	3.1
1	A	823	G	3.1
1	A	1040	U	3.1
6	C	88	ARG	3.1
13	J	43	ARG	3.1
17	N	35	ARG	3.1
15	L	73	GLU	3.1
18	O	7	GLU	3.1
1	A	993	G	3.0
14	K	87	THR	3.0
13	J	14	LYS	3.0
1	A	1212	U	3.0
4	Z	1	U	3.0
1	A	1013	G	3.0
1	A	1182	G	3.0
23	T	97	ALA	3.0
13	J	84	GLN	3.0
17	N	15	LYS	3.0
23	T	58	LYS	3.0
1	A	349	A	3.0
1	A	822	C	3.0
6	C	105	GLU	3.0
7	D	47	ARG	3.0
9	F	50	TYR	3.0
10	G	32	ARG	3.0
12	I	43	ALA	3.0
14	K	25	TYR	3.0
6	C	51	GLY	3.0
1	A	1127	G	3.0

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Mol	Chain	Res	Type	RSRZ
10	G	38	LEU	3.0
1	A	165	C	3.0
15	L	28	LYS	3.0
5	B	94	ASN	3.0
13	J	98	ILE	3.0
5	B	144	ARG	2.9
24	V	10	ARG	2.9
1	A	306	G	2.9
1	A	1224	G	2.9
15	L	111	LYS	2.9
1	A	1361(A)	C	2.9
12	I	48	GLU	2.9
16	M	12	ASN	2.9
14	K	121	PRO	2.9
9	F	49	ALA	2.9
7	D	112	VAL	2.9
14	K	75	TYR	2.9
5	B	109	SER	2.9
14	K	13	GLN	2.9
5	B	195	ASP	2.9
1	A	633	G	2.9
6	C	110	ASN	2.9
22	S	77	THR	2.9
12	I	110	GLU	2.9
15	L	65	GLU	2.9
16	M	51	ALA	2.9
1	A	437	U	2.9
6	C	155	GLY	2.9
12	I	114	TYR	2.9
6	C	49	SER	2.9
22	S	32	LYS	2.9
5	B	206	ASP	2.9
6	C	98	ASN	2.9
23	T	93	GLU	2.9
6	C	132	ARG	2.9
1	A	1094	G	2.9
1	A	1018	C	2.8
17	N	30	ALA	2.8
24	V	6	ARG	2.8
6	C	96	GLY	2.8
5	B	140	HIS	2.8
1	A	351	G	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	991	U	2.8
1	A	1025	U	2.8
1	A	1160	G	2.8
13	J	17	ASP	2.8
7	D	156	GLU	2.8
11	H	30	ARG	2.8
19	P	83	GLU	2.8
5	B	125	PRO	2.8
13	J	77	PRO	2.8
7	D	178	VAL	2.8
10	G	9	VAL	2.8
6	C	19	GLU	2.8
8	E	81	GLU	2.8
16	M	58	GLU	2.8
12	I	33	PHE	2.8
13	J	71	LEU	2.8
22	S	15	LEU	2.8
17	N	3	ARG	2.8
6	C	30	ARG	2.8
1	A	1384	C	2.8
11	H	126	LYS	2.8
9	F	21	LEU	2.8
22	S	39	THR	2.8
5	B	101	MET	2.7
12	I	54	ASP	2.7
12	I	9	ARG	2.7
16	M	44	ARG	2.7
1	A	723	U	2.7
21	R	85	LEU	2.7
1	A	268	C	2.7
1	A	1161	C	2.7
1	A	1226	C	2.7
1	A	1478	C	2.7
17	N	32	SER	2.7
19	P	54	GLU	2.7
12	I	10	ARG	2.7
1	A	1004	A	2.7
13	J	67	THR	2.7
7	D	153	ARG	2.7
5	B	75	LYS	2.7
7	D	86	LYS	2.7
6	C	56	ASP	2.7

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Mol	Chain	Res	Type	RSRZ
7	D	154	ASN	2.7
12	I	117	HIS	2.7
8	E	153	LYS	2.7
24	V	18	TYR	2.7
20	Q	93	GLN	2.7
13	J	8	LEU	2.7
5	B	110	GLN	2.6
8	E	68	GLU	2.6
16	M	67	GLU	2.6
1	A	1030(C)	G	2.6
5	B	205	ASP	2.6
6	C	3	ASN	2.6
7	D	73	ARG	2.6
9	F	97	PHE	2.6
19	P	41	PRO	2.6
12	I	22	GLY	2.6
1	A	975	A	2.6
13	J	83	GLU	2.6
21	R	38	GLU	2.6
1	A	1054	C	2.6
1	A	1137	C	2.6
10	G	151	TYR	2.6
15	L	115	LYS	2.6
1	A	841	U	2.6
20	Q	86	GLU	2.6
22	S	17	GLU	2.6
1	A	216	G	2.6
1	A	584	G	2.6
5	B	21	ARG	2.6
7	D	209	ARG	2.6
12	I	58	ARG	2.6
6	C	39	ILE	2.6
12	I	36	TYR	2.6
1	A	131	C	2.6
1	A	979	C	2.6
1	A	1038	C	2.6
10	G	56	GLN	2.6
7	D	145	GLU	2.6
12	I	2	GLU	2.6
21	R	83	GLU	2.6
10	G	10	ARG	2.6
1	A	1443	G	2.6

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Mol	Chain	Res	Type	RSRZ
5	B	105	PHE	2.6
6	C	23	TYR	2.6
1	A	1014	A	2.6
1	A	1123	A	2.6
12	I	87	GLN	2.6
13	J	36	GLY	2.6
5	B	37	ASN	2.6
5	B	77	ALA	2.6
9	F	39	LYS	2.6
14	K	70	LYS	2.6
18	O	48	LYS	2.6
24	V	9	ARG	2.6
6	C	194	GLY	2.5
11	H	70	GLN	2.5
21	R	31	LEU	2.5
1	A	662	G	2.5
1	A	1190	G	2.5
6	C	76	VAL	2.5
12	I	64	THR	2.5
1	A	848	C	2.5
1	A	1027	C	2.5
1	A	1325	C	2.5
13	J	11	PHE	2.5
1	A	1205	U	2.5
6	C	118	GLN	2.5
15	L	114	LYS	2.5
21	R	42	ARG	2.5
7	D	179	GLU	2.5
20	Q	82	MET	2.5
1	A	664	G	2.5
15	L	94	PRO	2.5
24	V	23	PRO	2.5
1	A	1282	C	2.5
22	S	7	LYS	2.5
7	D	12	CYS	2.5
5	B	136	VAL	2.5
20	Q	49	GLU	2.5
23	T	85	MET	2.5
5	B	19	HIS	2.5
23	T	68	LYS	2.5
23	T	87	LYS	2.5
1	A	497	A	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	1146	A	2.5
16	M	54	VAL	2.5
17	N	25	VAL	2.5
1	A	112	G	2.5
1	A	126	G	2.5
1	A	760	G	2.5
1	A	1316	G	2.5
1	A	1526	G	2.5
7	D	195	ALA	2.5
1	A	1264	C	2.5
6	C	10	PHE	2.5
21	R	25	THR	2.5
16	M	94	ARG	2.5
7	D	2	GLY	2.5
12	I	28	VAL	2.5
6	C	107	GLN	2.5
7	D	119	GLN	2.5
9	F	89	MET	2.4
5	B	193	ASP	2.4
6	C	93	LYS	2.4
1	A	233	C	2.4
15	L	120	TYR	2.4
12	I	8	GLY	2.4
13	J	44	VAL	2.4
13	J	61	GLU	2.4
5	B	22	LYS	2.4
13	J	63	PHE	2.4
14	K	122	LYS	2.4
16	M	20	THR	2.4
5	B	229	VAL	2.4
6	C	176	HIS	2.4
1	A	1006	C	2.4
1	A	413	G	2.4
1	A	1266	G	2.4
5	B	209	ARG	2.4
6	C	26	LYS	2.4
11	H	64	LYS	2.4
8	E	26	PHE	2.4
8	E	83	GLU	2.4
12	I	27	THR	2.4
1	A	88	A	2.4
1	A	1248	A	2.4

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Mol	Chain	Res	Type	RSRZ
16	M	14	ARG	2.4
24	V	24	ARG	2.4
6	C	128	PHE	2.4
1	A	5	U	2.4
1	A	421	U	2.4
1	A	1320	C	2.4
1	A	818	G	2.4
5	B	38	GLY	2.4
12	I	23	ASN	2.4
12	I	30	GLY	2.4
11	H	18	ARG	2.4
12	I	107	ARG	2.4
17	N	37	PHE	2.4
1	A	1502	A	2.4
3	Y	32	U	2.4
1	A	962	C	2.3
7	D	4	TYR	2.3
7	D	132	ARG	2.3
10	G	6	ARG	2.3
12	I	15	ALA	2.3
16	M	25	ILE	2.3
13	J	33	GLN	2.3
6	C	126	ARG	2.3
15	L	44	THR	2.3
5	B	113	HIS	2.3
23	T	59	ALA	2.3
19	P	39	TYR	2.3
6	C	62	ASP	2.3
14	K	81	ASP	2.3
9	F	64	GLN	2.3
12	I	101	PHE	2.3
15	L	78	GLN	2.3
1	A	1164	G	2.3
3	Y	28	G	2.3
7	D	18	LYS	2.3
6	C	77	ILE	2.3
10	G	7	ALA	2.3
5	B	63	MET	2.3
13	J	78	ASN	2.3
1	A	1041	A	2.3
6	C	136	GLN	2.3
1	A	1399	C	2.3

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Mol	Chain	Res	Type	RSRZ
5	B	74	LYS	2.3
6	C	97	LYS	2.3
16	M	27	LYS	2.3
1	A	1036	G	2.3
1	A	1166	G	2.3
1	A	1530	G	2.3
6	C	139	GLN	2.3
1	A	1252	A	2.3
5	B	36	ARG	2.3
16	M	69	GLU	2.3
18	O	6	GLU	2.3
1	A	1313	U	2.3
13	J	92	THR	2.3
21	R	17	SER	2.3
12	I	116	LYS	2.3
21	R	88	LYS	2.3
12	I	93	ARG	2.3
20	Q	92	ARG	2.3
21	R	18	ARG	2.3
21	R	54	ARG	2.3
1	A	1138	G	2.2
5	B	39	ILE	2.2
6	C	196	LEU	2.2
7	D	162	LEU	2.2
18	O	32	LEU	2.2
1	A	422	C	2.2
1	A	1362	C	2.2
5	B	153	ARG	2.2
16	M	114	ARG	2.2
21	R	32	ARG	2.2
5	B	52	GLU	2.2
12	I	35	GLU	2.2
5	B	97	TRP	2.2
1	A	606	G	2.2
1	A	1053	G	2.2
1	A	1131	G	2.2
1	A	1274	G	2.2
1	A	1295	G	2.2
1	A	1300	G	2.2
7	D	30	LYS	2.2
12	I	95	LYS	2.2
12	I	127	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	1135	U	2.2
1	A	1136	U	2.2
7	D	35	ARG	2.2
10	G	76	ARG	2.2
12	I	104	ARG	2.2
19	P	17	TYR	2.2
24	V	15	ARG	2.2
1	A	632	A	2.2
1	A	977	A	2.2
1	A	1286	A	2.2
1	A	1318	A	2.2
6	C	63	ASN	2.2
1	A	1296	C	2.2
5	B	131	PRO	2.2
21	R	53	ARG	2.2
1	A	498	U	2.2
5	B	146	GLN	2.2
6	C	170	GLN	2.2
5	B	172	ILE	2.2
1	A	1174	G	2.2
1	A	1467	G	2.2
5	B	170	GLU	2.2
10	G	139	GLU	2.2
5	B	188	ALA	2.2
10	G	55	GLY	2.2
14	K	118	GLY	2.2
12	I	75	ASP	2.2
5	B	76	GLN	2.2
14	K	104	GLN	2.2
6	C	94	LEU	2.2
5	B	177	ALA	2.2
16	M	72	ALA	2.2
6	C	85	ARG	2.2
22	S	74	PHE	2.2
1	A	383	A	2.2
1	A	1001	A	2.2
1	A	1213	A	2.2
1	A	1033	G	2.2
1	A	1185	G	2.2
1	A	1265	G	2.2
11	H	97	VAL	2.1
15	L	27	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
22	S	56	GLN	2.1
22	S	44	MET	2.1
12	I	52	ALA	2.1
12	I	94	ALA	2.1
22	S	21	GLU	2.1
12	I	29	ASN	2.1
22	S	59	PRO	2.1
22	S	10	PHE	2.1
1	A	170	U	2.1
1	A	1219	U	2.1
11	H	54	ASP	2.1
6	C	99	VAL	2.1
1	A	1269	A	2.1
10	G	85	TYR	2.1
5	B	8	LYS	2.1
5	B	154	LEU	2.1
16	M	13	LYS	2.1
1	A	1034	G	2.1
1	A	1177	G	2.1
1	A	1361	G	2.1
5	B	226	ARG	2.1
13	J	20	ALA	2.1
13	J	70	ARG	2.1
14	K	54	ARG	2.1
6	C	35	GLU	2.1
1	A	372	C	2.1
1	A	1477	C	2.1
5	B	181	PHE	2.1
14	K	42	TRP	2.1
12	I	25	LYS	2.1
11	H	37	ARG	2.1
1	A	496	A	2.1
5	B	134	GLU	2.1
6	C	166	GLU	2.1
12	I	86	VAL	2.1
1	A	756	C	2.1
3	Y	41	C	2.1
6	C	72	LYS	2.1
15	L	13	LYS	2.1
17	N	50	LYS	2.1
20	Q	87	LYS	2.1
5	B	108	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
13	J	23	ILE	2.1
11	H	84	ARG	2.1
9	F	63	TYR	2.1
23	T	49	ALA	2.1
1	A	997	U	2.1
5	B	45	GLN	2.1
5	B	228	GLY	2.1
15	L	29	GLY	2.1
8	E	149	GLU	2.1
13	J	41	PRO	2.1
13	J	95	GLU	2.1
19	P	15	PRO	2.1
21	R	28	GLU	2.1
5	B	124	SER	2.1
1	A	1287	A	2.1
19	P	50	LYS	2.1
23	T	48	LYS	2.1
5	B	175	ARG	2.1
6	C	21	ARG	2.1
13	J	28	ARG	2.1
16	M	102	ARG	2.1
18	O	72	ARG	2.1
1	A	717	C	2.1
1	A	1192	C	2.1
1	A	1200	C	2.1
1	A	1336	C	2.1
1	A	459	G	2.1
1	A	1022	G	2.1
1	A	1139	G	2.1
1	A	1156	G	2.1
1	A	1253	G	2.1
16	M	6	GLY	2.1
10	G	74	GLU	2.1
1	A	1528	U	2.0
1	A	1532	U	2.0
15	L	57	LYS	2.0
5	B	23	ARG	2.0
17	N	7	ILE	2.0
7	D	125	HIS	2.0
1	A	1183	A	2.0
22	S	61	TYR	2.0
14	K	123	LYS	2.0

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Mol	Chain	Res	Type	RSRZ
23	T	51	GLU	2.0
1	A	1141	C	2.0
12	I	53	VAL	2.0
1	A	266	G	2.0
1	A	1017	G	2.0
1	A	1142	G	2.0
1	A	1175	G	2.0
1	A	1385	G	2.0
13	J	40	LEU	2.0
23	T	8	ARG	2.0
7	D	113	SER	2.0
16	M	105	THR	2.0
8	E	23	GLY	2.0
13	J	21	GLN	2.0
1	A	1324	A	2.0
5	B	81	VAL	2.0
14	K	120	ARG	2.0
18	O	35	ARG	2.0
22	S	41	VAL	2.0
1	A	1260	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
26	MG	A	1616	1/1	0.53	0.43	20,20,20,20	1
26	MG	A	441	1/1	0.56	0.53	20,20,20,20	1
26	MG	A	1640	1/1	0.60	0.41	20,20,20,20	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
26	MG	A	1624	1/1	0.65	0.29	20,20,20,20	1
26	MG	A	1633	1/1	0.67	0.55	20,20,20,20	1
26	MG	A	1642	1/1	0.69	0.54	20,20,20,20	1
26	MG	A	1621	1/1	0.71	0.39	20,20,20,20	1
26	MG	A	1589	1/1	0.74	0.45	20,20,20,20	1
26	MG	A	1628	1/1	0.75	0.52	20,20,20,20	1
26	MG	A	1634	1/1	0.78	0.30	20,20,20,20	1
26	MG	A	210	1/1	0.78	0.11	20,20,20,20	1
26	MG	A	1644	1/1	0.79	0.21	20,20,20,20	1
26	MG	A	1645	1/1	0.79	0.46	20,20,20,20	1
26	MG	A	1638	1/1	0.80	0.21	20,20,20,20	1
26	MG	A	1652	1/1	0.80	0.45	20,20,20,20	1
26	MG	A	1631	1/1	0.81	0.64	20,20,20,20	1
26	MG	A	1622	1/1	0.81	0.18	20,20,20,20	1
26	MG	A	1590	1/1	0.82	0.26	20,20,20,20	0
26	MG	A	1618	1/1	0.82	0.28	20,20,20,20	0
26	MG	Y	456	1/1	0.82	0.20	20,20,20,20	1
26	MG	A	1571	1/1	0.83	0.28	20,20,20,20	1
26	MG	A	1548	1/1	0.83	0.15	20,20,20,20	0
26	MG	A	1620	1/1	0.83	0.38	20,20,20,20	1
26	MG	A	1630	1/1	0.84	0.19	20,20,20,20	1
26	MG	A	1646	1/1	0.84	0.35	20,20,20,20	1
26	MG	A	1569	1/1	0.84	0.34	20,20,20,20	1
26	MG	A	1562	1/1	0.84	0.27	20,20,20,20	1
26	MG	D	215	1/1	0.84	0.15	20,20,20,20	1
26	MG	A	1643	1/1	0.85	0.52	20,20,20,20	1
26	MG	A	1608	1/1	0.85	0.25	20,20,20,20	1
26	MG	A	1617	1/1	0.85	0.42	20,20,20,20	1
26	MG	A	1609	1/1	0.85	0.14	20,20,20,20	1
26	MG	A	1614	1/1	0.86	0.16	20,20,20,20	1
26	MG	A	1559	1/1	0.87	0.14	20,20,20,20	0
26	MG	A	1603	1/1	0.87	0.32	20,20,20,20	1
26	MG	A	1635	1/1	0.87	0.14	20,20,20,20	1
25	PAR	A	1545	42/42	0.87	0.22	59,59,59,59	0
26	MG	A	1639	1/1	0.87	0.27	20,20,20,20	1
26	MG	A	1641	1/1	0.88	0.08	20,20,20,20	1
26	MG	A	1552	1/1	0.88	0.29	20,20,20,20	0
26	MG	A	1648	1/1	0.88	0.10	20,20,20,20	1
26	MG	A	1570	1/1	0.88	0.20	20,20,20,20	1
26	MG	A	1655	1/1	0.88	0.27	20,20,20,20	1
26	MG	A	1597	1/1	0.88	0.28	20,20,20,20	1
26	MG	A	1555	1/1	0.88	0.19	20,20,20,20	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
26	MG	A	1588	1/1	0.89	0.22	20,20,20,20	1
26	MG	A	1556	1/1	0.89	0.21	20,20,20,20	0
26	MG	A	1598	1/1	0.89	0.28	20,20,20,20	1
26	MG	A	1647	1/1	0.90	0.17	20,20,20,20	1
26	MG	A	1573	1/1	0.90	0.20	20,20,20,20	0
26	MG	A	1604	1/1	0.90	0.15	20,20,20,20	1
26	MG	A	1601	1/1	0.91	0.21	20,20,20,20	1
26	MG	A	1563	1/1	0.91	0.28	20,20,20,20	1
26	MG	A	1565	1/1	0.91	0.15	20,20,20,20	0
26	MG	A	1591	1/1	0.91	0.32	20,20,20,20	1
26	MG	A	1593	1/1	0.91	0.23	20,20,20,20	0
26	MG	A	1567	1/1	0.91	0.25	20,20,20,20	1
26	MG	A	1615	1/1	0.91	0.42	20,20,20,20	1
26	MG	A	1576	1/1	0.91	0.24	20,20,20,20	1
26	MG	A	1549	1/1	0.91	0.42	20,20,20,20	1
26	MG	A	1564	1/1	0.92	0.23	20,20,20,20	0
26	MG	A	1561	1/1	0.92	0.23	20,20,20,20	0
26	MG	A	1566	1/1	0.92	0.26	20,20,20,20	0
26	MG	A	1606	1/1	0.92	0.27	20,20,20,20	1
26	MG	A	1553	1/1	0.92	0.24	20,20,20,20	0
26	MG	A	1580	1/1	0.92	0.12	20,20,20,20	0
26	MG	A	1610	1/1	0.92	0.40	20,20,20,20	1
26	MG	A	1582	1/1	0.92	0.25	20,20,20,20	1
26	MG	A	1629	1/1	0.92	0.27	20,20,20,20	1
26	MG	A	1551	1/1	0.92	0.17	20,20,20,20	1
26	MG	A	1550	1/1	0.93	0.30	20,20,20,20	1
26	MG	A	1602	1/1	0.93	0.47	20,20,20,20	1
26	MG	A	1653	1/1	0.93	0.32	20,20,20,20	1
26	MG	A	1572	1/1	0.93	0.38	20,20,20,20	1
26	MG	A	1656	1/1	0.93	0.31	20,20,20,20	1
26	MG	A	1568	1/1	0.93	0.20	20,20,20,20	0
26	MG	A	1583	1/1	0.93	0.36	20,20,20,20	1
26	MG	A	1592	1/1	0.94	0.18	20,20,20,20	0
26	MG	A	1577	1/1	0.94	0.20	20,20,20,20	1
26	MG	A	86	1/1	0.94	0.21	20,20,20,20	1
26	MG	A	1575	1/1	0.94	0.22	20,20,20,20	1
26	MG	A	1657	1/1	0.94	0.35	20,20,20,20	1
26	MG	A	71	1/1	0.94	0.25	20,20,20,20	1
26	MG	A	211	1/1	0.94	0.21	20,20,20,20	1
26	MG	A	1574	1/1	0.95	0.10	20,20,20,20	0
26	MG	A	1584	1/1	0.95	0.27	20,20,20,20	1
26	MG	A	1596	1/1	0.95	0.22	20,20,20,20	0

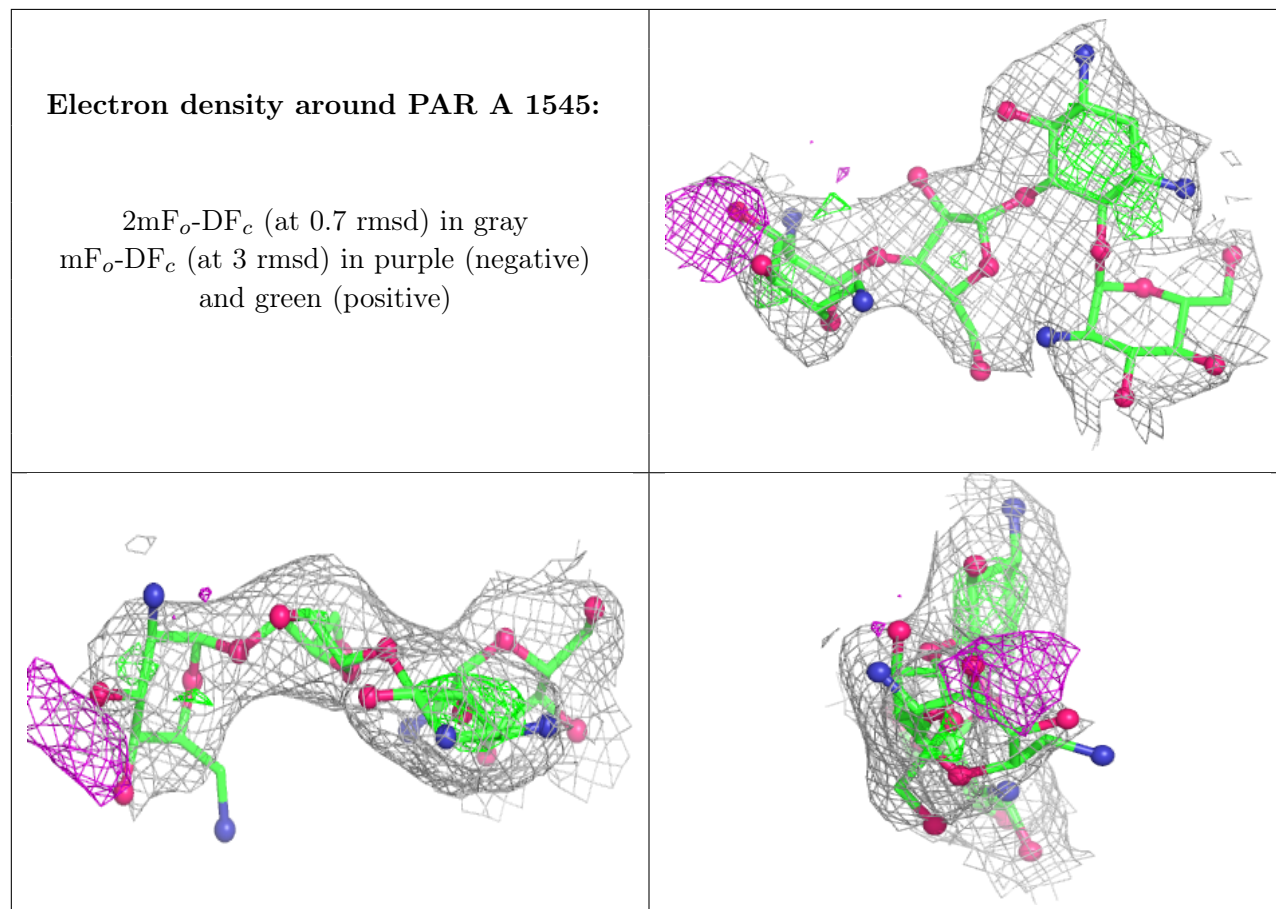
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
26	MG	A	1623	1/1	0.95	0.57	20,20,20,20	1
26	MG	A	1586	1/1	0.95	0.21	20,20,20,20	0
26	MG	A	1625	1/1	0.95	0.04	20,20,20,20	1
26	MG	A	1587	1/1	0.95	0.20	20,20,20,20	0
26	MG	A	1579	1/1	0.95	0.20	20,20,20,20	0
26	MG	A	1611	1/1	0.95	0.25	20,20,20,20	0
26	MG	A	1560	1/1	0.95	0.29	20,20,20,20	1
26	MG	A	1651	1/1	0.95	0.43	20,20,20,20	1
26	MG	A	1632	1/1	0.95	0.13	20,20,20,20	1
26	MG	A	213	1/1	0.95	0.13	20,20,20,20	1
26	MG	A	214	1/1	0.95	0.23	20,20,20,20	1
26	MG	A	1581	1/1	0.95	0.14	20,20,20,20	0
26	MG	A	1636	1/1	0.95	0.23	20,20,20,20	1
26	MG	A	1547	1/1	0.95	0.20	20,20,20,20	0
26	MG	D	210	1/1	0.95	0.37	20,20,20,20	1
26	MG	A	1619	1/1	0.95	0.62	20,20,20,20	1
26	MG	A	87	1/1	0.96	0.32	20,20,20,20	1
26	MG	A	1558	1/1	0.96	0.21	20,20,20,20	0
26	MG	A	1594	1/1	0.96	0.09	20,20,20,20	1
26	MG	A	1637	1/1	0.96	0.05	20,20,20,20	0
26	MG	A	1649	1/1	0.96	0.23	20,20,20,20	1
26	MG	A	1627	1/1	0.96	0.41	20,20,20,20	1
26	MG	A	1546	1/1	0.96	0.18	20,20,20,20	0
26	MG	A	1585	1/1	0.97	0.07	20,20,20,20	0
26	MG	A	1613	1/1	0.97	0.09	20,20,20,20	0
26	MG	A	1626	1/1	0.97	0.19	20,20,20,20	0
26	MG	A	1557	1/1	0.97	0.28	20,20,20,20	0
26	MG	A	1607	1/1	0.97	0.24	20,20,20,20	1
26	MG	A	1654	1/1	0.97	0.18	20,20,20,20	0
26	MG	J	449	1/1	0.97	0.08	20,20,20,20	1
26	MG	A	1612	1/1	0.98	0.22	20,20,20,20	0
26	MG	A	1600	1/1	0.98	0.24	20,20,20,20	0
26	MG	A	1554	1/1	0.98	0.30	20,20,20,20	0
26	MG	A	1578	1/1	0.98	0.44	20,20,20,20	1
26	MG	A	1650	1/1	0.98	0.05	20,20,20,20	0
26	MG	A	1595	1/1	0.98	0.23	20,20,20,20	0
26	MG	A	1599	1/1	0.98	0.13	20,20,20,20	0
26	MG	J	422	1/1	0.98	0.17	20,20,20,20	0
26	MG	A	1605	1/1	0.98	0.08	20,20,20,20	0
27	ZN	D	306	1/1	0.98	0.16	20,20,20,20	1
27	ZN	N	307	1/1	0.99	0.04	20,20,20,20	1

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.