



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:24 AM GMT

PDB ID : 3OTO
Title : Crystal Structure of the 30S ribosomal subunit from a KsgA mutant of *Thermus thermophilus* (HB8)
Authors : Demirci, H.; Murphy IV, F.; Belardinelli, R.; Kelley, A.C.; Ramakrishnan, V.; Gregory, S.T.; Dahlberg, A.E.; Jogl, G.
Deposited on : 2010-09-13
Resolution : 3.69 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

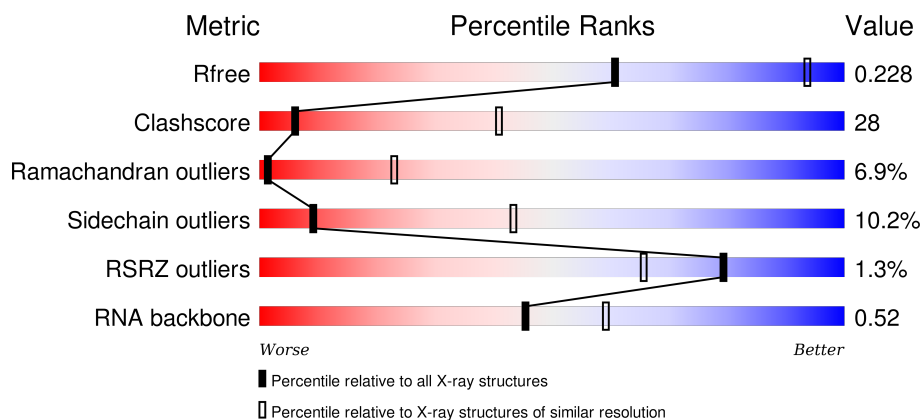
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.69 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}	91344	1101 (3.90-3.50)
Clashscore	102246	1224 (3.90-3.50)
Ramachandran outliers	100387	1172 (3.90-3.50)
Sidechain outliers	100360	1170 (3.90-3.50)
RSRZ outliers	91569	1108 (3.90-3.50)
RNA backbone	2183	1067 (4.60-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	<div> <div>2%</div> <div>30% 54% 14% .</div> </div>
2	B	256	<div> <div>38% 43% 11% 8%</div> </div>
3	C	239	<div> <div>2%</div> <div>36% 43% 7% . 14%</div> </div>
4	D	209	<div> <div>44% 49% 6%</div> </div>

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Mol	Chain	Length	Quality of chain
5	E	162	
6	F	101	
7	G	156	
8	H	138	
9	I	128	
10	J	105	
11	K	129	
12	L	135	
13	M	126	
14	N	61	
15	O	89	
16	P	88	
17	Q	105	
18	R	88	
19	S	93	
20	T	106	
21	U	27	

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
23	MG	A	1554	-	-	-	X
23	MG	A	1563	-	-	-	X
23	MG	A	1566	-	-	-	X
23	MG	A	1578	-	-	-	X
23	MG	A	1589	-	-	-	X
23	MG	A	1590	-	-	-	X
23	MG	A	1603	-	-	-	X
23	MG	A	1605	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
23	MG	A	1606	-	-	-	X
23	MG	A	1607	-	-	-	X
23	MG	A	1615	-	-	-	X
23	MG	A	1618	-	-	-	X
23	MG	A	1620	-	-	-	X
23	MG	A	1622	-	-	-	X
23	MG	A	1623	-	-	-	X
23	MG	A	1625	-	-	-	X
23	MG	A	1628	-	-	-	X
23	MG	A	1629	-	-	-	X
23	MG	A	94	-	-	-	X
23	MG	B	257	-	-	-	X
23	MG	M	127	-	-	-	X
24	K	A	1635	-	-	-	X
24	K	A	1636	-	-	-	X
24	K	A	1641	-	-	-	X
24	K	A	1644	-	-	-	X
24	K	A	1648	-	-	-	X
24	K	A	1651	-	-	-	X
24	K	A	1658	-	-	-	X
24	K	A	1666	-	-	-	X
24	K	A	1668	-	-	-	X
24	K	A	1669	-	-	-	X
24	K	A	1670	-	-	-	X

2 Entry composition

There are 24 unique types of molecules in this entry. The entry contains 51775 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 rRNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1513	Total	C	N	O	P	0	0	0
			32511	14472	6016	10511	1512			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	235	Total	C	N	O	S	0	0	0
			1873	1195	335	338	5			

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	115	Total	C	N	O	S	0	0	0
			921	569	190	160	2			

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

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

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

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

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

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

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

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

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

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

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

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

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

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
T	41	VAL	ILE	SEE REMARK 999	UNP P80380

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

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

- Molecule 22 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 23 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
23	B	1	Total	Mg	0	0
			1	1		
23	A	91	Total	Mg	0	0
			91	91		
23	D	1	Total	Mg	0	0
			1	1		
23	M	1	Total	Mg	0	0
			1	1		

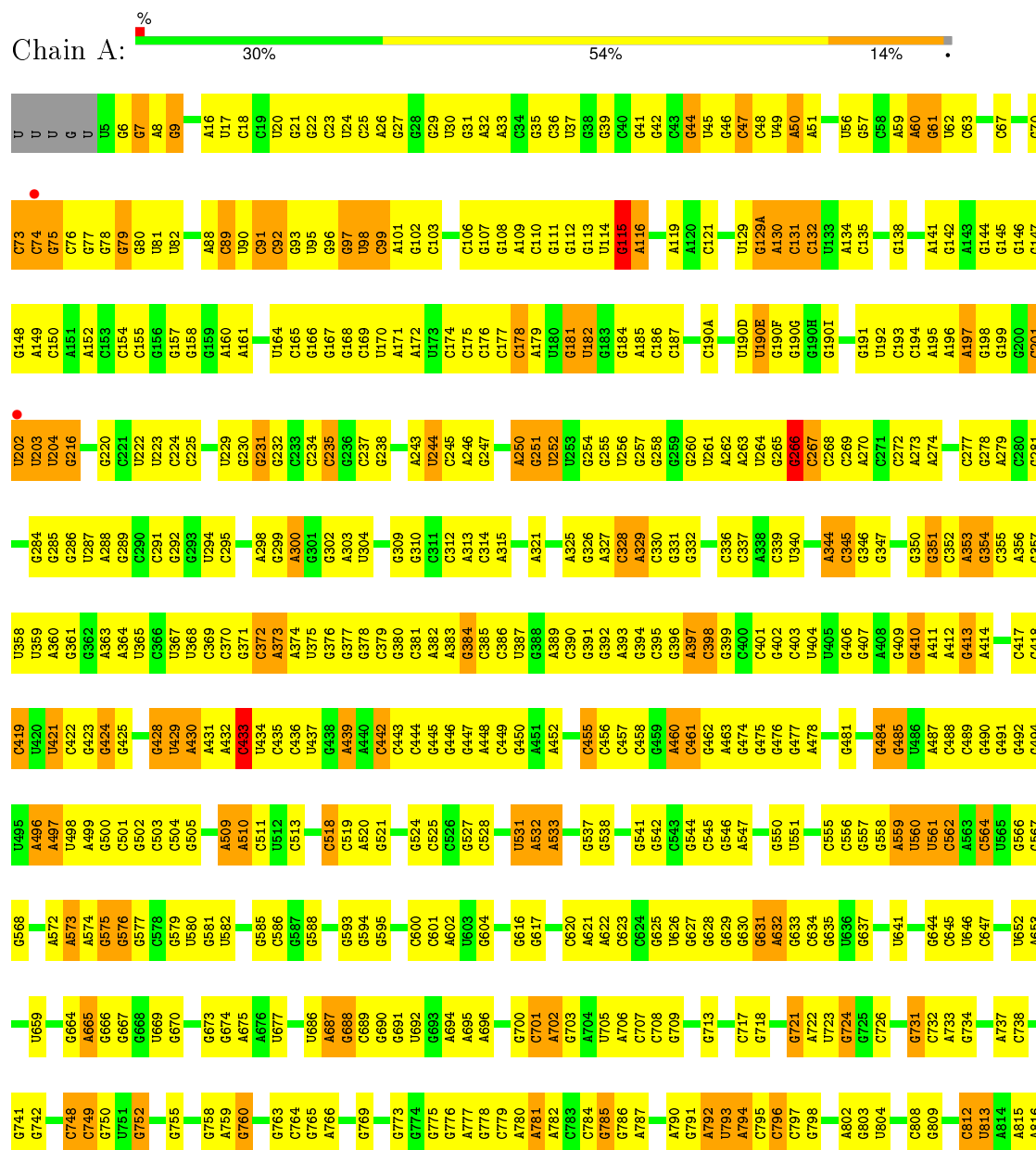
- Molecule 24 is POTASSIUM ION (three-letter code: K) (formula: K).

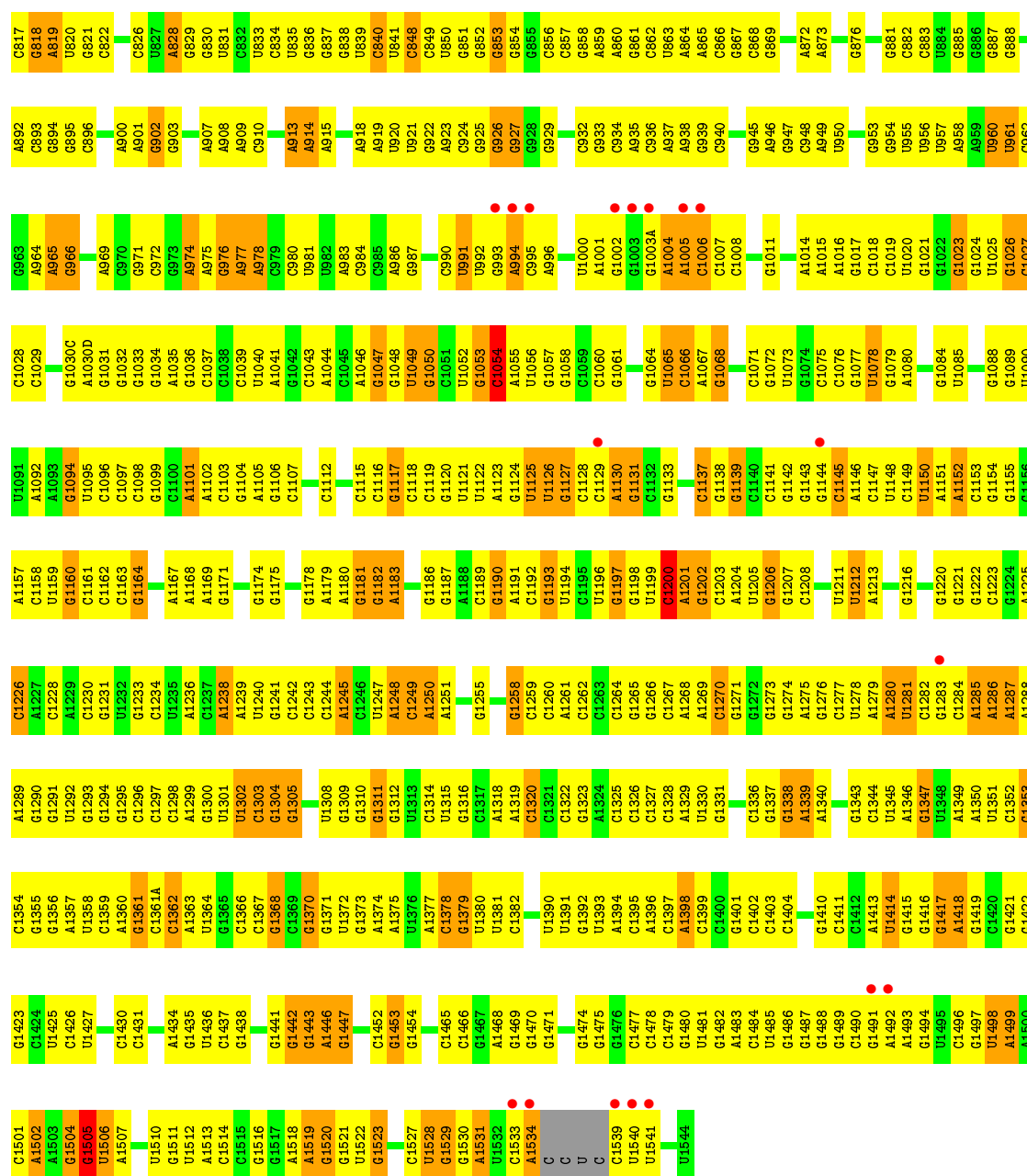
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
24	A	41	Total	K	0	0
			41	41		
24	E	1	Total	K	0	0
			1	1		

3 Residue-property plots

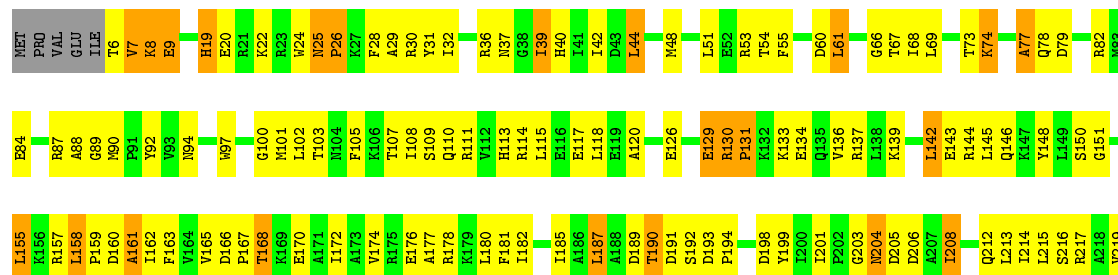
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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 ($\text{RSRZ} > 2$). 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.

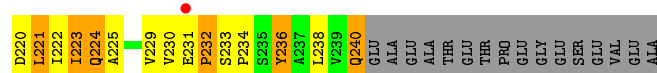
• Molecule 1: 16S rRNA



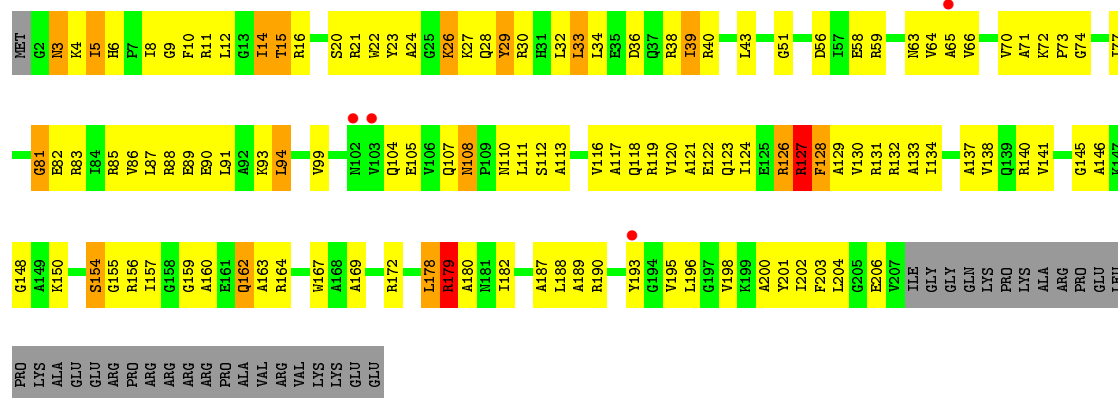


Chain B:

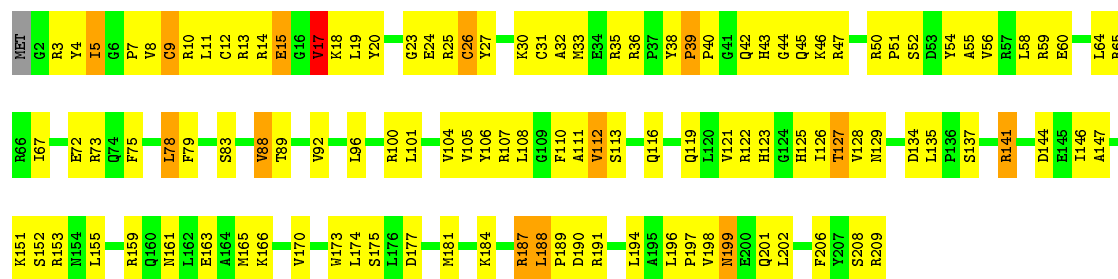




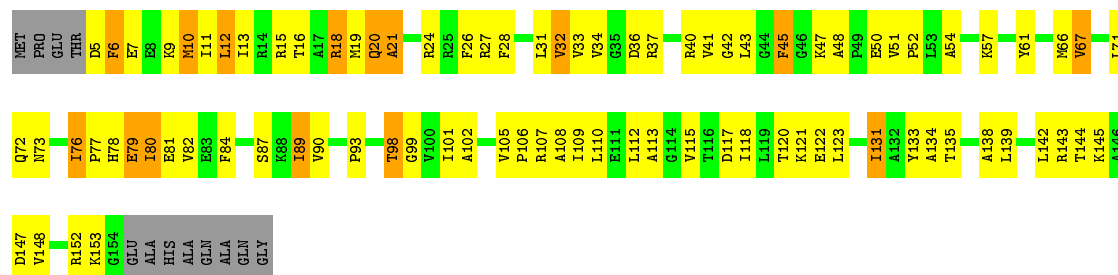
• Molecule 3: 30S RIBOSOMAL PROTEIN S3



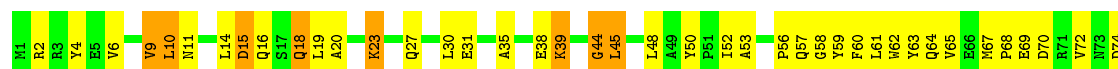
• Molecule 4: 30S RIBOSOMAL PROTEIN S4



• Molecule 5: 30S RIBOSOMAL PROTEIN S5



• Molecule 6: 30S RIBOSOMAL PROTEIN S6

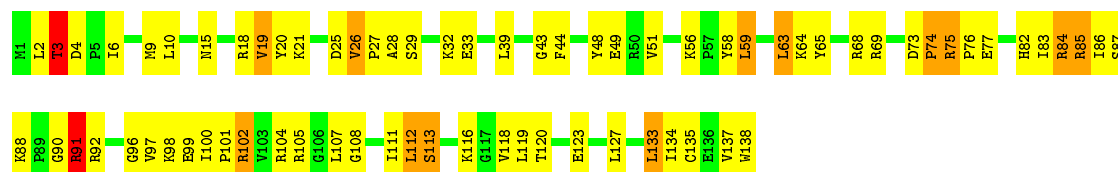




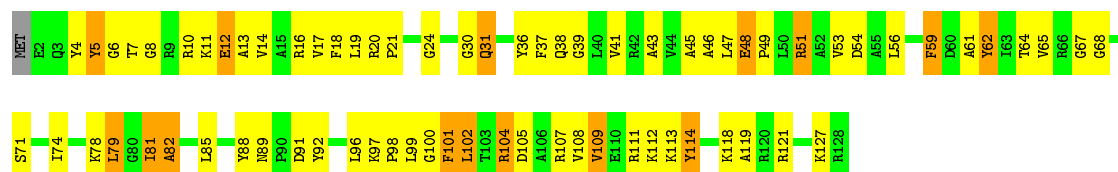
• Molecule 7: 30S RIBOSOMAL PROTEIN S7



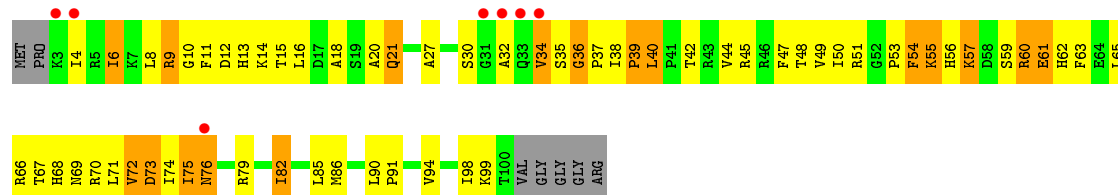
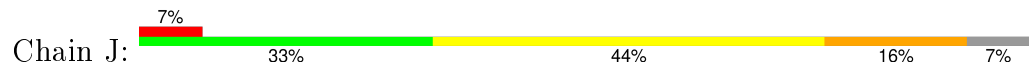
• Molecule 8: 30S RIBOSOMAL PROTEIN S8



• Molecule 9: 30S RIBOSOMAL PROTEIN S9

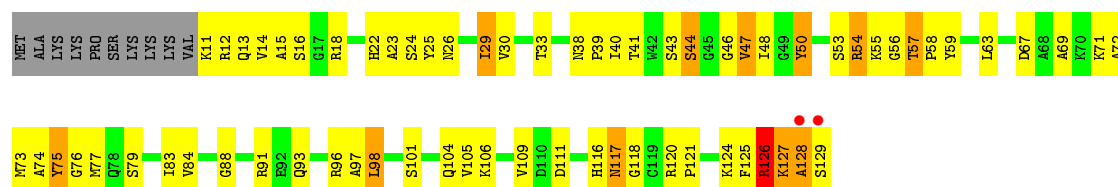


• Molecule 10: 30S RIBOSOMAL PROTEIN S10



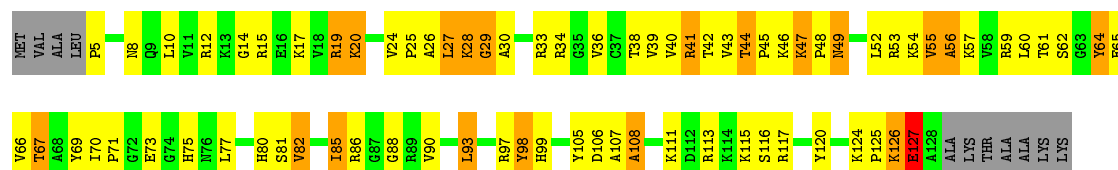
• Molecule 11: 30S RIBOSOMAL PROTEIN S11





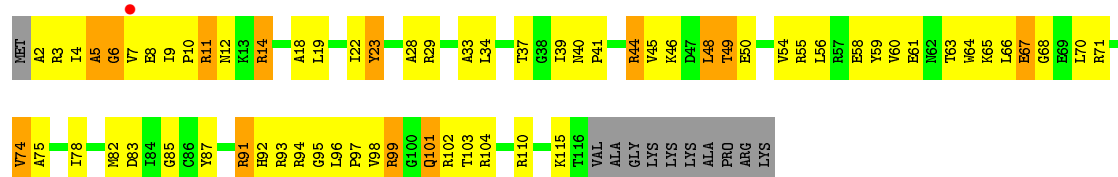
• Molecule 12: 30S RIBOSOMAL PROTEIN S12

Chain L: 36% 41% 14% 8%



• Molecule 13: 30S RIBOSOMAL PROTEIN S13

Chain M: 38% 43% 10% 9%



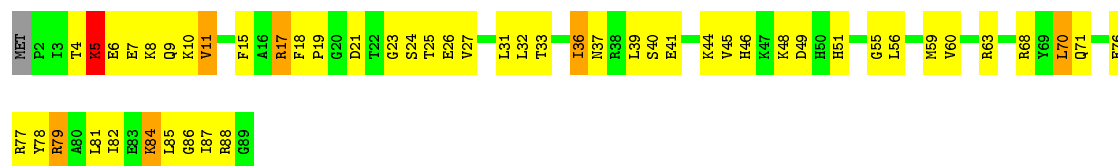
• Molecule 14: 30S RIBOSOMAL PROTEIN S14

Chain N: 3% 36% 56% 7%



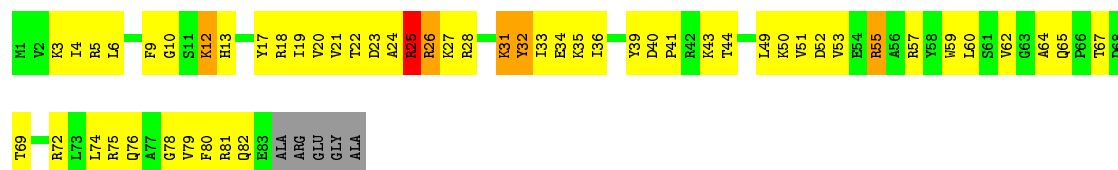
• Molecule 15: 30S RIBOSOMAL PROTEIN S15

Chain O: 42% 49% 7% 2%

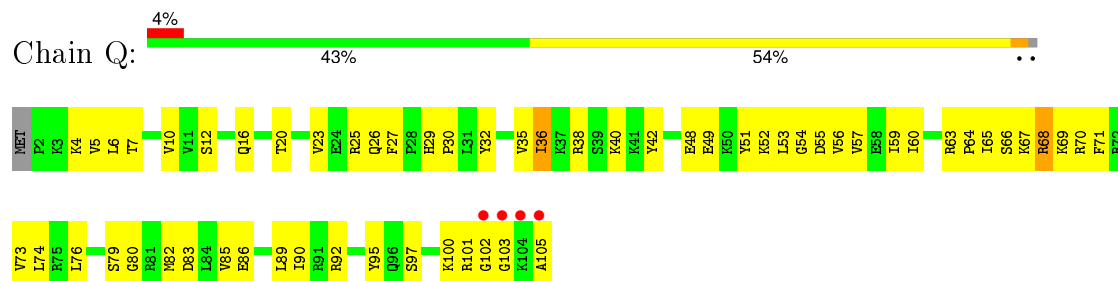


• Molecule 16: 30S RIBOSOMAL PROTEIN S16

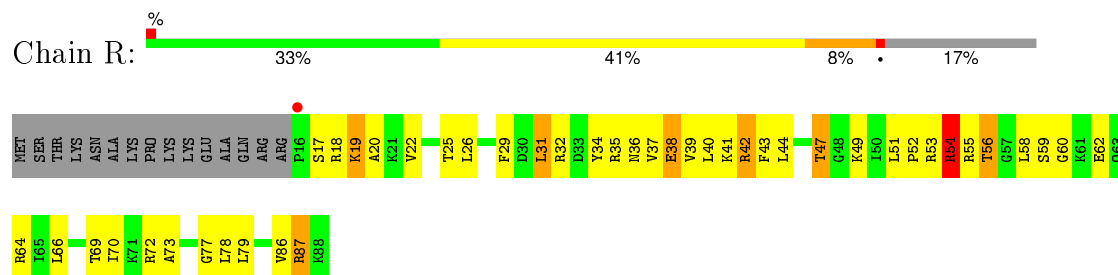
Chain P: 33% 55% 6% 6%



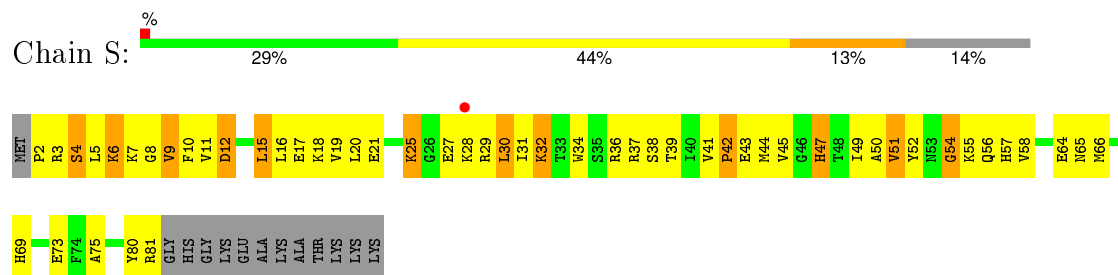
● Molecule 17: 30S RIBOSOMAL PROTEIN S17



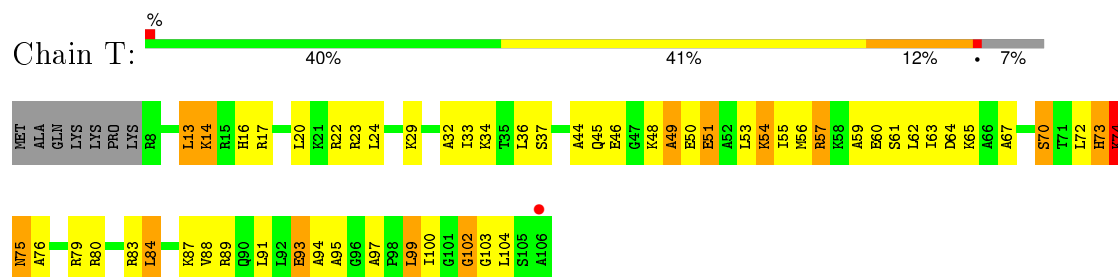
● Molecule 18: 30S RIBOSOMAL PROTEIN S18



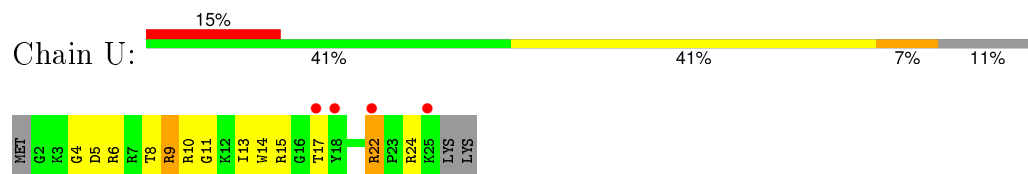
● Molecule 19: 30S RIBOSOMAL PROTEIN S19



● Molecule 20: 30S RIBOSOMAL PROTEIN S20



- Molecule 21: 30S RIBOSOMAL PROTEIN THX



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	402.09 Å 402.09 Å 173.25 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.84 – 3.69 29.84 – 3.69	Depositor EDS
% Data completeness (in resolution range)	92.7 (29.84-3.69) 97.8 (29.84-3.69)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.27 (at 3.65 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, R_{free}	0.173 , 0.231 0.176 , 0.228	Depositor DCC
R_{free} test set	7456 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	112.1	Xtriage
Anisotropy	0.382	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 85.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Outliers	0 of 148377 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	51775	wwPDB-VP
Average B, all atoms (Å ²)	127.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.71% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.45	0/36390	0.81	19/56793 (0.0%)
2	B	0.32	0/1908	0.49	0/2577
3	C	0.25	0/1636	0.44	0/2205
4	D	0.31	0/1733	0.47	0/2318
5	E	0.39	0/1162	0.58	0/1564
6	F	0.29	0/856	0.47	0/1154
7	G	0.26	0/1276	0.44	0/1709
8	H	0.42	0/1136	0.59	0/1527
9	I	0.28	0/1029	0.46	0/1378
10	J	0.27	0/805	0.47	0/1082
11	K	0.32	0/900	0.50	0/1213
12	L	0.34	0/986	0.55	0/1320
13	M	0.27	0/931	0.49	0/1248
14	N	0.26	0/501	0.46	0/664
15	O	0.33	0/745	0.51	0/992
16	P	0.33	0/716	0.52	0/963
17	Q	0.39	0/870	0.59	0/1159
18	R	0.30	0/603	0.50	0/799
19	S	0.23	0/661	0.45	0/890
20	T	0.31	0/764	0.50	0/1006
21	U	0.28	0/212	0.51	0/277
All	All	0.41	0/55820	0.73	19/82838 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	1	0

There are no bond length outliers.

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1505	G	C4-N9-C1'	8.15	137.09	126.50
1	A	1505	G	C6-C5-N7	-6.83	126.30	130.40
1	A	1505	G	C8-N9-C1'	-6.33	118.77	127.00
1	A	1505	G	N7-C8-N9	6.30	116.25	113.10
1	A	235	C	C6-N1-C2	5.81	122.62	120.30
1	A	1505	G	C8-N9-C4	-5.71	104.11	106.40
1	A	266	G	C2-N3-C4	-5.58	109.11	111.90
1	A	433	C	C5-C6-N1	5.50	123.75	121.00
1	A	1200	C	C2-N1-C1'	5.49	124.84	118.80
1	A	586	C	C6-N1-C2	5.47	122.49	120.30
1	A	115	G	C4-N9-C1'	5.42	133.55	126.50
1	A	1054	C	N1-C2-O2	5.40	122.14	118.90
1	A	1523	G	C5-C6-N1	-5.22	108.89	111.50
1	A	1054	C	C2-N1-C1'	5.18	124.50	118.80
1	A	853	G	C4-N9-C1'	5.17	133.23	126.50
1	A	115	G	C8-N9-C1'	-5.09	120.38	127.00
1	A	1505	G	N3-C4-C5	-5.09	126.06	128.60
1	A	115	G	N3-C4-N9	5.05	129.03	126.00
1	A	1505	G	N3-C4-N9	5.01	129.01	126.00

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	410	G	C3'

There are no planarity outliers.

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	32511	0	16413	1239	0
2	B	1873	0	1887	144	0
3	C	1612	0	1677	128	0
4	D	1703	0	1763	104	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	E	1146	0	1207	86	0
6	F	843	0	857	44	0
7	G	1257	0	1296	117	0
8	H	1116	0	1177	73	0
9	I	1011	0	1043	69	0
10	J	792	0	835	73	0
11	K	885	0	904	54	0
12	L	970	0	1057	95	0
13	M	921	0	978	65	0
14	N	492	0	530	48	0
15	O	734	0	771	59	0
16	P	700	0	720	47	0
17	Q	857	0	930	59	0
18	R	597	0	668	47	0
19	S	647	0	673	47	0
20	T	762	0	859	63	0
21	U	208	0	221	13	0
22	D	1	0	0	0	0
22	N	1	0	0	0	0
23	A	91	0	0	0	0
23	B	1	0	0	0	0
23	D	1	0	0	0	0
23	M	1	0	0	0	0
24	A	41	0	0	0	0
24	E	1	0	0	0	0
All	All	51775	0	36466	2487	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 28.

All (2487) 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)
15:O:17:ARG:HH11	15:O:17:ARG:HG3	1.12	1.08
1:A:1057:G:H5''	3:C:154:SER:HB2	1.32	1.08
1:A:559:A:H4'	1:A:560:U:H3'	1.35	1.06
11:K:15:ALA:HA	11:K:77:MET:HA	1.35	1.06
1:A:1443:G:H4'	1:A:1446:A:O5'	1.55	1.02
10:J:49:VAL:HG23	14:N:41:ARG:HB2	1.39	1.01
1:A:1250:A:H4'	9:I:68:GLY:H	1.26	1.00
1:A:409:G:H1	1:A:433:C:H42	1.04	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:10:LEU:HD22	8:H:83:ILE:HD11	1.42	0.98
1:A:60:A:H4'	1:A:61:G:O5'	1.60	0.97
1:A:630:G:H3'	1:A:631:G:H8	1.26	0.97
1:A:1368:G:H5''	9:I:112:LYS:HB3	1.47	0.96
18:R:36:ASN:HD22	18:R:39:VAL:HG12	1.27	0.96
18:R:19:LYS:HD2	18:R:20:ALA:H	1.28	0.96
1:A:141:A:H1'	1:A:182:U:O2	1.65	0.96
8:H:86:ILE:HG21	8:H:133:LEU:HD13	1.47	0.95
13:M:4:ILE:HD13	13:M:56:LEU:HD22	1.49	0.95
3:C:187:ALA:HB3	3:C:198:VAL:HB	1.47	0.94
1:A:975:A:H4'	1:A:976:G:H5''	1.48	0.94
1:A:77:G:H1	1:A:92:C:N4	1.64	0.94
1:A:266:G:H5''	1:A:267:C:H5	1.33	0.94
5:E:81:GLU:HG3	5:E:90:VAL:HG22	1.50	0.93
18:R:39:VAL:HG13	18:R:40:LEU:HD23	1.51	0.93
19:S:5:LEU:O	19:S:6:LYS:HB2	1.68	0.93
12:L:55:VAL:HG12	12:L:56:ALA:H	1.33	0.92
1:A:444:C:H42	1:A:490:G:H1	0.93	0.92
1:A:1225:A:H5''	1:A:1226:C:OP2	1.68	0.91
1:A:1285:A:H4'	1:A:1286:A:O5'	1.71	0.91
7:G:116:ALA:HA	7:G:119:ARG:HH21	1.35	0.90
1:A:75:G:H22	1:A:95:U:H3	1.18	0.90
1:A:1413:A:H2'	1:A:1414:U:H6	1.36	0.90
1:A:1147:C:H4'	9:I:5:TYR:HE1	1.37	0.89
3:C:126:ARG:O	3:C:127:ARG:HB2	1.70	0.89
1:A:432:A:HO2'	1:A:433:C:H6	0.90	0.88
1:A:560:U:H5'	1:A:566:G:N2	1.88	0.88
2:B:158:LEU:HD23	2:B:159:PRO:HD2	1.53	0.88
13:M:91:ARG:HH12	13:M:96:LEU:HD12	1.38	0.88
1:A:1125:U:H3'	1:A:1126:U:C5	2.09	0.87
3:C:26:LYS:HD2	3:C:27:LYS:H	1.40	0.87
1:A:266:G:H5''	1:A:267:C:C5	2.08	0.87
4:D:188:LEU:HD12	4:D:188:LEU:H	1.39	0.87
14:N:24:CYS:HB3	14:N:29:ARG:H	1.39	0.87
1:A:1204:A:H2'	1:A:1205:U:H5'	1.57	0.86
1:A:1047:G:H5''	14:N:4:LYS:HD2	1.55	0.86
13:M:23:TYR:HE2	13:M:70:LEU:HD22	1.36	0.86
1:A:748:C:H4'	1:A:749:C:O5'	1.74	0.86
1:A:89:C:H2'	1:A:89:C:O2	1.75	0.86
1:A:129:U:O3'	1:A:129(A):G:H3'	1.76	0.85
12:L:47:LYS:HB3	12:L:48:PRO:HD3	1.59	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:235:C:H5'	17:Q:70:ARG:HG2	1.57	0.84
2:B:204:ASN:ND2	2:B:206:ASP:H	1.76	0.84
2:B:114:ARG:HH11	2:B:118:LEU:HD21	1.42	0.84
1:A:76:C:H42	1:A:93:G:H1	1.23	0.84
1:A:501:C:H2'	1:A:502:G:H8	1.43	0.84
1:A:501:C:H2'	1:A:502:G:C8	2.13	0.83
12:L:5:PRO:HG2	12:L:15:ARG:NH2	1.93	0.83
1:A:1117:G:H5'	1:A:1118:C:OP2	1.77	0.83
5:E:51:VAL:HB	5:E:52:PRO:HD3	1.58	0.83
1:A:1250:A:H4'	9:I:68:GLY:N	1.94	0.82
1:A:991:U:H5	1:A:1212:U:C2	1.97	0.82
1:A:994:A:H62	1:A:1216:G:H4'	1.43	0.82
1:A:97:G:H2'	1:A:98:U:C6	2.14	0.82
14:N:29:ARG:HG3	14:N:30:ALA:H	1.44	0.81
7:G:17:VAL:HG12	7:G:18:TYR:HD2	1.45	0.81
5:E:76:ILE:HG22	5:E:93:PRO:HB3	1.59	0.81
9:I:53:VAL:HG21	9:I:85:LEU:HD21	1.61	0.81
16:P:67:THR:HG22	16:P:69:THR:H	1.46	0.81
9:I:48:GLU:HG2	9:I:51:ARG:HH21	1.46	0.81
3:C:64:VAL:HG23	3:C:99:VAL:HG11	1.62	0.81
17:Q:63:ARG:HG2	17:Q:64:PRO:HD2	1.63	0.81
3:C:70:VAL:HG12	3:C:72:LYS:H	1.43	0.80
1:A:1199:U:H5''	1:A:1200:C:OP2	1.80	0.80
1:A:1281:U:H5'	1:A:1282:C:C5	2.16	0.80
15:O:17:ARG:HG3	15:O:17:ARG:NH1	1.92	0.80
19:S:5:LEU:HD13	19:S:9:VAL:HG13	1.63	0.80
1:A:1238:A:H5'	1:A:1336:C:H41	1.44	0.80
2:B:103:THR:HG23	2:B:176:GLU:HG3	1.62	0.80
1:A:1413:A:H2'	1:A:1414:U:C6	2.16	0.80
1:A:79:G:C2	1:A:80:G:N7	2.51	0.79
10:J:44:VAL:HG11	10:J:66:ARG:HE	1.47	0.79
4:D:191:ARG:HH12	4:D:196:LEU:HB2	1.47	0.79
1:A:444:C:N4	1:A:490:G:H1	1.77	0.79
2:B:231:GLU:HB3	2:B:232:PRO:HD2	1.64	0.79
14:N:59:ALA:HB1	14:N:61:TRP:HZ3	1.47	0.79
1:A:177:C:H2'	1:A:178:C:H6	1.48	0.78
1:A:1137:C:H4'	1:A:1138:G:C2	2.17	0.78
1:A:1128:C:H42	1:A:1143:G:H22	1.28	0.78
1:A:1347:G:N2	1:A:1373:G:H2'	1.98	0.78
5:E:80:ILE:HD12	5:E:138:ALA:HB1	1.63	0.78
1:A:600:C:OP1	8:H:97:VAL:HG12	1.83	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1366:C:H2'	1:A:1367:C:H6	1.49	0.78
1:A:1065:U:H5''	1:A:1190:G:H22	1.48	0.78
1:A:812:C:H4'	1:A:813:U:O5'	1.83	0.78
1:A:630:G:H3'	1:A:631:G:C8	2.16	0.78
10:J:4:ILE:HD11	10:J:74:ILE:HD12	1.66	0.78
1:A:284:G:H2'	1:A:285:G:H8	1.50	0.77
1:A:266:G:H5'	1:A:268:C:H41	1.47	0.77
1:A:1065:U:H5''	1:A:1190:G:N2	1.99	0.77
3:C:21:ARG:HE	3:C:58:GLU:HG3	1.47	0.77
17:Q:67:LYS:HA	17:Q:70:ARG:HH12	1.49	0.77
3:C:22:TRP:HB3	3:C:59:ARG:HB2	1.67	0.77
5:E:76:ILE:HG23	5:E:78:HIS:H	1.50	0.77
1:A:328:C:O2	1:A:328:C:H2'	1.83	0.77
7:G:22:LEU:HD12	7:G:97:GLN:HE21	1.48	0.77
1:A:96:G:C2'	1:A:97:G:H5'	2.15	0.77
1:A:731:G:OP1	1:A:766:A:H1'	1.83	0.77
12:L:20:LYS:HD3	12:L:20:LYS:H	1.48	0.77
1:A:74:C:H3'	1:A:75:G:C5'	2.15	0.76
1:A:80:G:C2	1:A:81:U:C4	2.73	0.76
7:G:47:CYS:HA	7:G:50:ILE:HG12	1.67	0.76
2:B:126:GLU:HA	2:B:129:GLU:HG2	1.66	0.76
17:Q:40:LYS:HD3	17:Q:42:TYR:CZ	2.20	0.76
19:S:36:ARG:HB3	19:S:51:VAL:HG11	1.67	0.76
2:B:51:LEU:HD23	2:B:201:ILE:HD12	1.66	0.76
1:A:1418:A:H2'	1:A:1419:G:O4'	1.85	0.76
18:R:36:ASN:ND2	18:R:39:VAL:HG12	2.00	0.76
1:A:371:G:O2'	1:A:372:C:H5'	1.84	0.76
1:A:630:G:H5'	1:A:631:G:OP2	1.85	0.76
7:G:69:VAL:HG21	7:G:104:LEU:HD21	1.66	0.76
1:A:372:C:H4'	1:A:373:A:O5'	1.84	0.76
12:L:25:PRO:C	12:L:27:LEU:H	1.89	0.76
13:M:34:LEU:HD13	13:M:41:PRO:HA	1.67	0.76
15:O:17:ARG:HH11	15:O:17:ARG:CG	1.96	0.76
13:M:10:PRO:HB2	13:M:18:ALA:HB1	1.65	0.76
1:A:250:A:H4'	1:A:251:G:O5'	1.86	0.76
4:D:173:TRP:CE2	4:D:189:PRO:HG3	2.21	0.76
1:A:1361:G:C6	1:A:1361(A):C:N4	2.55	0.76
15:O:78:TYR:CZ	15:O:82:ILE:HD11	2.20	0.76
12:L:59:ARG:HA	12:L:65:GLU:HG2	1.66	0.76
1:A:149:A:H2'	1:A:150:C:H6	1.51	0.75
11:K:57:THR:HG22	11:K:59:TYR:H	1.51	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1065:U:H1'	1:A:1066:C:OP2	1.86	0.75
9:I:89:ASN:HB3	9:I:92:TYR:CD1	2.22	0.75
1:A:1122:U:H2'	1:A:1123:A:H5'	1.66	0.75
1:A:974:A:H8	1:A:974:A:OP1	1.69	0.75
1:A:432:A:O2'	1:A:433:C:H6	1.67	0.75
9:I:5:TYR:HD2	9:I:6:GLY:N	1.84	0.75
1:A:1189:C:H4'	3:C:10:PHE:HE1	1.52	0.75
1:A:76:C:N4	1:A:93:G:H1	1.85	0.75
1:A:707:C:H2'	1:A:708:C:H6	1.51	0.75
3:C:5:ILE:HG12	3:C:10:PHE:HD1	1.51	0.74
3:C:21:ARG:NH2	3:C:56:ASP:HB3	2.02	0.74
1:A:1493:A:H2'	1:A:1494:G:C8	2.22	0.74
3:C:64:VAL:HB	3:C:99:VAL:HG21	1.69	0.74
18:R:32:ARG:HA	18:R:69:THR:HG21	1.70	0.74
10:J:12:ASP:HB3	10:J:15:THR:HB	1.69	0.74
1:A:1305:G:N2	1:A:1331:G:H1'	2.02	0.74
5:E:102:ALA:HA	5:E:120:THR:OG1	1.88	0.74
15:O:8:LYS:O	15:O:11:VAL:HG13	1.87	0.74
7:G:16:LEU:H	7:G:16:LEU:HD22	1.51	0.74
4:D:7:PRO:HB2	4:D:10:ARG:HD2	1.68	0.74
1:A:664:G:H22	1:A:741:G:H1	1.36	0.74
1:A:97:G:OP2	1:A:97:G:H8	1.71	0.74
1:A:1001:A:H2'	1:A:1002:G:H8	1.53	0.74
18:R:86:VAL:HG12	18:R:87:ARG:HG3	1.68	0.74
15:O:24:SER:HB3	15:O:27:VAL:HG23	1.68	0.74
1:A:21:G:H2'	1:A:22:G:C8	2.23	0.73
1:A:750:G:N3	15:O:23:GLY:HA3	2.03	0.73
5:E:18:ARG:HG3	5:E:18:ARG:HH11	1.53	0.73
1:A:1329:A:P	13:M:28:ALA:HB3	2.28	0.73
11:K:50:TYR:HD2	11:K:54:ARG:HH11	1.37	0.73
5:E:144:THR:O	5:E:148:VAL:HG23	1.88	0.73
15:O:45:VAL:HG22	15:O:46:HIS:H	1.54	0.73
1:A:1147:C:H4'	9:I:5:TYR:CE1	2.23	0.73
1:A:70:G:C2'	1:A:73:C:H5'	2.19	0.73
6:F:50:TYR:CE1	18:R:77:GLY:HA2	2.24	0.73
7:G:111:ARG:HB2	7:G:119:ARG:HG2	1.71	0.72
1:A:106:C:O2	1:A:379:C:H4'	1.89	0.72
1:A:496:A:H4'	1:A:497:A:OP1	1.87	0.72
1:A:6:G:O2'	1:A:7:G:H5'	1.89	0.72
20:T:57:ARG:NH2	20:T:100:ILE:HD11	2.04	0.72
1:A:1054:C:O2'	1:A:1055:A:H5''	1.89	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:87:LYS:O	20:T:91:LEU:HD23	1.87	0.72
1:A:1453:G:H5'	1:A:1454:G:OP2	1.88	0.72
1:A:75:G:C2	1:A:76:C:C4	2.78	0.72
1:A:300:A:H8	1:A:300:A:O5'	1.72	0.72
1:A:574:A:H5''	1:A:575:G:OP2	1.89	0.72
15:O:21:ASP:OD1	15:O:24:SER:HB2	1.90	0.72
1:A:192:U:H2'	1:A:193:C:H6	1.55	0.72
7:G:135:VAL:HG12	7:G:139:GLU:HG3	1.71	0.72
3:C:156:ARG:H	3:C:163:ALA:HA	1.53	0.72
12:L:41:ARG:HB3	12:L:41:ARG:NH1	2.05	0.72
4:D:65:ARG:HG3	4:D:75:PHE:CD1	2.25	0.71
1:A:168:G:O2'	1:A:169:C:H5'	1.90	0.71
3:C:150:LYS:HG3	3:C:169:ALA:HB2	1.70	0.71
1:A:392:G:H2'	1:A:393:A:C8	2.25	0.71
1:A:1487:G:C2'	1:A:1488:G:H5'	2.21	0.71
3:C:201:TYR:O	3:C:202:ILE:HG13	1.90	0.71
1:A:975:A:H4'	1:A:976:G:C5'	2.19	0.71
19:S:51:VAL:HG12	19:S:52:TYR:H	1.53	0.71
20:T:45:GLN:HA	20:T:91:LEU:HD12	1.71	0.71
5:E:57:LYS:O	5:E:61:TYR:HD2	1.71	0.71
5:E:87:SER:HB3	5:E:131:ILE:CD1	2.21	0.71
7:G:3:ARG:O	7:G:4:ARG:HB2	1.91	0.71
8:H:20:TYR:CE1	8:H:76:PRO:HD2	2.26	0.71
1:A:1148:U:H2'	1:A:1149:C:O4'	1.91	0.71
1:A:538:G:OP1	12:L:113:ARG:HD2	1.90	0.71
10:J:34:VAL:HG22	10:J:74:ILE:HG23	1.73	0.70
1:A:1168:A:H2'	1:A:1169:A:C8	2.26	0.70
1:A:1203:C:H2'	1:A:1204:A:O4'	1.91	0.70
1:A:489:C:H2'	1:A:490:G:H8	1.57	0.70
1:A:177:C:H2'	1:A:178:C:C6	2.26	0.70
1:A:665:A:N3	1:A:732:C:H2'	2.07	0.70
1:A:409:G:H1	1:A:433:C:N4	1.85	0.70
1:A:457:C:H2'	1:A:458:C:H6	1.55	0.70
9:I:11:LYS:O	9:I:12:GLU:HB2	1.91	0.70
1:A:1068:G:H8	1:A:1068:G:OP2	1.75	0.70
1:A:95:U:H2'	1:A:96:G:C8	2.27	0.70
4:D:161:ASN:O	4:D:165:MET:HG2	1.92	0.70
1:A:1001:A:H2'	1:A:1002:G:C8	2.27	0.70
1:A:1234:C:H1'	1:A:1364:U:O2	1.90	0.70
1:A:190(F):G:H4'	1:A:190(G):G:OP2	1.91	0.70
1:A:475:G:C2	1:A:476:G:C5	2.80	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:436:C:H2'	1:A:437:U:H6	1.57	0.69
3:C:21:ARG:HH21	3:C:56:ASP:HB3	1.54	0.69
1:A:243:A:H4'	1:A:244:U:O5'	1.92	0.69
3:C:120:VAL:O	3:C:124:ILE:HG13	1.92	0.69
2:B:69:LEU:HD12	2:B:155:LEU:HD11	1.73	0.69
13:M:65:LYS:O	13:M:70:LEU:HD12	1.93	0.69
12:L:43:VAL:HG12	12:L:44:THR:H	1.58	0.69
1:A:1533:C:H2'	1:A:1534:A:H5'	1.75	0.69
1:A:1080:A:H5''	5:E:16:THR:HG21	1.73	0.69
1:A:1421:G:H2'	1:A:1422:G:H8	1.58	0.69
19:S:17:GLU:HA	19:S:20:LEU:HG	1.75	0.69
6:F:6:VAL:HG22	6:F:90:VAL:HG13	1.75	0.69
8:H:9:MET:HG3	8:H:26:VAL:HG21	1.75	0.69
1:A:977:A:H2'	1:A:978:A:H5'	1.75	0.69
1:A:92:C:C5	1:A:93:G:N7	2.61	0.69
1:A:990:C:H4'	1:A:1018:C:OP1	1.93	0.69
7:G:17:VAL:HG12	7:G:18:TYR:CD2	2.26	0.69
3:C:108:ASN:ND2	3:C:111:LEU:HG	2.06	0.69
1:A:16:A:H2'	1:A:17:U:H5'	1.75	0.69
1:A:359:U:H2'	1:A:360:A:C8	2.27	0.69
3:C:172:ARG:HE	3:C:203:PHE:HE2	1.41	0.69
2:B:204:ASN:HD22	2:B:206:ASP:H	1.40	0.68
1:A:1201:A:H1'	1:A:1202:G:OP2	1.93	0.68
13:M:5:ALA:HB3	13:M:22:ILE:HD13	1.74	0.68
20:T:53:LEU:HD12	20:T:100:ILE:HG23	1.74	0.68
1:A:1031:G:H2'	1:A:1032:G:C8	2.28	0.68
10:J:6:ILE:HD13	10:J:72:VAL:HB	1.76	0.68
1:A:1373:G:H5''	7:G:36:LYS:NZ	2.09	0.68
1:A:1485:U:H2'	1:A:1485:U:O2	1.92	0.68
1:A:1303:C:H2'	1:A:1304:G:H5'	1.73	0.68
1:A:1510:U:H2'	1:A:1511:G:C8	2.28	0.68
1:A:397:A:H5'	1:A:398:C:OP1	1.94	0.68
1:A:330:C:H2'	1:A:331:G:H5'	1.75	0.68
1:A:1103:C:H2'	1:A:1104:G:O4'	1.94	0.68
15:O:5:LYS:HD2	15:O:5:LYS:H	1.58	0.68
1:A:631:G:H5'	1:A:632:A:OP1	1.94	0.68
10:J:34:VAL:HG13	10:J:74:ILE:HA	1.74	0.68
1:A:461:C:H4'	1:A:462:G:OP2	1.94	0.67
3:C:27:LYS:HA	3:C:30:ARG:HH12	1.59	0.67
10:J:16:LEU:HD13	10:J:70:ARG:HG2	1.76	0.67
1:A:1487:G:O2'	1:A:1488:G:H5'	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:116:VAL:O	3:C:119:ARG:HB3	1.95	0.67
1:A:1262:C:H42	1:A:1273:G:H1	1.43	0.67
12:L:86:ARG:HH22	12:L:99:HIS:HD2	1.42	0.67
1:A:77:G:N1	1:A:92:C:N4	2.40	0.67
13:M:92:HIS:HA	13:M:110:ARG:NH2	2.10	0.67
1:A:628:G:O2'	1:A:629:G:H5'	1.94	0.67
8:H:118:VAL:O	8:H:119:LEU:HD23	1.94	0.67
14:N:23:ARG:NH1	14:N:30:ALA:HB2	2.08	0.67
1:A:106:C:C2'	1:A:107:G:H5'	2.24	0.67
15:O:39:LEU:HD12	15:O:56:LEU:HB2	1.77	0.67
1:A:1367:C:H4'	10:J:48:THR:HG21	1.76	0.67
9:I:78:LYS:HD3	9:I:101:PHE:HD2	1.59	0.67
1:A:113:G:H2'	1:A:114:U:C6	2.29	0.67
1:A:965:A:H1'	1:A:966:G:OP2	1.94	0.67
1:A:1031:G:H2'	1:A:1032:G:H8	1.60	0.67
1:A:924:C:H5'	1:A:1399:C:OP2	1.95	0.67
1:A:1046:A:H5'	1:A:1047:G:OP2	1.95	0.66
1:A:1126:U:H2'	1:A:1126:U:O2	1.94	0.66
14:N:23:ARG:HH12	14:N:30:ALA:HB2	1.60	0.66
1:A:1489:G:C2	1:A:1490:C:C2	2.83	0.66
1:A:946:A:H2'	1:A:947:G:C8	2.30	0.66
1:A:707:C:H2'	1:A:708:C:C6	2.30	0.66
1:A:299:G:H2'	1:A:300:A:C8	2.31	0.66
1:A:380:G:N2	1:A:382:A:H3'	2.11	0.66
1:A:1189:C:H4'	3:C:10:PHE:CE1	2.31	0.66
9:I:16:ARG:HH11	9:I:64:THR:HG21	1.59	0.66
12:L:34:ARG:O	12:L:61:THR:HG23	1.95	0.66
2:B:24:TRP:CZ3	2:B:26:PRO:HA	2.31	0.66
10:J:44:VAL:CG1	10:J:66:ARG:HE	2.08	0.66
11:K:33:THR:HG22	11:K:39:PRO:HA	1.78	0.66
1:A:1392:G:H2'	1:A:1393:U:H6	1.61	0.66
1:A:383:A:H2'	1:A:384:G:H5'	1.78	0.66
1:A:77:G:H1	1:A:92:C:H42	1.44	0.66
1:A:372:C:H1'	1:A:373:A:OP2	1.96	0.66
9:I:105:ASP:OD1	9:I:107:ARG:HG3	1.94	0.66
10:J:6:ILE:CD1	10:J:73:ASP:H	2.09	0.66
1:A:795:C:H5'	1:A:796:C:OP2	1.96	0.66
1:A:864:A:H2'	1:A:865:A:C8	2.31	0.66
9:I:48:GLU:HG2	9:I:51:ARG:NH2	2.10	0.66
12:L:24:VAL:HG13	12:L:98:TYR:HE2	1.61	0.66
1:A:1101:A:H4'	1:A:1102:A:O5'	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:100:ARG:O	4:D:104:VAL:HG23	1.96	0.65
1:A:447:G:H2'	1:A:485:G:N2	2.11	0.65
1:A:262:A:H5'	20:T:74:LYS:HG3	1.77	0.65
1:A:945:G:O6	1:A:1236:A:N1	2.29	0.65
1:A:836:G:C6	1:A:851:G:C6	2.83	0.65
1:A:960:U:H4'	1:A:961:U:O5'	1.95	0.65
7:G:65:ALA:O	7:G:69:VAL:HG23	1.96	0.65
1:A:1426:C:H2'	1:A:1427:U:C6	2.31	0.65
1:A:1539:C:H2'	1:A:1540:U:O4'	1.96	0.65
17:Q:97:SER:HA	17:Q:103:GLY:HA3	1.77	0.65
1:A:1225:A:N3	1:A:1225:A:H2'	2.11	0.65
1:A:16:A:C2'	1:A:17:U:H5'	2.26	0.65
1:A:445:G:H2'	1:A:446:G:H8	1.61	0.65
11:K:23:ALA:HB1	11:K:88:GLY:HA3	1.78	0.65
1:A:1026:G:N3	1:A:1026:G:H2'	2.11	0.65
1:A:1442:G:C6	1:A:1446:A:N6	2.65	0.65
1:A:616:G:H1'	1:A:625:G:N2	2.12	0.65
1:A:287:U:C2'	1:A:288:A:H5'	2.26	0.65
5:E:82:VAL:HG21	5:E:138:ALA:HA	1.78	0.65
1:A:1115:C:O2'	1:A:1116:C:H5'	1.95	0.65
1:A:75:G:N2	1:A:76:C:N3	2.45	0.65
17:Q:68:ARG:H	17:Q:70:ARG:HH11	1.44	0.65
5:E:89:ILE:HD13	5:E:90:VAL:H	1.61	0.65
17:Q:67:LYS:O	17:Q:68:ARG:HB2	1.97	0.65
1:A:96:G:H2'	1:A:97:G:O4'	1.97	0.65
1:A:792:A:OP2	1:A:792:A:H8	1.80	0.65
13:M:12:ASN:H	13:M:45:VAL:CG1	2.10	0.65
2:B:61:LEU:HD13	2:B:66:GLY:HA3	1.79	0.65
13:M:23:TYR:CE2	13:M:70:LEU:HD22	2.26	0.65
2:B:204:ASN:HD22	2:B:205:ASP:N	1.95	0.65
1:A:284:G:H2'	1:A:285:G:C8	2.32	0.65
12:L:39:VAL:HG12	12:L:40:VAL:N	2.12	0.65
10:J:8:LEU:HD12	10:J:20:ALA:HB2	1.77	0.65
5:E:11:ILE:HG21	5:E:105:VAL:HG13	1.78	0.65
1:A:620:C:C1'	4:D:135:LEU:HD13	2.27	0.65
1:A:627:G:H2'	1:A:628:G:H8	1.62	0.64
1:A:235:C:C5'	17:Q:70:ARG:HG2	2.28	0.64
12:L:43:VAL:HG12	12:L:44:THR:N	2.12	0.64
2:B:134:GLU:HA	2:B:137:ARG:HG2	1.78	0.64
3:C:155:GLY:O	3:C:196:LEU:HD22	1.97	0.64
2:B:36:ARG:O	2:B:39:ILE:HG12	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1320:C:N3	19:S:36:ARG:HD3	2.12	0.64
1:A:363:A:OP2	12:L:61:THR:HG21	1.97	0.64
3:C:128:PHE:HD2	3:C:129:ALA:H	1.43	0.64
10:J:38:ILE:HB	10:J:71:LEU:HB3	1.80	0.64
1:A:370:C:C2'	1:A:371:G:H5'	2.27	0.64
15:O:78:TYR:CE1	15:O:82:ILE:HD11	2.32	0.64
1:A:255:G:H1'	17:Q:16:GLN:OE1	1.97	0.64
2:B:180:LEU:O	2:B:181:PHE:HB2	1.96	0.64
10:J:14:LYS:O	10:J:18:ALA:HB3	1.97	0.64
1:A:1112:C:C2	3:C:178:LEU:HB2	2.33	0.64
1:A:532:A:H2'	1:A:532:A:N3	2.11	0.64
1:A:1374:A:C4	1:A:1375:A:C8	2.85	0.64
1:A:109:A:H2'	1:A:326:G:N2	2.13	0.64
1:A:1308:U:O2'	1:A:1309:G:H5'	1.98	0.64
1:A:1296:C:H4'	1:A:1302:U:C5	2.33	0.64
2:B:103:THR:HG23	2:B:176:GLU:CG	2.26	0.64
1:A:784:C:H2'	1:A:785:G:O4'	1.98	0.64
17:Q:59:ILE:HG23	17:Q:71:PHE:HB3	1.79	0.64
7:G:26:PHE:HD1	7:G:101:LEU:HD22	1.62	0.64
19:S:50:ALA:HA	19:S:58:VAL:O	1.97	0.64
1:A:1064:G:H1'	1:A:1190:G:N2	2.13	0.64
10:J:32:ALA:HB2	10:J:76:ASN:HD21	1.62	0.64
1:A:689:C:P	11:K:46:GLY:HA3	2.37	0.64
1:A:98:U:H2'	1:A:99:C:C6	2.33	0.63
2:B:110:GLN:HA	2:B:113:HIS:CD2	2.33	0.63
3:C:86:VAL:O	3:C:89:GLU:HB2	1.97	0.63
1:A:1053:G:HO2'	1:A:1199:U:H5	1.47	0.63
14:N:24:CYS:SG	14:N:39:LEU:HA	2.38	0.63
1:A:1366:C:H2'	1:A:1367:C:C6	2.31	0.63
1:A:1064:G:H21	1:A:1190:G:H2'	1.62	0.63
1:A:359:U:H2'	1:A:360:A:H8	1.61	0.63
1:A:1504:G:H4'	1:A:1505:G:H5'	1.80	0.63
2:B:115:LEU:HD12	2:B:145:LEU:CB	2.28	0.63
15:O:36:ILE:HD11	15:O:60:VAL:HA	1.79	0.63
7:G:116:ALA:CA	7:G:119:ARG:HH21	2.10	0.63
15:O:21:ASP:CG	15:O:24:SER:HB2	2.19	0.63
15:O:87:ILE:HG22	15:O:88:ARG:N	2.12	0.63
7:G:116:ALA:HA	7:G:119:ARG:NH2	2.12	0.63
9:I:108:VAL:HG12	9:I:109:VAL:H	1.63	0.63
1:A:1421:G:H2'	1:A:1422:G:C8	2.32	0.63
1:A:369:C:O2'	1:A:370:C:H5'	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1391:U:H2'	1:A:1392:G:C8	2.34	0.63
6:F:56:PRO:HD2	6:F:57:GLN:HG2	1.81	0.63
1:A:193:C:H4'	20:T:61:SER:HB2	1.81	0.63
7:G:146:GLU:HA	7:G:149:ARG:HG2	1.81	0.63
5:E:45:PHE:CD2	5:E:47:LYS:HE3	2.33	0.63
10:J:40:LEU:HD22	10:J:69:ASN:HB2	1.80	0.63
1:A:558:G:H3'	1:A:559:A:H3'	1.80	0.63
12:L:24:VAL:HG13	12:L:98:TYR:CE2	2.33	0.63
12:L:86:ARG:NH2	12:L:99:HIS:HD2	1.97	0.63
11:K:53:SER:O	11:K:55:LYS:N	2.32	0.63
14:N:53:LEU:O	14:N:56:VAL:HB	1.97	0.63
3:C:34:LEU:HG	14:N:25:VAL:HG21	1.79	0.63
7:G:63:LYS:O	7:G:66:VAL:HG12	1.98	0.63
15:O:87:ILE:HG22	15:O:88:ARG:H	1.64	0.63
1:A:986:A:H4'	19:S:55:LYS:HZ3	1.63	0.63
1:A:1250:A:C2	1:A:1287:A:N1	2.67	0.63
1:A:1425:U:H2'	1:A:1426:C:C6	2.33	0.63
3:C:148:GLY:HA3	3:C:172:ARG:O	1.98	0.63
1:A:429:U:H1'	1:A:430:A:H5''	1.80	0.63
7:G:54:THR:HG22	7:G:56:GLN:HG2	1.80	0.63
8:H:116:LYS:NZ	8:H:127:LEU:HB3	2.14	0.63
18:R:19:LYS:CD	18:R:20:ALA:H	2.07	0.62
2:B:74:LYS:NZ	2:B:206:ASP:HA	2.14	0.62
17:Q:97:SER:HA	17:Q:102:GLY:O	1.99	0.62
20:T:67:ALA:HA	20:T:73:HIS:H	1.62	0.62
1:A:1204:A:C2'	1:A:1205:U:H5'	2.27	0.62
1:A:1416:G:H22	1:A:1485:U:H1'	1.64	0.62
17:Q:49:GLU:O	17:Q:52:LYS:HE2	1.99	0.62
11:K:14:VAL:HG21	11:K:40:ILE:HD11	1.79	0.62
18:R:73:ALA:HB3	18:R:79:LEU:HD12	1.82	0.62
7:G:71:PRO:HG3	7:G:103:TRP:HZ3	1.63	0.62
1:A:392:G:H2'	1:A:393:A:H8	1.62	0.62
12:L:34:ARG:HG3	12:L:105:TYR:HE1	1.64	0.62
6:F:10:LEU:HB3	6:F:85:VAL:HA	1.80	0.62
15:O:48:LYS:HE2	15:O:48:LYS:HA	1.81	0.62
17:Q:68:ARG:H	17:Q:70:ARG:NH1	1.97	0.62
5:E:87:SER:HB3	5:E:131:ILE:HD12	1.80	0.62
8:H:69:ARG:HB2	8:H:74:PRO:O	1.99	0.62
1:A:1303:C:C2'	1:A:1304:G:H5'	2.29	0.62
14:N:59:ALA:HB1	14:N:61:TRP:CZ3	2.32	0.62
8:H:28:ALA:HA	8:H:59:LEU:HD12	1.81	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:25:ASN:C	2:B:25:ASN:HD22	2.03	0.62
1:A:687:A:H4'	1:A:688:G:O5'	1.99	0.62
6:F:23:LYS:O	6:F:27:GLN:HG2	2.00	0.62
1:A:738:C:OP1	6:F:92:LYS:HD3	1.99	0.62
1:A:833:U:H2'	1:A:834:C:C6	2.34	0.62
1:A:1372:U:H5''	9:I:71:SER:HB3	1.82	0.62
3:C:28:GLN:O	3:C:29:TYR:HB2	1.99	0.62
1:A:977:A:C8	1:A:1223:C:C4	2.88	0.62
18:R:22:VAL:O	18:R:26:LEU:HD13	1.99	0.62
2:B:146:GLN:O	2:B:150:SER:HB3	2.00	0.62
1:A:70:G:H2'	1:A:73:C:H5'	1.81	0.62
17:Q:63:ARG:HG2	17:Q:64:PRO:CD	2.30	0.62
1:A:1040:U:H2'	1:A:1041:A:C8	2.35	0.62
1:A:1381:U:H5	1:A:1382:C:C5	2.18	0.62
3:C:188:LEU:HD23	3:C:188:LEU:H	1.65	0.62
2:B:187:LEU:HD22	2:B:205:ASP:HB3	1.81	0.62
15:O:45:VAL:HG22	15:O:46:HIS:N	2.14	0.62
7:G:51:GLN:HB3	7:G:55:GLY:HA2	1.81	0.62
8:H:19:VAL:HG23	8:H:19:VAL:O	1.99	0.62
1:A:1202:G:C4	14:N:42:ILE:HD12	2.35	0.61
1:A:489:C:H2'	1:A:490:G:C8	2.35	0.61
1:A:345:C:OP2	1:A:345:C:H6	1.82	0.61
1:A:1359:C:O2'	1:A:1361:G:N7	2.33	0.61
1:A:264:U:H2'	1:A:265:G:H5'	1.81	0.61
6:F:62:TRP:C	6:F:63:TYR:HD2	2.04	0.61
9:I:19:LEU:HD23	9:I:61:ALA:HB2	1.82	0.61
1:A:424:G:H2'	1:A:425:G:H8	1.65	0.61
10:J:42:THR:HG23	10:J:67:THR:O	2.00	0.61
13:M:97:PRO:HB2	13:M:101:GLN:HG3	1.81	0.61
13:M:96:LEU:HB3	13:M:97:PRO:HD2	1.82	0.61
6:F:38:GLU:O	6:F:39:LYS:HB3	2.01	0.61
1:A:152:A:N6	1:A:170:U:C2	2.68	0.61
16:P:65:GLN:NE2	16:P:65:GLN:HA	2.14	0.61
14:N:8:GLU:HG3	14:N:11:LYS:HD2	1.81	0.61
1:A:22:G:H2'	1:A:23:C:C6	2.34	0.61
1:A:602:A:C2	1:A:637:G:C2	2.88	0.61
16:P:74:LEU:O	16:P:79:VAL:HG23	1.99	0.61
5:E:9:LYS:HB2	5:E:112:LEU:HD11	1.82	0.61
1:A:504:C:C2	1:A:542:G:N2	2.69	0.61
7:G:26:PHE:HA	7:G:101:LEU:HD13	1.82	0.61
2:B:110:GLN:HA	2:B:113:HIS:HD2	1.64	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:2:ARG:HH21	6:F:69:GLU:HG2	1.65	0.61
1:A:1310:G:H5'	1:A:1311:G:OP2	2.01	0.61
12:L:47:LYS:HB3	12:L:48:PRO:CD	2.30	0.61
16:P:18:ARG:HD3	16:P:35:LYS:HE2	1.80	0.61
18:R:54:ARG:NH2	18:R:54:ARG:HB2	2.16	0.61
1:A:130:A:C8	17:Q:63:ARG:HG3	2.36	0.61
1:A:434:U:H2'	1:A:435:C:O4'	2.01	0.61
1:A:113:G:H2'	1:A:114:U:H6	1.64	0.61
1:A:1474:G:H2'	1:A:1475:G:C8	2.35	0.61
19:S:11:VAL:HG21	19:S:41:VAL:HG13	1.83	0.61
11:K:126:ARG:O	11:K:127:LYS:HB2	2.00	0.61
12:L:62:SER:C	12:L:64:TYR:H	2.04	0.61
4:D:153:ARG:HG3	4:D:181:MET:SD	2.40	0.61
1:A:1148:U:C4	1:A:1149:C:N3	2.69	0.61
18:R:34:TYR:CD1	18:R:35:ARG:HG3	2.35	0.61
3:C:137:ALA:O	3:C:141:VAL:HG23	2.00	0.61
5:E:72:GLN:O	5:E:73:ASN:HB3	2.00	0.61
12:L:39:VAL:HG12	12:L:40:VAL:H	1.65	0.61
1:A:142:G:N3	1:A:196:A:H2	1.98	0.61
1:A:1054:C:H3'	1:A:1054:C:O2	2.00	0.61
1:A:1028:C:N4	1:A:1033:G:H22	1.98	0.61
1:A:721:G:N1	1:A:733:A:C2	2.69	0.61
5:E:19:MET:SD	5:E:24:ARG:HB3	2.40	0.61
1:A:1201:A:H4'	1:A:1202:G:O5'	2.01	0.60
1:A:1250:A:N1	1:A:1287:A:C2	2.68	0.60
5:E:10:MET:HA	5:E:32:VAL:HG23	1.83	0.60
4:D:191:ARG:NH1	4:D:196:LEU:HB2	2.16	0.60
1:A:633:G:H2'	1:A:634:C:C6	2.35	0.60
2:B:42:ILE:HG13	2:B:203:GLY:HA2	1.82	0.60
1:A:1056:U:O2'	1:A:1057:G:H5'	2.00	0.60
19:S:6:LYS:HG2	19:S:7:LYS:H	1.65	0.60
1:A:260:G:C5	1:A:261:U:C5	2.89	0.60
1:A:445:G:H2'	1:A:446:G:C8	2.36	0.60
1:A:24:U:H2'	1:A:25:C:C6	2.37	0.60
1:A:186:C:H2'	1:A:187:C:C6	2.37	0.60
13:M:70:LEU:C	13:M:70:LEU:HD23	2.21	0.60
17:Q:7:THR:O	17:Q:23:VAL:HG13	2.01	0.60
12:L:25:PRO:C	12:L:27:LEU:N	2.54	0.60
15:O:87:ILE:HG22	15:O:88:ARG:HD3	1.82	0.60
1:A:1152:A:H2'	1:A:1153:C:H6	1.66	0.60
7:G:27:ILE:HD12	7:G:40:ALA:HA	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:29:ARG:HG3	14:N:30:ALA:N	2.16	0.60
12:L:43:VAL:HG23	12:L:55:VAL:HG21	1.83	0.60
1:A:1126:U:C6	1:A:1126:U:OP1	2.54	0.60
1:A:106:C:H2'	1:A:107:G:H5'	1.83	0.60
1:A:629:G:H2'	1:A:630:G:O4'	2.02	0.60
1:A:287:U:H2'	1:A:288:A:H5'	1.82	0.60
17:Q:36:ILE:HD13	17:Q:36:ILE:H	1.66	0.60
3:C:85:ARG:HA	3:C:88:ARG:HB3	1.83	0.60
20:T:100:ILE:HG12	20:T:102:GLY:H	1.65	0.60
1:A:1273:G:H2'	1:A:1274:G:O4'	2.02	0.60
10:J:90:LEU:N	10:J:91:PRO:HD3	2.17	0.60
4:D:151:LYS:H	4:D:151:LYS:HD2	1.67	0.60
1:A:1142:G:H2'	1:A:1143:G:O4'	2.02	0.60
17:Q:97:SER:CA	17:Q:103:GLY:HA3	2.32	0.60
2:B:114:ARG:NH1	2:B:118:LEU:HD21	2.15	0.60
1:A:192:U:H5'	20:T:102:GLY:O	2.01	0.60
1:A:833:U:H2'	1:A:834:C:H6	1.67	0.60
1:A:1381:U:C5	1:A:1382:C:C5	2.89	0.60
15:O:26:GLU:OE1	15:O:77:ARG:HD2	2.02	0.60
6:F:67:MET:HB2	6:F:68:PRO:HD2	1.83	0.60
16:P:31:LYS:HG2	16:P:32:TYR:H	1.67	0.60
1:A:390:C:H4'	16:P:28:ARG:NH1	2.17	0.60
1:A:1404:C:H1'	1:A:1499:A:C2	2.37	0.60
1:A:1250:A:C2	1:A:1287:A:C6	2.90	0.60
8:H:6:ILE:H	8:H:6:ILE:HD12	1.66	0.60
1:A:70:G:C5	1:A:73:C:C4	2.90	0.60
1:A:722:A:N6	1:A:724:G:C2	2.70	0.60
16:P:20:VAL:HG21	16:P:32:TYR:CG	2.37	0.60
1:A:41:G:H2'	1:A:42:G:H8	1.66	0.60
1:A:781:A:C5	1:A:802:A:C2	2.90	0.60
7:G:43:PHE:O	7:G:47:CYS:HB2	2.02	0.59
2:B:97:TRP:CE2	2:B:101:MET:HG3	2.37	0.59
1:A:1163:C:H2'	1:A:1164:G:C8	2.36	0.59
2:B:44:LEU:H	2:B:44:LEU:HD13	1.67	0.59
3:C:6:HIS:CD2	3:C:8:ILE:HB	2.37	0.59
1:A:77:G:H2'	1:A:78:G:H8	1.67	0.59
20:T:100:ILE:HG12	20:T:102:GLY:N	2.16	0.59
1:A:1152:A:H5''	10:J:13:HIS:HB2	1.84	0.59
9:I:97:LYS:HB3	9:I:98:PRO:HD3	1.83	0.59
1:A:491:G:H2'	1:A:492:G:H8	1.67	0.59
1:A:1118:C:H1'	1:A:1179:A:C4	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1178:G:N2	1:A:1180:A:H3'	2.17	0.59
12:L:41:ARG:NH1	12:L:42:THR:H	1.99	0.59
1:A:978:A:OP1	1:A:978:A:H8	1.85	0.59
1:A:946:A:H2'	1:A:947:G:H8	1.65	0.59
1:A:41:G:H2'	1:A:42:G:C8	2.37	0.59
1:A:1436:U:C5	1:A:1437:C:C4	2.90	0.59
1:A:74:C:H3'	1:A:75:G:H5'	1.84	0.59
1:A:96:G:O2'	1:A:97:G:H5'	2.02	0.59
1:A:328:C:H1'	1:A:329:A:OP2	2.03	0.59
1:A:1040:U:H2'	1:A:1041:A:H8	1.67	0.59
1:A:1308:U:OP2	13:M:99:ARG:HG3	2.02	0.59
1:A:721:G:C6	1:A:733:A:C2	2.91	0.59
17:Q:29:HIS:HB2	17:Q:36:ILE:HD12	1.83	0.59
12:L:55:VAL:HG12	12:L:56:ALA:N	2.11	0.59
3:C:91:LEU:HD21	3:C:99:VAL:H	1.68	0.59
2:B:172:ILE:H	2:B:172:ILE:HD12	1.66	0.59
2:B:97:TRP:HH2	2:B:176:GLU:CD	2.06	0.59
1:A:243:A:C2	1:A:246:A:C8	2.91	0.59
1:A:1474:G:H2'	1:A:1475:G:H8	1.67	0.59
6:F:62:TRP:CH2	6:F:64:GLN:HB2	2.37	0.59
1:A:1269:A:H5'	1:A:1270:C:OP2	2.02	0.59
19:S:31:ILE:HB	19:S:49:ILE:HD13	1.85	0.59
18:R:40:LEU:N	18:R:40:LEU:HD23	2.18	0.59
1:A:73:C:N3	1:A:97:G:N2	2.50	0.59
1:A:261:U:O2	1:A:263:A:C8	2.55	0.59
7:G:51:GLN:HA	7:G:54:THR:O	2.03	0.59
1:A:291:C:O2'	1:A:292:G:H5'	2.03	0.59
1:A:559:A:H4'	1:A:560:U:C3'	2.24	0.59
3:C:23:TYR:CG	3:C:24:ALA:N	2.71	0.59
1:A:750:G:H21	15:O:23:GLY:HA3	1.67	0.59
5:E:110:LEU:HD13	5:E:118:ILE:HD13	1.83	0.59
1:A:1020:U:H2'	1:A:1021:G:C8	2.37	0.59
1:A:1112:C:N4	3:C:178:LEU:HD23	2.18	0.59
15:O:21:ASP:OD2	15:O:24:SER:HB2	2.03	0.59
20:T:50:GLU:H	20:T:99:LEU:HD12	1.68	0.59
2:B:101:MET:HA	2:B:108:ILE:HG21	1.84	0.59
2:B:87:ARG:O	2:B:88:ALA:HB3	2.02	0.59
1:A:1351:U:H4'	7:G:33:ASP:OD2	2.03	0.59
1:A:35:G:H2'	1:A:36:C:C6	2.38	0.59
10:J:6:ILE:HG23	10:J:98:ILE:HG12	1.85	0.59
2:B:230:VAL:HG12	2:B:231:GLU:N	2.17	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:41:VAL:HB	19:S:42:PRO:HD2	1.84	0.59
1:A:500:G:C5	1:A:546:G:N2	2.71	0.59
1:A:273:A:C2'	1:A:274:A:H5'	2.33	0.59
5:E:71:LEU:HD11	5:E:113:ALA:O	2.03	0.59
1:A:1351:U:H4'	7:G:33:ASP:CG	2.22	0.58
2:B:223:ILE:C	2:B:225:ALA:H	2.07	0.58
7:G:18:TYR:OH	7:G:58:PRO:HB2	2.03	0.58
1:A:273:A:H2'	1:A:274:A:H5'	1.84	0.58
1:A:355:C:C4	1:A:356:A:N7	2.71	0.58
1:A:627:G:O2'	1:A:628:G:H5'	2.03	0.58
18:R:44:LEU:HD21	18:R:70:ILE:HD13	1.84	0.58
1:A:277:C:H5'	17:Q:68:ARG:HH12	1.67	0.58
6:F:4:TYR:CE1	6:F:92:LYS:HG2	2.38	0.58
1:A:401:C:H2'	1:A:402:G:H8	1.68	0.58
12:L:54:LYS:N	12:L:54:LYS:HD2	2.19	0.58
14:N:41:ARG:HG3	14:N:42:ILE:N	2.19	0.58
8:H:6:ILE:N	8:H:6:ILE:HD12	2.19	0.58
13:M:5:ALA:HA	13:M:61:GLU:HG2	1.84	0.58
1:A:336:C:H2'	1:A:337:C:H6	1.69	0.58
15:O:18:PHE:HB2	15:O:19:PRO:HD2	1.83	0.58
3:C:22:TRP:CB	3:C:59:ARG:HB2	2.33	0.58
1:A:688:G:C4	1:A:700:G:N2	2.71	0.58
9:I:19:LEU:HB3	9:I:59:PHE:CE2	2.38	0.58
16:P:31:LYS:HG2	16:P:32:TYR:N	2.19	0.58
20:T:93:GLU:HG3	20:T:94:ALA:N	2.17	0.58
4:D:24:GLU:O	4:D:25:ARG:HB3	2.04	0.58
1:A:193:C:H2'	1:A:194:C:H6	1.69	0.58
1:A:428:G:H4'	1:A:429:U:O5'	2.03	0.58
16:P:60:LEU:HD23	16:P:64:ALA:HB3	1.85	0.58
18:R:38:GLU:CD	18:R:38:GLU:H	2.07	0.58
1:A:344:A:H4'	1:A:345:C:OP2	2.03	0.58
1:A:201:C:H42	1:A:216:G:H1	1.52	0.58
12:L:124:LYS:HD2	12:L:125:PRO:HD2	1.86	0.58
1:A:1024:G:H2'	1:A:1025:U:C6	2.39	0.58
7:G:111:ARG:HB3	7:G:113:GLU:HG2	1.86	0.58
2:B:134:GLU:C	2:B:136:VAL:H	2.07	0.58
1:A:1078:U:H5''	1:A:1079:G:OP2	2.03	0.58
1:A:1278:U:H5''	1:A:1279:A:O4'	2.04	0.58
1:A:96:G:C6	1:A:97:G:C2	2.92	0.58
9:I:48:GLU:N	9:I:49:PRO:HD2	2.18	0.58
1:A:1316:G:N2	1:A:1319:A:OP2	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:908:A:C2	1:A:909:A:C4	2.92	0.58
1:A:1399:C:O2	1:A:1401:G:C5	2.57	0.58
11:K:84:VAL:HG11	11:K:91:ARG:HD3	1.86	0.58
11:K:15:ALA:CA	11:K:77:MET:HA	2.24	0.57
1:A:88:A:C5	1:A:89:C:C5	2.92	0.57
1:A:17:U:H2'	1:A:18:C:C6	2.38	0.57
1:A:302:G:H5''	12:L:17:LYS:HE3	1.86	0.57
1:A:518:C:H5''	1:A:519:C:C6	2.39	0.57
5:E:101:ILE:HG22	5:E:101:ILE:O	2.04	0.57
1:A:1205:U:H4'	3:C:195:VAL:HG11	1.86	0.57
1:A:61:G:H2'	1:A:62:U:O4'	2.04	0.57
7:G:65:ALA:HB2	7:G:128:ALA:HB2	1.85	0.57
1:A:1430:C:H2'	1:A:1431:C:H6	1.68	0.57
15:O:33:THR:HG23	15:O:63:ARG:NH1	2.19	0.57
9:I:48:GLU:CG	9:I:51:ARG:HH21	2.14	0.57
1:A:1130:A:H5''	9:I:20:ARG:HH22	1.68	0.57
1:A:1047:G:O2'	1:A:1048:G:H5'	2.04	0.57
1:A:1311:G:N7	19:S:2:PRO:HA	2.20	0.57
1:A:1072:G:C5	1:A:1073:U:C4	2.92	0.57
1:A:1531:A:O5'	1:A:1531:A:H8	1.87	0.57
1:A:1157:A:H4'	1:A:1158:C:O5'	2.04	0.57
3:C:64:VAL:CG2	3:C:99:VAL:HG11	2.32	0.57
20:T:54:LYS:HA	20:T:57:ARG:NH1	2.19	0.57
12:L:34:ARG:HG3	12:L:105:TYR:CE1	2.39	0.57
2:B:24:TRP:HZ3	2:B:29:ALA:HB2	1.68	0.57
14:N:14:PRO:O	14:N:15:LYS:HB2	2.03	0.57
4:D:88:VAL:O	4:D:92:VAL:HG23	2.04	0.57
1:A:775:G:C2'	1:A:776:G:H5'	2.35	0.57
7:G:79:ARG:HG3	7:G:82:GLY:O	2.04	0.57
1:A:1298:C:H2'	7:G:114:ARG:NH1	2.18	0.57
1:A:1047:G:O5'	1:A:1047:G:H8	1.87	0.57
9:I:5:TYR:CD2	9:I:6:GLY:N	2.70	0.57
1:A:130:A:H1'	1:A:263:A:O2'	2.03	0.57
1:A:146:G:H2'	1:A:147:G:H8	1.68	0.57
12:L:27:LEU:C	12:L:29:GLY:H	2.08	0.57
5:E:72:GLN:NE2	5:E:144:THR:HG23	2.20	0.57
1:A:532:A:H3'	1:A:533:A:C5'	2.35	0.57
17:Q:5:VAL:O	17:Q:6:LEU:HD23	2.03	0.57
1:A:184:G:H2'	1:A:185:A:H8	1.68	0.57
13:M:75:ALA:HA	13:M:78:ILE:HD12	1.86	0.57
1:A:1200:C:O2	1:A:1200:C:H2'	2.04	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:357:G:C2	1:A:358:U:C5	2.93	0.57
6:F:10:LEU:HD12	6:F:59:TYR:HB3	1.86	0.57
1:A:594:G:H2'	1:A:595:G:H5'	1.87	0.57
1:A:1015:A:C6	1:A:1016:A:C6	2.93	0.57
2:B:97:TRP:HZ2	2:B:102:LEU:HD13	1.69	0.57
4:D:173:TRP:CD2	4:D:189:PRO:HG3	2.40	0.57
1:A:1504:G:H4'	1:A:1505:G:C5'	2.33	0.57
20:T:64:ASP:O	20:T:67:ALA:HB3	2.04	0.57
1:A:376:G:H5''	16:P:5:ARG:HB2	1.87	0.57
1:A:1126:U:H3	1:A:1127:G:N2	2.01	0.57
3:C:121:ALA:HB1	3:C:189:ALA:HB2	1.86	0.57
4:D:17:VAL:HG12	4:D:18:LYS:H	1.70	0.57
1:A:965:A:O2'	1:A:966:G:OP2	2.18	0.57
1:A:695:A:H2'	1:A:696:A:C8	2.40	0.57
1:A:1163:C:H2'	1:A:1164:G:H8	1.70	0.57
15:O:25:THR:CG2	15:O:70:LEU:HD23	2.35	0.57
1:A:559:A:H1'	1:A:560:U:OP2	2.04	0.56
1:A:77:G:C2	1:A:93:G:C2	2.92	0.56
1:A:98:U:C4	1:A:99:C:N4	2.72	0.56
2:B:231:GLU:HB3	2:B:232:PRO:CD	2.33	0.56
1:A:115:G:O5'	1:A:115:G:H8	1.88	0.56
1:A:222:U:H2'	1:A:223:U:C6	2.40	0.56
11:K:59:TYR:CE2	11:K:63:LEU:HD11	2.40	0.56
1:A:379:C:C2'	1:A:380:G:H5'	2.35	0.56
1:A:1505:G:O2'	1:A:1506:U:OP2	2.22	0.56
1:A:255:G:N2	1:A:272:C:C2	2.73	0.56
1:A:376:G:C4	1:A:389:A:C2	2.93	0.56
1:A:835:U:OP1	18:R:64:ARG:NH2	2.38	0.56
1:A:110:C:H2'	1:A:111:G:O4'	2.05	0.56
14:N:24:CYS:HB2	14:N:33:VAL:HG12	1.87	0.56
9:I:112:LYS:HD3	9:I:112:LYS:C	2.26	0.56
1:A:1240:U:OP1	7:G:119:ARG:NH2	2.32	0.56
1:A:1190:G:OP1	3:C:4:LYS:HA	2.05	0.56
1:A:463:A:C4	1:A:474:G:C8	2.93	0.56
15:O:39:LEU:CD1	15:O:56:LEU:HB2	2.36	0.56
1:A:1437:C:H2'	1:A:1438:G:H8	1.70	0.56
7:G:14:PRO:HA	7:G:21:VAL:HG12	1.87	0.56
20:T:13:LEU:HD12	20:T:13:LEU:C	2.26	0.56
1:A:645:C:H2'	1:A:645:C:O2	2.04	0.56
4:D:52:SER:O	4:D:56:VAL:HG23	2.06	0.56
12:L:126:LYS:HD2	12:L:126:LYS:H	1.69	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:51:ARG:HG3	10:J:59:SER:HB2	1.86	0.56
12:L:55:VAL:O	12:L:56:ALA:HB2	2.05	0.56
3:C:22:TRP:CD1	3:C:59:ARG:HD2	2.41	0.56
12:L:27:LEU:C	12:L:29:GLY:N	2.58	0.56
1:A:922:G:N2	1:A:1396:A:C4	2.74	0.56
2:B:168:THR:OG1	2:B:192:SER:HA	2.05	0.56
19:S:11:VAL:HG13	19:S:38:SER:HB2	1.87	0.56
1:A:56:U:H2'	1:A:57:G:C8	2.40	0.56
1:A:403:C:H2'	1:A:404:U:H6	1.71	0.56
1:A:1285:A:H1'	1:A:1286:A:OP2	2.06	0.56
1:A:279:A:H5''	1:A:281:G:O4'	2.06	0.56
2:B:158:LEU:CD2	2:B:159:PRO:HD2	2.33	0.56
7:G:29:LYS:HG3	7:G:101:LEU:HB3	1.87	0.56
1:A:184:G:H2'	1:A:185:A:C8	2.40	0.56
11:K:97:ALA:O	11:K:101:SER:HB3	2.04	0.56
3:C:190:ARG:HG3	3:C:195:VAL:HG12	1.87	0.56
14:N:25:VAL:HG13	14:N:26:ARG:H	1.68	0.56
8:H:6:ILE:HB	8:H:85:ARG:NH1	2.20	0.56
1:A:278:G:C6	17:Q:95:TYR:HD2	2.24	0.56
3:C:10:PHE:HE2	3:C:178:LEU:CD1	2.18	0.56
12:L:41:ARG:HB3	12:L:41:ARG:HH11	1.71	0.56
2:B:9:GLU:HA	2:B:48:MET:SD	2.45	0.56
15:O:7:GLU:HA	15:O:10:LYS:HE2	1.86	0.56
10:J:59:SER:O	10:J:60:ARG:HB2	2.05	0.56
1:A:1180:A:H5''	1:A:1181:G:OP2	2.06	0.56
2:B:103:THR:HG23	2:B:176:GLU:CD	2.26	0.56
1:A:419:C:N4	1:A:424:G:H1	2.04	0.56
3:C:180:ALA:HB1	3:C:182:ILE:HD11	1.86	0.56
7:G:22:LEU:CD1	7:G:97:GLN:HE21	2.17	0.56
1:A:435:C:H2'	1:A:436:C:C6	2.41	0.56
2:B:22:LYS:C	2:B:24:TRP:H	2.10	0.56
1:A:1502:A:H2	1:A:1505:G:H1	1.54	0.56
1:A:803:G:O5'	1:A:803:G:H8	1.89	0.56
4:D:19:LEU:HD22	4:D:67:ILE:HG12	1.87	0.56
1:A:1053:G:O2'	1:A:1199:U:H5	1.89	0.56
17:Q:67:LYS:O	17:Q:68:ARG:CB	2.53	0.56
1:A:562:C:H1'	12:L:15:ARG:HB3	1.87	0.56
1:A:1064:G:N2	1:A:1190:G:H2'	2.21	0.56
1:A:1123:A:H4'	10:J:37:PRO:HD2	1.87	0.56
11:K:43:SER:O	11:K:44:SER:HB3	2.05	0.56
1:A:1434:A:N6	1:A:1435:G:C2	2.73	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:66:MET:HE3	5:E:67:VAL:H	1.70	0.56
1:A:330:C:C2'	1:A:331:G:H5'	2.35	0.55
1:A:1124:G:HO2'	1:A:1145:C:N4	2.04	0.55
13:M:34:LEU:HA	13:M:37:THR:HG22	1.88	0.55
20:T:53:LEU:O	20:T:57:ARG:HD3	2.06	0.55
1:A:922:G:N2	1:A:1396:A:C5	2.74	0.55
1:A:432:A:O2'	1:A:433:C:C6	2.48	0.55
1:A:421:U:H5'	1:A:422:C:C5	2.41	0.55
1:A:103:C:O2'	1:A:172:A:N1	2.35	0.55
12:L:38:THR:HG22	12:L:39:VAL:HG23	1.87	0.55
15:O:55:GLY:O	15:O:59:MET:HG3	2.06	0.55
1:A:986:A:H4'	19:S:55:LYS:NZ	2.21	0.55
1:A:229:U:H5''	16:P:33:ILE:HD13	1.88	0.55
19:S:80:TYR:CE2	19:S:81:ARG:HB2	2.41	0.55
7:G:15:ASP:O	7:G:19:GLY:HA2	2.07	0.55
1:A:1352:C:H2'	1:A:1353:G:C8	2.41	0.55
1:A:932:C:H4'	7:G:4:ARG:NH2	2.22	0.55
1:A:1220:G:H2'	1:A:1221:G:O4'	2.05	0.55
6:F:19:LEU:HD23	6:F:23:LYS:HG3	1.87	0.55
19:S:11:VAL:HG22	19:S:39:THR:HB	1.86	0.55
17:Q:55:ASP:O	17:Q:57:VAL:HG13	2.07	0.55
2:B:160:ASP:O	2:B:161:ALA:HB2	2.06	0.55
3:C:15:THR:O	3:C:16:ARG:HB2	2.05	0.55
6:F:91:VAL:HG11	18:R:72:ARG:NH1	2.21	0.55
1:A:1477:C:H2'	1:A:1478:C:C6	2.42	0.55
9:I:100:GLY:C	9:I:102:LEU:H	2.08	0.55
18:R:39:VAL:HG13	18:R:40:LEU:CD2	2.32	0.55
1:A:101:A:O2'	1:A:102:G:H5'	2.06	0.55
1:A:1189:C:H5''	1:A:1190:G:OP2	2.07	0.55
1:A:475:G:H2'	1:A:476:G:C8	2.42	0.55
3:C:108:ASN:HD22	3:C:111:LEU:H	1.53	0.55
1:A:1522:U:O2'	1:A:1523:G:H5'	2.06	0.55
4:D:13:ARG:HD2	4:D:36:ARG:O	2.07	0.55
1:A:1085:U:C6	1:A:1094:G:N1	2.75	0.55
1:A:386:C:C2'	1:A:387:U:H5'	2.36	0.55
13:M:91:ARG:NH1	13:M:96:LEU:HB2	2.22	0.55
1:A:1493:A:H2'	1:A:1494:G:H8	1.71	0.55
2:B:69:LEU:HB3	2:B:162:ILE:HG22	1.88	0.55
2:B:115:LEU:HD12	2:B:145:LEU:HB3	1.88	0.55
8:H:96:GLY:H	8:H:99:GLU:CG	2.20	0.55
1:A:705:U:C5	1:A:706:A:N7	2.75	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:112:VAL:H	4:D:116:GLN:NE2	2.04	0.55
3:C:88:ARG:O	3:C:91:LEU:HB3	2.06	0.55
10:J:4:ILE:HG12	10:J:74:ILE:HB	1.88	0.55
1:A:193:C:O2	1:A:194:C:C6	2.60	0.55
20:T:49:ALA:HB3	20:T:99:LEU:HD12	1.89	0.55
1:A:977:A:H8	1:A:1223:C:N3	2.05	0.55
2:B:219:VAL:HA	2:B:222:ILE:HD12	1.89	0.55
9:I:36:TYR:CE2	9:I:37:PHE:CE2	2.95	0.55
2:B:240:GLN:HA	2:B:240:GLN:HE21	1.71	0.55
1:A:1315:U:O2	1:A:1360:A:H2	1.90	0.55
1:A:254:G:OP1	17:Q:67:LYS:O	2.24	0.55
1:A:264:U:H2'	1:A:265:G:C5'	2.37	0.55
2:B:118:LEU:HB2	2:B:142:LEU:HD12	1.88	0.55
1:A:1487:G:C4	1:A:1488:G:H8	2.25	0.55
8:H:116:LYS:HE2	8:H:127:LEU:HD13	1.88	0.55
1:A:79:G:N2	1:A:91:C:N3	2.54	0.55
1:A:314:C:O2'	1:A:315:A:H5'	2.06	0.55
1:A:524:G:H2'	1:A:525:C:C6	2.42	0.55
1:A:840:C:H4'	1:A:848:C:O2	2.07	0.55
8:H:43:GLY:O	8:H:64:LYS:HE2	2.07	0.55
1:A:434:U:C4	1:A:435:C:C4	2.95	0.55
9:I:78:LYS:HD3	9:I:101:PHE:CD2	2.40	0.55
1:A:737:A:H2'	1:A:738:C:C6	2.42	0.55
1:A:1265:G:H2'	1:A:1266:G:O4'	2.07	0.55
7:G:15:ASP:HB3	7:G:20:ASP:O	2.07	0.55
18:R:58:LEU:HD22	18:R:62:GLU:HB3	1.88	0.55
10:J:49:VAL:O	10:J:60:ARG:HA	2.07	0.55
4:D:20:TYR:CD2	4:D:27:TYR:HE1	2.25	0.55
1:A:421:U:H5'	1:A:422:C:H5	1.72	0.55
12:L:27:LEU:O	12:L:29:GLY:N	2.40	0.55
5:E:11:ILE:HD11	5:E:33:VAL:HG23	1.89	0.55
1:A:344:A:H5'	1:A:345:C:C5	2.42	0.55
5:E:84:PHE:HB3	5:E:134:ALA:HB2	1.89	0.55
21:U:22:ARG:O	21:U:22:ARG:HD3	2.07	0.55
14:N:24:CYS:HA	14:N:38:GLY:O	2.08	0.54
18:R:36:ASN:ND2	18:R:38:GLU:HG2	2.21	0.54
10:J:10:GLY:N	10:J:16:LEU:HD11	2.22	0.54
3:C:203:PHE:CD1	3:C:204:LEU:N	2.75	0.54
4:D:159:ARG:O	4:D:163:GLU:HB2	2.08	0.54
4:D:188:LEU:CD1	4:D:188:LEU:H	2.16	0.54
12:L:5:PRO:HG2	12:L:15:ARG:HH22	1.69	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:28:PHE:CD2	5:E:51:VAL:HG22	2.43	0.54
1:A:1065:U:C1'	1:A:1066:C:OP2	2.55	0.54
13:M:12:ASN:H	13:M:45:VAL:HG11	1.72	0.54
1:A:532:A:O2'	1:A:533:A:OP1	2.21	0.54
1:A:1357:A:H2'	1:A:1358:U:C6	2.42	0.54
1:A:264:U:C2'	1:A:265:G:H5'	2.36	0.54
1:A:1124:G:H5'	10:J:35:SER:HA	1.88	0.54
3:C:24:ALA:HB1	3:C:28:GLN:O	2.06	0.54
1:A:9:G:C2	1:A:26:A:C2	2.95	0.54
1:A:91:C:H2'	1:A:92:C:O5'	2.07	0.54
1:A:491:G:N3	1:A:492:G:C8	2.75	0.54
1:A:1158:C:H5'	2:B:133:LYS:HE2	1.88	0.54
2:B:230:VAL:HG12	2:B:231:GLU:H	1.70	0.54
1:A:1492:A:H2'	1:A:1493:A:O4'	2.06	0.54
5:E:57:LYS:O	5:E:61:TYR:CD2	2.59	0.54
1:A:499:A:H4'	1:A:500:G:OP1	2.06	0.54
6:F:96:PRO:HB2	6:F:98:LEU:HD21	1.89	0.54
1:A:1337:G:H5''	1:A:1338:G:OP1	2.07	0.54
1:A:665:A:C2	1:A:732:C:C2	2.96	0.54
1:A:936:C:H2'	1:A:937:A:O4'	2.07	0.54
1:A:1236:A:H4'	1:A:1304:G:H4'	1.90	0.54
1:A:80:G:N2	1:A:81:U:C4	2.75	0.54
7:G:111:ARG:CZ	7:G:122:HIS:HB3	2.38	0.54
1:A:1487:G:H2'	1:A:1488:G:H5'	1.88	0.54
12:L:28:LYS:O	12:L:30:ALA:N	2.40	0.54
7:G:24:THR:HA	7:G:27:ILE:HB	1.89	0.54
1:A:1174:G:C2	1:A:1175:G:C5	2.96	0.54
8:H:112:LEU:HD23	8:H:112:LEU:H	1.72	0.54
2:B:103:THR:CG2	2:B:176:GLU:HG3	2.36	0.54
1:A:103:C:OP1	20:T:17:ARG:NH1	2.35	0.54
1:A:22:G:H2'	1:A:23:C:H6	1.72	0.54
1:A:380:G:N2	1:A:382:A:H5''	2.23	0.54
1:A:170:U:O2'	1:A:171:A:H5'	2.07	0.54
1:A:1203:C:H6	1:A:1203:C:O5'	1.90	0.54
10:J:51:ARG:CZ	10:J:61:GLU:HB2	2.38	0.54
1:A:80:G:N2	1:A:81:U:N3	2.56	0.54
7:G:43:PHE:HD2	7:G:44:TYR:CE2	2.25	0.54
1:A:436:C:H2'	1:A:437:U:C6	2.40	0.54
1:A:1298:C:H2'	7:G:114:ARG:HH12	1.72	0.54
6:F:11:ASN:HB2	6:F:86:ARG:NH2	2.23	0.54
11:K:16:SER:HA	11:K:79:SER:O	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:17:VAL:HG21	7:G:44:TYR:CE2	2.43	0.54
13:M:37:THR:HG23	13:M:39:ILE:HG13	1.89	0.54
1:A:1391:U:H2'	1:A:1392:G:H8	1.73	0.54
16:P:4:ILE:HG12	16:P:21:VAL:HG22	1.89	0.54
4:D:127:THR:OG1	4:D:147:ALA:HB3	2.07	0.54
19:S:34:TRP:CD1	19:S:52:TYR:HB2	2.43	0.54
1:A:620:C:H2'	1:A:621:A:O4'	2.08	0.54
7:G:49:ILE:HG22	7:G:49:ILE:O	2.07	0.54
1:A:1289:A:H2'	1:A:1290:G:H5'	1.90	0.54
2:B:158:LEU:HD23	2:B:159:PRO:CD	2.32	0.53
19:S:56:GLN:HG2	19:S:57:HIS:N	2.23	0.53
13:M:33:ALA:O	13:M:37:THR:HB	2.09	0.53
14:N:8:GLU:O	14:N:8:GLU:HG2	2.07	0.53
1:A:1311:G:O6	19:S:2:PRO:HB3	2.07	0.53
6:F:68:PRO:HB2	6:F:70:ASP:OD1	2.08	0.53
3:C:73:PRO:HG3	3:C:105:GLU:CD	2.28	0.53
5:E:89:ILE:CD1	5:E:90:VAL:H	2.21	0.53
1:A:1392:G:H21	1:A:1502:A:H8	1.57	0.53
1:A:1130:A:H5''	9:I:20:ARG:NH2	2.24	0.53
10:J:49:VAL:CG2	14:N:41:ARG:HB2	2.27	0.53
1:A:96:G:H2'	1:A:97:G:H5'	1.90	0.53
1:A:484:G:H1'	1:A:485:G:OP2	2.08	0.53
1:A:617:G:H1	1:A:623:C:H42	1.55	0.53
10:J:82:ILE:HG23	10:J:85:LEU:HB2	1.90	0.53
1:A:1048:G:O3'	1:A:1049:U:H3'	2.08	0.53
1:A:1368:G:OP2	9:I:112:LYS:HD2	2.08	0.53
1:A:269:C:H2'	1:A:270:A:C8	2.44	0.53
1:A:278:G:C6	17:Q:95:TYR:CD2	2.96	0.53
1:A:765:G:H5''	1:A:766:A:OP1	2.08	0.53
1:A:381:C:H2'	1:A:382:A:O4'	2.08	0.53
12:L:28:LYS:HD3	12:L:33:ARG:HH22	1.72	0.53
1:A:409:G:C5	1:A:410:G:N7	2.77	0.53
1:A:994:A:H62	1:A:1216:G:C4'	2.18	0.53
7:G:17:VAL:HG12	7:G:18:TYR:N	2.23	0.53
1:A:370:C:H2'	1:A:371:G:H5'	1.90	0.53
6:F:4:TYR:HE1	6:F:92:LYS:HG2	1.73	0.53
2:B:139:LYS:HD3	2:B:139:LYS:O	2.09	0.53
3:C:6:HIS:HD2	3:C:8:ILE:HB	1.72	0.53
17:Q:25:ARG:HG3	17:Q:25:ARG:O	2.09	0.53
1:A:75:G:N2	1:A:76:C:C4	2.76	0.53
7:G:50:ILE:HG21	7:G:61:VAL:HG21	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:36:ILE:HG13	15:O:59:MET:HE2	1.90	0.53
1:A:429:U:H4'	1:A:430:A:O5'	2.08	0.53
11:K:79:SER:HB3	11:K:104:GLN:HB3	1.89	0.53
1:A:1244:C:OP2	21:U:9:ARG:HB2	2.08	0.53
1:A:1330:U:H2'	1:A:1331:G:H5'	1.90	0.53
1:A:1399:C:C2	1:A:1401:G:C5	2.96	0.53
1:A:1425:U:H2'	1:A:1426:C:H6	1.74	0.53
1:A:1378:C:H5''	1:A:1379:G:OP2	2.08	0.53
1:A:1128:C:H42	1:A:1143:G:N2	2.01	0.53
10:J:4:ILE:HG13	10:J:4:ILE:O	2.09	0.53
1:A:1488:G:H2'	1:A:1489:G:C8	2.44	0.53
8:H:119:LEU:HB3	8:H:123:GLU:HB3	1.91	0.53
1:A:1301:U:O2'	1:A:1302:U:H3'	2.09	0.53
13:M:95:GLY:O	13:M:96:LEU:HD23	2.09	0.53
1:A:113:G:H1	1:A:314:C:H42	1.57	0.53
16:P:21:VAL:HG21	16:P:59:TRP:CD1	2.44	0.53
16:P:6:LEU:HD23	16:P:17:TYR:CG	2.44	0.53
18:R:36:ASN:O	18:R:39:VAL:HG12	2.09	0.53
1:A:1414:U:H2'	1:A:1415:G:C8	2.44	0.53
1:A:659:U:OP1	15:O:8:LYS:HD3	2.07	0.53
12:L:28:LYS:C	12:L:30:ALA:H	2.13	0.53
11:K:12:ARG:CG	11:K:13:GLN:H	2.22	0.53
1:A:558:G:OP2	1:A:559:A:O2'	2.27	0.52
1:A:901:A:H5''	1:A:902:G:OP2	2.09	0.52
4:D:65:ARG:HG3	4:D:75:PHE:CG	2.43	0.52
1:A:977:A:H2'	1:A:978:A:C5'	2.37	0.52
1:A:689:C:C2'	1:A:690:G:H5'	2.39	0.52
1:A:775:G:O2'	1:A:776:G:H5'	2.08	0.52
5:E:12:LEU:HD22	5:E:12:LEU:O	2.10	0.52
1:A:1205:U:H2'	1:A:1206:G:C8	2.43	0.52
1:A:1328:C:H2'	1:A:1329:A:H8	1.73	0.52
13:M:5:ALA:O	13:M:6:GLY:C	2.47	0.52
10:J:38:ILE:HB	10:J:71:LEU:HD12	1.92	0.52
2:B:54:THR:HG21	2:B:201:ILE:HD11	1.91	0.52
1:A:1373:G:H5''	7:G:36:LYS:HZ2	1.74	0.52
10:J:16:LEU:HD21	10:J:94:VAL:HG13	1.91	0.52
1:A:376:G:N3	1:A:389:A:C2	2.77	0.52
1:A:1516:G:N2	1:A:1520:G:C4	2.77	0.52
1:A:860:A:H2'	1:A:861:G:O4'	2.08	0.52
1:A:913:A:H4'	1:A:914:A:O5'	2.09	0.52
2:B:28:PHE:CE2	2:B:190:THR:HA	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:17:ARG:NH1	15:O:17:ARG:CG	2.63	0.52
1:A:97:G:C5	1:A:98:U:O4	2.62	0.52
4:D:199:ASN:C	4:D:199:ASN:HD22	2.12	0.52
1:A:1416:G:O6	1:A:1417:G:N2	2.42	0.52
1:A:457:C:H2'	1:A:458:C:C6	2.40	0.52
1:A:424:G:H2'	1:A:425:G:C8	2.45	0.52
2:B:204:ASN:HD22	2:B:204:ASN:C	2.11	0.52
9:I:108:VAL:HG12	9:I:109:VAL:N	2.24	0.52
1:A:116:A:H61	1:A:313:A:H1'	1.73	0.52
1:A:595:G:C5	1:A:641:U:C5	2.97	0.52
4:D:105:VAL:HG13	4:D:110:PHE:HB2	1.92	0.52
1:A:260:G:C4	1:A:261:U:C5	2.97	0.52
1:A:457:C:C2	1:A:458:C:C5	2.98	0.52
2:B:24:TRP:CH2	2:B:26:PRO:HA	2.44	0.52
5:E:11:ILE:CG2	5:E:105:VAL:HG13	2.38	0.52
1:A:781:A:C4	1:A:802:A:C2	2.97	0.52
1:A:1276:G:O2'	1:A:1277:C:H5'	2.10	0.52
11:K:16:SER:HB2	11:K:106:LYS:NZ	2.24	0.52
13:M:49:THR:HG22	13:M:50:GLU:H	1.75	0.52
1:A:1283:G:O2'	1:A:1284:C:H5'	2.08	0.52
1:A:89:C:O2	1:A:89:C:C2'	2.53	0.52
16:P:67:THR:HG22	16:P:69:THR:N	2.22	0.52
1:A:1112:C:N3	3:C:178:LEU:HB2	2.25	0.52
1:A:750:G:N2	15:O:23:GLY:HA3	2.24	0.52
1:A:794:A:H2'	1:A:795:C:C6	2.45	0.52
1:A:232:G:H1'	1:A:262:A:N1	2.25	0.52
20:T:74:LYS:HB3	20:T:74:LYS:NZ	2.24	0.52
1:A:1279:A:H5''	1:A:1280:A:OP1	2.09	0.52
17:Q:26:GLN:O	17:Q:27:PHE:HB3	2.08	0.52
1:A:7:G:H5''	1:A:298:A:O4'	2.10	0.52
12:L:86:ARG:O	12:L:98:TYR:HB3	2.09	0.52
1:A:509:A:O2'	1:A:510:A:C8	2.63	0.52
1:A:1359:C:OP2	14:N:22:THR:HG21	2.10	0.52
1:A:994:A:N3	1:A:994:A:H2'	2.24	0.52
4:D:199:ASN:HD21	4:D:201:GLN:HB2	1.74	0.52
19:S:56:GLN:HG2	19:S:57:HIS:H	1.74	0.52
1:A:542:G:H5''	4:D:40:PRO:O	2.10	0.52
1:A:542:G:OP1	4:D:10:ARG:NH2	2.41	0.52
7:G:51:GLN:HB2	7:G:52:GLU:OE2	2.10	0.52
1:A:390:C:H4'	16:P:28:ARG:HH12	1.75	0.52
4:D:208:SER:HB3	5:E:101:ILE:HG12	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:111:ALA:HB1	4:D:116:GLN:HG2	1.91	0.52
1:A:949:A:C2	1:A:1233:G:N3	2.78	0.52
1:A:996:A:C6	1:A:1046:A:H1'	2.44	0.52
1:A:99:C:H2'	1:A:101:A:O4'	2.09	0.52
1:A:1488:G:H2'	1:A:1488:G:N3	2.25	0.52
5:E:33:VAL:HG12	5:E:34:VAL:N	2.25	0.52
10:J:75:ILE:HD13	10:J:76:ASN:H	1.75	0.52
11:K:121:PRO:HB2	11:K:125:PHE:HB2	1.92	0.52
18:R:34:TYR:CE1	18:R:35:ARG:HG3	2.45	0.52
17:Q:29:HIS:CG	17:Q:30:PRO:HD2	2.45	0.52
2:B:219:VAL:O	2:B:222:ILE:HB	2.10	0.52
16:P:21:VAL:O	16:P:33:ILE:HB	2.10	0.52
14:N:14:PRO:O	14:N:15:LYS:CB	2.58	0.52
8:H:96:GLY:H	8:H:99:GLU:HG3	1.74	0.52
1:A:1518:A:C2'	1:A:1519:A:H5'	2.39	0.52
1:A:1326:C:OP2	21:U:6:ARG:NE	2.36	0.52
4:D:121:VAL:O	4:D:134:ASP:HA	2.09	0.52
7:G:137:LYS:O	7:G:141:VAL:N	2.43	0.52
1:A:976:G:N2	1:A:1363:A:C4	2.78	0.52
9:I:114:TYR:CD2	10:J:60:ARG:HB2	2.45	0.52
1:A:503:C:H2'	1:A:504:C:C6	2.45	0.52
1:A:1392:G:O2'	1:A:1393:U:H5'	2.10	0.52
7:G:153:HIS:HA	7:G:155:ARG:CZ	2.40	0.52
1:A:1241:G:H2'	1:A:1242:C:C6	2.45	0.52
1:A:1154:G:H2'	1:A:1155:G:H8	1.74	0.52
1:A:164:U:H2'	1:A:165:C:C6	2.44	0.52
18:R:43:PHE:CG	18:R:66:LEU:HD11	2.45	0.52
1:A:858:G:O2'	1:A:859:A:H5'	2.10	0.52
14:N:24:CYS:SG	14:N:27:CYS:HB2	2.50	0.51
13:M:8:GLU:OE1	13:M:22:ILE:HG23	2.10	0.51
1:A:78:G:H1	1:A:91:C:N4	2.09	0.51
9:I:47:LEU:C	9:I:49:PRO:HD2	2.31	0.51
1:A:263:A:OP2	20:T:79:ARG:NH1	2.43	0.51
2:B:97:TRP:HH2	2:B:176:GLU:OE2	1.92	0.51
4:D:199:ASN:ND2	4:D:201:GLN:HB2	2.25	0.51
1:A:328:C:C1'	1:A:329:A:OP2	2.58	0.51
10:J:40:LEU:HD22	10:J:69:ASN:HD22	1.74	0.51
21:U:10:ARG:HG3	21:U:13:ILE:HD12	1.92	0.51
4:D:79:PHE:CD2	4:D:79:PHE:C	2.83	0.51
14:N:24:CYS:SG	14:N:43:CYS:SG	3.08	0.51
1:A:79:G:N2	1:A:91:C:C2	2.79	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1373:G:H5''	7:G:36:LYS:HZ3	1.73	0.51
12:L:41:ARG:HH11	12:L:42:THR:H	1.59	0.51
12:L:28:LYS:C	12:L:30:ALA:N	2.64	0.51
2:B:143:GLU:HA	2:B:146:GLN:HE21	1.74	0.51
1:A:1028:C:H2'	1:A:1029:C:O4'	2.10	0.51
19:S:30:LEU:HD23	19:S:31:ILE:N	2.25	0.51
1:A:595:G:C6	1:A:641:U:C5	2.98	0.51
1:A:9:G:OP1	5:E:122:GLU:HG3	2.10	0.51
1:A:9:G:OP2	5:E:121:LYS:HD2	2.10	0.51
6:F:97:PHE:O	6:F:98:LEU:HD23	2.11	0.51
1:A:1345:U:C2	1:A:1377:A:C2	2.98	0.51
5:E:40:ARG:HH11	5:E:40:ARG:HG2	1.75	0.51
1:A:558:G:C8	1:A:559:A:H2'	2.46	0.51
1:A:73:C:C2	1:A:97:G:N2	2.79	0.51
7:G:113:GLU:HB2	7:G:119:ARG:HG3	1.92	0.51
1:A:230:G:H2'	1:A:231:G:O4'	2.11	0.51
13:M:12:ASN:N	13:M:45:VAL:HG11	2.25	0.51
6:F:48:LEU:HG	6:F:57:GLN:HA	1.92	0.51
19:S:42:PRO:O	19:S:45:VAL:HG23	2.11	0.51
1:A:673:G:H2'	1:A:674:G:C8	2.46	0.51
8:H:4:ASP:OD2	8:H:85:ARG:NH1	2.43	0.51
1:A:279:A:OP2	17:Q:95:TYR:OH	2.19	0.51
1:A:1133:G:C2	1:A:1142:G:C2	2.98	0.51
1:A:1533:C:H3'	1:A:1533:C:H6	1.74	0.51
19:S:17:GLU:HA	19:S:20:LEU:CG	2.41	0.51
1:A:430:A:H2'	1:A:431:A:O4'	2.10	0.51
1:A:1264:C:H2'	1:A:1265:G:H8	1.75	0.51
17:Q:74:LEU:C	17:Q:74:LEU:HD23	2.30	0.51
1:A:97:G:C5	1:A:98:U:C4	2.99	0.51
1:A:391:G:C6	1:A:392:G:C5	2.99	0.51
1:A:1261:A:N7	1:A:1262:C:C5	2.79	0.51
1:A:119:A:C8	1:A:288:A:C2	2.98	0.51
7:G:91:VAL:HG12	7:G:96:GLN:HG3	1.91	0.51
19:S:12:ASP:HB2	19:S:38:SER:HB3	1.93	0.51
1:A:544:G:C5	1:A:545:C:C5	2.99	0.51
20:T:56:MET:CE	20:T:88:VAL:HG11	2.40	0.51
1:A:853:G:C2'	1:A:854:G:H5'	2.40	0.51
10:J:57:LYS:HD2	10:J:60:ARG:HH21	1.76	0.51
1:A:1158:C:O2	1:A:1158:C:H3'	2.11	0.51
5:E:79:GLU:O	8:H:104:ARG:CZ	2.59	0.51
1:A:1488:G:C2	1:A:1489:G:C5	2.99	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:419:C:H42	1:A:424:G:H1	1.58	0.51
3:C:38:ARG:HB3	3:C:94:LEU:HD21	1.93	0.51
3:C:64:VAL:HG12	3:C:65:ALA:N	2.26	0.51
8:H:27:PRO:HA	8:H:58:TYR:CD2	2.45	0.51
1:A:430:A:C2'	1:A:431:A:H5'	2.39	0.51
17:Q:4:LYS:HD3	17:Q:6:LEU:HD21	1.93	0.51
1:A:939:G:H2'	1:A:940:C:C6	2.45	0.51
1:A:1228:C:H3'	1:A:1228:C:H6	1.75	0.51
1:A:1048:G:H2'	1:A:1050:G:N7	2.26	0.51
12:L:20:LYS:CD	12:L:20:LYS:H	2.22	0.51
1:A:750:G:C2	15:O:23:GLY:HA3	2.45	0.51
1:A:513:C:H42	1:A:538:G:H1	1.59	0.51
1:A:1392:G:N2	1:A:1502:A:H8	2.08	0.51
1:A:255:G:C2	1:A:272:C:C2	2.99	0.51
10:J:75:ILE:O	10:J:76:ASN:HB2	2.10	0.51
1:A:1011:G:N2	1:A:1019:C:H1'	2.25	0.51
20:T:13:LEU:O	20:T:16:HIS:N	2.33	0.51
15:O:76:GLU:OE1	15:O:76:GLU:HA	2.11	0.51
2:B:178:ARG:HH12	8:H:68:ARG:HH22	1.59	0.51
1:A:1443:G:H2'	1:A:1443:G:N3	2.26	0.51
1:A:1198:G:H2'	1:A:1199:U:C6	2.46	0.51
8:H:137:VAL:O	8:H:138:TRP:HB3	2.11	0.51
1:A:1329:A:H5'	13:M:29:ARG:HD2	1.93	0.51
1:A:1158:C:N4	1:A:1160:G:C5	2.79	0.51
1:A:380:G:C2	1:A:382:A:H5''	2.45	0.51
20:T:48:LYS:O	20:T:50:GLU:N	2.44	0.51
1:A:475:G:H2'	1:A:476:G:H8	1.76	0.51
1:A:1349:A:C2	1:A:1374:A:C4	2.98	0.51
3:C:130:VAL:HG11	3:C:157:ILE:HG23	1.93	0.51
17:Q:83:ASP:O	17:Q:86:GLU:HB2	2.11	0.51
9:I:111:ARG:NH1	9:I:113:LYS:HA	2.25	0.51
1:A:1178:G:H21	1:A:1180:A:H3'	1.76	0.51
19:S:36:ARG:HH21	19:S:75:ALA:HB3	1.74	0.51
1:A:393:A:C2	1:A:394:G:C8	2.99	0.51
7:G:3:ARG:O	7:G:4:ARG:CB	2.59	0.51
4:D:107:ARG:HB3	4:D:174:LEU:HD11	1.93	0.51
1:A:1442:G:C5	1:A:1446:A:N6	2.79	0.50
11:K:57:THR:HG22	11:K:59:TYR:N	2.23	0.50
5:E:72:GLN:HE21	5:E:144:THR:HG23	1.76	0.50
8:H:20:TYR:HA	8:H:65:TYR:CZ	2.46	0.50
1:A:978:A:O2'	1:A:1322:C:N3	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1501:C:C4	1:A:1504:G:C4	2.98	0.50
1:A:622:A:C8	1:A:623:C:C5	2.99	0.50
8:H:112:LEU:HD23	8:H:112:LEU:N	2.26	0.50
4:D:198:VAL:HG12	4:D:199:ASN:N	2.25	0.50
5:E:148:VAL:HG21	8:H:107:LEU:HD13	1.92	0.50
12:L:97:ARG:HB2	12:L:98:TYR:CE1	2.46	0.50
5:E:33:VAL:CG1	5:E:34:VAL:N	2.74	0.50
2:B:105:PHE:O	2:B:109:SER:HB3	2.11	0.50
15:O:85:LEU:HB3	15:O:87:ILE:HD11	1.94	0.50
2:B:28:PHE:CD2	2:B:190:THR:HA	2.46	0.50
4:D:107:ARG:HH12	4:D:194:LEU:HD12	1.76	0.50
1:A:257:G:C4	1:A:258:G:C8	2.99	0.50
1:A:260:G:H2'	1:A:261:U:H6	1.76	0.50
1:A:1480:G:C6	1:A:1481:U:C4	2.99	0.50
1:A:149:A:H2'	1:A:150:C:C6	2.39	0.50
12:L:39:VAL:HG11	12:L:41:ARG:HG2	1.93	0.50
1:A:537:G:H2'	1:A:538:G:H8	1.75	0.50
1:A:978:A:C2	1:A:1319:A:C4	2.99	0.50
1:A:1505:G:O2'	1:A:1506:U:P	2.69	0.50
15:O:86:GLY:O	15:O:87:ILE:HD13	2.10	0.50
18:R:37:VAL:CG2	18:R:78:LEU:HB3	2.41	0.50
10:J:82:ILE:O	10:J:82:ILE:HG22	2.11	0.50
1:A:555:C:H2'	1:A:556:C:C6	2.46	0.50
3:C:20:SER:HB2	14:N:54:PRO:HG3	1.92	0.50
1:A:758:G:H8	1:A:758:G:O5'	1.95	0.50
8:H:86:ILE:HG22	8:H:87:SER:N	2.26	0.50
3:C:112:SER:O	3:C:116:VAL:HG23	2.11	0.50
8:H:120:THR:H	8:H:123:GLU:HB3	1.76	0.50
7:G:51:GLN:O	7:G:53:LYS:N	2.37	0.50
18:R:25:THR:C	18:R:26:LEU:HD12	2.31	0.50
2:B:84:GLU:OE1	2:B:216:SER:HA	2.11	0.50
1:A:521:G:H1	1:A:528:C:H42	1.58	0.50
1:A:325:A:OP2	20:T:70:SER:HB3	2.11	0.50
1:A:1126:U:H6	1:A:1126:U:OP1	1.91	0.50
3:C:23:TYR:CD1	10:J:10:GLY:HA2	2.46	0.50
1:A:1521:G:H2'	1:A:1522:U:C6	2.47	0.50
1:A:1375:A:N3	1:A:1375:A:H2'	2.26	0.50
1:A:429:U:C1'	1:A:430:A:H5''	2.41	0.50
4:D:50:ARG:HH12	4:D:52:SER:HA	1.75	0.50
7:G:95:ARG:HG2	7:G:99:LEU:HD12	1.93	0.50
3:C:77:ILE:C	3:C:83:ARG:HB3	2.32	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:87:TYR:N	19:S:73:GLU:O	2.45	0.50
6:F:30:LEU:HD23	6:F:30:LEU:N	2.25	0.50
1:A:1124:G:N2	1:A:1127:G:H21	2.09	0.50
2:B:51:LEU:CD2	2:B:201:ILE:HD12	2.39	0.50
1:A:1501:C:N4	1:A:1504:G:N3	2.59	0.50
1:A:35:G:H2'	1:A:36:C:H6	1.76	0.50
1:A:580:U:H2'	1:A:581:G:O4'	2.10	0.50
1:A:1150:U:O4	1:A:1151:A:N6	2.44	0.50
5:E:18:ARG:HG3	5:E:18:ARG:NH1	2.23	0.50
19:S:20:LEU:HD12	19:S:21:GLU:N	2.27	0.50
1:A:1266:G:N2	1:A:1269:A:OP2	2.45	0.50
1:A:1518:A:O2'	1:A:1519:A:H5'	2.12	0.50
1:A:797:C:O2'	1:A:798:G:H5'	2.11	0.50
1:A:646:U:H2'	1:A:647:C:C6	2.47	0.50
1:A:927:G:H1	1:A:1390:U:H3	1.59	0.50
13:M:3:ARG:HD2	13:M:9:ILE:HD11	1.93	0.50
1:A:559:A:C1'	1:A:560:U:OP2	2.60	0.50
1:A:1287:A:C6	1:A:1288:A:C6	3.00	0.50
8:H:82:HIS:CD2	8:H:138:TRP:NE1	2.79	0.50
1:A:77:G:H2'	1:A:78:G:C8	2.47	0.50
9:I:5:TYR:CD2	9:I:5:TYR:C	2.85	0.50
17:Q:23:VAL:HG21	17:Q:42:TYR:HD1	1.76	0.50
3:C:202:ILE:CG2	3:C:204:LEU:HD23	2.42	0.50
2:B:115:LEU:HD12	2:B:145:LEU:HB2	1.91	0.50
1:A:633:G:H2'	1:A:634:C:H6	1.77	0.50
18:R:31:LEU:HD21	18:R:66:LEU:HB2	1.94	0.50
9:I:4:TYR:CE2	9:I:88:TYR:HB2	2.47	0.50
5:E:5:ASP:CG	5:E:6:PHE:H	2.15	0.50
1:A:49:U:C2	1:A:361:G:N2	2.80	0.50
2:B:7:VAL:O	2:B:8:LYS:CB	2.59	0.50
1:A:1204:A:C6	1:A:1205:U:O2	2.65	0.50
1:A:1357:A:C4	1:A:1358:U:H5	2.30	0.50
1:A:106:C:H2'	1:A:107:G:C5'	2.42	0.50
1:A:1261:A:C8	1:A:1262:C:C5	3.00	0.50
12:L:33:ARG:O	12:L:85:ILE:HG23	2.12	0.50
1:A:792:A:C2	1:A:793:U:C4	3.00	0.50
13:M:45:VAL:HG13	13:M:46:LYS:N	2.26	0.50
1:A:594:G:C2'	1:A:595:G:H5'	2.42	0.50
7:G:45:ASP:O	7:G:49:ILE:HG13	2.11	0.50
1:A:1345:U:O2	1:A:1377:A:C6	2.65	0.50
1:A:277:C:C5'	17:Q:68:ARG:HH22	2.25	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1416:G:C2'	1:A:1417:G:H5'	2.42	0.49
5:E:98:THR:HG22	5:E:99:GLY:O	2.11	0.49
1:A:574:A:N3	1:A:883:C:H1'	2.27	0.49
8:H:120:THR:HG23	8:H:123:GLU:OE2	2.11	0.49
3:C:82:GLU:O	3:C:86:VAL:HG23	2.12	0.49
1:A:1339:A:H5''	1:A:1340:A:OP2	2.12	0.49
1:A:718:G:H5'	11:K:117:ASN:HB2	1.94	0.49
1:A:1186:G:N2	1:A:1187:G:H1'	2.27	0.49
1:A:1057:G:C5'	3:C:154:SER:HB2	2.22	0.49
5:E:51:VAL:HB	5:E:52:PRO:CD	2.37	0.49
5:E:80:ILE:HA	8:H:104:ARG:NH2	2.26	0.49
3:C:32:LEU:HB3	3:C:59:ARG:NH1	2.27	0.49
4:D:173:TRP:HB2	4:D:187:ARG:O	2.12	0.49
15:O:78:TYR:O	15:O:82:ILE:HG13	2.11	0.49
1:A:20:U:H2'	1:A:21:G:H5'	1.93	0.49
5:E:98:THR:HB	5:E:117:ASP:HB3	1.94	0.49
7:G:71:PRO:HG3	7:G:103:TRP:CZ3	2.45	0.49
1:A:1287:A:H2	1:A:1353:G:N3	2.10	0.49
1:A:490:G:C2	1:A:491:G:C8	3.01	0.49
1:A:328:C:O2	1:A:328:C:C2'	2.56	0.49
20:T:51:GLU:HA	20:T:54:LYS:HB2	1.93	0.49
1:A:620:C:N1	4:D:135:LEU:HD13	2.28	0.49
2:B:107:THR:C	2:B:109:SER:N	2.66	0.49
6:F:69:GLU:CD	6:F:69:GLU:H	2.15	0.49
1:A:1034:G:C2	1:A:1035:A:C5	3.01	0.49
1:A:1152:A:H2'	1:A:1153:C:C6	2.46	0.49
15:O:33:THR:HG23	15:O:63:ARG:HH11	1.77	0.49
1:A:1239:A:C4	1:A:1298:C:N4	2.80	0.49
18:R:53:ARG:C	18:R:55:ARG:H	2.16	0.49
1:A:1075:C:H2'	1:A:1076:C:H6	1.76	0.49
11:K:72:ALA:HA	11:K:75:TYR:HB2	1.94	0.49
1:A:1049:U:C4'	1:A:1050:G:OP2	2.60	0.49
1:A:410:G:OP2	4:D:25:ARG:HD2	2.11	0.49
1:A:97:G:C8	1:A:97:G:OP2	2.59	0.49
1:A:89:C:O2	1:A:90:U:O2	2.31	0.49
7:G:127:ALA:C	7:G:129:GLU:H	2.15	0.49
7:G:50:ILE:HG21	7:G:58:PRO:HA	1.95	0.49
6:F:62:TRP:C	6:F:63:TYR:CD2	2.85	0.49
1:A:1325:C:H4'	21:U:17:THR:HG21	1.94	0.49
4:D:31:CYS:C	4:D:33:MET:H	2.16	0.49
5:E:90:VAL:O	5:E:120:THR:HA	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:448:A:C4	1:A:487:A:N1	2.81	0.49
12:L:26:ALA:O	12:L:27:LEU:O	2.30	0.49
1:A:149:A:O2'	1:A:150:C:H5'	2.12	0.49
12:L:69:TYR:HE2	12:L:71:PRO:HA	1.78	0.49
15:O:39:LEU:O	15:O:39:LEU:HD13	2.13	0.49
1:A:1130:A:N1	1:A:1146:A:N3	2.60	0.49
1:A:1154:G:H2'	1:A:1155:G:C8	2.47	0.49
1:A:1186:G:C2	1:A:1187:G:N9	2.81	0.49
1:A:1329:A:H2'	1:A:1330:U:H6	1.77	0.49
12:L:71:PRO:HB2	12:L:120:TYR:HE2	1.77	0.49
1:A:926:G:H3'	1:A:1505:G:N2	2.27	0.49
13:M:12:ASN:N	13:M:45:VAL:CG1	2.74	0.49
1:A:688:G:H5'	11:K:46:GLY:C	2.32	0.49
11:K:47:VAL:HG12	11:K:48:ILE:N	2.27	0.49
1:A:828:A:H2'	1:A:829:G:O5'	2.13	0.49
1:A:1193:G:H2'	1:A:1194:U:H6	1.77	0.49
1:A:652:U:C2	1:A:752:G:N2	2.81	0.49
1:A:1283:G:H2'	1:A:1284:C:H6	1.77	0.49
1:A:474:G:N3	1:A:475:G:C8	2.80	0.49
1:A:112:G:O2'	1:A:113:G:H5'	2.12	0.49
3:C:123:GLN:OE1	3:C:133:ALA:HB1	2.12	0.49
11:K:14:VAL:HG21	11:K:40:ILE:CD1	2.42	0.49
16:P:25:ARG:H	16:P:25:ARG:HD3	1.77	0.49
3:C:134:ILE:O	3:C:138:VAL:HG23	2.13	0.49
1:A:166:G:C2	1:A:167:G:N7	2.81	0.49
1:A:958:A:N1	19:S:54:GLY:HA3	2.28	0.49
1:A:1529:G:OP2	1:A:1529:G:H3'	2.12	0.49
1:A:1357:A:H2'	1:A:1358:U:H6	1.76	0.49
1:A:62:U:H2'	1:A:63:C:C6	2.48	0.49
10:J:34:VAL:HG12	10:J:36:GLY:H	1.78	0.49
1:A:1148:U:H4'	9:I:14:VAL:HG11	1.94	0.49
16:P:21:VAL:O	16:P:21:VAL:HG12	2.13	0.49
1:A:939:G:H5''	7:G:102:ARG:NH2	2.28	0.49
1:A:1447:G:N3	1:A:1447:G:H2'	2.27	0.49
1:A:455:C:H6	1:A:455:C:O5'	1.95	0.49
1:A:1303:C:N4	1:A:1304:G:C6	2.81	0.49
1:A:1305:G:H5''	21:U:4:GLY:HA3	1.94	0.49
1:A:1124:G:H2'	1:A:1145:C:C5	2.48	0.49
19:S:34:TRP:HD1	19:S:52:TYR:CG	2.30	0.49
3:C:155:GLY:HA2	3:C:164:ARG:H	1.78	0.49
2:B:44:LEU:N	2:B:44:LEU:HD22	2.28	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:644:G:C5	1:A:645:C:C5	3.01	0.49
15:O:6:GLU:OE2	15:O:7:GLU:HG3	2.13	0.49
5:E:152:ARG:CZ	8:H:44:PHE:CE1	2.95	0.49
8:H:63:LEU:H	8:H:63:LEU:HD22	1.77	0.49
1:A:1352:C:H2'	1:A:1353:G:O4'	2.13	0.49
7:G:115:ARG:HB2	7:G:118:VAL:HG23	1.94	0.49
2:B:187:LEU:HA	2:B:201:ILE:HB	1.95	0.49
1:A:1200:C:O2	1:A:1200:C:C2'	2.60	0.48
2:B:51:LEU:HD21	2:B:201:ILE:HG23	1.95	0.48
2:B:100:GLY:HA2	2:B:176:GLU:OE1	2.12	0.48
1:A:977:A:C8	1:A:1223:C:N3	2.81	0.48
1:A:1262:C:H2'	1:A:1262:C:O2	2.12	0.48
1:A:1392:G:C4	1:A:1393:U:C5	3.01	0.48
20:T:75:ASN:OD1	20:T:75:ASN:N	2.46	0.48
1:A:721:G:H4'	1:A:722:A:O4'	2.13	0.48
1:A:49:U:O2'	1:A:50:A:H2'	2.13	0.48
1:A:790:A:C6	1:A:791:G:O6	2.65	0.48
20:T:20:LEU:O	20:T:23:ARG:HB3	2.13	0.48
5:E:143:ARG:HD2	8:H:77:GLU:OE2	2.13	0.48
1:A:1047:G:C2'	1:A:1048:G:H5'	2.43	0.48
1:A:487:A:C6	1:A:488:C:O2	2.66	0.48
2:B:158:LEU:HD22	2:B:182:ILE:HD11	1.94	0.48
1:A:1000:U:H2'	1:A:1001:A:C8	2.47	0.48
1:A:193:C:O2'	1:A:194:C:H5'	2.13	0.48
1:A:1486:G:H2'	1:A:1487:G:C1'	2.44	0.48
1:A:1164:G:C8	1:A:1164:G:OP2	2.66	0.48
5:E:152:ARG:CZ	8:H:44:PHE:HE1	2.26	0.48
1:A:197:A:N3	1:A:198:G:H1'	2.28	0.48
14:N:22:THR:HG23	14:N:33:VAL:CG2	2.42	0.48
1:A:1284:C:H3'	1:A:1285:A:H8	1.78	0.48
13:M:67:GLU:HB3	13:M:68:GLY:H	1.48	0.48
1:A:277:C:H5''	17:Q:68:ARG:HH22	1.78	0.48
1:A:488:C:H2'	1:A:489:C:C6	2.49	0.48
13:M:91:ARG:HB3	13:M:98:VAL:HG22	1.96	0.48
1:A:1092:A:H1'	1:A:1183:A:H62	1.78	0.48
1:A:1222:G:O2'	1:A:1223:C:H5'	2.12	0.48
1:A:1294:G:H2'	1:A:1295:G:H8	1.77	0.48
7:G:143:ARG:O	7:G:147:ALA:HB2	2.13	0.48
1:A:602:A:N1	1:A:637:G:C6	2.82	0.48
1:A:1434:A:N7	1:A:1435:G:C5	2.82	0.48
5:E:139:LEU:HA	5:E:142:LEU:HD12	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:46:ALA:HB1	7:G:121:ALA:N	2.28	0.48
16:P:76:GLN:C	16:P:78:GLY:H	2.15	0.48
9:I:13:ALA:HA	9:I:67:GLY:O	2.12	0.48
1:A:266:G:C5'	1:A:268:C:H41	2.22	0.48
7:G:111:ARG:NH1	7:G:122:HIS:HB3	2.29	0.48
3:C:202:ILE:HG22	3:C:204:LEU:HD23	1.95	0.48
5:E:33:VAL:HG21	5:E:109:ILE:HG12	1.95	0.48
7:G:40:ALA:CB	9:I:41:VAL:HG21	2.43	0.48
1:A:309:G:H2'	1:A:310:G:H8	1.79	0.48
20:T:37:SER:HB3	20:T:84:LEU:HD21	1.95	0.48
1:A:96:G:O6	1:A:97:G:C2	2.66	0.48
1:A:98:U:H6	1:A:98:U:H3'	1.77	0.48
2:B:51:LEU:HD22	2:B:55:PHE:CE1	2.48	0.48
1:A:1157:A:H1'	1:A:1181:G:H21	1.78	0.48
1:A:146:G:N3	1:A:147:G:C8	2.81	0.48
1:A:1347:G:H2'	9:I:108:VAL:O	2.13	0.48
13:M:40:ASN:ND2	13:M:41:PRO:HD2	2.28	0.48
3:C:29:TYR:CE2	3:C:33:LEU:HD22	2.49	0.48
8:H:63:LEU:N	8:H:63:LEU:HD13	2.28	0.48
1:A:266:G:C1'	1:A:267:C:OP2	2.62	0.48
1:A:1124:G:O2'	1:A:1145:C:N4	2.46	0.48
7:G:65:ALA:HB1	7:G:127:ALA:HB3	1.95	0.48
3:C:10:PHE:HE2	3:C:178:LEU:HD13	1.79	0.48
3:C:32:LEU:HB3	3:C:59:ARG:HH12	1.78	0.48
1:A:1488:G:N2	1:A:1489:G:C4	2.81	0.48
1:A:358:U:O2'	1:A:359:U:H5'	2.13	0.48
1:A:1392:G:H2'	1:A:1393:U:C6	2.44	0.48
1:A:1497:G:C5	1:A:1498:U:C4	3.02	0.48
9:I:46:ALA:HB2	9:I:74:ILE:HG23	1.95	0.48
1:A:1258:G:H2'	1:A:1259:C:C6	2.49	0.48
1:A:439:A:C4	1:A:497:A:C2	3.01	0.48
1:A:474:G:C2	1:A:475:G:C8	3.02	0.48
1:A:620:C:O2	4:D:135:LEU:HD22	2.14	0.48
1:A:377:G:OP1	16:P:3:LYS:HD3	2.13	0.48
11:K:29:ILE:HG12	11:K:30:VAL:N	2.27	0.48
1:A:1241:G:H2'	1:A:1242:C:H6	1.77	0.48
8:H:91:ARG:HG3	8:H:91:ARG:O	2.13	0.48
17:Q:54:GLY:HA3	17:Q:82:MET:HG2	1.94	0.48
1:A:46:G:C2	1:A:396:G:C2	3.01	0.48
1:A:920:U:H2'	1:A:921:U:C6	2.48	0.48
14:N:42:ILE:HG13	14:N:43:CYS:H	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:38:ILE:HG23	10:J:39:PRO:HD2	1.95	0.48
18:R:54:ARG:HB2	18:R:54:ARG:CZ	2.44	0.48
4:D:58:LEU:HD12	4:D:59:ARG:HD2	1.94	0.48
1:A:815:A:O2'	1:A:1527:C:H1'	2.14	0.48
12:L:12:ARG:HB3	12:L:12:ARG:HH11	1.79	0.48
17:Q:100:LYS:HG3	17:Q:100:LYS:O	2.14	0.48
13:M:23:TYR:HB2	13:M:67:GLU:OE1	2.14	0.48
1:A:99:C:H2'	1:A:101:A:C8	2.49	0.48
7:G:113:GLU:HB3	7:G:118:VAL:CG1	2.44	0.48
17:Q:63:ARG:O	17:Q:65:ILE:HD12	2.14	0.48
1:A:1190:G:H3'	3:C:3:ASN:HD21	1.79	0.48
2:B:130:ARG:HB3	2:B:131:PRO:HD2	1.96	0.48
20:T:17:ARG:CB	20:T:17:ARG:HH11	2.27	0.48
1:A:1410:G:H1'	1:A:1491:G:N2	2.28	0.48
1:A:407:G:H5'	4:D:3:ARG:HH12	1.77	0.48
18:R:25:THR:HG22	18:R:42:ARG:HH22	1.79	0.48
1:A:1024:G:C6	1:A:1025:U:O4	2.67	0.48
7:G:68:ASN:O	7:G:138:LYS:HD2	2.12	0.48
1:A:1007:C:H2'	1:A:1008:C:C6	2.48	0.48
1:A:1402:C:H2'	1:A:1403:C:C6	2.48	0.48
1:A:1046:A:H2	1:A:1047:G:C1'	2.27	0.48
1:A:448:A:C2	1:A:449:C:C4	3.01	0.48
1:A:1125:U:O2'	1:A:1126:U:P	2.72	0.48
2:B:73:THR:O	2:B:74:LYS:C	2.51	0.48
17:Q:23:VAL:HG21	17:Q:42:TYR:CD1	2.49	0.48
11:K:57:THR:HG23	11:K:58:PRO:HD2	1.96	0.48
1:A:965:A:C1'	1:A:966:G:OP2	2.62	0.48
1:A:1115:C:H2'	1:A:1116:C:H6	1.78	0.48
3:C:123:GLN:HB3	3:C:128:PHE:CB	2.43	0.48
1:A:1130:A:OP1	1:A:1131:G:N7	2.47	0.48
1:A:790:A:N1	1:A:791:G:C6	2.82	0.48
5:E:77:PRO:HG2	5:E:142:LEU:HD22	1.96	0.48
6:F:15:ASP:CG	6:F:16:GLN:N	2.68	0.48
1:A:974:A:OP2	14:N:41:ARG:NH1	2.35	0.47
1:A:1202:G:C4	14:N:42:ILE:CD1	2.97	0.47
9:I:111:ARG:HH12	9:I:113:LYS:HA	1.79	0.47
2:B:205:ASP:C	2:B:205:ASP:OD1	2.52	0.47
1:A:795:C:C5'	1:A:796:C:OP2	2.61	0.47
1:A:691:G:H2'	1:A:692:U:C6	2.49	0.47
1:A:986:A:C6	1:A:1220:G:N1	2.82	0.47
6:F:27:GLN:O	6:F:31:GLU:HG3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:14:TRP:CE3	21:U:15:ARG:HG3	2.49	0.47
3:C:130:VAL:HG23	3:C:131:ARG:H	1.78	0.47
5:E:20:GLN:O	5:E:21:ALA:O	2.32	0.47
1:A:677:U:H3	1:A:713:G:H22	1.62	0.47
1:A:956:U:H2'	1:A:957:U:O4'	2.14	0.47
12:L:82:VAL:HG23	12:L:106:ASP:OD1	2.13	0.47
2:B:30:ARG:HG2	2:B:31:TYR:CD1	2.49	0.47
12:L:43:VAL:CG1	12:L:44:THR:H	2.26	0.47
3:C:107:GLN:O	3:C:108:ASN:HB3	2.13	0.47
1:A:1296:C:H4'	1:A:1302:U:H5	1.77	0.47
1:A:1338:G:H2'	1:A:1339:A:C8	2.49	0.47
1:A:628:G:C2'	1:A:629:G:H5'	2.43	0.47
3:C:26:LYS:HD2	3:C:27:LYS:N	2.20	0.47
3:C:23:TYR:OH	10:J:9:ARG:HD3	2.13	0.47
1:A:820:U:H4'	1:A:821:G:OP2	2.14	0.47
1:A:1486:G:C6	1:A:1487:G:N1	2.82	0.47
1:A:1077:G:N2	1:A:1080:A:OP2	2.42	0.47
1:A:965:A:C2'	1:A:966:G:OP2	2.63	0.47
1:A:363:A:H62	12:L:28:LYS:NZ	2.12	0.47
2:B:134:GLU:C	2:B:136:VAL:N	2.68	0.47
1:A:1163:C:H2'	1:A:1164:G:O4'	2.15	0.47
18:R:66:LEU:C	18:R:66:LEU:HD23	2.35	0.47
1:A:980:C:HO2'	14:N:21:TYR:HE1	1.61	0.47
16:P:12:LYS:O	16:P:13:HIS:HB2	2.15	0.47
1:A:983:A:H1'	1:A:1049:U:O2	2.13	0.47
1:A:1286:A:H2'	1:A:1287:A:H4'	1.95	0.47
10:J:35:SER:HB2	10:J:73:ASP:O	2.15	0.47
17:Q:65:ILE:N	17:Q:65:ILE:HD12	2.30	0.47
1:A:1097:C:H1'	1:A:1169:A:H1'	1.96	0.47
1:A:287:U:O2'	1:A:288:A:H5'	2.13	0.47
11:K:124:LYS:C	11:K:125:PHE:HD1	2.18	0.47
1:A:1089:G:C5	1:A:1090:U:C5	3.02	0.47
11:K:69:ALA:O	11:K:73:MET:HG2	2.13	0.47
1:A:1485:U:C2'	1:A:1485:U:O2	2.61	0.47
1:A:504:C:C2	1:A:542:G:C2	3.03	0.47
20:T:50:GLU:HA	20:T:100:ILE:CG2	2.44	0.47
9:I:99:LEU:HB3	9:I:101:PHE:CD1	2.49	0.47
9:I:16:ARG:HH11	9:I:64:THR:CG2	2.26	0.47
1:A:1504:G:OP1	1:A:1507:A:H4'	2.14	0.47
1:A:532:A:H3'	1:A:533:A:H5'	1.96	0.47
6:F:60:PHE:O	6:F:61:LEU:HD23	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:126:ARG:HH22	11:K:129:SER:HB2	1.80	0.47
1:A:721:G:C6	1:A:733:A:H2	2.32	0.47
18:R:59:SER:H	18:R:62:GLU:HB2	1.79	0.47
18:R:59:SER:O	18:R:60:GLY:C	2.53	0.47
8:H:102:ARG:N	8:H:102:ARG:CD	2.78	0.47
13:M:82:MET:HB3	13:M:93:ARG:HH11	1.78	0.47
11:K:15:ALA:C	11:K:77:MET:HG3	2.35	0.47
4:D:25:ARG:C	4:D:27:TYR:N	2.67	0.47
13:M:6:GLY:HA3	13:M:67:GLU:HG3	1.97	0.47
1:A:97:G:O2'	1:A:98:U:H5'	2.14	0.47
7:G:38:LEU:HD12	7:G:38:LEU:O	2.14	0.47
12:L:47:LYS:CB	12:L:48:PRO:HD3	2.37	0.47
9:I:82:ALA:HB1	9:I:96:LEU:HD21	1.97	0.47
5:E:144:THR:HG22	5:E:145:LYS:H	1.78	0.47
1:A:500:G:C6	1:A:546:G:C2	3.03	0.47
11:K:79:SER:CB	11:K:104:GLN:HB3	2.43	0.47
1:A:509:A:H5'	4:D:54:TYR:CD2	2.49	0.47
19:S:3:ARG:O	19:S:4:SER:HB2	2.15	0.47
10:J:57:LYS:O	10:J:57:LYS:HD2	2.13	0.47
14:N:24:CYS:N	14:N:33:VAL:HG11	2.29	0.47
1:A:1150:U:O2	10:J:39:PRO:HG3	2.15	0.47
1:A:1126:U:N3	1:A:1127:G:C2	2.83	0.47
1:A:1150:U:H6	1:A:1150:U:O5'	1.96	0.47
2:B:74:LYS:HZ2	2:B:206:ASP:HA	1.79	0.47
2:B:51:LEU:HD22	2:B:55:PHE:HE1	1.80	0.47
16:P:69:THR:O	16:P:72:ARG:HB3	2.15	0.47
1:A:192:U:O4'	20:T:103:GLY:HA2	2.15	0.47
1:A:1487:G:H2'	1:A:1488:G:C5'	2.44	0.47
1:A:1487:G:C4	1:A:1488:G:C8	3.03	0.47
1:A:474:G:OP2	16:P:75:ARG:HD2	2.15	0.47
1:A:1425:U:H3	1:A:1475:G:H1	1.61	0.47
1:A:531:U:O3'	1:A:532:A:H4'	2.15	0.47
1:A:1264:C:H2'	1:A:1265:G:C8	2.50	0.47
4:D:50:ARG:NH1	4:D:52:SER:HA	2.29	0.47
1:A:838:G:N2	1:A:849:C:C2	2.82	0.47
1:A:1245:A:N1	1:A:1293:G:C2	2.83	0.47
17:Q:60:ILE:HB	17:Q:74:LEU:HD12	1.96	0.47
9:I:81:ILE:HG22	9:I:81:ILE:O	2.15	0.47
4:D:152:SER:HB2	4:D:155:LEU:HG	1.96	0.47
1:A:204:U:O2	1:A:204:U:H3'	2.15	0.47
1:A:892:A:C2	1:A:907:A:C4	3.02	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1056:U:H5'	3:C:163:ALA:HB2	1.97	0.47
1:A:974:A:C8	1:A:974:A:OP1	2.59	0.47
1:A:1314:C:OP2	19:S:6:LYS:HD3	2.15	0.47
1:A:144:G:C4	1:A:179:A:C2	3.02	0.47
1:A:625:G:C2	1:A:626:U:C2	3.02	0.47
1:A:694:A:H2'	1:A:695:A:O5'	2.14	0.47
19:S:80:TYR:O	19:S:81:ARG:C	2.53	0.47
1:A:838:G:H1	1:A:848:C:H42	1.63	0.47
2:B:92:TYR:CE2	2:B:151:GLY:HA3	2.50	0.47
11:K:67:ASP:OD2	11:K:71:LYS:HE3	2.15	0.47
4:D:177:ASP:C	4:D:177:ASP:OD1	2.52	0.47
1:A:1200:C:N4	1:A:1206:G:H1	2.13	0.47
1:A:181:G:C1'	1:A:182:U:OP2	2.63	0.47
10:J:12:ASP:HB3	10:J:15:THR:CB	2.44	0.47
1:A:929:G:OP1	1:A:1533:C:N4	2.45	0.47
16:P:26:ARG:HD3	16:P:31:LYS:HB3	1.97	0.47
16:P:20:VAL:HG21	16:P:32:TYR:CB	2.45	0.47
1:A:1265:G:H1	1:A:1270:C:H42	1.63	0.47
1:A:1298:C:N3	7:G:114:ARG:HD2	2.29	0.47
12:L:126:LYS:C	12:L:127:GLU:HG3	2.35	0.47
1:A:949:A:C4	1:A:1233:G:N2	2.83	0.47
9:I:43:ALA:HA	9:I:74:ILE:HD13	1.96	0.47
5:E:36:ASP:O	5:E:37:ARG:HB2	2.14	0.47
19:S:64:GLU:C	19:S:66:MET:H	2.18	0.47
1:A:191:G:C6	1:A:192:U:C4	3.03	0.47
1:A:575:G:H4'	1:A:576:G:OP1	2.15	0.47
2:B:25:ASN:HD22	2:B:26:PRO:N	2.12	0.47
13:M:11:ARG:HD2	13:M:12:ASN:N	2.29	0.47
1:A:964:A:O2'	10:J:55:LYS:HD3	2.15	0.47
1:A:1247:U:O2'	1:A:1248:A:H5'	2.14	0.47
20:T:34:LYS:CE	20:T:80:ARG:HH12	2.28	0.47
1:A:134:A:H2'	1:A:135:C:O4'	2.15	0.47
1:A:627:G:H2'	1:A:628:G:C8	2.48	0.46
12:L:47:LYS:CB	12:L:48:PRO:CD	2.93	0.46
1:A:564:C:OP1	12:L:15:ARG:NE	2.47	0.46
7:G:31:MET:SD	7:G:36:LYS:HB2	2.55	0.46
1:A:191:G:H21	20:T:104:LEU:HA	1.80	0.46
1:A:933:G:OP2	7:G:3:ARG:HB3	2.15	0.46
1:A:1167:A:C6	1:A:1168:A:C6	3.03	0.46
3:C:108:ASN:ND2	3:C:111:LEU:H	2.12	0.46
3:C:108:ASN:HD21	3:C:110:ASN:HB2	1.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:460:A:C2	1:A:462:G:C8	3.03	0.46
2:B:139:LYS:HD2	2:B:143:GLU:OE1	2.15	0.46
7:G:21:VAL:C	7:G:23:VAL:H	2.18	0.46
1:A:1007:C:C2	1:A:1023:G:N2	2.82	0.46
17:Q:66:SER:OG	17:Q:69:LYS:HG3	2.14	0.46
17:Q:56:VAL:O	17:Q:76:LEU:HD12	2.15	0.46
17:Q:89:LEU:HD23	17:Q:89:LEU:HA	1.79	0.46
20:T:36:LEU:HD12	20:T:62:LEU:HD12	1.96	0.46
1:A:1207:G:H2'	1:A:1208:C:C6	2.50	0.46
1:A:961:U:H2'	1:A:962:C:O4'	2.15	0.46
1:A:277:C:O2'	1:A:278:G:H5'	2.16	0.46
1:A:131:C:H2'	1:A:132:C:C6	2.50	0.46
1:A:1190:G:H3'	3:C:3:ASN:ND2	2.29	0.46
15:O:45:VAL:HG13	15:O:46:HIS:ND1	2.31	0.46
1:A:986:A:C2	1:A:1220:G:C2	3.02	0.46
11:K:127:LYS:O	11:K:128:ALA:HB2	2.14	0.46
1:A:1020:U:H2'	1:A:1021:G:H8	1.80	0.46
1:A:47:C:C6	1:A:365:U:H2'	2.50	0.46
1:A:862:C:O2'	1:A:863:U:H5'	2.15	0.46
12:L:19:ARG:HD2	12:L:19:ARG:N	2.30	0.46
17:Q:12:SER:HB3	17:Q:20:THR:HB	1.98	0.46
12:L:55:VAL:CG1	12:L:56:ALA:H	2.12	0.46
4:D:190:ASP:O	4:D:191:ARG:C	2.53	0.46
19:S:34:TRP:NE1	19:S:57:HIS:HE1	2.13	0.46
13:M:2:ALA:O	13:M:10:PRO:HD2	2.15	0.46
1:A:21:G:C2	1:A:22:G:C6	3.04	0.46
1:A:106:C:O2'	1:A:107:G:H5'	2.14	0.46
2:B:143:GLU:HA	2:B:146:GLN:NE2	2.31	0.46
11:K:24:SER:C	11:K:26:ASN:H	2.19	0.46
1:A:666:G:H5'	1:A:726:C:H1'	1.96	0.46
4:D:83:SER:HA	4:D:89:THR:HG23	1.97	0.46
4:D:141:ARG:H	4:D:141:ARG:HG2	1.47	0.46
1:A:1046:A:H2	1:A:1047:G:H1'	1.79	0.46
14:N:26:ARG:HD3	14:N:27:CYS:SG	2.56	0.46
1:A:1158:C:C5'	2:B:133:LYS:HE2	2.45	0.46
1:A:1418:A:H61	1:A:1482:G:H1'	1.80	0.46
1:A:397:A:N3	1:A:397:A:H3'	2.30	0.46
1:A:1026:G:N3	1:A:1026:G:C2'	2.76	0.46
1:A:1516:G:N2	1:A:1519:A:OP2	2.48	0.46
2:B:28:PHE:CD2	2:B:32:ILE:HD11	2.50	0.46
9:I:7:THR:HG22	9:I:8:GLY:N	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:118:GLN:O	3:C:122:GLU:HG3	2.14	0.46
1:A:1394:A:H4'	1:A:1395:C:OP2	2.16	0.46
1:A:1360:A:C2'	1:A:1361:G:O5'	2.64	0.46
1:A:1328:C:C2	1:A:1329:A:C8	3.04	0.46
7:G:60:LYS:HG3	7:G:64:GLN:HB2	1.97	0.46
1:A:900:A:N1	1:A:901:A:C2	2.84	0.46
1:A:813:U:H5'	1:A:903:G:O3'	2.16	0.46
1:A:1122:U:C2'	1:A:1123:A:H5'	2.41	0.46
12:L:113:ARG:NH2	12:L:120:TYR:CE1	2.84	0.46
1:A:463:A:H2'	1:A:474:G:H8	1.80	0.46
20:T:74:LYS:C	20:T:76:ALA:N	2.69	0.46
1:A:1295:G:N1	1:A:1296:C:C2	2.84	0.46
1:A:690:G:H2'	1:A:691:G:O4'	2.16	0.46
4:D:153:ARG:NH1	4:D:181:MET:HB2	2.31	0.46
1:A:1437:C:H2'	1:A:1438:G:C8	2.49	0.46
1:A:1186:G:C2	1:A:1187:G:C4	3.04	0.46
9:I:8:GLY:HA3	9:I:79:LEU:HB3	1.96	0.46
5:E:48:ALA:HB3	5:E:54:ALA:HA	1.97	0.46
9:I:30:GLY:O	9:I:31:GLN:O	2.33	0.46
9:I:114:TYR:HD1	9:I:114:TYR:O	1.98	0.46
1:A:1203:C:H5''	14:N:2:ALA:HB3	1.96	0.46
17:Q:67:LYS:HA	17:Q:70:ARG:NH1	2.25	0.46
1:A:990:C:H2'	1:A:991:U:O4'	2.16	0.46
1:A:994:A:N3	1:A:994:A:C2'	2.79	0.46
1:A:172:A:N7	1:A:174:C:C4	2.83	0.46
1:A:741:G:H2'	1:A:742:G:O4'	2.16	0.46
1:A:821:G:H2'	1:A:822:C:H6	1.81	0.46
1:A:345:C:H1'	1:A:346:G:N2	2.31	0.46
4:D:106:TYR:CE1	4:D:113:SER:HA	2.51	0.46
1:A:353:A:H2'	1:A:354:G:OP2	2.16	0.46
1:A:1098:C:H2'	1:A:1099:G:O4'	2.14	0.46
1:A:630:G:H5'	1:A:631:G:P	2.55	0.46
2:B:185:ILE:HD12	2:B:185:ILE:N	2.31	0.46
5:E:13:ILE:HD13	5:E:51:VAL:HG13	1.98	0.46
1:A:327:A:O2'	1:A:328:C:O4'	2.33	0.46
10:J:16:LEU:HD12	10:J:68:HIS:HB2	1.96	0.46
5:E:33:VAL:HA	5:E:42:GLY:O	2.16	0.46
1:A:376:G:H2'	1:A:377:G:H8	1.80	0.46
7:G:102:ARG:O	7:G:106:GLN:HB2	2.16	0.46
1:A:828:A:OP1	1:A:828:A:H4'	2.16	0.46
1:A:154:C:H2'	1:A:155:C:H6	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1513:A:H2'	1:A:1514:C:C6	2.50	0.46
1:A:224:C:H2'	1:A:225:C:C6	2.51	0.46
1:A:1353:G:C4	1:A:1354:C:C5	3.03	0.46
1:A:1118:C:H6	1:A:1118:C:O5'	1.99	0.46
10:J:16:LEU:HB3	10:J:70:ARG:HG3	1.97	0.46
9:I:10:ARG:C	9:I:12:GLU:H	2.19	0.46
12:L:98:TYR:N	12:L:98:TYR:CD1	2.84	0.46
1:A:686:U:C2	1:A:687:A:N7	2.84	0.46
8:H:116:LYS:HZ3	8:H:127:LEU:HB3	1.79	0.46
1:A:56:U:H2'	1:A:57:G:H8	1.78	0.46
1:A:803:G:C6	1:A:804:U:N3	2.84	0.46
6:F:91:VAL:HG11	18:R:72:ARG:HH12	1.81	0.46
4:D:111:ALA:HA	4:D:116:GLN:HE21	1.80	0.46
4:D:163:GLU:HA	4:D:166:LYS:HE3	1.98	0.46
15:O:76:GLU:O	15:O:79:ARG:N	2.49	0.46
20:T:33:ILE:HD13	20:T:63:ILE:HG12	1.98	0.46
1:A:1314:C:H2'	1:A:1315:U:C6	2.50	0.46
5:E:10:MET:HE1	5:E:13:ILE:HD11	1.97	0.46
1:A:192:U:H2'	1:A:193:C:C6	2.43	0.46
1:A:475:G:N1	1:A:476:G:C6	2.84	0.46
1:A:37:U:O2'	1:A:500:G:H4'	2.15	0.46
1:A:853:G:H2'	1:A:854:G:H5'	1.97	0.46
9:I:4:TYR:CD2	9:I:88:TYR:HB2	2.50	0.46
2:B:92:TYR:CE2	2:B:151:GLY:CA	2.99	0.46
2:B:92:TYR:CD2	2:B:151:GLY:HA3	2.51	0.46
1:A:895:G:H2'	1:A:896:C:C6	2.51	0.46
13:M:60:VAL:HG13	13:M:66:LEU:HD11	1.98	0.46
1:A:1314:C:C5	19:S:6:LYS:HE2	2.51	0.46
1:A:181:G:H1'	1:A:182:U:OP2	2.15	0.46
7:G:61:VAL:O	7:G:65:ALA:HB2	2.17	0.46
1:A:902:G:O2'	1:A:903:G:H5'	2.16	0.46
1:A:394:G:H2'	1:A:395:C:C6	2.51	0.46
1:A:16:A:H2'	1:A:17:U:C5'	2.45	0.46
13:M:92:HIS:HA	13:M:110:ARG:HH22	1.81	0.46
11:K:38:ASN:HA	11:K:39:PRO:HD3	1.80	0.46
1:A:1299:A:N7	1:A:1301:U:O2	2.48	0.46
2:B:219:VAL:HG12	2:B:223:ILE:HD11	1.96	0.46
1:A:769:G:H4'	1:A:1513:A:H4'	1.97	0.46
1:A:1120:G:C6	1:A:1121:U:C4	3.04	0.46
2:B:144:ARG:NH1	2:B:148:TYR:CE1	2.84	0.46
8:H:100:ILE:HA	8:H:101:PRO:HD3	1.69	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:29:ARG:HD2	19:S:29:ARG:N	2.31	0.46
1:A:1465:C:H2'	1:A:1466:C:O4'	2.16	0.46
12:L:20:LYS:HD3	12:L:20:LYS:N	2.24	0.45
3:C:23:TYR:CD2	3:C:24:ALA:N	2.84	0.45
4:D:65:ARG:HH11	4:D:72:GLU:HB2	1.81	0.45
4:D:65:ARG:NH1	4:D:72:GLU:HB2	2.30	0.45
13:M:11:ARG:HA	13:M:45:VAL:HG11	1.98	0.45
1:A:1294:G:H2'	1:A:1295:G:C8	2.51	0.45
1:A:428:G:C5	1:A:430:A:C6	3.04	0.45
5:E:71:LEU:CD2	5:E:115:VAL:HG22	2.46	0.45
20:T:13:LEU:HG	20:T:14:LYS:N	2.31	0.45
1:A:1228:C:OP1	13:M:115:LYS:HG2	2.17	0.45
13:M:14:ARG:HG3	13:M:44:ARG:HH21	1.81	0.45
1:A:29:G:O2'	1:A:30:U:H5'	2.16	0.45
1:A:867:G:C2	1:A:868:C:C6	3.04	0.45
1:A:976:G:N7	1:A:1359:C:H1'	2.31	0.45
1:A:409:G:OP1	4:D:24:GLU:O	2.34	0.45
1:A:147:G:C2	1:A:148:G:C8	3.04	0.45
7:G:16:LEU:H	7:G:16:LEU:CD2	2.27	0.45
20:T:74:LYS:HB3	20:T:74:LYS:HZ2	1.81	0.45
1:A:705:U:C5	1:A:706:A:C5	3.04	0.45
3:C:130:VAL:O	3:C:134:ILE:HG13	2.16	0.45
1:A:1030(C):G:C6	1:A:1030(D):A:C6	3.04	0.45
1:A:433:C:O2	1:A:433:C:H2'	2.17	0.45
1:A:77:G:O2'	1:A:78:G:H5'	2.17	0.45
1:A:92:C:C5	1:A:93:G:C8	3.04	0.45
1:A:1181:G:C6	1:A:1182:G:N1	2.84	0.45
7:G:65:ALA:HB1	7:G:127:ALA:CB	2.46	0.45
2:B:101:MET:HE3	2:B:108:ILE:HG12	1.98	0.45
20:T:44:ALA:C	20:T:46:GLU:H	2.20	0.45
3:C:113:ALA:HA	3:C:116:VAL:CG2	2.46	0.45
12:L:69:TYR:CD2	12:L:70:ILE:N	2.85	0.45
1:A:1502:A:H2	1:A:1505:G:N1	2.14	0.45
7:G:26:PHE:CA	7:G:101:LEU:HD13	2.46	0.45
3:C:89:GLU:O	3:C:93:LYS:HB2	2.16	0.45
1:A:894:G:C6	1:A:895:G:C5	3.04	0.45
8:H:100:ILE:HG23	8:H:101:PRO:HD2	1.98	0.45
1:A:867:G:C2	1:A:868:C:C5	3.05	0.45
4:D:128:VAL:O	4:D:129:ASN:HB2	2.17	0.45
10:J:71:LEU:HD13	10:J:72:VAL:N	2.32	0.45
7:G:50:ILE:CG2	7:G:61:VAL:HG21	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:101:MET:C	2:B:102:LEU:HD12	2.36	0.45
1:A:101:A:H2'	1:A:102:G:H8	1.82	0.45
1:A:491:G:C2	1:A:492:G:C5	3.05	0.45
1:A:1417:G:N2	1:A:1484:C:H42	2.14	0.45
1:A:1426:C:H2'	1:A:1427:U:H6	1.78	0.45
2:B:107:THR:C	2:B:109:SER:H	2.20	0.45
3:C:86:VAL:HG12	3:C:87:LEU:N	2.30	0.45
1:A:1228:C:N4	13:M:104:ARG:O	2.48	0.45
12:L:81:SER:HB3	12:L:106:ASP:HB2	1.98	0.45
19:S:3:ARG:HH22	19:S:69:HIS:CD2	2.35	0.45
1:A:176:C:O2	1:A:176:C:H2'	2.15	0.45
1:A:491:G:C2	1:A:492:G:C8	3.05	0.45
1:A:1413:A:H2'	1:A:1414:U:O4'	2.16	0.45
1:A:421:U:O4	3:C:126:ARG:HD2	2.17	0.45
2:B:101:MET:HB2	2:B:102:LEU:CD1	2.47	0.45
1:A:1112:C:C4	3:C:178:LEU:HD23	2.51	0.45
15:O:45:VAL:CG2	15:O:46:HIS:H	2.27	0.45
19:S:16:LEU:O	19:S:20:LEU:HG	2.16	0.45
15:O:87:ILE:CG2	15:O:88:ARG:H	2.29	0.45
1:A:521:G:H1	1:A:528:C:N4	2.14	0.45
1:A:364:A:H2'	1:A:365:U:O2	2.16	0.45
1:A:550:G:C5	1:A:551:U:C5	3.04	0.45
1:A:1197:G:H2'	1:A:1197:G:N3	2.32	0.45
14:N:22:THR:HG23	14:N:33:VAL:HG21	1.98	0.45
1:A:77:G:N1	1:A:93:G:C2	2.84	0.45
7:G:111:ARG:CB	7:G:119:ARG:HG2	2.44	0.45
1:A:1143:G:O5'	1:A:1143:G:H8	1.98	0.45
1:A:696:A:N3	1:A:786:G:O2'	2.39	0.45
1:A:413:G:N2	1:A:428:G:H1'	2.31	0.45
6:F:44:GLY:HA2	6:F:59:TYR:CE1	2.51	0.45
6:F:4:TYR:O	6:F:65:VAL:HG22	2.16	0.45
1:A:401:C:H1'	1:A:622:A:H1'	1.98	0.45
5:E:152:ARG:HB3	8:H:43:GLY:HA3	1.99	0.45
4:D:83:SER:HA	4:D:89:THR:CG2	2.45	0.45
1:A:1230:C:O2'	1:A:1231:G:H5'	2.17	0.45
1:A:1343:G:H2'	1:A:1344:C:C6	2.51	0.45
1:A:266:G:O2'	17:Q:67:LYS:HB3	2.17	0.45
1:A:1128:C:N4	1:A:1143:G:H22	2.06	0.45
1:A:379:C:H2'	1:A:380:G:H5'	1.97	0.45
20:T:45:GLN:O	20:T:45:GLN:HG2	2.16	0.45
1:A:689:C:O2'	1:A:690:G:H5'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:145:ALA:C	7:G:147:ALA:H	2.20	0.45
1:A:1498:U:H1'	1:A:1499:A:OP2	2.17	0.45
1:A:1015:A:H2'	1:A:1016:A:C8	2.51	0.45
1:A:674:G:H2'	1:A:675:A:C8	2.52	0.45
1:A:339:C:H2'	1:A:340:U:C6	2.52	0.45
1:A:1052:U:O5'	1:A:1052:U:H6	1.99	0.45
1:A:1201:A:H5''	1:A:1203:C:OP2	2.17	0.45
1:A:234:C:H2'	1:A:235:C:C6	2.51	0.45
8:H:26:VAL:HG23	8:H:27:PRO:HD2	1.98	0.45
1:A:430:A:C5	1:A:431:A:C8	3.04	0.45
3:C:188:LEU:CD2	3:C:188:LEU:H	2.30	0.45
4:D:153:ARG:HH12	4:D:181:MET:HB2	1.80	0.45
3:C:9:GLY:HA3	14:N:49:HIS:HB3	1.99	0.45
1:A:913:A:H1'	1:A:914:A:OP2	2.17	0.45
21:U:13:ILE:HG22	21:U:14:TRP:N	2.32	0.45
18:R:31:LEU:CD2	18:R:66:LEU:HB2	2.47	0.45
8:H:111:ILE:O	8:H:134:ILE:HB	2.17	0.45
1:A:560:U:H5'	1:A:566:G:H22	1.78	0.45
1:A:560:U:H4'	1:A:561:U:O5'	2.15	0.45
4:D:25:ARG:C	4:D:27:TYR:H	2.19	0.45
1:A:91:C:C2'	1:A:92:C:O5'	2.65	0.45
1:A:78:G:C2	1:A:92:C:N3	2.85	0.45
1:A:88:A:C5	1:A:89:C:C6	3.05	0.45
5:E:10:MET:SD	5:E:13:ILE:HG13	2.57	0.45
1:A:1347:G:H22	1:A:1373:G:H2'	1.75	0.45
3:C:11:ARG:HD3	3:C:178:LEU:O	2.17	0.45
1:A:192:U:C4'	20:T:103:GLY:HA2	2.47	0.45
3:C:107:GLN:O	3:C:108:ASN:CB	2.65	0.45
8:H:113:SER:HA	8:H:118:VAL:HA	1.99	0.45
5:E:105:VAL:HB	5:E:106:PRO:CD	2.47	0.45
7:G:26:PHE:O	7:G:30:ILE:HG13	2.16	0.45
11:K:127:LYS:N	11:K:127:LYS:HD2	2.33	0.45
16:P:26:ARG:HH11	16:P:26:ARG:HG3	1.81	0.45
1:A:1144:G:N2	1:A:1146:A:H61	2.14	0.45
15:O:6:GLU:OE1	15:O:6:GLU:N	2.50	0.45
4:D:36:ARG:HG2	4:D:38:TYR:CZ	2.52	0.45
1:A:830:G:C6	1:A:831:U:C4	3.04	0.45
2:B:193:ASP:C	2:B:193:ASP:OD1	2.56	0.45
4:D:14:ARG:HD3	4:D:14:ARG:O	2.17	0.45
1:A:91:C:H5	1:A:92:C:C6	2.35	0.44
7:G:50:ILE:HD12	7:G:61:VAL:HG11	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:130:A:H1'	1:A:263:A:HO2'	1.81	0.44
2:B:102:LEU:HD12	2:B:102:LEU:N	2.32	0.44
1:A:298:A:H2'	1:A:299:G:O4'	2.16	0.44
1:A:434:U:H2'	1:A:435:C:C6	2.52	0.44
20:T:75:ASN:O	20:T:76:ALA:C	2.55	0.44
1:A:986:A:C6	1:A:987:G:C6	3.04	0.44
1:A:67:C:O2'	1:A:171:A:H1'	2.18	0.44
11:K:29:ILE:HB	11:K:44:SER:HB3	1.99	0.44
1:A:1478:C:H2'	1:A:1479:C:C6	2.52	0.44
1:A:1292:U:H2'	1:A:1293:G:C8	2.51	0.44
2:B:92:TYR:CD1	2:B:94:ASN:HB2	2.52	0.44
19:S:44:MET:C	19:S:47:HIS:HD2	2.20	0.44
1:A:763:G:N2	1:A:764:C:C2	2.85	0.44
7:G:12:LEU:H	7:G:12:LEU:HD12	1.82	0.44
14:N:19:ARG:HG2	14:N:19:ARG:O	2.18	0.44
1:A:960:U:H4'	1:A:961:U:C5'	2.47	0.44
1:A:1304:G:C6	1:A:1305:G:N1	2.85	0.44
1:A:1327:C:H2'	1:A:1328:C:H6	1.83	0.44
1:A:73:C:O2'	1:A:75:G:N7	2.46	0.44
8:H:75:ARG:HA	8:H:76:PRO:HD3	1.90	0.44
6:F:63:TYR:O	6:F:65:VAL:HG13	2.17	0.44
1:A:1019:C:H2'	1:A:1020:U:O4'	2.17	0.44
8:H:90:GLY:O	8:H:91:ARG:HB2	2.17	0.44
1:A:138:G:H1	1:A:225:C:H42	1.65	0.44
1:A:175:C:H2'	1:A:176:C:H6	1.82	0.44
2:B:233:SER:HA	2:B:234:PRO:HD3	1.88	0.44
21:U:5:ASP:HB3	21:U:8:THR:OG1	2.17	0.44
8:H:6:ILE:H	8:H:6:ILE:CD1	2.31	0.44
2:B:185:ILE:H	2:B:185:ILE:HD12	1.82	0.44
1:A:1157:A:C4	1:A:1181:G:N2	2.85	0.44
1:A:370:C:C4	1:A:371:G:N7	2.85	0.44
1:A:537:G:H2'	1:A:538:G:C8	2.52	0.44
1:A:1096:C:H2'	1:A:1097:C:H6	1.82	0.44
8:H:29:SER:OG	8:H:32:LYS:HG3	2.17	0.44
1:A:947:G:H2'	1:A:948:C:O4'	2.17	0.44
1:A:737:A:H2'	1:A:738:C:H6	1.82	0.44
16:P:25:ARG:HD3	16:P:25:ARG:N	2.32	0.44
1:A:1144:G:C2	1:A:1146:A:N6	2.86	0.44
1:A:1291:G:H4'	9:I:39:GLY:HA3	1.98	0.44
3:C:77:ILE:HG23	3:C:81:GLY:HA2	1.98	0.44
8:H:102:ARG:H	8:H:102:ARG:CD	2.31	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:17:VAL:HG11	9:I:81:ILE:HG12	2.00	0.44
10:J:63:PHE:HZ	14:N:45:ARG:HG3	1.82	0.44
4:D:60:GLU:HG2	4:D:202:LEU:HB2	2.00	0.44
17:Q:79:SER:OG	17:Q:80:GLY:N	2.51	0.44
14:N:29:ARG:HH11	14:N:29:ARG:HG2	1.82	0.44
9:I:112:LYS:HD3	9:I:113:LYS:N	2.33	0.44
1:A:487:A:H2'	1:A:488:C:O4'	2.17	0.44
1:A:954:G:C6	1:A:955:U:N3	2.86	0.44
1:A:1240:U:H1'	7:G:38:LEU:HD21	1.99	0.44
1:A:1118:C:P	9:I:104:ARG:HE	2.41	0.44
1:A:177:C:C2	1:A:178:C:C5	3.05	0.44
1:A:1417:G:H21	1:A:1484:C:H42	1.66	0.44
1:A:1004:A:N6	1:A:1035:A:C5	2.85	0.44
4:D:50:ARG:HA	4:D:51:PRO:HD3	1.83	0.44
1:A:803:G:H2'	1:A:804:U:O4'	2.17	0.44
3:C:14:ILE:O	3:C:16:ARG:N	2.50	0.44
8:H:84:ARG:O	8:H:135:CYS:HB2	2.17	0.44
1:A:1053:G:H4'	1:A:1054:C:H5'	2.00	0.44
1:A:1249:C:H2'	1:A:1250:A:H5'	1.98	0.44
13:M:63:THR:HG23	13:M:64:TRP:CD2	2.53	0.44
1:A:265:G:O2'	1:A:266:G:H3'	2.18	0.44
2:B:53:ARG:HH12	2:B:199:TYR:HA	1.82	0.44
9:I:45:ALA:HA	9:I:48:GLU:HB2	1.99	0.44
8:H:97:VAL:HG13	8:H:98:LYS:N	2.33	0.44
1:A:1112:C:H1'	3:C:179:ARG:NH1	2.32	0.44
1:A:327:A:C2	1:A:329:A:C4	3.06	0.44
1:A:372:C:C1'	1:A:373:A:OP2	2.65	0.44
20:T:50:GLU:HA	20:T:100:ILE:HG22	1.99	0.44
20:T:49:ALA:HB3	20:T:99:LEU:CG	2.48	0.44
1:A:1486:G:C6	1:A:1487:G:C6	3.05	0.44
1:A:476:G:O2'	1:A:477:G:H5'	2.18	0.44
1:A:792:A:H1'	1:A:793:U:H5''	1.99	0.44
4:D:11:LEU:O	4:D:12:CYS:C	2.56	0.44
2:B:87:ARG:O	2:B:88:ALA:CB	2.66	0.44
13:M:50:GLU:OE2	13:M:50:GLU:HA	2.17	0.44
1:A:303:A:H2'	1:A:304:U:O4'	2.17	0.44
1:A:1361(A):C:O2	1:A:1362:C:C6	2.71	0.44
8:H:87:SER:OG	8:H:92:ARG:HA	2.17	0.44
1:A:70:G:O2'	1:A:73:C:H5'	2.18	0.44
10:J:6:ILE:HD12	10:J:73:ASP:H	1.81	0.44
1:A:1128:C:C4	1:A:1139:G:C6	3.04	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:456:C:C2	1:A:477:G:N2	2.85	0.44
1:A:909:A:H2'	1:A:910:C:O4'	2.18	0.44
3:C:123:GLN:HB3	3:C:128:PHE:HB2	2.00	0.44
11:K:125:PHE:N	11:K:125:PHE:CD1	2.85	0.44
1:A:428:G:H1'	1:A:429:U:OP2	2.17	0.44
1:A:1163:C:N4	1:A:1174:G:C2	2.85	0.44
1:A:35:G:C6	1:A:36:C:N4	2.86	0.44
1:A:1468:A:H2'	1:A:1469:G:O4'	2.17	0.44
7:G:62:PHE:C	7:G:62:PHE:CD2	2.91	0.44
12:L:43:VAL:CG1	12:L:44:THR:N	2.80	0.44
5:E:76:ILE:HG23	5:E:78:HIS:N	2.26	0.44
1:A:1191:A:OP1	3:C:3:ASN:OD1	2.35	0.44
12:L:20:LYS:CD	12:L:20:LYS:N	2.81	0.44
1:A:708:C:H2'	1:A:709:G:H8	1.82	0.44
1:A:1490:C:O2'	1:A:1491:G:H5'	2.17	0.44
7:G:137:LYS:O	7:G:138:LYS:C	2.55	0.44
1:A:234:C:H2'	1:A:235:C:H6	1.81	0.44
12:L:43:VAL:CG2	12:L:55:VAL:HG21	2.47	0.44
1:A:1418:A:OP2	1:A:1418:A:H3'	2.18	0.44
20:T:46:GLU:HB3	20:T:48:LYS:HE3	1.99	0.44
3:C:113:ALA:HA	3:C:116:VAL:HG23	1.99	0.44
1:A:984:C:H42	1:A:1221:G:H1	1.66	0.44
4:D:23:GLY:HA3	4:D:112:VAL:HG13	2.00	0.44
4:D:26:CYS:HA	4:D:31:CYS:HB2	1.99	0.44
1:A:157:G:H2'	1:A:158:G:C8	2.53	0.44
13:M:83:ASP:C	13:M:85:GLY:H	2.21	0.44
6:F:45:LEU:HA	6:F:58:GLY:O	2.17	0.44
2:B:215:LEU:HD23	2:B:215:LEU:HA	1.66	0.44
1:A:1358:U:O2'	1:A:1359:C:O4'	2.36	0.44
1:A:60:A:OP1	1:A:331:G:N1	2.41	0.44
1:A:181:G:C4'	1:A:182:U:OP2	2.66	0.44
7:G:47:CYS:O	7:G:50:ILE:HB	2.18	0.44
9:I:82:ALA:HA	9:I:85:LEU:HB3	2.00	0.44
1:A:1371:G:C5	1:A:1372:U:C5	3.06	0.44
1:A:284:G:C4	1:A:285:G:C8	3.06	0.44
7:G:16:LEU:HD22	7:G:16:LEU:N	2.25	0.44
1:A:107:G:C2	1:A:108:G:H1'	2.53	0.44
20:T:61:SER:O	20:T:65:LYS:HG3	2.18	0.44
1:A:477:G:C2	1:A:478:A:C5	3.05	0.44
12:L:90:VAL:CG2	12:L:99:HIS:HE1	2.30	0.44
1:A:865:A:H2'	1:A:866:C:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:692:U:OP1	11:K:124:LYS:HE3	2.18	0.44
7:G:70:LYS:HB2	7:G:96:GLN:HB3	2.00	0.44
1:A:374:A:C6	1:A:375:U:C4	3.06	0.44
2:B:220:ASP:C	2:B:222:ILE:H	2.21	0.44
1:A:1014:A:N7	1:A:1015:A:N6	2.66	0.44
1:A:1396:A:O4'	1:A:1398:A:H1'	2.17	0.44
16:P:39:TYR:CE2	16:P:41:PRO:HG3	2.52	0.44
1:A:157:G:H2'	1:A:158:G:H8	1.81	0.44
5:E:15:ARG:NH1	5:E:26:PHE:CE2	2.86	0.44
16:P:52:ASP:OD1	16:P:55:ARG:HB2	2.17	0.44
10:J:47:PHE:HD2	14:N:34:TYR:HE2	1.66	0.44
1:A:44:G:H2'	1:A:45:U:O4'	2.18	0.44
12:L:73:GLU:OE1	12:L:73:GLU:HA	2.18	0.44
13:M:70:LEU:C	13:M:70:LEU:CD2	2.87	0.43
7:G:18:TYR:OH	7:G:58:PRO:C	2.57	0.43
19:S:36:ARG:NH2	19:S:75:ALA:HB3	2.33	0.43
1:A:407:G:H1'	4:D:119:GLN:HE22	1.82	0.43
8:H:58:TYR:HB3	8:H:59:LEU:H	1.68	0.43
1:A:1084:G:H5'	1:A:1102:A:OP2	2.18	0.43
1:A:616:G:N3	1:A:625:G:C2	2.85	0.43
15:O:86:GLY:C	15:O:87:ILE:HD13	2.38	0.43
13:M:49:THR:HG22	13:M:50:GLU:N	2.33	0.43
5:E:139:LEU:HA	5:E:142:LEU:CD1	2.47	0.43
4:D:141:ARG:HB3	4:D:141:ARG:CZ	2.48	0.43
1:A:488:C:H2'	1:A:489:C:H6	1.82	0.43
1:A:990:C:H5'	1:A:1017:G:O2'	2.18	0.43
3:C:3:ASN:N	3:C:3:ASN:OD1	2.51	0.43
20:T:49:ALA:HB3	20:T:99:LEU:HG	2.00	0.43
2:B:61:LEU:HA	2:B:61:LEU:HD22	1.89	0.43
5:E:7:GLU:O	5:E:34:VAL:HA	2.18	0.43
16:P:20:VAL:CG2	16:P:32:TYR:HB2	2.47	0.43
4:D:38:TYR:CE1	4:D:45:GLN:HG3	2.53	0.43
4:D:146:ILE:HD12	4:D:146:ILE:N	2.33	0.43
13:M:49:THR:CG2	13:M:50:GLU:H	2.31	0.43
1:A:544:G:C6	1:A:545:C:C4	3.07	0.43
4:D:58:LEU:HD23	4:D:206:PHE:CE1	2.53	0.43
10:J:54:PHE:O	10:J:55:LYS:O	2.36	0.43
2:B:68:ILE:O	2:B:90:MET:HB3	2.18	0.43
1:A:585:G:H4'	12:L:8:ASN:OD1	2.18	0.43
1:A:1056:U:H2'	1:A:1057:G:H8	1.84	0.43
1:A:75:G:H2'	1:A:76:C:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:491:G:C4	1:A:492:G:C8	3.05	0.43
1:A:328:C:H4'	1:A:329:A:H5'	2.00	0.43
1:A:1418:A:C4	1:A:1483:A:C6	3.06	0.43
10:J:15:THR:HG22	10:J:94:VAL:HG23	2.01	0.43
1:A:299:G:C6	1:A:300:A:C6	3.07	0.43
1:A:346:G:C2'	1:A:347:G:H5'	2.48	0.43
3:C:6:HIS:HD2	3:C:9:GLY:H	1.65	0.43
9:I:20:ARG:HA	9:I:21:PRO:HD3	1.83	0.43
11:K:29:ILE:HB	11:K:44:SER:CB	2.48	0.43
1:A:778:G:H2'	1:A:779:C:O4'	2.18	0.43
11:K:93:GLN:HA	11:K:96:ARG:HB2	2.00	0.43
14:N:3:ARG:NH2	14:N:6:LEU:HD21	2.33	0.43
3:C:162:GLN:HG3	3:C:163:ALA:N	2.34	0.43
1:A:991:U:C5	1:A:1212:U:C2	2.90	0.43
7:G:60:LYS:O	7:G:61:VAL:C	2.57	0.43
1:A:130:A:O2'	1:A:131:C:H5''	2.18	0.43
2:B:97:TRP:CH2	2:B:176:GLU:OE2	2.70	0.43
1:A:284:G:N3	1:A:285:G:C8	2.86	0.43
17:Q:23:VAL:CG2	17:Q:42:TYR:HD1	2.31	0.43
18:R:32:ARG:HA	18:R:69:THR:CG2	2.44	0.43
3:C:113:ALA:HB1	3:C:200:ALA:HB3	2.00	0.43
5:E:131:ILE:HD12	5:E:131:ILE:HA	1.75	0.43
1:A:792:A:C6	1:A:794:A:N6	2.86	0.43
4:D:9:CYS:O	4:D:12:CYS:HB2	2.18	0.43
1:A:601:C:C2'	1:A:602:A:H5'	2.48	0.43
20:T:36:LEU:HD12	20:T:62:LEU:CD1	2.48	0.43
10:J:47:PHE:HD2	14:N:34:TYR:CE2	2.37	0.43
2:B:77:ALA:O	2:B:79:ASP:N	2.51	0.43
1:A:826:C:O2	8:H:15:ASN:ND2	2.52	0.43
1:A:1528:U:H2'	1:A:1528:U:H6	1.64	0.43
8:H:56:LYS:N	8:H:56:LYS:HD2	2.33	0.43
1:A:1318:A:H4'	19:S:10:PHE:CE2	2.53	0.43
1:A:1361(A):C:O2	1:A:1362:C:C5	2.71	0.43
1:A:96:G:O6	1:A:97:G:N1	2.52	0.43
2:B:54:THR:OG1	2:B:199:TYR:HB3	2.18	0.43
1:A:1182:G:H4'	1:A:1183:A:O5'	2.18	0.43
1:A:1417:G:O2'	1:A:1483:A:N6	2.52	0.43
20:T:49:ALA:HB3	20:T:99:LEU:CD1	2.47	0.43
16:P:75:ARG:HB2	16:P:80:PHE:HD1	1.84	0.43
2:B:69:LEU:HD23	2:B:69:LEU:C	2.39	0.43
8:H:9:MET:SD	8:H:32:LYS:HB3	2.58	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:72:LEU:O	20:T:74:LYS:N	2.46	0.43
1:A:1255:G:C6	1:A:1279:A:N7	2.86	0.43
11:K:12:ARG:HG2	11:K:13:GLN:H	1.83	0.43
2:B:144:ARG:NH1	2:B:148:TYR:HE1	2.16	0.43
12:L:45:PRO:HB3	12:L:53:ARG:HH12	1.83	0.43
7:G:85:TYR:CE1	7:G:154:TYR:HE1	2.36	0.43
8:H:108:GLY:HA3	8:H:138:TRP:HB3	1.99	0.43
7:G:108:ALA:O	7:G:119:ARG:HB3	2.18	0.43
1:A:89:C:N3	1:A:90:U:O2	2.51	0.43
2:B:185:ILE:HA	2:B:199:TYR:O	2.19	0.43
1:A:146:G:C2	1:A:147:G:C8	3.07	0.43
3:C:23:TYR:HA	10:J:11:PHE:CE1	2.54	0.43
1:A:20:U:C2'	1:A:21:G:H5'	2.47	0.43
1:A:750:G:H21	15:O:23:GLY:CA	2.30	0.43
20:T:49:ALA:O	20:T:50:GLU:C	2.57	0.43
20:T:44:ALA:HB1	20:T:91:LEU:HB3	1.99	0.43
1:A:818:G:O2'	1:A:819:A:H5'	2.19	0.43
12:L:60:LEU:HB2	12:L:64:TYR:O	2.19	0.43
9:I:100:GLY:O	9:I:102:LEU:N	2.50	0.43
11:K:16:SER:HB2	11:K:106:LYS:HZ2	1.83	0.43
16:P:40:ASP:HA	16:P:41:PRO:HD3	1.78	0.43
1:A:353:A:C2'	1:A:354:G:OP2	2.66	0.43
1:A:1468:A:H8	1:A:1468:A:O5'	2.02	0.43
1:A:1355:G:H2'	1:A:1356:G:C8	2.53	0.43
12:L:107:ALA:O	12:L:108:ALA:C	2.57	0.43
4:D:78:LEU:HD11	4:D:96:LEU:HB3	2.01	0.43
16:P:23:ASP:OD1	16:P:24:ALA:N	2.52	0.43
4:D:175:SER:HB3	4:D:184:LYS:HB2	2.01	0.43
4:D:30:LYS:C	4:D:32:ALA:H	2.22	0.43
1:A:1250:A:C6	1:A:1251:A:N1	2.87	0.43
8:H:6:ILE:O	8:H:10:LEU:HG	2.18	0.43
1:A:75:G:C2	1:A:96:G:N1	2.87	0.43
1:A:277:C:C2'	1:A:278:G:H5'	2.49	0.43
1:A:1118:C:C2	1:A:1179:A:C2	3.07	0.43
1:A:503:C:H2'	1:A:504:C:H6	1.84	0.43
1:A:300:A:C8	1:A:300:A:O5'	2.62	0.43
20:T:51:GLU:O	20:T:55:ILE:HG13	2.19	0.43
8:H:118:VAL:C	8:H:119:LEU:HD23	2.38	0.43
13:M:45:VAL:O	13:M:48:LEU:HB2	2.18	0.43
2:B:240:GLN:HE21	2:B:240:GLN:CA	2.26	0.43
18:R:53:ARG:NH1	18:R:60:GLY:HA2	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:938:A:H5'	7:G:76:ARG:HH22	1.83	0.43
8:H:102:ARG:HD2	8:H:102:ARG:H	1.83	0.43
4:D:43:HIS:HB3	4:D:46:LYS:HE2	2.00	0.43
6:F:52:ILE:O	6:F:53:ALA:HB3	2.19	0.43
1:A:294:U:H2'	1:A:295:C:C6	2.54	0.43
2:B:6:THR:CB	2:B:221:LEU:HD21	2.49	0.43
1:A:203:U:OP1	1:A:203:U:H3'	2.19	0.43
7:G:61:VAL:O	7:G:65:ALA:CB	2.67	0.43
1:A:370:C:O2'	1:A:371:G:H5'	2.19	0.43
2:B:107:THR:O	2:B:110:GLN:N	2.51	0.43
6:F:35:ALA:HA	6:F:67:MET:HB3	2.01	0.43
3:C:6:HIS:O	3:C:9:GLY:N	2.52	0.43
1:A:595:G:C6	1:A:641:U:C6	3.07	0.43
7:G:136:LYS:HD2	7:G:140:ASP:OD2	2.19	0.43
1:A:166:G:C2	1:A:167:G:C5	3.06	0.43
1:A:887:G:H2'	1:A:888:G:O4'	2.19	0.43
2:B:236:TYR:C	2:B:238:LEU:H	2.21	0.43
1:A:8:A:N6	4:D:209:ARG:HB2	2.34	0.43
13:M:63:THR:HG23	13:M:64:TRP:CG	2.54	0.43
1:A:994:A:H62	1:A:1216:G:C5'	2.32	0.43
1:A:285:G:C2	1:A:286:G:C8	3.07	0.43
7:G:26:PHE:CD1	7:G:101:LEU:HD22	2.48	0.43
17:Q:48:GLU:O	17:Q:49:GLU:C	2.55	0.43
1:A:1478:C:H2'	1:A:1479:C:H6	1.84	0.43
1:A:981:U:H5'	14:N:21:TYR:CZ	2.53	0.43
10:J:45:ARG:HH12	10:J:65:LEU:HD23	1.84	0.43
2:B:213:LEU:HD23	2:B:213:LEU:C	2.39	0.43
16:P:50:LYS:HG2	16:P:51:VAL:N	2.34	0.43
3:C:40:ARG:HA	3:C:43:LEU:HB2	2.01	0.43
18:R:47:THR:HB	18:R:49:LYS:HG3	2.01	0.43
10:J:59:SER:O	10:J:60:ARG:CB	2.67	0.43
1:A:1250:A:H4'	9:I:68:GLY:CA	2.48	0.43
3:C:117:ALA:HB1	3:C:187:ALA:HB2	1.99	0.43
1:A:70:G:N7	1:A:73:C:C4	2.87	0.43
1:A:268:C:H2'	1:A:269:C:C6	2.53	0.43
1:A:1416:G:H1	1:A:1485:U:H1'	1.83	0.43
1:A:20:U:H2'	1:A:21:G:C5'	2.49	0.43
1:A:381:C:C4	1:A:382:A:C5	3.07	0.43
12:L:41:ARG:HB3	12:L:41:ARG:CZ	2.49	0.43
1:A:865:A:H2'	1:A:866:C:H6	1.84	0.43
5:E:105:VAL:HB	5:E:106:PRO:HD3	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:36:ILE:HG22	15:O:37:ASN:N	2.33	0.43
1:A:41:G:C2	1:A:42:G:C5	3.07	0.43
2:B:190:THR:HG22	2:B:191:ASP:N	2.33	0.43
1:A:790:A:H2'	1:A:791:G:C8	2.54	0.43
1:A:918:A:H2'	1:A:919:A:O4'	2.19	0.43
15:O:41:GLU:O	15:O:44:LYS:HB2	2.18	0.43
11:K:22:HIS:CD2	11:K:22:HIS:O	2.72	0.43
18:R:36:ASN:HD22	18:R:39:VAL:CG1	2.14	0.42
18:R:18:ARG:O	18:R:19:LYS:HB2	2.17	0.42
1:A:89:C:C2	1:A:90:U:O2	2.71	0.42
1:A:1092:A:C4	1:A:1183:A:C6	3.07	0.42
3:C:70:VAL:HG12	3:C:71:ALA:N	2.34	0.42
9:I:16:ARG:NH1	9:I:64:THR:HG21	2.29	0.42
1:A:695:A:OP2	11:K:53:SER:N	2.51	0.42
7:G:70:LYS:HA	7:G:71:PRO:HD3	1.75	0.42
1:A:1379:G:C6	1:A:1380:U:C4	3.07	0.42
12:L:12:ARG:HB3	12:L:12:ARG:NH1	2.34	0.42
1:A:175:C:C4	1:A:176:C:C5	3.06	0.42
16:P:43:LYS:HD3	16:P:43:LYS:N	2.33	0.42
4:D:39:PRO:HB2	4:D:44:GLY:HA2	2.00	0.42
13:M:5:ALA:CB	13:M:22:ILE:HD13	2.44	0.42
1:A:178:C:O2'	1:A:179:A:H5'	2.20	0.42
1:A:1416:G:H2'	1:A:1417:G:H5'	2.00	0.42
11:K:56:GLY:O	11:K:57:THR:C	2.56	0.42
10:J:18:ALA:HA	10:J:21:GLN:CG	2.50	0.42
1:A:737:A:H2'	1:A:738:C:O4'	2.19	0.42
16:P:9:PHE:CE1	16:P:18:ARG:HD2	2.54	0.42
1:A:222:U:C2	1:A:223:U:C5	3.07	0.42
11:K:98:LEU:HA	11:K:101:SER:HB3	2.01	0.42
5:E:122:GLU:O	5:E:123:LEU:HD23	2.19	0.42
3:C:157:ILE:HD13	3:C:157:ILE:HA	1.93	0.42
1:A:593:G:H1	1:A:646:U:H3	1.66	0.42
15:O:15:PHE:CZ	15:O:84:LYS:HD3	2.54	0.42
20:T:29:LYS:O	20:T:32:ALA:HB3	2.19	0.42
1:A:190(A):C:C2	1:A:190(I):G:N2	2.87	0.42
6:F:80:ARG:NH1	6:F:88:VAL:HB	2.34	0.42
14:N:50:LYS:O	14:N:52:GLN:HG3	2.19	0.42
1:A:1357:A:C4	1:A:1358:U:C5	3.07	0.42
13:M:71:ARG:O	13:M:74:VAL:HG12	2.20	0.42
1:A:448:A:C4	1:A:487:A:C2	3.08	0.42
1:A:393:A:O2'	1:A:394:G:H5'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:63:LEU:H	11:K:63:LEU:HG	1.60	0.42
1:A:881:G:H2'	1:A:882:C:O4'	2.20	0.42
1:A:1148:U:N3	1:A:1149:C:C2	2.87	0.42
1:A:1511:G:C2'	1:A:1512:U:H5'	2.50	0.42
1:A:313:A:C6	1:A:314:C:N4	2.88	0.42
3:C:90:GLU:HA	3:C:93:LYS:CB	2.50	0.42
20:T:13:LEU:O	20:T:14:LYS:C	2.58	0.42
17:Q:10:VAL:HG23	17:Q:55:ASP:O	2.20	0.42
1:A:1119:C:O2	1:A:1155:G:C2	2.73	0.42
4:D:55:ALA:O	4:D:59:ARG:HG2	2.19	0.42
11:K:83:ILE:HA	11:K:109:VAL:O	2.19	0.42
11:K:74:ALA:C	11:K:76:GLY:H	2.21	0.42
8:H:33:GLU:HG3	8:H:48:TYR:CE1	2.54	0.42
1:A:667:G:H4'	15:O:51:HIS:ND1	2.34	0.42
3:C:156:ARG:HD3	3:C:160:ALA:O	2.20	0.42
1:A:1046:A:N3	1:A:1046:A:H2'	2.34	0.42
1:A:974:A:P	14:N:41:ARG:HH12	2.40	0.42
4:D:188:LEU:HD12	4:D:188:LEU:N	2.19	0.42
2:B:129:GLU:O	2:B:130:ARG:HB2	2.19	0.42
1:A:1502:A:H2'	1:A:1504:G:N7	2.34	0.42
14:N:49:HIS:C	14:N:51:GLY:H	2.22	0.42
1:A:622:A:C8	1:A:623:C:C6	3.08	0.42
15:O:4:THR:H	15:O:7:GLU:CD	2.23	0.42
1:A:1290:G:C6	1:A:1291:G:C6	3.07	0.42
1:A:862:C:C2'	1:A:863:U:H5'	2.49	0.42
1:A:44:G:N3	1:A:399:G:C2	2.87	0.42
1:A:160:A:N6	1:A:161:A:C2	2.87	0.42
1:A:962:C:O2	1:A:1201:A:C2	2.73	0.42
1:A:1330:U:OP1	13:M:23:TYR:O	2.38	0.42
1:A:77:G:C6	1:A:92:C:N4	2.87	0.42
1:A:1157:A:C4	1:A:1181:G:C2	3.07	0.42
5:E:10:MET:O	5:E:10:MET:HG3	2.18	0.42
1:A:6:G:H1	5:E:98:THR:HG1	1.61	0.42
1:A:1261:A:C8	1:A:1262:C:H5	2.37	0.42
1:A:1026:G:N2	1:A:1027:C:C6	2.87	0.42
2:B:37:ASN:HB2	2:B:39:ILE:HD11	2.00	0.42
10:J:18:ALA:HA	10:J:21:GLN:HG3	2.00	0.42
7:G:145:ALA:O	7:G:146:GLU:HB3	2.19	0.42
1:A:780:A:O2'	1:A:781:A:H5"	2.19	0.42
4:D:110:PHE:HE2	4:D:146:ILE:HG22	1.84	0.42
1:A:858:G:O6	1:A:869:G:C8	2.73	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:34:GLU:OE2	16:P:55:ARG:HD2	2.19	0.42
4:D:4:TYR:O	4:D:5:ILE:HB	2.19	0.42
1:A:1250:A:C2	1:A:1287:A:C2	3.07	0.42
13:M:45:VAL:CG1	13:M:46:LYS:N	2.82	0.42
17:Q:59:ILE:HG22	17:Q:71:PHE:CD1	2.54	0.42
15:O:87:ILE:CG2	15:O:88:ARG:N	2.80	0.42
1:A:1519:A:H8	1:A:1519:A:OP2	2.02	0.42
7:G:137:LYS:O	7:G:140:ASP:N	2.52	0.42
12:L:45:PRO:HB3	12:L:53:ARG:NH1	2.35	0.42
4:D:108:LEU:HA	4:D:108:LEU:HD23	1.80	0.42
2:B:20:GLU:O	2:B:40:HIS:CD2	2.72	0.42
13:M:54:VAL:O	13:M:55:ARG:C	2.58	0.42
12:L:77:LEU:HA	12:L:77:LEU:HD23	1.78	0.42
19:S:32:LYS:HE3	19:S:32:LYS:HB2	1.93	0.42
1:A:1357:A:C6	1:A:1358:U:O4	2.72	0.42
13:M:23:TYR:CD1	13:M:71:ARG:NH2	2.87	0.42
1:A:1182:G:C1'	1:A:1183:A:OP2	2.68	0.42
1:A:251:G:H4'	1:A:252:U:O5'	2.18	0.42
1:A:882:C:H2'	1:A:883:C:H6	1.83	0.42
1:A:363:A:H5'	12:L:34:ARG:HB2	2.01	0.42
2:B:25:ASN:HA	2:B:26:PRO:HD2	1.69	0.42
1:A:1115:C:H2'	1:A:1116:C:C6	2.54	0.42
1:A:1072:G:C6	1:A:1073:U:C4	3.07	0.42
1:A:852:G:H2'	1:A:853:G:O5'	2.20	0.42
1:A:1228:C:C6	1:A:1228:C:H3'	2.54	0.42
16:P:49:LEU:HD12	16:P:50:LYS:N	2.33	0.42
1:A:1105:A:O2'	1:A:1106:G:H5'	2.19	0.42
10:J:79:ARG:HG2	10:J:79:ARG:H	1.71	0.42
1:A:953:G:H2'	1:A:954:G:O4'	2.20	0.42
7:G:50:ILE:HD13	7:G:50:ILE:HA	1.78	0.42
1:A:1372:U:H2'	1:A:1373:G:O4'	2.20	0.42
1:A:378:G:H2'	1:A:379:C:C6	2.54	0.42
12:L:86:ARG:NH2	12:L:99:HIS:CD2	2.84	0.42
1:A:689:C:H2'	1:A:690:G:O4'	2.20	0.42
6:F:19:LEU:CD2	6:F:23:LYS:HG3	2.50	0.42
7:G:21:VAL:C	7:G:23:VAL:N	2.72	0.42
1:A:938:A:C6	1:A:939:G:C5	3.08	0.42
2:B:213:LEU:HD22	2:B:214:ILE:HD13	2.01	0.42
12:L:75:HIS:HD2	12:L:77:LEU:HB2	1.84	0.42
9:I:118:LYS:O	9:I:119:ALA:HB3	2.20	0.42
1:A:520:A:OP1	12:L:52:LEU:HD12	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:760:G:H22	17:Q:105:ALA:HA	1.84	0.42
1:A:1036:G:H2'	1:A:1037:C:O4'	2.19	0.42
12:L:115:LYS:O	12:L:117:ARG:N	2.48	0.42
1:A:1470:G:O2'	1:A:1471:G:H5'	2.20	0.42
8:H:49:GLU:O	8:H:51:VAL:HG13	2.20	0.42
14:N:24:CYS:HB3	14:N:29:ARG:N	2.21	0.42
5:E:135:THR:O	5:E:138:ALA:HB3	2.19	0.42
1:A:1487:G:C5	1:A:1488:G:C8	3.08	0.42
1:A:1349:A:H2'	1:A:1350:A:O4'	2.19	0.42
7:G:105:VAL:O	7:G:105:VAL:HG12	2.20	0.42
8:H:19:VAL:HG22	8:H:21:LYS:HG3	2.02	0.42
2:B:189:ASP:HB3	2:B:191:ASP:OD1	2.20	0.42
1:A:1154:G:N3	1:A:1155:G:C8	2.88	0.42
5:E:40:ARG:NH1	5:E:40:ARG:HG2	2.35	0.42
1:A:350:G:O2'	1:A:351:G:H5'	2.19	0.42
17:Q:90:ILE:C	17:Q:92:ARG:N	2.72	0.42
1:A:995:C:H6	1:A:995:C:O5'	2.03	0.42
1:A:59:A:N3	1:A:59:A:H2'	2.34	0.42
1:A:202:U:H3'	1:A:202:U:OP2	2.20	0.42
10:J:71:LEU:O	10:J:72:VAL:HB	2.20	0.42
2:B:97:TRP:CZ3	2:B:172:ILE:HG22	2.55	0.42
3:C:10:PHE:CD2	3:C:10:PHE:C	2.92	0.42
1:A:194:C:P	20:T:61:SER:HG	2.43	0.42
12:L:69:TYR:C	12:L:69:TYR:CD2	2.93	0.42
1:A:1346:A:N1	1:A:1374:A:H5''	2.35	0.42
7:G:92:SER:O	7:G:96:GLN:HG3	2.20	0.42
6:F:60:PHE:CZ	18:R:78:LEU:HD21	2.55	0.42
4:D:155:LEU:HD23	4:D:155:LEU:HA	1.82	0.42
17:Q:12:SER:HB3	17:Q:20:THR:CB	2.49	0.42
19:S:28:LYS:C	19:S:29:ARG:HD2	2.39	0.42
1:A:417:C:C5	1:A:418:C:C5	3.08	0.42
4:D:125:HIS:O	4:D:126:ILE:HD13	2.20	0.42
1:A:669:U:H2'	1:A:670:G:C8	2.54	0.42
20:T:24:LEU:HD12	20:T:24:LEU:HA	1.92	0.42
5:E:102:ALA:CA	5:E:120:THR:OG1	2.61	0.41
1:A:1118:C:C1'	1:A:1179:A:C4	3.02	0.41
4:D:196:LEU:C	4:D:198:VAL:H	2.23	0.41
1:A:1112:C:H1'	3:C:179:ARG:HH11	1.84	0.41
5:E:18:ARG:CG	5:E:18:ARG:HH11	2.27	0.41
12:L:39:VAL:CG1	12:L:40:VAL:N	2.82	0.41
7:G:29:LYS:O	7:G:105:VAL:HG11	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:87:ILE:O	15:O:88:ARG:HB2	2.20	0.41
11:K:40:ILE:HG22	11:K:41:THR:N	2.34	0.41
4:D:31:CYS:O	4:D:31:CYS:SG	2.78	0.41
2:B:77:ALA:HB2	2:B:165:VAL:HG11	2.01	0.41
12:L:45:PRO:HG2	12:L:49:ASN:O	2.19	0.41
19:S:15:LEU:O	19:S:19:VAL:HG12	2.20	0.41
10:J:50:ILE:O	14:N:41:ARG:HD2	2.20	0.41
1:A:1414:U:H2'	1:A:1414:U:O2	2.19	0.41
1:A:129(A):G:H1'	1:A:190(E):U:H2'	2.02	0.41
1:A:991:U:H5	1:A:1212:U:N3	2.16	0.41
1:A:893:C:H5''	1:A:1416:G:H5'	2.02	0.41
1:A:1422:G:C2	1:A:1423:G:C8	3.07	0.41
1:A:1392:G:C5	1:A:1393:U:C5	3.08	0.41
4:D:100:ARG:NH1	4:D:137:SER:HA	2.35	0.41
1:A:1540:U:C5	1:A:1541:U:C2	3.07	0.41
1:A:602:A:N3	1:A:637:G:C2	2.87	0.41
2:B:219:VAL:O	2:B:220:ASP:C	2.59	0.41
1:A:386:C:H2'	1:A:387:U:H5'	2.01	0.41
1:A:509:A:H3'	1:A:509:A:OP2	2.19	0.41
4:D:141:ARG:O	4:D:144:ASP:HB2	2.20	0.41
5:E:43:LEU:HD12	5:E:133:TYR:CE2	2.55	0.41
1:A:837:G:C2	1:A:850:U:O2	2.73	0.41
15:O:32:LEU:HD23	15:O:32:LEU:N	2.34	0.41
19:S:9:VAL:HG12	19:S:10:PHE:N	2.35	0.41
1:A:98:U:C6	1:A:98:U:H3'	2.55	0.41
1:A:88:A:C4	1:A:89:C:C6	3.08	0.41
1:A:1484:C:H2'	1:A:1485:U:O4'	2.19	0.41
4:D:8:VAL:C	4:D:10:ARG:H	2.23	0.41
20:T:54:LYS:HE2	20:T:54:LYS:HB3	1.94	0.41
1:A:1410:G:N2	1:A:1411:C:C2	2.88	0.41
3:C:116:VAL:HG21	3:C:202:ILE:HD11	2.02	0.41
1:A:1167:A:H8	1:A:1167:A:OP1	2.02	0.41
1:A:114:U:H2'	1:A:115:G:C8	2.55	0.41
9:I:100:GLY:C	9:I:102:LEU:N	2.74	0.41
16:P:39:TYR:HE2	16:P:41:PRO:HG3	1.84	0.41
1:A:914:A:C2	1:A:915:A:C8	3.08	0.41
4:D:101:LEU:O	4:D:105:VAL:HG23	2.20	0.41
6:F:16:GLN:NE2	6:F:20:ALA:HB2	2.35	0.41
12:L:10:LEU:HB3	17:Q:32:TYR:CE1	2.54	0.41
1:A:442:C:C4	1:A:443:C:H5	2.39	0.41
1:A:27:G:C6	1:A:557:G:C2	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:57:LYS:NZ	12:L:67:THR:HB	2.36	0.41
1:A:1043:C:H2'	1:A:1044:A:C8	2.55	0.41
8:H:82:HIS:CD2	8:H:138:TRP:HE1	2.39	0.41
18:R:19:LYS:HE2	18:R:19:LYS:HB3	1.92	0.41
13:M:4:ILE:O	13:M:5:ALA:O	2.38	0.41
1:A:95:U:H2'	1:A:96:G:H8	1.83	0.41
2:B:230:VAL:CG1	2:B:231:GLU:H	2.33	0.41
3:C:178:LEU:O	3:C:180:ALA:N	2.54	0.41
3:C:59:ARG:HG2	3:C:63:ASN:O	2.19	0.41
11:K:56:GLY:O	11:K:57:THR:O	2.38	0.41
3:C:23:TYR:CZ	3:C:24:ALA:O	2.74	0.41
1:A:541:G:H2'	1:A:542:G:O4'	2.20	0.41
1:A:573:A:C6	1:A:574:A:N1	2.88	0.41
1:A:1410:G:N2	1:A:1411:C:O2	2.54	0.41
7:G:71:PRO:O	7:G:96:GLN:HG2	2.20	0.41
18:R:41:LYS:HG3	18:R:42:ARG:N	2.35	0.41
3:C:137:ALA:HA	3:C:140:ARG:CZ	2.50	0.41
2:B:223:ILE:C	2:B:225:ALA:N	2.73	0.41
16:P:17:TYR:HE1	16:P:41:PRO:HG3	1.85	0.41
1:A:197:A:H1'	1:A:198:G:C1'	2.51	0.41
6:F:9:VAL:HG23	6:F:87:ARG:HB2	2.01	0.41
21:U:24:ARG:HG2	21:U:24:ARG:H	1.60	0.41
1:A:1250:A:C2	1:A:1251:A:C2	3.09	0.41
18:R:18:ARG:HA	18:R:18:ARG:HD3	1.88	0.41
12:L:46:LYS:O	12:L:47:LYS:C	2.59	0.41
3:C:91:LEU:C	3:C:91:LEU:HD23	2.40	0.41
1:A:691:G:H2'	1:A:692:U:H6	1.86	0.41
7:G:74:GLU:HG2	7:G:91:VAL:HG22	2.02	0.41
3:C:9:GLY:HA2	3:C:12:LEU:HG	2.01	0.41
16:P:4:ILE:HG13	16:P:64:ALA:HB1	2.03	0.41
15:O:7:GLU:O	15:O:10:LYS:HE2	2.20	0.41
2:B:19:HIS:CE1	2:B:189:ASP:OD1	2.73	0.41
7:G:120:ILE:O	7:G:121:ALA:C	2.56	0.41
1:A:46:G:O2'	1:A:365:U:H1'	2.19	0.41
20:T:33:ILE:HG12	20:T:62:LEU:HD22	2.01	0.41
1:A:224:C:H2'	1:A:225:C:H6	1.84	0.41
18:R:51:LEU:HD23	18:R:51:LEU:HA	1.80	0.41
8:H:25:ASP:OD1	8:H:25:ASP:N	2.53	0.41
1:A:1271:G:H5'	1:A:1314:C:H5''	2.03	0.41
8:H:10:LEU:HA	8:H:10:LEU:HD23	1.75	0.41
2:B:73:THR:HB	2:B:170:GLU:OE1	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:43:PHE:HD2	7:G:44:TYR:CD2	2.39	0.41
2:B:230:VAL:CG1	2:B:231:GLU:N	2.83	0.41
1:A:1421:G:N2	1:A:1480:G:C4	2.89	0.41
1:A:393:A:C4	1:A:394:G:C8	3.08	0.41
1:A:575:G:C6	1:A:821:G:N7	2.89	0.41
9:I:11:LYS:O	9:I:12:GLU:CB	2.64	0.41
1:A:428:G:C1'	1:A:429:U:OP2	2.68	0.41
6:F:4:TYR:CZ	6:F:72:VAL:HG21	2.55	0.41
1:A:423:G:N2	1:A:424:G:C8	2.89	0.41
1:A:375:U:O2'	1:A:376:G:H5'	2.20	0.41
2:B:212:GLN:O	2:B:213:LEU:C	2.58	0.41
6:F:76:ALA:O	6:F:80:ARG:HG3	2.21	0.41
5:E:107:ARG:O	5:E:108:ALA:C	2.57	0.41
1:A:962:C:O2	1:A:1201:A:H2	2.03	0.41
1:A:1315:U:C2	1:A:1323:G:N2	2.89	0.41
1:A:1368:G:OP1	10:J:62:HIS:HE1	2.04	0.41
1:A:70:G:C6	1:A:73:C:N3	2.89	0.41
1:A:76:C:N3	1:A:93:G:N2	2.65	0.41
10:J:44:VAL:HG11	10:J:66:ARG:NE	2.27	0.41
1:A:1370:G:C2	1:A:1371:G:C8	3.09	0.41
7:G:22:LEU:HD21	7:G:66:VAL:HG11	2.02	0.41
5:E:144:THR:HG22	5:E:145:LYS:N	2.35	0.41
1:A:574:A:H1'	1:A:883:C:O4'	2.21	0.41
1:A:933:G:OP2	7:G:3:ARG:O	2.39	0.41
1:A:695:A:C6	1:A:696:A:C6	3.08	0.41
1:A:786:G:C2	1:A:787:A:H1'	2.56	0.41
6:F:61:LEU:HB3	6:F:63:TYR:HE2	1.85	0.41
15:O:7:GLU:O	15:O:10:LYS:HG2	2.20	0.41
8:H:112:LEU:CD2	8:H:112:LEU:N	2.84	0.41
5:E:12:LEU:C	5:E:12:LEU:HD22	2.40	0.41
1:A:1267:C:C5	1:A:1268:A:C5	3.09	0.41
2:B:174:VAL:O	2:B:177:ALA:HB3	2.20	0.41
20:T:59:ALA:O	20:T:60:GLU:C	2.59	0.41
15:O:68:ARG:HB2	15:O:68:ARG:HH11	1.86	0.41
4:D:42:GLN:HG2	4:D:42:GLN:O	2.19	0.41
13:M:22:ILE:HG22	13:M:23:TYR:N	2.35	0.41
5:E:50:GLU:HG3	5:E:52:PRO:HD2	2.03	0.41
9:I:48:GLU:N	9:I:49:PRO:CD	2.84	0.41
1:A:902:G:H2'	1:A:903:G:H8	1.86	0.41
1:A:327:A:O2'	1:A:328:C:H6	2.03	0.41
4:D:119:GLN:HG2	4:D:123:HIS:CD2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:437:U:O2'	4:D:123:HIS:HD2	2.03	0.41
1:A:910:C:H5''	12:L:97:ARG:NH2	2.35	0.41
1:A:1374:A:C5	1:A:1375:A:N7	2.89	0.41
2:B:115:LEU:C	2:B:115:LEU:HD23	2.40	0.41
18:R:37:VAL:HG22	18:R:78:LEU:HB3	2.02	0.41
1:A:376:G:C2	1:A:389:A:C2	3.09	0.41
12:L:54:LYS:CD	12:L:54:LYS:N	2.84	0.41
1:A:1430:C:H2'	1:A:1431:C:C6	2.50	0.41
9:I:102:LEU:HD12	9:I:102:LEU:H	1.86	0.41
10:J:63:PHE:CD1	10:J:63:PHE:N	2.89	0.41
1:A:604:G:C6	1:A:635:G:C6	3.08	0.41
1:A:1206:G:C6	1:A:1207:G:C6	3.09	0.41
3:C:34:LEU:O	3:C:38:ARG:HG2	2.21	0.41
13:M:29:ARG:NH2	13:M:64:TRP:CD1	2.89	0.41
1:A:190(D):U:O2'	1:A:190(E):U:H5'	2.21	0.41
7:G:57:GLU:HB2	7:G:58:PRO:HD2	2.02	0.41
1:A:1133:G:H1	1:A:1141:C:H42	1.67	0.41
1:A:474:G:C4	1:A:475:G:C8	3.09	0.41
1:A:475:G:C2	1:A:476:G:N7	2.88	0.41
1:A:792:A:H2'	1:A:792:A:OP2	2.20	0.41
2:B:180:LEU:O	2:B:181:PHE:CB	2.68	0.41
10:J:40:LEU:HB3	10:J:69:ASN:O	2.21	0.41
1:A:413:G:N2	1:A:429:U:OP2	2.48	0.41
1:A:429:U:H5'	4:D:9:CYS:HB3	2.03	0.41
16:P:3:LYS:HG2	16:P:65:GLN:HB2	2.03	0.41
5:E:71:LEU:HD21	5:E:115:VAL:HG22	2.03	0.41
1:A:1071:C:O2'	1:A:1072:G:H5'	2.21	0.41
1:A:922:G:C2	1:A:1396:A:C6	3.09	0.41
1:A:922:G:C6	1:A:923:A:C6	3.08	0.41
1:A:403:C:O2'	1:A:404:U:H5'	2.20	0.41
1:A:385:C:H2'	1:A:386:C:H6	1.85	0.41
1:A:828:A:C2'	1:A:829:G:O5'	2.69	0.41
5:E:142:LEU:C	5:E:143:ARG:HG2	2.40	0.41
20:T:34:LYS:HE2	20:T:80:ARG:HH12	1.86	0.41
17:Q:85:VAL:HG12	17:Q:89:LEU:HG	2.03	0.41
1:A:1030(C):G:C6	1:A:1030(D):A:N6	2.89	0.41
3:C:159:GLY:HA2	3:C:193:TYR:CD1	2.56	0.41
9:I:18:PHE:HD1	9:I:62:TYR:CD2	2.39	0.41
17:Q:51:TYR:CG	17:Q:73:VAL:HG11	2.56	0.41
4:D:47:ARG:HA	4:D:47:ARG:HD2	1.71	0.41
8:H:83:ILE:HB	8:H:137:VAL:HG13	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:492:G:H2'	1:A:494:G:H8	1.86	0.41
3:C:10:PHE:HD2	3:C:11:ARG:HG3	1.86	0.41
3:C:5:ILE:HG13	3:C:5:ILE:H	1.70	0.41
15:O:9:GLN:O	15:O:11:VAL:N	2.53	0.41
1:A:463:A:C5	1:A:474:G:C8	3.09	0.41
1:A:1277:C:O2'	1:A:1279:A:H1'	2.21	0.41
1:A:1430:C:C2	1:A:1431:C:C5	3.09	0.41
7:G:48:LYS:HG3	7:G:49:ILE:N	2.36	0.41
1:A:417:C:C5	1:A:418:C:H5	2.39	0.41
1:A:1003(A):G:N2	1:A:1039:C:C4	2.89	0.41
1:A:567:G:C2	1:A:568:G:H1'	2.56	0.41
1:A:450:G:C8	1:A:481:G:C6	3.09	0.41
1:A:961:U:C2	1:A:983:A:C6	3.09	0.40
1:A:1419:G:H1	1:A:1481:U:H3	1.69	0.40
10:J:16:LEU:CD2	10:J:94:VAL:HG13	2.51	0.40
1:A:1487:G:C2'	1:A:1488:G:C5'	2.96	0.40
1:A:1261:A:N6	1:A:1275:A:C8	2.89	0.40
2:B:22:LYS:C	2:B:24:TRP:N	2.73	0.40
1:A:291:C:C2'	1:A:292:G:H5'	2.51	0.40
21:U:9:ARG:C	21:U:11:GLY:H	2.23	0.40
2:B:221:LEU:HD13	2:B:224:GLN:OE1	2.21	0.40
1:A:1106:G:O2'	1:A:1107:C:H5'	2.21	0.40
8:H:2:LEU:O	8:H:3:THR:C	2.59	0.40
1:A:1361(A):C:H1'	1:A:1362:C:H5''	2.03	0.40
19:S:5:LEU:O	19:S:6:LYS:CB	2.52	0.40
1:A:1284:C:C2	1:A:1285:A:N7	2.89	0.40
1:A:1182:G:H1'	1:A:1183:A:OP2	2.22	0.40
20:T:89:ARG:NH2	20:T:104:LEU:HB3	2.37	0.40
9:I:14:VAL:O	9:I:65:VAL:HG13	2.21	0.40
8:H:19:VAL:CG2	8:H:19:VAL:O	2.66	0.40
1:A:1029:C:N3	1:A:1033:G:N2	2.69	0.40
16:P:25:ARG:O	16:P:26:ARG:C	2.59	0.40
16:P:4:ILE:CD1	16:P:64:ALA:HB1	2.52	0.40
12:L:107:ALA:O	12:L:108:ALA:O	2.38	0.40
1:A:237:C:H2'	1:A:238:G:C8	2.57	0.40
1:A:701:C:C4'	1:A:702:A:OP2	2.69	0.40
1:A:1005:A:H5''	1:A:1006:C:OP2	2.21	0.40
3:C:36:ASP:HA	3:C:39:ILE:HD12	2.03	0.40
2:B:208:ILE:N	2:B:208:ILE:HD13	2.36	0.40
1:A:1204:A:C6	1:A:1205:U:C2	3.09	0.40
18:R:36:ASN:ND2	18:R:39:VAL:CG1	2.79	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:448:A:C2	1:A:449:C:C2	3.10	0.40
1:A:1118:C:O2	1:A:1179:A:C6	2.74	0.40
1:A:1179:A:H2'	1:A:1180:A:O4'	2.21	0.40
2:B:172:ILE:HD12	2:B:172:ILE:N	2.32	0.40
1:A:146:G:C2	1:A:177:C:N3	2.89	0.40
10:J:16:LEU:HD23	10:J:16:LEU:HA	1.93	0.40
6:F:48:LEU:HG	6:F:57:GLN:CA	2.51	0.40
1:A:1034:G:N1	1:A:1035:A:C6	2.89	0.40
1:A:1174:G:N2	1:A:1175:G:C4	2.89	0.40
16:P:60:LEU:HD23	16:P:60:LEU:HA	1.80	0.40
3:C:121:ALA:CB	3:C:189:ALA:HB2	2.52	0.40
8:H:96:GLY:N	8:H:99:GLU:HG3	2.36	0.40
1:A:1243:C:OP2	21:U:10:ARG:NH2	2.54	0.40
1:A:1119:C:O2	1:A:1155:G:N2	2.54	0.40
4:D:152:SER:HB2	4:D:155:LEU:CD1	2.51	0.40
13:M:55:ARG:HA	13:M:58:GLU:HG2	2.04	0.40
6:F:14:LEU:HB3	6:F:18:GLN:HB2	2.03	0.40
3:C:145:GLY:O	3:C:146:ALA:HB3	2.21	0.40
18:R:52:PRO:O	18:R:56:THR:HG23	2.22	0.40
11:K:111:ASP:OD2	11:K:111:ASP:O	2.38	0.40
1:A:1052:U:N3	1:A:1200:C:C4	2.90	0.40
13:M:19:LEU:HD11	13:M:56:LEU:HD21	2.04	0.40
1:A:131:C:O2	1:A:231:G:N2	2.50	0.40
1:A:1371:G:C4	1:A:1372:U:C5	3.09	0.40
1:A:149:A:N3	1:A:150:C:C6	2.89	0.40
1:A:819:A:H4'	1:A:820:U:OP2	2.21	0.40
1:A:574:A:H1'	1:A:883:C:C1'	2.51	0.40
1:A:357:G:H1'	1:A:368:U:O2	2.22	0.40
1:A:1512:U:H3	1:A:1523:G:H1	1.69	0.40
1:A:1521:G:H2'	1:A:1522:U:H6	1.85	0.40
1:A:255:G:C6	1:A:256:U:O4	2.74	0.40
1:A:1014:A:N7	1:A:1015:A:C6	2.89	0.40
2:B:167:PRO:HG2	2:B:192:SER:HB3	2.04	0.40
1:A:581:G:O2'	1:A:582:U:H5'	2.22	0.40
20:T:22:ARG:O	20:T:23:ARG:C	2.60	0.40
4:D:108:LEU:HD23	4:D:170:VAL:HG21	2.04	0.40
2:B:117:GLU:O	2:B:120:ALA:HB3	2.21	0.40
16:P:19:ILE:HG22	16:P:36:ILE:HG13	2.03	0.40
1:A:1088:G:O5'	1:A:1088:G:H8	2.05	0.40
12:L:93:LEU:N	12:L:93:LEU:HD23	2.37	0.40
1:A:1201:A:C1'	1:A:1202:G:OP2	2.65	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:631:G:H2'	1:A:631:G:N3	2.37	0.40
1:A:92:C:H5	1:A:93:G:N7	2.16	0.40
1:A:448:A:N1	1:A:449:C:C4	2.90	0.40
1:A:1124:G:N3	1:A:1127:G:N2	2.69	0.40
3:C:29:TYR:O	3:C:33:LEU:HB2	2.22	0.40
1:A:299:G:C5	1:A:300:A:C6	3.09	0.40
12:L:113:ARG:HH12	12:L:116:SER:H	1.69	0.40
1:A:1260:C:H2'	1:A:1261:A:OP2	2.21	0.40
1:A:601:C:O2'	1:A:602:A:H5'	2.21	0.40
2:B:166:ASP:OD1	2:B:167:PRO:HD2	2.21	0.40
1:A:1244:C:H42	1:A:1293:G:H1	1.69	0.40
21:U:6:ARG:HD2	21:U:15:ARG:HH12	1.87	0.40
1:A:925:G:C2	1:A:927:G:C8	3.10	0.40
4:D:15:GLU:CD	4:D:59:ARG:HH21	2.24	0.40
5:E:15:ARG:NH1	5:E:26:PHE:CZ	2.89	0.40
1:A:1058:G:N2	10:J:53:PRO:HG2	2.36	0.40
1:A:1061:G:H1'	10:J:56:HIS:CE1	2.56	0.40
7:G:77:SER:O	7:G:78:ARG:HB2	2.21	0.40
1:A:808:C:O2'	1:A:809:G:H5'	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	233/256 (91%)	168 (72%)	45 (19%)	20 (9%)	1	16
3	C	204/239 (85%)	152 (74%)	37 (18%)	15 (7%)	1	21
4	D	206/209 (99%)	168 (82%)	32 (16%)	6 (3%)	6	46
5	E	148/162 (91%)	119 (80%)	26 (18%)	3 (2%)	9	55
6	F	99/101 (98%)	80 (81%)	17 (17%)	2 (2%)	9	55

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	G	153/156 (98%)	105 (69%)	34 (22%)	14 (9%)	1	15
8	H	136/138 (99%)	115 (85%)	15 (11%)	6 (4%)	3	35
9	I	125/128 (98%)	86 (69%)	28 (22%)	11 (9%)	1	15
10	J	96/105 (91%)	60 (62%)	22 (23%)	14 (15%)	0	5
11	K	117/129 (91%)	85 (73%)	22 (19%)	10 (8%)	1	16
12	L	122/135 (90%)	87 (71%)	22 (18%)	13 (11%)	0	10
13	M	113/126 (90%)	91 (80%)	16 (14%)	6 (5%)	2	29
14	N	58/61 (95%)	40 (69%)	13 (22%)	5 (9%)	1	16
15	O	86/89 (97%)	70 (81%)	13 (15%)	3 (4%)	4	43
16	P	81/88 (92%)	63 (78%)	11 (14%)	7 (9%)	1	16
17	Q	102/105 (97%)	86 (84%)	14 (14%)	2 (2%)	9	55
18	R	71/88 (81%)	53 (75%)	14 (20%)	4 (6%)	2	28
19	S	78/93 (84%)	47 (60%)	19 (24%)	12 (15%)	0	5
20	T	97/106 (92%)	60 (62%)	28 (29%)	9 (9%)	1	15
21	U	22/27 (82%)	17 (77%)	5 (23%)	0	100	100
All	All	2347/2541 (92%)	1752 (75%)	433 (18%)	162 (7%)	1	23

All (162) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	7	VAL
2	B	8	LYS
3	C	15	THR
3	C	29	TYR
3	C	127	ARG
7	G	4	ARG
8	H	91	ARG
9	I	12	GLU
9	I	31	GLN
9	I	82	ALA
9	I	127	LYS
10	J	30	SER
10	J	55	LYS
10	J	60	ARG
11	K	127	LYS
11	K	128	ALA
12	L	27	LEU

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Mol	Chain	Res	Type
12	L	41	ARG
12	L	47	LYS
12	L	56	ALA
12	L	108	ALA
12	L	126	LYS
13	M	49	THR
14	N	15	LYS
16	P	31	LYS
17	Q	68	ARG
19	S	6	LYS
19	S	9	VAL
20	T	49	ALA
20	T	97	ALA
20	T	99	LEU
2	B	9	GLU
2	B	74	LYS
2	B	78	GLN
2	B	89	GLY
2	B	161	ALA
2	B	229	VAL
3	C	5	ILE
3	C	179	ARG
4	D	5	ILE
4	D	88	VAL
5	E	21	ALA
6	F	44	GLY
7	G	17	VAL
7	G	59	LEU
7	G	155	ARG
8	H	74	PRO
8	H	75	ARG
9	I	54	ASP
9	I	101	PHE
10	J	34	VAL
10	J	61	GLU
10	J	72	VAL
11	K	54	ARG
11	K	117	ASN
11	K	126	ARG
12	L	14	GLY
12	L	28	LYS
12	L	29	GLY

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Mol	Chain	Res	Type
12	L	127	GLU
13	M	5	ALA
13	M	6	GLY
14	N	17	LYS
14	N	60	SER
16	P	10	GLY
16	P	25	ARG
16	P	27	LYS
16	P	82	GLN
18	R	19	LYS
19	S	8	GLY
19	S	25	LYS
19	S	27	GLU
20	T	95	ALA
2	B	77	ALA
2	B	129	GLU
3	C	51	GLY
3	C	74	GLY
3	C	94	LEU
3	C	206	GLU
5	E	27	ARG
5	E	153	LYS
6	F	39	LYS
7	G	78	ARG
7	G	113	GLU
7	G	128	ALA
9	I	38	GLN
10	J	27	ALA
10	J	40	LEU
10	J	73	ASP
10	J	86	MET
11	K	44	SER
11	K	50	TYR
11	K	118	GLY
12	L	80	HIS
13	M	7	VAL
13	M	23	TYR
13	M	67	GLU
15	O	49	ASP
16	P	26	ARG
17	Q	101	ARG
18	R	17	SER

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Mol	Chain	Res	Type
18	R	54	ARG
19	S	4	SER
19	S	30	LEU
19	S	47	HIS
19	S	65	ASN
20	T	14	LYS
20	T	70	SER
20	T	93	GLU
20	T	102	GLY
2	B	131	PRO
2	B	155	LEU
2	B	198	ASP
3	C	39	ILE
3	C	108	ASN
3	C	154	SER
3	C	178	LEU
4	D	35	ARG
7	G	130	GLY
8	H	3	THR
9	I	51	ARG
11	K	57	THR
14	N	18	VAL
14	N	25	VAL
15	O	84	LYS
20	T	74	LYS
2	B	221	LEU
2	B	224	GLN
2	B	232	PRO
3	C	81	GLY
7	G	40	ALA
8	H	105	ARG
9	I	24	GLY
9	I	56	LEU
12	L	55	VAL
15	O	5	LYS
16	P	12	LYS
18	R	87	ARG
19	S	42	PRO
2	B	19	HIS
7	G	25	ALA
7	G	51	GLN
7	G	61	VAL

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Mol	Chain	Res	Type
8	H	73	ASP
9	I	81	ILE
10	J	39	PRO
2	B	26	PRO
7	G	55	GLY
11	K	47	VAL
2	B	130	ARG
2	B	194	PRO
3	C	66	VAL
4	D	39	PRO
10	J	76	ASN
4	D	197	PRO
12	L	88	GLY
19	S	51	VAL
10	J	36	GLY
10	J	82	ILE
4	D	17	VAL
7	G	57	GLU
19	S	54	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	194/220 (88%)	173 (89%)	21 (11%)	8	41
3	C	160/188 (85%)	148 (92%)	12 (8%)	17	57
4	D	180/181 (99%)	166 (92%)	14 (8%)	16	56
5	E	115/123 (94%)	98 (85%)	17 (15%)	4	26
6	F	90/90 (100%)	81 (90%)	9 (10%)	9	44
7	G	126/127 (99%)	116 (92%)	10 (8%)	15	55
8	H	119/119 (100%)	104 (87%)	15 (13%)	5	32
9	I	98/99 (99%)	87 (89%)	11 (11%)	7	39
10	J	87/92 (95%)	80 (92%)	7 (8%)	15	55

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	K	90/99 (91%)	80 (89%)	10 (11%)	8	39
12	L	104/111 (94%)	90 (86%)	14 (14%)	5	31
13	M	93/101 (92%)	81 (87%)	12 (13%)	5	32
14	N	49/50 (98%)	47 (96%)	2 (4%)	37	75
15	O	79/80 (99%)	69 (87%)	10 (13%)	5	32
16	P	72/74 (97%)	63 (88%)	9 (12%)	6	33
17	Q	96/97 (99%)	92 (96%)	4 (4%)	36	75
18	R	64/77 (83%)	57 (89%)	7 (11%)	8	40
19	S	71/80 (89%)	64 (90%)	7 (10%)	10	45
20	T	76/82 (93%)	67 (88%)	9 (12%)	6	36
21	U	19/22 (86%)	17 (90%)	2 (10%)	8	42
All	All	1982/2112 (94%)	1780 (90%)	202 (10%)	9	43

All (202) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	25	ASN
2	B	39	ILE
2	B	44	LEU
2	B	60	ASP
2	B	61	LEU
2	B	67	THR
2	B	82	ARG
2	B	111	ARG
2	B	142	LEU
2	B	157	ARG
2	B	158	LEU
2	B	163	PHE
2	B	168	THR
2	B	187	LEU
2	B	190	THR
2	B	204	ASN
2	B	208	ILE
2	B	217	ARG
2	B	223	ILE
2	B	236	TYR
2	B	240	GLN
3	C	3	ASN

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Mol	Chain	Res	Type
3	C	14	ILE
3	C	26	LYS
3	C	33	LEU
3	C	104	GLN
3	C	126	ARG
3	C	127	ARG
3	C	128	PHE
3	C	132	ARG
3	C	162	GLN
3	C	167	TRP
3	C	179	ARG
4	D	9	CYS
4	D	15	GLU
4	D	17	VAL
4	D	26	CYS
4	D	64	LEU
4	D	73	ARG
4	D	78	LEU
4	D	112	VAL
4	D	122	ARG
4	D	127	THR
4	D	141	ARG
4	D	187	ARG
4	D	188	LEU
4	D	199	ASN
5	E	6	PHE
5	E	10	MET
5	E	12	LEU
5	E	18	ARG
5	E	20	GLN
5	E	31	LEU
5	E	32	VAL
5	E	41	VAL
5	E	45	PHE
5	E	67	VAL
5	E	76	ILE
5	E	79	GLU
5	E	80	ILE
5	E	89	ILE
5	E	98	THR
5	E	131	ILE
5	E	147	ASP

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Mol	Chain	Res	Type
6	F	9	VAL
6	F	10	LEU
6	F	15	ASP
6	F	18	GLN
6	F	23	LYS
6	F	45	LEU
6	F	74	ASP
6	F	77	ARG
6	F	100	ASN
7	G	8	GLU
7	G	12	LEU
7	G	16	LEU
7	G	24	THR
7	G	37	ASN
7	G	41	ARG
7	G	62	PHE
7	G	66	VAL
7	G	114	ARG
7	G	153	HIS
8	H	3	THR
8	H	18	ARG
8	H	19	VAL
8	H	26	VAL
8	H	39	LEU
8	H	59	LEU
8	H	63	LEU
8	H	84	ARG
8	H	85	ARG
8	H	88	LYS
8	H	91	ARG
8	H	102	ARG
8	H	112	LEU
8	H	113	SER
8	H	133	LEU
9	I	5	TYR
9	I	48	GLU
9	I	59	PHE
9	I	62	TYR
9	I	79	LEU
9	I	91	ASP
9	I	102	LEU
9	I	104	ARG

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Mol	Chain	Res	Type
9	I	109	VAL
9	I	114	TYR
9	I	121	ARG
10	J	6	ILE
10	J	9	ARG
10	J	21	GLN
10	J	54	PHE
10	J	57	LYS
10	J	75	ILE
10	J	99	LYS
11	K	11	LYS
11	K	18	ARG
11	K	25	TYR
11	K	29	ILE
11	K	75	TYR
11	K	98	LEU
11	K	105	VAL
11	K	116	HIS
11	K	120	ARG
11	K	126	ARG
12	L	19	ARG
12	L	20	LYS
12	L	36	VAL
12	L	44	THR
12	L	49	ASN
12	L	64	TYR
12	L	66	VAL
12	L	67	THR
12	L	82	VAL
12	L	85	ILE
12	L	93	LEU
12	L	98	TYR
12	L	111	LYS
12	L	127	GLU
13	M	11	ARG
13	M	14	ARG
13	M	44	ARG
13	M	48	LEU
13	M	59	TYR
13	M	74	VAL
13	M	91	ARG
13	M	94	ARG

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Mol	Chain	Res	Type
13	M	99	ARG
13	M	101	GLN
13	M	102	ARG
13	M	103	THR
14	N	6	LEU
14	N	26	ARG
15	O	5	LYS
15	O	11	VAL
15	O	17	ARG
15	O	31	LEU
15	O	36	ILE
15	O	40	SER
15	O	70	LEU
15	O	71	GLN
15	O	79	ARG
15	O	81	LEU
16	P	22	THR
16	P	25	ARG
16	P	32	TYR
16	P	44	THR
16	P	53	VAL
16	P	55	ARG
16	P	57	ARG
16	P	62	VAL
16	P	81	ARG
17	Q	35	VAL
17	Q	36	ILE
17	Q	38	ARG
17	Q	53	LEU
18	R	29	PHE
18	R	31	LEU
18	R	38	GLU
18	R	42	ARG
18	R	47	THR
18	R	54	ARG
18	R	56	THR
19	S	12	ASP
19	S	15	LEU
19	S	18	LYS
19	S	25	LYS
19	S	32	LYS
19	S	37	ARG

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Mol	Chain	Res	Type
19	S	43	GLU
20	T	13	LEU
20	T	51	GLU
20	T	54	LYS
20	T	57	ARG
20	T	73	HIS
20	T	74	LYS
20	T	75	ASN
20	T	83	ARG
20	T	84	LEU
21	U	9	ARG
21	U	22	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (50) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	25	ASN
2	B	40	HIS
2	B	45	GLN
2	B	113	HIS
2	B	146	GLN
2	B	204	ASN
2	B	240	GLN
3	C	6	HIS
3	C	28	GLN
3	C	108	ASN
3	C	162	GLN
4	D	116	GLN
4	D	123	HIS
4	D	161	ASN
4	D	199	ASN
5	E	20	GLN
5	E	72	GLN
6	F	18	GLN
6	F	64	GLN
6	F	73	ASN
6	F	94	GLN
7	G	11	GLN
7	G	37	ASN
7	G	68	ASN
7	G	96	GLN
7	G	97	GLN

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Mol	Chain	Res	Type
7	G	106	GLN
8	H	82	HIS
9	I	23	ASN
9	I	124	GLN
10	J	21	GLN
10	J	69	ASN
10	J	76	ASN
11	K	22	HIS
11	K	38	ASN
12	L	49	ASN
12	L	75	HIS
12	L	80	HIS
12	L	99	HIS
13	M	62	ASN
15	O	13	GLN
16	P	13	HIS
16	P	65	GLN
16	P	76	GLN
16	P	82	GLN
18	R	36	ASN
19	S	47	HIS
19	S	57	HIS
20	T	42	GLN
20	T	73	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1511/1522 (99%)	281 (18%)	35 (2%)

All (281) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	7	G
1	A	9	G
1	A	31	G
1	A	32	A
1	A	33	A
1	A	39	G
1	A	44	G
1	A	47	C

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Mol	Chain	Res	Type
1	A	48	C
1	A	50	A
1	A	51	A
1	A	60	A
1	A	61	G
1	A	73	C
1	A	74	C
1	A	75	G
1	A	79	G
1	A	82	U
1	A	89	C
1	A	91	C
1	A	92	C
1	A	97	G
1	A	98	U
1	A	99	C
1	A	116	A
1	A	121	C
1	A	129(A)	G
1	A	130	A
1	A	131	C
1	A	132	C
1	A	145	G
1	A	178	C
1	A	182	U
1	A	190(E)	U
1	A	195	A
1	A	197	A
1	A	199	G
1	A	201	C
1	A	202	U
1	A	203	U
1	A	204	U
1	A	216	G
1	A	220	G
1	A	231	G
1	A	244	U
1	A	245	C
1	A	247	G
1	A	251	G
1	A	252	U
1	A	266	G

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Mol	Chain	Res	Type
1	A	267	C
1	A	289	G
1	A	300	A
1	A	312	C
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	351	G
1	A	352	C
1	A	353	A
1	A	354	G
1	A	367	U
1	A	373	A
1	A	384	G
1	A	397	A
1	A	398	C
1	A	406	G
1	A	410	G
1	A	411	A
1	A	412	A
1	A	413	G
1	A	414	A
1	A	419	C
1	A	421	U
1	A	424	G
1	A	429	U
1	A	430	A
1	A	433	C
1	A	439	A
1	A	442	C
1	A	452	A
1	A	455	C
1	A	460	A
1	A	461	C
1	A	485	G
1	A	497	A
1	A	498	U
1	A	505	G
1	A	509	A

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Mol	Chain	Res	Type
1	A	510	A
1	A	511	C
1	A	518	C
1	A	527	G
1	A	531	U
1	A	532	A
1	A	533	A
1	A	547	A
1	A	559	A
1	A	560	U
1	A	561	U
1	A	562	C
1	A	564	C
1	A	572	A
1	A	573	A
1	A	575	G
1	A	576	G
1	A	577	G
1	A	579	G
1	A	588	G
1	A	631	G
1	A	632	A
1	A	653	A
1	A	665	A
1	A	687	A
1	A	688	G
1	A	702	A
1	A	703	G
1	A	717	C
1	A	721	G
1	A	723	U
1	A	724	G
1	A	731	G
1	A	734	G
1	A	749	C
1	A	752	G
1	A	755	G
1	A	759	A
1	A	760	G
1	A	773	G
1	A	777	A
1	A	781	A

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Mol	Chain	Res	Type
1	A	782	A
1	A	785	G
1	A	792	A
1	A	793	U
1	A	794	A
1	A	796	C
1	A	813	U
1	A	816	A
1	A	817	C
1	A	818	G
1	A	819	A
1	A	828	A
1	A	839	U
1	A	840	C
1	A	841	U
1	A	848	C
1	A	856	C
1	A	857	C
1	A	872	A
1	A	873	A
1	A	876	G
1	A	885	G
1	A	902	G
1	A	914	A
1	A	926	G
1	A	927	G
1	A	934	C
1	A	935	A
1	A	950	U
1	A	960	U
1	A	961	U
1	A	966	G
1	A	969	A
1	A	971	G
1	A	972	C
1	A	974	A
1	A	976	G
1	A	977	A
1	A	978	A
1	A	991	U
1	A	992	U
1	A	993	G

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Mol	Chain	Res	Type
1	A	994	A
1	A	1005	A
1	A	1006	C
1	A	1023	G
1	A	1026	G
1	A	1027	C
1	A	1047	G
1	A	1050	G
1	A	1053	G
1	A	1054	C
1	A	1060	C
1	A	1065	U
1	A	1066	C
1	A	1068	G
1	A	1078	U
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	1117	G
1	A	1125	U
1	A	1126	U
1	A	1127	G
1	A	1129	C
1	A	1130	A
1	A	1131	G
1	A	1137	C
1	A	1139	G
1	A	1145	C
1	A	1150	U
1	A	1152	A
1	A	1159	U
1	A	1160	G
1	A	1161	C
1	A	1162	C
1	A	1164	G
1	A	1171	G
1	A	1181	G
1	A	1183	A
1	A	1190	G
1	A	1192	C
1	A	1193	G
1	A	1196	U

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Mol	Chain	Res	Type
1	A	1197	G
1	A	1200	C
1	A	1201	A
1	A	1202	G
1	A	1206	G
1	A	1211	U
1	A	1212	U
1	A	1213	A
1	A	1226	C
1	A	1238	A
1	A	1245	A
1	A	1248	A
1	A	1249	C
1	A	1250	A
1	A	1258	G
1	A	1270	C
1	A	1280	A
1	A	1281	U
1	A	1286	A
1	A	1287	A
1	A	1297	C
1	A	1300	G
1	A	1302	U
1	A	1303	C
1	A	1304	G
1	A	1305	G
1	A	1311	G
1	A	1312	G
1	A	1320	C
1	A	1338	G
1	A	1339	A
1	A	1347	G
1	A	1353	G
1	A	1361	G
1	A	1362	C
1	A	1368	G
1	A	1370	G
1	A	1378	C
1	A	1379	G
1	A	1397	C
1	A	1398	A
1	A	1414	U

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Mol	Chain	Res	Type
1	A	1417	G
1	A	1418	A
1	A	1441	G
1	A	1442	G
1	A	1443	G
1	A	1446	A
1	A	1447	G
1	A	1452	C
1	A	1453	G
1	A	1496	C
1	A	1499	A
1	A	1502	A
1	A	1504	G
1	A	1505	G
1	A	1506	U
1	A	1519	A
1	A	1520	G
1	A	1529	G
1	A	1530	G
1	A	1531	A
1	A	1534	A

All (35) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	60	A
1	A	115	G
1	A	129(A)	G
1	A	181	G
1	A	250	A
1	A	251	G
1	A	266	G
1	A	328	C
1	A	372	C
1	A	410	G
1	A	428	G
1	A	429	U
1	A	484	G
1	A	496	A
1	A	559	A
1	A	560	U
1	A	687	A

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Mol	Chain	Res	Type
1	A	701	C
1	A	748	C
1	A	812	C
1	A	913	A
1	A	960	U
1	A	965	A
1	A	1004	A
1	A	1049	U
1	A	1065	U
1	A	1067	A
1	A	1182	G
1	A	1201	A
1	A	1285	A
1	A	1443	G
1	A	1498	U
1	A	1504	G
1	A	1505	G
1	A	1528	U

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 138 ligands modelled in this entry, 138 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

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	1513/1522 (99%)	-0.28	20 (1%) 79 66	50, 108, 253, 361	0
2	B	235/256 (91%)	-0.63	1 (0%) 93 88	65, 115, 197, 256	0
3	C	206/239 (86%)	-0.34	4 (1%) 70 55	116, 170, 237, 271	0
4	D	208/209 (99%)	-0.52	0 100 100	63, 111, 160, 175	0
5	E	150/162 (92%)	-0.63	0 100 100	51, 78, 114, 154	0
6	F	101/101 (100%)	-0.65	0 100 100	87, 129, 155, 177	0
7	G	155/156 (99%)	-0.46	1 (0%) 90 83	99, 152, 220, 233	0
8	H	138/138 (100%)	-0.73	0 100 100	41, 72, 104, 137	0
9	I	127/128 (99%)	-0.45	0 100 100	78, 171, 216, 224	0
10	J	98/105 (93%)	0.08	7 (7%) 19 11	122, 178, 274, 291	0
11	K	119/129 (92%)	-0.50	2 (1%) 73 58	62, 106, 146, 183	0
12	L	124/135 (91%)	-0.49	0 100 100	48, 107, 143, 174	0
13	M	115/126 (91%)	-0.41	1 (0%) 85 75	96, 136, 170, 180	0
14	N	60/61 (98%)	-0.04	2 (3%) 50 35	125, 157, 213, 229	0
15	O	88/89 (98%)	-0.65	0 100 100	54, 95, 133, 171	0
16	P	83/88 (94%)	-0.67	0 100 100	69, 99, 137, 199	0
17	Q	104/105 (99%)	-0.46	4 (3%) 44 30	54, 83, 125, 223	0
18	R	73/88 (82%)	-0.60	1 (1%) 78 64	65, 99, 164, 209	0
19	S	80/93 (86%)	-0.07	1 (1%) 79 66	149, 183, 219, 231	0
20	T	99/106 (93%)	-0.66	1 (1%) 84 72	76, 107, 165, 190	0
21	U	24/27 (88%)	0.51	4 (16%) 2 2	121, 141, 162, 171	0
All	All	3900/4063 (95%)	-0.40	49 (1%) 79 66	41, 116, 222, 361	0

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
11	K	128	ALA	8.5
17	Q	103	GLY	6.9
1	A	1541	U	6.8
17	Q	104	LYS	6.5
10	J	33	GLN	5.7
1	A	1540	U	5.5
1	A	1003(A)	G	5.2
1	A	1129	C	4.2
1	A	74	C	4.0
1	A	1492	A	4.0
1	A	1005	A	3.9
17	Q	105	ALA	3.9
1	A	993	G	3.8
20	T	106	ALA	3.8
17	Q	102	GLY	3.7
10	J	32	ALA	3.6
3	C	102	ASN	3.4
3	C	193	TYR	3.4
1	A	202	U	3.2
11	K	129	SER	3.1
21	U	18	TYR	3.1
1	A	1534	A	3.0
21	U	25	LYS	3.0
1	A	1003	G	2.9
3	C	103	VAL	2.9
10	J	34	VAL	2.9
1	A	1006	C	2.8
10	J	76	ASN	2.7
1	A	1539	C	2.7
2	B	231	GLU	2.6
18	R	16	PRO	2.6
1	A	1002	G	2.6
1	A	1533	C	2.6
3	C	65	ALA	2.6
10	J	31	GLY	2.4
21	U	17	THR	2.4
13	M	7	VAL	2.4
14	N	12	ARG	2.4
7	G	5	ARG	2.3
14	N	13	THR	2.3
1	A	995	C	2.2
10	J	3	LYS	2.2
21	U	22	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
10	J	4	ILE	2.2
1	A	1144	G	2.1
1	A	1491	G	2.1
19	S	28	LYS	2.0
1	A	994	A	2.0
1	A	1283	G	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
24	K	A	1658	1/1	0.91	0.62	60.18	107,107,107,107	0
24	K	A	1666	1/1	0.74	0.55	42.77	74,74,74,74	0
24	K	A	1641	1/1	0.91	0.69	35.75	97,97,97,97	0
23	MG	A	1554	1/1	0.95	0.59	33.58	59,59,59,59	0
23	MG	A	1620	1/1	0.61	0.94	25.06	92,92,92,92	0
24	K	A	1668	1/1	0.90	0.43	20.26	95,95,95,95	0
23	MG	A	1605	1/1	0.94	1.19	19.49	56,56,56,56	0
24	K	A	1636	1/1	0.94	0.79	16.23	116,116,116,116	0
23	MG	A	1628	1/1	0.72	0.42	16.19	65,65,65,65	0
24	K	A	1644	1/1	0.96	0.49	13.94	55,55,55,55	0
23	MG	A	1603	1/1	0.70	0.49	12.15	100,100,100,100	0
23	MG	A	1606	1/1	0.84	0.42	11.86	65,65,65,65	0
24	K	A	1635	1/1	0.51	0.63	9.20	149,149,149,149	0
23	MG	A	1607	1/1	0.98	0.60	9.02	65,65,65,65	0
24	K	A	1651	1/1	0.92	0.48	8.85	138,138,138,138	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
23	MG	A	1590	1/1	0.96	0.33	7.99	39,39,39,39	0
23	MG	A	1622	1/1	0.86	0.55	7.97	87,87,87,87	0
23	MG	A	1618	1/1	0.93	0.49	7.56	64,64,64,64	0
24	K	A	1670	1/1	0.94	0.32	6.72	107,107,107,107	0
23	MG	A	1623	1/1	0.85	0.37	6.69	77,77,77,77	0
24	K	A	1669	1/1	0.95	0.46	5.99	98,98,98,98	0
23	MG	M	127	1/1	0.96	0.42	5.78	76,76,76,76	0
23	MG	A	1625	1/1	0.88	0.24	4.41	93,93,93,93	0
24	K	A	1648	1/1	0.97	0.25	4.40	63,63,63,63	0
23	MG	B	257	1/1	0.69	0.38	3.82	77,77,77,77	0
23	MG	A	1589	1/1	0.95	0.23	3.75	79,79,79,79	0
23	MG	A	94	1/1	0.94	0.23	3.73	66,66,66,66	0
23	MG	A	1629	1/1	0.97	0.41	3.13	61,61,61,61	0
23	MG	A	1563	1/1	0.95	0.26	2.86	20,20,20,20	0
23	MG	A	1566	1/1	0.90	0.37	2.51	90,90,90,90	0
23	MG	A	1578	1/1	0.80	0.51	2.41	50,50,50,50	0
23	MG	A	1615	1/1	0.97	0.18	2.39	55,55,55,55	0
23	MG	A	86	1/1	0.93	0.22	1.89	59,59,59,59	0
23	MG	A	1613	1/1	0.99	0.18	1.58	39,39,39,39	0
23	MG	A	1567	1/1	0.98	0.24	1.35	70,70,70,70	0
23	MG	A	1579	1/1	0.98	0.21	1.22	29,29,29,29	0
23	MG	A	1611	1/1	0.95	0.18	1.03	56,56,56,56	0
23	MG	A	1585	1/1	0.98	0.26	0.98	78,78,78,78	0
23	MG	A	1594	1/1	0.96	0.14	0.70	46,46,46,46	0
22	ZN	D	210	1/1	0.99	0.32	0.30	85,85,85,85	0
23	MG	A	1595	1/1	0.96	0.18	0.01	33,33,33,33	0
23	MG	A	1604	1/1	0.92	0.18	-0.41	52,52,52,52	0
23	MG	D	211	1/1	0.93	0.14	-0.71	73,73,73,73	0
22	ZN	N	141	1/1	0.99	0.07	-1.41	150,150,150,150	0
24	K	A	1650	1/1	0.97	0.11	-1.64	86,86,86,86	0
23	MG	A	1624	1/1	0.90	0.11	-1.77	38,38,38,38	0
23	MG	A	1621	1/1	0.98	0.11	-2.57	58,58,58,58	0
24	K	A	1647	1/1	0.93	0.17	-	85,85,85,85	0
24	K	A	1649	1/1	0.98	0.26	-	75,75,75,75	0
23	MG	A	1609	1/1	0.86	0.77	-	96,96,96,96	0
23	MG	A	1545	1/1	0.93	0.22	-	75,75,75,75	0
23	MG	A	1582	1/1	0.91	0.76	-	83,83,83,83	0
23	MG	A	1601	1/1	0.88	0.22	-	78,78,78,78	0
23	MG	A	1569	1/1	0.97	0.21	-	59,59,59,59	0
24	K	A	1632	1/1	0.93	0.16	-	102,102,102,102	0
23	MG	A	1556	1/1	0.89	0.49	-	93,93,93,93	0
24	K	E	163	1/1	0.93	0.29	-	115,115,115,115	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
23	MG	A	1565	1/1	0.90	0.40	-	87,87,87,87	0
23	MG	A	1597	1/1	0.89	0.26	-	47,47,47,47	0
23	MG	A	1559	1/1	0.85	0.90	-	53,53,53,53	0
23	MG	A	1576	1/1	0.81	0.53	-	78,78,78,78	0
24	K	A	1657	1/1	0.96	0.56	-	83,83,83,83	0
23	MG	A	1564	1/1	0.93	0.33	-	59,59,59,59	0
24	K	A	1653	1/1	0.98	0.15	-	98,98,98,98	0
24	K	A	1662	1/1	0.93	0.28	-	92,92,92,92	0
23	MG	A	1573	1/1	0.81	0.36	-	70,70,70,70	0
23	MG	A	1627	1/1	0.95	0.54	-	39,39,39,39	0
23	MG	A	1547	1/1	0.52	0.52	-	86,86,86,86	0
24	K	A	1645	1/1	0.96	0.37	-	75,75,75,75	0
24	K	A	1665	1/1	0.95	0.35	-	79,79,79,79	0
23	MG	A	1581	1/1	0.75	0.46	-	68,68,68,68	0
23	MG	A	1599	1/1	0.79	0.57	-	65,65,65,65	0
23	MG	A	1552	1/1	0.96	0.21	-	80,80,80,80	0
23	MG	A	1586	1/1	0.92	0.33	-	48,48,48,48	0
24	K	A	1661	1/1	0.93	0.14	-	79,79,79,79	0
23	MG	A	1555	1/1	0.84	0.26	-	95,95,95,95	0
24	K	A	1638	1/1	0.82	0.33	-	143,143,143,143	0
24	K	A	1633	1/1	0.95	0.19	-	135,135,135,135	0
23	MG	A	1560	1/1	0.77	0.52	-	89,89,89,89	0
23	MG	A	1614	1/1	0.98	0.14	-	56,56,56,56	0
23	MG	A	1553	1/1	0.92	0.70	-	94,94,94,94	0
23	MG	A	1574	1/1	0.64	0.93	-	68,68,68,68	0
24	K	A	1667	1/1	0.95	0.39	-	80,80,80,80	0
23	MG	A	1617	1/1	0.98	0.32	-	78,78,78,78	0
23	MG	A	1608	1/1	0.89	0.33	-	72,72,72,72	0
24	K	A	1654	1/1	0.91	0.34	-	85,85,85,85	0
23	MG	A	1551	1/1	0.79	0.55	-	50,50,50,50	0
23	MG	A	1602	1/1	0.94	0.44	-	63,63,63,63	0
23	MG	A	1558	1/1	0.57	0.43	-	81,81,81,81	0
23	MG	A	1588	1/1	0.84	0.22	-	59,59,59,59	0
24	K	A	1656	1/1	0.78	0.42	-	105,105,105,105	0
23	MG	A	85	1/1	0.97	0.38	-	35,35,35,35	0
23	MG	A	1570	1/1	0.90	0.69	-	34,34,34,34	0
24	K	A	1639	1/1	0.98	0.64	-	81,81,81,81	0
23	MG	A	1593	1/1	0.58	0.57	-	87,87,87,87	0
23	MG	A	1610	1/1	0.94	0.28	-	47,47,47,47	0
23	MG	A	1549	1/1	0.77	0.48	-	59,59,59,59	0
23	MG	A	1557	1/1	0.75	0.84	-	90,90,90,90	0
24	K	A	1659	1/1	0.97	0.30	-	76,76,76,76	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
23	MG	A	1562	1/1	0.92	0.73	-	54,54,54,54	0
24	K	A	1642	1/1	0.97	0.49	-	94,94,94,94	0
23	MG	A	1630	1/1	0.97	0.31	-	41,41,41,41	0
23	MG	A	1584	1/1	0.95	0.56	-	52,52,52,52	0
23	MG	A	1561	1/1	0.93	0.13	-	59,59,59,59	0
23	MG	A	1587	1/1	0.91	0.42	-	37,37,37,37	0
23	MG	A	1571	1/1	0.85	0.46	-	67,67,67,67	0
24	K	A	1663	1/1	0.94	0.55	-	99,99,99,99	0
23	MG	A	1546	1/1	0.90	0.75	-	76,76,76,76	0
23	MG	A	1575	1/1	0.95	0.59	-	32,32,32,32	0
24	K	A	1646	1/1	0.97	0.54	-	82,82,82,82	0
23	MG	A	1612	1/1	0.82	0.25	-	81,81,81,81	0
23	MG	A	100	1/1	0.99	0.20	-	126,126,126,126	0
23	MG	A	1548	1/1	0.75	0.94	-	81,81,81,81	0
23	MG	A	1577	1/1	0.88	0.59	-	63,63,63,63	0
23	MG	A	1580	1/1	0.96	0.43	-	79,79,79,79	0
23	MG	A	1583	1/1	0.72	0.39	-	67,67,67,67	0
23	MG	A	1626	1/1	0.96	0.16	-	62,62,62,62	0
24	K	A	1634	1/1	0.92	0.20	-	134,134,134,134	0
23	MG	A	1550	1/1	0.93	0.21	-	52,52,52,52	0
24	K	A	1652	1/1	0.88	0.23	-	100,100,100,100	0
23	MG	A	1596	1/1	0.69	1.22	-	54,54,54,54	0
23	MG	A	1619	1/1	0.77	0.47	-	91,91,91,91	0
24	K	A	1631	1/1	0.86	0.35	-	110,110,110,110	0
24	K	A	1664	1/1	0.86	0.23	-	111,111,111,111	0
23	MG	A	1591	1/1	0.84	0.34	-	82,82,82,82	0
24	K	A	1660	1/1	0.91	0.19	-	126,126,126,126	0
23	MG	A	1568	1/1	0.97	0.11	-	17,17,17,17	0
23	MG	A	1616	1/1	0.94	0.41	-	49,49,49,49	0
23	MG	A	71	1/1	0.85	0.81	-	74,74,74,74	0
24	K	A	1671	1/1	0.89	0.50	-	79,79,79,79	0
24	K	A	1643	1/1	0.96	0.27	-	122,122,122,122	0
23	MG	A	1572	1/1	0.96	0.40	-	35,35,35,35	0
24	K	A	1655	1/1	0.69	0.45	-	102,102,102,102	0
23	MG	A	1600	1/1	0.92	0.58	-	72,72,72,72	0
24	K	A	1640	1/1	0.93	0.53	-	108,108,108,108	0
24	K	A	1637	1/1	0.97	0.39	-	129,129,129,129	0
23	MG	A	1592	1/1	0.94	0.36	-	63,63,63,63	0
23	MG	A	1598	1/1	0.78	0.67	-	73,73,73,73	0

6.5 Other polymers [i](#)

There are no such residues in this entry.