



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 12:29 PM UTC

PDB ID : 3OTO / pdb_00003oto
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

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

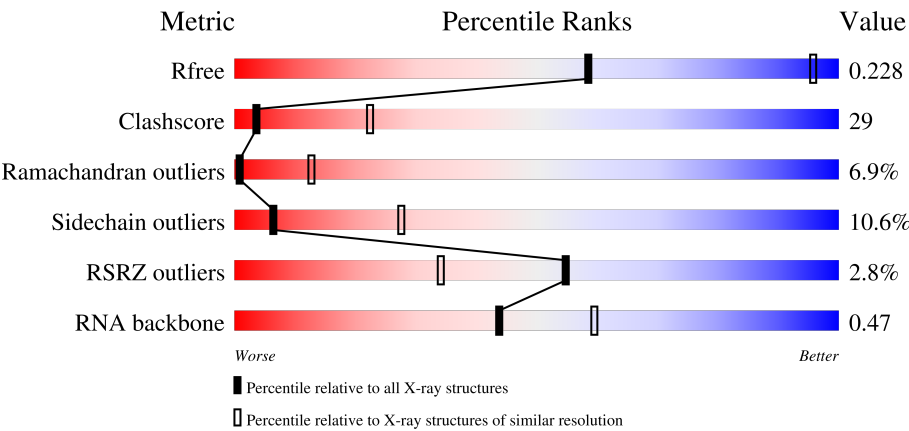
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.69 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.



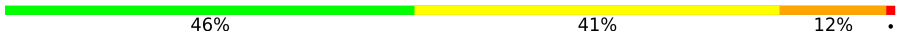
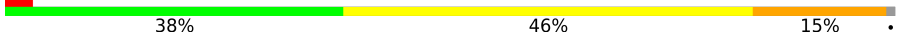
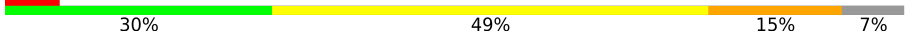
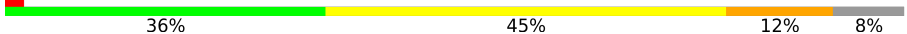
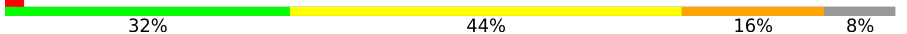
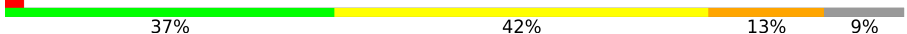
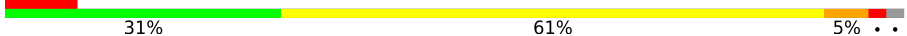
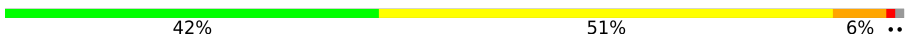
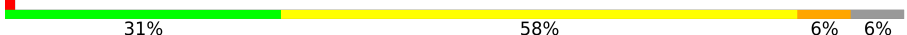
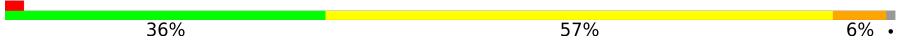
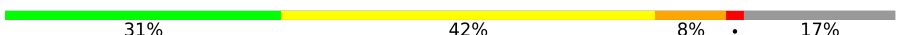
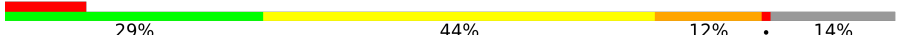
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1131 (3.80-3.60)
Clashscore	190562	1171 (3.80-3.60)
Ramachandran outliers	187476	1129 (3.80-3.60)
Sidechain outliers	187428	1126 (3.80-3.60)
RSRZ outliers	180081	1130 (3.80-3.60)
RNA backbone	3983	1007 (4.30-3.08)

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

Mol	Chain	Length	Quality of chain
1	A	1522	3% 30%55%14%
2	B	256	% 35%46%11%8%
3	C	239	3% 35%44%7%14%
4	D	209	4% 41%52%6%

Continued on next page...

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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
22	MG	A	1571	-	-	-	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 MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 23 is POTASSIUM ION (CCD ID: K) (formula: K).

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

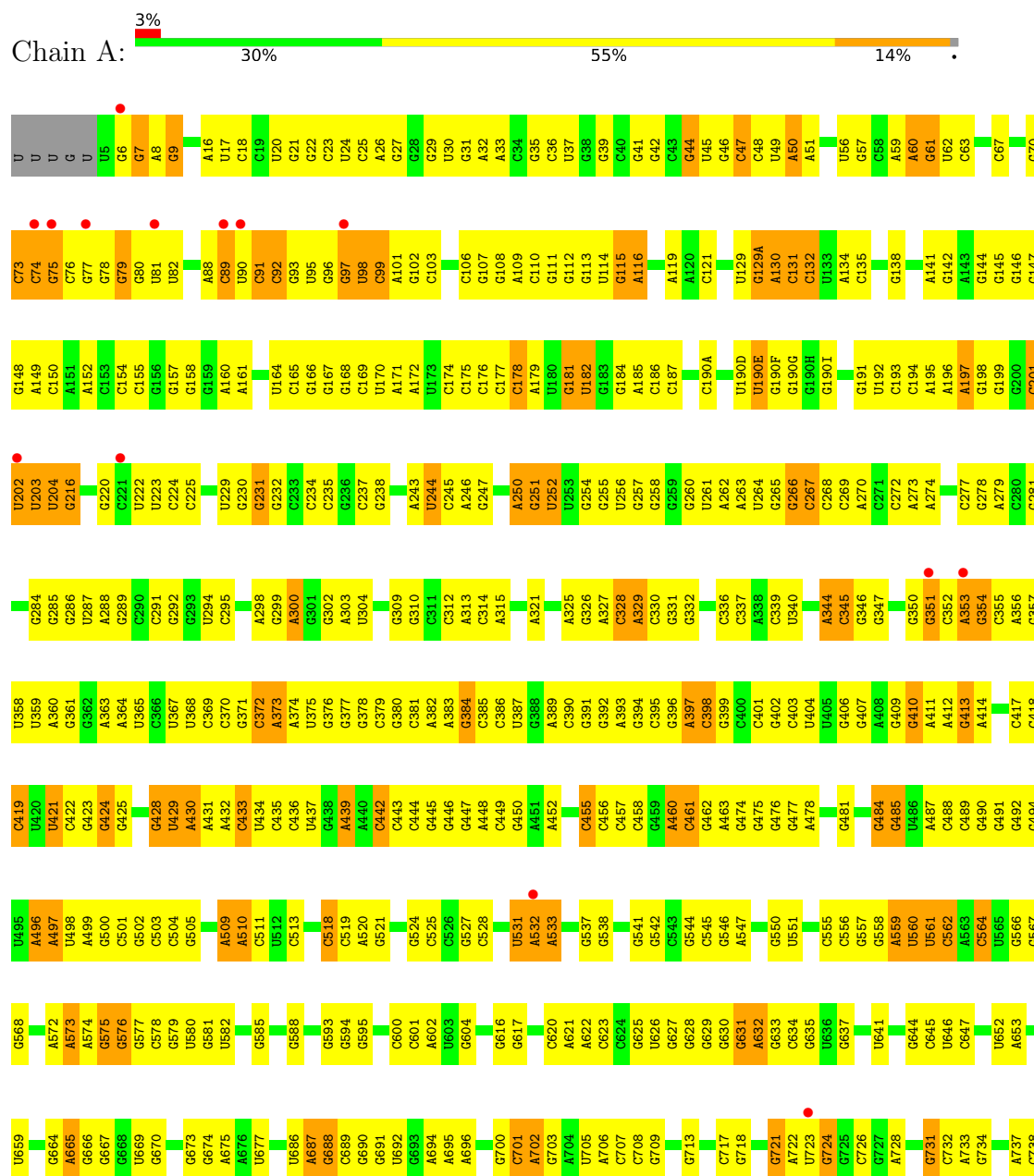
- Molecule 24 is ZINC ION (CCD ID: ZN) (formula: Zn).

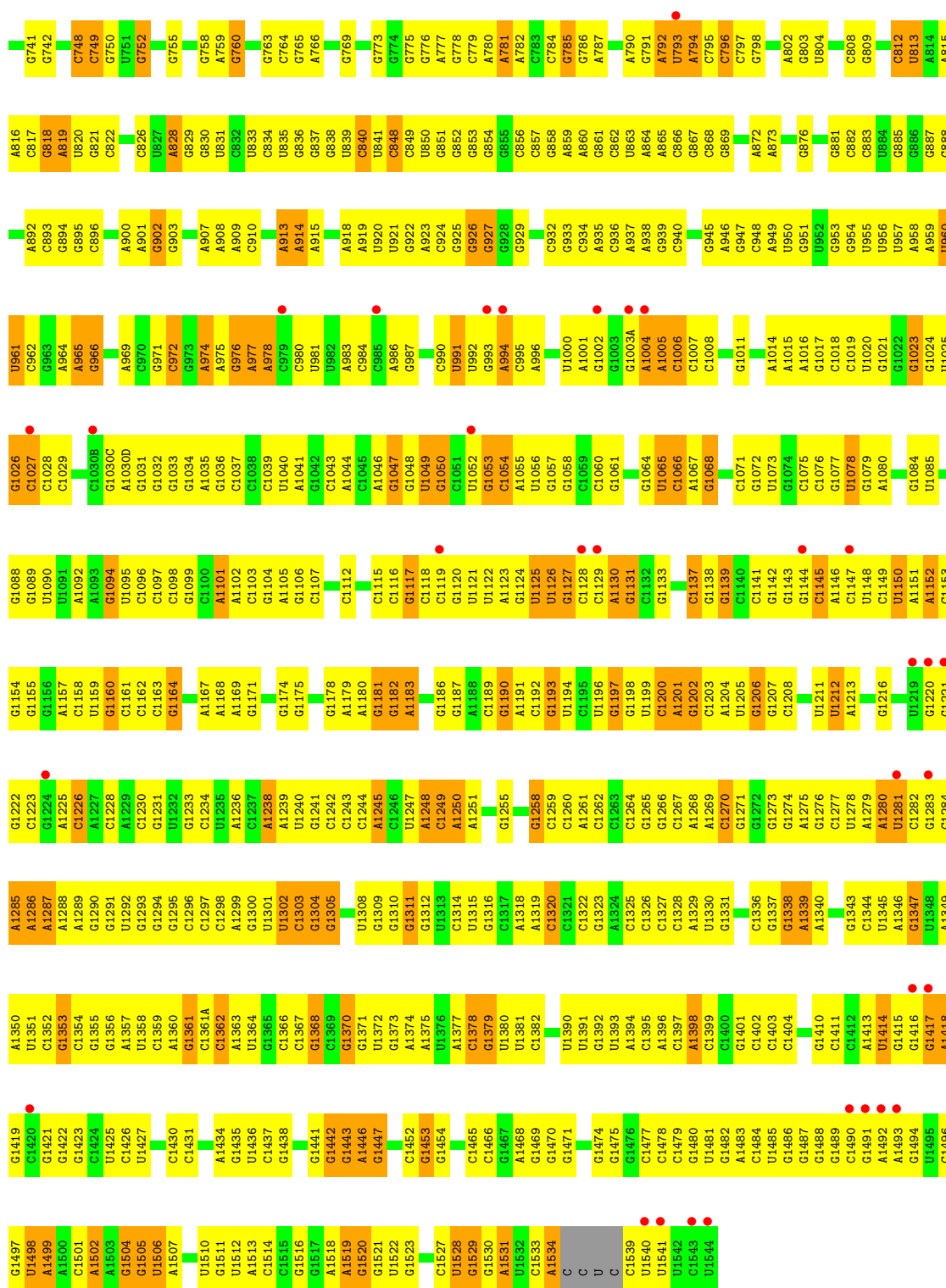
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
24	D	1	Total	Zn	0	0
			1	1		
24	N	1	Total	Zn	0	0
			1	1		

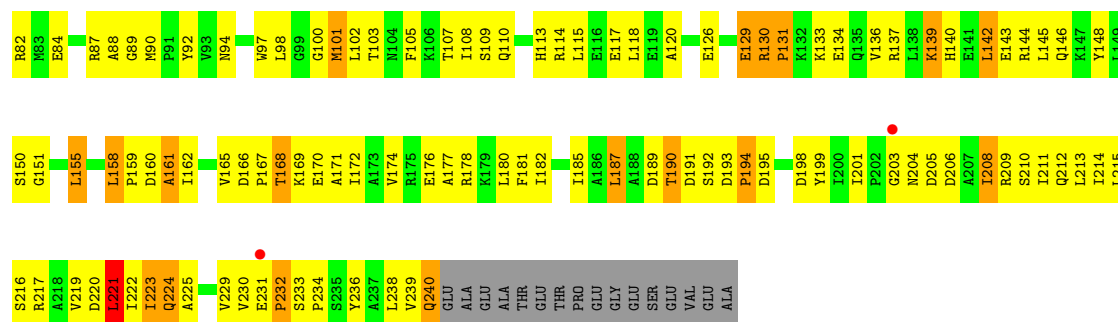
3 Residue-property plots

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

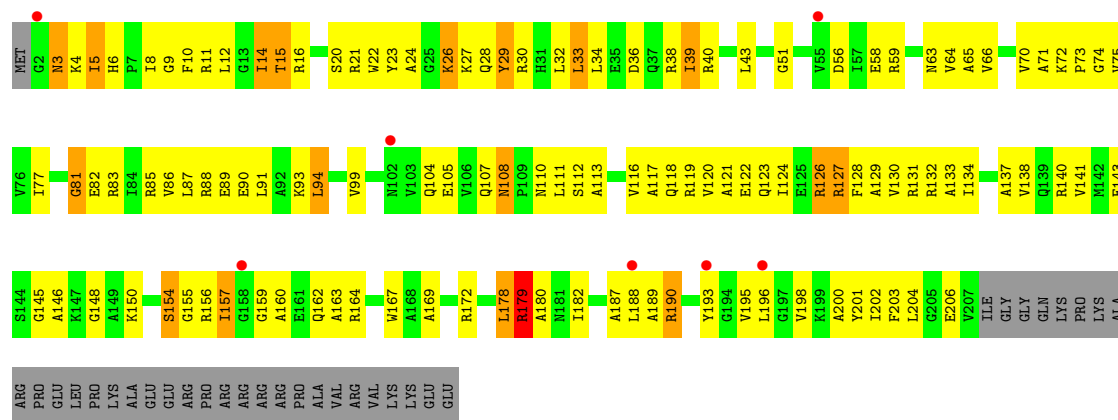
• Molecule 1: 16S rRNA



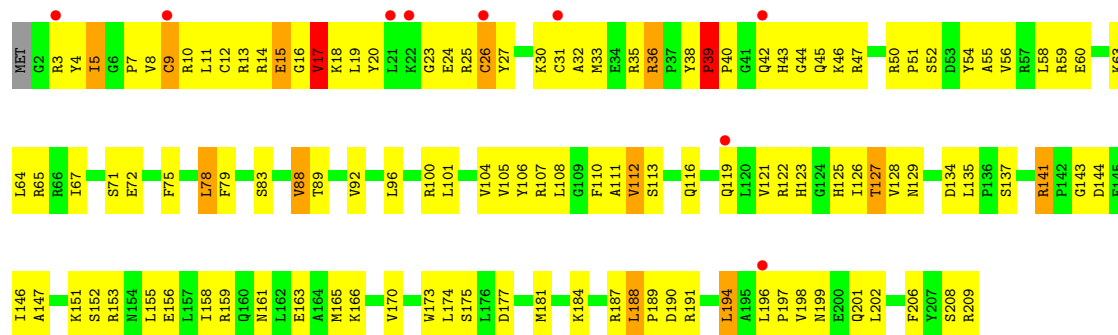




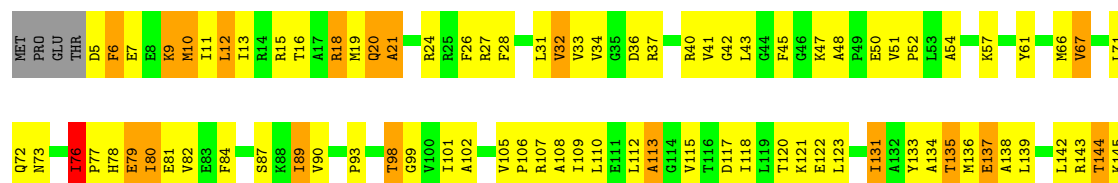
- Molecule 3: 30S RIBOSOMAL PROTEIN S3



- Molecule 4: 30S RIBOSOMAL PROTEIN S4



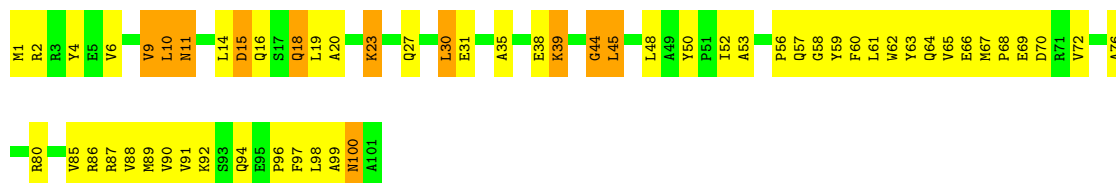
- Molecule 5: 30S RIBOSOMAL PROTEIN S5





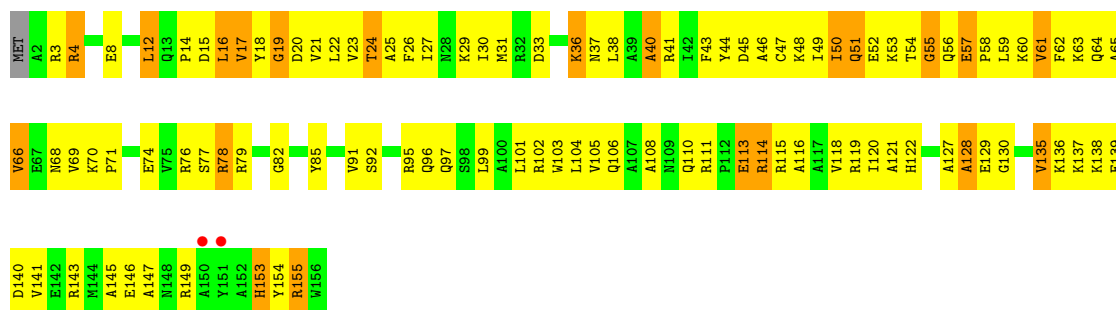
• Molecule 6: 30S RIBOSOMAL PROTEIN S6

Chain F: 43% 47% 11%



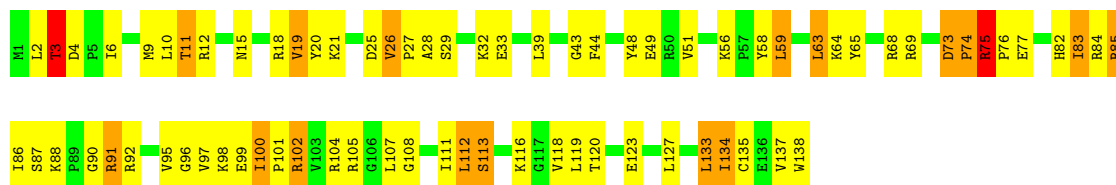
• Molecule 7: 30S RIBOSOMAL PROTEIN S7

Chain G: 32% 54% 13%



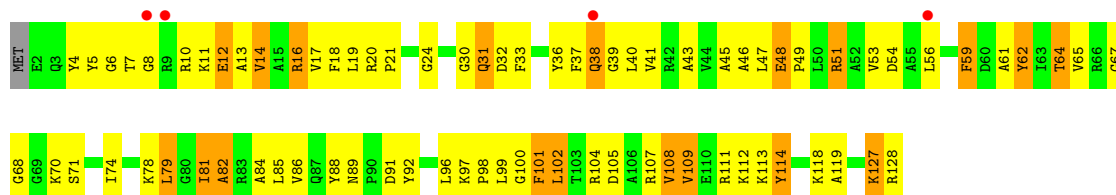
• Molecule 8: 30S RIBOSOMAL PROTEIN S8

Chain H: 46% 41% 12%



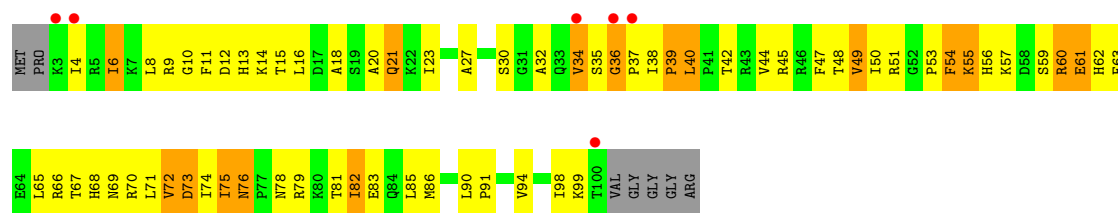
• Molecule 9: 30S RIBOSOMAL PROTEIN S9

Chain I: 3% 38% 46% 15%



• Molecule 10: 30S RIBOSOMAL PROTEIN S10

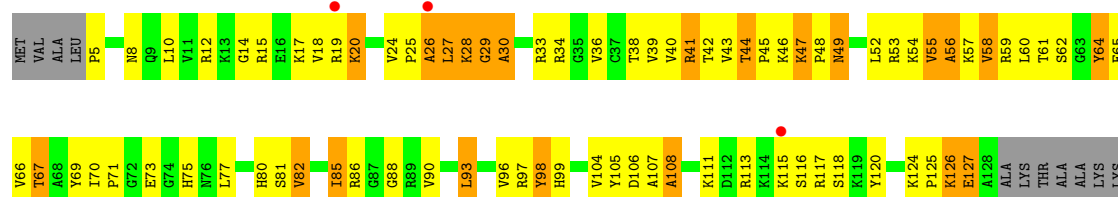
Chain J: 6% 30% 49% 15% 7%



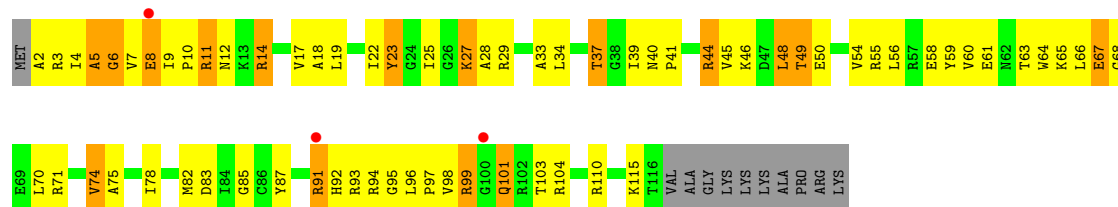
• Molecule 11: 30S RIBOSOMAL PROTEIN S11



• Molecule 12: 30S RIBOSOMAL PROTEIN S12



• Molecule 13: 30S RIBOSOMAL PROTEIN S13

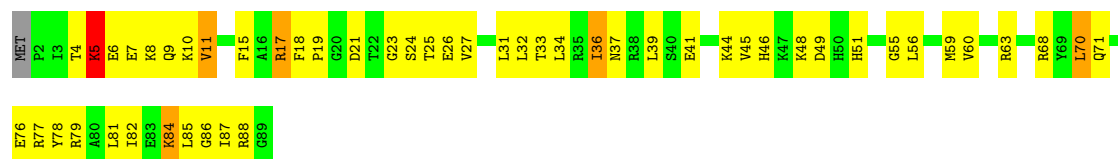


• Molecule 14: 30S RIBOSOMAL PROTEIN S14

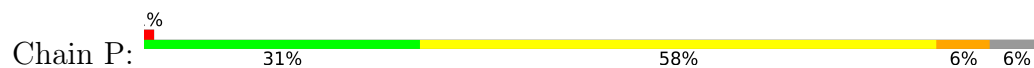


• Molecule 15: 30S RIBOSOMAL PROTEIN S15

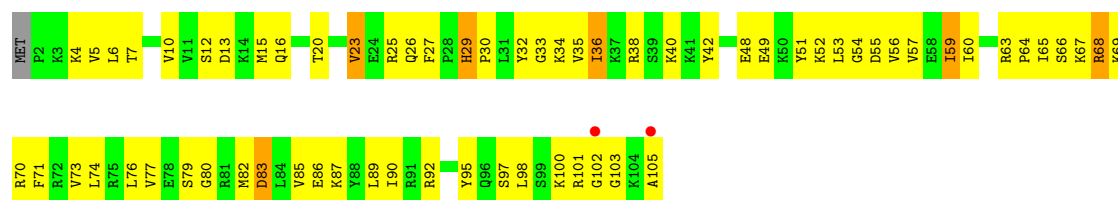




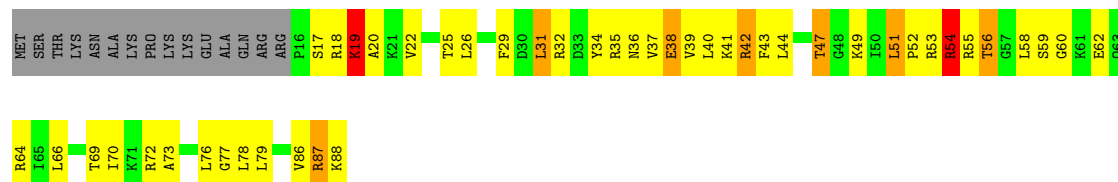
• Molecule 16: 30S RIBOSOMAL PROTEIN S16



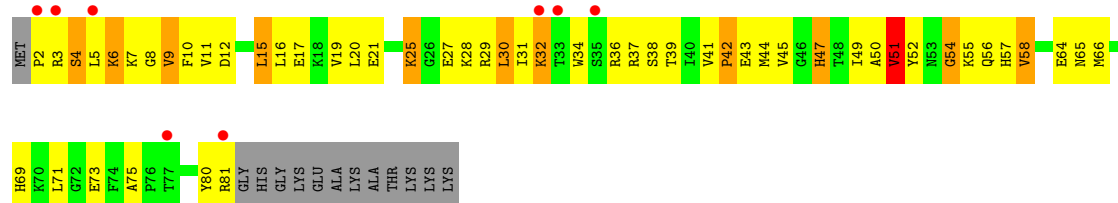
• Molecule 17: 30S RIBOSOMAL PROTEIN S17



• Molecule 18: 30S RIBOSOMAL PROTEIN S18

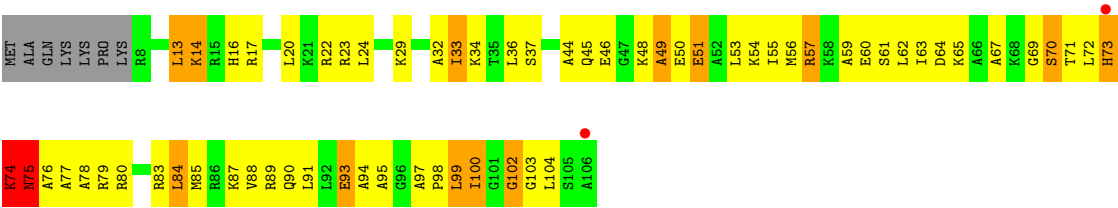


• Molecule 19: 30S RIBOSOMAL PROTEIN S19

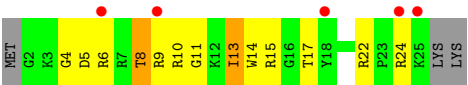


• Molecule 20: 30S RIBOSOMAL PROTEIN S20





● Molecule 21: 30S RIBOSOMAL PROTEIN THX



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	402.09Å 402.09Å 173.25Å 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) 97.6 (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 3.65Å)	Xtriage
Refinement program	PHENIX 1.6.4_486	Depositor
R, R_{free}	0.173 , 0.231 0.175 , 0.228	Depositor DCC
R_{free} test set	7456 reflections (5.02%)	wwPDB-VP
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 , 98.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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	0.25	0/36390	0.37	0/56793
2	B	0.42	0/1908	0.82	0/2577
3	C	0.32	0/1636	0.77	0/2205
4	D	0.39	0/1733	0.77	2/2318 (0.1%)
5	E	0.53	0/1162	0.92	3/1564 (0.2%)
6	F	0.35	0/856	0.79	2/1154 (0.2%)
7	G	0.34	0/1276	0.79	2/1709 (0.1%)
8	H	0.55	0/1136	0.96	5/1527 (0.3%)
9	I	0.36	0/1029	0.77	0/1378
10	J	0.37	0/805	0.84	0/1082
11	K	0.44	0/900	0.78	0/1213
12	L	0.43	0/986	0.90	5/1320 (0.4%)
13	M	0.35	0/931	0.83	1/1248 (0.1%)
14	N	0.33	0/501	0.78	0/664
15	O	0.44	0/745	0.72	0/992
16	P	0.44	0/716	0.84	0/963
17	Q	0.47	0/870	0.90	3/1159 (0.3%)
18	R	0.36	0/603	0.86	2/799 (0.3%)
19	S	0.30	0/661	0.76	1/890 (0.1%)
20	T	0.43	0/764	0.80	1/1006 (0.1%)
21	U	0.34	0/212	0.84	0/277
All	All	0.31	0/55820	0.56	27/82838 (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 (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	L	26	ALA	N-CA-C	-7.41	103.14	113.37
7	G	110	GLN	N-CA-C	-6.68	105.66	113.88
8	H	100	ILE	CA-C-N	6.58	126.49	119.85
8	H	100	ILE	C-N-CA	6.58	126.49	119.85
12	L	30	ALA	CA-C-N	5.85	125.53	119.56
12	L	30	ALA	C-N-CA	5.85	125.53	119.56
18	R	51	LEU	CA-C-N	5.80	125.75	119.78
18	R	51	LEU	C-N-CA	5.80	125.75	119.78
5	E	113	ALA	N-CA-C	-5.70	106.31	113.20
12	L	58	VAL	N-CA-C	5.59	115.94	108.27
8	H	75	ARG	CA-C-N	5.58	125.58	119.89
8	H	75	ARG	C-N-CA	5.58	125.58	119.89
19	S	58	VAL	N-CA-C	5.58	114.01	107.77
20	T	75	ASN	N-CA-C	-5.55	105.61	112.38
7	G	19	GLY	N-CA-C	-5.30	108.00	115.32
17	Q	83	ASP	N-CA-C	-5.26	105.62	111.36
12	L	18	VAL	N-CA-C	5.26	116.15	108.53
5	E	76	ILE	CA-C-N	5.17	124.96	119.28
5	E	76	ILE	C-N-CA	5.17	124.96	119.28
4	D	39	PRO	CA-C-N	5.10	126.21	119.84
4	D	39	PRO	C-N-CA	5.10	126.21	119.84
17	Q	29	HIS	CA-C-N	5.09	124.81	119.82
17	Q	29	HIS	C-N-CA	5.09	124.81	119.82
13	M	27	LYS	N-CA-C	-5.06	105.77	111.28
6	F	11	ASN	CA-C-N	5.05	125.12	119.87
6	F	11	ASN	C-N-CA	5.05	125.12	119.87
8	H	134	ILE	N-CA-C	5.05	115.72	110.82

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 [\(i\)](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32511	0	16413	1240	0
2	B	1873	0	1887	154	0
3	C	1612	0	1677	131	0
4	D	1703	0	1763	111	0
5	E	1146	0	1207	88	0
6	F	843	0	857	47	0
7	G	1257	0	1296	119	0
8	H	1116	0	1177	76	0
9	I	1011	0	1043	76	0
10	J	792	0	835	75	0
11	K	885	0	904	68	0
12	L	970	0	1057	97	0
13	M	921	0	978	67	0
14	N	492	0	530	53	0
15	O	734	0	771	62	0
16	P	700	0	720	51	0
17	Q	857	0	930	65	0
18	R	597	0	668	49	0
19	S	647	0	673	49	0
20	T	762	0	859	73	0
21	U	208	0	221	13	0
22	A	91	0	0	0	0
22	B	1	0	0	0	0
22	D	1	0	0	0	0
22	M	1	0	0	0	0
23	A	41	0	0	0	0
23	E	1	0	0	0	0
24	D	1	0	0	0	0
24	N	1	0	0	0	0
All	All	51775	0	36466	2576	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 29.

All (2576) 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:HG3	15:O:17:ARG:HH11	1.12	1.08
1:A:1057:G:H5"	3:C:154:SER:HB2	1.32	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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:H	4:D:188:LEU:HD12	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:89:C:O2	1:A:89:C:H2'	1.75	0.86
1:A:748:C:H4'	1:A:749:C:O5'	1.74	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: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
1:A:235:C:H5'	17:Q:70:ARG:HG2	1.57	0.84
2:B:114:ARG:HH11	2:B:118:LEU:HD21	1.42	0.84
2:B:204:ASN:ND2	2:B:206:ASP:H	1.76	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
1:A:1117:G:H5'	1:A:1118:C:OP2	1.77	0.83
12:L:5:PRO:HG2	12:L:15:ARG:NH2	1.93	0.83
5:E:51:VAL:HB	5:E:52:PRO:HD3	1.58	0.83
1:A:991:U:H5	1:A:1212:U:C2	1.97	0.82
1:A:1250:A:H4'	9:I:68:GLY:N	1.94	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
5:E:76:ILE:HG22	5:E:93:PRO:HB3	1.59	0.81
7:G:17:VAL:HG12	7:G:18:TYR:HD2	1.45	0.81
14:N:29:ARG:HG3	14:N:30:ALA:H	1.44	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
3:C:64:VAL:HG23	3:C:99:VAL:HG11	1.62	0.81
9:I:48:GLU:HG2	9:I:51:ARG:HH21	1.46	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:A:1065:U:H5''	1:A:1190:G:H22	1.48	0.78
1:A:1366:C:H2'	1:A:1367:C:H6	1.49	0.78
1:A:812:C:H4'	1:A:813:U:O5'	1.83	0.78
12:L:25:PRO:C	12:L:27:LEU:H	1.89	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
3:C:22:TRP:HB3	3:C:59:ARG:HB2	1.67	0.77
17:Q:67:LYS:HA	17:Q:70:ARG:HH12	1.49	0.77
1:A:328:C:O2	1:A:328:C:H2'	1.83	0.77
5:E:76:ILE:HG23	5:E:78:HIS:H	1.50	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:H	12:L:20:LYS:HD3	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
1:A:1418:A:H2'	1:A:1419:G:O4'	1.85	0.76
2:B:51:LEU:HD23	2:B:201:ILE:HD12	1.66	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
13:M:34:LEU:HD13	13:M:41:PRO:HA	1.67	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
13:M:10:PRO:HB2	13:M:18:ALA:HB1	1.65	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:17:ARG:HH11	15:O:17:ARG:CG	1.96	0.76
1:A:1361:G:C6	1:A:1361(A):C:N4	2.55	0.76
12:L:59:ARG:HA	12:L:65:GLU:HG2	1.66	0.76
15:O:78:TYR:CZ	15:O:82:ILE:HD11	2.20	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
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:432:A:O2'	1:A:433:C:H6	1.67	0.75
1:A:974:A:H8	1:A:974:A:OP1	1.69	0.75
1:A:1189:C:H4'	3:C:10:PHE:HE1	1.52	0.75
9:I:5:TYR:HD2	9:I:6:GLY:N	1.84	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
1:A:1493:A:H2'	1:A:1494:G:C8	2.22	0.74
3:C:21:ARG:NH2	3:C:56:ASP:HB3	2.02	0.74
3:C:64:VAL:HB	3:C:99:VAL:HG21	1.69	0.74
10:J:12:ASP:HB3	10:J:15:THR:HB	1.69	0.74
18:R:32:ARG:HA	18:R:69:THR:HG21	1.70	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
1:A:664:G:H22	1:A:741:G:H1	1.36	0.74
4:D:7:PRO:HB2	4:D:10:ARG:HD2	1.68	0.74
1:A:97:G:H8	1:A:97:G:OP2	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:HH11	5:E:18:ARG:HG3	1.53	0.73
1:A:1329:A:P	13:M:28:ALA:HB3	2.28	0.73
5:E:144:THR:O	5:E:148:VAL:HG23	1.88	0.73
11:K:50:TYR:HD2	11:K:54:ARG:HH11	1.37	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
7:G:111:ARG:HB2	7:G:119:ARG:HG2	1.71	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
1:A:1453:G:H5'	1:A:1454:G:OP2	1.88	0.72
20:T:87:LYS:O	20:T:91:LEU:HD23	1.87	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
1:A:192:U:H2'	1:A:193:C:H6	1.55	0.72
15:O:21:ASP:OD1	15:O:24:SER:HB2	1.90	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:NH1	12:L:41:ARG:HB3	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
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
20:T:45:GLN:HA	20:T:91:LEU:HD12	1.71	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:177:C:H2'	1:A:178:C:C6	2.26	0.70
1:A:489:C:H2'	1:A:490:G:H8	1.57	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:OP2	1:A:1068:G:H8	1.75	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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
1:A:1234:C:H1'	1:A:1364:U:O2	1.90	0.70
1:A:436:C:H2'	1:A:437:U:H6	1.57	0.69
1:A:243:A:H4'	1:A:244:U:O5'	1.92	0.69
3:C:21:ARG:HH21	3:C:56:ASP:HB3	1.54	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
1:A:1080:A:H5''	5:E:16:THR:HG21	1.73	0.69
1:A:1533:C:H2'	1:A:1534:A:H5'	1.75	0.69
12:L:43:VAL:HG12	12:L:44:THR:H	1.58	0.69
13:M:65:LYS:O	13:M:70:LEU:HD12	1.93	0.69
1:A:977:A:H2'	1:A:978:A:H5'	1.75	0.69
1:A:1421:G:H2'	1:A:1422:G:H8	1.58	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
19:S:17:GLU:HA	19:S:20:LEU:HG	1.75	0.69
1:A:16:A:H2'	1:A:17:U:H5'	1.75	0.69
1:A:92:C:C5	1:A:93:G:N7	2.61	0.69
1:A:359:U:H2'	1:A:360:A:C8	2.27	0.69
1:A:990:C:H4'	1:A:1018:C:OP1	1.93	0.69
3:C:108:ASN:ND2	3:C:111:LEU:HG	2.06	0.69
7:G:17:VAL:HG12	7:G:18:TYR:CD2	2.26	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:1031:G:H2'	1:A:1032:G:C8	2.28	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:1373:G:H5''	7:G:36:LYS:NZ	2.09	0.68
1:A:1485:U:O2	1:A:1485:U:H2'	1.92	0.68
10:J:6:ILE:HD13	10:J:72:VAL:HB	1.76	0.68
1:A:397:A:H5'	1:A:398:C:OP1	1.94	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:330:C:H2'	1:A:331:G:H5'	1.75	0.68
15:O:21:ASP:CG	15:O:24:SER:HB2	2.19	0.68
1:A:1103:C:H2'	1:A:1104:G:O4'	1.94	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:5:LYS:H	15:O:5:LYS:HD2	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
1:A:1262:C:H42	1:A:1273:G:H1	1.43	0.67
1:A:1487:G:O2'	1:A:1488:G:H5'	1.94	0.67
3:C:27:LYS:HA	3:C:30:ARG:HH12	1.59	0.67
3:C:116:VAL:O	3:C:119:ARG:HB3	1.95	0.67
10:J:16:LEU:HD13	10:J:70:ARG:HG2	1.76	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
1:A:106:C:C2'	1:A:107:G:H5'	2.24	0.67
14:N:23:ARG:NH1	14:N:30:ALA:HB2	2.08	0.67
15:O:39:LEU:HD12	15:O:56:LEU:HB2	1.77	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: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:1031:G:H2'	1:A:1032:G:H8	1.60	0.67
2:B:25:ASN:HD22	2:B:25:ASN:C	2.03	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:O2	1:A:1126:U:H2'	1.94	0.66
1:A:946:A:H2'	1:A:947:G:C8	2.30	0.66
1:A:1489:G:C2	1:A:1490:C:C2	2.83	0.66
14:N:23:ARG:HH12	14:N:30:ALA:HB2	1.60	0.66
1:A:299:G:H2'	1:A:300:A:C8	2.31	0.66
1:A:707:C:H2'	1:A:708:C:C6	2.30	0.66
6:F:62:TRP:C	6:F:63:TYR:HD2	2.04	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
2:B:24:TRP:CZ3	2:B:26:PRO:HA	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
1:A:383:A:H2'	1:A:384:G:H5'	1.78	0.66
1:A:1392:G:H2'	1:A:1393:U:H6	1.61	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
10:J:6:ILE:CD1	10:J:73:ASP:H	2.09	0.66
12:L:62:SER:C	12:L:64:TYR:H	2.04	0.66
1:A:1101:A:H4'	1:A:1102:A:O5'	1.95	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:262:A:H5'	20:T:74:LYS:HG3	1.77	0.65
1:A:447:G:H2'	1:A:485:G:N2	2.11	0.65
4:D:100:ARG:O	4:D:104:VAL:HG23	1.96	0.65
1:A:836:G:C6	1:A:851:G:C6	2.83	0.65
1:A:945:G:O6	1:A:1236:A:N1	2.29	0.65
1:A:960:U:H4'	1:A:961:U:O5'	1.95	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
7:G:65:ALA:O	7:G:69:VAL:HG23	1.96	0.65
17:Q:97:SER:HA	17:Q:103:GLY:HA3	1.77	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
1:A:1026:G:H2'	1:A:1026:G:N3	2.11	0.65
1:A:1225:A:H2'	1:A:1225:A:N3	2.11	0.65
11:K:23:ALA:HB1	11:K:88:GLY:HA3	1.78	0.65
1:A:287:U:C2'	1:A:288:A:H5'	2.26	0.65
1:A:616:G:H1'	1:A:625:G:N2	2.12	0.65
1:A:1442:G:C6	1:A:1446:A:N6	2.65	0.65
13:M:70:LEU:C	13:M:70:LEU:HD23	2.21	0.65
1:A:1115:C:O2'	1:A:1116:C:H5'	1.95	0.65
5:E:82:VAL:HG21	5:E:138:ALA:HA	1.78	0.65
1:A:75:G:N2	1:A:76:C:N3	2.45	0.65
5:E:89:ILE:HD13	5:E:90:VAL:H	1.61	0.65
17:Q:68:ARG:H	17:Q:70:ARG:HH11	1.44	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
2:B:61:LEU:HD13	2:B:66:GLY:HA3	1.79	0.65
13:M:12:ASN:H	13:M:45:VAL:CG1	2.10	0.65
1:A:284:G:H2'	1:A:285:G:C8	2.32	0.65
1:A:620:C:C1'	4:D:135:LEU:HD13	2.27	0.65
2:B:204:ASN:HD22	2:B:205:ASP:N	1.95	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:11:ILE:HG21	5:E:105:VAL:HG13	1.78	0.65
10:J:8:LEU:HD12	10:J:20:ALA:HB2	1.77	0.65
12:L:25:PRO:C	12:L:27:LEU:N	2.54	0.65
12:L:39:VAL:HG12	12:L:40:VAL:N	2.12	0.65
13:M:23:TYR:CE2	13:M:70:LEU:HD22	2.26	0.65
1:A:235:C:C5'	17:Q:70:ARG:HG2	2.28	0.64
1:A:627:G:H2'	1:A:628:G:H8	1.62	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
12:L:43:VAL:HG12	12:L:44:THR:N	2.12	0.64
2:B:36:ARG:O	2:B:39:ILE:HG12	1.98	0.64
1:A:363:A:OP2	12:L:61:THR:HG21	1.97	0.64
1:A:1320:C:N3	19:S:36:ARG:HD3	2.12	0.64
3:C:128:PHE:HD2	3:C:129:ALA:H	1.43	0.64
1:A:255:G:H1'	17:Q:16:GLN:OE1	1.97	0.64
1:A:370:C:C2'	1:A:371:G:H5'	2.27	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
10:J:38:ILE:HB	10:J:71:LEU:HB3	1.80	0.64
15:O:78:TYR:CE1	15:O:82:ILE:HD11	2.32	0.64
1:A:109:A:H2'	1:A:326:G:N2	2.13	0.64
1:A:532:A:H2'	1:A:532:A:N3	2.11	0.64
1:A:1112:C:C2	3:C:178:LEU:HB2	2.33	0.64
1:A:1374:A:C4	1:A:1375:A:C8	2.85	0.64
1:A:1296:C:H4'	1:A:1302:U:C5	2.33	0.64
1:A:1308:U:O2'	1:A:1309:G:H5'	1.98	0.64
2:B:97:TRP:HH2	2:B:176:GLU:CD	2.06	0.64
1:A:784:C:H2'	1:A:785:G:O4'	1.98	0.64
2:B:103:THR:HG23	2:B:176:GLU:CG	2.26	0.64
7:G:26:PHE:HD1	7:G:101:LEU:HD22	1.62	0.64
17:Q:59:ILE:HG23	17:Q:71:PHE:HB3	1.79	0.64
19:S:50:ALA:HA	19:S:58:VAL:O	1.97	0.64
1:A:689:C:P	11:K:46:GLY:HA3	2.37	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: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:359:U:H2'	1:A:360:A:H8	1.61	0.63
1:A:1053:G:HO2'	1:A:1199:U:H5	1.47	0.63
1:A:1064:G:H21	1:A:1190:G:H2'	1.62	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1366:C:H2'	1:A:1367:C:C6	2.31	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
14:N:24:CYS:SG	14:N:39:LEU:HA	2.38	0.63
15:O:36:ILE:HD11	15:O:60:VAL:HA	1.79	0.63
2:B:223:ILE:C	2:B:225:ALA:H	2.07	0.63
7:G:116:ALA:CA	7:G:119:ARG:HH21	2.10	0.63
15:O:87:ILE:HG22	15:O:88:ARG:N	2.12	0.63
1:A:369:C:O2'	1:A:370:C:H5'	1.98	0.63
1:A:1351:U:H4'	7:G:33:ASP:CG	2.22	0.63
1:A:1391:U:H2'	1:A:1392:G:C8	2.34	0.63
1:A:1421:G:H2'	1:A:1422:G:C8	2.32	0.63
6:F:56:PRO:HD2	6:F:57:GLN:HG2	1.81	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:193:C:H4'	20:T:61:SER:HB2	1.81	0.63
5:E:45:PHE:CD2	5:E:47:LYS:HE3	2.33	0.63
7:G:146:GLU:HA	7:G:149:ARG:HG2	1.81	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
11:K:53:SER:O	11:K:55:LYS:N	2.32	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
14:N:53:LEU:O	14:N:56:VAL:HB	1.97	0.63
1:A:986:A:H4'	19:S:55:LYS:HZ3	1.63	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
17:Q:67:LYS:O	17:Q:68:ARG:HB2	1.97	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
1:A:429:U:H1'	1:A:430:A:H5''	1.80	0.63
3:C:148:GLY:HA3	3:C:172:ARG:O	1.98	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
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
18:R:19:LYS:CD	18:R:20:ALA:H	2.07	0.62
18:R:38:GLU:H	18:R:38:GLU:CD	2.07	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1416:G:H22	1:A:1485:U:H1'	1.64	0.62
2:B:98:LEU:HB2	2:B:101:MET:HE3	1.81	0.62
2:B:134:GLU:C	2:B:136:VAL:H	2.07	0.62
17:Q:49:GLU:O	17:Q:52:LYS:HE2	1.99	0.62
7:G:71:PRO:HG3	7:G:103:TRP:HZ3	1.63	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
1:A:392:G:H2'	1:A:393:A:H8	1.62	0.62
6:F:10:LEU:HB3	6:F:85:VAL:HA	1.80	0.62
12:L:34:ARG:HG3	12:L:105:TYR:HE1	1.64	0.62
15:O:48:LYS:HA	15:O:48:LYS:HE2	1.81	0.62
5:E:10:MET:HE1	5:E:13:ILE:HD11	1.81	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
17:Q:68:ARG:H	17:Q:70:ARG:NH1	1.97	0.62
1:A:687:A:H4'	1:A:688:G:O5'	1.99	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:1303:C:C2'	1:A:1304:G:H5'	2.29	0.62
6:F:23:LYS:O	6:F:27:GLN:HG2	2.00	0.62
8:H:28:ALA:HA	8:H:59:LEU:HD12	1.81	0.62
14:N:59:ALA:HB1	14:N:61:TRP:CZ3	2.32	0.62
1:A:977:A:C8	1:A:1223:C:C4	2.88	0.62
1:A:1372:U:H5''	9:I:71:SER:HB3	1.82	0.62
2:B:146:GLN:O	2:B:150:SER:HB3	2.00	0.62
3:C:28:GLN:O	3:C:29:TYR:HB2	1.99	0.62
18:R:22:VAL:O	18:R:26:LEU:HD13	1.99	0.62
1:A:70:G:H2'	1:A:73:C:H5'	1.81	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
17:Q:63:ARG:HG2	17:Q:64:PRO:CD	2.30	0.62
2:B:187:LEU:HD22	2:B:205:ASP:HB3	1.81	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
15:O:45:VAL:HG22	15:O:46:HIS:N	2.14	0.62
1:A:345:C:OP2	1:A:345:C:H6	1.82	0.61
1:A:489:C:H2'	1:A:490:G:C8	2.35	0.61
1:A:1202:G:C4	14:N:42:ILE:HD12	2.35	0.61
1:A:264:U:H2'	1:A:265:G:H5'	1.81	0.61
1:A:424:G:H2'	1:A:425:G:H8	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1359:C:O2'	1:A:1361:G:N7	2.33	0.61
9:I:19:LEU:HD23	9:I:61:ALA:HB2	1.82	0.61
10:J:42:THR:HG23	10:J:67:THR:O	2.00	0.61
1:A:152:A:N6	1:A:170:U:C2	2.68	0.61
6:F:38:GLU:O	6:F:39:LYS:HB3	2.01	0.61
9:I:100:GLY:C	9:I:102:LEU:H	2.08	0.61
13:M:96:LEU:HB3	13:M:97:PRO:HD2	1.82	0.61
13:M:97:PRO:HB2	13:M:101:GLN:HG3	1.81	0.61
14:N:8:GLU:HG3	14:N:11:LYS:HD2	1.81	0.61
16:P:65:GLN:HA	16:P:65:GLN:NE2	2.14	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
5:E:9:LYS:HB2	5:E:112:LEU:HD11	1.82	0.61
16:P:74:LEU:O	16:P:79:VAL:HG23	1.99	0.61
20:T:13:LEU:C	20:T:13:LEU:HD12	2.26	0.61
1:A:504:C:C2	1:A:542:G:N2	2.69	0.61
1:A:1310:G:H5'	1:A:1311:G:OP2	2.01	0.61
2:B:110:GLN:HA	2:B:113:HIS:HD2	1.64	0.61
6:F:2:ARG:HH21	6:F:69:GLU:HG2	1.65	0.61
7:G:26:PHE:HA	7:G:101:LEU:HD13	1.82	0.61
9:I:112:LYS:HD3	9:I:112:LYS:C	2.26	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:HB2	18:R:54:ARG:NH2	2.16	0.61
1:A:113:G:H2'	1:A:114:U:H6	1.64	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:1474:G:H2'	1:A:1475:G:C8	2.35	0.61
4:D:153:ARG:HG3	4:D:181:MET:SD	2.40	0.61
11:K:126:ARG:O	11:K:127:LYS:HB2	2.00	0.61
12:L:27:LEU:C	12:L:29:GLY:H	2.08	0.61
19:S:11:VAL:HG21	19:S:41:VAL:HG13	1.83	0.61
1:A:1148:U:C4	1:A:1149:C:N3	2.69	0.61
3:C:137:ALA:O	3:C:141:VAL:HG23	2.00	0.61
18:R:34:TYR:CD1	18:R:35:ARG:HG3	2.35	0.61
1:A:142:G:N3	1:A:196:A:H2	1.98	0.61
5:E:72:GLN:O	5:E:73:ASN:HB3	2.00	0.61
12:L:27:LEU:C	12:L:29:GLY:N	2.58	0.61
12:L:39:VAL:HG12	12:L:40:VAL:H	1.65	0.61
1:A:721:G:N1	1:A:733:A:C2	2.69	0.61
1:A:1028:C:N4	1:A:1033:G:H22	1.98	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1054:C:O2	1:A:1054:C:H3'	2.00	0.61
5:E:19:MET:SD	5:E:24:ARG:HB3	2.40	0.61
1:A:633:G:H2'	1:A:634:C:C6	2.35	0.60
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
2:B:42:ILE:HG13	2:B:203:GLY:HA2	1.82	0.60
4:D:191:ARG:NH1	4:D:196:LEU:HB2	2.16	0.60
5:E:10:MET:HA	5:E:32:VAL:HG23	1.83	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
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: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:1152:A:H2'	1:A:1153:C:H6	1.66	0.60
2:B:22:LYS:C	2:B:24:TRP:H	2.10	0.60
2:B:103:THR:HG23	2:B:176:GLU:CD	2.26	0.60
7:G:27:ILE:HD12	7:G:40:ALA:HA	1.83	0.60
15:O:87:ILE:HG22	15:O:88:ARG:HD3	1.82	0.60
17:Q:7:THR:O	17:Q:23:VAL:HG13	2.01	0.60
1:A:106:C:H2'	1:A:107:G:H5'	1.83	0.60
1:A:1126:U:C6	1:A:1126:U:OP1	2.54	0.60
12:L:43:VAL:HG23	12:L:55:VAL:HG21	1.83	0.60
14:N:29:ARG:HG3	14:N:30:ALA:N	2.16	0.60
1:A:287:U:H2'	1:A:288:A:H5'	1.82	0.60
1:A:629:G:H2'	1:A:630:G:O4'	2.02	0.60
17:Q:36:ILE:H	17:Q:36:ILE:HD13	1.66	0.60
1:A:1273:G:H2'	1:A:1274:G:O4'	2.02	0.60
3:C:85:ARG:HA	3:C:88:ARG:HB3	1.83	0.60
4:D:151:LYS:H	4:D:151:LYS:HD2	1.67	0.60
10:J:90:LEU:N	10:J:91:PRO:HD3	2.17	0.60
20:T:100:ILE:HG12	20:T:102:GLY:H	1.65	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
1:A:192:U:H5'	20:T:102:GLY:O	2.01	0.60
1:A:390:C:H4'	16:P:28:ARG:NH1	2.17	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
1:A:1404:C:H1'	1:A:1499:A:C2	2.37	0.60
2:B:114:ARG:NH1	2:B:118:LEU:HD21	2.15	0.60
6:F:67:MET:HB2	6:F:68:PRO:HD2	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:26:GLU:OE1	15:O:77:ARG:HD2	2.02	0.60
16:P:31:LYS:HG2	16:P:32:TYR:H	1.67	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:41:G:H2'	1:A:42:G:H8	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
1:A:781:A:C5	1:A:802:A:C2	2.90	0.60
16:P:20:VAL:HG21	16:P:32:TYR:CG	2.37	0.60
1:A:1163:C:H2'	1:A:1164:G:C8	2.36	0.59
2:B:44:LEU:HD13	2:B:44:LEU:H	1.67	0.59
2:B:97:TRP:CE2	2:B:101:MET:HG3	2.37	0.59
3:C:6:HIS:CD2	3:C:8:ILE:HB	2.37	0.59
7:G:43:PHE:O	7:G:47:CYS:HB2	2.02	0.59
1:A:77:G:H2'	1:A:78:G:H8	1.67	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
20:T:100:ILE:HG12	20:T:102:GLY:N	2.16	0.59
1:A:41:G:H2'	1:A:42:G:C8	2.37	0.59
1:A:491:G:H2'	1:A:492:G:H8	1.67	0.59
1:A:946:A:H2'	1:A:947:G:H8	1.65	0.59
1:A:978:A:H8	1:A:978:A:OP1	1.85	0.59
1:A:1118:C:H1'	1:A:1179:A:C4	2.37	0.59
1:A:1178:G:N2	1:A:1180:A:H3'	2.17	0.59
1:A:1436:U:C5	1:A:1437:C:C4	2.90	0.59
12:L:41:ARG:NH1	12:L:42:THR:H	1.99	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:721:G:C6	1:A:733:A:C2	2.91	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
17:Q:29:HIS:HB2	17:Q:36:ILE:HD12	1.83	0.59
1:A:243:A:C2	1:A:246:A:C8	2.91	0.59
1:A:1269:A:H5'	1:A:1270:C:OP2	2.02	0.59
1:A:1474:G:H2'	1:A:1475:G:H8	1.67	0.59
2:B:172:ILE:H	2:B:172:ILE:HD12	1.66	0.59
3:C:91:LEU:HD21	3:C:99:VAL:H	1.68	0.59
6:F:62:TRP:CH2	6:F:64:GLN:HB2	2.37	0.59
12:L:55:VAL:HG12	12:L:56:ALA:N	2.11	0.59
19:S:31:ILE:HB	19:S:49:ILE:HD13	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:A:291:C:O2'	1:A:292:G:H5'	2.03	0.59
7:G:51:GLN:HA	7:G:54:THR:O	2.03	0.59
18:R:40:LEU:HD23	18:R:40:LEU:N	2.18	0.59
1:A:559:A:H4'	1:A:560:U:C3'	2.24	0.59
1:A:750:G:H21	15:O:23:GLY:HA3	1.67	0.59
1:A:1020:U:H2'	1:A:1021:G:C8	2.37	0.59
3:C:23:TYR:CG	3:C:24:ALA:N	2.71	0.59
5:E:110:LEU:HD13	5:E:118:ILE:HD13	1.83	0.59
11:K:72:ALA:HB1	11:K:77:MET:HE2	1.85	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
1:A:35:G:H2'	1:A:36:C:C6	2.38	0.59
1:A:1351:U:H4'	7:G:33:ASP:OD2	2.03	0.59
2:B:87:ARG:O	2:B:88:ALA:HB3	2.02	0.59
2:B:101:MET:HA	2:B:108:ILE:HG21	1.84	0.59
1:A:273:A:C2'	1:A:274:A:H5'	2.33	0.59
1:A:500:G:C5	1:A:546:G:N2	2.71	0.59
2:B:230:VAL:HG12	2:B:231:GLU:N	2.17	0.59
5:E:71:LEU:HD11	5:E:113:ALA:O	2.03	0.59
10:J:6:ILE:HG23	10:J:98:ILE:HG12	1.85	0.59
19:S:41:VAL:HB	19:S:42:PRO:HD2	1.84	0.59
2:B:74:LYS:HZ1	2:B:206:ASP:HA	1.68	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
7:G:18:TYR:OH	7:G:58:PRO:HB2	2.03	0.58
19:S:44:MET:HE1	19:S:71:LEU:HD21	1.83	0.58
1:A:627:G:O2'	1:A:628:G:H5'	2.03	0.58
11:K:32:ILE:HG21	11:K:77:MET:HE1	1.85	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
1:A:401:C:H2'	1:A:402:G:H8	1.68	0.58
6:F:4:TYR:CE1	6:F:92:LYS:HG2	2.38	0.58
12:L:54:LYS:N	12:L:54:LYS:HD2	2.19	0.58
1:A:336:C:H2'	1:A:337:C:H6	1.69	0.58
8:H:6:ILE:HD12	8:H:6:ILE:N	2.19	0.58
13:M:5:ALA:HA	13:M:61:GLU:HG2	1.84	0.58
14:N:41:ARG:HG3	14:N:42:ILE:N	2.19	0.58
15:O:18:PHE:HB2	15:O:19:PRO:HD2	1.83	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:688:G:C4	1:A:700:G:N2	2.71	0.58
3:C:22:TRP:CB	3:C:59:ARG:HB2	2.33	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
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
1:A:201:C:H42	1:A:216:G:H1	1.52	0.58
1:A:344:A:H4'	1:A:345:C:OP2	2.03	0.58
1:A:1024:G:H2'	1:A:1025:U:C6	2.39	0.58
12:L:124:LYS:HD2	12:L:125:PRO:HD2	1.86	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
7:G:111:ARG:HB3	7:G:113:GLU:HG2	1.86	0.58
1:A:96:G:C6	1:A:97:G:C2	2.92	0.58
1:A:908:A:C2	1:A:909:A:C4	2.92	0.58
1:A:1316:G:N2	1:A:1319:A:OP2	2.34	0.58
1:A:1399:C:O2	1:A:1401:G:C5	2.57	0.58
9:I:48:GLU:N	9:I:49:PRO:HD2	2.18	0.58
11:K:84:VAL:HG11	11:K:91:ARG:HD3	1.86	0.58
1:A:17:U:H2'	1:A:18:C:C6	2.38	0.57
1:A:88:A:C5	1:A:89:C:C5	2.92	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
1:A:951:G:HO2'	1:A:972:C:H5	1.52	0.57
3:C:73:PRO:HG3	3:C:105:GLU:CD	2.28	0.57
5:E:101:ILE:HG22	5:E:101:ILE:O	2.04	0.57
11:K:15:ALA:CA	11:K:77:MET:HA	2.24	0.57
1:A:61:G:H2'	1:A:62:U:O4'	2.04	0.57
1:A:1205:U:H4'	3:C:195:VAL:HG11	1.86	0.57
1:A:1430:C:H2'	1:A:1431:C:H6	1.68	0.57
4:D:199:ASN:HD22	4:D:199:ASN:C	2.12	0.57
7:G:65:ALA:HB2	7:G:128:ALA:HB2	1.85	0.57
15:O:33:THR:HG23	15:O:63:ARG:NH1	2.19	0.57
1:A:1130:A:H5''	9:I:20:ARG:HH22	1.68	0.57
9:I:48:GLU:CG	9:I:51:ARG:HH21	2.14	0.57
11:K:91:ARG:CZ	18:R:88:LYS:HZ1	2.17	0.57
1:A:1047:G:O2'	1:A:1048:G:H5'	2.04	0.57
1:A:1072:G:C5	1:A:1073:U:C4	2.92	0.57
1:A:1311:G:N7	19:S:2:PRO:HA	2.20	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1531:A:O5'	1:A:1531:A:H8	1.87	0.57
12:L:28:LYS:C	12:L:30:ALA:H	2.13	0.57
1:A:775:G:C2'	1:A:776:G:H5'	2.35	0.57
1:A:1157:A:H4'	1:A:1158:C:O5'	2.04	0.57
1:A:1298:C:H2'	7:G:114:ARG:NH1	2.18	0.57
2:B:24:TRP:HZ3	2:B:29:ALA:HB2	1.68	0.57
3:C:64:VAL:CG2	3:C:99:VAL:HG11	2.32	0.57
4:D:88:VAL:O	4:D:92:VAL:HG23	2.04	0.57
7:G:79:ARG:HG3	7:G:82:GLY:O	2.04	0.57
12:L:34:ARG:HG3	12:L:105:TYR:CE1	2.39	0.57
13:M:5:ALA:O	13:M:6:GLY:C	2.47	0.57
14:N:14:PRO:O	14:N:15:LYS:HB2	2.03	0.57
20:T:54:LYS:HA	20:T:57:ARG:NH1	2.19	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
1:A:184:G:H2'	1:A:185:A:H8	1.68	0.57
1:A:532:A:H3'	1:A:533:A:C5'	2.35	0.57
1:A:1047:G:H8	1:A:1047:G:O5'	1.87	0.57
5:E:72:GLN:NE2	5:E:144:THR:HG23	2.20	0.57
9:I:5:TYR:CD2	9:I:6:GLY:N	2.70	0.57
13:M:75:ALA:HA	13:M:78:ILE:HD12	1.86	0.57
17:Q:5:VAL:O	17:Q:6:LEU:HD23	2.03	0.57
1:A:357:G:C2	1:A:358:U:C5	2.93	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
1:A:1200:C:H2'	1:A:1200:C:O2	2.04	0.57
6:F:10:LEU:HD12	6:F:59:TYR:HB3	1.86	0.57
1:A:376:G:H5''	16:P:5:ARG:HB2	1.87	0.57
1:A:1504:G:H4'	1:A:1505:G:C5'	2.33	0.57
2:B:97:TRP:HZ2	2:B:102:LEU:HD13	1.69	0.57
2:B:204:ASN:HD22	2:B:204:ASN:C	2.11	0.57
4:D:24:GLU:O	4:D:25:ARG:HB3	2.04	0.57
4:D:173:TRP:CD2	4:D:189:PRO:HG3	2.40	0.57
20:T:64:ASP:O	20:T:67:ALA:HB3	2.04	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:695:A:H2'	1:A:696:A:C8	2.40	0.57
1:A:965:A:O2'	1:A:966:G:OP2	2.18	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
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
1:A:559:A:H1'	1:A:560:U:OP2	2.04	0.56
2:B:231:GLU:HB3	2:B:232:PRO:CD	2.33	0.56
1:A:110:C:H2'	1:A:111:G:O4'	2.05	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:379:C:C2'	1:A:380:G:H5'	2.35	0.56
1:A:835:U:OP1	18:R:64:ARG:NH2	2.38	0.56
1:A:1505:G:O2'	1:A:1506:U:OP2	2.22	0.56
11:K:59:TYR:CE2	11:K:63:LEU:HD11	2.40	0.56
1:A:463:A:C4	1:A:474:G:C8	2.93	0.56
1:A:645:C:H2'	1:A:645:C:O2	2.04	0.56
1:A:1190:G:OP1	3:C:4:LYS:HA	2.05	0.56
1:A:1240:U:OP1	7:G:119:ARG:NH2	2.32	0.56
1:A:1437:C:H2'	1:A:1438:G:H8	1.70	0.56
4:D:52:SER:O	4:D:56:VAL:HG23	2.06	0.56
7:G:14:PRO:HA	7:G:21:VAL:HG12	1.87	0.56
12:L:126:LYS:H	12:L:126:LYS:HD2	1.69	0.56
14:N:24:CYS:HB2	14:N:33:VAL:HG12	1.87	0.56
15:O:39:LEU:CD1	15:O:56:LEU:HB2	2.36	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
3:C:22:TRP:CD1	3:C:59:ARG:HD2	2.41	0.56
4:D:79:PHE:C	4:D:79:PHE:CD2	2.83	0.56
9:I:47:LEU:C	9:I:49:PRO:HD2	2.31	0.56
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
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
19:S:11:VAL:HG13	19:S:38:SER:HB2	1.87	0.56
1:A:184:G:H2'	1:A:185:A:C8	2.40	0.56
1:A:279:A:H5''	1:A:281:G:O4'	2.06	0.56
1:A:1285:A:H1'	1:A:1286:A:OP2	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
11:K:97:ALA:O	11:K:101:SER:HB3	2.04	0.56
1:A:278:G:C6	17:Q:95:TYR:HD2	2.24	0.56
2:B:9:GLU:HA	2:B:48:MET:SD	2.45	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:10:PHE:HE2	3:C:178:LEU:CD1	2.18	0.56
3:C:190:ARG:HG3	3:C:195:VAL:HG12	1.87	0.56
8:H:6:ILE:HB	8:H:85:ARG:NH1	2.20	0.56
12:L:41:ARG:HB3	12:L:41:ARG:HH11	1.71	0.56
14:N:25:VAL:HG13	14:N:26:ARG:H	1.68	0.56
15:O:7:GLU:HA	15:O:10:LYS:HE2	1.86	0.56
17:Q:74:LEU:HD23	17:Q:74:LEU:C	2.30	0.56
1:A:419:C:N4	1:A:424:G:H1	2.04	0.56
1:A:1180:A:H5''	1:A:1181:G:OP2	2.06	0.56
10:J:59:SER:O	10:J:60:ARG:HB2	2.05	0.56
1:A:435:C:H2'	1:A:436:C:C6	2.41	0.56
1:A:803:G:H8	1:A:803:G:O5'	1.89	0.56
1:A:1502:A:H2	1:A:1505:G:H1	1.54	0.56
3:C:180:ALA:HB1	3:C:182:ILE:HD11	1.86	0.56
4:D:19:LEU:HD22	4:D:67:ILE:HG12	1.87	0.56
7:G:22:LEU:CD1	7:G:97:GLN:HE21	2.17	0.56
1:A:562:C:H1'	12:L:15:ARG:HB3	1.87	0.56
1:A:1053:G:O2'	1:A:1199:U:H5	1.89	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
1:A:1434:A:N6	1:A:1435:G:C2	2.73	0.56
11:K:43:SER:O	11:K:44:SER:HB3	2.05	0.56
17:Q:67:LYS:O	17:Q:68:ARG:CB	2.53	0.56
1:A:330:C:C2'	1:A:331:G:H5'	2.35	0.55
1:A:922:G:N2	1:A:1396:A:C5	2.74	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:103:C:O2'	1:A:172:A:N1	2.35	0.55
1:A:229:U:H5''	16:P:33:ILE:HD13	1.88	0.55
1:A:421:U:H5'	1:A:422:C:C5	2.41	0.55
1:A:432:A:O2'	1:A:433:C:C6	2.48	0.55
1:A:986:A:H4'	19:S:55:LYS:NZ	2.21	0.55
7:G:15:ASP:O	7:G:19:GLY:HA2	2.07	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
19:S:80:TYR:CE2	19:S:81:ARG:HB2	2.41	0.55
1:A:130:A:OP2	1:A:190(E):U:O2'	2.17	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
1:A:1352:C:H2'	1:A:1353:G:C8	2.41	0.55
1:A:1477:C:H2'	1:A:1478:C:C6	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:19:LEU:HD23	6:F:23:LYS:HG3	1.87	0.55
6:F:91:VAL:HG11	18:R:72:ARG:NH1	2.21	0.55
17:Q:55:ASP:O	17:Q:57:VAL:HG13	2.07	0.55
19:S:11:VAL:HG22	19:S:39:THR:HB	1.86	0.55
1:A:101:A:O2'	1:A:102:G:H5'	2.06	0.55
1:A:386:C:C2'	1:A:387:U:H5'	2.36	0.55
1:A:475:G:H2'	1:A:476:G:C8	2.42	0.55
1:A:1085:U:C6	1:A:1094:G:N1	2.75	0.55
1:A:1189:C:H5''	1:A:1190:G:OP2	2.07	0.55
1:A:1522:U:O2'	1:A:1523:G:H5'	2.06	0.55
3:C:108:ASN:HD22	3:C:111:LEU:H	1.53	0.55
4:D:13:ARG:HD2	4:D:36:ARG:O	2.07	0.55
18:R:39:VAL:HG13	18:R:40:LEU:CD2	2.32	0.55
1:A:705:U:C5	1:A:706:A:N7	2.75	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
4:D:112:VAL:H	4:D:116:GLN:NE2	2.04	0.55
8:H:96:GLY:H	8:H:99:GLU:CG	2.20	0.55
13:M:91:ARG:NH1	13:M:96:LEU:HB2	2.22	0.55
1:A:193:C:O2	1:A:194:C:C6	2.60	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
2:B:240:GLN:HE21	2:B:240:GLN:HA	1.71	0.55
3:C:88:ARG:O	3:C:91:LEU:HB3	2.06	0.55
9:I:36:TYR:CE2	9:I:37:PHE:CE2	2.95	0.55
10:J:4:ILE:HG12	10:J:74:ILE:HB	1.88	0.55
20:T:49:ALA:HB3	20:T:99:LEU:HD12	1.89	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
1:A:1315:U:O2	1:A:1360:A:H2	1.90	0.55
1:A:1487:G:C4	1:A:1488:G:H8	2.25	0.55
2:B:118:LEU:HB2	2:B:142:LEU:HD12	1.88	0.55
8:H:116:LYS:HE2	8:H:127:LEU:HD13	1.88	0.55
18:R:25:THR:C	18:R:26:LEU:HD12	2.31	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:77:ILE:C	3:C:83:ARG:HB3	2.32	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
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
9:I:78:LYS:HD3	9:I:101:PHE:CD2	2.40	0.55
18:R:58:LEU:HD22	18:R:62:GLU:HB3	1.88	0.55
1:A:344:A:H5'	1:A:345:C:C5	2.42	0.55
1:A:421:U:H5'	1:A:422:C:H5	1.72	0.55
4:D:20:TYR:CD2	4:D:27:TYR:HE1	2.25	0.55
5:E:11:ILE:HD11	5:E:33:VAL:HG23	1.89	0.55
5:E:84:PHE:HB3	5:E:134:ALA:HB2	1.89	0.55
10:J:49:VAL:O	10:J:60:ARG:HA	2.07	0.55
12:L:27:LEU:O	12:L:29:GLY:N	2.40	0.55
21:U:22:ARG:O	21:U:22:ARG:HD3	2.07	0.55
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
5:E:5:ASP:CG	5:E:6:PHE:H	2.15	0.54
10:J:10:GLY:N	10:J:16:LEU:HD11	2.22	0.54
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
1:A:532:A:O2'	1:A:533:A:OP1	2.21	0.54
1:A:1065:U:C1'	1:A:1066:C:OP2	2.55	0.54
4:D:188:LEU:H	4:D:188:LEU:CD1	2.16	0.54
5:E:28:PHE:CD2	5:E:51:VAL:HG22	2.43	0.54
9:I:5:TYR:CD2	9:I:5:TYR:C	2.85	0.54
12:L:5:PRO:HG2	12:L:15:ARG:HH22	1.69	0.54
13:M:12:ASN:H	13:M:45:VAL:HG11	1.72	0.54
1:A:9:G:C2	1:A:26:A:C2	2.95	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
1:A:1357:A:H2'	1:A:1358:U:C6	2.42	0.54
3:C:24:ALA:HB1	3:C:28:GLN:O	2.06	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:499:A:H4'	1:A:500:G:OP1	2.06	0.54
1:A:1158:C:H5'	2:B:133:LYS:HE2	1.88	0.54
1:A:1337:G:H5''	1:A:1338:G:OP1	2.07	0.54
1:A:1492:A:H2'	1:A:1493:A:O4'	2.06	0.54
2:B:230:VAL:HG12	2:B:231:GLU:H	1.70	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:57:LYS:O	5:E:61:TYR:CD2	2.59	0.54
6:F:69:GLU:H	6:F:69:GLU:CD	2.15	0.54
6:F:96:PRO:HB2	6:F:98:LEU:HD21	1.89	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:80:G:N2	1:A:81:U:C4	2.75	0.54
1:A:1174:G:C2	1:A:1175:G:C5	2.96	0.54
1:A:1236:A:H4'	1:A:1304:G:H4'	1.90	0.54
1:A:1487:G:H2'	1:A:1488:G:H5'	1.88	0.54
7:G:24:THR:HA	7:G:27:ILE:HB	1.89	0.54
7:G:111:ARG:CZ	7:G:122:HIS:HB3	2.38	0.54
8:H:112:LEU:HD23	8:H:112:LEU:H	1.72	0.54
12:L:28:LYS:O	12:L:30:ALA:N	2.40	0.54
1:A:22:G:H2'	1:A:23:C:H6	1.72	0.54
1:A:103:C:OP1	20:T:17:ARG:NH1	2.35	0.54
1:A:170:U:O2'	1:A:171:A:H5'	2.07	0.54
1:A:380:G:N2	1:A:382:A:H5''	2.23	0.54
1:A:688:G:H5'	11:K:46:GLY:C	2.32	0.54
2:B:103:THR:CG2	2:B:176:GLU:HG3	2.36	0.54
7:G:127:ALA:C	7:G:129:GLU:H	2.15	0.54
18:R:53:ARG:C	18:R:55:ARG:H	2.16	0.54
1:A:80:G:N2	1:A:81:U:N3	2.56	0.54
1:A:436:C:H2'	1:A:437:U:C6	2.40	0.54
1:A:1203:C:O5'	1:A:1203:C:H6	1.90	0.54
1:A:1298:C:H2'	7:G:114:ARG:HH12	1.72	0.54
4:D:31:CYS:C	4:D:33:MET:H	2.16	0.54
6:F:11:ASN:HB2	6:F:86:ARG:NH2	2.23	0.54
7:G:43:PHE:HD2	7:G:44:TYR:CE2	2.25	0.54
10:J:51:ARG:CZ	10:J:61:GLU:HB2	2.38	0.54
11:K:16:SER:HA	11:K:79:SER:O	2.07	0.54
1:A:1391:U:H2'	1:A:1392:G:H8	1.73	0.54
4:D:127:THR:OG1	4:D:147:ALA:HB3	2.07	0.54
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
16:P:4:ILE:HG12	16:P:21:VAL:HG22	1.89	0.54
1:A:620:C:H2'	1:A:621:A:O4'	2.08	0.54
1:A:1289:A:H2'	1:A:1290:G:H5'	1.90	0.54
6:F:62:TRP:C	6:F:63:TYR:CD2	2.85	0.54
7:G:49:ILE:HG22	7:G:49:ILE:O	2.07	0.54
19:S:34:TRP:CD1	19:S:52:TYR:HB2	2.43	0.54
1:A:1311:G:O6	19:S:2:PRO:HB3	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1373:G:H5''	7:G:36:LYS:HZ2	1.73	0.53
2:B:158:LEU:HD23	2:B:159:PRO:CD	2.32	0.53
6:F:68:PRO:HB2	6:F:70:ASP:OD1	2.08	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
19:S:56:GLN:HG2	19:S:57:HIS:N	2.23	0.53
1:A:1130:A:H5''	9:I:20:ARG:NH2	2.24	0.53
1:A:1392:G:H21	1:A:1502:A:H8	1.57	0.53
5:E:89:ILE:CD1	5:E:90:VAL:H	2.21	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:49:VAL:CG2	14:N:41:ARG:HB2	2.27	0.53
10:J:82:ILE:HG23	10:J:85:LEU:HB2	1.90	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:381:C:H2'	1:A:382:A:O4'	2.08	0.53
1:A:765:G:H5''	1:A:766:A:OP1	2.08	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
12:L:28:LYS:HD3	12:L:33:ARG:HH22	1.72	0.53
1:A:370:C:H2'	1:A:371:G:H5'	1.90	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
2:B:139:LYS:O	2:B:139:LYS:HD3	2.09	0.53
3:C:6:HIS:HD2	3:C:8:ILE:HB	1.72	0.53
6:F:4:TYR:HE1	6:F:92:LYS:HG2	1.73	0.53
7:G:17:VAL:HG12	7:G:18:TYR:N	2.23	0.53
16:P:76:GLN:C	16:P:78:GLY:H	2.15	0.53
17:Q:25:ARG:HG3	17:Q:25:ARG:O	2.09	0.53
20:T:85:MET:HE2	20:T:104:LEU:HD23	1.90	0.53
1:A:75:G:N2	1:A:76:C:C4	2.76	0.53
1:A:429:U:H4'	1:A:430:A:O5'	2.08	0.53
1:A:1244:C:OP2	21:U:9:ARG:HB2	2.08	0.53
7:G:50:ILE:HG21	7:G:61:VAL:HG21	1.90	0.53
11:K:79:SER:HB3	11:K:104:GLN:HB3	1.89	0.53
1:A:1330:U:H2'	1:A:1331:G:H5'	1.90	0.53
1:A:1378:C:H5''	1:A:1379:G:OP2	2.08	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:1128:C:H42	1:A:1143:G:N2	2.01	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1301:U:O2'	1:A:1302:U:H3'	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:113:G:H1	1:A:314:C:H42	1.57	0.53
13:M:95:GLY:O	13:M:96:LEU:HD23	2.09	0.53
16:P:6:LEU:HD23	16:P:17:TYR:CG	2.44	0.53
16:P:21:VAL:HG21	16:P:59:TRP:CD1	2.44	0.53
1:A:659:U:OP1	15:O:8:LYS:HD3	2.07	0.53
1:A:1414:U:H2'	1:A:1415:G:C8	2.44	0.53
11:K:12:ARG:CG	11:K:13:GLN:H	2.22	0.53
18:R:36:ASN:O	18:R:39:VAL:HG12	2.09	0.53
1:A:558:G:OP2	1:A:559:A:O2'	2.27	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
1:A:901:A:H5''	1:A:902:G:OP2	2.09	0.52
1:A:977:A:H2'	1:A:978:A:C5'	2.37	0.52
4:D:65:ARG:HG3	4:D:75:PHE:CG	2.43	0.52
5:E:12:LEU:O	5:E:12:LEU:HD22	2.10	0.52
6:F:15:ASP:CG	6:F:16:GLN:N	2.68	0.52
1:A:376:G:N3	1:A:389:A:C2	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
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
1:A:1516:G:N2	1:A:1520:G:C4	2.77	0.52
2:B:28:PHE:CE2	2:B:190:THR:HA	2.45	0.52
2:B:54:THR:HG21	2:B:201:ILE:HD11	1.91	0.52
10:J:16:LEU:HD21	10:J:94:VAL:HG13	1.91	0.52
10:J:38:ILE:HB	10:J:71:LEU:HD12	1.92	0.52
1:A:97:G:C5	1:A:98:U:O4	2.62	0.52
1:A:424:G:H2'	1:A:425:G:C8	2.45	0.52
1:A:457:C:H2'	1:A:458:C:C6	2.40	0.52
1:A:1416:G:O6	1:A:1417:G:N2	2.42	0.52
15:O:17:ARG:NH1	15:O:17:ARG:CG	2.63	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
9:I:108:VAL:HG12	9:I:109:VAL:N	2.24	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
1:A:781:A:C4	1:A:802:A:C2	2.97	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1276:G:O2'	1:A:1277:C:H5'	2.10	0.52
2:B:24:TRP:CH2	2:B:26:PRO:HA	2.44	0.52
2:B:134:GLU:C	2:B:136:VAL:N	2.68	0.52
5:E:11:ILE:CG2	5:E:105:VAL:HG13	2.38	0.52
11:K:16:SER:HB2	11:K:106:LYS:NZ	2.24	0.52
11:K:32:ILE:CG2	11:K:77:MET:HE1	2.39	0.52
13:M:49:THR:HG22	13:M:50:GLU:H	1.75	0.52
18:R:66:LEU:HD23	18:R:66:LEU:C	2.35	0.52
1:A:89:C:O2	1:A:89:C:C2'	2.53	0.52
1:A:232:G:H1'	1:A:262:A:N1	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:1112:C:N3	3:C:178:LEU:HB2	2.25	0.52
1:A:1279:A:H5''	1:A:1280:A:OP1	2.09	0.52
1:A:1283:G:O2'	1:A:1284:C:H5'	2.08	0.52
11:K:124:LYS:C	11:K:125:PHE:HD1	2.18	0.52
16:P:67:THR:HG22	16:P:69:THR:N	2.22	0.52
17:Q:26:GLN:O	17:Q:27:PHE:HB3	2.08	0.52
20:T:74:LYS:HB3	20:T:74:LYS:NZ	2.24	0.52
1:A:7:G:H5''	1:A:298:A:O4'	2.10	0.52
1:A:509:A:O2'	1:A:510:A:C8	2.63	0.52
11:K:15:ALA:C	11:K:77:MET:HG3	2.35	0.52
12:L:86:ARG:O	12:L:98:TYR:HB3	2.09	0.52
18:R:59:SER:O	18:R:60:GLY:C	2.53	0.52
1:A:390:C:H4'	16:P:28:ARG:HH12	1.75	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
1:A:949:A:C2	1:A:1233:G:N3	2.78	0.52
1:A:994:A:H2'	1:A:994:A:N3	2.24	0.52
1:A:1359:C:OP2	14:N:22:THR:HG21	2.10	0.52
2:B:73:THR:O	2:B:74:LYS:C	2.51	0.52
4:D:111:ALA:HB1	4:D:116:GLN:HG2	1.91	0.52
4:D:199:ASN:HD21	4:D:201:GLN:HB2	1.74	0.52
4:D:208:SER:HB3	5:E:101:ILE:HG12	1.91	0.52
7:G:51:GLN:HB2	7:G:52:GLU:OE2	2.10	0.52
19:S:56:GLN:HG2	19:S:57:HIS:H	1.74	0.52
1:A:99:C:H2'	1:A:101:A:O4'	2.09	0.52
1:A:996:A:C6	1:A:1046:A:H1'	2.44	0.52
1:A:1326:C:OP2	21:U:6:ARG:NE	2.36	0.52
1:A:1488:G:H2'	1:A:1488:G:N3	2.25	0.52
1:A:1518:A:C2'	1:A:1519:A:H5'	2.39	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:219:VAL:O	2:B:222:ILE:HB	2.10	0.52
4:D:121:VAL:O	4:D:134:ASP:HA	2.09	0.52
5:E:33:VAL:HG12	5:E:34:VAL:N	2.25	0.52
7:G:137:LYS:O	7:G:141:VAL:N	2.43	0.52
8:H:96:GLY:H	8:H:99:GLU:HG3	1.74	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
14:N:14:PRO:O	14:N:15:LYS:CB	2.58	0.52
16:P:21:VAL:O	16:P:33:ILE:HB	2.10	0.52
17:Q:29:HIS:CG	17:Q:30:PRO:HD2	2.45	0.52
18:R:34:TYR:CE1	18:R:35:ARG:HG3	2.45	0.52
1:A:164:U:H2'	1:A:165:C:C6	2.44	0.52
1:A:503:C:H2'	1:A:504:C:C6	2.45	0.52
1:A:858:G:O2'	1:A:859:A:H5'	2.10	0.52
1:A:976:G:N2	1:A:1363:A:C4	2.78	0.52
1:A:1154:G:H2'	1:A:1155:G:H8	1.74	0.52
1:A:1241:G:H2'	1:A:1242:C:C6	2.45	0.52
1:A:1392:G:O2'	1:A:1393:U:H5'	2.10	0.52
2:B:107:THR:C	2:B:109:SER:N	2.66	0.52
7:G:153:HIS:HA	7:G:155:ARG:CZ	2.40	0.52
9:I:114:TYR:CD2	10:J:60:ARG:HB2	2.45	0.52
18:R:43:PHE:CG	18:R:66:LEU:HD11	2.45	0.52
1:A:78:G:H1	1:A:91:C:N4	2.09	0.51
1:A:263:A:OP2	20:T:79:ARG:NH1	2.43	0.51
1:A:328:C:C1'	1:A:329:A:OP2	2.58	0.51
2:B:97:TRP:HH2	2:B:176:GLU:OE2	1.92	0.51
2:B:205:ASP:C	2:B:205:ASP:OD1	2.52	0.51
4:D:177:ASP:OD1	4:D:177:ASP:C	2.52	0.51
4:D:199:ASN:ND2	4:D:201:GLN:HB2	2.25	0.51
10:J:40:LEU:HD22	10:J:69:ASN:HD22	1.74	0.51
13:M:8:GLU:OE1	13:M:22:ILE:HG23	2.10	0.51
14:N:24:CYS:SG	14:N:27:CYS:HB2	2.50	0.51
19:S:80:TYR:O	19:S:81:ARG:C	2.53	0.51
21:U:10:ARG:HG3	21:U:13:ILE:HD12	1.92	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
1:A:79:G:N2	1:A:91:C:C2	2.79	0.51
1:A:595:G:C6	1:A:641:U:C5	2.98	0.51
1:A:1028:C:H2'	1:A:1029:C:O4'	2.10	0.51
1:A:1345:U:C2	1:A:1377:A:C2	2.98	0.51
2:B:143:GLU:HA	2:B:146:GLN:HE21	1.74	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:40:ARG:HG2	5:E:40:ARG:HH11	1.75	0.51
6:F:97:PHE:O	6:F:98:LEU:HD23	2.11	0.51
12:L:41:ARG:HH11	12:L:42:THR:H	1.59	0.51
12:L:126:LYS:C	12:L:127:GLU:HG3	2.35	0.51
14:N:24:CYS:SG	14:N:43:CYS:SG	3.08	0.51
19:S:30:LEU:HD23	19:S:31:ILE:N	2.25	0.51
20:T:56:MET:HE1	20:T:104:LEU:HD21	1.91	0.51
1:A:73:C:C2	1:A:97:G:N2	2.79	0.51
1:A:230:G:H2'	1:A:231:G:O4'	2.11	0.51
1:A:558:G:C8	1:A:559:A:H2'	2.46	0.51
1:A:673:G:H2'	1:A:674:G:C8	2.46	0.51
6:F:48:LEU:HG	6:F:57:GLN:HA	1.92	0.51
7:G:113:GLU:HB2	7:G:119:ARG:HG3	1.92	0.51
13:M:12:ASN:N	13:M:45:VAL:HG11	2.25	0.51
19:S:42:PRO:O	19:S:45:VAL:HG23	2.11	0.51
19:S:64:GLU:C	19:S:66:MET:H	2.18	0.51
1:A:279:A:OP2	17:Q:95:TYR:OH	2.19	0.51
1:A:430:A:H2'	1:A:431:A:O4'	2.10	0.51
1:A:1133:G:C2	1:A:1142:G:C2	2.98	0.51
1:A:1264:C:H2'	1:A:1265:G:H8	1.75	0.51
1:A:1533:C:H3'	1:A:1533:C:H6	1.74	0.51
7:G:21:VAL:C	7:G:23:VAL:H	2.18	0.51
8:H:4:ASP:OD2	8:H:85:ARG:NH1	2.43	0.51
19:S:17:GLU:HA	19:S:20:LEU:CG	2.41	0.51
1:A:97:G:C5	1:A:98:U:C4	2.99	0.51
1:A:119:A:C8	1:A:288:A:C2	2.98	0.51
1:A:391:G:C6	1:A:392:G:C5	2.99	0.51
1:A:544:G:C5	1:A:545:C:C5	2.99	0.51
1:A:853:G:C2'	1:A:854:G:H5'	2.40	0.51
1:A:1261:A:N7	1:A:1262:C:C5	2.79	0.51
5:E:66:MET:HE3	5:E:67:VAL:H	1.75	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
20:T:56:MET:CE	20:T:88:VAL:HG11	2.40	0.51
1:A:419:C:H42	1:A:424:G:H1	1.58	0.51
1:A:1158:C:H3'	1:A:1158:C:O2	2.11	0.51
1:A:1488:G:C2	1:A:1489:G:C5	2.99	0.51
4:D:25:ARG:C	4:D:27:TYR:N	2.67	0.51
4:D:190:ASP:O	4:D:191:ARG:C	2.53	0.51
5:E:79:GLU:O	8:H:104:ARG:CZ	2.59	0.51
10:J:57:LYS:HD2	10:J:60:ARG:HH21	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:430:A:C2'	1:A:431:A:H5'	2.39	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
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
17:Q:4:LYS:HD3	17:Q:6:LEU:HD21	1.93	0.51
1:A:255:G:C2	1:A:272:C:C2	2.99	0.51
1:A:513:C:H42	1:A:538:G:H1	1.59	0.51
1:A:750:G:C2	15:O:23:GLY:HA3	2.45	0.51
1:A:1011:G:N2	1:A:1019:C:H1'	2.25	0.51
1:A:1048:G:H2'	1:A:1050:G:N7	2.26	0.51
1:A:1392:G:N2	1:A:1502:A:H8	2.08	0.51
2:B:178:ARG:HH12	8:H:68:ARG:HH22	1.59	0.51
10:J:4:ILE:HG13	10:J:4:ILE:O	2.09	0.51
10:J:75:ILE:O	10:J:76:ASN:HB2	2.10	0.51
12:L:20:LYS:H	12:L:20:LYS:CD	2.22	0.51
15:O:76:GLU:HA	15:O:76:GLU:OE1	2.11	0.51
20:T:13:LEU:O	20:T:16:HIS:N	2.33	0.51
1:A:380:G:C2	1:A:382:A:H5''	2.45	0.51
1:A:475:G:H2'	1:A:476:G:H8	1.76	0.51
1:A:1158:C:N4	1:A:1160:G:C5	2.79	0.51
1:A:1198:G:H2'	1:A:1199:U:C6	2.46	0.51
1:A:1329:A:H5'	13:M:29:ARG:HD2	1.93	0.51
1:A:1349:A:C2	1:A:1374:A:C4	2.98	0.51
1:A:1443:G:N3	1:A:1443:G:H2'	2.26	0.51
2:B:101:MET:C	2:B:102:LEU:HD12	2.36	0.51
3:C:130:VAL:HG11	3:C:157:ILE:HG23	1.93	0.51
8:H:137:VAL:O	8:H:138:TRP:HB3	2.11	0.51
17:Q:83:ASP:O	17:Q:86:GLU:HB2	2.11	0.51
20:T:48:LYS:O	20:T:50:GLU:N	2.44	0.51
1:A:393:A:C2	1:A:394:G:C8	2.99	0.51
1:A:1178:G:H21	1:A:1180:A:H3'	1.76	0.51
4:D:107:ARG:HB3	4:D:174:LEU:HD11	1.93	0.51
7:G:3:ARG:O	7:G:4:ARG:CB	2.59	0.51
9:I:111:ARG:NH1	9:I:113:LYS:HA	2.25	0.51
12:L:28:LYS:C	12:L:30:ALA:N	2.64	0.51
19:S:36:ARG:HH21	19:S:75:ALA:HB3	1.74	0.51
1:A:622:A:C8	1:A:623:C:C5	2.99	0.50
1:A:978:A:O2'	1:A:1322:C:N3	2.44	0.50
1:A:1442:G:C5	1:A:1446:A:N6	2.79	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
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
8:H:112:LEU:HD23	8:H:112:LEU:N	2.26	0.50
9:I:10:ARG:C	9:I:12:GLU:H	2.19	0.50
11:K:24:SER:C	11:K:26:ASN:H	2.19	0.50
11:K:57:THR:HG22	11:K:59:TYR:N	2.23	0.50
1:A:257:G:C4	1:A:258:G:C8	2.99	0.50
2:B:28:PHE:CD2	2:B:190:THR:HA	2.46	0.50
2:B:105:PHE:O	2:B:109:SER:HB3	2.11	0.50
4:D:107:ARG:HH12	4:D:194:LEU:HD12	1.76	0.50
4:D:198:VAL:HG12	4:D:199:ASN:N	2.25	0.50
5:E:33:VAL:CG1	5:E:34:VAL:N	2.74	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
15:O:85:LEU:HB3	15:O:87:ILE:HD11	1.94	0.50
1:A:149:A:H2'	1:A:150:C:C6	2.39	0.50
1:A:260:G:H2'	1:A:261:U:H6	1.76	0.50
1:A:537:G:H2'	1:A:538:G:H8	1.75	0.50
1:A:555:C:H2'	1:A:556:C:C6	2.46	0.50
1:A:758:G:H8	1:A:758:G:O5'	1.95	0.50
1:A:978:A:C2	1:A:1319:A:C4	2.99	0.50
1:A:1124:G:HO2'	1:A:1145:C:N4	2.10	0.50
1:A:1480:G:C6	1:A:1481:U:C4	2.99	0.50
1:A:1505:G:O2'	1:A:1506:U:P	2.69	0.50
3:C:20:SER:HB2	14:N:54:PRO:HG3	1.92	0.50
10:J:82:ILE:HG22	10:J:82:ILE:O	2.11	0.50
12:L:39:VAL:HG11	12:L:41:ARG:HG2	1.93	0.50
15:O:36:ILE:HG13	15:O:59:MET:HE2	1.92	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
20:T:44:ALA:C	20:T:46:GLU:H	2.20	0.50
1:A:325:A:OP2	20:T:70:SER:HB3	2.11	0.50
1:A:521:G:H1	1:A:528:C:H42	1.58	0.50
1:A:1373:G:H5''	7:G:36:LYS:HZ3	1.74	0.50
2:B:84:GLU:OE1	2:B:216:SER:HA	2.11	0.50
3:C:112:SER:O	3:C:116:VAL:HG23	2.11	0.50
7:G:51:GLN:O	7:G:53:LYS:N	2.37	0.50
8:H:86:ILE:HG22	8:H:87:SER:N	2.26	0.50
8:H:120:THR:H	8:H:123:GLU:HB3	1.76	0.50
1:A:429:U:C1'	1:A:430:A:H5''	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1126:U:OP1	1:A:1126:U:H6	1.91	0.50
1:A:1375:A:N3	1:A:1375:A:H2'	2.26	0.50
1:A:1521:G:H2'	1:A:1522:U:C6	2.47	0.50
3:C:23:TYR:CD1	10:J:10:GLY:HA2	2.46	0.50
4:D:50:ARG:HH12	4:D:52:SER:HA	1.75	0.50
6:F:30:LEU:N	6:F:30:LEU:HD23	2.25	0.50
7:G:95:ARG:HG2	7:G:99:LEU:HD12	1.93	0.50
13:M:87:TYR:N	19:S:73:GLU:O	2.45	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:1124:G:N2	1:A:1127:G:H21	2.09	0.50
1:A:1501:C:N4	1:A:1504:G:N3	2.59	0.50
2:B:51:LEU:CD2	2:B:201:ILE:HD12	2.39	0.50
1:A:646:U:H2'	1:A:647:C:C6	2.47	0.50
1:A:797:C:O2'	1:A:798:G:H5'	2.11	0.50
1:A:927:G:H1	1:A:1390:U:H3	1.59	0.50
1:A:1150:U:O4	1:A:1151:A:N6	2.44	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
5:E:18:ARG:HG3	5:E:18:ARG:NH1	2.23	0.50
13:M:3:ARG:HD2	13:M:9:ILE:HD11	1.93	0.50
19:S:20:LEU:HD12	19:S:21:GLU:N	2.27	0.50
19:S:44:MET:C	19:S:47:HIS:HD2	2.20	0.50
20:T:56:MET:HE2	20:T:88:VAL:HG21	1.93	0.50
1:A:49:U:C2	1:A:361:G:N2	2.80	0.50
1:A:77:G:H2'	1:A:78:G:C8	2.47	0.50
1:A:559:A:C1'	1:A:560:U:OP2	2.60	0.50
1:A:633:G:H2'	1:A:634:C:H6	1.77	0.50
1:A:1287:A:C6	1:A:1288:A:C6	3.00	0.50
2:B:7:VAL:O	2:B:8:LYS:CB	2.59	0.50
2:B:115:LEU:HD12	2:B:145:LEU:HB2	1.91	0.50
3:C:202:ILE:CG2	3:C:204:LEU:HD23	2.42	0.50
8:H:82:HIS:CD2	8:H:138:TRP:NE1	2.79	0.50
9:I:4:TYR:CE2	9:I:88:TYR:HB2	2.47	0.50
17:Q:23:VAL:HG21	17:Q:42:TYR:HD1	1.76	0.50
18:R:31:LEU:HD21	18:R:66:LEU:HB2	1.94	0.50
1:A:106:C:H2'	1:A:107:G:C5'	2.42	0.50
1:A:594:G:C2'	1:A:595:G:H5'	2.42	0.50
1:A:792:A:C2	1:A:793:U:C4	3.00	0.50
1:A:1204:A:C6	1:A:1205:U:O2	2.65	0.50
1:A:1261:A:C8	1:A:1262:C:C5	3.00	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1345:U:O2	1:A:1377:A:C6	2.65	0.50
1:A:1357:A:C4	1:A:1358:U:H5	2.30	0.50
7:G:45:ASP:O	7:G:49:ILE:HG13	2.11	0.50
12:L:33:ARG:O	12:L:85:ILE:HG23	2.12	0.50
13:M:45:VAL:HG13	13:M:46:LYS:N	2.26	0.50
1:A:277:C:C5'	17:Q:68:ARG:HH22	2.25	0.49
1:A:574:A:N3	1:A:883:C:H1'	2.27	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:1339:A:H5''	1:A:1340:A:OP2	2.12	0.49
1:A:1416:G:C2'	1:A:1417:G:H5'	2.42	0.49
3:C:82:GLU:O	3:C:86:VAL:HG23	2.12	0.49
5:E:98:THR:HG22	5:E:99:GLY:O	2.11	0.49
8:H:120:THR:HG23	8:H:123:GLU:OE2	2.11	0.49
1:A:20:U:H2'	1:A:21:G:H5'	1.93	0.49
1:A:1057:G:C5'	3:C:154:SER:HB2	2.22	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
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
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
7:G:145:ALA:C	7:G:147:ALA:H	2.20	0.49
15:O:78:TYR:O	15:O:82:ILE:HG13	2.11	0.49
1:A:328:C:O2	1:A:328:C:C2'	2.56	0.49
1:A:490:G:C2	1:A:491:G:C8	3.01	0.49
1:A:620:C:N1	4:D:135:LEU:HD13	2.28	0.49
1:A:1034:G:C2	1:A:1035:A:C5	3.01	0.49
1:A:1075:C:H2'	1:A:1076:C:H6	1.76	0.49
1:A:1152:A:H2'	1:A:1153:C:C6	2.46	0.49
1:A:1239:A:C4	1:A:1298:C:N4	2.80	0.49
1:A:1287:A:H2	1:A:1353:G:N3	2.10	0.49
11:K:72:ALA:HA	11:K:75:TYR:HB2	1.94	0.49
15:O:33:THR:HG23	15:O:63:ARG:HH11	1.77	0.49
20:T:51:GLU:HA	20:T:54:LYS:HB2	1.93	0.49
1:A:89:C:O2	1:A:90:U:O2	2.31	0.49
1:A:97:G:OP2	1:A:97:G:C8	2.59	0.49
1:A:410:G:OP2	4:D:25:ARG:HD2	2.11	0.49
1:A:1049:U:C4'	1:A:1050:G:OP2	2.60	0.49
1:A:1325:C:H4'	21:U:17:THR:HG21	1.94	0.49
7:G:50:ILE:HG21	7:G:58:PRO:HA	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:149:A:O2'	1:A:150:C:H5'	2.12	0.49
1:A:448:A:C4	1:A:487:A:N1	2.81	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
4:D:25:ARG:C	4:D:27:TYR:H	2.19	0.49
5:E:90:VAL:O	5:E:120:THR:HA	2.11	0.49
12:L:26:ALA:O	12:L:27:LEU:O	2.30	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
20:T:75:ASN:O	20:T:76:ALA:C	2.55	0.49
1:A:652:U:C2	1:A:752:G:N2	2.81	0.49
1:A:828:A:H2'	1:A:829:G:O5'	2.13	0.49
1:A:926:G:H3'	1:A:1505:G:N2	2.27	0.49
1:A:1193:G:H2'	1:A:1194:U:H6	1.77	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
13:M:12:ASN:N	13:M:45:VAL:CG1	2.74	0.49
1:A:112:G:O2'	1:A:113:G:H5'	2.12	0.49
1:A:166:G:C2	1:A:167:G:N7	2.81	0.49
1:A:474:G:N3	1:A:475:G:C8	2.80	0.49
1:A:958:A:N1	19:S:54:GLY:HA3	2.28	0.49
1:A:1283:G:H2'	1:A:1284:C:H6	1.77	0.49
1:A:1529:G:H3'	1:A:1529:G:OP2	2.12	0.49
2:B:107:THR:C	2:B:109:SER:H	2.20	0.49
3:C:123:GLN:OE1	3:C:133:ALA:HB1	2.12	0.49
3:C:134:ILE:O	3:C:138:VAL:HG23	2.13	0.49
11:K:14:VAL:HG21	11:K:40:ILE:CD1	2.42	0.49
16:P:25:ARG:HD3	16:P:25:ARG:H	1.77	0.49
1:A:62:U:H2'	1:A:63:C:C6	2.48	0.49
1:A:455:C:O5'	1:A:455:C:H6	1.95	0.49
1:A:939:G:H5''	7:G:102:ARG:NH2	2.28	0.49
1:A:1148:U:H4'	9:I:14:VAL:HG11	1.94	0.49
1:A:1357:A:H2'	1:A:1358:U:H6	1.76	0.49
1:A:1447:G:H2'	1:A:1447:G:N3	2.27	0.49
4:D:11:LEU:O	4:D:12:CYS:C	2.56	0.49
10:J:34:VAL:HG12	10:J:36:GLY:H	1.78	0.49
16:P:21:VAL:O	16:P:21:VAL:HG12	2.13	0.49
1:A:644:G:C5	1:A:645:C:C5	3.01	0.49
1:A:1124:G:H2'	1:A:1145:C:C5	2.48	0.49
1:A:1303:C:N4	1:A:1304:G:C6	2.81	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1305:G:H5''	21:U:4:GLY:HA3	1.94	0.49
2:B:44:LEU:N	2:B:44:LEU:HD22	2.28	0.49
3:C:155:GLY:HA2	3:C:164:ARG:H	1.78	0.49
5:E:152:ARG:CZ	8:H:44:PHE:CE1	2.95	0.49
8:H:63:LEU:HD22	8:H:63:LEU:H	1.77	0.49
15:O:6:GLU:OE2	15:O:7:GLU:HG3	2.13	0.49
19:S:34:TRP:HD1	19:S:52:TYR:CG	2.30	0.49
1:A:1352:C:H2'	1:A:1353:G:O4'	2.13	0.49
2:B:187:LEU:HA	2:B:201:ILE:HB	1.95	0.49
7:G:62:PHE:C	7:G:62:PHE:CD2	2.91	0.49
7:G:115:ARG:HB2	7:G:118:VAL:HG23	1.94	0.49
1:A:49:U:O2'	1:A:50:A:H2'	2.13	0.48
1:A:721:G:H4'	1:A:722:A:O4'	2.13	0.48
1:A:790:A:C6	1:A:791:G:O6	2.65	0.48
1:A:977:A:C8	1:A:1223:C:N3	2.81	0.48
1:A:1200:C:O2	1:A:1200:C:C2'	2.60	0.48
1:A:1262:C:O2	1:A:1262:C:H2'	2.12	0.48
1:A:1392:G:C4	1:A:1393:U:C5	3.01	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
5:E:143:ARG:HD2	8:H:77:GLU:OE2	2.13	0.48
7:G:137:LYS:O	7:G:138:LYS:C	2.55	0.48
20:T:20:LEU:O	20:T:23:ARG:HB3	2.13	0.48
20:T:75:ASN:OD1	20:T:75:ASN:N	2.46	0.48
1:A:193:C:O2'	1:A:194:C:H5'	2.13	0.48
1:A:197:A:N3	1:A:198:G:H1'	2.28	0.48
1:A:487:A:C6	1:A:488:C:O2	2.66	0.48
1:A:1000:U:H2'	1:A:1001:A:C8	2.47	0.48
1:A:1047:G:C2'	1:A:1048:G:H5'	2.43	0.48
1:A:1164:G:C8	1:A:1164:G:OP2	2.66	0.48
1:A:1486:G:H2'	1:A:1487:G:C1'	2.44	0.48
2:B:158:LEU:HD22	2:B:182:ILE:HD11	1.94	0.48
5:E:152:ARG:CZ	8:H:44:PHE:HE1	2.26	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
1:A:602:A:N1	1:A:637:G:C6	2.82	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:1284:C:H3'	1:A:1285:A:H8	1.78	0.48
1:A:1294:G:H2'	1:A:1295:G:H8	1.77	0.48
1:A:1434:A:N7	1:A:1435:G:C5	2.82	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:220:ASP:C	2:B:222:ILE:H	2.21	0.48
5:E:139:LEU:HA	5:E:142:LEU:HD12	1.95	0.48
7:G:46:ALA:HB1	7:G:121:ALA:N	2.28	0.48
7:G:143:ARG:O	7:G:147:ALA:HB2	2.13	0.48
9:I:13:ALA:HA	9:I:67:GLY:O	2.12	0.48
13:M:67:GLU:HB3	13:M:68:GLY:H	1.48	0.48
13:M:91:ARG:HB3	13:M:98:VAL:HG22	1.96	0.48
14:N:22:THR:HG23	14:N:33:VAL:CG2	2.42	0.48
1:A:266:G:C5'	1:A:268:C:H41	2.22	0.48
1:A:309:G:H2'	1:A:310:G:H8	1.79	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:18:TYR:OH	7:G:58:PRO:C	2.57	0.48
7:G:40:ALA:CB	9:I:41:VAL:HG21	2.43	0.48
7:G:111:ARG:NH1	7:G:122:HIS:HB3	2.29	0.48
11:K:74:ALA:C	11:K:76:GLY:H	2.21	0.48
15:O:86:GLY:C	15:O:87:ILE:HD13	2.38	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:H3'	1:A:98:U:H6	1.77	0.48
1:A:146:G:N3	1:A:147:G:C8	2.81	0.48
1:A:1157:A:H1'	1:A:1181:G:H21	1.78	0.48
1:A:1347:G:H2'	9:I:108:VAL:O	2.13	0.48
2:B:51:LEU:HD22	2:B:55:PHE:CE1	2.48	0.48
3:C:29:TYR:CE2	3:C:33:LEU:HD22	2.49	0.48
8:H:63:LEU:HD13	8:H:63:LEU:N	2.28	0.48
13:M:40:ASN:ND2	13:M:41:PRO:HD2	2.28	0.48
13:M:83:ASP:C	13:M:85:GLY:H	2.21	0.48
1:A:266:G:C1'	1:A:267:C:OP2	2.62	0.48
1:A:358:U:O2'	1:A:359:U:H5'	2.13	0.48
1:A:1124:G:O2'	1:A:1145:C:N4	2.46	0.48
1:A:1258:G:H2'	1:A:1259:C:C6	2.49	0.48
1:A:1392:G:H2'	1:A:1393:U:C6	2.44	0.48
1:A:1488:G:N2	1:A:1489:G:C4	2.81	0.48
1:A:1497:G:C5	1:A:1498:U:C4	3.02	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
7:G:60:LYS:O	7:G:61:VAL:C	2.57	0.48
7:G:65:ALA:HB1	7:G:127:ALA:HB3	1.95	0.48
9:I:46:ALA:HB2	9:I:74:ILE:HG23	1.95	0.48
11:K:47:VAL:HG12	11:K:48:ILE:N	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:46:G:C2	1:A:396:G:C2	3.01	0.48
1:A:377:G:OP1	16:P:3:LYS:HD3	2.13	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:920:U:H2'	1:A:921:U:C6	2.48	0.48
1:A:1241:G:H2'	1:A:1242:C:H6	1.77	0.48
2:B:69:LEU:C	2:B:69:LEU:HD23	2.39	0.48
2:B:193:ASP:C	2:B:193:ASP:OD1	2.56	0.48
8:H:91:ARG:O	8:H:91:ARG:HG3	2.13	0.48
11:K:29:ILE:HG12	11:K:30:VAL:N	2.27	0.48
17:Q:54:GLY:HA3	17:Q:82:MET:HG2	1.94	0.48
1:A:815:A:O2'	1:A:1527:C:H1'	2.14	0.48
4:D:58:LEU:HD12	4:D:59:ARG:HD2	1.94	0.48
10:J:38:ILE:HG23	10:J:39:PRO:HD2	1.95	0.48
12:L:12:ARG:HB3	12:L:12:ARG:HH11	1.79	0.48
14:N:42:ILE:HG13	14:N:43:CYS:H	1.79	0.48
18:R:54:ARG:HB2	18:R:54:ARG:CZ	2.44	0.48
20:T:49:ALA:O	20:T:50:GLU:C	2.57	0.48
1:A:99:C:H2'	1:A:101:A:C8	2.49	0.48
1:A:407:G:H5'	4:D:3:ARG:HH12	1.77	0.48
1:A:1007:C:H2'	1:A:1008:C:C6	2.48	0.48
1:A:1024:G:C6	1:A:1025:U:O4	2.67	0.48
1:A:1190:G:H3'	3:C:3:ASN:HD21	1.79	0.48
1:A:1402:C:H2'	1:A:1403:C:C6	2.48	0.48
1:A:1410:G:H1'	1:A:1491:G:N2	2.28	0.48
2:B:130:ARG:HB3	2:B:131:PRO:HD2	1.96	0.48
4:D:30:LYS:C	4:D:32:ALA:H	2.22	0.48
7:G:68:ASN:O	7:G:138:LYS:HD2	2.12	0.48
7:G:113:GLU:HB3	7:G:118:VAL:CG1	2.44	0.48
8:H:118:VAL:C	8:H:119:LEU:HD23	2.38	0.48
12:L:107:ALA:O	12:L:108:ALA:C	2.57	0.48
13:M:23:TYR:HB2	13:M:67:GLU:OE1	2.14	0.48
17:Q:63:ARG:O	17:Q:65:ILE:HD12	2.14	0.48
17:Q:100:LYS:HG3	17:Q:100:LYS:O	2.14	0.48
18:R:25:THR:HG22	18:R:42:ARG:HH22	1.79	0.48
20:T:17:ARG:CB	20:T:17:ARG:HH11	2.27	0.48
1:A:448:A:C2	1:A:449:C:C4	3.01	0.48
1:A:790:A:N1	1:A:791:G:C6	2.82	0.48
1:A:965:A:C1'	1:A:966:G:OP2	2.62	0.48
1:A:1046:A:H2	1:A:1047:G:C1'	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1115:C:H2'	1:A:1116:C:H6	1.78	0.48
1:A:1125:U:O2'	1:A:1126:U:P	2.72	0.48
1:A:1130:A:OP1	1:A:1131:G:N7	2.47	0.48
3:C:123:GLN:HB3	3:C:128:PHE:CB	2.43	0.48
5:E:77:PRO:HG2	5:E:142:LEU:HD22	1.96	0.48
11:K:57:THR:HG23	11:K:58:PRO:HD2	1.96	0.48
17:Q:23:VAL:HG21	17:Q:42:TYR:CD1	2.49	0.48
1:A:677:U:H3	1:A:713:G:H22	1.62	0.47
1:A:691:G:H2'	1:A:692:U:C6	2.49	0.47
1:A:795:C:C5'	1:A:796:C:OP2	2.61	0.47
1:A:956:U:H2'	1:A:957:U:O4'	2.14	0.47
1:A:974:A:OP2	14:N:41:ARG:NH1	2.35	0.47
1:A:986:A:C6	1:A:1220:G:N1	2.82	0.47
1:A:1202:G:C4	14:N:42:ILE:CD1	2.97	0.47
2:B:30:ARG:HG2	2:B:31:TYR:CD1	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
6:F:27:GLN:O	6:F:31:GLU:HG3	2.14	0.47
9:I:111:ARG:HH12	9:I:113:LYS:HA	1.79	0.47
12:L:82:VAL:HG23	12:L:106:ASP:OD1	2.13	0.47
21:U:14:TRP:CE3	21:U:15:ARG:HG3	2.49	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
2:B:213:LEU:HD23	2:B:213:LEU:C	2.39	0.47
3:C:107:GLN:O	3:C:108:ASN:HB3	2.13	0.47
12:L:43:VAL:CG1	12:L:44:THR:H	2.26	0.47
17:Q:48:GLU:O	17:Q:49:GLU:C	2.55	0.47
1:A:363:A:H62	12:L:28:LYS:NZ	2.12	0.47
1:A:628:G:C2'	1:A:629:G:H5'	2.43	0.47
1:A:820:U:H4'	1:A:821:G:OP2	2.14	0.47
1:A:965:A:C2'	1:A:966:G:OP2	2.63	0.47
1:A:980:C:HO2'	14:N:21:TYR:HE1	1.61	0.47
1:A:1077:G:N2	1:A:1080:A:OP2	2.42	0.47
1:A:1163:C:H2'	1:A:1164:G:O4'	2.15	0.47
1:A:1486:G:C6	1:A:1487:G:N1	2.82	0.47
2:B:236:TYR:C	2:B:238:LEU:H	2.21	0.47
3:C:23:TYR:OH	10:J:9:ARG:HD3	2.13	0.47
3:C:26:LYS:HD2	3:C:27:LYS:N	2.20	0.47
16:P:12:LYS:O	16:P:13:HIS:HB2	2.15	0.47
1:A:287:U:O2'	1:A:288:A:H5'	2.13	0.47
1:A:983:A:H1'	1:A:1049:U:O2	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1089:G:C5	1:A:1090:U:C5	3.02	0.47
1:A:1097:C:H1'	1:A:1169:A:H1'	1.96	0.47
1:A:1286:A:H2'	1:A:1287:A:H4'	1.95	0.47
2:B:25:ASN:C	2:B:25:ASN:ND2	2.72	0.47
10:J:35:SER:HB2	10:J:73:ASP:O	2.15	0.47
11:K:69:ALA:O	11:K:73:MET:HG2	2.13	0.47
17:Q:65:ILE:HD12	17:Q:65:ILE:N	2.30	0.47
1:A:504:C:C2	1:A:542:G:C2	3.03	0.47
1:A:532:A:H3'	1:A:533:A:H5'	1.96	0.47
1:A:721:G:C6	1:A:733:A:H2	2.32	0.47
1:A:1485:U:O2	1:A:1485:U:C2'	2.61	0.47
1:A:1504:G:OP1	1:A:1507:A:H4'	2.14	0.47
2:B:223:ILE:C	2:B:225:ALA:N	2.73	0.47
6:F:60:PHE:O	6:F:61:LEU:HD23	2.14	0.47
8:H:102:ARG:CD	8:H:102:ARG:N	2.78	0.47
9:I:16:ARG:HH11	9:I:64:THR:CG2	2.26	0.47
9:I:99:LEU:HB3	9:I:101:PHE:CD1	2.49	0.47
11:K:56:GLY:O	11:K:57:THR:C	2.56	0.47
11:K:126:ARG:HH22	11:K:129:SER:HB2	1.80	0.47
13:M:70:LEU:C	13:M:70:LEU:CD2	2.87	0.47
13:M:82:MET:HB3	13:M:93:ARG:HH11	1.78	0.47
18:R:59:SER:H	18:R:62:GLU:HB2	1.79	0.47
20:T:50:GLU:HA	20:T:100:ILE:CG2	2.44	0.47
1:A:97:G:O2'	1:A:98:U:H5'	2.14	0.47
1:A:500:G:C6	1:A:546:G:C2	3.03	0.47
1:A:509:A:H5'	4:D:54:TYR:CD2	2.49	0.47
5:E:144:THR:HG22	5:E:145:LYS:H	1.78	0.47
7:G:38:LEU:HD12	7:G:38:LEU:O	2.14	0.47
9:I:82:ALA:HB1	9:I:96:LEU:HD21	1.97	0.47
11:K:79:SER:CB	11:K:104:GLN:HB3	2.43	0.47
12:L:47:LYS:CB	12:L:48:PRO:HD3	2.37	0.47
13:M:6:GLY:HA3	13:M:67:GLU:HG3	1.97	0.47
19:S:3:ARG:O	19:S:4:SER:HB2	2.15	0.47
20:T:13:LEU:O	20:T:14:LYS:C	2.58	0.47
1:A:192:U:O4'	20:T:103:GLY:HA2	2.15	0.47
1:A:204:U:O2	1:A:204:U:H3'	2.15	0.47
1:A:474:G:OP2	16:P:75:ARG:HD2	2.15	0.47
1:A:531:U:O3'	1:A:532:A:H4'	2.15	0.47
1:A:838:G:N2	1:A:849:C:C2	2.82	0.47
1:A:892:A:C2	1:A:907:A:C4	3.02	0.47
1:A:1126:U:N3	1:A:1127:G:C2	2.83	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1150:U:O2	10:J:39:PRO:HG3	2.15	0.47
1:A:1150:U:O5'	1:A:1150:U:H6	1.96	0.47
1:A:1245:A:N1	1:A:1293:G:C2	2.83	0.47
1:A:1264:C:H2'	1:A:1265:G:C8	2.50	0.47
1:A:1425:U:H3	1:A:1475:G:H1	1.61	0.47
1:A:1487:G:C4	1:A:1488:G:C8	3.03	0.47
1:A:1487:G:H2'	1:A:1488:G:C5'	2.44	0.47
2:B:51:LEU:HD22	2:B:55:PHE:HE1	1.80	0.47
4:D:50:ARG:NH1	4:D:52:SER:HA	2.29	0.47
4:D:152:SER:HB2	4:D:155:LEU:HG	1.96	0.47
9:I:81:ILE:HG22	9:I:81:ILE:O	2.15	0.47
10:J:57:LYS:HD2	10:J:57:LYS:O	2.13	0.47
14:N:24:CYS:N	14:N:33:VAL:HG11	2.29	0.47
14:N:49:HIS:C	14:N:51:GLY:H	2.22	0.47
15:O:4:THR:H	15:O:7:GLU:CD	2.23	0.47
16:P:69:THR:O	16:P:72:ARG:HB3	2.15	0.47
17:Q:60:ILE:HB	17:Q:74:LEU:HD12	1.96	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
1:A:838:G:H1	1:A:848:C:H42	1.63	0.47
1:A:974:A:OP1	1:A:974:A:C8	2.59	0.47
1:A:1056:U:H5'	3:C:163:ALA:HB2	1.97	0.47
1:A:1314:C:OP2	19:S:6:LYS:HD3	2.15	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
13:M:54:VAL:O	13:M:55:ARG:C	2.58	0.47
1:A:181:G:C1'	1:A:182:U:OP2	2.63	0.47
1:A:929:G:OP1	1:A:1533:C:N4	2.45	0.47
1:A:949:A:C4	1:A:1233:G:N2	2.83	0.47
1:A:1200:C:N4	1:A:1206:G:H1	2.13	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
5:E:36:ASP:O	5:E:37:ARG:HB2	2.14	0.47
6:F:89:MET:HE2	18:R:76:LEU:HD11	1.97	0.47
9:I:43:ALA:HA	9:I:74:ILE:HD13	1.96	0.47
10:J:12:ASP:HB3	10:J:15:THR:CB	2.44	0.47
16:P:20:VAL:HG21	16:P:32:TYR:CB	2.45	0.47
16:P:26:ARG:HD3	16:P:31:LYS:HB3	1.97	0.47
1:A:134:A:H2'	1:A:135:C:O4'	2.15	0.47
1:A:191:G:C6	1:A:192:U:C4	3.03	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:575:G:H4'	1:A:576:G:OP1	2.15	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
2:B:25:ASN:HD22	2:B:26:PRO:N	2.12	0.47
2:B:115:LEU:HD23	2:B:115:LEU:C	2.40	0.47
4:D:196:LEU:C	4:D:198:VAL:H	2.23	0.47
13:M:11:ARG:HD2	13:M:12:ASN:N	2.29	0.47
20:T:34:LYS:CE	20:T:80:ARG:HH12	2.28	0.47
1:A:191:G:H21	20:T:104:LEU:HA	1.80	0.46
1:A:460:A:C2	1:A:462:G:C8	3.03	0.46
1:A:564:C:OP1	12:L:15:ARG:NE	2.47	0.46
1:A:627:G:H2'	1:A:628:G:C8	2.48	0.46
1:A:933:G:OP2	7:G:3:ARG:HB3	2.15	0.46
1:A:1007:C:C2	1:A:1023:G:N2	2.82	0.46
1:A:1167:A:C6	1:A:1168:A:C6	3.03	0.46
2:B:139:LYS:HD2	2:B:143:GLU:OE1	2.15	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
7:G:31:MET:SD	7:G:36:LYS:HB2	2.55	0.46
12:L:47:LYS:CB	12:L:48:PRO:CD	2.93	0.46
17:Q:56:VAL:O	17:Q:76:LEU:HD12	2.15	0.46
17:Q:66:SER:OG	17:Q:69:LYS:HG3	2.14	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:47:C:C6	1:A:365:U:H2'	2.50	0.46
1:A:131:C:H2'	1:A:132:C:C6	2.50	0.46
1:A:277:C:O2'	1:A:278:G:H5'	2.16	0.46
1:A:862:C:O2'	1:A:863:U:H5'	2.15	0.46
1:A:961:U:H2'	1:A:962:C:O4'	2.15	0.46
1:A:986:A:C2	1:A:1220:G:C2	3.02	0.46
1:A:1020:U:H2'	1:A:1021:G:H8	1.80	0.46
1:A:1190:G:H3'	3:C:3:ASN:ND2	2.29	0.46
1:A:1207:G:H2'	1:A:1208:C:C6	2.50	0.46
11:K:127:LYS:O	11:K:128:ALA:HB2	2.14	0.46
12:L:19:ARG:N	12:L:19:ARG:HD2	2.30	0.46
12:L:69:TYR:C	12:L:69:TYR:CD2	2.93	0.46
15:O:45:VAL:HG13	15:O:46:HIS:ND1	2.31	0.46
17:Q:12:SER:HB3	17:Q:20:THR:HB	1.98	0.46
17:Q:90:ILE:C	17:Q:92:ARG:N	2.72	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:666:G:H5'	1:A:726:C:H1'	1.96	0.46
2:B:143:GLU:HA	2:B:146:GLN:NE2	2.31	0.46
2:B:219:VAL:O	2:B:220:ASP:C	2.59	0.46
3:C:10:PHE:C	3:C:10:PHE:CD2	2.92	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
12:L:55:VAL:CG1	12:L:56:ALA:H	2.12	0.46
13:M:2:ALA:O	13:M:10:PRO:HD2	2.15	0.46
19:S:28:LYS:C	19:S:29:ARG:HD2	2.39	0.46
19:S:34:TRP:NE1	19:S:57:HIS:HE1	2.13	0.46
1:A:397:A:H3'	1:A:397:A:N3	2.30	0.46
1:A:1026:G:N3	1:A:1026:G:C2'	2.76	0.46
1:A:1046:A:H2	1:A:1047:G:H1'	1.79	0.46
1:A:1158:C:C5'	2:B:133:LYS:HE2	2.45	0.46
1:A:1394:A:H4'	1:A:1395:C:OP2	2.16	0.46
1:A:1418:A:H61	1:A:1482:G:H1'	1.80	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
3:C:118:GLN:O	3:C:122:GLU:HG3	2.14	0.46
9:I:7:THR:HG22	9:I:8:GLY:N	2.29	0.46
14:N:26:ARG:HD3	14:N:27:CYS:SG	2.56	0.46
1:A:463:A:H2'	1:A:474:G:H8	1.80	0.46
1:A:690:G:H2'	1:A:691:G:O4'	2.16	0.46
1:A:813:U:H5'	1:A:903:G:O3'	2.16	0.46
1:A:900:A:N1	1:A:901:A:C2	2.84	0.46
1:A:1122:U:C2'	1:A:1123:A:H5'	2.41	0.46
1:A:1186:G:C2	1:A:1187:G:C4	3.04	0.46
1:A:1295:G:N1	1:A:1296:C:C2	2.84	0.46
1:A:1328:C:C2	1:A:1329:A:C8	3.04	0.46
1:A:1360:A:C2'	1:A:1361:G:O5'	2.64	0.46
1:A:1437:C:H2'	1:A:1438:G:C8	2.49	0.46
4:D:8:VAL:C	4:D:10:ARG:H	2.23	0.46
4:D:153:ARG:NH1	4:D:181:MET:HB2	2.31	0.46
5:E:48:ALA:HB3	5:E:54:ALA:HA	1.97	0.46
7:G:21:VAL:C	7:G:23:VAL:N	2.72	0.46
7:G:60:LYS:HG3	7:G:64:GLN:HB2	1.97	0.46
9:I:8:GLY:HA3	9:I:79:LEU:HB3	1.96	0.46
9:I:30:GLY:O	9:I:31:GLN:O	2.33	0.46
12:L:113:ARG:NH2	12:L:120:TYR:CE1	2.84	0.46
1:A:172:A:N7	1:A:174:C:C4	2.83	0.46
1:A:345:C:H1'	1:A:346:G:N2	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:353:A:H2'	1:A:354:G:OP2	2.16	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: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:1098:C:H2'	1:A:1099:G:O4'	2.14	0.46
1:A:1203:C:H5''	14:N:2:ALA:HB3	1.96	0.46
4:D:106:TYR:CE1	4:D:113:SER:HA	2.51	0.46
7:G:120:ILE:O	7:G:121:ALA:C	2.56	0.46
9:I:100:GLY:C	9:I:102:LEU:N	2.74	0.46
9:I:114:TYR:O	9:I:114:TYR:HD1	1.98	0.46
17:Q:67:LYS:HA	17:Q:70:ARG:NH1	2.25	0.46
1:A:154:C:H2'	1:A:155:C:H6	1.81	0.46
1:A:224:C:H2'	1:A:225:C:C6	2.51	0.46
1:A:327:A:O2'	1:A:328:C:O4'	2.33	0.46
1:A:376:G:H2'	1:A:377:G:H8	1.80	0.46
1:A:630:G:H5'	1:A:631:G:P	2.55	0.46
1:A:828:A:H4'	1:A:828:A:OP1	2.16	0.46
1:A:1513:A:H2'	1:A:1514:C:C6	2.50	0.46
2:B:185:ILE:N	2:B:185:ILE:HD12	2.31	0.46
3:C:91:LEU:HD23	3:C:91:LEU:C	2.40	0.46
5:E:13:ILE:HD13	5:E:51:VAL:HG13	1.98	0.46
5:E:33:VAL:HA	5:E:42:GLY:O	2.16	0.46
7:G:102:ARG:O	7:G:106:GLN:HB2	2.16	0.46
10:J:16:LEU:HD12	10:J:68:HIS:HB2	1.96	0.46
12:L:46:LYS:O	12:L:47:LYS:C	2.59	0.46
1:A:56:U:H2'	1:A:57:G:H8	1.78	0.46
1:A:686:U:C2	1:A:687:A:N7	2.84	0.46
1:A:803:G:C6	1:A:804:U:N3	2.84	0.46
1:A:959:A:O2'	1:A:984:C:O2'	2.29	0.46
1:A:1118:C:O5'	1:A:1118:C:H6	1.99	0.46
1:A:1353:G:C4	1:A:1354:C:C5	3.03	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
5:E:107:ARG:O	5:E:108:ALA:C	2.57	0.46
6:F:91:VAL:HG11	18:R:72:ARG:HH12	1.81	0.46
8:H:116:LYS:HZ3	8:H:127:LEU:HB3	1.79	0.46
10:J:16:LEU:HB3	10:J:70:ARG:HG3	1.97	0.46
12:L:98:TYR:CD1	12:L:98:TYR:N	2.84	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:37:U:O2'	1:A:500:G:H4'	2.15	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:853:G:H2'	1:A:854:G:H5'	1.97	0.46
1:A:895:G:H2'	1:A:896:C:C6	2.51	0.46
1:A:1314:C:H2'	1:A:1315:U:C6	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
9:I:4:TYR:CD2	9:I:88:TYR:HB2	2.50	0.46
13:M:60:VAL:HG13	13:M:66:LEU:HD11	1.98	0.46
20:T:59:ALA:O	20:T:60:GLU:C	2.59	0.46
1:A:16:A:H2'	1:A:17:U:C5'	2.45	0.46
1:A:181:G:H1'	1:A:182:U:OP2	2.15	0.46
1:A:394:G:H2'	1:A:395:C:C6	2.51	0.46
1:A:769:G:H4'	1:A:1513:A:H4'	1.97	0.46
1:A:902:G:O2'	1:A:903:G:H5'	2.16	0.46
1:A:1120:G:C6	1:A:1121:U:C4	3.04	0.46
1:A:1299:A:N7	1:A:1301:U:O2	2.48	0.46
1:A:1314:C:C5	19:S:6:LYS:HE2	2.51	0.46
1:A:1465:C:H2'	1:A:1466:C:O4'	2.16	0.46
2:B:144:ARG:NH1	2:B:148:TYR:CE1	2.84	0.46
2:B:219:VAL:HG12	2:B:223:ILE:HD11	1.96	0.46
5:E:12:LEU:HD22	5:E:12:LEU:C	2.40	0.46
7:G:61:VAL:O	7:G:65:ALA:HB2	2.17	0.46
8:H:100:ILE:HA	8:H:101:PRO:HD3	1.69	0.46
11:K:38:ASN:HA	11:K:39:PRO:HD3	1.80	0.46
13:M:92:HIS:HA	13:M:110:ARG:HH22	1.81	0.46
19:S:29:ARG:HD2	19:S:29:ARG:N	2.31	0.46
21:U:9:ARG:C	21:U:11:GLY:H	2.23	0.46
1:A:29:G:O2'	1:A:30:U:H5'	2.16	0.45
1:A:428:G:C5	1:A:430:A:C6	3.04	0.45
1:A:867:G:C2	1:A:868:C:C6	3.04	0.45
1:A:1228:C:OP1	13:M:115:LYS:HG2	2.17	0.45
1:A:1294:G:H2'	1:A:1295:G:C8	2.51	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
5:E:71:LEU:CD2	5:E:115:VAL:HG22	2.46	0.45
12:L:20:LYS:HD3	12:L:20:LYS:N	2.24	0.45
13:M:11:ARG:HA	13:M:45:VAL:HG11	1.98	0.45
13:M:14:ARG:HG3	13:M:44:ARG:HH21	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:13:LEU:HG	20:T:14:LYS:N	2.31	0.45
1:A:147:G:C2	1:A:148:G:C8	3.04	0.45
1:A:409:G:OP1	4:D:24:GLU:O	2.34	0.45
1:A:705:U:C5	1:A:706:A:C5	3.04	0.45
1:A:976:G:N7	1:A:1359:C:H1'	2.31	0.45
1:A:1030(C):G:C6	1:A:1030(D):A:C6	3.04	0.45
3:C:130:VAL:O	3:C:134:ILE:HG13	2.16	0.45
5:E:142:LEU:C	5:E:143:ARG:HG2	2.40	0.45
7:G:16:LEU:H	7:G:16:LEU:CD2	2.27	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:433:C:O2	1:A:433:C:H2'	2.17	0.45
1:A:867:G:C2	1:A:868:C:C5	3.05	0.45
1:A:894:G:C6	1:A:895:G:C5	3.04	0.45
1:A:1181:G:C6	1:A:1182:G:N1	2.84	0.45
1:A:1502:A:H2	1:A:1505:G:N1	2.14	0.45
3:C:89:GLU:O	3:C:93:LYS:HB2	2.16	0.45
3:C:113:ALA:HA	3:C:116:VAL:CG2	2.46	0.45
4:D:128:VAL:O	4:D:129:ASN:HB2	2.17	0.45
7:G:26:PHE:CA	7:G:101:LEU:HD13	2.46	0.45
7:G:65:ALA:HB1	7:G:127:ALA:CB	2.46	0.45
8:H:100:ILE:HG23	8:H:101:PRO:HD2	1.98	0.45
12:L:69:TYR:CD2	12:L:70:ILE:N	2.85	0.45
7:G:50:ILE:CG2	7:G:61:VAL:HG21	2.47	0.45
8:H:2:LEU:O	8:H:3:THR:C	2.59	0.45
10:J:71:LEU:HD13	10:J:72:VAL:N	2.32	0.45
1:A:101:A:H2'	1:A:102:G:H8	1.82	0.45
1:A:176:C:H2'	1:A:176:C:O2	2.15	0.45
1:A:491:G:C2	1:A:492:G:C5	3.05	0.45
1:A:1228:C:N4	13:M:104:ARG:O	2.48	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:22:LYS:C	2:B:24:TRP:N	2.73	0.45
3:C:86:VAL:HG12	3:C:87:LEU:N	2.30	0.45
12:L:81:SER:HB3	12:L:106:ASP:HB2	1.98	0.45
16:P:25:ARG:O	16:P:26:ARG:C	2.59	0.45
19:S:3:ARG:HH22	19:S:69:HIS:CD2	2.35	0.45
1:A:364:A:H2'	1:A:365:U:O2	2.16	0.45
1:A:421:U:O4	3:C:126:ARG:HD2	2.17	0.45
1:A:491:G:C2	1:A:492:G:C8	3.05	0.45
1:A:521:G:H1	1:A:528:C:N4	2.14	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:550:G:C5	1:A:551:U:C5	3.04	0.45
1:A:1112:C:C4	3:C:178:LEU:HD23	2.51	0.45
1:A:1197:G:N3	1:A:1197:G:H2'	2.32	0.45
1:A:1413:A:H2'	1:A:1414:U:O4'	2.16	0.45
2:B:101:MET:HB2	2:B:102:LEU:CD1	2.47	0.45
15:O:45:VAL:CG2	15:O:46:HIS:H	2.27	0.45
15:O:87:ILE:CG2	15:O:88:ARG:H	2.29	0.45
19:S:16:LEU:O	19:S:20:LEU:HG	2.16	0.45
1:A:77:G:N1	1:A:93:G:C2	2.84	0.45
1:A:401:C:H1'	1:A:622:A:H1'	1.98	0.45
1:A:413:G:N2	1:A:428:G:H1'	2.31	0.45
1:A:1143:G:H8	1:A:1143:G:O5'	1.98	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
4:D:83:SER:HA	4:D:89:THR:CG2	2.45	0.45
5:E:152:ARG:HB3	8:H:43:GLY:HA3	1.99	0.45
6:F:4:TYR:O	6:F:65:VAL:HG22	2.16	0.45
6:F:44:GLY:HA2	6:F:59:TYR:CE1	2.51	0.45
7:G:111:ARG:CB	7:G:119:ARG:HG2	2.44	0.45
14:N:22:THR:HG23	14:N:33:VAL:HG21	1.98	0.45
20:T:22:ARG:O	20:T:23:ARG:C	2.60	0.45
1:A:266:G:O2'	17:Q:67:LYS:HB3	2.17	0.45
1:A:339:C:H2'	1:A:340:U:C6	2.52	0.45
1:A:379:C:H2'	1:A:380:G:H5'	1.97	0.45
1:A:674:G:H2'	1:A:675:A:C8	2.52	0.45
1:A:689:C:O2'	1:A:690:G:H5'	2.17	0.45
1:A:1015:A:H2'	1:A:1016:A:C8	2.51	0.45
1:A:1128:C:N4	1:A:1143:G:H22	2.06	0.45
1:A:1498:U:H1'	1:A:1499:A:OP2	2.17	0.45
4:D:15:GLU:CD	4:D:59:ARG:HH21	2.24	0.45
20:T:45:GLN:O	20:T:45:GLN:HG2	2.16	0.45
1:A:234:C:H2'	1:A:235:C:C6	2.51	0.45
1:A:430:A:C5	1:A:431:A:C8	3.04	0.45
1:A:913:A:H1'	1:A:914:A:OP2	2.17	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
3:C:9:GLY:HA3	14:N:49:HIS:HB3	1.99	0.45
3:C:129:ALA:O	3:C:130:VAL:C	2.60	0.45
3:C:188:LEU:H	3:C:188:LEU:CD2	2.30	0.45
4:D:153:ARG:HH12	4:D:181:MET:HB2	1.80	0.45
8:H:26:VAL:HG23	8:H:27:PRO:HD2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:111:ILE:O	8:H:134:ILE:HB	2.17	0.45
18:R:31:LEU:CD2	18:R:66:LEU:HB2	2.47	0.45
20:T:98:PRO:O	20:T:99:LEU:C	2.60	0.45
21:U:13:ILE:HG22	21:U:14:TRP:N	2.32	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
1:A:91:C:C2'	1:A:92:C:O5'	2.65	0.45
1:A:192:U:C4'	20:T:103:GLY:HA2	2.47	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
1:A:830:G:C6	1:A:831:U:C4	3.04	0.45
1:A:1144:G:N2	1:A:1146:A:H61	2.14	0.45
1:A:1347:G:H22	1:A:1373:G:H2'	1.75	0.45
2:B:210:SER:O	2:B:211:ILE:C	2.60	0.45
2:B:212:GLN:O	2:B:213:LEU:C	2.58	0.45
3:C:11:ARG:HD3	3:C:178:LEU:O	2.17	0.45
3:C:107:GLN:O	3:C:108:ASN:CB	2.65	0.45
4:D:14:ARG:O	4:D:14:ARG:HD3	2.17	0.45
4:D:36:ARG:HG2	4:D:38:TYR:CZ	2.52	0.45
5:E:10:MET:SD	5:E:13:ILE:HG13	2.57	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
8:H:113:SER:HA	8:H:118:VAL:HA	1.99	0.45
11:K:127:LYS:N	11:K:127:LYS:HD2	2.33	0.45
15:O:6:GLU:OE1	15:O:6:GLU:N	2.50	0.45
16:P:26:ARG:HH11	16:P:26:ARG:HG3	1.81	0.45
20:T:90:GLN:C	20:T:93:GLU:HB3	2.42	0.45
1:A:67:C:O2'	1:A:171:A:H1'	2.18	0.44
1:A:91:C:H5	1:A:92:C:C6	2.35	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
1:A:763:G:N2	1:A:764:C:C2	2.85	0.44
1:A:986:A:C6	1:A:987:G:C6	3.04	0.44
1:A:1292:U:H2'	1:A:1293:G:C8	2.51	0.44
1:A:1478:C:H2'	1:A:1479:C:C6	2.52	0.44
2:B:92:TYR:CD1	2:B:94:ASN:HB2	2.52	0.44
2:B:102:LEU:HD12	2:B:102:LEU:N	2.32	0.44
2:B:169:LYS:C	2:B:171:ALA:H	2.26	0.44
7:G:12:LEU:H	7:G:12:LEU:HD12	1.82	0.44
7:G:50:ILE:HD12	7:G:61:VAL:HG11	1.98	0.44
9:I:89:ASN:C	9:I:91:ASP:H	2.25	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:29:ILE:HB	11:K:44:SER:HB3	1.99	0.44
14:N:19:ARG:O	14:N:19:ARG:HG2	2.18	0.44
14:N:44:LEU:HD13	14:N:44:LEU:C	2.42	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
1:A:960:U:H4'	1:A:961:U:C5'	2.47	0.44
1:A:1019:C:H2'	1:A:1020:U:O4'	2.17	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
2:B:233:SER:HA	2:B:234:PRO:HD3	1.88	0.44
6:F:63:TYR:O	6:F:65:VAL:HG13	2.17	0.44
7:G:51:GLN:C	7:G:53:LYS:H	2.25	0.44
8:H:75:ARG:HA	8:H:76:PRO:HD3	1.90	0.44
8:H:90:GLY:O	8:H:91:ARG:HB2	2.17	0.44
14:N:16:PHE:O	14:N:17:LYS:C	2.60	0.44
21:U:5:ASP:HB3	21:U:8:THR:OG1	2.17	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:737:A:H2'	1:A:738:C:H6	1.82	0.44
1:A:947:G:H2'	1:A:948:C:O4'	2.17	0.44
1:A:1096:C:H2'	1:A:1097:C:H6	1.82	0.44
1:A:1144:G:C2	1:A:1146:A:N6	2.86	0.44
1:A:1157:A:C4	1:A:1181:G:N2	2.85	0.44
1:A:1291:G:H4'	9:I:39:GLY:HA3	1.98	0.44
2:B:185:ILE:HD12	2:B:185:ILE:H	1.82	0.44
3:C:77:ILE:HG23	3:C:81:GLY:HA2	1.98	0.44
4:D:60:GLU:HG2	4:D:202:LEU:HB2	2.00	0.44
8:H:6:ILE:H	8:H:6:ILE:CD1	2.31	0.44
8:H:29:SER:OG	8:H:32:LYS:HG3	2.17	0.44
8:H:102:ARG:CD	8:H:102:ARG:H	2.31	0.44
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
16:P:23:ASP:C	16:P:23:ASP:OD1	2.60	0.44
16:P:25:ARG:HD3	16:P:25:ARG:N	2.32	0.44
17:Q:13:ASP:C	17:Q:15:MET:H	2.26	0.44
17:Q:79:SER:OG	17:Q:80:GLY:N	2.51	0.44
20:T:74:LYS:C	20:T:76:ALA:N	2.69	0.44
1:A:177:C:C2	1:A:178:C:C5	3.05	0.44
1:A:487:A:H2'	1:A:488:C:O4'	2.17	0.44
1:A:803:G:H2'	1:A:804:U:O4'	2.17	0.44
1:A:954:G:C6	1:A:955:U:N3	2.86	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1004:A:N6	1:A:1035:A:C5	2.85	0.44
1:A:1118:C:P	9:I:104:ARG:HE	2.41	0.44
1:A:1240:U:H1'	7:G:38:LEU:HD21	1.99	0.44
1:A:1417:G:H21	1:A:1484:C:H42	1.66	0.44
2:B:100:GLY:O	2:B:101:MET:C	2.61	0.44
3:C:14:ILE:O	3:C:16:ARG:N	2.50	0.44
4:D:50:ARG:HA	4:D:51:PRO:HD3	1.83	0.44
6:F:1:MET:HE3	6:F:66:GLU:HG2	1.99	0.44
7:G:37:ASN:HD22	7:G:37:ASN:C	2.25	0.44
8:H:84:ARG:O	8:H:135:CYS:HB2	2.17	0.44
9:I:112:LYS:HD3	9:I:113:LYS:N	2.33	0.44
11:K:16:SER:HB2	11:K:106:LYS:HZ2	1.82	0.44
14:N:29:ARG:HG2	14:N:29:ARG:HH11	1.82	0.44
1:A:265:G:O2'	1:A:266:G:H3'	2.18	0.44
1:A:303:A:H2'	1:A:304:U:O4'	2.17	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
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
1:A:1053:G:H4'	1:A:1054:C:H5'	2.00	0.44
1:A:1112:C:H1'	3:C:179:ARG:NH1	2.32	0.44
1:A:1249:C:H2'	1:A:1250:A:H5'	1.98	0.44
1:A:1486:G:C6	1:A:1487:G:C6	3.05	0.44
2:B:53:ARG:HH12	2:B:199:TYR:HA	1.82	0.44
2:B:87:ARG:O	2:B:88:ALA:CB	2.66	0.44
8:H:97:VAL:HG13	8:H:98:LYS:N	2.33	0.44
9:I:45:ALA:HA	9:I:48:GLU:HB2	1.99	0.44
10:J:81:THR:C	10:J:83:GLU:H	2.25	0.44
13:M:50:GLU:HA	13:M:50:GLU:OE2	2.17	0.44
13:M:63:THR:HG23	13:M:64:TRP:CD2	2.53	0.44
20:T:49:ALA:HB3	20:T:99:LEU:CG	2.48	0.44
20:T:50:GLU:HA	20:T:100:ILE:HG22	1.99	0.44
1:A:35:G:C6	1:A:36:C:N4	2.86	0.44
1:A:70:G:O2'	1:A:73:C:H5'	2.18	0.44
1:A:428:G:H1'	1:A:429:U:OP2	2.17	0.44
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
1:A:1128:C:C4	1:A:1139:G:C6	3.04	0.44
1:A:1163:C:N4	1:A:1174:G:C2	2.85	0.44
1:A:1361(A):C:O2	1:A:1362:C:C6	2.71	0.44
1:A:1468:A:H2'	1:A:1469:G:O4'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:123:GLN:HB3	3:C:128:PHE:HB2	2.00	0.44
8:H:87:SER:OG	8:H:92:ARG:HA	2.17	0.44
10:J:6:ILE:HD12	10:J:73:ASP:H	1.81	0.44
11:K:74:ALA:C	11:K:76:GLY:N	2.76	0.44
11:K:125:PHE:N	11:K:125:PHE:CD1	2.85	0.44
1:A:708:C:H2'	1:A:709:G:H8	1.82	0.44
1:A:1191:A:OP1	3:C:3:ASN:OD1	2.35	0.44
1:A:1490:C:O2'	1:A:1491:G:H5'	2.17	0.44
5:E:76:ILE:HG23	5:E:78:HIS:N	2.26	0.44
12:L:20:LYS:CD	12:L:20:LYS:N	2.81	0.44
12:L:43:VAL:CG1	12:L:44:THR:N	2.80	0.44
1:A:157:G:H2'	1:A:158:G:C8	2.53	0.44
1:A:234:C:H2'	1:A:235:C:H6	1.81	0.44
1:A:984:C:H42	1:A:1221:G:H1	1.66	0.44
1:A:1418:A:H3'	1:A:1418:A:OP2	2.18	0.44
2:B:215:LEU:HA	2:B:215:LEU:HD23	1.66	0.44
3:C:113:ALA:HA	3:C:116:VAL:HG23	1.99	0.44
3:C:143:GLU:C	3:C:145:GLY:H	2.25	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
6:F:45:LEU:HA	6:F:58:GLY:O	2.17	0.44
11:K:14:VAL:C	11:K:16:SER:H	2.26	0.44
12:L:43:VAL:CG2	12:L:55:VAL:HG21	2.47	0.44
20:T:46:GLU:HB3	20:T:48:LYS:HE3	1.99	0.44
1:A:44:G:H2'	1:A:45:U:O4'	2.18	0.44
1:A:60:A:OP1	1:A:331:G:N1	2.41	0.44
1:A:107:G:C2	1:A:108:G:H1'	2.53	0.44
1:A:157:G:H2'	1:A:158:G:H8	1.81	0.44
1:A:181:G:C4'	1:A:182:U:OP2	2.66	0.44
1:A:284:G:C4	1:A:285:G:C8	3.06	0.44
1:A:374:A:C6	1:A:375:U:C4	3.06	0.44
1:A:477:G:C2	1:A:478:A:C5	3.05	0.44
1:A:692:U:OP1	11:K:124:LYS:HE3	2.18	0.44
1:A:865:A:H2'	1:A:866:C:C6	2.52	0.44
1:A:1014:A:N7	1:A:1015:A:N6	2.66	0.44
1:A:1358:U:O2'	1:A:1359:C:O4'	2.36	0.44
1:A:1371:G:C5	1:A:1372:U:C5	3.06	0.44
1:A:1396:A:O4'	1:A:1398:A:H1'	2.17	0.44
2:B:208:ILE:O	2:B:209:ARG:C	2.61	0.44
4:D:8:VAL:C	4:D:10:ARG:N	2.74	0.44
5:E:15:ARG:NH1	5:E:26:PHE:CE2	2.86	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:16:LEU:HD22	7:G:16:LEU:N	2.25	0.44
7:G:47:CYS:O	7:G:50:ILE:HB	2.18	0.44
7:G:70:LYS:HB2	7:G:96:GLN:HB3	2.00	0.44
9:I:82:ALA:HA	9:I:85:LEU:HB3	2.00	0.44
10:J:47:PHE:HD2	14:N:34:TYR:HE2	1.66	0.44
12:L:73:GLU:OE1	12:L:73:GLU:HA	2.18	0.44
12:L:90:VAL:CG2	12:L:99:HIS:HE1	2.30	0.44
16:P:39:TYR:CE2	16:P:41:PRO:HG3	2.52	0.44
16:P:52:ASP:OD1	16:P:55:ARG:HB2	2.17	0.44
20:T:61:SER:O	20:T:65:LYS:HG3	2.18	0.44
1:A:407:G:H1'	4:D:119:GLN:HE22	1.82	0.43
1:A:616:G:N3	1:A:625:G:C2	2.85	0.43
1:A:1084:G:H5'	1:A:1102:A:OP2	2.18	0.43
4:D:141:ARG:HB3	4:D:141:ARG:CZ	2.48	0.43
5:E:139:LEU:HA	5:E:142:LEU:CD1	2.47	0.43
8:H:58:TYR:HB3	8:H:59:LEU:H	1.68	0.43
13:M:49:THR:HG22	13:M:50:GLU:N	2.33	0.43
15:O:34:LEU:HD13	15:O:34:LEU:C	2.43	0.43
19:S:36:ARG:NH2	19:S:75:ALA:HB3	2.33	0.43
20:T:77:ALA:O	20:T:78:ALA:C	2.60	0.43
1:A:488:C:H2'	1:A:489:C:H6	1.82	0.43
1:A:544:G:C6	1:A:545:C:C4	3.07	0.43
1:A:585:G:H4'	12:L:8:ASN:OD1	2.18	0.43
1:A:990:C:H5'	1:A:1017:G:O2'	2.18	0.43
2:B:61:LEU:HD22	2:B:61:LEU:HA	1.89	0.43
2:B:68:ILE:O	2:B:90:MET:HB3	2.18	0.43
3:C:3:ASN:OD1	3:C:3:ASN:N	2.51	0.43
4:D:38:TYR:CE1	4:D:45:GLN:HG3	2.53	0.43
4:D:58:LEU:HD23	4:D:206:PHE:CE1	2.53	0.43
4:D:146:ILE:N	4:D:146:ILE:HD12	2.33	0.43
5:E:7:GLU:O	5:E:34:VAL:HA	2.18	0.43
10:J:54:PHE:O	10:J:55:LYS:O	2.36	0.43
13:M:49:THR:CG2	13:M:50:GLU:H	2.31	0.43
16:P:20:VAL:CG2	16:P:32:TYR:HB2	2.47	0.43
17:Q:33:GLY:O	17:Q:34:LYS:C	2.61	0.43
17:Q:86:GLU:O	17:Q:87:LYS:C	2.61	0.43
20:T:49:ALA:HB3	20:T:99:LEU:HG	2.00	0.43
1:A:75:G:H2'	1:A:76:C:C6	2.53	0.43
1:A:299:G:C6	1:A:300:A:C6	3.07	0.43
1:A:328:C:H4'	1:A:329:A:H5'	2.00	0.43
1:A:346:G:C2'	1:A:347:G:H5'	2.48	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:778:G:H2'	1:A:779:C:O4'	2.18	0.43
1:A:1056:U:H2'	1:A:1057:G:H8	1.84	0.43
1:A:1418:A:C4	1:A:1483:A:C6	3.06	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
10:J:15:THR:HG22	10:J:94:VAL:HG23	2.01	0.43
11:K:29:ILE:HB	11:K:44:SER:CB	2.48	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
1:A:130:A:O2'	1:A:131:C:H5''	2.18	0.43
1:A:284:G:N3	1:A:285:G:C8	2.86	0.43
1:A:601:C:C2'	1:A:602:A:H5'	2.48	0.43
1:A:792:A:C6	1:A:794:A:N6	2.86	0.43
1:A:826:C:O2	8:H:15:ASN:ND2	2.52	0.43
1:A:991:U:C5	1:A:1212:U:C2	2.90	0.43
1:A:1528:U:H6	1:A:1528:U:H2'	1.64	0.43
2:B:77:ALA:O	2:B:79:ASP:N	2.51	0.43
2:B:97:TRP:CH2	2:B:176:GLU:OE2	2.70	0.43
3:C:113:ALA:HB1	3:C:200:ALA:HB3	2.00	0.43
3:C:162:GLN:HG3	3:C:163:ALA:N	2.34	0.43
4:D:9:CYS:O	4:D:12:CYS:HB2	2.18	0.43
5:E:131:ILE:HD12	5:E:131:ILE:HA	1.75	0.43
8:H:56:LYS:HD2	8:H:56:LYS:N	2.33	0.43
9:I:84:ALA:C	9:I:86:VAL:H	2.26	0.43
10:J:47:PHE:HD2	14:N:34:TYR:CE2	2.37	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
20:T:36:LEU:HD12	20:T:62:LEU:CD1	2.48	0.43
1:A:96:G:O6	1:A:97:G:N1	2.52	0.43
1:A:1182:G:H4'	1:A:1183:A:O5'	2.18	0.43
1:A:1255:G:C6	1:A:1279:A:N7	2.86	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:1417:G:O2'	1:A:1483:A:N6	2.52	0.43
2:B:54:THR:OG1	2:B:199:TYR:HB3	2.18	0.43
2:B:144:ARG:NH1	2:B:148:TYR:HE1	2.16	0.43
7:G:85:TYR:CE1	7:G:154:TYR:HE1	2.36	0.43
8:H:9:MET:SD	8:H:32:LYS:HB3	2.58	0.43
11:K:12:ARG:HG2	11:K:13:GLN:H	1.83	0.43
12:L:45:PRO:HB3	12:L:53:ARG:HH12	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:75:ARG:HB2	16:P:80:PHE:HD1	1.84	0.43
20:T:49:ALA:HB3	20:T:99:LEU:CD1	2.47	0.43
20:T:72:LEU:O	20:T:74:LYS:N	2.46	0.43
1:A:20:U:C2'	1:A:21:G:H5'	2.47	0.43
1:A:89:C:N3	1:A:90:U:O2	2.51	0.43
1:A:146:G:C2	1:A:147:G:C8	3.07	0.43
1:A:353:A:C2'	1:A:354:G:OP2	2.66	0.43
1:A:578:C:O2'	1:A:728:A:N3	2.48	0.43
1:A:750:G:H21	15:O:23:GLY:CA	2.30	0.43
1:A:818:G:O2'	1:A:819:A:H5'	2.19	0.43
1:A:1355:G:H2'	1:A:1356:G:C8	2.53	0.43
1:A:1468:A:O5'	1:A:1468:A:H8	2.02	0.43
2:B:185:ILE:HA	2:B:199:TYR:O	2.19	0.43
3:C:23:TYR:HA	10:J:11:PHE:CE1	2.54	0.43
4:D:78:LEU:HD11	4:D:96:LEU:HB3	2.01	0.43
4:D:175:SER:HB3	4:D:184:LYS:HB2	2.01	0.43
7:G:108:ALA:O	7:G:119:ARG:HB3	2.18	0.43
8:H:108:GLY:HA3	8:H:138:TRP:HB3	1.99	0.43
9:I:100:GLY:O	9:I:102:LEU:N	2.50	0.43
12:L:60:LEU:HB2	12:L:64:TYR:O	2.19	0.43
16:P:23:ASP:OD1	16:P:24:ALA:N	2.52	0.43
16:P:40:ASP:HA	16:P:41:PRO:HD3	1.78	0.43
17:Q:5:VAL:C	17:Q:6:LEU:HD23	2.43	0.43
20:T:44:ALA:HB1	20:T:91:LEU:HB3	1.99	0.43
1:A:75:G:C2	1:A:96:G:N1	2.87	0.43
1:A:203:U:H3'	1:A:203:U:OP1	2.19	0.43
1:A:277:C:C2'	1:A:278:G:H5'	2.49	0.43
1:A:294:U:H2'	1:A:295:C:C6	2.54	0.43
1:A:300:A:O5'	1:A:300:A:C8	2.62	0.43
1:A:503:C:H2'	1:A:504:C:H6	1.84	0.43
1:A:938:A:H5'	7:G:76:ARG:HH22	1.83	0.43
1:A:1118:C:C2	1:A:1179:A:C2	3.07	0.43
1:A:1250:A:C6	1:A:1251:A:N1	2.87	0.43
2:B:6:THR:CB	2:B:221:LEU:HD21	2.49	0.43
2:B:240:GLN:HE21	2:B:240:GLN:CA	2.26	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
8:H:6:ILE:O	8:H:10:LEU:HG	2.18	0.43
8:H:102:ARG:H	8:H:102:ARG:HD2	1.83	0.43
13:M:45:VAL:O	13:M:48:LEU:HB2	2.18	0.43
13:M:59:TYR:CD1	13:M:59:TYR:C	2.95	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:53:ARG:NH1	18:R:60:GLY:HA2	2.33	0.43
20:T:51:GLU:O	20:T:55:ILE:HG13	2.19	0.43
1:A:8:A:N6	4:D:209:ARG:HB2	2.34	0.43
1:A:166:G:C2	1:A:167:G:C5	3.06	0.43
1:A:370:C:O2'	1:A:371:G:H5'	2.19	0.43
1:A:595:G:C6	1:A:641:U:C6	3.07	0.43
1:A:887:G:H2'	1:A:888:G:O4'	2.19	0.43
2:B:107:THR:O	2:B:110:GLN:N	2.51	0.43
3:C:6:HIS:O	3:C:9:GLY:N	2.52	0.43
6:F:35:ALA:HA	6:F:67:MET:HB3	2.01	0.43
7:G:61:VAL:O	7:G:65:ALA:CB	2.67	0.43
7:G:136:LYS:HD2	7:G:140:ASP:OD2	2.19	0.43
1:A:285:G:C2	1:A:286:G:C8	3.07	0.43
1:A:981:U:H5'	14:N:21:TYR:CZ	2.53	0.43
1:A:994:A:H62	1:A:1216:G:C5'	2.32	0.43
1:A:1478:C:H2'	1:A:1479:C:H6	1.84	0.43
3:C:40:ARG:HA	3:C:43:LEU:HB2	2.01	0.43
4:D:71:SER:O	4:D:72:GLU:C	2.61	0.43
7:G:26:PHE:CD1	7:G:101:LEU:HD22	2.48	0.43
8:H:96:GLY:O	8:H:97:VAL:C	2.61	0.43
10:J:45:ARG:HH12	10:J:65:LEU:HD23	1.84	0.43
13:M:63:THR:HG23	13:M:64:TRP:CG	2.54	0.43
16:P:50:LYS:HG2	16:P:51:VAL:N	2.34	0.43
17:Q:97:SER:C	17:Q:98:LEU:HD23	2.43	0.43
18:R:47:THR:HB	18:R:49:LYS:HG3	2.01	0.43
1:A:20:U:H2'	1:A:21:G:C5'	2.49	0.43
1:A:41:G:C2	1:A:42:G:C5	3.07	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:381:C:C4	1:A:382:A:C5	3.07	0.43
1:A:790:A:H2'	1:A:791:G:C8	2.54	0.43
1:A:865:A:H2'	1:A:866:C:H6	1.84	0.43
1:A:918:A:H2'	1:A:919:A:O4'	2.19	0.43
1:A:1250:A:H4'	9:I:68:GLY:CA	2.48	0.43
1:A:1416:G:H1	1:A:1485:U:H1'	1.83	0.43
2:B:190:THR:HG22	2:B:191:ASP:N	2.33	0.43
3:C:117:ALA:HB1	3:C:187:ALA:HB2	1.99	0.43
4:D:143:GLY:O	4:D:144:ASP:C	2.62	0.43
5:E:105:VAL:HB	5:E:106:PRO:HD3	1.99	0.43
10:J:59:SER:O	10:J:60:ARG:CB	2.67	0.43
10:J:76:ASN:C	10:J:78:ASN:H	2.26	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:22:HIS:CD2	11:K:22:HIS:O	2.72	0.43
12:L:41:ARG:HB3	12:L:41:ARG:CZ	2.49	0.43
14:N:42:ILE:O	14:N:43:CYS:C	2.59	0.43
15:O:41:GLU:O	15:O:44:LYS:HB2	2.18	0.43
20:T:74:LYS:HB3	20:T:74:LYS:HZ2	1.82	0.43
1:A:89:C:C2	1:A:90:U:O2	2.71	0.42
1:A:175:C:C4	1:A:176:C:C5	3.06	0.42
1:A:695:A:OP2	11:K:53:SER:N	2.51	0.42
1:A:1092:A:C4	1:A:1183:A:C6	3.07	0.42
1:A:1379:G:C6	1:A:1380:U:C4	3.07	0.42
3:C:70:VAL:HG12	3:C:71:ALA:N	2.34	0.42
4:D:39:PRO:HB2	4:D:44:GLY:HA2	2.00	0.42
7:G:70:LYS:HA	7:G:71:PRO:HD3	1.75	0.42
9:I:16:ARG:NH1	9:I:64:THR:HG21	2.29	0.42
12:L:12:ARG:HB3	12:L:12:ARG:NH1	2.34	0.42
14:N:11:LYS:O	14:N:12:ARG:C	2.61	0.42
16:P:43:LYS:HD3	16:P:43:LYS:N	2.33	0.42
18:R:18:ARG:O	18:R:19:LYS:HB2	2.17	0.42
18:R:36:ASN:HD22	18:R:39:VAL:CG1	2.14	0.42
1:A:178:C:O2'	1:A:179:A:H5'	2.20	0.42
1:A:190(A):C:C2	1:A:190(I):G:N2	2.87	0.42
1:A:222:U:C2	1:A:223:U:C5	3.07	0.42
1:A:593:G:H1	1:A:646:U:H3	1.66	0.42
1:A:737:A:H2'	1:A:738:C:O4'	2.19	0.42
1:A:1416:G:H2'	1:A:1417:G:H5'	2.00	0.42
3:C:157:ILE:HD13	3:C:157:ILE:HA	1.93	0.42
4:D:16:GLY:O	4:D:33:MET:HE2	2.18	0.42
5:E:122:GLU:O	5:E:123:LEU:HD23	2.19	0.42
6:F:80:ARG:NH1	6:F:88:VAL:HB	2.34	0.42
8:H:11:THR:O	8:H:12:ARG:C	2.62	0.42
10:J:18:ALA:HA	10:J:21:GLN:CG	2.50	0.42
11:K:98:LEU:HA	11:K:101:SER:HB3	2.01	0.42
13:M:5:ALA:CB	13:M:22:ILE:HD13	2.44	0.42
14:N:50:LYS:O	14:N:52:GLN:HG3	2.19	0.42
15:O:15:PHE:CZ	15:O:84:LYS:HD3	2.54	0.42
16:P:9:PHE:CE1	16:P:18:ARG:HD2	2.54	0.42
20:T:29:LYS:O	20:T:32:ALA:HB3	2.19	0.42
1:A:313:A:C6	1:A:314:C:N4	2.88	0.42
1:A:393:A:O2'	1:A:394:G:H5'	2.19	0.42
1:A:448:A:C4	1:A:487:A:C2	3.08	0.42
1:A:667:G:H4'	15:O:51:HIS:ND1	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:881:G:H2'	1:A:882:C:O4'	2.20	0.42
1:A:1119:C:O2	1:A:1155:G:C2	2.73	0.42
1:A:1148:U:N3	1:A:1149:C:C2	2.87	0.42
1:A:1357:A:C4	1:A:1358:U:C5	3.07	0.42
1:A:1511:G:C2'	1:A:1512:U:H5'	2.50	0.42
2:B:118:LEU:C	2:B:120:ALA:H	2.27	0.42
3:C:90:GLU:HA	3:C:93:LYS:CB	2.50	0.42
4:D:55:ALA:O	4:D:59:ARG:HG2	2.19	0.42
8:H:33:GLU:HG3	8:H:48:TYR:CE1	2.54	0.42
8:H:73:ASP:OD2	8:H:73:ASP:C	2.62	0.42
11:K:63:LEU:H	11:K:63:LEU:HG	1.60	0.42
11:K:83:ILE:HA	11:K:109:VAL:O	2.19	0.42
12:L:117:ARG:O	12:L:118:SER:C	2.63	0.42
13:M:71:ARG:O	13:M:74:VAL:HG12	2.20	0.42
17:Q:10:VAL:HG23	17:Q:55:ASP:O	2.20	0.42
17:Q:85:VAL:O	17:Q:86:GLU:C	2.62	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:622:A:C8	1:A:623:C:C6	3.08	0.42
1:A:862:C:C2'	1:A:863:U:H5'	2.49	0.42
1:A:974:A:P	14:N:41:ARG:HH12	2.40	0.42
1:A:1046:A:N3	1:A:1046:A:H2'	2.34	0.42
1:A:1290:G:C6	1:A:1291:G:C6	3.07	0.42
1:A:1502:A:H2'	1:A:1504:G:N7	2.34	0.42
2:B:129:GLU:O	2:B:130:ARG:HB2	2.19	0.42
3:C:156:ARG:HD3	3:C:160:ALA:O	2.20	0.42
4:D:188:LEU:HD12	4:D:188:LEU:N	2.19	0.42
11:K:105:VAL:O	11:K:106:LYS:C	2.61	0.42
1:A:6:G:H1	5:E:98:THR:HG1	1.61	0.42
1:A:77:G:C6	1:A:92:C:N4	2.87	0.42
1:A:780:A:O2'	1:A:781:A:H5''	2.19	0.42
1:A:858:G:O6	1:A:869:G:C8	2.73	0.42
1:A:962:C:O2	1:A:1201:A:C2	2.73	0.42
1:A:1026:G:N2	1:A:1027:C:C6	2.87	0.42
1:A:1157:A:C4	1:A:1181:G:C2	3.07	0.42
1:A:1261:A:C8	1:A:1262:C:H5	2.37	0.42
1:A:1330:U:OP1	13:M:23:TYR:O	2.38	0.42
2:B:37:ASN:HB2	2:B:39:ILE:HD11	2.00	0.42
4:D:4:TYR:O	4:D:5:ILE:HB	2.19	0.42
4:D:110:PHE:HE2	4:D:146:ILE:HG22	1.84	0.42
7:G:145:ALA:O	7:G:146:GLU:HB3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:18:ALA:HA	10:J:21:GLN:HG3	2.00	0.42
11:K:34:ASP:C	11:K:36:ASP:H	2.28	0.42
16:P:34:GLU:OE2	16:P:55:ARG:HD2	2.19	0.42
1:A:1250:A:C2	1:A:1287:A:C2	3.07	0.42
1:A:1519:A:OP2	1:A:1519:A:H8	2.02	0.42
2:B:20:GLU:O	2:B:40:HIS:CD2	2.72	0.42
4:D:108:LEU:HD23	4:D:108:LEU:HA	1.80	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
12:L:77:LEU:HD23	12:L:77:LEU:HA	1.78	0.42
13:M:45:VAL:CG1	13:M:46:LYS:N	2.82	0.42
15:O:87:ILE:CG2	15:O:88:ARG:N	2.80	0.42
17:Q:59:ILE:HG22	17:Q:71:PHE:CD1	2.54	0.42
19:S:32:LYS:HE3	19:S:32:LYS:HB2	1.93	0.42
1:A:251:G:H4'	1:A:252:U:O5'	2.18	0.42
1:A:363:A:H5'	12:L:34:ARG:HB2	2.01	0.42
1:A:852:G:H2'	1:A:853:G:O5'	2.20	0.42
1:A:882:C:H2'	1:A:883:C:H6	1.83	0.42
1:A:1072:G:C6	1:A:1073:U:C4	3.07	0.42
1:A:1105:A:O2'	1:A:1106:G:H5'	2.19	0.42
1:A:1115:C:H2'	1:A:1116:C:C6	2.54	0.42
1:A:1182:G:C1'	1:A:1183:A:OP2	2.68	0.42
1:A:1228:C:H3'	1:A:1228:C:C6	2.54	0.42
1:A:1357:A:C6	1:A:1358:U:O4	2.72	0.42
2:B:25:ASN:HA	2:B:26:PRO:HD2	1.69	0.42
4:D:156:GLU:C	4:D:158:ILE:H	2.27	0.42
10:J:79:ARG:H	10:J:79:ARG:HG2	1.71	0.42
11:K:124:LYS:C	11:K:125:PHE:CD1	2.98	0.42
13:M:23:TYR:C	13:M:25:ILE:H	2.27	0.42
13:M:23:TYR:CD1	13:M:71:ARG:NH2	2.87	0.42
16:P:49:LEU:HD12	16:P:50:LYS:N	2.33	0.42
1:A:378:G:H2'	1:A:379:C:C6	2.54	0.42
1:A:520:A:OP1	12:L:52:LEU:HD12	2.20	0.42
1:A:689:C:H2'	1:A:690:G:O4'	2.20	0.42
1:A:760:G:H22	17:Q:105:ALA:HA	1.84	0.42
1:A:938:A:C6	1:A:939:G:C5	3.08	0.42
1:A:953:G:H2'	1:A:954:G:O4'	2.20	0.42
1:A:1036:G:H2'	1:A:1037:C:O4'	2.19	0.42
1:A:1372:U:H2'	1:A:1373:G:O4'	2.20	0.42
1:A:1470:G:O2'	1:A:1471:G:H5'	2.20	0.42
2:B:213:LEU:HD22	2:B:214:ILE:HD13	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:195:VAL:C	3:C:196:LEU:HD23	2.45	0.42
6:F:19:LEU:CD2	6:F:23:LYS:HG3	2.50	0.42
7:G:50:ILE:HD13	7:G:50:ILE:HA	1.78	0.42
8:H:49:GLU:O	8:H:51:VAL:HG13	2.20	0.42
9:I:118:LYS:O	9:I:119:ALA:HB3	2.20	0.42
11:K:53:SER:C	11:K:55:LYS:N	2.77	0.42
12:L:75:HIS:HD2	12:L:77:LEU:HB2	1.84	0.42
12:L:86:ARG:NH2	12:L:99:HIS:CD2	2.84	0.42
12:L:115:LYS:O	12:L:117:ARG:N	2.48	0.42
15:O:36:ILE:HG22	15:O:37:ASN:N	2.33	0.42
1:A:59:A:H2'	1:A:59:A:N3	2.34	0.42
1:A:202:U:H3'	1:A:202:U:OP2	2.20	0.42
1:A:350:G:O2'	1:A:351:G:H5'	2.19	0.42
1:A:995:C:H6	1:A:995:C:O5'	2.03	0.42
1:A:1154:G:N3	1:A:1155:G:C8	2.88	0.42
1:A:1349:A:H2'	1:A:1350:A:O4'	2.19	0.42
1:A:1487:G:C5	1:A:1488:G:C8	3.08	0.42
2:B:189:ASP:HB3	2:B:191:ASP:OD1	2.20	0.42
5:E:40:ARG:HG2	5:E:40:ARG:NH1	2.35	0.42
5:E:135:THR:O	5:E:138:ALA:HB3	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
11:K:111:ASP:O	11:K:112:THR:C	2.62	0.42
14:N:24:CYS:HB3	14:N:29:ARG:N	2.21	0.42
1:A:417:C:C5	1:A:418:C:C5	3.08	0.42
1:A:669:U:H2'	1:A:670:G:C8	2.54	0.42
1:A:1346:A:N1	1:A:1374:A:H5''	2.35	0.42
2:B:97:TRP:CZ3	2:B:172:ILE:HG22	2.55	0.42
4:D:125:HIS:O	4:D:126:ILE:HD13	2.20	0.42
4:D:155:LEU:HD23	4:D:155:LEU:HA	1.82	0.42
6:F:60:PHE:CZ	18:R:78:LEU:HD21	2.55	0.42
7:G:92:SER:O	7:G:96:GLN:HG3	2.20	0.42
10:J:71:LEU:O	10:J:72:VAL:HB	2.20	0.42
17:Q:12:SER:HB3	17:Q:20:THR:CB	2.49	0.42
20:T:24:LEU:HD12	20:T:24:LEU:HA	1.92	0.42
20:T:74:LYS:C	20:T:76:ALA:H	2.25	0.42
1:A:1112:C:H1'	3:C:179:ARG:HH11	1.84	0.41
1:A:1118:C:C1'	1:A:1179:A:C4	3.02	0.41
2:B:77:ALA:HB2	2:B:165:VAL:HG11	2.01	0.41
4:D:31:CYS:O	4:D:31:CYS:SG	2.78	0.41
5:E:18:ARG:HH11	5:E:18:ARG:CG	2.27	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:102:ALA:CA	5:E:120:THR:OG1	2.61	0.41
7:G:29:LYS:O	7:G:105:VAL:HG11	2.20	0.41
11:K:40:ILE:HG22	11:K:41:THR:N	2.34	0.41
12:L:39:VAL:CG1	12:L:40:VAL:N	2.82	0.41
12:L:45:PRO:HG2	12:L:49:ASN:O	2.19	0.41
15:O:87:ILE:O	15:O:88:ARG:HB2	2.20	0.41
19:S:15:LEU:O	19:S:19:VAL:HG12	2.20	0.41
20:T:84:LEU:O	20:T:85:MET:C	2.63	0.41
1:A:129(A):G:H1'	1:A:190(E):U:H2'	2.02	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
1:A:602:A:N3	1:A:637:G:C2	2.87	0.41
1:A:837:G:C2	1:A:850:U:O2	2.73	0.41
1:A:893:C:H5''	1:A:1416:G:H5'	2.02	0.41
1:A:991:U:H5	1:A:1212:U:N3	2.16	0.41
1:A:1392:G:C5	1:A:1393:U:C5	3.08	0.41
1:A:1414:U:H2'	1:A:1414:U:O2	2.19	0.41
1:A:1422:G:C2	1:A:1423:G:C8	3.07	0.41
1:A:1540:U:C5	1:A:1541:U:C2	3.07	0.41
4:D:100:ARG:NH1	4:D:137:SER:HA	2.35	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
10:J:50:ILE:O	14:N:41:ARG:HD2	2.20	0.41
14:N:54:PRO:C	14:N:56:VAL:H	2.28	0.41
15:O:32:LEU:N	15:O:32:LEU:HD23	2.34	0.41
1:A:27:G:C6	1:A:557:G:C2	3.08	0.41
1:A:88:A:C4	1:A:89:C:C6	3.08	0.41
1:A:98:U:C6	1:A:98:U:H3'	2.55	0.41
1:A:114:U:H2'	1:A:115:G:C8	2.55	0.41
1:A:442:C:C4	1:A:443:C:H5	2.39	0.41
1:A:914:A:C2	1:A:915:A:C8	3.08	0.41
1:A:1043:C:H2'	1:A:1044:A:C8	2.55	0.41
1:A:1167:A:H8	1:A:1167:A:OP1	2.02	0.41
1:A:1410:G:N2	1:A:1411:C:C2	2.88	0.41
1:A:1484:C:H2'	1:A:1485:U:O4'	2.19	0.41
2:B:139:LYS:HD3	2:B:139:LYS:C	2.44	0.41
3:C:116:VAL:HG21	3:C:202:ILE:HD11	2.02	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
12:L:57:LYS:NZ	12:L:67:THR:HB	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:9:GLN:C	15:O:11:VAL:N	2.77	0.41
16:P:39:TYR:HE2	16:P:41:PRO:HG3	1.84	0.41
19:S:9:VAL:HG12	19:S:10:PHE:N	2.35	0.41
20:T:54:LYS:HE2	20:T:54:LYS:HB3	1.94	0.41
1:A:95:U:H2'	1:A:96:G:H8	1.83	0.41
1:A:197:A:H1'	1:A:198:G:C1'	2.51	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
2:B:194:PRO:O	2:B:195:ASP:C	2.64	0.41
2:B:230:VAL:CG1	2:B:231:GLU:H	2.33	0.41
2:B:239:VAL:C	2:B:240:GLN:HG2	2.45	0.41
3:C:23:TYR:CZ	3:C:24:ALA:O	2.74	0.41
3:C:59:ARG:HG2	3:C:63:ASN:O	2.19	0.41
3:C:137:ALA:HA	3:C:140:ARG:CZ	2.50	0.41
3:C:178:LEU:O	3:C:180:ALA:N	2.54	0.41
6:F:9:VAL:HG23	6:F:87:ARG:HB2	2.01	0.41
7:G:71:PRO:O	7:G:96:GLN:HG2	2.20	0.41
8:H:82:HIS:CD2	8:H:138:TRP:HE1	2.39	0.41
9:I:32:ASP:CG	9:I:33:PHE:N	2.78	0.41
11:K:56:GLY:O	11:K:57:THR:O	2.38	0.41
13:M:4:ILE:O	13:M:5:ALA:O	2.38	0.41
16:P:17:TYR:HE1	16:P:41:PRO:HG3	1.85	0.41
18:R:19:LYS:HE2	18:R:19:LYS:HB3	1.92	0.41
18:R:41:LYS:HG3	18:R:42:ARG:N	2.35	0.41
21:U:24:ARG:H	21:U:24:ARG:HG2	1.60	0.41
1:A:46:G:O2'	1:A:365:U:H1'	2.19	0.41
1:A:224:C:H2'	1:A:225:C:H6	1.84	0.41
1:A:691:G:H2'	1:A:692:U:H6	1.86	0.41
1:A:1250:A:C2	1:A:1251:A:C2	3.09	0.41
2:B:19:HIS:CE1	2:B:189:ASP:OD1	2.73	0.41
3:C:9:GLY:HA2	3:C:12:LEU:HG	2.01	0.41
7:G:74:GLU:HG2	7:G:91:VAL:HG22	2.02	0.41
8:H:25:ASP:OD1	8:H:25:ASP:N	2.53	0.41
9:I:127:LYS:O	9:I:128:ARG:C	2.62	0.41
15:O:7:GLU:O	15:O:10:LYS:HE2	2.20	0.41
16:P:4:ILE:HG13	16:P:64:ALA:HB1	2.03	0.41
18:R:18:ARG:HD3	18:R:18:ARG:HA	1.88	0.41
18:R:51:LEU:HA	18:R:51:LEU:HD23	1.80	0.41
20:T:33:ILE:HG12	20:T:62:LEU:HD22	2.01	0.41
1:A:375:U:O2'	1:A:376:G:H5'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:393:A:C4	1:A:394:G:C8	3.08	0.41
1:A:423:G:N2	1:A:424:G:C8	2.89	0.41
1:A:428:G:C1'	1:A:429:U:OP2	2.68	0.41
1:A:575:G:C6	1:A:821:G:N7	2.89	0.41
1:A:1271:G:H5'	1:A:1314:C:H5''	2.03	0.41
1:A:1421:G:N2	1:A:1480:G:C4	2.89	0.41
2:B:73:THR:HB	2:B:170:GLU:OE1	2.20	0.41
2:B:230:VAL:CG1	2:B:231:GLU:N	2.83	0.41
6:F:4:TYR:CZ	6:F:72:VAL:HG21	2.55	0.41
6:F:76:ALA:O	6:F:80:ARG:HG3	2.21	0.41
7:G:43:PHE:HD2	7:G:44:TYR:CD2	2.39	0.41
8:H:10:LEU:HD23	8:H:10:LEU:HA	1.75	0.41
9:I:11:LYS:O	9:I:12:GLU:CB	2.64	0.41
11:K:92:GLU:C	11:K:94:ALA:H	2.28	0.41
16:P:76:GLN:C	16:P:78:GLY:N	2.79	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
1:A:574:A:H1'	1:A:883:C:O4'	2.21	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
1:A:933:G:OP2	7:G:3:ARG:O	2.39	0.41
1:A:962:C:O2	1:A:1201:A:H2	2.03	0.41
1:A:1267:C:C5	1:A:1268:A:C5	3.09	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:1370:G:C2	1:A:1371:G:C8	3.09	0.41
2:B:174:VAL:O	2:B:177:ALA:HB3	2.20	0.41
4:D:42:GLN:O	4:D:42:GLN:HG2	2.19	0.41
4:D:199:ASN:C	4:D:199:ASN:ND2	2.76	0.41
5:E:144:THR:HG22	5:E:145:LYS:N	2.35	0.41
6:F:61:LEU:HB3	6:F:63:TYR:HE2	1.85	0.41
7:G:22:LEU:HD21	7:G:66:VAL:HG11	2.02	0.41
8:H:112:LEU:N	8:H:112:LEU:CD2	2.84	0.41
9:I:70:LYS:O	9:I:71:SER:C	2.64	0.41
10:J:44:VAL:HG11	10:J:66:ARG:NE	2.27	0.41
11:K:66:LEU:O	11:K:67:ASP:C	2.64	0.41
15:O:7:GLU:O	15:O:10:LYS:HG2	2.20	0.41
15:O:68:ARG:HB2	15:O:68:ARG:HH11	1.86	0.41
20:T:69:GLY:C	20:T:71:THR:H	2.28	0.41
1:A:327:A:O2'	1:A:328:C:H6	2.03	0.41
1:A:376:G:C2	1:A:389:A:C2	3.09	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:604:G:C6	1:A:635:G:C6	3.08	0.41
1:A:902:G:H2'	1:A:903:G:H8	1.86	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
1:A:1430:C:H2'	1:A:1431:C:C6	2.50	0.41
4:D:119:GLN:HG2	4:D:123:HIS:CD2	2.56	0.41
5:E:50:GLU:HG3	5:E:52:PRO:HD2	2.03	0.41
6:F:99:ALA:O	6:F:100:ASN:C	2.62	0.41
9:I:48:GLU:N	9:I:49:PRO:CD	2.84	0.41
9:I:102:LEU:H	9:I:102:LEU:HD12	1.86	0.41
10:J:63:PHE:CD1	10:J:63:PHE:N	2.89	0.41
12:L:29:GLY:O	12:L:30:ALA:C	2.63	0.41
12:L:54:LYS:N	12:L:54:LYS:CD	2.84	0.41
13:M:22:ILE:HG22	13:M:23:TYR:N	2.35	0.41
18:R:37:VAL:HG22	18:R:78:LEU:HB3	2.02	0.41
1:A:190(D):U:O2'	1:A:190(E):U:H5'	2.21	0.41
1:A:385:C:H2'	1:A:386:C:H6	1.85	0.41
1:A:403:C:O2'	1:A:404:U:H5'	2.20	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
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:OP2	1:A:792:A:H2'	2.20	0.41
1:A:828:A:C2'	1:A:829:G:O5'	2.69	0.41
1:A:922:G:C6	1:A:923:A:C6	3.08	0.41
1:A:922:G:C2	1:A:1396:A:C6	3.09	0.41
1:A:1030(C):G:C6	1:A:1030(D):A:N6	2.89	0.41
1:A:1071:C:O2'	1:A:1072:G:H5'	2.21	0.41
1:A:1133:G:H1	1:A:1141:C:H42	1.67	0.41
1:A:1206:G:C6	1:A:1207:G:C6	3.09	0.41
2:B:180:LEU:O	2:B:181:PHE:CB	2.68	0.41
3:C:34:LEU:O	3:C:38:ARG:HG2	2.21	0.41
3:C:159:GLY:HA2	3:C:193:TYR:CD1	2.56	0.41
4:D:47:ARG:HD2	4:D:47:ARG:HA	1.71	0.41
5:E:71:LEU:HD21	5:E:115:VAL:HG22	2.03	0.41
7:G:57:GLU:HB2	7:G:58:PRO:HD2	2.02	0.41
9:I:18:PHE:HD1	9:I:62:TYR:CD2	2.39	0.41
9:I:112:LYS:C	9:I:112:LYS:CD	2.91	0.41
10:J:40:LEU:HB3	10:J:69:ASN:O	2.21	0.41
11:K:53:SER:O	11:K:54:ARG:C	2.64	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:29:ARG:NH2	13:M:64:TRP:CD1	2.89	0.41
16:P:3:LYS:HG2	16:P:65:GLN:HB2	2.03	0.41
17:Q:51:TYR:CG	17:Q:73:VAL:HG11	2.56	0.41
17:Q:85:VAL:HG12	17:Q:89:LEU:HG	2.03	0.41
20:T:34:LYS:HE2	20:T:80:ARG:HH12	1.86	0.41
1:A:417:C:C5	1:A:418:C:H5	2.39	0.41
1:A:450:G:C8	1:A:481:G:C6	3.09	0.41
1:A:463:A:C5	1:A:474:G:C8	3.09	0.41
1:A:492:G:H2'	1:A:494:G:H8	1.86	0.41
1:A:567:G:C2	1:A:568:G:H1'	2.56	0.41
1:A:1003(A):G:N2	1:A:1039:C:C4	2.89	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
2:B:27:LYS:HD2	2:B:193:ASP:CG	2.46	0.41
3:C:5:ILE:H	3:C:5:ILE:HG13	1.70	0.41
3:C:10:PHE:HD2	3:C:11:ARG:HG3	1.86	0.41
7:G:48:LYS:HG3	7:G:49:ILE:N	2.36	0.41
8:H:83:ILE:HB	8:H:137:VAL:HG13	2.01	0.41
15:O:9:GLN:O	15:O:11:VAL:N	2.53	0.41
1:A:291:C:C2'	1:A:292:G:H5'	2.51	0.40
1:A:961:U:C2	1:A:983:A:C6	3.09	0.40
1:A:1106:G:O2'	1:A:1107:C:H5'	2.21	0.40
1:A:1261:A:N6	1:A:1275:A:C8	2.89	0.40
1:A:1419:G:H1	1:A:1481:U:H3	1.69	0.40
1:A:1487:G:C2'	1:A:1488:G:C5'	2.96	0.40
2:B:221:LEU:HD13	2:B:224:GLN:OE1	2.21	0.40
5:E:136:MET:O	5:E:137:GLU:C	2.64	0.40
10:J:16:LEU:CD2	10:J:94:VAL:HG13	2.51	0.40
20:T:44:ALA:C	20:T:46:GLU:N	2.79	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
1:A:1029:C:N3	1:A:1033:G:N2	2.69	0.40
1:A:1182:G:H1'	1:A:1183:A:OP2	2.22	0.40
1:A:1284:C:C2	1:A:1285:A:N7	2.89	0.40
1:A:1361(A):C:H1'	1:A:1362:C:H5''	2.03	0.40
2:B:208:ILE:N	2:B:208:ILE:HD13	2.36	0.40
3:C:36:ASP:HA	3:C:39:ILE:HD12	2.03	0.40
8:H:19:VAL:O	8:H:19:VAL:CG2	2.66	0.40
9:I:14:VAL:O	9:I:65:VAL:HG13	2.21	0.40
12:L:107:ALA:O	12:L:108:ALA:O	2.38	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:76:GLU:O	15:O:77:ARG:C	2.63	0.40
16:P:4:ILE:CD1	16:P:64:ALA:HB1	2.52	0.40
19:S:5:LEU:O	19:S:6:LYS:CB	2.52	0.40
20:T:89:ARG:NH2	20:T:104:LEU:HB3	2.37	0.40
1:A:146:G:C2	1:A:177:C:N3	2.89	0.40
1:A:401:C:O2'	1:A:621:A:N3	2.49	0.40
1:A:448:A:C2	1:A:449:C:C2	3.10	0.40
1:A:1034:G:N1	1:A:1035:A:C6	2.89	0.40
1:A:1118:C:O2	1:A:1179:A:C6	2.74	0.40
1:A:1119:C:O2	1:A:1155:G:N2	2.54	0.40
1:A:1174:G:N2	1:A:1175:G:C4	2.89	0.40
1:A:1179:A:H2'	1:A:1180:A:O4'	2.21	0.40
1:A:1204:A:C6	1:A:1205:U:C2	3.09	0.40
1:A:1243:C:OP2	21:U:10:ARG:NH2	2.54	0.40
2:B:172:ILE:HD12	2:B:172:ILE:N	2.32	0.40
3:C:121:ALA:CB	3:C:189:ALA:HB2	2.52	0.40
3:C:145:GLY:O	3:C:146:ALA:HB3	2.21	0.40
4:D:152:SER:HB2	4:D:155:LEU:CD1	2.51	0.40
6:F:14:LEU:HB3	6:F:18:GLN:HB2	2.03	0.40
6:F:48:LEU:HG	6:F:57:GLN:CA	2.51	0.40
8:H:96:GLY:N	8:H:99:GLU:HG3	2.36	0.40
9:I:38:GLN:C	9:I:40:LEU:H	2.29	0.40
10:J:16:LEU:HD23	10:J:16:LEU:HA	1.93	0.40
11:K:111:ASP:O	11:K:111:ASP:OD2	2.38	0.40
13:M:55:ARG:HA	13:M:58:GLU:HG2	2.04	0.40
16:P:40:ASP:OD2	16:P:40:ASP:C	2.64	0.40
16:P:60:LEU:HD23	16:P:60:LEU:HA	1.80	0.40
18:R:36:ASN:ND2	18:R:39:VAL:CG1	2.79	0.40
18:R:52:PRO:O	18:R:56:THR:HG23	2.22	0.40
1:A:131:C:O2	1:A:231:G:N2	2.50	0.40
1:A:149:A:N3	1:A:150:C:C6	2.89	0.40
1:A:255:G:C6	1:A:256:U:O4	2.74	0.40
1:A:357:G:H1'	1:A:368:U:O2	2.22	0.40
1:A:574:A:H1'	1:A:883:C:C1'	2.51	0.40
1:A:581:G:O2'	1:A:582:U:H5'	2.22	0.40
1:A:819:A:H4'	1:A:820:U:OP2	2.21	0.40
1:A:1014:A:N7	1:A:1015:A:C6	2.89	0.40
1:A:1052:U:N3	1:A:1200:C:C4	2.90	0.40
1:A:1088:G:H8	1:A:1088:G:O5'	2.05	0.40
1:A:1371:G:C4	1:A:1372:U:C5	3.09	0.40
1:A:1512:U:H3	1:A:1523:G:H1	1.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1521:G:H2'	1:A:1522:U:H6	1.85	0.40
2:B:117:GLU:O	2:B:120:ALA:HB3	2.21	0.40
2:B:167:PRO:HG2	2:B:192:SER:HB3	2.04	0.40
4:D:43:HIS:O	4:D:44:GLY:C	2.64	0.40
4:D:108:LEU:HD23	4:D:170:VAL:HG21	2.04	0.40
5:E:50:GLU:O	5:E:51:VAL:C	2.63	0.40
5:E:102:ALA:HA	5:E:120:THR:HG1	1.84	0.40
12:L:93:LEU:N	12:L:93:LEU:HD23	2.37	0.40
13:M:19:LEU:HD11	13:M:56:LEU:HD21	2.04	0.40
16:P:19:ILE:HG22	16:P:36:ILE:HG13	2.03	0.40
16:P:42:ARG:O	16:P:43:LYS:C	2.64	0.40
19:S:10:PHE:CD2	19:S:10:PHE:C	2.99	0.40
20:T:48:LYS:O	20:T:49:ALA:C	2.64	0.40
1:A:92:C:H5	1:A:93:G:N7	2.16	0.40
1:A:299:G:C5	1:A:300:A:C6	3.09	0.40
1:A:448:A:N1	1:A:449:C:C4	2.90	0.40
1:A:601:C:O2'	1:A:602:A:H5'	2.21	0.40
1:A:631:G:N3	1:A:631:G:H2'	2.37	0.40
1:A:808:C:O2'	1:A:809:G:H5'	2.22	0.40
1:A:925:G:C2	1:A:927:G:C8	3.10	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
1:A:1124:G:N3	1:A:1127:G:N2	2.69	0.40
1:A:1201:A:C1'	1:A:1202:G:OP2	2.65	0.40
1:A:1244:C:H42	1:A:1293:G:H1	1.69	0.40
1:A:1260:C:H2'	1:A:1261:A:OP2	2.21	0.40
2:B:166:ASP:OD1	2:B:167:PRO:HD2	2.21	0.40
3:C:29:TYR:O	3:C:33:LEU:HB2	2.22	0.40
5:E:15:ARG:NH1	5:E:26:PHE:CZ	2.89	0.40
7:G:77:SER:O	7:G:78:ARG:HB2	2.21	0.40
12:L:113:ARG:HH12	12:L:116:SER:H	1.69	0.40
21:U:6:ARG:HD2	21:U:15:ARG:HH12	1.87	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

of similar resolution.

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	233/256 (91%)	168 (72%)	45 (19%)	20 (9%)	0	8
3	C	204/239 (85%)	152 (74%)	37 (18%)	15 (7%)	1	11
4	D	206/209 (99%)	168 (82%)	32 (16%)	6 (3%)	3	26
5	E	148/162 (91%)	119 (80%)	26 (18%)	3 (2%)	6	32
6	F	99/101 (98%)	80 (81%)	17 (17%)	2 (2%)	6	32
7	G	153/156 (98%)	105 (69%)	34 (22%)	14 (9%)	0	8
8	H	136/138 (99%)	115 (85%)	15 (11%)	6 (4%)	2	19
9	I	125/128 (98%)	86 (69%)	28 (22%)	11 (9%)	0	8
10	J	96/105 (91%)	60 (62%)	22 (23%)	14 (15%)	0	2
11	K	117/129 (91%)	85 (73%)	22 (19%)	10 (8%)	0	8
12	L	122/135 (90%)	87 (71%)	22 (18%)	13 (11%)	0	5
13	M	113/126 (90%)	91 (80%)	16 (14%)	6 (5%)	1	16
14	N	58/61 (95%)	40 (69%)	13 (22%)	5 (9%)	0	8
15	O	86/89 (97%)	70 (81%)	13 (15%)	3 (4%)	3	24
16	P	81/88 (92%)	63 (78%)	11 (14%)	7 (9%)	0	8
17	Q	102/105 (97%)	86 (84%)	14 (14%)	2 (2%)	6	32
18	R	71/88 (81%)	53 (75%)	14 (20%)	4 (6%)	1	16
19	S	78/93 (84%)	47 (60%)	19 (24%)	12 (15%)	0	2
20	T	97/106 (92%)	60 (62%)	28 (29%)	9 (9%)	0	7
21	U	22/27 (82%)	17 (77%)	5 (23%)	0	100	100
All	All	2347/2541 (92%)	1752 (75%)	433 (18%)	162 (7%)	1	13

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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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%)	174 (90%)	20 (10%)	7	29
3	C	160/188 (85%)	148 (92%)	12 (8%)	12	39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	D	180/181 (99%)	166 (92%)	14 (8%)	11	37
5	E	115/123 (94%)	94 (82%)	21 (18%)	2	11
6	F	90/90 (100%)	81 (90%)	9 (10%)	7	30
7	G	126/127 (99%)	115 (91%)	11 (9%)	9	34
8	H	119/119 (100%)	103 (87%)	16 (13%)	4	20
9	I	98/99 (99%)	87 (89%)	11 (11%)	6	25
10	J	87/92 (95%)	80 (92%)	7 (8%)	11	37
11	K	90/99 (91%)	81 (90%)	9 (10%)	7	30
12	L	104/111 (94%)	89 (86%)	15 (14%)	3	18
13	M	93/101 (92%)	79 (85%)	14 (15%)	3	16
14	N	49/50 (98%)	47 (96%)	2 (4%)	27	52
15	O	79/80 (99%)	71 (90%)	8 (10%)	7	29
16	P	72/74 (97%)	64 (89%)	8 (11%)	6	25
17	Q	96/97 (99%)	89 (93%)	7 (7%)	13	40
18	R	64/77 (83%)	56 (88%)	8 (12%)	4	21
19	S	71/80 (89%)	65 (92%)	6 (8%)	10	35
20	T	76/82 (93%)	66 (87%)	10 (13%)	4	20
21	U	19/22 (86%)	17 (90%)	2 (10%)	6	28
All	All	1982/2112 (94%)	1772 (89%)	210 (11%)	6	27

All (210) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	15	VAL
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	101	MET
2	B	139	LYS
2	B	140	HIS
2	B	142	LEU
2	B	158	LEU
2	B	168	THR

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Mol	Chain	Res	Type
2	B	187	LEU
2	B	190	THR
2	B	208	ILE
2	B	217	ARG
2	B	221	LEU
2	B	223	ILE
2	B	240	GLN
3	C	3	ASN
3	C	14	ILE
3	C	26	LYS
3	C	33	LEU
3	C	75	VAL
3	C	104	GLN
3	C	126	ARG
3	C	132	ARG
3	C	157	ILE
3	C	167	TRP
3	C	179	ARG
3	C	190	ARG
4	D	9	CYS
4	D	15	GLU
4	D	17	VAL
4	D	26	CYS
4	D	36	ARG
4	D	63	LYS
4	D	64	LEU
4	D	78	LEU
4	D	112	VAL
4	D	122	ARG
4	D	127	THR
4	D	141	ARG
4	D	188	LEU
4	D	194	LEU
5	E	6	PHE
5	E	9	LYS
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

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Mol	Chain	Res	Type
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	135	THR
5	E	137	GLU
5	E	144	THR
5	E	147	ASP
5	E	148	VAL
6	F	9	VAL
6	F	10	LEU
6	F	15	ASP
6	F	18	GLN
6	F	23	LYS
6	F	30	LEU
6	F	45	LEU
6	F	94	GLN
6	F	100	ASN
7	G	8	GLU
7	G	12	LEU
7	G	16	LEU
7	G	24	THR
7	G	36	LYS
7	G	41	ARG
7	G	50	ILE
7	G	66	VAL
7	G	114	ARG
7	G	135	VAL
7	G	153	HIS
8	H	3	THR
8	H	11	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	83	ILE
8	H	85	ARG

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Mol	Chain	Res	Type
8	H	88	LYS
8	H	95	VAL
8	H	102	ARG
8	H	112	LEU
8	H	113	SER
8	H	133	LEU
9	I	14	VAL
9	I	16	ARG
9	I	48	GLU
9	I	59	PHE
9	I	62	TYR
9	I	64	THR
9	I	79	LEU
9	I	102	LEU
9	I	108	VAL
9	I	109	VAL
9	I	114	TYR
10	J	6	ILE
10	J	21	GLN
10	J	23	ILE
10	J	49	VAL
10	J	54	PHE
10	J	75	ILE
10	J	99	LYS
11	K	11	LYS
11	K	25	TYR
11	K	29	ILE
11	K	48	ILE
11	K	75	TYR
11	K	98	LEU
11	K	105	VAL
11	K	120	ARG
11	K	124	LYS
12	L	20	LYS
12	L	36	VAL
12	L	44	THR
12	L	49	ASN
12	L	58	VAL
12	L	64	TYR
12	L	66	VAL
12	L	67	THR
12	L	82	VAL

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Mol	Chain	Res	Type
12	L	85	ILE
12	L	93	LEU
12	L	96	VAL
12	L	98	TYR
12	L	104	VAL
12	L	111	LYS
13	M	8	GLU
13	M	11	ARG
13	M	14	ARG
13	M	17	VAL
13	M	27	LYS
13	M	37	THR
13	M	44	ARG
13	M	48	LEU
13	M	74	VAL
13	M	91	ARG
13	M	94	ARG
13	M	99	ARG
13	M	101	GLN
13	M	103	THR
14	N	6	LEU
14	N	25	VAL
15	O	5	LYS
15	O	11	VAL
15	O	17	ARG
15	O	31	LEU
15	O	36	ILE
15	O	70	LEU
15	O	71	GLN
15	O	81	LEU
16	P	2	VAL
16	P	22	THR
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	23	VAL
17	Q	35	VAL
17	Q	36	ILE
17	Q	38	ARG

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Mol	Chain	Res	Type
17	Q	53	LEU
17	Q	59	ILE
17	Q	77	VAL
18	R	19	LYS
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	15	LEU
19	S	25	LYS
19	S	32	LYS
19	S	37	ARG
19	S	43	GLU
19	S	51	VAL
20	T	13	LEU
20	T	33	ILE
20	T	51	GLU
20	T	57	ARG
20	T	73	HIS
20	T	74	LYS
20	T	75	ASN
20	T	83	ARG
20	T	84	LEU
20	T	100	ILE
21	U	8	THR
21	U	13	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (54) 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

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Mol	Chain	Res	Type
3	C	108	ASN
3	C	136	GLN
3	C	162	GLN
3	C	176	HIS
4	D	116	GLN
4	D	119	GLN
4	D	123	HIS
4	D	154	ASN
4	D	161	ASN
4	D	199	ASN
5	E	20	GLN
5	E	72	GLN
5	E	73	ASN
6	F	18	GLN
6	F	27	GLN
6	F	64	GLN
6	F	94	GLN
7	G	11	GLN
7	G	37	ASN
7	G	68	ASN
7	G	96	GLN
7	G	97	GLN
7	G	106	GLN
8	H	82	HIS
9	I	23	ASN
9	I	73	GLN
10	J	21	GLN
10	J	69	ASN
10	J	76	ASN
11	K	22	HIS
11	K	38	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

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Mol	Chain	Res	Type
19	S	57	HIS
20	T	42	GLN
20	T	73	HIS

5.3.3 RNA ⓘ

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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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
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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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%)	-0.04	47 (3%) 51 32	50, 108, 253, 361	0
2	B	235/256 (91%)	-0.24	2 (0%) 81 58	65, 115, 197, 256	0
3	C	206/239 (86%)	0.05	7 (3%) 48 30	116, 170, 237, 271	0
4	D	208/209 (99%)	-0.01	9 (4%) 40 25	63, 111, 160, 175	0
5	E	150/162 (92%)	-0.39	0 100 100	51, 78, 114, 154	0
6	F	101/101 (100%)	-0.37	0 100 100	87, 129, 155, 177	0
7	G	155/156 (99%)	-0.08	2 (1%) 75 50	99, 152, 220, 233	0
8	H	138/138 (100%)	-0.54	0 100 100	41, 72, 104, 137	0
9	I	127/128 (99%)	0.17	4 (3%) 51 32	78, 171, 216, 224	0
10	J	98/105 (93%)	0.47	6 (6%) 27 18	122, 178, 274, 291	0
11	K	119/129 (92%)	-0.22	2 (1%) 69 43	62, 106, 146, 183	0
12	L	124/135 (91%)	-0.03	3 (2%) 59 37	48, 107, 143, 174	0
13	M	115/126 (91%)	0.09	3 (2%) 57 35	96, 136, 170, 180	0
14	N	60/61 (98%)	0.40	5 (8%) 17 14	125, 157, 213, 229	0
15	O	88/89 (98%)	-0.41	0 100 100	54, 95, 133, 171	0
16	P	83/88 (94%)	-0.21	1 (1%) 76 51	69, 99, 137, 199	0
17	Q	104/105 (99%)	-0.29	2 (1%) 66 42	54, 83, 125, 223	0
18	R	73/88 (82%)	-0.34	0 100 100	65, 99, 164, 209	0
19	S	80/93 (86%)	0.48	8 (10%) 12 13	149, 183, 219, 231	0
20	T	99/106 (93%)	-0.15	2 (2%) 65 41	76, 107, 165, 190	0
21	U	24/27 (88%)	0.92	5 (20%) 2 3	121, 141, 162, 171	0
All	All	3900/4063 (95%)	-0.07	108 (2%) 55 34	41, 116, 222, 361	0

All (108) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
20	T	106	ALA	6.8
1	A	1129	C	5.6
1	A	1003(A)	G	5.2
1	A	1491	G	5.2
9	I	9	ARG	5.1
19	S	3	ARG	5.1
11	K	128	ALA	4.7
1	A	202	U	4.6
12	L	115	LYS	4.5
1	A	1541	U	4.4
19	S	33	THR	4.4
1	A	1004	A	4.2
1	A	1492	A	4.1
1	A	1417	G	4.1
1	A	81	U	3.9
19	S	5	LEU	3.9
1	A	1540	U	3.8
1	A	6	G	3.8
19	S	2	PRO	3.8
1	A	77	G	3.5
10	J	34	VAL	3.5
14	N	2	ALA	3.5
1	A	993	G	3.4
14	N	3	ARG	3.4
1	A	74	C	3.3
1	A	1030(B)	C	3.3
11	K	129	SER	3.3
1	A	532	A	3.3
13	M	8	GLU	3.2
4	D	31	CYS	3.2
1	A	793	U	3.2
1	A	90	U	3.2
21	U	24	ARG	3.1
21	U	6	ARG	3.1
17	Q	102	GLY	3.1
19	S	35	SER	3.1
21	U	18	TYR	3.1
1	A	75	G	3.1
1	A	1416	G	3.1
4	D	22	LYS	3.1
21	U	25	LYS	3.1
9	I	8	GLY	3.0
1	A	221	C	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	985	C	2.9
13	M	91	ARG	2.9
10	J	37	PRO	2.9
1	A	723	U	2.9
10	J	36	GLY	2.9
1	A	979	C	2.8
1	A	1224	G	2.8
3	C	2	GLY	2.8
13	M	100	GLY	2.7
7	G	150	ALA	2.7
4	D	9	CYS	2.7
4	D	119	GLN	2.6
10	J	3	LYS	2.6
1	A	1220	G	2.6
1	A	994	A	2.6
1	A	1052	U	2.6
4	D	42	GLN	2.6
1	A	1281	U	2.6
19	S	81	ARG	2.5
1	A	1027	C	2.5
1	A	1543	C	2.5
19	S	77	THR	2.5
1	A	89	C	2.5
1	A	1002	G	2.5
1	A	1221	G	2.4
1	A	1128	C	2.4
1	A	1420	C	2.4
2	B	231	GLU	2.4
3	C	196	LEU	2.4
1	A	1490	C	2.3
2	B	203	GLY	2.3
19	S	32	LYS	2.3
4	D	21	LEU	2.3
14	N	57	ARG	2.3
14	N	6	LEU	2.2
12	L	26	ALA	2.2
1	A	97	G	2.2
10	J	100	THR	2.2
1	A	1144	G	2.2
9	I	38	GLN	2.2
9	I	56	LEU	2.2
12	L	19	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
3	C	193	TYR	2.2
1	A	351	G	2.1
3	C	102	ASN	2.1
1	A	1119	C	2.1
1	A	1147	C	2.1
10	J	4	ILE	2.1
3	C	158	GLY	2.1
4	D	3	ARG	2.1
16	P	68	ASP	2.1
1	A	1544	U	2.1
3	C	188	LEU	2.1
4	D	26	CYS	2.1
21	U	9	ARG	2.1
17	Q	105	ALA	2.1
20	T	73	HIS	2.1
1	A	1283	G	2.1
3	C	55	VAL	2.1
14	N	18	VAL	2.0
1	A	1219	U	2.0
4	D	196	LEU	2.0
1	A	353	A	2.0
1	A	1493	A	2.0
7	G	151	TYR	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
22	MG	A	1581	1/1	0.57	0.28	68,68,68,68	0
22	MG	A	1620	1/1	0.57	0.30	92,92,92,92	0
23	K	A	1631	1/1	0.57	0.32	110,110,110,110	0
22	MG	A	1603	1/1	0.58	0.27	100,100,100,100	0
22	MG	A	1558	1/1	0.62	0.14	81,81,81,81	0
22	MG	A	1557	1/1	0.64	0.39	90,90,90,90	0
22	MG	A	1574	1/1	0.65	0.35	68,68,68,68	0
23	K	A	1642	1/1	0.66	0.17	94,94,94,94	0
23	K	A	1655	1/1	0.68	0.19	102,102,102,102	0
23	K	A	1638	1/1	0.69	0.17	143,143,143,143	0
23	K	A	1637	1/1	0.70	0.25	129,129,129,129	0
23	K	A	1658	1/1	0.71	0.25	107,107,107,107	0
22	MG	A	1582	1/1	0.72	0.33	83,83,83,83	0
22	MG	A	1593	1/1	0.72	0.28	87,87,87,87	0
22	MG	A	1622	1/1	0.72	0.35	87,87,87,87	0
23	K	A	1635	1/1	0.73	0.37	149,149,149,149	0
23	K	A	1653	1/1	0.73	0.19	98,98,98,98	0
23	K	A	1643	1/1	0.74	0.25	122,122,122,122	0
23	K	A	1634	1/1	0.74	0.17	134,134,134,134	0
22	MG	A	1612	1/1	0.76	0.38	81,81,81,81	0
23	K	A	1661	1/1	0.78	0.15	79,79,79,79	0
22	MG	A	1571	1/1	0.79	0.41	67,67,67,67	0
23	K	A	1636	1/1	0.80	0.29	116,116,116,116	0
22	MG	A	1576	1/1	0.80	0.26	78,78,78,78	0
22	MG	A	1606	1/1	0.80	0.33	65,65,65,65	0
22	MG	A	1556	1/1	0.81	0.41	93,93,93,93	0
23	K	A	1656	1/1	0.81	0.27	105,105,105,105	0
22	MG	A	1588	1/1	0.81	0.26	59,59,59,59	0
22	MG	A	1626	1/1	0.81	0.18	62,62,62,62	0
23	K	A	1641	1/1	0.82	0.28	97,97,97,97	0
22	MG	A	1591	1/1	0.83	0.20	82,82,82,82	0
22	MG	A	1609	1/1	0.83	0.61	96,96,96,96	0
22	MG	A	1599	1/1	0.83	0.14	65,65,65,65	0
23	K	A	1654	1/1	0.83	0.16	85,85,85,85	0
22	MG	A	1600	1/1	0.83	0.20	72,72,72,72	0
22	MG	A	1601	1/1	0.83	0.10	78,78,78,78	0
22	MG	A	1592	1/1	0.83	0.36	63,63,63,63	0
22	MG	D	211	1/1	0.83	0.21	73,73,73,73	0
22	MG	A	1566	1/1	0.84	0.28	90,90,90,90	0
22	MG	A	1546	1/1	0.84	0.36	76,76,76,76	0
23	K	A	1657	1/1	0.85	0.25	83,83,83,83	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
22	MG	A	1551	1/1	0.85	0.16	50,50,50,50	0
23	K	A	1652	1/1	0.85	0.15	100,100,100,100	0
23	K	A	1667	1/1	0.85	0.21	80,80,80,80	0
22	MG	A	1580	1/1	0.86	0.11	79,79,79,79	0
22	MG	A	1545	1/1	0.86	0.09	75,75,75,75	0
23	K	A	1659	1/1	0.87	0.14	76,76,76,76	0
22	MG	A	1548	1/1	0.87	0.24	81,81,81,81	0
22	MG	A	1559	1/1	0.87	0.27	53,53,53,53	0
22	MG	A	1555	1/1	0.88	0.54	95,95,95,95	0
22	MG	A	1619	1/1	0.88	0.12	91,91,91,91	0
22	MG	A	1562	1/1	0.88	0.32	54,54,54,54	0
23	K	A	1648	1/1	0.88	0.16	63,63,63,63	0
22	MG	A	1565	1/1	0.88	0.15	87,87,87,87	0
22	MG	A	71	1/1	0.88	0.44	74,74,74,74	0
22	MG	A	1553	1/1	0.88	0.33	94,94,94,94	0
23	K	A	1668	1/1	0.88	0.22	95,95,95,95	0
23	K	A	1670	1/1	0.88	0.19	107,107,107,107	0
23	K	E	163	1/1	0.88	0.16	115,115,115,115	0
22	MG	A	1614	1/1	0.89	0.13	56,56,56,56	0
23	K	A	1646	1/1	0.89	0.36	82,82,82,82	0
23	K	A	1660	1/1	0.89	0.26	126,126,126,126	0
22	MG	A	1560	1/1	0.89	0.44	89,89,89,89	0
22	MG	A	1577	1/1	0.90	0.28	63,63,63,63	0
22	MG	A	1549	1/1	0.90	0.14	59,59,59,59	0
22	MG	A	1607	1/1	0.90	0.16	65,65,65,65	0
22	MG	B	257	1/1	0.90	0.19	77,77,77,77	0
22	MG	A	1598	1/1	0.90	0.34	73,73,73,73	0
22	MG	A	1613	1/1	0.91	0.23	39,39,39,39	0
22	MG	A	1611	1/1	0.91	0.07	56,56,56,56	0
22	MG	A	1608	1/1	0.91	0.35	72,72,72,72	0
23	K	A	1650	1/1	0.91	0.16	86,86,86,86	0
22	MG	A	1627	1/1	0.91	0.22	39,39,39,39	0
22	MG	A	1628	1/1	0.91	0.18	65,65,65,65	0
23	K	A	1647	1/1	0.92	0.11	85,85,85,85	0
22	MG	A	1596	1/1	0.92	0.33	54,54,54,54	0
23	K	A	1664	1/1	0.92	0.12	111,111,111,111	0
22	MG	A	1584	1/1	0.92	0.21	52,52,52,52	0
23	K	A	1651	1/1	0.92	0.33	138,138,138,138	0
22	MG	A	100	1/1	0.92	0.38	126,126,126,126	0
23	K	A	1671	1/1	0.92	0.29	79,79,79,79	0
23	K	A	1640	1/1	0.92	0.26	108,108,108,108	0
22	MG	A	1564	1/1	0.93	0.24	59,59,59,59	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
23	K	A	1662	1/1	0.93	0.29	92,92,92,92	0
23	K	A	1663	1/1	0.93	0.18	99,99,99,99	0
23	K	A	1632	1/1	0.93	0.10	102,102,102,102	0
23	K	A	1649	1/1	0.93	0.16	75,75,75,75	0
22	MG	A	1605	1/1	0.93	0.43	56,56,56,56	0
22	MG	A	1575	1/1	0.93	0.15	32,32,32,32	0
22	MG	A	1587	1/1	0.93	0.22	37,37,37,37	0
22	MG	A	1554	1/1	0.93	0.37	59,59,59,59	0
22	MG	A	1583	1/1	0.94	0.38	67,67,67,67	0
22	MG	A	1573	1/1	0.94	0.10	70,70,70,70	0
22	MG	A	1578	1/1	0.94	0.33	50,50,50,50	0
22	MG	A	1618	1/1	0.94	0.17	64,64,64,64	0
22	MG	A	1561	1/1	0.94	0.22	59,59,59,59	0
23	K	A	1666	1/1	0.94	0.16	74,74,74,74	0
22	MG	A	1590	1/1	0.94	0.27	39,39,39,39	0
22	MG	A	1563	1/1	0.94	0.19	20,20,20,20	0
23	K	A	1669	1/1	0.94	0.18	98,98,98,98	0
22	MG	A	94	1/1	0.94	0.42	66,66,66,66	0
22	MG	A	1625	1/1	0.94	0.43	93,93,93,93	0
22	MG	A	1572	1/1	0.94	0.20	35,35,35,35	0
22	MG	A	1630	1/1	0.95	0.17	41,41,41,41	0
22	MG	A	1547	1/1	0.95	0.21	86,86,86,86	0
22	MG	A	86	1/1	0.95	0.17	59,59,59,59	0
22	MG	A	1586	1/1	0.95	0.20	48,48,48,48	0
23	K	A	1639	1/1	0.95	0.33	81,81,81,81	0
22	MG	A	1604	1/1	0.95	0.16	52,52,52,52	0
22	MG	A	1629	1/1	0.95	0.19	61,61,61,61	0
23	K	A	1645	1/1	0.96	0.15	75,75,75,75	0
22	MG	A	1623	1/1	0.96	0.28	77,77,77,77	0
22	MG	A	1579	1/1	0.96	0.20	29,29,29,29	0
22	MG	A	1552	1/1	0.96	0.24	80,80,80,80	0
22	MG	A	1567	1/1	0.96	0.34	70,70,70,70	0
22	MG	A	1589	1/1	0.96	0.32	79,79,79,79	0
23	K	A	1633	1/1	0.96	0.07	135,135,135,135	0
22	MG	A	1585	1/1	0.96	0.21	78,78,78,78	0
22	MG	A	1617	1/1	0.96	0.15	78,78,78,78	0
22	MG	A	1597	1/1	0.97	0.39	47,47,47,47	0
22	MG	A	1610	1/1	0.97	0.17	47,47,47,47	0
23	K	A	1665	1/1	0.97	0.16	79,79,79,79	0
22	MG	M	127	1/1	0.97	0.16	76,76,76,76	0
22	MG	A	1615	1/1	0.97	0.10	55,55,55,55	0
22	MG	A	1602	1/1	0.97	0.21	63,63,63,63	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
22	MG	A	85	1/1	0.97	0.15	35,35,35,35	0
22	MG	A	1550	1/1	0.97	0.14	52,52,52,52	0
22	MG	A	1624	1/1	0.97	0.04	38,38,38,38	0
23	K	A	1644	1/1	0.97	0.22	55,55,55,55	0
22	MG	A	1570	1/1	0.98	0.24	34,34,34,34	0
22	MG	A	1616	1/1	0.98	0.15	49,49,49,49	0
22	MG	A	1568	1/1	0.98	0.10	17,17,17,17	0
22	MG	A	1621	1/1	0.98	0.03	58,58,58,58	0
22	MG	A	1569	1/1	0.98	0.11	59,59,59,59	0
22	MG	A	1595	1/1	0.98	0.07	33,33,33,33	0
24	ZN	D	210	1/1	0.98	0.18	85,85,85,85	0
22	MG	A	1594	1/1	0.99	0.06	46,46,46,46	0
24	ZN	N	141	1/1	1.00	0.02	150,150,150,150	0

6.5 Other polymers [i](#)

There are no such residues in this entry.