



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 07:06 pm GMT

PDB ID : 4DV2
Title : Crystal structure of the *Thermus thermophilus* 30S ribosomal subunit with a 16S rRNA mutation, C912A
Authors : Demirci, H.; Murphy IV, F.; Murphy, E.; Gregory, S.T.; Dahlberg, A.E.; Jogl, G.
Deposited on : 2012-02-22
Resolution : 3.65 Å(reported)

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

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

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk28620

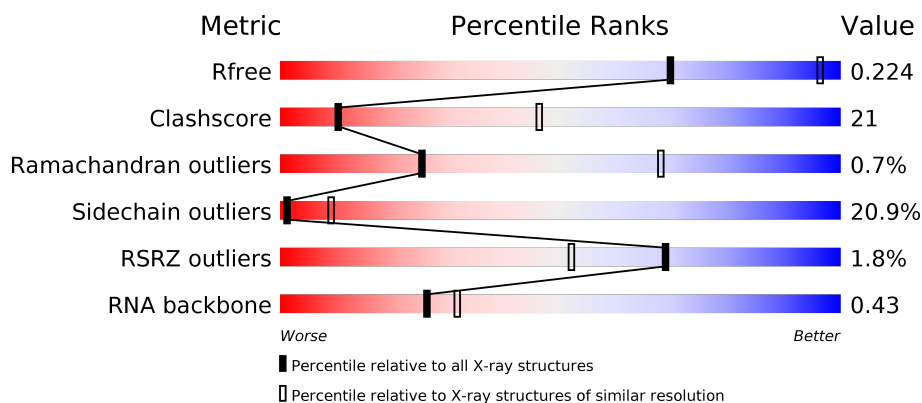
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.65 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.






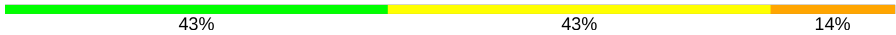
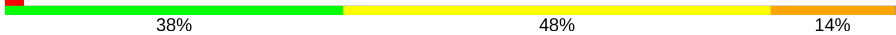
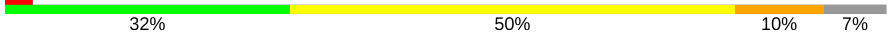
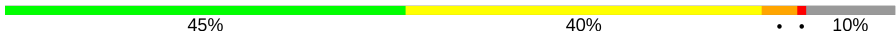
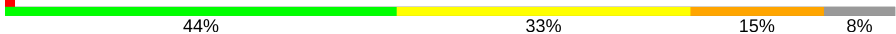
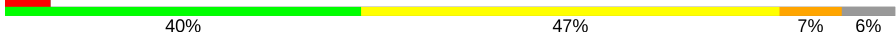
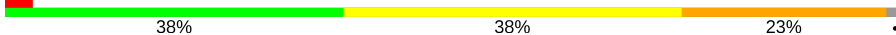
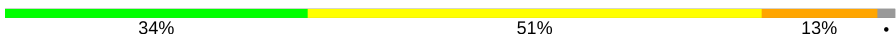
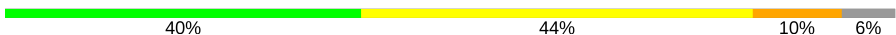
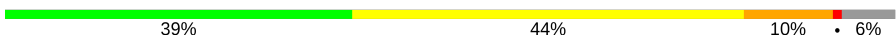
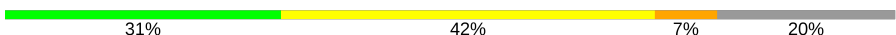



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	1143 (3.80-3.48)
Clashscore	112137	1092 (3.78-3.50)
Ramachandran outliers	110173	1051 (3.78-3.50)
Sidechain outliers	110143	1051 (3.78-3.50)
RSRZ outliers	101464	1000 (3.78-3.50)
RNA backbone	2435	1002 (4.30-2.90)

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

Mol	Chain	Length	Quality of chain
1	A	1522	<div> <div>2%</div> <div>20% 42% 29% 8%</div> </div>
2	B	256	<div> <div>41% 38% 13% 9%</div> </div>
3	C	239	<div> <div>5%</div> <div>30% 44% 12% 14%</div> </div>
4	D	209	<div> <div>%</div> <div>54% 36% 9%</div> </div>

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

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
22	MG	A	1615	-	-	-	X
22	MG	A	1642	-	-	-	X
22	MG	A	1645	-	-	-	X
22	MG	A	1649	-	-	-	X
22	MG	A	1711	-	-	-	X
22	MG	A	1714	-	-	-	X
22	MG	A	1718	-	-	-	X
22	MG	A	1727	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
22	MG	A	1730	-	-	-	X
22	MG	A	1759	-	-	-	X
22	MG	A	1775	-	-	-	X
22	MG	A	1781	-	-	-	X
22	MG	A	1809	-	-	-	X
22	MG	A	1822	-	-	-	X
22	MG	A	1824	-	-	-	X
22	MG	A	1834	-	-	-	X
22	MG	A	1842	-	-	-	X
22	MG	A	1845	-	-	-	X
22	MG	A	1846	-	-	-	X
22	MG	A	1863	-	-	-	X
22	MG	B	301	-	-	-	X
22	MG	D	302	-	-	-	X
22	MG	Q	201	-	-	-	X
22	MG	T	202	-	-	-	X

2 Entry composition

There are 24 unique types of molecules in this entry. The entry contains 52441 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	1512	Total	C	N	O	P	0	6	0
			32646	14541	6041	10546	1518			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	912	A	C	ENGINEERED MUTATION	GB M26923.1
A	1534	C	A	CONFLICT	GB M26923.1
A	1535	A	C	CONFLICT	GB M26923.1

- Molecule 2 is a protein called ribosomal protein S2.

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

- Molecule 3 is a protein called 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 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 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 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 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 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 ribosomal protein S9.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
9	I	127	Total	C	N	O	0	0	0
			1010	639	197	174			

- Molecule 10 is a protein called 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 ribosomal protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	116	Total	C	N	O	S	0	0	0
			864	537	164	160	3			

- Molecule 12 is a protein called ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	124	Total	C	N	O	S	0	0	0
			972	612	195	163	2			

- Molecule 13 is a protein called ribosomal protein S13.

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

- Molecule 14 is a protein called 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 ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	O	87	Total	C	N	O	S	0	0	0
			729	457	146	124	2			

- Molecule 16 is a protein called 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 ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	Q	99	Total	C	N	O	S	0	0	0
			823	528	152	141	2			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	96	GLN	GLU	CONFLICT	UNP Q5SHP7

- Molecule 18 is a protein called ribosomal protein S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	R	70	Total	C	N	O	0	0	0
			574	367	112	95			

- Molecule 19 is a protein called 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 ribosomal protein S20.

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

- Molecule 21 is a protein called 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 (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
22	P	2	Total	Mg	0	0
			2	2		
22	J	1	Total	Mg	0	0
			1	1		
22	Q	2	Total	Mg	0	0
			2	2		
22	D	4	Total	Mg	0	0
			4	4		
22	E	1	Total	Mg	0	0
			1	1		
22	B	2	Total	Mg	0	0
			2	2		
22	I	1	Total	Mg	0	0
			1	1		
22	C	2	Total	Mg	0	0
			2	2		
22	A	268	Total	Mg	0	0
			268	268		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
22	T	2	Total 2	Mg 2	0	0
22	L	1	Total 1	Mg 1	0	0
22	F	1	Total 1	Mg 1	0	0
22	M	2	Total 2	Mg 2	0	0

- Molecule 23 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

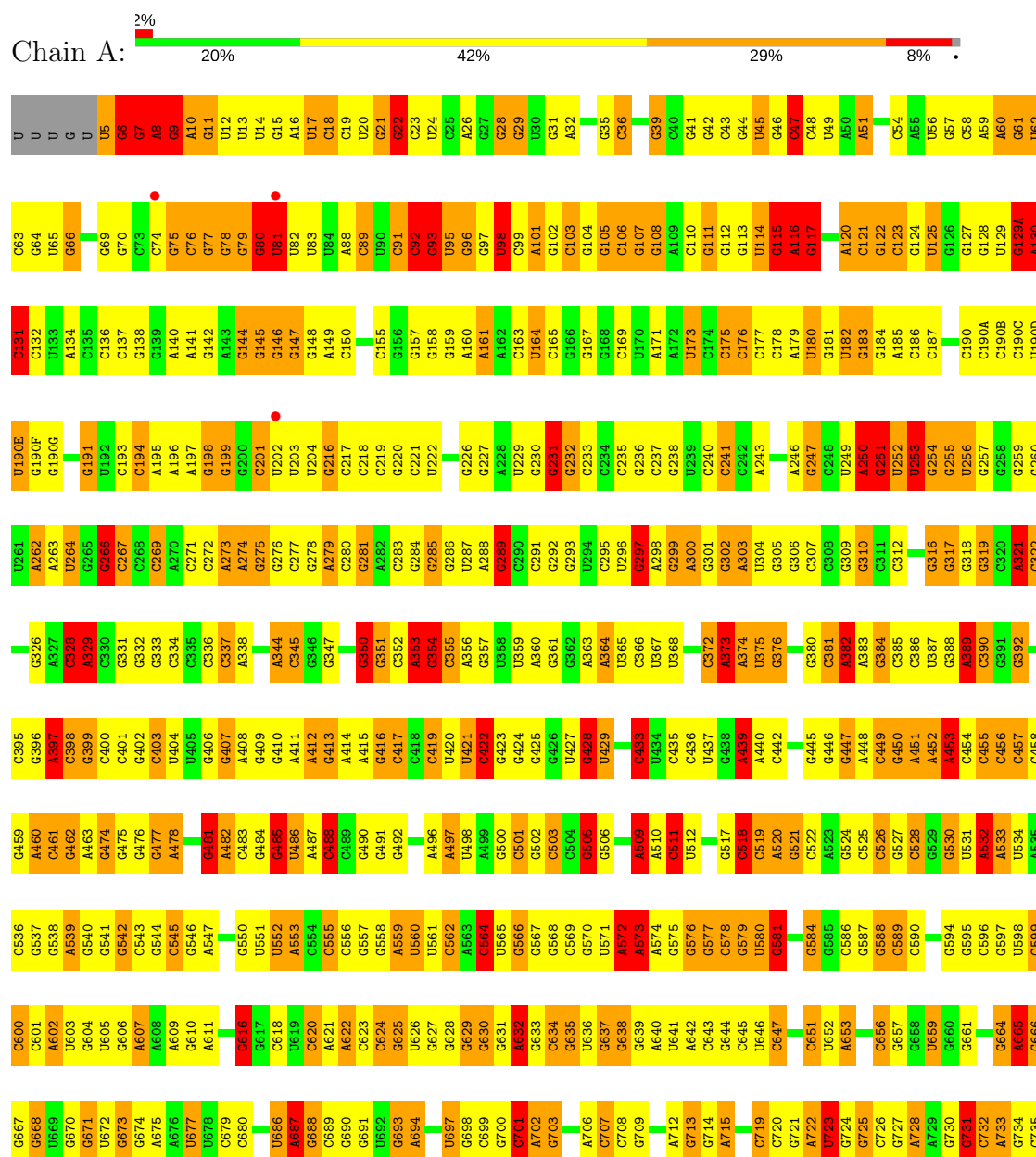
- Molecule 24 is water.

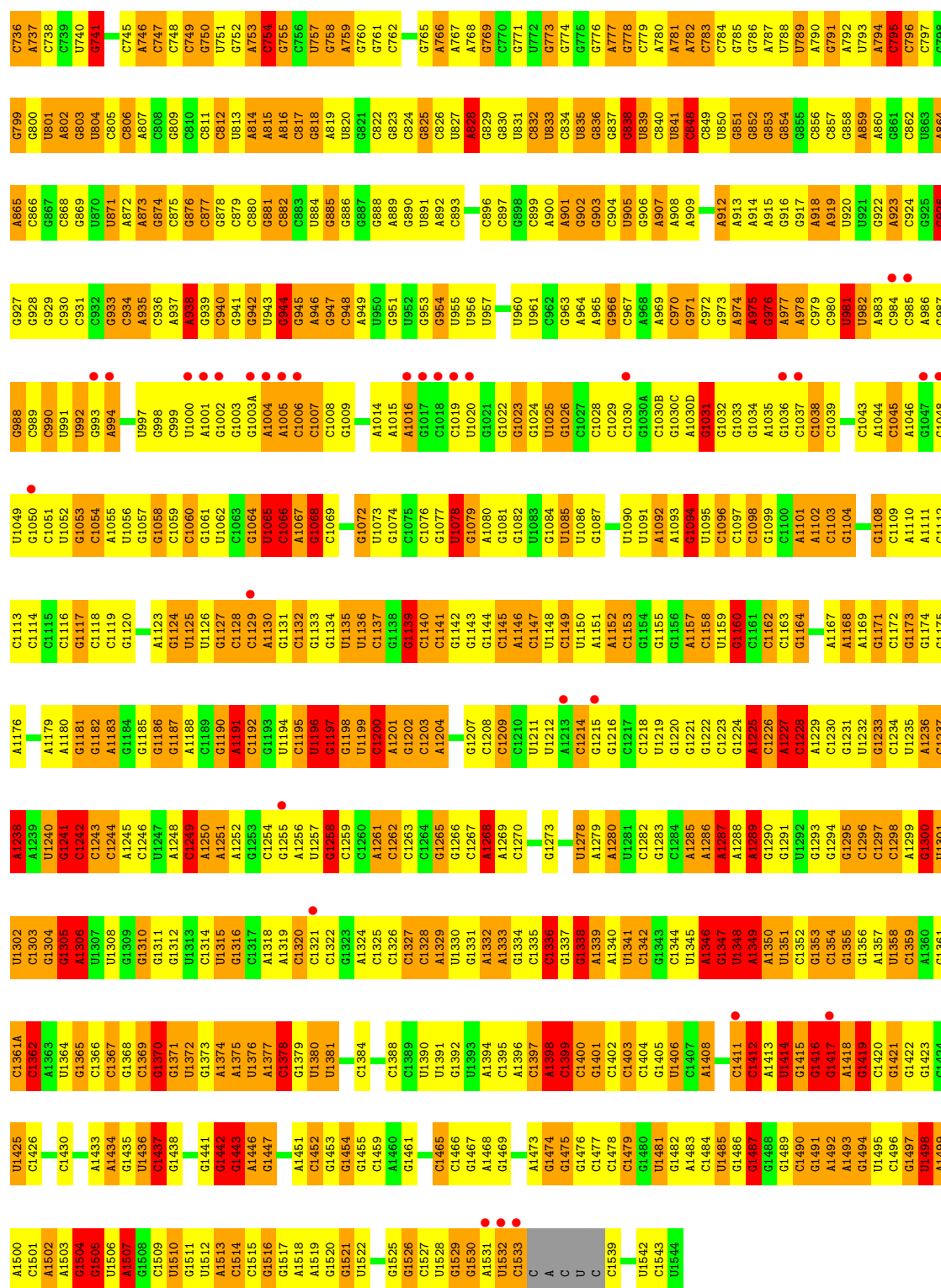
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
24	A	391	Total 391	O 391	0	0
24	B	1	Total 1	O 1	0	0
24	D	3	Total 3	O 3	0	0
24	E	4	Total 4	O 4	0	0
24	G	2	Total 2	O 2	0	0
24	J	2	Total 2	O 2	0	0
24	K	1	Total 1	O 1	0	0
24	M	3	Total 3	O 3	0	0
24	N	4	Total 4	O 4	0	0
24	P	4	Total 4	O 4	0	0
24	T	1	Total 1	O 1	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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

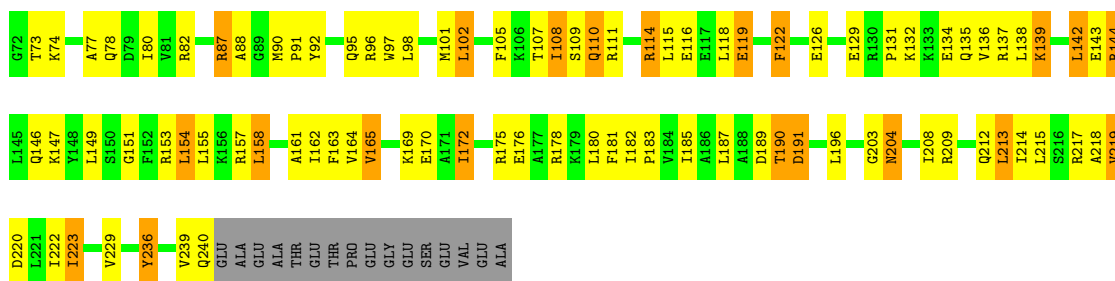




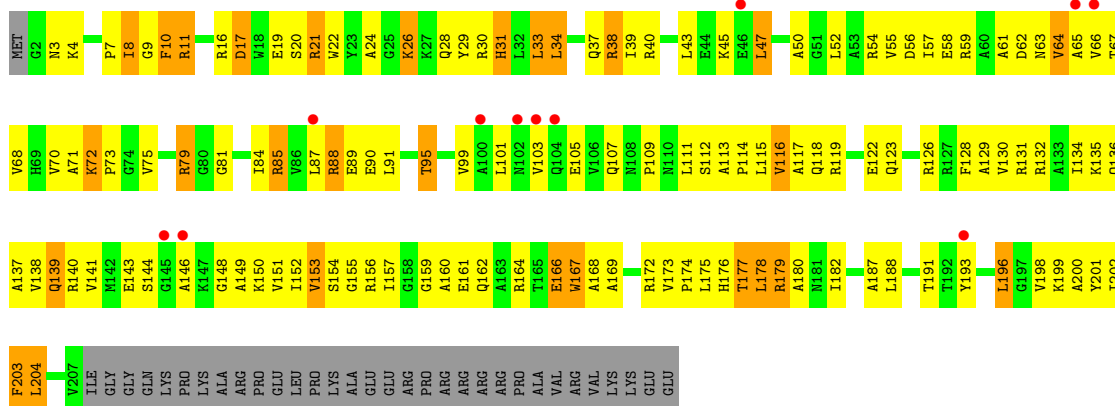
• Molecule 2: ribosomal protein S2

Chain B: 41% 38% 13% 9%

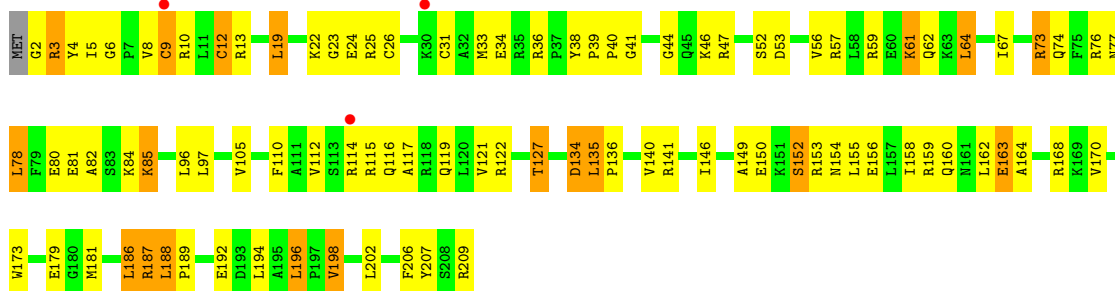
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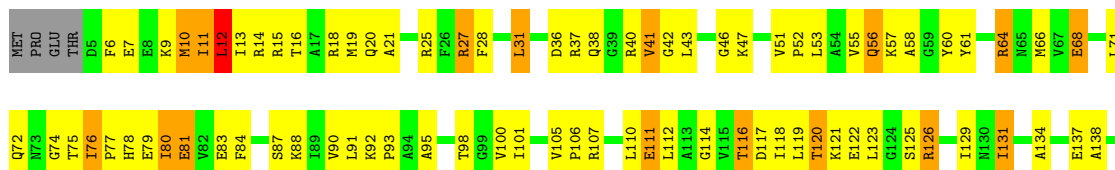
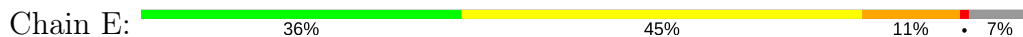
- Molecule 3: ribosomal protein S3



- Molecule 4: ribosomal protein S4

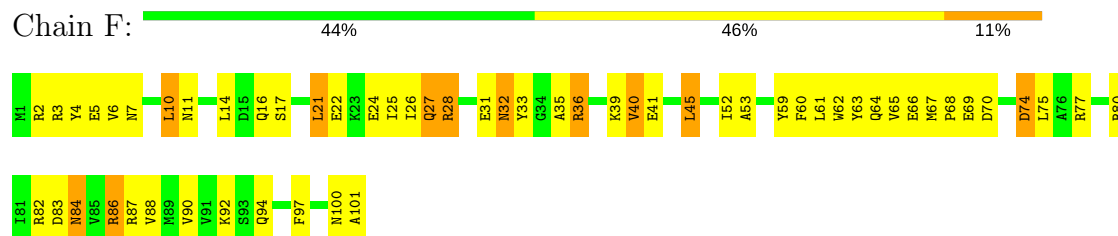


- Molecule 5: ribosomal protein S5

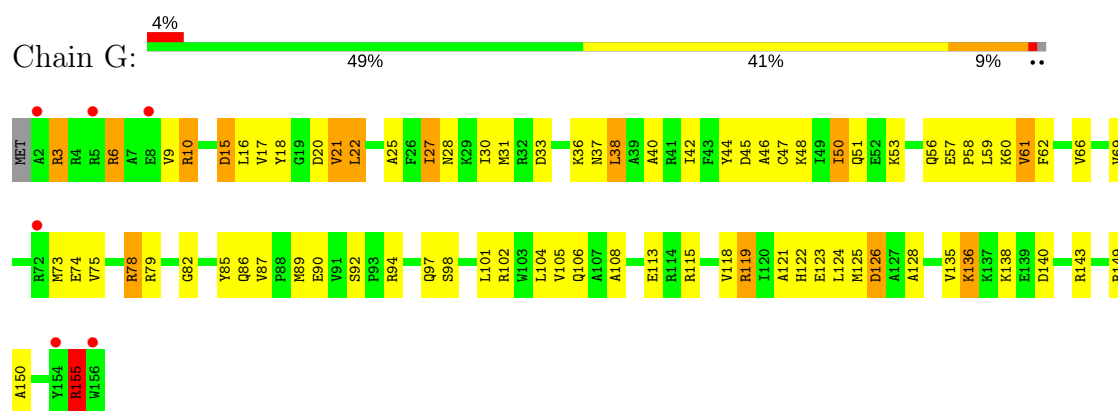




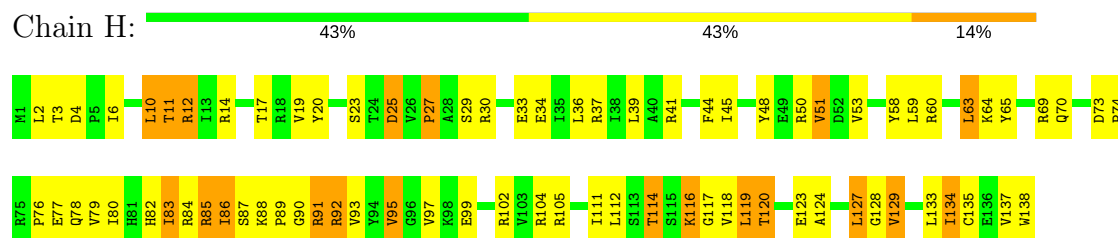
• Molecule 6: ribosomal protein S6



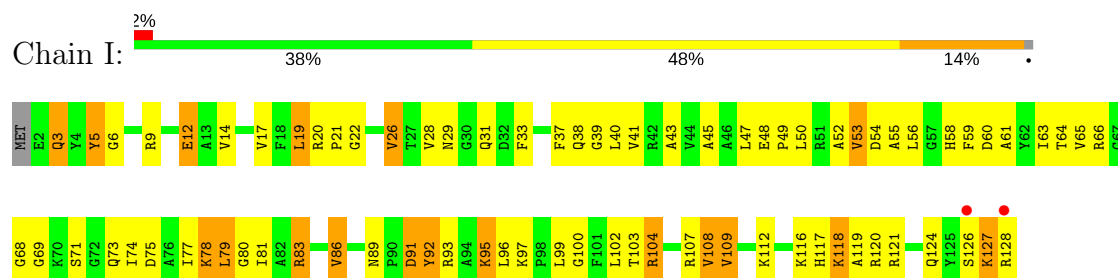
• Molecule 7: ribosomal protein S7



• Molecule 8: ribosomal protein S8

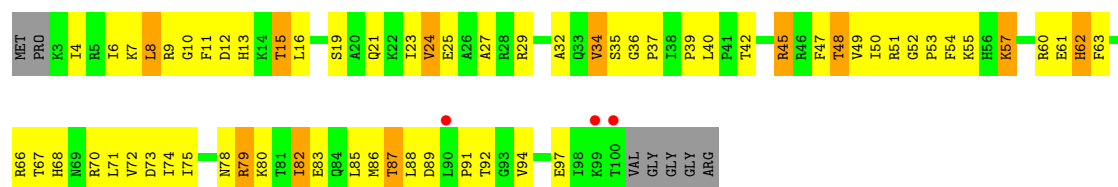


• Molecule 9: ribosomal protein S9

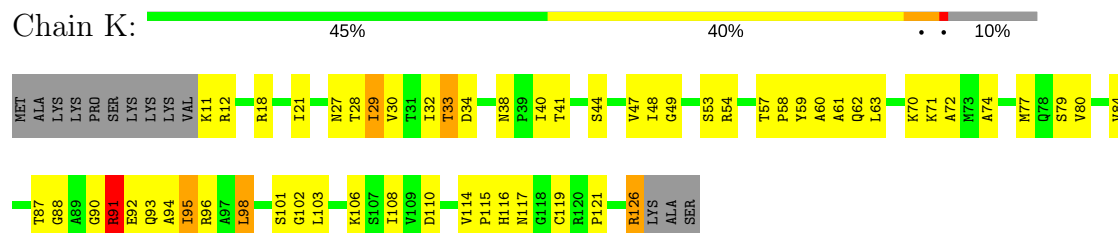


• Molecule 10: ribosomal protein S10





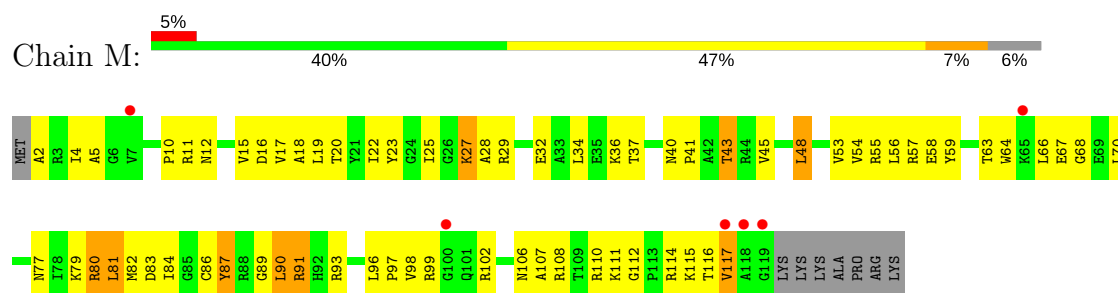
• Molecule 11: ribosomal protein S11



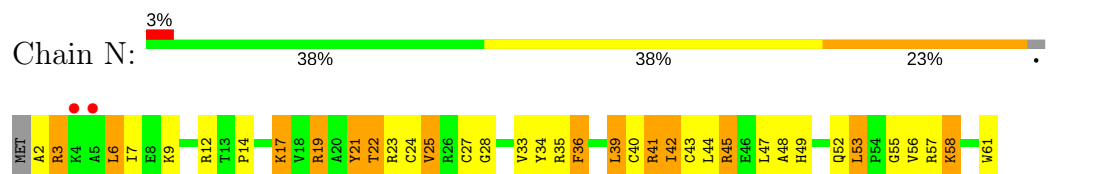
• Molecule 12: ribosomal protein S12



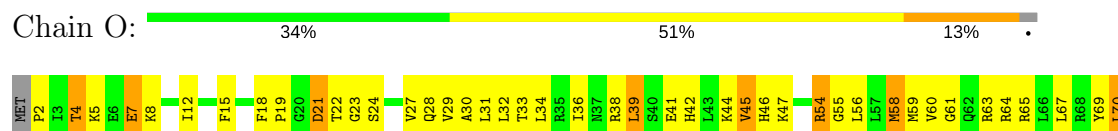
• Molecule 13: ribosomal protein S13



• Molecule 14: ribosomal protein S14



• Molecule 15: ribosomal protein S15





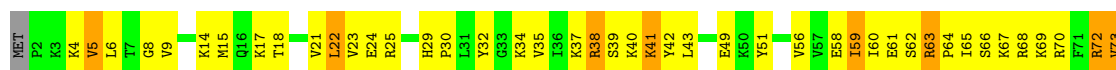
- Molecule 16: ribosomal protein S16

Chain P: 40% 44% 10% 6%



- Molecule 17: ribosomal protein S17

Chain Q: 39% 44% 10% 6%



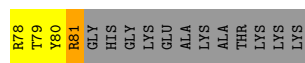
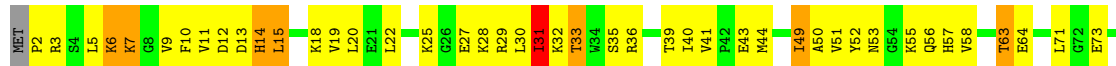
- Molecule 18: ribosomal protein S18

Chain R: 31% 42% 7% 20%



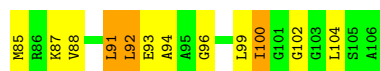
- Molecule 19: ribosomal protein S19

Chain S: 34% 42% 9% 14%

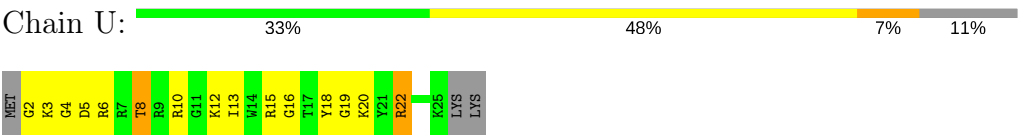


- Molecule 20: ribosomal protein S20

Chain T: 47% 39% 8% 7%



● Molecule 21: 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	403.74Å 403.74Å 173.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.77 – 3.65 29.77 – 3.65	Depositor EDS
% Data completeness (in resolution range)	97.0 (29.77-3.65) 96.8 (29.77-3.65)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.97 (at 3.65Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_978)	Depositor
R, R_{free}	0.165 , 0.223 0.164 , 0.224	Depositor DCC
R_{free} test set	7634 reflections (4.98%)	DCC
Wilson B-factor (Å ²)	137.5	Xtriage
Anisotropy	0.320	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.23 , 127.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	52441	wwPDB-VP
Average B, all atoms (Å ²)	173.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.78% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MA6, 0TD, MG, 2MG, 5MC, UR3, 4OC, M2G, 7MG, PSU

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	1.20	163/36142 (0.5%)	1.88	1794/56401 (3.2%)
2	B	0.79	0/1935	0.96	1/2609 (0.0%)
3	C	0.58	0/1636	0.82	1/2205 (0.0%)
4	D	0.74	2/1733 (0.1%)	0.93	4/2318 (0.2%)
5	E	0.93	0/1162	1.12	4/1564 (0.3%)
6	F	0.65	0/856	0.84	0/1154
7	G	0.65	0/1276	0.83	0/1709
8	H	1.08	1/1136 (0.1%)	1.21	5/1527 (0.3%)
9	I	0.69	0/1029	0.86	1/1379 (0.1%)
10	J	0.57	0/805	0.83	0/1082
11	K	0.77	0/879	0.97	2/1187 (0.2%)
12	L	0.81	0/977	1.02	2/1306 (0.2%)
13	M	0.69	0/947	0.86	0/1270
14	N	0.59	0/501	0.85	0/664
15	O	0.80	0/740	1.05	3/987 (0.3%)
16	P	0.87	1/716 (0.1%)	1.00	1/963 (0.1%)
17	Q	1.01	0/836	1.21	6/1117 (0.5%)
18	R	0.74	0/579	0.98	1/768 (0.1%)
19	S	0.47	0/661	0.78	0/890
20	T	0.74	0/765	1.01	1/1007 (0.1%)
21	U	0.71	0/212	0.90	0/277
All	All	1.07	167/55523 (0.3%)	1.65	1826/82384 (2.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	1
3	C	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
5	E	0	1
8	H	0	2
10	J	0	2
12	L	0	1
13	M	0	1
20	T	0	1
All	All	0	11

All (167) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	279	A	N3-C4	-11.90	1.27	1.34
1	A	279	A	N9-C4	-11.72	1.30	1.37
1	A	573	A	N7-C5	-10.54	1.32	1.39
1	A	1500	A	N3-C4	-9.71	1.29	1.34
1	A	1507	A	N9-C4	-9.58	1.32	1.37
1	A	1509	C	N1-C6	-9.51	1.31	1.37
1	A	586	C	N1-C6	-9.12	1.31	1.37
1	A	828	A	N9-C4	-8.42	1.32	1.37
1	A	1066	C	N1-C6	-7.96	1.32	1.37
1	A	574	A	C5-C4	-7.92	1.33	1.38
1	A	1079	G	N7-C5	-7.83	1.34	1.39
1	A	876	G	C5-C4	-7.72	1.32	1.38
1	A	1509	C	N3-C4	-7.68	1.28	1.33
1	A	824	C	N1-C6	-7.63	1.32	1.37
1	A	1287	A	N9-C4	7.54	1.42	1.37
1	A	79	G	N9-C4	7.48	1.44	1.38
1	A	856	C	N1-C6	-7.44	1.32	1.37
1	A	266	G	N9-C4	-7.29	1.32	1.38
1	A	566	G	N7-C5	-7.26	1.34	1.39
1	A	882	C	N3-C4	-7.24	1.28	1.33
1	A	882	C	N1-C6	-7.21	1.32	1.37
1	A	279	A	N7-C5	-7.18	1.34	1.39
1	A	572	A	N3-C4	-7.18	1.30	1.34
8	H	135	CYS	CB-SG	-7.07	1.70	1.82
1	A	780	A	N9-C4	-7.07	1.33	1.37
1	A	1500	A	N9-C4	-7.03	1.33	1.37
1	A	1514	C	N1-C6	-7.01	1.32	1.37
1	A	1103	C	N1-C6	-6.95	1.32	1.37
1	A	125	U	C2-N3	-6.94	1.32	1.37
1	A	1103	C	C2-N3	-6.89	1.30	1.35
1	A	481	G	N9-C4	6.87	1.43	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1510	U	C2-N3	-6.83	1.32	1.37
1	A	860	A	N3-C4	-6.81	1.30	1.34
1	A	1332	A	C6-N1	-6.79	1.30	1.35
1	A	572	A	C5-C4	-6.73	1.34	1.38
1	A	382	A	N7-C5	-6.72	1.35	1.39
4	D	12	CYS	CB-SG	6.71	1.93	1.82
1	A	640	A	N3-C4	-6.62	1.30	1.34
1	A	279	A	C5-C6	-6.61	1.35	1.41
1	A	722	A	C5-C6	-6.59	1.35	1.41
1	A	1064	G	N3-C4	-6.57	1.30	1.35
1	A	715	A	N9-C4	-6.56	1.33	1.37
1	A	802	A	C5-C4	-6.56	1.34	1.38
1	A	1502	A	C5-C6	-6.56	1.35	1.41
1	A	634	C	N1-C6	-6.53	1.33	1.37
1	A	715	A	N3-C4	-6.44	1.30	1.34
1	A	108	G	N9-C8	6.43	1.42	1.37
1	A	753	A	N3-C4	-6.38	1.31	1.34
1	A	904	C	N1-C6	-6.35	1.33	1.37
1	A	572	A	P-OP1	6.33	1.59	1.49
1	A	737	A	N9-C4	-6.33	1.34	1.37
1	A	817	C	N1-C6	-6.29	1.33	1.37
1	A	687	A	N7-C5	-6.27	1.35	1.39
1	A	602	A	N9-C4	-6.24	1.34	1.37
1	A	571	U	C5-C6	-6.23	1.28	1.34
1	A	785	G	C5-C6	-6.16	1.36	1.42
1	A	1103	C	C2-O2	-6.13	1.19	1.24
1	A	919	A	N9-C4	-6.12	1.34	1.37
1	A	570	G	C6-N1	-6.12	1.35	1.39
1	A	865	A	C6-N6	-6.11	1.29	1.33
1	A	1077	G	N9-C8	-6.09	1.33	1.37
1	A	1306	A	N9-C8	-6.08	1.32	1.37
1	A	570	G	N1-C2	-6.08	1.32	1.37
1	A	130	A	N9-C4	-6.06	1.34	1.37
1	A	321	A	N9-C4	-6.06	1.34	1.37
1	A	578	C	N1-C6	-6.04	1.33	1.37
1	A	912	A	N9-C4	-6.02	1.34	1.37
1	A	235	C	N1-C6	-6.01	1.33	1.37
1	A	1513	A	N9-C4	-6.00	1.34	1.37
1	A	1370	G	N9-C4	5.99	1.42	1.38
1	A	291	C	N1-C6	-5.97	1.33	1.37
1	A	639	G	C6-N1	-5.94	1.35	1.39
1	A	1377	A	N3-C4	-5.91	1.31	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	285	G	N3-C4	-5.90	1.31	1.35
1	A	562	C	N1-C6	-5.89	1.33	1.37
1	A	797	C	N1-C6	-5.88	1.33	1.37
16	P	59	TRP	CB-CG	-5.86	1.39	1.50
1	A	1504	G	C5-C4	-5.84	1.34	1.38
1	A	1074	G	N9-C4	5.84	1.42	1.38
1	A	876	G	C5-C6	-5.82	1.36	1.42
1	A	130	A	N3-C4	-5.79	1.31	1.34
1	A	1513	A	N3-C4	-5.78	1.31	1.34
1	A	572	A	N1-C2	-5.74	1.29	1.34
1	A	1401	G	C5-C4	-5.74	1.34	1.38
1	A	569	C	N3-C4	-5.73	1.29	1.33
1	A	1514	C	N3-C4	-5.71	1.29	1.33
1	A	889	A	N3-C4	-5.70	1.31	1.34
1	A	771	G	C5-C6	-5.65	1.36	1.42
1	A	807	A	N7-C5	-5.65	1.35	1.39
1	A	1346	A	C3'-O3'	5.64	1.50	1.42
1	A	1332	A	N3-C4	-5.63	1.31	1.34
1	A	1078	U	C4-O4	-5.62	1.19	1.23
1	A	1377	A	C5-C4	-5.60	1.34	1.38
1	A	733	A	N9-C4	-5.60	1.34	1.37
1	A	80	G	N9-C4	5.58	1.42	1.38
1	A	107	G	N7-C5	-5.58	1.35	1.39
1	A	1094	G	N1-C2	-5.58	1.33	1.37
1	A	862	C	C4-C5	-5.58	1.38	1.43
1	A	644	G	C5-C4	-5.56	1.34	1.38
1	A	1227	A	N9-C4	-5.56	1.34	1.37
1	A	833	U	C4-O4	5.55	1.28	1.23
1	A	884	U	C2-N3	-5.55	1.33	1.37
1	A	130	A	N7-C5	-5.55	1.35	1.39
1	A	860	A	N9-C4	-5.53	1.34	1.37
1	A	712	A	N3-C4	-5.53	1.31	1.34
1	A	144	G	C6-N1	5.51	1.43	1.39
1	A	766	A	C5-C6	-5.50	1.36	1.41
1	A	1376	U	C2-N3	-5.49	1.33	1.37
1	A	580	U	N1-C2	-5.48	1.33	1.38
1	A	915	A	N9-C4	-5.47	1.34	1.37
1	A	1377	A	N9-C4	-5.46	1.34	1.37
1	A	92	C	P-O5'	5.45	1.65	1.59
1	A	746	A	N7-C5	5.44	1.42	1.39
1	A	897	C	N3-C4	-5.44	1.30	1.33
1	A	901	A	N9-C4	-5.44	1.34	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1094	G	C6-N1	-5.44	1.35	1.39
1	A	131	C	N1-C6	-5.44	1.33	1.37
1	A	250	A	C5-C4	5.36	1.42	1.38
4	D	26	CYS	CB-SG	5.35	1.91	1.82
1	A	728	A	N3-C4	-5.33	1.31	1.34
1	A	1504	G	N7-C5	-5.33	1.36	1.39
1	A	481	G	N3-C4	5.32	1.39	1.35
1	A	860	A	N7-C5	-5.32	1.36	1.39
1	A	825	G	N9-C8	-5.32	1.34	1.37
1	A	599	C	N1-C6	-5.32	1.33	1.37
1	A	1064	G	N9-C4	-5.31	1.33	1.38
1	A	731	G	N9-C4	-5.30	1.33	1.38
1	A	828	A	C5-C6	-5.30	1.36	1.41
1	A	1502	A	N9-C4	-5.30	1.34	1.37
1	A	828	A	N7-C5	-5.29	1.36	1.39
1	A	574	A	N9-C8	-5.29	1.33	1.37
1	A	644	G	C6-N1	-5.28	1.35	1.39
1	A	801	U	C2-N3	-5.26	1.34	1.37
1	A	1241	G	N3-C4	-5.26	1.31	1.35
1	A	564	C	N1-C6	-5.26	1.33	1.37
1	A	752	G	N9-C4	-5.26	1.33	1.38
1	A	606	G	N9-C4	5.25	1.42	1.38
1	A	1417	G	N9-C4	5.24	1.42	1.38
1	A	575	G	N3-C4	-5.24	1.31	1.35
1	A	904	C	C4-C5	-5.23	1.38	1.43
1	A	634	C	N3-C4	-5.20	1.30	1.33
1	A	868	C	N1-C6	-5.19	1.34	1.37
1	A	728	A	N9-C4	-5.19	1.34	1.37
1	A	310	G	C5-C6	-5.19	1.37	1.42
1	A	903	G	C2-N2	-5.18	1.29	1.34
1	A	822	C	N1-C6	-5.17	1.34	1.37
1	A	288	A	N9-C4	-5.16	1.34	1.37
1	A	1080	A	N7-C5	-5.16	1.36	1.39
1	A	900	A	N7-C5	-5.15	1.36	1.39
1	A	93	G	N9-C4	5.15	1.42	1.38
1	A	817	C	N3-C4	-5.14	1.30	1.33
1	A	780	A	N3-C4	-5.14	1.31	1.34
1	A	274	A	C5-C4	-5.13	1.35	1.38
1	A	885	G	N7-C5	-5.11	1.36	1.39
1	A	594	G	N7-C5	-5.09	1.36	1.39
1	A	641	U	N3-C4	-5.09	1.33	1.38
1	A	357	G	C5-C4	-5.09	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	904	C	N3-C4	-5.06	1.30	1.33
1	A	719	C	C2-N3	-5.05	1.31	1.35
1	A	604	G	C6-O6	5.05	1.28	1.24
1	A	570	G	C5-C4	-5.04	1.34	1.38
1	A	389	A	N7-C5	-5.04	1.36	1.39
1	A	651	C	C2-O2	5.04	1.28	1.24
1	A	1529	G	N3-C4	-5.01	1.31	1.35
1	A	306	G	C6-N1	5.01	1.43	1.39
1	A	1329	A	N7-C5	-5.01	1.36	1.39
1	A	1510	U	N1-C6	-5.00	1.33	1.38

All (1826) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1505	G	C8-N9-C4	-16.48	99.81	106.40
1	A	117	G	N1-C6-O6	15.84	129.41	119.90
1	A	279	A	C5-N7-C8	-15.12	96.34	103.90
1	A	722	A	N1-C6-N6	14.64	127.39	118.60
1	A	948	C	C6-N1-C2	14.42	126.07	120.30
1	A	873	A	C8-N9-C4	-14.18	100.13	105.80
1	A	722	A	C2-N3-C4	-13.96	103.62	110.60
1	A	279	A	N7-C8-N9	13.24	120.42	113.80
1	A	117	G	C6-C5-N7	-13.20	122.48	130.40
1	A	1502	A	C4-C5-N7	13.12	117.26	110.70
1	A	117	G	C5-C6-N1	-13.12	104.94	111.50
1	A	1370	G	C8-N9-C4	-13.09	101.16	106.40
1	A	1505	G	N7-C8-N9	12.88	119.54	113.10
1	A	1502	A	C5-N7-C8	-12.68	97.56	103.90
1	A	1502	A	N1-C6-N6	12.56	126.14	118.60
1	A	572	A	N9-C4-C5	12.55	110.82	105.80
1	A	481	G	N3-C4-N9	12.49	133.49	126.00
1	A	232	G	C4-C5-N7	12.25	115.70	110.80
1	A	753	A	N1-C2-N3	11.98	135.29	129.30
1	A	1103	C	C2-N3-C4	-11.95	113.92	119.90
1	A	526	C	C6-N1-C2	11.82	125.03	120.30
1	A	331	G	N1-C6-O6	11.80	126.98	119.90
1	A	1181	G	C8-N9-C4	11.78	111.11	106.40
1	A	382	A	C8-N9-C4	-11.66	101.14	105.80
1	A	144	G	N1-C6-O6	11.60	126.86	119.90
1	A	1455	G	N1-C6-O6	11.57	126.84	119.90
1	A	572	A	N1-C6-N6	-11.56	111.66	118.60
1	A	279	A	C6-C5-N7	-11.54	124.22	132.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	938	A	N1-C6-N6	-11.52	111.69	118.60
1	A	569	C	C5-C6-N1	-11.49	115.26	121.00
1	A	805	C	N3-C4-C5	11.40	126.46	121.90
1	A	865	A	C5-C6-N1	11.40	123.40	117.70
1	A	279	A	N1-C6-N6	11.38	125.43	118.60
1	A	912	A	C2-N3-C4	-11.38	104.91	110.60
1	A	232	G	N9-C4-C5	-11.37	100.85	105.40
1	A	106	C	C6-N1-C2	-11.31	115.78	120.30
1	A	15	G	N1-C6-O6	11.14	126.59	119.90
1	A	884	U	C5-C6-N1	-11.07	117.17	122.70
1	A	922	G	N1-C6-O6	-11.01	113.30	119.90
1	A	1452	C	C6-N1-C2	10.97	124.69	120.30
1	A	331	G	C5-C6-N1	-10.96	106.02	111.50
1	A	573	A	C8-N9-C4	-10.95	101.42	105.80
1	A	255	G	N1-C6-O6	10.93	126.46	119.90
1	A	1287	A	C8-N9-C4	-10.88	101.45	105.80
1	A	21	G	C8-N9-C4	10.87	110.75	106.40
1	A	573	A	C4-C5-C6	10.77	122.39	117.00
1	A	125	U	C5-C6-N1	-10.76	117.32	122.70
1	A	1332	A	N1-C6-N6	-10.75	112.15	118.60
1	A	802	A	C8-N9-C4	10.71	110.08	105.80
1	A	912	A	C5-C6-N1	-10.67	112.36	117.70
1	A	131	C	C5-C6-N1	-10.66	115.67	121.00
1	A	147	G	N1-C6-O6	10.64	126.29	119.90
1	A	903	G	N1-C2-N3	10.62	130.27	123.90
1	A	481	G	N3-C4-C5	-10.55	123.33	128.60
1	A	859	A	N1-C6-N6	10.51	124.91	118.60
1	A	293	G	N1-C6-O6	10.48	126.19	119.90
1	A	628	G	N3-C4-C5	-10.47	123.37	128.60
1	A	771	G	C4-C5-N7	10.46	114.98	110.80
1	A	945	G	C5-C6-N1	10.40	116.70	111.50
1	A	9	G	N1-C6-O6	10.39	126.14	119.90
1	A	828	A	C2-N3-C4	-10.37	105.42	110.60
1	A	1370	G	N7-C8-N9	10.34	118.27	113.10
1	A	1308	U	N3-C2-O2	10.33	129.43	122.20
1	A	130	A	C4-C5-C6	10.28	122.14	117.00
1	A	1526	G	C5-C6-O6	-10.24	122.46	128.60
1	A	805	C	C6-N1-C2	10.23	124.39	120.30
1	A	1502	A	C6-C5-N7	-10.23	125.14	132.30
1	A	771	G	N9-C4-C5	-10.19	101.32	105.40
1	A	1060	C	N3-C2-O2	-10.17	114.78	121.90
1	A	117	G	C4-C5-C6	10.12	124.87	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	130	A	N1-C6-N6	10.08	124.65	118.60
1	A	266	G	N3-C4-N9	-10.08	119.95	126.00
1	A	703	G	C4-C5-N7	-10.07	106.77	110.80
1	A	279	A	C8-N9-C4	-10.06	101.78	105.80
1	A	1369	C	C6-N1-C2	-10.05	116.28	120.30
1	A	797	C	C6-N1-C2	10.04	124.31	120.30
1	A	852	G	C5-C6-N1	-9.99	106.51	111.50
1	A	746	A	C8-N9-C4	9.88	109.75	105.80
1	A	29	G	C2-N3-C4	-9.87	106.97	111.90
1	A	651	C	C6-N1-C2	9.85	124.24	120.30
1	A	912	A	N1-C6-N6	9.83	124.50	118.60
1	A	1370	G	N3-C4-C5	-9.81	123.70	128.60
1	A	79	G	N3-C4-C5	-9.75	123.72	128.60
1	A	1526	G	N1-C6-O6	9.73	125.74	119.90
1	A	833	U	N3-C4-C5	-9.72	108.77	114.60
1	A	117	G	C8-N9-C1'	-9.71	114.38	127.00
1	A	638	G	N1-C6-O6	9.68	125.71	119.90
1	A	1452	C	N1-C2-N3	-9.66	112.44	119.20
1	A	945	G	C5-C6-O6	-9.66	122.81	128.60
1	A	828	A	N1-C6-N6	9.65	124.39	118.60
1	A	266	G	N3-C4-C5	9.54	133.37	128.60
1	A	1370	G	C4-N9-C1'	9.51	138.86	126.50
1	A	786	G	N1-C6-O6	9.50	125.60	119.90
1	A	80	G	C8-N9-C4	-9.49	102.61	106.40
1	A	875	C	C5-C6-N1	-9.47	116.26	121.00
1	A	839	U	N1-C2-O2	9.47	129.43	122.80
1	A	1149	C	C6-N1-C2	-9.46	116.51	120.30
1	A	722	A	N9-C4-C5	-9.45	102.02	105.80
1	A	1505	G	N9-C4-C5	9.43	109.17	105.40
1	A	482	A	N1-C6-N6	9.40	124.24	118.60
1	A	281	G	C5-N7-C8	-9.39	99.60	104.30
1	A	283	C	C6-N1-C2	-9.39	116.54	120.30
1	A	771	G	C2-N3-C4	-9.37	107.21	111.90
1	A	232	G	C6-C5-N7	-9.37	124.78	130.40
1	A	1060	C	N1-C2-O2	9.37	124.52	118.90
1	A	18	C	C5-C6-N1	-9.36	116.32	121.00
1	A	292	G	N1-C6-O6	9.36	125.52	119.90
1	A	565	U	N3-C4-C5	9.36	120.22	114.60
1	A	307	C	N1-C2-O2	9.35	124.51	118.90
1	A	302	G	C5-C6-N1	9.34	116.17	111.50
1	A	1452	C	N1-C2-O2	9.33	124.50	118.90
1	A	785	G	C5-C6-O6	-9.33	123.00	128.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	565	U	C6-N1-C2	9.31	126.59	121.00
1	A	851	G	C4-N9-C1'	9.29	138.58	126.50
1	A	860	A	N1-C2-N3	9.28	133.94	129.30
1	A	1074	G	C8-N9-C4	-9.27	102.69	106.40
1	A	1336	C	C2-N1-C1'	9.26	128.99	118.80
1	A	856	C	N3-C4-C5	-9.24	118.20	121.90
1	A	326	G	N3-C4-C5	-9.19	124.00	128.60
1	A	833	U	C4-C5-C6	9.19	125.21	119.70
1	A	288	A	C2-N3-C4	-9.15	106.03	110.60
1	A	885	G	N1-C6-O6	9.14	125.38	119.90
1	A	1417	G	C8-N9-C4	-9.13	102.75	106.40
1	A	713	G	N1-C6-O6	9.12	125.37	119.90
1	A	589	C	C6-N1-C2	9.11	123.94	120.30
1	A	722	A	C6-C5-N7	-9.11	125.92	132.30
1	A	789	U	C5-C4-O4	9.11	131.36	125.90
1	A	693	G	N1-C6-O6	9.10	125.36	119.90
1	A	128	G	N1-C6-O6	9.08	125.35	119.90
1	A	645	C	C5-C6-N1	9.08	125.54	121.00
1	A	283	C	C5-C6-N1	9.08	125.54	121.00
1	A	262	A	N1-C6-N6	-9.08	113.16	118.60
1	A	1103	C	C5-C6-N1	-9.05	116.47	121.00
1	A	785	G	C4-C5-N7	9.05	114.42	110.80
1	A	279	A	C4-C5-N7	9.03	115.22	110.70
1	A	1395	C	C6-N1-C2	9.03	123.91	120.30
1	A	232	G	N3-C2-N2	8.97	126.18	119.90
1	A	572	A	C5-C6-N1	8.96	122.18	117.70
1	A	1372	U	C5-C6-N1	8.96	127.18	122.70
1	A	1510	U	C5-C6-N1	-8.96	118.22	122.70
1	A	872	A	C5-N7-C8	-8.92	99.44	103.90
1	A	719	C	C5-C6-N1	-8.91	116.55	121.00
1	A	240	C	N3-C4-N4	8.91	124.24	118.00
1	A	865	A	C2-N3-C4	8.91	115.05	110.60
1	A	17	U	N3-C4-O4	8.89	125.62	119.40
1	A	589	C	C5-C6-N1	-8.89	116.56	121.00
1	A	284	G	N1-C6-O6	8.88	125.23	119.90
1	A	737	A	C2-N3-C4	-8.87	106.16	110.60
1	A	366	C	N1-C2-O2	8.87	124.22	118.90
1	A	734	G	N9-C4-C5	-8.87	101.85	105.40
1	A	295	C	C6-N1-C2	8.84	123.83	120.30
1	A	814	A	C2-N3-C4	-8.84	106.18	110.60
1	A	580	U	N1-C2-O2	-8.83	116.62	122.80
1	A	904	C	C6-N1-C2	-8.83	116.77	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	703	G	C5-C6-O6	8.82	133.90	128.60
1	A	1388	C	C6-N1-C2	8.81	123.83	120.30
1	A	279	A	C2-N3-C4	-8.80	106.20	110.60
1	A	292	G	C5-C6-O6	-8.79	123.33	128.60
1	A	789	U	N3-C2-O2	-8.78	116.05	122.20
1	A	255	G	C6-C5-N7	-8.78	125.13	130.40
1	A	873	A	N7-C8-N9	8.78	118.19	113.80
1	A	1282	C	C6-N1-C2	-8.76	116.80	120.30
1	A	572	A	C8-N9-C4	-8.74	102.30	105.80
1	A	825	G	C8-N9-C4	8.71	109.88	106.40
1	A	643	C	C6-N1-C2	-8.69	116.82	120.30
1	A	1350	A	C8-N9-C4	-8.69	102.32	105.80
1	A	1358	U	N1-C2-N3	8.68	120.11	114.90
1	A	735	C	C6-N1-C2	8.66	123.77	120.30
1	A	569	C	C6-N1-C2	8.66	123.76	120.30
1	A	103	C	N3-C4-C5	-8.65	118.44	121.90
1	A	1346	A	C5-C6-N1	8.65	122.02	117.70
1	A	661	G	C2-N3-C4	-8.64	107.58	111.90
1	A	1329	A	C8-N9-C4	-8.64	102.34	105.80
1	A	576	G	N3-C4-C5	-8.63	124.28	128.60
1	A	1310	G	N1-C6-O6	8.62	125.07	119.90
1	A	252	U	C5-C6-N1	-8.61	118.39	122.70
1	A	913	A	C8-N9-C4	-8.61	102.36	105.80
1	A	1336	C	N1-C2-O2	8.60	124.06	118.90
1	A	836	G	N1-C6-O6	8.59	125.06	119.90
1	A	130	A	C6-C5-N7	-8.57	126.30	132.30
1	A	20	U	C5-C4-O4	-8.54	120.77	125.90
1	A	572	A	C2-N3-C4	8.54	114.87	110.60
1	A	779	C	C2-N3-C4	-8.54	115.63	119.90
1	A	715	A	C2-N3-C4	-8.52	106.34	110.60
1	A	645	C	C6-N1-C2	-8.52	116.89	120.30
1	A	941	G	N1-C6-O6	8.51	125.01	119.90
1	A	1452	C	C6-N1-C1'	-8.51	110.59	120.80
1	A	920	U	C5-C4-O4	8.50	131.00	125.90
1	A	232	G	N3-C4-N9	8.49	131.09	126.00
1	A	1361(A)	C	C5-C6-N1	8.48	125.24	121.00
1	A	117	G	C4-N9-C1'	8.48	137.53	126.50
1	A	802	A	N7-C8-N9	-8.47	109.57	113.80
1	A	777	A	N1-C6-N6	8.45	123.67	118.60
1	A	571	U	C6-N1-C2	8.44	126.07	121.00
1	A	1187	G	C8-N9-C4	-8.44	103.02	106.40
1	A	1447	G	C8-N9-C4	-8.44	103.02	106.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	586	C	C5-C6-N1	-8.43	116.78	121.00
1	A	901	A	C2-N3-C4	-8.43	106.39	110.60
1	A	79	G	C2-N3-C4	8.41	116.11	111.90
1	A	852	G	C2-N3-C4	-8.40	107.70	111.90
1	A	1347	G	C8-N9-C4	8.40	109.76	106.40
1	A	784	C	C6-N1-C2	-8.38	116.95	120.30
1	A	1358	U	N3-C2-O2	-8.38	116.33	122.20
1	A	661	G	N1-C6-O6	8.38	124.93	119.90
1	A	129(A)	G	C6-C5-N7	-8.37	125.38	130.40
1	A	1530	G	N3-C4-C5	8.36	132.78	128.60
1	A	785	G	N1-C6-O6	8.36	124.92	119.90
1	A	175	C	C6-N1-C2	8.35	123.64	120.30
1	A	129(A)	G	C4-N9-C1'	8.34	137.34	126.50
1	A	1414	U	C2-N1-C1'	8.34	127.71	117.70
1	A	730	G	N1-C2-N2	-8.34	108.69	116.20
1	A	328	C	N1-C2-O2	8.33	123.90	118.90
1	A	638	G	C5-C6-N1	-8.32	107.34	111.50
1	A	1052	U	C5-C6-N1	8.31	126.86	122.70
1	A	281	G	C4-C5-N7	8.31	114.12	110.80
1	A	789	U	N1-C2-N3	8.30	119.88	114.90
1	A	881	G	N1-C6-O6	8.30	124.88	119.90
1	A	117	G	N9-C4-C5	-8.30	102.08	105.40
1	A	1181	G	N7-C8-N9	-8.29	108.95	113.10
1	A	789	U	N3-C4-C5	-8.29	109.63	114.60
1	A	21	G	N9-C4-C5	-8.28	102.09	105.40
1	A	310	G	C5-C6-O6	-8.26	123.64	128.60
1	A	309	G	C8-N9-C4	8.26	109.70	106.40
1	A	1502	A	N7-C8-N9	8.25	117.93	113.80
1	A	948	C	C5-C6-N1	-8.25	116.88	121.00
1	A	453	A	C8-N9-C4	8.23	109.09	105.80
1	A	382	A	N7-C8-N9	8.23	117.92	113.80
1	A	1347	G	N3-C4-N9	8.23	130.94	126.00
1	A	771	G	C6-C5-N7	-8.23	125.46	130.40
1	A	331	G	C6-C5-N7	-8.22	125.47	130.40
1	A	851	G	C8-N9-C1'	-8.22	116.31	127.00
1	A	518	C	N1-C2-O2	8.21	123.83	118.90
1	A	201	C	C6-N1-C2	-8.21	117.02	120.30
1	A	852	G	N1-C6-O6	8.21	124.82	119.90
1	A	255	G	C5-C6-O6	-8.20	123.68	128.60
1	A	36	C	C6-N1-C2	-8.20	117.02	120.30
1	A	1327	C	C6-N1-C2	8.19	123.58	120.30
1	A	235	C	C5-C6-N1	-8.19	116.90	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1186	G	C5-C6-N1	-8.17	107.42	111.50
1	A	635	G	N1-C6-O6	8.16	124.80	119.90
1	A	753	A	C2-N3-C4	-8.16	106.52	110.60
1	A	1417	G	N3-C4-C5	-8.15	124.53	128.60
1	A	1336	C	C5-C6-N1	8.13	125.06	121.00
1	A	1344	C	C2-N3-C4	-8.13	115.84	119.90
1	A	789	U	C6-N1-C2	-8.12	116.13	121.00
1	A	774	G	C5-C6-O6	-8.12	123.73	128.60
1	A	875	C	C6-N1-C2	8.12	123.55	120.30
1	A	730	G	N1-C2-N3	8.10	128.76	123.90
1	A	1507	A	C2-N3-C4	-8.10	106.55	110.60
1	A	1502	A	N9-C4-C5	-8.10	102.56	105.80
17	Q	22	LEU	CB-CG-CD2	-8.10	97.24	111.00
1	A	1076	C	C6-N1-C2	-8.09	117.06	120.30
1	A	201	C	C2-N1-C1'	8.09	127.70	118.80
1	A	872	A	C4-C5-N7	8.09	114.75	110.70
1	A	851	G	N3-C4-C5	-8.08	124.56	128.60
1	A	309	G	N9-C4-C5	-8.07	102.17	105.40
1	A	703	G	N9-C4-C5	8.07	108.63	105.40
1	A	562	C	N1-C2-O2	8.07	123.74	118.90
1	A	936	C	C6-N1-C2	8.07	123.53	120.30
1	A	598	U	C5-C6-N1	-8.02	118.69	122.70
1	A	667	G	N1-C6-O6	8.01	124.71	119.90
1	A	1509	C	C4-C5-C6	8.01	121.41	117.40
1	A	558	G	C8-N9-C4	-8.01	103.20	106.40
1	A	629	G	C8-N9-C4	-8.00	103.20	106.40
1	A	1447	G	N7-C8-N9	8.00	117.10	113.10
1	A	9	G	C5-C6-O6	-7.99	123.80	128.60
1	A	721	G	C4-N9-C1'	7.99	136.89	126.50
1	A	1375	A	N1-C6-N6	-7.99	113.81	118.60
1	A	117	G	C2-N3-C4	-7.99	107.91	111.90
1	A	80	G	N3-C4-C5	-7.98	124.61	128.60
1	A	562	C	C6-N1-C2	7.98	123.49	120.30
1	A	721	G	C8-N9-C1'	-7.97	116.64	127.00
1	A	606	G	N3-C4-C5	-7.96	124.62	128.60
1	A	766	A	N1-C6-N6	7.95	123.37	118.60
1	A	1149	C	C5-C6-N1	7.95	124.97	121.00
1	A	659	U	C5-C6-N1	-7.94	118.73	122.70
1	A	1087	G	N1-C6-O6	7.92	124.65	119.90
1	A	701	C	C6-N1-C2	7.92	123.47	120.30
1	A	1129	C	C6-N1-C2	-7.92	117.13	120.30
1	A	771	G	C5-C6-O6	-7.91	123.85	128.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1238	A	N9-C4-C5	7.91	108.97	105.80
1	A	1338	G	N1-C6-O6	-7.90	115.16	119.90
1	A	1530	G	C8-N9-C4	7.90	109.56	106.40
1	A	18	C	C6-N1-C2	7.89	123.46	120.30
1	A	779	C	C5-C6-N1	-7.89	117.06	121.00
1	A	752	G	N3-C4-N9	-7.88	121.27	126.00
1	A	931	C	C5-C6-N1	-7.88	117.06	121.00
1	A	872	A	C2-N3-C4	-7.88	106.66	110.60
1	A	929	G	C2-N3-C4	-7.87	107.96	111.90
1	A	814	A	N1-C2-N3	7.87	133.23	129.30
1	A	1344	C	C5-C6-N1	-7.86	117.07	121.00
1	A	753	A	N9-C4-C5	7.85	108.94	105.80
1	A	872	A	N1-C6-N6	7.85	123.31	118.60
1	A	1412	C	C6-N1-C2	-7.85	117.16	120.30
1	A	589	C	C2-N3-C4	-7.84	115.98	119.90
1	A	1103	C	N3-C2-O2	-7.84	116.42	121.90
1	A	368	U	N3-C4-O4	-7.83	113.92	119.40
1	A	331	G	C2-N3-C4	-7.82	107.99	111.90
1	A	310	G	C4-C5-N7	7.81	113.92	110.80
1	A	722	A	C5-C6-N1	-7.80	113.80	117.70
1	A	933	G	N1-C6-O6	7.80	124.58	119.90
1	A	860	A	C2-N3-C4	-7.78	106.71	110.60
1	A	1332	A	N9-C4-C5	7.78	108.91	105.80
1	A	1476	G	C8-N9-C4	-7.78	103.29	106.40
1	A	778	G	N3-C2-N2	-7.77	114.46	119.90
1	A	859	A	C4-C5-C6	7.77	120.88	117.00
1	A	907	A	N1-C2-N3	7.76	133.18	129.30
1	A	138	G	C8-N9-C4	7.75	109.50	106.40
1	A	130	A	C5-C6-N1	-7.75	113.83	117.70
1	A	1236	A	N1-C6-N6	7.75	123.25	118.60
1	A	1346	A	C2-N3-C4	7.73	114.47	110.60
1	A	194	C	N1-C2-O2	7.73	123.54	118.90
1	A	725	G	N1-C6-O6	7.72	124.53	119.90
1	A	326	G	C4-C5-N7	-7.72	107.71	110.80
1	A	788	U	C2-N1-C1'	7.71	126.95	117.70
1	A	667	G	C2-N3-C4	-7.71	108.04	111.90
1	A	1344	C	N3-C4-C5	7.71	124.98	121.90
1	A	299	G	N1-C6-O6	7.71	124.52	119.90
1	A	851	G	N3-C4-N9	7.70	130.62	126.00
1	A	107	G	N1-C6-O6	7.70	124.52	119.90
1	A	23	C	N3-C2-O2	-7.69	116.52	121.90
1	A	142	G	C2-N3-C4	7.69	115.75	111.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	930	C	N3-C4-C5	7.69	124.98	121.90
1	A	777	A	C5-N7-C8	-7.69	100.06	103.90
1	A	546	G	N3-C4-C5	-7.68	124.76	128.60
1	A	115	G	N1-C6-O6	7.68	124.51	119.90
1	A	580	U	N1-C2-N3	7.67	119.50	114.90
4	D	12	CYS	CA-CB-SG	7.67	127.81	114.00
1	A	922	G	C5-C6-O6	7.67	133.20	128.60
1	A	1442	G	C4-N9-C1'	7.67	136.47	126.50
1	A	22	G	N1-C2-N3	7.66	128.50	123.90
1	A	1354	C	C6-N1-C2	-7.66	117.23	120.30
1	A	913	A	N1-C6-N6	-7.65	114.01	118.60
1	A	698	G	N3-C4-C5	-7.65	124.78	128.60
1	A	112	G	N3-C2-N2	-7.64	114.55	119.90
1	A	571	U	C5-C6-N1	-7.64	118.88	122.70
1	A	610	G	C4-N9-C1'	7.62	136.41	126.50
1	A	1414	U	C5-C6-N1	7.62	126.51	122.70
1	A	719	C	N3-C4-N4	-7.61	112.67	118.00
1	A	5	U	C6-N1-C2	7.60	125.56	121.00
1	A	975	A	C5-C6-N1	-7.60	113.90	117.70
1	A	107	G	C6-C5-N7	-7.59	125.84	130.40
1	A	872	A	N7-C8-N9	7.59	117.60	113.80
1	A	945	G	C4-C5-N7	7.58	113.83	110.80
1	A	946	A	N1-C6-N6	-7.58	114.05	118.60
1	A	948	C	C2-N1-C1'	-7.58	110.46	118.80
1	A	481	G	C5-N7-C8	7.57	108.09	104.30
1	A	309	G	N3-C4-N9	7.57	130.54	126.00
1	A	938	A	C5-C6-N6	7.57	129.75	123.70
1	A	1502	A	C2-N3-C4	-7.56	106.82	110.60
1	A	24	U	N3-C2-O2	7.56	127.49	122.20
1	A	555	C	C6-N1-C2	-7.55	117.28	120.30
1	A	190	C	N3-C2-O2	-7.55	116.61	121.90
1	A	1477	C	C6-N1-C2	-7.55	117.28	120.30
1	A	131	C	C4-C5-C6	7.54	121.17	117.40
1	A	774	G	N1-C6-O6	7.52	124.41	119.90
1	A	526	C	C5-C6-N1	-7.52	117.24	121.00
1	A	1200	C	C2-N1-C1'	7.52	127.07	118.80
1	A	777	A	C6-C5-N7	-7.52	127.04	132.30
1	A	1367	C	C6-N1-C2	-7.51	117.29	120.30
1	A	600	C	N3-C4-C5	7.51	124.90	121.90
8	H	12	ARG	NE-CZ-NH1	-7.51	116.55	120.30
1	A	820	U	N1-C2-N3	7.50	119.40	114.90
1	A	266	G	C5-N7-C8	-7.50	100.55	104.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	877	C	C4-C5-C6	7.50	121.15	117.40
1	A	1181	G	C4-N9-C1'	-7.49	116.76	126.50
1	A	569	C	C2-N3-C4	-7.49	116.16	119.90
1	A	732	C	C6-N1-C2	7.48	123.29	120.30
1	A	1258	G	N3-C4-C5	-7.48	124.86	128.60
1	A	190	C	C6-N1-C2	-7.47	117.31	120.30
1	A	771	G	C8-N9-C4	7.47	109.39	106.40
1	A	1510	U	N3-C2-O2	-7.47	116.97	122.20
1	A	283	C	N3-C4-C5	-7.47	118.91	121.90
1	A	586	C	C2-N3-C4	-7.47	116.17	119.90
1	A	903	G	N3-C2-N2	-7.46	114.68	119.90
1	A	715	A	N1-C2-N3	7.46	133.03	129.30
1	A	1238	A	C4-C5-N7	-7.46	106.97	110.70
1	A	22	G	C6-C5-N7	-7.45	125.93	130.40
1	A	276	G	C8-N9-C4	7.45	109.38	106.40
1	A	635	G	N1-C2-N3	7.44	128.36	123.90
1	A	788	U	N3-C2-O2	-7.44	117.00	122.20
1	A	778	G	C5-C6-N1	-7.43	107.78	111.50
1	A	1437	C	N1-C2-O2	7.43	123.36	118.90
1	A	574	A	N7-C8-N9	-7.43	110.09	113.80
1	A	720	C	N1-C2-O2	7.41	123.35	118.90
1	A	1509	C	C2-N3-C4	-7.41	116.20	119.90
1	A	1346	A	C5-N7-C8	7.41	107.60	103.90
1	A	39	G	C5-C6-N1	7.40	115.20	111.50
1	A	1080	A	N1-C6-N6	-7.39	114.16	118.60
1	A	522	C	C6-N1-C2	7.39	123.26	120.30
1	A	885	G	C5-C6-N1	-7.38	107.81	111.50
1	A	8	A	C8-N9-C4	-7.37	102.85	105.80
1	A	885	G	C2-N3-C4	-7.37	108.22	111.90
1	A	232	G	C5-C6-O6	-7.36	124.18	128.60
1	A	1443	G	N1-C6-O6	7.36	124.32	119.90
1	A	173	U	N1-C2-N3	7.36	119.32	114.90
1	A	328	C	N3-C2-O2	-7.36	116.75	121.90
1	A	1238	A	N1-C6-N6	-7.36	114.19	118.60
1	A	1200	C	C5-C6-N1	7.35	124.68	121.00
1	A	812	C	N3-C4-C5	-7.35	118.96	121.90
1	A	628	G	C4-C5-N7	-7.35	107.86	110.80
1	A	605	U	C5-C4-O4	7.34	130.30	125.90
1	A	449	C	N1-C2-O2	7.34	123.30	118.90
1	A	232	G	N1-C6-O6	7.32	124.29	119.90
1	A	871	U	N1-C2-O2	7.32	127.92	122.80
1	A	1336	C	N3-C4-N4	7.32	123.12	118.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	587	G	N1-C6-O6	-7.32	115.51	119.90
1	A	820	U	N1-C2-O2	-7.32	117.68	122.80
1	A	713	G	C5-C6-O6	-7.31	124.21	128.60
1	A	131	C	C6-N1-C2	7.31	123.22	120.30
1	A	1529	G	C4-N9-C1'	7.30	136.00	126.50
1	A	771	G	N1-C6-O6	7.30	124.28	119.90
1	A	451	A	C4-C5-C6	-7.28	113.36	117.00
1	A	1268	A	C8-N9-C4	-7.27	102.89	105.80
8	H	12	ARG	NE-CZ-NH2	7.27	123.93	120.30
1	A	60	A	C8-N9-C4	7.26	108.71	105.80
1	A	574	A	C5-C6-N1	7.26	121.33	117.70
1	A	721	G	C6-C5-N7	-7.26	126.04	130.40
1	A	928	G	C5-C6-O6	-7.26	124.24	128.60
1	A	481	G	C2-N3-C4	7.26	115.53	111.90
1	A	774	G	C4-C5-N7	7.25	113.70	110.80
1	A	7	G	N3-C4-C5	-7.25	124.97	128.60
1	A	1516[A]	G	C8-N9-C4	-7.25	103.50	106.40
1	A	1516[B]	G	C8-N9-C4	-7.25	103.50	106.40
1	A	129(A)	G	C8-N9-C1'	-7.25	117.58	127.00
1	A	1336	C	C6-N1-C1'	-7.24	112.11	120.80
1	A	292	G	C6-C5-N7	-7.23	126.06	130.40
1	A	28	G	N1-C6-O6	7.22	124.23	119.90
1	A	602	A	C2-N3-C4	-7.21	107.00	110.60
1	A	1443	G	C5-C6-O6	-7.20	124.28	128.60
1	A	719	C	C2-N3-C4	-7.20	116.30	119.90
1	A	665	A	C8-N9-C4	-7.20	102.92	105.80
1	A	235	C	C6-N1-C2	7.19	123.18	120.30
1	A	819	A	C8-N9-C4	-7.19	102.92	105.80
1	A	251	G	C6-C5-N7	-7.19	126.09	130.40
1	A	1103	C	N3-C4-C5	7.19	124.78	121.90
1	A	874	G	N1-C2-N3	7.19	128.21	123.90
1	A	1346	A	C6-N1-C2	-7.18	114.29	118.60
1	A	1187	G	N7-C8-N9	7.18	116.69	113.10
1	A	306	G	N1-C6-O6	7.18	124.21	119.90
1	A	1443	G	N9-C4-C5	-7.17	102.53	105.40
1	A	180	U	C2-N1-C1'	7.17	126.30	117.70
1	A	589	C	N3-C4-C5	7.16	124.76	121.90
1	A	392	G	C6-C5-N7	-7.16	126.11	130.40
1	A	975	A	N1-C6-N6	7.15	122.89	118.60
1	A	1455	G	C5-C6-O6	-7.15	124.31	128.60
1	A	799	G	C4-C5-N7	7.15	113.66	110.80
1	A	865	A	N1-C2-N3	-7.14	125.73	129.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1332	A	C5-C6-N6	7.14	129.41	123.70
1	A	653	A	C5-C6-N6	7.14	129.41	123.70
1	A	600	C	C6-N1-C2	7.14	123.15	120.30
1	A	1306	A	N1-C6-N6	7.13	122.88	118.60
1	A	1434	A	N1-C6-N6	7.13	122.88	118.60
1	A	703	G	N3-C4-C5	-7.13	125.04	128.60
1	A	279	A	C4-C5-C6	7.12	120.56	117.00
1	A	104	G	N1-C6-O6	7.11	124.17	119.90
1	A	651	C	N3-C4-C5	7.11	124.74	121.90
1	A	1329	A	N7-C8-N9	7.11	117.35	113.80
1	A	638	G	C6-C5-N7	-7.10	126.14	130.40
1	A	8	A	N9-C4-C5	7.10	108.64	105.80
1	A	569	C	N3-C4-C5	7.10	124.74	121.90
1	A	194	C	N3-C2-O2	-7.09	116.93	121.90
1	A	21	G	N7-C8-N9	-7.09	109.55	113.10
1	A	610	G	C8-N9-C1'	-7.09	117.78	127.00
1	A	731	G	C5-C6-O6	-7.09	124.35	128.60
1	A	1181	G	N3-C4-C5	7.09	132.15	128.60
1	A	1327	C	C5-C6-N1	-7.09	117.45	121.00
1	A	1080	A	N9-C4-C5	7.09	108.64	105.80
1	A	1299	A	C4-C5-N7	7.08	114.24	110.70
1	A	776	G	N3-C4-C5	7.08	132.14	128.60
1	A	872	A	C6-C5-N7	-7.08	127.35	132.30
1	A	190(F)	G	C4-N9-C1'	-7.07	117.30	126.50
1	A	93	G	N3-C4-C5	-7.07	125.07	128.60
1	A	721	G	N3-C4-N9	7.06	130.24	126.00
1	A	878	G	N1-C2-N3	7.06	128.13	123.90
1	A	850	U	C5-C4-O4	7.05	130.13	125.90
1	A	901	A	C5-C6-N1	-7.05	114.17	117.70
1	A	180	U	N3-C4-O4	7.05	124.33	119.40
1	A	449	C	N3-C2-O2	-7.04	116.97	121.90
1	A	642	A	C8-N9-C4	-7.04	102.98	105.80
1	A	128	G	C5-C6-O6	-7.04	124.38	128.60
1	A	474	G	C6-C5-N7	-7.04	126.17	130.40
1	A	569	C	N3-C4-N4	-7.04	113.07	118.00
1	A	18	C	C2-N3-C4	-7.04	116.38	119.90
1	A	526	C	N3-C4-C5	7.03	124.71	121.90
1	A	129(A)	G	N3-C4-N9	7.02	130.21	126.00
1	A	326	G	N1-C2-N3	7.02	128.11	123.90
1	A	264	U	N1-C2-N3	7.01	119.11	114.90
1	A	1064	G	C2-N3-C4	-7.01	108.39	111.90
1	A	722	A	N1-C2-N3	7.00	132.80	129.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	745	C	C6-N1-C2	7.00	123.10	120.30
1	A	1306	A	C4-C5-C6	7.00	120.50	117.00
1	A	408	A	C8-N9-C4	-7.00	103.00	105.80
1	A	1195	C	N3-C4-N4	6.99	122.89	118.00
1	A	886	G	C4-C5-N7	6.98	113.59	110.80
1	A	577	G	C2-N3-C4	-6.98	108.41	111.90
1	A	366	C	C2-N1-C1'	6.98	126.48	118.80
1	A	722	A	C4-C5-N7	6.98	114.19	110.70
1	A	1365	G	C8-N9-C4	-6.98	103.61	106.40
1	A	882	C	N3-C2-O2	-6.97	117.02	121.90
1	A	805	C	C4-C5-C6	-6.96	113.92	117.40
1	A	1305	G	C8-N9-C4	-6.96	103.62	106.40
1	A	181	G	C8-N9-C4	-6.96	103.62	106.40
1	A	303	A	N1-C2-N3	6.96	132.78	129.30
1	A	577	G	N1-C6-O6	6.95	124.07	119.90
1	A	286	G	C5-C6-N1	6.94	114.97	111.50
1	A	482	A	C6-C5-N7	-6.94	127.44	132.30
1	A	722	A	C8-N9-C4	6.94	108.58	105.80
1	A	230	G	N9-C4-C5	-6.93	102.63	105.40
1	A	128	G	C6-C5-N7	-6.92	126.25	130.40
1	A	758	G	N3-C4-C5	6.92	132.06	128.60
1	A	809	G	C8-N9-C4	-6.90	103.64	106.40
1	A	570	G	N3-C4-C5	-6.90	125.15	128.60
1	A	803	G	N1-C6-O6	-6.88	115.77	119.90
1	A	874	G	C8-N9-C4	6.88	109.15	106.40
1	A	1388	C	C2-N1-C1'	-6.88	111.23	118.80
1	A	721	G	C4-C5-C6	6.88	122.93	118.80
1	A	785	G	C6-C5-N7	-6.88	126.27	130.40
1	A	416	G	N1-C6-O6	6.88	124.03	119.90
1	A	1235	U	N1-C2-O2	-6.88	117.99	122.80
1	A	1078	U	C5-C6-N1	6.87	126.14	122.70
1	A	1543	C	C6-N1-C2	6.87	123.05	120.30
1	A	231	G	C8-N9-C4	6.86	109.14	106.40
1	A	703	G	C8-N9-C4	-6.86	103.66	106.40
1	A	1287	A	N7-C8-N9	6.86	117.23	113.80
1	A	854	G	N1-C2-N3	6.86	128.01	123.90
1	A	15	G	C5-C6-N1	-6.84	108.08	111.50
1	A	825	G	N7-C8-N9	-6.84	109.68	113.10
1	A	871	U	N3-C2-O2	-6.84	117.41	122.20
1	A	173	U	C6-N1-C2	-6.84	116.90	121.00
1	A	283	C	C2-N3-C4	6.84	123.32	119.90
1	A	1194	U	C5-C6-N1	6.84	126.12	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1347	G	N7-C8-N9	-6.84	109.68	113.10
1	A	284	G	C5-C6-O6	-6.83	124.50	128.60
1	A	477	G	N1-C6-O6	6.83	124.00	119.90
1	A	777	A	C4-C5-N7	6.83	114.11	110.70
1	A	169	C	C6-N1-C2	-6.82	117.57	120.30
1	A	1149	C	C2-N1-C1'	6.82	126.31	118.80
1	A	1442	G	C8-N9-C1'	-6.82	118.13	127.00
1	A	309	G	C8-N9-C1'	-6.81	118.14	127.00
1	A	876	G	C5-C6-O6	-6.81	124.51	128.60
1	A	121	C	C5-C6-N1	-6.81	117.59	121.00
1	A	1502	A	C5-C6-N6	-6.81	118.25	123.70
1	A	1411	C	C5-C6-N1	6.81	124.40	121.00
1	A	882	C	N1-C2-N3	6.80	123.96	119.20
1	A	1268	A	N9-C4-C5	6.80	108.52	105.80
1	A	1332	A	N1-C2-N3	6.80	132.70	129.30
1	A	804	U	C5-C4-O4	6.80	129.98	125.90
1	A	400	C	N1-C2-O2	6.80	122.98	118.90
1	A	888	G	N3-C2-N2	-6.80	115.14	119.90
1	A	111	G	C5-C6-N1	-6.79	108.11	111.50
1	A	92	C	C2-N1-C1'	6.79	126.27	118.80
1	A	198	G	N1-C6-O6	6.79	123.97	119.90
1	A	796	C	N3-C2-O2	-6.78	117.15	121.90
1	A	92	C	N1-C2-O2	6.78	122.97	118.90
1	A	785	G	N9-C4-C5	-6.78	102.69	105.40
1	A	1131	G	N1-C6-O6	6.78	123.97	119.90
1	A	366	C	N3-C2-O2	-6.78	117.16	121.90
1	A	1377	A	C8-N9-C4	6.78	108.51	105.80
1	A	144	G	C5-C6-N1	-6.77	108.11	111.50
1	A	222	U	C6-N1-C2	6.77	125.06	121.00
1	A	1380	U	N1-C2-N3	6.77	118.96	114.90
1	A	1447	G	C5-C6-O6	-6.77	124.54	128.60
1	A	636	U	C5-C6-N1	-6.76	119.32	122.70
1	A	190(A)	C	C6-N1-C2	-6.76	117.60	120.30
1	A	79	G	N3-C4-N9	6.75	130.05	126.00
1	A	1289	A	C8-N9-C4	-6.75	103.10	105.80
1	A	190(F)	G	N3-C4-N9	-6.75	121.95	126.00
1	A	604	G	C5-C6-N1	-6.75	108.12	111.50
1	A	851	G	C4-C5-C6	6.75	122.85	118.80
1	A	664	G	C5-C6-O6	6.75	132.65	128.60
1	A	1250	A	N1-C6-N6	-6.75	114.55	118.60
1	A	122	G	C4-C5-N7	6.74	113.50	110.80
1	A	565	U	N1-C2-N3	-6.74	110.85	114.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	283	C	N3-C4-N4	6.74	122.72	118.00
1	A	128	G	C4-C5-N7	6.74	113.50	110.80
1	A	745	C	N3-C4-C5	6.74	124.60	121.90
1	A	941	G	C5-C6-O6	-6.73	124.56	128.60
1	A	1192	C	C5-C4-N4	6.73	124.91	120.20
1	A	1299	A	C5-N7-C8	-6.73	100.54	103.90
1	A	317	G	N1-C6-O6	6.73	123.94	119.90
1	A	562	C	C5-C6-N1	-6.72	117.64	121.00
4	D	19	LEU	CA-CB-CG	-6.72	99.83	115.30
1	A	1414	U	N1-C2-O2	6.72	127.50	122.80
1	A	75	G	N3-C4-N9	-6.72	121.97	126.00
1	A	1474	G	N1-C6-O6	6.72	123.93	119.90
1	A	856	C	N1-C2-O2	-6.71	114.87	118.90
1	A	23	C	N1-C2-N3	6.71	123.90	119.20
1	A	665	A	N9-C4-C5	6.71	108.48	105.80
1	A	693	G	C6-C5-N7	-6.71	126.37	130.40
1	A	1405	G	C4-C5-N7	-6.71	108.11	110.80
1	A	629	G	N3-C4-C5	-6.71	125.25	128.60
1	A	1200	C	C6-N1-C2	-6.71	117.62	120.30
1	A	885	G	C6-C5-N7	-6.71	126.38	130.40
1	A	1372	U	C6-N1-C2	-6.69	116.98	121.00
1	A	573	A	N3-C4-C5	-6.69	122.12	126.80
1	A	447	G	C5-C6-O6	6.69	132.61	128.60
1	A	587	G	N9-C4-C5	6.68	108.07	105.40
1	A	93	G	C8-N9-C4	-6.68	103.73	106.40
1	A	293	G	C2-N3-C4	-6.68	108.56	111.90
1	A	281	G	N7-C8-N9	6.68	116.44	113.10
1	A	830	G	C5-C6-N1	-6.68	108.16	111.50
1	A	230	G	C8-N9-C4	6.67	109.07	106.40
1	A	328	C	N3-C4-N4	-6.67	113.33	118.00
1	A	1376	U	C5-C4-O4	6.67	129.90	125.90
1	A	1455	G	C6-C5-N7	-6.67	126.40	130.40
1	A	201	C	C5-C6-N1	6.67	124.33	121.00
1	A	259	G	C8-N9-C4	-6.67	103.73	106.40
1	A	456	C	N1-C2-O2	6.67	122.90	118.90
1	A	1342	C	N1-C2-O2	-6.66	114.90	118.90
1	A	1297	C	N3-C4-C5	6.66	124.56	121.90
1	A	1327	C	C2-N1-C1'	-6.66	111.47	118.80
1	A	1139	G	N3-C4-C5	-6.66	125.27	128.60
1	A	1398	A	N1-C2-N3	6.66	132.63	129.30
1	A	39	G	C2-N3-C4	6.66	115.23	111.90
1	A	602	A	C8-N9-C4	6.66	108.46	105.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	828	A	C5-N7-C8	-6.66	100.57	103.90
1	A	1060	C	C6-N1-C2	-6.66	117.64	120.30
1	A	260	G	C4-C5-N7	6.65	113.46	110.80
1	A	58	C	C6-N1-C2	-6.64	117.64	120.30
1	A	542	G	N3-C4-C5	-6.64	125.28	128.60
1	A	276	G	N3-C2-N2	-6.64	115.25	119.90
1	A	628	G	C4-C5-C6	6.64	122.78	118.80
1	A	827	U	C2-N3-C4	-6.64	123.02	127.00
1	A	1388	C	C5-C6-N1	-6.64	117.68	121.00
1	A	1358	U	C6-N1-C2	-6.64	117.02	121.00
1	A	1200	C	N1-C2-O2	6.63	122.88	118.90
1	A	1065	U	N3-C2-O2	6.63	126.84	122.20
1	A	106	C	N1-C2-N3	6.63	123.84	119.20
1	A	799	G	C5-C6-O6	-6.63	124.62	128.60
1	A	181	G	N3-C4-C5	-6.63	125.29	128.60
1	A	750	G	N3-C4-C5	-6.62	125.29	128.60
1	A	1287	A	C4-C5-C6	6.61	120.31	117.00
1	A	1376	U	N3-C2-O2	-6.61	117.57	122.20
1	A	1378	C	C5-C6-N1	6.61	124.30	121.00
1	A	777	A	N7-C8-N9	6.61	117.10	113.80
1	A	122	G	N1-C6-O6	6.60	123.86	119.90
1	A	375	U	N1-C2-N3	6.60	118.86	114.90
1	A	752	G	N3-C4-C5	6.60	131.90	128.60
1	A	1238	A	C5-C6-N6	6.60	128.98	123.70
1	A	1512	U	N3-C4-O4	6.60	124.02	119.40
17	Q	98	LEU	CA-CB-CG	6.60	130.47	115.30
1	A	262	A	C6-C5-N7	6.59	136.92	132.30
1	A	886	G	N1-C6-O6	6.59	123.86	119.90
1	A	279	A	C4-N9-C1'	6.59	138.17	126.30
1	A	1525	G	N7-C8-N9	-6.59	109.80	113.10
1	A	147	G	C2-N3-C4	-6.59	108.61	111.90
1	A	758	G	C8-N9-C4	6.59	109.03	106.40
1	A	797	C	N3-C4-C5	6.58	124.53	121.90
1	A	771	G	N1-C2-N2	-6.58	110.27	116.20
1	A	1077	G	N1-C2-N2	-6.58	110.28	116.20
1	A	1147	C	C6-N1-C2	-6.58	117.67	120.30
1	A	1303	C	N3-C4-N4	-6.58	113.39	118.00
1	A	1346	A	N7-C8-N9	-6.57	110.51	113.80
1	A	279	A	N1-C2-N3	6.57	132.59	129.30
1	A	595	G	C4-C5-N7	-6.57	108.17	110.80
1	A	147	G	C5-C6-N1	-6.57	108.22	111.50
1	A	20	U	N3-C4-O4	6.57	124.00	119.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	262	A	C4-C5-C6	-6.57	113.72	117.00
1	A	811	C	C6-N1-C2	6.57	122.93	120.30
1	A	819	A	N7-C8-N9	6.57	117.08	113.80
1	A	835	U	C5-C4-O4	6.56	129.84	125.90
1	A	29	G	N1-C2-N3	6.55	127.83	123.90
1	A	622	A	C6-N1-C2	6.55	122.53	118.60
1	A	1452	C	C5-C4-N4	-6.55	115.61	120.20
1	A	281	G	C5-C6-O6	-6.55	124.67	128.60
1	A	820	U	C6-N1-C1'	6.55	130.37	121.20
1	A	850	U	N3-C2-O2	-6.55	117.61	122.20
1	A	853	G	C6-C5-N7	-6.55	126.47	130.40
1	A	703	G	C5-C6-N1	-6.54	108.23	111.50
1	A	1087	G	N3-C4-C5	6.54	131.87	128.60
1	A	116	A	N1-C6-N6	6.54	122.53	118.60
1	A	142	G	N1-C6-O6	-6.53	115.98	119.90
1	A	1505	G	C5-N7-C8	-6.53	101.03	104.30
1	A	572	A	C6-N1-C2	-6.53	114.68	118.60
1	A	736	C	N3-C2-O2	-6.52	117.33	121.90
1	A	975	A	N7-C8-N9	6.52	117.06	113.80
15	O	81	LEU	CA-CB-CG	6.52	130.30	115.30
1	A	1509	C	N1-C2-N3	6.52	123.76	119.20
1	A	171	A	N3-C4-C5	-6.51	122.24	126.80
1	A	832	C	C5-C4-N4	-6.51	115.64	120.20
1	A	873	A	N9-C4-C5	6.51	108.41	105.80
1	A	81	U	C5-C6-N1	6.51	125.95	122.70
1	A	439	A	C8-N9-C4	-6.51	103.20	105.80
1	A	9	G	C6-C5-N7	-6.51	126.50	130.40
1	A	789	U	C4-C5-C6	6.51	123.60	119.70
1	A	864	A	C5-C6-N6	6.50	128.90	123.70
1	A	873	A	C5-C6-N1	6.50	120.95	117.70
1	A	856	C	C4-C5-C6	6.50	120.65	117.40
1	A	326	G	C4-N9-C1'	6.50	134.94	126.50
1	A	886	G	C5-C6-O6	-6.49	124.70	128.60
1	A	266	G	C2-N3-C4	-6.49	108.66	111.90
1	A	81	U	C6-N1-C2	-6.49	117.11	121.00
1	A	721	G	N1-C2-N2	-6.49	110.36	116.20
1	A	720	C	N3-C2-O2	-6.48	117.36	121.90
1	A	667	G	N3-C4-C5	6.48	131.84	128.60
1	A	635	G	C5-C6-N1	-6.48	108.26	111.50
1	A	142	G	C5-C6-N1	6.47	114.74	111.50
1	A	1139	G	C8-N9-C4	-6.47	103.81	106.40
1	A	828	A	N1-C2-N3	6.47	132.53	129.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1521	G	N1-C6-O6	-6.47	116.02	119.90
1	A	890	G	C5-C6-O6	6.46	132.48	128.60
1	A	917	G	C2-N3-C4	-6.46	108.67	111.90
1	A	1294	G	C8-N9-C4	-6.45	103.82	106.40
1	A	146	G	N1-C6-O6	6.45	123.77	119.90
1	A	331	G	N9-C4-C5	-6.45	102.82	105.40
1	A	402	G	C8-N9-C4	-6.45	103.82	106.40
1	A	576	G	C4-C5-C6	6.45	122.67	118.80
1	A	190(C)	C	C6-N1-C2	-6.45	117.72	120.30
1	A	598	U	C6-N1-C2	6.44	124.86	121.00
1	A	576	G	N3-C4-N9	6.44	129.86	126.00
1	A	190(F)	G	N3-C4-C5	6.44	131.82	128.60
1	A	558	G	C4-C5-N7	6.44	113.38	110.80
1	A	1443	G	C4-C5-N7	6.44	113.38	110.80
1	A	1168	A	C8-N9-C4	6.43	108.37	105.80
1	A	1369	C	C5-C6-N1	6.43	124.22	121.00
1	A	945	G	C4-C5-C6	-6.43	114.94	118.80
1	A	597	G	N1-C2-N3	6.43	127.76	123.90
1	A	778	G	C4-C5-N7	-6.43	108.23	110.80
1	A	1103	C	N1-C2-N3	6.43	123.70	119.20
1	A	860	A	C4-C5-C6	6.42	120.21	117.00
1	A	859	A	C6-C5-N7	-6.42	127.81	132.30
1	A	131	C	C2-N3-C4	-6.42	116.69	119.90
1	A	81	U	C2-N1-C1'	6.41	125.39	117.70
1	A	917	G	N1-C2-N3	6.41	127.75	123.90
1	A	796	C	C5-C6-N1	-6.41	117.80	121.00
1	A	1390	U	N3-C4-C5	-6.40	110.76	114.60
1	A	562	C	C6-N1-C1'	-6.40	113.12	120.80
1	A	251	G	N1-C6-O6	6.40	123.74	119.90
1	A	814	A	C8-N9-C4	6.39	108.36	105.80
1	A	276	G	N1-C6-O6	6.39	123.73	119.90
1	A	1295	G	C8-N9-C4	-6.39	103.84	106.40
1	A	707	C	C6-N1-C2	6.38	122.85	120.30
1	A	818	G	N3-C4-N9	-6.38	122.17	126.00
1	A	1361(A)	C	N1-C2-O2	6.38	122.73	118.90
1	A	575	G	C8-N9-C4	6.38	108.95	106.40
1	A	518	C	C2-N1-C1'	6.37	125.80	118.80
1	A	788	U	N3-C4-O4	6.37	123.86	119.40
1	A	381	C	N1-C2-O2	6.36	122.72	118.90
1	A	757	U	C5-C6-N1	-6.36	119.52	122.70
1	A	93	G	N3-C4-N9	6.36	129.82	126.00
1	A	971	G	C8-N9-C4	6.36	108.94	106.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	819	A	C4-C5-C6	6.36	120.18	117.00
1	A	773	G	N9-C4-C5	-6.35	102.86	105.40
1	A	1528	U	C5-C4-O4	-6.35	122.09	125.90
1	A	653	A	N9-C4-C5	6.35	108.34	105.80
1	A	723	U	C5-C6-N1	6.35	125.87	122.70
1	A	819	A	N1-C2-N3	6.35	132.47	129.30
1	A	825	G	C5-C6-O6	-6.35	124.79	128.60
1	A	909	A	C8-N9-C4	-6.35	103.26	105.80
1	A	777	A	C5-C6-N6	-6.34	118.62	123.70
1	A	839	U	C2-N1-C1'	6.34	125.31	117.70
1	A	941	G	C4-C5-N7	6.34	113.34	110.80
1	A	281	G	N1-C6-O6	6.34	123.71	119.90
1	A	1336	C	C2-N3-C4	6.34	123.07	119.90
1	A	567	G	C4-C5-N7	-6.34	108.26	110.80
1	A	864	A	N1-C6-N6	-6.33	114.80	118.60
1	A	112	G	N3-C4-N9	-6.33	122.20	126.00
1	A	618	C	C6-N1-C2	6.33	122.83	120.30
1	A	176	C	C6-N1-C2	6.33	122.83	120.30
1	A	774	G	C6-C5-N7	-6.33	126.60	130.40
1	A	752	G	C5-C6-O6	6.33	132.40	128.60
1	A	108	G	C8-N9-C4	-6.32	103.87	106.40
1	A	1339	A	C2-N3-C4	6.31	113.76	110.60
1	A	1077	G	C8-N9-C4	6.30	108.92	106.40
1	A	255	G	C4-C5-N7	6.30	113.32	110.80
1	A	975	A	C5-N7-C8	-6.30	100.75	103.90
1	A	481	G	C8-N9-C1'	-6.30	118.81	127.00
1	A	713	G	C6-C5-N7	-6.30	126.62	130.40
1	A	875	C	C2-N3-C4	-6.29	116.75	119.90
1	A	726	C	C2-N3-C4	-6.29	116.76	119.90
1	A	558	G	C5-N7-C8	-6.29	101.16	104.30
1	A	881	G	C6-C5-N7	-6.29	126.63	130.40
1	A	1370	G	N3-C4-N9	6.28	129.77	126.00
1	A	703	G	C4-C5-C6	6.28	122.57	118.80
1	A	10	A	C2-N3-C4	-6.28	107.46	110.60
1	A	522	C	C2-N1-C1'	-6.28	111.89	118.80
1	A	310	G	N1-C6-O6	6.28	123.67	119.90
1	A	828	A	C5-C6-N6	-6.28	118.68	123.70
1	A	1455	G	C4-C5-N7	6.28	113.31	110.80
1	A	897	C	C5-C6-N1	-6.27	117.86	121.00
1	A	946	A	C6-N1-C2	-6.27	114.84	118.60
1	A	396	G	N3-C4-C5	-6.27	125.47	128.60
1	A	929	G	C8-N9-C4	6.27	108.91	106.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	389	A	N1-C2-N3	6.27	132.43	129.30
1	A	600	C	C5-C6-N1	-6.27	117.87	121.00
1	A	306	G	C5-C6-N1	-6.26	108.37	111.50
1	A	899	C	C6-N1-C2	-6.26	117.80	120.30
1	A	541	G	N3-C2-N2	-6.26	115.52	119.90
1	A	890	G	N1-C6-O6	-6.26	116.14	119.90
1	A	1134	G	C8-N9-C4	-6.26	103.90	106.40
1	A	180	U	C5-C4-O4	-6.25	122.15	125.90
1	A	302	G	N3-C4-N9	6.25	129.75	126.00
1	A	1136	U	C6-N1-C2	-6.25	117.25	121.00
1	A	625	G	N3-C4-C5	-6.24	125.48	128.60
1	A	17	U	C4-C5-C6	6.24	123.44	119.70
1	A	227	G	N3-C4-C5	6.23	131.72	128.60
1	A	881	G	C8-N9-C4	6.22	108.89	106.40
1	A	190(G)	G	N7-C8-N9	6.22	116.21	113.10
1	A	907	A	C2-N3-C4	-6.21	107.49	110.60
1	A	93	G	N7-C8-N9	6.21	116.21	113.10
1	A	190(F)	G	N7-C8-N9	-6.21	109.99	113.10
1	A	586	C	C4-C5-C6	6.21	120.50	117.40
1	A	815	A	C5-C6-N6	-6.21	118.73	123.70
1	A	283	C	C2-N1-C1'	6.21	125.63	118.80
1	A	641	U	C5-C6-N1	-6.21	119.59	122.70
1	A	129(A)	G	N7-C8-N9	6.21	116.20	113.10
1	A	733	A	C5-N7-C8	-6.21	100.80	103.90
1	A	66	G	C6-C5-N7	-6.20	126.68	130.40
1	A	1384	C	N3-C4-C5	-6.20	119.42	121.90
1	A	765	G	C5-C6-N1	-6.20	108.40	111.50
1	A	839	U	N3-C2-O2	-6.20	117.86	122.20
1	A	643	C	N3-C2-O2	-6.20	117.56	121.90
1	A	912	A	N3-C4-C5	6.20	131.14	126.80
1	A	279	A	C5-C6-N1	-6.19	114.61	117.70
1	A	703	G	C5-N7-C8	6.19	107.39	104.30
1	A	853	G	C4-N9-C1'	6.19	134.55	126.50
1	A	693	G	C5-C6-O6	-6.19	124.89	128.60
1	A	558	G	N7-C8-N9	6.19	116.19	113.10
1	A	1078	U	C6-N1-C2	-6.19	117.29	121.00
1	A	1303	C	N3-C4-C5	6.19	124.38	121.90
1	A	144	G	N3-C4-C5	6.18	131.69	128.60
1	A	907	A	N1-C6-N6	-6.18	114.89	118.60
1	A	1064	G	N3-C2-N2	-6.18	115.57	119.90
1	A	838	G	C8-N9-C4	6.18	108.87	106.40
1	A	1443	G	C8-N9-C4	6.18	108.87	106.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1447	G	C5-N7-C8	-6.18	101.21	104.30
1	A	913	A	P-O3'-C3'	6.18	127.12	119.70
1	A	309	G	N1-C2-N3	6.18	127.61	123.90
1	A	1347	G	C2-N3-C4	6.18	114.99	111.90
1	A	302	G	C6-N1-C2	-6.17	121.39	125.10
1	A	522	C	C5-C6-N1	-6.17	117.91	121.00
1	A	373	A	N7-C8-N9	6.17	116.89	113.80
1	A	912	A	C6-C5-N7	-6.17	127.98	132.30
1	A	1436	U	N3-C2-O2	-6.17	117.88	122.20
1	A	653	A	N1-C6-N6	-6.16	114.90	118.60
1	A	828	A	C4-C5-N7	6.16	113.78	110.70
1	A	975	A	C2-N3-C4	-6.16	107.52	110.60
1	A	1437	C	C5-C6-N1	6.16	124.08	121.00
1	A	256	U	C5-C4-O4	-6.16	122.20	125.90
1	A	570	G	C6-N1-C2	-6.16	121.41	125.10
1	A	125	U	C2-N3-C4	-6.16	123.31	127.00
1	A	145	G	C5-C6-N1	-6.16	108.42	111.50
1	A	375	U	C6-N1-C2	-6.15	117.31	121.00
1	A	587	G	C6-C5-N7	6.15	134.09	130.40
5	E	152	ARG	NE-CZ-NH2	-6.15	117.22	120.30
1	A	864	A	N9-C4-C5	6.15	108.26	105.80
1	A	1490	C	C5-C6-N1	6.14	124.07	121.00
1	A	913	A	N7-C8-N9	6.14	116.87	113.80
1	A	70	G	N3-C4-C5	6.14	131.67	128.60
1	A	773	G	C6-C5-N7	-6.14	126.72	130.40
1	A	227	G	N3-C2-N2	-6.14	115.60	119.90
1	A	815	A	N1-C6-N6	6.13	122.28	118.60
1	A	851	G	C6-C5-N7	-6.13	126.72	130.40
1	A	1225	A	C8-N9-C4	-6.13	103.35	105.80
1	A	1441	G	C8-N9-C4	-6.13	103.95	106.40
1	A	575	G	N1-C6-O6	6.12	123.57	119.90
1	A	78	G	N3-C2-N2	-6.12	115.62	119.90
1	A	483	C	C5-C4-N4	6.12	124.48	120.20
1	A	59	A	C5-C6-N6	-6.11	118.81	123.70
1	A	1469	G	N7-C8-N9	6.11	116.16	113.10
1	A	942	G	N1-C6-O6	6.11	123.57	119.90
1	A	1190	G	P-O3'-C3'	6.11	127.03	119.70
1	A	573	A	C6-C5-N7	-6.11	128.02	132.30
1	A	827	U	N3-C2-O2	-6.11	117.92	122.20
1	A	288	A	C5-C6-N1	-6.11	114.65	117.70
1	A	722	A	C5-C6-N6	-6.11	118.82	123.70
1	A	606	G	C2-N3-C4	6.10	114.95	111.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	635	G	C4-C5-C6	6.10	122.46	118.80
1	A	751	U	C6-N1-C2	6.10	124.66	121.00
1	A	1066	C	C5-C6-N1	-6.10	117.95	121.00
1	A	199	G	N1-C6-O6	6.10	123.56	119.90
1	A	720	C	C6-N1-C1'	-6.10	113.48	120.80
1	A	353	A	N7-C8-N9	-6.09	110.75	113.80
1	A	929	G	N3-C4-C5	6.09	131.65	128.60
1	A	746	A	N7-C8-N9	-6.09	110.75	113.80
1	A	1077	G	N3-C2-N2	6.09	124.16	119.90
1	A	1371	G	C8-N9-C4	-6.09	103.96	106.40
1	A	229	U	N1-C2-N3	6.09	118.55	114.90
1	A	293	G	C5-C6-N1	-6.09	108.46	111.50
1	A	23	C	C4-C5-C6	6.08	120.44	117.40
1	A	336	C	C5-C4-N4	-6.08	115.94	120.20
1	A	127	G	N1-C6-O6	6.08	123.55	119.90
1	A	482	A	C5-C6-N6	-6.08	118.83	123.70
1	A	769	G	C8-N9-C4	6.08	108.83	106.40
1	A	833	U	N3-C2-O2	-6.08	117.94	122.20
1	A	873	A	C5-N7-C8	-6.08	100.86	103.90
1	A	938	A	N9-C4-C5	6.08	108.23	105.80
1	A	199	G	C2-N3-C4	-6.08	108.86	111.90
1	A	922	G	C4-C5-N7	-6.08	108.37	110.80
1	A	928	G	N1-C6-O6	6.07	123.54	119.90
1	A	610	G	N1-C2-N3	6.07	127.54	123.90
1	A	922	G	C6-C5-N7	6.07	134.04	130.40
1	A	1132	C	C6-N1-C2	-6.07	117.87	120.30
1	A	1079	G	C8-N9-C4	-6.07	103.97	106.40
1	A	376	G	C5-N7-C8	6.06	107.33	104.30
1	A	829	G	C8-N9-C1'	-6.06	119.12	127.00
1	A	1196	U	N1-C2-O2	6.06	127.04	122.80
1	A	734	G	C8-N9-C4	6.06	108.82	106.40
1	A	309	G	N1-C2-N2	-6.05	110.75	116.20
1	A	1306	A	C6-C5-N7	-6.05	128.07	132.30
1	A	227	G	N1-C2-N2	6.04	121.64	116.20
1	A	232	G	N1-C2-N2	-6.04	110.76	116.20
1	A	1529	G	C8-N9-C1'	-6.04	119.14	127.00
1	A	302	G	N9-C4-C5	-6.04	102.98	105.40
1	A	723	U	C2-N1-C1'	6.04	124.95	117.70
1	A	825	G	N1-C6-O6	6.04	123.53	119.90
1	A	875	C	C4-C5-C6	6.04	120.42	117.40
1	A	578	C	C5-C6-N1	-6.04	117.98	121.00
1	A	1249	C	C5-C6-N1	6.04	124.02	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	66	G	N1-C6-O6	6.04	123.52	119.90
8	H	119	LEU	CA-CB-CG	6.04	129.18	115.30
1	A	190(F)	G	C6-C5-N7	6.03	134.02	130.40
1	A	503	C	N1-C2-O2	-6.03	115.28	118.90
1	A	1371	G	C2-N3-C4	6.03	114.92	111.90
1	A	266	G	N7-C8-N9	6.03	116.11	113.10
1	A	128	G	C5-N7-C8	-6.03	101.29	104.30
1	A	673	G	C8-N9-C4	-6.03	103.99	106.40
1	A	697	U	N3-C2-O2	-6.03	117.98	122.20
1	A	130	A	C8-N9-C1'	-6.02	116.86	127.70
1	A	481	G	C8-N9-C4	6.02	108.81	106.40
1	A	561	U	C5-C6-N1	-6.01	119.69	122.70
1	A	293	G	N3-C2-N2	-6.01	115.69	119.90
1	A	916	G	C6-N1-C2	-6.01	121.49	125.10
1	A	977	A	C2-N3-C4	6.01	113.61	110.60
1	A	1442	G	C6-C5-N7	-6.01	126.79	130.40
1	A	1338	G	C5-C6-O6	6.01	132.21	128.60
1	A	912	A	C6-N1-C2	6.01	122.20	118.60
1	A	1298	C	C6-N1-C2	6.01	122.70	120.30
1	A	129(A)	G	C4-C5-N7	6.00	113.20	110.80
1	A	907	A	C5-C6-N6	6.00	128.50	123.70
1	A	1077	G	N9-C4-C5	-6.00	103.00	105.40
1	A	1514	C	N1-C2-O2	-6.00	115.30	118.90
1	A	1469	G	C6-C5-N7	-5.99	126.80	130.40
1	A	302	G	C8-N9-C4	5.99	108.80	106.40
1	A	387	U	C5-C4-O4	5.99	129.50	125.90
1	A	587	G	C4-C5-N7	-5.99	108.41	110.80
1	A	735	C	C5-C6-N1	-5.99	118.01	121.00
1	A	137	C	N3-C4-C5	5.98	124.29	121.90
1	A	1197	G	C8-N9-C1'	-5.98	119.22	127.00
1	A	328	C	C2-N1-C1'	5.98	125.38	118.80
1	A	881	G	C2-N3-C4	-5.98	108.91	111.90
1	A	930	C	C2-N3-C4	-5.98	116.91	119.90
1	A	1334	G	C5-C6-O6	5.98	132.19	128.60
1	A	1268	A	N1-C6-N6	-5.97	115.02	118.60
1	A	734	G	N1-C6-O6	5.97	123.48	119.90
1	A	1060	C	C2-N1-C1'	5.97	125.37	118.80
1	A	827	U	C5-C6-N1	-5.97	119.71	122.70
1	A	1526	G	N3-C2-N2	-5.97	115.72	119.90
1	A	240	C	C5-C4-N4	-5.97	116.02	120.20
1	A	630	G	C5-C6-N1	-5.97	108.52	111.50
1	A	1434	A	N9-C4-C5	-5.97	103.41	105.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	900	A	C2-N3-C4	-5.96	107.62	110.60
1	A	933	G	C5-C6-O6	-5.96	125.02	128.60
1	A	296	U	C5-C6-N1	-5.96	119.72	122.70
1	A	328	C	N3-C4-C5	5.96	124.28	121.90
1	A	331	G	N3-C4-C5	5.96	131.58	128.60
1	A	1230	C	N1-C2-O2	5.96	122.48	118.90
1	A	1539	C	N1-C2-O2	5.96	122.48	118.90
1	A	1542	U	C6-N1-C2	5.96	124.58	121.00
1	A	1064	G	N1-C2-N3	5.96	127.48	123.90
1	A	144	G	C5-C6-O6	-5.96	125.02	128.60
1	A	552	U	C5-C6-N1	-5.96	119.72	122.70
1	A	900	A	N1-C2-N3	5.96	132.28	129.30
1	A	924	C	C6-N1-C2	-5.96	117.92	120.30
1	A	1469	G	C8-N9-C4	-5.96	104.02	106.40
1	A	877	C	C2-N3-C4	-5.96	116.92	119.90
1	A	121	C	C2-N3-C4	-5.95	116.92	119.90
1	A	1346	A	P-O3'-C3'	5.95	126.84	119.70
1	A	1117	G	C8-N9-C4	5.95	108.78	106.40
1	A	1310	G	C6-C5-N7	-5.95	126.83	130.40
1	A	753	A	N1-C6-N6	-5.94	115.03	118.60
1	A	28	G	C5-C6-O6	-5.94	125.04	128.60
1	A	180	U	C5-C6-N1	5.94	125.67	122.70
1	A	1308	U	N1-C2-O2	-5.94	118.64	122.80
1	A	128	G	N7-C8-N9	5.94	116.07	113.10
1	A	569	C	C4-C5-C6	5.94	120.37	117.40
1	A	815	A	C8-N9-C4	5.94	108.17	105.80
1	A	1197	G	C4-N9-C1'	5.94	134.22	126.50
1	A	1507	A	N3-C4-C5	5.94	130.96	126.80
1	A	1066	C	C2-N3-C4	-5.94	116.93	119.90
1	A	1370	G	C6-C5-N7	-5.94	126.84	130.40
1	A	897	C	C2-N3-C4	-5.93	116.93	119.90
1	A	39	G	N1-C6-O6	-5.93	116.34	119.90
1	A	607	A	N1-C6-N6	5.93	122.16	118.60
1	A	557	G	N1-C6-O6	5.92	123.45	119.90
1	A	7	G	N3-C4-N9	5.92	129.55	126.00
1	A	7	G	C6-N1-C2	-5.92	121.55	125.10
1	A	422	C	N1-C2-O2	5.92	122.45	118.90
1	A	1461	G	C8-N9-C4	5.92	108.77	106.40
1	A	1501	C	N1-C2-O2	5.92	122.45	118.90
1	A	803	G	N1-C2-N2	-5.92	110.88	116.20
1	A	831	U	N3-C4-O4	5.92	123.54	119.40
1	A	638	G	C2-N3-C4	-5.91	108.94	111.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	750	G	C6-N1-C2	-5.91	121.55	125.10
1	A	570	G	C4-N9-C1'	5.91	134.18	126.50
1	A	725	G	C5-C6-O6	-5.91	125.05	128.60
1	A	730	G	C8-N9-C1'	-5.91	119.32	127.00
1	A	310	G	N9-C4-C5	-5.91	103.04	105.40
1	A	600	C	C2-N3-C4	-5.90	116.95	119.90
1	A	98	U	C6-N1-C2	-5.90	117.46	121.00
1	A	58	C	C5-C6-N1	5.90	123.95	121.00
1	A	816	A	C2-N3-C4	-5.90	107.65	110.60
1	A	823	G	N1-C2-N3	5.90	127.44	123.90
1	A	1367	C	C5-C6-N1	5.90	123.95	121.00
1	A	376	G	C4-C5-N7	-5.89	108.44	110.80
1	A	1241	G	N3-C4-N9	-5.89	122.46	126.00
1	A	1411	C	C2-N1-C1'	5.89	125.28	118.80
1	A	191	G	C2-N3-C4	-5.89	108.95	111.90
1	A	725	G	C4-C5-N7	5.89	113.16	110.80
1	A	886	G	N9-C4-C5	-5.89	103.04	105.40
1	A	125	U	N3-C2-O2	-5.89	118.08	122.20
1	A	351	G	N1-C6-O6	5.89	123.43	119.90
1	A	580	U	N3-C4-C5	-5.89	111.07	114.60
1	A	828	A	C6-C5-N7	-5.88	128.18	132.30
1	A	1399	C	C6-N1-C2	5.88	122.65	120.30
1	A	16	A	N1-C6-N6	-5.88	115.07	118.60
1	A	929	G	N1-C6-O6	5.88	123.43	119.90
1	A	1094	G	N3-C4-N9	5.88	129.53	126.00
1	A	1361(A)	C	C6-N1-C2	-5.88	117.95	120.30
1	A	701	C	N1-C2-O2	5.88	122.42	118.90
1	A	836	G	C5-C6-N1	-5.87	108.56	111.50
1	A	945	G	C5-N7-C8	-5.87	101.36	104.30
1	A	930	C	C5-C6-N1	-5.87	118.06	121.00
1	A	788	U	C6-N1-C2	-5.87	117.48	121.00
1	A	389	A	C4-C5-C6	5.87	119.93	117.00
1	A	599	C	C6-N1-C2	5.87	122.65	120.30
1	A	1411	C	C6-N1-C2	-5.87	117.95	120.30
1	A	250	A	N1-C6-N6	5.86	122.12	118.60
1	A	380	G	N3-C4-N9	-5.86	122.48	126.00
1	A	407	G	C6-C5-N7	5.86	133.92	130.40
1	A	638	G	N9-C4-C5	-5.86	103.06	105.40
1	A	108	G	N3-C4-N9	-5.86	122.48	126.00
1	A	241	C	C6-N1-C2	5.86	122.64	120.30
1	A	734	G	C4-C5-N7	5.86	113.14	110.80
1	A	1416	G	C8-N9-C4	-5.86	104.06	106.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	749	C	C5-C6-N1	5.86	123.93	121.00
1	A	1525	G	C5-N7-C8	5.86	107.23	104.30
1	A	106	C	N3-C2-O2	-5.86	117.80	121.90
1	A	839	U	C6-N1-C1'	-5.86	113.00	121.20
1	A	877	C	C5-C6-N1	-5.86	118.07	121.00
1	A	930	C	C6-N1-C2	5.86	122.64	120.30
1	A	262	A	C5-C6-N6	5.85	128.38	123.70
1	A	812	C	C4-C5-C6	5.85	120.33	117.40
1	A	136	C	C6-N1-C2	-5.85	117.96	120.30
1	A	773	G	N1-C6-O6	5.85	123.41	119.90
1	A	812	C	C5-C4-N4	5.85	124.30	120.20
1	A	872	A	N9-C4-C5	-5.85	103.46	105.80
1	A	720	C	C2-N1-C1'	5.85	125.23	118.80
1	A	1442	G	N3-C4-N9	5.85	129.51	126.00
1	A	628	G	N3-C4-N9	5.85	129.51	126.00
1	A	1509	C	C5-C6-N1	-5.85	118.08	121.00
1	A	606	G	C8-N9-C4	-5.84	104.06	106.40
1	A	1087	G	C4-C5-N7	5.84	113.14	110.80
1	A	249	U	C6-N1-C2	-5.84	117.50	121.00
1	A	584	G	N1-C6-O6	5.84	123.40	119.90
1	A	11	G	C5-C6-O6	-5.84	125.10	128.60
1	A	227	G	N3-C4-N9	-5.83	122.50	126.00
1	A	1310	G	N9-C4-C5	-5.83	103.07	105.40
1	A	1525	G	C8-N9-C4	5.83	108.73	106.40
1	A	373	A	N1-C2-N3	5.83	132.22	129.30
1	A	1265	G	C8-N9-C4	-5.83	104.07	106.40
1	A	112	G	C5-C6-N1	-5.83	108.59	111.50
1	A	1067	A	P-O3'-C3'	5.83	126.69	119.70
1	A	622	A	N1-C2-N3	-5.83	126.39	129.30
1	A	125	U	N3-C4-O4	-5.82	115.32	119.40
1	A	862	C	C5-C4-N4	-5.82	116.12	120.20
1	A	1417	G	N7-C8-N9	5.82	116.01	113.10
1	A	1187	G	C6-C5-N7	-5.82	126.91	130.40
1	A	1494	G	C8-N9-C4	5.82	108.73	106.40
1	A	865	A	N1-C6-N6	-5.82	115.11	118.60
1	A	1416	G	N7-C8-N9	5.82	116.01	113.10
1	A	734	G	C6-C5-N7	-5.82	126.91	130.40
1	A	1530	G	C4-N9-C1'	-5.82	118.94	126.50
1	A	5	U	P-O3'-C3'	5.81	126.68	119.70
1	A	482	A	N7-C8-N9	5.81	116.71	113.80
1	A	562	C	N3-C2-O2	-5.81	117.83	121.90
1	A	890	G	C4-C5-N7	-5.81	108.47	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1468	A	N1-C6-N6	5.81	122.09	118.60
1	A	581	G	C2-N3-C4	-5.81	109.00	111.90
1	A	17	U	N3-C4-C5	-5.80	111.12	114.60
1	A	183	G	C6-C5-N7	-5.80	126.92	130.40
1	A	22	G	C2-N3-C4	-5.80	109.00	111.90
1	A	501	C	C6-N1-C2	-5.80	117.98	120.30
1	A	827	U	N1-C2-N3	5.80	118.38	114.90
1	A	753	A	C6-N1-C2	-5.80	115.12	118.60
1	A	854	G	C2-N3-C4	-5.80	109.00	111.90
1	A	1180	A	C8-N9-C4	-5.80	103.48	105.80
1	A	36	C	N3-C4-C5	-5.79	119.58	121.90
1	A	1421	G	C8-N9-C4	-5.79	104.08	106.40
1	A	860	A	C6-C5-N7	-5.79	128.25	132.30
1	A	877	C	N1-C2-N3	5.79	123.25	119.20
1	A	1419	G	C8-N9-C4	-5.79	104.08	106.40
1	A	786	G	C5-C6-O6	-5.79	125.13	128.60
1	A	437	U	C5-C6-N1	-5.79	119.81	122.70
1	A	876	G	C8-N9-C4	5.79	108.71	106.40
1	A	890	G	N9-C4-C5	5.79	107.71	105.40
1	A	1136	U	C5-C6-N1	5.79	125.59	122.70
1	A	1525	G	C4-C5-N7	-5.79	108.49	110.80
1	A	289	G	N1-C6-O6	5.78	123.37	119.90
1	A	1246	C	C6-N1-C2	-5.78	117.99	120.30
20	T	94	ALA	N-CA-C	-5.78	95.38	111.00
1	A	295	C	C5-C6-N1	-5.78	118.11	121.00
1	A	647	C	C6-N1-C2	5.78	122.61	120.30
1	A	803	G	C5-C6-N1	5.78	114.39	111.50
1	A	1300	G	N1-C6-O6	-5.78	116.43	119.90
1	A	1362	C	C6-N1-C2	-5.78	117.99	120.30
1	A	190(G)	G	N1-C6-O6	5.77	123.36	119.90
1	A	322	C	C6-N1-C2	5.77	122.61	120.30
1	A	933	G	C4-C5-N7	5.77	113.11	110.80
1	A	712	A	N1-C2-N3	5.77	132.18	129.30
1	A	931	C	C6-N1-C2	5.77	122.61	120.30
1	A	190(G)	G	C8-N9-C4	-5.77	104.09	106.40
1	A	666	G	C2-N3-C4	-5.77	109.02	111.90
1	A	722	A	C4-C5-C6	5.77	119.88	117.00
1	A	1348	U	C2-N1-C1'	5.77	124.62	117.70
1	A	190(F)	G	C8-N9-C4	5.76	108.71	106.40
1	A	255	G	C4-N9-C1'	5.76	134.00	126.50
1	A	812	C	N3-C2-O2	-5.76	117.86	121.90
1	A	876	G	N7-C8-N9	-5.76	110.22	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1078	U	C5-C4-O4	-5.76	122.44	125.90
1	A	1528	U	N3-C4-O4	5.76	123.44	119.40
1	A	1249	C	C6-N1-C2	-5.76	118.00	120.30
1	A	1310	G	C5-C6-O6	-5.76	125.14	128.60
1	A	1347	G	N3-C4-C5	-5.76	125.72	128.60
1	A	738	C	N3-C2-O2	-5.76	117.87	121.90
1	A	309	G	C5-C6-O6	-5.76	125.14	128.60
1	A	707	C	C5-C6-N1	-5.76	118.12	121.00
1	A	1158	C	N3-C4-C5	-5.76	119.60	121.90
1	A	198	G	C4-C5-N7	5.76	113.10	110.80
1	A	977	A	N1-C6-N6	-5.76	115.15	118.60
1	A	26	A	N1-C2-N3	5.75	132.18	129.30
1	A	728	A	C2-N3-C4	-5.75	107.72	110.60
1	A	1173	G	C8-N9-C4	5.75	108.70	106.40
1	A	1067	A	C2-N3-C4	5.75	113.47	110.60
1	A	1074	G	N7-C8-N9	5.75	115.97	113.10
1	A	408	A	N9-C4-C5	5.74	108.10	105.80
1	A	1067	A	N3-C4-C5	-5.74	122.78	126.80
1	A	574	A	C8-N9-C4	5.74	108.10	105.80
1	A	888	G	C4-C5-N7	-5.74	108.50	110.80
1	A	1349	A	N1-C6-N6	-5.74	115.16	118.60
1	A	76	C	C5-C4-N4	5.74	124.22	120.20
1	A	893	C	C6-N1-C2	-5.74	118.00	120.30
11	K	91	ARG	N-CA-C	-5.74	95.50	111.00
1	A	284	G	C6-C5-N7	-5.74	126.96	130.40
1	A	884	U	C6-N1-C2	5.74	124.44	121.00
1	A	926	G	N3-C4-C5	-5.74	125.73	128.60
1	A	190(E)	U	C5-C4-O4	-5.74	122.46	125.90
1	A	250	A	C5-C6-N1	-5.74	114.83	117.70
1	A	1191	A	C6-N1-C2	-5.74	115.16	118.60
1	A	1403	C	N3-C2-O2	5.74	125.92	121.90
1	A	106	C	C4-C5-C6	5.73	120.27	117.40
1	A	453	A	N7-C8-N9	-5.73	110.93	113.80
1	A	664	G	N1-C6-O6	-5.73	116.46	119.90
1	A	1203	C	C5-C6-N1	5.73	123.87	121.00
1	A	721	G	N3-C4-C5	-5.73	125.74	128.60
1	A	1346	A	N3-C4-C5	-5.73	122.79	126.80
1	A	29	G	C5-C6-N1	-5.72	108.64	111.50
1	A	269	C	C5-C6-N1	-5.72	118.14	121.00
1	A	912	A	C5-N7-C8	-5.72	101.04	103.90
17	Q	32	TYR	CB-CG-CD2	-5.72	117.57	121.00
1	A	853	G	C8-N9-C1'	-5.72	119.57	127.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1204	A	N1-C6-N6	-5.72	115.17	118.60
1	A	1074	G	N3-C4-C5	-5.72	125.74	128.60
1	A	253	U	N3-C2-O2	5.72	126.20	122.20
1	A	1479	C	C6-N1-C2	-5.72	118.01	120.30
1	A	765	G	N1-C6-O6	5.71	123.33	119.90
1	A	903	G	C6-N1-C2	-5.71	121.67	125.10
1	A	1401	G	C5-C6-N1	5.71	114.36	111.50
1	A	382	A	N9-C4-C5	5.71	108.08	105.80
1	A	564	C	N1-C2-N3	-5.71	115.20	119.20
1	A	1455	G	N3-C2-N2	-5.71	115.91	119.90
1	A	251	G	N7-C8-N9	5.70	115.95	113.10
1	A	29	G	N3-C4-C5	5.70	131.45	128.60
1	A	147	G	C6-C5-N7	-5.70	126.98	130.40
1	A	373	A	C5-N7-C8	-5.70	101.05	103.90
1	A	795	C	N3-C2-O2	5.70	125.89	121.90
1	A	941	G	C2-N3-C4	-5.70	109.05	111.90
1	A	1510	U	C4-C5-C6	5.70	123.12	119.70
1	A	665	A	N1-C2-N3	5.70	132.15	129.30
1	A	580	U	C5-C4-O4	5.69	129.32	125.90
1	A	571	U	N1-C2-O2	5.69	126.78	122.80
1	A	1347	G	C5-N7-C8	5.69	107.14	104.30
1	A	1487	G	C5-C6-O6	-5.69	125.19	128.60
1	A	818	G	N3-C2-N2	-5.69	115.92	119.90
1	A	651	C	N3-C2-O2	5.69	125.88	121.90
1	A	639	G	N1-C6-O6	-5.68	116.49	119.90
1	A	1087	G	C5-N7-C8	-5.68	101.46	104.30
12	L	85	ILE	CB-CA-C	-5.68	100.23	111.60
1	A	826	C	N3-C4-C5	5.68	124.17	121.90
1	A	908	A	N1-C2-N3	5.68	132.14	129.30
1	A	1258	G	C8-N9-C4	-5.68	104.13	106.40
1	A	144	G	C4-C5-N7	5.68	113.07	110.80
1	A	567	G	C5-C6-O6	5.68	132.01	128.60
1	A	637	G	C6-C5-N7	-5.67	127.00	130.40
1	A	1336	C	N3-C4-C5	-5.67	119.63	121.90
1	A	316	G	N1-C6-O6	5.67	123.30	119.90
1	A	881	G	C5-C6-O6	-5.67	125.20	128.60
1	A	553	A	N1-C2-N3	5.67	132.13	129.30
1	A	653	A	N1-C2-N3	5.67	132.13	129.30
1	A	190(D)	U	C5-C6-N1	-5.67	119.87	122.70
1	A	450	G	C5-C6-O6	5.67	132.00	128.60
1	A	897	C	N3-C2-O2	-5.67	117.93	121.90
9	I	107	ARG	NE-CZ-NH1	5.67	123.13	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	948	C	N3-C4-C5	5.66	124.17	121.90
1	A	380	G	C5-C6-N1	-5.66	108.67	111.50
1	A	762	C	N3-C4-N4	5.66	121.96	118.00
1	A	1434	A	C5-C6-N6	-5.66	119.17	123.70
1	A	575	G	C2-N3-C4	-5.66	109.07	111.90
1	A	1351	U	C6-N1-C2	-5.66	117.61	121.00
1	A	975	A	C6-C5-N7	-5.66	128.34	132.30
1	A	1077	G	C6-C5-N7	-5.66	127.01	130.40
1	A	10	A	C8-N9-C4	5.65	108.06	105.80
1	A	1098	C	C5-C6-N1	-5.65	118.17	121.00
1	A	310	G	C8-N9-C4	5.65	108.66	106.40
1	A	326	G	C8-N9-C1'	-5.65	119.66	127.00
1	A	564	C	C2-N3-C4	5.65	122.72	119.90
1	A	805	C	N1-C2-N3	-5.65	115.25	119.20
1	A	416	G	C6-C5-N7	-5.65	127.01	130.40
1	A	500	G	N1-C6-O6	5.65	123.29	119.90
1	A	1052	U	C6-N1-C2	-5.65	117.61	121.00
1	A	155	C	C6-N1-C2	-5.65	118.04	120.30
1	A	198	G	C6-C5-N7	-5.64	127.01	130.40
1	A	287	U	N1-C2-N3	5.64	118.29	114.90
1	A	373	A	C6-C5-N7	-5.64	128.35	132.30
1	A	21	G	N1-C6-O6	5.64	123.29	119.90
1	A	1240	U	C5-C4-O4	5.64	129.28	125.90
1	A	589	C	N3-C4-N4	-5.64	114.05	118.00
1	A	1374	A	C5-C6-N1	-5.64	114.88	117.70
1	A	400	C	N3-C4-C5	5.64	124.16	121.90
1	A	776	G	C2-N3-C4	-5.64	109.08	111.90
1	A	1064	G	N3-C4-N9	-5.64	122.62	126.00
5	E	41	VAL	CB-CA-C	-5.64	100.69	111.40
1	A	191	G	N3-C4-C5	5.63	131.42	128.60
1	A	482	A	C4-C5-C6	5.63	119.82	117.00
1	A	970	C	N1-C2-O2	5.63	122.28	118.90
1	A	558	G	N1-C6-O6	5.63	123.28	119.90
1	A	24	U	C5-C4-O4	-5.63	122.52	125.90
1	A	750	G	N3-C4-N9	5.63	129.38	126.00
1	A	1354	C	C5-C6-N1	5.63	123.82	121.00
1	A	231	G	N3-C4-N9	5.63	129.38	126.00
1	A	14	U	C6-N1-C2	-5.63	117.62	121.00
1	A	926	G	C8-N9-C4	-5.62	104.15	106.40
1	A	194	C	C6-N1-C2	-5.62	118.05	120.30
1	A	1374	A	N1-C2-N3	5.62	132.11	129.30
1	A	227	G	C8-N9-C1'	5.62	134.30	127.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	231	G	N9-C4-C5	-5.62	103.15	105.40
1	A	640	A	C8-N9-C4	-5.62	103.55	105.80
1	A	804	U	N1-C2-N3	5.62	118.27	114.90
1	A	9	G	C4-C5-N7	5.61	113.05	110.80
1	A	677	U	C5-C4-O4	5.61	129.26	125.90
1	A	108	G	N3-C2-N2	-5.61	115.98	119.90
1	A	190(B)	C	C5-C6-N1	5.61	123.80	121.00
1	A	277	C	C6-N1-C2	5.61	122.54	120.30
1	A	269	C	C4-C5-C6	5.60	120.20	117.40
1	A	1098	C	C6-N1-C2	5.60	122.54	120.30
1	A	1238	A	N1-C2-N3	5.59	132.10	129.30
1	A	1528	U	N3-C2-O2	5.59	126.11	122.20
1	A	930	C	N3-C4-N4	-5.59	114.09	118.00
1	A	1195	C	C2-N1-C1'	5.59	124.95	118.80
1	A	1411	C	N1-C2-O2	5.59	122.25	118.90
1	A	546	G	N3-C4-N9	5.59	129.35	126.00
1	A	70	G	N1-C6-O6	5.59	123.25	119.90
1	A	509	A	C3'-C2'-C1'	-5.59	97.03	101.50
1	A	1465	C	N1-C2-O2	5.58	122.25	118.90
1	A	635	G	C8-N9-C1'	-5.58	119.74	127.00
1	A	190(G)	G	C6-C5-N7	-5.58	127.05	130.40
1	A	253	U	N1-C2-O2	-5.58	118.89	122.80
1	A	350	G	C8-N9-C4	-5.58	104.17	106.40
1	A	396	G	N1-C2-N2	-5.58	111.18	116.20
1	A	546	G	C4-N9-C1'	5.58	133.75	126.50
1	A	1103	C	C6-N1-C2	5.58	122.53	120.30
1	A	616	G	C5-C6-N1	-5.57	108.71	111.50
1	A	971	G	N7-C8-N9	-5.57	110.31	113.10
1	A	316	G	C6-C5-N7	-5.57	127.06	130.40
1	A	741	G	N1-C6-O6	5.57	123.24	119.90
1	A	830	G	C8-N9-C4	-5.57	104.17	106.40
1	A	1304	G	C8-N9-C4	-5.57	104.17	106.40
1	A	552	U	C2-N3-C4	-5.57	123.66	127.00
1	A	567	G	N1-C2-N3	5.57	127.24	123.90
1	A	387	U	N3-C2-O2	-5.57	118.30	122.20
1	A	1031	G	C8-N9-C4	-5.57	104.17	106.40
1	A	1481	U	C6-N1-C2	-5.57	117.66	121.00
1	A	923	A	N1-C6-N6	5.57	121.94	118.60
1	A	941	G	C6-C5-N7	-5.56	127.06	130.40
1	A	23	C	C2-N3-C4	-5.56	117.12	119.90
1	A	350	G	N7-C8-N9	5.56	115.88	113.10
1	A	1374	A	C5-C6-N6	5.56	128.15	123.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	22	G	N1-C2-N2	-5.56	111.20	116.20
1	A	521	G	N1-C6-O6	-5.56	116.57	119.90
1	A	59	A	C5-C6-N1	5.55	120.48	117.70
1	A	238	G	C8-N9-C4	-5.55	104.18	106.40
1	A	733	A	N7-C8-N9	5.55	116.58	113.80
1	A	644	G	C5-C6-N1	5.55	114.28	111.50
1	A	481	G	N9-C4-C5	-5.55	103.18	105.40
1	A	1371	G	N1-C2-N3	-5.55	120.57	123.90
1	A	201	C	N1-C2-O2	5.55	122.23	118.90
1	A	837	G	C8-N9-C4	5.55	108.62	106.40
1	A	436	C	N1-C2-O2	5.54	122.23	118.90
1	A	1251	A	C8-N9-C4	-5.54	103.58	105.80
1	A	433	C	C6-N1-C2	-5.54	118.08	120.30
1	A	1477	C	C5-C6-N1	5.54	123.77	121.00
1	A	632	A	C5-N7-C8	-5.54	101.13	103.90
1	A	1468	A	C4-C5-N7	5.54	113.47	110.70
1	A	309	G	C6-N1-C2	-5.54	121.78	125.10
1	A	355	C	C6-N1-C2	-5.54	118.09	120.30
1	A	380	G	C4-C5-N7	-5.54	108.59	110.80
1	A	804	U	C6-N1-C1'	5.54	128.95	121.20
1	A	1521	G	C5-N7-C8	5.54	107.07	104.30
1	A	299	G	C5-C6-O6	-5.53	125.28	128.60
1	A	1082	G	C2-N3-C4	-5.53	109.13	111.90
1	A	19	C	N3-C4-C5	5.53	124.11	121.90
1	A	125	U	C6-N1-C2	5.53	124.32	121.00
1	A	131	C	N3-C2-O2	-5.53	118.03	121.90
1	A	882	C	C6-N1-C2	-5.53	118.09	120.30
1	A	963	G	C8-N9-C4	-5.53	104.19	106.40
1	A	576	G	C5-N7-C8	5.53	107.06	104.30
1	A	597	G	C6-N1-C2	-5.53	121.78	125.10
1	A	882	C	C4-C5-C6	5.53	120.16	117.40
1	A	573	A	N7-C8-N9	5.53	116.56	113.80
1	A	1390	U	C5-C4-O4	5.53	129.22	125.90
1	A	376	G	N7-C8-N9	-5.52	110.34	113.10
1	A	299	G	C8-N9-C4	5.52	108.61	106.40
1	A	723	U	C6-N1-C2	-5.52	117.69	121.00
1	A	120	A	C2-N3-C4	-5.52	107.84	110.60
1	A	1241	G	N3-C4-C5	5.52	131.36	128.60
1	A	762	C	C5-C4-N4	-5.52	116.34	120.20
1	A	19	C	C6-N1-C2	5.51	122.51	120.30
1	A	610	G	C6-C5-N7	-5.51	127.09	130.40
1	A	618	C	N1-C2-N3	-5.51	115.34	119.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1062	U	C6-N1-C2	-5.51	117.69	121.00
1	A	1147	C	N3-C4-C5	-5.51	119.69	121.90
1	A	1377	A	C5-C6-N1	5.51	120.45	117.70
1	A	1469	G	N1-C6-O6	5.51	123.20	119.90
1	A	396	G	N3-C4-N9	5.50	129.30	126.00
1	A	75	G	C4-N9-C1'	-5.50	119.34	126.50
1	A	795	C	C6-N1-C2	5.50	122.50	120.30
1	A	749	C	C5-C4-N4	-5.50	116.35	120.20
1	A	17	U	N1-C2-O2	-5.50	118.95	122.80
1	A	734	G	N3-C4-N9	5.50	129.30	126.00
1	A	403	C	C5-C6-N1	-5.49	118.25	121.00
1	A	1425	U	C5-C4-O4	5.49	129.20	125.90
1	A	61	G	N1-C6-O6	5.49	123.19	119.90
1	A	229	U	C6-N1-C2	-5.49	117.70	121.00
1	A	250	A	C2-N3-C4	-5.49	107.85	110.60
1	A	606	G	C4-C5-N7	-5.49	108.60	110.80
1	A	1370	G	C8-N9-C1'	-5.49	119.86	127.00
1	A	392	G	N1-C6-O6	5.49	123.19	119.90
1	A	74	C	C6-N1-C2	-5.49	118.11	120.30
1	A	852	G	C6-C5-N7	-5.49	127.11	130.40
1	A	723	U	N1-C2-O2	5.48	126.64	122.80
1	A	260	G	C5-C6-O6	-5.48	125.31	128.60
1	A	884	U	C4-C5-C6	5.48	122.98	119.70
1	A	392	G	C4-N9-C1'	5.47	133.62	126.50
1	A	474	G	N1-C6-O6	5.47	123.19	119.90
1	A	488	C	N1-C2-O2	5.47	122.19	118.90
1	A	194	C	C2-N1-C1'	5.47	124.82	118.80
1	A	481	G	N3-C2-N2	5.47	123.73	119.90
1	A	865	A	C4-C5-C6	-5.47	114.27	117.00
8	H	10	LEU	CB-CG-CD2	-5.47	101.71	111.00
1	A	734	G	C8-N9-C1'	-5.46	119.90	127.00
1	A	1375	A	C5-N7-C8	5.46	106.63	103.90
1	A	562	C	C4-C5-C6	5.46	120.13	117.40
1	A	636	U	C4-C5-C6	5.46	122.97	119.70
1	A	1296	C	C6-N1-C2	5.46	122.48	120.30
1	A	701	C	C5-C6-N1	-5.46	118.27	121.00
1	A	913	A	N9-C4-C5	5.46	107.98	105.80
1	A	260	G	C6-C5-N7	-5.46	127.13	130.40
1	A	275	G	N9-C4-C5	-5.46	103.22	105.40
1	A	326	G	C4-C5-C6	5.46	122.07	118.80
1	A	869	G	N3-C4-N9	-5.45	122.73	126.00
1	A	15	G	C5-C6-O6	-5.45	125.33	128.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	238	G	C5-C6-N1	-5.45	108.78	111.50
1	A	641	U	N1-C2-N3	5.45	118.17	114.90
1	A	600	C	N3-C4-N4	-5.45	114.19	118.00
1	A	75	G	N3-C4-C5	5.45	131.32	128.60
1	A	353	A	C5-N7-C8	5.45	106.62	103.90
1	A	627	G	C4-C5-N7	5.44	112.98	110.80
1	A	637	G	N1-C6-O6	5.44	123.16	119.90
1	A	697	U	C5-C4-O4	5.44	129.16	125.90
1	A	912	A	C4-C5-N7	5.44	113.42	110.70
1	A	919	A	C5-N7-C8	-5.44	101.18	103.90
1	A	505	G	C8-N9-C4	5.44	108.58	106.40
1	A	1233	G	C6-C5-N7	-5.44	127.14	130.40
1	A	1250	A	N9-C4-C5	5.44	107.97	105.80
1	A	937	A	C8-N9-C4	-5.44	103.62	105.80
1	A	157	G	N1-C6-O6	5.43	123.16	119.90
1	A	518	C	C6-N1-C1'	-5.43	114.28	120.80
1	A	627	G	C5-C6-O6	-5.43	125.34	128.60
1	A	771	G	N1-C2-N3	5.43	127.16	123.90
1	A	786	G	C6-C5-N7	-5.43	127.14	130.40
1	A	806	C	N3-C4-C5	5.43	124.07	121.90
1	A	1501	C	N3-C4-C5	5.43	124.07	121.90
1	A	509	A	C5-C6-N1	5.43	120.42	117.70
1	A	571	U	N1-C2-N3	-5.43	111.64	114.90
1	A	809	G	N7-C8-N9	5.43	115.82	113.10
1	A	400	C	N3-C4-N4	-5.43	114.20	118.00
1	A	511	C	C5-C6-N1	-5.42	118.29	121.00
1	A	570	G	C5-C6-N1	5.42	114.21	111.50
1	A	1417	G	N1-C6-O6	-5.42	116.65	119.90
1	A	720	C	N3-C4-C5	5.42	124.07	121.90
1	A	727	G	C5-C6-O6	5.42	131.85	128.60
1	A	292	G	C4-C5-N7	5.42	112.97	110.80
1	A	416	G	C5-C6-O6	-5.42	125.35	128.60
1	A	1064	G	N3-C4-C5	5.42	131.31	128.60
1	A	1474	G	C6-C5-N7	-5.42	127.15	130.40
1	A	47	C	C2-N1-C1'	5.42	124.76	118.80
1	A	397	A	C8-N9-C4	-5.42	103.63	105.80
1	A	532	A	C8-N9-C4	-5.42	103.63	105.80
1	A	777	A	C8-N9-C4	-5.42	103.63	105.80
1	A	815	A	N7-C8-N9	-5.42	111.09	113.80
1	A	1234	C	N3-C4-N4	5.42	121.79	118.00
1	A	1485	U	C6-N1-C2	-5.42	117.75	121.00
1	A	293	G	C5-C6-O6	-5.42	125.35	128.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	305	G	C2-N3-C4	-5.42	109.19	111.90
1	A	1080	A	C4-C5-N7	-5.42	107.99	110.70
1	A	450	G	C4-C5-N7	-5.41	108.63	110.80
1	A	639	G	N1-C2-N3	5.41	127.15	123.90
1	A	715	A	C5-C6-N6	5.41	128.03	123.70
1	A	1117	G	N3-C4-C5	5.41	131.31	128.60
1	A	928	G	C4-C5-N7	5.41	112.96	110.80
15	O	54	ARG	NE-CZ-NH1	5.41	123.00	120.30
1	A	75	G	C8-N9-C1'	5.41	134.03	127.00
1	A	76	C	C2-N1-C1'	-5.41	112.85	118.80
1	A	1079	G	C5-C6-O6	5.41	131.84	128.60
1	A	276	G	N7-C8-N9	-5.41	110.40	113.10
1	A	518	C	N3-C2-O2	-5.41	118.12	121.90
1	A	891	U	C2-N1-C1'	5.41	124.19	117.70
1	A	115	G	C5-C6-O6	-5.40	125.36	128.60
1	A	157	G	C5-C6-N1	-5.40	108.80	111.50
1	A	198	G	C5-C6-O6	-5.40	125.36	128.60
1	A	1072	G	N3-C2-N2	-5.40	116.12	119.90
1	A	256	U	C5-C6-N1	5.40	125.40	122.70
1	A	981	U	C5-C6-N1	5.40	125.40	122.70
1	A	478	A	N1-C6-N6	5.40	121.84	118.60
1	A	1065	U	N1-C2-O2	-5.40	119.02	122.80
1	A	240	C	N3-C4-C5	-5.40	119.74	121.90
1	A	331	G	C8-N9-C4	5.40	108.56	106.40
1	A	859	A	N3-C4-N9	5.40	131.72	127.40
1	A	121	C	N1-C2-O2	-5.39	115.66	118.90
1	A	891	U	C6-N1-C1'	-5.39	113.65	121.20
1	A	656	C	C2-N3-C4	-5.39	117.20	119.90
1	A	252	U	C2-N3-C4	-5.39	123.77	127.00
1	A	787	A	N1-C6-N6	-5.39	115.37	118.60
1	A	399	G	C2-N3-C4	-5.39	109.20	111.90
1	A	869	G	N3-C4-C5	5.39	131.29	128.60
1	A	481	G	N7-C8-N9	-5.38	110.41	113.10
1	A	329	A	N1-C6-N6	5.38	121.83	118.60
1	A	392	G	C4-C5-C6	5.38	122.03	118.80
1	A	407	G	C4-N9-C1'	-5.38	119.50	126.50
1	A	802	A	N9-C4-C5	-5.38	103.65	105.80
1	A	176	C	N3-C2-O2	5.38	125.67	121.90
1	A	447	G	C4-C5-N7	-5.38	108.65	110.80
1	A	833	U	C5-C4-O4	5.38	129.13	125.90
2	B	102	LEU	CA-CB-CG	-5.38	102.93	115.30
1	A	291	C	C2-N3-C4	-5.38	117.21	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	937	A	N1-C6-N6	-5.38	115.37	118.60
1	A	866	C	C5-C6-N1	-5.37	118.31	121.00
1	A	917	G	N3-C2-N2	-5.37	116.14	119.90
1	A	144	G	C5-N7-C8	-5.37	101.61	104.30
1	A	227	G	N1-C6-O6	5.37	123.12	119.90
1	A	773	G	C4-C5-N7	5.37	112.95	110.80
1	A	778	G	C2-N3-C4	-5.37	109.21	111.90
1	A	755	G	C5-C6-O6	-5.37	125.38	128.60
1	A	747	C	N3-C4-C5	5.37	124.05	121.90
1	A	779	C	C4-C5-C6	5.37	120.08	117.40
1	A	1344	C	C6-N1-C2	5.37	122.45	120.30
1	A	929	G	N9-C4-C5	-5.37	103.25	105.40
1	A	18	C	C4-C5-C6	5.37	120.08	117.40
1	A	366	C	C6-N1-C1'	-5.36	114.36	120.80
1	A	530	G	C4-N9-C1'	5.36	133.47	126.50
1	A	815	A	C6-N1-C2	-5.36	115.38	118.60
1	A	1327	C	N3-C4-N4	-5.36	114.25	118.00
1	A	601	C	C6-N1-C2	5.36	122.44	120.30
1	A	603	U	C4-C5-C6	5.36	122.92	119.70
1	A	565	U	N3-C2-O2	5.36	125.95	122.20
1	A	761	G	N3-C2-N2	5.36	123.65	119.90
1	A	1341	U	C2-N1-C1'	-5.36	111.27	117.70
1	A	93	G	C4-N9-C1'	5.36	133.47	126.50
1	A	145	G	C4-C5-N7	-5.36	108.66	110.80
1	A	848	C	N3-C4-C5	5.36	124.04	121.90
1	A	105	G	N1-C2-N2	-5.35	111.38	116.20
1	A	595	G	C5-C6-O6	5.35	131.81	128.60
1	A	637	G	C8-N9-C1'	-5.35	120.04	127.00
1	A	880	C	N3-C4-N4	5.35	121.75	118.00
1	A	1528	U	C6-N1-C2	5.35	124.21	121.00
1	A	888	G	C5-C6-N1	-5.35	108.83	111.50
1	A	1447	G	C4-C5-N7	5.35	112.94	110.80
1	A	129(A)	G	N1-C6-O6	5.35	123.11	119.90
1	A	753	A	C8-N9-C4	-5.35	103.66	105.80
1	A	1481	U	C5-C4-O4	5.35	129.11	125.90
1	A	1452	C	C2-N1-C1'	5.34	124.68	118.80
1	A	1501	C	N3-C2-O2	-5.34	118.16	121.90
1	A	15	G	C6-C5-N7	-5.34	127.19	130.40
1	A	249	U	N3-C4-C5	-5.34	111.40	114.60
1	A	260	G	C5-N7-C8	-5.34	101.63	104.30
1	A	796	C	C2-N3-C4	-5.34	117.23	119.90
1	A	120	A	N1-C2-N3	5.34	131.97	129.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	653	A	C8-N9-C4	-5.33	103.67	105.80
1	A	1361(A)	C	C4-C5-C6	-5.33	114.73	117.40
1	A	337	C	C4-C5-C6	5.33	120.06	117.40
1	A	354	G	N3-C4-C5	-5.33	125.94	128.60
1	A	719	C	C2-N1-C1'	-5.33	112.94	118.80
1	A	266	G	C8-N9-C4	-5.33	104.27	106.40
1	A	731	G	C5-N7-C8	-5.33	101.64	104.30
1	A	1094	G	N3-C2-N2	5.33	123.63	119.90
11	K	117	ASN	N-CA-C	5.33	125.38	111.00
1	A	456	C	N3-C2-O2	-5.33	118.17	121.90
1	A	859	A	C5-C6-N6	-5.33	119.44	123.70
1	A	1479	C	C5-C6-N1	5.33	123.66	121.00
1	A	1339	A	N1-C6-N6	-5.32	115.41	118.60
1	A	722	A	N3-C4-C5	5.32	130.53	126.80
1	A	373	A	N1-C6-N6	5.32	121.79	118.60
1	A	715	A	N3-C4-N9	-5.32	123.14	127.40
3	C	47	LEU	CA-CB-CG	5.32	127.53	115.30
1	A	364	A	C6-N1-C2	-5.32	115.41	118.60
1	A	874	G	C6-N1-C2	-5.32	121.91	125.10
1	A	719	C	C5-C4-N4	5.31	123.92	120.20
1	A	726	C	N3-C4-C5	5.31	124.03	121.90
1	A	771	G	C5-N7-C8	-5.31	101.64	104.30
1	A	1287	A	N9-C4-C5	5.31	107.92	105.80
1	A	699	C	N3-C2-O2	5.31	125.62	121.90
1	A	1058	G	C4-N9-C1'	5.31	133.40	126.50
1	A	511	C	N3-C4-C5	5.31	124.02	121.90
1	A	1455	G	C5-C6-N1	-5.31	108.85	111.50
1	A	238	G	N3-C4-N9	-5.30	122.82	126.00
1	A	353	A	C8-N9-C4	5.30	107.92	105.80
1	A	979	C	C6-N1-C2	-5.30	118.18	120.30
1	A	120	A	C8-N9-C4	5.30	107.92	105.80
1	A	1334	G	N1-C6-O6	-5.30	116.72	119.90
1	A	1405	G	C6-C5-N7	5.30	133.58	130.40
1	A	89	C	C6-N1-C2	-5.30	118.18	120.30
1	A	147	G	C8-N9-C4	5.30	108.52	106.40
1	A	1081	G	C8-N9-C4	-5.30	104.28	106.40
1	A	558	G	C6-C5-N7	-5.29	127.22	130.40
1	A	820	U	C2-N1-C1'	-5.29	111.35	117.70
1	A	888	G	N9-C4-C5	5.29	107.52	105.40
1	A	912	A	N9-C4-C5	-5.29	103.68	105.80
17	Q	5	VAL	CB-CA-C	-5.29	101.34	111.40
1	A	95	U	C6-N1-C1'	5.29	128.61	121.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	639	G	N1-C2-N2	-5.29	111.44	116.20
1	A	1080	A	C5-C6-N6	5.29	127.93	123.70
1	A	908	A	C2-N3-C4	-5.29	107.96	110.60
1	A	22	G	C4-N9-C1'	5.28	133.37	126.50
1	A	1414	U	N3-C2-O2	-5.28	118.50	122.20
1	A	187	C	N3-C4-N4	5.28	121.70	118.00
1	A	252	U	C6-N1-C2	5.28	124.17	121.00
1	A	853	G	N1-C2-N3	5.28	127.07	123.90
1	A	1077	G	N3-C4-N9	5.28	129.17	126.00
1	A	293	G	N3-C4-C5	5.28	131.24	128.60
1	A	543	C	N1-C2-O2	-5.28	115.73	118.90
1	A	725	G	C5-N7-C8	-5.28	101.66	104.30
1	A	850	U	C6-N1-C2	-5.28	117.83	121.00
1	A	1158	C	N3-C2-O2	-5.28	118.21	121.90
1	A	1162	C	N1-C2-O2	5.27	122.06	118.90
1	A	1191	A	N1-C6-N6	-5.27	115.44	118.60
1	A	542	G	N3-C4-N9	5.27	129.16	126.00
1	A	545	C	C6-N1-C2	-5.27	118.19	120.30
1	A	1542	U	N1-C2-N3	-5.27	111.74	114.90
1	A	395	C	N3-C4-C5	-5.27	119.79	121.90
1	A	326	G	C6-N1-C2	-5.27	121.94	125.10
1	A	730	G	C4-C5-C6	5.27	121.96	118.80
1	A	1249	C	C2-N1-C1'	5.27	124.59	118.80
1	A	1332	A	C4-C5-N7	-5.27	108.07	110.70
1	A	1061	G	C8-N9-C4	-5.26	104.29	106.40
1	A	111	G	N3-C4-N9	-5.26	122.84	126.00
1	A	1350	A	N9-C4-C5	5.26	107.90	105.80
1	A	190(G)	G	C5-C6-N1	-5.26	108.87	111.50
1	A	274	A	C6-N1-C2	-5.26	115.44	118.60
1	A	694	A	C5-C6-N1	-5.26	115.07	117.70
4	D	97	LEU	CB-CG-CD2	-5.26	102.06	111.00
1	A	318	G	N3-C2-N2	-5.26	116.22	119.90
1	A	140	A	N1-C6-N6	5.25	121.75	118.60
1	A	232	G	C5-N7-C8	-5.25	101.67	104.30
1	A	1529	G	C5-C6-N1	-5.25	108.87	111.50
1	A	266	G	C5-C6-N1	-5.25	108.87	111.50
1	A	1250	A	C5-C6-N6	5.25	127.90	123.70
1	A	1507	A	N1-C6-N6	5.25	121.75	118.60
1	A	575	G	N9-C4-C5	-5.25	103.30	105.40
1	A	231	G	C8-N9-C1'	-5.25	120.18	127.00
1	A	860	A	N7-C8-N9	5.25	116.42	113.80
1	A	1306	A	N7-C8-N9	5.25	116.42	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	136	C	N3-C2-O2	-5.25	118.23	121.90
1	A	454	C	C5-C6-N1	5.25	123.62	121.00
1	A	758	G	C4-C5-N7	5.25	112.90	110.80
1	A	364	A	C4-C5-C6	5.24	119.62	117.00
1	A	853	G	C2-N3-C4	-5.24	109.28	111.90
1	A	1333	A	N1-C6-N6	5.24	121.75	118.60
1	A	439	A	N7-C8-N9	5.24	116.42	113.80
1	A	1416	G	N3-C4-C5	-5.24	125.98	128.60
1	A	26	A	C2-N3-C4	-5.24	107.98	110.60
1	A	326	G	C5-C6-O6	5.24	131.74	128.60
1	A	733	A	N3-C4-N9	-5.24	123.21	127.40
1	A	454	C	C6-N1-C2	-5.24	118.20	120.30
1	A	570	G	C8-N9-C1'	-5.24	120.19	127.00
1	A	918	A	C2-N3-C4	-5.24	107.98	110.60
1	A	1478	C	C6-N1-C2	-5.24	118.20	120.30
1	A	76	C	C5-C6-N1	-5.24	118.38	121.00
1	A	130	A	C4-N9-C1'	5.24	135.72	126.30
1	A	570	G	N3-C4-N9	5.24	129.14	126.00
1	A	693	G	C4-C5-N7	5.24	112.89	110.80
12	L	10	LEU	CB-CG-CD2	5.24	119.90	111.00
1	A	1390	U	N1-C2-N3	5.23	118.04	114.90
1	A	485	G	P-O3'-C3'	5.23	125.98	119.70
1	A	706	A	C8-N9-C4	5.23	107.89	105.80
1	A	62	U	N3-C2-O2	-5.23	118.54	122.20
1	A	138	G	N1-C6-O6	5.22	123.03	119.90
1	A	397	A	N7-C8-N9	5.22	116.41	113.80
1	A	634	C	N1-C2-N3	5.22	122.86	119.20
1	A	694	A	C2-N3-C4	-5.22	107.99	110.60
1	A	1068	G	C6-C5-N7	-5.22	127.27	130.40
1	A	1104	G	N1-C6-O6	5.22	123.03	119.90
5	E	10	MET	CG-SD-CE	5.22	108.56	100.20
1	A	131	C	C6-N1-C1'	-5.22	114.53	120.80
1	A	819	A	C6-C5-N7	-5.22	128.65	132.30
1	A	1248	A	C2-N3-C4	5.22	113.21	110.60
1	A	1455	G	C2-N3-C4	-5.22	109.29	111.90
1	A	726	C	C5-C4-N4	-5.22	116.55	120.20
1	A	1238	A	C5-N7-C8	5.22	106.51	103.90
1	A	1209	C	N3-C2-O2	-5.22	118.25	121.90
1	A	1132	C	C5-C6-N1	5.22	123.61	121.00
1	A	1262	C	C6-N1-C2	-5.22	118.21	120.30
1	A	1513	A	N1-C2-N3	5.22	131.91	129.30
1	A	173	U	N3-C2-O2	-5.22	118.55	122.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	610	G	C4-C5-C6	5.22	121.93	118.80
1	A	817	C	C6-N1-C1'	-5.22	114.54	120.80
1	A	836	G	C8-N9-C1'	-5.22	120.22	127.00
1	A	970	C	N3-C2-O2	-5.22	118.25	121.90
1	A	853	G	N1-C2-N2	-5.21	111.51	116.20
1	A	1375	A	C4-C5-N7	-5.21	108.09	110.70
1	A	285	G	N3-C4-N9	-5.21	122.87	126.00
1	A	651	C	N1-C2-N3	-5.21	115.55	119.20
1	A	171	A	C6-N1-C2	-5.21	115.48	118.60
1	A	753	A	C5-C6-N6	5.20	127.86	123.70
1	A	1530	G	N1-C6-O6	5.20	123.02	119.90
17	Q	63	ARG	NE-CZ-NH1	-5.20	117.70	120.30
1	A	300	A	N9-C4-C5	5.20	107.88	105.80
1	A	730	G	C4-N9-C1'	5.20	133.25	126.50
1	A	1528	U	C6-N1-C1'	-5.20	113.93	121.20
1	A	635	G	C2-N3-C4	-5.19	109.30	111.90
1	A	402	G	N9-C4-C5	5.19	107.48	105.40
1	A	833	U	N1-C2-N3	5.19	118.02	114.90
1	A	259	G	N1-C2-N3	5.19	127.01	123.90
1	A	318	G	N1-C6-O6	5.19	123.01	119.90
1	A	462	G	N3-C4-N9	5.19	129.11	126.00
1	A	564	C	C5-C6-N1	5.19	123.59	121.00
5	E	12	LEU	CA-CB-CG	5.19	127.23	115.30
1	A	1237	C	C4-C5-C6	5.19	119.99	117.40
1	A	144	G	C6-N1-C2	5.18	128.21	125.10
1	A	334	C	N1-C2-O2	5.18	122.01	118.90
1	A	642	A	N9-C4-C5	5.18	107.87	105.80
1	A	1230	C	N3-C2-O2	-5.18	118.27	121.90
1	A	917	G	C6-N1-C2	-5.18	121.99	125.10
1	A	1155	G	C8-N9-C4	-5.18	104.33	106.40
1	A	1345	U	N1-C2-O2	-5.18	119.18	122.80
1	A	1395	C	C5-C6-N1	-5.18	118.41	121.00
1	A	260	G	C8-N9-C4	-5.17	104.33	106.40
1	A	576	G	C4-C5-N7	-5.17	108.73	110.80
1	A	725	G	N3-C4-C5	5.17	131.19	128.60
1	A	738	C	N1-C2-O2	5.17	122.00	118.90
1	A	1378	C	C6-N1-C2	-5.17	118.23	120.30
1	A	368	U	C5-C4-O4	5.17	129.00	125.90
1	A	1328	C	C5-C4-N4	-5.17	116.58	120.20
1	A	727	G	N1-C6-O6	-5.17	116.80	119.90
1	A	59	A	C4-C5-N7	5.17	113.28	110.70
1	A	147	G	C5-C6-O6	-5.17	125.50	128.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1347	G	N9-C4-C5	-5.17	103.33	105.40
1	A	637	G	N3-C4-N9	5.17	129.10	126.00
1	A	351	G	C4-C5-N7	5.16	112.87	110.80
1	A	935	A	C8-N9-C4	5.16	107.86	105.80
1	A	946	A	N1-C2-N3	5.16	131.88	129.30
1	A	1087	G	C2-N3-C4	-5.16	109.32	111.90
1	A	1233	G	C5-C6-O6	-5.16	125.50	128.60
1	A	755	G	C6-N1-C2	-5.16	122.01	125.10
1	A	75	G	N3-C2-N2	-5.16	116.29	119.90
1	A	1158	C	N1-C2-O2	5.15	121.99	118.90
1	A	1345	U	C5-C6-N1	-5.15	120.12	122.70
1	A	114	U	C5-C6-N1	-5.15	120.12	122.70
1	A	190(F)	G	C8-N9-C1'	5.15	133.69	127.00
1	A	259	G	N7-C8-N9	5.15	115.67	113.10
1	A	1454	G	C4-C5-N7	5.15	112.86	110.80
1	A	295	C	N3-C4-C5	5.15	123.96	121.90
1	A	1086	U	N3-C2-O2	5.15	125.80	122.20
17	Q	74	LEU	CB-CG-CD1	-5.15	102.25	111.00
1	A	389	A	C8-N9-C4	-5.15	103.74	105.80
1	A	1052	U	N3-C4-O4	5.14	123.00	119.40
1	A	257	G	C6-C5-N7	-5.14	127.31	130.40
1	A	328	C	P-O3'-C3'	5.14	125.87	119.70
1	A	1452	C	C2-N3-C4	5.14	122.47	119.90
1	A	1510	U	N1-C2-N3	5.14	117.98	114.90
1	A	1529	G	N7-C8-N9	5.14	115.67	113.10
4	D	26	CYS	CA-CB-SG	5.14	123.26	114.00
1	A	383	A	N1-C2-N3	-5.14	126.73	129.30
1	A	788	U	N1-C2-O2	5.14	126.40	122.80
1	A	337	C	N3-C4-C5	-5.14	119.84	121.90
1	A	785	G	C2-N3-C4	-5.14	109.33	111.90
1	A	905	U	N3-C2-O2	-5.14	118.60	122.20
1	A	909	A	N7-C8-N9	5.14	116.37	113.80
1	A	243	A	N1-C2-N3	5.14	131.87	129.30
1	A	835	U	N3-C2-O2	-5.14	118.60	122.20
1	A	829	G	C4-N9-C1'	5.13	133.17	126.50
1	A	1442	G	N3-C4-C5	-5.13	126.03	128.60
15	O	69	TYR	CB-CA-C	-5.13	100.13	110.40
1	A	267	C	C6-N1-C2	-5.13	118.25	120.30
1	A	1242	C	C6-N1-C2	-5.13	118.25	120.30
1	A	221	C	N3-C4-C5	5.13	123.95	121.90
1	A	645	C	N3-C4-C5	-5.13	119.85	121.90
1	A	609	A	C5-C6-N1	-5.12	115.14	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	326	G	N1-C2-N2	-5.12	111.59	116.20
1	A	1191	A	C5-C6-N1	5.12	120.26	117.70
1	A	1268	A	N3-C4-C5	-5.12	123.21	126.80
1	A	668	G	C8-N9-C4	5.12	108.45	106.40
1	A	123	C	N3-C4-C5	-5.12	119.85	121.90
1	A	976	G	C4-C5-N7	-5.12	108.75	110.80
1	A	637	G	C4-N9-C1'	5.12	133.15	126.50
1	A	791	G	C4-C5-C6	5.12	121.87	118.80
18	R	50	ILE	CB-CA-C	-5.12	101.37	111.60
1	A	96	G	N3-C4-C5	5.12	131.16	128.60
1	A	322	C	N3-C2-O2	5.12	125.48	121.90
1	A	759	A	C8-N9-C4	-5.11	103.75	105.80
1	A	1507	A	C8-N9-C4	5.11	107.85	105.80
1	A	319	G	N1-C6-O6	5.11	122.97	119.90
1	A	611	A	N1-C6-N6	-5.11	115.53	118.60
1	A	1108	G	N3-C4-C5	-5.11	126.05	128.60
1	A	783	C	C6-N1-C2	5.11	122.34	120.30
1	A	860	A	C8-N9-C4	-5.11	103.76	105.80
1	A	1403	C	N1-C2-O2	-5.11	115.83	118.90
1	A	264	U	N3-C2-O2	-5.11	118.62	122.20
1	A	289	G	C8-N9-C4	-5.11	104.36	106.40
1	A	1345	U	C2-N3-C4	-5.11	123.94	127.00
1	A	11	G	C6-N1-C2	-5.10	122.04	125.10
1	A	79	G	C8-N9-C4	-5.10	104.36	106.40
1	A	709	G	N3-C4-C5	5.10	131.15	128.60
1	A	1377	A	C2-N3-C4	5.10	113.15	110.60
8	H	134	ILE	CB-CA-C	-5.10	101.41	111.60
1	A	799	G	N9-C4-C5	-5.10	103.36	105.40
1	A	1468	A	C5-C6-N6	-5.10	119.62	123.70
1	A	251	G	C4-C5-N7	5.09	112.84	110.80
1	A	396	G	N1-C2-N3	5.09	126.95	123.90
1	A	1248	A	N1-C2-N3	-5.09	126.76	129.30
1	A	1341	U	N3-C2-O2	5.09	125.76	122.20
1	A	1061	G	N7-C8-N9	5.08	115.64	113.10
1	A	1187	G	N1-C6-O6	5.08	122.95	119.90
1	A	187	C	N3-C4-C5	-5.08	119.87	121.90
1	A	331	G	C4-C5-C6	5.08	121.85	118.80
1	A	881	G	N9-C4-C5	-5.08	103.37	105.40
1	A	791	G	C8-N9-C4	-5.08	104.37	106.40
1	A	164	U	C5-C4-O4	5.07	128.94	125.90
1	A	896	C	C6-N1-C2	-5.07	118.27	120.30
1	A	1236	A	N1-C2-N3	-5.07	126.76	129.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1398	A	C4-C5-N7	-5.07	108.16	110.70
16	P	51	VAL	N-CA-C	5.07	124.70	111.00
1	A	1233	G	C4-C5-N7	5.07	112.83	110.80
1	A	291	C	C4-C5-C6	5.07	119.94	117.40
1	A	1186	G	N3-C4-N9	-5.07	122.96	126.00
1	A	1192	C	N3-C4-N4	-5.07	114.45	118.00
1	A	19	C	C5-C6-N1	-5.07	118.47	121.00
1	A	428	G	P-O3'-C3'	5.07	125.78	119.70
1	A	1102	A	C8-N9-C4	5.07	107.83	105.80
1	A	1108	G	C6-C5-N7	-5.07	127.36	130.40
1	A	565	U	C5-C4-O4	-5.06	122.86	125.90
1	A	800	G	N3-C4-N9	5.06	129.04	126.00
1	A	1399	C	N3-C2-O2	5.06	125.44	121.90
1	A	577	G	C5-C6-O6	-5.06	125.56	128.60
1	A	1487	G	N1-C6-O6	5.06	122.94	119.90
1	A	129(A)	G	C5-C6-O6	-5.06	125.56	128.60
1	A	947	G	C2-N3-C4	-5.06	109.37	111.90
1	A	196	A	N1-C6-N6	-5.06	115.56	118.60
1	A	1228	C	C6-N1-C2	-5.06	118.28	120.30
1	A	1300	G	C6-C5-N7	5.06	133.44	130.40
1	A	630	G	N1-C6-O6	5.06	122.94	119.90
1	A	1190	G	C8-N9-C4	5.06	108.42	106.40
1	A	672	U	C6-N1-C2	5.05	124.03	121.00
1	A	944	G	C8-N9-C4	-5.05	104.38	106.40
1	A	1199	U	N3-C2-O2	5.05	125.74	122.20
1	A	364	A	N1-C2-N3	5.05	131.83	129.30
1	A	1076	C	C2-N1-C1'	5.05	124.36	118.80
1	A	76	C	C4-C5-C6	5.05	119.93	117.40
1	A	138	G	N7-C8-N9	-5.05	110.57	113.10
1	A	837	G	N9-C4-C5	-5.05	103.38	105.40
1	A	1160	G	N3-C4-N9	5.05	129.03	126.00
1	A	1485	U	C5-C4-O4	5.05	128.93	125.90
1	A	306	G	N3-C2-N2	-5.05	116.37	119.90
1	A	606	G	C4-N9-C1'	5.05	133.06	126.50
1	A	1308	U	C5-C4-O4	-5.05	122.87	125.90
1	A	77	G	N3-C2-N2	5.04	123.43	119.90
1	A	668	G	C8-N9-C1'	-5.04	120.44	127.00
1	A	6	G	C5-C6-O6	-5.04	125.57	128.60
1	A	1350	A	N7-C8-N9	5.04	116.32	113.80
1	A	31	G	C5-C6-O6	-5.04	125.58	128.60
1	A	1160	G	C5-C6-O6	-5.04	125.58	128.60
1	A	107	G	N9-C4-C5	-5.04	103.39	105.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	897	C	N3-C4-C5	5.04	123.91	121.90
1	A	905	U	C5-C6-N1	5.04	125.22	122.70
1	A	58	C	N3-C4-C5	5.03	123.91	121.90
1	A	190(G)	G	C4-N9-C1'	5.03	133.04	126.50
1	A	661	G	N3-C4-C5	5.03	131.11	128.60
1	A	928	G	C6-C5-N7	-5.03	127.38	130.40
1	A	1344	C	N3-C4-N4	-5.03	114.48	118.00
1	A	22	G	C4-C5-C6	5.03	121.82	118.80
1	A	1246	C	C5-C6-N1	5.03	123.51	121.00
1	A	1355	G	C8-N9-C4	-5.03	104.39	106.40
1	A	115	G	N3-C2-N2	-5.02	116.38	119.90
1	A	1498	UR3	P-O3'-C3'	5.02	125.73	119.70
1	A	380	G	C5-C6-O6	5.02	131.61	128.60
1	A	947	G	C8-N9-C4	5.02	108.41	106.40
1	A	1139	G	C4-C5-N7	-5.02	108.79	110.80
1	A	884	U	C5-C4-O4	5.02	128.91	125.90
1	A	101	A	N1-C6-N6	-5.02	115.59	118.60
1	A	7	G	C5-C6-N1	5.02	114.01	111.50
1	A	201	C	N3-C2-O2	-5.02	118.39	121.90
1	A	1287	A	C4-N9-C1'	5.02	135.33	126.30
1	A	1226	C	C6-N1-C2	-5.01	118.29	120.30
1	A	297	G	N3-C4-C5	-5.01	126.09	128.60
1	A	754	C	N3-C2-O2	-5.01	118.39	121.90
1	A	300	A	C8-N9-C4	-5.01	103.80	105.80
1	A	230	G	C8-N9-C1'	-5.01	120.49	127.00
1	A	474	G	C4-C5-N7	5.01	112.80	110.80
1	A	570	G	N1-C6-O6	-5.01	116.90	119.90
1	A	831	U	C4-C5-C6	5.01	122.70	119.70
1	A	80	G	N7-C8-N9	5.00	115.60	113.10
1	A	255	G	C8-N9-C1'	-5.00	120.49	127.00
1	A	9	G	N9-C4-C5	-5.00	103.40	105.40
1	A	511	C	N3-C4-N4	-5.00	114.50	118.00
1	A	773	G	C2-N3-C4	-5.00	109.40	111.90
1	A	830	G	N9-C4-C5	5.00	107.40	105.40

There are no chirality outliers.

All (11) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	77	ALA	Peptide
3	C	166	GLU	Peptide
3	C	179	ARG	Peptide

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Mol	Chain	Res	Type	Group
5	E	20	GLN	Peptide
8	H	27	PRO	Peptide
8	H	90	GLY	Peptide
10	J	35	SER	Peptide
10	J	87	THR	Peptide
12	L	25	PRO	Peptide
13	M	117	VAL	Peptide
20	T	93	GLU	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32646	0	16503	874	1
2	B	1900	0	1951	105	0
3	C	1612	0	1677	109	0
4	D	1703	0	1763	68	0
5	E	1146	0	1207	71	0
6	F	843	0	857	46	0
7	G	1257	0	1296	60	0
8	H	1116	0	1177	71	0
9	I	1010	0	1037	78	0
10	J	792	0	835	59	0
11	K	864	0	881	41	0
12	L	972	0	1058	59	0
13	M	937	0	995	52	0
14	N	492	0	529	47	0
15	O	729	0	768	41	0
16	P	700	0	720	41	0
17	Q	823	0	893	58	0
18	R	574	0	644	37	0
19	S	647	0	673	35	0
20	T	763	0	861	37	0
21	U	208	0	221	14	0
22	A	268	0	0	0	0
22	B	2	0	0	0	0
22	C	2	0	0	0	0
22	D	4	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	E	1	0	0	0	0
22	F	1	0	0	0	0
22	I	1	0	0	0	0
22	J	1	0	0	0	0
22	L	1	0	0	0	0
22	M	2	0	0	0	0
22	P	2	0	0	0	0
22	Q	2	0	0	0	0
22	T	2	0	0	0	0
23	D	1	0	0	0	0
23	N	1	0	0	0	0
24	A	391	0	0	6	0
24	B	1	0	0	2	0
24	D	3	0	0	0	0
24	E	4	0	0	0	0
24	G	2	0	0	1	0
24	J	2	0	0	2	0
24	K	1	0	0	0	0
24	M	3	0	0	1	0
24	N	4	0	0	1	0
24	P	4	0	0	3	0
24	T	1	0	0	1	0
All	All	52441	0	36546	1810	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 21.

All (1810) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:967:5MC:H4'	9:I:128:ARG:HG3	1.33	1.06
1:A:75:G:N2	1:A:76:C:N3	2.07	1.02
1:A:949:A:N6	24:A:2225:HOH:O	1.90	1.02
1:A:1152:A:H5''	10:J:13:HIS:HB2	1.44	1.00
20:T:50:GLU:HA	20:T:100:ILE:HG13	1.47	0.95
1:A:1532:U:H2'	1:A:1533:C:H3'	1.50	0.92
1:A:1073:U:OP2	5:E:57:LYS:NZ	2.01	0.92
1:A:184:G:H2'	1:A:185:A:H8	1.35	0.91
1:A:1347:G:H3'	9:I:108:VAL:O	1.70	0.91
3:C:182:ILE:HG12	3:C:203:PHE:HB2	1.51	0.91
13:M:23:TYR:HE2	13:M:70:LEU:HD22	1.36	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1125:U:OP2	1:A:1145:C:N4	2.04	0.89
1:A:130:A:OP2	1:A:190(E):U:O2'	1.89	0.89
8:H:4:ASP:OD2	8:H:85:ARG:NH1	2.06	0.89
3:C:138:VAL:HG13	3:C:149:ALA:HB3	1.54	0.88
10:J:55:LYS:HB2	10:J:57:LYS:HE3	1.56	0.88
16:P:21:VAL:HG12	16:P:33:ILE:HD12	1.56	0.87
1:A:1415:G:H2'	1:A:1416:G:H8	1.38	0.87
1:A:1417:G:O2'	1:A:1483:A:N6	2.06	0.87
1:A:1426:C:H42	1:A:1474:G:H1	1.23	0.86
20:T:100:ILE:HG22	20:T:102:GLY:H	1.39	0.86
1:A:1368:G:H5''	9:I:112:LYS:HB3	1.56	0.86
3:C:137:ALA:HA	3:C:140:ARG:HD2	1.55	0.86
1:A:1415:G:H2'	1:A:1416:G:C8	2.09	0.85
1:A:446:G:H1	1:A:488:C:H42	1.21	0.84
11:K:121:PRO:HG2	11:K:126:ARG:HG2	1.60	0.84
10:J:12:ASP:HB3	10:J:15:THR:HB	1.60	0.84
1:A:517:G:N1	1:A:533:A:OP2	2.09	0.84
8:H:41:ARG:NH1	8:H:123:GLU:OE2	2.11	0.84
12:L:24:VAL:HG13	12:L:98:TYR:HE2	1.42	0.83
1:A:91:C:O2'	1:A:92:C:OP1	1.95	0.83
1:A:1515[B]:C:H42	1:A:1520[B]:G:H1	1.27	0.82
3:C:150:LYS:HB2	3:C:173:VAL:HG21	1.60	0.81
1:A:664:G:H22	1:A:741:G:H1	1.27	0.81
1:A:101:A:H2'	1:A:102:G:H8	1.46	0.81
1:A:501:C:H2'	1:A:502:G:C8	2.15	0.81
19:S:41:VAL:HG22	19:S:44:MET:HG3	1.61	0.81
1:A:1195:C:H3'	1:A:1196:U:H5''	1.60	0.81
1:A:1436:U:H2'	1:A:1437:C:H6	1.46	0.80
1:A:686:U:HO2'	1:A:687:A:H8	1.26	0.80
1:A:1149:C:O2'	1:A:1280:A:N1	2.15	0.80
1:A:279:A:H8	1:A:279:A:H5'	1.47	0.80
1:A:279:A:OP2	17:Q:95:TYR:OH	1.98	0.80
7:G:56:GLN:HG2	7:G:60:LYS:HD3	1.64	0.80
1:A:1518[B]:MA6:H102	1:A:1519[B]:MA6:H103	1.65	0.79
8:H:6:ILE:HB	8:H:85:ARG:HH12	1.45	0.79
15:O:39:LEU:HD13	15:O:56:LEU:HB2	1.64	0.79
1:A:103:C:OP1	20:T:17:ARG:NH1	2.15	0.79
1:A:951:G:OP2	13:M:102:ARG:NH2	2.16	0.79
1:A:1009:G:H1	1:A:1020:U:H3	1.30	0.79
4:D:57:ARG:HG2	4:D:202:LEU:HD12	1.65	0.79
1:A:184:G:H2'	1:A:185:A:C8	2.17	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:140:ASP:HA	7:G:143:ARG:HB2	1.65	0.79
1:A:384:G:H2'	1:A:385:C:C6	2.18	0.78
3:C:85:ARG:HD2	3:C:88:ARG:HH11	1.48	0.78
1:A:1426:C:N3	1:A:1474:G:N2	2.29	0.78
20:T:45:GLN:HG3	20:T:91:LEU:HD11	1.65	0.77
1:A:1198:G:H2'	1:A:1199:U:C6	2.20	0.77
1:A:1314:C:H5	19:S:6:LYS:HD3	1.49	0.77
4:D:64:LEU:HD23	4:D:198:VAL:HG21	1.65	0.77
1:A:1266:G:N2	1:A:1269:A:OP2	2.15	0.77
1:A:505:G:O6	1:A:526:C:N4	2.17	0.77
13:M:23:TYR:CE2	13:M:70:LEU:HD22	2.20	0.77
1:A:1250:A:O2'	1:A:1370:G:O2'	2.02	0.77
10:J:53:PRO:HA	14:N:41:ARG:HH22	1.51	0.76
1:A:79:G:N1	1:A:80:G:N7	2.34	0.76
3:C:130:VAL:HG11	3:C:153:VAL:HG21	1.65	0.76
12:L:34:ARG:O	12:L:61:THR:OG1	2.04	0.76
16:P:3:LYS:HG3	16:P:24:ALA:HB2	1.67	0.76
3:C:43:LEU:HA	3:C:47:LEU:HD13	1.68	0.75
8:H:85:ARG:NE	8:H:87:SER:O	2.17	0.75
1:A:1404:5MC:H1'	1:A:1499:A:C2	2.21	0.75
1:A:1415:G:N2	1:A:1486:G:N3	2.34	0.75
3:C:180:ALA:HB1	3:C:203:PHE:HE1	1.51	0.75
16:P:80:PHE:N	24:P:204:HOH:O	2.10	0.75
1:A:36:C:H5''	12:L:123:LYS:HD3	1.69	0.75
10:J:47:PHE:HB3	14:N:34:TYR:HE2	1.49	0.75
1:A:115:G:O2'	1:A:116:A:OP2	2.05	0.75
1:A:953:G:H5'	1:A:965:A:H61	1.52	0.75
12:L:24:VAL:HG13	12:L:98:TYR:CE2	2.21	0.75
14:N:24:CYS:HB2	14:N:39:LEU:HA	1.67	0.74
1:A:1373:G:H5''	7:G:36:LYS:HE2	1.70	0.74
1:A:1497:G:H2'	1:A:1498:UR3:H5'	1.70	0.74
1:A:1249:C:O2'	9:I:73:GLN:NE2	2.19	0.74
1:A:584:G:OP2	17:Q:87:LYS:NZ	2.21	0.73
1:A:455:C:H2'	1:A:456:C:H6	1.53	0.73
14:N:40:CYS:O	14:N:44:LEU:N	2.17	0.73
1:A:1435:G:H2'	1:A:1436:U:C6	2.24	0.73
1:A:1310:G:OP1	13:M:77:ASN:ND2	2.22	0.73
8:H:6:ILE:HB	8:H:85:ARG:NH1	2.04	0.73
13:M:22:ILE:HG22	13:M:23:TYR:H	1.52	0.73
13:M:96:LEU:O	13:M:110:ARG:NH1	2.22	0.73
1:A:1241:G:H2'	1:A:1242:C:H6	1.54	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:13:ARG:NH1	4:D:38:TYR:O	2.22	0.72
8:H:114:THR:HB	8:H:116:LYS:H	1.54	0.72
1:A:1003:G:N2	1:A:1039:C:N3	2.35	0.72
1:A:1242:C:H42	1:A:1295:G:H1	1.37	0.72
1:A:81:U:H2'	1:A:83:U:OP2	1.89	0.72
1:A:1145:C:O2'	1:A:1146:A:O5'	2.07	0.72
1:A:1316:G:N2	1:A:1319:A:OP2	2.22	0.72
1:A:1188:A:O3'	14:N:58:LYS:NZ	2.22	0.72
1:A:992:U:H3	1:A:1044:A:N6	1.87	0.72
1:A:1399:C:H4'	1:A:1400:5MC:H5''	1.71	0.72
1:A:1192:C:O2	5:E:25:ARG:NH2	2.22	0.72
1:A:9:G:OP2	5:E:121:LYS:NZ	2.16	0.72
1:A:1113:C:H42	1:A:1187:G:H1	1.37	0.72
1:A:1347:G:HO2'	1:A:1348:U:H6	1.38	0.72
1:A:113:G:H1'	1:A:354:G:H5'	1.70	0.72
1:A:836:G:OP1	18:R:61:LYS:NZ	2.23	0.71
9:I:5:TYR:HD1	9:I:6:GLY:N	1.88	0.71
20:T:44:ALA:HB1	20:T:91:LEU:HB3	1.72	0.71
13:M:91:ARG:HB3	13:M:98:VAL:HG22	1.72	0.71
19:S:12:ASP:OD1	19:S:35:SER:OG	2.08	0.71
2:B:16:HIS:CD2	2:B:204:ASN:H	2.08	0.71
10:J:61:GLU:HA	24:J:302:HOH:O	1.91	0.71
12:L:27:LEU:HG	12:L:28:LYS:H	1.56	0.71
1:A:1498:UR3:O2'	1:A:1499:A:OP2	2.06	0.71
13:M:10:PRO:HB2	13:M:18:ALA:HB1	1.73	0.71
1:A:1201:A:H4'	1:A:1202:G:C5'	2.21	0.71
11:K:57:THR:HG23	11:K:60:ALA:H	1.53	0.71
1:A:1300:G:O2'	1:A:1301:U:OP2	2.09	0.70
10:J:39:PRO:HA	10:J:70:ARG:HG3	1.72	0.70
17:Q:75:ARG:HH22	17:Q:77:VAL:HG13	1.57	0.70
1:A:216:G:H2'	1:A:217:C:C6	2.27	0.70
13:M:108:ARG:NH2	13:M:112:GLY:O	2.23	0.70
16:P:57:ARG:NE	16:P:79:VAL:O	2.19	0.70
10:J:79:ARG:HH12	10:J:82:ILE:HB	1.56	0.70
7:G:10:ARG:HH11	7:G:10:ARG:HB2	1.57	0.70
3:C:129:ALA:HB3	3:C:132:ARG:HG3	1.73	0.70
1:A:1078:U:H5''	1:A:1079:G:OP2	1.92	0.69
7:G:113:GLU:O	7:G:119:ARG:HD3	1.92	0.69
3:C:134:ILE:HG23	3:C:151:VAL:HB	1.75	0.69
1:A:103:C:P	20:T:17:ARG:HH12	2.16	0.69
21:U:5:ASP:HB3	21:U:8:THR:OG1	1.92	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:298:A:N6	24:A:2047:HOH:O	2.09	0.69
1:A:411:A:OP2	4:D:25:ARG:NH2	2.25	0.69
5:E:137:GLU:O	5:E:141:GLN:HG3	1.93	0.69
20:T:33:ILE:HG12	20:T:62:LEU:HD13	1.75	0.69
21:U:6:ARG:HD3	21:U:15:ARG:HH12	1.57	0.69
1:A:255:G:H1	1:A:271:C:H42	1.38	0.69
1:A:975:A:H5'	1:A:975:A:H8	1.57	0.69
7:G:69:VAL:HG21	7:G:104:LEU:HD21	1.75	0.69
17:Q:4:LYS:HG2	17:Q:6:LEU:HD21	1.75	0.69
17:Q:66:SER:O	17:Q:70:ARG:NH1	2.26	0.69
21:U:10:ARG:HA	21:U:13:ILE:HD12	1.74	0.69
1:A:1144:G:H22	1:A:1146:A:H62	1.40	0.68
7:G:47:CYS:HB3	7:G:58:PRO:HG2	1.76	0.68
8:H:10:LEU:HD22	8:H:83:ILE:HD12	1.74	0.68
8:H:20:TYR:CE1	8:H:76:PRO:HG2	2.29	0.68
1:A:537:G:H5''	12:L:113:ARG:HH21	1.57	0.68
20:T:60:GLU:HA	20:T:63:ILE:HD12	1.74	0.68
1:A:359:U:H2'	1:A:360:A:C8	2.29	0.68
8:H:87:SER:HA	8:H:93:VAL:HG13	1.76	0.68
13:M:20:THR:HG22	24:M:303:HOH:O	1.94	0.68
2:B:18:GLY:HA3	2:B:41:ILE:HA	1.74	0.68
1:A:198:G:H1	1:A:219:C:H42	1.42	0.68
8:H:25:ASP:OD1	8:H:25:ASP:N	2.26	0.68
1:A:972:C:H4'	10:J:57:LYS:HG2	1.76	0.68
13:M:54:VAL:HG22	13:M:57:ARG:HH12	1.59	0.68
1:A:501:C:H2'	1:A:502:G:H8	1.59	0.67
1:A:1053:G:N2	1:A:1058:G:O6	2.26	0.67
1:A:130:A:O2'	1:A:131:C:H5''	1.94	0.67
5:E:142:LEU:O	5:E:143:ARG:HD3	1.95	0.67
2:B:139:LYS:O	2:B:139:LYS:NZ	2.27	0.67
4:D:187:ARG:HD2	4:D:188:LEU:H	1.56	0.67
1:A:559:A:OP1	5:E:126:ARG:NH2	2.26	0.67
1:A:1510:U:H2'	1:A:1511:G:C8	2.30	0.67
4:D:80:GLU:O	4:D:84:LYS:HG2	1.95	0.67
8:H:20:TYR:HE1	8:H:76:PRO:HG2	1.58	0.67
14:N:24:CYS:HB2	14:N:39:LEU:HD23	1.77	0.67
1:A:781:A:H2'	1:A:782:A:H5'	1.76	0.67
5:E:84:PHE:HB2	5:E:134:ALA:HB2	1.76	0.67
4:D:13:ARG:NH2	4:D:40:PRO:HA	2.10	0.67
1:A:966:M2G:HM22	1:A:967:5MC:H1'	1.77	0.66
6:F:2:ARG:O	6:F:66:GLU:HA	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:50:LEU:HB3	9:I:55:ALA:HB3	1.76	0.66
1:A:1338:G:H2'	1:A:1339:A:C8	2.30	0.66
1:A:1418:A:H61	1:A:1482:G:H1'	1.60	0.66
1:A:1195:C:H3'	1:A:1196:U:C5'	2.24	0.66
2:B:97:TRP:HH2	2:B:176:GLU:CD	1.99	0.66
10:J:62:HIS:ND1	24:J:301:HOH:O	2.27	0.66
1:A:1250:A:HO2'	1:A:1370:G:HO2'	1.41	0.66
5:E:126:ARG:HH11	5:E:126:ARG:HG3	1.59	0.66
4:D:19:LEU:HD21	4:D:67:ILE:HG12	1.78	0.66
20:T:92:LEU:O	20:T:96:GLY:HA2	1.95	0.66
19:S:53:ASN:HB2	19:S:55:LYS:H	1.60	0.66
1:A:838:G:H1	1:A:848:C:H42	1.44	0.66
7:G:20:ASP:OD2	7:G:22:LEU:N	2.27	0.66
1:A:1118:C:H1'	1:A:1179:A:C4	2.31	0.65
1:A:216:G:H2'	1:A:217:C:H6	1.61	0.65
1:A:1497:G:C2'	1:A:1498:UR3:H5'	2.26	0.65
1:A:1139:G:O2'	1:A:1140:C:OP2	2.13	0.65
14:N:23:ARG:NH1	14:N:28:GLY:O	2.29	0.65
1:A:279:A:C8	1:A:279:A:H5'	2.31	0.65
1:A:1007:C:H1'	1:A:1023:G:H1	1.60	0.65
2:B:158:LEU:H	2:B:158:LEU:HD12	1.60	0.65
7:G:15:ASP:OD2	7:G:44:TYR:OH	2.13	0.65
9:I:19:LEU:HD21	9:I:59:PHE:HB3	1.79	0.65
1:A:1515[B]:C:N4	1:A:1520[B]:G:H1	1.94	0.65
1:A:457:C:H2'	1:A:458:C:C6	2.32	0.65
3:C:123:GLN:HA	3:C:126:ARG:HD2	1.78	0.65
17:Q:86:GLU:HG3	17:Q:90:ILE:HD11	1.79	0.65
1:A:1143:G:H2'	1:A:1144:G:C8	2.32	0.65
14:N:2:ALA:N	14:N:27:CYS:O	2.29	0.65
1:A:77:G:H2'	1:A:78:G:C8	2.32	0.65
17:Q:24:GLU:HA	17:Q:39:SER:HB3	1.79	0.65
1:A:17:U:H2'	1:A:18:C:C6	2.33	0.65
1:A:485:G:O2'	1:A:486:U:OP2	2.15	0.64
8:H:17:THR:O	8:H:78:GLN:NE2	2.30	0.64
12:L:87:GLY:HA2	12:L:98:TYR:HA	1.78	0.64
17:Q:40:LYS:HD3	17:Q:42:TYR:CZ	2.32	0.64
1:A:77:G:H2'	1:A:78:G:H8	1.62	0.64
7:G:18:TYR:HE2	7:G:59:LEU:HB2	1.62	0.64
20:T:87:LYS:O	20:T:91:LEU:HB2	1.96	0.64
1:A:1305:G:O2'	1:A:1306:A:H8	1.80	0.64
1:A:1347:G:N2	1:A:1374:A:OP2	2.26	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:11:ARG:HA	3:C:178:LEU:HD11	1.77	0.64
17:Q:51:TYR:HE1	17:Q:73:VAL:HB	1.62	0.64
1:A:572:A:H5'	1:A:573:A:OP2	1.98	0.64
12:L:84:LEU:HD23	12:L:101:VAL:HG21	1.79	0.64
1:A:1006:C:N4	1:A:1024:G:H21	1.95	0.64
1:A:973:G:H3'	1:A:974:A:H5''	1.79	0.64
1:A:279:A:H5''	1:A:281:G:O4'	1.97	0.64
9:I:21:PRO:HA	9:I:59:PHE:HA	1.79	0.64
1:A:1098:C:OP2	2:B:144:ARG:NH2	2.31	0.64
1:A:1241:G:H2'	1:A:1242:C:C6	2.33	0.64
1:A:967:5MC:O2'	9:I:128:ARG:NH1	2.31	0.64
17:Q:5:VAL:HG22	17:Q:60:ILE:HD12	1.80	0.64
1:A:250:A:H4'	1:A:251:G:O5'	1.98	0.63
5:E:42:GLY:N	5:E:66:MET:SD	2.71	0.63
1:A:1314:C:C5	19:S:6:LYS:HD3	2.33	0.63
1:A:447:G:H1	1:A:485:G:HO2'	1.44	0.63
1:A:1240:U:OP1	7:G:119:ARG:NH2	2.30	0.63
1:A:217:C:H2'	1:A:218:C:H6	1.63	0.63
9:I:108:VAL:HG12	9:I:109:VAL:H	1.63	0.63
12:L:53:ARG:HD3	12:L:93:LEU:HD21	1.80	0.63
6:F:94:GLN:HB2	18:R:32:ARG:HD3	1.80	0.63
1:A:1305:G:O2'	1:A:1306:A:O5'	2.16	0.63
1:A:551:U:O2'	12:L:86:ARG:HD2	1.97	0.63
1:A:980:C:H3'	1:A:981:U:H6	1.63	0.63
6:F:41:GLU:OE1	18:R:35:ARG:NH1	2.31	0.63
11:K:101:SER:HG	11:K:103:LEU:H	1.45	0.63
1:A:588:G:H1	1:A:651:C:H42	1.44	0.63
2:B:61:LEU:HD13	2:B:66:GLY:HA3	1.80	0.63
7:G:115:ARG:HB2	7:G:118:VAL:HG23	1.80	0.63
12:L:27:LEU:O	12:L:29:GLY:N	2.32	0.63
1:A:129:U:O3'	1:A:129(A):G:H3'	1.98	0.63
1:A:1318:A:H4'	19:S:10:PHE:CE2	2.34	0.63
1:A:1244:C:H42	1:A:1293:G:H1	1.44	0.63
1:A:1255:G:C6	1:A:1279:A:N7	2.67	0.63
2:B:131:PRO:HG2	2:B:134:GLU:HG2	1.80	0.63
13:M:4:ILE:HG12	13:M:56:LEU:HD12	1.81	0.63
15:O:2:PRO:O	15:O:38:ARG:NH1	2.32	0.63
1:A:78:G:C2	1:A:92:C:N4	2.66	0.63
3:C:29:TYR:HD2	3:C:33:LEU:HD22	1.64	0.63
12:L:27:LEU:C	12:L:29:GLY:H	2.03	0.63
1:A:512:U:OP1	4:D:46:LYS:NZ	2.31	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:126:ARG:CG	5:E:126:ARG:HH11	2.12	0.62
10:J:24:VAL:HG21	10:J:37:PRO:HG3	1.80	0.62
12:L:55:VAL:HG12	12:L:69:TYR:HA	1.80	0.62
1:A:1168:A:H2'	1:A:1169:A:C8	2.34	0.62
12:L:93:LEU:O	12:L:96:VAL:HG23	1.99	0.62
1:A:1111:A:N1	3:C:177:THR:HB	2.13	0.62
1:A:407:G:H5''	4:D:115:ARG:HB3	1.82	0.62
1:A:1465:C:H2'	1:A:1466:C:O4'	2.00	0.62
1:A:1096:C:H2'	1:A:1097:C:H6	1.65	0.62
1:A:481:G:HO2'	1:A:482:A:H8	1.48	0.62
1:A:1045:C:H2'	1:A:1046:A:H8	1.64	0.62
1:A:1436:U:H2'	1:A:1437:C:C6	2.32	0.62
1:A:299:G:H2'	1:A:300:A:C8	2.35	0.62
1:A:457:C:H2'	1:A:458:C:H6	1.64	0.62
1:A:1001:A:H2'	1:A:1002:G:H8	1.65	0.62
19:S:19:VAL:HG13	19:S:22:LEU:HD12	1.81	0.62
1:A:1361(A):C:HO2'	1:A:1362:C:H6	1.48	0.61
7:G:40:ALA:HB1	9:I:41:VAL:HG21	1.82	0.61
2:B:116:GLU:HG2	2:B:153:ARG:HH12	1.65	0.61
1:A:992:U:H3	1:A:1044:A:H61	1.47	0.61
2:B:240:GLN:OE1	2:B:240:GLN:N	2.33	0.61
9:I:26:VAL:HG23	9:I:33:PHE:HB2	1.82	0.61
9:I:38:GLN:OE1	9:I:39:GLY:N	2.34	0.61
14:N:39:LEU:HD13	14:N:43:CYS:HB3	1.83	0.61
17:Q:95:TYR:HA	17:Q:98:LEU:HD11	1.81	0.61
4:D:156:GLU:O	4:D:160:GLN:HG2	1.99	0.61
8:H:82:HIS:HD1	8:H:138:TRP:HE1	1.48	0.61
1:A:1328:C:H2'	1:A:1329:A:H8	1.64	0.61
1:A:75:G:N2	1:A:96:G:H1	1.98	0.61
3:C:58:GLU:H	3:C:65:ALA:HB3	1.65	0.61
10:J:45:ARG:HH11	10:J:45:ARG:HB3	1.65	0.61
12:L:25:PRO:C	12:L:27:LEU:H	2.03	0.61
1:A:578:C:O2'	1:A:728:A:N3	2.28	0.61
2:B:98:LEU:HB2	2:B:101:MET:SD	2.40	0.61
7:G:17:VAL:HG12	7:G:18:TYR:HD1	1.66	0.61
3:C:132:ARG:HA	3:C:135:LYS:HE2	1.82	0.61
14:N:12:ARG:HG3	14:N:14:PRO:HD3	1.82	0.61
1:A:1243:C:H2'	1:A:1244:C:H6	1.65	0.60
1:A:1473:A:H2'	1:A:1474:G:C8	2.36	0.60
1:A:427:U:OP1	4:D:13:ARG:NH2	2.34	0.60
17:Q:60:ILE:O	17:Q:62:SER:OG	2.20	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1113:C:N4	1:A:1187:G:H1	1.99	0.60
1:A:989:C:H42	1:A:1216:G:H1	1.49	0.60
1:A:247:G:OP2	17:Q:100:LYS:HG3	2.00	0.60
9:I:96:LEU:HD23	9:I:102:LEU:HD21	1.82	0.60
9:I:28:VAL:HG12	9:I:29:ASN:OD1	2.01	0.60
8:H:127:LEU:O	8:H:127:LEU:HD12	2.01	0.60
17:Q:18:THR:HG23	17:Q:69:LYS:HE3	1.84	0.60
18:R:86:VAL:HG12	18:R:87:ARG:H	1.67	0.60
21:U:6:ARG:HD3	21:U:15:ARG:NH1	2.17	0.60
1:A:1347:G:O2'	1:A:1348:U:O5'	2.19	0.60
1:A:275:G:H5'	17:Q:14:LYS:HD3	1.84	0.60
1:A:92:C:H2'	1:A:92:C:O2	2.00	0.60
3:C:56:ASP:HB2	3:C:67:THR:HB	1.83	0.60
8:H:111:ILE:HG22	8:H:134:ILE:HD12	1.83	0.60
9:I:45:ALA:HA	9:I:48:GLU:HB2	1.83	0.60
11:K:108:ILE:HB	18:R:87:ARG:O	2.02	0.60
11:K:84:VAL:HG11	11:K:91:ARG:HD3	1.84	0.60
2:B:181:PHE:CE2	8:H:70:GLN:HB3	2.37	0.60
1:A:970:C:OP1	10:J:57:LYS:NZ	2.26	0.60
6:F:11:ASN:HB2	6:F:86:ARG:NH2	2.17	0.60
17:Q:63:ARG:O	17:Q:65:ILE:HD12	2.02	0.60
1:A:1504:G:OP1	1:A:1507:A:H4'	2.00	0.60
2:B:98:LEU:HA	24:B:401:HOH:O	2.02	0.60
4:D:187:ARG:HD2	4:D:188:LEU:N	2.16	0.60
4:D:39:PRO:HG2	4:D:44:GLY:HA2	1.82	0.60
1:A:1152:A:H2'	1:A:1153:C:C6	2.37	0.59
7:G:75:VAL:HG11	7:G:86:GLN:HB3	1.83	0.59
1:A:1368:G:OP2	9:I:112:LYS:HD3	2.01	0.59
1:A:5:U:H4'	1:A:6:G:O5'	2.02	0.59
11:K:21:ILE:HD12	11:K:95:ILE:HG23	1.84	0.59
1:A:1326:C:OP2	21:U:6:ARG:NH1	2.35	0.59
1:A:1499:A:H1'	1:A:1520[A]:G:OP1	2.02	0.59
1:A:668:G:H1'	15:O:46:HIS:HD2	1.67	0.59
7:G:46:ALA:O	7:G:50:ILE:HB	2.02	0.59
1:A:1402:4OC:H2'	1:A:1403:C:C6	2.38	0.59
1:A:877:C:O2'	8:H:3:THR:HG23	2.03	0.59
1:A:345:C:OP2	1:A:345:C:H6	1.86	0.59
1:A:376:G:OP2	16:P:67:THR:HG21	2.03	0.59
17:Q:29:HIS:CG	17:Q:30:PRO:HD2	2.37	0.59
1:A:101:A:H2'	1:A:102:G:C8	2.34	0.59
1:A:1257:U:O2'	1:A:1258:G:H8	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1442:G:N7	1:A:1446:A:N6	2.50	0.59
1:A:802:A:H2'	1:A:803:G:O4'	2.03	0.59
1:A:79:G:C4	1:A:91:C:N3	2.70	0.59
2:B:23:ARG:O	2:B:24:TRP:HD1	1.86	0.59
4:D:36:ARG:HG2	4:D:38:TYR:OH	2.02	0.59
8:H:83:ILE:HG12	8:H:137:VAL:HG13	1.84	0.59
9:I:3:GLN:O	9:I:3:GLN:NE2	2.35	0.59
1:A:1238:A:OP1	1:A:1336:C:N4	2.32	0.59
2:B:15:VAL:HG21	2:B:209:ARG:HG2	1.83	0.59
1:A:1349:A:OP1	9:I:118:LYS:NZ	2.35	0.59
1:A:1187:G:H1'	14:N:61:TRP:OXT	2.02	0.59
1:A:836:G:C6	1:A:851:G:C6	2.90	0.59
13:M:59:TYR:CE1	13:M:63:THR:HG21	2.37	0.59
1:A:1127:G:H1	1:A:1145:C:H42	1.50	0.59
1:A:1221:G:H5'	19:S:36:ARG:HH11	1.66	0.59
1:A:1356:G:H2'	1:A:1357:A:C8	2.38	0.59
1:A:719:C:H42	18:R:74:ARG:HH12	1.50	0.59
12:L:84:LEU:O	12:L:101:VAL:HG23	2.02	0.59
15:O:18:PHE:HB2	15:O:19:PRO:HD2	1.84	0.59
16:P:43:LYS:HG2	16:P:48:TRP:CG	2.37	0.59
1:A:344:A:H5'	1:A:345:C:C5	2.38	0.59
3:C:39:ILE:HG21	3:C:57:ILE:HD11	1.84	0.59
9:I:28:VAL:N	9:I:31:GLN:O	2.30	0.59
1:A:1033:G:H2'	1:A:1034:G:C8	2.38	0.58
3:C:155:GLY:HA2	3:C:164:ARG:O	2.03	0.58
9:I:71:SER:HA	9:I:74:ILE:HG13	1.84	0.58
13:M:107:ALA:HB3	13:M:111:LYS:HE3	1.85	0.58
19:S:56:GLN:HG2	19:S:57:HIS:H	1.68	0.58
1:A:1347:G:O2'	1:A:1348:U:H6	1.85	0.58
1:A:1025:U:O2'	1:A:1026:G:O4'	2.21	0.58
1:A:1152:A:H2'	1:A:1153:C:H6	1.68	0.58
2:B:189:ASP:HB3	2:B:203:GLY:O	2.03	0.58
12:L:82:VAL:HG13	12:L:106:ASP:OD1	2.03	0.58
13:M:22:ILE:HG22	13:M:23:TYR:N	2.18	0.58
18:R:87:ARG:H	18:R:87:ARG:NH1	2.00	0.58
1:A:1474:G:H2'	1:A:1475:G:C8	2.38	0.58
1:A:92:C:O2	1:A:93:G:C8	2.57	0.58
3:C:148:GLY:HA3	3:C:172:ARG:O	2.03	0.58
4:D:112:VAL:HG23	4:D:116:GLN:OE1	2.02	0.58
1:A:967:5MC:C4'	9:I:128:ARG:HG3	2.22	0.58
17:Q:8:GLY:O	17:Q:56:VAL:HA	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:31:ILE:HG21	19:S:49:ILE:HD13	1.85	0.58
19:S:3:ARG:NH2	19:S:73:GLU:OE2	2.35	0.58
19:S:7:LYS:NZ	19:S:7:LYS:HB3	2.17	0.58
1:A:948:C:H42	1:A:1233:G:H1	1.49	0.58
2:B:55:PHE:CD2	2:B:58:ILE:HD12	2.38	0.58
3:C:30:ARG:HE	3:C:31:HIS:CE1	2.20	0.58
1:A:1328:C:H2'	1:A:1329:A:C8	2.39	0.58
1:A:528:C:H41	12:L:49:ASN:HD21	1.52	0.58
1:A:1160:G:O4'	2:B:132:LYS:NZ	2.36	0.58
1:A:933:G:OP2	7:G:3:ARG:HB3	2.03	0.58
1:A:753:A:H4'	1:A:754:C:O5'	2.03	0.58
11:K:59:TYR:O	11:K:62:GLN:HB3	2.04	0.58
2:B:82:ARG:HA	2:B:92:TYR:CE1	2.39	0.58
1:A:1366:C:O3'	10:J:60:ARG:NH2	2.36	0.58
1:A:328:C:O2	1:A:328:C:H2'	2.02	0.58
16:P:74:LEU:HB3	16:P:79:VAL:HG21	1.86	0.58
7:G:22:LEU:O	7:G:25:ALA:HB3	2.04	0.58
1:A:1358:U:H5''	14:N:35:ARG:HG3	1.85	0.57
1:A:1443:G:H5''	1:A:1446:A:H5''	1.85	0.57
1:A:310:G:OP2	16:P:27:LYS:NZ	2.35	0.57
8:H:124:ALA:O	8:H:128:GLY:N	2.34	0.57
16:P:39:TYR:HE2	16:P:41:PRO:HB3	1.69	0.57
5:E:92:LYS:O	5:E:118:ILE:HG13	2.04	0.57
19:S:18:LYS:O	19:S:22:LEU:HG	2.05	0.57
1:A:263:A:OP2	20:T:79:ARG:NH1	2.37	0.57
1:A:463:A:H2'	1:A:474:G:H8	1.70	0.57
1:A:1057:G:H5''	3:C:154:SER:HB2	1.86	0.57
9:I:96:LEU:HB3	9:I:102:LEU:HG	1.85	0.57
1:A:1006:C:H42	1:A:1024:G:H21	1.51	0.57
1:A:719:C:H42	18:R:74:ARG:NH1	2.02	0.57
1:A:76:C:H41	1:A:93:G:H1	1.49	0.57
1:A:1370:G:H5''	9:I:109:VAL:HG11	1.86	0.57
19:S:51:VAL:HG12	19:S:52:TYR:H	1.68	0.57
1:A:1347:G:H2'	1:A:1373:G:H1	1.68	0.57
1:A:372:C:H4'	1:A:373:A:O5'	2.05	0.57
1:A:946:A:H2'	1:A:947:G:C8	2.39	0.57
1:A:1370:G:C5'	9:I:109:VAL:HG11	2.34	0.57
20:T:63:ILE:HG21	20:T:81:LYS:HG3	1.85	0.57
1:A:1305:G:N2	1:A:1331:G:H1'	2.19	0.57
1:A:1216:G:OP1	14:N:3:ARG:NH2	2.38	0.57
1:A:945:G:O6	1:A:1236:A:N1	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:403:C:H4'	4:D:122:ARG:NH1	2.19	0.57
20:T:79:ARG:O	20:T:83:ARG:HG3	2.04	0.57
1:A:77:G:C2	1:A:93:G:C2	2.93	0.57
13:M:99:ARG:HH12	19:S:2:PRO:HD2	1.70	0.57
1:A:1267:C:H1'	21:U:20:LYS:HE3	1.86	0.57
1:A:1357:A:H2'	1:A:1358:U:C6	2.40	0.57
1:A:355:C:H5'	1:A:389:A:OP2	2.05	0.57
1:A:60:A:H4'	1:A:61:G:O5'	2.05	0.57
3:C:38:ARG:HH11	3:C:38:ARG:HB2	1.69	0.57
4:D:9:CYS:O	4:D:12:CYS:HB2	2.04	0.57
1:A:1255:G:O2'	1:A:1258:G:H1'	2.04	0.57
1:A:237:C:OP2	17:Q:40:LYS:NZ	2.36	0.57
1:A:926:G:H3'	1:A:1505:G:H21	1.70	0.56
1:A:1127:G:H1	1:A:1145:C:N4	2.03	0.56
1:A:1261:A:H1'	1:A:1283:G:H5''	1.87	0.56
1:A:407:G:OP1	4:D:115:ARG:HD3	2.05	0.56
4:D:78:LEU:O	4:D:81:GLU:HB3	2.05	0.56
1:A:91:C:H2'	1:A:92:C:C5	2.40	0.56
2:B:23:ARG:NH1	2:B:23:ARG:HB2	2.20	0.56
1:A:95:U:H2'	1:A:96:G:C8	2.40	0.56
5:E:27:ARG:HH11	5:E:27:ARG:HG2	1.70	0.56
9:I:50:LEU:HD11	9:I:81:ILE:HD12	1.87	0.56
8:H:83:ILE:HD11	8:H:137:VAL:HG22	1.88	0.56
9:I:17:VAL:HG21	9:I:80:GLY:HA3	1.88	0.56
1:A:1031:G:H2'	1:A:1032:G:C8	2.41	0.56
1:A:1352:C:H2'	1:A:1353:G:C8	2.41	0.56
1:A:620:C:H2'	1:A:621:A:O4'	2.06	0.56
3:C:159:GLY:HA2	3:C:193:TYR:CZ	2.40	0.56
10:J:49:VAL:HG13	14:N:41:ARG:HB2	1.87	0.56
1:A:44:G:OP2	16:P:12:LYS:HB2	2.06	0.56
16:P:66:PRO:HG2	16:P:71:ARG:NH1	2.20	0.56
1:A:1337:G:H5''	1:A:1338:G:OP1	2.06	0.56
1:A:131:C:O2	1:A:231:G:N2	2.39	0.56
1:A:552:U:H2'	1:A:553:A:C8	2.41	0.56
9:I:48:GLU:N	9:I:49:PRO:HD2	2.21	0.56
17:Q:75:ARG:HH12	17:Q:77:VAL:HA	1.71	0.56
1:A:106:C:C2'	1:A:107:G:H5'	2.35	0.56
1:A:1133:G:N2	1:A:1141:C:O2	2.38	0.56
1:A:1172:C:H2'	1:A:1173:G:H8	1.71	0.56
21:U:13:ILE:O	21:U:16:GLY:N	2.34	0.56
1:A:1043:C:H2'	1:A:1044:A:C8	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:976:G:C8	1:A:1358:U:O2	2.59	0.56
1:A:1484:C:H2'	1:A:1485:U:O4'	2.06	0.56
3:C:139:GLN:O	3:C:143:GLU:N	2.33	0.56
1:A:130:A:H5'	17:Q:63:ARG:HE	1.71	0.56
14:N:22:THR:HB	14:N:33:VAL:HB	1.87	0.56
1:A:509:A:H3'	1:A:509:A:C8	2.41	0.56
1:A:975:A:H5'	1:A:975:A:C8	2.38	0.56
1:A:1255:G:N2	1:A:1259:C:O2	2.37	0.55
1:A:1242:C:N4	1:A:1295:G:H1	2.03	0.55
1:A:236:G:OP1	17:Q:40:LYS:NZ	2.38	0.55
2:B:23:ARG:N	2:B:23:ARG:HH11	2.04	0.55
4:D:155:LEU:HB2	4:D:158:ILE:HG12	1.88	0.55
7:G:38:LEU:O	7:G:42:ILE:HG13	2.06	0.55
12:L:89:ARG:HH21	12:L:97:ARG:HB3	1.71	0.55
20:T:73:HIS:O	20:T:76:ALA:HB3	2.06	0.55
1:A:344:A:H4'	1:A:345:C:OP2	2.06	0.55
3:C:8:ILE:HD11	3:C:16:ARG:NH2	2.22	0.55
12:L:55:VAL:HA	12:L:70:ILE:HG13	1.87	0.55
13:M:15:VAL:HG21	13:M:48:LEU:HD21	1.89	0.55
1:A:976:G:OP2	1:A:1358:U:O2'	2.22	0.55
15:O:70:LEU:HD13	15:O:78:TYR:HB2	1.89	0.55
10:J:57:LYS:H	10:J:57:LYS:HD2	1.70	0.55
15:O:55:GLY:O	15:O:59:MET:HG3	2.06	0.55
17:Q:6:LEU:HD23	17:Q:6:LEU:N	2.22	0.55
1:A:1254:C:OP1	10:J:45:ARG:HD2	2.06	0.55
1:A:1329:A:P	13:M:28:ALA:HB3	2.47	0.55
1:A:147:G:H1	1:A:175:C:H42	1.53	0.55
1:A:373:A:H1'	1:A:481:G:H1'	1.88	0.55
1:A:401:C:H1'	1:A:622:A:H1'	1.89	0.55
1:A:673:G:H2'	1:A:674:G:C8	2.42	0.55
2:B:115:LEU:O	2:B:119:GLU:HB2	2.06	0.55
1:A:1367:C:H5'	10:J:60:ARG:HE	1.71	0.55
1:A:64:G:H4'	1:A:65:U:H5''	1.88	0.55
7:G:123:GLU:O	7:G:126:ASP:N	2.40	0.55
13:M:2:ALA:O	13:M:10:PRO:HD2	2.06	0.55
14:N:19:ARG:HH11	14:N:19:ARG:HB3	1.70	0.55
1:A:359:U:H2'	1:A:360:A:H8	1.70	0.55
3:C:131:ARG:HA	3:C:134:ILE:HD12	1.89	0.55
5:E:101:ILE:O	5:E:120:THR:HB	2.07	0.55
17:Q:86:GLU:O	17:Q:89:LEU:N	2.40	0.55
19:S:5:LEU:HD13	19:S:9:VAL:HG13	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:191:G:H21	20:T:104:LEU:HA	1.72	0.55
1:A:1505:G:H3'	1:A:1505:G:C8	2.42	0.55
1:A:77:G:C6	1:A:93:G:N1	2.74	0.55
1:A:1435:G:H2'	1:A:1436:U:H6	1.72	0.55
5:E:68:GLU:HG3	5:E:68:GLU:O	2.07	0.55
5:E:78:HIS:HD1	8:H:104:ARG:HG3	1.71	0.55
6:F:36:ARG:HH11	6:F:36:ARG:HB3	1.71	0.55
10:J:87:THR:HG23	10:J:89:ASP:H	1.72	0.55
11:K:41:THR:HG21	11:K:71:LYS:HB3	1.88	0.55
1:A:1128:C:O2'	1:A:1130:A:N7	2.40	0.55
1:A:1143:G:H2'	1:A:1144:G:H8	1.71	0.55
1:A:1437:C:H5''	1:A:1438:G:OP2	2.06	0.55
1:A:411:A:N7	1:A:413:G:N3	2.54	0.55
3:C:116:VAL:O	3:C:119:ARG:HB3	2.07	0.55
7:G:20:ASP:OD2	7:G:21:VAL:N	2.40	0.55
1:A:1188:A:H4'	24:N:202:HOH:O	2.06	0.54
1:A:463:A:H2'	1:A:474:G:C8	2.42	0.54
8:H:119:LEU:HD12	8:H:124:ALA:HB2	1.89	0.54
1:A:1147:C:O2'	9:I:5:TYR:OH	2.14	0.54
15:O:15:PHE:CD2	15:O:30:ALA:HB2	2.41	0.54
1:A:1257:U:O2'	1:A:1258:G:O5'	2.26	0.54
1:A:1498:UR3:O4'	1:A:1519[A]:MA6:H2	2.06	0.54
1:A:579:G:O3'	15:O:54:ARG:NH2	2.38	0.54
2:B:22:LYS:O	2:B:23:ARG:HD3	2.07	0.54
5:E:88:LYS:HB3	5:E:123:LEU:HB2	1.89	0.54
11:K:94:ALA:O	11:K:98:LEU:HB2	2.07	0.54
1:A:1181:G:O2'	1:A:1182:G:O5'	2.22	0.54
1:A:1416:G:C2'	1:A:1417:G:H5'	2.38	0.54
1:A:384:G:H2'	1:A:385:C:C5	2.41	0.54
1:A:633:G:H2'	1:A:634:C:C6	2.43	0.54
1:A:746:A:O2'	1:A:747:C:H5'	2.06	0.54
11:K:71:LYS:O	11:K:74:ALA:HB3	2.07	0.54
1:A:1200:C:H1'	1:A:1204:A:N6	2.23	0.54
1:A:1378:C:H2'	1:A:1379:G:O4'	2.08	0.54
1:A:1499:A:C1'	1:A:1520[A]:G:H5'	2.37	0.54
1:A:838:G:H1	1:A:848:C:N4	2.05	0.54
4:D:117:ALA:O	4:D:121:VAL:HG23	2.07	0.54
12:L:46:LYS:NZ	12:L:47:LYS:HE3	2.23	0.54
1:A:1355:G:H2'	1:A:1356:G:H8	1.71	0.54
3:C:131:ARG:O	3:C:134:ILE:HB	2.08	0.54
4:D:52:SER:O	4:D:56:VAL:HG23	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1237:C:N4	1:A:1336:C:O2	2.41	0.54
1:A:1369:C:H2'	1:A:1370:G:C8	2.42	0.54
2:B:17:PHE:HA	2:B:44:LEU:HD11	1.90	0.54
3:C:43:LEU:O	3:C:47:LEU:HB2	2.07	0.54
7:G:79:ARG:NE	7:G:82:GLY:O	2.37	0.54
1:A:1342:C:O2'	9:I:124:GLN:HG2	2.07	0.54
1:A:1048:G:H5''	14:N:3:ARG:HH21	1.73	0.54
1:A:1085:U:C6	1:A:1094:G:N1	2.76	0.54
1:A:1406:U:H4'	1:A:1518[B]:MA6:H1'	1.90	0.54
1:A:36:C:OP1	12:L:123:LYS:NZ	2.28	0.54
1:A:853:G:C2'	1:A:854:G:H5'	2.37	0.54
4:D:127:THR:OG1	4:D:149:ALA:HB2	2.08	0.54
5:E:72:GLN:O	5:E:75:THR:HG22	2.07	0.54
1:A:560:U:H5'	1:A:566:G:C2	2.42	0.54
3:C:152:ILE:HB	3:C:199:LYS:HB2	1.90	0.54
3:C:26:LYS:H	3:C:26:LYS:HD3	1.72	0.54
10:J:82:ILE:HD12	10:J:82:ILE:H	1.72	0.54
13:M:25:ILE:HD11	13:M:66:LEU:HD11	1.90	0.54
18:R:87:ARG:HH11	18:R:87:ARG:HA	1.73	0.54
1:A:1332:A:H2'	1:A:1333:A:C8	2.43	0.54
1:A:390:C:O3'	16:P:28:ARG:NH2	2.41	0.54
1:A:707:C:H2'	1:A:708:C:C6	2.43	0.54
1:A:75:G:N2	1:A:96:G:N1	2.56	0.54
6:F:35:ALA:HA	6:F:67:MET:HB3	1.87	0.54
1:A:707:C:H2'	1:A:708:C:H6	1.72	0.54
2:B:172:ILE:H	2:B:172:ILE:HD12	1.71	0.54
2:B:191:ASP:N	2:B:191:ASP:OD1	2.37	0.54
4:D:209:ARG:HG2	4:D:209:ARG:O	2.08	0.54
18:R:86:VAL:HG12	18:R:87:ARG:NH1	2.23	0.54
1:A:1197:G:H5''	24:A:2054:HOH:O	2.08	0.53
1:A:1422:G:H2'	1:A:1423:G:H8	1.73	0.53
5:E:105:VAL:HG11	5:E:131:ILE:HG22	1.90	0.53
10:J:4:ILE:HG22	10:J:6:ILE:HD11	1.90	0.53
1:A:1181:G:C2	1:A:1182:G:N2	2.76	0.53
1:A:1329:A:C2	1:A:1330:U:C2	2.96	0.53
5:E:27:ARG:HG2	5:E:27:ARG:NH1	2.24	0.53
2:B:91:PRO:HB3	2:B:154:LEU:HB3	1.91	0.53
4:D:114:ARG:HG3	4:D:114:ARG:HH11	1.74	0.53
16:P:79:VAL:N	24:P:204:HOH:O	2.40	0.53
1:A:1014:A:H4'	19:S:14:HIS:CE1	2.43	0.53
1:A:1244:C:H5''	1:A:1245:A:OP2	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:381:C:H2'	1:A:382:A:O4'	2.09	0.53
1:A:62:U:OP1	1:A:385:C:O2'	2.25	0.53
2:B:126:GLU:HG3	2:B:129:GLU:HB2	1.90	0.53
9:I:22:GLY:HA3	9:I:60:ASP:HB2	1.89	0.53
1:A:1128:C:OP1	9:I:66:ARG:NH2	2.41	0.53
13:M:11:ARG:HA	13:M:45:VAL:HG11	1.90	0.53
1:A:1526:G:H2'	1:A:1527:C:H6	1.74	0.53
1:A:241:C:H42	1:A:285:G:H1	1.57	0.53
1:A:677:U:H3	1:A:713:G:H22	1.55	0.53
14:N:24:CYS:H	14:N:33:VAL:HG21	1.73	0.53
1:A:665:A:N3	1:A:732:C:H2'	2.23	0.53
2:B:139:LYS:NZ	2:B:143:GLU:HG3	2.23	0.53
4:D:121:VAL:HG11	4:D:136:PRO:HA	1.88	0.53
13:M:16:ASP:OD1	13:M:16:ASP:N	2.41	0.53
15:O:29:VAL:HG11	15:O:81:LEU:HD11	1.91	0.53
17:Q:21:VAL:HG21	17:Q:59:ILE:HG13	1.91	0.53
17:Q:66:SER:HB3	17:Q:69:LYS:HG3	1.90	0.53
1:A:1305:G:O2'	1:A:1306:A:P	2.67	0.53
3:C:70:VAL:HG12	3:C:72:LYS:H	1.73	0.53
5:E:84:PHE:CB	5:E:134:ALA:HB2	2.38	0.53
10:J:52:GLY:O	14:N:41:ARG:NH2	2.41	0.53
1:A:1305:G:H5''	21:U:4:GLY:HA3	1.90	0.53
1:A:1320:C:N4	19:S:36:ARG:HG3	2.24	0.53
1:A:1329:A:OP1	13:M:28:ALA:HB3	2.08	0.53
1:A:404:U:O4	4:D:2:GLY:N	2.42	0.53
1:A:778:G:H8	1:A:778:G:O5'	1.92	0.53
2:B:180:LEU:O	2:B:181:PHE:HB2	2.09	0.53
2:B:7:VAL:N	2:B:8:LYS:HZ3	2.06	0.53
3:C:114:PRO:O	3:C:118:GLN:NE2	2.42	0.53
4:D:150:GLU:HA	4:D:153:ARG:HG3	1.91	0.53
9:I:28:VAL:O	9:I:31:GLN:N	2.39	0.53
18:R:46:GLU:OE1	18:R:46:GLU:N	2.37	0.53
20:T:81:LYS:O	20:T:85:MET:HG3	2.09	0.53
1:A:1190:G:OP1	3:C:4:LYS:HA	2.07	0.53
1:A:1399:C:O2	1:A:1401:G:C5	2.62	0.53
1:A:47:C:H6	1:A:365:U:H2'	1.74	0.53
1:A:939:G:H5''	7:G:102:ARG:NH1	2.24	0.53
2:B:19:HIS:ND1	2:B:20:GLU:HG2	2.24	0.53
6:F:4:TYR:HD1	6:F:92:LYS:HA	1.74	0.53
1:A:1250:A:H4'	9:I:68:GLY:O	2.09	0.53
12:L:58:VAL:O	12:L:65:GLU:HA	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:4:THR:N	15:O:7:GLU:OE1	2.28	0.53
1:A:1032:G:H2'	1:A:1033:G:O4'	2.08	0.53
1:A:1064:G:H1'	1:A:1190:G:H21	1.74	0.53
1:A:56:U:H2'	1:A:57:G:H8	1.74	0.53
8:H:83:ILE:CD1	8:H:137:VAL:HG22	2.39	0.53
15:O:29:VAL:HG21	15:O:67:LEU:HD23	1.91	0.53
1:A:1311:G:H1	1:A:1326:C:H42	1.57	0.52
1:A:1397:C:O2'	1:A:1398:A:OP1	2.26	0.52
1:A:273:A:N6	1:A:274:A:C6	2.77	0.52
1:A:416:G:H2'	1:A:417:C:C6	2.44	0.52
3:C:202:ILE:HG22	3:C:204:LEU:HD23	1.91	0.52
1:A:686:U:O2'	1:A:687:A:H8	1.88	0.52
1:A:731:G:OP1	1:A:766:A:H1'	2.08	0.52
2:B:51:LEU:O	2:B:55:PHE:HB2	2.09	0.52
4:D:152:SER:HA	4:D:155:LEU:HG	1.91	0.52
1:A:409:G:OP2	4:D:22:LYS:HD3	2.10	0.52
13:M:84:ILE:HG13	13:M:86:CYS:H	1.74	0.52
13:M:96:LEU:HB3	13:M:97:PRO:HD2	1.91	0.52
18:R:22:VAL:HG23	18:R:56:THR:HA	1.89	0.52
1:A:1285:A:H4'	1:A:1286:A:O5'	2.09	0.52
1:A:579:G:H5'	1:A:728:A:H1'	1.90	0.52
1:A:864:A:H2'	1:A:865:A:C8	2.44	0.52
1:A:885:G:H1	1:A:912:A:H2	1.57	0.52
11:K:72:ALA:HB1	11:K:77:MET:HG3	1.91	0.52
1:A:1391:U:H2'	1:A:1392:G:C8	2.44	0.52
1:A:421:U:H5'	1:A:422:C:H5	1.74	0.52
1:A:502:G:P	12:L:118:SER:HG	2.32	0.52
1:A:790:A:H2'	1:A:791:G:C8	2.44	0.52
2:B:36:ARG:O	2:B:39:ILE:HD12	2.09	0.52
3:C:156:ARG:NH1	3:C:160:ALA:O	2.40	0.52
3:C:187:ALA:HB3	3:C:198:VAL:HB	1.91	0.52
12:L:45:PRO:HD3	12:L:51:ALA:O	2.09	0.52
1:A:949:A:C2	1:A:1233:G:N3	2.78	0.52
1:A:589:C:O2'	1:A:590:C:H5'	2.09	0.52
1:A:902:G:H2'	1:A:903:G:H8	1.75	0.52
1:A:943:U:C2'	1:A:944:G:H5'	2.39	0.52
12:L:53:ARG:NH1	12:L:92:0TD:OD2	2.43	0.52
21:U:12:LYS:O	21:U:22:ARG:NH1	2.41	0.52
1:A:1499:A:H1'	1:A:1520[A]:G:H5'	1.90	0.52
1:A:459:G:H1'	1:A:463:A:H61	1.75	0.52
1:A:551:U:H2'	1:A:552:U:C6	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:39:LYS:HG2	20:T:55:ILE:HD13	1.91	0.52
1:A:1172:C:H2'	1:A:1173:G:C8	2.45	0.52
5:E:91:LEU:HB3	5:E:118:ILE:HD11	1.91	0.52
6:F:97:PHE:HE1	18:R:61:LYS:HE2	1.74	0.52
8:H:77:GLU:HG2	8:H:78:GLN:H	1.73	0.52
12:L:8:ASN:O	12:L:12:ARG:HG2	2.09	0.52
1:A:581:G:O3'	15:O:64:ARG:NH2	2.42	0.52
1:A:350:G:H5''	1:A:350:G:H8	1.74	0.52
1:A:766:A:H2'	1:A:767:A:O4'	2.10	0.52
3:C:11:ARG:NH2	3:C:175:LEU:O	2.41	0.52
12:L:113:ARG:HB3	12:L:122:THR:HG21	1.92	0.52
18:R:43:PHE:C	18:R:51:LEU:HD12	2.29	0.52
1:A:423:G:N3	1:A:423:G:H3'	2.24	0.52
2:B:23:ARG:CZ	2:B:23:ARG:HB2	2.39	0.52
1:A:673:G:H5''	6:F:87:ARG:NH1	2.25	0.52
1:A:1045:C:H2'	1:A:1046:A:C8	2.44	0.52
2:B:134:GLU:HA	2:B:137:ARG:HG3	1.92	0.52
3:C:136:GLN:HA	3:C:139:GLN:HG3	1.90	0.52
9:I:5:TYR:CD1	9:I:6:GLY:N	2.75	0.52
11:K:54:ARG:O	11:K:57:THR:HG22	2.08	0.52
19:S:22:LEU:HD22	19:S:28:LYS:HB2	1.92	0.52
1:A:1118:C:O2'	1:A:1119:C:H5'	2.10	0.51
1:A:337:C:H2'	1:A:338:A:H8	1.74	0.51
1:A:981:U:H5''	1:A:982:U:H5''	1.92	0.51
4:D:46:LYS:HG2	4:D:47:ARG:H	1.75	0.51
5:E:107:ARG:O	5:E:111:GLU:HB2	2.10	0.51
1:A:1305:G:O2'	1:A:1306:A:C8	2.58	0.51
1:A:47:C:C6	1:A:365:U:H2'	2.46	0.51
3:C:130:VAL:O	3:C:134:ILE:HG13	2.10	0.51
12:L:27:LEU:C	12:L:29:GLY:N	2.63	0.51
1:A:528:C:N4	12:L:49:ASN:HD21	2.08	0.51
1:A:1338:G:C6	1:A:1339:A:C6	2.98	0.51
1:A:1502:A:C2	1:A:1504:G:C4	2.97	0.51
1:A:254:G:OP1	17:Q:67:LYS:O	2.28	0.51
1:A:1000:U:H2'	1:A:1001:A:C8	2.46	0.51
1:A:1188:A:H5''	24:A:2233:HOH:O	2.10	0.51
1:A:1376:U:OP1	7:G:98:SER:OG	2.20	0.51
1:A:412:A:H5''	1:A:413:G:OP1	2.09	0.51
6:F:100:ASN:HB2	18:R:23:LYS:HG3	1.92	0.51
10:J:79:ARG:O	10:J:79:ARG:NH1	2.43	0.51
13:M:82:MET:HA	13:M:89:GLY:HA3	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1163:C:H2'	1:A:1164:G:O4'	2.11	0.51
1:A:236:G:H2'	1:A:237:C:O4'	2.10	0.51
2:B:23:ARG:O	2:B:24:TRP:CD1	2.63	0.51
11:K:32:ILE:HD12	11:K:72:ALA:HB2	1.93	0.51
12:L:89:ARG:NH2	12:L:97:ARG:HB3	2.25	0.51
13:M:27:LYS:HE2	13:M:27:LYS:HA	1.93	0.51
1:A:1221:G:OP1	19:S:36:ARG:HD3	2.10	0.51
1:A:1358:U:O2'	1:A:1359:C:OP1	2.28	0.51
7:G:22:LEU:HD21	7:G:66:VAL:HG21	1.93	0.51
9:I:118:LYS:NZ	9:I:118:LYS:O	2.41	0.51
15:O:75:PRO:O	15:O:79:ARG:HG3	2.11	0.51
21:U:10:ARG:O	21:U:13:ILE:HB	2.10	0.51
1:A:1351:U:H4'	7:G:33:ASP:CG	2.31	0.51
11:K:90:GLY:HA2	11:K:93:GLN:HB2	1.92	0.51
20:T:71:THR:O	20:T:72:LEU:HD23	2.10	0.51
5:E:36:ASP:OD1	5:E:38:GLN:N	2.38	0.51
5:E:60:TYR:HE1	5:E:64:ARG:HE	1.58	0.51
1:A:1355:G:H2'	1:A:1356:G:C8	2.46	0.51
1:A:1412:C:C5	1:A:1413:A:C6	2.99	0.51
1:A:1483:A:H2'	1:A:1484:C:O4'	2.11	0.51
1:A:204:U:H4'	1:A:216:G:O4'	2.09	0.51
1:A:79:G:C2	1:A:80:G:C8	2.99	0.51
2:B:24:TRP:HZ3	2:B:29:ALA:HB2	1.75	0.51
7:G:115:ARG:HD2	7:G:115:ARG:H	1.76	0.51
7:G:118:VAL:O	7:G:122:HIS:HB2	2.10	0.51
9:I:103:THR:HG22	9:I:104:ARG:O	2.11	0.51
14:N:3:ARG:NH1	14:N:3:ARG:HB3	2.26	0.51
9:I:79:LEU:O	9:I:83:ARG:HG2	2.11	0.51
10:J:27:ALA:HB2	10:J:85:LEU:HD21	1.93	0.51
14:N:9:LYS:HD2	14:N:23:ARG:HB2	1.91	0.51
16:P:8:ARG:NH2	16:P:15:PRO:HB3	2.26	0.51
1:A:1225:A:N3	1:A:1225:A:H2'	2.26	0.50
2:B:161:ALA:HB1	2:B:185:ILE:HD11	1.92	0.50
4:D:23:GLY:HA3	4:D:112:VAL:HG12	1.93	0.50
7:G:10:ARG:HB2	7:G:10:ARG:NH1	2.25	0.50
8:H:95:VAL:HG12	8:H:99:GLU:HB2	1.92	0.50
1:A:1125:U:H5	10:J:73:ASP:OD2	1.94	0.50
13:M:12:ASN:H	13:M:45:VAL:HB	1.76	0.50
18:R:70:ILE:HG22	18:R:71:LYS:N	2.26	0.50
7:G:22:LEU:HD12	7:G:97:GLN:HE22	1.77	0.50
7:G:28:ASN:O	7:G:31:MET:HB3	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:59:SER:H	18:R:62:GLU:HB2	1.76	0.50
1:A:1003(A):G:N1	1:A:1038:C:N3	2.59	0.50
1:A:985:C:N3	1:A:1221:G:N2	2.59	0.50
1:A:1222:G:OP2	1:A:1322:C:N4	2.41	0.50
1:A:144:G:H1	1:A:178:C:H42	1.57	0.50
7:G:40:ALA:CB	9:I:41:VAL:HG21	2.40	0.50
9:I:91:ASP:N	9:I:91:ASP:OD1	2.44	0.50
12:L:11:VAL:HG12	12:L:12:ARG:N	2.26	0.50
1:A:1092:A:N3	1:A:1183:A:N6	2.60	0.50
1:A:616:G:H1'	1:A:625:G:N2	2.26	0.50
1:A:736:C:H2'	1:A:737:A:C8	2.47	0.50
1:A:757:U:H2'	1:A:758:G:O4'	2.12	0.50
1:A:795:C:H5''	1:A:796:C:OP2	2.12	0.50
2:B:21:ARG:HA	2:B:39:ILE:HG23	1.94	0.50
3:C:58:GLU:HB3	10:J:92:THR:HG21	1.91	0.50
5:E:81:GLU:OE2	5:E:88:LYS:HE2	2.11	0.50
11:K:32:ILE:O	11:K:40:ILE:N	2.44	0.50
15:O:56:LEU:HA	15:O:59:MET:HE2	1.93	0.50
19:S:50:ALA:HA	19:S:58:VAL:O	2.12	0.50
1:A:1214:C:O2'	1:A:1215:G:H5'	2.11	0.50
1:A:620:C:C2	4:D:135:LEU:HD13	2.46	0.50
1:A:835:U:H3	1:A:851:G:H1	1.59	0.50
2:B:136:VAL:HA	2:B:139:LYS:HB3	1.93	0.50
2:B:142:LEU:HD22	2:B:146:GLN:NE2	2.27	0.50
6:F:60:PHE:CZ	18:R:78:LEU:HD21	2.46	0.50
7:G:17:VAL:HG12	7:G:18:TYR:CD1	2.45	0.50
1:A:1104:G:H4'	2:B:111:ARG:NH2	2.27	0.50
1:A:1257:U:HO2'	1:A:1258:G:P	2.34	0.50
1:A:1314:C:H2'	1:A:1315:U:C6	2.46	0.50
1:A:518:C:H4'	1:A:519:C:O5'	2.11	0.50
1:A:946:A:H2'	1:A:947:G:H8	1.76	0.50
3:C:116:VAL:HG21	3:C:202:ILE:HD11	1.92	0.50
3:C:95:THR:OG1	3:C:95:THR:O	2.30	0.50
6:F:36:ARG:NH1	6:F:36:ARG:HB3	2.27	0.50
15:O:55:GLY:HA2	15:O:58:MET:HG3	1.92	0.50
1:A:1148:U:H4'	9:I:14:VAL:HG11	1.94	0.50
1:A:1443:G:H4'	1:A:1446:A:H5''	1.93	0.50
3:C:180:ALA:HB1	3:C:203:PHE:CE1	2.40	0.50
6:F:33:TYR:CD1	6:F:75:LEU:HA	2.46	0.50
13:M:4:ILE:HG12	13:M:56:LEU:CD1	2.40	0.50
1:A:123:C:OP1	1:A:312:C:H5'	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:29:TYR:CD2	3:C:33:LEU:HD22	2.46	0.50
10:J:6:ILE:HD13	10:J:72:VAL:HB	1.93	0.50
17:Q:63:ARG:HG2	17:Q:64:PRO:CD	2.42	0.50
17:Q:67:LYS:O	17:Q:68:ARG:HB2	2.11	0.50
1:A:1058:G:H2'	1:A:1059:C:O4'	2.12	0.50
1:A:1101:A:H4'	1:A:1102:A:O5'	2.12	0.50
1:A:114:U:O2'	1:A:115:G:H5'	2.12	0.50
1:A:1201:A:H4'	1:A:1202:G:O5'	2.11	0.50
1:A:552:U:H2'	1:A:553:A:H8	1.76	0.50
1:A:580:U:H2'	1:A:581:G:O4'	2.12	0.50
1:A:600:C:H42	1:A:638:G:H1	1.60	0.50
1:A:789:U:O2	1:A:791:G:C8	2.65	0.50
1:A:953:G:H2'	1:A:954:G:O4'	2.12	0.50
2:B:142:LEU:HD13	2:B:146:GLN:HE22	1.76	0.50
3:C:156:ARG:HA	3:C:160:ALA:HB3	1.94	0.50
3:C:167:TRP:HE3	3:C:168:ALA:H	1.58	0.50
18:R:50:ILE:HD13	18:R:70:ILE:HD13	1.94	0.50
1:A:1505:G:H8	1:A:1505:G:H3'	1.77	0.49
1:A:385:C:H2'	1:A:386:C:H6	1.77	0.49
1:A:918:A:H2'	1:A:919:A:O4'	2.12	0.49
1:A:980:C:H3'	1:A:981:U:C6	2.46	0.49
1:A:10:A:OP2	5:E:126:ARG:HD3	2.12	0.49
17:Q:83:ASP:N	17:Q:83:ASP:OD1	2.45	0.49
1:A:1065:U:H4'	1:A:1066:C:O5'	2.12	0.49
1:A:1481:U:C2	1:A:1482:G:C8	3.00	0.49
1:A:442:C:H42	1:A:492:G:H1	1.59	0.49
1:A:44:G:N2	1:A:399:G:C4	2.80	0.49
1:A:45:U:H2'	1:A:46:G:C8	2.47	0.49
1:A:451:A:N6	1:A:481:G:C4	2.80	0.49
1:A:485:G:O2'	1:A:486:U:P	2.71	0.49
1:A:814:A:H2'	1:A:816:A:H5''	1.94	0.49
1:A:96:G:O2'	1:A:97:G:H5'	2.12	0.49
3:C:19:GLU:HB3	3:C:40:ARG:NH2	2.27	0.49
4:D:36:ARG:HA	4:D:38:TYR:CE2	2.46	0.49
13:M:108:ARG:CZ	13:M:114:ARG:HG2	2.41	0.49
1:A:1521:G:H2'	1:A:1522:U:O4'	2.11	0.49
1:A:409:G:H1	1:A:433:C:H42	1.60	0.49
7:G:16:LEU:HD11	9:I:45:ALA:HB2	1.95	0.49
5:E:116:THR:HG23	5:E:117:ASP:OD1	2.12	0.49
6:F:3:ARG:HA	6:F:65:VAL:O	2.13	0.49
12:L:46:LYS:HZ2	12:L:47:LYS:HE3	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:53:LEU:HD12	14:N:56:VAL:HG21	1.94	0.49
18:R:34:TYR:CE1	18:R:35:ARG:HG3	2.47	0.49
1:A:117:G:O5'	1:A:117:G:H8	1.95	0.49
1:A:1339:A:H2'	1:A:1340:A:O4'	2.12	0.49
1:A:1398:A:H5'	1:A:1401:G:H4'	1.94	0.49
9:I:26:VAL:HG12	9:I:61:ALA:HB3	1.93	0.49
18:R:86:VAL:HG12	18:R:87:ARG:HH12	1.76	0.49
1:A:1518[A]:MA6:H93	1:A:1519[A]:MA6:H92	1.93	0.49
1:A:1163:C:H2'	1:A:1164:G:C8	2.48	0.49
1:A:496:A:H4'	1:A:497:A:OP1	2.12	0.49
1:A:56:U:H2'	1:A:57:G:C8	2.47	0.49
5:E:144:THR:O	5:E:147:ASP:HB2	2.13	0.49
10:J:48:THR:OG1	10:J:62:HIS:HB3	2.13	0.49
15:O:39:LEU:CD1	15:O:56:LEU:HB2	2.37	0.49
16:P:20:VAL:CG1	16:P:32:TYR:HB2	2.43	0.49
1:A:1287:A:H2'	1:A:1288:A:C8	2.48	0.49
1:A:255:G:H2'	1:A:256:U:C6	2.47	0.49
1:A:477:G:H2'	1:A:478:A:C8	2.48	0.49
1:A:629:G:H2'	1:A:630:G:O4'	2.13	0.49
5:E:46:GLY:H	5:E:58:ALA:HB2	1.78	0.49
11:K:48:ILE:HG22	11:K:49:GLY:H	1.78	0.49
11:K:91:ARG:HB3	11:K:91:ARG:HH11	1.77	0.49
1:A:1269:A:N1	1:A:1312:G:O2'	2.42	0.49
1:A:193:C:H2'	1:A:194:C:H6	1.78	0.49
3:C:8:ILE:HD11	3:C:16:ARG:HH21	1.78	0.49
1:A:299:G:C6	1:A:300:A:C6	3.01	0.49
5:E:118:ILE:O	5:E:119:LEU:HD23	2.11	0.49
9:I:53:VAL:HG21	9:I:59:PHE:HE1	1.77	0.49
1:A:182:U:H3'	1:A:182:U:P	2.53	0.48
1:A:21:G:H2'	1:A:22:G:C8	2.48	0.48
1:A:456:C:C2	1:A:457:C:C5	3.01	0.48
9:I:126:SER:HB2	9:I:127:LYS:HD2	1.95	0.48
9:I:69:GLY:O	9:I:73:GLN:HG3	2.13	0.48
13:M:36:LYS:HD3	13:M:59:TYR:CE2	2.48	0.48
1:A:231:G:O2'	1:A:232:G:H5'	2.13	0.48
1:A:865:A:C2	1:A:918:A:H4'	2.48	0.48
1:A:91:C:HO2'	1:A:92:C:P	2.32	0.48
3:C:150:LYS:HB3	3:C:201:TYR:HB2	1.94	0.48
3:C:52:LEU:HD13	3:C:68:VAL:HG13	1.95	0.48
10:J:10:GLY:O	10:J:67:THR:HA	2.12	0.48
15:O:39:LEU:HB3	15:O:56:LEU:HD12	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:63:ARG:HG2	17:Q:64:PRO:HD2	1.94	0.48
19:S:11:VAL:HG22	19:S:39:THR:HB	1.93	0.48
1:A:1347:G:H2'	1:A:1373:G:N1	2.27	0.48
1:A:1366:C:H2'	1:A:1367:C:H6	1.77	0.48
1:A:1418:A:N6	1:A:1482:G:H1'	2.27	0.48
1:A:491:G:N2	1:A:492:G:H1'	2.28	0.48
1:A:679:C:H2'	1:A:680:C:H6	1.79	0.48
5:E:78:HIS:ND1	8:H:104:ARG:HG3	2.28	0.48
8:H:11:THR:OG1	8:H:14:ARG:NH1	2.34	0.48
1:A:1022:G:N2	1:A:1023:G:O6	2.46	0.48
1:A:1300:G:HO2'	1:A:1301:U:P	2.34	0.48
1:A:1499:A:H8	1:A:1499:A:O5'	1.96	0.48
1:A:459:G:H1'	1:A:463:A:N6	2.28	0.48
1:A:689:C:OP1	11:K:44:SER:OG	2.21	0.48
1:A:912:A:O5'	1:A:912:A:H8	1.96	0.48
2:B:144:ARG:O	2:B:147:LYS:N	2.46	0.48
5:E:7:GLU:OE1	5:E:37:ARG:NE	2.46	0.48
6:F:39:LYS:HB2	6:F:39:LYS:HE3	1.44	0.48
8:H:34:GLU:HB3	8:H:118:VAL:HG21	1.95	0.48
9:I:97:LYS:HB2	9:I:102:LEU:HD12	1.94	0.48
18:R:74:ARG:HB3	18:R:81:PHE:CE1	2.48	0.48
19:S:40:ILE:HA	19:S:44:MET:SD	2.53	0.48
1:A:1065:U:H5''	1:A:1190:G:N2	2.28	0.48
1:A:1152:A:H5'	10:J:70:ARG:NH2	2.28	0.48
1:A:1191:A:H2'	1:A:1192:C:H6	1.78	0.48
1:A:1244:C:N4	1:A:1293:G:H1	2.11	0.48
1:A:1402:4OC:H2'	1:A:1403:C:O4'	2.13	0.48
1:A:1416:G:H2'	1:A:1417:G:H5'	1.95	0.48
4:D:173:TRP:HB2	4:D:187:ARG:O	2.14	0.48
15:O:36:ILE:HD13	15:O:59:MET:HE3	1.95	0.48
16:P:82:GLN:H	16:P:82:GLN:HG2	1.50	0.48
1:A:1029:C:H42	1:A:1033:G:N2	2.11	0.48
1:A:1265:G:C6	1:A:1266:G:C6	3.00	0.48
1:A:1417:G:C8	1:A:1417:G:OP2	2.67	0.48
1:A:78:G:N2	1:A:92:C:C4	2.82	0.48
2:B:101:MET:HB2	2:B:102:LEU:HD12	1.94	0.48
2:B:17:PHE:CD1	2:B:18:GLY:N	2.81	0.48
3:C:112:SER:O	3:C:115:LEU:HB2	2.13	0.48
4:D:78:LEU:HD21	4:D:96:LEU:HB3	1.95	0.48
7:G:97:GLN:O	7:G:101:LEU:HD12	2.13	0.48
10:J:27:ALA:HB2	10:J:85:LEU:HD11	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:25:PRO:C	12:L:27:LEU:N	2.64	0.48
1:A:1249:C:H2'	1:A:1250:A:H5'	1.95	0.48
1:A:1350:A:C5	1:A:1351:U:C5	3.02	0.48
1:A:264:U:H4'	17:Q:63:ARG:HD3	1.96	0.48
1:A:550:G:C5	1:A:551:U:C5	3.02	0.48
8:H:104:ARG:CZ	8:H:138:TRP:CZ2	2.96	0.48
9:I:33:PHE:CE2	9:I:47:LEU:HD11	2.49	0.48
11:K:18:ARG:O	11:K:33:THR:HG23	2.14	0.48
12:L:6:THR:HB	12:L:8:ASN:H	1.79	0.48
17:Q:15:MET:HE3	17:Q:18:THR:HB	1.96	0.48
20:T:72:LEU:HD21	20:T:80:ARG:HH12	1.79	0.48
1:A:1516[A]:G:H2'	1:A:1518[A]:MA6:OP2	2.14	0.48
1:A:303:A:H2'	1:A:304:U:O4'	2.13	0.48
1:A:646:U:H2'	1:A:647:C:C6	2.49	0.48
1:A:679:C:H2'	1:A:680:C:C6	2.49	0.48
3:C:157:ILE:HD13	3:C:166:GLU:HG2	1.96	0.48
4:D:164:ALA:O	4:D:168:ARG:HD3	2.13	0.48
11:K:110:ASP:HB2	18:R:88:LYS:HD2	1.94	0.48
15:O:12:ILE:HG23	15:O:27:VAL:CG1	2.43	0.48
1:A:217:C:H2'	1:A:218:C:C6	2.47	0.48
1:A:481:G:O2'	1:A:482:A:H8	1.97	0.48
1:A:502:G:H2'	1:A:503:C:O4'	2.14	0.48
1:A:625:G:H2'	1:A:626:U:C6	2.49	0.48
1:A:77:G:N1	1:A:93:G:C2	2.82	0.48
4:D:19:LEU:HA	4:D:19:LEU:HD23	1.45	0.48
12:L:28:LYS:C	12:L:30:ALA:H	2.16	0.48
13:M:67:GLU:HG3	13:M:68:GLY:H	1.78	0.48
15:O:12:ILE:HG12	15:O:31:LEU:HD11	1.94	0.48
1:A:106:C:H2'	1:A:107:G:H5'	1.95	0.48
1:A:1437:C:H2'	1:A:1437:C:O2	2.13	0.48
1:A:176:C:H2'	1:A:177:C:C6	2.49	0.48
1:A:76:C:C6	1:A:77:G:C8	3.02	0.48
7:G:73:MET:SD	7:G:90:GLU:HA	2.54	0.48
9:I:79:LEU:HD21	9:I:102:LEU:O	2.14	0.48
1:A:1058:G:C2	1:A:1059:C:C2	3.02	0.47
1:A:1049:U:H5'	1:A:1201:A:OP2	2.14	0.47
1:A:1413:A:H2'	1:A:1414:U:C6	2.49	0.47
1:A:35:G:C6	1:A:36:C:N4	2.82	0.47
1:A:484:G:O2'	1:A:485:G:OP2	2.26	0.47
1:A:501:C:O3'	12:L:118:SER:OG	2.31	0.47
12:L:35:GLY:HA3	12:L:60:LEU:HD13	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:53:VAL:O	16:P:54:GLU:C	2.51	0.47
1:A:1116:C:O2'	9:I:108:VAL:HG21	2.14	0.47
1:A:1144:G:N2	1:A:1146:A:H62	2.11	0.47
1:A:1157:A:C8	1:A:1158:C:C4	3.02	0.47
1:A:1203:C:H6	1:A:1203:C:O5'	1.97	0.47
1:A:1347:G:O2'	1:A:1348:U:P	2.72	0.47
2:B:219:VAL:HG13	2:B:223:ILE:HD11	1.96	0.47
10:J:87:THR:HG23	10:J:89:ASP:N	2.29	0.47
1:A:723:U:O2	1:A:723:U:H2'	2.14	0.47
1:A:833:U:H2'	1:A:834:C:C6	2.48	0.47
1:A:757:U:O2'	1:A:879:C:O2	2.31	0.47
2:B:62:ALA:HB1	2:B:222:ILE:HG23	1.95	0.47
2:B:21:ARG:HG3	2:B:22:LYS:H	1.80	0.47
5:E:10:MET:SD	5:E:13:ILE:HG23	2.55	0.47
6:F:53:ALA:HB3	6:F:86:ARG:NH1	2.29	0.47
12:L:46:LYS:HG2	12:L:47:LYS:HG3	1.96	0.47
1:A:115:G:H5''	24:A:2260:HOH:O	2.14	0.47
1:A:1496:C:H2'	1:A:1497:G:O4'	2.14	0.47
1:A:902:G:H2'	1:A:903:G:C8	2.49	0.47
13:M:106:ASN:HA	13:M:108:ARG:HG2	1.97	0.47
16:P:18:ARG:O	16:P:20:VAL:HG23	2.14	0.47
16:P:53:VAL:O	16:P:55:ARG:N	2.47	0.47
20:T:39:LYS:O	20:T:43:LEU:HD23	2.14	0.47
1:A:1007:C:H2'	1:A:1008:C:C6	2.50	0.47
1:A:1064:G:N2	1:A:1190:G:O2'	2.48	0.47
1:A:1160:G:O6	1:A:1181:G:C6	2.67	0.47
1:A:164:U:H2'	1:A:165:C:C6	2.49	0.47
1:A:945:G:N1	1:A:1337:G:C2	2.82	0.47
1:A:986:A:H2'	1:A:987:G:C8	2.49	0.47
3:C:22:TRP:CD1	3:C:59:ARG:HG3	2.49	0.47
6:F:27:GLN:O	6:F:31:GLU:HG3	2.14	0.47
9:I:97:LYS:HE2	9:I:97:LYS:HB2	1.68	0.47
10:J:15:THR:HG23	10:J:94:VAL:HG13	1.95	0.47
11:K:63:LEU:HD23	11:K:63:LEU:HA	1.52	0.47
16:P:9:PHE:HD1	16:P:18:ARG:HG3	1.79	0.47
17:Q:86:GLU:CG	17:Q:90:ILE:HD11	2.44	0.47
20:T:30:LYS:O	20:T:34:LYS:HG2	2.14	0.47
5:E:83:GLU:HG2	5:E:88:LYS:HG3	1.96	0.47
11:K:29:ILE:HD12	11:K:30:VAL:N	2.30	0.47
16:P:3:LYS:HD2	16:P:65:GLN:O	2.15	0.47
1:A:316:G:H1	1:A:337:C:H42	1.61	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:923:A:OP1	5:E:21:ALA:HB2	2.15	0.47
15:O:30:ALA:HA	15:O:85:LEU:HD11	1.96	0.47
16:P:20:VAL:HG13	16:P:32:TYR:HB2	1.96	0.47
17:Q:40:LYS:HD3	17:Q:42:TYR:OH	2.15	0.47
1:A:1157:A:C4	1:A:1181:G:N2	2.82	0.47
1:A:124:G:H2'	1:A:125:U:C6	2.49	0.47
1:A:1526:G:C4	1:A:1527:C:C5	3.03	0.47
1:A:79:G:N1	1:A:80:G:C5	2.83	0.47
4:D:152:SER:O	4:D:155:LEU:HG	2.14	0.47
5:E:6:PHE:HD2	5:E:36:ASP:HB3	1.80	0.47
18:R:39:VAL:HG13	18:R:40:LEU:HD23	1.96	0.47
20:T:36:LEU:HA	20:T:36:LEU:HD23	1.61	0.47
20:T:36:LEU:O	20:T:39:LYS:HB3	2.14	0.47
1:A:1029:C:H42	1:A:1033:G:H21	1.61	0.47
1:A:1068:G:H8	1:A:1068:G:OP2	1.98	0.47
1:A:1336:C:H6	1:A:1336:C:H5''	1.80	0.47
1:A:113:G:C1'	1:A:354:G:H5'	2.41	0.47
1:A:88:A:H2'	1:A:89:C:O4'	2.14	0.47
1:A:8:A:C2	4:D:209:ARG:HD2	2.50	0.47
4:D:206:PHE:CD2	4:D:207:TYR:CE2	3.03	0.47
8:H:33:GLU:OE2	8:H:50:ARG:NH2	2.48	0.47
8:H:36:LEU:HA	8:H:39:LEU:HD12	1.96	0.47
9:I:74:ILE:HA	9:I:77:ILE:HD12	1.96	0.47
10:J:6:ILE:O	10:J:71:LEU:HD12	2.15	0.47
10:J:49:VAL:CG1	14:N:41:ARG:HB2	2.44	0.47
15:O:87:ILE:HG22	15:O:88:ARG:N	2.30	0.47
16:P:38:TYR:HE2	16:P:50:LYS:HE2	1.80	0.47
1:A:1096:C:H2'	1:A:1097:C:C6	2.49	0.47
1:A:1366:C:H2'	1:A:1367:C:C6	2.49	0.47
2:B:217:ARG:HA	2:B:217:ARG:HD3	1.71	0.47
2:B:54:THR:O	2:B:58:ILE:HG13	2.15	0.47
3:C:123:GLN:O	3:C:128:PHE:HB2	2.15	0.47
3:C:64:VAL:HG12	3:C:65:ALA:H	1.80	0.47
7:G:124:LEU:HD23	7:G:124:LEU:HA	1.63	0.47
9:I:126:SER:OG	9:I:127:LYS:N	2.48	0.47
16:P:4:ILE:HG22	16:P:70:ALA:HB1	1.96	0.47
1:A:1053:G:H4'	1:A:1054:C:H5'	1.97	0.47
1:A:1103:C:H2'	1:A:1104:G:O4'	2.15	0.47
1:A:110:C:H2'	1:A:111:G:O4'	2.15	0.47
1:A:1174:G:H2'	1:A:1175:G:H8	1.80	0.47
1:A:376:G:H5''	16:P:5:ARG:HB2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:24:ALA:HB1	3:C:28:GLN:HB2	1.97	0.47
5:E:37:ARG:O	5:E:114:GLY:HA3	2.14	0.47
1:A:1349:A:OP1	9:I:120:ARG:HB2	2.15	0.47
10:J:15:THR:HG23	10:J:94:VAL:CG1	2.45	0.47
10:J:61:GLU:OE1	14:N:45:ARG:NH1	2.42	0.47
13:M:34:LEU:HG	13:M:41:PRO:HA	1.97	0.47
1:A:1150:U:O4	1:A:1151:A:N6	2.48	0.46
1:A:1218:C:H2'	1:A:1219:U:C6	2.49	0.46
3:C:117:ALA:HB1	3:C:187:ALA:HB2	1.97	0.46
14:N:9:LYS:HE2	14:N:12:ARG:HH12	1.80	0.46
15:O:18:PHE:CE2	15:O:21:ASP:HB2	2.50	0.46
1:A:1003(A):G:N2	1:A:1038:C:O2	2.49	0.46
2:B:97:TRP:HH2	2:B:176:GLU:OE2	1.96	0.46
3:C:199:LYS:HB3	3:C:201:TYR:HE1	1.81	0.46
7:G:150:ALA:HA	11:K:59:TYR:CD2	2.51	0.46
10:J:21:GLN:O	10:J:25:GLU:HG3	2.15	0.46
18:R:79:LEU:CD2	18:R:80:PRO:HD2	2.45	0.46
1:A:978:A:N7	1:A:1361:G:N2	2.64	0.46
1:A:1414:U:H2'	1:A:1414:U:O2	2.15	0.46
1:A:1434:A:N7	1:A:1435:G:C5	2.83	0.46
1:A:1498:UR3:H4'	1:A:1519[A]:MA6:N1	2.31	0.46
1:A:397:A:N3	1:A:397:A:H3'	2.30	0.46
1:A:997:U:H2'	1:A:998:G:C8	2.51	0.46
4:D:73:ARG:O	4:D:77:ASN:HB2	2.15	0.46
5:E:31:LEU:HD23	5:E:31:LEU:HA	1.60	0.46
6:F:26:ILE:HG21	6:F:63:TYR:HE2	1.81	0.46
1:A:1376:U:O4	7:G:10:ARG:NH1	2.49	0.46
8:H:112:LEU:HD23	8:H:112:LEU:N	2.29	0.46
5:E:152:ARG:O	8:H:64:LYS:NZ	2.48	0.46
8:H:84:ARG:HG3	8:H:85:ARG:N	2.28	0.46
1:A:1202:G:N3	14:N:42:ILE:HD12	2.31	0.46
1:A:1435:G:C2	1:A:1436:U:C4	3.04	0.46
1:A:78:G:N2	1:A:79:G:H1'	2.30	0.46
1:A:892:A:C2	1:A:907:A:C4	3.04	0.46
1:A:966:M2G:HM22	1:A:967:5MC:C2	2.50	0.46
1:A:988:G:N1	1:A:989:C:O2	2.48	0.46
2:B:118:LEU:O	2:B:122:PHE:N	2.49	0.46
8:H:114:THR:OG1	8:H:117:GLY:O	2.22	0.46
10:J:32:ALA:O	10:J:34:VAL:HG23	2.15	0.46
15:O:74:ASP:CG	15:O:77:ARG:HG3	2.36	0.46
18:R:36:ASN:OD1	18:R:39:VAL:HG12	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1145:C:HO2'	1:A:1146:A:P	2.37	0.46
1:A:1214:C:H3'	1:A:1215:G:C8	2.50	0.46
2:B:98:LEU:HD13	24:B:401:HOH:O	2.16	0.46
3:C:21:ARG:HG3	3:C:58:GLU:HG2	1.97	0.46
11:K:101:SER:OG	11:K:102:GLY:N	2.49	0.46
1:A:1425:U:O2'	1:A:1426:C:H5'	2.16	0.46
1:A:564:C:O2'	8:H:91:ARG:NH2	2.44	0.46
1:A:78:G:N2	1:A:92:C:C5	2.84	0.46
2:B:31:TYR:CD1	2:B:31:TYR:N	2.84	0.46
6:F:10:LEU:HB3	6:F:84:ASN:O	2.16	0.46
8:H:51:VAL:HG21	8:H:60:ARG:NH2	2.31	0.46
10:J:34:VAL:HG13	10:J:74:ILE:HA	1.97	0.46
1:A:1202:G:O2'	14:N:27:CYS:SG	2.64	0.46
1:A:1371:G:O3'	9:I:69:GLY:HA3	2.15	0.46
1:A:1422:G:H2'	1:A:1423:G:C8	2.51	0.46
1:A:297:G:H5''	1:A:298:A:OP2	2.15	0.46
1:A:881:G:H2'	1:A:882:C:O4'	2.15	0.46
1:A:989:C:N3	1:A:1216:G:N2	2.64	0.46
9:I:126:SER:CB	9:I:127:LYS:HD2	2.46	0.46
12:L:25:PRO:HA	12:L:27:LEU:H	1.81	0.46
16:P:75:ARG:HH11	16:P:75:ARG:HG3	1.81	0.46
20:T:83:ARG:NH2	24:T:301:HOH:O	2.49	0.46
1:A:1015:A:N6	1:A:1016:A:C6	2.84	0.46
1:A:1196:U:H3'	1:A:1197:G:H5'	1.98	0.46
1:A:991:U:O2'	1:A:992:U:P	2.74	0.46
4:D:140:VAL:HG11	4:D:146:ILE:HD11	1.98	0.46
6:F:33:TYR:CE1	6:F:75:LEU:HA	2.51	0.46
12:L:60:LEU:HA	12:L:60:LEU:HD13	1.52	0.46
13:M:29:ARG:HB3	13:M:64:TRP:CH2	2.51	0.46
16:P:43:LYS:HG2	16:P:48:TRP:CD2	2.50	0.46
1:A:1030:C:H42	1:A:1031:G:H22	1.64	0.46
1:A:1174:G:C2	1:A:1175:G:C5	3.04	0.46
1:A:1278:U:H5'	1:A:1279:A:H5'	1.96	0.46
1:A:1369:C:H2'	1:A:1370:G:H8	1.80	0.46
1:A:1518[B]:MA6:H93	1:A:1519[B]:MA6:C2	2.46	0.46
1:A:129(A):G:H1'	1:A:190(E):U:H2'	1.97	0.46
1:A:316:G:H2'	1:A:317:G:H8	1.81	0.46
1:A:446:G:N2	1:A:488:C:N3	2.50	0.46
2:B:134:GLU:HB2	2:B:137:ARG:HE	1.80	0.46
3:C:151:VAL:O	3:C:152:ILE:HD13	2.15	0.46
11:K:27:ASN:OD1	11:K:28:THR:N	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:981:U:H4'	14:N:21:TYR:CE2	2.51	0.46
17:Q:4:LYS:CG	17:Q:6:LEU:HD21	2.44	0.46
18:R:51:LEU:HD23	18:R:52:PRO:HD2	1.98	0.46
19:S:15:LEU:HD21	19:S:71:LEU:HD11	1.97	0.46
1:A:1067:A:N1	1:A:1108:G:O2'	2.44	0.46
1:A:106:C:O2'	1:A:107:G:H5'	2.16	0.46
1:A:1093:A:N3	1:A:1109:C:O2'	2.41	0.46
1:A:130:A:H1'	1:A:263:A:O2'	2.16	0.46
5:E:80:ILE:HD11	5:E:138:ALA:HA	1.98	0.46
10:J:91:PRO:HB2	10:J:94:VAL:CG2	2.46	0.46
12:L:20:LYS:HG3	12:L:20:LYS:H	1.57	0.46
12:L:58:VAL:HG12	12:L:59:ARG:O	2.14	0.46
13:M:40:ASN:HD22	13:M:43:THR:HG23	1.81	0.46
1:A:1090:U:H2'	1:A:1091:U:H6	1.81	0.45
1:A:1243:C:H2'	1:A:1244:C:C6	2.48	0.45
1:A:1300:G:OP2	1:A:1335:C:N4	2.50	0.45
1:A:1417:G:H21	1:A:1484:C:H42	1.63	0.45
1:A:280:C:H4'	1:A:281:G:OP2	2.15	0.45
1:A:877:C:O2	8:H:3:THR:HG21	2.15	0.45
5:E:95:ALA:O	5:E:98:THR:OG1	2.28	0.45
11:K:59:TYR:CE1	11:K:63:LEU:HD11	2.51	0.45
1:A:130:A:H5'	17:Q:63:ARG:NE	2.30	0.45
1:A:1332:A:H2'	1:A:1333:A:H8	1.81	0.45
1:A:344:A:H5'	1:A:345:C:H5	1.79	0.45
2:B:24:TRP:HA	2:B:190:THR:O	2.16	0.45
8:H:10:LEU:HA	8:H:10:LEU:HD23	1.48	0.45
8:H:65:TYR:HA	8:H:79:VAL:HG23	1.98	0.45
11:K:90:GLY:HA2	11:K:93:GLN:H	1.80	0.45
17:Q:38:ARG:HD2	17:Q:38:ARG:N	2.32	0.45
20:T:75:ASN:HA	20:T:78:ALA:HB3	1.98	0.45
1:A:452:A:H2'	1:A:453:A:C8	2.52	0.45
1:A:939:G:H2'	1:A:940:C:C6	2.51	0.45
2:B:122:PHE:CZ	2:B:139:LYS:HE2	2.51	0.45
1:A:1117:G:H5''	9:I:104:ARG:NH2	2.30	0.45
11:K:44:SER:O	11:K:47:VAL:HB	2.16	0.45
16:P:39:TYR:CD1	16:P:73:LEU:HD13	2.51	0.45
16:P:38:TYR:CE2	16:P:50:LYS:HE2	2.51	0.45
1:A:120:A:H2'	1:A:122:G:C8	2.52	0.45
1:A:1417:G:H21	1:A:1484:C:N4	2.15	0.45
1:A:419:C:H42	1:A:424:G:H1	1.63	0.45
1:A:51:A:C6	1:A:353:A:C2	3.05	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:926:G:H3'	1:A:1505:G:N2	2.31	0.45
2:B:97:TRP:CZ3	2:B:98:LEU:O	2.70	0.45
10:J:8:LEU:HD11	10:J:72:VAL:HG22	1.98	0.45
1:A:1035:A:H2'	1:A:1036:G:C8	2.51	0.45
1:A:544:G:C6	1:A:545:C:C4	3.04	0.45
2:B:55:PHE:HD2	2:B:58:ILE:HD12	1.80	0.45
1:A:542:G:H5'	4:D:41:GLY:HA3	1.99	0.45
5:E:51:VAL:HB	5:E:52:PRO:HD3	1.98	0.45
6:F:14:LEU:HD21	6:F:84:ASN:OD1	2.15	0.45
8:H:97:VAL:HG23	8:H:129:VAL:O	2.17	0.45
10:J:89:ASP:OD2	10:J:91:PRO:HD2	2.15	0.45
13:M:80:ARG:NH1	13:M:81:LEU:HB3	2.32	0.45
1:A:1361(A):C:O2'	1:A:1362:C:H6	2.00	0.45
1:A:588:G:H1	1:A:651:C:N4	2.12	0.45
1:A:838:G:N2	1:A:849:C:C2	2.85	0.45
5:E:87:SER:HB3	5:E:131:ILE:HD13	1.98	0.45
6:F:10:LEU:HD11	6:F:61:LEU:HD11	1.98	0.45
6:F:4:TYR:HB2	6:F:65:VAL:HG22	1.98	0.45
7:G:102:ARG:O	7:G:106:GLN:HG3	2.16	0.45
8:H:102:ARG:HG3	8:H:102:ARG:O	2.17	0.45
9:I:83:ARG:O	9:I:86:VAL:HG12	2.17	0.45
11:K:47:VAL:HG12	11:K:48:ILE:N	2.31	0.45
1:A:1174:G:H2'	1:A:1175:G:C8	2.51	0.45
1:A:1406:U:O2'	1:A:1517[B]:G:N2	2.50	0.45
2:B:87:ARG:HB3	2:B:87:ARG:HH11	1.82	0.45
3:C:117:ALA:HB2	3:C:200:ALA:CB	2.46	0.45
3:C:64:VAL:HB	3:C:99:VAL:HG23	1.99	0.45
5:E:36:ASP:OD2	5:E:40:ARG:HB2	2.16	0.45
8:H:87:SER:CA	8:H:93:VAL:HG13	2.44	0.45
11:K:70:LYS:HB3	11:K:70:LYS:HE2	1.76	0.45
12:L:46:LYS:HD2	12:L:94:PRO:HG3	1.99	0.45
16:P:34:GLU:OE2	16:P:55:ARG:HD2	2.17	0.45
17:Q:60:ILE:HG13	17:Q:61:GLU:N	2.31	0.45
17:Q:43:LEU:HD12	17:Q:68:ARG:HB3	1.99	0.45
18:R:26:LEU:HD23	18:R:29:PHE:CE2	2.52	0.45
1:A:1112:C:H1'	3:C:179:ARG:NH2	2.31	0.45
1:A:1288:A:H2'	1:A:1289:A:H8	1.82	0.45
1:A:1481:U:C4	1:A:1482:G:N7	2.84	0.45
1:A:445:G:C2	1:A:490:G:C2	3.05	0.45
2:B:108:ILE:HA	2:B:108:ILE:HD12	1.74	0.45
2:B:162:ILE:HG22	2:B:164:VAL:HG23	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:24:TRP:CZ3	2:B:26:PRO:HA	2.52	0.45
8:H:86:ILE:HG22	8:H:87:SER:N	2.30	0.45
13:M:54:VAL:O	13:M:58:GLU:HG2	2.16	0.45
18:R:76:LEU:HA	18:R:76:LEU:HD23	1.58	0.45
1:A:955:U:H1'	1:A:1227:A:N6	2.31	0.45
1:A:1346:A:H62	1:A:1375:A:H62	1.65	0.45
1:A:1397:C:HO2'	1:A:1398:A:P	2.40	0.45
1:A:452:A:O2'	1:A:453:A:O5'	2.34	0.45
1:A:832:C:H2'	1:A:833:U:O4'	2.17	0.45
2:B:21:ARG:HA	2:B:39:ILE:HA	1.98	0.45
4:D:73:ARG:HD3	4:D:77:ASN:OD1	2.16	0.45
7:G:108:ALA:O	7:G:119:ARG:HG2	2.17	0.45
9:I:75:ASP:O	9:I:78:LYS:HB3	2.17	0.45
9:I:9:ARG:CG	9:I:14:VAL:HG13	2.47	0.45
10:J:7:LYS:HB3	10:J:97:GLU:HB2	1.98	0.45
11:K:80:VAL:HG21	11:K:103:LEU:HD13	1.99	0.45
12:L:17:LYS:HE3	12:L:17:LYS:HB2	1.74	0.45
21:U:18:TYR:HE2	21:U:22:ARG:HE	1.65	0.45
1:A:1417:G:N2	1:A:1484:C:H42	2.15	0.45
1:A:1513:A:H2'	1:A:1514:C:C6	2.52	0.45
1:A:7:G:H5'	1:A:298:A:H5'	1.98	0.45
1:A:410:G:C2	1:A:429:U:C2	3.05	0.45
2:B:101:MET:O	2:B:105:PHE:HD1	2.00	0.45
3:C:66:VAL:HG21	3:C:91:LEU:HD21	1.99	0.45
6:F:22:GLU:OE1	6:F:82:ARG:NH2	2.50	0.45
8:H:36:LEU:HA	8:H:36:LEU:HD23	1.70	0.45
13:M:79:LYS:O	13:M:83:ASP:HB2	2.17	0.45
1:A:1124:G:H2'	1:A:1145:C:H41	1.81	0.44
1:A:659:U:OP2	15:O:8:LYS:NZ	2.42	0.44
1:A:75:G:N2	1:A:96:G:H22	2.15	0.44
1:A:980:C:H5''	1:A:981:U:C5	2.52	0.44
2:B:107:THR:HG23	2:B:110:GLN:OE1	2.17	0.44
3:C:37:GLN:HE22	14:N:52:GLN:CD	2.21	0.44
5:E:90:VAL:HG23	5:E:121:LYS:O	2.16	0.44
7:G:37:ASN:HB3	24:G:201:HOH:O	2.17	0.44
8:H:27:PRO:HA	8:H:58:TYR:CD2	2.51	0.44
9:I:117:HIS:HB2	9:I:121:ARG:HG2	1.98	0.44
1:A:1215:G:H2'	1:A:1215:G:N3	2.32	0.44
1:A:11:G:C5	1:A:12:U:C5	3.05	0.44
1:A:448:A:P	1:A:485:G:H22	2.40	0.44
1:A:853:G:H2'	1:A:854:G:H5'	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:85:ARG:HA	3:C:88:ARG:HD2	1.99	0.44
5:E:98:THR:HB	5:E:117:ASP:HB3	1.99	0.44
7:G:136:LYS:HB3	7:G:136:LYS:HE3	1.77	0.44
7:G:89:MET:HA	7:G:155:ARG:NH1	2.32	0.44
8:H:120:THR:H	8:H:123:GLU:HB2	1.83	0.44
10:J:91:PRO:HB2	10:J:94:VAL:HG21	1.99	0.44
11:K:114:VAL:HG23	11:K:115:PRO:HD2	2.00	0.44
15:O:60:VAL:HG12	15:O:61:GLY:N	2.33	0.44
20:T:33:ILE:CD1	20:T:63:ILE:HA	2.47	0.44
1:A:1124:G:C8	1:A:1145:C:C5	3.06	0.44
1:A:28:G:C6	1:A:29:G:C5	3.06	0.44
1:A:966:M2G:N7	1:A:967:5MC:HM52	2.33	0.44
1:A:981:U:H5'	14:N:21:TYR:OH	2.17	0.44
3:C:112:SER:HB3	3:C:115:LEU:HD12	1.97	0.44
3:C:84:ILE:HG23	3:C:88:ARG:NH1	2.32	0.44
10:J:51:ARG:NH1	10:J:61:GLU:OE1	2.50	0.44
12:L:33:ARG:NH1	12:L:61:THR:HB	2.32	0.44
1:A:333:G:H4'	20:T:16:HIS:CE1	2.52	0.44
1:A:460:A:O2'	1:A:461:C:H5''	2.18	0.44
1:A:519:C:H2'	1:A:520:A:C8	2.51	0.44
1:A:803:G:H2'	1:A:804:U:O4'	2.17	0.44
1:A:923:A:O5'	1:A:923:A:H8	2.00	0.44
3:C:10:PHE:HD2	3:C:10:PHE:O	2.00	0.44
3:C:4:LYS:NZ	3:C:4:LYS:HB2	2.32	0.44
6:F:69:GLU:N	6:F:69:GLU:OE1	2.48	0.44
7:G:108:ALA:HB2	7:G:123:GLU:HG2	1.99	0.44
8:H:85:ARG:HG3	8:H:85:ARG:HH11	1.82	0.44
13:M:40:ASN:ND2	13:M:43:THR:HG23	2.33	0.44
18:R:79:LEU:HA	18:R:79:LEU:HD23	1.66	0.44
1:A:415:A:H2'	1:A:416:G:O4'	2.17	0.44
1:A:828:A:H4'	1:A:828:A:OP1	2.16	0.44
1:A:93:G:C2	1:A:95:U:N3	2.86	0.44
2:B:215:LEU:HD23	2:B:215:LEU:HA	1.43	0.44
3:C:91:LEU:HG	3:C:99:VAL:HG11	2.00	0.44
4:D:3:ARG:NH1	4:D:74:GLN:OE1	2.51	0.44
5:E:112:LEU:HA	5:E:112:LEU:HD23	1.70	0.44
7:G:85:TYR:O	7:G:87:VAL:HG13	2.17	0.44
8:H:82:HIS:ND1	8:H:138:TRP:NE1	2.50	0.44
8:H:20:TYR:HA	8:H:65:TYR:CE2	2.53	0.44
3:C:9:GLY:HA3	14:N:49:HIS:HD1	1.81	0.44
10:J:11:PHE:HB3	14:N:55:GLY:HA2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:719:C:N4	18:R:74:ARG:HH12	2.14	0.44
1:A:1417:G:H8	1:A:1417:G:OP2	2.01	0.44
1:A:505:G:H2'	1:A:506:G:C8	2.52	0.44
1:A:579:G:H2'	1:A:580:U:C6	2.53	0.44
3:C:119:ARG:O	3:C:122:GLU:HB2	2.18	0.44
4:D:159:ARG:O	4:D:163:GLU:HB2	2.18	0.44
5:E:144:THR:O	5:E:148:VAL:HG23	2.17	0.44
9:I:89:ASN:O	9:I:92:TYR:HB2	2.17	0.44
9:I:9:ARG:HG3	9:I:14:VAL:HG13	1.99	0.44
15:O:70:LEU:HA	15:O:70:LEU:HD23	1.51	0.44
1:A:1054:C:OP1	1:A:1197:G:OP1	2.36	0.44
1:A:1219:U:C4	1:A:1220:G:N7	2.86	0.44
1:A:1515[A]:C:N3	1:A:1520[A]:G:N2	2.66	0.44
1:A:524:G:H2'	1:A:525:C:C6	2.53	0.44
3:C:79:ARG:HG3	3:C:79:ARG:H	1.73	0.44
5:E:121:LYS:HG2	5:E:123:LEU:HD21	1.99	0.44
10:J:63:PHE:HE1	14:N:45:ARG:HA	1.83	0.44
14:N:6:LEU:O	14:N:23:ARG:NE	2.39	0.44
15:O:36:ILE:HD12	15:O:60:VAL:HG23	1.99	0.44
1:A:1223:C:P	19:S:78:ARG:HH22	2.41	0.44
1:A:1069:C:O2'	1:A:1192:C:H1'	2.18	0.44
1:A:1185:G:O2'	1:A:1186:G:H5'	2.18	0.44
1:A:651:C:O2'	1:A:652:U:H5'	2.18	0.44
2:B:17:PHE:HD1	2:B:18:GLY:N	2.15	0.44
2:B:55:PHE:HE2	2:B:218:ALA:HA	1.83	0.44
2:B:25:ASN:O	2:B:27:LYS:N	2.51	0.44
5:E:92:LYS:HB3	5:E:119:LEU:HB2	1.99	0.44
5:E:28:PHE:O	5:E:47:LYS:HA	2.18	0.44
5:E:51:VAL:HG12	5:E:52:PRO:N	2.32	0.44
6:F:10:LEU:HD12	6:F:59:TYR:HB3	1.99	0.44
9:I:118:LYS:O	9:I:120:ARG:N	2.44	0.44
11:K:58:PRO:O	11:K:61:ALA:HB3	2.18	0.44
1:A:1257:U:O2'	1:A:1258:G:C8	2.70	0.44
1:A:1290:G:H2'	1:A:1291:G:H8	1.83	0.44
1:A:279:A:OP1	1:A:280:C:O2'	2.32	0.44
1:A:321:A:N6	1:A:329:A:OP2	2.50	0.44
1:A:80:G:H2'	1:A:81:U:H5'	2.00	0.44
1:A:990:C:N3	1:A:1216:G:N2	2.66	0.44
4:D:186:LEU:HG	4:D:186:LEU:H	1.47	0.44
1:A:673:G:H5''	6:F:87:ARG:CZ	2.47	0.44
1:A:825:G:H21	8:H:11:THR:HG21	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:87:THR:HG22	11:K:88:GLY:N	2.32	0.44
12:L:120:TYR:CD2	12:L:120:TYR:N	2.86	0.44
16:P:12:LYS:O	16:P:13:HIS:HB2	2.17	0.44
1:A:1136:U:H4'	1:A:1137:C:OP2	2.17	0.43
1:A:1196:U:OP1	1:A:1197:G:H5'	2.18	0.43
1:A:1329:A:H2'	1:A:1330:U:O4'	2.18	0.43
1:A:1354:C:H2'	1:A:1355:G:H8	1.83	0.43
1:A:1375:A:C2	1:A:1376:U:C2	3.06	0.43
1:A:1473:A:C6	1:A:1474:G:C6	3.06	0.43
1:A:176:C:H2'	1:A:177:C:C5	2.53	0.43
1:A:701:C:H4'	1:A:702:A:O5'	2.18	0.43
4:D:121:VAL:HG12	4:D:134:ASP:O	2.17	0.43
5:E:12:LEU:HD22	5:E:12:LEU:O	2.18	0.43
8:H:114:THR:HG21	8:H:129:VAL:HB	2.00	0.43
12:L:11:VAL:HG22	17:Q:29:HIS:CD2	2.53	0.43
13:M:23:TYR:HB2	13:M:67:GLU:OE2	2.18	0.43
16:P:65:GLN:HA	16:P:66:PRO:HD2	1.76	0.43
18:R:63:GLN:O	18:R:66:LEU:HB3	2.18	0.43
19:S:31:ILE:HG23	19:S:32:LYS:N	2.33	0.43
20:T:100:ILE:HG22	20:T:102:GLY:N	2.20	0.43
1:A:602:A:C2	1:A:637:G:C2	3.06	0.43
1:A:988:G:C6	1:A:989:C:C2	3.07	0.43
1:A:98:U:OP2	1:A:98:U:H6	2.00	0.43
5:E:60:TYR:O	5:E:64:ARG:HG2	2.18	0.43
6:F:80:ARG:HG3	6:F:88:VAL:HB	2.00	0.43
13:M:37:THR:HG23	13:M:55:ARG:HB3	2.00	0.43
13:M:80:ARG:HB3	13:M:80:ARG:HH11	1.83	0.43
1:A:1221:G:H5'	19:S:36:ARG:NH1	2.32	0.43
1:A:1254:C:H4'	1:A:1357:A:OP1	2.18	0.43
1:A:1311:G:H1	1:A:1326:C:N4	2.16	0.43
1:A:1349:A:C2	1:A:1374:A:C4	3.06	0.43
1:A:773:G:N2	1:A:806:C:O2	2.50	0.43
2:B:139:LYS:HZ2	2:B:143:GLU:HG3	1.83	0.43
4:D:173:TRP:CD1	4:D:189:PRO:HD3	2.54	0.43
8:H:63:LEU:HD23	8:H:65:TYR:OH	2.18	0.43
8:H:78:GLN:HA	8:H:78:GLN:OE1	2.18	0.43
11:K:98:LEU:HD23	11:K:98:LEU:HA	1.70	0.43
14:N:23:ARG:HD3	14:N:28:GLY:O	2.19	0.43
1:A:1341:U:O5'	1:A:1341:U:H6	2.00	0.43
1:A:1374:A:C4	1:A:1375:A:C8	3.07	0.43
1:A:147:G:C2	1:A:148:G:C8	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1399:C:C2	1:A:1502:A:N6	2.86	0.43
1:A:403:C:H4'	4:D:122:ARG:HH11	1.82	0.43
1:A:448:A:C4	1:A:487:A:C2	3.06	0.43
1:A:539:A:H2'	1:A:540:G:C8	2.53	0.43
1:A:622:A:H2'	1:A:623:C:H5'	2.00	0.43
2:B:180:LEU:HD23	2:B:180:LEU:HA	1.59	0.43
5:E:71:LEU:HD23	5:E:71:LEU:HA	1.66	0.43
1:A:671:G:H5'	6:F:77:ARG:NH2	2.33	0.43
6:F:4:TYR:CD1	6:F:92:LYS:HA	2.53	0.43
8:H:89:PRO:HA	8:H:92:ARG:NH1	2.33	0.43
11:K:92:GLU:HB3	11:K:96:ARG:NH2	2.33	0.43
15:O:39:LEU:HB3	15:O:56:LEU:CD1	2.47	0.43
15:O:78:TYR:CZ	15:O:82:ILE:HD12	2.54	0.43
16:P:68:ASP:OD1	16:P:68:ASP:N	2.50	0.43
17:Q:67:LYS:HA	17:Q:70:ARG:HH12	1.84	0.43
1:A:1371:G:C5	1:A:1372:U:C5	3.07	0.43
1:A:1408:A:C6	1:A:1494:G:C6	3.07	0.43
1:A:253:U:H2'	1:A:254:G:H8	1.84	0.43
3:C:113:ALA:O	3:C:116:VAL:HG23	2.18	0.43
4:D:31:CYS:C	4:D:33:MET:H	2.21	0.43
5:E:11:ILE:HA	5:E:11:ILE:HD13	1.61	0.43
5:E:122:GLU:HG2	5:E:131:ILE:HG13	1.99	0.43
12:L:60:LEU:HB2	12:L:64:TYR:O	2.19	0.43
12:L:84:LEU:HB3	12:L:104:VAL:HG11	2.00	0.43
13:M:80:ARG:HH12	13:M:81:LEU:HB3	1.83	0.43
14:N:17:LYS:HE2	14:N:17:LYS:HB2	1.79	0.43
17:Q:22:LEU:HD12	17:Q:23:VAL:N	2.34	0.43
1:A:1320:C:C4	19:S:36:ARG:HG3	2.53	0.43
20:T:74:LYS:HB2	20:T:76:ALA:H	1.82	0.43
1:A:1001:A:H2'	1:A:1002:G:C8	2.48	0.43
1:A:1007:C:O2	1:A:1023:G:N1	2.51	0.43
1:A:1370:G:C2	1:A:1371:G:N7	2.87	0.43
1:A:1419:G:H2'	1:A:1420:C:O4'	2.18	0.43
1:A:455:C:H2'	1:A:456:C:C6	2.43	0.43
1:A:657:G:H4'	15:O:28:GLN:HG2	2.01	0.43
2:B:55:PHE:HA	2:B:58:ILE:HD12	2.00	0.43
3:C:17:ASP:O	3:C:54:ARG:NH1	2.48	0.43
3:C:40:ARG:HE	3:C:55:VAL:HB	1.81	0.43
3:C:81:GLY:O	3:C:84:ILE:HG22	2.17	0.43
3:C:87:LEU:HA	3:C:87:LEU:HD13	1.82	0.43
4:D:207:TYR:HD2	4:D:207:TYR:HA	1.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:47:CYS:HB3	7:G:58:PRO:CG	2.47	0.43
12:L:77:LEU:HD23	12:L:77:LEU:HA	1.63	0.43
17:Q:5:VAL:C	17:Q:6:LEU:HD23	2.39	0.43
1:A:1067:A:N6	1:A:1109:C:H5'	2.34	0.43
1:A:289:G:H8	1:A:289:G:H5'	1.83	0.43
1:A:49:U:C2	1:A:361:G:N2	2.86	0.43
1:A:9:G:H5'	5:E:122:GLU:OE2	2.19	0.43
2:B:149:LEU:O	2:B:153:ARG:HB2	2.18	0.43
5:E:76:ILE:HG22	5:E:93:PRO:HG3	2.00	0.43
6:F:45:LEU:HD23	6:F:45:LEU:HA	1.80	0.43
1:A:1167:A:C6	1:A:1168:A:C6	3.07	0.43
1:A:1220:G:H2'	1:A:1221:G:O4'	2.19	0.43
1:A:145:G:C2	1:A:146:G:C5	3.07	0.43
1:A:475:G:H2'	1:A:476:G:C8	2.54	0.43
1:A:631:G:H5''	1:A:632:A:OP1	2.19	0.43
1:A:673:G:O3'	6:F:87:ARG:NH2	2.52	0.43
1:A:687:A:H4'	1:A:688:G:O5'	2.19	0.43
1:A:78:G:C6	1:A:79:G:C8	3.07	0.43
1:A:902:G:O2'	1:A:903:G:H5'	2.19	0.43
1:A:8:A:N1	4:D:209:ARG:HD2	2.34	0.43
7:G:45:ASP:HA	7:G:48:LYS:HG3	1.99	0.43
8:H:112:LEU:HD22	8:H:133:LEU:HA	2.01	0.43
9:I:37:PHE:CZ	9:I:74:ILE:HG12	2.53	0.43
17:Q:75:ARG:NH2	17:Q:77:VAL:HG13	2.30	0.43
19:S:33:THR:HG22	19:S:35:SER:H	1.84	0.43
1:A:992:U:N3	1:A:1044:A:N6	2.60	0.43
1:A:1346:A:OP1	9:I:120:ARG:NH1	2.45	0.43
1:A:1421:G:H2'	1:A:1422:G:O4'	2.19	0.43
1:A:1491:G:N2	1:A:1492:A:H62	2.16	0.43
1:A:675:A:H1'	11:K:116:HIS:CG	2.53	0.43
1:A:980:C:H5''	1:A:981:U:H5	1.84	0.43
2:B:204:ASN:N	2:B:204:ASN:OD1	2.51	0.43
5:E:77:PRO:HD2	5:E:142:LEU:HD13	2.01	0.43
7:G:118:VAL:HG12	7:G:122:HIS:HD1	1.83	0.43
7:G:18:TYR:OH	7:G:58:PRO:HB2	2.19	0.43
17:Q:83:ASP:OD1	17:Q:84:LEU:N	2.49	0.43
1:A:120:A:H2'	1:A:122:G:N7	2.34	0.43
1:A:1268:A:O3'	21:U:19:GLY:HA2	2.19	0.43
1:A:1305:G:H22	1:A:1331:G:H1'	1.81	0.43
2:B:114:ARG:HD3	2:B:114:ARG:O	2.19	0.43
4:D:82:ALA:HA	4:D:85:LYS:HG3	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:53:ARG:HH12	12:L:92:OTD:CG	2.31	0.43
15:O:15:PHE:CZ	15:O:85:LEU:HD21	2.53	0.43
15:O:70:LEU:O	15:O:73:GLU:N	2.50	0.43
20:T:20:LEU:O	20:T:23:ARG:HB3	2.18	0.43
1:A:1526:G:H2'	1:A:1527:C:C6	2.53	0.42
1:A:321:A:H2'	1:A:322:C:C6	2.54	0.42
1:A:337:C:H2'	1:A:338:A:C8	2.54	0.42
1:A:631:G:O3'	1:A:632:A:H8	2.01	0.42
2:B:10:LEU:H	2:B:10:LEU:HD12	1.84	0.42
2:B:92:TYR:O	2:B:151:GLY:HA3	2.19	0.42
3:C:10:PHE:CE2	3:C:178:LEU:HB2	2.54	0.42
6:F:11:ASN:HB2	6:F:86:ARG:CZ	2.49	0.42
6:F:62:TRP:CH2	6:F:64:GLN:HB2	2.54	0.42
7:G:115:ARG:HB2	7:G:118:VAL:CG2	2.47	0.42
8:H:83:ILE:HD12	8:H:83:ILE:HG23	1.73	0.42
1:A:376:G:H5''	16:P:5:ARG:HD2	2.00	0.42
1:A:1123:A:H2'	1:A:1124:G:C8	2.54	0.42
1:A:1148:U:H2'	1:A:1149:C:O4'	2.19	0.42
1:A:1491:G:C5	1:A:1493:A:C2	3.07	0.42
1:A:1514:C:H2'	1:A:1515[A]:C:O4'	2.19	0.42
1:A:688:G:C5	1:A:700:G:C2	3.07	0.42
2:B:172:ILE:H	2:B:172:ILE:CD1	2.26	0.42
2:B:88:ALA:O	2:B:90:MET:N	2.52	0.42
3:C:24:ALA:HB3	3:C:29:TYR:CD1	2.54	0.42
3:C:19:GLU:O	3:C:56:ASP:HA	2.19	0.42
5:E:80:ILE:HD11	5:E:138:ALA:HB1	2.01	0.42
5:E:6:PHE:CD2	5:E:36:ASP:HB3	2.54	0.42
13:M:82:MET:HA	13:M:89:GLY:CA	2.49	0.42
16:P:32:TYR:HD2	16:P:32:TYR:O	2.02	0.42
1:A:376:G:H4'	16:P:5:ARG:HD2	2.01	0.42
17:Q:43:LEU:HD23	17:Q:43:LEU:HA	1.77	0.42
17:Q:17:LYS:N	17:Q:49:GLU:OE2	2.36	0.42
17:Q:59:ILE:HD13	17:Q:59:ILE:HA	1.64	0.42
1:A:160:A:N6	1:A:161:A:C2	2.88	0.42
1:A:62:U:H2'	1:A:63:C:C6	2.55	0.42
1:A:665:A:H3'	1:A:725:G:N2	2.34	0.42
1:A:75:G:N2	1:A:96:G:N2	2.68	0.42
2:B:222:ILE:HD13	2:B:222:ILE:HG21	1.77	0.42
5:E:106:PRO:O	5:E:110:LEU:HG	2.18	0.42
8:H:53:VAL:HB	8:H:58:TYR:CE1	2.54	0.42
10:J:36:GLY:HA3	10:J:37:PRO:HD3	1.70	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:48:ILE:HD13	11:K:63:LEU:HB3	2.01	0.42
15:O:7:GLU:HG3	15:O:7:GLU:H	1.63	0.42
19:S:80:TYR:CG	19:S:81:ARG:N	2.87	0.42
1:A:1370:G:C2	1:A:1371:G:C8	3.08	0.42
1:A:439:A:C4	1:A:497:A:C2	3.07	0.42
1:A:740:U:O2'	1:A:741:G:H5'	2.19	0.42
1:A:768:A:C5	1:A:769:G:C8	3.08	0.42
1:A:905:U:H2'	1:A:906:G:H5'	2.01	0.42
1:A:865:A:H2	1:A:918:A:H4'	1.84	0.42
2:B:102:LEU:HB3	2:B:180:LEU:HD12	2.01	0.42
2:B:10:LEU:C	2:B:12:GLU:H	2.21	0.42
2:B:217:ARG:O	2:B:220:ASP:HB2	2.20	0.42
3:C:7:PRO:O	3:C:11:ARG:NE	2.52	0.42
5:E:74:GLY:HA3	5:E:116:THR:HG22	2.00	0.42
5:E:11:ILE:HB	5:E:31:LEU:HB3	2.00	0.42
6:F:67:MET:HB2	6:F:68:PRO:HD2	2.02	0.42
1:A:599:C:O2'	8:H:129:VAL:HG12	2.20	0.42
9:I:54:ASP:O	9:I:58:HIS:ND1	2.52	0.42
9:I:97:LYS:O	9:I:100:GLY:N	2.51	0.42
14:N:36:PHE:CD1	14:N:36:PHE:C	2.93	0.42
1:A:1149:C:O5'	1:A:1149:C:H6	2.03	0.42
1:A:994:A:C8	1:A:1216:G:H4'	2.54	0.42
1:A:1304:G:OP1	21:U:2:GLY:N	2.53	0.42
1:A:266:G:H8	1:A:266:G:H5''	1.83	0.42
1:A:424:G:H2'	1:A:425:G:C8	2.55	0.42
1:A:511:C:O2'	1:A:534:U:H1'	2.20	0.42
1:A:690:G:C6	1:A:691:G:C6	3.07	0.42
1:A:76:C:N4	1:A:93:G:H1	2.16	0.42
3:C:115:LEU:HA	3:C:115:LEU:HD23	1.77	0.42
3:C:34:LEU:HD21	14:N:25:VAL:HG21	2.01	0.42
1:A:403:C:O3'	4:D:122:ARG:HD3	2.19	0.42
13:M:34:LEU:HD13	13:M:34:LEU:HA	1.88	0.42
13:M:87:TYR:O	13:M:90:LEU:N	2.52	0.42
15:O:4:THR:HG23	15:O:7:GLU:OE1	2.20	0.42
16:P:4:ILE:HG13	16:P:64:ALA:HB1	2.01	0.42
1:A:1324:A:H2'	1:A:1325:C:O4'	2.18	0.42
1:A:1474:G:O5'	1:A:1474:G:H8	2.02	0.42
1:A:1520[A]:G:H2'	1:A:1521:G:C8	2.54	0.42
1:A:77:G:C4	1:A:93:G:N2	2.87	0.42
2:B:7:VAL:O	2:B:8:LYS:HB3	2.19	0.42
3:C:155:GLY:O	3:C:196:LEU:HG	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:87:LEU:O	3:C:91:LEU:HB2	2.18	0.42
7:G:6:ARG:O	7:G:6:ARG:HG3	2.20	0.42
9:I:102:LEU:HD23	9:I:102:LEU:HA	1.70	0.42
10:J:47:PHE:HB3	14:N:34:TYR:CE2	2.40	0.42
12:L:127:GLU:HG2	12:L:127:GLU:H	1.68	0.42
13:M:4:ILE:HG22	13:M:5:ALA:N	2.35	0.42
1:A:105:G:H2'	1:A:106:C:C6	2.54	0.42
1:A:1169:A:H2'	1:A:1171:G:O4'	2.19	0.42
1:A:1208:C:C4	1:A:1209:C:C5	3.08	0.42
1:A:429:U:OP1	4:D:36:ARG:NH1	2.52	0.42
1:A:912:A:H5''	12:L:46:LYS:HZ1	1.84	0.42
1:A:97:G:C2'	1:A:98:U:H5'	2.49	0.42
3:C:11:ARG:HB3	3:C:16:ARG:HB2	2.02	0.42
4:D:162:LEU:HD23	4:D:162:LEU:HA	1.64	0.42
6:F:5:GLU:HG2	6:F:62:TRP:CZ2	2.55	0.42
8:H:11:THR:O	8:H:12:ARG:C	2.58	0.42
9:I:52:ALA:HB1	9:I:95:LYS:HD2	2.01	0.42
10:J:6:ILE:C	10:J:71:LEU:HD12	2.39	0.42
14:N:39:LEU:HA	14:N:39:LEU:HD23	1.77	0.42
1:A:1037:C:N3	1:A:1038:C:N4	2.68	0.42
1:A:1191:A:H2'	1:A:1192:C:C6	2.55	0.42
1:A:1374:A:H2'	1:A:1375:A:C8	2.54	0.42
1:A:149:A:H2'	1:A:150:C:C6	2.55	0.42
1:A:363:A:N6	1:A:364:A:N1	2.67	0.42
1:A:461:C:H4'	1:A:462:G:OP2	2.20	0.42
1:A:79:G:C2	1:A:80:G:N7	2.87	0.42
1:A:943:U:H2'	1:A:944:G:H5'	2.00	0.42
8:H:51:VAL:HG11	8:H:60:ARG:HB2	2.01	0.42
9:I:14:VAL:O	9:I:65:VAL:HG23	2.20	0.42
20:T:43:LEU:HG	20:T:55:ILE:CD1	2.50	0.42
20:T:60:GLU:O	20:T:63:ILE:HB	2.19	0.42
1:A:1109:C:H2'	1:A:1110:A:O4'	2.19	0.42
1:A:1402:4OC:H1'	1:A:1402:4OC:HM23	1.48	0.42
1:A:145:G:H2'	1:A:146:G:H8	1.85	0.42
1:A:539:A:H2'	1:A:540:G:H8	1.83	0.42
1:A:77:G:C2	1:A:93:G:N3	2.88	0.42
1:A:782:A:C6	1:A:801:U:C2	3.08	0.42
1:A:956:U:H2'	1:A:957:U:O4'	2.20	0.42
2:B:236:TYR:CD2	2:B:239:VAL:HG21	2.55	0.42
2:B:46:LYS:HE3	2:B:46:LYS:HB2	1.95	0.42
2:B:51:LEU:HA	2:B:51:LEU:HD23	1.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:11:ILE:HG23	5:E:11:ILE:HD12	1.59	0.42
7:G:79:ARG:HH21	7:G:82:GLY:HA2	1.84	0.42
1:A:1056:U:O2'	1:A:1057:G:H5'	2.20	0.42
1:A:1098:C:H2'	1:A:1099:G:O4'	2.20	0.42
1:A:374:A:C6	1:A:375:U:C4	3.08	0.42
2:B:95:GLN:NE2	2:B:147:LYS:HE2	2.35	0.42
2:B:24:TRP:CZ3	2:B:29:ALA:HB2	2.54	0.42
5:E:131:ILE:HD13	5:E:131:ILE:HA	1.54	0.42
5:E:55:VAL:HG12	5:E:56:GLN:N	2.34	0.42
9:I:28:VAL:HA	9:I:63:ILE:O	2.19	0.42
12:L:24:VAL:HG12	12:L:26:ALA:H	1.85	0.42
14:N:6:LEU:HB3	14:N:23:ARG:HH21	1.85	0.42
1:A:1250:A:H2'	1:A:1251:A:C8	2.55	0.41
1:A:1311:G:C2	1:A:1327:C:N3	2.88	0.41
1:A:596:C:O5'	1:A:596:C:H6	2.02	0.41
3:C:73:PRO:HG3	3:C:105:GLU:OE1	2.20	0.41
3:C:161:GLU:HG2	3:C:161:GLU:O	2.20	0.41
10:J:42:THR:HG23	10:J:67:THR:C	2.41	0.41
10:J:19:SER:CB	10:J:94:VAL:HG11	2.50	0.41
11:K:106:LYS:HA	11:K:106:LYS:HD3	1.95	0.41
1:A:1004:A:H4'	1:A:1005:A:OP1	2.20	0.41
1:A:1114:C:H42	1:A:1186:G:H1	1.68	0.41
1:A:1196:U:H3'	1:A:1197:G:C5'	2.50	0.41
1:A:141:A:H1'	1:A:182:U:O2	2.19	0.41
1:A:532:A:H2'	1:A:533:A:H5''	2.01	0.41
1:A:623:C:H2'	1:A:624:C:O4'	2.19	0.41
1:A:689:C:H2'	1:A:690:G:O4'	2.19	0.41
2:B:88:ALA:HB3	2:B:219:VAL:HG22	2.01	0.41
3:C:150:LYS:O	3:C:201:TYR:HB2	2.20	0.41
12:L:46:LYS:HE3	12:L:47:LYS:NZ	2.35	0.41
14:N:36:PHE:C	14:N:36:PHE:HD1	2.22	0.41
14:N:48:ALA:HA	14:N:53:LEU:HB2	2.02	0.41
20:T:40:ALA:HB2	20:T:55:ILE:CG2	2.50	0.41
1:A:1084:G:O2'	1:A:1085:U:OP1	2.26	0.41
1:A:1201:A:H4'	1:A:1202:G:H5''	2.00	0.41
1:A:1221:G:C4	1:A:1222:G:C8	3.08	0.41
1:A:428:G:H1'	1:A:429:U:OP2	2.20	0.41
1:A:794:A:C5	1:A:795:C:C4	3.09	0.41
2:B:95:GLN:OE1	2:B:95:GLN:HA	2.19	0.41
4:D:105:VAL:HG13	4:D:110:PHE:HB2	2.02	0.41
4:D:196:LEU:O	4:D:198:VAL:N	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:4:TYR:HE2	4:D:6:GLY:O	2.03	0.41
8:H:48:TYR:CD1	8:H:59:LEU:HD22	2.55	0.41
17:Q:60:ILE:HG22	17:Q:72:ARG:O	2.20	0.41
1:A:986:A:O2'	19:S:52:TYR:OH	2.14	0.41
1:A:1257:U:O2'	1:A:1258:G:P	2.78	0.41
1:A:1354:C:H2'	1:A:1355:G:C8	2.55	0.41
1:A:1417:G:O3'	1:A:1418:A:H8	2.03	0.41
1:A:1434:A:H2'	1:A:1435:G:O4'	2.20	0.41
1:A:901:A:C5	1:A:902:G:H1'	2.56	0.41
2:B:74:LYS:O	2:B:78:GLN:HG3	2.20	0.41
4:D:8:VAL:O	4:D:10:ARG:N	2.54	0.41
6:F:70:ASP:N	6:F:70:ASP:OD1	2.49	0.41
7:G:78:ARG:HG3	7:G:87:VAL:HG21	2.01	0.41
1:A:1279:A:H5''	10:J:7:LYS:HE2	2.02	0.41
17:Q:35:VAL:HG12	17:Q:35:VAL:O	2.21	0.41
1:A:191:G:O2'	20:T:102:GLY:O	2.24	0.41
1:A:1376:U:H2'	1:A:1377:A:C8	2.56	0.41
1:A:1443:G:C4'	1:A:1446:A:H5''	2.50	0.41
1:A:1416:G:N2	1:A:1484:C:O2	2.53	0.41
1:A:1408:A:N6	1:A:1494:G:C6	2.89	0.41
1:A:255:G:O6	1:A:266:G:O6	2.38	0.41
1:A:446:G:H1	1:A:488:C:N4	2.03	0.41
1:A:750:G:N3	15:O:23:GLY:HA3	2.34	0.41
1:A:973:G:C3'	1:A:974:A:H5''	2.49	0.41
1:A:980:C:H5'	1:A:981:U:OP2	2.20	0.41
2:B:102:LEU:HB2	2:B:176:GLU:OE1	2.20	0.41
2:B:134:GLU:O	2:B:138:LEU:HD12	2.21	0.41
1:A:1103:C:H5'	2:B:98:LEU:HD12	2.03	0.41
3:C:154:SER:OG	3:C:155:GLY:N	2.48	0.41
3:C:175:LEU:HD21	3:C:201:TYR:CE2	2.56	0.41
6:F:21:LEU:O	6:F:25:ILE:HG12	2.20	0.41
8:H:80:ILE:HD13	8:H:80:ILE:HG21	1.72	0.41
9:I:93:ARG:HG3	9:I:102:LEU:HD11	2.03	0.41
1:A:1048:G:N2	1:A:1050:G:C4	2.88	0.41
1:A:1443:G:C5'	1:A:1446:A:H5''	2.50	0.41
1:A:1486:G:N2	1:A:1487:G:N3	2.68	0.41
1:A:289:G:P	24:A:1909:HOH:O	2.79	0.41
1:A:397:A:H5'	1:A:398:C:P	2.61	0.41
1:A:460:A:C6	1:A:462:G:C5	3.09	0.41
1:A:506:G:H1	1:A:525:C:H42	1.68	0.41
1:A:302:G:N3	1:A:556:C:H4'	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:854:G:H3'	1:A:871:U:O4	2.21	0.41
1:A:938:A:H2'	1:A:939:G:O4'	2.20	0.41
1:A:981:U:H5''	1:A:982:U:C5'	2.50	0.41
3:C:113:ALA:HA	3:C:116:VAL:CG2	2.51	0.41
4:D:187:ARG:NH2	4:D:188:LEU:HD12	2.36	0.41
6:F:4:TYR:HD1	6:F:92:LYS:CA	2.34	0.41
6:F:74:ASP:OD2	6:F:74:ASP:N	2.48	0.41
7:G:27:ILE:HA	7:G:30:ILE:HD12	2.03	0.41
8:H:27:PRO:HB3	8:H:58:TYR:CE2	2.56	0.41
8:H:73:ASP:HA	8:H:74:PRO:HD2	1.75	0.41
10:J:72:VAL:O	10:J:73:ASP:HB2	2.20	0.41
11:K:48:ILE:HG13	11:K:48:ILE:H	1.36	0.41
1:A:1228:C:O3'	13:M:116:THR:HG23	2.20	0.41
13:M:19:LEU:O	13:M:22:ILE:HG13	2.20	0.41
1:A:1030(C):G:C6	1:A:1030(D):A:N1	2.89	0.41
1:A:1228:C:OP1	13:M:115:LYS:NZ	2.39	0.41
1:A:1372:U:N3	1:A:1373:G:C4	2.89	0.41
1:A:262:A:C6	1:A:263:A:C6	3.08	0.41
1:A:413:G:H3'	1:A:413:G:C8	2.55	0.41
1:A:555:C:H2'	1:A:556:C:C6	2.55	0.41
1:A:634:C:H2'	1:A:635:G:H8	1.85	0.41
1:A:7:G:H5'	1:A:298:A:O4'	2.20	0.41
1:A:92:C:O2	1:A:92:C:C2'	2.66	0.41
3:C:149:ALA:O	3:C:169:ALA:HB1	2.20	0.41
3:C:61:ALA:C	3:C:63:ASN:H	2.24	0.41
4:D:110:PHE:CZ	4:D:181:MET:O	2.73	0.41
1:A:620:C:N1	4:D:135:LEU:HD13	2.35	0.41
5:E:12:LEU:HD13	5:E:31:LEU:HB2	2.02	0.41
6:F:4:TYR:CE1	6:F:92:LYS:HB3	2.56	0.41
7:G:61:VAL:HG22	7:G:128:ALA:HB1	2.03	0.41
8:H:2:LEU:HD23	8:H:2:LEU:HA	1.88	0.41
10:J:34:VAL:HG22	10:J:75:ILE:H	1.86	0.41
17:Q:58:GLU:O	17:Q:59:ILE:HD13	2.20	0.41
1:A:1133:G:C2	1:A:1142:G:C2	3.08	0.41
1:A:1320:C:H2'	1:A:1321:C:O4'	2.20	0.41
1:A:1433:A:C8	1:A:1467:G:N2	2.89	0.41
1:A:474:G:H8	1:A:474:G:O5'	2.04	0.41
1:A:517:G:N2	1:A:530:G:OP1	2.50	0.41
1:A:841:U:H3	2:B:37:ASN:HA	1.84	0.41
1:A:938:A:N3	1:A:1376:U:O2'	2.40	0.41
2:B:213:LEU:HD23	2:B:214:ILE:HG12	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:80:ILE:HD12	2:B:80:ILE:N	2.36	0.41
3:C:141:VAL:O	3:C:146:ALA:HB3	2.21	0.41
3:C:72:LYS:HB2	3:C:75:VAL:HG23	2.02	0.41
6:F:6:VAL:HG22	6:F:90:VAL:HG22	2.03	0.41
7:G:135:VAL:HA	7:G:138:LYS:HB3	2.03	0.41
5:E:152:ARG:NE	8:H:44:PHE:CE1	2.89	0.41
8:H:77:GLU:HG2	8:H:78:GLN:N	2.35	0.41
1:A:1251:A:H4'	9:I:12:GLU:OE2	2.21	0.41
12:L:6:THR:OG1	12:L:9:GLN:HG3	2.21	0.41
15:O:76:GLU:O	15:O:77:ARG:C	2.59	0.41
19:S:80:TYR:CE1	19:S:81:ARG:HB3	2.56	0.41
1:A:999:C:O2'	1:A:1000:U:H5'	2.21	0.41
1:A:1003:G:N2	1:A:1039:C:C2	2.89	0.41
1:A:179:A:H2'	1:A:180:U:C6	2.56	0.41
1:A:278:G:OP2	17:Q:41:LYS:NZ	2.44	0.41
1:A:985:C:C4	1:A:1221:G:N2	2.89	0.41
2:B:71:VAL:O	2:B:165:VAL:HG23	2.20	0.41
3:C:71:ALA:CB	3:C:109:PRO:HB3	2.51	0.41
3:C:178:LEU:HA	3:C:178:LEU:HD23	1.69	0.41
3:C:68:VAL:HG12	3:C:70:VAL:HG22	2.03	0.41
11:K:34:ASP:OD1	11:K:38:ASN:N	2.54	0.41
20:T:33:ILE:HD11	20:T:63:ILE:HA	2.03	0.41
1:A:255:G:C2	1:A:272:C:C2	3.08	0.41
2:B:132:LYS:HA	2:B:135:GLN:HB3	2.03	0.41
3:C:8:ILE:HA	3:C:11:ARG:HB2	2.03	0.41
3:C:174:PRO:O	3:C:177:THR:HG23	2.21	0.41
6:F:10:LEU:H	6:F:10:LEU:HD12	1.86	0.41
9:I:116:LYS:HB3	9:I:121:ARG:O	2.20	0.41
9:I:43:ALA:HA	9:I:74:ILE:HD13	2.02	0.41
12:L:41:ARG:HD3	12:L:43:VAL:HG22	2.02	0.41
12:L:98:TYR:CD1	12:L:98:TYR:N	2.88	0.41
15:O:44:LYS:HB3	15:O:44:LYS:HE2	1.82	0.41
17:Q:29:HIS:ND1	17:Q:30:PRO:HD2	2.35	0.41
18:R:47:THR:O	18:R:49:LYS:N	2.54	0.41
19:S:63:THR:HG22	19:S:64:GLU:H	1.86	0.41
1:A:1236:A:OP1	21:U:3:LYS:HG3	2.21	0.41
1:A:1380:U:H1'	1:A:1381:U:OP2	2.21	0.41
1:A:1495:U:H2'	1:A:1496:C:C6	2.56	0.41
1:A:184:G:C4	1:A:185:A:N7	2.89	0.41
1:A:35:G:C6	1:A:36:C:C4	3.09	0.41
1:A:462:G:C6	1:A:463:A:C5	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:409:G:OP1	4:D:24:GLU:O	2.38	0.41
7:G:44:TYR:O	7:G:48:LYS:HG3	2.21	0.41
8:H:63:LEU:N	8:H:63:LEU:HD13	2.36	0.41
10:J:79:ARG:NH2	10:J:82:ILE:HD13	2.36	0.41
13:M:54:VAL:HG22	13:M:57:ARG:NH1	2.32	0.41
1:A:463:A:O2'	16:P:82:GLN:HG2	2.20	0.41
6:F:101:ALA:HA	18:R:28:GLU:HG3	2.03	0.41
18:R:58:LEU:HD23	18:R:58:LEU:HA	1.70	0.41
1:A:1004:A:HO2'	1:A:1005:A:P	2.44	0.40
1:A:1135:U:O2'	1:A:1136:U:H2'	2.21	0.40
1:A:948:C:N4	1:A:1233:G:H1	2.18	0.40
1:A:1251:A:H2'	1:A:1252:A:C8	2.56	0.40
1:A:1261:A:H5''	1:A:1262:C:OP2	2.21	0.40
1:A:1338:G:C6	1:A:1339:A:N6	2.89	0.40
1:A:1402:4OC:H2'	1:A:1403:C:H6	1.83	0.40
1:A:232:G:H2'	1:A:233:C:C6	2.56	0.40
1:A:42:G:H2'	1:A:43:C:O4'	2.20	0.40
1:A:934:C:H42	1:A:938:A:H61	1.69	0.40
6:F:28:ARG:O	6:F:32:ASN:HB2	2.21	0.40
14:N:7:ILE:HG22	14:N:7:ILE:O	2.21	0.40
15:O:42:HIS:O	15:O:46:HIS:HB2	2.20	0.40
17:Q:37:LYS:C	17:Q:38:ARG:HD2	2.41	0.40
17:Q:84:LEU:N	17:Q:84:LEU:HD23	2.36	0.40
19:S:41:VAL:HG23	19:S:43:GLU:HG2	2.01	0.40
1:A:1014:A:H2'	1:A:1015:A:C8	2.57	0.40
1:A:1474:G:H2'	1:A:1475:G:H8	1.80	0.40
1:A:35:G:C5	1:A:36:C:C5	3.09	0.40
1:A:782:A:H2'	1:A:783:C:O4'	2.21	0.40
1:A:991:U:HO2'	1:A:992:U:P	2.45	0.40
3:C:123:GLN:O	3:C:126:ARG:HB2	2.21	0.40
4:D:61:LYS:HD3	4:D:62:GLN:HG2	2.03	0.40
7:G:22:LEU:CD2	7:G:66:VAL:HG21	2.51	0.40
9:I:126:SER:OG	9:I:127:LYS:HD2	2.21	0.40
10:J:53:PRO:HA	14:N:41:ARG:NH2	2.28	0.40
16:P:81:ARG:N	24:P:201:HOH:O	2.53	0.40
17:Q:65:ILE:N	17:Q:65:ILE:HD12	2.36	0.40
1:A:1200:C:H1'	1:A:1204:A:H62	1.86	0.40
1:A:1231:G:H2'	1:A:1232:U:O4'	2.22	0.40
1:A:1263:C:C2	1:A:1273:G:N2	2.89	0.40
8:H:137:VAL:HG12	8:H:138:TRP:N	2.36	0.40
1:A:1202:G:C4	14:N:42:ILE:HD12	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:59:MET:HB2	15:O:59:MET:HE2	1.93	0.40
16:P:60:LEU:HD23	16:P:60:LEU:HA	1.68	0.40
17:Q:59:ILE:CD1	17:Q:73:VAL:HG13	2.51	0.40
1:A:102:G:H2'	1:A:103:C:H6	1.86	0.40
1:A:1157:A:H8	1:A:1158:C:C4	2.39	0.40
1:A:241:C:N4	1:A:285:G:H1	2.20	0.40
1:A:416:G:C5	1:A:417:C:C4	3.10	0.40
1:A:449:C:C5	1:A:450:G:C5	3.09	0.40
1:A:714:G:H2'	1:A:715:A:C8	2.56	0.40
1:A:581:G:O6	1:A:758:G:C8	2.75	0.40
1:A:934:C:N4	1:A:938:A:H61	2.19	0.40
2:B:182:ILE:HA	2:B:183:PRO:HD3	1.98	0.40
3:C:157:ILE:HB	3:C:164:ARG:HH12	1.86	0.40
3:C:172:ARG:NH1	3:C:174:PRO:HG3	2.37	0.40
3:C:50:ALA:HA	3:C:72:LYS:HD3	2.04	0.40
5:E:80:ILE:HA	8:H:104:ARG:NH2	2.36	0.40
9:I:118:LYS:HZ2	9:I:121:ARG:HB3	1.86	0.40
14:N:41:ARG:HA	14:N:44:LEU:HB3	2.03	0.40
15:O:33:THR:OG1	15:O:63:ARG:HD2	2.21	0.40
16:P:43:LYS:HA	16:P:48:TRP:HB3	2.03	0.40
20:T:10:LEU:HD22	20:T:11:SER:H	1.87	0.40
20:T:82:SER:O	20:T:83:ARG:C	2.60	0.40
1:A:1288:A:H2'	1:A:1289:A:C8	2.56	0.40
1:A:1296:C:H4'	1:A:1302:U:C5	2.56	0.40
1:A:1399:C:C2	1:A:1401:G:C5	3.09	0.40
1:A:449:C:H3'	1:A:450:G:H8	1.87	0.40
1:A:778:G:C8	1:A:778:G:O5'	2.73	0.40
1:A:794:A:C6	1:A:795:C:C4	3.10	0.40
1:A:865:A:H8	1:A:865:A:O5'	2.05	0.40
2:B:9:GLU:HG2	2:B:10:LEU:H	1.86	0.40
6:F:40:VAL:HB	6:F:63:TYR:CD1	2.57	0.40
7:G:46:ALA:HB1	7:G:121:ALA:HB2	2.04	0.40
1:A:1367:C:P	10:J:60:ARG:HH21	2.45	0.40
18:R:30:ASP:OD2	18:R:32:ARG:HB3	2.22	0.40
18:R:79:LEU:HD22	18:R:80:PRO:HD2	2.02	0.40
19:S:41:VAL:CG2	19:S:44:MET:HG3	2.41	0.40

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:92:C:O2'	1:A:1338:G:O2'[3_545]	2.18	0.02

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	232/256 (91%)	195 (84%)	33 (14%)	4 (2%)	11	52
3	C	204/239 (85%)	172 (84%)	32 (16%)	0	100	100
4	D	206/209 (99%)	197 (96%)	9 (4%)	0	100	100
5	E	148/162 (91%)	137 (93%)	10 (7%)	1 (1%)	25	68
6	F	99/101 (98%)	93 (94%)	6 (6%)	0	100	100
7	G	153/156 (98%)	139 (91%)	13 (8%)	1 (1%)	25	68
8	H	136/138 (99%)	125 (92%)	11 (8%)	0	100	100
9	I	125/128 (98%)	109 (87%)	15 (12%)	1 (1%)	22	65
10	J	96/105 (91%)	82 (85%)	12 (12%)	2 (2%)	8	47
11	K	114/129 (88%)	104 (91%)	10 (9%)	0	100	100
12	L	121/135 (90%)	111 (92%)	8 (7%)	2 (2%)	11	52
13	M	116/126 (92%)	99 (85%)	17 (15%)	0	100	100
14	N	58/61 (95%)	51 (88%)	7 (12%)	0	100	100
15	O	85/89 (96%)	80 (94%)	4 (5%)	1 (1%)	15	58
16	P	81/88 (92%)	77 (95%)	4 (5%)	0	100	100
17	Q	97/105 (92%)	88 (91%)	9 (9%)	0	100	100
18	R	68/88 (77%)	59 (87%)	9 (13%)	0	100	100
19	S	78/93 (84%)	69 (88%)	7 (9%)	2 (3%)	6	42
20	T	97/106 (92%)	81 (84%)	14 (14%)	2 (2%)	8	47
21	U	22/27 (82%)	19 (86%)	3 (14%)	0	100	100
All	All	2336/2541 (92%)	2087 (89%)	233 (10%)	16 (1%)	25	68

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	21	ARG
7	G	155	ARG
19	S	31	ILE
9	I	119	ALA
10	J	86	MET
12	L	28	LYS
2	B	87	ARG
20	T	73	HIS
2	B	16	HIS
12	L	27	LEU
19	S	14	HIS
10	J	34	VAL
5	E	129	ILE
20	T	88	VAL
2	B	229	VAL
15	O	45	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	202/220 (92%)	153 (76%)	49 (24%)	1	6
3	C	160/188 (85%)	120 (75%)	40 (25%)	1	5
4	D	180/181 (99%)	151 (84%)	29 (16%)	3	19
5	E	115/123 (94%)	84 (73%)	31 (27%)	0	4
6	F	90/90 (100%)	73 (81%)	17 (19%)	2	11
7	G	126/127 (99%)	100 (79%)	26 (21%)	1	9
8	H	119/119 (100%)	95 (80%)	24 (20%)	1	10
9	I	98/99 (99%)	75 (76%)	23 (24%)	1	6
10	J	87/92 (95%)	65 (75%)	22 (25%)	0	5
11	K	88/99 (89%)	77 (88%)	11 (12%)	5	30
12	L	103/110 (94%)	78 (76%)	25 (24%)	1	6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	M	94/101 (93%)	81 (86%)	13 (14%)	4	27
14	N	49/50 (98%)	33 (67%)	16 (33%)	0	2
15	O	79/80 (99%)	59 (75%)	20 (25%)	0	5
16	P	72/74 (97%)	59 (82%)	13 (18%)	2	13
17	Q	94/97 (97%)	80 (85%)	14 (15%)	3	24
18	R	61/77 (79%)	50 (82%)	11 (18%)	2	13
19	S	71/80 (89%)	56 (79%)	15 (21%)	1	9
20	T	76/82 (93%)	63 (83%)	13 (17%)	2	16
21	U	19/22 (86%)	17 (90%)	2 (10%)	8	38
All	All	1983/2111 (94%)	1569 (79%)	414 (21%)	1	9

All (414) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	7	VAL
2	B	8	LYS
2	B	10	LEU
2	B	11	LEU
2	B	12	GLU
2	B	16	HIS
2	B	17	PHE
2	B	23	ARG
2	B	24	TRP
2	B	39	ILE
2	B	53	ARG
2	B	55	PHE
2	B	60	ASP
2	B	61	LEU
2	B	67	THR
2	B	69	LEU
2	B	73	THR
2	B	96	ARG
2	B	108	ILE
2	B	109	SER
2	B	110	GLN
2	B	114	ARG
2	B	119	GLU
2	B	122	PHE
2	B	139	LYS

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Mol	Chain	Res	Type
2	B	142	LEU
2	B	144	ARG
2	B	154	LEU
2	B	155	LEU
2	B	157	ARG
2	B	158	LEU
2	B	163	PHE
2	B	165	VAL
2	B	169	LYS
2	B	170	GLU
2	B	172	ILE
2	B	175	ARG
2	B	178	ARG
2	B	187	LEU
2	B	190	THR
2	B	191	ASP
2	B	196	LEU
2	B	204	ASN
2	B	208	ILE
2	B	212	GLN
2	B	213	LEU
2	B	219	VAL
2	B	223	ILE
2	B	236	TYR
3	C	3	ASN
3	C	8	ILE
3	C	10	PHE
3	C	11	ARG
3	C	17	ASP
3	C	20	SER
3	C	21	ARG
3	C	26	LYS
3	C	31	HIS
3	C	33	LEU
3	C	34	LEU
3	C	38	ARG
3	C	45	LYS
3	C	62	ASP
3	C	64	VAL
3	C	72	LYS
3	C	79	ARG
3	C	85	ARG

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Mol	Chain	Res	Type
3	C	88	ARG
3	C	89	GLU
3	C	90	GLU
3	C	95	THR
3	C	101	LEU
3	C	103	VAL
3	C	107	GLN
3	C	111	LEU
3	C	116	VAL
3	C	139	GLN
3	C	144	SER
3	C	153	VAL
3	C	162	GLN
3	C	167	TRP
3	C	176	HIS
3	C	177	THR
3	C	178	LEU
3	C	188	LEU
3	C	191	THR
3	C	196	LEU
3	C	203	PHE
3	C	204	LEU
4	D	3	ARG
4	D	5	ILE
4	D	9	CYS
4	D	34	GLU
4	D	53	ASP
4	D	59	ARG
4	D	61	LYS
4	D	64	LEU
4	D	73	ARG
4	D	76	ARG
4	D	78	LEU
4	D	85	LYS
4	D	119	GLN
4	D	127	THR
4	D	134	ASP
4	D	135	LEU
4	D	141	ARG
4	D	152	SER
4	D	154	ASN
4	D	163	GLU

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Mol	Chain	Res	Type
4	D	170	VAL
4	D	179	GLU
4	D	186	LEU
4	D	187	ARG
4	D	188	LEU
4	D	192	GLU
4	D	194	LEU
4	D	196	LEU
4	D	198	VAL
5	E	9	LYS
5	E	11	ILE
5	E	12	LEU
5	E	14	ARG
5	E	15	ARG
5	E	16	THR
5	E	18	ARG
5	E	19	MET
5	E	27	ARG
5	E	31	LEU
5	E	41	VAL
5	E	43	LEU
5	E	53	LEU
5	E	56	GLN
5	E	61	TYR
5	E	64	ARG
5	E	68	GLU
5	E	76	ILE
5	E	79	GLU
5	E	80	ILE
5	E	81	GLU
5	E	100	VAL
5	E	111	GLU
5	E	116	THR
5	E	120	THR
5	E	125	SER
5	E	126	ARG
5	E	131	ILE
5	E	148	VAL
5	E	150	ARG
5	E	151	LEU
6	F	7	ASN
6	F	10	LEU

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Mol	Chain	Res	Type
6	F	16	GLN
6	F	17	SER
6	F	21	LEU
6	F	24	GLU
6	F	27	GLN
6	F	28	ARG
6	F	32	ASN
6	F	36	ARG
6	F	40	VAL
6	F	45	LEU
6	F	52	ILE
6	F	74	ASP
6	F	83	ASP
6	F	84	ASN
6	F	86	ARG
7	G	3	ARG
7	G	6	ARG
7	G	9	VAL
7	G	10	ARG
7	G	15	ASP
7	G	21	VAL
7	G	22	LEU
7	G	27	ILE
7	G	38	LEU
7	G	50	ILE
7	G	51	GLN
7	G	53	LYS
7	G	57	GLU
7	G	61	VAL
7	G	62	PHE
7	G	74	GLU
7	G	78	ARG
7	G	92	SER
7	G	94	ARG
7	G	105	VAL
7	G	119	ARG
7	G	125	MET
7	G	126	ASP
7	G	136	LYS
7	G	149	ARG
7	G	155	ARG
8	H	11	THR

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Mol	Chain	Res	Type
8	H	19	VAL
8	H	23	SER
8	H	25	ASP
8	H	29	SER
8	H	30	ARG
8	H	37	ARG
8	H	45	ILE
8	H	51	VAL
8	H	63	LEU
8	H	69	ARG
8	H	83	ILE
8	H	85	ARG
8	H	86	ILE
8	H	88	LYS
8	H	91	ARG
8	H	92	ARG
8	H	95	VAL
8	H	105	ARG
8	H	114	THR
8	H	116	LYS
8	H	120	THR
8	H	127	LEU
8	H	129	VAL
9	I	3	GLN
9	I	5	TYR
9	I	12	GLU
9	I	19	LEU
9	I	20	ARG
9	I	26	VAL
9	I	40	LEU
9	I	53	VAL
9	I	56	LEU
9	I	64	THR
9	I	78	LYS
9	I	79	LEU
9	I	83	ARG
9	I	86	VAL
9	I	91	ASP
9	I	92	TYR
9	I	95	LYS
9	I	99	LEU
9	I	104	ARG

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Mol	Chain	Res	Type
9	I	108	VAL
9	I	109	VAL
9	I	118	LYS
9	I	127	LYS
10	J	8	LEU
10	J	9	ARG
10	J	15	THR
10	J	16	LEU
10	J	23	ILE
10	J	24	VAL
10	J	29	ARG
10	J	40	LEU
10	J	45	ARG
10	J	48	THR
10	J	50	ILE
10	J	54	PHE
10	J	57	LYS
10	J	62	HIS
10	J	66	ARG
10	J	68	HIS
10	J	78	ASN
10	J	79	ARG
10	J	80	LYS
10	J	82	ILE
10	J	83	GLU
10	J	88	LEU
11	K	11	LYS
11	K	12	ARG
11	K	29	ILE
11	K	33	THR
11	K	53	SER
11	K	79	SER
11	K	91	ARG
11	K	95	ILE
11	K	98	LEU
11	K	119	CYS
11	K	126	ARG
12	L	6	THR
12	L	10	LEU
12	L	12	ARG
12	L	18	VAL
12	L	20	LYS

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Mol	Chain	Res	Type
12	L	21	LYS
12	L	23	LYS
12	L	33	ARG
12	L	34	ARG
12	L	37	CYS
12	L	41	ARG
12	L	43	VAL
12	L	47	LYS
12	L	49	ASN
12	L	52	LEU
12	L	60	LEU
12	L	61	THR
12	L	64	TYR
12	L	65	GLU
12	L	79	GLU
12	L	80	HIS
12	L	89	ARG
12	L	112	ASP
12	L	113	ARG
12	L	122	THR
13	M	17	VAL
13	M	27	LYS
13	M	32	GLU
13	M	43	THR
13	M	48	LEU
13	M	53	VAL
13	M	80	ARG
13	M	81	LEU
13	M	87	TYR
13	M	90	LEU
13	M	91	ARG
13	M	93	ARG
13	M	117	VAL
14	N	3	ARG
14	N	6	LEU
14	N	17	LYS
14	N	19	ARG
14	N	21	TYR
14	N	22	THR
14	N	25	VAL
14	N	36	PHE
14	N	39	LEU

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Mol	Chain	Res	Type
14	N	41	ARG
14	N	42	ILE
14	N	45	ARG
14	N	47	LEU
14	N	53	LEU
14	N	57	ARG
14	N	58	LYS
15	O	4	THR
15	O	5	LYS
15	O	7	GLU
15	O	21	ASP
15	O	22	THR
15	O	24	SER
15	O	32	LEU
15	O	34	LEU
15	O	39	LEU
15	O	41	GLU
15	O	45	VAL
15	O	47	LYS
15	O	58	MET
15	O	65	ARG
15	O	70	LEU
15	O	71	GLN
15	O	78	TYR
15	O	82	ILE
15	O	83	GLU
15	O	85	LEU
16	P	2	VAL
16	P	26	ARG
16	P	32	TYR
16	P	33	ILE
16	P	45	THR
16	P	54	GLU
16	P	55	ARG
16	P	62	VAL
16	P	68	ASP
16	P	74	LEU
16	P	79	VAL
16	P	80	PHE
16	P	82	GLN
17	Q	9	VAL
17	Q	25	ARG

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Mol	Chain	Res	Type
17	Q	34	LYS
17	Q	38	ARG
17	Q	41	LYS
17	Q	59	ILE
17	Q	72	ARG
17	Q	73	VAL
17	Q	75	ARG
17	Q	86	GLU
17	Q	87	LYS
17	Q	92	ARG
17	Q	96	GLN
17	Q	98	LEU
18	R	25	THR
18	R	32	ARG
18	R	42	ARG
18	R	47	THR
18	R	53	ARG
18	R	68	LYS
18	R	70	ILE
18	R	82	THR
18	R	84	LYS
18	R	87	ARG
18	R	88	LYS
19	S	6	LYS
19	S	7	LYS
19	S	13	ASP
19	S	15	LEU
19	S	20	LEU
19	S	25	LYS
19	S	27	GLU
19	S	29	ARG
19	S	30	LEU
19	S	31	ILE
19	S	33	THR
19	S	49	ILE
19	S	63	THR
19	S	79	THR
19	S	81	ARG
20	T	19	SER
20	T	24	LEU
20	T	36	LEU
20	T	56	MET

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Mol	Chain	Res	Type
20	T	62	LEU
20	T	70	SER
20	T	72	LEU
20	T	75	ASN
20	T	84	LEU
20	T	91	LEU
20	T	92	LEU
20	T	99	LEU
20	T	100	ILE
21	U	8	THR
21	U	22	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	16	HIS
3	C	37	GLN
9	I	73	GLN
10	J	56	HIS
10	J	62	HIS
11	K	26	ASN
15	O	46	HIS
19	S	14	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1503/1522 (98%)	402 (26%)	0

All (402) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	6	G
1	A	7	G
1	A	8	A
1	A	9	G
1	A	13	U
1	A	22	G
1	A	32	A
1	A	39	G

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Mol	Chain	Res	Type
1	A	41	G
1	A	45	U
1	A	47	C
1	A	48	C
1	A	51	A
1	A	54	C
1	A	66	G
1	A	69	G
1	A	80	G
1	A	81	U
1	A	82	U
1	A	91	C
1	A	92	C
1	A	93	G
1	A	98	U
1	A	99	C
1	A	108	G
1	A	115	G
1	A	116	A
1	A	117	G
1	A	121	C
1	A	129(A)	G
1	A	130	A
1	A	131	C
1	A	132	C
1	A	134	A
1	A	158	G
1	A	159	G
1	A	161	A
1	A	163	C
1	A	167	G
1	A	173	U
1	A	182	U
1	A	183	G
1	A	186	C
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	216	G

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Mol	Chain	Res	Type
1	A	220	G
1	A	226	G
1	A	231	G
1	A	246	A
1	A	247	G
1	A	250	A
1	A	251	G
1	A	252	U
1	A	253	U
1	A	254	G
1	A	266	G
1	A	267	C
1	A	269	C
1	A	273	A
1	A	289	G
1	A	297	G
1	A	301	G
1	A	319	G
1	A	321	A
1	A	328	C
1	A	329	A
1	A	332	G
1	A	344	A
1	A	345	C
1	A	347	G
1	A	350	G
1	A	351	G
1	A	352	C
1	A	353	A
1	A	354	G
1	A	356	A
1	A	367	U
1	A	372	C
1	A	373	A
1	A	374	A
1	A	382	A
1	A	384	G
1	A	388	G
1	A	389	A
1	A	390	C
1	A	392	G
1	A	397	A

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Mol	Chain	Res	Type
1	A	398	C
1	A	406	G
1	A	412	A
1	A	413	G
1	A	414	A
1	A	417	C
1	A	419	C
1	A	420	U
1	A	421	U
1	A	422	C
1	A	428	G
1	A	429	U
1	A	433	C
1	A	435	C
1	A	439	A
1	A	440	A
1	A	452	A
1	A	453	A
1	A	455	C
1	A	457	C
1	A	460	A
1	A	461	C
1	A	481	G
1	A	485	G
1	A	486	U
1	A	488	C
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	519	C
1	A	520	A
1	A	521	G
1	A	527	7MG
1	A	528	C
1	A	531	U
1	A	532	A
1	A	533	A
1	A	536	C

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Mol	Chain	Res	Type
1	A	538	G
1	A	539	A
1	A	547	A
1	A	559	A
1	A	560	U
1	A	562	C
1	A	564	C
1	A	568	G
1	A	572	A
1	A	573	A
1	A	576	G
1	A	577	G
1	A	579	G
1	A	581	G
1	A	588	G
1	A	607	A
1	A	616	G
1	A	620	C
1	A	624	C
1	A	632	A
1	A	653	A
1	A	656	C
1	A	665	A
1	A	666	G
1	A	670	G
1	A	671	G
1	A	686	U
1	A	687	A
1	A	688	G
1	A	693	G
1	A	694	A
1	A	697	U
1	A	701	C
1	A	702	A
1	A	703	G
1	A	722	A
1	A	723	U
1	A	724	G
1	A	731	G
1	A	733	A
1	A	741	G
1	A	748	C

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Mol	Chain	Res	Type
1	A	749	C
1	A	754	C
1	A	755	G
1	A	759	A
1	A	760	G
1	A	777	A
1	A	781	A
1	A	782	A
1	A	792	A
1	A	793	U
1	A	794	A
1	A	795	C
1	A	799	G
1	A	812	C
1	A	813	U
1	A	815	A
1	A	817	C
1	A	818	G
1	A	828	A
1	A	838	G
1	A	839	U
1	A	840	C
1	A	841	U
1	A	848	C
1	A	852	G
1	A	857	C
1	A	858	G
1	A	859	A
1	A	873	A
1	A	874	G
1	A	876	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	938	A
1	A	940	C
1	A	942	G
1	A	944	G
1	A	954	G

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Mol	Chain	Res	Type
1	A	960	U
1	A	961	U
1	A	964	A
1	A	966	M2G
1	A	969	A
1	A	971	G
1	A	974	A
1	A	975	A
1	A	976	G
1	A	977	A
1	A	978	A
1	A	981	U
1	A	982	U
1	A	983	A
1	A	984	C
1	A	988	G
1	A	990	C
1	A	992	U
1	A	993	G
1	A	994	A
1	A	1004	A
1	A	1005	A
1	A	1006	C
1	A	1007	C
1	A	1016	A
1	A	1019	C
1	A	1023	G
1	A	1025	U
1	A	1026	G
1	A	1028	C
1	A	1030(B)	C
1	A	1031	G
1	A	1038	C
1	A	1045	C
1	A	1051	C
1	A	1053	G
1	A	1054	C
1	A	1055	A
1	A	1060	C
1	A	1065	U
1	A	1066	C
1	A	1068	G

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Mol	Chain	Res	Type
1	A	1072	G
1	A	1078	U
1	A	1085	U
1	A	1092	A
1	A	1094	G
1	A	1095	U
1	A	1096	C
1	A	1101	A
1	A	1120	G
1	A	1124	G
1	A	1125	U
1	A	1126	U
1	A	1127	G
1	A	1128	C
1	A	1129	C
1	A	1130	A
1	A	1132	C
1	A	1135	U
1	A	1137	C
1	A	1139	G
1	A	1140	C
1	A	1141	C
1	A	1145	C
1	A	1146	A
1	A	1152	A
1	A	1153	C
1	A	1157	A
1	A	1159	U
1	A	1160	G
1	A	1162	C
1	A	1164	G
1	A	1171	G
1	A	1176	A
1	A	1182	G
1	A	1183	A
1	A	1191	A
1	A	1196	U
1	A	1197	G
1	A	1198	G
1	A	1200	C
1	A	1201	A
1	A	1202	G

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Mol	Chain	Res	Type
1	A	1207	2MG
1	A	1211	U
1	A	1212	U
1	A	1214	C
1	A	1224	G
1	A	1225	A
1	A	1226	C
1	A	1227	A
1	A	1228	C
1	A	1229	A
1	A	1238	A
1	A	1241	G
1	A	1242	C
1	A	1243	C
1	A	1244	C
1	A	1249	C
1	A	1256	A
1	A	1258	G
1	A	1261	A
1	A	1268	A
1	A	1270	C
1	A	1278	U
1	A	1280	A
1	A	1285	A
1	A	1286	A
1	A	1287	A
1	A	1289	A
1	A	1297	C
1	A	1298	C
1	A	1300	G
1	A	1301	U
1	A	1302	U
1	A	1303	C
1	A	1305	G
1	A	1306	A
1	A	1315	U
1	A	1316	G
1	A	1320	C
1	A	1336	C
1	A	1338	G
1	A	1346	A
1	A	1347	G

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Mol	Chain	Res	Type
1	A	1348	U
1	A	1349	A
1	A	1353	G
1	A	1359	C
1	A	1362	C
1	A	1364	U
1	A	1365	G
1	A	1370	G
1	A	1378	C
1	A	1381	U
1	A	1394	A
1	A	1396	A
1	A	1397	C
1	A	1398	A
1	A	1399	C
1	A	1400	5MC
1	A	1406	U
1	A	1408	A
1	A	1411	C
1	A	1412	C
1	A	1414	U
1	A	1415	G
1	A	1416	G
1	A	1417	G
1	A	1418	A
1	A	1419	G
1	A	1430	C
1	A	1437	C
1	A	1442	G
1	A	1443	G
1	A	1446	A
1	A	1447	G
1	A	1451	A
1	A	1452	C
1	A	1453	G
1	A	1454	G
1	A	1459	C
1	A	1475	G
1	A	1479	C
1	A	1487	G
1	A	1489	G
1	A	1490	C

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Mol	Chain	Res	Type
1	A	1491	G
1	A	1492	A
1	A	1493	A
1	A	1497	G
1	A	1498	UR3
1	A	1499	A
1	A	1503	A
1	A	1504	G
1	A	1505	G
1	A	1506	U
1	A	1507	A
1	A	1529	G
1	A	1530	G
1	A	1531	A
1	A	1532	U
1	A	1533	C

There are no RNA pucker outliers to report.

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

17 non-standard protein/DNA/RNA residues are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	2MG	A	1207	1	19,26,27	2.21	4 (21%)	20,38,41	2.02	3 (15%)
1	5MC	A	1400	1	15,22,23	1.39	3 (20%)	17,32,35	1.03	2 (11%)
1	4OC	A	1402	1	16,23,24	1.48	2 (12%)	19,32,35	0.69	0
1	5MC	A	1404	1	15,22,23	1.39	3 (20%)	17,32,35	0.97	1 (5%)
1	5MC	A	1407	1	15,22,23	1.50	3 (20%)	17,32,35	0.81	1 (5%)
1	UR3	A	1498	1,22	14,22,23	1.60	3 (21%)	16,32,35	1.28	1 (6%)
1	MA6	A	1518[A]	1	16,26,27	0.53	0	18,38,41	1.27	2 (11%)
1	MA6	A	1518[B]	1	16,26,27	1.06	2 (12%)	18,38,41	1.00	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MA6	A	1519[A]	1	16,26,27	1.03	2 (12%)	18,38,41	1.38	4 (22%)
1	MA6	A	1519[B]	1	16,26,27	1.26	3 (18%)	18,38,41	0.91	2 (11%)
1	PSU	A	1540	1	16,21,22	0.93	1 (6%)	20,30,33	3.60	5 (25%)
1	PSU	A	1541	1	16,21,22	1.00	1 (6%)	20,30,33	3.52	5 (25%)
1	PSU	A	516	1,22	16,21,22	1.06	1 (6%)	20,30,33	3.36	8 (40%)
1	7MG	A	527	1	20,26,27	2.52	7 (35%)	22,39,42	1.55	6 (27%)
1	M2G	A	966	1	20,27,28	1.93	6 (30%)	21,40,43	1.99	5 (23%)
1	5MC	A	967	1	15,22,23	1.20	3 (20%)	17,32,35	0.91	1 (5%)
12	0TD	L	92	12	5,9,10	2.17	1 (20%)	3,11,13	3.02	2 (66%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	2MG	A	1207	1	-	0/5/27/28	0/3/3/3
1	5MC	A	1400	1	-	0/3/25/26	0/2/2/2
1	4OC	A	1402	1	-	1/7/29/30	0/2/2/2
1	5MC	A	1404	1	-	0/3/25/26	0/2/2/2
1	5MC	A	1407	1	-	0/3/25/26	0/2/2/2
1	UR3	A	1498	1,22	-	0/3/25/26	0/2/2/2
1	MA6	A	1518[A]	1	-	0/7/29/30	0/3/3/3
1	MA6	A	1518[B]	1	-	0/7/29/30	0/3/3/3
1	MA6	A	1519[A]	1	-	0/7/29/30	0/3/3/3
1	MA6	A	1519[B]	1	-	0/7/29/30	0/3/3/3
1	PSU	A	1540	1	-	0/7/25/26	0/2/2/2
1	PSU	A	1541	1	-	0/7/25/26	0/2/2/2
1	PSU	A	516	1,22	-	0/7/25/26	0/2/2/2
1	7MG	A	527	1	-	0/7/37/38	0/3/3/3
1	M2G	A	966	1	-	0/7/29/30	0/3/3/3
1	5MC	A	967	1	-	0/3/25/26	0/2/2/2
12	0TD	L	92	12	-	0/2/12/14	0/0/0/0

All (45) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	527	7MG	C8-N9	-5.99	1.36	1.45
1	A	1498	UR3	C4-N3	-3.98	1.32	1.38
1	A	527	7MG	CM7-N7	-2.86	1.41	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1498	UR3	C6-N1	-2.77	1.32	1.35
1	A	967	5MC	O5'-C5'	-2.55	1.41	1.44
1	A	1404	5MC	O5'-C5'	-2.35	1.41	1.44
1	A	1402	4OC	O5'-C5'	-2.31	1.41	1.44
1	A	966	M2G	O5'-C5'	-2.31	1.41	1.44
1	A	967	5MC	C6-C5	-2.20	1.34	1.40
1	A	527	7MG	C2-N3	-2.14	1.31	1.35
1	A	1207	2MG	O5'-C5'	-2.13	1.41	1.44
1	A	1498	UR3	C3U-N3	-2.11	1.42	1.47
1	A	1400	5MC	C4-N3	2.01	1.38	1.35
1	A	1207	2MG	C2-N1	2.02	1.41	1.34
1	A	967	5MC	C5-C4	2.05	1.44	1.41
1	A	1407	5MC	C2-N3	2.08	1.42	1.38
1	A	966	M2G	C2-N1	2.09	1.38	1.34
1	A	1519[A]	MA6	C5-C4	2.12	1.45	1.40
1	A	1519[B]	MA6	C2-N3	2.23	1.35	1.32
1	A	1519[B]	MA6	C5-C4	2.25	1.45	1.40
1	A	1518[B]	MA6	C2-N1	2.25	1.38	1.33
1	A	1404	5MC	C2-N3	2.35	1.42	1.38
1	A	1518[B]	MA6	C4-N3	2.48	1.39	1.35
1	A	1400	5MC	C5-C4	2.52	1.45	1.41
1	A	527	7MG	C6-N1	2.52	1.37	1.33
1	A	966	M2G	C6-C5	2.60	1.46	1.41
1	A	516	PSU	C4-N3	2.70	1.37	1.33
1	A	1519[A]	MA6	C2-N1	2.74	1.39	1.33
1	A	1402	4OC	CM4-N4	2.75	1.50	1.45
1	A	1407	5MC	C4-N4	2.82	1.41	1.34
1	A	1404	5MC	C5-C4	2.91	1.45	1.41
1	A	1540	PSU	C4-N3	2.96	1.38	1.33
1	A	1519[B]	MA6	C2-N1	3.06	1.39	1.33
1	A	1400	5MC	C2-N3	3.10	1.44	1.38
1	A	1541	PSU	C4-N3	3.16	1.38	1.33
1	A	966	M2G	C2-N2	3.37	1.40	1.34
1	A	527	7MG	C4-N3	3.48	1.38	1.34
1	A	1407	5MC	C5-C4	3.71	1.46	1.41
1	A	527	7MG	C2-N2	3.97	1.42	1.34
1	A	966	M2G	C4-N3	4.28	1.42	1.35
1	A	966	M2G	C6-N1	4.38	1.41	1.33
12	L	92	0TD	CA-C	4.44	1.56	1.50
1	A	1207	2MG	C6-N1	5.75	1.43	1.33
1	A	527	7MG	C6-C5	6.12	1.48	1.41
1	A	1207	2MG	C2-N2	6.67	1.39	1.34

All (49) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1541	PSU	N1-C2-N3	-12.20	119.63	128.40
1	A	1540	PSU	N1-C2-N3	-11.90	119.84	128.40
1	A	516	PSU	N1-C2-N3	-10.54	120.82	128.40
1	A	1207	2MG	C5-C6-N1	-7.33	113.04	123.48
1	A	516	PSU	C5-C4-N3	-7.17	119.55	125.43
1	A	1540	PSU	C5-C4-N3	-6.94	119.73	125.43
1	A	966	M2G	C5-C6-N1	-6.26	114.57	123.48
1	A	1541	PSU	C5-C4-N3	-6.26	120.30	125.43
12	L	92	0TD	CSB-SB-CB	-4.47	93.27	101.60
1	A	527	7MG	C4-N9-C1'	-3.04	119.22	126.58
1	A	516	PSU	C5-C6-N1	-2.95	120.56	124.39
1	A	527	7MG	C5-C4-N3	-2.91	121.62	126.47
1	A	527	7MG	C5-C6-N1	-2.60	119.29	123.37
1	A	516	PSU	O4'-C1'-C5	-2.52	106.03	109.93
1	A	1540	PSU	C5-C6-N1	-2.49	121.16	124.39
1	A	1541	PSU	C5-C6-N1	-2.40	121.28	124.39
1	A	1518[A]	MA6	N1-C6-N6	-2.36	114.50	117.00
1	A	966	M2G	N1-C2-N2	-2.27	114.82	117.16
12	L	92	0TD	O-C-CA	-2.26	119.87	125.15
1	A	1407	5MC	N4-C4-N3	-2.17	113.79	117.00
1	A	1498	UR3	C5-C4-N3	-2.16	112.91	117.34
1	A	967	5MC	N4-C4-N3	-2.14	113.84	117.00
1	A	1519[A]	MA6	C1'-N9-C4	-2.11	122.99	126.64
1	A	516	PSU	C5-C1'-C2'	-2.10	111.92	115.55
1	A	1404	5MC	N4-C4-N3	-2.00	114.05	117.00
1	A	527	7MG	N3-C4-N9	2.01	129.55	126.98
1	A	527	7MG	C2-N3-C4	2.07	119.78	113.95
1	A	1400	5MC	C5-C4-N3	2.08	124.58	121.22
1	A	1519[B]	MA6	C2-N1-C6	2.08	116.93	111.82
1	A	966	M2G	CM2-N2-C2	2.10	123.34	121.34
1	A	1518[B]	MA6	C2-N1-C6	2.12	117.01	111.82
1	A	1519[B]	MA6	N3-C2-N1	2.13	130.72	128.86
1	A	1519[A]	MA6	C5-C6-N6	2.22	127.55	122.58
1	A	527	7MG	N2-C2-N1	2.28	120.88	117.24
1	A	1400	5MC	CM5-C5-C6	2.31	123.29	118.67
1	A	966	M2G	N3-C2-N2	2.31	119.54	117.15
1	A	516	PSU	O4'-C1'-C2'	2.33	108.19	104.45
1	A	1518[A]	MA6	C2-N1-C6	2.46	117.86	111.82
1	A	1519[A]	MA6	C2-N1-C6	2.56	118.11	111.82
1	A	516	PSU	C6-N1-C2	2.62	119.56	115.36
1	A	1207	2MG	C4-C5-N7	2.87	112.18	109.41
1	A	1519[A]	MA6	N3-C2-N1	2.98	131.46	128.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1540	PSU	C6-N1-C2	3.24	120.55	115.36
1	A	1541	PSU	C6-N1-C2	3.33	120.68	115.36
1	A	1207	2MG	C6-N1-C2	3.66	121.73	115.18
1	A	966	M2G	C6-N1-C2	5.06	122.20	116.18
1	A	516	PSU	C4-N3-C2	5.12	119.64	115.16
1	A	1541	PSU	C4-N3-C2	5.72	120.16	115.16
1	A	1540	PSU	C4-N3-C2	5.98	120.39	115.16

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	1402	4OC	N3-C4-N4-CM4

There are no ring outliers.

11 monomers are involved in 24 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1400	5MC	1	0
1	A	1402	4OC	4	0
1	A	1404	5MC	1	0
1	A	1498	UR3	5	0
1	A	1518[A]	MA6	2	0
1	A	1518[B]	MA6	3	0
1	A	1519[A]	MA6	3	0
1	A	1519[B]	MA6	2	0
1	A	966	M2G	3	0
1	A	967	5MC	6	0
12	L	92	0TD	2	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 291 ligands modelled in this entry, 291 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	1498/1522 (98%)	-0.28	35 (2%) 61 43	85, 156, 308, 384	0
2	B	234/256 (91%)	-0.64	0 100 100	105, 165, 249, 269	0
3	C	206/239 (86%)	-0.06	11 (5%) 27 17	164, 235, 290, 329	0
4	D	208/209 (99%)	-0.52	3 (1%) 75 60	99, 159, 211, 239	0
5	E	150/162 (92%)	-0.68	0 100 100	79, 122, 163, 194	0
6	F	101/101 (100%)	-0.78	0 100 100	130, 175, 208, 240	0
7	G	155/156 (99%)	-0.36	6 (3%) 40 26	150, 203, 269, 323	0
8	H	138/138 (100%)	-0.72	0 100 100	74, 108, 152, 181	0
9	I	127/128 (99%)	-0.43	2 (1%) 72 56	173, 226, 272, 298	0
10	J	98/105 (93%)	-0.23	3 (3%) 49 33	194, 237, 302, 326	0
11	K	116/129 (89%)	-0.71	0 100 100	111, 146, 197, 222	0
12	L	123/135 (91%)	-0.57	1 (0%) 86 74	79, 155, 195, 227	0
13	M	118/126 (93%)	-0.27	6 (5%) 29 18	139, 190, 229, 290	0
14	N	60/61 (98%)	-0.15	2 (3%) 47 32	185, 222, 274, 306	0
15	O	87/89 (97%)	-0.72	0 100 100	92, 132, 179, 209	0
16	P	83/88 (94%)	-0.59	0 100 100	110, 146, 187, 230	0
17	Q	99/105 (94%)	-0.82	0 100 100	95, 125, 176, 185	0
18	R	70/88 (79%)	-0.69	0 100 100	107, 145, 200, 231	0
19	S	80/93 (86%)	0.03	0 100 100	197, 254, 313, 320	0
20	T	99/106 (93%)	-0.74	0 100 100	112, 149, 204, 232	0
21	U	24/27 (88%)	0.22	0 100 100	169, 204, 229, 239	0
All	All	3874/4063 (95%)	-0.41	69 (1%) 69 52	74, 166, 278, 384	0

All (69) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1018	C	8.4
1	A	1036	G	7.0
3	C	65	ALA	6.9
1	A	993	G	6.4
1	A	1017	G	5.7
1	A	1129	C	5.7
1	A	1037	C	5.4
13	M	118	ALA	5.3
1	A	1050	G	5.3
1	A	1006	C	5.1
1	A	1019	C	5.0
3	C	193	TYR	4.9
3	C	102	ASN	4.6
1	A	1005	A	4.5
3	C	146	ALA	4.2
10	J	90	LEU	3.9
1	A	985	C	3.6
14	N	4	LYS	3.6
3	C	104	GLN	3.6
3	C	103	VAL	3.5
3	C	145	GLY	3.4
10	J	99	LYS	3.4
7	G	5	ARG	3.3
1	A	1001	A	3.3
7	G	154	TYR	3.2
7	G	156	TRP	3.2
13	M	7	VAL	3.1
13	M	117	VAL	3.1
14	N	5	ALA	3.1
1	A	1002	G	3.1
1	A	1213	A	3.1
1	A	1533	C	3.1
3	C	46	GLU	3.1
13	M	65	LYS	3.0
7	G	8	GLU	3.0
1	A	1411	C	2.9
7	G	2	ALA	2.9
1	A	1532	U	2.9
7	G	72	ARG	2.8
1	A	1321	C	2.8
1	A	1215	G	2.7
1	A	1531	A	2.6
1	A	1047	G	2.6

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Mol	Chain	Res	Type	RSRZ
9	I	128	ARG	2.5
1	A	1003(A)	G	2.4
1	A	1004	A	2.4
1	A	81	U	2.4
1	A	1030	C	2.4
1	A	984	C	2.3
1	A	202	U	2.3
3	C	66	VAL	2.3
1	A	74	C	2.3
10	J	100	THR	2.2
1	A	994	A	2.2
1	A	1020	U	2.2
3	C	100	ALA	2.2
13	M	119	GLY	2.2
4	D	9	CYS	2.2
3	C	87	LEU	2.2
1	A	1048	G	2.1
4	D	114	ARG	2.1
13	M	100	GLY	2.1
1	A	1000	U	2.1
1	A	1417	G	2.1
1	A	1016	A	2.1
9	I	126	SER	2.1
1	A	1255	G	2.1
12	L	114	LYS	2.0
4	D	30	LYS	2.0

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
1	7MG	A	527	24/25	0.97	0.12	-	116,135,155,161	0
1	PSU	A	516	20/21	0.95	0.12	-	162,181,197,197	0
1	MA6	A	1518[A]	24/25	0.98	0.21	-	118,131,141,143	24
1	MA6	A	1519[B]	24/25	0.97	0.22	-	106,118,129,130	24
1	MA6	A	1518[B]	24/25	0.98	0.21	-	126,135,138,138	24

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
12	0TD	L	92	10/11	0.96	0.24	-	157,170,178,331	0
1	5MC	A	1400	21/22	0.94	0.16	-	114,142,154,174	0
1	PSU	A	1540	20/21	0.89	0.35	-	271,280,285,287	0
1	5MC	A	1404	21/22	0.94	0.22	-	112,135,164,183	0
1	5MC	A	967	21/22	0.95	0.12	-	162,170,190,199	0
1	4OC	A	1402	22/23	0.95	0.22	-	124,137,170,187	0
1	M2G	A	966	25/26	0.93	0.15	-	165,177,184,186	0
1	5MC	A	1407	21/22	0.96	0.10	-	149,172,180,188	0
1	2MG	A	1207	24/25	0.91	0.27	-	263,291,297,309	0
1	PSU	A	1541	20/21	0.90	0.23	-	223,263,279,284	0
1	MA6	A	1519[A]	24/25	0.97	0.22	-	109,115,125,137	24
1	UR3	A	1498	21/22	0.96	0.20	-	117,143,151,155	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
22	MG	A	1842	1/1	0.91	0.57	36.46	244,244,244,244	0
22	MG	A	1714	1/1	0.93	0.78	28.37	116,116,116,116	0
22	MG	A	1822	1/1	0.96	0.74	19.16	333,333,333,333	0
22	MG	A	1845	1/1	0.82	0.71	12.49	106,106,106,106	0
22	MG	A	1863	1/1	0.75	0.43	9.06	103,103,103,103	0
22	MG	A	1846	1/1	0.83	0.44	7.56	131,131,131,131	0
22	MG	A	1645	1/1	0.98	0.52	6.43	132,132,132,132	0
22	MG	A	1649	1/1	0.89	0.33	5.43	145,145,145,145	0
22	MG	B	301	1/1	0.95	0.65	5.21	154,154,154,154	0
22	MG	A	1730	1/1	0.98	0.25	4.86	107,107,107,107	0
22	MG	D	302	1/1	0.88	0.38	4.83	142,142,142,142	0
22	MG	A	1718	1/1	0.97	0.32	4.51	96,96,96,96	0
22	MG	A	1642	1/1	0.99	0.21	4.17	176,176,176,176	0
22	MG	A	1781	1/1	0.97	0.28	3.67	116,116,116,116	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
22	MG	Q	201	1/1	0.74	0.41	3.60	140,140,140,140	0
22	MG	T	202	1/1	0.92	0.29	3.40	96,96,96,96	0
22	MG	A	1711	1/1	0.86	0.28	3.11	85,85,85,85	0
22	MG	A	1834	1/1	0.97	0.28	2.76	232,232,232,232	0
22	MG	A	1775	1/1	0.96	0.21	2.56	101,101,101,101	0
22	MG	A	1809	1/1	0.98	0.28	2.50	330,330,330,330	0
22	MG	A	1727	1/1	0.92	0.41	2.34	178,178,178,178	0
22	MG	A	1615	1/1	0.98	0.19	2.32	86,86,86,86	0
22	MG	A	1759	1/1	0.95	0.19	2.18	98,98,98,98	0
22	MG	A	1824	1/1	0.94	0.22	2.03	435,435,435,435	0
22	MG	A	1765	1/1	0.96	0.23	1.69	390,390,390,390	0
22	MG	A	1604	1/1	0.99	0.17	1.54	141,141,141,141	0
22	MG	A	1721	1/1	0.97	0.20	1.49	128,128,128,128	0
22	MG	A	1780	1/1	0.94	0.21	1.43	162,162,162,162	0
22	MG	A	1771	1/1	0.94	0.23	1.41	158,158,158,158	0
22	MG	A	1866	1/1	0.96	0.29	1.38	149,149,149,149	0
22	MG	A	1712	1/1	0.94	0.23	1.30	103,103,103,103	0
22	MG	A	1734	1/1	0.96	0.18	1.20	99,99,99,99	0
22	MG	A	1706	1/1	0.98	0.22	1.00	151,151,151,151	0
22	MG	A	1753	1/1	0.92	0.27	0.92	169,169,169,169	0
22	MG	A	1683	1/1	0.99	0.15	0.78	237,237,237,237	0
22	MG	B	302	1/1	0.97	0.24	0.67	166,166,166,166	0
22	MG	A	1610	1/1	0.99	0.18	0.56	110,110,110,110	0
22	MG	A	1657	1/1	0.98	0.19	0.55	124,124,124,124	0
22	MG	A	1622	1/1	0.99	0.19	0.37	75,75,75,75	0
22	MG	A	1616	1/1	0.99	0.19	0.37	79,79,79,79	0
22	MG	C	302	1/1	0.99	0.22	0.23	163,163,163,163	0
22	MG	A	1638	1/1	0.99	0.18	0.17	124,124,124,124	0
22	MG	A	1772	1/1	0.92	0.27	0.10	126,126,126,126	0
22	MG	A	1697	1/1	0.95	0.21	0.08	139,139,139,139	0
22	MG	J	201	1/1	0.94	0.20	0.06	497,497,497,497	0
22	MG	A	1702	1/1	0.94	0.11	-0.23	322,322,322,322	0
23	ZN	D	301	1/1	0.98	0.33	-0.44	127,127,127,127	0
22	MG	A	1722	1/1	0.98	0.15	-0.44	129,129,129,129	0
23	ZN	N	101	1/1	0.97	0.15	-0.45	395,395,395,395	0
22	MG	C	301	1/1	0.96	0.14	-0.55	150,150,150,150	0
22	MG	A	1760	1/1	0.98	0.14	-0.61	137,137,137,137	0
22	MG	A	1705	1/1	0.96	0.16	-0.62	118,118,118,118	0
22	MG	A	1833	1/1	0.97	0.14	-0.64	450,450,450,450	0
22	MG	A	1700	1/1	0.87	0.22	-0.95	438,438,438,438	0
22	MG	A	1690	1/1	0.93	0.14	-1.35	160,160,160,160	0
22	MG	A	1630	1/1	0.99	0.12	-1.38	129,129,129,129	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
22	MG	D	303	1/1	0.75	0.10	-1.45	141,141,141,141	0
22	MG	A	1684	1/1	0.98	0.09	-1.81	128,128,128,128	0
22	MG	A	1752	1/1	0.98	0.09	-2.18	90,90,90,90	0
22	MG	A	1633	1/1	0.97	0.09	-2.66	105,105,105,105	0
22	MG	A	1699	1/1	0.98	0.09	-4.01	117,117,117,117	0
22	MG	A	1652	1/1	0.97	0.12	-	126,126,126,126	0
22	MG	A	1831	1/1	0.97	0.26	-	191,191,191,191	0
22	MG	A	1611	1/1	0.95	0.07	-	182,182,182,182	0
22	MG	A	1607	1/1	0.96	0.04	-	165,165,165,165	0
22	MG	A	1713	1/1	0.89	0.28	-	106,106,106,106	0
22	MG	A	1602	1/1	0.98	0.47	-	168,168,168,168	0
22	MG	A	1821	1/1	0.97	0.37	-	399,399,399,399	0
22	MG	A	1789	1/1	0.92	0.14	-	174,174,174,174	0
22	MG	A	1673	1/1	0.97	0.20	-	130,130,130,130	0
22	MG	D	304	1/1	0.74	0.11	-	106,106,106,106	0
22	MG	A	1627	1/1	0.97	0.14	-	96,96,96,96	0
22	MG	A	1766	1/1	0.97	0.14	-	282,282,282,282	0
22	MG	A	1614	1/1	0.99	0.17	-	152,152,152,152	0
22	MG	A	1756	1/1	0.94	0.30	-	140,140,140,140	0
22	MG	A	1674	1/1	0.98	0.04	-	168,168,168,168	0
22	MG	A	1758	1/1	0.92	0.32	-	107,107,107,107	0
22	MG	A	1641	1/1	0.98	0.36	-	78,78,78,78	0
22	MG	A	1794	1/1	0.98	0.34	-	422,422,422,422	0
22	MG	A	1733	1/1	0.97	0.16	-	91,91,91,91	0
22	MG	A	1768	1/1	0.87	0.57	-	118,118,118,118	0
22	MG	A	1783	1/1	0.87	0.38	-	133,133,133,133	0
22	MG	A	1848	1/1	0.94	0.06	-	166,166,166,166	0
22	MG	F	201	1/1	0.97	0.60	-	149,149,149,149	0
22	MG	A	1837	1/1	0.94	0.35	-	226,226,226,226	0
22	MG	A	1836	1/1	0.97	0.35	-	231,231,231,231	0
22	MG	A	1640	1/1	0.83	0.36	-	111,111,111,111	0
22	MG	A	1665	1/1	0.93	0.13	-	117,117,117,117	0
22	MG	A	1808	1/1	0.99	0.21	-	278,278,278,278	0
22	MG	A	1773	1/1	0.95	0.13	-	164,164,164,164	0
22	MG	A	1830	1/1	0.98	0.10	-	199,199,199,199	0
22	MG	A	1679	1/1	0.93	0.62	-	177,177,177,177	0
22	MG	A	1813	1/1	0.90	0.31	-	210,210,210,210	0
22	MG	A	1646	1/1	0.85	0.32	-	143,143,143,143	0
22	MG	A	1680	1/1	0.93	0.28	-	139,139,139,139	0
22	MG	A	1606	1/1	0.99	0.08	-	114,114,114,114	0
22	MG	A	1791	1/1	0.94	0.15	-	160,160,160,160	0
22	MG	A	1698	1/1	0.98	0.17	-	192,192,192,192	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
22	MG	A	1732	1/1	0.99	0.18	-	134,134,134,134	0
22	MG	A	1608	1/1	0.94	0.52	-	127,127,127,127	0
22	MG	A	1854	1/1	0.82	0.25	-	94,94,94,94	0
22	MG	A	1835	1/1	0.97	0.20	-	317,317,317,317	0
22	MG	A	1774	1/1	0.79	0.13	-	134,134,134,134	0
22	MG	A	1763	1/1	0.92	0.19	-	240,240,240,240	0
22	MG	A	1659	1/1	0.85	0.53	-	95,95,95,95	0
22	MG	M	201	1/1	0.92	0.74	-	388,388,388,388	0
22	MG	A	1852	1/1	0.95	0.37	-	121,121,121,121	0
22	MG	A	1865	1/1	0.90	0.29	-	120,120,120,120	0
22	MG	A	1660	1/1	0.99	0.07	-	129,129,129,129	0
22	MG	A	1747	1/1	0.98	0.17	-	137,137,137,137	0
22	MG	A	1639	1/1	0.94	0.16	-	173,173,173,173	0
22	MG	A	1670	1/1	0.98	0.12	-	129,129,129,129	0
22	MG	A	1637	1/1	0.94	0.15	-	329,329,329,329	0
22	MG	A	1816	1/1	0.60	0.50	-	170,170,170,170	0
22	MG	A	1744	1/1	0.88	0.13	-	151,151,151,151	0
22	MG	A	1856	1/1	0.58	0.34	-	108,108,108,108	0
22	MG	A	1613	1/1	0.98	0.11	-	117,117,117,117	0
22	MG	A	1818	1/1	0.91	0.46	-	247,247,247,247	0
22	MG	A	1827	1/1	0.97	0.26	-	148,148,148,148	0
22	MG	A	1666	1/1	0.98	0.13	-	147,147,147,147	0
22	MG	A	1797	1/1	0.77	0.48	-	367,367,367,367	0
22	MG	A	1668	1/1	0.90	0.17	-	111,111,111,111	0
22	MG	A	1694	1/1	0.96	0.28	-	376,376,376,376	0
22	MG	A	1716	1/1	0.98	0.11	-	95,95,95,95	0
22	MG	A	1742	1/1	0.75	0.25	-	132,132,132,132	0
22	MG	A	1715	1/1	0.96	0.45	-	148,148,148,148	0
22	MG	A	1755	1/1	0.93	0.24	-	131,131,131,131	0
22	MG	A	1820	1/1	0.80	0.29	-	495,495,495,495	0
22	MG	A	1625	1/1	0.87	0.21	-	214,214,214,214	0
22	MG	A	1858	1/1	0.84	0.36	-	90,90,90,90	0
22	MG	A	1799	1/1	0.96	0.12	-	287,287,287,287	0
22	MG	A	1749	1/1	0.95	0.30	-	121,121,121,121	0
22	MG	T	201	1/1	0.92	0.19	-	155,155,155,155	0
22	MG	A	1729	1/1	0.90	0.59	-	120,120,120,120	0
22	MG	A	1785	1/1	0.95	0.35	-	394,394,394,394	0
22	MG	A	1736	1/1	0.91	0.28	-	99,99,99,99	0
22	MG	A	1671	1/1	0.86	0.23	-	162,162,162,162	0
22	MG	A	1620	1/1	0.98	0.25	-	136,136,136,136	0
22	MG	A	1628	1/1	0.97	0.28	-	69,69,69,69	0
22	MG	A	1605	1/1	0.97	0.22	-	102,102,102,102	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
22	MG	A	1825	1/1	0.97	0.19	-	404,404,404,404	0
22	MG	A	1726	1/1	0.74	0.50	-	106,106,106,106	0
22	MG	A	1682	1/1	0.97	0.45	-	137,137,137,137	0
22	MG	A	1807	1/1	0.72	0.27	-	141,141,141,141	0
22	MG	A	1738	1/1	0.96	0.32	-	102,102,102,102	0
22	MG	A	1741	1/1	0.96	0.16	-	111,111,111,111	0
22	MG	A	1853	1/1	0.73	0.15	-	91,91,91,91	0
22	MG	A	1651	1/1	0.99	0.14	-	173,173,173,173	0
22	MG	A	1709	1/1	0.95	0.17	-	165,165,165,165	0
22	MG	A	1740	1/1	0.96	0.14	-	107,107,107,107	0
22	MG	A	1707	1/1	0.93	0.57	-	120,120,120,120	0
22	MG	A	1805	1/1	0.68	0.23	-	153,153,153,153	0
22	MG	A	1847	1/1	0.95	0.56	-	145,145,145,145	0
22	MG	A	1757	1/1	0.96	0.17	-	123,123,123,123	0
22	MG	A	1720	1/1	0.87	0.34	-	109,109,109,109	0
22	MG	A	1728	1/1	0.95	0.23	-	129,129,129,129	0
22	MG	A	1704	1/1	0.91	0.56	-	118,118,118,118	0
22	MG	A	1719	1/1	0.98	0.11	-	143,143,143,143	0
22	MG	A	1623	1/1	0.82	0.35	-	125,125,125,125	0
22	MG	A	1681	1/1	1.00	0.14	-	162,162,162,162	0
22	MG	A	1653	1/1	0.98	0.09	-	118,118,118,118	0
22	MG	A	1691	1/1	0.94	0.20	-	136,136,136,136	0
22	MG	A	1802	1/1	0.90	0.21	-	137,137,137,137	0
22	MG	A	1735	1/1	0.78	0.22	-	114,114,114,114	0
22	MG	A	1654	1/1	0.93	0.17	-	117,117,117,117	0
22	MG	A	1644	1/1	0.94	0.21	-	253,253,253,253	0
22	MG	A	1678	1/1	0.90	0.23	-	143,143,143,143	0
22	MG	A	1754	1/1	0.96	0.13	-	107,107,107,107	0
22	MG	A	1761	1/1	0.93	0.38	-	156,156,156,156	0
22	MG	A	1855	1/1	0.92	0.20	-	139,139,139,139	0
22	MG	Q	202	1/1	0.81	0.36	-	105,105,105,105	0
22	MG	A	1618	1/1	0.80	0.43	-	125,125,125,125	0
22	MG	A	1844	1/1	0.99	0.16	-	276,276,276,276	0
22	MG	A	1693	1/1	-0.03	0.25	-	146,146,146,146	0
22	MG	A	1703	1/1	0.79	0.38	-	138,138,138,138	0
22	MG	D	305	1/1	0.85	1.11	-	122,122,122,122	0
22	MG	A	1859	1/1	0.72	0.59	-	132,132,132,132	0
22	MG	A	1662	1/1	0.99	0.13	-	144,144,144,144	0
22	MG	A	1617	1/1	0.98	0.17	-	97,97,97,97	0
22	MG	A	1656	1/1	0.87	0.61	-	133,133,133,133	0
22	MG	A	1779	1/1	0.63	0.33	-	159,159,159,159	0
22	MG	A	1619	1/1	0.99	0.25	-	95,95,95,95	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
22	MG	A	1777	1/1	0.92	0.12	-	93,93,93,93	0
22	MG	A	1663	1/1	0.97	0.14	-	148,148,148,148	0
22	MG	A	1796	1/1	0.82	1.11	-	383,383,383,383	0
22	MG	A	1851	1/1	0.79	0.41	-	126,126,126,126	0
22	MG	A	1689	1/1	0.88	0.13	-	238,238,238,238	0
22	MG	A	1737	1/1	0.93	0.25	-	142,142,142,142	0
22	MG	A	1632	1/1	0.99	0.29	-	231,231,231,231	0
22	MG	A	1810	1/1	0.97	0.07	-	122,122,122,122	0
22	MG	A	1840	1/1	0.79	0.14	-	149,149,149,149	0
22	MG	A	1603	1/1	0.92	0.32	-	111,111,111,111	0
22	MG	A	1688	1/1	0.93	0.51	-	113,113,113,113	0
22	MG	A	1686	1/1	0.93	0.35	-	124,124,124,124	0
22	MG	A	1770	1/1	0.95	0.13	-	166,166,166,166	0
22	MG	A	1806	1/1	0.92	0.10	-	408,408,408,408	0
22	MG	A	1731	1/1	0.93	0.47	-	103,103,103,103	0
22	MG	A	1624	1/1	0.90	0.65	-	68,68,68,68	0
22	MG	A	1643	1/1	0.98	0.17	-	102,102,102,102	0
22	MG	A	1843	1/1	0.91	0.21	-	163,163,163,163	0
22	MG	A	1710	1/1	0.89	0.19	-	162,162,162,162	0
22	MG	A	1717	1/1	0.87	0.31	-	146,146,146,146	0
22	MG	A	1857	1/1	0.88	0.20	-	115,115,115,115	0
22	MG	A	1782	1/1	0.69	0.51	-	144,144,144,144	0
22	MG	A	1787	1/1	0.87	0.23	-	140,140,140,140	0
22	MG	A	1814	1/1	0.99	0.21	-	224,224,224,224	0
22	MG	A	1725	1/1	0.83	0.33	-	142,142,142,142	0
22	MG	A	1669	1/1	0.93	0.20	-	145,145,145,145	0
22	MG	A	1708	1/1	0.98	0.10	-	113,113,113,113	0
22	MG	P	102	1/1	0.66	0.40	-	128,128,128,128	0
22	MG	A	1677	1/1	0.80	0.33	-	125,125,125,125	0
22	MG	A	1800	1/1	0.90	0.20	-	389,389,389,389	0
22	MG	A	1621	1/1	0.95	0.18	-	118,118,118,118	0
22	MG	A	1795	1/1	0.91	0.37	-	253,253,253,253	0
22	MG	A	1798	1/1	0.98	0.33	-	208,208,208,208	0
22	MG	A	1823	1/1	0.71	0.30	-	168,168,168,168	0
22	MG	A	1860	1/1	0.95	0.17	-	115,115,115,115	0
22	MG	A	1751	1/1	0.76	1.45	-	136,136,136,136	0
22	MG	A	1838	1/1	0.91	0.23	-	386,386,386,386	0
22	MG	A	1724	1/1	0.91	0.53	-	146,146,146,146	0
22	MG	A	1675	1/1	0.98	0.27	-	275,275,275,275	0
22	MG	A	1784	1/1	0.93	0.34	-	318,318,318,318	0
22	MG	A	1828	1/1	0.92	0.40	-	156,156,156,156	0
22	MG	A	1626	1/1	0.83	0.60	-	150,150,150,150	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
22	MG	A	1867	1/1	0.89	0.49	-	139,139,139,139	0
22	MG	A	1672	1/1	0.46	0.94	-	130,130,130,130	0
22	MG	A	1701	1/1	0.98	0.16	-	216,216,216,216	0
22	MG	A	1692	1/1	0.96	0.12	-	167,167,167,167	0
22	MG	A	1746	1/1	0.83	0.38	-	126,126,126,126	0
22	MG	A	1778	1/1	0.89	0.12	-	137,137,137,137	0
22	MG	A	1636	1/1	0.97	0.46	-	112,112,112,112	0
22	MG	A	1829	1/1	0.78	0.63	-	286,286,286,286	0
22	MG	A	1804	1/1	0.92	0.23	-	305,305,305,305	0
22	MG	A	1786	1/1	0.80	0.35	-	234,234,234,234	0
22	MG	A	1739	1/1	0.87	0.37	-	126,126,126,126	0
22	MG	E	201	1/1	0.97	0.17	-	152,152,152,152	0
22	MG	A	1635	1/1	0.95	0.39	-	151,151,151,151	0
22	MG	A	1767	1/1	0.91	0.11	-	184,184,184,184	0
22	MG	A	1609	1/1	0.92	0.36	-	113,113,113,113	0
22	MG	A	1839	1/1	0.93	0.17	-	318,318,318,318	0
22	MG	A	1868	1/1	0.94	0.19	-	139,139,139,139	0
22	MG	A	1612	1/1	0.95	0.04	-	136,136,136,136	0
22	MG	A	1764	1/1	0.99	0.13	-	290,290,290,290	0
22	MG	A	1850	1/1	0.55	0.53	-	134,134,134,134	0
22	MG	A	1695	1/1	0.98	0.17	-	125,125,125,125	0
22	MG	A	1762	1/1	0.78	0.20	-	219,219,219,219	0
22	MG	A	1743	1/1	0.95	0.29	-	135,135,135,135	0
22	MG	A	1696	1/1	0.98	0.15	-	193,193,193,193	0
22	MG	A	1664	1/1	0.92	0.17	-	126,126,126,126	0
22	MG	A	1631	1/1	0.65	0.69	-	118,118,118,118	0
22	MG	A	1748	1/1	0.89	0.24	-	144,144,144,144	0
22	MG	A	1676	1/1	0.95	0.17	-	136,136,136,136	0
22	MG	A	1648	1/1	0.96	0.26	-	82,82,82,82	0
22	MG	A	1864	1/1	0.76	0.14	-	123,123,123,123	0
22	MG	A	1667	1/1	0.93	0.27	-	274,274,274,274	0
22	MG	A	1861	1/1	0.92	0.25	-	135,135,135,135	0
22	MG	A	1634	1/1	1.00	0.19	-	73,73,73,73	0
22	MG	A	1629	1/1	0.91	0.49	-	106,106,106,106	0
22	MG	A	1801	1/1	0.80	0.25	-	152,152,152,152	0
22	MG	A	1788	1/1	0.95	0.17	-	330,330,330,330	0
22	MG	A	1790	1/1	0.91	0.29	-	159,159,159,159	0
22	MG	A	1745	1/1	0.89	0.49	-	127,127,127,127	0
22	MG	A	1819	1/1	0.84	0.81	-	141,141,141,141	0
22	MG	A	1658	1/1	0.93	0.18	-	123,123,123,123	0
22	MG	A	1811	1/1	0.92	0.21	-	242,242,242,242	0
22	MG	A	1793	1/1	0.97	0.15	-	182,182,182,182	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
22	MG	A	1862	1/1	0.94	0.17	-	99,99,99,99	0
22	MG	A	1661	1/1	0.86	0.10	-	148,148,148,148	0
22	MG	A	1815	1/1	0.97	0.13	-	197,197,197,197	0
22	MG	A	1685	1/1	0.92	0.43	-	116,116,116,116	0
22	MG	A	1650	1/1	0.97	0.21	-	118,118,118,118	0
22	MG	A	1841	1/1	0.90	0.40	-	175,175,175,175	0
22	MG	A	1832	1/1	0.90	0.52	-	364,364,364,364	0
22	MG	A	1769	1/1	0.87	0.16	-	142,142,142,142	0
22	MG	A	1647	1/1	0.98	0.12	-	110,110,110,110	0
22	MG	A	1792	1/1	0.94	0.12	-	398,398,398,398	0
22	MG	A	1803	1/1	0.86	0.35	-	147,147,147,147	0
22	MG	A	1849	1/1	0.87	0.27	-	123,123,123,123	0
22	MG	A	1776	1/1	0.92	0.15	-	129,129,129,129	0
22	MG	I	201	1/1	0.92	0.19	-	143,143,143,143	0
22	MG	M	202	1/1	0.40	0.82	-	122,122,122,122	0
22	MG	A	1723	1/1	0.99	0.13	-	122,122,122,122	0
22	MG	P	101	1/1	0.83	0.34	-	90,90,90,90	0
22	MG	A	1826	1/1	0.93	0.16	-	447,447,447,447	0
22	MG	A	1687	1/1	0.97	0.06	-	151,151,151,151	0
22	MG	L	201	1/1	0.97	0.07	-	122,122,122,122	0
22	MG	A	1812	1/1	0.93	0.26	-	365,365,365,365	0
22	MG	A	1817	1/1	0.96	0.15	-	297,297,297,297	0
22	MG	A	1601	1/1	0.82	0.50	-	137,137,137,137	0
22	MG	A	1750	1/1	0.97	0.33	-	128,128,128,128	0
22	MG	A	1655	1/1	0.92	0.23	-	141,141,141,141	0

6.5 Other polymers [i](#)

There are no such residues in this entry.