



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 06:20 am GMT

PDB ID : 4DV4
Title : Crystal structure of the *Thermus thermophilus* 30S ribosomal subunit with a 16S rRNA mutation, A914G
Authors : Demirci, H.; Murphy IV, F.; Murphy, E.; Gregory, S.T.; Dahlberg, A.E.; Jogle, 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)	:	recalc28949

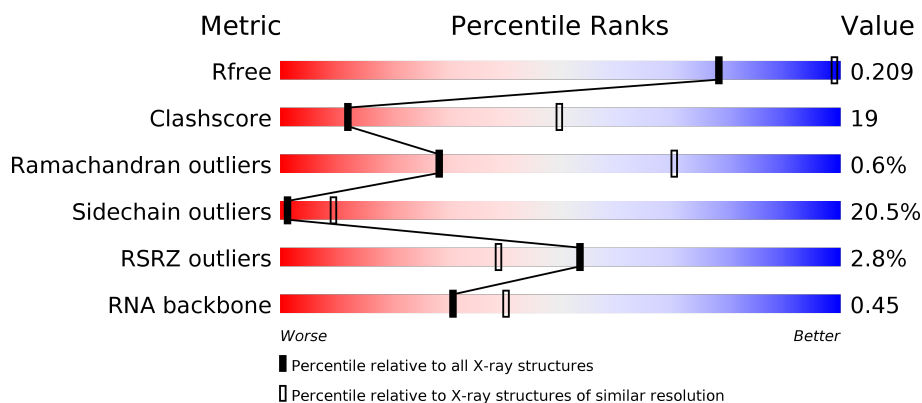
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

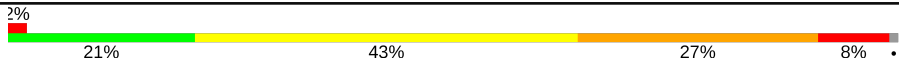



The reported resolution of this entry is 3.65 Å.

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	1134 (3.82-3.50)
Clashscore	112137	1267 (3.82-3.50)
Ramachandran outliers	110173	1219 (3.82-3.50)
Sidechain outliers	110143	1218 (3.82-3.50)
RSRZ outliers	101464	1160 (3.82-3.50)
RNA backbone	2435	1004 (4.40-2.90)

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	
2	B	256	
3	C	239	
4	D	209	

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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	1619	-	-	-	X
22	MG	A	1637	-	-	-	X
22	MG	A	1659	-	-	-	X
22	MG	A	1668	-	-	-	X
22	MG	A	1689	-	-	-	X
22	MG	A	1700	-	-	-	X
22	MG	A	1708	-	-	-	X
22	MG	A	1711	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
22	MG	A	1715	-	-	-	X
22	MG	A	1717	-	-	-	X
22	MG	A	1722	-	-	-	X
22	MG	A	1743	-	-	-	X
22	MG	A	1746	-	-	-	X
22	MG	A	1751	-	-	-	X
22	MG	A	1768	-	-	-	X
22	MG	A	1776	-	-	-	X
22	MG	A	1810	-	-	-	X
22	MG	A	1811	-	-	-	X
22	MG	A	1827	-	-	-	X
22	MG	A	1856	-	-	-	X
22	MG	B	301	-	-	-	X
22	MG	D	302	-	-	-	X
22	MG	J	201	-	-	-	X
22	MG	P	103	-	-	-	X
22	MG	Q	202	-	-	-	X

2 Entry composition

There are 24 unique types of molecules in this entry. The entry contains 52434 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
			32645	14540	6039	10548	1518			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	914	G	A	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	3	Total	Mg	0	0
			3	3		
22	J	2	Total	Mg	0	0
			2	2		
22	Q	2	Total	Mg	0	0
			2	2		
22	D	3	Total	Mg	0	0
			3	3		
22	E	1	Total	Mg	0	0
			1	1		
22	B	2	Total	Mg	0	0
			2	2		
22	C	2	Total	Mg	0	0
			2	2		
22	A	268	Total	Mg	0	0
			268	268		
22	N	1	Total	Mg	0	0
			1	1		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
22	S	1	Total 1	Mg 1	0	0
22	F	1	Total 1	Mg 1	0	0
22	M	1	Total 1	Mg 1	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

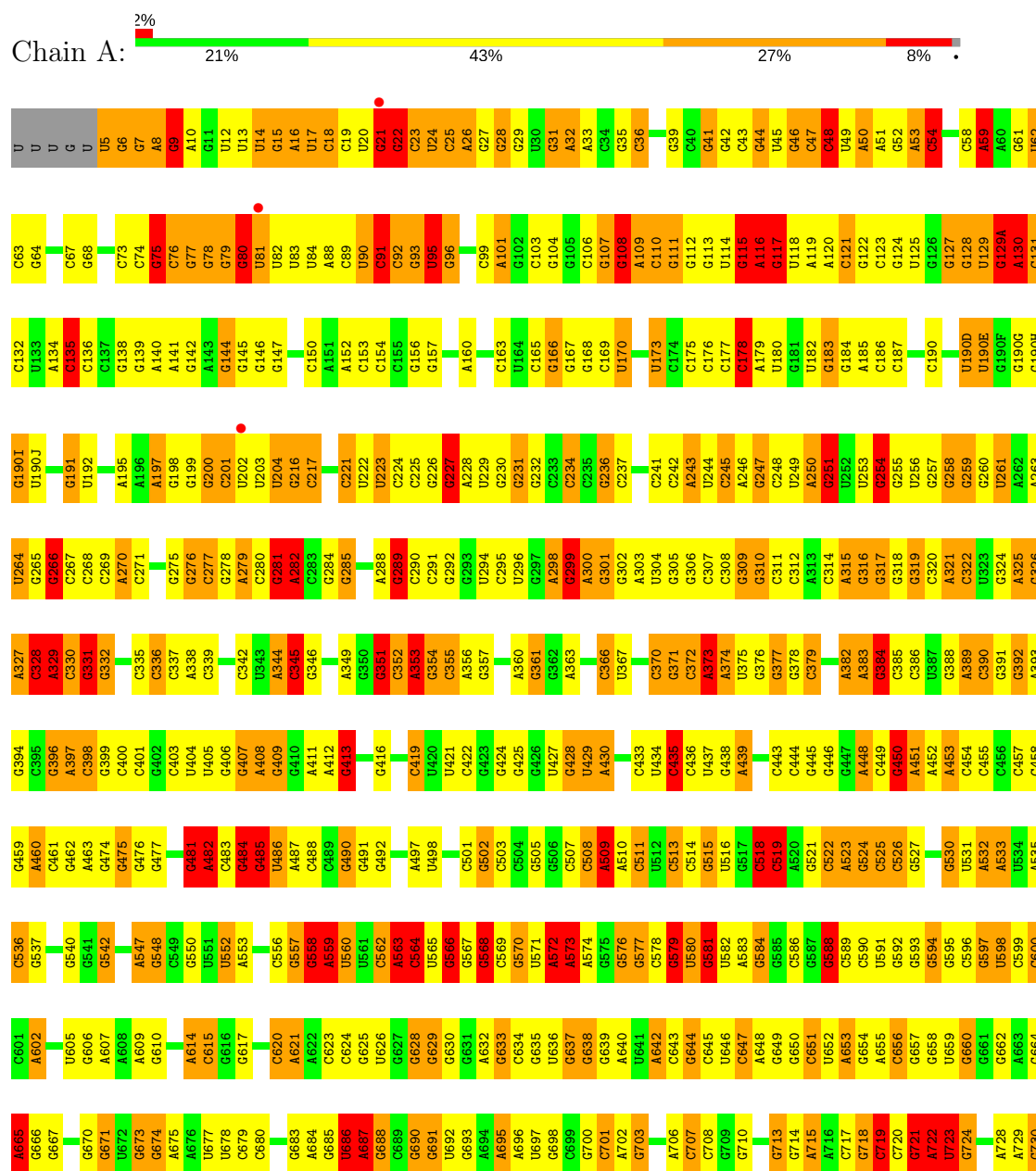
- Molecule 24 is water.

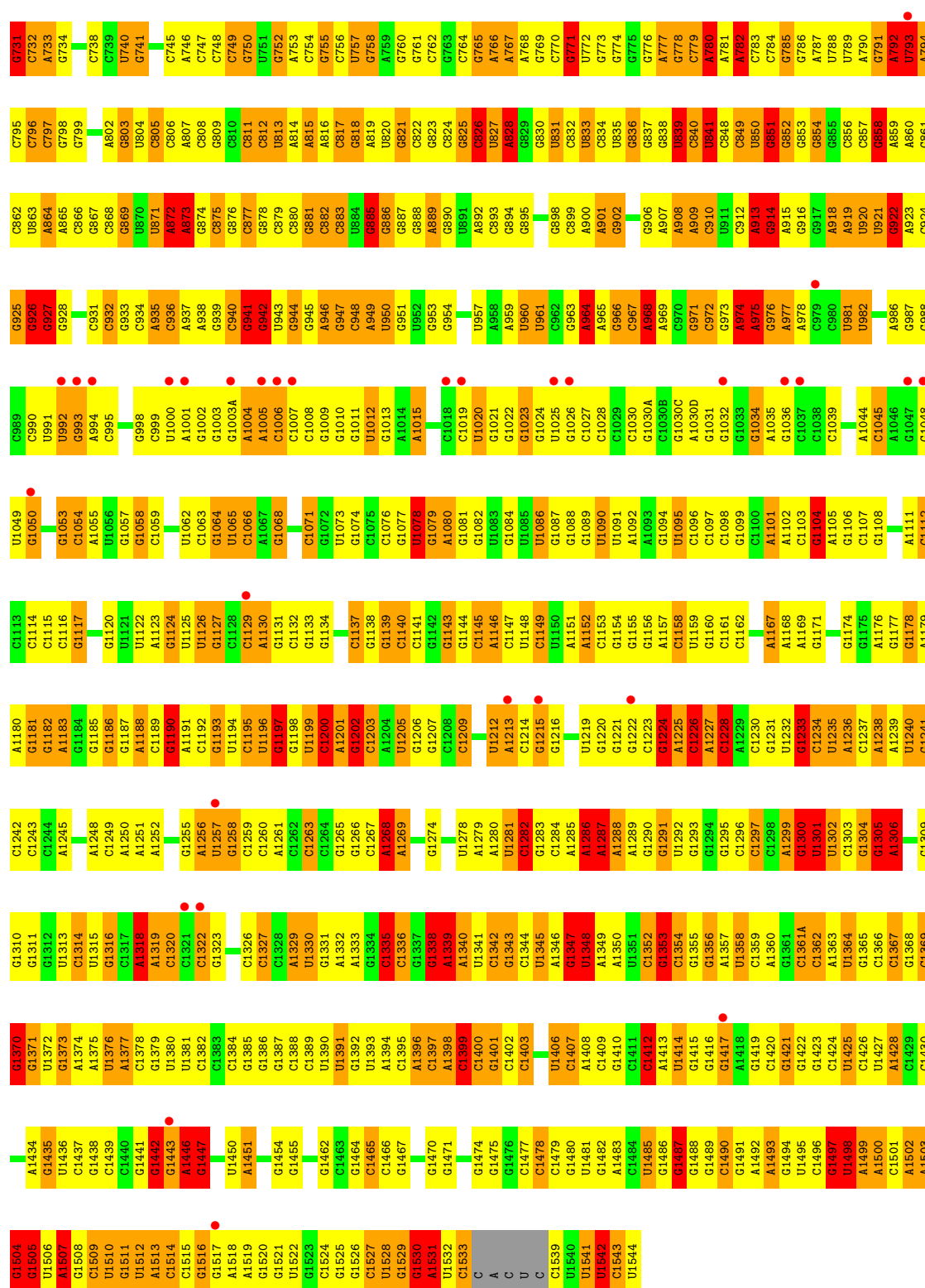
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
24	A	383	Total 383	O 383	0	0
24	E	3	Total 3	O 3	0	0
24	G	2	Total 2	O 2	0	0
24	I	1	Total 1	O 1	0	0
24	J	3	Total 3	O 3	0	0
24	L	1	Total 1	O 1	0	0
24	M	7	Total 7	O 7	0	0
24	N	2	Total 2	O 2	0	0
24	P	8	Total 8	O 8	0	0
24	Q	1	Total 1	O 1	0	0
24	T	1	Total 1	O 1	0	0

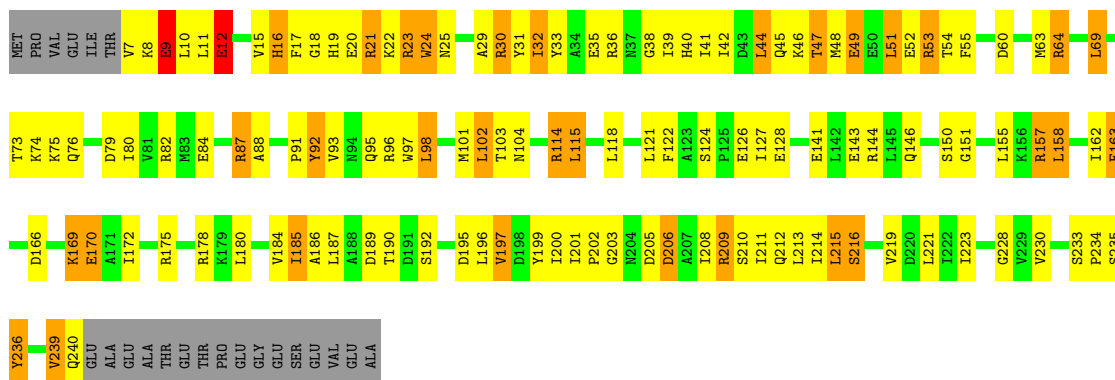
3 Residue-property plots

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

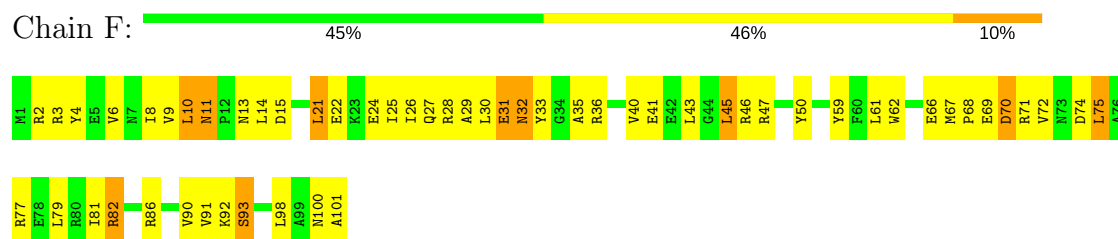




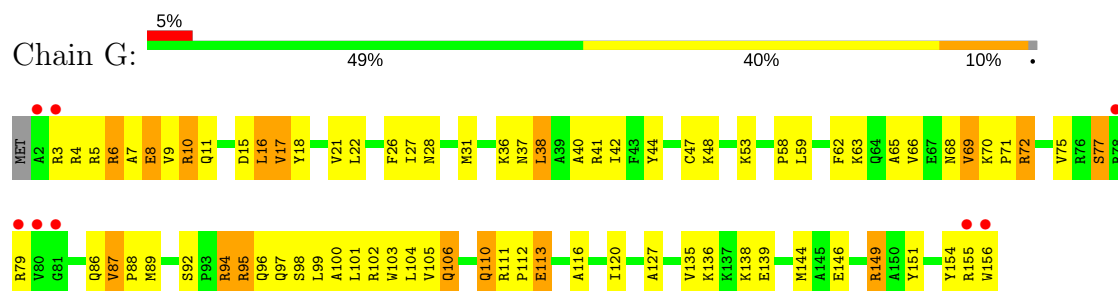


GLY

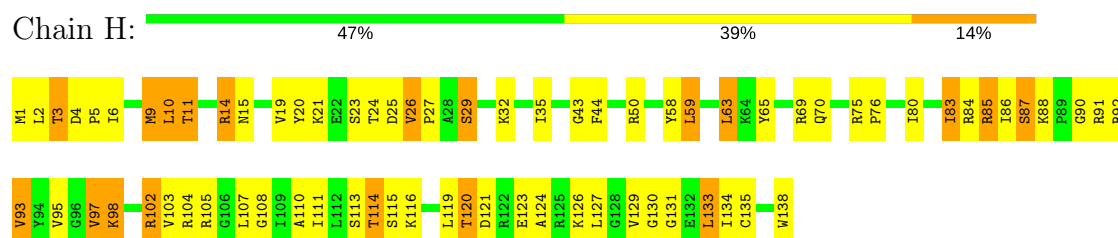
- Molecule 6: ribosomal protein S6



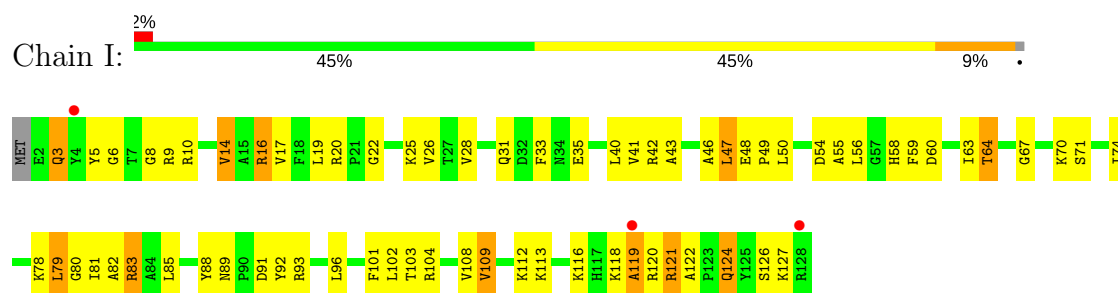
- Molecule 7: ribosomal protein S7



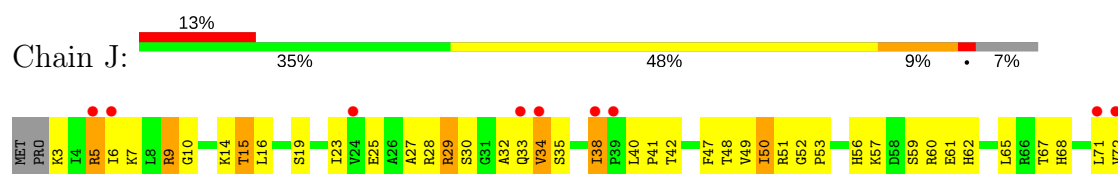
- Molecule 8: ribosomal protein S8

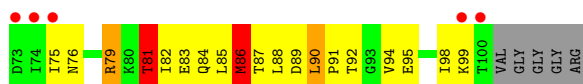


- Molecule 9: ribosomal protein S9

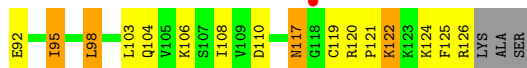


- Molecule 10: ribosomal protein S10

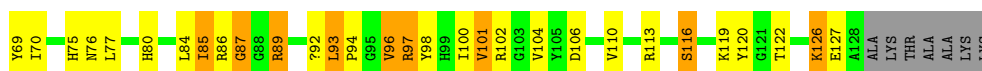
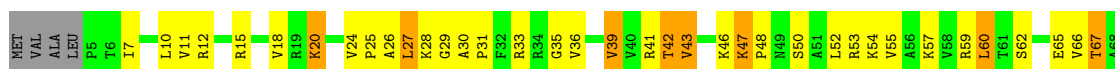




- Molecule 11: ribosomal protein S11



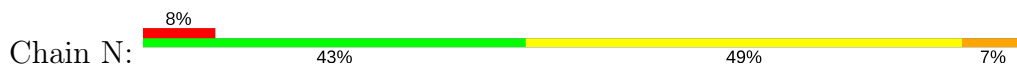
- Molecule 12: ribosomal protein S12



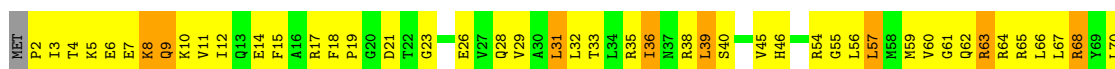
- Molecule 13: ribosomal protein S13



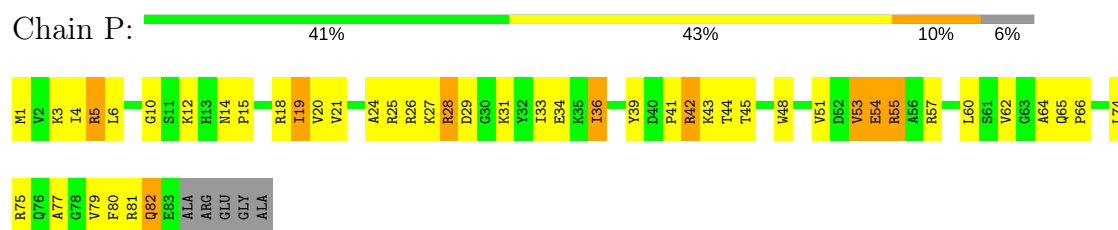
- Molecule 14: ribosomal protein S14



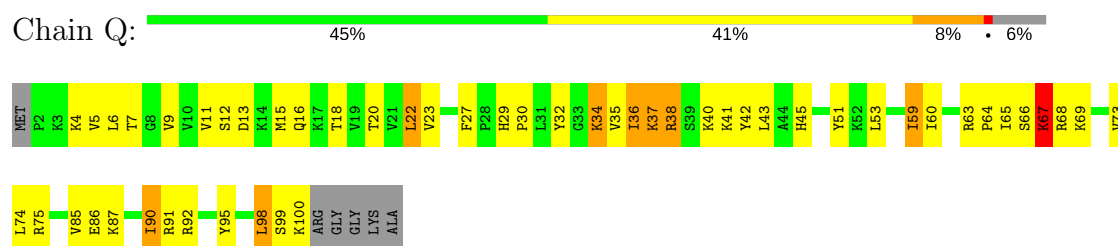
- Molecule 15: ribosomal protein S15



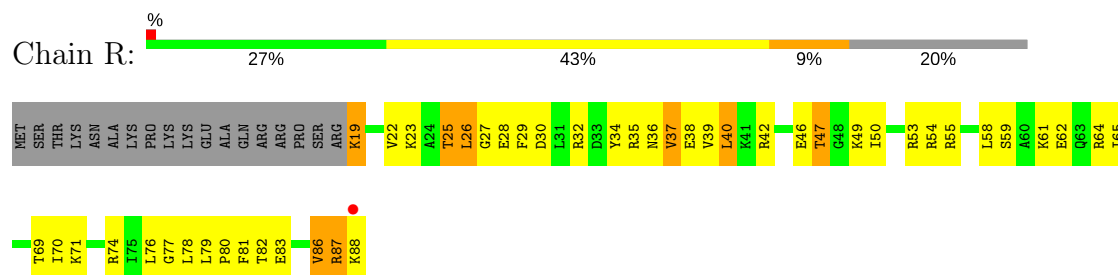
- Molecule 16: ribosomal protein S16



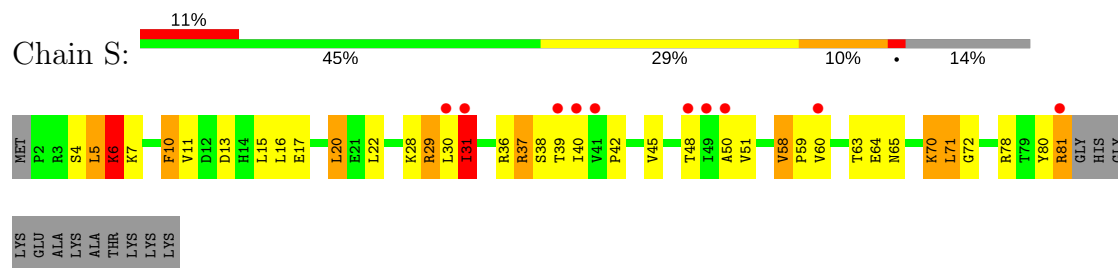
- Molecule 17: ribosomal protein S17



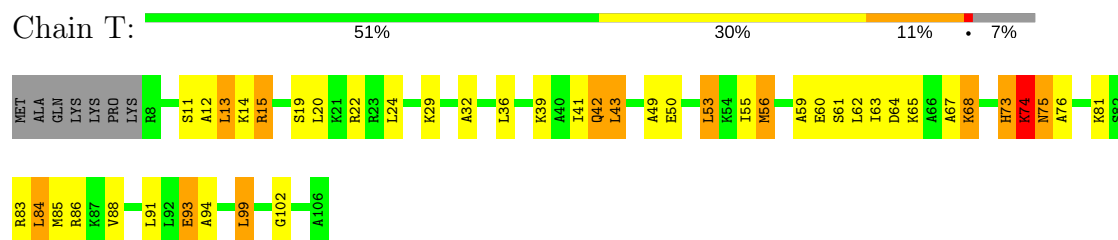
- Molecule 18: ribosomal protein S18



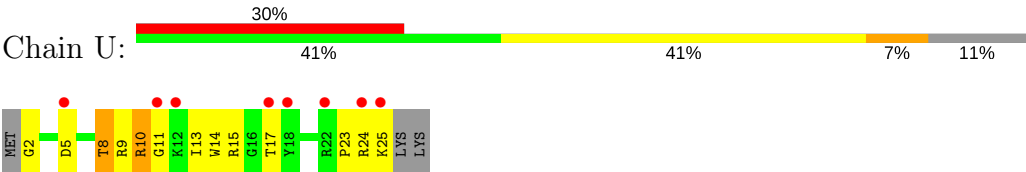
- Molecule 19: ribosomal protein S19



- Molecule 20: ribosomal protein S20



- 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	402.64Å 402.64Å 174.75Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.66 – 3.65 34.66 – 3.65	Depositor EDS
% Data completeness (in resolution range)	98.2 (34.66-3.65) 98.0 (34.66-3.65)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.80 (at 3.66Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_978)	Depositor
R, R_{free}	0.153 , 0.208 0.152 , 0.209	Depositor DCC
R_{free} test set	7743 reflections (4.99%)	DCC
Wilson B-factor (Å ²)	138.2	Xtriage
Anisotropy	0.202	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.23 , 129.2	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	52434	wwPDB-VP
Average B, all atoms (Å ²)	168.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.89% 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	1.22	174/36140 (0.5%)	1.94	1937/56398 (3.4%)
2	B	0.81	2/1935 (0.1%)	0.96	4/2609 (0.2%)
3	C	0.62	0/1636	0.81	0/2205
4	D	0.77	1/1733 (0.1%)	1.00	5/2318 (0.2%)
5	E	0.97	1/1162 (0.1%)	1.12	5/1564 (0.3%)
6	F	0.69	0/856	0.83	2/1154 (0.2%)
7	G	0.68	0/1276	0.90	1/1709 (0.1%)
8	H	1.03	0/1136	1.12	2/1527 (0.1%)
9	I	0.56	0/1029	0.81	0/1379
10	J	0.63	0/805	0.87	1/1082 (0.1%)
11	K	0.83	1/879 (0.1%)	0.98	2/1187 (0.2%)
12	L	0.82	0/977	1.10	2/1306 (0.2%)
13	M	0.63	0/947	0.83	0/1270
14	N	0.65	0/501	0.87	0/664
15	O	0.81	0/740	1.02	2/987 (0.2%)
16	P	0.88	0/716	1.10	3/963 (0.3%)
17	Q	1.03	0/836	1.15	4/1117 (0.4%)
18	R	0.81	0/579	0.96	0/768
19	S	0.61	0/661	0.81	1/890 (0.1%)
20	T	0.80	0/765	1.07	2/1007 (0.2%)
21	U	0.58	0/212	0.91	0/277
All	All	1.09	179/55521 (0.3%)	1.69	1973/82381 (2.4%)

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
4	D	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
7	G	0	1
8	H	0	1
10	J	0	2
12	L	0	2
13	M	0	1
15	O	0	1
18	R	0	1
20	T	0	2
All	All	0	13

All (179) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	279	A	N9-C4	-13.57	1.29	1.37
1	A	300	A	N3-C4	-9.42	1.29	1.34
1	A	1442	G	N9-C4	9.30	1.45	1.38
1	A	301	G	C6-N1	-9.24	1.33	1.39
1	A	822	C	N1-C6	-8.85	1.31	1.37
4	D	12	CYS	CB-SG	8.85	1.97	1.82
1	A	1525	G	N1-C2	-8.58	1.30	1.37
1	A	938	A	N3-C4	-8.45	1.29	1.34
1	A	1502	A	C5-C6	-8.40	1.33	1.41
1	A	279	A	N7-C5	-8.29	1.34	1.39
1	A	574	A	N9-C4	-8.05	1.33	1.37
1	A	279	A	N3-C4	-8.03	1.30	1.34
1	A	569	C	N3-C4	-7.91	1.28	1.33
1	A	569	C	N1-C6	-7.78	1.32	1.37
1	A	816	A	N9-C4	-7.62	1.33	1.37
1	A	300	A	N9-C4	-7.62	1.33	1.37
1	A	817	C	N1-C6	-7.47	1.32	1.37
1	A	1504	G	N7-C5	-7.47	1.34	1.39
1	A	1501	C	N3-C4	-7.43	1.28	1.33
1	A	1377	A	N9-C4	-7.38	1.33	1.37
1	A	1500	A	C6-N1	-7.36	1.30	1.35
1	A	833	U	C4-O4	7.33	1.29	1.23
1	A	1103	C	N1-C6	-7.24	1.32	1.37
1	A	1514	C	N1-C6	-7.19	1.32	1.37
1	A	298	A	N3-C4	-7.19	1.30	1.34
1	A	107	G	C5-C6	-7.18	1.35	1.42
1	A	109	A	N9-C4	-7.18	1.33	1.37
1	A	797	C	N1-C6	-7.16	1.32	1.37
1	A	1509	C	N3-C4	-7.14	1.28	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	869	G	C8-N7	-7.13	1.26	1.30
1	A	1442	G	N3-C4	7.10	1.40	1.35
1	A	856	C	N1-C6	-7.08	1.32	1.37
1	A	938	A	N9-C4	-7.05	1.33	1.37
1	A	946	A	C6-N1	-7.02	1.30	1.35
1	A	559	A	C6-N1	-6.99	1.30	1.35
1	A	1524	C	N1-C6	-6.95	1.32	1.37
1	A	780	A	N9-C4	-6.91	1.33	1.37
1	A	1526	G	C5-C4	-6.87	1.33	1.38
1	A	572	A	C6-N1	-6.86	1.30	1.35
1	A	574	A	N3-C4	-6.81	1.30	1.34
1	A	586	C	N1-C6	-6.78	1.33	1.37
1	A	1501	C	N1-C6	-6.76	1.33	1.37
1	A	1377	A	N3-C4	-6.73	1.30	1.34
1	A	729	A	N7-C5	-6.71	1.35	1.39
1	A	946	A	N3-C4	-6.71	1.30	1.34
1	A	779	C	N1-C6	-6.70	1.33	1.37
1	A	880	C	N1-C6	-6.62	1.33	1.37
1	A	328	C	N1-C6	-6.61	1.33	1.37
1	A	1064	G	N9-C4	-6.60	1.32	1.38
1	A	301	G	N3-C4	-6.58	1.30	1.35
1	A	482	A	N7-C5	-6.57	1.35	1.39
1	A	1502	A	N7-C5	-6.56	1.35	1.39
1	A	875	C	N1-C6	-6.54	1.33	1.37
1	A	266	G	N9-C4	-6.45	1.32	1.38
1	A	300	A	N7-C5	-6.45	1.35	1.39
11	K	119	CYS	CB-SG	-6.44	1.71	1.82
1	A	124	G	N3-C4	-6.41	1.30	1.35
1	A	889	A	N3-C4	-6.37	1.31	1.34
1	A	327	A	N7-C5	-6.37	1.35	1.39
1	A	308	C	N1-C6	-6.34	1.33	1.37
1	A	766	A	N3-C4	-6.33	1.31	1.34
1	A	572	A	N3-C4	-6.31	1.31	1.34
1	A	860	A	N3-C4	-6.28	1.31	1.34
1	A	1500	A	N3-C4	-6.27	1.31	1.34
1	A	243	A	C5-C6	-6.25	1.35	1.41
1	A	1064	G	N3-C4	-6.25	1.31	1.35
1	A	602	A	N9-C4	-6.23	1.34	1.37
1	A	451	A	N9-C4	-6.21	1.34	1.37
1	A	124	G	C6-N1	-6.17	1.35	1.39
1	A	753	A	N3-C4	-6.14	1.31	1.34
1	A	864	A	N7-C5	-6.12	1.35	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	572	A	C5-C4	-6.12	1.34	1.38
1	A	758	G	C5-C6	-6.05	1.36	1.42
1	A	797	C	N3-C4	-6.04	1.29	1.33
1	A	1076	C	N1-C6	-6.03	1.33	1.37
1	A	1077	G	N9-C8	-6.03	1.33	1.37
1	A	642	A	N9-C4	-6.03	1.34	1.37
1	A	120	A	N9-C4	-6.02	1.34	1.37
1	A	654	G	C5-C6	-6.00	1.36	1.42
1	A	915	A	N9-C4	-5.98	1.34	1.37
1	A	868	C	N3-C4	-5.98	1.29	1.33
1	A	872	A	P-O5'	-5.97	1.53	1.59
1	A	1513	A	N9-C4	-5.97	1.34	1.37
1	A	922	G	C6-N1	-5.93	1.35	1.39
1	A	719	C	N1-C6	-5.89	1.33	1.37
1	A	1401	G	C5-C4	-5.88	1.34	1.38
1	A	836	G	C6-O6	5.82	1.29	1.24
1	A	1504	G	N9-C8	-5.82	1.33	1.37
1	A	563	A	N7-C5	-5.81	1.35	1.39
1	A	1531	A	N9-C4	5.79	1.41	1.37
1	A	779	C	N3-C4	-5.79	1.29	1.33
1	A	116	A	N9-C4	-5.75	1.34	1.37
1	A	782	A	N7-C5	-5.73	1.35	1.39
1	A	19	C	N3-C4	-5.73	1.29	1.33
1	A	67	C	N1-C6	-5.71	1.33	1.37
1	A	931	C	N3-C4	-5.71	1.29	1.33
1	A	481	G	N9-C4	5.71	1.42	1.38
1	A	1525	G	C6-N1	-5.69	1.35	1.39
2	B	12	GLU	CG-CD	5.68	1.60	1.51
1	A	876	G	C5-C4	-5.68	1.34	1.38
1	A	1508	G	N7-C5	-5.67	1.35	1.39
1	A	1394	A	N9-C4	-5.67	1.34	1.37
1	A	722	A	C5-C6	-5.66	1.35	1.41
1	A	753	A	N9-C4	-5.66	1.34	1.37
1	A	1248	A	N9-C4	5.65	1.41	1.37
1	A	860	A	N9-C4	-5.64	1.34	1.37
1	A	122	G	N7-C5	-5.64	1.35	1.39
1	A	722	A	N9-C4	-5.64	1.34	1.37
1	A	1500	A	C5-C4	-5.63	1.34	1.38
1	A	787	A	C5-C6	-5.63	1.35	1.41
1	A	576	G	N3-C4	-5.62	1.31	1.35
1	A	563	A	N3-C4	-5.62	1.31	1.34
1	A	130	A	N3-C4	-5.62	1.31	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	329	A	C5-C6	-5.62	1.35	1.41
1	A	328	C	N3-C4	-5.61	1.30	1.33
1	A	1370	G	N9-C4	5.61	1.42	1.38
1	A	564	C	N1-C6	-5.60	1.33	1.37
1	A	1379	G	C6-N1	-5.59	1.35	1.39
1	A	835	U	C4-O4	5.59	1.28	1.23
1	A	565	U	C4-C5	-5.57	1.38	1.43
1	A	232	G	C6-N1	5.54	1.43	1.39
1	A	828	A	N7-C5	-5.53	1.35	1.39
1	A	1401	G	C6-N1	-5.53	1.35	1.39
1	A	1190	G	N7-C5	-5.52	1.35	1.39
1	A	1500	A	N1-C2	-5.52	1.29	1.34
1	A	460	A	N9-C4	5.50	1.41	1.37
1	A	109	A	N3-C4	-5.48	1.31	1.34
1	A	728	A	N3-C4	-5.48	1.31	1.34
1	A	782	A	C6-N1	-5.47	1.31	1.35
1	A	243	A	C6-N1	-5.46	1.31	1.35
1	A	872	A	N7-C5	-5.46	1.35	1.39
1	A	382	A	N7-C5	-5.46	1.35	1.39
1	A	382	A	C5-C6	-5.44	1.36	1.41
1	A	570	G	N1-C2	-5.42	1.33	1.37
1	A	797	C	C2-N3	-5.41	1.31	1.35
1	A	832	C	N1-C6	-5.41	1.33	1.37
1	A	1514	C	N3-C4	-5.40	1.30	1.33
1	A	16	A	C6-N1	-5.39	1.31	1.35
2	B	9	GLU	CG-CD	5.38	1.60	1.51
5	E	115	VAL	CB-CG2	-5.37	1.41	1.52
1	A	289	G	N7-C5	-5.36	1.36	1.39
1	A	559	A	N3-C4	-5.35	1.31	1.34
1	A	80	G	N9-C4	5.34	1.42	1.38
1	A	266	G	N3-C4	-5.33	1.31	1.35
1	A	654	G	N9-C4	-5.32	1.33	1.38
1	A	16	A	N3-C4	-5.31	1.31	1.34
1	A	873	A	N7-C5	-5.30	1.36	1.39
1	A	875	C	N3-C4	-5.30	1.30	1.33
1	A	1527	C	N3-C4	-5.28	1.30	1.33
1	A	397	A	N3-C4	-5.27	1.31	1.34
1	A	782	A	N3-C4	-5.26	1.31	1.34
1	A	116	A	N3-C4	-5.24	1.31	1.34
1	A	1346	A	N9-C4	-5.24	1.34	1.37
1	A	16	A	N9-C4	-5.23	1.34	1.37
1	A	787	A	N7-C5	-5.22	1.36	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	938	A	C6-N1	-5.19	1.31	1.35
1	A	758	G	N7-C5	-5.18	1.36	1.39
1	A	131	C	N3-C4	-5.18	1.30	1.33
1	A	1525	G	C5-C4	-5.18	1.34	1.38
1	A	131	C	N1-C6	-5.17	1.34	1.37
1	A	825	G	C5-C4	-5.17	1.34	1.38
1	A	1442	G	C2-N3	5.17	1.36	1.32
1	A	584	G	N7-C5	-5.14	1.36	1.39
1	A	787	A	N9-C4	-5.14	1.34	1.37
1	A	1301	U	C3'-O3'	5.10	1.49	1.42
1	A	1306	A	N9-C4	-5.10	1.34	1.37
1	A	644	G	C5-C6	-5.09	1.37	1.42
1	A	1455	G	C5-C6	-5.09	1.37	1.42
1	A	1375	A	N3-C4	-5.08	1.31	1.34
1	A	327	A	C5-C6	-5.08	1.36	1.41
1	A	322	C	N1-C6	-5.07	1.34	1.37
1	A	803	G	N3-C4	-5.06	1.31	1.35
1	A	1501	C	C2-N3	-5.05	1.31	1.35
1	A	243	A	N3-C4	-5.05	1.31	1.34
1	A	279	A	C5-C6	-5.02	1.36	1.41
1	A	122	G	C5-C6	-5.01	1.37	1.42
1	A	1531	A	N3-C4	5.01	1.37	1.34
1	A	1510	U	C2-N3	-5.01	1.34	1.37
1	A	1396	A	N9-C4	-5.00	1.34	1.37

All (1973) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	758	G	N1-C6-O6	21.49	132.79	119.90
1	A	758	G	C5-C6-O6	-16.07	118.96	128.60
1	A	1442	G	N3-C4-N9	15.41	135.25	126.00
1	A	722	A	C2-N3-C4	-14.89	103.16	110.60
1	A	232	G	N1-C6-O6	14.78	128.76	119.90
1	A	862	C	C6-N1-C2	14.54	126.12	120.30
1	A	117	G	C6-C5-N7	-13.95	122.03	130.40
1	A	1516[A]	G	C8-N9-C4	-13.93	100.83	106.40
1	A	1516[B]	G	C8-N9-C4	-13.93	100.83	106.40
1	A	117	G	N1-C6-O6	13.79	128.17	119.90
1	A	481	G	N3-C4-N9	13.77	134.26	126.00
1	A	279	A	C5-N7-C8	-13.46	97.17	103.90
1	A	758	G	C6-C5-N7	-13.44	122.34	130.40
1	A	1442	G	C4-N9-C1'	13.30	143.79	126.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1505	G	C8-N9-C4	-13.22	101.11	106.40
1	A	1442	G	N3-C4-C5	-13.20	122.00	128.60
1	A	1502	A	N1-C6-N6	13.20	126.52	118.60
1	A	758	G	N9-C4-C5	-13.18	100.13	105.40
1	A	1502	A	C5-N7-C8	-13.15	97.32	103.90
1	A	1531	A	N1-C6-N6	12.99	126.39	118.60
1	A	1305	G	C8-N9-C4	-12.95	101.22	106.40
1	A	724	G	C4-C5-N7	12.88	115.95	110.80
1	A	107	G	C4-C5-N7	12.88	115.95	110.80
1	A	128	G	N1-C6-O6	12.87	127.62	119.90
1	A	279	A	C2-N3-C4	-12.73	104.23	110.60
1	A	1516[A]	G	N9-C4-C5	12.68	110.47	105.40
1	A	1516[B]	G	N9-C4-C5	12.68	110.47	105.40
1	A	565	U	C5-C4-O4	-12.64	118.32	125.90
1	A	569	C	C5-C6-N1	-12.39	114.81	121.00
1	A	1502	A	C4-C5-N7	12.39	116.89	110.70
1	A	946	A	N1-C6-N6	-12.22	111.27	118.60
1	A	734	G	N1-C6-O6	12.11	127.17	119.90
1	A	1455	G	N1-C6-O6	12.11	127.17	119.90
1	A	600	C	C6-N1-C2	12.07	125.13	120.30
1	A	1502	A	C6-C5-N7	-12.06	123.86	132.30
1	A	1442	G	C8-N9-C1'	-11.92	111.50	127.00
1	A	703	G	C4-C5-N7	-11.72	106.11	110.80
1	A	820	U	N1-C2-O2	-11.71	114.60	122.80
1	A	862	C	N3-C4-C5	11.70	126.58	121.90
1	A	122	G	N1-C6-O6	11.69	126.91	119.90
1	A	825	G	C8-N9-C4	11.64	111.06	106.40
1	A	572	A	N1-C6-N6	-11.59	111.65	118.60
1	A	117	G	C4-N9-C1'	11.56	141.52	126.50
1	A	279	A	N7-C8-N9	11.52	119.56	113.80
1	A	266	G	C6-C5-N7	-11.49	123.51	130.40
1	A	266	G	C5-N7-C8	-11.48	98.56	104.30
1	A	724	G	C5-C6-O6	-11.47	121.72	128.60
1	A	938	A	N1-C6-N6	-11.43	111.74	118.60
1	A	117	G	C8-N9-C1'	-11.39	112.19	127.00
1	A	816	A	C2-N3-C4	-11.38	104.91	110.60
1	A	820	U	N1-C2-N3	11.37	121.72	114.90
1	A	129	U	N3-C4-C5	-11.36	107.78	114.60
1	A	833	U	N3-C4-C5	-11.36	107.79	114.60
1	A	1190	G	C4-N9-C1'	11.32	141.22	126.50
1	A	1510	U	C5-C6-N1	-11.28	117.06	122.70
1	A	693	G	N1-C6-O6	11.17	126.60	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	948	C	C6-N1-C2	11.14	124.76	120.30
1	A	758	G	C4-C5-N7	11.13	115.25	110.80
1	A	600	C	C5-C6-N1	-11.11	115.45	121.00
1	A	805	C	N3-C4-C5	11.04	126.32	121.90
1	A	774	G	C5-C6-O6	-11.03	121.98	128.60
1	A	17	U	C5-C6-N1	-11.02	117.19	122.70
1	A	481	G	N3-C4-C5	-10.93	123.14	128.60
1	A	117	G	C4-C5-C6	10.90	125.34	118.80
1	A	317	G	N1-C6-O6	10.89	126.43	119.90
1	A	836	G	N1-C6-O6	10.69	126.31	119.90
1	A	76	C	C2-N1-C1'	-10.59	107.16	118.80
1	A	128	G	C5-C6-O6	-10.59	122.25	128.60
1	A	1502	A	N7-C8-N9	10.56	119.08	113.80
1	A	266	G	C4-C5-N7	10.48	114.99	110.80
1	A	771	G	N1-C6-O6	10.47	126.18	119.90
1	A	774	G	C4-C5-N7	10.43	114.97	110.80
1	A	833	U	C4-C5-C6	10.43	125.96	119.70
1	A	703	G	C5-C6-O6	10.38	134.83	128.60
1	A	774	G	N1-C6-O6	10.38	126.12	119.90
1	A	873	A	C8-N9-C4	-10.36	101.66	105.80
1	A	279	A	N1-C6-N6	10.25	124.75	118.60
1	A	445	G	N1-C6-O6	10.22	126.03	119.90
1	A	835	U	C5-C4-O4	10.18	132.01	125.90
1	A	599	C	C6-N1-C2	10.14	124.36	120.30
1	A	285	G	C2-N3-C4	-10.12	106.84	111.90
1	A	76	C	N1-C2-O2	-10.07	112.86	118.90
1	A	482	A	N1-C6-N6	10.02	124.61	118.60
1	A	1305	G	N7-C8-N9	9.99	118.09	113.10
1	A	1379	G	N3-C4-C5	-9.97	123.61	128.60
1	A	572	A	N9-C4-C5	9.95	109.78	105.80
1	A	109	A	C2-N3-C4	-9.95	105.63	110.60
1	A	876	G	C5-C6-O6	-9.89	122.67	128.60
1	A	758	G	C2-N3-C4	-9.88	106.96	111.90
1	A	1531	A	N7-C8-N9	9.88	118.74	113.80
1	A	1531	A	C6-C5-N7	-9.88	125.38	132.30
1	A	107	G	C5-C6-O6	-9.86	122.68	128.60
1	A	880	C	C4-C5-C6	9.86	122.33	117.40
1	A	1189	C	C6-N1-C2	9.85	124.24	120.30
1	A	833	U	C5-C4-O4	9.84	131.81	125.90
1	A	80	G	C8-N9-C4	-9.77	102.49	106.40
1	A	1299	A	C4-N9-C1'	9.74	143.83	126.30
1	A	797	C	N3-C4-C5	9.73	125.79	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	922	G	N3-C4-C5	-9.67	123.77	128.60
1	A	812	C	N3-C4-C5	-9.66	118.03	121.90
1	A	1103	C	C6-N1-C2	9.64	124.16	120.30
1	A	1455	G	C5-C6-O6	-9.57	122.86	128.60
1	A	295	C	C6-N1-C2	9.56	124.12	120.30
1	A	565	U	N1-C2-N3	-9.54	109.17	114.90
1	A	731	G	N1-C6-O6	9.53	125.62	119.90
1	A	841	U	C5-C6-N1	9.53	127.46	122.70
1	A	635	G	N1-C6-O6	9.53	125.61	119.90
1	A	935	A	N1-C6-N6	-9.50	112.90	118.60
1	A	167	G	N1-C6-O6	9.46	125.58	119.90
1	A	724	G	C5-N7-C8	-9.44	99.58	104.30
1	A	836	G	C5-C6-N1	-9.44	106.78	111.50
1	A	451	A	C8-N9-C4	9.43	109.57	105.80
1	A	626	U	C6-N1-C2	-9.39	115.36	121.00
1	A	128	G	C6-C5-N7	-9.39	124.77	130.40
1	A	892	A	C2-N3-C4	-9.39	105.91	110.60
1	A	1112	C	N1-C2-O2	9.38	124.53	118.90
1	A	1508	G	C8-N9-C4	-9.38	102.65	106.40
1	A	107	G	N1-C6-O6	9.35	125.51	119.90
1	A	1442	G	C6-C5-N7	-9.35	124.79	130.40
1	A	875	C	C5-C6-N1	-9.34	116.33	121.00
1	A	46	G	C5-C6-N1	-9.32	106.84	111.50
1	A	279	A	C6-C5-N7	-9.31	125.78	132.30
1	A	825	G	N7-C8-N9	-9.30	108.45	113.10
1	A	295	C	N3-C4-C5	9.29	125.61	121.90
1	A	1190	G	C4-C5-C6	9.26	124.36	118.80
1	A	863	U	C5-C4-O4	9.26	131.45	125.90
1	A	266	G	N7-C8-N9	9.25	117.73	113.10
1	A	778	G	C2-N3-C4	-9.25	107.28	111.90
1	A	326	G	C5-C6-O6	9.24	134.15	128.60
1	A	1417	G	C8-N9-C4	-9.24	102.70	106.40
1	A	129	U	C6-N1-C2	-9.23	115.46	121.00
1	A	850	U	C5-C4-O4	9.21	131.42	125.90
1	A	115	G	N1-C6-O6	9.19	125.41	119.90
1	A	907	A	N1-C2-N3	9.18	133.89	129.30
1	A	300	A	N1-C2-N3	9.17	133.89	129.30
1	A	481	G	C2-N3-C4	9.17	116.48	111.90
4	D	12	CYS	CA-CB-SG	9.16	130.48	114.00
1	A	175	C	C6-N1-C2	9.14	123.96	120.30
1	A	647	C	C6-N1-C2	9.14	123.96	120.30
1	A	326	G	C4-C5-N7	-9.12	107.15	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	859	A	N1-C6-N6	9.11	124.07	118.60
1	A	1373	G	C4-C5-N7	-9.08	107.17	110.80
1	A	353	A	N1-C6-N6	-9.07	113.16	118.60
1	A	1190	G	C8-N9-C1'	-9.06	115.22	127.00
1	A	872	A	N1-C6-N6	9.06	124.04	118.60
1	A	922	G	C8-N9-C4	-9.05	102.78	106.40
1	A	1103	C	C5-C6-N1	-9.05	116.48	121.00
1	A	232	G	N9-C4-C5	-9.03	101.79	105.40
1	A	722	A	N1-C6-N6	9.03	124.02	118.60
1	A	128	G	C4-C5-N7	9.02	114.41	110.80
1	A	5	U	C5-C6-N1	-9.00	118.20	122.70
1	A	1149	C	C6-N1-C2	-9.00	116.70	120.30
1	A	867	G	C5-C6-O6	-8.99	123.20	128.60
1	A	525	C	C6-N1-C2	8.99	123.90	120.30
1	A	242	C	C6-N1-C2	8.99	123.90	120.30
1	A	1190	G	C8-N9-C4	-8.98	102.81	106.40
1	A	1190	G	C5-C6-N1	-8.98	107.01	111.50
1	A	482	A	C6-C5-N7	-8.97	126.02	132.30
1	A	1299	A	C8-N9-C1'	-8.96	111.57	127.70
1	A	319	G	C6-C5-N7	-8.95	125.03	130.40
1	A	445	G	C6-C5-N7	-8.94	125.04	130.40
1	A	1080	A	N1-C6-N6	-8.94	113.24	118.60
1	A	591	U	C5-C6-N1	-8.93	118.23	122.70
1	A	576	G	N1-C2-N3	8.91	129.25	123.90
1	A	782	A	N1-C2-N3	8.91	133.76	129.30
1	A	1370	G	C6-C5-N7	-8.91	125.05	130.40
1	A	518	C	N1-C2-O2	8.91	124.25	118.90
1	A	129	U	N1-C2-N3	8.89	120.23	114.90
1	A	1107	C	C6-N1-C2	-8.88	116.75	120.30
1	A	1395	C	N1-C2-O2	-8.86	113.58	118.90
1	A	107	G	C6-C5-N7	-8.86	125.08	130.40
1	A	723	U	C5-C6-N1	8.84	127.12	122.70
1	A	259	G	C8-N9-C4	-8.82	102.87	106.40
1	A	1505	G	N9-C4-C5	8.78	108.91	105.40
1	A	1543	C	C6-N1-C2	8.78	123.81	120.30
1	A	722	A	C5-C6-N1	-8.78	113.31	117.70
1	A	753	A	N1-C2-N3	8.78	133.69	129.30
1	A	779	C	N1-C2-O2	-8.78	113.63	118.90
1	A	1455	G	C6-C5-N7	-8.78	125.13	130.40
1	A	877	C	N3-C4-C5	8.77	125.41	121.90
1	A	833	U	N3-C2-O2	-8.76	116.07	122.20
1	A	1200	C	N1-C2-O2	8.74	124.15	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	569	C	C2-N3-C4	-8.74	115.53	119.90
1	A	299	G	C4-C5-N7	8.72	114.29	110.80
1	A	1370	G	N1-C6-O6	8.72	125.13	119.90
1	A	119	A	C8-N9-C4	-8.69	102.32	105.80
1	A	481	G	C5-N7-C8	8.69	108.64	104.30
1	A	92	C	N3-C4-C5	8.68	125.37	121.90
1	A	839	U	N1-C2-O2	8.68	128.88	122.80
1	A	117	G	C5-C6-N1	-8.67	107.17	111.50
1	A	76	C	C6-N1-C1'	8.66	131.20	120.80
1	A	266	G	C2-N3-C4	-8.66	107.57	111.90
1	A	279	A	C8-N9-C4	-8.66	102.34	105.80
1	A	1352	C	C6-N1-C2	-8.65	116.84	120.30
1	A	232	G	C5-C6-O6	-8.64	123.41	128.60
1	A	721	G	C6-C5-N7	-8.64	125.22	130.40
1	A	481	G	C8-N9-C4	8.63	109.85	106.40
1	A	250	A	C5-C6-N1	-8.63	113.39	117.70
1	A	145	G	N1-C6-O6	8.63	125.08	119.90
1	A	710	G	C5-C6-O6	-8.63	123.42	128.60
1	A	482	A	C4-C5-C6	8.62	121.31	117.00
1	A	1505	G	N3-C4-C5	-8.62	124.29	128.60
1	A	703	G	N9-C4-C5	8.62	108.85	105.40
1	A	108	G	C8-N9-C4	-8.60	102.96	106.40
1	A	686	U	C5-C6-N1	-8.60	118.40	122.70
1	A	1318	A	C8-N9-C4	8.60	109.24	105.80
1	A	569	C	C4-C5-C6	8.59	121.69	117.40
1	A	146	G	N1-C6-O6	8.59	125.05	119.90
1	A	1299	A	C6-C5-N7	-8.58	126.29	132.30
1	A	1501	C	N3-C4-C5	8.58	125.33	121.90
1	A	300	A	C8-N9-C4	-8.57	102.37	105.80
1	A	788	U	N3-C4-O4	8.57	125.40	119.40
1	A	1370	G	C8-N9-C4	-8.57	102.97	106.40
1	A	184	G	N1-C6-O6	8.57	125.04	119.90
1	A	115	G	C5-C6-O6	-8.56	123.46	128.60
1	A	242	C	C5-C6-N1	-8.56	116.72	121.00
1	A	266	G	N1-C6-O6	8.55	125.03	119.90
1	A	317	G	C6-C5-N7	-8.54	125.28	130.40
1	A	232	G	C6-C5-N7	-8.54	125.28	130.40
1	A	771	G	C5-C6-O6	-8.54	123.48	128.60
1	A	1295	G	C8-N9-C4	-8.54	102.99	106.40
1	A	730	G	C4-C5-N7	-8.52	107.39	110.80
1	A	947	G	C8-N9-C4	8.52	109.81	106.40
1	A	1228	C	N1-C2-O2	8.52	124.01	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	482	A	N7-C8-N9	8.51	118.06	113.80
1	A	920	U	C5-C4-O4	8.51	131.00	125.90
1	A	139	G	N1-C6-O6	8.51	125.00	119.90
1	A	357	G	N1-C6-O6	8.50	125.00	119.90
1	A	693	G	C5-C6-O6	-8.49	123.51	128.60
1	A	366	C	N1-C2-O2	8.48	123.99	118.90
1	A	868	C	C6-N1-C2	-8.48	116.91	120.30
1	A	250	A	C2-N3-C4	-8.47	106.36	110.60
1	A	1370	G	C4-N9-C1'	8.47	137.51	126.50
1	A	718	G	N1-C6-O6	8.46	124.98	119.90
1	A	1516[A]	G	N3-C4-N9	-8.45	120.93	126.00
1	A	1516[B]	G	N3-C4-N9	-8.45	120.93	126.00
1	A	862	C	N3-C2-O2	8.44	127.81	121.90
1	A	277	C	C6-N1-C2	8.44	123.68	120.30
1	A	1377	A	N1-C2-N3	8.43	133.51	129.30
1	A	1199	U	N3-C2-O2	-8.43	116.30	122.20
1	A	1516[A]	G	C8-N9-C1'	8.42	137.95	127.00
1	A	1516[B]	G	C8-N9-C1'	8.42	137.95	127.00
1	A	319	G	C4-C5-N7	8.42	114.17	110.80
1	A	481	G	C5-C6-N1	8.42	115.71	111.50
1	A	776	G	N3-C4-C5	8.42	132.81	128.60
1	A	774	G	C6-C5-N7	-8.40	125.36	130.40
1	A	129	U	C5-C4-O4	8.39	130.94	125.90
1	A	869	G	N1-C6-O6	-8.38	114.87	119.90
1	A	1335	C	N1-C2-O2	8.37	123.92	118.90
1	A	686	U	C5-C4-O4	8.37	130.92	125.90
1	A	451	A	N9-C4-C5	-8.37	102.45	105.80
1	A	167	G	N9-C4-C5	-8.35	102.06	105.40
1	A	734	G	N9-C4-C5	-8.33	102.07	105.40
1	A	482	A	C5-C6-N1	-8.33	113.54	117.70
1	A	1332	A	C8-N9-C4	-8.32	102.47	105.80
1	A	1080	A	N9-C4-C5	8.31	109.12	105.80
1	A	1112	C	N3-C2-O2	-8.30	116.09	121.90
1	A	644	G	C4-C5-N7	8.29	114.12	110.80
1	A	918	A	C6-N1-C2	-8.29	113.63	118.60
1	A	719	C	N1-C2-O2	8.26	123.86	118.90
1	A	1332	A	N1-C6-N6	-8.25	113.65	118.60
1	A	1158	C	C6-N1-C2	-8.25	117.00	120.30
1	A	169	C	C6-N1-C2	-8.24	117.00	120.30
1	A	703	G	C5-N7-C8	8.23	108.42	104.30
1	A	481	G	N7-C8-N9	-8.23	108.98	113.10
1	A	975	A	N1-C6-N6	8.23	123.54	118.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	888	G	C4-C5-N7	-8.22	107.51	110.80
1	A	755	G	N1-C6-O6	8.21	124.82	119.90
1	A	309	G	C5-C6-O6	-8.20	123.68	128.60
1	A	1379	G	N1-C6-O6	-8.20	114.98	119.90
1	A	931	C	C5-C6-N1	-8.19	116.90	121.00
1	A	1202	G	N1-C6-O6	-8.19	114.98	119.90
1	A	144	G	N1-C6-O6	8.18	124.81	119.90
1	A	377	G	N3-C4-N9	8.18	130.91	126.00
1	A	329	A	C2-N3-C4	-8.17	106.52	110.60
1	A	586	C	C5-C6-N1	-8.16	116.92	121.00
1	A	880	C	N3-C4-N4	8.16	123.72	118.00
1	A	918	A	C5-C6-N1	8.16	121.78	117.70
1	A	573	A	N1-C6-N6	8.15	123.49	118.60
1	A	852	G	C5-C6-N1	-8.15	107.42	111.50
1	A	877	C	C2-N3-C4	-8.15	115.83	119.90
1	A	1379	G	C5-C6-N1	8.14	115.57	111.50
1	A	1190	G	N7-C8-N9	8.13	117.16	113.10
1	A	1531	A	C5-C6-N1	-8.12	113.64	117.70
1	A	129(A)	G	N3-C4-N9	8.12	130.87	126.00
1	A	621	A	C8-N9-C4	-8.12	102.55	105.80
1	A	946	A	N9-C4-C5	8.11	109.04	105.80
1	A	117	G	N3-C4-N9	8.09	130.85	126.00
1	A	900	A	C5-N7-C8	-8.05	99.87	103.90
1	A	1370	G	N3-C4-C5	-8.05	124.57	128.60
1	A	1529	G	C8-N9-C4	-8.04	103.18	106.40
1	A	1202	G	C4-C5-N7	-8.03	107.59	110.80
1	A	279	A	C5-C6-N1	-8.03	113.69	117.70
1	A	129	U	N1-C2-O2	-8.02	117.19	122.80
1	A	251	G	N1-C2-N3	8.02	128.71	123.90
1	A	18	C	C6-N1-C2	8.01	123.50	120.30
1	A	319	G	C5-C6-O6	-8.01	123.80	128.60
1	A	931	C	C2-N3-C4	-8.01	115.90	119.90
1	A	1239	A	C8-N9-C4	8.00	109.00	105.80
1	A	17	U	C2-N3-C4	-8.00	122.20	127.00
1	A	183	G	C6-C5-N7	-8.00	125.60	130.40
1	A	657	G	N1-C6-O6	8.00	124.70	119.90
1	A	782	A	C8-N9-C4	-8.00	102.60	105.80
1	A	797	C	C2-N3-C4	-7.99	115.90	119.90
1	A	291	C	C5-C4-N4	-7.99	114.61	120.20
1	A	1542	U	C6-N1-C2	7.99	125.80	121.00
1	A	129(A)	G	C6-C5-N7	-7.99	125.61	130.40
1	A	750	G	N3-C4-N9	7.99	130.79	126.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	734	G	C5-C6-O6	-7.99	123.81	128.60
1	A	1377	A	N9-C4-C5	7.97	108.99	105.80
1	A	721	G	C4-N9-C1'	7.97	136.86	126.50
1	A	299	G	C5-C6-O6	-7.97	123.82	128.60
1	A	1200	C	C2-N1-C1'	7.97	127.56	118.80
1	A	1112	C	C2-N1-C1'	7.95	127.55	118.80
1	A	559	A	C6-N1-C2	-7.95	113.83	118.60
1	A	825	G	C5-C6-O6	-7.95	123.83	128.60
1	A	1502	A	C5-C6-N6	-7.95	117.34	123.70
1	A	625	G	C5-C6-N1	7.94	115.47	111.50
1	A	389	A	N1-C6-N6	-7.94	113.84	118.60
1	A	656	C	N3-C4-C5	7.92	125.07	121.90
1	A	875	C	C6-N1-C2	7.92	123.47	120.30
1	A	710	G	N1-C6-O6	7.91	124.65	119.90
1	A	774	G	N9-C4-C5	-7.91	102.24	105.40
1	A	719	C	N3-C2-O2	-7.90	116.37	121.90
1	A	1525	G	N1-C6-O6	-7.90	115.16	119.90
1	A	722	A	C6-C5-N7	-7.90	126.77	132.30
1	A	95	U	C6-N1-C2	-7.88	116.27	121.00
1	A	609	A	C2-N3-C4	-7.87	106.67	110.60
1	A	942	G	C6-C5-N7	-7.86	125.69	130.40
1	A	698	G	C4-N9-C1'	7.85	136.71	126.50
1	A	649	G	C5-C6-O6	-7.83	123.90	128.60
1	A	511	C	C6-N1-C2	7.83	123.43	120.30
1	A	1289	A	C8-N9-C4	-7.82	102.67	105.80
1	A	1139	G	C8-N9-C4	-7.81	103.28	106.40
1	A	722	A	N1-C2-N3	7.81	133.20	129.30
1	A	450	G	C8-N9-C4	7.80	109.52	106.40
1	A	856	C	C5-C6-N1	-7.79	117.10	121.00
1	A	570	G	N3-C4-C5	-7.79	124.70	128.60
1	A	129	U	C6-N1-C1'	7.79	132.10	121.20
1	A	1403	C	N3-C4-C5	-7.79	118.78	121.90
1	A	298	A	N1-C2-N3	7.78	133.19	129.30
1	A	948	C	C2-N1-C1'	-7.78	110.24	118.80
1	A	1500	A	N9-C4-C5	7.78	108.91	105.80
1	A	300	A	C6-N1-C2	-7.77	113.94	118.60
1	A	1268	A	N1-C6-N6	-7.77	113.94	118.60
1	A	1377	A	C2-N3-C4	-7.77	106.72	110.60
1	A	878	G	C4-C5-N7	7.75	113.90	110.80
1	A	584	G	N1-C2-N2	7.74	123.17	116.20
4	D	94	LEU	CA-CB-CG	-7.74	97.50	115.30
1	A	797	C	C6-N1-C2	7.74	123.39	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	129(A)	G	C4-N9-C1'	7.73	136.55	126.50
1	A	941	G	C8-N9-C4	-7.73	103.31	106.40
1	A	107	G	N9-C4-C5	-7.72	102.31	105.40
1	A	584	G	C5-C6-O6	-7.71	123.97	128.60
1	A	413	G	C2-N3-C4	7.71	115.75	111.90
1	A	445	G	C5-C6-O6	-7.71	123.98	128.60
1	A	812	C	C6-N1-C2	-7.70	117.22	120.30
1	A	129(A)	G	C8-N9-C1'	-7.70	116.99	127.00
1	A	654	G	C5-C6-O6	-7.70	123.98	128.60
1	A	559	A	N1-C2-N3	7.69	133.15	129.30
1	A	650	G	C8-N9-C4	7.69	109.47	106.40
1	A	815	A	C8-N9-C4	7.68	108.87	105.80
1	A	724	G	N9-C4-C5	-7.68	102.33	105.40
1	A	658	G	C8-N9-C4	7.68	109.47	106.40
1	A	945	G	C5-C6-N1	7.67	115.33	111.50
1	A	615	C	C6-N1-C2	-7.67	117.23	120.30
1	A	946	A	C6-N1-C2	-7.66	114.01	118.60
1	A	1527	C	N3-C4-C5	7.66	124.96	121.90
1	A	771	G	C4-C5-N7	7.64	113.86	110.80
1	A	643	C	N3-C4-C5	7.63	124.95	121.90
1	A	15	G	C4-C5-N7	7.63	113.85	110.80
1	A	657	G	N1-C2-N3	7.63	128.48	123.90
1	A	7	G	C6-C5-N7	-7.62	125.83	130.40
1	A	1531	A	C8-N9-C4	-7.62	102.75	105.80
1	A	320	C	C6-N1-C2	7.62	123.35	120.30
1	A	300	A	C5-N7-C8	-7.61	100.09	103.90
1	A	752	G	C5-C6-O6	7.61	133.17	128.60
1	A	565	U	C6-N1-C2	7.60	125.56	121.00
1	A	1487	G	N3-C4-C5	-7.60	124.80	128.60
1	A	1112	C	C6-N1-C1'	-7.60	111.68	120.80
1	A	835	U	N3-C2-O2	-7.60	116.88	122.20
1	A	860	A	N1-C2-N3	7.60	133.10	129.30
1	A	299	G	N1-C6-O6	7.59	124.46	119.90
1	A	703	G	C4-C5-C6	7.59	123.36	118.80
1	A	824	C	C6-N1-C2	7.59	123.34	120.30
5	E	119	LEU	CA-CB-CG	-7.59	97.85	115.30
1	A	593	G	C2-N3-C4	-7.58	108.11	111.90
1	A	1505	G	N7-C8-N9	7.58	116.89	113.10
1	A	693	G	C4-C5-N7	7.58	113.83	110.80
1	A	862	C	C5-C4-N4	-7.58	114.90	120.20
1	A	117	G	N1-C2-N3	7.58	128.45	123.90
1	A	721	G	C4-C5-C6	7.58	123.34	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1370	G	N7-C8-N9	7.57	116.89	113.10
1	A	1490	C	C5-C6-N1	7.57	124.78	121.00
1	A	54	C	N3-C4-C5	7.56	124.92	121.90
1	A	190(G)	G	N1-C6-O6	7.56	124.44	119.90
1	A	275	G	N1-C6-O6	7.56	124.44	119.90
1	A	1339	A	N1-C6-N6	-7.56	114.06	118.60
4	D	135	LEU	CA-CB-CG	-7.55	97.94	115.30
1	A	656	C	C2-N3-C4	-7.55	116.13	119.90
1	A	329	A	N1-C6-N6	7.54	123.13	118.60
1	A	584	G	N1-C2-N3	-7.54	119.38	123.90
1	A	730	G	N9-C4-C5	7.54	108.42	105.40
1	A	875	C	C2-N3-C4	-7.52	116.14	119.90
1	A	1377	A	N1-C6-N6	-7.52	114.09	118.60
1	A	1190	G	C6-C5-N7	-7.52	125.89	130.40
1	A	654	G	C2-N3-C4	-7.52	108.14	111.90
1	A	511	C	C5-C6-N1	-7.51	117.24	121.00
1	A	117	G	C2-N3-C4	-7.51	108.14	111.90
1	A	1403	C	N3-C4-N4	7.51	123.26	118.00
1	A	319	G	N1-C6-O6	7.51	124.41	119.90
1	A	1087	G	C4-C5-N7	7.51	113.80	110.80
1	A	22	G	N1-C6-O6	7.50	124.40	119.90
1	A	1327	C	C6-N1-C2	7.49	123.30	120.30
1	A	250	A	N1-C6-N6	7.49	123.09	118.60
1	A	167	G	C6-C5-N7	-7.49	125.91	130.40
1	A	16	A	C2-N3-C4	-7.48	106.86	110.60
1	A	389	A	N9-C4-C5	7.48	108.79	105.80
1	A	835	U	C4-C5-C6	7.47	124.18	119.70
1	A	654	G	N3-C2-N2	-7.46	114.68	119.90
1	A	598	U	C5-C6-N1	-7.44	118.98	122.70
1	A	264	U	N1-C2-N3	7.44	119.36	114.90
1	A	816	A	N3-C4-C5	7.43	132.00	126.80
1	A	926	G	C5-C6-N1	-7.43	107.78	111.50
1	A	1156	G	C8-N9-C4	-7.43	103.43	106.40
1	A	1108	G	C8-N9-C4	-7.43	103.43	106.40
1	A	703	G	C5-C6-N1	-7.42	107.79	111.50
1	A	872	A	C4-C5-C6	7.42	120.71	117.00
1	A	830	G	C5-C6-N1	-7.42	107.79	111.50
1	A	581	G	N3-C4-C5	7.42	132.31	128.60
1	A	131	C	N3-C2-O2	-7.41	116.71	121.90
1	A	301	G	C8-N9-C4	-7.41	103.44	106.40
1	A	1500	A	N1-C6-N6	-7.40	114.16	118.60
1	A	1525	G	C5-C6-N1	7.40	115.20	111.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	864	A	C5-N7-C8	7.39	107.59	103.90
1	A	697	U	C6-N1-C2	7.38	125.43	121.00
1	A	316	G	N1-C6-O6	7.38	124.33	119.90
1	A	635	G	C5-C6-N1	-7.37	107.81	111.50
1	A	771	G	C6-C5-N7	-7.37	125.98	130.40
1	A	232	G	C5-C6-N1	-7.36	107.82	111.50
1	A	724	G	N1-C6-O6	7.36	124.31	119.90
1	A	1237	C	C6-N1-C2	-7.36	117.36	120.30
1	A	629	G	N3-C4-C5	-7.35	124.92	128.60
1	A	317	G	C5-C6-O6	-7.35	124.19	128.60
1	A	839	U	N3-C2-O2	-7.35	117.05	122.20
1	A	5	U	C6-N1-C2	7.35	125.41	121.00
1	A	879	C	C2-N3-C4	-7.35	116.23	119.90
1	A	77	G	N3-C4-C5	-7.34	124.93	128.60
1	A	326	G	N3-C4-C5	-7.34	124.93	128.60
1	A	667	G	N1-C6-O6	7.34	124.31	119.90
1	A	806	C	C5-C4-N4	-7.34	115.06	120.20
1	A	788	U	C5-C4-O4	-7.34	121.50	125.90
1	A	247	G	N1-C6-O6	7.34	124.30	119.90
1	A	1501	C	C2-N3-C4	-7.34	116.23	119.90
1	A	540	G	N1-C6-O6	7.33	124.30	119.90
1	A	557	G	C8-N9-C4	-7.33	103.47	106.40
1	A	931	C	N3-C2-O2	-7.33	116.77	121.90
1	A	299	G	N9-C4-C5	-7.32	102.47	105.40
1	A	227	G	C6-C5-N7	-7.31	126.01	130.40
1	A	769	G	C8-N9-C4	7.31	109.32	106.40
1	A	261	U	C6-N1-C2	-7.31	116.61	121.00
1	A	629	G	C8-N9-C4	-7.31	103.48	106.40
1	A	721	G	C5-C6-N1	-7.31	107.85	111.50
1	A	1342	C	N3-C4-N4	7.30	123.11	118.00
1	A	485	G	C4-C5-N7	-7.30	107.88	110.80
1	A	1333	A	N1-C2-N3	7.29	132.95	129.30
1	A	1305	G	N9-C4-C5	7.29	108.32	105.40
1	A	326	G	N1-C2-N3	7.29	128.27	123.90
1	A	518	C	C2-N1-C1'	7.28	126.81	118.80
1	A	1230	C	C5-C6-N1	7.28	124.64	121.00
1	A	724	G	C6-C5-N7	-7.28	126.03	130.40
1	A	919	A	C8-N9-C4	7.28	108.71	105.80
1	A	257	G	C6-C5-N7	-7.27	126.04	130.40
1	A	799	G	C4-C5-N7	7.27	113.71	110.80
1	A	856	C	C6-N1-C2	7.27	123.21	120.30
1	A	789	U	N3-C4-C5	-7.27	110.24	114.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	906	G	C8-N9-C4	7.26	109.30	106.40
1	A	377	G	C8-N9-C1'	-7.26	117.57	127.00
1	A	964	A	C8-N9-C4	-7.25	102.90	105.80
1	A	518	C	N3-C2-O2	-7.25	116.82	121.90
1	A	122	G	C5-C6-O6	-7.25	124.25	128.60
1	A	80	G	N3-C4-C5	-7.25	124.98	128.60
1	A	460	A	C2-N3-C4	7.25	114.22	110.60
1	A	227	G	N1-C6-O6	7.24	124.25	119.90
1	A	693	G	N9-C4-C5	-7.24	102.50	105.40
1	A	718	G	C6-C5-N7	-7.24	126.05	130.40
1	A	400	C	N3-C4-C5	7.23	124.79	121.90
1	A	91	C	C6-N1-C2	-7.23	117.41	120.30
1	A	1235	U	N3-C4-O4	7.23	124.46	119.40
1	A	938	A	C5-C6-N6	7.23	129.48	123.70
1	A	1502	A	C2-N3-C4	-7.23	106.99	110.60
1	A	1525	G	N3-C4-C5	-7.22	124.99	128.60
1	A	758	G	C8-N9-C4	7.21	109.28	106.40
1	A	7	G	N1-C6-O6	7.21	124.22	119.90
1	A	298	A	C6-N1-C2	-7.20	114.28	118.60
1	A	122	G	C6-C5-N7	-7.20	126.08	130.40
1	A	872	A	C2-N3-C4	-7.20	107.00	110.60
1	A	80	G	C6-C5-N7	-7.20	126.08	130.40
1	A	864	A	C5-C6-N1	-7.19	114.11	117.70
1	A	377	G	C4-N9-C1'	7.18	135.84	126.50
1	A	445	G	C4-C5-N7	7.18	113.67	110.80
1	A	1516[A]	G	C5-C6-O6	7.18	132.91	128.60
1	A	1516[B]	G	C5-C6-O6	7.18	132.91	128.60
1	A	762	C	C5-C4-N4	-7.17	115.18	120.20
1	A	7	G	N9-C4-C5	-7.17	102.53	105.40
1	A	1329	A	N1-C6-N6	7.17	122.90	118.60
1	A	407	G	C8-N9-C4	7.16	109.27	106.40
1	A	1528	U	C5-C6-N1	-7.16	119.12	122.70
1	A	524	G	N1-C6-O6	7.15	124.19	119.90
1	A	77	G	N1-C6-O6	-7.15	115.61	119.90
1	A	1030	C	C6-N1-C2	-7.15	117.44	120.30
1	A	300	A	N7-C8-N9	7.15	117.37	113.80
1	A	117	G	N9-C4-C5	-7.14	102.54	105.40
1	A	548	G	N1-C6-O6	7.14	124.19	119.90
1	A	322	C	N3-C4-N4	7.14	123.00	118.00
1	A	596	C	C6-N1-C2	7.14	123.16	120.30
1	A	617	G	N1-C2-N2	-7.14	109.78	116.20
4	D	56	VAL	CB-CA-C	-7.14	97.84	111.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	K	98	LEU	CA-CB-CG	7.13	131.71	115.30
1	A	779	C	N1-C2-N3	7.13	124.19	119.20
1	A	559	A	C6-C5-N7	-7.13	127.31	132.30
1	A	886	G	N1-C6-O6	7.13	124.17	119.90
1	A	1299	A	C4-C5-C6	7.13	120.56	117.00
1	A	1370	G	N3-C4-N9	7.13	130.28	126.00
1	A	562	C	C6-N1-C2	7.12	123.15	120.30
1	A	626	U	N3-C2-O2	-7.12	117.22	122.20
1	A	879	C	C5-C4-N4	-7.12	115.22	120.20
1	A	289	G	C8-N9-C4	-7.12	103.55	106.40
1	A	878	G	C5-N7-C8	-7.12	100.74	104.30
1	A	92	C	C6-N1-C2	7.12	123.15	120.30
1	A	311	C	N3-C2-O2	-7.12	116.92	121.90
1	A	1500	A	C8-N9-C4	-7.12	102.95	105.80
1	A	1532	U	C5-C6-N1	7.12	126.26	122.70
1	A	9	G	N1-C6-O6	7.11	124.17	119.90
1	A	389	A	C4-C5-N7	-7.10	107.15	110.70
1	A	1086	U	N1-C2-O2	7.10	127.77	122.80
1	A	1378	C	C5-C6-N1	7.10	124.55	121.00
1	A	15	G	N3-C4-N9	7.10	130.26	126.00
1	A	900	A	C2-N3-C4	-7.09	107.05	110.60
1	A	1282	C	C6-N1-C2	-7.09	117.47	120.30
1	A	734	G	C4-C5-N7	7.08	113.63	110.80
1	A	626	U	N1-C2-N3	7.08	119.15	114.90
1	A	119	A	N9-C4-C5	7.08	108.63	105.80
1	A	167	G	C5-C6-O6	-7.08	124.35	128.60
1	A	931	C	N1-C2-N3	7.07	124.15	119.20
1	A	116	A	C2-N3-C4	-7.06	107.07	110.60
1	A	17	U	C6-N1-C2	7.06	125.23	121.00
1	A	481	G	C8-N9-C1'	-7.06	117.83	127.00
1	A	1379	G	N3-C4-N9	7.06	130.23	126.00
1	A	289	G	N1-C6-O6	7.06	124.13	119.90
1	A	615	C	C5-C4-N4	-7.05	115.26	120.20
1	A	671	G	N1-C6-O6	7.05	124.13	119.90
1	A	199	G	N1-C6-O6	7.04	124.12	119.90
1	A	52	G	C6-C5-N7	-7.03	126.18	130.40
1	A	583	A	N1-C6-N6	7.03	122.82	118.60
1	A	1178	G	C8-N9-C4	-7.03	103.59	106.40
1	A	693	G	C6-C5-N7	-7.03	126.18	130.40
1	A	947	G	N9-C4-C5	-7.03	102.59	105.40
1	A	592	G	C5-C6-N1	-7.02	107.99	111.50
1	A	1299	A	N7-C8-N9	7.02	117.31	113.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	279	A	C4-C5-N7	7.02	114.21	110.70
1	A	957	U	C6-N1-C2	-7.02	116.79	121.00
1	A	778	G	C5-C6-N1	-7.02	107.99	111.50
1	A	941	G	C5-N7-C8	-7.02	100.79	104.30
1	A	881	G	C6-C5-N7	-7.01	126.19	130.40
1	A	1403	C	C2-N1-C1'	7.01	126.51	118.80
1	A	1335	C	N3-C2-O2	-7.01	116.99	121.90
1	A	451	A	C4-C5-C6	-7.01	113.50	117.00
1	A	141	A	N1-C6-N6	7.00	122.80	118.60
1	A	782	A	N9-C4-C5	7.00	108.60	105.80
1	A	1531	A	C4-C5-N7	6.99	114.20	110.70
1	A	481	G	N9-C4-C5	-6.99	102.60	105.40
1	A	259	G	N7-C8-N9	6.99	116.59	113.10
1	A	1377	A	N3-C4-N9	-6.99	121.81	127.40
1	A	1509	C	N1-C2-N3	6.99	124.09	119.20
1	A	570	G	C4-N9-C1'	6.98	135.57	126.50
1	A	305	G	C8-N9-C4	-6.98	103.61	106.40
1	A	932	C	C6-N1-C2	-6.98	117.51	120.30
1	A	502	G	N1-C6-O6	6.97	124.08	119.90
1	A	606	G	C8-N9-C4	-6.96	103.61	106.40
1	A	92	C	N1-C2-O2	6.96	123.08	118.90
1	A	169	C	N3-C4-C5	-6.96	119.12	121.90
1	A	872	A	C6-C5-N7	-6.96	127.43	132.30
15	O	63	ARG	NE-CZ-NH2	-6.96	116.82	120.30
1	A	1087	G	C5-N7-C8	-6.96	100.82	104.30
1	A	614	A	C5-C6-N1	6.95	121.18	117.70
1	A	649	G	N1-C6-O6	6.95	124.07	119.90
1	A	774	G	C5-N7-C8	-6.95	100.83	104.30
1	A	1502	A	C8-N9-C4	-6.95	103.02	105.80
1	A	23	C	C6-N1-C2	-6.94	117.52	120.30
1	A	569	C	C6-N1-C2	6.94	123.08	120.30
1	A	108	G	N7-C8-N9	6.94	116.57	113.10
1	A	765	G	N3-C4-C5	6.94	132.07	128.60
1	A	289	G	C6-C5-N7	-6.93	126.24	130.40
1	A	289	G	N7-C8-N9	6.93	116.56	113.10
1	A	975	A	C5-N7-C8	-6.93	100.44	103.90
1	A	383	A	C8-N9-C4	-6.92	103.03	105.80
1	A	773	G	C5-C6-O6	-6.92	124.45	128.60
1	A	1370	G	C4-C5-C6	6.92	122.95	118.80
1	A	275	G	C5-C6-N1	-6.91	108.05	111.50
1	A	1202	G	C5-C6-O6	6.90	132.74	128.60
1	A	1305	G	C4-C5-C6	6.89	122.94	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	523	A	N1-C6-N6	6.89	122.73	118.60
1	A	783	C	C6-N1-C2	6.89	123.06	120.30
2	B	23	ARG	N-CA-C	-6.89	92.40	111.00
1	A	107	G	C5-N7-C8	-6.88	100.86	104.30
1	A	511	C	N3-C4-C5	6.88	124.65	121.90
1	A	1212	U	C2-N1-C1'	6.88	125.96	117.70
1	A	928	G	N1-C6-O6	6.87	124.02	119.90
1	A	1333	A	C6-N1-C2	-6.87	114.48	118.60
1	A	22	G	C6-C5-N7	-6.86	126.28	130.40
1	A	869	G	C5-C6-O6	6.86	132.72	128.60
1	A	1462	G	N1-C6-O6	6.86	124.02	119.90
1	A	807	A	C2-N3-C4	-6.86	107.17	110.60
1	A	559	A	C4-C5-C6	6.86	120.43	117.00
1	A	229	U	C6-N1-C2	-6.86	116.89	121.00
1	A	944	G	N1-C2-N2	-6.86	110.03	116.20
1	A	760	G	C5-C6-O6	6.85	132.71	128.60
1	A	311	C	C6-N1-C2	-6.85	117.56	120.30
1	A	686	U	N3-C4-O4	-6.85	114.61	119.40
1	A	15	G	C5-C6-O6	-6.84	124.49	128.60
1	A	1088	G	N3-C4-C5	6.84	132.02	128.60
1	A	483	C	N3-C4-C5	-6.84	119.16	121.90
1	A	1531	A	C4-C5-C6	6.84	120.42	117.00
1	A	599	C	C5-C4-N4	-6.83	115.42	120.20
1	A	734	G	C6-C5-N7	-6.83	126.30	130.40
1	A	243	A	C5-N7-C8	-6.83	100.48	103.90
1	A	820	U	C4-C5-C6	6.82	123.79	119.70
1	A	1367	C	C6-N1-C2	-6.82	117.57	120.30
1	A	650	G	N1-C6-O6	6.82	123.99	119.90
1	A	776	G	C2-N3-C4	-6.81	108.49	111.90
1	A	1442	G	C2-N3-C4	6.81	115.31	111.90
1	A	617	G	C8-N9-C1'	-6.80	118.16	127.00
1	A	301	G	N9-C4-C5	6.80	108.12	105.40
1	A	7	G	C5-C6-O6	-6.79	124.52	128.60
1	A	254	G	C8-N9-C4	6.79	109.11	106.40
1	A	701	C	N1-C2-O2	6.79	122.97	118.90
1	A	784	C	C6-N1-C2	-6.79	117.58	120.30
1	A	329	A	C6-C5-N7	-6.79	127.55	132.30
1	A	698	G	C8-N9-C1'	-6.78	118.18	127.00
1	A	753	A	N1-C6-N6	-6.78	114.53	118.60
1	A	747	C	N3-C4-C5	6.78	124.61	121.90
1	A	1370	G	C5-C6-O6	-6.77	124.54	128.60
1	A	695	A	C2-N3-C4	-6.77	107.22	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	697	U	N3-C4-O4	-6.77	114.66	119.40
1	A	876	G	N1-C6-O6	6.76	123.96	119.90
1	A	779	C	C2-N3-C4	-6.76	116.52	119.90
1	A	1516[A]	G	C4-C5-N7	-6.76	108.10	110.80
1	A	1516[B]	G	C4-C5-N7	-6.76	108.10	110.80
1	A	851	G	N3-C4-N9	6.76	130.06	126.00
1	A	292	G	C5-C6-O6	-6.76	124.55	128.60
1	A	586	C	C4-C5-C6	6.75	120.78	117.40
1	A	261	U	N1-C2-N3	6.75	118.95	114.90
1	A	353	A	C5-C6-N6	6.75	129.10	123.70
1	A	771	G	N9-C4-C5	-6.75	102.70	105.40
1	A	887	G	C5-C6-O6	-6.75	124.55	128.60
1	A	922	G	C4-N9-C1'	6.75	135.28	126.50
1	A	857	C	C6-N1-C2	-6.75	117.60	120.30
1	A	1531	A	C5-N7-C8	-6.75	100.53	103.90
1	A	703	G	N3-C4-C5	-6.74	125.23	128.60
1	A	733	A	C2-N3-C4	-6.74	107.23	110.60
1	A	839	U	C2-N1-C1'	6.74	125.79	117.70
1	A	248	C	C5-C6-N1	-6.74	117.63	121.00
1	A	382	A	C8-N9-C4	-6.74	103.11	105.80
1	A	582	U	C5-C4-O4	-6.74	121.86	125.90
1	A	1088	G	N3-C4-N9	-6.73	121.96	126.00
1	A	760	G	C2-N3-C4	-6.73	108.53	111.90
1	A	796	C	C5-C6-N1	-6.73	117.63	121.00
1	A	1417	G	N9-C4-C5	6.73	108.09	105.40
1	A	145	G	C5-C6-O6	-6.73	124.56	128.60
1	A	342	C	N3-C4-C5	-6.73	119.21	121.90
1	A	769	G	C5-C6-O6	-6.72	124.56	128.60
11	K	117	ASN	N-CA-C	6.72	129.14	111.00
1	A	128	G	C5-N7-C8	-6.72	100.94	104.30
1	A	1087	G	N1-C6-O6	6.71	123.93	119.90
1	A	1167	A	C8-N9-C4	-6.71	103.11	105.80
1	A	605	U	N3-C4-C5	-6.71	110.57	114.60
1	A	150	C	C6-N1-C2	-6.71	117.62	120.30
1	A	593	G	C5-C6-N1	-6.71	108.14	111.50
1	A	698	G	C6-C5-N7	-6.70	126.38	130.40
1	A	721	G	C8-N9-C1'	-6.70	118.29	127.00
1	A	755	G	C6-C5-N7	-6.70	126.38	130.40
1	A	22	G	C5-C6-N1	-6.70	108.15	111.50
1	A	299	G	C6-C5-N7	-6.70	126.38	130.40
1	A	482	A	C2-N3-C4	-6.70	107.25	110.60
1	A	1058	G	C4-C5-N7	-6.69	108.12	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1286	A	C8-N9-C4	-6.69	103.12	105.80
1	A	1377	A	C5-C6-N6	6.69	129.05	123.70
1	A	306	G	C5-C6-N1	-6.68	108.16	111.50
1	A	662	G	C8-N9-C1'	-6.67	118.33	127.00
1	A	1399	C	C6-N1-C2	6.67	122.97	120.30
1	A	1530	G	C4-C5-N7	6.67	113.47	110.80
1	A	1385	G	C4-C5-N7	-6.67	108.13	110.80
1	A	327	A	C5-C6-N1	6.67	121.03	117.70
1	A	1442	G	N9-C4-C5	-6.66	102.73	105.40
1	A	488	C	N3-C4-C5	6.66	124.56	121.90
1	A	797	C	C5-C6-N1	-6.66	117.67	121.00
1	A	1350	A	C8-N9-C4	-6.66	103.14	105.80
1	A	116	A	C5-C6-N1	-6.66	114.37	117.70
1	A	907	A	C2-N3-C4	-6.66	107.27	110.60
1	A	129	U	C4-C5-C6	6.66	123.69	119.70
1	A	140	A	C2-N3-C4	-6.66	107.27	110.60
1	A	899	C	N3-C4-N4	6.66	122.66	118.00
1	A	851	G	C4-N9-C1'	6.65	135.15	126.50
1	A	947	G	N3-C4-N9	6.65	129.99	126.00
1	A	1080	A	C4-C5-N7	-6.64	107.38	110.70
1	A	1447	G	C4-C5-N7	6.64	113.46	110.80
1	A	819	A	C4-C5-C6	6.64	120.32	117.00
1	A	111	G	N1-C6-O6	6.64	123.88	119.90
1	A	1510	U	C4-C5-C6	6.64	123.68	119.70
1	A	573	A	C5-C6-N6	-6.64	118.39	123.70
1	A	902	G	C5-C6-N1	6.63	114.81	111.50
1	A	1358	U	N3-C2-O2	-6.63	117.56	122.20
1	A	326	G	C4-C5-C6	6.62	122.77	118.80
1	A	511	C	N3-C4-N4	-6.61	113.37	118.00
1	A	860	A	C6-N1-C2	-6.61	114.63	118.60
1	A	1470	G	N1-C6-O6	6.61	123.87	119.90
1	A	523	A	C2-N3-C4	-6.61	107.30	110.60
1	A	813	U	C5-C6-N1	6.60	126.00	122.70
1	A	1081	G	N1-C6-O6	6.60	123.86	119.90
1	A	47	C	C6-N1-C2	6.60	122.94	120.30
1	A	859	A	C5-N7-C8	-6.60	100.60	103.90
1	A	509	A	C8-N9-C4	-6.60	103.16	105.80
1	A	932	C	N3-C2-O2	-6.59	117.28	121.90
1	A	565	U	N3-C2-O2	6.59	126.81	122.20
1	A	129(A)	G	N9-C4-C5	-6.59	102.77	105.40
1	A	167	G	C4-C5-N7	6.59	113.43	110.80
1	A	285	G	N1-C2-N3	6.59	127.85	123.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	813	U	C5-C4-O4	-6.59	121.95	125.90
1	A	450	G	N7-C8-N9	-6.57	109.81	113.10
1	A	873	A	N9-C4-C5	6.57	108.43	105.80
1	A	117	G	C5-C6-O6	-6.57	124.66	128.60
1	A	777	A	N1-C6-N6	6.56	122.54	118.60
1	A	671	G	C6-C5-N7	-6.56	126.46	130.40
1	A	959	A	C8-N9-C4	-6.56	103.17	105.80
1	A	16	A	N1-C2-N3	6.56	132.58	129.30
1	A	226	G	N9-C4-C5	-6.56	102.78	105.40
1	A	888	G	C5-C6-N1	-6.55	108.22	111.50
1	A	1181	G	C4-N9-C1'	-6.55	117.98	126.50
1	A	599	C	C5-C6-N1	-6.55	117.73	121.00
17	Q	98	LEU	CA-CB-CG	6.55	130.36	115.30
1	A	1233	G	N1-C6-O6	6.54	123.83	119.90
1	A	1442	G	C5-C6-O6	-6.54	124.67	128.60
1	A	1513	A	C2-N3-C4	-6.54	107.33	110.60
1	A	141	A	N9-C4-C5	-6.54	103.18	105.80
1	A	600	C	N3-C4-N4	-6.54	113.42	118.00
1	A	813	U	N3-C4-O4	6.54	123.98	119.40
1	A	583	A	C5-C6-N6	-6.54	118.47	123.70
1	A	609	A	C5-C6-N1	-6.54	114.43	117.70
1	A	226	G	C8-N9-C4	6.54	109.01	106.40
1	A	942	G	N1-C6-O6	6.53	123.82	119.90
1	A	696	A	C6-N1-C2	-6.53	114.68	118.60
1	A	697	U	C2-N1-C1'	-6.53	109.86	117.70
1	A	786	G	C8-N9-C4	-6.53	103.79	106.40
1	A	1330	U	C5-C4-O4	-6.53	121.98	125.90
1	A	353	A	N9-C4-C5	6.52	108.41	105.80
1	A	782	A	C4-C5-C6	6.52	120.26	117.00
1	A	454	C	N1-C2-O2	6.52	122.81	118.90
1	A	898	G	C8-N9-C4	6.52	109.01	106.40
1	A	10	A	N1-C6-N6	-6.51	114.69	118.60
1	A	760	G	C4-C5-N7	-6.51	108.20	110.80
1	A	854	G	C8-N9-C1'	-6.51	118.54	127.00
1	A	758	G	C5-C6-N1	-6.51	108.25	111.50
1	A	881	G	C5-C6-O6	-6.51	124.70	128.60
1	A	1508	G	C5-C6-N1	6.51	114.75	111.50
1	A	76	C	C5-C6-N1	-6.50	117.75	121.00
1	A	1269	A	C2-N3-C4	-6.50	107.35	110.60
1	A	396	G	N3-C4-C5	-6.50	125.35	128.60
1	A	944	G	N3-C4-C5	-6.50	125.35	128.60
1	A	562	C	N1-C2-O2	6.49	122.80	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	814	A	C8-N9-C4	6.49	108.40	105.80
1	A	686	U	N3-C2-O2	-6.49	117.66	122.20
1	A	1510	U	C5-C4-O4	6.49	129.79	125.90
1	A	729	A	N1-C6-N6	6.49	122.49	118.60
1	A	317	G	N9-C4-C5	-6.49	102.81	105.40
1	A	594	G	N1-C2-N2	-6.49	110.36	116.20
1	A	1376	U	C5-C6-N1	-6.49	119.46	122.70
1	A	880	C	C5-C4-N4	-6.48	115.66	120.20
1	A	589	C	C5-C6-N1	-6.48	117.76	121.00
1	A	728	A	N1-C2-N3	6.48	132.54	129.30
1	A	753	A	C6-N1-C2	-6.48	114.71	118.60
1	A	1274	G	C8-N9-C4	-6.48	103.81	106.40
1	A	58	C	C6-N1-C2	-6.47	117.71	120.30
1	A	889	A	N1-C2-N3	6.47	132.54	129.30
1	A	322	C	C4-C5-C6	6.47	120.64	117.40
1	A	858	G	N3-C2-N2	6.47	124.43	119.90
1	A	279	A	N1-C2-N3	6.46	132.53	129.30
1	A	7	G	C4-C5-N7	6.46	113.38	110.80
1	A	53	A	C6-N1-C2	-6.46	114.72	118.60
1	A	1305	G	C5-C6-N1	-6.46	108.27	111.50
1	A	46	G	N1-C6-O6	6.45	123.77	119.90
1	A	1379	G	C6-N1-C2	-6.45	121.23	125.10
1	A	132	C	N3-C2-O2	-6.45	117.39	121.90
1	A	755	G	C4-N9-C1'	6.44	134.88	126.50
1	A	242	C	C2-N3-C4	-6.44	116.68	119.90
1	A	14	U	C6-N1-C2	-6.44	117.14	121.00
1	A	728	A	C6-C5-N7	-6.44	127.79	132.30
1	A	750	G	N3-C4-C5	-6.43	125.38	128.60
1	A	119	A	N1-C6-N6	-6.43	114.74	118.60
1	A	858	G	N1-C6-O6	-6.43	116.04	119.90
1	A	1318	A	C4-C5-C6	-6.43	113.78	117.00
1	A	708	C	N3-C4-C5	6.43	124.47	121.90
1	A	67	C	C6-N1-C2	-6.42	117.73	120.30
5	E	152	ARG	NE-CZ-NH2	-6.42	117.09	120.30
1	A	1416	G	C8-N9-C4	-6.42	103.83	106.40
1	A	370	C	N1-C2-O2	6.42	122.75	118.90
1	A	425	G	N3-C4-C5	-6.42	125.39	128.60
1	A	1098	C	C6-N1-C2	6.42	122.87	120.30
1	A	1269	A	C8-N9-C4	6.42	108.37	105.80
1	A	626	U	C2-N1-C1'	6.42	125.40	117.70
1	A	1514	C	N3-C2-O2	-6.42	117.41	121.90
1	A	657	G	C6-C5-N7	-6.41	126.55	130.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	722	A	C4-C5-N7	6.41	113.91	110.70
1	A	558	G	C5-C6-O6	-6.41	124.75	128.60
1	A	941	G	N7-C8-N9	6.41	116.31	113.10
1	A	732	C	C6-N1-C2	6.41	122.86	120.30
1	A	1380	U	C5-C6-N1	-6.41	119.50	122.70
1	A	450	G	C5-C6-O6	6.40	132.44	128.60
1	A	752	G	C4-C5-N7	-6.40	108.24	110.80
1	A	869	G	C5-N7-C8	6.40	107.50	104.30
1	A	32	A	N1-C2-N3	6.39	132.50	129.30
1	A	703	G	C8-N9-C4	-6.39	103.84	106.40
1	A	941	G	C4-C5-N7	6.39	113.36	110.80
1	A	851	G	N3-C4-C5	-6.39	125.41	128.60
1	A	576	G	C8-N9-C1'	-6.38	118.70	127.00
1	A	887	G	C4-C5-N7	6.38	113.35	110.80
1	A	552	U	N1-C2-N3	6.38	118.73	114.90
1	A	248	C	C2-N3-C4	-6.38	116.71	119.90
1	A	833	U	N1-C2-N3	6.38	118.72	114.90
1	A	400	C	C6-N1-C2	6.37	122.85	120.30
1	A	757	U	N3-C4-C5	-6.37	110.78	114.60
1	A	789	U	C5-C4-O4	6.37	129.72	125.90
1	A	277	C	N3-C4-C5	6.37	124.45	121.90
1	A	859	A	N7-C8-N9	6.37	116.98	113.80
1	A	1455	G	C4-C5-N7	6.37	113.35	110.80
1	A	1508	G	N3-C4-C5	-6.37	125.42	128.60
1	A	583	A	C4-C5-N7	6.36	113.88	110.70
1	A	357	G	C2-N3-C4	-6.36	108.72	111.90
1	A	26	A	C2-N3-C4	-6.35	107.42	110.60
1	A	1359	C	C6-N1-C2	-6.35	117.76	120.30
1	A	871	U	N1-C2-N3	-6.35	111.09	114.90
1	A	1107	C	N3-C4-C5	-6.35	119.36	121.90
1	A	451	A	C4-C5-N7	6.35	113.87	110.70
1	A	755	G	C8-N9-C1'	-6.35	118.75	127.00
1	A	576	G	C4-N9-C1'	6.35	134.75	126.50
1	A	910	C	C6-N1-C2	6.35	122.84	120.30
1	A	861	G	C6-N1-C2	-6.34	121.29	125.10
1	A	1508	G	N7-C8-N9	6.34	116.27	113.10
1	A	832	C	N1-C2-O2	-6.34	115.10	118.90
1	A	1139	G	N3-C4-C5	-6.34	125.43	128.60
1	A	1299	A	N1-C2-N3	6.33	132.47	129.30
1	A	7	G	N1-C2-N2	-6.33	110.50	116.20
1	A	251	G	N1-C2-N2	-6.33	110.50	116.20
1	A	628	G	N3-C4-C5	-6.33	125.44	128.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1442	G	N3-C2-N2	6.33	124.33	119.90
1	A	862	C	N1-C2-N3	-6.32	114.78	119.20
1	A	481	G	C5-C6-O6	-6.32	124.81	128.60
1	A	160	A	C8-N9-C4	-6.31	103.28	105.80
1	A	818	G	C2-N3-C4	6.31	115.05	111.90
1	A	1514	C	C2-N3-C4	-6.31	116.75	119.90
1	A	657	G	C4-C5-C6	6.31	122.58	118.80
1	A	811	C	N3-C4-C5	-6.31	119.38	121.90
1	A	52	G	N3-C4-N9	6.30	129.78	126.00
1	A	893	C	C6-N1-C2	-6.30	117.78	120.30
2	B	221	LEU	CA-CB-CG	6.30	129.79	115.30
1	A	377	G	C6-C5-N7	-6.30	126.62	130.40
1	A	945	G	C4-C5-N7	6.29	113.32	110.80
1	A	900	A	C4-C5-N7	6.29	113.85	110.70
1	A	974	A	N1-C6-N6	-6.29	114.83	118.60
1	A	515	G	C6-C5-N7	-6.29	126.63	130.40
1	A	1082	G	N1-C6-O6	6.29	123.67	119.90
1	A	1509	C	C5-C6-N1	-6.29	117.86	121.00
5	E	115	VAL	CB-CA-C	-6.29	99.45	111.40
1	A	1108	G	N9-C4-C5	6.29	107.92	105.40
1	A	1200	C	C6-N1-C1'	-6.29	113.26	120.80
1	A	91	C	C5-C6-N1	6.29	124.14	121.00
1	A	15	G	C6-C5-N7	-6.28	126.63	130.40
1	A	796	C	C2-N3-C4	-6.28	116.76	119.90
1	A	924	C	N1-C2-O2	-6.28	115.13	118.90
1	A	1330	U	N3-C4-O4	6.28	123.80	119.40
1	A	765	G	C5-C6-N1	-6.28	108.36	111.50
1	A	280	C	N3-C4-N4	-6.27	113.61	118.00
1	A	802	A	N1-C6-N6	6.27	122.36	118.60
1	A	1528	U	C6-N1-C2	6.27	124.76	121.00
1	A	854	G	C4-N9-C1'	6.27	134.65	126.50
1	A	388	G	C4-C5-N7	-6.26	108.29	110.80
1	A	754	C	N3-C2-O2	-6.26	117.52	121.90
1	A	526	C	C6-N1-C2	6.26	122.81	120.30
1	A	731	G	C5-C6-O6	-6.26	124.84	128.60
1	A	76	C	C5-C4-N4	6.26	124.58	120.20
1	A	119	A	C6-N1-C2	-6.26	114.84	118.60
1	A	584	G	C2-N3-C4	6.26	115.03	111.90
1	A	1186	G	C5-C6-N1	-6.26	108.37	111.50
15	O	57	LEU	CB-CG-CD1	-6.26	100.36	111.00
1	A	782	A	C2-N3-C4	-6.25	107.47	110.60
1	A	924	C	C6-N1-C2	-6.25	117.80	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1332	A	N9-C4-C5	6.25	108.30	105.80
17	Q	99	SER	N-CA-C	6.25	127.87	111.00
1	A	570	G	C8-N9-C4	-6.24	103.90	106.40
1	A	1373	G	C5-C6-O6	6.24	132.35	128.60
1	A	332	G	N3-C2-N2	-6.24	115.53	119.90
1	A	124	G	N1-C2-N3	6.24	127.64	123.90
1	A	617	G	N9-C4-C5	-6.24	102.90	105.40
1	A	290	C	C2-N3-C4	-6.24	116.78	119.90
1	A	662	G	C6-C5-N7	-6.24	126.66	130.40
1	A	1232	U	N1-C2-O2	-6.23	118.44	122.80
1	A	328	C	C2-N3-C4	6.23	123.02	119.90
1	A	1501	C	C5-C6-N1	-6.23	117.88	121.00
1	A	183	G	C4-C5-N7	6.23	113.29	110.80
1	A	659	U	C2-N3-C4	-6.23	123.26	127.00
1	A	1376	U	N3-C2-O2	-6.23	117.84	122.20
1	A	713	G	C8-N9-C4	-6.22	103.91	106.40
1	A	882	C	N1-C2-N3	6.22	123.56	119.20
1	A	229	U	N1-C2-N3	6.22	118.63	114.90
1	A	1525	G	C2-N3-C4	6.22	115.01	111.90
1	A	1509	C	C2-N3-C4	-6.22	116.79	119.90
1	A	658	G	N9-C4-C5	-6.22	102.91	105.40
1	A	377	G	N3-C4-C5	-6.22	125.49	128.60
1	A	658	G	N1-C6-O6	6.22	123.63	119.90
1	A	881	G	N1-C2-N3	6.22	127.63	123.90
1	A	1205	U	N3-C2-O2	-6.21	117.85	122.20
1	A	931	C	N3-C4-N4	-6.21	113.65	118.00
1	A	565	U	N3-C4-C5	6.21	118.33	114.60
1	A	873	A	N1-C6-N6	-6.21	114.88	118.60
1	A	650	G	C5-C6-O6	-6.21	124.88	128.60
1	A	654	G	N1-C6-O6	6.20	123.62	119.90
1	A	24	U	C5-C6-N1	-6.20	119.60	122.70
1	A	605	U	C4-C5-C6	6.20	123.42	119.70
1	A	635	G	C2-N3-C4	-6.20	108.80	111.90
1	A	728	A	N1-C6-N6	6.20	122.32	118.60
1	A	1299	A	C5-N7-C8	-6.20	100.80	103.90
1	A	1373	G	C5-N7-C8	6.20	107.40	104.30
20	T	94	ALA	N-CA-C	-6.20	94.27	111.00
1	A	257	G	N1-C6-O6	6.20	123.62	119.90
1	A	401	C	N3-C4-C5	6.20	124.38	121.90
17	Q	22	LEU	CA-CB-CG	-6.20	101.05	115.30
1	A	184	G	C5-C6-O6	-6.19	124.89	128.60
1	A	266	G	C4-N9-C1'	6.19	134.54	126.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	24	U	C6-N1-C2	6.18	124.71	121.00
1	A	80	G	N7-C8-N9	6.18	116.19	113.10
1	A	925	G	C8-N9-C4	-6.17	103.93	106.40
1	A	122	G	C4-C5-N7	6.17	113.27	110.80
1	A	250	A	N3-C4-C5	6.17	131.12	126.80
1	A	623	C	C6-N1-C2	6.17	122.77	120.30
1	A	64	G	C4-C5-N7	6.17	113.27	110.80
1	A	835	U	C5-C6-N1	-6.17	119.62	122.70
1	A	863	U	C2-N1-C1'	-6.17	110.30	117.70
1	A	946	A	N1-C2-N3	6.17	132.38	129.30
1	A	872	A	C5-C6-N1	-6.16	114.62	117.70
1	A	77	G	C5-C6-N1	6.15	114.58	111.50
1	A	78	G	N1-C6-O6	6.15	123.59	119.90
1	A	142	G	N3-C4-C5	-6.15	125.52	128.60
1	A	577	G	N3-C4-C5	6.15	131.68	128.60
1	A	1412	C	C6-N1-C2	-6.15	117.84	120.30
1	A	708	C	C6-N1-C2	6.15	122.76	120.30
1	A	1447	G	C5-N7-C8	-6.15	101.23	104.30
1	A	141	A	C2-N3-C4	-6.14	107.53	110.60
1	A	590	C	C6-N1-C2	6.14	122.76	120.30
1	A	285	G	C5-C6-N1	-6.14	108.43	111.50
1	A	294	U	C6-N1-C2	6.14	124.69	121.00
1	A	780	A	N1-C2-N3	6.14	132.37	129.30
1	A	279	A	N3-C4-N9	-6.14	122.49	127.40
1	A	153	C	C6-N1-C2	-6.13	117.85	120.30
1	A	633	G	C4-C5-N7	6.13	113.25	110.80
1	A	589	C	C2-N3-C4	-6.13	116.83	119.90
1	A	1530	G	N3-C4-C5	6.13	131.67	128.60
1	A	226	G	C5-C6-O6	-6.13	124.92	128.60
1	A	253	U	N1-C2-O2	-6.13	118.51	122.80
1	A	574	A	N3-C4-N9	-6.13	122.49	127.40
1	A	1238	A	N1-C6-N6	6.13	122.28	118.60
1	A	1268	A	N9-C4-C5	6.13	108.25	105.80
1	A	451	A	N3-C4-C5	6.13	131.09	126.80
1	A	729	A	C6-C5-N7	-6.13	128.01	132.30
1	A	1071	C	C6-N1-C2	6.13	122.75	120.30
1	A	1129	C	C6-N1-C2	-6.13	117.85	120.30
1	A	43	C	C6-N1-C2	6.12	122.75	120.30
1	A	787	A	C4-C5-N7	6.12	113.76	110.70
1	A	450	G	C4-C5-N7	-6.12	108.35	110.80
1	A	830	G	N1-C6-O6	6.12	123.57	119.90
1	A	882	C	C2-N3-C4	-6.12	116.84	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	760	G	N3-C4-N9	-6.12	122.33	126.00
1	A	925	G	N7-C8-N9	6.12	116.16	113.10
1	A	439	A	C8-N9-C4	-6.11	103.36	105.80
1	A	662	G	C4-N9-C1'	6.11	134.44	126.50
1	A	1192	C	N3-C4-C5	6.11	124.34	121.90
1	A	16	A	N7-C8-N9	-6.11	110.75	113.80
1	A	526	C	N1-C2-O2	6.11	122.56	118.90
1	A	120	A	C8-N9-C4	6.10	108.24	105.80
1	A	590	C	C5-C6-N1	-6.10	117.95	121.00
1	A	319	G	C4-N9-C1'	6.10	134.43	126.50
1	A	1497	G	N3-C4-C5	-6.10	125.55	128.60
1	A	119	A	C5-C6-N1	6.10	120.75	117.70
1	A	568	G	C8-N9-C4	-6.10	103.96	106.40
1	A	720	C	N1-C2-O2	6.10	122.56	118.90
1	A	868	C	N1-C2-N3	6.10	123.47	119.20
1	A	573	A	C8-N9-C4	-6.09	103.36	105.80
1	A	276	G	C8-N9-C4	6.09	108.84	106.40
1	A	1421	G	C8-N9-C4	-6.09	103.96	106.40
1	A	519	C	N1-C2-O2	6.09	122.55	118.90
1	A	1442	G	C4-C5-C6	6.09	122.45	118.80
1	A	573	A	C6-C5-N7	-6.09	128.04	132.30
1	A	660	G	C4-C5-N7	6.09	113.23	110.80
1	A	753	A	C2-N3-C4	-6.09	107.56	110.60
1	A	971	G	N1-C6-O6	6.08	123.55	119.90
1	A	1403	C	C6-N1-C1'	-6.08	113.50	120.80
1	A	268	C	N3-C4-C5	-6.08	119.47	121.90
1	A	320	C	C5-C6-N1	-6.08	117.96	121.00
1	A	1162	C	C6-N1-C2	6.08	122.73	120.30
1	A	47	C	C6-N1-C1'	-6.07	113.52	120.80
1	A	232	G	C8-N9-C4	6.07	108.83	106.40
1	A	46	G	C2-N3-C4	-6.07	108.87	111.90
1	A	975	A	C4-C5-N7	6.07	113.73	110.70
1	A	1442	G	N7-C8-N9	6.07	116.13	113.10
1	A	807	A	N1-C2-N3	6.06	132.33	129.30
1	A	167	G	C8-N9-C1'	-6.06	119.12	127.00
1	A	574	A	N3-C4-C5	6.06	131.04	126.80
1	A	1131	G	C8-N9-C4	-6.06	103.98	106.40
1	A	141	A	N3-C4-C5	6.06	131.04	126.80
1	A	305	G	C5-C6-O6	6.06	132.24	128.60
1	A	572	A	C5-C6-N1	6.06	120.73	117.70
1	A	789	U	C6-N1-C2	-6.05	117.37	121.00
1	A	881	G	C6-N1-C2	-6.05	121.47	125.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1161	C	C6-N1-C2	-6.05	117.88	120.30
1	A	644	G	C5-C6-O6	-6.05	124.97	128.60
1	A	1224	G	C4-N9-C1'	-6.05	118.63	126.50
1	A	370	C	N3-C2-O2	-6.05	117.67	121.90
1	A	816	A	N3-C4-N9	-6.05	122.56	127.40
1	A	662	G	N3-C4-N9	6.05	129.63	126.00
1	A	558	G	N1-C6-O6	6.04	123.53	119.90
1	A	591	U	C2-N3-C4	-6.04	123.37	127.00
1	A	322	C	N3-C4-C5	-6.04	119.48	121.90
1	A	1131	G	C6-C5-N7	-6.03	126.78	130.40
1	A	636	U	N3-C4-O4	6.03	123.62	119.40
1	A	24	U	C2-N3-C4	-6.03	123.38	127.00
1	A	817	C	C2-N1-C1'	6.03	125.43	118.80
1	A	835	U	N3-C4-C5	-6.03	110.98	114.60
1	A	867	G	N3-C4-N9	6.03	129.62	126.00
1	A	16	A	C8-N9-C4	6.02	108.21	105.80
1	A	1542	U	N1-C2-N3	-6.02	111.29	114.90
1	A	569	C	N1-C2-O2	-6.02	115.29	118.90
1	A	687	A	P-O3'-C3'	6.02	126.92	119.70
1	A	1314	C	C6-N1-C2	-6.02	117.89	120.30
1	A	1529	G	N7-C8-N9	6.02	116.11	113.10
1	A	644	G	C5-N7-C8	-6.02	101.29	104.30
1	A	720	C	C2-N1-C1'	6.02	125.42	118.80
1	A	1081	G	C5-C6-O6	-6.02	124.99	128.60
1	A	643	C	N3-C4-N4	-6.02	113.79	118.00
1	A	799	G	N9-C4-C5	-6.01	102.99	105.40
1	A	697	U	C5-C6-N1	-6.01	119.69	122.70
1	A	279	A	C4-C5-C6	6.01	120.01	117.00
1	A	597	G	N3-C4-N9	6.01	129.61	126.00
1	A	1058	G	C5-C6-O6	6.01	132.21	128.60
1	A	758	G	C4-C5-C6	6.01	122.41	118.80
1	A	639	G	C2-N3-C4	-6.01	108.90	111.90
1	A	1371	G	C8-N9-C4	-6.01	104.00	106.40
1	A	660	G	C6-C5-N7	-6.00	126.80	130.40
1	A	231	G	N1-C6-O6	6.00	123.50	119.90
1	A	231	G	N9-C4-C5	-6.00	103.00	105.40
1	A	251	G	N3-C4-C5	-5.99	125.60	128.60
1	A	1395	C	N3-C2-O2	5.99	126.10	121.90
1	A	1336	C	N1-C2-O2	5.99	122.49	118.90
1	A	68	G	N3-C4-N9	-5.99	122.41	126.00
1	A	110	C	N3-C2-O2	5.99	126.09	121.90
1	A	366	C	N3-C2-O2	-5.98	117.71	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	518	C	C6-N1-C1'	-5.98	113.62	120.80
1	A	851	G	C8-N9-C1'	-5.98	119.22	127.00
1	A	80	G	C4-C5-C6	5.98	122.39	118.80
1	A	110	C	C6-N1-C2	5.98	122.69	120.30
1	A	815	A	N7-C8-N9	-5.97	110.81	113.80
1	A	27	G	C5-N7-C8	-5.97	101.31	104.30
1	A	1446	A	C8-N9-C4	5.97	108.19	105.80
1	A	584	G	N1-C6-O6	5.97	123.48	119.90
1	A	894	G	N1-C6-O6	5.97	123.48	119.90
1	A	1477	C	C6-N1-C2	-5.96	117.91	120.30
1	A	129(A)	G	C4-C5-N7	5.96	113.19	110.80
1	A	1322	C	C2-N1-C1'	5.96	125.36	118.80
1	A	59	A	C4-C5-N7	5.96	113.68	110.70
1	A	817	C	C2-N3-C4	-5.96	116.92	119.90
1	A	281	G	P-O3'-C3'	5.96	126.85	119.70
1	A	859	A	C5-C6-N6	-5.96	118.94	123.70
1	A	754	C	C2-N1-C1'	5.96	125.35	118.80
1	A	281	G	C5-C6-N1	-5.95	108.52	111.50
1	A	861	G	C5-C6-O6	-5.95	125.03	128.60
1	A	1354	C	C6-N1-C2	-5.95	117.92	120.30
1	A	357	G	C5-C6-O6	-5.95	125.03	128.60
1	A	639	G	N1-C2-N3	5.95	127.47	123.90
1	A	620	C	C5-C4-N4	-5.95	116.03	120.20
1	A	899	C	C2-N1-C1'	5.95	125.34	118.80
1	A	909	A	C5-C6-N6	-5.95	118.94	123.70
1	A	944	G	C4-N9-C1'	5.95	134.23	126.50
1	A	329	A	N1-C2-N3	5.94	132.27	129.30
1	A	127	G	C8-N9-C4	5.94	108.78	106.40
1	A	304	U	C5-C6-N1	-5.94	119.73	122.70
1	A	757	U	C4-C5-C6	5.94	123.26	119.70
1	A	92	C	C6-N1-C1'	-5.93	113.68	120.80
1	A	569	C	N3-C4-N4	-5.93	113.85	118.00
1	A	778	G	N1-C6-O6	5.93	123.46	119.90
1	A	617	G	N3-C4-N9	5.93	129.56	126.00
1	A	111	G	N3-C4-N9	-5.93	122.44	126.00
1	A	59	A	C5-N7-C8	-5.93	100.94	103.90
1	A	540	G	C5-C6-O6	-5.93	125.05	128.60
1	A	569	C	C2-N1-C1'	-5.93	112.28	118.80
1	A	722	A	C5-N7-C8	-5.93	100.94	103.90
1	A	941	G	C5-C6-O6	-5.92	125.05	128.60
1	A	722	A	N9-C4-C5	-5.92	103.43	105.80
1	A	857	C	N3-C4-C5	-5.92	119.53	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	53	A	C5-C6-N1	5.92	120.66	117.70
1	A	121	C	N1-C2-O2	-5.92	115.35	118.90
1	A	379	C	C2-N3-C4	-5.92	116.94	119.90
2	B	44	LEU	CA-CB-CG	-5.92	101.70	115.30
1	A	873	A	C5-C6-N1	5.91	120.66	117.70
1	A	43	C	C5-C6-N1	-5.91	118.05	121.00
1	A	724	G	N7-C8-N9	5.91	116.05	113.10
1	A	851	G	C6-C5-N7	-5.90	126.86	130.40
1	A	197	A	C8-N9-C4	5.90	108.16	105.80
1	A	718	G	N7-C8-N9	5.90	116.05	113.10
1	A	27	G	C4-C5-N7	5.90	113.16	110.80
1	A	931	C	C4-C5-C6	5.90	120.35	117.40
1	A	294	U	C5-C6-N1	-5.89	119.75	122.70
1	A	691	G	C4-C5-N7	5.89	113.16	110.80
1	A	828	A	N1-C6-N6	5.89	122.14	118.60
1	A	578	C	C6-N1-C2	-5.89	117.94	120.30
1	A	95	U	C5-C6-N1	5.89	125.64	122.70
1	A	910	C	N3-C4-C5	5.89	124.26	121.90
1	A	720	C	C6-N1-C2	-5.89	117.94	120.30
1	A	553	A	C8-N9-C4	5.88	108.15	105.80
1	A	864	A	N7-C8-N9	-5.88	110.86	113.80
1	A	947	G	N3-C2-N2	5.88	124.02	119.90
1	A	1428	A	N1-C6-N6	5.88	122.13	118.60
1	A	488	C	C6-N1-C2	5.88	122.65	120.30
1	A	1226	C	N1-C2-O2	5.88	122.43	118.90
1	A	25	C	C6-N1-C2	5.88	122.65	120.30
1	A	881	G	N3-C4-N9	5.88	129.53	126.00
1	A	1531	A	C6-N1-C2	5.88	122.13	118.60
1	A	824	C	C5-C6-N1	-5.88	118.06	121.00
1	A	329	A	C4-C5-C6	5.87	119.94	117.00
1	A	583	A	C5-N7-C8	-5.87	100.97	103.90
1	A	633	G	C5-C6-O6	-5.87	125.08	128.60
1	A	814	A	C6-N1-C2	-5.87	115.08	118.60
1	A	542	G	N3-C4-C5	-5.87	125.67	128.60
12	L	15	ARG	NE-CZ-NH1	5.87	123.23	120.30
1	A	761	G	N3-C4-N9	-5.87	122.48	126.00
1	A	1490	C	C4-C5-C6	-5.86	114.47	117.40
1	A	597	G	N1-C2-N3	5.86	127.42	123.90
12	L	26	ALA	N-CA-C	-5.86	95.19	111.00
1	A	144	G	C5-C6-N1	-5.86	108.57	111.50
1	A	407	G	N3-C4-C5	5.86	131.53	128.60
1	A	907	A	N9-C4-C5	5.85	108.14	105.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	811	C	C6-N1-C1'	-5.85	113.78	120.80
1	A	823	G	N1-C2-N3	5.85	127.41	123.90
1	A	1316	G	C8-N9-C4	5.85	108.74	106.40
1	A	310	G	C5-C6-O6	-5.85	125.09	128.60
1	A	446	G	C4-N9-C1'	5.85	134.10	126.50
1	A	1149	C	C5-C6-N1	5.85	123.92	121.00
1	A	250	A	C6-N1-C2	5.84	122.11	118.60
1	A	907	A	C8-N9-C4	-5.84	103.46	105.80
1	A	1516[A]	G	N7-C8-N9	5.84	116.02	113.10
1	A	1516[B]	G	N7-C8-N9	5.84	116.02	113.10
1	A	295	C	N3-C4-N4	-5.84	113.91	118.00
1	A	906	G	N9-C4-C5	-5.84	103.06	105.40
1	A	530	G	C8-N9-C4	-5.84	104.07	106.40
1	A	935	A	N9-C4-C5	5.83	108.13	105.80
1	A	450	G	C5-N7-C8	5.83	107.21	104.30
1	A	32	A	C6-N1-C2	-5.83	115.11	118.60
1	A	632	A	C8-N9-C4	-5.83	103.47	105.80
1	A	1103	C	C2-N3-C4	-5.83	116.99	119.90
1	A	482	A	C5-N7-C8	-5.82	100.99	103.90
1	A	1299	A	C8-N9-C4	-5.82	103.47	105.80
1	A	307	C	C5-C6-N1	5.82	123.91	121.00
1	A	363	A	C8-N9-C4	-5.82	103.47	105.80
1	A	8	A	N9-C4-C5	5.82	108.13	105.80
1	A	580	U	N3-C4-O4	5.82	123.47	119.40
1	A	360	A	C8-N9-C4	-5.82	103.47	105.80
1	A	572	A	C6-N1-C2	-5.82	115.11	118.60
1	A	1203	C	C5-C6-N1	5.81	123.91	121.00
1	A	938	A	N9-C4-C5	5.81	108.12	105.80
1	A	981	U	N3-C4-O4	5.81	123.47	119.40
1	A	1178	G	N9-C4-C5	5.81	107.72	105.40
1	A	1530	G	N1-C6-O6	5.81	123.39	119.90
1	A	221	C	N3-C4-N4	-5.81	113.93	118.00
1	A	279	A	N3-C4-C5	5.81	130.86	126.80
1	A	319	G	C5-N7-C8	-5.80	101.40	104.30
1	A	327	A	C6-N1-C2	-5.80	115.12	118.60
1	A	654	G	N3-C4-C5	5.80	131.50	128.60
1	A	684	A	N9-C4-C5	5.80	108.12	105.80
1	A	722	A	N3-C4-C5	5.80	130.86	126.80
1	A	849	C	N3-C4-C5	5.80	124.22	121.90
1	A	1295	G	N7-C8-N9	5.80	116.00	113.10
1	A	574	A	C2-N3-C4	-5.80	107.70	110.60
1	A	326	G	C4-N9-C1'	5.80	134.04	126.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	413	G	C5-C6-O6	-5.79	125.12	128.60
1	A	615	C	C2-N1-C1'	5.79	125.17	118.80
1	A	947	G	N1-C2-N2	-5.79	110.98	116.20
1	A	1190	G	N3-C4-C5	-5.79	125.70	128.60
1	A	914	G	N1-C2-N2	5.79	121.41	116.20
1	A	577	G	C2-N3-C4	-5.79	109.01	111.90
1	A	1478	C	C5-C6-N1	5.78	123.89	121.00
1	A	486	U	C6-N1-C2	5.78	124.47	121.00
1	A	80	G	N1-C6-O6	5.78	123.37	119.90
1	A	908	A	C2-N3-C4	-5.78	107.71	110.60
1	A	1376	U	N3-C4-O4	-5.78	115.35	119.40
1	A	597	G	N3-C4-C5	-5.78	125.71	128.60
1	A	639	G	C8-N9-C4	5.78	108.71	106.40
1	A	1370	G	C8-N9-C1'	-5.78	119.49	127.00
1	A	199	G	N3-C2-N2	-5.77	115.86	119.90
1	A	1356	G	C4-C5-N7	5.77	113.11	110.80
1	A	141	A	C4-C5-N7	5.77	113.58	110.70
1	A	667	G	C6-C5-N7	-5.77	126.94	130.40
1	A	972	C	N3-C4-C5	-5.77	119.59	121.90
1	A	1228	C	C2-N1-C1'	5.77	125.15	118.80
1	A	936	C	C4-C5-C6	5.77	120.28	117.40
1	A	345	C	C6-N1-C2	-5.77	117.99	120.30
1	A	509	A	C3'-C2'-C1'	-5.76	96.89	101.50
1	A	550	G	N1-C2-N3	5.76	127.36	123.90
1	A	779	C	C5-C6-N1	-5.76	118.12	121.00
1	A	1318	A	N9-C4-C5	-5.76	103.50	105.80
1	A	1379	G	C2-N3-C4	5.76	114.78	111.90
1	A	1386	G	N1-C2-N3	5.76	127.36	123.90
1	A	232	G	C4-C5-C6	5.76	122.26	118.80
1	A	776	G	N3-C4-N9	-5.76	122.54	126.00
1	A	945	G	C5-N7-C8	-5.76	101.42	104.30
1	A	1318	A	N1-C2-N3	-5.76	126.42	129.30
1	A	251	G	N3-C4-N9	5.75	129.45	126.00
1	A	250	A	N9-C4-C5	-5.75	103.50	105.80
1	A	946	A	C5-C6-N6	5.75	128.30	123.70
1	A	315	A	N1-C2-N3	5.75	132.18	129.30
1	A	602	A	N1-C2-N3	5.75	132.18	129.30
1	A	130	A	N1-C6-N6	5.75	122.05	118.60
1	A	1195	C	N1-C2-O2	-5.75	115.45	118.90
16	P	19	ILE	CB-CA-C	-5.75	100.10	111.60
1	A	1064	G	C2-N3-C4	-5.75	109.03	111.90
1	A	799	G	C6-C5-N7	-5.75	126.95	130.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	741	G	C4-N9-C1'	-5.74	119.03	126.50
1	A	799	G	C2-N3-C4	-5.74	109.03	111.90
1	A	319	G	C8-N9-C1'	-5.74	119.54	127.00
1	A	588	G	N9-C4-C5	-5.74	103.10	105.40
1	A	1228	C	N3-C2-O2	-5.74	117.88	121.90
1	A	876	G	C8-N9-C4	5.74	108.69	106.40
1	A	1361(A)	C	N1-C2-O2	5.74	122.34	118.90
1	A	302	G	C5-C6-O6	-5.73	125.16	128.60
1	A	734	G	C8-N9-C4	5.73	108.69	106.40
1	A	1104	G	N3-C4-C5	-5.73	125.73	128.60
1	A	200	G	N1-C6-O6	5.73	123.34	119.90
1	A	835	U	N1-C2-N3	5.73	118.34	114.90
1	A	888	G	C5-N7-C8	5.73	107.16	104.30
1	A	767	A	C5-C6-N1	5.72	120.56	117.70
1	A	326	G	C5-N7-C8	5.72	107.16	104.30
1	A	945	G	C8-N9-C4	-5.72	104.11	106.40
1	A	454	C	C5-C6-N1	5.72	123.86	121.00
1	A	490	G	C5-C6-O6	-5.71	125.17	128.60
1	A	925	G	C6-C5-N7	-5.71	126.97	130.40
1	A	109	A	N1-C2-N3	5.71	132.16	129.30
1	A	1490	C	C2-N1-C1'	5.71	125.08	118.80
1	A	596	C	N1-C2-O2	5.71	122.33	118.90
1	A	753	A	N9-C4-C5	5.71	108.08	105.80
1	A	284	G	C5-C6-O6	-5.71	125.18	128.60
1	A	572	A	C4-C5-N7	-5.71	107.85	110.70
1	A	1268	A	C5-C6-N6	5.71	128.26	123.70
1	A	199	G	N3-C4-C5	5.70	131.45	128.60
1	A	1104	G	N3-C4-N9	5.70	129.42	126.00
1	A	1533	C	C2-N1-C1'	5.70	125.07	118.80
1	A	266	G	C5-C6-N1	-5.70	108.65	111.50
1	A	270	A	N1-C6-N6	5.70	122.02	118.60
1	A	731	G	C4-C5-N7	5.70	113.08	110.80
1	A	867	G	C4-C5-N7	5.70	113.08	110.80
1	A	595	G	N1-C2-N3	5.70	127.32	123.90
1	A	662	G	N1-C6-O6	5.70	123.32	119.90
1	A	756	C	C6-N1-C2	5.70	122.58	120.30
1	A	223	U	N1-C2-O2	-5.70	118.81	122.80
1	A	817	C	C6-N1-C1'	-5.70	113.97	120.80
1	A	831	U	N3-C4-C5	-5.70	111.18	114.60
1	A	914	G	N3-C2-N2	-5.70	115.91	119.90
1	A	1232	U	N1-C2-N3	5.69	118.32	114.90
1	A	1341	U	C2-N1-C1'	-5.69	110.87	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	658	G	C2-N3-C4	-5.69	109.05	111.90
1	A	328	C	C5-C6-N1	5.69	123.85	121.00
1	A	1199	U	N1-C2-O2	5.69	126.78	122.80
1	A	14	U	N1-C2-N3	5.69	118.31	114.90
1	A	1354	C	C5-C6-N1	5.69	123.84	121.00
1	A	167	G	C8-N9-C4	5.68	108.67	106.40
1	A	485	G	C4-N9-C1'	-5.68	119.11	126.50
1	A	867	G	C6-C5-N7	-5.68	126.99	130.40
1	A	859	A	C6-C5-N7	-5.68	128.32	132.30
1	A	878	G	N1-C6-O6	5.68	123.31	119.90
1	A	1167	A	N7-C8-N9	5.68	116.64	113.80
1	A	1235	U	C5-C4-O4	-5.68	122.50	125.90
1	A	666	G	C2-N3-C4	-5.67	109.06	111.90
1	A	755	G	C4-C5-C6	5.67	122.20	118.80
1	A	243	A	C2-N3-C4	-5.67	107.76	110.60
1	A	946	A	C4-C5-N7	-5.67	107.86	110.70
1	A	481	G	C6-N1-C2	-5.67	121.70	125.10
1	A	1079	G	N3-C4-C5	-5.67	125.77	128.60
1	A	1345	U	C5-C6-N1	-5.67	119.86	122.70
1	A	1181	G	C8-N9-C4	5.67	108.67	106.40
1	A	125	U	C5-C6-N1	-5.67	119.87	122.70
1	A	597	G	C4-C5-C6	5.67	122.20	118.80
1	A	257	G	C4-N9-C1'	5.67	133.87	126.50
1	A	511	C	C2-N1-C1'	-5.66	112.57	118.80
1	A	691	G	C5-N7-C8	-5.66	101.47	104.30
1	A	48	C	C6-N1-C2	5.66	122.56	120.30
1	A	1231	G	C4-C5-N7	5.66	113.06	110.80
1	A	73	C	N3-C4-C5	-5.66	119.64	121.90
1	A	357	G	C6-C5-N7	-5.66	127.01	130.40
1	A	586	C	C6-N1-C2	5.66	122.56	120.30
1	A	779	C	C4-C5-C6	5.66	120.23	117.40
1	A	1045	C	C6-N1-C2	-5.65	118.04	120.30
1	A	565	U	N3-C4-O4	5.65	123.36	119.40
1	A	797	C	N3-C4-N4	-5.65	114.04	118.00
1	A	906	G	N1-C6-O6	5.65	123.29	119.90
1	A	1384	C	C6-N1-C2	-5.65	118.04	120.30
1	A	1491	G	N1-C6-O6	-5.65	116.51	119.90
1	A	90	U	C5-C6-N1	-5.65	119.88	122.70
1	A	719	C	C5-C6-N1	-5.65	118.18	121.00
1	A	830	G	C2-N3-C4	-5.65	109.08	111.90
1	A	1478	C	C6-N1-C2	-5.65	118.04	120.30
1	A	670	G	C5-C6-O6	-5.65	125.21	128.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	146	G	C8-N9-C4	5.64	108.66	106.40
1	A	728	A	C4-C5-C6	5.64	119.82	117.00
1	A	8	A	N1-C6-N6	-5.64	115.21	118.60
1	A	68	G	C4-N9-C1'	-5.63	119.18	126.50
1	A	548	G	N3-C2-N2	-5.63	115.96	119.90
1	A	1332	A	C5-C6-N6	5.63	128.21	123.70
1	A	336	C	C5-C4-N4	-5.63	116.26	120.20
1	A	1394	A	C2-N3-C4	-5.63	107.78	110.60
1	A	357	G	C4-C5-N7	5.63	113.05	110.80
1	A	724	G	N1-C2-N3	-5.63	120.52	123.90
1	A	796	C	N3-C2-O2	-5.63	117.96	121.90
1	A	446	G	C8-N9-C1'	-5.63	119.69	127.00
1	A	598	U	N3-C4-O4	-5.63	115.46	119.40
1	A	698	G	C4-C5-C6	5.63	122.18	118.80
1	A	384	G	C6-N1-C2	-5.62	121.72	125.10
1	A	856	C	C4-C5-C6	5.62	120.21	117.40
1	A	922	G	N3-C4-N9	5.62	129.38	126.00
1	A	927	G	C5-C6-N1	-5.62	108.69	111.50
1	A	104	G	C2-N3-C4	-5.62	109.09	111.90
1	A	1187	G	C4-N9-C1'	5.62	133.80	126.50
1	A	1388	C	C6-N1-C2	5.62	122.55	120.30
1	A	1230	C	C6-N1-C2	-5.62	118.05	120.30
1	A	761	G	N3-C4-C5	5.61	131.41	128.60
1	A	1078	U	C5-C6-N1	5.61	125.51	122.70
1	A	1399	C	C5-C6-N1	-5.61	118.19	121.00
1	A	780	A	C8-N9-C4	5.61	108.05	105.80
1	A	1197	G	C5-C6-O6	-5.61	125.23	128.60
1	A	306	G	C8-N9-C4	5.61	108.64	106.40
1	A	690	G	C5-C6-O6	5.61	131.97	128.60
1	A	894	G	C6-C5-N7	-5.61	127.03	130.40
1	A	558	G	C6-C5-N7	-5.61	127.04	130.40
1	A	657	G	C8-N9-C1'	-5.61	119.71	127.00
1	A	792	A	P-O3'-C3'	5.61	126.43	119.70
1	A	900	A	N7-C8-N9	5.61	116.60	113.80
8	H	10	LEU	CB-CG-CD2	-5.61	101.47	111.00
8	H	59	LEU	CB-CG-CD2	-5.61	101.47	111.00
1	A	300	A	C2-N3-C4	-5.60	107.80	110.60
1	A	579	G	N9-C4-C5	-5.60	103.16	105.40
1	A	116	A	C8-N9-C4	5.60	108.04	105.80
1	A	731	G	C6-C5-N7	-5.60	127.04	130.40
1	A	854	G	N1-C2-N3	5.60	127.26	123.90
1	A	7	G	N3-C4-N9	5.60	129.36	126.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	573	A	C2-N3-C4	5.60	113.40	110.60
1	A	913	A	P-O3'-C3'	5.60	126.42	119.70
1	A	1287	A	N9-C4-C5	5.60	108.04	105.80
1	A	707	C	C6-N1-C2	5.60	122.54	120.30
1	A	93	G	N3-C4-N9	5.59	129.36	126.00
1	A	373	A	C4-C5-C6	5.59	119.80	117.00
1	A	586	C	C2-N1-C1'	-5.59	112.65	118.80
1	A	805	C	C6-N1-C2	5.59	122.54	120.30
1	A	1348	U	C6-N1-C1'	-5.59	113.37	121.20
1	A	190(H)	G	N3-C4-C5	5.59	131.40	128.60
1	A	64	G	C6-C5-N7	-5.59	127.05	130.40
1	A	1512	U	N3-C4-C5	-5.59	111.25	114.60
1	A	588	G	C8-N9-C1'	-5.58	119.74	127.00
1	A	610	G	N1-C6-O6	-5.58	116.55	119.90
1	A	280	C	N3-C4-C5	5.58	124.13	121.90
1	A	552	U	C2-N3-C4	-5.58	123.65	127.00
1	A	710	G	C4-C5-N7	5.58	113.03	110.80
1	A	719	C	C4-C5-C6	5.58	120.19	117.40
1	A	887	G	C5-N7-C8	-5.58	101.51	104.30
1	A	1202	G	N9-C4-C5	5.58	107.63	105.40
1	A	1212	U	C5-C6-N1	5.58	125.49	122.70
1	A	621	A	N7-C8-N9	5.58	116.59	113.80
1	A	640	A	C6-N1-C2	-5.58	115.25	118.60
1	A	875	C	C4-C5-C6	5.58	120.19	117.40
1	A	326	G	N1-C2-N2	-5.58	111.18	116.20
1	A	416	G	C6-C5-N7	-5.58	127.05	130.40
1	A	573	A	C4-C5-C6	5.58	119.79	117.00
1	A	659	U	C5-C6-N1	-5.58	119.91	122.70
1	A	760	G	C4-N9-C1'	-5.58	119.25	126.50
1	A	1465	C	N1-C2-O2	5.58	122.25	118.90
1	A	595	G	C4-C5-N7	-5.58	108.57	110.80
1	A	721	G	N3-C4-N9	5.58	129.35	126.00
1	A	27	G	C5-C6-O6	-5.57	125.26	128.60
1	A	234	C	C6-N1-C1'	-5.57	114.11	120.80
1	A	901	A	C8-N9-C4	-5.57	103.57	105.80
1	A	351	G	N1-C6-O6	5.57	123.24	119.90
1	A	796	C	C4-C5-C6	5.57	120.19	117.40
4	D	26	CYS	CA-CB-SG	5.57	124.03	114.00
1	A	878	G	C5-C6-O6	-5.57	125.26	128.60
1	A	918	A	N3-C4-C5	-5.57	122.90	126.80
1	A	301	G	N1-C6-O6	-5.57	116.56	119.90
1	A	721	G	N1-C2-N2	-5.57	111.19	116.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1490	C	N1-C2-O2	5.57	122.24	118.90
1	A	134	A	C2-N3-C4	-5.57	107.82	110.60
1	A	326	G	N9-C4-C5	5.57	107.63	105.40
1	A	666	G	C8-N9-C4	-5.57	104.17	106.40
1	A	1238	A	C5-C6-N6	-5.56	119.25	123.70
1	A	730	G	C5-C6-O6	5.56	131.94	128.60
1	A	361	G	C5-C6-O6	-5.56	125.26	128.60
1	A	878	G	C6-C5-N7	-5.56	127.07	130.40
1	A	599	C	C2-N3-C4	-5.55	117.12	119.90
1	A	901	A	C2-N3-C4	-5.55	107.82	110.60
1	A	389	A	N3-C4-C5	-5.55	122.92	126.80
1	A	1080	A	C5-C6-N6	5.55	128.14	123.70
7	G	102	ARG	NE-CZ-NH2	-5.55	117.53	120.30
1	A	786	G	N3-C2-N2	-5.54	116.02	119.90
1	A	1525	G	C6-N1-C2	-5.54	121.77	125.10
1	A	1087	G	C5-C6-O6	-5.54	125.27	128.60
1	A	317	G	C4-C5-N7	5.54	113.02	110.80
1	A	1359	C	C2-N1-C1'	5.54	124.89	118.80
1	A	131	C	C2-N3-C4	-5.54	117.13	119.90
1	A	277	C	C2-N1-C1'	-5.54	112.71	118.80
1	A	890	G	C8-N9-C4	5.54	108.61	106.40
1	A	787	A	C2-N3-C4	-5.53	107.83	110.60
1	A	975	A	C5-C6-N1	-5.53	114.93	117.70
1	A	1363	A	C8-N9-C4	-5.53	103.59	105.80
1	A	445	G	N9-C4-C5	-5.53	103.19	105.40
1	A	639	G	C5-C6-O6	-5.53	125.28	128.60
1	A	1202	G	C6-C5-N7	5.53	133.72	130.40
1	A	304	U	C6-N1-C2	5.52	124.31	121.00
1	A	309	G	C4-C5-N7	5.52	113.01	110.80
1	A	328	C	C2-N1-C1'	5.52	124.87	118.80
1	A	945	G	N7-C8-N9	5.52	115.86	113.10
1	A	1500	A	N3-C4-C5	-5.52	122.94	126.80
1	A	234	C	C5-C4-N4	-5.52	116.34	120.20
1	A	1342	C	N3-C4-C5	-5.52	119.69	121.90
1	A	482	A	C8-N9-C4	-5.51	103.59	105.80
1	A	828	A	C5-C6-N6	-5.51	119.29	123.70
1	A	1487	G	C8-N9-C4	-5.51	104.19	106.40
1	A	52	G	N3-C4-C5	-5.51	125.84	128.60
1	A	157	G	N3-C4-C5	5.51	131.35	128.60
1	A	730	G	N1-C6-O6	-5.51	116.59	119.90
1	A	1414	U	N3-C2-O2	-5.51	118.34	122.20
1	A	718	G	C4-N9-C1'	5.51	133.66	126.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	408	A	C8-N9-C4	-5.50	103.60	105.80
1	A	863	U	N3-C4-O4	-5.50	115.55	119.40
1	A	64	G	C2-N3-C4	-5.50	109.15	111.90
1	A	524	G	C5-C6-O6	-5.50	125.30	128.60
1	A	852	G	N1-C6-O6	5.50	123.20	119.90
1	A	1434	A	N1-C6-N6	5.50	121.90	118.60
1	A	1380	U	N3-C4-O4	-5.50	115.55	119.40
1	A	303	A	C8-N9-C4	5.50	108.00	105.80
1	A	77	G	N3-C4-N9	5.49	129.30	126.00
1	A	508	C	N3-C4-C5	5.49	124.10	121.90
1	A	733	A	C8-N9-C4	5.49	108.00	105.80
1	A	793	U	C6-N1-C2	-5.49	117.71	121.00
1	A	64	G	N9-C4-C5	-5.49	103.20	105.40
1	A	778	G	N1-C2-N3	5.49	127.19	123.90
1	A	944	G	N3-C2-N2	5.49	123.74	119.90
1	A	787	A	C5-N7-C8	-5.49	101.16	103.90
1	A	1082	G	C2-N3-C4	-5.49	109.16	111.90
1	A	576	G	C4-C5-C6	5.48	122.09	118.80
1	A	852	G	C2-N3-C4	-5.48	109.16	111.90
1	A	1524	C	N1-C2-O2	-5.48	115.61	118.90
1	A	170	U	N1-C2-N3	5.48	118.19	114.90
1	A	939	G	C6-N1-C2	-5.48	121.81	125.10
1	A	1187	G	C8-N9-C4	-5.48	104.21	106.40
1	A	1543	C	N1-C2-O2	5.48	122.19	118.90
1	A	79	G	N3-C4-C5	-5.48	125.86	128.60
1	A	806	C	N3-C4-C5	5.48	124.09	121.90
1	A	413	G	N3-C4-N9	5.48	129.29	126.00
1	A	101	A	N1-C6-N6	-5.48	115.31	118.60
1	A	285	G	N3-C4-C5	5.48	131.34	128.60
1	A	647	C	N1-C2-N3	-5.48	115.37	119.20
1	A	243	A	N1-C2-N3	5.47	132.04	129.30
1	A	1155	G	C8-N9-C4	-5.47	104.21	106.40
1	A	249	U	C5-C4-O4	5.47	129.18	125.90
1	A	104	G	N1-C2-N3	5.47	127.18	123.90
5	E	41	VAL	CB-CA-C	-5.47	101.01	111.40
1	A	36	C	N3-C2-O2	-5.47	118.07	121.90
2	B	197	VAL	CB-CA-C	-5.47	101.01	111.40
1	A	236	G	C5-C6-O6	5.46	131.88	128.60
1	A	740	U	C5-C6-N1	-5.46	119.97	122.70
1	A	1200	C	C5-C6-N1	5.46	123.73	121.00
1	A	1236	A	C5-C6-N6	-5.46	119.33	123.70
1	A	946	A	C5-C6-N1	5.46	120.43	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1234	C	N3-C4-C5	5.46	124.08	121.90
19	S	6	LYS	N-CA-C	5.46	125.74	111.00
1	A	666	G	N1-C2-N3	5.46	127.18	123.90
1	A	1465	C	N3-C2-O2	-5.46	118.08	121.90
1	A	511	C	C2-N3-C4	-5.46	117.17	119.90
1	A	802	A	C5-C6-N6	-5.46	119.33	123.70
1	A	878	G	C2-N3-C4	-5.46	109.17	111.90
1	A	965	A	C8-N9-C4	5.46	107.98	105.80
1	A	183	G	N1-C6-O6	5.45	123.17	119.90
1	A	750	G	C6-N1-C2	-5.45	121.83	125.10
1	A	24	U	N3-C4-C5	5.45	117.87	114.60
1	A	61	G	N3-C4-C5	-5.45	125.88	128.60
1	A	185	A	C8-N9-C4	5.45	107.98	105.80
1	A	1522	U	N3-C4-C5	-5.45	111.33	114.60
1	A	124	G	C2-N3-C4	-5.45	109.18	111.90
1	A	435	C	C6-N1-C2	-5.45	118.12	120.30
1	A	73	C	C6-N1-C2	-5.44	118.12	120.30
1	A	191	G	N1-C6-O6	5.44	123.17	119.90
1	A	383	A	N7-C8-N9	5.44	116.52	113.80
1	A	867	G	N1-C6-O6	5.44	123.17	119.90
1	A	243	A	C4-C5-N7	5.44	113.42	110.70
1	A	439	A	N7-C8-N9	5.44	116.52	113.80
1	A	921	U	N3-C4-C5	-5.44	111.33	114.60
1	A	1084	G	C4-C5-N7	-5.44	108.62	110.80
1	A	824	C	N3-C4-C5	5.44	124.08	121.90
1	A	28	G	C5-C6-O6	-5.43	125.34	128.60
16	P	5	ARG	NE-CZ-NH2	-5.43	117.58	120.30
1	A	1240	U	N3-C2-O2	-5.43	118.40	122.20
1	A	1287	A	C8-N9-C4	-5.43	103.63	105.80
1	A	595	G	C5-C6-O6	5.43	131.86	128.60
1	A	243	A	C5-C6-N6	-5.43	119.36	123.70
1	A	389	A	C5-N7-C8	5.43	106.61	103.90
1	A	660	G	N1-C6-O6	5.43	123.16	119.90
1	A	875	C	N3-C4-C5	5.43	124.07	121.90
1	A	755	G	C5-C6-N1	-5.43	108.79	111.50
1	A	892	A	N1-C2-N3	5.43	132.01	129.30
1	A	920	U	N3-C4-C5	-5.43	111.34	114.60
1	A	1212	U	C6-N1-C1'	-5.43	113.60	121.20
1	A	264	U	C6-N1-C2	-5.43	117.74	121.00
1	A	306	G	N1-C6-O6	5.43	123.16	119.90
1	A	389	A	C5-C6-N6	5.43	128.04	123.70
1	A	636	U	C4-C5-C6	5.43	122.96	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	948	C	N3-C2-O2	5.43	125.70	121.90
1	A	1530	G	C5-C6-O6	-5.43	125.34	128.60
1	A	1539	C	C5-C6-N1	5.43	123.71	121.00
1	A	230	G	C8-N9-C1'	-5.42	119.95	127.00
1	A	542	G	C4-N9-C1'	5.42	133.55	126.50
1	A	803	G	N1-C2-N3	5.42	127.15	123.90
1	A	1403	C	N3-C2-O2	5.42	125.70	121.90
1	A	1502	A	C4-N9-C1'	5.42	136.06	126.30
1	A	1197	G	N3-C2-N2	-5.42	116.11	119.90
1	A	820	U	C2-N3-C4	-5.42	123.75	127.00
1	A	1288	A	N1-C6-N6	-5.42	115.35	118.60
1	A	17	U	C2-N1-C1'	-5.41	111.20	117.70
1	A	127	G	N1-C6-O6	5.41	123.15	119.90
1	A	1238	A	C5-N7-C8	-5.41	101.19	103.90
1	A	257	G	C8-N9-C1'	-5.41	119.97	127.00
1	A	428	G	P-O3'-C3'	5.41	126.19	119.70
1	A	526	C	N3-C4-C5	5.41	124.06	121.90
1	A	1228	C	C6-N1-C1'	-5.41	114.31	120.80
1	A	9	G	C6-C5-N7	-5.41	127.16	130.40
1	A	314	C	N3-C4-C5	5.40	124.06	121.90
1	A	780	A	C6-N1-C2	-5.40	115.36	118.60
1	A	876	G	C4-C5-N7	5.40	112.96	110.80
1	A	1220	G	C8-N9-C4	-5.40	104.24	106.40
1	A	59	A	C5-C6-N1	5.40	120.40	117.70
1	A	123	C	C6-N1-C2	-5.40	118.14	120.30
1	A	827	U	N3-C2-O2	-5.40	118.42	122.20
1	A	300	A	C6-C5-N7	-5.40	128.52	132.30
1	A	851	G	C4-C5-C6	5.39	122.04	118.80
1	A	1509	C	C4-C5-C6	5.39	120.10	117.40
1	A	327	A	C5-C6-N6	-5.39	119.39	123.70
1	A	975	A	C6-N1-C2	5.39	121.83	118.60
1	A	1395	C	C2-N1-C1'	-5.39	112.87	118.80
1	A	46	G	C4-C5-C6	5.39	122.03	118.80
1	A	922	G	C6-N1-C2	-5.38	121.87	125.10
1	A	275	G	C6-C5-N7	-5.38	127.17	130.40
1	A	909	A	C6-N1-C2	-5.38	115.37	118.60
5	E	12	LEU	CA-CB-CG	5.38	127.67	115.30
1	A	79	G	N3-C4-N9	5.38	129.22	126.00
1	A	655	A	C5-C6-N1	5.38	120.39	117.70
1	A	1390	U	C4-C5-C6	5.37	122.92	119.70
1	A	836	G	C4-C5-C6	5.37	122.02	118.80
1	A	44	G	C2-N3-C4	-5.37	109.22	111.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	389	A	C8-N9-C4	-5.37	103.65	105.80
1	A	617	G	C4-N9-C1'	5.37	133.48	126.50
1	A	822	C	C6-N1-C2	5.37	122.45	120.30
1	A	1263	C	N3-C4-C5	5.37	124.05	121.90
1	A	1181	G	N3-C4-C5	5.37	131.28	128.60
1	A	29	G	C2-N3-C4	-5.36	109.22	111.90
1	A	752	G	N7-C8-N9	-5.36	110.42	113.10
1	A	1238	A	C6-C5-N7	-5.36	128.55	132.30
1	A	371	G	C5-C6-N1	5.36	114.18	111.50
1	A	1071	C	N3-C4-C5	5.36	124.05	121.90
1	A	147	G	C8-N9-C4	5.36	108.55	106.40
1	A	332	G	C5-C6-O6	-5.36	125.38	128.60
1	A	1340	A	N1-C2-N3	5.36	131.98	129.30
1	A	1447	G	C5-C6-O6	-5.36	125.39	128.60
1	A	444	C	N3-C4-C5	5.36	124.04	121.90
1	A	893	C	C2-N3-C4	5.36	122.58	119.90
1	A	1353	G	N3-C4-C5	-5.36	125.92	128.60
1	A	901	A	N9-C4-C5	5.35	107.94	105.80
1	A	232	G	N3-C4-N9	5.35	129.21	126.00
1	A	317	G	C2-N3-C4	-5.35	109.23	111.90
1	A	588	G	C8-N9-C4	5.35	108.54	106.40
1	A	1153	C	C5-C6-N1	-5.35	118.33	121.00
1	A	17	U	N3-C4-C5	5.34	117.81	114.60
1	A	190(J)	U	C5-C6-N1	-5.34	120.03	122.70
1	A	1527	C	C2-N3-C4	-5.34	117.23	119.90
1	A	1529	G	N3-C2-N2	-5.34	116.16	119.90
1	A	780	A	C2-N3-C4	-5.34	107.93	110.60
1	A	862	C	C5-C6-N1	-5.34	118.33	121.00
1	A	111	G	N1-C2-N2	5.34	121.01	116.20
20	T	74	LYS	CA-C-N	-5.34	105.45	117.20
1	A	785	G	C5-C6-O6	-5.34	125.40	128.60
1	A	1081	G	C4-C5-N7	5.34	112.94	110.80
1	A	15	G	C4-N9-C1'	5.34	133.44	126.50
1	A	13	U	N3-C2-O2	5.33	125.93	122.20
1	A	190(G)	G	C2-N3-C4	-5.33	109.23	111.90
1	A	635	G	C6-C5-N7	-5.33	127.20	130.40
1	A	635	G	N3-C2-N2	-5.33	116.17	119.90
1	A	1397	C	C2-N3-C4	5.33	122.57	119.90
1	A	1153	C	N3-C4-N4	-5.33	114.27	118.00
1	A	122	G	C5-C6-N1	-5.33	108.83	111.50
1	A	231	G	C4-C5-N7	5.33	112.93	110.80
1	A	557	G	N1-C2-N3	5.33	127.10	123.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1202	G	C2-N3-C4	5.33	114.56	111.90
1	A	760	G	N1-C2-N3	5.33	127.10	123.90
1	A	809	G	C5-C6-O6	-5.33	125.40	128.60
1	A	1333	A	C4-C5-C6	5.33	119.66	117.00
1	A	1376	U	C5-C4-O4	5.33	129.10	125.90
1	A	140	A	N1-C2-N3	5.33	131.96	129.30
1	A	326	G	C5-C6-N1	-5.32	108.84	111.50
1	A	448	A	N1-C2-N3	5.32	131.96	129.30
1	A	290	C	N1-C2-N3	5.32	122.93	119.20
1	A	1369	C	C6-N1-C2	-5.32	118.17	120.30
1	A	1507	A	C4-N9-C1'	5.32	135.88	126.30
1	A	639	G	N9-C4-C5	-5.32	103.27	105.40
1	A	229	U	N1-C2-O2	-5.32	119.08	122.80
1	A	922	G	N1-C2-N3	5.32	127.09	123.90
1	A	1261	A	C8-N9-C4	-5.31	103.67	105.80
1	A	10	A	N7-C8-N9	-5.31	111.14	113.80
1	A	295	C	C5-C6-N1	-5.31	118.34	121.00
1	A	809	G	C4-C5-N7	5.31	112.92	110.80
1	A	33	A	C5-C6-N1	5.31	120.35	117.70
1	A	256	U	C5-C4-O4	-5.31	122.72	125.90
1	A	698	G	N3-C4-C5	-5.31	125.95	128.60
1	A	741	G	N3-C2-N2	-5.31	116.18	119.90
1	A	1352	C	N3-C2-O2	-5.31	118.19	121.90
1	A	127	G	N9-C4-C5	-5.30	103.28	105.40
1	A	309	G	C5-C6-N1	5.30	114.15	111.50
1	A	893	C	N3-C4-C5	-5.30	119.78	121.90
1	A	1425	U	C5-C6-N1	-5.30	120.05	122.70
1	A	1237	C	N3-C2-O2	-5.30	118.19	121.90
1	A	1511	G	C4-N9-C1'	5.30	133.39	126.50
1	A	717	C	N1-C2-O2	-5.30	115.72	118.90
1	A	867	G	C6-N1-C2	-5.30	121.92	125.10
1	A	1502	A	N9-C4-C5	-5.30	103.68	105.80
1	A	1503	A	C8-N9-C4	5.30	107.92	105.80
1	A	190(G)	G	C5-C6-N1	-5.29	108.85	111.50
1	A	150	C	N3-C4-C5	-5.29	119.78	121.90
1	A	165	C	C6-N1-C2	5.29	122.42	120.30
1	A	570	G	N3-C4-N9	5.29	129.18	126.00
1	A	671	G	C5-C6-N1	-5.29	108.85	111.50
1	A	1435	G	N3-C4-C5	-5.29	125.95	128.60
1	A	15	G	N9-C4-C5	-5.29	103.28	105.40
1	A	522	C	N1-C2-O2	-5.29	115.72	118.90
1	A	767	A	C8-N9-C4	-5.29	103.68	105.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	638	G	N1-C2-N3	5.29	127.07	123.90
1	A	1131	G	N1-C6-O6	5.29	123.07	119.90
1	A	1187	G	N7-C8-N9	5.29	115.75	113.10
1	A	41	G	N3-C4-N9	5.29	129.17	126.00
1	A	396	G	C2-N3-C4	5.29	114.54	111.90
1	A	377	G	C4-C5-C6	5.29	121.97	118.80
1	A	523	A	N9-C4-C5	-5.29	103.69	105.80
1	A	1187	G	C6-C5-N7	-5.29	127.23	130.40
1	A	1338	G	C6-N1-C2	-5.29	121.93	125.10
1	A	1532	U	C4-C5-C6	-5.29	116.53	119.70
6	F	45	LEU	CA-CB-CG	-5.28	103.16	115.30
1	A	814	A	N7-C8-N9	-5.28	111.16	113.80
1	A	928	G	C5-C6-O6	-5.28	125.43	128.60
1	A	876	G	N3-C2-N2	-5.28	116.21	119.90
1	A	920	U	C2-N1-C1'	-5.28	111.37	117.70
10	J	90	LEU	N-CA-C	5.27	125.24	111.00
1	A	107	G	N1-C2-N3	-5.27	120.74	123.90
1	A	336	C	N3-C4-N4	5.27	121.69	118.00
1	A	485	G	C6-C5-N7	5.27	133.56	130.40
1	A	1434	A	C5-C6-N6	-5.27	119.48	123.70
1	A	67	C	N1-C2-N3	5.27	122.89	119.20
1	A	625	G	C6-N1-C2	-5.27	121.94	125.10
1	A	771	G	C5-N7-C8	-5.27	101.67	104.30
1	A	75	G	N1-C6-O6	5.27	123.06	119.90
1	A	583	A	C6-C5-N7	-5.27	128.61	132.30
1	A	767	A	N1-C6-N6	-5.27	115.44	118.60
1	A	824	C	C2-N3-C4	-5.27	117.27	119.90
1	A	1202	G	C5-N7-C8	5.27	106.93	104.30
1	A	21	G	N1-C6-O6	-5.27	116.74	119.90
1	A	640	A	C5-C6-N1	5.27	120.33	117.70
1	A	281	G	C8-N9-C1'	-5.26	120.16	127.00
1	A	1237	C	N3-C4-C5	-5.26	119.79	121.90
1	A	226	G	N1-C6-O6	5.26	123.06	119.90
1	A	633	G	N9-C4-C5	-5.26	103.30	105.40
1	A	820	U	C6-N1-C1'	5.26	128.57	121.20
1	A	1417	G	C4-C5-N7	-5.26	108.69	110.80
1	A	1498	UR3	P-O3'-C3'	5.26	126.02	119.70
1	A	15	G	C8-N9-C1'	-5.26	120.16	127.00
1	A	1390	U	N3-C4-C5	-5.26	111.44	114.60
1	A	1289	A	N1-C6-N6	-5.26	115.44	118.60
17	Q	67	LYS	N-CA-C	-5.26	96.81	111.00
1	A	336	C	C6-N1-C2	5.26	122.40	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	291	C	N3-C4-N4	5.25	121.68	118.00
1	A	12	U	C5-C6-N1	-5.25	120.08	122.70
1	A	355	C	C5-C6-N1	5.25	123.62	121.00
1	A	670	G	N1-C6-O6	5.25	123.05	119.90
1	A	678	U	N3-C4-O4	5.25	123.07	119.40
1	A	577	G	C5-N7-C8	-5.25	101.68	104.30
1	A	777	A	C6-C5-N7	-5.25	128.63	132.30
1	A	1240	U	C5-C4-O4	5.25	129.05	125.90
1	A	657	G	C6-N1-C2	-5.24	121.95	125.10
1	A	852	G	C8-N9-C4	5.24	108.50	106.40
1	A	957	U	N3-C4-C5	-5.24	111.46	114.60
1	A	1364	U	N1-C2-N3	5.24	118.04	114.90
1	A	29	G	N1-C2-N3	5.24	127.04	123.90
1	A	256	U	N3-C4-C5	5.24	117.74	114.60
1	A	576	G	C5-C6-N1	-5.24	108.88	111.50
1	A	880	C	C5-C6-N1	-5.24	118.38	121.00
1	A	1190	G	N1-C2-N3	5.24	127.04	123.90
1	A	696	A	C5-C6-N1	5.24	120.32	117.70
1	A	730	G	C5-N7-C8	5.24	106.92	104.30
1	A	864	A	C4-C5-C6	5.24	119.62	117.00
1	A	767	A	C6-N1-C2	-5.23	115.46	118.60
1	A	769	G	N9-C4-C5	-5.23	103.31	105.40
1	A	1376	U	N1-C2-O2	5.23	126.46	122.80
1	A	1487	G	C6-N1-C2	-5.23	121.96	125.10
1	A	1500	A	C2-N3-C4	5.23	113.22	110.60
1	A	400	C	N3-C4-N4	-5.23	114.34	118.00
1	A	594	G	N1-C2-N3	5.23	127.03	123.90
1	A	319	G	N9-C4-C5	-5.22	103.31	105.40
1	A	793	U	C6-N1-C1'	5.22	128.51	121.20
1	A	820	U	C6-N1-C2	-5.22	117.87	121.00
1	A	975	A	N9-C4-C5	-5.22	103.71	105.80
1	A	116	A	N1-C2-N3	5.22	131.91	129.30
1	A	353	A	C4-C5-N7	-5.22	108.09	110.70
1	A	373	A	N1-C2-N3	5.22	131.91	129.30
1	A	168	G	C4-N9-C1'	5.22	133.28	126.50
1	A	13	U	N1-C2-O2	-5.21	119.15	122.80
1	A	128	G	N9-C4-C5	-5.21	103.31	105.40
1	A	20	U	N3-C4-O4	5.21	123.05	119.40
1	A	721	G	N7-C8-N9	5.21	115.70	113.10
1	A	746	A	N1-C2-N3	5.21	131.91	129.30
1	A	873	A	N7-C8-N9	5.21	116.40	113.80
1	A	15	G	C5-N7-C8	-5.20	101.70	104.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	872	A	N1-C2-N3	5.20	131.90	129.30
1	A	1155	G	N7-C8-N9	5.20	115.70	113.10
1	A	893	C	C5-C6-N1	5.20	123.60	121.00
1	A	598	U	C5-C4-O4	5.20	129.02	125.90
1	A	1341	U	C5-C6-N1	-5.20	120.10	122.70
1	A	178	C	N1-C2-O2	5.20	122.02	118.90
1	A	229	U	N3-C4-O4	5.20	123.04	119.40
1	A	889	A	N9-C4-C5	5.20	107.88	105.80
1	A	597	G	C6-C5-N7	-5.19	127.28	130.40
1	A	686	U	N1-C2-N3	5.19	118.02	114.90
1	A	570	G	C6-N1-C2	-5.19	121.98	125.10
1	A	145	G	N1-C2-N2	5.19	120.87	116.20
1	A	826	C	C6-N1-C2	5.19	122.38	120.30
1	A	282	A	N1-C6-N6	-5.19	115.49	118.60
1	A	1238	A	C4-C5-N7	5.18	113.29	110.70
1	A	741	G	N3-C4-N9	-5.18	122.89	126.00
1	A	1087	G	N3-C4-C5	5.18	131.19	128.60
1	A	1195	C	N3-C2-O2	5.18	125.53	121.90
1	A	715	A	C2-N3-C4	-5.18	108.01	110.60
1	A	900	A	N1-C2-N3	5.18	131.89	129.30
1	A	142	G	N3-C4-N9	5.18	129.11	126.00
1	A	62	U	C4-C5-C6	5.18	122.81	119.70
1	A	485	G	C5-N7-C8	5.18	106.89	104.30
1	A	577	G	C4-C5-N7	5.18	112.87	110.80
1	A	812	C	C4-C5-C6	5.18	119.99	117.40
1	A	168	G	C8-N9-C1'	-5.17	120.27	127.00
1	A	816	A	N1-C2-N3	5.17	131.89	129.30
1	A	14	U	N3-C4-C5	-5.17	111.50	114.60
1	A	890	G	N7-C8-N9	-5.17	110.52	113.10
1	A	192	U	C6-N1-C2	5.17	124.10	121.00
1	A	574	A	C5-C6-N1	-5.17	115.12	117.70
1	A	129(A)	G	N3-C2-N2	5.16	123.51	119.90
1	A	975	A	C2-N3-C4	-5.16	108.02	110.60
1	A	157	G	N3-C4-N9	-5.16	122.91	126.00
1	A	975	A	N3-C4-C5	5.16	130.41	126.80
1	A	885	G	N3-C2-N2	-5.16	116.29	119.90
1	A	602	A	C6-N1-C2	-5.15	115.51	118.60
1	A	1131	G	N7-C8-N9	5.15	115.68	113.10
1	A	1188	A	C8-N9-C4	5.15	107.86	105.80
1	A	724	G	N3-C2-N2	5.15	123.51	119.90
1	A	938	A	N1-C2-N3	5.15	131.88	129.30
1	A	104	G	C6-C5-N7	-5.15	127.31	130.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	592	G	C4-C5-N7	-5.15	108.74	110.80
1	A	173	U	N1-C2-N3	5.15	117.99	114.90
1	A	750	G	N1-C2-N3	5.15	126.99	123.90
1	A	1064	G	N1-C2-N3	5.15	126.99	123.90
1	A	413	G	N3-C4-C5	-5.15	126.03	128.60
1	A	382	A	C6-C5-N7	-5.14	128.70	132.30
1	A	665	A	C5-C6-N1	5.14	120.27	117.70
1	A	821	G	C5-C6-O6	-5.14	125.51	128.60
1	A	318	G	N3-C2-N2	-5.14	116.30	119.90
1	A	1137	C	C6-N1-C2	-5.14	118.24	120.30
1	A	1505	G	C4-C5-C6	5.14	121.89	118.80
1	A	331	G	C8-N9-C1'	-5.14	120.32	127.00
1	A	109	A	N3-C4-C5	5.14	130.40	126.80
16	P	36	ILE	C-N-CA	-5.14	111.51	122.30
1	A	300	A	N9-C4-C5	5.14	107.86	105.80
1	A	1131	G	C4-C5-C6	5.14	121.88	118.80
1	A	576	G	C4-C5-N7	-5.14	108.75	110.80
1	A	1104	G	C6-C5-N7	-5.14	127.32	130.40
1	A	1282	C	N3-C4-C5	-5.14	119.84	121.90
1	A	1314	C	N3-C4-C5	-5.14	119.84	121.90
1	A	637	G	N3-C4-N9	5.13	129.08	126.00
1	A	242	C	N3-C4-C5	5.13	123.95	121.90
1	A	1239	A	N9-C4-C5	-5.13	103.75	105.80
1	A	1533	C	C2-N3-C4	5.13	122.47	119.90
1	A	325	A	N1-C2-N3	5.13	131.87	129.30
1	A	530	G	N7-C8-N9	5.13	115.67	113.10
1	A	792	A	N1-C6-N6	5.13	121.68	118.60
1	A	1361(A)	C	C5-C6-N1	5.13	123.57	121.00
1	A	1397	C	C5-C6-N1	5.13	123.57	121.00
1	A	120	A	C2-N3-C4	-5.13	108.03	110.60
1	A	394	G	C4-C5-N7	-5.13	108.75	110.80
1	A	135	C	N3-C2-O2	5.13	125.49	121.90
1	A	173	U	N3-C4-O4	-5.13	115.81	119.40
1	A	752	G	C8-N9-C4	5.13	108.45	106.40
1	A	1224	G	C8-N9-C4	5.13	108.45	106.40
1	A	805	C	C4-C5-C6	-5.13	114.84	117.40
1	A	799	G	N1-C6-O6	5.12	122.97	119.90
1	A	1526	G	C5-C6-N1	5.12	114.06	111.50
1	A	231	G	C6-C5-N7	-5.12	127.33	130.40
1	A	1300	G	P-O3'-C3'	5.12	125.85	119.70
1	A	227	G	C5-C6-O6	-5.12	125.53	128.60
1	A	229	U	N3-C4-C5	-5.12	111.53	114.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	154	C	C5-C4-N4	-5.12	116.62	120.20
1	A	394	G	N7-C8-N9	-5.12	110.54	113.10
1	A	868	C	C2-N3-C4	-5.12	117.34	119.90
1	A	902	G	C6-C5-N7	5.12	133.47	130.40
1	A	717	C	N3-C2-O2	5.12	125.48	121.90
1	A	869	G	N7-C8-N9	-5.12	110.54	113.10
1	A	568	G	N1-C6-O6	-5.11	116.83	119.90
1	A	573	A	N3-C4-C5	-5.11	123.22	126.80
1	A	886	G	C5-C6-O6	-5.11	125.53	128.60
1	A	894	G	C2-N3-C4	-5.11	109.34	111.90
1	A	1389	C	C6-N1-C2	5.11	122.35	120.30
1	A	883	C	C6-N1-C2	-5.11	118.25	120.30
1	A	1206	G	C5-C6-N1	-5.11	108.94	111.50
1	A	1385	G	C5-N7-C8	5.11	106.86	104.30
6	F	98	LEU	CA-CB-CG	-5.11	103.54	115.30
1	A	568	G	N9-C4-C5	5.11	107.44	105.40
1	A	850	U	N1-C2-N3	5.11	117.97	114.90
1	A	1288	A	N9-C4-C5	5.11	107.84	105.80
1	A	1467	G	N9-C4-C5	5.11	107.44	105.40
1	A	1539	C	N3-C4-N4	5.11	121.58	118.00
1	A	915	A	C2-N3-C4	-5.11	108.05	110.60
1	A	617	G	N3-C2-N2	5.11	123.47	119.90
1	A	1090	U	C4-C5-C6	5.10	122.76	119.70
1	A	101	A	C8-N9-C4	-5.10	103.76	105.80
1	A	79	G	C8-N9-C4	-5.10	104.36	106.40
1	A	199	G	C2-N3-C4	-5.10	109.35	111.90
1	A	1507	A	C8-N9-C4	-5.10	103.76	105.80
1	A	190(I)	G	C4-C5-C6	5.10	121.86	118.80
1	A	615	C	N3-C4-N4	5.10	121.57	118.00
1	A	1500	A	C6-N1-C2	-5.10	115.54	118.60
1	A	305	G	C5-C6-N1	-5.10	108.95	111.50
1	A	760	G	N3-C4-C5	5.09	131.15	128.60
1	A	557	G	N9-C4-C5	5.09	107.44	105.40
1	A	312	C	N3-C4-C5	5.09	123.94	121.90
1	A	850	U	N3-C4-C5	-5.09	111.55	114.60
1	A	306	G	N3-C2-N2	-5.09	116.34	119.90
1	A	1378	C	C2-N3-C4	5.09	122.44	119.90
1	A	1505	G	C4-C5-N7	-5.09	108.77	110.80
1	A	484	G	P-O3'-C3'	5.09	125.81	119.70
1	A	818	G	N9-C4-C5	5.09	107.44	105.40
1	A	1299	A	N1-C6-N6	5.09	121.65	118.60
1	A	373	A	N1-C6-N6	-5.08	115.55	118.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	566	G	N1-C2-N3	5.08	126.95	123.90
1	A	851	G	N1-C6-O6	5.08	122.95	119.90
1	A	900	A	C5-C6-N6	-5.08	119.64	123.70
1	A	557	G	N3-C4-C5	-5.08	126.06	128.60
1	A	825	G	C5-C6-N1	5.08	114.04	111.50
1	A	765	G	C6-N1-C2	5.08	128.15	125.10
1	A	1289	A	N9-C4-C5	5.08	107.83	105.80
1	A	968	A	N1-C2-N3	-5.08	126.76	129.30
1	A	481	G	N3-C2-N2	5.07	123.45	119.90
1	A	683	G	N3-C4-C5	-5.07	126.06	128.60
1	A	648	A	C6-N1-C2	-5.07	115.56	118.60
1	A	59	A	C5-C6-N6	-5.07	119.64	123.70
1	A	379	C	C5-C6-N1	-5.07	118.47	121.00
1	A	1064	G	N3-C4-N9	-5.07	122.96	126.00
1	A	1543	C	N3-C4-C5	5.07	123.93	121.90
1	A	1299	A	C6-N1-C2	-5.07	115.56	118.60
1	A	146	G	C5-C6-N1	-5.07	108.97	111.50
1	A	1301	U	P-O3'-C3'	5.07	125.78	119.70
1	A	27	G	C6-C5-N7	-5.07	127.36	130.40
1	A	169	C	C2-N3-C4	5.07	122.43	119.90
1	A	764	C	N3-C2-O2	-5.07	118.36	121.90
1	A	864	A	C5-C6-N6	5.07	127.75	123.70
1	A	559	A	C5-C6-N6	-5.06	119.65	123.70
1	A	691	G	C6-C5-N7	-5.06	127.36	130.40
1	A	1531	A	N9-C4-C5	-5.06	103.77	105.80
1	A	254	G	N7-C8-N9	-5.06	110.57	113.10
1	A	258	G	C6-C5-N7	-5.06	127.36	130.40
1	A	750	G	N1-C2-N2	-5.06	111.64	116.20
1	A	864	A	C6-N1-C2	5.06	121.64	118.60
1	A	416	G	N1-C6-O6	5.06	122.94	119.90
1	A	425	G	C8-N9-C4	-5.06	104.38	106.40
1	A	901	A	N1-C2-N3	5.06	131.83	129.30
1	A	52	G	N1-C2-N3	5.06	126.94	123.90
1	A	1117	G	N9-C4-C5	-5.06	103.38	105.40
1	A	1291	G	C8-N9-C4	5.06	108.42	106.40
1	A	201	C	C2-N1-C1'	5.06	124.36	118.80
1	A	1443	G	C4-C5-N7	5.06	112.82	110.80
1	A	1249	C	N1-C2-O2	5.06	121.93	118.90
1	A	1340	A	C2-N3-C4	-5.06	108.07	110.60
1	A	522	C	C2-N1-C1'	-5.05	113.24	118.80
1	A	1287	A	N1-C2-N3	5.05	131.83	129.30
1	A	64	G	N1-C6-O6	5.05	122.93	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	673	G	N1-C6-O6	5.05	122.93	119.90
1	A	1533	C	N1-C2-O2	5.05	121.93	118.90
1	A	416	G	C8-N9-C4	-5.05	104.38	106.40
1	A	400	C	N1-C2-O2	5.05	121.93	118.90
1	A	762	C	C5-C6-N1	5.05	123.53	121.00
1	A	880	C	C2-N3-C4	-5.05	117.38	119.90
1	A	674	G	C2-N3-C4	-5.05	109.38	111.90
1	A	1391	U	N1-C2-O2	5.05	126.33	122.80
1	A	1531	A	C4-N9-C1'	5.05	135.38	126.30
1	A	138	G	C8-N9-C4	5.04	108.42	106.40
1	A	854	G	C4-C5-C6	5.04	121.83	118.80
1	A	46	G	N1-C2-N3	5.04	126.92	123.90
1	A	964	A	N7-C8-N9	5.04	116.32	113.80
1	A	96	G	C8-N9-C4	-5.04	104.39	106.40
1	A	128	G	N7-C8-N9	5.04	115.62	113.10
1	A	167	G	N3-C4-N9	5.04	129.02	126.00
1	A	285	G	N1-C6-O6	5.04	122.92	119.90
1	A	924	C	N3-C4-C5	-5.03	119.89	121.90
1	A	1348	U	C2-N1-C1'	5.03	123.74	117.70
1	A	289	G	C5-N7-C8	-5.03	101.78	104.30
1	A	1064	G	N3-C4-C5	5.03	131.12	128.60
1	A	879	C	N3-C4-N4	5.03	121.52	118.00
1	A	1117	G	C5-C6-O6	-5.03	125.58	128.60
1	A	392	G	C6-C5-N7	-5.03	127.38	130.40
1	A	863	U	C6-N1-C1'	5.03	128.24	121.20
1	A	243	A	C6-C5-N7	-5.03	128.78	132.30
1	A	298	A	N9-C4-C5	5.02	107.81	105.80
1	A	789	U	N3-C2-O2	-5.02	118.68	122.20
1	A	1343	G	N3-C2-N2	-5.02	116.38	119.90
1	A	1382	C	N1-C2-O2	5.02	121.91	118.90
1	A	1544	U	N3-C2-O2	5.02	125.72	122.20
1	A	570	G	C8-N9-C1'	-5.02	120.47	127.00
1	A	814	A	N1-C2-N3	5.02	131.81	129.30
1	A	948	C	N3-C4-N4	-5.02	114.48	118.00
1	A	228	A	N1-C6-N6	5.02	121.61	118.60
1	A	377	G	N1-C2-N2	-5.02	111.68	116.20
1	A	109	A	N1-C6-N6	5.02	121.61	118.60
1	A	626	U	N3-C4-O4	5.02	122.91	119.40
1	A	657	G	C5-C6-O6	-5.02	125.59	128.60
1	A	234	C	C2-N1-C1'	5.02	124.32	118.80
1	A	811	C	C2-N1-C1'	5.02	124.32	118.80
1	A	895	G	C8-N9-C4	-5.02	104.39	106.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1529	G	C4-N9-C1'	5.02	133.02	126.50
1	A	1339	A	C6-C5-N7	5.02	135.81	132.30
1	A	1462	G	C2-N3-C4	-5.02	109.39	111.90
1	A	483	C	C4-C5-C6	5.01	119.91	117.40
1	A	783	C	C5-C6-N1	-5.01	118.49	121.00
1	A	141	A	C8-N9-C4	5.01	107.81	105.80
1	A	881	G	C4-C5-C6	5.01	121.81	118.80
1	A	639	G	N1-C6-O6	5.01	122.91	119.90
1	A	653	A	C8-N9-C4	-5.01	103.80	105.80
1	A	769	G	N1-C6-O6	5.01	122.91	119.90
1	A	793	U	N3-C4-C5	-5.01	111.59	114.60
1	A	257	G	N3-C4-N9	5.01	129.00	126.00
1	A	655	A	C6-N1-C2	-5.01	115.59	118.60
1	A	1408	A	N1-C6-N6	5.01	121.61	118.60
1	A	1098	C	C5-C6-N1	-5.01	118.50	121.00
1	A	1199	U	C2-N1-C1'	5.01	123.71	117.70
1	A	1314	C	N3-C4-N4	5.01	121.50	118.00
1	A	1347	G	C8-N9-C1'	5.01	133.51	127.00
1	A	1467	G	C4-C5-N7	-5.01	108.80	110.80
1	A	392	G	N1-C6-O6	5.00	122.90	119.90
1	A	1417	G	N7-C8-N9	5.00	115.60	113.10
1	A	190(G)	G	N3-C2-N2	-5.00	116.40	119.90
1	A	573	A	N7-C8-N9	5.00	116.30	113.80
1	A	700	G	N1-C2-N2	-5.00	111.70	116.20
1	A	762	C	N3-C4-N4	5.00	121.50	118.00
1	A	720	C	N3-C2-O2	-5.00	118.40	121.90
1	A	811	C	N3-C4-N4	5.00	121.50	118.00

There are no chirality outliers.

All (13) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	170	GLU	Peptide
4	D	195	ALA	Peptide
7	G	154	TYR	Peptide
8	H	90	GLY	Peptide
10	J	86	MET	Peptide
10	J	90	LEU	Peptide
12	L	27	LEU	Peptide
12	L	87	GLY	Peptide
13	M	105	THR	Peptide
15	O	2	PRO	Peptide

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Mol	Chain	Res	Type	Group
18	R	86	VAL	Peptide
20	T	12	ALA	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	32645	0	16507	767	0
2	B	1900	0	1951	95	0
3	C	1612	0	1677	92	0
4	D	1703	0	1763	97	0
5	E	1146	0	1207	71	0
6	F	843	0	857	43	0
7	G	1257	0	1296	63	0
8	H	1116	0	1177	73	0
9	I	1010	0	1037	67	0
10	J	792	0	835	62	0
11	K	864	0	881	40	0
12	L	972	0	1058	57	0
13	M	937	0	995	50	0
14	N	492	0	529	29	0
15	O	729	0	768	46	0
16	P	700	0	720	37	0
17	Q	823	0	893	47	0
18	R	574	0	644	37	0
19	S	647	0	673	28	0
20	T	763	0	861	29	0
21	U	208	0	221	12	0
22	A	268	0	0	0	0
22	B	2	0	0	0	0
22	C	2	0	0	0	0
22	D	3	0	0	0	0
22	E	1	0	0	0	0
22	F	1	0	0	0	0
22	J	2	0	0	0	0
22	M	1	0	0	0	0
22	N	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	P	3	0	0	0	0
22	Q	2	0	0	0	0
22	S	1	0	0	0	0
23	D	1	0	0	0	0
23	N	1	0	0	0	0
24	A	383	0	0	11	0
24	E	3	0	0	0	0
24	G	2	0	0	2	0
24	I	1	0	0	1	0
24	J	3	0	0	3	0
24	L	1	0	0	0	0
24	M	7	0	0	1	0
24	N	2	0	0	0	0
24	P	8	0	0	1	0
24	Q	1	0	0	0	0
24	T	1	0	0	0	0
All	All	52434	0	36550	1661	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 19.

All (1661) 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)
18:R:39:VAL:HG13	18:R:40:LEU:HD23	1.46	0.98
8:H:9:MET:HG3	8:H:26:VAL:HG21	1.41	0.98
1:A:1399:C:H4'	1:A:1400:5MC:H5''	1.53	0.90
14:N:39:LEU:HD22	14:N:43:CYS:HB3	1.54	0.88
1:A:1309:G:OP2	13:M:99:ARG:NH1	2.07	0.87
3:C:131:ARG:HA	3:C:134:ILE:HD12	1.55	0.87
3:C:11:ARG:HH11	3:C:178:LEU:HD23	1.39	0.86
1:A:992:U:H3	1:A:1044:A:H62	1.23	0.85
21:U:10:ARG:HH11	21:U:10:ARG:HB2	1.40	0.85
1:A:21:G:N2	1:A:885:G:O3'	2.10	0.85
16:P:15:PRO:HD2	16:P:42:ARG:HD3	1.59	0.85
1:A:1368:G:H5''	9:I:112:LYS:HB3	1.59	0.84
2:B:9:GLU:OE1	2:B:10:LEU:N	2.09	0.84
6:F:68:PRO:HB2	6:F:71:ARG:HG3	1.60	0.83
1:A:692:U:OP1	11:K:124:LYS:NZ	2.11	0.83
18:R:36:ASN:HD22	18:R:39:VAL:HG12	1.43	0.83
5:E:11:ILE:HG22	5:E:31:LEU:HB3	1.60	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:70:ASP:OD1	6:F:70:ASP:N	2.10	0.83
1:A:427:U:OP1	4:D:13:ARG:NH2	2.11	0.82
11:K:110:ASP:HB2	18:R:88:LYS:HG2	1.62	0.82
1:A:310:G:OP2	16:P:27:LYS:NZ	2.10	0.82
1:A:481:G:HO2'	1:A:482:A:H8	1.27	0.82
1:A:532:A:O2'	1:A:533:A:OP1	1.98	0.82
1:A:1007:C:O2	1:A:1023:G:N1	2.11	0.81
1:A:836:G:OP1	18:R:61:LYS:NZ	2.14	0.81
1:A:869:G:N7	24:A:2164:HOH:O	2.14	0.81
8:H:4:ASP:OD2	8:H:85:ARG:NH1	2.13	0.80
17:Q:15:MET:HE3	17:Q:18:THR:HB	1.62	0.79
12:L:87:GLY:HA2	12:L:98:TYR:HA	1.63	0.79
5:E:144:THR:HG22	5:E:146:ALA:H	1.47	0.79
1:A:1435:G:H2'	1:A:1436:U:C6	2.17	0.79
19:S:58:VAL:HG12	19:S:59:PRO:HD2	1.65	0.79
1:A:21:G:O2'	1:A:22:G:OP1	2.01	0.79
2:B:223:ILE:HG22	2:B:228:GLY:HA3	1.65	0.79
1:A:973:G:H3'	1:A:974:A:H5''	1.62	0.78
1:A:1369:C:H2'	1:A:1370:G:C8	2.19	0.78
2:B:12:GLU:HG3	2:B:213:LEU:HD21	1.62	0.78
12:L:41:ARG:HH12	12:L:43:VAL:HG13	1.47	0.78
1:A:1338:G:H2'	1:A:1339:A:C8	2.18	0.78
5:E:93:PRO:HD2	8:H:105:ARG:HH21	1.49	0.78
1:A:1195:C:H3'	1:A:1196:U:C5'	2.13	0.77
1:A:144:G:H1	1:A:178:C:H42	1.30	0.77
1:A:1195:C:H3'	1:A:1196:U:H5''	1.65	0.77
12:L:27:LEU:C	12:L:29:GLY:H	1.87	0.77
18:R:47:THR:HG22	18:R:83:GLU:H	1.49	0.77
1:A:1090:U:H2'	1:A:1091:U:H6	1.50	0.77
3:C:5:ILE:HD13	3:C:10:PHE:HB2	1.65	0.77
4:D:11:LEU:HD13	4:D:66:ARG:HD3	1.67	0.76
1:A:656:C:O2'	15:O:28:GLN:NE2	2.19	0.75
2:B:15:VAL:HG13	2:B:209:ARG:HG3	1.69	0.75
1:A:982:U:OP2	14:N:23:ARG:NH2	2.20	0.75
8:H:21:LYS:O	8:H:65:TYR:OH	2.02	0.75
1:A:407:G:OP1	4:D:115:ARG:NH1	2.20	0.75
12:L:20:LYS:H	12:L:20:LYS:HD3	1.51	0.75
8:H:29:SER:HB3	8:H:32:LYS:HD2	1.68	0.75
3:C:174:PRO:HB2	3:C:177:THR:HG23	1.69	0.74
15:O:87:ILE:HG22	15:O:88:ARG:H	1.50	0.74
17:Q:12:SER:HB3	17:Q:20:THR:HB	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:677:U:H3	1:A:713:G:H22	1.35	0.74
1:A:966:M2G:HM13	1:A:967:5MC:H1'	1.69	0.74
12:L:113:ARG:HH12	12:L:116:SER:H	1.36	0.74
7:G:40:ALA:HB3	9:I:41:VAL:HG21	1.70	0.73
1:A:1030(D):A:H62	1:A:1031:G:H21	1.34	0.73
9:I:26:VAL:HB	9:I:33:PHE:HB2	1.67	0.73
21:U:9:ARG:HH22	21:U:23:PRO:HD2	1.53	0.73
4:D:22:LYS:HB2	4:D:26:CYS:SG	2.29	0.73
5:E:142:LEU:O	5:E:143:ARG:NH1	2.20	0.73
3:C:91:LEU:HD21	3:C:99:VAL:HG22	1.68	0.73
1:A:600:C:H42	1:A:638:G:H1	1.35	0.73
4:D:78:LEU:HD21	4:D:96:LEU:HB3	1.71	0.73
8:H:111:ILE:HG22	8:H:134:ILE:HB	1.71	0.73
1:A:1497:G:H2'	1:A:1498:UR3:H5'	1.71	0.72
3:C:35:GLU:OE2	3:C:59:ARG:NH1	2.22	0.72
1:A:1124:G:H2'	1:A:1145:C:H41	1.55	0.72
1:A:758:G:N7	24:A:1965:HOH:O	2.21	0.72
3:C:11:ARG:HG2	3:C:178:LEU:HG	1.72	0.72
9:I:108:VAL:HG12	9:I:109:VAL:H	1.55	0.72
1:A:976:G:OP2	1:A:1358:U:H1'	1.90	0.72
1:A:1345:U:OP1	9:I:120:ARG:NH1	2.23	0.72
1:A:1127:G:O6	1:A:1144:G:N1	2.23	0.71
1:A:1064:G:N2	1:A:1190:G:H2'	2.05	0.71
4:D:187:ARG:CZ	4:D:188:LEU:H	2.02	0.71
1:A:298:A:N6	24:A:2036:HOH:O	2.13	0.71
1:A:660:G:H1	1:A:745:C:H42	1.38	0.71
1:A:838:G:H2'	1:A:839:U:H5''	1.71	0.71
16:P:21:VAL:HG12	16:P:33:ILE:HD12	1.72	0.71
1:A:1101:A:H4'	1:A:1102:A:O5'	1.90	0.71
17:Q:63:ARG:HG2	17:Q:64:PRO:HD2	1.73	0.71
1:A:977:A:H2'	1:A:978:A:H5''	1.73	0.71
9:I:50:LEU:HB3	9:I:55:ALA:HB3	1.73	0.71
13:M:10:PRO:HB2	13:M:18:ALA:HB1	1.73	0.71
13:M:11:ARG:HA	13:M:45:VAL:HG11	1.71	0.70
15:O:35:ARG:HB3	15:O:59:MET:HE1	1.72	0.70
15:O:6:GLU:OE2	15:O:6:GLU:N	2.18	0.70
1:A:542:G:OP1	4:D:10:ARG:NH2	2.24	0.70
12:L:93:LEU:HD12	12:L:96:VAL:HG21	1.72	0.70
1:A:1241:G:H2'	1:A:1242:C:H6	1.56	0.70
13:M:34:LEU:HG	13:M:41:PRO:HB3	1.74	0.70
13:M:48:LEU:HB3	13:M:53:VAL:HG23	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:64:LEU:HA	4:D:67:ILE:HD12	1.72	0.70
1:A:1441:G:H4'	1:A:1442:G:C5	2.25	0.70
12:L:113:ARG:NH1	12:L:116:SER:H	1.89	0.70
17:Q:43:LEU:HB2	17:Q:68:ARG:O	1.91	0.70
1:A:1442:G:N2	1:A:1447:G:N7	2.40	0.70
1:A:31:G:N2	1:A:48:C:OP1	2.22	0.70
1:A:411:A:N7	1:A:413:G:N3	2.40	0.70
7:G:75:VAL:HG22	7:G:88:PRO:HA	1.72	0.70
1:A:1347:G:H3'	9:I:108:VAL:O	1.92	0.69
1:A:281:G:O2'	1:A:282:A:OP2	2.06	0.69
1:A:113:G:H1'	1:A:354:G:H5'	1.74	0.69
1:A:1243:C:OP1	21:U:10:ARG:NH1	2.24	0.69
5:E:147:ASP:OD1	5:E:147:ASP:N	2.19	0.69
1:A:1426:C:H42	1:A:1474:G:H1	1.41	0.68
1:A:719:C:H1'	18:R:49:LYS:HG2	1.75	0.68
1:A:953:G:N7	13:M:104:ARG:NH2	2.41	0.68
1:A:1314:C:H2'	1:A:1315:U:C6	2.29	0.68
4:D:61:LYS:NZ	4:D:62:GLN:OE1	2.27	0.68
1:A:509:A:H3'	1:A:509:A:C8	2.29	0.68
3:C:156:ARG:NE	3:C:160:ALA:O	2.24	0.68
11:K:124:LYS:HG3	11:K:125:PHE:CD1	2.29	0.68
3:C:180:ALA:HB3	3:C:203:PHE:CE1	2.28	0.68
7:G:69:VAL:HG21	7:G:104:LEU:HD21	1.76	0.68
12:L:57:LYS:HD3	12:L:67:THR:HG23	1.76	0.68
1:A:452:A:O2'	1:A:453:A:O4'	2.11	0.68
12:L:20:LYS:CD	12:L:20:LYS:H	2.07	0.68
12:L:10:LEU:HB3	17:Q:32:TYR:CE1	2.28	0.68
1:A:536:C:H2'	1:A:537:G:C8	2.29	0.67
1:A:580:U:H2'	1:A:581:G:O4'	1.93	0.67
10:J:25:GLU:O	10:J:29:ARG:NE	2.27	0.67
10:J:48:THR:HA	10:J:62:HIS:HB3	1.76	0.67
21:U:10:ARG:NH1	21:U:10:ARG:HB2	2.09	0.67
2:B:208:ILE:HA	2:B:211:ILE:HD12	1.75	0.67
10:J:15:THR:HG23	10:J:94:VAL:HG22	1.77	0.67
3:C:71:ALA:HB1	3:C:109:PRO:HG3	1.76	0.67
4:D:107:ARG:HH21	4:D:194:LEU:HD11	1.59	0.67
7:G:16:LEU:H	7:G:16:LEU:HD22	1.58	0.67
14:N:8:GLU:HA	14:N:11:LYS:HD2	1.76	0.67
1:A:1004:A:H5''	1:A:1025:U:N3	2.10	0.67
7:G:70:LYS:O	7:G:72:ARG:NH1	2.28	0.67
12:L:10:LEU:HB3	17:Q:32:TYR:CD1	2.30	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:50:TYR:CE1	18:R:77:GLY:HA2	2.29	0.67
1:A:964:A:N6	24:A:2266:HOH:O	2.19	0.67
1:A:1425:U:H3	1:A:1475:G:H1	1.42	0.67
1:A:1495:U:H2'	1:A:1496:C:C6	2.29	0.67
3:C:21:ARG:HG3	3:C:58:GLU:HG2	1.77	0.67
16:P:60:LEU:HD23	16:P:64:ALA:HB3	1.77	0.67
12:L:47:LYS:HG2	12:L:48:PRO:HD3	1.75	0.67
1:A:501:C:H2'	1:A:502:G:C8	2.30	0.66
1:A:1257:U:H4'	1:A:1258:G:O5'	1.95	0.66
1:A:1352:C:H42	1:A:1370:G:H1	1.43	0.66
1:A:1426:C:H2'	1:A:1427:U:H6	1.59	0.66
1:A:1147:C:H4'	9:I:5:TYR:HE1	1.59	0.66
3:C:37:GLN:HE22	14:N:47:LEU:HD11	1.60	0.66
10:J:57:LYS:NZ	24:J:303:HOH:O	2.28	0.66
17:Q:45:HIS:HD2	17:Q:65:ILE:HG12	1.60	0.66
1:A:1112:C:O2'	3:C:179:ARG:NH1	2.27	0.66
16:P:26:ARG:HG2	16:P:27:LYS:H	1.60	0.66
10:J:3:LYS:HB3	10:J:3:LYS:NZ	2.11	0.66
20:T:60:GLU:HA	20:T:63:ILE:HD12	1.78	0.66
20:T:56:MET:HE2	20:T:85:MET:HA	1.77	0.66
2:B:84:GLU:OE2	2:B:233:SER:OG	2.11	0.66
1:A:321:A:N7	1:A:328:C:H6	1.94	0.66
4:D:83:SER:HA	4:D:89:THR:HG23	1.77	0.66
1:A:1314:C:H5	19:S:6:LYS:HE2	1.60	0.66
1:A:1305:G:N2	1:A:1331:G:H1'	2.11	0.66
1:A:1049:U:H4'	1:A:1050:G:O5'	1.96	0.65
1:A:1126:U:H3	1:A:1149:C:H1'	1.61	0.65
1:A:972:C:H4'	10:J:57:LYS:HD3	1.78	0.65
3:C:6:HIS:NE2	3:C:8:ILE:HB	2.11	0.65
1:A:1406:U:O2'	1:A:1517[B]:G:N2	2.29	0.65
4:D:163:GLU:HA	4:D:166:LYS:HD3	1.78	0.65
13:M:20:THR:HG22	24:M:307:HOH:O	1.96	0.65
11:K:57:THR:HG23	11:K:60:ALA:H	1.62	0.65
1:A:1065:U:H5''	1:A:1190:G:N2	2.11	0.65
1:A:177:C:OP1	20:T:65:LYS:NZ	2.30	0.65
1:A:1498:UR3:O2'	1:A:1499:A:OP2	2.13	0.65
1:A:519:C:OP2	12:L:50:SER:OG	2.08	0.65
2:B:97:TRP:HZ2	2:B:102:LEU:HD22	1.62	0.65
2:B:146:GLN:O	2:B:150:SER:OG	2.13	0.65
4:D:23:GLY:HA3	4:D:112:VAL:HG12	1.78	0.65
1:A:1301:U:O2'	1:A:1302:U:O5'	2.14	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:50:ILE:H	10:J:50:ILE:HD12	1.62	0.64
2:B:42:ILE:HG21	2:B:202:PRO:HB2	1.79	0.64
14:N:47:LEU:HB3	14:N:53:LEU:HD21	1.79	0.64
1:A:1376:U:OP1	7:G:98:SER:OG	2.16	0.64
8:H:110:ALA:HB3	8:H:121:ASP:HB3	1.79	0.64
8:H:114:THR:HG22	8:H:130:GLY:O	1.98	0.64
9:I:8:GLY:HA3	9:I:79:LEU:HB3	1.79	0.64
3:C:37:GLN:NE2	14:N:47:LEU:HD11	2.12	0.64
17:Q:40:LYS:HD2	17:Q:42:TYR:CZ	2.32	0.64
1:A:1133:G:H2'	1:A:1134:G:H8	1.63	0.64
1:A:80:G:O2'	1:A:81:U:OP1	2.12	0.64
7:G:88:PRO:HB2	7:G:155:ARG:NH2	2.12	0.64
18:R:36:ASN:ND2	18:R:39:VAL:HG12	2.12	0.64
1:A:833:U:H2'	1:A:834:C:C6	2.32	0.63
2:B:223:ILE:HG21	2:B:230:VAL:HB	1.80	0.63
7:G:38:LEU:O	7:G:42:ILE:HG13	1.98	0.63
16:P:43:LYS:HG2	16:P:48:TRP:CG	2.33	0.63
10:J:42:THR:HG23	10:J:67:THR:O	1.97	0.63
1:A:1193:G:H2'	1:A:1194:U:H6	1.64	0.63
1:A:411:A:H62	1:A:413:G:N2	1.97	0.63
13:M:117:VAL:HG12	13:M:118:ALA:H	1.62	0.63
14:N:48:ALA:HB1	14:N:56:VAL:HG11	1.80	0.63
6:F:8:ILE:HB	6:F:61:LEU:HB2	1.81	0.63
16:P:4:ILE:HG12	16:P:21:VAL:HG22	1.80	0.63
1:A:1296:C:H4'	1:A:1302:U:C5	2.33	0.63
1:A:1314:C:C5	19:S:6:LYS:HE2	2.33	0.63
2:B:158:LEU:H	2:B:158:LEU:HD12	1.62	0.63
6:F:13:ASN:N	6:F:13:ASN:OD1	2.30	0.63
12:L:27:LEU:C	12:L:29:GLY:N	2.52	0.63
1:A:22:G:H2'	1:A:23:C:H6	1.64	0.63
9:I:118:LYS:O	9:I:120:ARG:N	2.31	0.63
1:A:1366:C:H2'	1:A:1367:C:H6	1.64	0.63
16:P:10:GLY:HA3	16:P:14:ASN:O	1.99	0.63
13:M:12:ASN:H	13:M:45:VAL:HG12	1.64	0.62
1:A:1504:G:OP1	1:A:1507:A:H4'	1.99	0.62
3:C:179:ARG:HG2	3:C:206:GLU:HG3	1.80	0.62
6:F:10:LEU:HD11	6:F:59:TYR:HD2	1.64	0.62
8:H:85:ARG:NE	8:H:87:SER:O	2.31	0.62
13:M:4:ILE:HD13	13:M:56:LEU:HB3	1.80	0.62
1:A:536:C:H2'	1:A:537:G:H8	1.64	0.62
4:D:190:ASP:H	4:D:193:ASP:HB2	1.63	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1412:C:H2'	1:A:1413:A:C8	2.33	0.62
10:J:7:LYS:HA	10:J:71:LEU:CD1	2.29	0.62
1:A:1144:G:N2	1:A:1145:C:O2	2.33	0.62
8:H:10:LEU:HD22	8:H:83:ILE:HD13	1.80	0.62
1:A:1241:G:H2'	1:A:1242:C:C6	2.34	0.62
15:O:55:GLY:O	15:O:59:MET:HG3	2.00	0.62
2:B:80:ILE:H	2:B:80:ILE:HD12	1.64	0.62
9:I:55:ALA:HB1	9:I:59:PHE:HB2	1.81	0.62
2:B:172:ILE:H	2:B:172:ILE:HD12	1.65	0.62
1:A:1372:U:H5''	9:I:71:SER:HB3	1.80	0.62
1:A:826:C:O2	8:H:15:ASN:ND2	2.33	0.61
4:D:200:GLU:CD	4:D:200:GLU:H	2.02	0.61
10:J:61:GLU:HA	24:J:302:HOH:O	2.00	0.61
10:J:89:ASP:CG	10:J:91:PRO:HD3	2.20	0.61
1:A:707:C:H4'	11:K:20:TYR:CD1	2.35	0.61
1:A:1124:G:N2	1:A:1127:G:H21	1.99	0.61
1:A:792:A:H4'	1:A:793:U:O5'	2.00	0.61
3:C:34:LEU:HD23	14:N:25:VAL:HG21	1.82	0.61
15:O:7:GLU:OE1	15:O:38:ARG:NH2	2.33	0.61
18:R:46:GLU:CD	18:R:46:GLU:H	2.03	0.61
1:A:1392:G:H21	1:A:1502:A:H8	1.49	0.61
2:B:74:LYS:HE3	2:B:205:ASP:HB2	1.82	0.61
1:A:1086:U:H3	1:A:1099:G:H22	1.47	0.61
5:E:152:ARG:HB3	8:H:43:GLY:HA3	1.81	0.61
1:A:881:G:P	12:L:12:ARG:HH22	2.24	0.61
5:E:145:LYS:HG3	8:H:107:LEU:HD22	1.82	0.61
12:L:53:ARG:NH1	12:L:92:0TD:OD2	2.33	0.61
1:A:1518[B]:MA6:H93	1:A:1519[B]:MA6:N1	2.16	0.61
1:A:376:G:H5''	16:P:5:ARG:HD2	1.82	0.61
1:A:1064:G:H22	1:A:1190:G:H2'	1.63	0.61
1:A:949:A:H5''	1:A:950:U:OP2	2.01	0.61
8:H:5:PRO:HB2	8:H:6:ILE:HD12	1.83	0.61
8:H:114:THR:HG21	8:H:129:VAL:HG23	1.83	0.61
1:A:279:A:H8	1:A:279:A:H5'	1.66	0.61
1:A:1205:U:OP1	3:C:190:ARG:NH2	2.34	0.61
3:C:147:LYS:HE3	3:C:203:PHE:HE2	1.66	0.61
8:H:97:VAL:HG12	8:H:98:LYS:HG3	1.84	0.60
11:K:65:ALA:HB1	11:K:98:LEU:HB2	1.83	0.60
1:A:328:C:H4'	1:A:329:A:O5'	2.02	0.60
1:A:1465:C:H2'	1:A:1466:C:O4'	2.01	0.60
1:A:371:G:O2'	1:A:372:C:H5'	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1020:U:H2'	1:A:1021:G:H8	1.67	0.60
1:A:1290:G:H2'	1:A:1291:G:H8	1.65	0.60
10:J:62:HIS:N	24:J:301:HOH:O	2.12	0.60
2:B:53:ARG:HG2	2:B:54:THR:N	2.16	0.60
1:A:1397:C:O2'	1:A:1398:A:OP1	2.14	0.60
1:A:21:G:HO2'	1:A:22:G:P	2.23	0.60
1:A:1228:C:O3'	13:M:116:THR:HG23	2.02	0.60
1:A:436:C:H2'	1:A:437:U:H6	1.67	0.60
3:C:8:ILE:HG23	3:C:16:ARG:HE	1.67	0.60
1:A:1356:G:H2'	1:A:1357:A:C8	2.37	0.60
1:A:1499:A:H1'	1:A:1520[A]:G:H5'	1.84	0.60
1:A:419:C:H42	1:A:424:G:H1	1.48	0.60
1:A:518:C:H4'	1:A:519:C:O5'	2.02	0.60
3:C:70:VAL:HG21	3:C:76:VAL:HG21	1.84	0.60
9:I:88:TYR:CD2	9:I:89:ASN:HB2	2.37	0.60
13:M:12:ASN:H	13:M:45:VAL:CG1	2.14	0.60
1:A:1318:A:H2'	19:S:37:ARG:HD2	1.82	0.60
6:F:69:GLU:CD	6:F:69:GLU:H	2.05	0.59
7:G:26:PHE:CD1	7:G:101:LEU:HD22	2.36	0.59
11:K:121:PRO:HD2	11:K:126:ARG:HD2	1.84	0.59
20:T:29:LYS:O	20:T:32:ALA:HB3	2.01	0.59
4:D:156:GLU:O	4:D:160:GLN:HB2	2.02	0.59
1:A:1398:A:H5''	1:A:1401:G:H4'	1.84	0.59
1:A:1414:U:H2'	1:A:1415:G:H8	1.67	0.59
1:A:24:U:H2'	1:A:25:C:C6	2.37	0.59
1:A:372:C:H4'	1:A:373:A:O5'	2.01	0.59
5:E:97:GLY:N	5:E:117:ASP:OD2	2.36	0.59
10:J:6:ILE:HB	10:J:72:VAL:HG21	1.84	0.59
14:N:27:CYS:SG	14:N:29:ARG:HB2	2.42	0.59
1:A:501:C:H2'	1:A:502:G:H8	1.64	0.59
10:J:7:LYS:HE2	10:J:9:ARG:HH21	1.67	0.59
1:A:1130:A:O2'	9:I:3:GLN:NE2	2.32	0.59
1:A:413:G:H1	4:D:36:ARG:HH11	1.48	0.59
9:I:113:LYS:H	9:I:119:ALA:HA	1.68	0.59
1:A:864:A:H2'	1:A:865:A:C8	2.38	0.59
1:A:91:C:H2'	1:A:92:C:C6	2.37	0.59
1:A:975:A:H4'	1:A:976:G:O5'	2.02	0.59
1:A:9:G:OP2	5:E:121:LYS:NZ	2.33	0.59
9:I:28:VAL:O	9:I:31:GLN:N	2.36	0.59
1:A:1004:A:O2'	1:A:1005:A:OP1	2.20	0.59
1:A:1362:C:O2'	24:A:2162:HOH:O	2.17	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:614:A:H2'	1:A:615:C:C6	2.37	0.59
1:A:738:C:OP2	6:F:92:LYS:NZ	2.31	0.59
7:G:89:MET:HA	7:G:155:ARG:HD3	1.84	0.59
1:A:1116:C:O2'	9:I:108:VAL:HG21	2.03	0.59
1:A:563:A:H5''	1:A:564:C:OP1	2.03	0.59
9:I:43:ALA:HA	9:I:74:ILE:HD13	1.85	0.59
3:C:11:ARG:NH2	3:C:175:LEU:O	2.33	0.58
11:K:120:ARG:HG2	11:K:120:ARG:HH11	1.67	0.58
1:A:222:U:H2'	1:A:223:U:C6	2.38	0.58
1:A:778:G:H8	1:A:778:G:O5'	1.85	0.58
2:B:240:GLN:OE1	2:B:240:GLN:N	2.36	0.58
1:A:450:G:H4'	16:P:41:PRO:HB2	1.84	0.58
12:L:55:VAL:HG12	12:L:69:TYR:HA	1.84	0.58
19:S:39:THR:HG22	19:S:40:ILE:O	2.02	0.58
21:U:15:ARG:HH11	21:U:15:ARG:HB2	1.67	0.58
5:E:80:ILE:HD11	5:E:138:ALA:HB1	1.84	0.58
1:A:933:G:OP2	7:G:3:ARG:HB3	2.04	0.58
10:J:3:LYS:HA	10:J:75:ILE:HG12	1.85	0.58
10:J:32:ALA:O	10:J:34:VAL:HG23	2.03	0.58
20:T:39:LYS:O	20:T:43:LEU:HB2	2.03	0.58
1:A:937:A:N6	1:A:1345:U:O4	2.36	0.58
1:A:1111:A:H61	3:C:177:THR:HB	1.68	0.58
6:F:71:ARG:O	6:F:74:ASP:N	2.36	0.58
8:H:97:VAL:H	8:H:98:LYS:NZ	2.01	0.58
1:A:1147:C:H4'	9:I:5:TYR:CE1	2.38	0.58
1:A:1368:G:OP2	9:I:112:LYS:HD3	2.03	0.58
1:A:951:G:OP2	13:M:102:ARG:NH2	2.33	0.58
3:C:154:SER:OG	3:C:155:GLY:N	2.30	0.58
7:G:15:ASP:OD1	7:G:44:TYR:OH	2.20	0.58
12:L:84:LEU:HD23	12:L:101:VAL:HG21	1.85	0.58
1:A:1048:G:H1	1:A:1209:C:H42	1.49	0.58
1:A:1286:A:H2'	1:A:1287:A:H4'	1.85	0.58
1:A:1426:C:H2'	1:A:1427:U:C6	2.38	0.58
7:G:37:ASN:ND2	24:G:202:HOH:O	2.21	0.58
10:J:3:LYS:N	10:J:75:ILE:HG23	2.19	0.58
1:A:1297:C:OP1	13:M:44:ARG:NH2	2.37	0.58
1:A:1057:G:H5''	3:C:154:SER:HB2	1.85	0.57
10:J:50:ILE:HA	10:J:60:ARG:HG2	1.86	0.57
1:A:1134:G:H1	1:A:1140:C:H42	1.50	0.57
1:A:450:G:N7	1:A:481:G:O6	2.37	0.57
1:A:652:U:O4	1:A:752:G:O2'	2.19	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:79:G:C2	1:A:80:G:C8	2.92	0.57
5:E:92:LYS:O	5:E:118:ILE:HG13	2.04	0.57
1:A:1071:C:H42	1:A:1104:G:H1	1.51	0.57
4:D:9:CYS:O	4:D:12:CYS:HB2	2.04	0.57
15:O:60:VAL:HG12	15:O:61:GLY:N	2.19	0.57
1:A:1315:U:HO2'	1:A:1360:A:HO2'	1.52	0.57
1:A:1372:U:H2'	1:A:1373:G:O4'	2.04	0.57
2:B:213:LEU:HG	2:B:214:ILE:HD13	1.85	0.57
4:D:191:ARG:HH12	4:D:196:LEU:HB2	1.69	0.57
1:A:1055:A:N7	1:A:1200:C:N4	2.48	0.57
1:A:250:A:H4'	1:A:251:G:O5'	2.04	0.57
3:C:14:ILE:HG22	3:C:15:THR:HG23	1.85	0.57
7:G:18:TYR:CD2	7:G:59:LEU:HD13	2.38	0.57
8:H:6:ILE:N	8:H:6:ILE:HD12	2.19	0.57
18:R:36:ASN:HD22	18:R:39:VAL:H	1.52	0.57
1:A:685:G:H2'	1:A:686:U:H5''	1.85	0.57
17:Q:87:LYS:HA	17:Q:90:ILE:HD12	1.86	0.57
1:A:572:A:H5'	1:A:573:A:OP2	2.04	0.57
1:A:462:G:H21	16:P:82:GLN:HE21	1.52	0.57
3:C:62:ASP:HA	3:C:97:LYS:HD3	1.86	0.57
1:A:451:A:N6	1:A:481:G:C4	2.73	0.57
1:A:673:G:H2'	1:A:674:G:C8	2.40	0.57
2:B:45:GLN:O	2:B:48:MET:HB2	2.04	0.57
2:B:76:GLN:HG3	2:B:206:ASP:OD1	2.05	0.57
13:M:2:ALA:O	13:M:10:PRO:HD2	2.05	0.57
16:P:43:LYS:HG2	16:P:48:TRP:CD2	2.40	0.57
1:A:77:G:O2'	1:A:78:G:H5'	2.04	0.56
1:A:838:G:C2'	1:A:839:U:H5''	2.34	0.56
3:C:5:ILE:CD1	3:C:10:PHE:HB2	2.32	0.56
4:D:4:TYR:CE2	4:D:11:LEU:HD11	2.40	0.56
10:J:84:GLN:HG2	10:J:88:LEU:HD11	1.86	0.56
1:A:1145:C:HO2'	1:A:1146:A:P	2.28	0.56
1:A:1197:G:H5''	24:A:2043:HOH:O	2.04	0.56
1:A:1516[A]:G:N1	1:A:1519[A]:MA6:OP2	2.36	0.56
1:A:130:A:H1'	1:A:263:A:O2'	2.04	0.56
1:A:269:C:H2'	1:A:270:A:C8	2.40	0.56
1:A:518:C:H2'	1:A:530:G:C8	2.40	0.56
1:A:581:G:N7	24:A:1965:HOH:O	2.33	0.56
1:A:79:G:N1	1:A:80:G:C5	2.73	0.56
10:J:49:VAL:O	10:J:61:GLU:N	2.36	0.56
11:K:20:TYR:CD2	11:K:83:ILE:HB	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:22:G:H2'	1:A:23:C:C6	2.40	0.56
3:C:148:GLY:HA3	3:C:172:ARG:O	2.05	0.56
1:A:1152:A:OP1	10:J:68:HIS:NE2	2.38	0.56
12:L:30:ALA:HB1	12:L:31:PRO:HD2	1.87	0.56
12:L:24:VAL:HG13	12:L:98:TYR:HE2	1.69	0.56
1:A:1342:C:H2'	1:A:1343:G:C8	2.39	0.56
3:C:180:ALA:HB2	3:C:206:GLU:HA	1.87	0.56
3:C:79:ARG:HH11	3:C:79:ARG:HB2	1.71	0.56
9:I:49:PRO:HD3	9:I:101:PHE:CE2	2.40	0.56
16:P:39:TYR:HE2	16:P:41:PRO:HG3	1.71	0.56
1:A:1256:A:H4'	1:A:1257:U:O5'	2.05	0.56
1:A:481:G:O2'	1:A:482:A:H8	1.86	0.56
9:I:89:ASN:HB3	9:I:92:TYR:CD1	2.41	0.56
10:J:6:ILE:HG23	10:J:98:ILE:HG12	1.88	0.56
1:A:1006:C:N4	1:A:1022:G:H22	2.02	0.56
1:A:1493:A:O2'	1:A:1494:G:H8	1.88	0.56
1:A:279:A:C8	1:A:279:A:H5'	2.40	0.56
1:A:975:A:H5'	1:A:975:A:H8	1.71	0.56
10:J:49:VAL:HG13	14:N:41:ARG:HB2	1.87	0.56
12:L:25:PRO:HB3	12:L:27:LEU:HD22	1.86	0.56
1:A:1437:C:H2'	1:A:1438:G:H8	1.71	0.56
2:B:114:ARG:HH11	2:B:118:LEU:HD11	1.71	0.56
5:E:69:VAL:HG22	5:E:139:LEU:HB3	1.87	0.56
11:K:104:GLN:HG2	11:K:106:LYS:HE2	1.86	0.56
14:N:8:GLU:HA	14:N:11:LYS:CD	2.35	0.56
1:A:1290:G:H2'	1:A:1291:G:C8	2.40	0.56
1:A:1435:G:H2'	1:A:1436:U:H6	1.69	0.56
1:A:778:G:H2'	1:A:779:C:O4'	2.04	0.56
3:C:6:HIS:HE2	3:C:8:ILE:HB	1.71	0.56
5:E:80:ILE:HG22	8:H:104:ARG:HH21	1.70	0.56
10:J:50:ILE:CD1	10:J:50:ILE:H	2.18	0.56
13:M:4:ILE:HG23	13:M:57:ARG:HA	1.87	0.56
1:A:1133:G:H1	1:A:1141:C:H42	1.54	0.56
1:A:1343:G:H2'	1:A:1344:C:C6	2.40	0.56
1:A:1419:G:H1	1:A:1481:U:H3	1.54	0.56
5:E:17:ALA:HA	5:E:26:PHE:HB3	1.87	0.56
12:L:70:ILE:HG21	12:L:75:HIS:HD2	1.71	0.56
1:A:1377:A:C5	7:G:7:ALA:HB1	2.41	0.56
4:D:28:SER:O	4:D:30:LYS:N	2.38	0.56
7:G:40:ALA:CB	9:I:41:VAL:HG21	2.36	0.56
19:S:71:LEU:HD22	19:S:72:GLY:N	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1035:A:H2'	1:A:1036:G:C8	2.39	0.56
1:A:1420:C:H2'	1:A:1421:G:H8	1.70	0.56
1:A:707:C:OP1	11:K:85:ARG:NH1	2.39	0.56
1:A:1258:G:OP2	1:A:1258:G:H8	1.89	0.55
1:A:629:G:H2'	1:A:630:G:O4'	2.06	0.55
8:H:2:LEU:HD23	8:H:3:THR:N	2.21	0.55
10:J:91:PRO:HB2	10:J:94:VAL:HB	1.88	0.55
11:K:58:PRO:O	11:K:61:ALA:N	2.39	0.55
1:A:804:U:H5''	1:A:805:C:OP2	2.07	0.55
9:I:126:SER:OG	9:I:127:LYS:N	2.39	0.55
20:T:81:LYS:O	20:T:85:MET:HG3	2.06	0.55
1:A:338:A:H2'	1:A:339:C:O4'	2.06	0.55
8:H:9:MET:HE2	8:H:32:LYS:HG2	1.88	0.55
10:J:57:LYS:O	10:J:60:ARG:NH1	2.39	0.55
15:O:7:GLU:O	15:O:11:VAL:HG23	2.07	0.55
17:Q:4:LYS:HG3	17:Q:5:VAL:N	2.19	0.55
1:A:1349:A:OP2	9:I:118:LYS:HD3	2.07	0.55
1:A:1422:G:N2	1:A:1479:C:N3	2.55	0.55
1:A:77:G:C4	1:A:93:G:N2	2.75	0.55
2:B:17:PHE:HD1	2:B:18:GLY:N	2.04	0.55
2:B:20:GLU:HA	2:B:23:ARG:NH1	2.22	0.55
5:E:152:ARG:NE	8:H:44:PHE:HE1	2.03	0.55
1:A:942:G:H21	9:I:124:GLN:HE22	1.54	0.55
1:A:513:C:H2'	1:A:514:C:O4'	2.06	0.55
1:A:89:C:O2'	1:A:90:U:H5'	2.07	0.55
1:A:946:A:H2'	1:A:947:G:C8	2.42	0.55
1:A:881:G:OP2	12:L:12:ARG:NH2	2.39	0.55
13:M:15:VAL:HG21	13:M:48:LEU:HD21	1.87	0.55
17:Q:63:ARG:HG2	17:Q:64:PRO:CD	2.35	0.55
1:A:1511:G:H2'	1:A:1512:U:O4'	2.07	0.55
1:A:558:G:H5''	1:A:559:A:H3'	1.87	0.55
1:A:988:G:O2'	1:A:1015:A:N6	2.30	0.55
11:K:32:ILE:O	11:K:40:ILE:N	2.38	0.55
1:A:1349:A:C2	1:A:1374:A:C4	2.95	0.55
1:A:1145:C:O2'	1:A:1146:A:O5'	2.20	0.55
1:A:750:G:H1'	15:O:23:GLY:H	1.70	0.55
6:F:27:GLN:HA	6:F:30:LEU:HD12	1.88	0.55
10:J:79:ARG:HH22	10:J:82:ILE:HB	1.71	0.55
1:A:35:G:H2'	1:A:36:C:C6	2.42	0.55
1:A:411:A:C8	1:A:413:G:H1'	2.41	0.55
2:B:122:PHE:HA	2:B:127:ILE:HD11	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:167:TRP:CE3	3:C:167:TRP:HA	2.41	0.55
5:E:93:PRO:O	8:H:105:ARG:NH2	2.40	0.55
10:J:27:ALA:HB2	10:J:85:LEU:HD21	1.87	0.55
10:J:52:GLY:O	14:N:41:ARG:NH2	2.39	0.55
1:A:1497:G:C2'	1:A:1498:UR3:H5'	2.36	0.54
4:D:155:LEU:HB3	4:D:158:ILE:HG13	1.89	0.54
9:I:48:GLU:N	9:I:49:PRO:HD2	2.22	0.54
10:J:79:ARG:NH2	10:J:82:ILE:HB	2.22	0.54
12:L:70:ILE:HG21	12:L:75:HIS:CD2	2.42	0.54
10:J:81:THR:O	10:J:85:LEU:HG	2.07	0.54
1:A:276:G:O2'	17:Q:68:ARG:NH1	2.40	0.54
18:R:19:LYS:O	18:R:19:LYS:HD3	2.07	0.54
1:A:620:C:H2'	1:A:621:A:O4'	2.07	0.54
3:C:119:ARG:O	3:C:122:GLU:HB2	2.08	0.54
3:C:141:VAL:HG11	3:C:202:ILE:HG12	1.90	0.54
5:E:18:ARG:HG2	5:E:19:MET:N	2.22	0.54
16:P:19:ILE:HG22	16:P:36:ILE:HG13	1.90	0.54
1:A:1342:C:H2'	1:A:1343:G:H8	1.70	0.54
1:A:1147:C:O2	9:I:16:ARG:NH2	2.40	0.54
1:A:968:A:C8	1:A:1062:U:H4'	2.43	0.54
6:F:100:ASN:H	18:R:23:LYS:HZ1	1.55	0.54
9:I:3:GLN:OE1	9:I:20:ARG:NH2	2.40	0.54
12:L:110:VAL:HG23	12:L:120:TYR:HB3	1.89	0.54
13:M:16:ASP:OD1	13:M:16:ASP:N	2.41	0.54
1:A:560:U:H5'	1:A:566:G:N2	2.23	0.54
6:F:29:ALA:HA	6:F:32:ASN:HB2	1.89	0.54
15:O:18:PHE:CZ	15:O:21:ASP:HB2	2.42	0.54
1:A:1006:C:H2'	1:A:1007:C:H6	1.71	0.54
1:A:1236:A:H4'	1:A:1304:G:H4'	1.89	0.54
1:A:8:A:N6	4:D:209:ARG:HB2	2.23	0.54
4:D:82:ALA:HB1	4:D:92:VAL:HG12	1.90	0.54
1:A:1197:G:H22	10:J:56:HIS:CE1	2.26	0.54
1:A:1291:G:H2'	1:A:1292:U:C6	2.42	0.54
1:A:547:A:OP2	4:D:2:GLY:N	2.40	0.54
1:A:664:G:H22	1:A:741:G:H1	1.54	0.54
20:T:49:ALA:HB3	20:T:99:LEU:HD12	1.90	0.54
1:A:1516[A]:G:H2'	1:A:1518[A]:MA6:OP2	2.08	0.54
1:A:644:G:C5	1:A:645:C:C5	2.95	0.54
2:B:9:GLU:HG3	2:B:12:GLU:HG2	1.90	0.54
3:C:174:PRO:HB2	3:C:177:THR:CG2	2.38	0.54
1:A:1285:A:H4'	1:A:1286:A:O5'	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:101:ALA:HA	18:R:28:GLU:HG2	1.90	0.54
1:A:113:G:H2'	1:A:114:U:C6	2.43	0.53
1:A:782:A:OP1	1:A:1521:G:N2	2.41	0.53
3:C:110:ASN:OD1	3:C:140:ARG:HB3	2.08	0.53
1:A:1111:A:N1	3:C:177:THR:HB	2.24	0.53
5:E:92:LYS:HB3	5:E:119:LEU:HB2	1.91	0.53
11:K:92:GLU:OE2	11:K:95:ILE:HD12	2.07	0.53
1:A:186:C:H2'	1:A:187:C:C6	2.43	0.53
1:A:200:G:H2'	1:A:201:C:O4'	2.09	0.53
1:A:436:C:H2'	1:A:437:U:C6	2.42	0.53
1:A:8:A:C6	4:D:209:ARG:HB2	2.43	0.53
1:A:1352:C:N3	1:A:1370:G:N2	2.44	0.53
9:I:103:THR:HG22	9:I:104:ARG:O	2.09	0.53
3:C:136:GLN:HG3	3:C:140:ARG:HH21	1.72	0.53
3:C:79:ARG:NH1	3:C:79:ARG:HB2	2.23	0.53
7:G:100:ALA:O	7:G:104:LEU:HG	2.09	0.53
18:R:36:ASN:ND2	18:R:39:VAL:H	2.06	0.53
20:T:61:SER:O	20:T:65:LYS:HG2	2.08	0.53
1:A:1096:C:H2'	1:A:1097:C:H6	1.73	0.53
1:A:1373:G:H5''	7:G:36:LYS:HB2	1.89	0.53
1:A:404:U:H2'	1:A:405:U:H6	1.74	0.53
2:B:162:ILE:O	2:B:185:ILE:HD12	2.09	0.53
1:A:1315:U:O2'	1:A:1360:A:O2'	2.23	0.53
2:B:97:TRP:CZ2	2:B:101:MET:HB2	2.44	0.53
2:B:60:ASP:O	2:B:64:ARG:HB2	2.09	0.53
19:S:30:LEU:HA	19:S:48:THR:O	2.09	0.53
21:U:5:ASP:O	21:U:11:GLY:HA3	2.08	0.53
1:A:1225:A:N3	1:A:1225:A:H2'	2.23	0.53
1:A:1243:C:H5''	21:U:8:THR:HG22	1.89	0.53
1:A:1438:G:H2'	1:A:1439:C:H6	1.74	0.53
2:B:124:SER:HB3	2:B:126:GLU:OE2	2.09	0.53
2:B:91:PRO:HG2	2:B:155:LEU:CD2	2.38	0.53
4:D:18:LYS:HE2	4:D:20:TYR:HE2	1.73	0.53
13:M:89:GLY:O	13:M:93:ARG:HG2	2.09	0.53
18:R:30:ASP:OD1	18:R:32:ARG:N	2.37	0.53
1:A:1305:G:OP2	1:A:1305:G:C8	2.62	0.53
1:A:1417:G:O2'	1:A:1483:A:N6	2.42	0.53
1:A:88:A:H2'	1:A:89:C:O4'	2.09	0.53
2:B:36:ARG:O	2:B:39:ILE:HG22	2.09	0.53
4:D:102:ASP:OD1	4:D:103:ASN:N	2.40	0.53
5:E:88:LYS:HB3	5:E:123:LEU:HB2	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:8:ILE:HD13	6:F:26:ILE:HD13	1.90	0.53
5:E:100:VAL:O	5:E:107:ARG:NH2	2.42	0.53
6:F:3:ARG:HB3	6:F:93:SER:HB2	1.90	0.53
7:G:87:VAL:HG13	7:G:151:TYR:HB3	1.91	0.53
15:O:15:PHE:CZ	15:O:85:LEU:HD21	2.44	0.53
1:A:1053:G:HO2'	1:A:1199:U:H5	1.57	0.52
2:B:35:GLU:OE1	2:B:38:GLY:HA2	2.09	0.52
4:D:3:ARG:NH1	4:D:70:ILE:HA	2.24	0.52
8:H:114:THR:HB	8:H:116:LYS:H	1.74	0.52
14:N:21:TYR:HE2	14:N:23:ARG:HE	1.56	0.52
17:Q:37:LYS:O	17:Q:38:ARG:HD2	2.08	0.52
18:R:39:VAL:O	18:R:42:ARG:HB2	2.09	0.52
1:A:1361(A):C:HO2'	1:A:1362:C:H6	1.58	0.52
1:A:1498:UR3:O4'	1:A:1519[A]:MA6:H2	2.09	0.52
1:A:758:G:O5'	1:A:758:G:H8	1.92	0.52
1:A:966:M2G:H2'	1:A:967:5MC:H6	1.73	0.52
2:B:157:ARG:HG2	2:B:158:LEU:N	2.24	0.52
6:F:22:GLU:OE1	6:F:82:ARG:NH1	2.42	0.52
11:K:34:ASP:OD1	11:K:38:ASN:N	2.41	0.52
1:A:1367:C:O5'	9:I:112:LYS:NZ	2.42	0.52
4:D:155:LEU:HD23	4:D:156:GLU:H	1.73	0.52
1:A:932:C:H5'	7:G:4:ARG:HG2	1.90	0.52
12:L:42:THR:HG23	12:L:52:LEU:HB3	1.90	0.52
1:A:1240:U:H1'	7:G:38:LEU:HD21	1.92	0.52
1:A:373:A:H1'	1:A:481:G:N3	2.25	0.52
1:A:77:G:C2	1:A:78:G:C4	2.97	0.52
4:D:101:LEU:O	4:D:105:VAL:HG23	2.09	0.52
1:A:1178:G:N2	1:A:1181:G:OP2	2.43	0.52
1:A:560:U:H5'	1:A:566:G:C2	2.45	0.52
7:G:47:CYS:HB3	7:G:58:PRO:HG2	1.91	0.52
15:O:5:LYS:O	15:O:8:LYS:HB2	2.09	0.52
1:A:960:U:H1'	1:A:1223:C:H5'	1.92	0.52
1:A:1361(A):C:H2'	1:A:1362:C:H5''	1.92	0.52
1:A:378:G:H2'	1:A:379:C:C6	2.44	0.52
11:K:33:THR:HA	11:K:39:PRO:HA	1.91	0.52
1:A:1004:A:H5''	1:A:1025:U:C2	2.44	0.52
4:D:177:ASP:OD2	4:D:179:GLU:HB2	2.09	0.52
5:E:90:VAL:C	5:E:91:LEU:HD23	2.30	0.52
11:K:59:TYR:O	11:K:62:GLN:HB3	2.09	0.52
1:A:1283:G:H2'	1:A:1284:C:H6	1.75	0.52
1:A:409:G:H1	1:A:433:C:H42	1.56	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:476:G:H2'	1:A:477:G:C8	2.45	0.52
1:A:770:C:O2'	1:A:771:G:H5'	2.10	0.52
8:H:4:ASP:OD1	8:H:6:ILE:N	2.38	0.52
20:T:13:LEU:HD12	20:T:14:LYS:N	2.24	0.52
1:A:999:C:H2'	1:A:1000:U:C6	2.45	0.52
1:A:1314:C:OP2	19:S:6:LYS:NZ	2.38	0.52
1:A:75:G:N1	1:A:76:C:N3	2.58	0.52
4:D:3:ARG:HH11	4:D:70:ILE:HA	1.75	0.52
5:E:13:ILE:HG22	5:E:30:ALA:HA	1.92	0.52
7:G:18:TYR:CE2	7:G:59:LEU:HB2	2.45	0.52
8:H:9:MET:CG	8:H:26:VAL:HG21	2.28	0.52
10:J:10:GLY:HA3	10:J:16:LEU:HD21	1.91	0.52
12:L:25:PRO:HG3	12:L:27:LEU:HD13	1.92	0.52
4:D:57:ARG:HG3	4:D:202:LEU:HD13	1.90	0.51
9:I:25:LYS:HE2	9:I:60:ASP:OD2	2.09	0.51
15:O:18:PHE:HB2	15:O:19:PRO:HD2	1.91	0.51
21:U:15:ARG:NH1	21:U:15:ARG:HB2	2.26	0.51
1:A:1305:G:OP1	21:U:2:GLY:N	2.43	0.51
1:A:1305:G:O2'	1:A:1306:A:OP2	2.23	0.51
1:A:1488:G:H2'	1:A:1489:G:H8	1.75	0.51
2:B:47:THR:HG23	2:B:202:PRO:HG2	1.92	0.51
2:B:82:ARG:NE	2:B:92:TYR:OH	2.35	0.51
1:A:1376:U:O4	7:G:10:ARG:NH1	2.43	0.51
11:K:54:ARG:O	11:K:57:THR:HG22	2.09	0.51
17:Q:7:THR:O	17:Q:23:VAL:HG13	2.10	0.51
1:A:1009:G:H1	1:A:1020:U:H3	1.58	0.51
1:A:1008:C:O2	1:A:1023:G:N2	2.43	0.51
1:A:1414:U:H2'	1:A:1415:G:C8	2.44	0.51
1:A:176:C:O2'	1:A:177:C:H5'	2.09	0.51
1:A:518:C:H2'	1:A:530:G:H8	1.76	0.51
2:B:114:ARG:NH1	2:B:118:LEU:HD21	2.25	0.51
4:D:3:ARG:NH2	4:D:74:GLN:OE1	2.43	0.51
7:G:106:GLN:O	7:G:110:GLN:HB2	2.10	0.51
10:J:3:LYS:HB3	10:J:3:LYS:HZ3	1.75	0.51
14:N:25:VAL:HG12	14:N:38:GLY:O	2.10	0.51
1:A:1415:G:H1	1:A:1485:U:H3	1.57	0.51
1:A:1392:G:N2	1:A:1502:A:H8	2.09	0.51
1:A:1510:U:H2'	1:A:1511:G:C8	2.46	0.51
1:A:427:U:OP2	4:D:36:ARG:NH2	2.43	0.51
12:L:46:LYS:HG2	12:L:47:LYS:HD3	1.92	0.51
1:A:949:A:OP1	13:M:101:GLN:HB3	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:8:GLU:O	14:N:11:LYS:HB2	2.10	0.51
17:Q:27:PHE:CZ	17:Q:36:ILE:HD11	2.45	0.51
1:A:1009:G:N2	1:A:1010:G:N3	2.58	0.51
1:A:1427:U:H2'	1:A:1428:A:C8	2.46	0.51
1:A:28:G:O2'	1:A:296:U:OP1	2.28	0.51
1:A:383:A:C5	1:A:384:G:H1'	2.45	0.51
3:C:6:HIS:HD2	14:N:49:HIS:HB3	1.74	0.51
15:O:36:ILE:HG12	15:O:59:MET:HE2	1.91	0.51
1:A:243:A:C2	1:A:246:A:C8	2.99	0.51
1:A:474:G:H4'	16:P:81:ARG:NH2	2.26	0.51
5:E:43:LEU:HD21	5:E:133:TYR:CE2	2.45	0.51
12:L:41:ARG:NH1	12:L:43:VAL:HG13	2.22	0.51
1:A:1213:A:N6	1:A:1215:G:C4	2.78	0.51
1:A:1401:G:C2	1:A:1402:4OC:H1'	2.45	0.51
1:A:836:G:C6	1:A:851:G:C6	2.99	0.51
4:D:141:ARG:N	4:D:144:ASP:OD2	2.40	0.51
13:M:59:TYR:O	13:M:63:THR:OG1	2.28	0.51
15:O:3:ILE:CD1	15:O:35:ARG:HG3	2.41	0.51
18:R:26:LEU:HD12	18:R:27:GLY:H	1.75	0.51
1:A:428:G:H4'	1:A:429:U:O5'	2.11	0.51
1:A:566:G:H4'	1:A:567:G:OP1	2.11	0.51
1:A:757:U:H2'	1:A:758:G:O4'	2.11	0.51
1:A:828:A:H4'	1:A:828:A:OP1	2.11	0.51
1:A:76:C:H42	1:A:95:U:H3	1.57	0.51
1:A:1301:U:HO2'	1:A:1302:U:P	2.33	0.51
1:A:966:M2G:C5	1:A:967:5MC:HM52	2.46	0.51
2:B:98:LEU:HB2	2:B:101:MET:SD	2.51	0.51
5:E:102:ALA:H	5:E:107:ARG:HH12	1.59	0.51
5:E:122:GLU:O	5:E:123:LEU:HD23	2.11	0.51
7:G:68:ASN:O	7:G:138:LYS:HD3	2.11	0.51
8:H:97:VAL:N	8:H:98:LYS:NZ	2.59	0.51
20:T:65:LYS:O	20:T:68:LYS:HB3	2.11	0.51
1:A:1305:G:H22	1:A:1331:G:H1'	1.76	0.51
1:A:1402:4OC:HM22	1:A:1403:C:H5'	1.92	0.51
1:A:127:G:N2	1:A:234:C:O2	2.28	0.51
1:A:31:G:O2'	1:A:48:C:N4	2.44	0.51
15:O:39:LEU:HD13	15:O:56:LEU:HD13	1.93	0.51
15:O:6:GLU:CD	15:O:6:GLU:H	2.06	0.51
19:S:11:VAL:HG13	19:S:15:LEU:HD11	1.92	0.51
1:A:335:C:H2'	1:A:336:C:C6	2.46	0.50
1:A:370:C:C2'	1:A:371:G:H5'	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:390:C:H2'	1:A:391:G:C8	2.46	0.50
1:A:476:G:H2'	1:A:477:G:H8	1.76	0.50
1:A:91:C:C6	1:A:92:C:H5	2.29	0.50
2:B:212:GLN:O	2:B:216:SER:HB3	2.11	0.50
3:C:178:LEU:HD22	3:C:179:ARG:N	2.26	0.50
6:F:36:ARG:NH1	6:F:66:GLU:OE1	2.44	0.50
1:A:115:G:H1'	1:A:116:A:N7	2.26	0.50
3:C:36:ASP:OD2	3:C:59:ARG:NH2	2.44	0.50
8:H:102:ARG:HH11	8:H:105:ARG:HD3	1.74	0.50
1:A:1250:A:H5''	9:I:67:GLY:HA2	1.92	0.50
1:A:130:A:H5'	17:Q:63:ARG:HE	1.76	0.50
1:A:216:G:H2'	1:A:217:C:C6	2.46	0.50
1:A:321:A:H2'	1:A:322:C:C6	2.46	0.50
6:F:10:LEU:CD1	6:F:59:TYR:HB3	2.41	0.50
16:P:53:VAL:O	16:P:55:ARG:N	2.44	0.50
1:A:103:C:OP2	20:T:14:LYS:HD2	2.12	0.50
1:A:1313:U:H5	19:S:4:SER:HB2	1.76	0.50
1:A:1343:G:H2'	1:A:1344:C:H6	1.76	0.50
1:A:1417:G:H2'	1:A:1482:G:H22	1.76	0.50
1:A:224:C:H2'	1:A:225:C:H6	1.76	0.50
1:A:344:A:H5'	1:A:345:C:C5	2.46	0.50
1:A:81:U:H5'	1:A:82:U:OP2	2.12	0.50
1:A:9:G:OP1	5:E:122:GLU:HG3	2.12	0.50
1:A:1222:G:OP2	1:A:1322:C:N4	2.43	0.50
1:A:393:A:OP2	16:P:12:LYS:NZ	2.44	0.50
2:B:115:LEU:HD11	2:B:146:GLN:HG3	1.94	0.50
2:B:17:PHE:HD1	2:B:18:GLY:H	1.59	0.50
1:A:409:G:OP1	4:D:24:GLU:O	2.29	0.50
7:G:136:LYS:HE2	7:G:136:LYS:C	2.32	0.50
1:A:1464:G:O2'	1:A:1465:C:H5'	2.11	0.50
1:A:384:G:H2'	1:A:385:C:C6	2.46	0.50
1:A:588:G:H1	1:A:651:C:H42	1.60	0.50
3:C:15:THR:O	3:C:15:THR:OG1	2.25	0.50
3:C:11:ARG:NH1	3:C:178:LEU:HD23	2.19	0.50
1:A:108:G:C6	20:T:15:ARG:HD2	2.47	0.50
1:A:1152:A:OP1	10:J:68:HIS:CD2	2.65	0.50
4:D:64:LEU:HD23	4:D:198:VAL:HG21	1.92	0.50
9:I:82:ALA:HB1	9:I:102:LEU:HD23	1.93	0.50
20:T:13:LEU:HD12	20:T:14:LYS:H	1.76	0.50
1:A:385:C:H2'	1:A:386:C:C6	2.47	0.50
1:A:77:G:N2	1:A:78:G:C4	2.79	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:875:C:O2'	8:H:14:ARG:NH1	2.45	0.50
3:C:87:LEU:O	3:C:91:LEU:HB3	2.12	0.50
15:O:3:ILE:HD11	15:O:35:ARG:HG3	1.94	0.50
16:P:34:GLU:OE1	16:P:55:ARG:NH1	2.42	0.50
19:S:80:TYR:CD1	19:S:81:ARG:N	2.78	0.50
1:A:1251:A:H2'	1:A:1252:A:C8	2.47	0.50
1:A:374:A:H5''	1:A:375:U:OP2	2.12	0.50
1:A:532:A:HO2'	1:A:533:A:P	2.30	0.50
1:A:706:A:H1'	11:K:29:ILE:HD11	1.94	0.50
1:A:771:G:N2	1:A:808:C:O2	2.45	0.50
4:D:12:CYS:SG	4:D:19:LEU:O	2.70	0.50
8:H:113:SER:HB2	8:H:134:ILE:HD11	1.93	0.50
19:S:50:ALA:HA	19:S:58:VAL:O	2.12	0.50
1:A:110:C:H2'	1:A:111:G:O4'	2.11	0.49
1:A:1201:A:H4'	1:A:1202:G:O5'	2.12	0.49
1:A:403:C:H2'	1:A:404:U:H6	1.76	0.49
1:A:993:G:H2'	1:A:995:C:H41	1.76	0.49
6:F:10:LEU:HD12	6:F:59:TYR:HB3	1.94	0.49
8:H:119:LEU:HD12	8:H:124:ALA:HB2	1.94	0.49
1:A:324:G:OP1	20:T:22:ARG:HD3	2.12	0.49
1:A:254:G:OP1	17:Q:67:LYS:O	2.29	0.49
4:D:62:GLN:O	4:D:66:ARG:HG3	2.13	0.49
1:A:457:C:H2'	1:A:458:C:H6	1.76	0.49
1:A:556:C:H2'	1:A:557:G:O4'	2.12	0.49
5:E:76:ILE:HB	5:E:77:PRO:HD2	1.93	0.49
7:G:146:GLU:OE2	7:G:149:ARG:HG3	2.12	0.49
13:M:23:TYR:HB3	13:M:67:GLU:H	1.77	0.49
1:A:130:A:C8	17:Q:63:ARG:HG3	2.47	0.49
1:A:337:C:H2'	1:A:338:A:H8	1.77	0.49
1:A:62:U:O2'	1:A:63:C:H5'	2.12	0.49
1:A:81:U:H2'	1:A:83:U:OP2	2.12	0.49
7:G:70:LYS:HG2	7:G:96:GLN:HB3	1.95	0.49
13:M:96:LEU:O	13:M:110:ARG:NH1	2.42	0.49
1:A:270:A:H2'	1:A:271:C:C6	2.48	0.49
1:A:353:A:H5'	1:A:353:A:H8	1.76	0.49
1:A:908:A:O2'	1:A:909:A:H5'	2.12	0.49
7:G:72:ARG:HH11	7:G:72:ARG:N	2.10	0.49
10:J:79:ARG:HA	10:J:79:ARG:NE	2.28	0.49
16:P:74:LEU:HD22	16:P:79:VAL:HG21	1.95	0.49
1:A:1124:G:C2	1:A:1127:G:N2	2.80	0.49
1:A:1329:A:P	13:M:28:ALA:HB3	2.52	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1435:G:O5'	1:A:1435:G:H8	1.95	0.49
1:A:547:A:H4'	1:A:548:G:O5'	2.12	0.49
1:A:80:G:H2'	1:A:81:U:O5'	2.12	0.49
3:C:105:GLU:OE2	3:C:107:GLN:NE2	2.45	0.49
13:M:95:GLY:O	13:M:96:LEU:HD23	2.12	0.49
18:R:86:VAL:HG12	18:R:87:ARG:H	1.77	0.49
1:A:790:A:H2'	1:A:791:G:C8	2.48	0.49
1:A:908:A:C2	1:A:909:A:C4	3.00	0.49
13:M:11:ARG:HD2	13:M:45:VAL:CG1	2.43	0.49
18:R:58:LEU:HD13	18:R:62:GLU:HB3	1.94	0.49
1:A:1406:U:C6	1:A:1407:5MC:HM52	2.48	0.49
1:A:646:U:H2'	1:A:647:C:C6	2.48	0.49
3:C:150:LYS:HB3	3:C:201:TYR:HB2	1.95	0.49
1:A:409:G:OP2	4:D:22:LYS:HD2	2.13	0.49
5:E:43:LEU:HD23	5:E:43:LEU:O	2.13	0.49
7:G:5:ARG:HH12	7:G:8:GLU:HG3	1.77	0.49
10:J:79:ARG:HH11	10:J:83:GLU:HB2	1.78	0.49
15:O:6:GLU:HA	15:O:9:GLN:HB2	1.95	0.49
21:U:15:ARG:HG2	21:U:17:THR:HG23	1.95	0.49
1:A:337:C:H2'	1:A:338:A:C8	2.48	0.49
1:A:509:A:C3'	1:A:509:A:C8	2.95	0.49
1:A:522:C:H1'	1:A:536:C:H5''	1.95	0.49
1:A:687:A:H4'	1:A:688:G:O5'	2.13	0.49
1:A:93:G:O2'	1:A:95:U:H5'	2.13	0.49
4:D:32:ALA:O	4:D:36:ARG:N	2.41	0.49
4:D:8:VAL:O	4:D:11:LEU:N	2.32	0.49
6:F:10:LEU:HD12	6:F:10:LEU:H	1.77	0.49
16:P:15:PRO:CD	16:P:42:ARG:HD3	2.39	0.49
1:A:255:G:H1'	17:Q:16:GLN:OE1	2.13	0.49
17:Q:35:VAL:HG12	17:Q:35:VAL:O	2.11	0.49
19:S:28:LYS:HG2	19:S:29:ARG:N	2.27	0.49
1:A:21:G:N2	1:A:886:G:P	2.86	0.49
1:A:448:A:C2	1:A:449:C:C4	3.01	0.49
1:A:674:G:O2'	1:A:675:A:H5'	2.13	0.49
8:H:86:ILE:HG21	8:H:133:LEU:HD13	1.95	0.49
15:O:17:ARG:HB2	15:O:18:PHE:CD2	2.48	0.49
1:A:679:C:H2'	1:A:680:C:C6	2.47	0.48
2:B:39:ILE:HG23	2:B:41:ILE:HD11	1.94	0.48
3:C:155:GLY:HA3	3:C:163:ALA:HB1	1.95	0.48
5:E:33:VAL:HG13	5:E:112:LEU:HD12	1.95	0.48
8:H:102:ARG:NH1	8:H:105:ARG:HD3	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:108:ARG:HD3	13:M:114:ARG:NH1	2.28	0.48
18:R:25:THR:O	18:R:26:LEU:HB2	2.12	0.48
2:B:87:ARG:HH21	2:B:219:VAL:HG12	1.78	0.48
3:C:156:ARG:H	3:C:163:ALA:HA	1.77	0.48
5:E:17:ALA:HB2	5:E:26:PHE:HD2	1.77	0.48
18:R:74:ARG:HB3	18:R:81:PHE:CE1	2.47	0.48
1:A:1443:G:O5'	1:A:1443:G:H8	1.97	0.48
1:A:926:G:N2	1:A:1542:U:OP1	2.34	0.48
1:A:259:G:H2'	1:A:260:G:C8	2.48	0.48
1:A:858:G:O6	1:A:869:G:C8	2.66	0.48
2:B:84:GLU:OE1	2:B:216:SER:HA	2.12	0.48
7:G:104:LEU:HA	7:G:104:LEU:HD23	1.52	0.48
8:H:98:LYS:HE2	8:H:98:LYS:H	1.77	0.48
1:A:628:G:H2'	1:A:629:G:H8	1.79	0.48
2:B:20:GLU:HA	2:B:23:ARG:HH11	1.79	0.48
1:A:438:G:H4'	4:D:123:HIS:CD2	2.48	0.48
4:D:25:ARG:C	4:D:27:TYR:H	2.16	0.48
7:G:5:ARG:HG2	7:G:6:ARG:H	1.79	0.48
8:H:120:THR:HG23	8:H:123:GLU:CD	2.34	0.48
10:J:25:GLU:HA	10:J:28:ARG:HB2	1.96	0.48
11:K:80:VAL:HG21	11:K:103:LEU:HD13	1.94	0.48
11:K:91:ARG:HH12	18:R:88:LYS:HE2	1.78	0.48
12:L:93:LEU:O	12:L:96:VAL:HG23	2.13	0.48
1:A:113:G:H2'	1:A:114:U:H6	1.78	0.48
3:C:20:SER:HA	3:C:57:ILE:O	2.13	0.48
1:A:1117:G:H5''	9:I:104:ARG:NH2	2.28	0.48
13:M:62:ASN:OD1	13:M:62:ASN:N	2.40	0.48
15:O:12:ILE:O	15:O:15:PHE:N	2.46	0.48
18:R:22:VAL:HG23	18:R:55:ARG:O	2.14	0.48
1:A:1492:A:H3'	1:A:1493:A:O4'	2.14	0.48
1:A:811:C:O2'	1:A:901:A:N1	2.42	0.48
5:E:131:ILE:O	5:E:134:ALA:N	2.45	0.48
7:G:135:VAL:O	7:G:139:GLU:HG3	2.14	0.48
9:I:25:LYS:HG3	9:I:60:ASP:OD1	2.14	0.48
9:I:5:TYR:CD2	9:I:6:GLY:N	2.82	0.48
10:J:7:LYS:HA	10:J:71:LEU:HD11	1.95	0.48
13:M:34:LEU:HD12	13:M:39:ILE:O	2.14	0.48
16:P:6:LEU:HD12	16:P:6:LEU:N	2.28	0.48
1:A:1488:G:H2'	1:A:1489:G:C8	2.49	0.48
2:B:170:GLU:O	2:B:172:ILE:N	2.46	0.48
4:D:31:CYS:SG	4:D:31:CYS:O	2.71	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:94:ARG:O	7:G:97:GLN:HB3	2.14	0.48
8:H:69:ARG:NH1	8:H:75:ARG:O	2.46	0.48
14:N:16:PHE:HD1	14:N:19:ARG:HH11	1.61	0.48
20:T:56:MET:HG3	20:T:88:VAL:HG21	1.94	0.48
1:A:352:C:H5''	1:A:352:C:H6	1.78	0.48
1:A:841:U:H6	1:A:841:U:P	2.37	0.48
1:A:872:A:C8	1:A:874:G:C8	3.02	0.48
2:B:189:ASP:OD1	2:B:205:ASP:HB3	2.13	0.48
2:B:84:GLU:OE2	2:B:235:SER:OG	2.29	0.48
3:C:174:PRO:O	3:C:177:THR:HG23	2.13	0.48
8:H:104:ARG:HD2	8:H:138:TRP:CD2	2.48	0.48
1:A:1279:A:H5''	10:J:7:LYS:NZ	2.28	0.48
17:Q:95:TYR:HA	17:Q:98:LEU:CD1	2.44	0.48
1:A:1092:A:N3	1:A:1183:A:N6	2.62	0.48
1:A:1329:A:H5''	13:M:29:ARG:HD2	1.95	0.48
1:A:1409:C:H2'	1:A:1410:G:C8	2.49	0.48
2:B:236:TYR:O	2:B:239:VAL:HB	2.13	0.48
5:E:87:SER:HB3	5:E:131:ILE:HD13	1.94	0.48
8:H:113:SER:O	8:H:131:GLY:HA3	2.14	0.48
1:A:1437:C:H2'	1:A:1438:G:C8	2.48	0.48
8:H:98:LYS:CE	8:H:98:LYS:H	2.27	0.48
1:A:1347:G:O2'	1:A:1348:U:P	2.71	0.47
1:A:664:G:OP1	18:R:64:ARG:HD2	2.13	0.47
2:B:163:PHE:CD1	2:B:185:ILE:HB	2.49	0.47
3:C:108:ASN:HB3	3:C:111:LEU:H	1.79	0.47
4:D:108:LEU:HD22	4:D:176:LEU:HB2	1.94	0.47
4:D:192:GLU:C	4:D:194:LEU:H	2.17	0.47
4:D:36:ARG:HG2	4:D:38:TYR:OH	2.14	0.47
5:E:77:PRO:HD2	5:E:142:LEU:HD13	1.95	0.47
5:E:40:ARG:HH11	5:E:40:ARG:HG2	1.79	0.47
6:F:4:TYR:HE1	6:F:92:LYS:HG2	1.79	0.47
7:G:111:ARG:HG2	7:G:112:PRO:HD2	1.95	0.47
15:O:15:PHE:CZ	15:O:84:LYS:HD3	2.49	0.47
1:A:1031:G:H2'	1:A:1032:G:C8	2.49	0.47
1:A:1181:G:O2'	1:A:1182:G:H5'	2.14	0.47
1:A:1450:U:O2'	1:A:1451:A:H8	1.97	0.47
1:A:793:U:O2	1:A:1516[A]:G:O2'	2.24	0.47
1:A:977:A:C2'	1:A:978:A:H5''	2.43	0.47
3:C:156:ARG:NH1	3:C:193:TYR:O	2.47	0.47
5:E:105:VAL:HG12	5:E:106:PRO:N	2.29	0.47
7:G:5:ARG:NH1	7:G:8:GLU:HG3	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:16:LEU:HD22	10:J:94:VAL:HG13	1.96	0.47
12:L:110:VAL:CG2	12:L:120:TYR:HB3	2.43	0.47
17:Q:11:VAL:HG12	17:Q:85:VAL:HG22	1.97	0.47
1:A:1530:G:H4'	1:A:1530:G:OP1	2.13	0.47
8:H:84:ARG:O	8:H:135:CYS:HB2	2.14	0.47
9:I:118:LYS:HG3	9:I:121:ARG:HB3	1.97	0.47
12:L:127:GLU:OE2	12:L:127:GLU:N	2.46	0.47
1:A:1474:G:H2'	1:A:1475:G:C8	2.49	0.47
1:A:77:G:C5	1:A:93:G:N1	2.81	0.47
6:F:8:ILE:HG21	6:F:61:LEU:HD12	1.96	0.47
10:J:38:ILE:H	10:J:38:ILE:HD13	1.79	0.47
11:K:122:LYS:HB3	11:K:122:LYS:HE2	1.48	0.47
20:T:59:ALA:O	20:T:63:ILE:HG13	2.14	0.47
1:A:112:G:C2	1:A:113:G:C8	3.02	0.47
1:A:1409:C:H2'	1:A:1410:G:H8	1.78	0.47
1:A:328:C:H1'	1:A:329:A:OP2	2.14	0.47
1:A:95:U:H2'	1:A:96:G:H8	1.79	0.47
4:D:187:ARG:HA	4:D:187:ARG:NH1	2.29	0.47
4:D:199:ASN:O	4:D:202:LEU:HB2	2.15	0.47
1:A:921:U:O2'	5:E:19:MET:O	2.29	0.47
12:L:76:ASN:ND2	12:L:106:ASP:O	2.47	0.47
10:J:47:PHE:CZ	14:N:37:PHE:HE1	2.32	0.47
1:A:1391:U:H2'	1:A:1392:G:C8	2.49	0.47
1:A:1517[B]:G:N7	1:A:1518[B]:MA6:H103	2.29	0.47
1:A:413:G:H1	4:D:36:ARG:NH1	2.11	0.47
3:C:108:ASN:C	3:C:110:ASN:N	2.68	0.47
3:C:47:LEU:HB3	3:C:50:ALA:HB3	1.96	0.47
5:E:131:ILE:HD13	5:E:131:ILE:HA	1.66	0.47
5:E:80:ILE:HG22	8:H:104:ARG:NH2	2.30	0.47
7:G:17:VAL:HG12	7:G:18:TYR:CD1	2.49	0.47
10:J:40:LEU:HB3	10:J:41:PRO:HD2	1.96	0.47
1:A:116:A:H2'	1:A:117:G:H8	1.79	0.47
1:A:1228:C:H4'	13:M:116:THR:HA	1.96	0.47
1:A:278:G:OP2	17:Q:41:LYS:NZ	2.37	0.47
1:A:7:G:H5'	1:A:298:A:H5'	1.96	0.47
5:E:96:PRO:HA	5:E:117:ASP:OD2	2.14	0.47
1:A:1228:C:OP1	13:M:108:ARG:NH2	2.48	0.47
1:A:1402:4OC:O2	1:A:1500:A:N1	2.48	0.47
1:A:80:G:HO2'	1:A:81:U:P	2.32	0.47
1:A:840:C:H4'	1:A:841:U:OP1	2.13	0.47
1:A:925:G:C2	1:A:927:G:C8	3.03	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:6:HIS:CD2	14:N:49:HIS:HB3	2.50	0.47
6:F:25:ILE:HD13	6:F:28:ARG:HD2	1.97	0.47
6:F:33:TYR:CD1	6:F:75:LEU:HD23	2.49	0.47
16:P:26:ARG:HD2	16:P:31:LYS:O	2.15	0.47
1:A:1133:G:H2'	1:A:1134:G:C8	2.48	0.47
1:A:396:G:O2'	1:A:398:C:OP1	2.23	0.47
1:A:448:A:C4	1:A:487:A:C2	3.03	0.47
1:A:75:G:C2	1:A:76:C:C2	3.03	0.47
1:A:377:G:OP1	16:P:3:LYS:HD3	2.15	0.47
17:Q:29:HIS:CE1	17:Q:30:PRO:HD2	2.50	0.47
1:A:321:A:H2'	1:A:322:C:H6	1.79	0.47
1:A:633:G:H2'	1:A:634:C:C6	2.49	0.47
1:A:707:C:H5''	11:K:85:ARG:HH12	1.79	0.47
1:A:922:G:C2	1:A:1396:A:C6	3.02	0.47
2:B:24:TRP:CG	2:B:25:ASN:N	2.83	0.47
4:D:190:ASP:HB2	4:D:193:ASP:OD2	2.15	0.47
1:A:1080:A:O3'	5:E:16:THR:OG1	2.31	0.47
7:G:26:PHE:HD1	7:G:101:LEU:HD22	1.78	0.47
10:J:48:THR:HG1	10:J:62:HIS:CG	2.28	0.47
17:Q:40:LYS:HD2	17:Q:42:TYR:CE1	2.49	0.47
18:R:37:VAL:CG2	18:R:78:LEU:HB3	2.45	0.47
1:A:109:A:C4	1:A:327:A:C2	3.03	0.47
1:A:628:G:H2'	1:A:629:G:C8	2.50	0.47
1:A:841:U:OP2	1:A:841:U:H6	1.99	0.47
1:A:1188:A:H5''	24:I:201:HOH:O	2.14	0.46
1:A:1330:U:H2'	1:A:1331:G:H5'	1.95	0.46
8:H:1:MET:HG2	8:H:2:LEU:O	2.15	0.46
9:I:28:VAL:HA	9:I:63:ILE:O	2.16	0.46
17:Q:29:HIS:HA	17:Q:30:PRO:HD3	1.77	0.46
1:A:344:A:H4'	1:A:345:C:OP2	2.15	0.46
1:A:706:A:C1'	11:K:29:ILE:HD11	2.45	0.46
7:G:113:GLU:HG2	7:G:113:GLU:H	1.52	0.46
1:A:1227:A:OP2	13:M:111:LYS:HE2	2.15	0.46
16:P:28:ARG:HG3	16:P:29:ASP:N	2.29	0.46
19:S:42:PRO:O	19:S:45:VAL:HG23	2.15	0.46
1:A:1345:U:H3'	24:A:2229:HOH:O	2.14	0.46
1:A:1438:G:H2'	1:A:1439:C:C6	2.49	0.46
1:A:224:C:H2'	1:A:225:C:C6	2.50	0.46
1:A:45:U:H2'	1:A:46:G:C8	2.50	0.46
1:A:913:A:H4'	1:A:914:G:O5'	2.15	0.46
1:A:77:G:C6	1:A:93:G:N1	2.83	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:986:A:H2'	1:A:987:G:O4'	2.16	0.46
2:B:187:LEU:HD11	2:B:203:GLY:HA3	1.97	0.46
7:G:41:ARG:HH11	7:G:41:ARG:HB3	1.80	0.46
12:L:53:ARG:HG3	12:L:53:ARG:HH11	1.80	0.46
1:A:190(D):U:O2'	1:A:190(E):U:H5'	2.15	0.46
1:A:419:C:N4	1:A:424:G:H1	2.12	0.46
1:A:509:A:H8	1:A:509:A:H3'	1.80	0.46
2:B:88:ALA:HB2	2:B:219:VAL:HG13	1.98	0.46
5:E:144:THR:HB	5:E:147:ASP:OD1	2.15	0.46
12:L:46:LYS:HE2	12:L:94:PRO:HG2	1.97	0.46
12:L:46:LYS:HB2	12:L:92:OTD:O	2.15	0.46
20:T:68:LYS:HE3	20:T:68:LYS:HA	1.98	0.46
1:A:1068:G:OP1	1:A:1387:G:O2'	2.33	0.46
1:A:1225:A:H5'	1:A:1226:C:OP2	2.14	0.46
1:A:128:G:C6	1:A:129:U:N3	2.83	0.46
1:A:642:A:C8	8:H:115:SER:HA	2.51	0.46
1:A:877:C:O2'	8:H:3:THR:HG23	2.16	0.46
1:A:1318:A:H4'	19:S:10:PHE:CD2	2.51	0.46
1:A:1006:C:H42	1:A:1022:G:H22	1.63	0.46
1:A:1442:G:C6	1:A:1446:A:N7	2.83	0.46
1:A:731:G:OP1	1:A:766:A:H1'	2.14	0.46
8:H:20:TYR:HA	8:H:65:TYR:CE2	2.51	0.46
10:J:47:PHE:HB3	14:N:34:TYR:CE2	2.50	0.46
1:A:1498:UR3:C4'	1:A:1519[A]:MA6:H2	2.45	0.46
1:A:24:U:H2'	1:A:25:C:H6	1.79	0.46
1:A:552:U:H4'	12:L:86:ARG:HG3	1.96	0.46
3:C:188:LEU:HD11	3:C:195:VAL:HG22	1.98	0.46
5:E:102:ALA:H	5:E:107:ARG:NH1	2.12	0.46
5:E:110:LEU:HD13	5:E:118:ILE:HD13	1.98	0.46
5:E:6:PHE:HE2	5:E:36:ASP:HB3	1.81	0.46
8:H:80:ILE:HG21	8:H:83:ILE:HG13	1.96	0.46
20:T:64:ASP:O	20:T:67:ALA:HB3	2.15	0.46
1:A:1320:C:N4	19:S:36:ARG:HG3	2.30	0.46
1:A:279:A:OP2	17:Q:95:TYR:OH	2.24	0.46
1:A:78:G:N2	1:A:79:G:H1'	2.31	0.46
9:I:118:LYS:C	9:I:120:ARG:H	2.19	0.46
17:Q:74:LEU:HD12	17:Q:74:LEU:HA	1.48	0.46
1:A:1250:A:H2'	1:A:1251:A:C8	2.51	0.46
1:A:330:C:H2'	1:A:331:G:H5'	1.98	0.46
1:A:960:U:H4'	1:A:961:U:C5'	2.46	0.46
2:B:187:LEU:HD22	2:B:201:ILE:HB	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:11:ARG:HD3	3:C:178:LEU:HD23	1.97	0.46
3:C:16:ARG:CZ	3:C:54:ARG:HH12	2.29	0.46
7:G:92:SER:HB3	7:G:95:ARG:HB2	1.97	0.46
11:K:33:THR:HG22	11:K:39:PRO:HA	1.98	0.46
15:O:26:GLU:OE1	15:O:70:LEU:HD11	2.16	0.46
20:T:50:GLU:HB2	20:T:99:LEU:HD13	1.96	0.46
1:A:1420:C:H2'	1:A:1421:G:C8	2.50	0.46
1:A:204:U:H4'	1:A:216:G:O4'	2.16	0.46
1:A:75:G:C6	1:A:76:C:C4	3.04	0.46
2:B:212:GLN:NE2	2:B:235:SER:OG	2.49	0.46
4:D:155:LEU:HD23	4:D:156:GLU:N	2.31	0.46
6:F:4:TYR:CE1	6:F:92:LYS:HG2	2.52	0.46
8:H:25:ASP:OD1	8:H:25:ASP:N	2.48	0.46
9:I:88:TYR:CE2	9:I:89:ASN:HB2	2.51	0.46
12:L:47:LYS:H	12:L:47:LYS:HD3	1.81	0.46
13:M:11:ARG:HD2	13:M:45:VAL:HG11	1.97	0.46
1:A:803:G:C6	1:A:804:U:C4	3.04	0.45
3:C:173:VAL:HG12	3:C:175:LEU:HD21	1.98	0.45
3:C:6:HIS:CD2	3:C:9:GLY:H	2.33	0.45
4:D:98:GLU:HG3	4:D:194:LEU:HD21	1.98	0.45
1:A:6:G:H2'	5:E:119:LEU:HD13	1.98	0.45
8:H:35:ILE:HD11	8:H:134:ILE:HD13	1.98	0.45
15:O:39:LEU:HB3	15:O:56:LEU:HD13	1.97	0.45
15:O:4:THR:HG23	15:O:7:GLU:OE2	2.16	0.45
16:P:51:VAL:HG12	16:P:53:VAL:N	2.31	0.45
1:A:1030(A):G:H2'	1:A:1030(C):G:OP2	2.15	0.45
1:A:1223:C:H3'	1:A:1224:G:C5'	2.45	0.45
1:A:1413:A:H2'	1:A:1414:U:H6	1.82	0.45
1:A:413:G:H2'	1:A:428:G:N2	2.31	0.45
1:A:602:A:C2	1:A:637:G:C2	3.04	0.45
1:A:1074:G:O3'	2:B:103:THR:HG21	2.15	0.45
2:B:158:LEU:N	2:B:158:LEU:HD12	2.29	0.45
3:C:134:ILE:O	3:C:138:VAL:HG23	2.16	0.45
7:G:26:PHE:HA	7:G:101:LEU:HD13	1.98	0.45
8:H:63:LEU:HD13	8:H:63:LEU:N	2.30	0.45
11:K:20:TYR:HD2	11:K:83:ILE:HB	1.81	0.45
11:K:95:ILE:HG21	11:K:108:ILE:HD13	1.98	0.45
12:L:77:LEU:HD23	12:L:77:LEU:HA	1.54	0.45
18:R:34:TYR:CE1	18:R:35:ARG:HG3	2.50	0.45
1:A:1122:U:H5	1:A:1123:A:C8	2.35	0.45
1:A:748:C:H4'	1:A:749:C:O5'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:35:GLU:O	3:C:39:ILE:HG13	2.16	0.45
14:N:7:ILE:O	14:N:7:ILE:HG22	2.16	0.45
1:A:882:C:O2'	1:A:883:C:H5'	2.15	0.45
1:A:943:U:H2'	1:A:944:G:H5'	1.98	0.45
5:E:98:THR:HB	5:E:117:ASP:HB3	1.98	0.45
8:H:59:LEU:HA	8:H:59:LEU:HD23	1.74	0.45
12:L:35:GLY:HA3	12:L:60:LEU:HD13	1.98	0.45
1:A:1063:C:H2'	1:A:1064:G:C8	2.52	0.45
1:A:129:U:O3'	1:A:129(A):G:H3'	2.16	0.45
1:A:1505:G:H3'	1:A:1505:G:C8	2.52	0.45
1:A:173:U:H6	1:A:198:G:HO2'	1.63	0.45
1:A:443:C:H42	1:A:491:G:H1	1.64	0.45
1:A:91:C:H2'	1:A:92:C:H6	1.78	0.45
3:C:108:ASN:CB	3:C:111:LEU:H	2.29	0.45
3:C:150:LYS:HD2	3:C:173:VAL:HG11	1.98	0.45
8:H:80:ILE:CG2	8:H:83:ILE:HG13	2.47	0.45
1:A:1071:C:N4	1:A:1104:G:H1	2.14	0.45
1:A:1300:G:C6	1:A:1335:C:C5	3.05	0.45
1:A:1314:C:H2'	1:A:1315:U:H6	1.77	0.45
1:A:1531:A:O5'	1:A:1531:A:H8	2.00	0.45
1:A:918:A:H2'	1:A:919:A:C8	2.51	0.45
1:A:922:G:C6	1:A:923:A:C6	3.04	0.45
4:D:68:TYR:CE2	4:D:97:LEU:HB3	2.51	0.45
7:G:28:ASN:O	7:G:31:MET:HB3	2.17	0.45
8:H:86:ILE:HD13	8:H:86:ILE:HA	1.59	0.45
1:A:279:A:C4	17:Q:98:LEU:HD22	2.52	0.45
1:A:579:G:O3'	15:O:54:ARG:NH2	2.48	0.45
13:M:37:THR:HG21	13:M:56:LEU:HD23	1.99	0.45
15:O:33:THR:HG23	15:O:63:ARG:NH1	2.32	0.45
15:O:29:VAL:HG21	15:O:67:LEU:HD21	1.98	0.45
19:S:5:LEU:C	19:S:6:LYS:HD3	2.37	0.45
1:A:1281:U:H5'	1:A:1282:C:H5	1.81	0.45
1:A:1502:A:H2	1:A:1505:G:H1	1.65	0.45
9:I:22:GLY:HA3	9:I:60:ASP:HB2	1.98	0.45
10:J:75:ILE:HG22	10:J:76:ASN:OD1	2.16	0.45
1:A:1279:A:H5''	10:J:7:LYS:HZ1	1.81	0.45
1:A:1035:A:C6	1:A:1036:G:C6	3.04	0.45
1:A:1185:G:C2	1:A:1186:G:C5	3.05	0.45
1:A:1053:G:O2'	1:A:1199:U:H5	2.00	0.45
1:A:1222:G:N2	1:A:1223:C:O2	2.50	0.45
1:A:1443:G:H5''	1:A:1446:A:H5'	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:15:G:H1'	5:E:19:MET:HE1	1.99	0.45
1:A:250:A:O5'	1:A:250:A:H8	2.00	0.45
1:A:91:C:O2'	1:A:92:C:H5'	2.17	0.45
5:E:36:ASP:OD1	5:E:38:GLN:N	2.47	0.45
6:F:75:LEU:O	6:F:79:LEU:HD12	2.16	0.45
9:I:108:VAL:HG12	9:I:109:VAL:N	2.27	0.45
9:I:92:TYR:O	9:I:96:LEU:HB2	2.16	0.45
12:L:126:LYS:HB2	12:L:126:LYS:HE2	1.62	0.45
15:O:45:VAL:HG12	15:O:46:HIS:H	1.82	0.45
18:R:47:THR:CG2	18:R:83:GLU:H	2.26	0.45
19:S:63:THR:HG22	19:S:64:GLU:H	1.82	0.45
1:A:1203:C:O5'	1:A:1203:C:H6	2.00	0.45
1:A:1316:G:N2	1:A:1319:A:OP2	2.50	0.45
2:B:126:GLU:H	2:B:126:GLU:HG3	1.61	0.45
2:B:47:THR:O	2:B:51:LEU:HB2	2.17	0.45
4:D:187:ARG:HD2	4:D:187:ARG:HA	1.50	0.45
4:D:35:ARG:O	4:D:36:ARG:HG3	2.17	0.45
6:F:2:ARG:NE	6:F:69:GLU:HG2	2.32	0.45
6:F:75:LEU:HD13	6:F:79:LEU:HD11	1.99	0.45
9:I:50:LEU:O	9:I:54:ASP:N	2.49	0.45
1:A:1003:G:N2	1:A:1039:C:O2	2.50	0.44
1:A:988:G:HO2'	1:A:1015:A:H61	1.56	0.44
1:A:1120:G:C2	1:A:1154:G:N3	2.85	0.44
1:A:1355:G:C6	1:A:1368:G:C6	3.04	0.44
1:A:14:U:O2	1:A:16:A:C8	2.71	0.44
1:A:317:G:N2	1:A:336:C:O2	2.48	0.44
1:A:35:G:H2'	1:A:36:C:H6	1.82	0.44
1:A:567:G:H2'	1:A:568:G:O4'	2.16	0.44
1:A:695:A:H61	1:A:797:C:H1'	1.82	0.44
2:B:18:GLY:HA3	2:B:42:ILE:H	1.81	0.44
2:B:69:LEU:HD21	2:B:93:VAL:HG23	1.99	0.44
4:D:4:TYR:HE2	4:D:11:LEU:HD11	1.78	0.44
4:D:25:ARG:C	4:D:27:TYR:N	2.69	0.44
4:D:80:GLU:O	4:D:84:LYS:HD2	2.17	0.44
5:E:84:PHE:CE1	5:E:133:TYR:HB3	2.52	0.44
7:G:77:SER:HA	7:G:86:GLN:HA	2.00	0.44
11:K:52:GLY:O	11:K:55:LYS:HB2	2.16	0.44
16:P:74:LEU:O	16:P:77:ALA:HB3	2.18	0.44
19:S:51:VAL:HG21	19:S:71:LEU:HD21	1.98	0.44
1:A:1054:C:OP1	1:A:1197:G:OP1	2.35	0.44
1:A:1199:U:H5''	1:A:1200:C:OP2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1281:U:H5'	1:A:1282:C:C5	2.52	0.44
1:A:1338:G:H2'	1:A:1339:A:H8	1.75	0.44
1:A:1338:G:C6	1:A:1339:A:C6	3.05	0.44
2:B:17:PHE:HA	2:B:44:LEU:HD11	1.99	0.44
12:L:7:ILE:HD13	12:L:7:ILE:HA	1.72	0.44
20:T:20:LEU:N	20:T:20:LEU:HD23	2.32	0.44
1:A:117:G:P	24:A:1912:HOH:O	2.75	0.44
1:A:236:G:H2'	1:A:237:C:O4'	2.18	0.44
9:I:8:GLY:N	9:I:83:ARG:HD2	2.33	0.44
13:M:97:PRO:HA	13:M:110:ARG:HD3	1.98	0.44
17:Q:5:VAL:HA	17:Q:59:ILE:O	2.17	0.44
1:A:191:G:O2'	20:T:102:GLY:O	2.23	0.44
1:A:1020:U:H2'	1:A:1021:G:C8	2.50	0.44
1:A:1028:C:N3	1:A:1034:G:N2	2.66	0.44
1:A:1361(A):C:O2'	1:A:1362:C:H6	2.00	0.44
1:A:434:U:C4	1:A:435:C:C4	3.06	0.44
2:B:186:ALA:HB3	2:B:197:VAL:HG11	2.00	0.44
3:C:15:THR:OG1	3:C:178:LEU:HD11	2.18	0.44
5:E:90:VAL:O	5:E:91:LEU:HD23	2.18	0.44
8:H:86:ILE:HD12	8:H:86:ILE:HG23	1.59	0.44
9:I:17:VAL:HG21	9:I:80:GLY:HA3	2.00	0.44
12:L:7:ILE:O	12:L:10:LEU:N	2.46	0.44
15:O:68:ARG:HB2	15:O:68:ARG:HE	1.22	0.44
15:O:85:LEU:HD23	15:O:85:LEU:N	2.32	0.44
1:A:1318:A:O2'	19:S:37:ARG:HB3	2.17	0.44
1:A:1190:G:OP1	3:C:4:LYS:HA	2.17	0.44
1:A:1234:C:H2'	1:A:1235:U:H6	1.82	0.44
1:A:1245:A:N1	1:A:1293:G:C2	2.85	0.44
1:A:1370:G:C2	1:A:1371:G:N7	2.85	0.44
1:A:1424:C:H2'	1:A:1425:U:C6	2.52	0.44
1:A:690:G:H2'	1:A:691:G:O4'	2.16	0.44
1:A:865:A:H1'	1:A:918:A:O2'	2.18	0.44
2:B:16:HIS:CD2	2:B:17:PHE:O	2.70	0.44
2:B:54:THR:OG1	2:B:199:TYR:HB3	2.18	0.44
3:C:112:SER:O	3:C:115:LEU:HB2	2.17	0.44
4:D:186:LEU:O	4:D:187:ARG:HD2	2.17	0.44
6:F:77:ARG:O	6:F:81:ILE:HG13	2.18	0.44
7:G:156:TRP:CD1	7:G:156:TRP:O	2.71	0.44
1:A:1048:G:H1	1:A:1209:C:N4	2.13	0.44
1:A:949:A:C2	1:A:1233:G:N3	2.86	0.44
1:A:1258:G:OP2	1:A:1258:G:C8	2.69	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:17:U:H2'	1:A:18:C:C6	2.52	0.44
1:A:329:A:H3'	1:A:330:C:C5'	2.47	0.44
1:A:521:G:OP1	12:L:54:LYS:HE2	2.17	0.44
1:A:660:G:H1	1:A:745:C:N4	2.10	0.44
5:E:119:LEU:HD23	5:E:119:LEU:HA	1.41	0.44
5:E:121:LYS:HG3	5:E:122:GLU:N	2.33	0.44
5:E:142:LEU:HD23	5:E:142:LEU:HA	1.70	0.44
10:J:5:ARG:HD2	10:J:99:LYS:O	2.18	0.44
13:M:8:GLU:CD	13:M:22:ILE:HA	2.37	0.44
19:S:70:LYS:NZ	19:S:70:LYS:HB3	2.33	0.44
1:A:1065:U:H4'	1:A:1066:C:O5'	2.17	0.44
1:A:1095:U:H2'	1:A:1096:C:C6	2.53	0.44
1:A:407:G:C6	1:A:408:A:C6	3.05	0.44
1:A:50:A:N6	1:A:361:G:H4'	2.33	0.44
1:A:665:A:H1'	1:A:733:A:O4'	2.16	0.44
1:A:793:U:H4'	1:A:794:A:OP2	2.18	0.44
3:C:58:GLU:HB3	10:J:92:THR:HG21	1.99	0.44
5:E:112:LEU:HA	5:E:112:LEU:HD23	1.72	0.44
11:K:122:LYS:H	11:K:122:LYS:HG2	1.49	0.44
16:P:65:GLN:HA	16:P:66:PRO:HD2	1.80	0.44
17:Q:51:TYR:CE1	17:Q:73:VAL:HB	2.53	0.44
1:A:1026:G:C8	1:A:1027:C:C5	3.06	0.44
1:A:1486:G:H2'	1:A:1487:G:O4'	2.17	0.44
1:A:475:G:H2'	1:A:476:G:C8	2.52	0.44
3:C:114:PRO:O	3:C:118:GLN:HG3	2.18	0.44
4:D:19:LEU:HD11	4:D:67:ILE:HG13	1.99	0.44
1:A:1078:U:H5''	1:A:1079:G:OP2	2.18	0.44
1:A:1304:G:O3'	21:U:2:GLY:N	2.51	0.44
1:A:299:G:H2'	1:A:300:A:C8	2.53	0.44
1:A:594:G:H1	1:A:645:C:H42	1.66	0.44
2:B:17:PHE:CD1	2:B:18:GLY:N	2.84	0.44
4:D:67:ILE:HG22	4:D:114:ARG:HH12	1.83	0.44
6:F:21:LEU:HG	6:F:21:LEU:O	2.18	0.44
1:A:503:C:OP2	12:L:116:SER:HB3	2.18	0.44
12:L:84:LEU:HG	12:L:85:ILE:N	2.32	0.44
13:M:51:ALA:HA	13:M:54:VAL:HG12	1.99	0.44
15:O:9:GLN:O	15:O:10:LYS:C	2.56	0.44
16:P:19:ILE:H	16:P:19:ILE:HG13	1.59	0.44
1:A:1284:C:OP2	1:A:1285:A:O2'	2.30	0.43
1:A:1349:A:P	9:I:118:LYS:HD3	2.58	0.43
3:C:69:HIS:HA	3:C:104:GLN:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:163:GLU:O	4:D:166:LYS:HG2	2.18	0.43
4:D:187:ARG:HH22	4:D:188:LEU:HG	1.82	0.43
9:I:112:LYS:HE2	9:I:113:LYS:O	2.18	0.43
9:I:116:LYS:HB3	9:I:121:ARG:O	2.18	0.43
15:O:31:LEU:HA	15:O:31:LEU:HD12	1.89	0.43
1:A:1111:A:C5	1:A:1112:C:C5	3.06	0.43
1:A:1519[B]:MA6:H5'	1:A:1520[B]:G:OP2	2.17	0.43
1:A:46:G:H2'	1:A:366:C:C5	2.53	0.43
1:A:1111:A:N6	3:C:177:THR:HB	2.33	0.43
4:D:30:LYS:C	4:D:32:ALA:H	2.21	0.43
4:D:30:LYS:O	4:D:32:ALA:N	2.51	0.43
5:E:10:MET:SD	5:E:13:ILE:HG23	2.58	0.43
5:E:80:ILE:O	5:E:80:ILE:HG13	2.17	0.43
7:G:138:LYS:HG2	7:G:139:GLU:CG	2.48	0.43
8:H:10:LEU:HA	8:H:10:LEU:HD23	1.58	0.43
15:O:29:VAL:HG21	15:O:67:LEU:CD2	2.49	0.43
16:P:53:VAL:O	16:P:54:GLU:C	2.56	0.43
17:Q:65:ILE:HG21	17:Q:69:LYS:HE2	2.00	0.43
18:R:79:LEU:HA	18:R:80:PRO:HD3	1.67	0.43
20:T:36:LEU:HD23	20:T:36:LEU:HA	1.53	0.43
1:A:1347:G:C2'	1:A:1348:U:OP2	2.66	0.43
1:A:1480:G:C6	1:A:1481:U:C4	3.06	0.43
1:A:109:A:C6	1:A:326:G:C6	3.07	0.43
1:A:391:G:C6	1:A:392:G:C5	3.06	0.43
1:A:779:C:H2'	1:A:780:A:O4'	2.18	0.43
3:C:43:LEU:HD23	3:C:43:LEU:HA	1.67	0.43
5:E:35:GLY:HA3	5:E:112:LEU:HB3	1.99	0.43
6:F:11:ASN:ND2	6:F:13:ASN:OD1	2.29	0.43
7:G:138:LYS:HG2	7:G:139:GLU:HG2	1.99	0.43
15:O:39:LEU:HD13	15:O:56:LEU:HB2	1.99	0.43
1:A:115:G:H4'	1:A:116:A:O5'	2.18	0.43
1:A:1241:G:C4	1:A:1242:C:C5	3.06	0.43
1:A:912:C:H5''	12:L:46:LYS:HE3	2.01	0.43
1:A:940:C:H5''	1:A:941:G:OP2	2.18	0.43
3:C:39:ILE:HD12	3:C:57:ILE:HD13	2.00	0.43
12:L:11:VAL:H	12:L:11:VAL:HG23	1.52	0.43
12:L:120:TYR:N	12:L:120:TYR:CD2	2.86	0.43
13:M:22:ILE:N	13:M:22:ILE:HD12	2.34	0.43
13:M:82:MET:HA	13:M:89:GLY:HA3	2.01	0.43
17:Q:22:LEU:HA	17:Q:22:LEU:HD12	1.44	0.43
17:Q:59:ILE:HD13	17:Q:59:ILE:HA	1.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1001:A:H2'	1:A:1002:G:H8	1.83	0.43
1:A:1392:G:O2'	1:A:1393:U:H5'	2.19	0.43
1:A:1406:U:C5	1:A:1407:5MC:HM52	2.53	0.43
2:B:29:ALA:HA	2:B:32:ILE:HG13	2.00	0.43
2:B:73:THR:HG21	2:B:96:ARG:HD2	1.99	0.43
5:E:103:GLY:O	5:E:107:ARG:HB2	2.18	0.43
12:L:42:THR:CG2	12:L:52:LEU:HB3	2.48	0.43
13:M:37:THR:CG2	13:M:55:ARG:HB3	2.49	0.43
15:O:70:LEU:HD23	15:O:78:TYR:HB2	2.00	0.43
17:Q:32:TYR:N	17:Q:32:TYR:CD2	2.82	0.43
1:A:1179:A:H2'	1:A:1180:A:O4'	2.18	0.43
1:A:1284:C:H3'	1:A:1285:A:H2'	2.00	0.43
1:A:315:A:O2'	1:A:330:C:O2'	2.29	0.43
1:A:990:C:C2	1:A:1216:G:N2	2.87	0.43
2:B:187:LEU:HA	2:B:187:LEU:HD22	1.56	0.43
2:B:46:LYS:HA	2:B:49:GLU:OE2	2.19	0.43
7:G:71:PRO:HD3	7:G:103:TRP:HZ3	1.83	0.43
8:H:20:TYR:CE1	8:H:76:PRO:HD2	2.54	0.43
9:I:79:LEU:HA	9:I:79:LEU:HD23	1.91	0.43
1:A:1012:U:H2'	1:A:1013:G:O4'	2.19	0.43
1:A:1268:A:H2'	1:A:1269:A:C8	2.54	0.43
1:A:1296:C:H4'	1:A:1302:U:H5	1.78	0.43
1:A:1505:G:H8	1:A:1505:G:H3'	1.84	0.43
1:A:269:C:H2'	1:A:270:A:H8	1.84	0.43
1:A:118:U:H3'	1:A:288:A:H61	1.83	0.43
1:A:299:G:N1	24:A:2036:HOH:O	2.36	0.43
2:B:233:SER:HA	2:B:234:PRO:HD3	1.87	0.43
3:C:69:HIS:HB3	3:C:106:VAL:HG23	2.01	0.43
4:D:200:GLU:CD	4:D:200:GLU:N	2.72	0.43
4:D:19:LEU:HD21	4:D:67:ILE:HG12	2.00	0.43
5:E:146:ALA:HB3	5:E:147:ASP:OD1	2.19	0.43
8:H:103:VAL:HG12	8:H:108:GLY:HA3	2.00	0.43
9:I:8:GLY:HA2	9:I:79:LEU:HD13	2.01	0.43
10:J:6:ILE:HB	10:J:72:VAL:CG2	2.49	0.43
11:K:54:ARG:HG2	11:K:54:ARG:H	1.71	0.43
17:Q:43:LEU:HD12	17:Q:68:ARG:HB3	2.00	0.43
18:R:22:VAL:O	18:R:25:THR:N	2.52	0.43
1:A:1313:U:C5	19:S:4:SER:HB2	2.54	0.43
1:A:1021:G:C6	1:A:1022:G:C8	3.07	0.43
1:A:106:C:C2'	1:A:107:G:H5'	2.48	0.43
1:A:1286:A:H5'	21:U:25:LYS:HD3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:144:G:H1	1:A:178:C:N4	2.09	0.43
1:A:241:C:H42	1:A:285:G:H1	1.66	0.43
1:A:524:G:H2'	1:A:525:C:C6	2.53	0.43
2:B:163:PHE:HA	2:B:163:PHE:HD1	1.63	0.43
2:B:16:His:HD2	2:B:17:PHE:O	2.02	0.43
3:C:130:VAL:O	3:C:134:ILE:HG13	2.19	0.43
7:G:37:ASN:HB3	24:G:202:HOH:O	2.19	0.43
8:H:69:ARG:HH11	8:H:69:ARG:HG3	1.84	0.43
13:M:39:ILE:HG22	13:M:40:ASN:O	2.18	0.43
19:S:17:GLU:HA	19:S:20:LEU:HG	2.00	0.43
1:A:1114:C:H2'	1:A:1115:C:H6	1.83	0.43
1:A:1311:G:H1	1:A:1326:C:H42	1.66	0.43
1:A:909:A:H2'	1:A:910:C:O4'	2.18	0.43
2:B:87:ARG:HH21	2:B:219:VAL:CG1	2.32	0.43
4:D:19:LEU:HD23	4:D:20:TYR:H	1.83	0.43
4:D:96:LEU:HD12	4:D:96:LEU:HA	1.71	0.43
4:D:201:GLN:NE2	5:E:117:ASP:OD1	2.52	0.43
7:G:59:LEU:O	7:G:62:PHE:HB3	2.19	0.43
9:I:9:ARG:HB3	9:I:14:VAL:HG13	1.99	0.43
12:L:27:LEU:CA	12:L:29:GLY:H	2.32	0.43
17:Q:6:LEU:HD13	17:Q:23:VAL:HG11	2.01	0.43
17:Q:29:His:CG	17:Q:30:PRO:HD2	2.54	0.43
1:A:652:U:C2	1:A:752:G:N2	2.87	0.43
3:C:8:ILE:HG23	3:C:16:ARG:HG2	2.00	0.43
6:F:6:VAL:HG22	6:F:90:VAL:HG22	2.01	0.43
17:Q:90:ILE:O	17:Q:91:ARG:C	2.56	0.43
18:R:47:THR:HA	18:R:83:GLU:HB2	2.01	0.43
1:A:1157:A:H4'	1:A:1158:C:O5'	2.19	0.42
1:A:1258:G:H2'	1:A:1259:C:C6	2.54	0.42
1:A:1305:G:H4'	1:A:1306:A:O5'	2.19	0.42
1:A:1513:A:H2'	1:A:1514:C:C6	2.53	0.42
1:A:491:G:H2'	1:A:492:G:H8	1.84	0.42
1:A:714:G:H2'	1:A:715:A:C8	2.54	0.42
2:B:74:LYS:NZ	2:B:74:LYS:HB3	2.33	0.42
6:F:6:VAL:HG13	6:F:90:VAL:CG2	2.49	0.42
9:I:127:LYS:HA	9:I:127:LYS:HD3	1.64	0.42
10:J:50:ILE:HD13	14:N:41:ARG:HD2	2.01	0.42
1:A:277:C:H5'	17:Q:68:ARG:NH1	2.34	0.42
20:T:43:LEU:HD22	20:T:43:LEU:HA	1.62	0.42
1:A:455:C:H6	1:A:455:C:O5'	2.02	0.42
1:A:459:G:H1'	1:A:463:A:N6	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:83:U:C4	1:A:84:U:C5	3.07	0.42
4:D:108:LEU:HA	4:D:108:LEU:HD23	1.77	0.42
1:A:825:G:H21	8:H:11:THR:HG21	1.83	0.42
1:A:707:C:H4'	11:K:20:TYR:CE1	2.54	0.42
11:K:95:ILE:H	11:K:95:ILE:HG13	1.37	0.42
20:T:41:ILE:HG22	20:T:42:GLN:N	2.34	0.42
1:A:1478:C:H5	1:A:1479:C:C5	2.37	0.42
2:B:87:ARG:NH1	2:B:233:SER:HB2	2.35	0.42
3:C:113:ALA:N	3:C:114:PRO:HD2	2.35	0.42
3:C:182:ILE:HA	3:C:202:ILE:O	2.19	0.42
3:C:56:ASP:OD1	3:C:56:ASP:N	2.52	0.42
5:E:44:GLY:N	5:E:62:ALA:HB2	2.34	0.42
1:A:1092:A:H5''	7:G:4:ARG:CZ	2.49	0.42
7:G:88:PRO:HB2	7:G:155:ARG:CZ	2.49	0.42
9:I:112:LYS:HA	9:I:119:ALA:HB2	2.01	0.42
1:A:1367:C:H5'	10:J:60:ARG:HE	1.85	0.42
11:K:106:LYS:HD3	11:K:106:LYS:HA	1.84	0.42
11:K:46:GLY:HA2	11:K:50:TYR:O	2.19	0.42
13:M:9:ILE:N	13:M:9:ILE:HD12	2.34	0.42
17:Q:41:LYS:HB2	17:Q:41:LYS:HE2	1.89	0.42
1:A:1004:A:H5''	1:A:1025:U:C4	2.54	0.42
1:A:1151:A:O2'	1:A:1152:A:OP2	2.28	0.42
1:A:1287:A:H2	1:A:1353:G:N3	2.18	0.42
1:A:345:C:OP2	1:A:345:C:H6	2.03	0.42
1:A:507:C:OP2	1:A:508:C:O2'	2.29	0.42
1:A:597:G:H2'	1:A:598:U:H5'	2.01	0.42
4:D:13:ARG:HD2	4:D:38:TYR:O	2.20	0.42
4:D:187:ARG:HH11	4:D:187:ARG:HA	1.84	0.42
4:D:70:ILE:HG22	4:D:71:SER:O	2.18	0.42
9:I:46:ALA:O	9:I:81:ILE:HD12	2.20	0.42
9:I:55:ALA:HA	9:I:58:HIS:HB3	2.02	0.42
15:O:57:LEU:HA	15:O:57:LEU:HD12	1.83	0.42
1:A:260:G:H2'	1:A:261:U:C6	2.54	0.42
1:A:803:G:H2'	1:A:804:U:O4'	2.19	0.42
1:A:827:U:H5''	1:A:828:A:OP2	2.19	0.42
11:K:40:ILE:HG22	11:K:75:TYR:CE1	2.54	0.42
18:R:59:SER:H	18:R:62:GLU:HB2	1.84	0.42
19:S:16:LEU:HG	19:S:20:LEU:HD23	2.02	0.42
1:A:1011:G:H2'	1:A:1012:U:O4'	2.19	0.42
1:A:1096:C:H2'	1:A:1097:C:C6	2.54	0.42
1:A:1343:G:C5	1:A:1344:C:C4	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1527:C:H2'	1:A:1528:U:C6	2.55	0.42
1:A:321:A:N7	1:A:328:C:C6	2.81	0.42
1:A:413:G:O6	4:D:36:ARG:HD2	2.19	0.42
1:A:722:A:O3'	1:A:723:U:C6	2.71	0.42
1:A:770:C:C2'	1:A:771:G:H5'	2.49	0.42
1:A:778:G:C8	1:A:778:G:O5'	2.71	0.42
2:B:223:ILE:O	2:B:228:GLY:N	2.52	0.42
4:D:9:CYS:SG	4:D:31:CYS:O	2.77	0.42
4:D:79:PHE:O	4:D:82:ALA:N	2.53	0.42
7:G:92:SER:HB3	7:G:95:ARG:H	1.84	0.42
8:H:69:ARG:HG3	8:H:69:ARG:NH1	2.34	0.42
10:J:86:MET:SD	10:J:87:THR:N	2.92	0.42
1:A:1009:G:N2	1:A:1010:G:H1'	2.35	0.42
1:A:1058:G:C6	1:A:1059:C:N3	2.87	0.42
1:A:22:G:C4	1:A:23:C:C5	3.08	0.42
1:A:484:G:O2'	1:A:485:G:OP2	2.25	0.42
1:A:815:A:N6	1:A:1509:C:H1'	2.35	0.42
1:A:22:G:C5	1:A:914:G:O6	2.71	0.42
1:A:998:G:C2	1:A:1044:A:C5	3.08	0.42
2:B:187:LEU:HD22	2:B:201:ILE:O	2.20	0.42
2:B:215:LEU:HD23	2:B:215:LEU:HA	1.67	0.42
2:B:49:GLU:H	2:B:49:GLU:HG3	1.59	0.42
6:F:10:LEU:HD11	6:F:59:TYR:CD2	2.48	0.42
6:F:25:ILE:HD13	6:F:25:ILE:HA	1.96	0.42
6:F:41:GLU:OE1	18:R:35:ARG:NH1	2.49	0.42
8:H:6:ILE:CD1	8:H:6:ILE:N	2.81	0.42
15:O:67:LEU:HD13	15:O:82:ILE:HD11	2.02	0.42
1:A:430:A:OP1	4:D:8:VAL:N	2.50	0.42
1:A:976:G:C8	1:A:1358:U:C2	3.08	0.42
2:B:169:LYS:HB3	2:B:169:LYS:HE3	1.91	0.42
5:E:6:PHE:HA	5:E:6:PHE:HD2	1.68	0.42
8:H:116:LYS:CD	8:H:127:LEU:HD12	2.50	0.42
10:J:14:LYS:HB2	10:J:14:LYS:NZ	2.35	0.42
11:K:59:TYR:CE1	11:K:63:LEU:HD21	2.55	0.42
18:R:76:LEU:HD23	18:R:76:LEU:HA	1.70	0.42
1:A:1010:G:N2	1:A:1019:C:N3	2.44	0.42
1:A:109:A:H2'	1:A:326:G:N2	2.33	0.42
1:A:179:A:H2'	1:A:180:U:C6	2.55	0.42
1:A:794:A:N6	1:A:795:C:N4	2.67	0.42
1:A:839:U:H5'	1:A:840:C:C5	2.55	0.42
1:A:9:G:C2	1:A:26:A:N1	2.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:63:LYS:HE3	4:D:198:VAL:HG23	2.00	0.42
4:D:13:ARG:HA	4:D:33:MET:SD	2.60	0.42
4:D:94:LEU:HD23	4:D:94:LEU:HA	1.46	0.42
5:E:88:LYS:HD2	5:E:123:LEU:HD12	2.02	0.42
8:H:87:SER:HA	8:H:93:VAL:HG12	2.02	0.42
9:I:16:ARG:HH11	9:I:64:THR:HG23	1.84	0.42
12:L:60:LEU:HA	12:L:60:LEU:HD13	1.80	0.42
16:P:60:LEU:HD23	16:P:60:LEU:HA	1.53	0.42
17:Q:22:LEU:HD12	17:Q:23:VAL:N	2.35	0.42
19:S:22:LEU:HD12	19:S:31:ILE:HD11	2.02	0.42
1:A:1474:G:N1	1:A:1475:G:C6	2.88	0.42
1:A:1499:A:C1'	1:A:1520[A]:G:H5'	2.47	0.42
1:A:152:A:N6	1:A:170:U:C2	2.87	0.42
1:A:329:A:H3'	1:A:330:C:H5'	2.01	0.42
1:A:355:C:C4	1:A:356:A:N7	2.88	0.42
1:A:837:G:C2	1:A:850:U:O2	2.73	0.42
8:H:29:SER:HB3	8:H:32:LYS:CD	2.43	0.42
10:J:19:SER:O	10:J:23:ILE:HD12	2.20	0.42
13:M:72:ALA:HA	13:M:75:ALA:HB3	2.02	0.42
14:N:40:CYS:H	14:N:43:CYS:HB2	1.84	0.42
15:O:81:LEU:HA	15:O:81:LEU:HD23	1.63	0.42
16:P:75:ARG:HA	24:P:206:HOH:O	2.20	0.42
1:A:135:C:H5''	1:A:136:C:OP2	2.20	0.41
1:A:1497:G:O2'	1:A:1518[A]:MA6:H92	2.19	0.41
1:A:309:G:H2'	1:A:310:G:H8	1.85	0.41
1:A:405:U:O4	4:D:2:GLY:HA3	2.20	0.41
1:A:570:G:C6	1:A:873:A:C2	3.07	0.41
1:A:16:A:C2	1:A:920:U:O2	2.73	0.41
2:B:53:ARG:HH11	2:B:199:TYR:HD2	1.68	0.41
3:C:136:GLN:HG3	3:C:140:ARG:NH2	2.35	0.41
6:F:67:MET:HB2	6:F:68:PRO:HD2	2.02	0.41
8:H:97:VAL:H	8:H:98:LYS:HZ3	1.65	0.41
14:N:26:ARG:HH11	14:N:47:LEU:HD21	1.85	0.41
17:Q:45:HIS:CD2	17:Q:65:ILE:HG12	2.47	0.41
18:R:59:SER:N	18:R:62:GLU:OE1	2.52	0.41
1:A:1185:G:N2	1:A:1186:G:C4	2.88	0.41
1:A:463:A:C8	1:A:474:G:N7	2.89	0.41
1:A:571:U:H5''	1:A:572:A:OP2	2.19	0.41
1:A:597:G:C5	1:A:598:U:C6	3.08	0.41
1:A:854:G:H3'	1:A:871:U:O4	2.20	0.41
2:B:30:ARG:HG2	2:B:31:TYR:CD1	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:92:TYR:CD1	2:B:151:GLY:HA3	2.55	0.41
5:E:31:LEU:HA	5:E:31:LEU:HD23	1.67	0.41
9:I:6:GLY:CA	9:I:83:ARG:HB2	2.50	0.41
1:A:1124:G:H5'	10:J:35:SER:O	2.20	0.41
10:J:52:GLY:HA2	10:J:53:PRO:HD2	1.73	0.41
10:J:79:ARG:NH2	10:J:82:ILE:HD12	2.35	0.41
13:M:18:ALA:O	13:M:21:TYR:HB2	2.20	0.41
1:A:1090:U:H2'	1:A:1091:U:C6	2.40	0.41
1:A:1167:A:N6	1:A:1168:A:N1	2.68	0.41
1:A:1255:G:O2'	1:A:1258:G:H1'	2.19	0.41
1:A:1371:G:C6	1:A:1372:U:C4	3.09	0.41
1:A:1399:C:O2	1:A:1401:G:C5	2.73	0.41
1:A:264:U:H2'	1:A:265:G:O4'	2.20	0.41
1:A:115:G:O2'	1:A:289:G:H5''	2.20	0.41
1:A:299:G:C6	1:A:300:A:C6	3.08	0.41
1:A:41:G:H2'	1:A:42:G:C8	2.55	0.41
1:A:5:U:H4'	1:A:6:G:O5'	2.20	0.41
1:A:77:G:C6	1:A:93:G:C6	3.08	0.41
2:B:143:GLU:HA	2:B:146:GLN:OE1	2.20	0.41
2:B:30:ARG:HD2	2:B:31:TYR:CZ	2.55	0.41
3:C:127:ARG:HG2	3:C:193:TYR:OH	2.21	0.41
4:D:100:ARG:CZ	4:D:137:SER:HA	2.50	0.41
1:A:509:A:H5'	4:D:54:TYR:HD2	1.85	0.41
5:E:11:ILE:O	5:E:11:ILE:HD13	2.21	0.41
5:E:151:LEU:HD23	5:E:151:LEU:HA	1.52	0.41
7:G:44:TYR:HA	7:G:44:TYR:HD2	1.76	0.41
7:G:59:LEU:HG	7:G:63:LYS:HE2	2.01	0.41
16:P:28:ARG:HG3	16:P:29:ASP:OD2	2.20	0.41
17:Q:29:HIS:CG	17:Q:30:PRO:CD	3.04	0.41
1:A:1425:U:H2'	1:A:1426:C:C6	2.55	0.41
1:A:378:G:H2'	1:A:379:C:H6	1.83	0.41
1:A:481:G:O2'	1:A:482:A:C8	2.64	0.41
1:A:795:C:H5''	1:A:796:C:OP2	2.20	0.41
2:B:158:LEU:H	2:B:158:LEU:CD1	2.20	0.41
2:B:98:LEU:HB2	2:B:101:MET:HG3	2.02	0.41
4:D:88:VAL:O	4:D:89:THR:C	2.57	0.41
7:G:22:LEU:HD12	7:G:22:LEU:HA	1.80	0.41
8:H:126:LYS:HB3	8:H:126:LYS:HE2	1.77	0.41
8:H:27:PRO:HA	8:H:58:TYR:CD2	2.56	0.41
11:K:33:THR:HG22	11:K:39:PRO:CA	2.51	0.41
16:P:39:TYR:CE2	16:P:41:PRO:HG3	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:55:ILE:HD13	20:T:55:ILE:HA	1.69	0.41
1:A:1105:A:H2'	1:A:1106:G:C8	2.56	0.41
1:A:1180:A:OP1	9:I:103:THR:HG23	2.21	0.41
1:A:1222:G:C2	1:A:1223:C:C2	3.08	0.41
1:A:1435:G:H1	1:A:1466:C:H42	1.67	0.41
1:A:1518[A]:MA6:H93	1:A:1519[A]:MA6:C9	2.50	0.41
1:A:190:C:H42	1:A:190(I):G:H1	1.68	0.41
1:A:374:A:N3	1:A:374:A:H2'	2.35	0.41
1:A:403:C:H2'	1:A:404:U:C6	2.55	0.41
3:C:178:LEU:HD13	3:C:178:LEU:C	2.40	0.41
5:E:105:VAL:HG11	5:E:131:ILE:HG22	2.02	0.41
5:E:92:LYS:HA	5:E:93:PRO:HD3	1.90	0.41
9:I:9:ARG:HD3	9:I:14:VAL:HG13	2.02	0.41
1:A:1027:C:H2'	1:A:1028:C:C6	2.56	0.41
1:A:116:A:H2'	1:A:117:G:C8	2.55	0.41
1:A:1518[B]:MA6:H93	1:A:1519[B]:MA6:C6	2.50	0.41
1:A:244:U:H4'	1:A:245:C:H5''	2.02	0.41
1:A:266:G:H5''	1:A:266:G:H8	1.86	0.41
1:A:490:G:C6	1:A:491:G:N7	2.89	0.41
1:A:730:G:N2	1:A:765:G:H5''	2.35	0.41
1:A:865:A:H2'	1:A:866:C:C6	2.54	0.41
1:A:953:G:H2'	1:A:954:G:O4'	2.20	0.41
1:A:976:G:H4'	1:A:977:A:OP1	2.21	0.41
3:C:153:VAL:HG13	3:C:198:VAL:HG22	2.03	0.41
4:D:207:TYR:HD2	4:D:207:TYR:HA	1.65	0.41
4:D:57:ARG:HG3	4:D:202:LEU:CD1	2.50	0.41
6:F:46:ARG:HB3	6:F:46:ARG:NH1	2.35	0.41
14:N:24:CYS:HB3	14:N:29:ARG:HB3	2.03	0.41
16:P:18:ARG:O	16:P:20:VAL:HG23	2.20	0.41
16:P:82:GLN:H	16:P:82:GLN:HG2	1.76	0.41
18:R:29:PHE:CD1	18:R:39:VAL:HG21	2.56	0.41
1:A:1267:C:O2	1:A:1327:C:H4'	2.21	0.41
1:A:1354:C:H6	1:A:1354:C:O5'	2.03	0.41
1:A:767:A:H2'	1:A:768:A:C8	2.55	0.41
1:A:21:G:N2	1:A:886:G:OP1	2.53	0.41
3:C:20:SER:O	14:N:54:PRO:HB3	2.20	0.41
4:D:142:PRO:HB3	4:D:187:ARG:NH1	2.36	0.41
4:D:25:ARG:O	4:D:25:ARG:HG2	2.21	0.41
5:E:82:VAL:HG21	5:E:138:ALA:HA	2.03	0.41
16:P:3:LYS:HG3	16:P:24:ALA:HB2	2.02	0.41
1:A:1124:G:C8	1:A:1145:C:C5	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:210:SER:O	2:B:214:ILE:HG12	2.21	0.41
2:B:40:HIS:O	2:B:41:ILE:HD13	2.20	0.41
14:N:31:ARG:O	14:N:33:VAL:HG23	2.20	0.41
10:J:47:PHE:CZ	14:N:37:PHE:CE1	3.09	0.41
18:R:70:ILE:HG22	18:R:71:LYS:N	2.36	0.41
1:A:1221:G:OP1	19:S:36:ARG:HD3	2.20	0.41
1:A:227:G:H1'	24:A:2159:HOH:O	2.20	0.41
1:A:452:A:HO2'	1:A:453:A:H8	1.59	0.41
3:C:3:ASN:N	3:C:3:ASN:OD1	2.54	0.41
3:C:88:ARG:HH21	3:C:100:ALA:HB1	1.86	0.41
5:E:107:ARG:O	5:E:111:GLU:HB2	2.21	0.41
6:F:35:ALA:HA	6:F:67:MET:HB3	2.02	0.41
7:G:101:LEU:HD23	7:G:101:LEU:HA	1.93	0.41
7:G:116:ALA:O	7:G:120:ILE:HG12	2.21	0.41
7:G:99:LEU:HD23	7:G:99:LEU:HA	1.60	0.41
8:H:102:ARG:HG3	8:H:102:ARG:O	2.21	0.41
8:H:75:ARG:HA	8:H:76:PRO:HD3	1.64	0.41
8:H:97:VAL:N	8:H:98:LYS:HZ1	2.18	0.41
1:A:1343:G:H4'	9:I:122:ALA:HB3	2.03	0.41
9:I:96:LEU:HD23	9:I:102:LEU:HD21	2.03	0.41
12:L:59:ARG:HE	12:L:65:GLU:HG3	1.86	0.41
15:O:64:ARG:HH21	15:O:68:ARG:HH22	1.68	0.41
17:Q:34:LYS:HG3	17:Q:34:LYS:O	2.18	0.41
1:A:1073:U:O2	2:B:104:ASN:ND2	2.54	0.41
1:A:1515[B]:C:H42	1:A:1520[B]:G:H1	1.68	0.41
1:A:128:G:C2	1:A:234:C:C2	3.09	0.41
1:A:261:U:O2	1:A:263:A:C8	2.74	0.41
1:A:508:C:H6	1:A:508:C:O5'	2.04	0.41
1:A:665:A:N3	1:A:732:C:H2'	2.35	0.41
1:A:791:G:H2'	1:A:792:A:H5'	2.01	0.41
3:C:23:TYR:OH	10:J:9:ARG:NH1	2.54	0.41
8:H:70:GLN:OE1	8:H:70:GLN:HA	2.20	0.41
11:K:29:ILE:HG21	11:K:29:ILE:HD13	1.83	0.41
15:O:45:VAL:HB	15:O:46:HIS:ND1	2.36	0.41
20:T:84:LEU:HA	20:T:84:LEU:HD22	1.64	0.41
1:A:1313:U:O4	19:S:4:SER:OG	2.12	0.41
1:A:53:A:C2	1:A:54:C:H1'	2.57	0.41
1:A:721:G:OP2	18:R:53:ARG:HG3	2.20	0.41
1:A:738:C:OP1	6:F:92:LYS:HD3	2.21	0.41
4:D:5:ILE:H	4:D:5:ILE:HG13	1.70	0.41
6:F:28:ARG:O	6:F:31:GLU:HG3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:45:LEU:O	6:F:46:ARG:HG2	2.20	0.41
9:I:47:LEU:HB3	9:I:50:LEU:HD12	2.02	0.41
9:I:93:ARG:HB3	9:I:93:ARG:NH1	2.36	0.41
12:L:39:VAL:HG12	12:L:57:LYS:HG2	2.03	0.41
15:O:18:PHE:HD1	15:O:19:PRO:O	2.04	0.41
15:O:26:GLU:OE1	15:O:77:ARG:HD2	2.21	0.41
15:O:67:LEU:HA	15:O:67:LEU:HD23	1.82	0.41
19:S:63:THR:HG22	19:S:64:GLU:N	2.36	0.41
1:A:987:G:N2	1:A:1219:U:O2	2.54	0.40
1:A:1422:G:H2'	1:A:1423:G:H8	1.86	0.40
1:A:316:G:OP2	1:A:351:G:O2'	2.39	0.40
1:A:376:G:C4	1:A:389:A:C2	3.09	0.40
1:A:451:A:N7	1:A:481:G:C2	2.89	0.40
1:A:515:G:C6	1:A:516:PSU:C2	3.09	0.40
1:A:651:C:O2'	1:A:652:U:H5'	2.21	0.40
1:A:794:A:C6	1:A:795:C:C4	3.08	0.40
1:A:797:C:H2'	1:A:798:G:H8	1.86	0.40
1:A:831:U:OP2	2:B:22:LYS:NZ	2.47	0.40
1:A:833:U:H2'	1:A:834:C:H6	1.82	0.40
1:A:77:G:C5	1:A:93:G:C2	3.09	0.40
1:A:942:G:N2	1:A:943:U:C2	2.89	0.40
1:A:947:G:H2'	1:A:948:C:O4'	2.21	0.40
2:B:10:LEU:C	2:B:12:GLU:H	2.23	0.40
2:B:155:LEU:HA	2:B:155:LEU:HD23	1.72	0.40
4:D:127:THR:HB	4:D:147:ALA:HB3	2.03	0.40
5:E:43:LEU:HD21	5:E:133:TYR:CD2	2.56	0.40
7:G:26:PHE:CE1	7:G:105:VAL:HG23	2.56	0.40
7:G:16:LEU:HG	9:I:42:ARG:HA	2.02	0.40
12:L:11:VAL:HG13	17:Q:29:HIS:CD2	2.57	0.40
13:M:56:LEU:HD23	13:M:56:LEU:HA	1.75	0.40
15:O:64:ARG:HG2	15:O:88:ARG:HH11	1.85	0.40
1:A:1143:G:H2'	1:A:1144:G:C8	2.57	0.40
1:A:1430:C:C2	1:A:1471:G:N2	2.89	0.40
1:A:59:A:H3'	1:A:331:G:H22	1.87	0.40
1:A:44:G:N2	1:A:399:G:C4	2.89	0.40
1:A:523:A:H8	1:A:523:A:O5'	2.04	0.40
1:A:838:G:N2	1:A:849:C:C2	2.88	0.40
1:A:858:G:O6	1:A:869:G:H3'	2.21	0.40
1:A:92:C:O2	1:A:93:G:C8	2.74	0.40
2:B:180:LEU:HD23	2:B:180:LEU:HA	1.86	0.40
2:B:21:ARG:HA	2:B:39:ILE:HA	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:825:G:N2	8:H:11:THR:HG21	2.36	0.40
1:A:1148:U:O3'	9:I:14:VAL:HG11	2.22	0.40
13:M:34:LEU:CD1	13:M:39:ILE:HB	2.50	0.40
13:M:67:GLU:O	13:M:71:ARG:HB2	2.21	0.40
20:T:73:HIS:O	20:T:76:ALA:HB3	2.21	0.40
1:A:115:G:H8	1:A:115:G:O5'	2.04	0.40
1:A:1177:G:H8	1:A:1177:G:O5'	2.04	0.40
1:A:1265:G:C6	1:A:1266:G:C6	3.10	0.40
1:A:475:G:H2'	1:A:476:G:H8	1.86	0.40
1:A:765:G:C6	1:A:812:C:C2	3.09	0.40
1:A:90:U:H2'	1:A:90:U:H6	1.80	0.40
2:B:166:ASP:O	2:B:170:GLU:HG2	2.22	0.40
3:C:167:TRP:HB3	3:C:168:ALA:H	1.65	0.40
4:D:131:ARG:HA	4:D:131:ARG:HD3	1.88	0.40
7:G:65:ALA:HB1	7:G:127:ALA:HB3	2.03	0.40
8:H:23:SER:HA	8:H:63:LEU:HD22	2.02	0.40
8:H:97:VAL:HG23	8:H:129:VAL:C	2.41	0.40
12:L:89:ARG:HE	12:L:89:ARG:HB3	1.36	0.40
13:M:15:VAL:O	13:M:19:LEU:HG	2.22	0.40
1:A:1089:G:C6	1:A:1090:U:N3	2.89	0.40
1:A:1124:G:H2'	1:A:1145:C:N4	2.30	0.40
1:A:1345:U:C2	1:A:1377:A:C2	3.09	0.40
1:A:1424:C:H2'	1:A:1425:U:H6	1.85	0.40
1:A:1533:C:O2	1:A:1533:C:H2'	2.20	0.40
1:A:156:G:N1	1:A:166:G:C6	2.90	0.40
1:A:186:C:H2'	1:A:187:C:H6	1.86	0.40
1:A:707:C:HO2'	11:K:20:TYR:HE1	1.66	0.40
1:A:852:G:N1	1:A:853:G:N7	2.70	0.40
3:C:180:ALA:HB3	3:C:203:PHE:HE1	1.83	0.40
6:F:41:GLU:HB2	6:F:62:TRP:HB3	2.02	0.40
11:K:53:SER:O	11:K:55:LYS:N	2.55	0.40
12:L:89:ARG:HH21	12:L:97:ARG:CG	2.34	0.40
13:M:29:ARG:HB3	13:M:64:TRP:CH2	2.56	0.40
20:T:74:LYS:HB3	20:T:75:ASN:H	1.14	0.40
1:A:1505:G:H2'	1:A:1541:PSU:OP2	2.22	0.40
1:A:41:G:C2	1:A:42:G:C5	3.09	0.40
1:A:771:G:H2'	1:A:772:U:C6	2.56	0.40
3:C:88:ARG:HA	3:C:91:LEU:HD22	2.03	0.40
4:D:80:GLU:H	4:D:80:GLU:HG2	1.67	0.40
10:J:51:ARG:HG3	10:J:59:SER:O	2.21	0.40
1:A:1059:C:O3'	14:N:45:ARG:NH2	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:17:ARG:HD3	15:O:26:GLU:OE2	2.21	0.40
16:P:19:ILE:CG2	16:P:36:ILE:HG13	2.51	0.40
17:Q:95:TYR:HA	17:Q:98:LEU:HD13	2.03	0.40
20:T:53:LEU:HA	20:T:53:LEU:HD22	1.70	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	232/256 (91%)	201 (87%)	28 (12%)	3 (1%)	14	57
3	C	204/239 (85%)	173 (85%)	31 (15%)	0	100	100
4	D	206/209 (99%)	194 (94%)	12 (6%)	0	100	100
5	E	148/162 (91%)	139 (94%)	9 (6%)	0	100	100
6	F	99/101 (98%)	93 (94%)	6 (6%)	0	100	100
7	G	153/156 (98%)	141 (92%)	12 (8%)	0	100	100
8	H	136/138 (99%)	129 (95%)	7 (5%)	0	100	100
9	I	125/128 (98%)	112 (90%)	12 (10%)	1 (1%)	22	66
10	J	96/105 (91%)	76 (79%)	17 (18%)	3 (3%)	5	41
11	K	114/129 (88%)	99 (87%)	14 (12%)	1 (1%)	20	64
12	L	121/135 (90%)	108 (89%)	12 (10%)	1 (1%)	22	66
13	M	116/126 (92%)	99 (85%)	16 (14%)	1 (1%)	20	64
14	N	58/61 (95%)	49 (84%)	9 (16%)	0	100	100
15	O	85/89 (96%)	78 (92%)	7 (8%)	0	100	100
16	P	81/88 (92%)	73 (90%)	8 (10%)	0	100	100
17	Q	97/105 (92%)	87 (90%)	10 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	R	68/88 (77%)	58 (85%)	9 (13%)	1 (2%)	12	55
19	S	78/93 (84%)	73 (94%)	4 (5%)	1 (1%)	14	57
20	T	97/106 (92%)	83 (86%)	12 (12%)	2 (2%)	8	49
21	U	22/27 (82%)	21 (96%)	0	1 (4%)	3	30
All	All	2336/2541 (92%)	2086 (89%)	235 (10%)	15 (1%)	28	70

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	21	ARG
19	S	31	ILE
20	T	99	LEU
9	I	119	ALA
10	J	86	MET
12	L	28	LYS
20	T	73	HIS
10	J	81	THR
11	K	117	ASN
18	R	26	LEU
2	B	87	ARG
2	B	95	GLN
21	U	24	ARG
10	J	34	VAL
13	M	84	ILE

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%)	152 (75%)	50 (25%)	1	6
3	C	160/188 (85%)	127 (79%)	33 (21%)	1	9
4	D	180/181 (99%)	142 (79%)	38 (21%)	1	9
5	E	115/123 (94%)	90 (78%)	25 (22%)	1	8

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	F	90/90 (100%)	71 (79%)	19 (21%)	1	9
7	G	126/127 (99%)	101 (80%)	25 (20%)	1	10
8	H	119/119 (100%)	95 (80%)	24 (20%)	1	10
9	I	98/99 (99%)	79 (81%)	19 (19%)	1	11
10	J	87/92 (95%)	75 (86%)	12 (14%)	4	27
11	K	88/99 (89%)	76 (86%)	12 (14%)	4	28
12	L	103/110 (94%)	77 (75%)	26 (25%)	0	5
13	M	94/101 (93%)	75 (80%)	19 (20%)	1	10
14	N	49/50 (98%)	39 (80%)	10 (20%)	1	9
15	O	79/80 (99%)	64 (81%)	15 (19%)	2	11
16	P	72/74 (97%)	59 (82%)	13 (18%)	2	13
17	Q	94/97 (97%)	78 (83%)	16 (17%)	2	17
18	R	61/77 (79%)	49 (80%)	12 (20%)	1	10
19	S	71/80 (89%)	54 (76%)	17 (24%)	1	6
20	T	76/82 (93%)	58 (76%)	18 (24%)	1	6
21	U	19/22 (86%)	15 (79%)	4 (21%)	1	9
All	All	1983/2111 (94%)	1576 (80%)	407 (20%)	1	9

All (407) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	7	VAL
2	B	8	LYS
2	B	9	GLU
2	B	11	LEU
2	B	12	GLU
2	B	16	HIS
2	B	19	HIS
2	B	24	TRP
2	B	30	ARG
2	B	32	ILE
2	B	33	TYR
2	B	47	THR
2	B	49	GLU
2	B	51	LEU
2	B	52	GLU

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Mol	Chain	Res	Type
2	B	53	ARG
2	B	55	PHE
2	B	63	MET
2	B	64	ARG
2	B	69	LEU
2	B	75	LYS
2	B	79	ASP
2	B	92	TYR
2	B	98	LEU
2	B	102	LEU
2	B	114	ARG
2	B	115	LEU
2	B	121	LEU
2	B	128	GLU
2	B	141	GLU
2	B	144	ARG
2	B	157	ARG
2	B	158	LEU
2	B	163	PHE
2	B	169	LYS
2	B	175	ARG
2	B	178	ARG
2	B	184	VAL
2	B	185	ILE
2	B	190	THR
2	B	192	SER
2	B	195	ASP
2	B	196	LEU
2	B	200	ILE
2	B	206	ASP
2	B	209	ARG
2	B	215	LEU
2	B	216	SER
2	B	236	TYR
2	B	239	VAL
3	C	3	ASN
3	C	15	THR
3	C	26	LYS
3	C	32	LEU
3	C	47	LEU
3	C	56	ASP
3	C	63	ASN

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Mol	Chain	Res	Type
3	C	70	VAL
3	C	75	VAL
3	C	79	ARG
3	C	84	ILE
3	C	91	LEU
3	C	95	THR
3	C	99	VAL
3	C	110	ASN
3	C	119	ARG
3	C	120	VAL
3	C	130	VAL
3	C	131	ARG
3	C	154	SER
3	C	156	ARG
3	C	162	GLN
3	C	166	GLU
3	C	167	TRP
3	C	172	ARG
3	C	175	LEU
3	C	177	THR
3	C	179	ARG
3	C	191	THR
3	C	192	THR
3	C	193	TYR
3	C	195	VAL
3	C	204	LEU
4	D	5	ILE
4	D	9	CYS
4	D	10	ARG
4	D	19	LEU
4	D	25	ARG
4	D	26	CYS
4	D	34	GLU
4	D	52	SER
4	D	59	ARG
4	D	64	LEU
4	D	76	ARG
4	D	80	GLU
4	D	83	SER
4	D	84	LYS
4	D	96	LEU
4	D	122	ARG

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Mol	Chain	Res	Type
4	D	132	ARG
4	D	137	SER
4	D	145	GLU
4	D	150	GLU
4	D	155	LEU
4	D	157	LEU
4	D	158	ILE
4	D	160	GLN
4	D	162	LEU
4	D	163	GLU
4	D	166	LYS
4	D	170	VAL
4	D	177	ASP
4	D	178	VAL
4	D	186	LEU
4	D	187	ARG
4	D	190	ASP
4	D	192	GLU
4	D	194	LEU
4	D	196	LEU
4	D	198	VAL
4	D	202	LEU
5	E	6	PHE
5	E	11	ILE
5	E	12	LEU
5	E	14	ARG
5	E	20	GLN
5	E	26	PHE
5	E	31	LEU
5	E	32	VAL
5	E	33	VAL
5	E	41	VAL
5	E	43	LEU
5	E	55	VAL
5	E	63	ARG
5	E	64	ARG
5	E	68	GLU
5	E	75	THR
5	E	79	GLU
5	E	100	VAL
5	E	107	ARG
5	E	116	THR

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Mol	Chain	Res	Type
5	E	120	THR
5	E	147	ASP
5	E	148	VAL
5	E	149	GLU
5	E	150	ARG
6	F	9	VAL
6	F	10	LEU
6	F	11	ASN
6	F	14	LEU
6	F	15	ASP
6	F	21	LEU
6	F	24	GLU
6	F	31	GLU
6	F	32	ASN
6	F	40	VAL
6	F	43	LEU
6	F	47	ARG
6	F	70	ASP
6	F	72	VAL
6	F	75	LEU
6	F	82	ARG
6	F	86	ARG
6	F	91	VAL
6	F	93	SER
7	G	6	ARG
7	G	8	GLU
7	G	9	VAL
7	G	10	ARG
7	G	11	GLN
7	G	16	LEU
7	G	17	VAL
7	G	21	VAL
7	G	27	ILE
7	G	38	LEU
7	G	48	LYS
7	G	53	LYS
7	G	66	VAL
7	G	69	VAL
7	G	72	ARG
7	G	77	SER
7	G	79	ARG
7	G	87	VAL

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Mol	Chain	Res	Type
7	G	94	ARG
7	G	95	ARG
7	G	106	GLN
7	G	110	GLN
7	G	113	GLU
7	G	144	MET
7	G	149	ARG
8	H	3	THR
8	H	9	MET
8	H	11	THR
8	H	14	ARG
8	H	19	VAL
8	H	24	THR
8	H	26	VAL
8	H	29	SER
8	H	50	ARG
8	H	63	LEU
8	H	83	ILE
8	H	85	ARG
8	H	87	SER
8	H	88	LYS
8	H	91	ARG
8	H	92	ARG
8	H	93	VAL
8	H	95	VAL
8	H	97	VAL
8	H	98	LYS
8	H	102	ARG
8	H	114	THR
8	H	120	THR
8	H	133	LEU
9	I	3	GLN
9	I	10	ARG
9	I	14	VAL
9	I	16	ARG
9	I	19	LEU
9	I	35	GLU
9	I	40	LEU
9	I	47	LEU
9	I	56	LEU
9	I	64	THR
9	I	70	LYS

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Mol	Chain	Res	Type
9	I	78	LYS
9	I	79	LEU
9	I	83	ARG
9	I	85	LEU
9	I	91	ASP
9	I	109	VAL
9	I	121	ARG
9	I	124	GLN
10	J	5	ARG
10	J	9	ARG
10	J	15	THR
10	J	29	ARG
10	J	30	SER
10	J	33	GLN
10	J	38	ILE
10	J	50	ILE
10	J	65	LEU
10	J	79	ARG
10	J	81	THR
10	J	95	GLU
11	K	11	LYS
11	K	14	VAL
11	K	29	ILE
11	K	47	VAL
11	K	48	ILE
11	K	62	GLN
11	K	70	LYS
11	K	78	GLN
11	K	79	SER
11	K	83	ILE
11	K	95	ILE
11	K	122	LYS
12	L	18	VAL
12	L	20	LYS
12	L	33	ARG
12	L	36	VAL
12	L	39	VAL
12	L	42	THR
12	L	43	VAL
12	L	47	LYS
12	L	60	LEU
12	L	62	SER

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Mol	Chain	Res	Type
12	L	66	VAL
12	L	67	THR
12	L	80	HIS
12	L	85	ILE
12	L	89	ARG
12	L	93	LEU
12	L	96	VAL
12	L	97	ARG
12	L	100	ILE
12	L	101	VAL
12	L	102	ARG
12	L	104	VAL
12	L	116	SER
12	L	119	LYS
12	L	122	THR
12	L	126	LYS
13	M	14	ARG
13	M	44	ARG
13	M	45	VAL
13	M	47	ASP
13	M	48	LEU
13	M	54	VAL
13	M	61	GLU
13	M	63	THR
13	M	64	TRP
13	M	66	LEU
13	M	67	GLU
13	M	80	ARG
13	M	81	LEU
13	M	82	MET
13	M	99	ARG
13	M	105	THR
13	M	108	ARG
13	M	109	THR
13	M	110	ARG
14	N	6	LEU
14	N	9	LYS
14	N	22	THR
14	N	24	CYS
14	N	29	ARG
14	N	31	ARG
14	N	50	LYS

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Mol	Chain	Res	Type
14	N	53	LEU
14	N	57	ARG
14	N	58	LYS
15	O	8	LYS
15	O	9	GLN
15	O	14	GLU
15	O	31	LEU
15	O	32	LEU
15	O	36	ILE
15	O	39	LEU
15	O	40	SER
15	O	62	GLN
15	O	65	ARG
15	O	66	LEU
15	O	68	ARG
15	O	73	GLU
15	O	81	LEU
15	O	87	ILE
16	P	1	MET
16	P	25	ARG
16	P	28	ARG
16	P	42	ARG
16	P	44	THR
16	P	45	THR
16	P	53	VAL
16	P	54	GLU
16	P	55	ARG
16	P	57	ARG
16	P	62	VAL
16	P	80	PHE
16	P	82	GLN
17	Q	9	VAL
17	Q	13	ASP
17	Q	34	LYS
17	Q	36	ILE
17	Q	37	LYS
17	Q	38	ARG
17	Q	53	LEU
17	Q	59	ILE
17	Q	60	ILE
17	Q	66	SER
17	Q	67	LYS

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Mol	Chain	Res	Type
17	Q	75	ARG
17	Q	86	GLU
17	Q	90	ILE
17	Q	92	ARG
17	Q	100	LYS
18	R	19	LYS
18	R	25	THR
18	R	37	VAL
18	R	38	GLU
18	R	40	LEU
18	R	47	THR
18	R	50	ILE
18	R	54	ARG
18	R	65	ILE
18	R	69	THR
18	R	82	THR
18	R	87	ARG
19	S	5	LEU
19	S	6	LYS
19	S	7	LYS
19	S	10	PHE
19	S	13	ASP
19	S	20	LEU
19	S	29	ARG
19	S	31	ILE
19	S	37	ARG
19	S	38	SER
19	S	58	VAL
19	S	60	VAL
19	S	65	ASN
19	S	70	LYS
19	S	71	LEU
19	S	78	ARG
19	S	81	ARG
20	T	11	SER
20	T	13	LEU
20	T	15	ARG
20	T	19	SER
20	T	24	LEU
20	T	42	GLN
20	T	43	LEU
20	T	53	LEU

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Mol	Chain	Res	Type
20	T	56	MET
20	T	62	LEU
20	T	68	LYS
20	T	74	LYS
20	T	75	ASN
20	T	83	ARG
20	T	84	LEU
20	T	86	ARG
20	T	91	LEU
20	T	93	GLU
21	U	8	THR
21	U	10	ARG
21	U	13	ILE
21	U	14	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	6	HIS
4	D	42	GLN
4	D	161	ASN
15	O	28	GLN
16	P	82	GLN
17	Q	45	HIS
18	R	36	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1503/1522 (98%)	358 (23%)	0

All (358) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	6	G
1	A	9	G
1	A	21	G
1	A	22	G
1	A	31	G
1	A	32	A

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Mol	Chain	Res	Type
1	A	39	G
1	A	47	C
1	A	48	C
1	A	49	U
1	A	50	A
1	A	51	A
1	A	54	C
1	A	59	A
1	A	74	C
1	A	75	G
1	A	80	G
1	A	81	U
1	A	91	C
1	A	95	U
1	A	99	C
1	A	101	A
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	135	C
1	A	163	C
1	A	166	G
1	A	178	C
1	A	182	U
1	A	183	G
1	A	190(D)	U
1	A	190(E)	U
1	A	195	A
1	A	197	A
1	A	202	U
1	A	203	U
1	A	204	U
1	A	216	G
1	A	217	C
1	A	221	C
1	A	227	G
1	A	231	G

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Mol	Chain	Res	Type
1	A	245	C
1	A	247	G
1	A	251	G
1	A	254	G
1	A	258	G
1	A	266	G
1	A	267	C
1	A	281	G
1	A	282	A
1	A	289	G
1	A	299	G
1	A	301	G
1	A	319	G
1	A	321	A
1	A	325	A
1	A	328	C
1	A	329	A
1	A	330	C
1	A	331	G
1	A	332	G
1	A	344	A
1	A	345	C
1	A	346	G
1	A	349	A
1	A	351	G
1	A	352	C
1	A	353	A
1	A	354	G
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	390	C
1	A	397	A
1	A	398	C
1	A	406	G
1	A	409	G
1	A	412	A
1	A	413	G
1	A	419	C

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Mol	Chain	Res	Type
1	A	421	U
1	A	422	C
1	A	429	U
1	A	430	A
1	A	435	C
1	A	439	A
1	A	450	G
1	A	453	A
1	A	460	A
1	A	461	C
1	A	475	G
1	A	481	G
1	A	482	A
1	A	484	G
1	A	485	G
1	A	486	U
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	513	C
1	A	518	C
1	A	519	C
1	A	526	C
1	A	527	7MG
1	A	531	U
1	A	532	A
1	A	533	A
1	A	535	A
1	A	536	C
1	A	547	A
1	A	558	G
1	A	559	A
1	A	560	U
1	A	562	C
1	A	563	A
1	A	564	C
1	A	566	G
1	A	568	G
1	A	572	A

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Mol	Chain	Res	Type
1	A	573	A
1	A	576	G
1	A	577	G
1	A	579	G
1	A	581	G
1	A	584	G
1	A	588	G
1	A	607	A
1	A	624	C
1	A	651	C
1	A	653	A
1	A	665	A
1	A	671	G
1	A	686	U
1	A	687	A
1	A	688	G
1	A	701	C
1	A	702	A
1	A	703	G
1	A	718	G
1	A	719	C
1	A	721	G
1	A	722	A
1	A	723	U
1	A	724	G
1	A	731	G
1	A	740	U
1	A	749	C
1	A	755	G
1	A	771	G
1	A	777	A
1	A	780	A
1	A	781	A
1	A	782	A
1	A	785	G
1	A	791	G
1	A	792	A
1	A	793	U
1	A	794	A
1	A	813	U
1	A	817	C
1	A	818	G

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Mol	Chain	Res	Type
1	A	821	G
1	A	826	C
1	A	828	A
1	A	839	U
1	A	840	C
1	A	841	U
1	A	848	C
1	A	851	G
1	A	858	G
1	A	872	A
1	A	873	A
1	A	885	G
1	A	889	A
1	A	902	G
1	A	913	A
1	A	914	G
1	A	916	G
1	A	922	G
1	A	926	G
1	A	927	G
1	A	934	C
1	A	935	A
1	A	936	C
1	A	940	C
1	A	941	G
1	A	942	G
1	A	949	A
1	A	950	U
1	A	960	U
1	A	961	U
1	A	963	G
1	A	964	A
1	A	966	M2G
1	A	967	5MC
1	A	968	A
1	A	969	A
1	A	971	G
1	A	974	A
1	A	975	A
1	A	976	G
1	A	977	A
1	A	981	U

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Mol	Chain	Res	Type
1	A	982	U
1	A	991	U
1	A	992	U
1	A	993	G
1	A	994	A
1	A	1003(A)	G
1	A	1004	A
1	A	1005	A
1	A	1006	C
1	A	1012	U
1	A	1015	A
1	A	1020	U
1	A	1023	G
1	A	1024	G
1	A	1034	G
1	A	1045	C
1	A	1050	G
1	A	1053	G
1	A	1054	C
1	A	1065	U
1	A	1066	C
1	A	1068	G
1	A	1078	U
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	1104	G
1	A	1124	G
1	A	1125	U
1	A	1126	U
1	A	1127	G
1	A	1129	C
1	A	1130	A
1	A	1132	C
1	A	1137	C
1	A	1138	G
1	A	1139	G
1	A	1140	C
1	A	1143	G
1	A	1145	C
1	A	1146	A
1	A	1152	A

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Mol	Chain	Res	Type
1	A	1159	U
1	A	1160	G
1	A	1169	A
1	A	1171	G
1	A	1174	G
1	A	1176	A
1	A	1182	G
1	A	1183	A
1	A	1190	G
1	A	1191	A
1	A	1193	G
1	A	1196	U
1	A	1197	G
1	A	1198	G
1	A	1200	C
1	A	1201	A
1	A	1202	G
1	A	1207	2MG
1	A	1209	C
1	A	1212	U
1	A	1213	A
1	A	1214	C
1	A	1215	G
1	A	1224	G
1	A	1225	A
1	A	1226	C
1	A	1227	A
1	A	1228	C
1	A	1233	G
1	A	1238	A
1	A	1241	G
1	A	1256	A
1	A	1257	U
1	A	1258	G
1	A	1260	C
1	A	1263	C
1	A	1268	A
1	A	1278	U
1	A	1280	A
1	A	1281	U
1	A	1282	C
1	A	1286	A

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Mol	Chain	Res	Type
1	A	1287	A
1	A	1288	A
1	A	1297	C
1	A	1299	A
1	A	1300	G
1	A	1301	U
1	A	1302	U
1	A	1303	C
1	A	1304	G
1	A	1305	G
1	A	1306	A
1	A	1310	G
1	A	1318	A
1	A	1319	A
1	A	1320	C
1	A	1323	G
1	A	1335	C
1	A	1336	C
1	A	1338	G
1	A	1339	A
1	A	1340	A
1	A	1347	G
1	A	1348	U
1	A	1353	G
1	A	1362	C
1	A	1364	U
1	A	1365	G
1	A	1370	G
1	A	1381	U
1	A	1398	A
1	A	1399	C
1	A	1400	5MC
1	A	1406	U
1	A	1407	5MC
1	A	1412	C
1	A	1442	G
1	A	1446	A
1	A	1447	G
1	A	1451	A
1	A	1454	G
1	A	1485	U
1	A	1487	G

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Mol	Chain	Res	Type
1	A	1490	C
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	1541	PSU
1	A	1542	U
1	A	1543	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	2.48	4 (21%)	20,38,41	2.00	3 (15%)
1	5MC	A	1400	1	15,22,23	0.84	0	17,32,35	1.18	2 (11%)
1	4OC	A	1402	1	16,23,24	1.18	2 (12%)	19,32,35	0.82	1 (5%)
1	5MC	A	1404	1	15,22,23	1.55	3 (20%)	17,32,35	1.46	2 (11%)
1	5MC	A	1407	1	15,22,23	1.57	2 (13%)	17,32,35	0.97	1 (5%)
1	UR3	A	1498	1	14,22,23	1.02	1 (7%)	16,32,35	1.46	2 (12%)
1	MA6	A	1518[A]	1	16,26,27	0.72	0	18,38,41	1.23	1 (5%)
1	MA6	A	1518[B]	1	16,26,27	0.77	0	18,38,41	0.98	0

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	0.87	1 (6%)	18,38,41	1.22	2 (11%)
1	MA6	A	1519[B]	1	16,26,27	1.35	3 (18%)	18,38,41	0.85	0
1	PSU	A	1540	1	16,21,22	1.10	1 (6%)	20,30,33	4.17	5 (25%)
1	PSU	A	1541	1	16,21,22	0.96	2 (12%)	20,30,33	3.77	6 (30%)
1	PSU	A	516	1,22	16,21,22	1.08	1 (6%)	20,30,33	3.92	6 (30%)
1	7MG	A	527	1,22	20,26,27	2.90	7 (35%)	22,39,42	1.89	3 (13%)
1	M2G	A	966	1	20,27,28	1.58	4 (20%)	21,40,43	2.67	6 (28%)
1	5MC	A	967	1	15,22,23	1.25	2 (13%)	17,32,35	1.05	2 (11%)
12	0TD	L	92	12	5,9,10	1.74	1 (20%)	3,11,13	3.61	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	-	0/7/29/30	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	-	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	1,22	-	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 (34) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	527	7MG	C8-N9	-8.75	1.32	1.45
1	A	527	7MG	CM7-N7	-3.40	1.40	1.46
1	A	1407	5MC	C6-C5	-2.82	1.32	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	527	7MG	C8-N7	-2.58	1.31	1.43
1	A	1402	4OC	O5'-C5'	-2.58	1.41	1.44
1	A	527	7MG	O6-C6	-2.44	1.18	1.24
1	A	1519[A]	MA6	C4-N3	-2.34	1.32	1.35
1	A	1404	5MC	C6-C5	-2.18	1.34	1.40
1	A	1404	5MC	O5'-C5'	-2.12	1.41	1.44
1	A	1541	PSU	O4'-C1'	-2.01	1.41	1.44
1	A	1402	4OC	C5-C4	2.08	1.44	1.39
1	A	1498	UR3	O3'-C3'	2.35	1.48	1.43
1	A	966	M2G	C2-N1	2.36	1.38	1.34
1	A	967	5MC	C4-N4	2.39	1.40	1.34
1	A	967	5MC	C2-N3	2.45	1.43	1.38
1	A	1207	2MG	C2-N1	2.48	1.43	1.34
1	A	1519[B]	MA6	C2-N3	2.58	1.36	1.32
1	A	527	7MG	C6-C5	2.62	1.44	1.41
1	A	1519[B]	MA6	C2-N1	2.67	1.38	1.33
1	A	966	M2G	C4-N3	2.87	1.40	1.35
1	A	1207	2MG	C4-N3	2.94	1.40	1.35
1	A	1541	PSU	C4-N3	3.05	1.38	1.33
1	A	1519[B]	MA6	C4-N3	3.18	1.40	1.35
1	A	516	PSU	C4-N3	3.22	1.38	1.33
12	L	92	0TD	CA-C	3.51	1.54	1.50
1	A	966	M2G	C2-N2	3.59	1.40	1.34
1	A	1540	PSU	C4-N3	3.60	1.39	1.33
1	A	1407	5MC	C5-C4	3.78	1.46	1.41
1	A	966	M2G	C6-N1	4.19	1.40	1.33
1	A	527	7MG	C2-N2	4.30	1.42	1.34
1	A	1404	5MC	C5-C4	4.66	1.48	1.41
1	A	527	7MG	C4-N3	5.44	1.41	1.34
1	A	1207	2MG	C2-N2	6.66	1.39	1.34
1	A	1207	2MG	C6-N1	6.81	1.45	1.33

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1540	PSU	N1-C2-N3	-14.21	118.18	128.40
1	A	516	PSU	N1-C2-N3	-13.49	118.70	128.40
1	A	1541	PSU	N1-C2-N3	-13.01	119.05	128.40
1	A	966	M2G	C5-C6-N1	-7.71	112.51	123.48
1	A	1540	PSU	C5-C4-N3	-7.33	119.42	125.43
1	A	1207	2MG	C5-C6-N1	-7.18	113.26	123.48
1	A	516	PSU	C5-C4-N3	-6.92	119.75	125.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1541	PSU	C5-C4-N3	-6.50	120.10	125.43
12	L	92	0TD	CSB-SB-CB	-5.34	91.63	101.60
1	A	527	7MG	C5-C4-N3	-4.95	118.21	126.47
1	A	1404	5MC	N4-C4-N3	-4.26	110.70	117.00
1	A	966	M2G	N1-C2-N2	-4.07	112.97	117.16
1	A	1498	UR3	C5-C4-N3	-2.85	111.48	117.34
1	A	1402	4OC	CM4-N4-C4	-2.84	120.49	122.94
1	A	1400	5MC	CM5-C5-C4	-2.67	118.91	121.65
12	L	92	0TD	O-C-CA	-2.59	119.12	125.15
1	A	1407	5MC	N4-C4-N3	-2.57	113.21	117.00
1	A	1540	PSU	C5-C1'-C2'	-2.49	111.26	115.55
1	A	1498	UR3	C3U-N3-C2	-2.46	113.79	119.75
1	A	1541	PSU	C5-C6-N1	-2.40	121.28	124.39
1	A	516	PSU	C5-C6-N1	-2.36	121.33	124.39
1	A	966	M2G	C2-N3-C4	-2.33	112.46	115.11
1	A	967	5MC	CM5-C5-C4	-2.01	119.58	121.65
1	A	966	M2G	C4-C5-N7	2.04	111.38	109.41
1	A	1207	2MG	C4-C5-N7	2.05	111.39	109.41
1	A	1519[A]	MA6	C2-N1-C6	2.09	116.96	111.82
1	A	516	PSU	O4'-C1'-C2'	2.33	108.19	104.45
1	A	527	7MG	C2-N3-C4	2.40	120.70	113.95
1	A	1518[A]	MA6	C2-N1-C6	2.61	118.22	111.82
1	A	1541	PSU	O4'-C1'-C2'	2.65	108.70	104.45
1	A	1519[A]	MA6	N3-C2-N1	2.66	131.17	128.86
1	A	967	5MC	CM5-C5-C6	2.70	124.05	118.67
1	A	1404	5MC	C5-C4-N3	2.72	125.62	121.22
1	A	1400	5MC	CM5-C5-C6	2.91	124.47	118.67
1	A	516	PSU	C6-N1-C2	3.26	120.58	115.36
1	A	1540	PSU	C6-N1-C2	3.52	120.99	115.36
1	A	1541	PSU	C6-N1-C2	3.73	121.32	115.36
1	A	1207	2MG	C6-N1-C2	3.79	121.97	115.18
1	A	966	M2G	N3-C2-N2	4.37	121.66	117.15
1	A	1541	PSU	C4-N3-C2	5.94	120.35	115.16
1	A	527	7MG	N3-C4-N9	6.25	134.96	126.98
1	A	966	M2G	C6-N1-C2	6.28	123.66	116.18
1	A	516	PSU	C4-N3-C2	7.03	121.31	115.16
1	A	1540	PSU	C4-N3-C2	7.53	121.74	115.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

13 monomers are involved in 26 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1400	5MC	1	0
1	A	1402	4OC	3	0
1	A	1407	5MC	2	0
1	A	1498	UR3	5	0
1	A	1518[A]	MA6	3	0
1	A	1518[B]	MA6	3	0
1	A	1519[A]	MA6	4	0
1	A	1519[B]	MA6	3	0
1	A	1541	PSU	1	0
1	A	516	PSU	1	0
1	A	966	M2G	3	0
1	A	967	5MC	3	0
12	L	92	0TD	2	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 289 ligands modelled in this entry, 289 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	1498/1522 (98%)	-0.30	34 (2%) 61 46	88, 150, 286, 387	0
2	B	234/256 (91%)	-0.54	0 100 100	110, 168, 268, 286	0
3	C	206/239 (86%)	0.11	14 (6%) 18 12	162, 213, 261, 290	0
4	D	208/209 (99%)	-0.39	5 (2%) 59 44	108, 155, 199, 234	0
5	E	150/162 (92%)	-0.58	0 100 100	86, 126, 170, 198	0
6	F	101/101 (100%)	-0.59	0 100 100	121, 179, 212, 250	0
7	G	155/156 (99%)	-0.28	8 (5%) 28 19	143, 190, 248, 259	0
8	H	138/138 (100%)	-0.59	0 100 100	82, 115, 151, 197	0
9	I	127/128 (99%)	-0.10	3 (2%) 59 44	157, 217, 260, 283	0
10	J	98/105 (93%)	0.62	14 (14%) 3 3	188, 246, 325, 368	0
11	K	116/129 (89%)	-0.30	1 (0%) 84 73	116, 151, 201, 215	0
12	L	123/135 (91%)	-0.36	0 100 100	95, 157, 200, 225	0
13	M	118/126 (93%)	-0.09	3 (2%) 58 43	151, 183, 216, 272	0
14	N	60/61 (98%)	0.21	5 (8%) 12 9	166, 205, 258, 282	0
15	O	87/89 (97%)	-0.34	1 (1%) 80 67	94, 140, 184, 196	0
16	P	83/88 (94%)	-0.44	0 100 100	103, 146, 190, 220	0
17	Q	99/105 (94%)	-0.57	0 100 100	84, 126, 176, 199	0
18	R	70/88 (79%)	-0.49	1 (1%) 75 62	106, 150, 201, 227	0
19	S	80/93 (86%)	0.34	10 (12%) 4 4	185, 234, 275, 291	0
20	T	99/106 (93%)	-0.55	0 100 100	115, 152, 198, 234	0
21	U	24/27 (88%)	1.25	8 (33%) 0 1	165, 177, 208, 219	0
All	All	3874/4063 (95%)	-0.28	107 (2%) 53 39	82, 163, 261, 387	0

All (107) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1129	C	6.9
1	A	993	G	6.9
1	A	1037	C	5.6
21	U	18	TYR	5.2
10	J	34	VAL	4.8
10	J	39	PRO	4.7
10	J	73	ASP	4.6
1	A	1047	G	4.6
4	D	35	ARG	4.5
7	G	80	VAL	4.2
10	J	33	GLN	4.2
1	A	1036	G	4.1
10	J	38	ILE	4.0
1	A	1018	C	4.0
21	U	17	THR	3.9
1	A	1048	G	3.8
19	S	49	ILE	3.8
1	A	1003(A)	G	3.6
1	A	1001	A	3.6
1	A	1019	C	3.6
1	A	1006	C	3.5
10	J	74	ILE	3.4
7	G	156	TRP	3.4
1	A	1005	A	3.4
19	S	31	ILE	3.4
3	C	68	VAL	3.4
1	A	202	U	3.3
3	C	76	VAL	3.3
14	N	18	VAL	3.3
3	C	193	TYR	3.2
3	C	161	GLU	3.2
3	C	66	VAL	3.0
9	I	128	ARG	3.0
13	M	117	VAL	3.0
7	G	2	ALA	3.0
15	O	88	ARG	3.0
21	U	25	LYS	3.0
1	A	994	A	2.9
14	N	3	ARG	2.9
1	A	1443	G	2.9
7	G	81	GLY	2.9
7	G	78	ARG	2.8
13	M	119	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
3	C	65	ALA	2.8
19	S	48	THR	2.8
3	C	162	GLN	2.8
10	J	99	LYS	2.7
3	C	102	ASN	2.7
19	S	50	ALA	2.7
3	C	157	ILE	2.7
1	A	1215	G	2.7
3	C	103	VAL	2.6
19	S	40	ILE	2.6
1	A	992	U	2.6
10	J	72	VAL	2.6
3	C	156	ARG	2.6
9	I	119	ALA	2.6
14	N	17	LYS	2.6
21	U	12	LYS	2.6
21	U	22	ARG	2.6
19	S	30	LEU	2.6
1	A	1222	G	2.6
1	A	1257	U	2.5
10	J	5	ARG	2.5
21	U	24	ARG	2.5
1	A	1000	U	2.5
1	A	1050	G	2.4
1	A	1417	G	2.4
10	J	100	THR	2.4
10	J	75	ILE	2.4
1	A	1213	A	2.4
4	D	34	GLU	2.4
1	A	1025	U	2.4
11	K	118	GLY	2.4
10	J	6	ILE	2.4
7	G	155	ARG	2.4
1	A	1032	G	2.4
19	S	41	VAL	2.3
19	S	39	THR	2.3
4	D	36	ARG	2.3
3	C	78	GLY	2.3
9	I	4	TYR	2.3
1	A	81	U	2.2
1	A	1007	C	2.2
18	R	88	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
3	C	67	THR	2.2
21	U	11	GLY	2.2
13	M	118	ALA	2.2
1	A	1026	G	2.2
1	A	1322	C	2.2
4	D	37	PRO	2.1
1	A	979	C	2.1
14	N	4	LYS	2.1
21	U	5	ASP	2.1
4	D	33	MET	2.1
1	A	1321	C	2.1
14	N	14	PRO	2.1
10	J	71	LEU	2.1
7	G	3	ARG	2.1
19	S	60	VAL	2.1
3	C	87	LEU	2.0
19	S	81	ARG	2.0
1	A	1517[A]	G	2.0
7	G	79	ARG	2.0
1	A	793	U	2.0
10	J	24	VAL	2.0
1	A	21	G	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	PSU	A	1541	20/21	0.89	0.25	-	220,227,234,235	0
1	MA6	A	1518[A]	24/25	0.95	0.39	-	121,138,144,149	24
1	M2G	A	966	25/26	0.95	0.20	-	167,195,202,204	0
1	5MC	A	1404	21/22	0.94	0.17	-	127,137,174,177	0
1	UR3	A	1498	21/22	0.95	0.27	-	132,143,155,163	0
1	MA6	A	1518[B]	24/25	0.95	0.39	-	123,140,152,155	24
1	7MG	A	527	24/25	0.94	0.17	-	125,139,158,159	0
1	5MC	A	1407	21/22	0.94	0.21	-	155,176,182,195	0
1	2MG	A	1207	24/25	0.94	0.14	-	201,225,261,267	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
1	PSU	A	516	20/21	0.92	0.14	-	130,162,189,195	0
12	0TD	L	92	10/11	0.97	0.57	-	144,153,175,322	0
1	5MC	A	967	21/22	0.96	0.16	-	158,165,199,200	0
1	MA6	A	1519[B]	24/25	0.96	0.31	-	115,125,129,130	24
1	4OC	A	1402	22/23	0.97	0.19	-	130,141,155,213	0
1	PSU	A	1540	20/21	0.86	0.42	-	212,224,250,256	0
1	MA6	A	1519[A]	24/25	0.96	0.31	-	114,123,128,180	24
1	5MC	A	1400	21/22	0.95	0.18	-	117,141,147,151	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	D	302	1/1	0.97	0.64	11.78	122,122,122,122	0
22	MG	A	1619	1/1	0.87	0.66	10.76	178,178,178,178	0
22	MG	A	1810	1/1	0.94	0.69	7.93	386,386,386,386	0
22	MG	J	201	1/1	0.80	0.74	7.88	127,127,127,127	0
22	MG	A	1715	1/1	0.98	0.35	6.45	88,88,88,88	0
22	MG	A	1717	1/1	0.80	0.35	6.28	120,120,120,120	0
22	MG	A	1708	1/1	0.91	0.42	6.18	127,127,127,127	0
22	MG	B	301	1/1	0.95	0.35	6.16	138,138,138,138	0
22	MG	A	1659	1/1	0.85	0.27	5.61	148,148,148,148	0
22	MG	Q	202	1/1	0.75	0.35	5.34	146,146,146,146	0
22	MG	A	1689	1/1	0.59	0.38	4.48	124,124,124,124	0
22	MG	A	1700	1/1	0.94	0.40	4.39	110,110,110,110	0
22	MG	A	1856	1/1	0.93	0.17	4.23	136,136,136,136	0
22	MG	A	1743	1/1	0.93	0.59	3.70	112,112,112,112	0
22	MG	A	1768	1/1	0.97	0.30	3.69	112,112,112,112	0
22	MG	A	1722	1/1	0.82	0.30	3.43	115,115,115,115	0
22	MG	A	1637	1/1	0.84	0.25	2.72	127,127,127,127	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
22	MG	A	1811	1/1	0.98	0.18	2.32	255,255,255,255	0
22	MG	P	103	1/1	0.75	0.39	2.29	132,132,132,132	0
22	MG	A	1827	1/1	0.99	0.25	2.03	304,304,304,304	0
22	MG	A	1668	1/1	0.98	0.30	2.01	271,271,271,271	0
22	MG	A	1733	1/1	0.94	0.21	1.91	102,102,102,102	0
22	MG	A	1761	1/1	0.74	0.16	1.83	157,157,157,157	0
22	MG	A	1711	1/1	0.94	0.51	1.83	139,139,139,139	0
22	MG	C	301	1/1	0.99	0.34	1.82	165,165,165,165	0
22	MG	J	202	1/1	0.97	0.37	1.58	344,344,344,344	0
22	MG	A	1757	1/1	0.92	0.22	1.58	105,105,105,105	0
22	MG	A	1696	1/1	0.93	0.37	1.47	399,399,399,399	0
22	MG	A	1763	1/1	0.91	0.23	1.40	362,362,362,362	0
22	MG	A	1695	1/1	0.98	0.18	1.36	134,134,134,134	0
22	MG	A	1766	1/1	0.94	0.18	1.25	131,131,131,131	0
22	MG	A	1751	1/1	0.88	0.41	1.20	139,139,139,139	0
22	MG	A	1645	1/1	0.98	0.22	1.16	76,76,76,76	0
22	MG	A	1776	1/1	0.82	0.45	1.11	135,135,135,135	0
22	MG	A	1731	1/1	0.95	0.25	0.89	109,109,109,109	0
22	MG	A	1642	1/1	0.96	0.29	0.86	158,158,158,158	0
22	MG	A	1610	1/1	0.99	0.21	0.84	119,119,119,119	0
23	ZN	D	301	1/1	0.99	0.34	0.63	117,117,117,117	0
22	MG	A	1746	1/1	0.83	0.43	0.58	181,181,181,181	0
22	MG	A	1719	1/1	0.97	0.16	0.52	108,108,108,108	0
22	MG	A	1760	1/1	0.98	0.12	0.37	147,147,147,147	0
22	MG	B	302	1/1	0.97	0.27	0.20	147,147,147,147	0
22	MG	A	1615	1/1	0.97	0.20	-0.20	87,87,87,87	0
22	MG	A	1825	1/1	0.97	0.17	-0.20	470,470,470,470	0
22	MG	A	1775	1/1	0.97	0.17	-0.26	110,110,110,110	0
22	MG	A	1799	1/1	0.78	0.24	-0.27	466,466,466,466	0
23	ZN	N	101	1/1	0.97	0.17	-0.34	233,233,233,233	0
22	MG	A	1847	1/1	0.98	0.11	-0.35	155,155,155,155	0
22	MG	A	1866	1/1	0.77	0.18	-0.36	123,123,123,123	0
22	MG	A	1727	1/1	0.98	0.12	-0.55	91,91,91,91	0
22	MG	A	1701	1/1	0.98	0.13	-0.65	146,146,146,146	0
22	MG	A	1687	1/1	0.89	0.20	-0.75	162,162,162,162	0
22	MG	A	1639	1/1	0.98	0.12	-0.91	163,163,163,163	0
22	MG	A	1703	1/1	0.98	0.13	-0.96	142,142,142,142	0
22	MG	A	1820	1/1	0.86	0.23	-0.96	459,459,459,459	0
22	MG	A	1759	1/1	0.99	0.11	-0.97	155,155,155,155	0
22	MG	A	1835	1/1	0.99	0.15	-0.99	349,349,349,349	0
22	MG	D	303	1/1	0.98	0.10	-1.02	119,119,119,119	0
22	MG	A	1698	1/1	0.98	0.10	-1.04	218,218,218,218	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
22	MG	A	1635	1/1	0.97	0.13	-1.12	101,101,101,101	0
22	MG	A	1750	1/1	0.96	0.08	-1.48	102,102,102,102	0
22	MG	A	1620	1/1	1.00	0.13	-1.49	116,116,116,116	0
22	MG	A	1691	1/1	0.98	0.10	-1.66	128,128,128,128	0
22	MG	A	1680	1/1	0.97	0.10	-1.74	128,128,128,128	0
22	MG	A	1860	1/1	0.91	0.10	-1.85	167,167,167,167	0
22	MG	A	1630	1/1	0.93	0.11	-1.87	139,139,139,139	0
22	MG	A	1627	1/1	0.99	0.10	-2.12	110,110,110,110	0
22	MG	A	1654	1/1	0.98	0.09	-2.74	121,121,121,121	0
22	MG	A	1707	1/1	0.97	0.13	-3.13	83,83,83,83	0
22	MG	A	1867	1/1	0.98	0.19	-	139,139,139,139	0
22	MG	A	1849	1/1	0.95	0.13	-	133,133,133,133	0
22	MG	A	1736	1/1	0.96	0.20	-	156,156,156,156	0
22	MG	A	1684	1/1	0.99	0.15	-	158,158,158,158	0
22	MG	A	1772	1/1	0.83	0.21	-	115,115,115,115	0
22	MG	A	1854	1/1	0.83	0.42	-	112,112,112,112	0
22	MG	A	1826	1/1	0.94	0.24	-	225,225,225,225	0
22	MG	A	1814	1/1	0.92	0.36	-	113,113,113,113	0
22	MG	A	1830	1/1	0.87	0.42	-	512,512,512,512	0
22	MG	A	1838	1/1	0.96	0.14	-	187,187,187,187	0
22	MG	A	1803	1/1	0.95	0.35	-	386,386,386,386	0
22	MG	A	1786	1/1	0.96	0.20	-	179,179,179,179	0
22	MG	A	1836	1/1	0.86	0.46	-	98,98,98,98	0
22	MG	A	1686	1/1	0.75	0.16	-	166,166,166,166	0
22	MG	A	1828	1/1	0.96	0.11	-	351,351,351,351	0
22	MG	A	1753	1/1	0.97	0.19	-	128,128,128,128	0
22	MG	A	1718	1/1	0.98	0.11	-	103,103,103,103	0
22	MG	A	1681	1/1	0.99	0.13	-	152,152,152,152	0
22	MG	A	1611	1/1	0.96	0.19	-	171,171,171,171	0
22	MG	A	1665	1/1	0.97	0.09	-	271,271,271,271	0
22	MG	A	1729	1/1	0.90	0.35	-	105,105,105,105	0
22	MG	A	1855	1/1	0.84	0.19	-	114,114,114,114	0
22	MG	A	1804	1/1	0.96	0.64	-	366,366,366,366	0
22	MG	A	1726	1/1	0.94	0.20	-	130,130,130,130	0
22	MG	A	1818	1/1	0.48	0.88	-	126,126,126,126	0
22	MG	A	1832	1/1	0.97	0.16	-	390,390,390,390	0
22	MG	A	1813	1/1	0.76	0.41	-	105,105,105,105	0
22	MG	A	1778	1/1	0.84	0.73	-	132,132,132,132	0
22	MG	A	1791	1/1	0.84	0.27	-	244,244,244,244	0
22	MG	A	1631	1/1	1.00	0.14	-	93,93,93,93	0
22	MG	M	201	1/1	0.97	0.21	-	375,375,375,375	0
22	MG	A	1802	1/1	0.89	0.09	-	250,250,250,250	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
22	MG	A	1744	1/1	0.93	0.14	-	150,150,150,150	0
22	MG	A	1702	1/1	0.90	0.51	-	124,124,124,124	0
22	MG	A	1625	1/1	0.87	0.27	-	124,124,124,124	0
22	MG	A	1662	1/1	0.90	0.18	-	128,128,128,128	0
22	MG	A	1678	1/1	0.99	0.13	-	182,182,182,182	0
22	MG	A	1658	1/1	0.99	0.19	-	111,111,111,111	0
22	MG	A	1829	1/1	0.98	0.26	-	202,202,202,202	0
22	MG	P	102	1/1	0.53	0.38	-	141,141,141,141	0
22	MG	A	1661	1/1	0.97	0.12	-	141,141,141,141	0
22	MG	A	1693	1/1	0.97	0.31	-	150,150,150,150	0
22	MG	A	1800	1/1	0.99	0.13	-	62,62,62,62	0
22	MG	A	1690	1/1	0.97	0.15	-	387,387,387,387	0
22	MG	A	1796	1/1	0.93	0.46	-	168,168,168,168	0
22	MG	A	1617	1/1	0.98	0.22	-	113,113,113,113	0
22	MG	A	1724	1/1	0.92	0.37	-	133,133,133,133	0
22	MG	P	101	1/1	0.91	0.43	-	90,90,90,90	0
22	MG	A	1841	1/1	0.78	0.16	-	149,149,149,149	0
22	MG	A	1653	1/1	0.88	0.27	-	127,127,127,127	0
22	MG	A	1740	1/1	0.95	0.15	-	129,129,129,129	0
22	MG	A	1779	1/1	0.93	0.30	-	374,374,374,374	0
22	MG	A	1797	1/1	0.95	0.12	-	176,176,176,176	0
22	MG	A	1812	1/1	0.94	0.09	-	429,429,429,429	0
22	MG	A	1676	1/1	0.96	0.48	-	151,151,151,151	0
22	MG	A	1846	1/1	0.97	0.10	-	150,150,150,150	0
22	MG	A	1748	1/1	0.95	0.35	-	136,136,136,136	0
22	MG	A	1710	1/1	0.86	0.60	-	111,111,111,111	0
22	MG	A	1616	1/1	0.97	0.25	-	195,195,195,195	0
22	MG	A	1862	1/1	0.96	0.28	-	155,155,155,155	0
22	MG	A	1754	1/1	0.77	0.32	-	134,134,134,134	0
22	MG	A	1604	1/1	0.99	0.25	-	151,151,151,151	0
22	MG	A	1824	1/1	0.98	0.88	-	407,407,407,407	0
22	MG	A	1765	1/1	0.93	0.25	-	127,127,127,127	0
22	MG	A	1782	1/1	0.92	0.28	-	244,244,244,244	0
22	MG	A	1608	1/1	0.94	0.29	-	99,99,99,99	0
22	MG	A	1664	1/1	0.96	0.07	-	129,129,129,129	0
22	MG	A	1842	1/1	0.95	0.19	-	161,161,161,161	0
22	MG	A	1720	1/1	0.99	0.08	-	114,114,114,114	0
22	MG	A	1613	1/1	0.97	0.13	-	160,160,160,160	0
22	MG	A	1674	1/1	0.84	0.29	-	171,171,171,171	0
22	MG	A	1632	1/1	0.99	0.40	-	90,90,90,90	0
22	MG	A	1773	1/1	0.80	0.27	-	142,142,142,142	0
22	MG	A	1808	1/1	0.95	0.51	-	265,265,265,265	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
22	MG	A	1758	1/1	0.84	0.23	-	150,150,150,150	0
22	MG	E	201	1/1	0.91	0.43	-	163,163,163,163	0
22	MG	A	1672	1/1	0.98	0.08	-	166,166,166,166	0
22	MG	A	1819	1/1	0.95	0.19	-	294,294,294,294	0
22	MG	A	1809	1/1	0.83	0.29	-	466,466,466,466	0
22	MG	A	1714	1/1	0.73	0.49	-	124,124,124,124	0
22	MG	A	1694	1/1	0.99	0.33	-	194,194,194,194	0
22	MG	A	1851	1/1	0.90	0.41	-	136,136,136,136	0
22	MG	A	1735	1/1	0.91	0.32	-	122,122,122,122	0
22	MG	A	1785	1/1	0.94	0.09	-	364,364,364,364	0
22	MG	A	1655	1/1	0.91	0.23	-	113,113,113,113	0
22	MG	A	1712	1/1	0.82	0.43	-	151,151,151,151	0
22	MG	A	1669	1/1	0.94	0.27	-	144,144,144,144	0
22	MG	A	1749	1/1	0.95	0.14	-	114,114,114,114	0
22	MG	A	1704	1/1	0.97	0.18	-	95,95,95,95	0
22	MG	A	1848	1/1	0.79	0.41	-	144,144,144,144	0
22	MG	C	302	1/1	0.98	0.16	-	181,181,181,181	0
22	MG	A	1626	1/1	0.94	0.21	-	112,112,112,112	0
22	MG	A	1805	1/1	0.95	0.14	-	162,162,162,162	0
22	MG	A	1745	1/1	0.87	0.78	-	155,155,155,155	0
22	MG	A	1670	1/1	0.91	0.34	-	109,109,109,109	0
22	MG	A	1732	1/1	0.97	0.18	-	81,81,81,81	0
22	MG	A	1859	1/1	0.89	0.48	-	143,143,143,143	0
22	MG	F	201	1/1	0.93	0.35	-	144,144,144,144	0
22	MG	A	1790	1/1	0.97	0.19	-	356,356,356,356	0
22	MG	A	1643	1/1	0.95	0.13	-	146,146,146,146	0
22	MG	A	1863	1/1	0.82	0.89	-	121,121,121,121	0
22	MG	A	1792	1/1	0.91	0.33	-	145,145,145,145	0
22	MG	A	1747	1/1	0.78	0.24	-	118,118,118,118	0
22	MG	A	1730	1/1	0.99	0.12	-	129,129,129,129	0
22	MG	A	1699	1/1	0.74	0.45	-	171,171,171,171	0
22	MG	A	1815	1/1	0.93	0.37	-	286,286,286,286	0
22	MG	A	1845	1/1	0.85	0.85	-	157,157,157,157	0
22	MG	A	1767	1/1	0.72	0.48	-	167,167,167,167	0
22	MG	A	1764	1/1	0.96	0.24	-	220,220,220,220	0
22	MG	A	1705	1/1	0.92	0.08	-	156,156,156,156	0
22	MG	A	1780	1/1	0.79	0.37	-	154,154,154,154	0
22	MG	A	1833	1/1	0.90	0.26	-	230,230,230,230	0
22	MG	A	1647	1/1	0.99	0.26	-	138,138,138,138	0
22	MG	A	1762	1/1	0.96	0.17	-	184,184,184,184	0
22	MG	A	1801	1/1	0.93	0.28	-	135,135,135,135	0
22	MG	A	1794	1/1	0.91	0.25	-	211,211,211,211	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
22	MG	A	1624	1/1	0.96	0.49	-	113,113,113,113	0
22	MG	A	1679	1/1	0.96	0.29	-	150,150,150,150	0
22	MG	A	1831	1/1	0.95	0.16	-	244,244,244,244	0
22	MG	A	1709	1/1	0.80	0.43	-	118,118,118,118	0
22	MG	A	1605	1/1	0.94	0.31	-	105,105,105,105	0
22	MG	A	1858	1/1	0.73	0.37	-	115,115,115,115	0
22	MG	A	1649	1/1	0.93	0.18	-	130,130,130,130	0
22	MG	A	1629	1/1	0.99	0.51	-	147,147,147,147	0
22	MG	A	1634	1/1	0.99	0.29	-	290,290,290,290	0
22	MG	A	1795	1/1	0.98	0.27	-	247,247,247,247	0
22	MG	A	1843	1/1	0.94	0.16	-	186,186,186,186	0
22	MG	A	1739	1/1	0.72	0.68	-	132,132,132,132	0
22	MG	A	1725	1/1	0.69	0.91	-	126,126,126,126	0
22	MG	A	1721	1/1	0.98	0.18	-	127,127,127,127	0
22	MG	A	1650	1/1	0.98	0.11	-	112,112,112,112	0
22	MG	A	1609	1/1	0.93	0.26	-	115,115,115,115	0
22	MG	A	1685	1/1	0.91	0.80	-	109,109,109,109	0
22	MG	A	1633	1/1	0.93	0.24	-	113,113,113,113	0
22	MG	A	1677	1/1	0.95	0.11	-	130,130,130,130	0
22	MG	A	1614	1/1	0.98	0.08	-	144,144,144,144	0
22	MG	A	1660	1/1	0.98	0.08	-	116,116,116,116	0
22	MG	A	1771	1/1	0.93	0.10	-	114,114,114,114	0
22	MG	A	1770	1/1	0.90	0.20	-	99,99,99,99	0
22	MG	A	1652	1/1	0.81	0.28	-	150,150,150,150	0
22	MG	A	1816	1/1	0.75	0.30	-	422,422,422,422	0
22	MG	A	1789	1/1	0.89	0.15	-	215,215,215,215	0
22	MG	A	1852	1/1	0.94	0.19	-	102,102,102,102	0
22	MG	A	1752	1/1	0.94	0.20	-	108,108,108,108	0
22	MG	A	1787	1/1	0.85	0.32	-	175,175,175,175	0
22	MG	A	1675	1/1	0.84	0.43	-	123,123,123,123	0
22	MG	A	1798	1/1	0.91	0.21	-	212,212,212,212	0
22	MG	A	1602	1/1	0.96	0.50	-	145,145,145,145	0
22	MG	A	1723	1/1	0.92	0.08	-	151,151,151,151	0
22	MG	Q	201	1/1	0.72	0.18	-	136,136,136,136	0
22	MG	A	1606	1/1	0.99	0.09	-	113,113,113,113	0
22	MG	A	1612	1/1	0.98	0.04	-	174,174,174,174	0
22	MG	A	1755	1/1	0.88	0.33	-	118,118,118,118	0
22	MG	A	1793	1/1	0.92	0.28	-	134,134,134,134	0
22	MG	A	1864	1/1	0.91	0.27	-	129,129,129,129	0
22	MG	A	1713	1/1	0.89	0.35	-	92,92,92,92	0
22	MG	A	1638	1/1	0.92	0.37	-	95,95,95,95	0
22	MG	A	1641	1/1	0.98	0.30	-	188,188,188,188	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
22	MG	A	1781	1/1	0.94	0.07	-	174,174,174,174	0
22	MG	A	1688	1/1	0.96	0.19	-	121,121,121,121	0
22	MG	A	1656	1/1	0.66	0.54	-	110,110,110,110	0
22	MG	A	1784	1/1	0.99	0.07	-	153,153,153,153	0
22	MG	A	1806	1/1	0.89	0.26	-	242,242,242,242	0
22	MG	A	1857	1/1	0.93	0.18	-	141,141,141,141	0
22	MG	A	1840	1/1	0.84	0.63	-	136,136,136,136	0
22	MG	D	304	1/1	0.83	0.16	-	111,111,111,111	0
22	MG	A	1692	1/1	0.98	0.09	-	175,175,175,175	0
22	MG	A	1646	1/1	0.93	0.28	-	134,134,134,134	0
22	MG	A	1601	1/1	0.85	0.36	-	122,122,122,122	0
22	MG	A	1769	1/1	0.89	0.14	-	134,134,134,134	0
22	MG	A	1788	1/1	0.84	0.17	-	420,420,420,420	0
22	MG	A	1734	1/1	0.89	0.24	-	94,94,94,94	0
22	MG	A	1673	1/1	0.99	0.06	-	211,211,211,211	0
22	MG	A	1774	1/1	0.99	0.05	-	142,142,142,142	0
22	MG	A	1728	1/1	0.81	0.28	-	128,128,128,128	0
22	MG	A	1737	1/1	0.82	0.50	-	133,133,133,133	0
22	MG	A	1640	1/1	0.87	0.33	-	145,145,145,145	0
22	MG	A	1667	1/1	0.98	0.09	-	123,123,123,123	0
22	MG	A	1621	1/1	0.82	0.80	-	111,111,111,111	0
22	MG	A	1706	1/1	0.91	0.17	-	207,207,207,207	0
22	MG	A	1741	1/1	0.97	0.37	-	118,118,118,118	0
22	MG	A	1697	1/1	0.98	0.38	-	335,335,335,335	0
22	MG	A	1865	1/1	0.99	0.17	-	180,180,180,180	0
22	MG	A	1622	1/1	0.90	0.83	-	67,67,67,67	0
22	MG	A	1742	1/1	0.98	0.12	-	129,129,129,129	0
22	MG	A	1823	1/1	0.99	0.07	-	276,276,276,276	0
22	MG	A	1683	1/1	0.96	0.13	-	175,175,175,175	0
22	MG	A	1666	1/1	0.87	0.17	-	118,118,118,118	0
22	MG	A	1821	1/1	0.39	0.75	-	119,119,119,119	0
22	MG	A	1807	1/1	0.91	0.48	-	254,254,254,254	0
22	MG	S	101	1/1	0.87	0.85	-	156,156,156,156	0
22	MG	A	1623	1/1	0.95	0.08	-	148,148,148,148	0
22	MG	A	1603	1/1	0.93	0.18	-	117,117,117,117	0
22	MG	A	1839	1/1	0.97	0.28	-	170,170,170,170	0
22	MG	A	1738	1/1	0.84	0.23	-	115,115,115,115	0
22	MG	A	1853	1/1	0.74	0.39	-	161,161,161,161	0
22	MG	N	102	1/1	0.89	0.18	-	184,184,184,184	0
22	MG	A	1783	1/1	0.90	1.10	-	179,179,179,179	0
22	MG	A	1844	1/1	0.94	0.17	-	123,123,123,123	0
22	MG	A	1756	1/1	0.90	0.25	-	127,127,127,127	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
22	MG	A	1663	1/1	0.93	0.10	-	102,102,102,102	0
22	MG	A	1628	1/1	0.79	0.35	-	110,110,110,110	0
22	MG	A	1837	1/1	0.86	0.36	-	150,150,150,150	0
22	MG	A	1618	1/1	0.95	0.33	-	147,147,147,147	0
22	MG	A	1834	1/1	0.84	0.26	-	157,157,157,157	0
22	MG	A	1817	1/1	0.76	0.35	-	144,144,144,144	0
22	MG	A	1850	1/1	0.90	1.04	-	150,150,150,150	0
22	MG	A	1822	1/1	0.38	1.21	-	147,147,147,147	0
22	MG	A	1651	1/1	0.97	0.23	-	184,184,184,184	0
22	MG	A	1648	1/1	0.98	0.25	-	176,176,176,176	0
22	MG	A	1644	1/1	0.96	0.18	-	126,126,126,126	0
22	MG	A	1682	1/1	0.86	0.30	-	126,126,126,126	0
22	MG	A	1607	1/1	0.86	0.10	-	183,183,183,183	0
22	MG	A	1716	1/1	0.97	0.44	-	139,139,139,139	0
22	MG	A	1657	1/1	0.96	0.16	-	136,136,136,136	0
22	MG	A	1777	1/1	0.68	0.77	-	144,144,144,144	0
22	MG	A	1868	1/1	0.92	0.20	-	144,144,144,144	0
22	MG	A	1636	1/1	0.98	0.27	-	127,127,127,127	0
22	MG	A	1671	1/1	0.96	0.39	-	120,120,120,120	0
22	MG	A	1861	1/1	0.93	0.14	-	163,163,163,163	0

6.5 Other polymers

There are no such residues in this entry.