



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 27, 2014 – 04:00 PM GMT

PDB ID : 3V28
Title : Crystal structure of HPF bound to the 70S ribosome. This PDB entry contains coordinates for the 30S subunit with bound HPF of the 2nd ribosome in the ASU
Authors : Polikanov, Y.S.; Blaha, G.M.; Steitz, T.A.
Deposited on : 2011-12-11
Resolution : 3.10 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

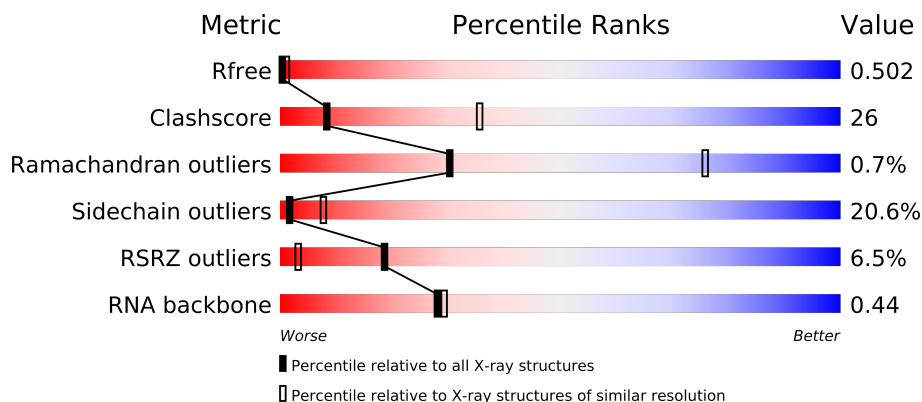
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 3.10 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}	66092	1007 (3.18-3.02)
Clashscore	79885	1078 (3.16-3.04)
Ramachandran outliers	78287	1044 (3.16-3.04)
Sidechain outliers	78261	1044 (3.16-3.04)
RSRZ outliers	66119	1008 (3.18-3.02)
RNA backbone	1838	1047 (3.60-2.60)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	1522	
2	B	256	
3	C	239	
4	D	209	
5	E	162	
6	F	101	
7	G	156	
8	H	138	
9	I	128	
10	J	105	
11	K	129	
12	L	132	

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Mol	Chain	Length	Quality of chain
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	
22	X	101	

2 Entry composition

There are 25 unique types of molecules in this entry. The entry contains 50808 atoms, of which 0 are hydrogen and 0 are deuterium.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 16S Ribosomal RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1497	Total	C	N	O	P	0	0	0
			32185	14324	5968	10396	1497			

- Molecule 2 is a protein called 30S Ribosomal Protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	229	Total	C	N	O	S	0	0	0
			1775	1132	318	320	5			

- Molecule 3 is a protein called 30S Ribosomal Protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	206	Total	C	N	O	S	0	0	0
			1450	906	279	264	1			

- Molecule 4 is a protein called 30S Ribosomal Protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	208	Total	C	N	O	S	0	0	0
			1526	963	283	274	6			

- Molecule 5 is a protein called 30S Ribosomal Protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	148	Total	C	N	O	S	0	0	0
			1105	699	204	198	4			

- Molecule 6 is a protein called 30S Ribosomal Protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	100	Total	C	N	O	S	0	0	0
			777	493	137	144	3			

- Molecule 7 is a protein called 30S Ribosomal Protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	155	Total	C	N	O	S	0	0	0
			1164	726	224	208	6			

- Molecule 8 is a protein called 30S Ribosomal Protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	H	138	Total	C	N	O	S	0	0	0
			1045	665	188	190	2			

- Molecule 9 is a protein called 30S Ribosomal Protein S9.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
9	I	125	Total	C	N	O	0	0	0
			852	533	163	156			

- Molecule 10 is a protein called 30S Ribosomal Protein S10.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
10	J	96	Total	C	N	O	0	0	0
			663	410	132	121			

- Molecule 11 is a protein called 30S Ribosomal Protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	114	Total	C	N	O	S	0	0	0
			828	516	155	154	3			

- Molecule 12 is a protein called 30S Ribosomal Protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	122	Total	C	N	O	S	0	0	0
			905	567	178	159	1			

- Molecule 13 is a protein called 30S Ribosomal Protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	M	114	Total	C	N	O	S	0	0	0
			804	497	164	142	1			

- Molecule 14 is a protein called 30S Ribosomal Protein S14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	N	60	Total	C	N	O	S	0	0	0
			478	303	99	72	4			

- Molecule 15 is a protein called 30S Ribosomal Protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	O	88	Total	C	N	O	S	0	0	0
			724	453	143	126	2			

- Molecule 16 is a protein called 30S Ribosomal Protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	P	82	Total	C	N	O	S	0	0	0
			651	416	123	111	1			

- Molecule 17 is a protein called 30S Ribosomal Protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	Q	99	Total	C	N	O	S	0	0	0
			823	528	151	142	2			

- Molecule 18 is a protein called 30S Ribosomal Protein S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	R	68	Total	C	N	O	0	0	0
			514	329	98	87			

- Molecule 19 is a protein called 30S Ribosomal Protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	S	81	Total	C	N	O	S	0	0	0
			560	351	108	99	2			

- Molecule 20 is a protein called 30S Ribosomal Protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	T	97	Total	C	N	O	S	0	0	0
			713	438	152	121	2			

- Molecule 21 is a protein called 30S Ribosomal Protein THX.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	U	23	Total	C	N	O	0	0	0
			199	122	48	29			

- Molecule 22 is a protein called Probable sigma(54) modulation protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	X	95	Total	C	N	O	S	0	0	0
			601	378	108	114	1			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	96	HIS	-	EXPRESSION TAG	UNP P0AFX0
X	97	HIS	-	EXPRESSION TAG	UNP P0AFX0
X	98	HIS	-	EXPRESSION TAG	UNP P0AFX0
X	99	HIS	-	EXPRESSION TAG	UNP P0AFX0
X	100	HIS	-	EXPRESSION TAG	UNP P0AFX0
X	101	HIS	-	EXPRESSION TAG	UNP P0AFX0

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
23	Q	1	Total	Mg	0	0
			1	1		
23	A	168	Total	Mg	0	0
			168	168		
23	E	1	Total	Mg	0	0
			1	1		

- Molecule 24 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 25 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
25	A	282	Total	O	0	0
			282	282		

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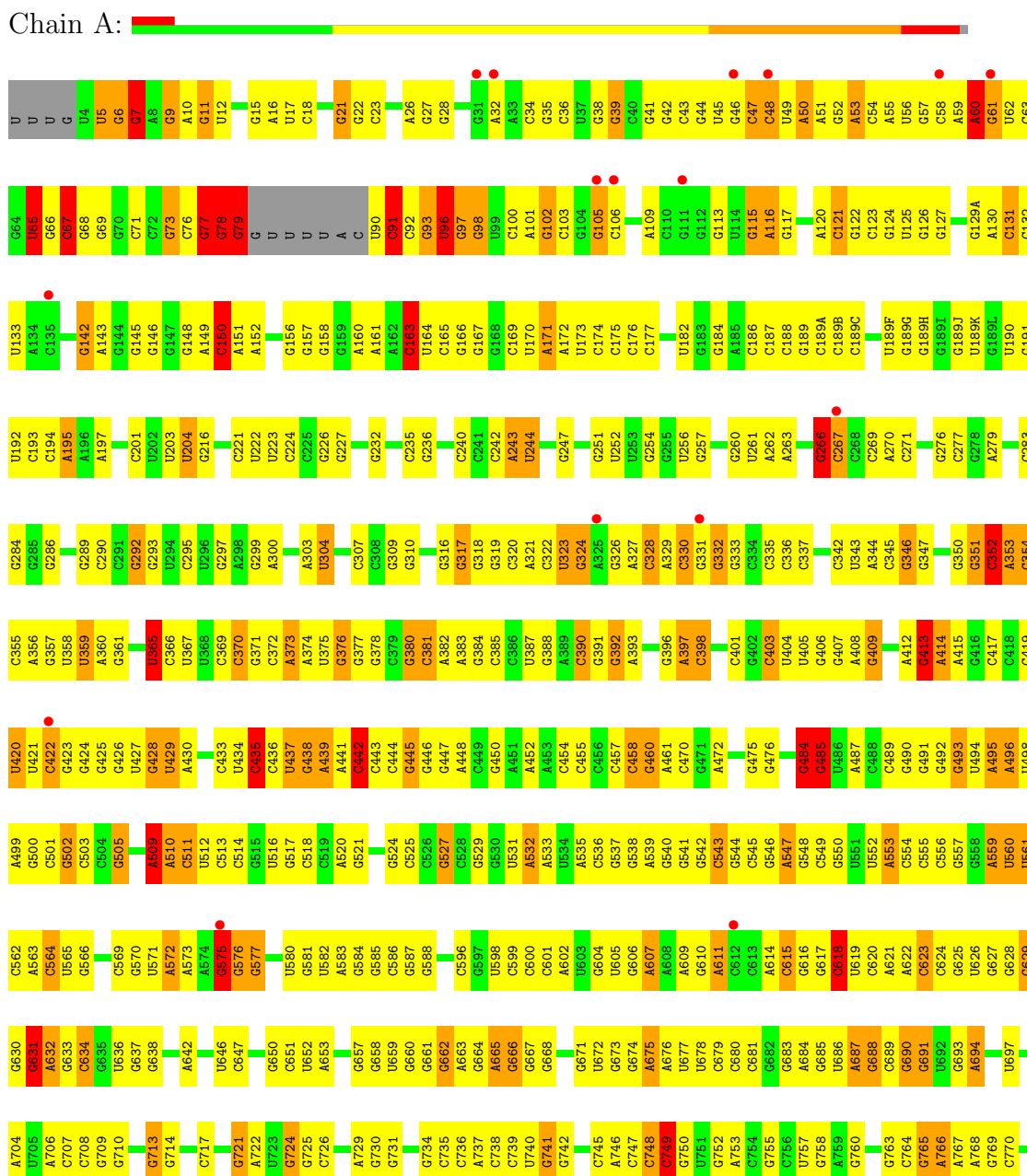
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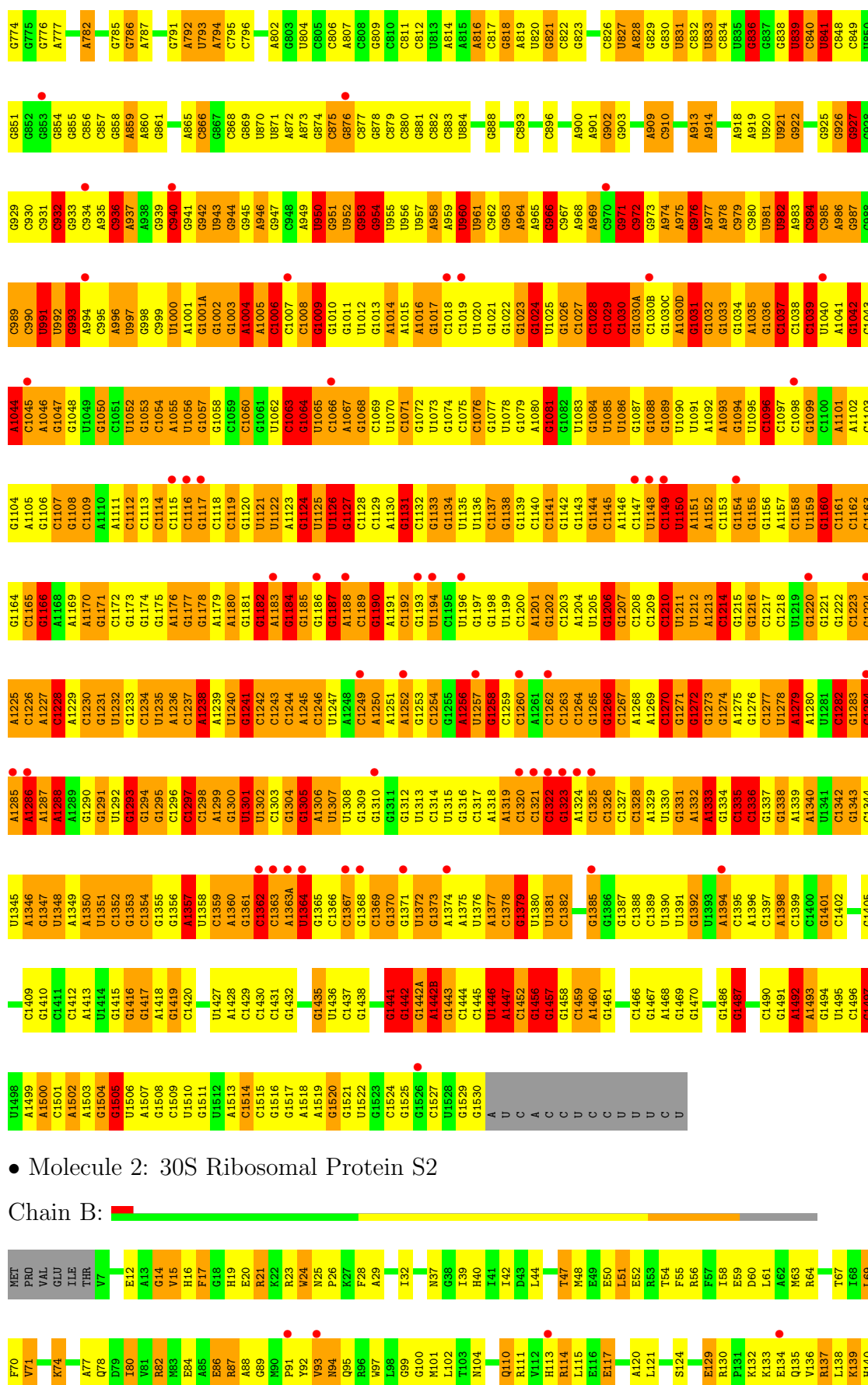
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
25	C	1	Total 1	O 1	0	0
25	D	1	Total 1	O 1	0	0
25	E	2	Total 2	O 2	0	0
25	K	1	Total 1	O 1	0	0
25	L	2	Total 2	O 2	0	0
25	N	1	Total 1	O 1	0	0
25	Q	1	Total 1	O 1	0	0
25	T	2	Total 2	O 2	0	0
25	X	1	Total 1	O 1	0	0

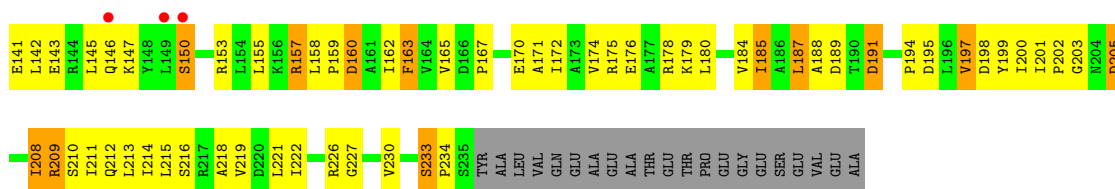
3 Residue-property plots

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

• Molecule 1: 16S Ribosomal RNA

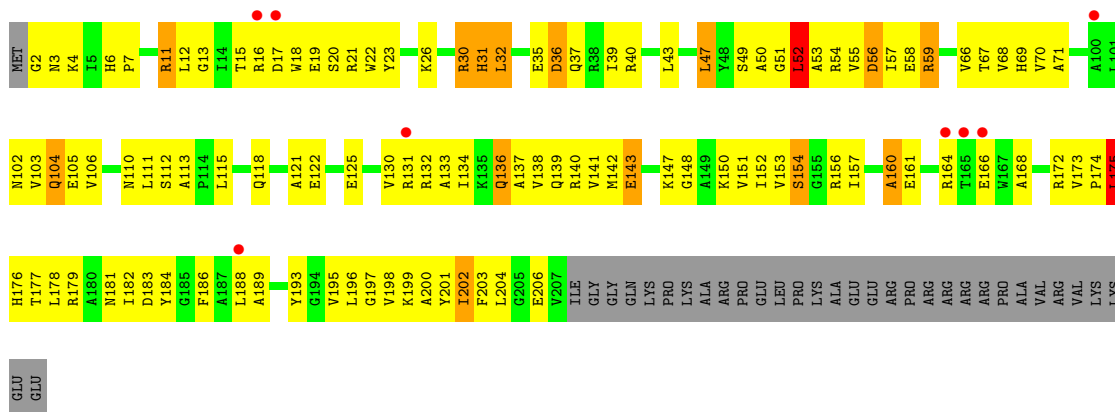






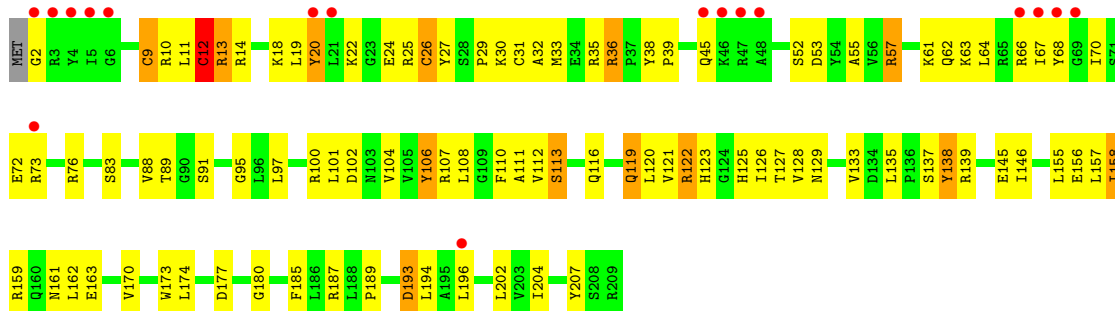
• Molecule 3: 30S Ribosomal Protein S3

Chain C:



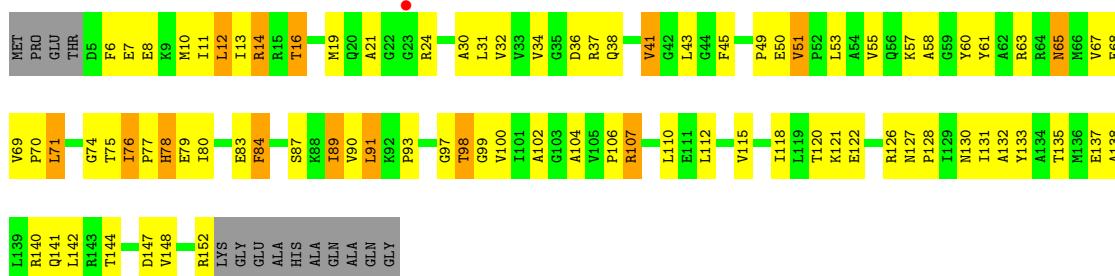
• Molecule 4: 30S Ribosomal Protein S4

Chain D:



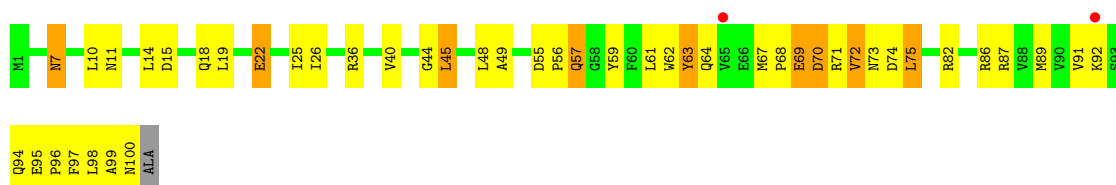
• Molecule 5: 30S Ribosomal Protein S5

Chain E:



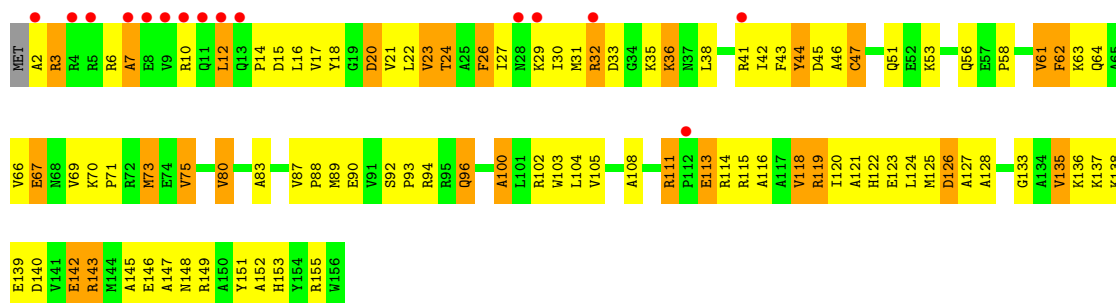
• Molecule 6: 30S Ribosomal Protein S6

Chain F:



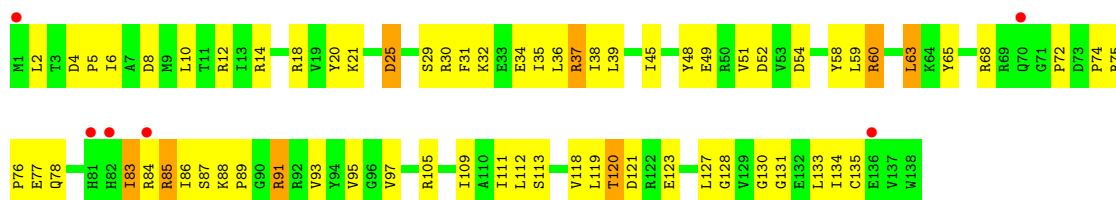
• Molecule 7: 30S Ribosomal Protein S7

Chain G:



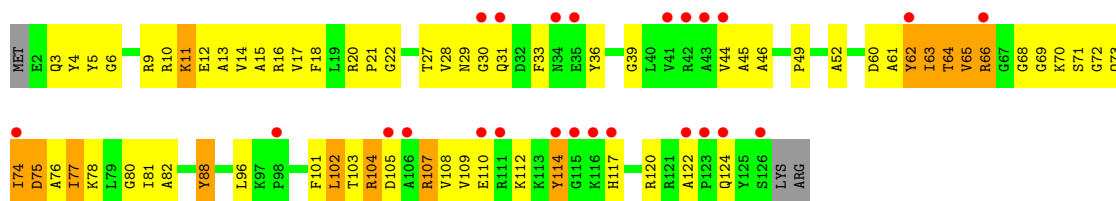
• Molecule 8: 30S Ribosomal Protein S8

Chain H:



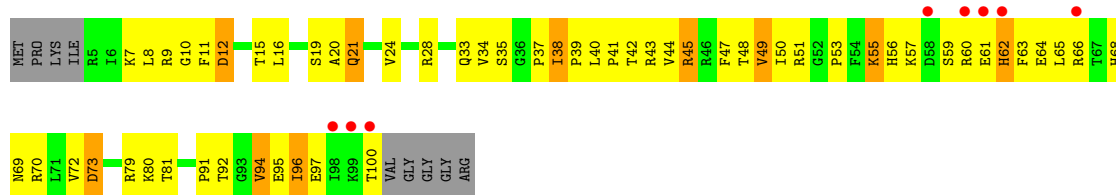
• Molecule 9: 30S Ribosomal Protein S9

Chain I:



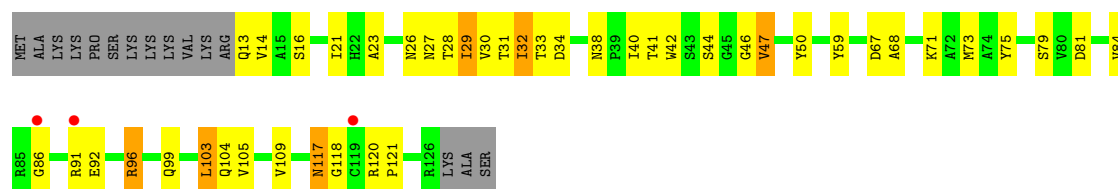
• Molecule 10: 30S Ribosomal Protein S10

Chain J:



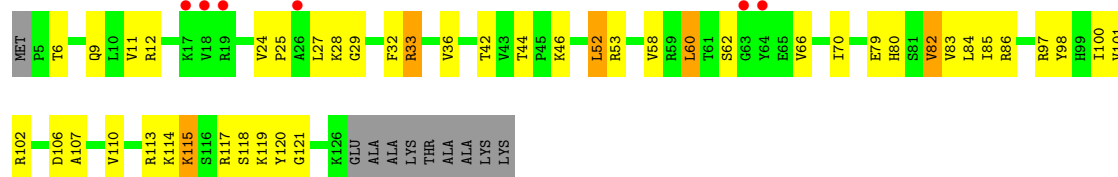
• Molecule 11: 30S Ribosomal Protein S11

Chain K:



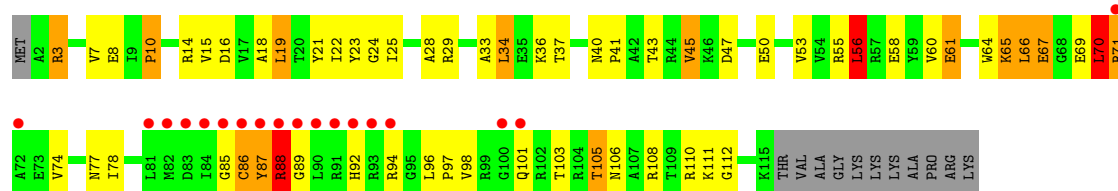
- Molecule 12: 30S Ribosomal Protein S12

Chain L:



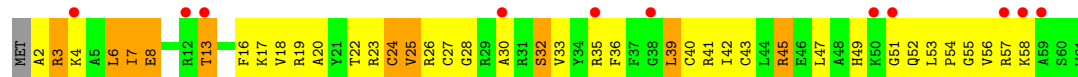
- Molecule 13: 30S Ribosomal Protein S13

Chain M:



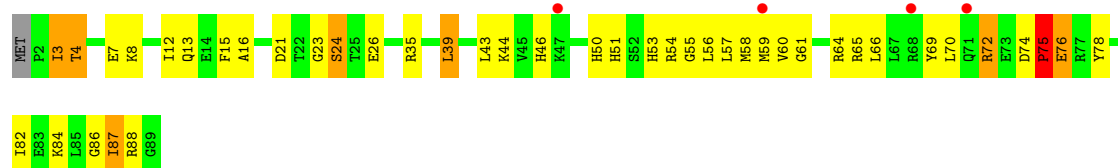
- Molecule 14: 30S Ribosomal Protein S14

Chain N:



- Molecule 15: 30S Ribosomal Protein S15

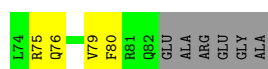
Chain O:



- Molecule 16: 30S Ribosomal Protein S16

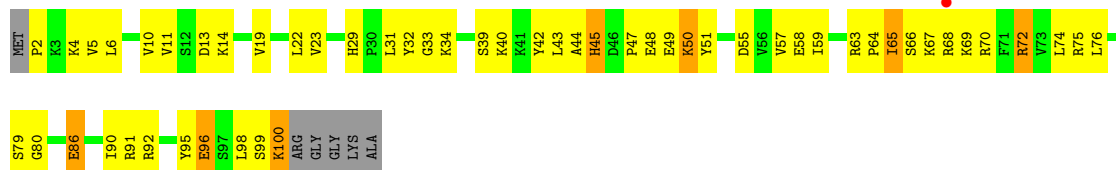
Chain P:





• Molecule 17: 30S Ribosomal Protein S17

Chain Q:



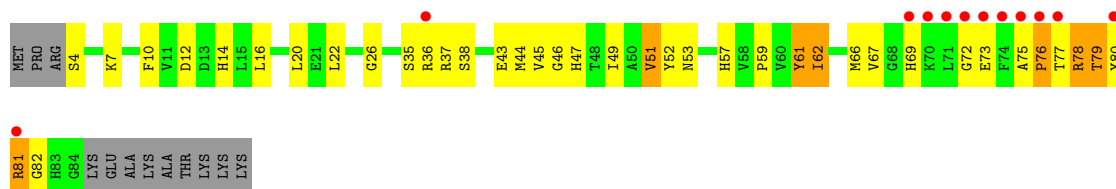
• Molecule 18: 30S Ribosomal Protein S18

Chain R:



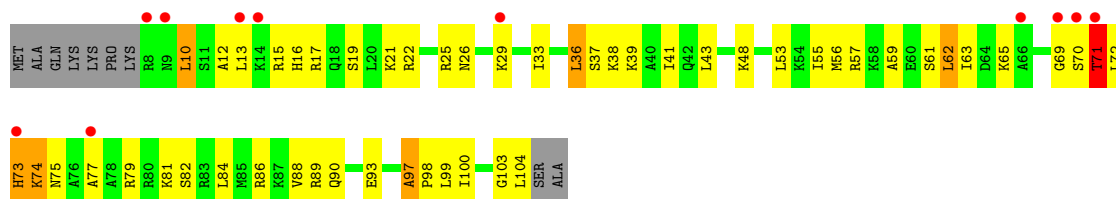
• Molecule 19: 30S Ribosomal Protein S19

Chain S:



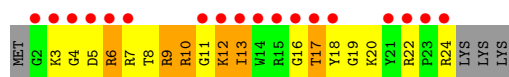
• Molecule 20: 30S Ribosomal Protein S20

Chain T:



• Molecule 21: 30S Ribosomal Protein THX

Chain U:



• Molecule 22: Probable sigma(54) modulation protein

Chain X:



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	208.97Å 447.24Å 617.67Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.98 – 3.10 49.98 – 3.10	Depositor EDS
% Data completeness (in resolution range)	96.0 (49.98-3.10) 96.0 (49.98-3.10)	Depositor EDS
R_{merge}	0.23	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.39 (at 3.12Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.2_869)	Depositor
R, R_{free}	0.216 , 0.258 0.499 , 0.502	Depositor DCC
R_{free} test set	49855 reflections (5.02%)	DCC
Wilson B-factor (Å ²)	65.0	Xtriage
Anisotropy	0.263	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.25 , 64.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtriage
Outliers	1 of 993194 reflections (0.000%)	Xtriage
F_o, F_c correlation	0.47	EDS
Total number of atoms	50808	wwPDB-VP
Average B, all atoms (Å ²)	104.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.51% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.11	53/36028 (0.1%)	1.55	750/56231 (1.3%)
2	B	0.75	0/1809	0.79	1/2450 (0.0%)
3	C	0.78	0/1474	0.86	2/2003 (0.1%)
4	D	0.72	2/1556 (0.1%)	0.87	3/2113 (0.1%)
5	E	0.63	0/1121	0.82	1/1517 (0.1%)
6	F	0.62	0/790	0.73	0/1077
7	G	0.96	0/1183	0.90	0/1599
8	H	0.58	0/1065	0.75	0/1445
9	I	1.00	0/867	0.91	1/1180 (0.1%)
10	J	0.90	0/676	0.97	0/924
11	K	0.61	0/843	0.75	1/1144 (0.1%)
12	L	0.64	0/921	0.80	0/1247
13	M	1.03	0/814	1.03	2/1107 (0.2%)
14	N	0.77	1/487 (0.2%)	0.87	1/649 (0.2%)
15	O	0.66	0/735	0.85	0/981
16	P	0.56	0/667	0.82	0/905
17	Q	0.69	1/836 (0.1%)	0.85	0/1117
18	R	0.63	0/519	0.76	1/699 (0.1%)
19	S	0.98	0/574	0.93	0/781
20	T	0.62	0/715	0.84	1/947 (0.1%)
21	U	0.91	0/203	0.97	0/266
22	X	0.77	0/606	0.82	0/828
All	All	1.00	57/54489 (0.1%)	1.37	764/81210 (0.9%)

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	4

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Mol	Chain	#Chirality outliers	#Planarity outliers
3	C	0	1
4	D	0	1
7	G	0	2
9	I	0	1
10	J	0	2
13	M	0	2
15	O	0	1
17	Q	0	1
19	S	0	1
20	T	0	1
All	All	0	17

All (57) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1442(A)	G	N9-C4	17.19	1.51	1.38
1	A	1442(A)	G	C2-N3	14.30	1.44	1.32
1	A	1442(A)	G	N3-C4	12.97	1.44	1.35
4	D	12	CYS	CB-SG	11.03	2.00	1.82
1	A	1442(A)	G	C2-N2	8.08	1.42	1.34
1	A	1116	C	N1-C6	8.07	1.42	1.37
1	A	1492	A	N9-C4	8.06	1.42	1.37
1	A	1340	A	N9-C4	7.78	1.42	1.37
1	A	1493	A	N9-C4	7.47	1.42	1.37
1	A	1442(B)	A	N9-C4	7.33	1.42	1.37
1	A	69	G	O3'-P	-7.24	1.52	1.61
1	A	986	A	N9-C4	7.21	1.42	1.37
1	A	1333	A	N9-C4	6.97	1.42	1.37
4	D	9	CYS	CB-SG	6.96	1.94	1.82
1	A	946	A	N9-C4	6.74	1.41	1.37
1	A	1310	G	N7-C5	6.62	1.43	1.39
1	A	78	G	C6-N1	6.44	1.44	1.39
1	A	1456	G	N3-C4	6.21	1.39	1.35
1	A	1447	A	N9-C4	6.16	1.41	1.37
1	A	951	G	N9-C4	6.05	1.42	1.38
1	A	1442(A)	G	C5-C6	5.94	1.48	1.42
1	A	1243	C	N1-C6	5.91	1.40	1.37
1	A	1030(D)	A	N9-C4	5.82	1.41	1.37
1	A	1124	G	N9-C4	5.81	1.42	1.38
1	A	1004	A	N9-C4	5.74	1.41	1.37
1	A	1335	C	N1-C2	5.72	1.45	1.40
1	A	1492	A	N3-C4	5.70	1.38	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1330	U	N1-C2	5.59	1.43	1.38
1	A	1290	G	N3-C4	5.56	1.39	1.35
17	Q	49	GLU	CG-CD	5.55	1.60	1.51
1	A	1354	C	C2-N3	5.54	1.40	1.35
1	A	1001	A	N9-C4	5.54	1.41	1.37
1	A	1149	C	N1-C2	5.44	1.45	1.40
1	A	1294	G	C6-N1	5.43	1.43	1.39
1	A	1456	G	N9-C4	5.41	1.42	1.38
1	A	1180	A	N9-C4	5.41	1.41	1.37
1	A	1360	A	N9-C4	5.40	1.41	1.37
1	A	1149	C	N1-C6	5.40	1.40	1.37
1	A	1124	G	C5-C4	5.33	1.42	1.38
1	A	1377	A	N9-C4	5.27	1.41	1.37
1	A	1290	G	N9-C4	5.25	1.42	1.38
1	A	1279	A	N9-C4	5.24	1.41	1.37
1	A	1291	G	N3-C4	5.24	1.39	1.35
1	A	1370	G	C6-N1	5.24	1.43	1.39
1	A	1030(A)	G	N9-C4	5.21	1.42	1.38
1	A	1256	A	N9-C4	5.15	1.41	1.37
1	A	1332	A	C5-C4	5.14	1.42	1.38
1	A	1235	U	N1-C2	5.13	1.43	1.38
1	A	1447	A	N3-C4	5.09	1.38	1.34
1	A	839	U	N1-C2	5.08	1.43	1.38
1	A	1124	G	N3-C4	5.08	1.39	1.35
1	A	1050	G	N3-C4	5.07	1.39	1.35
1	A	1033	G	N3-C4	5.04	1.39	1.35
1	A	1333	A	C5-C4	5.04	1.42	1.38
1	A	986	A	N3-C4	5.03	1.37	1.34
14	N	43	CYS	CB-SG	-5.03	1.73	1.81
1	A	1266	G	N9-C4	5.01	1.42	1.38

All (764) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1442(A)	G	N3-C4-C5	-26.14	115.53	128.60
1	A	1442(A)	G	N3-C4-N9	25.18	141.10	126.00
1	A	1442(A)	G	N3-C2-N2	23.08	136.06	119.90
1	A	1442(A)	G	C4-N9-C1'	18.90	151.07	126.50
1	A	1149	C	N1-C2-O2	16.98	129.09	118.90
1	A	1442(A)	G	C2-N3-C4	16.91	120.35	111.90
1	A	1442(A)	G	N1-C2-N2	-16.62	101.24	116.20
1	A	1442(A)	G	C8-N9-C1'	-15.76	106.52	127.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1442(A)	G	N1-C6-O6	-13.95	111.53	119.90
1	A	1442(A)	G	C5-C6-N1	13.88	118.44	111.50
1	A	1340	A	C8-N9-C4	-12.24	100.90	105.80
1	A	1006	C	C6-N1-C2	-12.10	115.46	120.30
1	A	1003	G	C5-C6-O6	12.08	135.85	128.60
1	A	1352	C	C6-N1-C2	-11.78	115.59	120.30
1	A	979	C	C6-N1-C2	-11.59	115.66	120.30
1	A	1149	C	N3-C4-N4	-11.53	109.93	118.00
1	A	1379	G	C6-C5-N7	-11.38	123.57	130.40
1	A	1003	G	C8-N9-C4	-10.94	102.02	106.40
1	A	1149	C	C5-C4-N4	10.89	127.82	120.20
1	A	1379	G	N9-C4-C5	-10.79	101.08	105.40
1	A	1149	C	N3-C2-O2	-10.72	114.39	121.90
1	A	1266	G	C8-N9-C4	-10.65	102.14	106.40
1	A	1037	C	C2-N3-C4	10.62	125.21	119.90
1	A	1171	G	C5-C6-O6	10.42	134.85	128.60
1	A	1163	C	C6-N1-C2	-10.31	116.17	120.30
1	A	1379	G	C4-C5-N7	10.31	114.93	110.80
1	A	1379	G	N3-C4-N9	10.31	132.19	126.00
1	A	1442(A)	G	C8-N9-C4	-10.13	102.35	106.40
1	A	1063	C	C6-N1-C2	-9.95	116.32	120.30
1	A	1033	G	N3-C4-N9	9.94	131.96	126.00
1	A	458	C	C6-N1-C2	-9.93	116.33	120.30
1	A	1266	G	N7-C8-N9	9.76	117.98	113.10
1	A	1054	C	C6-N1-C2	-9.66	116.44	120.30
1	A	1006	C	C5-C6-N1	9.62	125.81	121.00
1	A	1124	G	N3-C2-N2	9.62	126.63	119.90
1	A	1335	C	N1-C2-O2	9.54	124.62	118.90
1	A	1124	G	C5-C6-O6	9.53	134.32	128.60
1	A	1379	G	C5-C6-O6	-9.45	122.93	128.60
1	A	972	C	C6-N1-C2	-9.39	116.54	120.30
1	A	1044	A	C5-C6-N6	9.39	131.21	123.70
1	A	1335	C	N3-C2-O2	-9.36	115.35	121.90
1	A	1044	A	N1-C6-N6	-9.34	112.99	118.60
1	A	1502	A	C5-N7-C8	-9.29	99.26	103.90
1	A	1116	C	C2-N3-C4	9.21	124.51	119.90
1	A	1033	G	C4-C5-N7	9.15	114.46	110.80
1	A	818	G	C4-C5-N7	-9.06	107.18	110.80
1	A	1293	G	C5-C6-N1	9.04	116.02	111.50
1	A	1030(B)	C	C6-N1-C2	-8.96	116.72	120.30
1	A	1343	G	C5-C6-O6	-8.89	123.27	128.60
1	A	634	C	C6-N1-C2	-8.88	116.75	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1456	G	C2-N3-C4	8.87	116.33	111.90
1	A	1003	G	N1-C6-O6	-8.86	114.58	119.90
1	A	435	C	N1-C2-O2	8.83	124.20	118.90
1	A	1033	G	N9-C4-C5	-8.81	101.88	105.40
1	A	910	C	C6-N1-C2	8.73	123.79	120.30
1	A	1077	G	C8-N9-C4	8.64	109.86	106.40
1	A	1379	G	N1-C6-O6	8.64	125.09	119.90
1	A	818	G	C5-C6-O6	8.62	133.78	128.60
1	A	117	G	N9-C4-C5	-8.55	101.98	105.40
1	A	1243	C	C6-N1-C2	-8.53	116.89	120.30
1	A	1340	A	N9-C4-C5	8.53	109.21	105.80
1	A	1108	G	C4-C5-N7	-8.46	107.41	110.80
1	A	1442(A)	G	N7-C8-N9	8.43	117.31	113.10
1	A	1442(A)	G	C6-N1-C2	-8.41	120.05	125.10
1	A	1343	G	N1-C6-O6	8.38	124.93	119.90
1	A	1158	C	N1-C2-O2	8.36	123.91	118.90
4	D	12	CYS	CA-CB-SG	8.36	129.04	114.00
1	A	1033	G	C5-C6-O6	-8.35	123.59	128.60
1	A	1052	U	N1-C2-O2	8.33	128.63	122.80
1	A	357	G	N1-C6-O6	-8.32	114.91	119.90
1	A	1171	G	N1-C6-O6	-8.31	114.91	119.90
1	A	1192	C	C6-N1-C2	-8.30	116.98	120.30
1	A	1230	C	C6-N1-C2	-8.30	116.98	120.30
1	A	1283	G	C8-N9-C4	-8.29	103.09	106.40
1	A	1216	G	N3-C4-C5	8.26	132.73	128.60
1	A	943	U	C5-C4-O4	8.25	130.85	125.90
1	A	839	U	N1-C2-O2	8.23	128.56	122.80
1	A	1050	G	N3-C2-N2	8.20	125.64	119.90
1	A	52	G	C5-C6-O6	8.19	133.51	128.60
1	A	1351	U	C5-C6-N1	-8.18	118.61	122.70
1	A	28	G	N1-C6-O6	8.13	124.78	119.90
1	A	1442(B)	A	N3-C4-C5	-8.08	121.14	126.80
1	A	936	C	C2-N1-C1'	8.05	127.66	118.80
1	A	1282	C	C6-N1-C2	-8.03	117.09	120.30
1	A	1305	G	N1-C6-O6	8.03	124.72	119.90
1	A	986	A	C2-N3-C4	8.03	114.61	110.60
1	A	1502	A	C6-C5-N7	-8.01	126.69	132.30
1	A	1456	G	N3-C4-N9	7.97	130.78	126.00
1	A	1039	C	N1-C2-O2	7.95	123.67	118.90
1	A	242	C	N1-C2-O2	-7.93	114.14	118.90
1	A	1081	G	N9-C4-C5	-7.92	102.23	105.40
1	A	117	G	N1-C6-O6	7.89	124.63	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	77	G	C4-C5-N7	7.88	113.95	110.80
1	A	1116	C	C5-C4-N4	7.87	125.71	120.20
1	A	1409	C	C6-N1-C2	7.86	123.44	120.30
1	A	529	G	N1-C6-O6	7.85	124.61	119.90
1	A	1442(A)	G	C6-C5-N7	-7.84	125.69	130.40
1	A	925	G	C8-N9-C4	7.79	109.52	106.40
1	A	1050	G	N3-C4-N9	7.78	130.67	126.00
1	A	1054	C	N3-C2-O2	-7.74	116.48	121.90
1	A	1033	G	C6-C5-N7	-7.73	125.76	130.40
1	A	44	G	N1-C6-O6	7.71	124.53	119.90
1	A	896	C	C6-N1-C2	7.70	123.38	120.30
1	A	1216	G	N3-C4-N9	-7.70	121.38	126.00
1	A	27	G	C5-C6-O6	-7.69	123.98	128.60
1	A	1353	G	C2-N3-C4	7.69	115.74	111.90
1	A	572	A	C8-N9-C4	7.68	108.87	105.80
1	A	1357	A	C8-N9-C4	-7.67	102.73	105.80
1	A	691	G	N9-C4-C5	-7.66	102.34	105.40
1	A	1223	C	C6-N1-C2	-7.65	117.24	120.30
1	A	1165	C	C2-N3-C4	7.65	123.72	119.90
3	C	52	LEU	CA-CB-CG	7.64	132.87	115.30
1	A	359	U	C2-N3-C4	-7.62	122.43	127.00
1	A	1502	A	C4-C5-N7	7.62	114.51	110.70
1	A	1206	G	C5-C6-O6	-7.58	124.05	128.60
1	A	1081	G	N1-C6-O6	7.56	124.44	119.90
1	A	1032	G	N3-C4-N9	-7.55	121.47	126.00
1	A	357	G	N9-C4-C5	7.53	108.41	105.40
1	A	1108	G	N1-C6-O6	-7.53	115.38	119.90
1	A	21	G	C5-C6-O6	7.52	133.12	128.60
1	A	1446	U	N1-C2-N3	-7.52	110.39	114.90
1	A	691	G	C8-N9-C4	7.49	109.40	106.40
1	A	1030	C	N1-C2-O2	7.49	123.39	118.90
1	A	1343	G	C6-C5-N7	-7.49	125.91	130.40
1	A	1003	G	N9-C4-C5	7.48	108.39	105.40
1	A	1165	C	C5-C4-N4	7.48	125.44	120.20
1	A	1184	G	C5-C6-O6	7.47	133.08	128.60
1	A	1263	C	C5-C4-N4	-7.45	114.98	120.20
1	A	1336	C	C6-N1-C2	-7.45	117.32	120.30
1	A	1108	G	C5-C6-O6	7.43	133.06	128.60
1	A	998	G	C4-C5-N7	-7.41	107.84	110.80
1	A	577	G	C8-N9-C4	7.41	109.36	106.40
1	A	972	C	C5-C6-N1	7.39	124.70	121.00
1	A	1063	C	C5-C6-N1	7.37	124.69	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	946	A	C6-N1-C2	-7.37	114.18	118.60
1	A	47	C	N3-C2-O2	7.36	127.05	121.90
1	A	1163	C	C5-C6-N1	7.35	124.68	121.00
1	A	1120	G	N3-C4-N9	-7.35	121.59	126.00
1	A	1446	U	C5-C4-O4	-7.33	121.50	125.90
1	A	1124	G	C5-C6-N1	-7.33	107.84	111.50
1	A	1231	G	N3-C4-C5	-7.33	124.94	128.60
1	A	460	G	N7-C8-N9	7.32	116.76	113.10
1	A	1352	C	N3-C2-O2	-7.32	116.78	121.90
1	A	1442	G	C5-N7-C8	7.31	107.95	104.30
1	A	1124	G	N1-C2-N2	-7.25	109.67	116.20
1	A	299	G	N3-C4-C5	7.24	132.22	128.60
1	A	1126	U	N1-C2-O2	7.24	127.86	122.80
1	A	1502	A	N1-C6-N6	7.24	122.94	118.60
1	A	1502	A	C2-N3-C4	-7.22	106.99	110.60
1	A	936	C	C5-C4-N4	-7.21	115.15	120.20
1	A	1124	G	C6-N1-C2	7.18	129.41	125.10
1	A	21	G	N1-C6-O6	-7.16	115.61	119.90
1	A	1149	C	C2-N3-C4	7.15	123.47	119.90
1	A	91	C	C5-C6-N1	7.14	124.57	121.00
1	A	1029	C	C5-C4-N4	7.14	125.20	120.20
1	A	1284	C	C6-N1-C2	-7.14	117.45	120.30
1	A	1502	A	N1-C2-N3	7.13	132.87	129.30
1	A	27	G	N1-C6-O6	7.11	124.17	119.90
1	A	839	U	C2-N1-C1'	7.11	126.24	117.70
1	A	991	U	N1-C2-O2	7.11	127.78	122.80
1	A	1024	G	C4-C5-N7	7.11	113.64	110.80
1	A	909	A	N1-C6-N6	7.11	122.87	118.60
1	A	529	G	C6-C5-N7	-7.10	126.14	130.40
1	A	936	C	C6-N1-C1'	-7.10	112.28	120.80
1	A	940	C	C5-C6-N1	7.09	124.54	121.00
1	A	681	C	C6-N1-C2	7.09	123.13	120.30
1	A	460	G	C8-N9-C4	-7.06	103.58	106.40
1	A	942	G	C5-C6-O6	7.06	132.84	128.60
1	A	163	C	N3-C4-C5	-7.05	119.08	121.90
1	A	442	C	C6-N1-C2	-7.04	117.48	120.30
1	A	1230	C	C5-C6-N1	7.03	124.51	121.00
1	A	1330	U	N1-C2-O2	7.02	127.72	122.80
1	A	1045	C	C2-N3-C4	7.02	123.41	119.90
1	A	936	C	N1-C2-O2	7.02	123.11	118.90
1	A	1321	C	N3-C4-C5	-7.01	119.10	121.90
1	A	1177	G	N7-C8-N9	7.00	116.60	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	52	G	N1-C6-O6	-7.00	115.70	119.90
1	A	117	G	C6-C5-N7	-6.99	126.21	130.40
1	A	997	U	C2-N3-C4	6.99	131.19	127.00
1	A	1350	A	C8-N9-C4	-6.98	103.01	105.80
1	A	1502	A	N7-C8-N9	6.97	117.28	113.80
1	A	357	G	C6-N1-C2	-6.96	120.93	125.10
1	A	1153	C	C2-N1-C1'	-6.95	111.15	118.80
1	A	1241	G	N7-C8-N9	6.93	116.56	113.10
1	A	1457	G	C5-C6-N1	6.92	114.96	111.50
1	A	713	G	N1-C6-O6	-6.92	115.75	119.90
1	A	721	G	N1-C6-O6	6.91	124.05	119.90
1	A	1237	C	C6-N1-C2	-6.89	117.54	120.30
1	A	1442(A)	G	C4-C5-C6	6.87	122.92	118.80
1	A	1044	A	C6-N1-C2	6.87	122.72	118.60
1	A	1160	G	N9-C4-C5	-6.87	102.65	105.40
1	A	1017	G	N1-C6-O6	-6.86	115.78	119.90
1	A	691	G	N1-C6-O6	6.83	124.00	119.90
1	A	1266	G	N3-C4-C5	-6.83	125.19	128.60
1	A	921	U	C2-N3-C4	6.83	131.10	127.00
1	A	1081	G	C8-N9-C4	6.83	109.13	106.40
1	A	365	U	C5-C6-N1	-6.81	119.29	122.70
1	A	1443	G	N9-C4-C5	-6.81	102.67	105.40
1	A	1114	C	N1-C2-O2	6.81	122.99	118.90
1	A	1357	A	N7-C8-N9	6.81	117.20	113.80
1	A	940	C	N1-C2-O2	6.81	122.98	118.90
1	A	1108	G	N3-C4-C5	-6.80	125.20	128.60
1	A	1030(B)	C	C5-C6-N1	6.80	124.40	121.00
1	A	1231	G	C5-C6-N1	6.80	114.90	111.50
1	A	1024	G	N1-C6-O6	6.79	123.97	119.90
1	A	776	G	C5-C6-N1	-6.78	108.11	111.50
1	A	1370	G	N3-C2-N2	-6.78	115.16	119.90
1	A	150	C	C5-C6-N1	6.76	124.38	121.00
1	A	1235	U	C5-C4-O4	-6.76	121.84	125.90
1	A	34	C	C6-N1-C2	6.76	123.00	120.30
1	A	818	G	N9-C4-C5	6.75	108.10	105.40
1	A	1325	C	C2-N3-C4	6.74	123.27	119.90
1	A	1158	C	C2-N1-C1'	6.71	126.18	118.80
1	A	77	G	C5-C6-O6	-6.70	124.58	128.60
1	A	1288	A	C8-N9-C4	6.67	108.47	105.80
1	A	972	C	N1-C2-O2	6.67	122.90	118.90
1	A	1029	C	C2-N3-C4	6.67	123.23	119.90
1	A	361	G	N1-C6-O6	6.66	123.90	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1030(A)	G	C2-N3-C4	6.65	115.23	111.90
1	A	1378	C	C6-N1-C2	-6.65	117.64	120.30
1	A	953	G	C8-N9-C4	6.64	109.06	106.40
1	A	1166	G	C4-C5-N7	-6.63	108.15	110.80
1	A	1231	G	C2-N3-C4	6.63	115.22	111.90
1	A	979	C	C5-C6-N1	6.63	124.31	121.00
1	A	484	G	N1-C6-O6	-6.62	115.93	119.90
1	A	357	G	C5-C6-N1	6.62	114.81	111.50
1	A	831	U	C6-N1-C2	-6.62	117.03	121.00
1	A	1443	G	C5-C6-O6	-6.61	124.63	128.60
1	A	1206	G	N3-C4-N9	6.61	129.96	126.00
1	A	1210	C	N1-C2-O2	6.60	122.86	118.90
1	A	932	C	C2-N1-C1'	6.59	126.06	118.80
1	A	1192	C	C5-C6-N1	6.58	124.29	121.00
1	A	1003	G	N7-C8-N9	6.58	116.39	113.10
1	A	951	G	N3-C4-C5	-6.58	125.31	128.60
1	A	1050	G	N9-C4-C5	-6.57	102.77	105.40
1	A	1392	G	N1-C2-N2	-6.55	110.31	116.20
1	A	979	C	C2-N1-C1'	6.54	126.00	118.80
1	A	102	G	C8-N9-C4	-6.53	103.79	106.40
1	A	1284	C	N3-C4-C5	-6.52	119.29	121.90
1	A	117	G	N3-C4-N9	6.51	129.91	126.00
1	A	1270	C	C5-C6-N1	6.51	124.25	121.00
1	A	1382	C	N1-C2-O2	6.51	122.80	118.90
1	A	54	C	C2-N3-C4	-6.48	116.66	119.90
1	A	1178	G	N7-C8-N9	6.48	116.34	113.10
1	A	1325	C	N1-C2-O2	6.48	122.79	118.90
1	A	1056	U	N3-C4-C5	-6.47	110.72	114.60
1	A	839	U	N3-C2-O2	-6.47	117.67	122.20
1	A	1120	G	N9-C4-C5	6.47	107.99	105.40
1	A	1185	G	C4-C5-N7	-6.47	108.21	110.80
1	A	1166	G	C4-N9-C1'	-6.47	118.09	126.50
1	A	1305	G	C5-C6-N1	-6.46	108.27	111.50
1	A	1442(B)	A	C4-N9-C1'	6.46	137.92	126.30
1	A	352	C	N1-C2-O2	6.45	122.77	118.90
1	A	1024	G	C6-C5-N7	-6.43	126.54	130.40
1	A	322	C	C6-N1-C2	6.42	122.87	120.30
1	A	1367	C	C6-N1-C2	-6.42	117.73	120.30
1	A	117	G	C4-C5-N7	6.41	113.36	110.80
1	A	1241	G	N3-C4-N9	6.41	129.84	126.00
1	A	330	C	C6-N1-C2	-6.40	117.74	120.30
1	A	1024	G	N7-C8-N9	6.38	116.29	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	295	C	C6-N1-C2	6.38	122.85	120.30
1	A	163	C	C6-N1-C2	-6.37	117.75	120.30
1	A	1232	U	C6-N1-C2	-6.37	117.18	121.00
1	A	1178	G	C8-N9-C4	-6.36	103.85	106.40
1	A	1330	U	C2-N1-C1'	6.35	125.32	117.70
1	A	971	G	C8-N9-C4	-6.34	103.86	106.40
1	A	976	G	C4-N9-C1'	-6.34	118.26	126.50
1	A	1194	U	C6-N1-C2	-6.31	117.21	121.00
1	A	1267	C	C6-N1-C2	-6.31	117.78	120.30
1	A	73	G	C5-C6-O6	-6.30	124.82	128.60
1	A	721	G	C5-C6-N1	-6.30	108.35	111.50
1	A	1166	G	C5-C6-O6	6.29	132.38	128.60
1	A	888	G	C5-C6-O6	6.29	132.37	128.60
1	A	1148	U	C5-C6-N1	6.29	125.84	122.70
1	A	117	G	C5-C6-O6	-6.27	124.83	128.60
1	A	435	C	N3-C2-O2	-6.27	117.51	121.90
1	A	976	G	N3-C4-N9	-6.27	122.24	126.00
1	A	1017	G	C6-C5-N7	6.26	134.16	130.40
1	A	1379	G	C8-N9-C1'	-6.26	118.86	127.00
1	A	495	A	N1-C6-N6	-6.26	114.85	118.60
1	A	1443	G	C4-C5-N7	6.26	113.30	110.80
1	A	1060	C	C6-N1-C2	-6.25	117.80	120.30
1	A	1076	C	C6-N1-C2	6.25	122.80	120.30
1	A	765	G	C8-N9-C4	-6.25	103.90	106.40
1	A	1047	G	C6-N1-C2	6.24	128.84	125.10
1	A	1235	U	C2-N3-C4	-6.24	123.26	127.00
1	A	63	C	C6-N1-C2	-6.23	117.81	120.30
1	A	866	C	N3-C4-C5	-6.21	119.42	121.90
1	A	1246	C	C5-C6-N1	6.21	124.11	121.00
1	A	1301	U	C6-N1-C2	-6.21	117.27	121.00
1	A	1184	G	C6-N1-C2	6.21	128.83	125.10
1	A	963	G	N3-C4-N9	6.21	129.72	126.00
1	A	998	G	N9-C4-C5	6.21	107.88	105.40
1	A	1343	G	C4-C5-N7	6.21	113.28	110.80
1	A	1119	C	C6-N1-C2	-6.21	117.82	120.30
1	A	976	G	N3-C4-C5	6.21	131.70	128.60
1	A	1340	A	N7-C8-N9	6.21	116.90	113.80
1	A	529	G	C5-C6-O6	-6.20	124.88	128.60
1	A	770	C	C5-C6-N1	-6.20	117.90	121.00
1	A	1042	G	C6-C5-N7	6.19	134.12	130.40
1	A	1343	G	N3-C4-N9	6.19	129.72	126.00
1	A	1442(B)	A	C4-C5-C6	6.17	120.09	117.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	954	G	C8-N9-C4	6.17	108.87	106.40
1	A	1527	C	C6-N1-C2	6.17	122.77	120.30
1	A	358	U	N1-C2-N3	6.17	118.60	114.90
1	A	818	G	N1-C6-O6	-6.16	116.20	119.90
1	A	39	G	C4-C5-N7	-6.16	108.34	110.80
1	A	1009	G	N1-C6-O6	6.15	123.59	119.90
1	A	1246	C	N1-C2-O2	6.15	122.59	118.90
1	A	1392	G	N3-C2-N2	6.15	124.20	119.90
1	A	1214	C	N3-C4-C5	-6.14	119.44	121.90
1	A	1231	G	C6-N1-C2	-6.14	121.42	125.10
1	A	804	U	C5-C6-N1	-6.13	119.63	122.70
1	A	458	C	N3-C2-O2	-6.13	117.61	121.90
1	A	1286	A	N1-C2-N3	6.13	132.36	129.30
1	A	1333	A	C8-N9-C4	-6.12	103.35	105.80
1	A	444	C	C6-N1-C2	6.11	122.74	120.30
1	A	1008	C	N3-C4-N4	6.10	122.27	118.00
1	A	1165	C	N3-C4-C5	-6.10	119.46	121.90
1	A	1283	G	N1-C6-O6	-6.10	116.24	119.90
1	A	1131	G	C8-N9-C4	6.10	108.84	106.40
1	A	1277	C	C5-C4-N4	6.10	124.47	120.20
1	A	1004	A	C8-N9-C4	-6.10	103.36	105.80
1	A	557	G	N3-C4-C5	-6.09	125.55	128.60
1	A	1166	G	C6-C5-N7	6.09	134.06	130.40
1	A	1171	G	C6-N1-C2	6.09	128.75	125.10
1	A	1456	G	N3-C4-C5	-6.09	125.56	128.60
1	A	1314	C	N1-C2-O2	6.08	122.55	118.90
1	A	1330	U	N3-C2-O2	-6.07	117.95	122.20
1	A	1030	C	N3-C2-O2	-6.07	117.65	121.90
1	A	741	G	C8-N9-C4	6.06	108.82	106.40
1	A	1266	G	C2-N3-C4	6.06	114.93	111.90
1	A	1322	C	C6-N1-C2	-6.05	117.88	120.30
1	A	1267	C	C5-C6-N1	6.05	124.03	121.00
1	A	836	G	C5-C6-O6	-6.04	124.98	128.60
1	A	1442	G	C8-N9-C1'	-6.04	119.15	127.00
1	A	1033	G	N3-C2-N2	6.03	124.12	119.90
1	A	940	C	C2-N1-C1'	6.03	125.43	118.80
1	A	1008	C	C5-C4-N4	-6.03	115.98	120.20
1	A	1379	G	C4-N9-C1'	6.03	134.34	126.50
1	A	901	A	C2-N3-C4	-6.02	107.59	110.60
1	A	365	U	C2-N1-C1'	-6.02	110.48	117.70
1	A	946	A	N1-C6-N6	-6.01	114.99	118.60
1	A	1096	C	N3-C4-C5	6.01	124.31	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1158	C	N3-C2-O2	-6.01	117.69	121.90
1	A	1293	G	N3-C4-N9	6.01	129.61	126.00
1	A	1320	C	N3-C2-O2	-6.01	117.69	121.90
1	A	986	A	C5-C6-N1	6.00	120.70	117.70
1	A	1081	G	C4-C5-N7	6.00	113.20	110.80
1	A	1028	C	C2-N3-C4	6.00	122.90	119.90
1	A	1417	G	N3-C4-N9	5.99	129.60	126.00
1	A	1442(B)	A	C8-N9-C4	-5.99	103.40	105.80
1	A	1133	G	C4-C5-N7	-5.99	108.40	110.80
1	A	122	G	N1-C6-O6	5.99	123.49	119.90
1	A	1121	U	C5-C6-N1	5.99	125.69	122.70
1	A	1045	C	N1-C2-O2	5.99	122.49	118.90
1	A	204	U	C5-C6-N1	5.99	125.69	122.70
1	A	1487	G	C2-N3-C4	-5.98	108.91	111.90
1	A	1277	C	C6-N1-C2	-5.97	117.91	120.30
1	A	376	G	N1-C6-O6	5.97	123.48	119.90
1	A	1154	G	C4-C5-N7	-5.97	108.41	110.80
1	A	831	U	N1-C2-N3	5.96	118.47	114.90
1	A	972	C	N3-C2-O2	-5.95	117.74	121.90
1	A	420	U	C6-N1-C2	-5.94	117.44	121.00
1	A	1234	C	N1-C2-O2	5.94	122.46	118.90
1	A	1081	G	C2-N3-C4	-5.94	108.93	111.90
1	A	1108	G	N9-C4-C5	5.94	107.77	105.40
1	A	1456	G	N3-C2-N2	5.94	124.06	119.90
1	A	1148	U	C6-N1-C2	-5.93	117.44	121.00
1	A	944	G	N3-C4-N9	5.93	129.56	126.00
1	A	1320	C	C6-N1-C2	-5.93	117.93	120.30
1	A	1274	G	N1-C6-O6	5.92	123.45	119.90
1	A	1297	C	N3-C4-C5	-5.92	119.53	121.90
1	A	433	C	C5-C6-N1	-5.91	118.05	121.00
1	A	1071	C	C6-N1-C2	-5.91	117.94	120.30
1	A	1342	C	N1-C2-O2	5.90	122.44	118.90
1	A	1024	G	C5-C6-O6	-5.89	125.07	128.60
1	A	1153	C	C6-N1-C1'	5.89	127.87	120.80
1	A	721	G	C6-C5-N7	-5.88	126.87	130.40
1	A	1312	G	C6-N1-C2	5.88	128.63	125.10
1	A	240	C	C5-C6-N1	-5.87	118.06	121.00
1	A	1042	G	N1-C2-N2	5.87	121.49	116.20
1	A	1270	C	C6-N1-C2	-5.87	117.95	120.30
2	B	129	GLU	N-CA-C	-5.87	95.16	111.00
1	A	317	G	N1-C6-O6	5.86	123.42	119.90
1	A	1120	G	N3-C2-N2	-5.86	115.80	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	M	70	LEU	CA-CB-CG	5.86	128.77	115.30
1	A	357	G	C8-N9-C4	-5.85	104.06	106.40
1	A	982	U	C5-C6-N1	5.85	125.63	122.70
1	A	1282	C	C2-N1-C1'	5.85	125.24	118.80
1	A	1030(A)	G	N3-C4-C5	-5.85	125.67	128.60
1	A	307	C	C6-N1-C2	-5.85	117.96	120.30
1	A	880	C	C6-N1-C2	5.84	122.64	120.30
1	A	1367	C	N1-C2-O2	5.84	122.40	118.90
1	A	577	G	N3-C4-C5	5.84	131.52	128.60
1	A	1351	U	C6-N1-C2	5.84	124.50	121.00
1	A	1008	C	C5-C6-N1	5.84	123.92	121.00
1	A	1354	C	C6-N1-C2	-5.83	117.97	120.30
1	A	1064	G	C8-N9-C4	-5.83	104.07	106.40
1	A	1254	C	C4-C5-C6	5.83	120.32	117.40
13	M	56	LEU	CA-CB-CG	5.83	128.71	115.30
1	A	610	G	C8-N9-C1'	-5.83	119.42	127.00
1	A	1306	A	C8-N9-C4	-5.82	103.47	105.80
1	A	304	U	C5-C4-O4	5.82	129.39	125.90
1	A	1306	A	N7-C8-N9	5.82	116.71	113.80
1	A	1145	C	C5-C4-N4	5.80	124.26	120.20
1	A	1183	A	C8-N9-C4	-5.80	103.48	105.80
1	A	1272	G	N9-C4-C5	-5.80	103.08	105.40
1	A	749	C	C6-N1-C2	-5.80	117.98	120.30
1	A	993	G	N3-C4-C5	-5.80	125.70	128.60
1	A	1031	G	C8-N9-C4	-5.80	104.08	106.40
1	A	1405	G	N3-C2-N2	5.80	123.96	119.90
1	A	1008	C	C2-N1-C1'	5.80	125.18	118.80
1	A	610	G	C4-N9-C1'	5.78	134.02	126.50
1	A	1024	G	C5-N7-C8	-5.78	101.41	104.30
1	A	982	U	C6-N1-C2	-5.78	117.53	121.00
18	R	85	LEU	CA-CB-CG	5.78	128.59	115.30
1	A	1160	G	C5-C6-O6	-5.78	125.13	128.60
1	A	1442(B)	A	N3-C4-N9	5.77	132.02	127.40
1	A	1442(B)	A	C6-N1-C2	-5.77	115.14	118.60
1	A	1273	G	N7-C8-N9	5.76	115.98	113.10
1	A	1350	A	N7-C8-N9	5.76	116.68	113.80
1	A	359	U	C5-C6-N1	-5.76	119.82	122.70
1	A	998	G	N3-C2-N2	-5.75	115.87	119.90
1	A	1182	G	N3-C4-N9	-5.75	122.55	126.00
1	A	952	U	C5-C4-O4	5.75	129.35	125.90
1	A	1116	C	N3-C4-N4	-5.75	113.97	118.00
1	A	950	U	N3-C2-O2	-5.75	118.17	122.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1114	C	N3-C2-O2	-5.75	117.88	121.90
1	A	292	G	N3-C4-C5	-5.74	125.73	128.60
1	A	1293	G	N9-C4-C5	-5.74	103.10	105.40
1	A	1077	G	N7-C8-N9	-5.74	110.23	113.10
1	A	1163	C	C2-N3-C4	5.74	122.77	119.90
1	A	1124	G	C4-N9-C1'	5.74	133.96	126.50
1	A	1353	G	N3-C4-C5	-5.73	125.73	128.60
1	A	980	C	N3-C4-N4	-5.73	113.99	118.00
1	A	67	C	C6-N1-C2	-5.73	118.01	120.30
1	A	204	U	C2-N1-C1'	5.73	124.57	117.70
1	A	1054	C	N1-C2-O2	5.72	122.33	118.90
1	A	1352	C	N1-C2-N3	5.72	123.20	119.20
1	A	1171	G	C8-N9-C4	-5.72	104.11	106.40
1	A	357	G	C2-N3-C4	5.72	114.76	111.90
1	A	691	G	C5-C6-O6	-5.71	125.17	128.60
1	A	1284	C	C2-N3-C4	5.71	122.75	119.90
1	A	1493	A	C8-N9-C4	-5.71	103.52	105.80
1	A	323	U	C5-C6-N1	5.70	125.55	122.70
1	A	7	G	N3-C4-C5	5.70	131.45	128.60
1	A	972	C	C2-N1-C1'	5.70	125.07	118.80
1	A	1017	G	C5-C6-O6	5.70	132.02	128.60
1	A	1367	C	N3-C2-O2	-5.70	117.91	121.90
1	A	638	G	C8-N9-C4	5.70	108.68	106.40
1	A	1443	G	N3-C4-N9	5.69	129.41	126.00
1	A	615	C	C6-N1-C2	-5.69	118.03	120.30
1	A	979	C	N3-C4-C5	-5.69	119.62	121.90
1	A	1243	C	C6-N1-C1'	5.68	127.62	120.80
1	A	1249	C	C6-N1-C2	-5.68	118.03	120.30
1	A	1378	C	C5-C6-N1	5.68	123.84	121.00
1	A	1514	C	C6-N1-C2	-5.68	118.03	120.30
1	A	1232	U	C5-C6-N1	5.68	125.54	122.70
1	A	358	U	N3-C4-O4	-5.67	115.43	119.40
1	A	403	C	C2-N3-C4	-5.67	117.06	119.90
1	A	53	A	C6-N1-C2	-5.66	115.20	118.60
1	A	1441	G	C8-N9-C4	-5.66	104.14	106.40
1	A	1390	U	N1-C2-O2	-5.66	118.84	122.80
1	A	1006	C	N1-C2-O2	-5.65	115.51	118.90
1	A	455	C	C5-C6-N1	5.65	123.83	121.00
1	A	694	A	N1-C6-N6	5.65	121.99	118.60
1	A	951	G	N3-C4-N9	5.65	129.39	126.00
1	A	940	C	C6-N1-C2	-5.64	118.04	120.30
1	A	1029	C	N3-C4-C5	-5.64	119.64	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1165	C	N1-C2-O2	5.63	122.28	118.90
1	A	1171	G	N7-C8-N9	5.63	115.92	113.10
1	A	361	G	C5-C6-N1	-5.63	108.69	111.50
1	A	976	G	C8-N9-C1'	5.63	134.31	127.00
1	A	1021	G	C5-C6-O6	-5.62	125.23	128.60
1	A	986	A	C5-C6-N6	-5.62	119.20	123.70
1	A	713	G	C5-C6-N1	5.62	114.31	111.50
1	A	438	G	N3-C4-N9	5.60	129.36	126.00
1	A	150	C	C6-N1-C2	-5.60	118.06	120.30
1	A	1362	C	N1-C2-O2	5.60	122.26	118.90
1	A	1457	G	C5-C6-O6	-5.59	125.24	128.60
1	A	286	G	N1-C6-O6	-5.59	116.54	119.90
1	A	1420	C	C6-N1-C2	-5.59	118.06	120.30
1	A	998	G	C6-C5-N7	5.59	133.75	130.40
1	A	1032	G	C5-C6-O6	5.59	131.95	128.60
1	A	1385	G	N1-C6-O6	5.58	123.25	119.90
1	A	1456	G	N1-C2-N3	-5.58	120.55	123.90
1	A	1133	G	N9-C4-C5	5.58	107.63	105.40
1	A	1230	C	N1-C2-O2	5.58	122.25	118.90
1	A	1497	G	C8-N9-C4	-5.58	104.17	106.40
1	A	1232	U	N3-C4-O4	5.58	123.30	119.40
1	A	358	U	C5-C4-O4	5.57	129.24	125.90
1	A	571	U	C5-C6-N1	5.57	125.49	122.70
1	A	485	G	C4-N9-C1'	-5.57	119.26	126.50
1	A	1317	C	N1-C2-O2	5.57	122.24	118.90
1	A	1177	G	C8-N9-C4	-5.57	104.17	106.40
1	A	1343	G	C4-N9-C1'	5.56	133.73	126.50
1	A	1241	G	C6-C5-N7	-5.56	127.06	130.40
1	A	1254	C	N1-C2-O2	-5.56	115.56	118.90
1	A	1163	C	N3-C4-C5	-5.56	119.68	121.90
1	A	901	A	N1-C6-N6	5.55	121.93	118.60
1	A	1216	G	C4-N9-C1'	-5.55	119.29	126.50
1	A	252	U	C5-C6-N1	-5.54	119.93	122.70
1	A	792	A	C8-N9-C4	5.54	108.02	105.80
1	A	1120	G	N1-C2-N2	5.54	121.19	116.20
1	A	946	A	C5-C6-N1	5.54	120.47	117.70
1	A	1328	C	C6-N1-C2	5.54	122.52	120.30
1	A	1241	G	C4-N9-C1'	5.54	133.70	126.50
1	A	942	G	C4-C5-N7	-5.53	108.59	110.80
1	A	1283	G	N7-C8-N9	5.53	115.87	113.10
1	A	782	A	C8-N9-C4	-5.53	103.59	105.80
1	A	1160	G	C4-C5-N7	5.53	113.01	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1442	G	N3-C4-N9	5.53	129.31	126.00
1	A	171	A	N9-C4-C5	5.52	108.01	105.80
1	A	809	G	C8-N9-C4	5.52	108.61	106.40
1	A	78	G	N1-C6-O6	5.52	123.21	119.90
1	A	359	U	N1-C2-N3	5.52	118.21	114.90
1	A	925	G	N9-C4-C5	-5.52	103.19	105.40
1	A	1032	G	N3-C4-C5	5.52	131.36	128.60
1	A	1057	G	C5-C6-O6	-5.51	125.29	128.60
1	A	1182	G	C8-N9-C1'	5.51	134.16	127.00
1	A	1323	G	N7-C8-N9	5.51	115.85	113.10
1	A	960	U	C6-N1-C2	-5.50	117.70	121.00
1	A	1277	C	C2-N3-C4	5.49	122.65	119.90
1	A	569	C	N1-C2-O2	5.49	122.19	118.90
1	A	925	G	N1-C6-O6	5.49	123.19	119.90
1	A	1101	A	N1-C6-N6	-5.49	115.31	118.60
1	A	1032	G	C6-N1-C2	5.49	128.39	125.10
1	A	71	C	C6-N1-C2	-5.48	118.11	120.30
1	A	1340	A	N1-C6-N6	-5.48	115.31	118.60
1	A	1237	C	C2-N3-C4	5.47	122.64	119.90
1	A	1320	C	N1-C2-O2	5.47	122.18	118.90
1	A	240	C	C2-N3-C4	-5.47	117.17	119.90
1	A	1031	G	C2-N3-C4	5.47	114.64	111.90
1	A	1166	G	N1-C6-O6	-5.47	116.62	119.90
1	A	1228	C	C2-N3-C4	5.47	122.63	119.90
1	A	443	C	N1-C2-O2	5.46	122.18	118.90
1	A	896	C	C5-C6-N1	-5.46	118.27	121.00
1	A	356	A	C2-N3-C4	5.46	113.33	110.60
1	A	1305	G	N3-C4-C5	5.46	131.33	128.60
1	A	105	G	N9-C4-C5	5.46	107.58	105.40
1	A	1326	C	C2-N3-C4	5.46	122.63	119.90
1	A	28	G	C5-C6-O6	-5.46	125.33	128.60
1	A	509	A	C8-N9-C4	-5.45	103.62	105.80
1	A	1301	U	N3-C4-C5	-5.45	111.33	114.60
1	A	812	C	C6-N1-C2	5.44	122.48	120.30
1	A	78	G	C5-C6-N1	-5.44	108.78	111.50
1	A	1241	G	C8-N9-C4	-5.44	104.22	106.40
1	A	1322	C	C5-C6-N1	5.44	123.72	121.00
1	A	936	C	N3-C4-N4	5.43	121.80	118.00
1	A	77	G	N9-C4-C5	-5.43	103.23	105.40
1	A	553	A	C8-N9-C4	-5.42	103.63	105.80
1	A	1145	C	C2-N3-C4	5.42	122.61	119.90
1	A	1238	A	C5-N7-C8	5.41	106.61	103.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	610	G	N3-C4-N9	5.41	129.25	126.00
1	A	841	U	C5-C6-N1	5.41	125.40	122.70
1	A	1045	C	C5-C6-N1	5.41	123.70	121.00
1	A	1099	G	C8-N9-C4	-5.40	104.24	106.40
1	A	43	C	C2-N3-C4	5.40	122.60	119.90
1	A	261	U	C2-N1-C1'	-5.40	111.22	117.70
1	A	1246	C	C2-N1-C1'	5.39	124.73	118.80
1	A	1361	G	N3-C4-C5	-5.39	125.91	128.60
1	A	1467	G	C8-N9-C4	-5.38	104.25	106.40
1	A	791	G	N1-C6-O6	5.38	123.13	119.90
1	A	381	C	N3-C4-C5	-5.38	119.75	121.90
1	A	1235	U	N3-C2-O2	-5.38	118.43	122.20
1	A	1361	G	N1-C6-O6	-5.38	116.67	119.90
1	A	79	G	C5-C6-O6	-5.38	125.37	128.60
1	A	1216	G	C8-N9-C1'	5.38	133.99	127.00
1	A	226	G	C8-N9-C4	5.38	108.55	106.40
1	A	260	G	N3-C4-N9	-5.38	122.78	126.00
1	A	1182	G	N1-C2-N2	5.37	121.03	116.20
1	A	11	G	N1-C6-O6	5.37	123.12	119.90
1	A	171	A	C8-N9-C4	-5.37	103.65	105.80
1	A	1163	C	C2-N1-C1'	5.36	124.70	118.80
1	A	346	G	C4-N9-C1'	5.36	133.47	126.50
1	A	1231	G	C8-N9-C4	-5.36	104.26	106.40
1	A	49	U	C5-C6-N1	-5.35	120.03	122.70
1	A	370	C	C6-N1-C2	5.34	122.44	120.30
1	A	1141	C	N1-C2-O2	-5.34	115.69	118.90
5	E	71	LEU	CA-CB-CG	5.34	127.58	115.30
1	A	1160	G	C5-C6-N1	5.34	114.17	111.50
1	A	577	G	N9-C4-C5	-5.33	103.27	105.40
1	A	984	C	N3-C4-N4	5.33	121.73	118.00
1	A	1120	G	C6-C5-N7	5.33	133.60	130.40
1	A	266	G	C2-N3-C4	-5.32	109.24	111.90
1	A	982	U	N3-C4-O4	5.32	123.13	119.40
1	A	1031	G	N3-C4-C5	-5.32	125.94	128.60
14	N	43	CYS	CA-CB-SG	-5.32	104.43	114.00
1	A	1351	U	C2-N1-C1'	-5.32	111.32	117.70
1	A	1000	U	C6-N1-C2	-5.31	117.81	121.00
1	A	1468	A	C8-N9-C4	5.31	107.92	105.80
1	A	150	C	C2-N3-C4	5.31	122.55	119.90
1	A	611	A	N1-C6-N6	-5.31	115.42	118.60
1	A	1060	C	C5-C6-N1	5.30	123.65	121.00
1	A	981	U	N3-C4-O4	5.30	123.11	119.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	7	G	N3-C4-N9	-5.30	122.82	126.00
1	A	454	C	C4-C5-C6	5.30	120.05	117.40
1	A	1258	G	C6-N1-C2	5.30	128.28	125.10
1	A	675	A	N1-C6-N6	5.29	121.78	118.60
1	A	927	G	N1-C6-O6	5.29	123.08	119.90
1	A	1003	G	C6-N1-C2	5.29	128.27	125.10
1	A	1150	U	C5-C4-O4	5.29	129.07	125.90
1	A	102	G	N9-C4-C5	5.29	107.51	105.40
1	A	163	C	C2-N1-C1'	5.28	124.61	118.80
1	A	1166	G	C8-N9-C1'	5.28	133.86	127.00
1	A	78	G	N3-C4-C5	5.27	131.24	128.60
1	A	1009	G	C5-C6-O6	-5.27	125.44	128.60
1	A	954	G	N9-C4-C5	-5.27	103.29	105.40
1	A	1006	C	N3-C4-N4	5.27	121.69	118.00
1	A	1467	G	N3-C4-C5	-5.27	125.97	128.60
4	D	26	CYS	CA-CB-SG	5.27	123.48	114.00
1	A	419	C	N3-C2-O2	5.27	125.59	121.90
1	A	1333	A	N7-C8-N9	5.27	116.43	113.80
1	A	893	C	C6-N1-C2	5.26	122.40	120.30
1	A	1350	A	C4-C5-C6	5.26	119.63	117.00
1	A	260	G	N3-C4-C5	5.26	131.23	128.60
1	A	1370	G	N3-C4-N9	-5.26	122.85	126.00
1	A	413	G	C4-C5-N7	-5.25	108.70	110.80
1	A	631	G	N1-C6-O6	5.25	123.05	119.90
1	A	1185	G	C2-N3-C4	5.25	114.53	111.90
1	A	1343	G	N9-C4-C5	-5.25	103.30	105.40
1	A	1293	G	C8-N9-C4	5.25	108.50	106.40
1	A	982	U	N3-C4-C5	-5.25	111.45	114.60
1	A	1492	A	C2-N3-C4	5.25	113.22	110.60
1	A	190	U	C5-C6-N1	5.24	125.32	122.70
1	A	1014	A	N7-C8-N9	5.24	116.42	113.80
1	A	1330	U	C6-N1-C2	-5.24	117.86	121.00
1	A	984	C	C5-C6-N1	5.24	123.62	121.00
1	A	1293	G	C6-N1-C2	-5.24	121.96	125.10
1	A	981	U	C5-C6-N1	5.24	125.32	122.70
1	A	484	G	C5-C6-O6	5.23	131.74	128.60
1	A	1165	C	C6-N1-C1'	5.23	127.07	120.80
1	A	39	G	C6-N1-C2	-5.22	121.97	125.10
1	A	1081	G	C6-C5-N7	-5.22	127.27	130.40
1	A	1315	U	C6-N1-C2	-5.22	117.87	121.00
1	A	776	G	N3-C4-N9	-5.21	122.87	126.00
1	A	361	G	C6-N1-C2	5.21	128.22	125.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1182	G	N3-C2-N2	-5.20	116.26	119.90
1	A	1206	G	C6-N1-C2	-5.20	121.98	125.10
1	A	823	G	C8-N9-C4	5.20	108.48	106.40
1	A	1182	G	C4-N9-C1'	-5.20	119.74	126.50
1	A	1120	G	C4-C5-N7	-5.20	108.72	110.80
1	A	1350	A	N1-C2-N3	5.20	131.90	129.30
1	A	1405	G	N3-C4-N9	5.19	129.12	126.00
1	A	96	U	N1-C2-N3	-5.19	111.78	114.90
1	A	1262	C	C6-N1-C1'	-5.19	114.57	120.80
1	A	502	G	C8-N9-C4	-5.19	104.32	106.40
1	A	1187	G	N1-C6-O6	5.19	123.01	119.90
1	A	240	C	N3-C4-N4	-5.19	114.37	118.00
1	A	932	C	N1-C2-O2	5.19	122.01	118.90
1	A	1093	A	N9-C4-C5	-5.18	103.73	105.80
4	D	26	CYS	N-CA-C	-5.18	97.00	111.00
1	A	1500	A	C8-N9-C4	-5.18	103.73	105.80
1	A	1127	G	C5-C6-O6	5.18	131.71	128.60
1	A	324	G	N3-C4-C5	-5.18	126.01	128.60
1	A	557	G	N3-C4-N9	5.18	129.11	126.00
1	A	1037	C	N1-C2-N3	-5.18	115.58	119.20
3	C	175	LEU	CA-CB-CG	5.18	127.20	115.30
1	A	1120	G	C8-N9-C1'	5.17	133.73	127.00
1	A	1267	C	C2-N3-C4	5.17	122.49	119.90
1	A	543	C	C2-N3-C4	5.17	122.48	119.90
1	A	1325	C	N3-C4-C5	-5.17	119.83	121.90
1	A	1189	C	N3-C4-N4	-5.17	114.38	118.00
1	A	1382	C	N3-C2-O2	-5.17	118.28	121.90
1	A	1249	C	C5-C6-N1	5.17	123.58	121.00
1	A	936	C	C5-C6-N1	5.16	123.58	121.00
1	A	1223	C	N3-C4-C5	-5.16	119.83	121.90
9	I	96	LEU	N-CA-C	5.16	124.93	111.00
1	A	749	C	C6-N1-C1'	5.16	126.99	120.80
1	A	966	G	N7-C8-N9	5.16	115.68	113.10
1	A	1443	G	C5-C6-N1	5.16	114.08	111.50
1	A	1312	G	N1-C6-O6	5.15	122.99	119.90
1	A	1284	C	C5-C6-N1	5.15	123.58	121.00
1	A	43	C	N3-C2-O2	5.15	125.50	121.90
1	A	1176	A	N1-C6-N6	-5.15	115.51	118.60
1	A	1052	U	N1-C2-N3	-5.14	111.81	114.90
1	A	1467	G	N9-C4-C5	5.14	107.46	105.40
1	A	986	A	N3-C4-N9	5.14	131.51	127.40
1	A	304	U	C6-N1-C2	-5.14	117.92	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1206	G	N3-C4-C5	-5.14	126.03	128.60
1	A	365	U	N3-C4-O4	-5.13	115.81	119.40
1	A	575	G	C8-N9-C4	5.13	108.45	106.40
1	A	689	C	C6-N1-C2	-5.13	118.25	120.30
1	A	1270	C	N1-C2-O2	5.13	121.98	118.90
1	A	1330	U	C5-C6-N1	5.13	125.27	122.70
1	A	44	G	C5-C6-N1	-5.13	108.93	111.50
1	A	1108	G	C5-N7-C8	5.13	106.86	104.30
1	A	1241	G	N3-C4-C5	-5.13	126.03	128.60
1	A	1442(A)	G	N9-C4-C5	-5.13	103.35	105.40
1	A	1442(B)	A	C2-N3-C4	5.12	113.16	110.60
1	A	1028	C	C5-C6-N1	5.12	123.56	121.00
1	A	77	G	C6-C5-N7	-5.12	127.33	130.40
1	A	357	G	C6-C5-N7	5.12	133.47	130.40
1	A	365	U	C5-C4-O4	5.12	128.97	125.90
1	A	1002	G	C8-N9-C4	-5.12	104.35	106.40
1	A	1253	G	C5-C6-O6	5.11	131.67	128.60
1	A	380	G	N3-C4-N9	-5.11	122.93	126.00
1	A	1277	C	C6-N1-C1'	5.11	126.93	120.80
1	A	1116	C	C5-C6-N1	5.11	123.55	121.00
1	A	1160	G	N3-C4-N9	5.11	129.06	126.00
1	A	681	C	N1-C2-N3	-5.11	115.63	119.20
1	A	1004	A	N3-C4-C5	-5.11	123.23	126.80
1	A	1301	U	C5-C4-O4	5.11	128.96	125.90
1	A	1045	C	C6-N1-C2	-5.10	118.26	120.30
1	A	1241	G	C4-C5-N7	5.10	112.84	110.80
1	A	355	C	N1-C2-O2	-5.10	115.84	118.90
1	A	618	C	C6-N1-C2	-5.10	118.26	120.30
1	A	1153	C	C5-C6-N1	-5.10	118.45	121.00
11	K	118	GLY	N-CA-C	5.10	125.84	113.10
1	A	242	C	N3-C2-O2	5.09	125.47	121.90
1	A	1262	C	C2-N1-C1'	5.09	124.40	118.80
1	A	697	U	C5-C6-N1	-5.09	120.15	122.70
1	A	1297	C	C6-N1-C2	-5.09	118.26	120.30
1	A	60	A	C8-N9-C4	-5.09	103.76	105.80
1	A	65	U	C5-C6-N1	5.09	125.25	122.70
1	A	204	U	N1-C2-O2	5.09	126.36	122.80
1	A	390	C	C2-N3-C4	-5.09	117.36	119.90
1	A	514	C	C5-C6-N1	5.08	123.54	121.00
1	A	1124	G	C8-N9-C1'	-5.08	120.39	127.00
1	A	1249	C	N1-C2-O2	5.08	121.95	118.90
1	A	1340	A	N3-C4-C5	-5.08	123.24	126.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	993	G	N3-C4-N9	5.08	129.05	126.00
1	A	982	U	C2-N1-C1'	5.07	123.79	117.70
1	A	78	G	C6-N1-C2	5.07	128.14	125.10
1	A	1416	G	C5-C6-N1	-5.07	108.97	111.50
1	A	1008	C	N1-C2-O2	5.07	121.94	118.90
1	A	1505	G	N3-C4-N9	-5.07	122.96	126.00
1	A	292	G	N3-C4-N9	5.06	129.04	126.00
1	A	487	A	N1-C6-N6	5.06	121.64	118.60
1	A	1124	G	N3-C4-N9	5.06	129.04	126.00
1	A	150	C	N3-C4-C5	-5.06	119.88	121.90
1	A	922	G	N1-C6-O6	5.06	122.94	119.90
1	A	1017	G	C2-N3-C4	5.06	114.43	111.90
1	A	992	U	P-O3'-C3'	5.06	125.77	119.70
1	A	1364	U	C2-N3-C4	5.06	130.03	127.00
1	A	297	G	C5-C6-O6	5.06	131.63	128.60
1	A	662	G	N1-C6-O6	5.06	122.93	119.90
20	T	97	ALA	C-N-CD	-5.05	109.48	120.60
1	A	1033	G	N1-C6-O6	5.05	122.93	119.90
1	A	358	U	C2-N3-C4	-5.05	123.97	127.00
1	A	1447	A	C2-N3-C4	5.05	113.12	110.60
1	A	1435	G	N1-C6-O6	5.04	122.93	119.90
1	A	54	C	N1-C2-N3	5.04	122.73	119.20
1	A	987	G	N1-C6-O6	5.04	122.93	119.90
1	A	1258	G	C5-C6-O6	5.04	131.62	128.60
1	A	776	G	N3-C4-C5	5.04	131.12	128.60
1	A	818	G	C5-N7-C8	5.04	106.82	104.30
1	A	1340	A	C5-C6-N6	5.04	127.73	123.70
1	A	1122	U	C5-C6-N1	5.03	125.22	122.70
1	A	98	G	N7-C8-N9	5.03	115.62	113.10
1	A	986	A	N3-C4-C5	-5.03	123.28	126.80
1	A	1379	G	N1-C2-N2	-5.03	111.67	116.20
1	A	1442	G	C4-C5-N7	-5.03	108.79	110.80
1	A	951	G	C8-N9-C4	-5.03	104.39	106.40
1	A	1190	G	N3-C4-C5	5.02	131.11	128.60
1	A	839	U	C6-N1-C1'	-5.02	114.17	121.20
1	A	1442(B)	A	C8-N9-C1'	-5.02	118.67	127.70
1	A	1524	C	C6-N1-C2	5.02	122.31	120.30
1	A	740	U	C5-C4-O4	5.01	128.91	125.90
1	A	1377	A	N1-C6-N6	-5.01	115.59	118.60
1	A	60	A	N9-C4-C5	5.01	107.80	105.80
1	A	1101	A	N7-C8-N9	-5.00	111.30	113.80
1	A	1216	G	C4-C5-C6	-5.00	115.80	118.80

There are no chirality outliers.

All (17) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	129	GLU	Peptide
2	B	130	ARG	Peptide
2	B	14	GLY	Peptide
2	B	71	VAL	Peptide
3	C	160	ALA	Peptide
4	D	29	PRO	Peptide
7	G	146	GLU	Peptide
7	G	7	ALA	Peptide
9	I	102	LEU	Peptide
10	J	21	GLN	Peptide
10	J	92	THR	Peptide
13	M	65	LYS	Peptide
13	M	86	CYS	Peptide
15	O	75	PRO	Peptide
17	Q	96	GLU	Peptide
19	S	76	PRO	Peptide
20	T	48	LYS	Peptide

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32185	0	16244	1259	0
2	B	1775	0	1743	121	0
3	C	1450	0	1314	123	0
4	D	1526	0	1415	85	0
5	E	1105	0	1130	60	0
6	F	777	0	737	34	0
7	G	1164	0	1106	99	0
8	H	1045	0	1033	51	0
9	I	852	0	742	79	0
10	J	663	0	558	70	0
11	K	828	0	822	28	0
12	L	905	0	916	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
13	M	804	0	752	60	0
14	N	478	0	496	58	0
15	O	724	0	749	31	0
16	P	651	0	638	36	0
17	Q	823	0	891	47	0
18	R	514	0	530	21	0
19	S	560	0	466	40	0
20	T	713	0	766	39	0
21	U	199	0	208	23	0
22	X	601	0	485	16	0
23	A	168	0	0	0	0
23	E	1	0	0	0	0
23	Q	1	0	0	0	0
24	D	1	0	0	0	0
24	N	1	0	0	0	0
25	A	282	0	0	25	0
25	C	1	0	0	2	0
25	D	1	0	0	0	0
25	E	2	0	0	0	0
25	K	1	0	0	1	0
25	L	2	0	0	1	0
25	N	1	0	0	0	0
25	Q	1	0	0	0	0
25	T	2	0	0	0	0
25	X	1	0	0	0	0
All	All	50808	0	33741	2164	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 26.

All (2164) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1441:G:H2'	1:A:1459:C:N4	1.50	1.25
1:A:1441:G:C2'	1:A:1459:C:H41	1.54	1.19
1:A:989:C:N4	1:A:1216:G:H1	1.46	1.14
1:A:1441:G:C2'	1:A:1459:C:N4	2.17	1.01
1:A:949:A:H61	1:A:1232:U:H3	1.05	1.00
1:A:1089:G:H1	1:A:1096:C:N4	1.58	1.00
1:A:1459:C:C5	1:A:1460:A:N6	2.30	0.98
1:A:1459:C:C3'	1:A:1460:A:C8	2.48	0.96
10:J:50:ILE:HA	10:J:60:ARG:HG2	1.47	0.96
1:A:1459:C:H3'	1:A:1460:A:N7	1.81	0.95

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:839:U:H5'	1:A:840:C:H5	1.28	0.95
1:A:1457:G:H2'	1:A:1458:G:H8	1.27	0.95
8:H:6:ILE:HB	8:H:85:ARG:HH12	1.29	0.94
1:A:950:U:H3	1:A:1231:G:H1	1.05	0.94
13:M:3:ARG:HE	13:M:45:VAL:HG12	1.29	0.94
1:A:1089:G:H1	1:A:1096:C:H42	0.96	0.94
1:A:1113:C:N4	1:A:1187:G:H1	1.64	0.94
2:B:88:ALA:HB2	2:B:219:VAL:HG13	1.50	0.93
13:M:19:LEU:HB3	13:M:25:ILE:HG21	1.47	0.93
1:A:1128:C:H42	1:A:1143:G:H1	1.11	0.93
1:A:939:G:H1	1:A:1344:C:H42	1.15	0.93
1:A:1350:A:H61	1:A:1372:U:H3	1.11	0.93
1:A:932:C:N4	1:A:1385:G:H1	1.66	0.93
1:A:1262:C:H42	1:A:1273:G:H1	1.16	0.93
1:A:1113:C:H42	1:A:1187:G:H1	0.93	0.92
1:A:1349:A:N7	1:A:1373:G:N2	2.15	0.92
2:B:20:GLU:O	2:B:40:HIS:N	2.02	0.92
1:A:954:G:N2	1:A:1227:A:N7	2.17	0.92
1:A:932:C:N4	1:A:1385:G:N1	2.17	0.92
6:F:15:ASP:HB2	6:F:18:GLN:H	1.34	0.92
1:A:1441:G:H2'	1:A:1459:C:H41	0.76	0.92
1:A:1262:C:N4	1:A:1273:G:H1	1.67	0.91
1:A:1006:C:H42	1:A:1024:G:H21	1.09	0.91
1:A:1443:G:O6	1:A:1459:C:O2	1.89	0.91
1:A:581:G:OP2	25:A:2054:HOH:O	1.87	0.91
1:A:949:A:N6	1:A:1232:U:H3	1.68	0.91
1:A:1055:A:N7	1:A:1200:C:N4	2.17	0.90
1:A:1346:A:OP1	9:I:120:ARG:NH1	2.05	0.90
11:K:29:ILE:HG23	11:K:44:SER:HB3	1.51	0.90
1:A:1502:A:OP1	25:A:2045:HOH:O	1.88	0.90
1:A:1371:G:H5''	9:I:69:GLY:H	1.35	0.89
1:A:1170:A:H3'	1:A:1171:G:H8	1.37	0.89
2:B:19:HIS:ND1	2:B:189:ASP:OD2	2.04	0.89
1:A:955:U:H1'	1:A:1227:A:H61	1.36	0.89
1:A:673:G:H2'	1:A:674:G:C8	2.07	0.89
1:A:989:C:N3	1:A:1216:G:N2	2.22	0.88
1:A:937:A:N6	1:A:1345:U:O4	2.06	0.88
2:B:50:GLU:O	2:B:54:THR:OG1	1.89	0.88
1:A:1444:C:N4	1:A:1459:C:O2	2.07	0.88
1:A:1130:A:H61	1:A:1144:G:H1'	1.39	0.88
1:A:860:A:OP2	25:A:1876:HOH:O	1.91	0.87
1:A:559:A:H4'	1:A:560:U:H3'	1.57	0.87

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:986:A:N3	19:S:52:TYR:OH	2.07	0.86
1:A:758:G:N7	25:A:2055:HOH:O	2.06	0.86
1:A:953:G:O6	1:A:1228:C:N3	2.09	0.86
1:A:1030:C:N4	1:A:1031:G:C6	2.43	0.86
1:A:949:A:H1'	1:A:1364:U:N3	1.91	0.86
7:G:123:GLU:HA	7:G:126:ASP:HB2	1.56	0.85
1:A:782:A:OP1	25:A:1952:HOH:O	1.93	0.85
1:A:1459:C:O3'	1:A:1460:A:C8	2.30	0.85
19:S:16:LEU:HA	19:S:20:LEU:HB2	1.59	0.85
1:A:932:C:N3	1:A:1385:G:N2	2.25	0.84
5:E:122:GLU:O	5:E:126:ARG:NH1	2.09	0.84
1:A:1458:G:C2	1:A:1459:C:O4'	2.30	0.84
1:A:1327:C:OP1	21:U:20:LYS:N	2.11	0.84
1:A:1466:C:OP2	25:A:1869:HOH:O	1.94	0.84
1:A:1356:G:H2'	1:A:1357:A:C8	2.12	0.84
1:A:1459:C:H3'	1:A:1460:A:C8	2.11	0.84
16:P:19:ILE:HG22	16:P:36:ILE:HG13	1.59	0.84
9:I:16:ARG:HB2	9:I:64:THR:HG23	1.57	0.83
10:J:8:LEU:HD11	10:J:20:ALA:HB2	1.59	0.83
1:A:1300:G:H1	1:A:1334:G:H2'	1.43	0.83
1:A:973:G:H3'	1:A:974:A:H5''	1.59	0.83
1:A:1368:G:H5''	9:I:112:LYS:HB3	1.60	0.83
1:A:48:C:OP2	25:A:1855:HOH:O	1.95	0.83
7:G:14:PRO:HG3	7:G:21:VAL:HG12	1.61	0.82
1:A:1508:G:OP1	25:A:2030:HOH:O	1.97	0.82
3:C:20:SER:HB3	3:C:22:TRP:HE1	1.43	0.82
1:A:390:C:O3'	16:P:28:ARG:NH2	2.12	0.82
1:A:1156:G:H21	1:A:1179:A:H61	1.24	0.82
9:I:28:VAL:HB	9:I:36:TYR:HB3	1.59	0.81
1:A:1457:G:C4	1:A:1458:G:C8	2.68	0.81
1:A:1288:A:N1	1:A:1371:G:H1'	1.94	0.81
1:A:1251:A:N6	1:A:1285:A:N1	2.27	0.81
1:A:1141:C:H2'	1:A:1142:G:H8	1.44	0.81
1:A:427:U:OP1	4:D:13:ARG:NH2	2.14	0.81
1:A:1237:C:O2'	1:A:1300:G:N2	2.11	0.81
3:C:137:ALA:HA	3:C:140:ARG:HD3	1.62	0.81
1:A:1009:G:O6	1:A:1020:U:O2	1.98	0.81
1:A:977:A:HO2'	1:A:981:U:H3	1.26	0.80
1:A:581:G:N7	25:A:2055:HOH:O	2.14	0.80
1:A:940:C:H42	1:A:1343:G:H1	1.25	0.80
1:A:1235:U:H5''	21:U:3:LYS:HB2	1.63	0.80
7:G:42:ILE:HA	7:G:45:ASP:HB2	1.63	0.80

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1050:G:O6	1:A:1208:C:N3	2.15	0.80
1:A:1027:C:C2	1:A:1034:G:N2	2.47	0.80
7:G:42:ILE:HB	7:G:116:ALA:HB3	1.64	0.79
13:M:86:CYS:HB3	13:M:89:GLY:H	1.44	0.79
6:F:61:LEU:HB3	6:F:63:TYR:HE2	1.46	0.79
1:A:1350:A:N6	1:A:1372:U:H3	1.81	0.79
1:A:977:A:O2'	1:A:981:U:N3	2.12	0.79
1:A:90:U:H2'	1:A:91:C:C6	2.18	0.79
1:A:1457:G:H2'	1:A:1458:G:C8	2.17	0.79
1:A:1075:C:OP1	2:B:179:LYS:NZ	2.13	0.79
2:B:87:ARG:HE	2:B:233:SER:HB2	1.47	0.78
1:A:839:U:H5'	1:A:840:C:C5	2.18	0.78
1:A:1128:C:N4	1:A:1143:G:H1	1.80	0.78
1:A:1170:A:H3'	1:A:1171:G:C8	2.18	0.78
8:H:4:ASP:OD1	8:H:85:ARG:NH1	2.16	0.78
1:A:1179:A:H4'	9:I:103:THR:HA	1.66	0.78
17:Q:76:LEU:HD11	17:Q:79:SER:HB2	1.62	0.78
8:H:29:SER:HB3	8:H:32:LYS:HG3	1.65	0.78
1:A:1377:A:H2'	7:G:7:ALA:HB1	1.64	0.78
3:C:43:LEU:HD23	3:C:47:LEU:HD13	1.65	0.78
9:I:13:ALA:HB1	9:I:73:GLN:HG3	1.66	0.77
2:B:71:VAL:HG13	2:B:93:VAL:HG23	1.66	0.77
1:A:176:C:OP1	20:T:29:LYS:NZ	2.15	0.77
7:G:16:LEU:HD22	9:I:45:ALA:H	1.49	0.77
1:A:1349:A:H2'	1:A:1350:A:H8	1.50	0.77
14:N:32:SER:HB3	14:N:41:ARG:HB3	1.67	0.77
1:A:266:G:O2'	1:A:267:C:OP2	2.02	0.77
1:A:1237:C:N4	1:A:1337:G:H1	1.82	0.77
1:A:235:C:H5'	17:Q:70:ARG:HG2	1.64	0.77
1:A:953:G:N1	1:A:1228:C:O2	2.17	0.76
6:F:7:ASN:HD21	18:R:34:TYR:HE1	1.31	0.76
1:A:1235:U:O2'	1:A:1305:G:OP1	2.03	0.76
1:A:547:A:OP1	25:A:1991:HOH:O	2.04	0.76
1:A:1222:G:OP2	1:A:1322:C:N4	2.19	0.76
7:G:46:ALA:HA	7:G:121:ALA:HB2	1.68	0.76
1:A:1005:A:H1'	1:A:1036:G:H22	1.50	0.76
1:A:1130:A:H4'	9:I:3:GLN:HE22	1.51	0.76
1:A:1273:G:H3'	1:A:1274:G:H8	1.50	0.76
1:A:1254:C:H42	1:A:1283:G:H1	1.33	0.76
1:A:1154:G:H2'	1:A:1155:G:H8	1.52	0.75
1:A:1004:A:N6	1:A:1035:A:N7	2.34	0.75
1:A:177:C:OP1	20:T:65:LYS:NZ	2.19	0.75

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:K:79:SER:HA	11:K:104:GLN:HB2	1.68	0.75
2:B:54:THR:HG23	2:B:199:TYR:HB3	1.69	0.75
1:A:1251:A:N6	1:A:1354:C:O2'	2.17	0.75
7:G:69:VAL:HG21	7:G:104:LEU:HD13	1.69	0.75
1:A:750:G:N3	15:O:23:GLY:HA3	2.01	0.75
2:B:197:VAL:O	8:H:68:ARG:NH2	2.20	0.75
3:C:17:ASP:O	3:C:54:ARG:NH2	2.19	0.75
9:I:15:ALA:HB2	9:I:65:VAL:HG23	1.69	0.74
19:S:36:ARG:NH1	19:S:75:ALA:O	2.19	0.74
1:A:166:G:H2'	1:A:167:G:H8	1.52	0.74
1:A:192:U:H2'	1:A:193:C:H6	1.51	0.74
1:A:1459:C:O3'	1:A:1460:A:H8	1.67	0.74
1:A:1262:C:N3	1:A:1273:G:N2	2.34	0.74
7:G:73:MET:HG2	7:G:145:ALA:HB1	1.69	0.74
1:A:1457:G:C5	1:A:1458:G:N7	2.55	0.74
1:A:1010:G:H2'	1:A:1011:G:H8	1.52	0.74
1:A:949:A:H1'	1:A:1364:U:H3	1.50	0.74
13:M:86:CYS:HB3	13:M:89:GLY:N	2.01	0.74
1:A:1006:C:H2'	1:A:1007:C:C2	2.23	0.74
1:A:437:U:H5''	4:D:155:LEU:HD11	1.69	0.74
1:A:447:G:OP2	25:A:1822:HOH:O	2.05	0.74
1:A:946:A:H61	1:A:1235:U:H3	1.35	0.74
1:A:1346:A:H2	1:A:1347:G:H21	1.33	0.74
9:I:4:TYR:CZ	9:I:88:TYR:HB2	2.23	0.74
1:A:1030:C:N3	1:A:1031:G:C2	2.56	0.74
4:D:159:ARG:O	4:D:163:GLU:N	2.18	0.74
1:A:1444:C:H42	1:A:1458:G:H1	1.36	0.73
1:A:1073:U:H2'	1:A:1074:G:H8	1.51	0.73
1:A:940:C:N4	1:A:1343:G:H1	1.84	0.73
7:G:43:PHE:HA	7:G:46:ALA:HB3	1.70	0.73
7:G:88:PRO:HG2	7:G:152:ALA:HA	1.70	0.73
14:N:7:ILE:HG22	14:N:23:ARG:HE	1.52	0.73
1:A:1376:U:H2'	1:A:1377:A:C8	2.24	0.73
1:A:484:G:O2'	1:A:485:G:OP2	2.06	0.73
14:N:16:PHE:H	14:N:19:ARG:HB2	1.54	0.73
1:A:1324:A:H5'	1:A:1363:C:H5''	1.71	0.73
1:A:1165:C:N4	1:A:1171:G:H1	1.86	0.73
2:B:60:ASP:O	2:B:64:ARG:HG3	1.89	0.73
7:G:138:LYS:NZ	7:G:142:GLU:OE1	2.20	0.72
1:A:1442:G:N7	1:A:1442(A):G:C6	2.57	0.72
1:A:427:U:OP2	4:D:36:ARG:NH2	2.22	0.72
1:A:1147:C:O2	9:I:16:ARG:NH2	2.23	0.72

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1443:G:O6	1:A:1459:C:C2	2.42	0.72
19:S:46:GLY:HA2	19:S:61:TYR:CE1	2.25	0.72
3:C:36:ASP:HA	3:C:39:ILE:HD12	1.70	0.72
15:O:16:ALA:HB1	15:O:21:ASP:HB3	1.72	0.72
1:A:1231:G:N2	1:A:1232:U:H1'	2.05	0.72
1:A:964:A:H2'	1:A:969:A:H1'	1.71	0.72
1:A:97:G:HO2'	1:A:98:G:H8	1.37	0.72
2:B:87:ARG:HH21	2:B:233:SER:H	1.37	0.72
7:G:41:ARG:NH2	9:I:39:GLY:O	2.23	0.72
1:A:148:G:H2'	1:A:149:A:H8	1.54	0.72
3:C:13:GLY:HA3	14:N:57:ARG:HH22	1.55	0.72
1:A:1131:G:H1	1:A:1143:G:H21	1.38	0.71
1:A:939:G:H1	1:A:1344:C:N4	1.87	0.71
2:B:137:ARG:HB2	2:B:137:ARG:HH11	1.55	0.71
20:T:10:LEU:HG	20:T:12:ALA:H	1.54	0.71
1:A:976:G:N2	1:A:1363(A):A:OP1	2.23	0.71
1:A:642:A:N3	8:H:113:SER:OG	2.22	0.71
13:M:71:ARG:HA	13:M:74:VAL:HB	1.71	0.71
13:M:70:LEU:O	13:M:74:VAL:N	2.24	0.71
1:A:538:G:H5''	12:L:114:LYS:HB2	1.72	0.71
3:C:6:HIS:HD2	3:C:7:PRO:HD2	1.55	0.71
1:A:576:G:OP1	25:A:1949:HOH:O	2.08	0.71
1:A:1156:G:H21	1:A:1179:A:N6	1.88	0.71
7:G:15:ASP:N	7:G:20:ASP:O	2.18	0.71
10:J:8:LEU:O	10:J:69:ASN:HA	1.89	0.71
1:A:1176:A:H2'	1:A:1177:G:C8	2.26	0.71
1:A:735:C:H2'	1:A:736:C:H6	1.54	0.71
14:N:24:CYS:HB2	14:N:40:CYS:N	2.06	0.71
11:K:31:THR:HG22	11:K:42:TRP:HB2	1.72	0.71
1:A:903:G:OP1	25:A:1959:HOH:O	2.09	0.71
13:M:15:VAL:HG22	13:M:41:PRO:HA	1.72	0.71
1:A:1347:G:N2	1:A:1374:A:O5'	2.24	0.71
1:A:1342:C:H2'	1:A:1343:G:C8	2.25	0.70
13:M:3:ARG:NH2	13:M:45:VAL:O	2.21	0.70
1:A:605:U:H2'	1:A:606:G:C8	2.26	0.70
1:A:1499:A:OP2	25:A:1862:HOH:O	2.08	0.70
3:C:150:LYS:HB2	3:C:173:VAL:HG21	1.73	0.70
2:B:219:VAL:HA	2:B:222:ILE:HD12	1.73	0.70
15:O:54:ARG:HG2	15:O:58:MET:HE2	1.70	0.70
1:A:1273:G:H3'	1:A:1274:G:C8	2.27	0.70
1:A:1301:U:OP1	13:M:21:TYR:OH	2.07	0.70
1:A:1286:A:H2	21:U:22:ARG:HH21	1.37	0.70

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
10:J:79:ARG:O	10:J:81:THR:N	2.21	0.70
1:A:1173:G:H2'	1:A:1174:G:H8	1.55	0.70
1:A:1237:C:H42	1:A:1337:G:H1	1.39	0.70
1:A:222:U:H2'	1:A:223:U:C6	2.27	0.70
3:C:134:ILE:HG23	3:C:151:VAL:HB	1.74	0.70
3:C:182:ILE:HG12	3:C:203:PHE:HA	1.73	0.70
1:A:1231:G:N1	1:A:1232:U:O2	2.25	0.70
4:D:57:ARG:HE	4:D:202:LEU:HD22	1.57	0.70
4:D:104:VAL:HA	4:D:107:ARG:HB2	1.73	0.70
2:B:167:PRO:O	2:B:171:ALA:N	2.25	0.69
13:M:86:CYS:O	19:S:73:GLU:HB3	1.91	0.69
4:D:9:CYS:HA	4:D:12:CYS:HB2	1.73	0.69
1:A:1161:C:H2'	1:A:1162:C:C6	2.27	0.69
1:A:1154:G:H2'	1:A:1155:G:C8	2.28	0.69
10:J:44:VAL:HG13	10:J:66:ARG:HG2	1.75	0.69
10:J:8:LEU:HD13	10:J:16:LEU:HG	1.73	0.69
1:A:1242:C:O2'	1:A:1303:C:OP1	2.11	0.69
7:G:139:GLU:O	7:G:143:ARG:NE	2.25	0.69
1:A:1089:G:N2	1:A:1096:C:N3	2.36	0.69
1:A:405:U:O4	4:D:2:GLY:N	2.26	0.69
10:J:50:ILE:HD12	10:J:50:ILE:H	1.57	0.69
1:A:1376:U:H5'	7:G:102:ARG:HH22	1.57	0.69
1:A:1460:A:P	1:A:1460:A:H8	2.15	0.69
3:C:40:ARG:HA	3:C:43:LEU:HD12	1.75	0.69
5:E:50:GLU:HB2	5:E:53:LEU:HD22	1.74	0.69
15:O:39:LEU:HB3	15:O:56:LEU:HD23	1.75	0.69
3:C:103:VAL:HG12	3:C:104:GLN:H	1.58	0.69
1:A:434:U:H2'	1:A:435:C:C6	2.27	0.69
1:A:1502:A:H2	1:A:1505:G:N1	1.92	0.68
1:A:426:G:OP1	4:D:38:TYR:OH	2.12	0.68
1:A:977:A:N6	1:A:1224:G:OP1	2.26	0.68
10:J:39:PRO:HA	10:J:70:ARG:HG2	1.75	0.68
1:A:952:U:H3	1:A:1229:A:H61	1.39	0.68
2:B:135:GLN:HA	2:B:138:LEU:HD12	1.73	0.68
1:A:223:U:H2'	1:A:224:C:H6	1.58	0.68
1:A:1002:G:H22	1:A:1039:C:H1'	1.58	0.68
1:A:975:A:O3'	1:A:1358:U:O2'	2.12	0.68
1:A:1238:A:N1	1:A:1241:G:N2	2.33	0.68
7:G:66:VAL:HG22	7:G:100:ALA:HB1	1.74	0.68
1:A:1444:C:N4	1:A:1458:G:H1	1.92	0.68
5:E:80:ILE:HG13	5:E:91:LEU:HB2	1.76	0.68
18:R:35:ARG:HB3	18:R:35:ARG:NH1	2.09	0.68

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1459:C:C3'	1:A:1460:A:N7	2.52	0.68
3:C:20:SER:HB3	3:C:22:TRP:NE1	2.08	0.68
1:A:959:A:H61	19:S:78:ARG:HA	1.59	0.68
1:A:1165:C:H42	1:A:1171:G:H1	1.40	0.67
1:A:73:G:H1	1:A:96:U:H3	1.41	0.67
1:A:1150:U:O4	1:A:1151:A:N6	2.27	0.67
2:B:157:ARG:NH2	2:B:160:ASP:OD1	2.23	0.67
4:D:133:VAL:HG11	4:D:138:TYR:HD1	1.58	0.67
1:A:1158:C:N3	1:A:1181:G:N2	2.42	0.67
5:E:57:LYS:HG2	5:E:61:TYR:CE2	2.30	0.67
7:G:142:GLU:HB3	7:G:143:ARG:HH21	1.60	0.67
1:A:548:G:OP1	25:A:1993:HOH:O	2.13	0.67
2:B:222:ILE:O	2:B:226:ARG:HG2	1.94	0.67
3:C:36:ASP:O	3:C:39:ILE:HB	1.94	0.67
1:A:1144:G:H21	1:A:1146:A:N6	1.92	0.67
1:A:1309:G:OP1	13:M:92:HIS:NE2	2.28	0.67
3:C:11:ARG:HH11	3:C:11:ARG:HB2	1.59	0.67
1:A:1351:U:H2'	1:A:1352:C:H6	1.60	0.67
1:A:1030(A):G:O2'	1:A:1030(C):G:N7	2.27	0.67
1:A:330:C:O2	25:A:1866:HOH:O	2.11	0.67
3:C:32:LEU:HD11	3:C:59:ARG:HD2	1.76	0.66
3:C:157:ILE:O	3:C:164:ARG:NH2	2.28	0.66
1:A:1084:G:H21	1:A:1102:A:N6	1.93	0.66
1:A:425:G:O3'	4:D:45:GLN:NE2	2.28	0.66
1:A:976:G:P	14:N:32:SER:H	2.19	0.66
1:A:1297:C:H4'	1:A:1298:C:H5'	1.76	0.66
1:A:1435:G:H2'	1:A:1436:U:C6	2.30	0.66
15:O:8:LYS:HG2	15:O:12:ILE:HD11	1.78	0.66
1:A:1231:G:C2	1:A:1232:U:H1'	2.31	0.66
1:A:1381:U:H3'	1:A:1382:C:H6	1.61	0.66
1:A:1067:A:N3	1:A:1068:G:H1'	2.11	0.66
15:O:70:LEU:HG	15:O:78:TYR:HB2	1.77	0.66
3:C:156:ARG:NE	3:C:161:GLU:OE2	2.28	0.66
1:A:382:A:H2'	1:A:383:A:C8	2.30	0.66
4:D:32:ALA:HA	4:D:35:ARG:HB2	1.77	0.66
22:X:4:ASN:HB2	22:X:38:TYR:HA	1.78	0.66
1:A:365:U:H5''	1:A:366:C:OP1	1.95	0.66
15:O:3:ILE:HD13	15:O:3:ILE:H	1.61	0.66
1:A:1046:A:H3'	1:A:1047:G:H8	1.60	0.66
1:A:1073:U:H2'	1:A:1074:G:C8	2.29	0.66
19:S:46:GLY:N	19:S:62:ILE:O	2.28	0.66
1:A:171:A:H2'	1:A:172:A:C8	2.29	0.66

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:D:157:LEU:O	4:D:161:ASN:ND2	2.20	0.66
1:A:1457:G:N3	1:A:1458:G:C8	2.63	0.66
1:A:1457:G:C4	1:A:1458:G:N7	2.64	0.66
1:A:1112:C:N3	3:C:178:LEU:HB2	2.10	0.66
20:T:10:LEU:HD21	20:T:12:ALA:HB3	1.76	0.66
1:A:1106:G:H5''	3:C:172:ARG:HD3	1.77	0.66
1:A:1211:U:H4'	1:A:1212:U:OP2	1.96	0.65
21:U:17:THR:OG1	21:U:18:TYR:N	2.29	0.65
1:A:1245:A:H61	1:A:1292:U:H3	1.43	0.65
17:Q:6:LEU:HD23	17:Q:23:VAL:HG11	1.77	0.65
1:A:1332:A:H2'	1:A:1333:A:C8	2.31	0.65
5:E:12:LEU:HB3	5:E:31:LEU:HB3	1.78	0.65
1:A:1306:A:H3'	1:A:1307:U:H6	1.62	0.65
1:A:1078:U:H1'	5:E:130:ASN:HD21	1.61	0.65
1:A:1028:C:N3	1:A:1033:G:C6	2.65	0.65
22:X:17:ARG:HA	22:X:20:VAL:HG12	1.78	0.65
1:A:1258:G:H2'	1:A:1259:C:C6	2.32	0.65
21:U:10:ARG:HE	21:U:10:ARG:HA	1.61	0.65
2:B:115:LEU:HD13	2:B:145:LEU:HB3	1.78	0.65
5:E:43:LEU:O	5:E:65:ASN:ND2	2.30	0.65
1:A:1377:A:H2'	7:G:7:ALA:CB	2.27	0.65
7:G:43:PHE:HD1	7:G:46:ALA:HB3	1.61	0.65
4:D:108:LEU:HD11	4:D:174:LEU:HD22	1.79	0.65
1:A:1015:A:N3	1:A:1218:C:O2'	2.27	0.65
1:A:186:C:H2'	1:A:187:C:C6	2.32	0.65
1:A:1373:G:H5'	7:G:36:LYS:HG3	1.79	0.65
1:A:1502:A:H2	1:A:1505:G:H1	1.42	0.65
1:A:1500:A:OP1	25:A:2030:HOH:O	2.15	0.65
5:E:71:LEU:HD11	5:E:74:GLY:H	1.62	0.65
4:D:20:TYR:HA	4:D:26:CYS:SG	2.36	0.65
1:A:996:A:H2'	1:A:997:U:C6	2.32	0.64
1:A:1142:G:C6	1:A:1143:G:H1'	2.32	0.64
1:A:1128:C:H4'	9:I:16:ARG:HH22	1.62	0.64
14:N:24:CYS:SG	14:N:27:CYS:N	2.70	0.64
1:A:1210:C:H3'	1:A:1211:U:H5''	1.80	0.64
1:A:538:G:OP2	12:L:115:LYS:HB2	1.97	0.64
9:I:22:GLY:HA3	9:I:60:ASP:HB2	1.79	0.64
1:A:1111:A:N1	3:C:177:THR:HG23	2.12	0.64
3:C:54:ARG:HH11	3:C:56:ASP:HB2	1.63	0.64
14:N:7:ILE:HG22	14:N:23:ARG:NE	2.12	0.64
11:K:41:THR:HG21	11:K:71:LYS:HD2	1.79	0.64
2:B:87:ARG:HD2	2:B:219:VAL:HG11	1.77	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1381:U:H3'	1:A:1382:C:C6	2.33	0.64
1:A:1181:G:H4'	1:A:1184:G:H5'	1.78	0.64
1:A:59:A:H5''	1:A:60:A:H5''	1.80	0.64
11:K:73:MET:HG3	11:K:103:LEU:HD21	1.80	0.64
1:A:1130:A:N6	1:A:1144:G:H1'	2.11	0.64
1:A:1326:C:H5''	21:U:18:TYR:O	1.98	0.64
20:T:97:ALA:HB3	20:T:99:LEU:H	1.62	0.64
9:I:17:VAL:HG11	9:I:81:ILE:HA	1.80	0.64
1:A:991:U:H3'	1:A:1212:U:H3	1.62	0.63
1:A:1027:C:N1	1:A:1034:G:N2	2.45	0.63
1:A:926:G:H21	22:X:94:GLN:HE22	1.44	0.63
1:A:1387:G:H2'	1:A:1388:C:C6	2.33	0.63
9:I:9:ARG:HH11	9:I:104:ARG:HE	1.45	0.63
1:A:171:A:H2'	1:A:172:A:H8	1.63	0.63
11:K:84:VAL:HG11	11:K:91:ARG:HD2	1.80	0.63
1:A:102:G:H2'	1:A:103:C:H6	1.62	0.63
1:A:1121:U:O4	1:A:1152:A:N1	2.31	0.63
5:E:98:THR:HG22	5:E:99:GLY:H	1.63	0.63
13:M:89:GLY:HA2	13:M:92:HIS:CD2	2.33	0.63
14:N:23:ARG:NH1	14:N:30:ALA:HB2	2.14	0.63
1:A:1243:C:H5''	21:U:8:THR:HG21	1.80	0.63
1:A:989:C:H42	1:A:1216:G:H1	0.72	0.63
1:A:952:U:H3	1:A:1229:A:N6	1.97	0.63
20:T:33:ILE:O	20:T:37:SER:OG	2.12	0.63
16:P:29:ASP:OD2	16:P:29:ASP:N	2.31	0.62
1:A:352:C:O2'	1:A:354:G:OP1	2.12	0.62
19:S:80:TYR:O	19:S:81:ARG:HG3	1.99	0.62
7:G:111:ARG:NH1	7:G:119:ARG:O	2.32	0.62
4:D:30:LYS:HA	4:D:35:ARG:HD2	1.80	0.62
1:A:324:G:OP1	20:T:70:SER:HB2	1.99	0.62
1:A:920:U:H2'	1:A:921:U:C6	2.34	0.62
1:A:1444:C:N3	1:A:1459:C:H1'	2.14	0.62
1:A:1359:C:OP2	14:N:35:ARG:HD2	1.99	0.62
1:A:166:G:H2'	1:A:167:G:C8	2.34	0.62
1:A:1103:C:H2'	1:A:1104:G:O4'	1.99	0.62
2:B:167:PRO:HG3	2:B:188:ALA:HB2	1.81	0.62
4:D:138:TYR:HD2	4:D:139:ARG:N	1.98	0.62
1:A:1356:G:H2'	1:A:1357:A:H8	1.61	0.62
1:A:1155:G:H2'	1:A:1156:G:C8	2.34	0.62
7:G:149:ARG:HB2	11:K:59:TYR:CD1	2.35	0.62
1:A:1347:G:N1	1:A:1374:A:OP2	2.28	0.62
1:A:1239:A:H62	1:A:1299:A:N6	1.97	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1157:A:H4'	1:A:1158:C:O5'	2.00	0.62
1:A:918:A:H2'	1:A:919:A:C8	2.33	0.62
1:A:1005:A:H1'	1:A:1036:G:N2	2.13	0.62
1:A:1323:G:O2'	1:A:1362:C:O2'	2.18	0.62
1:A:735:C:H2'	1:A:736:C:C6	2.33	0.62
1:A:158:G:N2	1:A:163:C:O2	2.32	0.62
1:A:662:G:O2'	1:A:836:G:OP1	2.17	0.62
1:A:1113:C:N3	1:A:1187:G:N2	2.45	0.62
1:A:1239:A:H62	1:A:1299:A:H61	1.48	0.62
14:N:24:CYS:HB2	14:N:40:CYS:H	1.65	0.62
2:B:78:GLN:O	2:B:94:ASN:ND2	2.32	0.62
1:A:664:G:P	18:R:64:ARG:HH21	2.21	0.62
21:U:3:LYS:HG2	21:U:10:ARG:HG3	1.82	0.62
1:A:1238:A:OP2	1:A:1335:C:H1'	1.99	0.62
1:A:745:C:H2'	1:A:746:A:H8	1.63	0.62
1:A:542:G:H2'	1:A:543:C:C6	2.35	0.62
1:A:1135:U:H2'	1:A:1137:C:O4'	1.99	0.62
1:A:971:G:OP1	1:A:972:C:H5''	2.00	0.62
3:C:181:ASN:ND2	3:C:181:ASN:O	2.33	0.62
1:A:1165:C:N3	1:A:1171:G:N2	2.48	0.61
1:A:957:U:O2'	1:A:959:A:N7	2.32	0.61
3:C:131:ARG:NH2	3:C:166:GLU:OE2	2.32	0.61
1:A:971:G:O2'	1:A:1365:G:H4'	2.00	0.61
4:D:155:LEU:HB3	4:D:158:ILE:HB	1.82	0.61
1:A:1452:C:O2'	1:A:1456:G:OP2	2.18	0.61
3:C:184:TYR:HE1	3:C:199:LYS:HB3	1.65	0.61
1:A:1379:G:H21	1:A:1381:U:H5	1.47	0.61
1:A:1055:A:N1	1:A:1056:U:H1'	2.14	0.61
3:C:18:TRP:CD1	14:N:54:PRO:HA	2.35	0.61
1:A:663:A:O3'	18:R:64:ARG:NH2	2.33	0.61
10:J:63:PHE:HD1	14:N:58:LYS:HA	1.65	0.61
11:K:13:GLN:N	11:K:75:TYR:O	2.32	0.61
10:J:47:PHE:O	10:J:63:PHE:N	2.31	0.61
7:G:47:CYS:SG	7:G:58:PRO:HB3	2.41	0.61
1:A:1441:G:N2	1:A:1459:C:H5	1.98	0.61
5:E:102:ALA:HB1	5:E:106:PRO:HG2	1.82	0.61
10:J:45:ARG:O	10:J:65:LEU:N	2.33	0.61
1:A:1217:C:H2'	1:A:1218:C:C6	2.36	0.61
1:A:376:G:H1	1:A:387:U:H3	1.47	0.61
1:A:1442(A):G:N3	1:A:1442(B):A:H2'	2.15	0.61
1:A:955:U:H1'	1:A:1227:A:N6	2.13	0.61
1:A:1238:A:N6	1:A:1296:C:O2	2.33	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1007:C:O2	1:A:1023:G:N2	2.34	0.61
1:A:1306:A:H3'	1:A:1307:U:C6	2.36	0.61
1:A:1016:A:C5	1:A:1017:G:H1'	2.35	0.61
1:A:142:G:H2'	1:A:143:A:H8	1.64	0.61
1:A:243:A:H4'	1:A:244:U:O5'	2.00	0.61
1:A:532:A:N1	3:C:193:TYR:HB3	2.16	0.61
7:G:12:LEU:HD21	7:G:24:THR:HB	1.82	0.61
1:A:833:U:H2'	1:A:834:C:C6	2.36	0.61
1:A:1128:C:H1'	1:A:1146:A:H61	1.65	0.61
2:B:178:ARG:HH22	8:H:68:ARG:HH22	1.48	0.61
17:Q:13:ASP:CG	17:Q:14:LYS:H	2.04	0.61
18:R:44:LEU:HD21	18:R:70:ILE:HD13	1.82	0.61
1:A:1131:G:H1	1:A:1143:G:N2	1.98	0.61
2:B:54:THR:O	2:B:58:ILE:HG13	2.00	0.61
1:A:1242:C:H4'	1:A:1303:C:O3'	2.01	0.61
1:A:407:G:H4'	4:D:116:GLN:HA	1.83	0.61
1:A:542:G:H2'	1:A:543:C:H6	1.66	0.61
2:B:15:VAL:HG23	2:B:209:ARG:HG2	1.82	0.61
2:B:77:ALA:HB2	2:B:211:ILE:HG12	1.81	0.60
1:A:994:A:H2	14:N:4:LYS:HD3	1.66	0.60
1:A:745:C:OP1	1:A:851:G:O2'	2.18	0.60
1:A:376:G:OP2	16:P:67:THR:HG21	2.00	0.60
12:L:27:LEU:O	12:L:29:GLY:N	2.34	0.60
4:D:89:THR:HB	4:D:204:ILE:HD11	1.83	0.60
1:A:1442(A):G:C6	1:A:1442(B):A:C2	2.89	0.60
1:A:878:G:H5'	8:H:89:PRO:HG2	1.81	0.60
6:F:61:LEU:HB3	6:F:63:TYR:CE2	2.33	0.60
1:A:59:A:H1'	1:A:354:G:N2	2.17	0.60
1:A:509:A:H3'	25:A:1944:HOH:O	2.00	0.60
16:P:49:LEU:HD11	16:P:51:VAL:HG23	1.83	0.60
17:Q:48:GLU:HB2	17:Q:50:LYS:HG2	1.83	0.60
1:A:41:G:H2'	1:A:42:G:C8	2.36	0.60
1:A:1401:G:OP1	22:X:80:LYS:HE2	2.02	0.60
14:N:25:VAL:H	14:N:39:LEU:HD23	1.65	0.60
1:A:745:C:H2'	1:A:746:A:C8	2.37	0.60
12:L:79:GLU:O	12:L:80:HIS:HB2	2.01	0.60
1:A:1128:C:H5'	9:I:16:ARG:HH12	1.66	0.60
1:A:1236:A:H4'	1:A:1304:G:H5'	1.84	0.60
1:A:1027:C:C4	1:A:1034:G:N1	2.70	0.60
1:A:41:G:H2'	1:A:42:G:H8	1.67	0.60
5:E:6:PHE:HB2	5:E:34:VAL:HG22	1.82	0.60
1:A:1063:C:H2'	1:A:1064:G:C8	2.36	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1046:A:H3'	1:A:1047:G:C8	2.37	0.60
1:A:677:U:H3	1:A:713:G:H22	1.48	0.60
1:A:981:U:H2'	1:A:982:U:C5	2.36	0.60
1:A:1441:G:N2	1:A:1459:C:C5	2.70	0.60
1:A:1179:A:H2'	1:A:1180:A:O4'	2.02	0.60
1:A:174:C:H2'	1:A:175:C:H6	1.65	0.60
1:A:450:G:OP1	16:P:43:LYS:NZ	2.35	0.60
1:A:1442(A):G:C2	1:A:1442(B):A:H2'	2.37	0.60
1:A:1305:G:H1'	1:A:1306:A:C8	2.36	0.60
3:C:137:ALA:O	3:C:141:VAL:HG23	2.02	0.60
9:I:46:ALA:HB1	9:I:77:ILE:HB	1.84	0.60
9:I:49:PRO:HG2	9:I:78:LYS:HA	1.84	0.60
1:A:552:U:H4'	12:L:86:ARG:HG2	1.84	0.60
1:A:972:C:H2'	10:J:55:LYS:HB2	1.84	0.59
10:J:49:VAL:HG21	14:N:41:ARG:HB2	1.83	0.59
3:C:35:GLU:O	3:C:39:ILE:HG13	2.02	0.59
1:A:438:G:OP1	4:D:125:HIS:HE1	1.85	0.59
12:L:24:VAL:HG13	12:L:98:TYR:HE2	1.67	0.59
10:J:20:ALA:O	10:J:24:VAL:N	2.35	0.59
1:A:1014:A:H2'	1:A:1015:A:C8	2.37	0.59
5:E:76:ILE:HG12	5:E:77:PRO:HD2	1.83	0.59
1:A:683:G:H2'	1:A:684:A:C8	2.37	0.59
1:A:1306:A:H1'	1:A:1332:A:C2	2.37	0.59
1:A:1072:G:H2'	1:A:1073:U:C6	2.37	0.59
3:C:11:ARG:HD3	3:C:178:LEU:O	2.02	0.59
1:A:542:G:P	4:D:10:ARG:HH22	2.26	0.59
1:A:927:G:O2'	1:A:1503:A:N7	2.35	0.59
10:J:37:PRO:HA	10:J:72:VAL:HG12	1.83	0.59
1:A:316:G:OP2	1:A:351:G:O2'	2.20	0.59
1:A:973:G:H4'	14:N:41:ARG:HH22	1.68	0.59
7:G:16:LEU:HD22	9:I:45:ALA:N	2.16	0.59
1:A:169:C:H2'	1:A:170:U:H6	1.68	0.59
4:D:26:CYS:HA	4:D:31:CYS:HB2	1.83	0.59
1:A:509:A:H5''	4:D:55:ALA:HB2	1.83	0.59
4:D:72:GLU:OE1	4:D:207:TYR:OH	2.13	0.59
1:A:583:A:H2'	1:A:584:G:O4'	2.02	0.59
9:I:9:ARG:HB2	9:I:14:VAL:HG13	1.83	0.59
1:A:1117:G:H1'	1:A:1184:G:H22	1.66	0.59
1:A:1015:A:H2'	1:A:1016:A:O4'	2.02	0.59
1:A:765:G:H5''	1:A:766:A:OP1	2.03	0.59
1:A:1371:G:H5''	9:I:69:GLY:N	2.13	0.59
1:A:1373:G:H4'	7:G:31:MET:HE3	1.84	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1158:C:O2'	1:A:1160:G:OP1	2.12	0.59
1:A:166:G:N7	25:A:1926:HOH:O	2.32	0.59
3:C:115:LEU:HA	3:C:118:GLN:HG2	1.85	0.59
13:M:24:GLY:HA3	13:M:66:LEU:HD22	1.84	0.59
1:A:627:G:H2'	1:A:628:G:H8	1.68	0.59
1:A:737:A:H2'	1:A:738:C:C6	2.37	0.59
1:A:1249:C:N4	1:A:1287:A:H5'	2.18	0.59
16:P:28:ARG:HH11	16:P:28:ARG:HG2	1.66	0.59
1:A:615:C:H2'	1:A:616:G:H8	1.68	0.59
1:A:753:A:OP1	15:O:69:TYR:OH	2.19	0.59
1:A:1203:C:OP1	14:N:3:ARG:NH1	2.33	0.59
9:I:31:GLN:CD	9:I:36:TYR:HD1	2.05	0.59
1:A:833:U:H2'	1:A:834:C:H6	1.67	0.59
1:A:913:A:H4'	1:A:914:A:O5'	2.03	0.59
6:F:70:ASP:OD1	6:F:70:ASP:N	2.36	0.59
1:A:408:A:OP1	4:D:113:SER:OG	2.17	0.59
1:A:382:A:H2'	1:A:383:A:H8	1.68	0.59
1:A:1189:C:OP1	14:N:58:LYS:NZ	2.29	0.59
3:C:70:VAL:O	3:C:105:GLU:HA	2.03	0.59
18:R:31:LEU:HD23	18:R:31:LEU:H	1.67	0.59
1:A:857:C:H2'	1:A:858:G:O4'	2.03	0.59
3:C:138:VAL:HG22	3:C:151:VAL:HG23	1.85	0.59
1:A:944:G:H2'	1:A:1338:G:O6	2.02	0.59
1:A:1246:C:N3	1:A:1291:G:O6	2.36	0.59
1:A:377:G:H2'	1:A:378:G:C8	2.37	0.59
6:F:62:TRP:CH2	6:F:64:GLN:HB2	2.37	0.59
7:G:64:GLN:HG3	7:G:128:ALA:HB1	1.85	0.59
1:A:1131:G:H2'	1:A:1132:C:C6	2.38	0.58
9:I:29:ASN:HD21	9:I:65:VAL:H	1.51	0.58
14:N:24:CYS:HA	14:N:39:LEU:HA	1.85	0.58
1:A:1269:A:OP1	21:U:24:ARG:HB2	2.03	0.58
2:B:69:LEU:HD22	2:B:91:PRO:HB2	1.85	0.58
1:A:1442:G:N7	1:A:1442(A):G:C5	2.71	0.58
1:A:1124:G:O2'	10:J:38:ILE:HG21	2.03	0.58
7:G:14:PRO:HA	7:G:21:VAL:HA	1.84	0.58
1:A:1121:U:H2'	1:A:1122:U:H5'	1.85	0.58
1:A:102:G:H2'	1:A:103:C:C6	2.38	0.58
8:H:31:PHE:CE2	8:H:35:ILE:HD11	2.38	0.58
2:B:195:ASP:O	8:H:74:PRO:HG3	2.02	0.58
3:C:137:ALA:HA	3:C:140:ARG:HB2	1.84	0.58
17:Q:67:LYS:HA	17:Q:70:ARG:HH12	1.69	0.58
1:A:979:C:H42	14:N:18:VAL:HG12	1.66	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:606:G:H5''	1:A:607:A:H5'	1.85	0.58
1:A:100:C:H2'	1:A:101:A:C8	2.38	0.58
4:D:193:ASP:N	4:D:193:ASP:OD1	2.35	0.58
2:B:136:VAL:HA	2:B:139:LYS:HB3	1.85	0.58
1:A:542:G:OP1	4:D:10:ARG:NH2	2.35	0.58
1:A:353:A:H5'	1:A:353:A:H8	1.69	0.58
1:A:951:G:N2	1:A:952:U:H1'	2.19	0.58
1:A:174:C:H2'	1:A:175:C:C6	2.37	0.58
19:S:51:VAL:O	19:S:57:HIS:HA	2.04	0.58
11:K:27:ASN:OD1	11:K:28:THR:N	2.36	0.58
1:A:300:A:H1'	1:A:565:U:O2	2.04	0.58
2:B:28:PHE:HD2	2:B:194:PRO:HG3	1.68	0.58
19:S:36:ARG:HB3	19:S:72:GLY:CA	2.34	0.58
7:G:92:SER:HB2	7:G:93:PRO:HD2	1.85	0.58
1:A:1097:C:O2'	1:A:1170:A:H1'	2.04	0.58
8:H:10:LEU:HD22	8:H:83:ILE:HD11	1.85	0.58
3:C:18:TRP:HD1	14:N:54:PRO:HA	1.69	0.58
3:C:160:ALA:HB3	3:C:164:ARG:NH2	2.19	0.58
1:A:814:A:H2'	1:A:816:A:H5''	1.85	0.58
1:A:194:C:H2'	1:A:195:A:H5''	1.85	0.58
1:A:652:U:C2	1:A:752:G:N2	2.71	0.58
1:A:56:U:H2'	1:A:57:G:C8	2.38	0.58
1:A:785:G:C2'	1:A:786:G:H5'	2.34	0.58
19:S:36:ARG:HB3	19:S:72:GLY:N	2.18	0.58
20:T:63:ILE:HD12	20:T:81:LYS:HG2	1.85	0.58
1:A:1161:C:O2'	1:A:1162:C:H5'	2.04	0.57
1:A:709:G:H2'	1:A:710:G:H8	1.69	0.57
1:A:303:A:H2'	1:A:304:U:O4'	2.04	0.57
1:A:1441:G:C2	1:A:1459:C:H5	2.21	0.57
8:H:6:ILE:O	8:H:10:LEU:HG	2.04	0.57
21:U:12:LYS:HB3	21:U:22:ARG:HH11	1.69	0.57
1:A:626:U:H2'	1:A:627:G:C8	2.39	0.57
2:B:17:PHE:H	2:B:17:PHE:HD2	1.50	0.57
1:A:1130:A:H61	1:A:1144:G:C1'	2.15	0.57
1:A:1007:C:H2'	1:A:1008:C:C5	2.39	0.57
1:A:1030(D):A:H62	1:A:1031:G:H21	1.53	0.57
3:C:132:ARG:O	3:C:136:GLN:N	2.32	0.57
1:A:448:A:OP2	1:A:485:G:N1	2.31	0.57
1:A:940:C:H1'	1:A:1374:A:H2	1.68	0.57
4:D:174:LEU:HD23	4:D:185:PHE:HA	1.87	0.57
1:A:359:U:H2'	1:A:360:A:H8	1.69	0.57
1:A:38:G:C2	1:A:397:A:C2	2.92	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1457:G:C6	1:A:1458:G:C5	2.92	0.57
2:B:87:ARG:HH11	2:B:219:VAL:HG12	1.69	0.57
2:B:54:THR:HG21	2:B:201:ILE:HD11	1.87	0.57
7:G:41:ARG:O	7:G:45:ASP:N	2.37	0.57
7:G:62:PHE:HA	7:G:124:LEU:HD22	1.86	0.57
17:Q:65:ILE:HD13	17:Q:69:LYS:HE2	1.86	0.57
1:A:763:G:H2'	1:A:764:C:H6	1.70	0.57
14:N:22:THR:HG21	14:N:35:ARG:HG2	1.86	0.57
1:A:76:C:H3'	1:A:77:G:H5''	1.87	0.57
6:F:7:ASN:OD1	6:F:7:ASN:N	2.37	0.57
13:M:37:THR:HG21	13:M:56:LEU:HA	1.87	0.57
1:A:932:C:H5'	7:G:3:ARG:HD3	1.86	0.57
1:A:1078:U:H2'	1:A:1079:G:O4'	2.05	0.57
10:J:40:LEU:HD11	10:J:69:ASN:HB3	1.86	0.57
1:A:186:C:H2'	1:A:187:C:H6	1.69	0.57
1:A:1305:G:H1'	1:A:1306:A:H8	1.70	0.57
1:A:1297:C:C4'	1:A:1298:C:H5'	2.34	0.57
1:A:437:U:OP1	4:D:155:LEU:HG	2.04	0.57
1:A:683:G:H2'	1:A:684:A:H8	1.70	0.57
1:A:359:U:H2'	1:A:360:A:C8	2.39	0.57
19:S:22:LEU:HA	19:S:26:GLY:O	2.05	0.57
1:A:1166:G:O2'	1:A:1169:A:N7	2.28	0.56
1:A:1343:G:H4'	9:I:122:ALA:HB3	1.86	0.56
6:F:96:PRO:HB3	18:R:30:ASP:CG	2.26	0.56
1:A:555:C:H2'	1:A:556:C:C6	2.40	0.56
20:T:73:HIS:HB3	20:T:74:LYS:HG2	1.87	0.56
1:A:1443:G:O6	1:A:1459:C:H1'	2.05	0.56
5:E:80:ILE:HD12	5:E:138:ALA:HB1	1.86	0.56
18:R:35:ARG:HB3	18:R:35:ARG:HH11	1.68	0.56
17:Q:45:HIS:CD2	17:Q:65:ILE:HG12	2.40	0.56
1:A:601:C:H2'	1:A:602:A:H8	1.69	0.56
1:A:858:G:O6	1:A:869:G:H3'	2.05	0.56
1:A:1237:C:N3	1:A:1337:G:N2	2.53	0.56
1:A:1160:G:C6	1:A:1181:G:N1	2.74	0.56
1:A:192:U:H2'	1:A:193:C:C6	2.35	0.56
5:E:19:MET:SD	5:E:24:ARG:HB3	2.46	0.56
2:B:88:ALA:HB1	2:B:222:ILE:HG21	1.88	0.56
2:B:74:LYS:O	2:B:78:GLN:HB2	2.05	0.56
1:A:828:A:H2'	1:A:829:G:O4'	2.05	0.56
7:G:10:ARG:O	7:G:94:ARG:NH2	2.38	0.56
6:F:67:MET:HE1	6:F:75:LEU:HD13	1.86	0.56
1:A:1142:G:C5	1:A:1143:G:H1'	2.40	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1392:G:H21	1:A:1502:A:H8	1.52	0.56
3:C:18:TRP:HE1	14:N:56:VAL:N	2.02	0.56
12:L:102:ARG:HA	12:L:107:ALA:HB1	1.86	0.56
6:F:69:GLU:O	6:F:72:VAL:HG13	2.06	0.56
1:A:991:U:H3'	1:A:1212:U:N3	2.20	0.56
1:A:1124:G:H2'	1:A:1126:U:O4	2.05	0.56
3:C:6:HIS:CD2	3:C:7:PRO:HD2	2.38	0.56
10:J:51:ARG:HB2	10:J:59:SER:OG	2.05	0.56
1:A:142:G:H2'	1:A:143:A:C8	2.40	0.56
1:A:377:G:OP1	16:P:3:LYS:HD2	2.06	0.56
1:A:335:C:H2'	1:A:336:C:C6	2.41	0.56
1:A:1458:G:N3	1:A:1458:G:H2'	2.20	0.56
1:A:1342:C:H2'	1:A:1343:G:H8	1.70	0.56
1:A:559:A:OP1	5:E:126:ARG:NH2	2.32	0.56
1:A:1072:G:C5	1:A:1073:U:C4	2.94	0.56
1:A:148:G:H2'	1:A:149:A:C8	2.39	0.56
1:A:1521:G:H2'	1:A:1522:U:C6	2.41	0.56
11:K:23:ALA:O	11:K:86:GLY:HA3	2.06	0.56
13:M:94:ARG:HH11	13:M:96:LEU:HD12	1.70	0.56
1:A:966:G:OP2	1:A:966:G:H8	1.88	0.56
1:A:1222:G:H5''	19:S:78:ARG:HE	1.70	0.56
1:A:1084:G:H21	1:A:1102:A:H62	1.54	0.56
1:A:540:G:H2'	1:A:541:G:O4'	2.06	0.56
3:C:125:GLU:HG3	3:C:189:ALA:HB1	1.88	0.56
1:A:1388:C:H2'	1:A:1389:C:C6	2.40	0.56
1:A:1516:G:H2'	1:A:1518:A:OP2	2.06	0.56
2:B:82:ARG:HG2	2:B:92:TYR:OH	2.05	0.56
1:A:631:G:H2'	1:A:632:A:C8	2.41	0.56
1:A:1492:A:H2'	1:A:1492:A:N3	2.21	0.56
22:X:76:GLY:O	22:X:80:LYS:HG2	2.05	0.55
1:A:1254:C:N3	1:A:1283:G:N2	2.54	0.55
1:A:1033:G:C8	1:A:1034:G:C8	2.94	0.55
1:A:434:U:H2'	1:A:435:C:H6	1.69	0.55
7:G:113:GLU:HG3	7:G:119:ARG:HG3	1.88	0.55
2:B:97:TRP:HH2	2:B:176:GLU:CD	2.10	0.55
1:A:189(F):U:O2	17:Q:63:ARG:NH2	2.38	0.55
7:G:71:PRO:HG3	7:G:103:TRP:CZ3	2.42	0.55
3:C:154:SER:O	3:C:196:LEU:HD13	2.07	0.55
5:E:12:LEU:HD22	5:E:13:ILE:N	2.21	0.55
1:A:266:G:H5''	1:A:267:C:C5	2.41	0.55
1:A:428:G:H4'	1:A:429:U:O5'	2.06	0.55
1:A:997:U:O4	1:A:1044:A:N1	2.39	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1060:C:O3'	10:J:59:SER:OG	2.15	0.55
20:T:90:GLN:O	20:T:93:GLU:HB3	2.06	0.55
1:A:553:A:H2'	1:A:554:C:C6	2.41	0.55
8:H:36:LEU:HA	8:H:39:LEU:HD23	1.87	0.55
1:A:97:G:O2'	1:A:98:G:H8	1.90	0.55
1:A:615:C:H2'	1:A:616:G:C8	2.42	0.55
1:A:616:G:C2	1:A:617:G:C8	2.95	0.55
1:A:626:U:H2'	1:A:627:G:H8	1.72	0.55
6:F:55:ASP:HB3	6:F:86:ARG:HH12	1.72	0.55
1:A:946:A:N6	1:A:1235:U:H3	2.03	0.55
1:A:17:U:H2'	1:A:18:C:C6	2.41	0.55
3:C:172:ARG:HH21	3:C:174:PRO:HG3	1.71	0.55
3:C:11:ARG:HB3	3:C:15:THR:HB	1.88	0.55
2:B:137:ARG:HB2	2:B:137:ARG:NH1	2.20	0.55
3:C:118:GLN:HA	3:C:121:ALA:HB3	1.87	0.55
5:E:51:VAL:O	5:E:55:VAL:HG23	2.07	0.55
1:A:1060:C:H4'	10:J:51:ARG:HB3	1.87	0.55
1:A:575:G:OP1	1:A:575:G:H4'	2.06	0.55
2:B:187:LEU:HD23	2:B:201:ILE:HB	1.87	0.55
6:F:11:ASN:HB3	6:F:14:LEU:HG	1.89	0.55
1:A:1504:G:OP1	1:A:1507:A:H4'	2.06	0.55
1:A:223:U:H2'	1:A:224:C:C6	2.41	0.55
1:A:277:C:H5''	17:Q:68:ARG:NH2	2.22	0.55
1:A:920:U:C2	1:A:921:U:C5	2.95	0.55
3:C:2:GLY:N	25:C:301:HOH:O	2.40	0.55
1:A:999:C:H2'	1:A:1000:U:C6	2.41	0.55
1:A:932:C:C5'	7:G:3:ARG:HD3	2.37	0.55
1:A:978:A:H5''	1:A:979:C:OP2	2.06	0.55
3:C:152:ILE:HD12	3:C:199:LYS:HB2	1.88	0.55
1:A:1189:C:P	10:J:51:ARG:HH22	2.30	0.55
17:Q:40:LYS:HD3	17:Q:42:TYR:CZ	2.42	0.55
17:Q:4:LYS:HD2	17:Q:5:VAL:H	1.71	0.55
7:G:75:VAL:HA	7:G:87:VAL:O	2.07	0.55
1:A:678:U:H2'	1:A:679:C:C6	2.41	0.55
5:E:76:ILE:HG22	5:E:93:PRO:HB3	1.89	0.55
10:J:48:THR:HA	10:J:62:HIS:HA	1.89	0.55
1:A:537:G:H5''	12:L:113:ARG:NH1	2.21	0.55
1:A:1486:G:H2'	1:A:1487:G:O4'	2.07	0.55
1:A:840:C:H4'	1:A:841:U:OP1	2.06	0.54
1:A:1002:G:N2	1:A:1039:C:H1'	2.19	0.54
17:Q:22:LEU:HD11	17:Q:39:SER:HB3	1.89	0.54
18:R:36:ASN:HD22	18:R:36:ASN:C	2.10	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:668:G:O2'	15:O:46:HIS:HB3	2.07	0.54
1:A:1459:C:C4	1:A:1460:A:N6	2.75	0.54
1:A:1320:C:H2'	1:A:1321:C:O4'	2.08	0.54
2:B:95:GLN:HG3	2:B:147:LYS:HD3	1.89	0.54
1:A:21:G:H2'	1:A:22:G:C8	2.42	0.54
1:A:1127:G:H5'	9:I:66:ARG:HH22	1.72	0.54
1:A:148:G:O2'	1:A:149:A:H5'	2.08	0.54
1:A:429:U:H3'	4:D:22:LYS:NZ	2.22	0.54
9:I:17:VAL:HG21	9:I:80:GLY:HA3	1.89	0.54
3:C:122:GLU:HA	3:C:125:GLU:HB2	1.88	0.54
2:B:80:ILE:HD11	2:B:215:LEU:HB2	1.88	0.54
2:B:71:VAL:O	2:B:165:VAL:HG23	2.07	0.54
1:A:1030(A):G:H2'	1:A:1030(C):G:OP2	2.08	0.54
1:A:1242:C:O2'	1:A:1303:C:H5''	2.08	0.54
7:G:23:VAL:HG22	7:G:43:PHE:HE2	1.71	0.54
1:A:160:A:H2'	1:A:161:A:O4'	2.07	0.54
1:A:1490:C:H2'	1:A:1491:G:O4'	2.07	0.54
1:A:1298:C:H5''	1:A:1299:A:C8	2.43	0.54
1:A:392:G:H5'	16:P:13:HIS:CE1	2.42	0.54
3:C:186:PHE:HE1	3:C:197:GLY:HA2	1.71	0.54
4:D:18:LYS:HA	4:D:33:MET:HG3	1.90	0.54
1:A:826:C:H2'	1:A:827:U:C6	2.42	0.54
17:Q:92:ARG:O	17:Q:95:TYR:HB2	2.07	0.54
1:A:7:G:H21	5:E:121:LYS:HG2	1.73	0.54
3:C:181:ASN:ND2	3:C:204:LEU:O	2.41	0.54
7:G:18:TYR:CE1	7:G:58:PRO:HB2	2.43	0.54
1:A:65:U:H2'	1:A:381:C:H5	1.73	0.54
1:A:1443:G:H1	1:A:1459:C:C2'	2.20	0.54
1:A:1250:A:H2	1:A:1370:G:H1'	1.73	0.54
1:A:605:U:H2'	1:A:606:G:H8	1.72	0.54
15:O:75:PRO:O	15:O:78:TYR:HB3	2.07	0.54
1:A:769:G:H4'	1:A:1513:A:H4'	1.90	0.54
1:A:1260:C:OP1	1:A:1284:C:H4'	2.08	0.54
1:A:1181:G:N2	1:A:1182:G:H22	2.06	0.54
4:D:173:TRP:CD2	4:D:189:PRO:HG3	2.43	0.54
1:A:922:G:N3	1:A:1398:A:H2	2.06	0.54
1:A:1266:G:H8	1:A:1266:G:OP2	1.90	0.54
9:I:70:LYS:HA	9:I:73:GLN:HB2	1.90	0.54
1:A:1507:A:O3'	25:A:2029:HOH:O	2.18	0.54
1:A:1157:A:C2	1:A:1180:A:H2'	2.43	0.54
3:C:43:LEU:O	3:C:47:LEU:HB2	2.08	0.54
1:A:60:A:H4'	1:A:61:G:O5'	2.08	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1076:C:H42	1:A:1081:G:H1	1.56	0.54
2:B:24:TRP:HZ3	2:B:29:ALA:HB2	1.73	0.54
1:A:393:A:OP2	16:P:12:LYS:HD2	2.08	0.54
13:M:19:LEU:HA	13:M:22:ILE:HD12	1.89	0.53
9:I:29:ASN:H	9:I:63:ILE:HG22	1.73	0.53
3:C:30:ARG:HG3	3:C:31:HIS:CD2	2.43	0.53
1:A:15:G:H8	1:A:1396:A:HO2'	1.56	0.53
1:A:279:A:C5	17:Q:98:LEU:HD23	2.42	0.53
1:A:950:U:O4	1:A:1231:G:O6	2.26	0.53
8:H:85:ARG:NE	8:H:87:SER:O	2.41	0.53
7:G:26:PHE:HZ	7:G:105:VAL:HB	1.73	0.53
1:A:1305:G:H2'	21:U:4:GLY:O	2.08	0.53
1:A:1304:G:N2	1:A:1332:A:OP2	2.38	0.53
5:E:127:ASN:O	5:E:131:ILE:HG12	2.09	0.53
1:A:1394:A:N1	1:A:1500:A:O2'	2.36	0.53
19:S:46:GLY:HA2	19:S:61:TYR:HE1	1.73	0.53
7:G:114:ARG:O	7:G:119:ARG:NH1	2.36	0.53
7:G:113:GLU:HB2	7:G:118:VAL:HB	1.90	0.53
15:O:69:TYR:HA	15:O:72:ARG:HD3	1.89	0.53
1:A:35:G:H2'	1:A:36:C:C6	2.43	0.53
1:A:1189:C:OP1	10:J:51:ARG:NH2	2.35	0.53
1:A:598:U:H2'	1:A:599:C:C6	2.43	0.53
1:A:35:G:N2	1:A:550:G:H1'	2.23	0.53
1:A:262:A:H2'	1:A:263:A:C8	2.43	0.53
6:F:7:ASN:ND2	18:R:34:TYR:HE1	2.05	0.53
1:A:157:G:H1	1:A:164:U:H3	1.55	0.53
1:A:447:G:H2'	1:A:485:G:N2	2.22	0.53
3:C:148:GLY:HA3	3:C:172:ARG:H	1.73	0.53
1:A:407:G:O2'	4:D:116:GLN:HG3	2.09	0.53
1:A:1192:C:H6	1:A:1192:C:H3'	1.74	0.53
1:A:407:G:H1	1:A:435:C:H42	1.55	0.53
10:J:45:ARG:HB3	10:J:65:LEU:HB3	1.91	0.53
12:L:24:VAL:HG13	12:L:98:TYR:CE2	2.43	0.53
8:H:120:THR:H	8:H:123:GLU:HB2	1.73	0.53
1:A:1457:G:C6	1:A:1458:G:N7	2.76	0.53
1:A:1349:A:H5'	9:I:120:ARG:HB3	1.90	0.53
3:C:23:TYR:CE2	10:J:95:GLU:HB2	2.44	0.53
17:Q:50:LYS:HD3	17:Q:51:TYR:CE1	2.44	0.53
1:A:414:A:H2'	1:A:415:A:C8	2.44	0.53
8:H:6:ILE:HB	8:H:85:ARG:NH1	2.12	0.53
1:A:581:G:N2	1:A:760:G:N7	2.57	0.53
13:M:87:TYR:HB2	19:S:73:GLU:HA	1.90	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:E:69:VAL:O	5:E:71:LEU:N	2.41	0.53
1:A:611:A:H61	1:A:629:G:H1	1.55	0.53
1:A:738:C:H2'	1:A:739:C:H6	1.73	0.53
3:C:112:SER:OG	3:C:112:SER:O	2.25	0.53
1:A:323:U:O3'	20:T:22:ARG:HD3	2.09	0.53
1:A:646:U:H2'	1:A:647:C:H6	1.74	0.53
1:A:380:G:N2	1:A:384:G:C5	2.77	0.53
1:A:951:G:C6	1:A:1231:G:C6	2.97	0.53
2:B:51:LEU:O	2:B:55:PHE:HD2	1.92	0.53
1:A:1030:C:N4	1:A:1031:G:C5	2.71	0.53
1:A:1208:C:H2'	1:A:1209:C:C6	2.43	0.53
7:G:140:ASP:O	7:G:143:ARG:HD2	2.08	0.53
7:G:111:ARG:HH22	7:G:122:HIS:HB3	1.74	0.53
6:F:97:PHE:HD2	18:R:31:LEU:HD21	1.74	0.53
1:A:943:U:H2'	1:A:944:G:C8	2.44	0.53
2:B:162:ILE:HD11	2:B:184:VAL:HG22	1.89	0.53
1:A:932:C:N4	1:A:1385:G:C6	2.77	0.53
1:A:1316:G:H4'	14:N:18:VAL:HG21	1.90	0.53
1:A:169:C:H2'	1:A:170:U:C6	2.43	0.53
1:A:59:A:H3'	1:A:331:G:H22	1.73	0.53
1:A:1265:G:H2'	1:A:1266:G:C8	2.44	0.53
11:K:32:ILE:HD11	11:K:68:ALA:HB1	1.91	0.53
5:E:68:GLU:CD	5:E:70:PRO:HG3	2.30	0.53
1:A:742:G:OP2	15:O:35:ARG:NH2	2.42	0.53
1:A:493:G:HO2'	1:A:494:U:H6	1.55	0.53
4:D:13:ARG:HD2	4:D:38:TYR:O	2.09	0.52
1:A:91:C:H2'	1:A:92:C:C6	2.44	0.52
1:A:1324:A:C5'	1:A:1363:C:H5''	2.39	0.52
1:A:1244:C:H2'	1:A:1245:A:C8	2.44	0.52
1:A:1247:U:H1'	1:A:1291:G:N2	2.23	0.52
6:F:22:GLU:O	6:F:26:ILE:HG13	2.08	0.52
1:A:292:G:N7	1:A:293:G:H1'	2.24	0.52
7:G:26:PHE:CZ	7:G:105:VAL:HB	2.45	0.52
1:A:1298:C:H4'	1:A:1299:A:C4	2.44	0.52
1:A:1300:G:N1	1:A:1334:G:H2'	2.19	0.52
1:A:1252:A:H2	1:A:1355:G:H1'	1.72	0.52
1:A:79:G:N2	1:A:91:C:O2	2.43	0.52
1:A:336:C:H2'	1:A:337:C:H6	1.73	0.52
1:A:609:A:H5'	16:P:18:ARG:HH22	1.74	0.52
10:J:10:GLY:HA3	10:J:94:VAL:HG22	1.91	0.52
9:I:28:VAL:HB	9:I:36:TYR:CB	2.34	0.52
4:D:32:ALA:O	4:D:36:ARG:N	2.42	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1162:C:H2'	1:A:1163:C:H6	1.75	0.52
11:K:73:MET:HE2	11:K:103:LEU:HD13	1.92	0.52
12:L:32:PHE:HE1	12:L:86:ARG:HG3	1.74	0.52
1:A:1412:C:H2'	1:A:1413:A:C8	2.45	0.52
1:A:1191:A:OP2	3:C:3:ASN:ND2	2.42	0.52
1:A:1442(A):G:C5	1:A:1442(B):A:C2	2.96	0.52
1:A:437:U:O3'	4:D:125:HIS:NE2	2.39	0.52
1:A:501:C:H1'	1:A:549:C:H1'	1.92	0.52
1:A:1441:G:C3'	1:A:1459:C:N4	2.73	0.52
1:A:1030(C):G:N7	1:A:1031:G:N2	2.58	0.52
21:U:12:LYS:O	21:U:16:GLY:N	2.37	0.52
21:U:12:LYS:HB3	21:U:22:ARG:NH1	2.24	0.52
1:A:1060:C:N4	25:C:301:HOH:O	2.42	0.52
1:A:1459:C:C2'	1:A:1460:A:C8	2.93	0.52
1:A:1098:C:H5'	1:A:1169:A:H1'	1.92	0.52
1:A:586:C:H2'	1:A:587:G:H5'	1.92	0.52
1:A:1125:U:H5'	1:A:1126:U:C5	2.44	0.52
1:A:18:C:H5''	5:E:127:ASN:HD21	1.74	0.52
1:A:1369:C:H2'	1:A:1370:G:C8	2.45	0.52
9:I:20:ARG:HB3	9:I:60:ASP:O	2.10	0.52
1:A:785:G:H2'	1:A:786:G:H5'	1.92	0.52
6:F:96:PRO:HB3	18:R:30:ASP:OD2	2.09	0.52
2:B:21:ARG:NE	2:B:21:ARG:H	2.08	0.52
3:C:55:VAL:HG12	3:C:57:ILE:HG13	1.91	0.52
1:A:1048:G:C6	1:A:1210:C:N4	2.77	0.52
1:A:1053:G:N7	1:A:1199:U:H2'	2.25	0.52
1:A:1305:G:OP2	1:A:1305:G:C8	2.63	0.52
1:A:860:A:N6	1:A:861:G:C2	2.78	0.52
3:C:153:VAL:HA	3:C:197:GLY:O	2.10	0.52
7:G:113:GLU:OE2	7:G:119:ARG:HA	2.09	0.52
2:B:97:TRP:CZ2	2:B:101:MET:HB2	2.44	0.52
8:H:121:ASP:OD1	8:H:121:ASP:N	2.40	0.52
1:A:1109:C:O5'	1:A:1109:C:H6	1.93	0.52
11:K:26:ASN:O	25:K:201:HOH:O	2.18	0.52
1:A:1327:C:H2'	1:A:1328:C:O4'	2.09	0.52
3:C:134:ILE:HG22	3:C:168:ALA:HB3	1.91	0.52
11:K:21:ILE:HB	11:K:84:VAL:HG22	1.90	0.52
19:S:49:ILE:O	19:S:59:PRO:HA	2.09	0.52
19:S:16:LEU:CA	19:S:20:LEU:HB2	2.37	0.52
1:A:1239:A:H4'	1:A:1240:U:OP1	2.09	0.52
1:A:1492:A:OP1	1:A:1492:A:H4'	2.10	0.52
1:A:1458:G:H3'	1:A:1459:C:H5''	1.92	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1459:C:C5'	1:A:1460:A:OP2	2.57	0.52
1:A:1004:A:H2	1:A:1037:C:N4	2.08	0.52
1:A:1238:A:N7	1:A:1299:A:N1	2.57	0.52
1:A:977:A:H1'	1:A:982:U:H3	1.74	0.52
7:G:142:GLU:CB	7:G:143:ARG:HH21	2.22	0.52
5:E:14:ARG:HE	5:E:16:THR:HG22	1.74	0.52
1:A:1128:C:N3	1:A:1143:G:N2	2.47	0.51
1:A:676:A:O2'	1:A:677:U:H5'	2.10	0.51
1:A:1029:C:N3	1:A:1032:G:O6	2.43	0.51
18:R:66:LEU:O	18:R:70:ILE:HG13	2.11	0.51
12:L:25:PRO:C	12:L:27:LEU:H	2.11	0.51
1:A:971:G:H1	1:A:1363(A):A:H5'	1.75	0.51
9:I:10:ARG:CB	9:I:75:ASP:HB2	2.39	0.51
1:A:1052:U:H2'	1:A:1055:A:OP1	2.09	0.51
20:T:61:SER:O	20:T:65:LYS:HG2	2.11	0.51
1:A:826:C:H4'	8:H:12:ARG:HD3	1.91	0.51
2:B:16:HIS:CD2	2:B:209:ARG:HG3	2.45	0.51
1:A:666:G:H5'	1:A:726:C:H1'	1.93	0.51
16:P:72:ARG:HG2	16:P:73:LEU:HD23	1.92	0.51
1:A:1347:G:H1'	1:A:1348:U:H5	1.75	0.51
1:A:958:A:N3	1:A:985:C:O2'	2.37	0.51
1:A:746:A:H2'	1:A:747:C:C6	2.45	0.51
10:J:12:ASP:C	10:J:68:HIS:HD2	2.13	0.51
1:A:954:G:N2	1:A:1227:A:H62	2.08	0.51
2:B:55:PHE:CD1	2:B:58:ILE:HD12	2.45	0.51
1:A:1157:A:N1	1:A:1180:A:H2'	2.25	0.51
9:I:28:VAL:O	9:I:36:TYR:HB2	2.10	0.51
1:A:475:G:H2'	1:A:476:G:C8	2.46	0.51
1:A:1137:C:H5'	1:A:1138:G:C6	2.45	0.51
3:C:30:ARG:HB3	14:N:36:PHE:O	2.11	0.51
17:Q:66:SER:O	17:Q:69:LYS:N	2.26	0.51
1:A:806:C:H2'	1:A:807:A:H8	1.76	0.51
1:A:1220:G:H2'	1:A:1221:G:C8	2.45	0.51
1:A:939:G:N3	1:A:1375:A:H2	2.08	0.51
1:A:1157:A:H61	1:A:1178:G:H21	1.58	0.51
15:O:87:ILE:HG22	15:O:88:ARG:H	1.75	0.51
16:P:75:ARG:HA	16:P:80:PHE:HD1	1.75	0.51
1:A:659:U:H2'	1:A:660:G:O4'	2.11	0.51
1:A:123:C:O2'	1:A:290:C:O2	2.20	0.51
1:A:586:C:O2'	1:A:878:G:H4'	2.11	0.51
13:M:14:ARG:CZ	13:M:41:PRO:HB2	2.40	0.51
1:A:757:U:OP1	1:A:822:C:O2'	2.28	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1084:G:H5'	1:A:1102:A:OP2	2.10	0.51
8:H:31:PHE:O	8:H:35:ILE:HG13	2.11	0.51
12:L:110:VAL:HG23	12:L:120:TYR:HB3	1.92	0.51
1:A:50:A:H8	1:A:50:A:OP1	1.93	0.51
9:I:9:ARG:NH1	9:I:104:ARG:HE	2.09	0.51
1:A:1305:G:H8	21:U:5:ASP:HA	1.76	0.51
1:A:1241:G:H5''	1:A:1242:C:OP2	2.10	0.51
1:A:1240:U:O5'	1:A:1241:G:H8	1.93	0.51
9:I:31:GLN:NE2	9:I:36:TYR:HD1	2.09	0.51
3:C:36:ASP:O	3:C:40:ARG:HG2	2.11	0.51
7:G:69:VAL:HA	7:G:138:LYS:HB2	1.93	0.51
1:A:1188:A:H2'	1:A:1189:C:H5'	1.93	0.51
12:L:32:PHE:O	12:L:33:ARG:HD2	2.10	0.51
18:R:36:ASN:ND2	18:R:39:VAL:H	2.09	0.51
4:D:128:VAL:HA	4:D:145:GLU:O	2.11	0.51
1:A:990:C:C4	1:A:991:U:C4	2.99	0.51
1:A:838:G:N2	1:A:849:C:C2	2.79	0.51
13:M:18:ALA:HB2	13:M:45:VAL:HG21	1.92	0.51
2:B:84:GLU:HB3	2:B:219:VAL:HG21	1.93	0.51
2:B:20:GLU:HG3	2:B:191:ASP:OD1	2.10	0.51
1:A:1359:C:OP1	14:N:22:THR:OG1	2.20	0.51
7:G:137:LYS:HA	7:G:140:ASP:CG	2.32	0.51
1:A:184:G:C4'	1:A:224:C:H4'	2.41	0.51
15:O:39:LEU:HD13	15:O:56:LEU:HD23	1.92	0.51
2:B:12:GLU:O	2:B:16:HIS:ND1	2.40	0.51
1:A:865:A:H2'	1:A:866:C:C6	2.46	0.51
13:M:10:PRO:HG2	13:M:45:VAL:HG11	1.93	0.51
1:A:1347:G:O2'	1:A:1373:G:N1	2.38	0.51
5:E:135:THR:O	5:E:138:ALA:HB3	2.11	0.51
19:S:10:PHE:CE2	19:S:38:SER:HB3	2.45	0.51
1:A:1063:C:OP2	1:A:1064:G:O2'	2.27	0.51
20:T:16:HIS:O	20:T:19:SER:N	2.44	0.51
8:H:63:LEU:HB2	8:H:65:TYR:CE1	2.46	0.51
1:A:1345:U:OP1	9:I:120:ARG:HD3	2.11	0.51
1:A:1004:A:H2'	1:A:1036:G:O6	2.11	0.51
1:A:1284:C:H3'	1:A:1285:A:H2'	1.93	0.51
1:A:616:G:C2	1:A:617:G:N7	2.79	0.51
20:T:69:GLY:O	20:T:73:HIS:NE2	2.43	0.51
1:A:6:G:O2'	1:A:7:G:H5''	2.11	0.51
16:P:11:SER:OG	16:P:12:LYS:N	2.44	0.51
1:A:460:G:O6	1:A:470:C:H5''	2.11	0.51
8:H:63:LEU:HB2	8:H:65:TYR:HE1	1.75	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:L:6:THR:OG1	12:L:9:GLN:HG3	2.10	0.51
1:A:838:G:H2'	1:A:839:U:H5''	1.93	0.50
1:A:1006:C:O2	1:A:1024:G:H1'	2.10	0.50
1:A:966:G:H5''	1:A:969:A:N7	2.26	0.50
1:A:1254:C:N4	1:A:1283:G:H1	2.06	0.50
1:A:658:G:C2	1:A:749:C:N3	2.79	0.50
10:J:62:HIS:H	10:J:62:HIS:CD2	2.29	0.50
1:A:1192:C:C5	1:A:1193:G:C8	2.99	0.50
1:A:189:G:H2'	1:A:189(A):C:H6	1.76	0.50
3:C:56:ASP:O	3:C:67:THR:HB	2.11	0.50
15:O:82:ILE:O	15:O:86:GLY:N	2.44	0.50
1:A:688:G:O2'	1:A:704:A:N1	2.36	0.50
12:L:83:VAL:HG13	12:L:100:ILE:HG23	1.93	0.50
1:A:586:C:C2'	1:A:587:G:H5'	2.41	0.50
1:A:1055:A:C2	1:A:1056:U:H1'	2.46	0.50
1:A:1029:C:O2	1:A:1032:G:N1	2.44	0.50
1:A:1285:A:H4'	1:A:1286:A:O5'	2.11	0.50
1:A:750:G:C2	15:O:23:GLY:HA3	2.46	0.50
1:A:436:C:O2'	1:A:437:U:OP2	2.25	0.50
14:N:23:ARG:HD2	14:N:28:GLY:C	2.31	0.50
17:Q:45:HIS:HD2	17:Q:65:ILE:HG12	1.76	0.50
7:G:87:VAL:HG22	7:G:151:TYR:HB3	1.93	0.50
1:A:1058:G:N2	10:J:53:PRO:HG3	2.26	0.50
1:A:1346:A:H1'	1:A:1347:G:H5''	1.94	0.50
1:A:1378:C:H5''	1:A:1379:G:OP2	2.11	0.50
1:A:1016:A:O2'	1:A:1217:C:O2'	2.25	0.50
7:G:115:ARG:O	7:G:119:ARG:HD3	2.12	0.50
1:A:601:C:H2'	1:A:602:A:C8	2.46	0.50
6:F:69:GLU:N	6:F:69:GLU:OE1	2.45	0.50
1:A:1510:U:H2'	1:A:1511:G:C8	2.46	0.50
10:J:28:ARG:CB	10:J:34:VAL:HG21	2.42	0.50
1:A:1457:G:N1	1:A:1458:G:C5	2.79	0.50
1:A:1141:C:H2'	1:A:1142:G:C8	2.34	0.50
1:A:673:G:O3'	6:F:87:ARG:NH2	2.44	0.50
9:I:28:VAL:HG23	9:I:33:PHE:HA	1.94	0.50
1:A:1173:G:C5	1:A:1174:G:N7	2.79	0.50
2:B:167:PRO:CG	2:B:188:ALA:HB2	2.42	0.50
1:A:187:C:H5''	20:T:86:ARG:HG3	1.93	0.50
10:J:63:PHE:HA	14:N:58:LYS:HA	1.94	0.50
1:A:1459:C:O5'	1:A:1460:A:OP2	2.30	0.50
2:B:187:LEU:HD13	2:B:205:ASP:HA	1.93	0.50
1:A:1328:C:H5''	13:M:28:ALA:HB3	1.94	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
9:I:114:TYR:CD2	9:I:114:TYR:N	2.80	0.50
1:A:1117:G:H1'	1:A:1184:G:N2	2.26	0.50
1:A:749:C:H2'	1:A:750:G:H8	1.77	0.50
1:A:407:G:O6	1:A:435:C:N4	2.45	0.50
7:G:24:THR:HG22	7:G:27:ILE:HD11	1.93	0.50
1:A:1088:G:N2	1:A:1089:G:H1'	2.27	0.50
1:A:976:G:OP2	14:N:32:SER:N	2.43	0.50
9:I:71:SER:HA	9:I:74:ILE:HB	1.94	0.50
1:A:1352:C:H1'	1:A:1371:G:N2	2.26	0.50
3:C:186:PHE:HA	3:C:198:VAL:O	2.11	0.50
1:A:1151:A:N3	10:J:70:ARG:NH2	2.60	0.50
1:A:918:A:H2'	1:A:919:A:H8	1.74	0.50
1:A:811:C:H4'	1:A:900:A:N6	2.27	0.50
14:N:2:ALA:HB1	14:N:6:LEU:HD13	1.92	0.50
16:P:20:VAL:HG23	16:P:34:GLU:O	2.12	0.50
1:A:1391:U:H2'	1:A:1392:G:C8	2.46	0.50
2:B:80:ILE:HG13	2:B:215:LEU:HD12	1.93	0.50
1:A:1339:A:N6	1:A:1340:A:N3	2.59	0.50
1:A:544:G:C2	1:A:545:C:C2	3.00	0.50
21:U:6:ARG:HA	21:U:11:GLY:HA3	1.92	0.50
13:M:3:ARG:HB3	13:M:8:GLU:O	2.12	0.50
1:A:1309:G:C6	1:A:1329:A:C6	3.00	0.50
7:G:143:ARG:O	7:G:147:ALA:N	2.37	0.50
13:M:69:GLU:C	13:M:71:ARG:H	2.15	0.50
7:G:113:GLU:HB2	7:G:119:ARG:HG3	1.92	0.50
5:E:104:ALA:O	5:E:107:ARG:HG2	2.12	0.50
14:N:26:ARG:HH11	14:N:47:LEU:HD21	1.76	0.50
1:A:1025:U:O2	1:A:1036:G:O6	2.30	0.49
1:A:966:G:H5''	1:A:969:A:C8	2.46	0.49
1:A:438:G:H4'	4:D:123:HIS:ND1	2.27	0.49
1:A:1111:A:O5'	1:A:1111:A:H8	1.94	0.49
1:A:414:A:H2'	1:A:415:A:H8	1.77	0.49
1:A:1278:U:H5'	1:A:1279:A:O4'	2.12	0.49
2:B:84:GLU:OE1	2:B:216:SER:HA	2.12	0.49
2:B:28:PHE:CZ	2:B:189:ASP:HA	2.47	0.49
1:A:1370:G:H5''	9:I:12:GLU:OE2	2.12	0.49
4:D:9:CYS:SG	4:D:22:LYS:NZ	2.70	0.49
1:A:55:A:C5	1:A:56:U:C5	3.00	0.49
1:A:502:G:C2	1:A:503:C:C2	3.00	0.49
15:O:15:PHE:CE2	15:O:84:LYS:HD2	2.48	0.49
13:M:33:ALA:HA	13:M:36:LYS:CB	2.43	0.49
1:A:191:G:N2	20:T:103:GLY:HA2	2.26	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:218:ALA:O	2:B:222:ILE:HG13	2.12	0.49
1:A:448:A:P	1:A:485:G:H22	2.35	0.49
3:C:175:LEU:HD12	3:C:175:LEU:H	1.77	0.49
1:A:1001(A):G:H2'	1:A:1002:G:H8	1.77	0.49
1:A:103:C:P	20:T:17:ARG:HH21	2.36	0.49
3:C:139:GLN:O	3:C:143:GLU:HB2	2.13	0.49
2:B:219:VAL:O	2:B:222:ILE:HB	2.12	0.49
1:A:1371:G:H2'	1:A:1372:U:O4'	2.12	0.49
1:A:757:U:H2'	1:A:758:G:O4'	2.11	0.49
21:U:12:LYS:HZ1	21:U:19:GLY:HA3	1.76	0.49
1:A:77:G:O6	1:A:78:G:N1	2.45	0.49
7:G:103:TRP:CE2	7:G:137:LYS:HD2	2.47	0.49
1:A:1094:G:H22	1:A:1105:A:H62	1.61	0.49
13:M:50:GLU:O	13:M:53:VAL:HG12	2.12	0.49
1:A:1513:A:H2'	1:A:1514:C:C6	2.47	0.49
2:B:213:LEU:HD22	2:B:214:ILE:HD13	1.95	0.49
4:D:25:ARG:O	4:D:27:TYR:N	2.43	0.49
8:H:51:VAL:HG11	8:H:60:ARG:HG3	1.94	0.49
6:F:49:ALA:HB2	18:R:78:LEU:O	2.12	0.49
5:E:91:LEU:HD12	5:E:120:THR:HG22	1.94	0.49
1:A:35:G:N1	1:A:550:G:C2	2.81	0.49
22:X:53:THR:HG23	22:X:62:HIS:HB3	1.94	0.49
1:A:1212:U:H5'	1:A:1213:A:OP1	2.13	0.49
1:A:1023:G:OP2	1:A:1023:G:H8	1.95	0.49
1:A:254:G:OP1	17:Q:67:LYS:O	2.30	0.49
7:G:137:LYS:HD3	7:G:140:ASP:HB2	1.95	0.49
7:G:51:GLN:HG3	7:G:58:PRO:HD3	1.95	0.49
1:A:951:G:C5	1:A:1231:G:C6	3.01	0.49
1:A:974:A:H8	1:A:974:A:OP1	1.95	0.49
7:G:29:LYS:HB3	7:G:105:VAL:HG11	1.93	0.49
1:A:674:G:H2'	1:A:675:A:C8	2.47	0.49
1:A:1251:A:H4'	9:I:12:GLU:OE2	2.12	0.49
7:G:71:PRO:HB3	7:G:138:LYS:O	2.13	0.49
4:D:108:LEU:CD1	4:D:174:LEU:HD13	2.43	0.49
10:J:51:ARG:CZ	10:J:61:GLU:HB3	2.43	0.49
17:Q:65:ILE:H	17:Q:65:ILE:HD12	1.78	0.49
20:T:26:ASN:OD1	20:T:71:THR:HG23	2.12	0.49
1:A:950:U:N3	1:A:1231:G:N1	2.42	0.49
2:B:185:ILE:HA	2:B:199:TYR:O	2.13	0.49
17:Q:76:LEU:HD21	17:Q:79:SER:N	2.27	0.49
1:A:93:G:O2'	1:A:96:U:H5'	2.13	0.49
1:A:186:C:O3'	20:T:82:SER:HB2	2.13	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:993:G:H2'	1:A:995:C:H41	1.78	0.49
1:A:1469:G:H2'	1:A:1470:G:C8	2.48	0.49
1:A:396:G:O2'	1:A:398:C:OP1	2.19	0.49
1:A:1210:C:H3'	1:A:1211:U:C5'	2.43	0.49
1:A:952:U:O2	1:A:1229:A:N1	2.46	0.49
1:A:986:A:H2'	1:A:987:G:C8	2.47	0.49
1:A:1026:G:N3	1:A:1027:C:H5'	2.28	0.49
1:A:448:A:OP2	1:A:485:G:N2	2.45	0.49
17:Q:86:GLU:HG2	17:Q:90:ILE:HD11	1.95	0.49
1:A:868:C:H2'	1:A:869:G:O4'	2.13	0.49
1:A:1240:U:H3'	1:A:1241:G:O4'	2.13	0.49
3:C:32:LEU:HD21	3:C:59:ARG:CZ	2.43	0.49
3:C:148:GLY:CA	3:C:172:ARG:H	2.25	0.49
19:S:12:ASP:HB2	19:S:38:SER:OG	2.13	0.49
17:Q:66:SER:HB3	17:Q:69:LYS:HB2	1.95	0.49
1:A:830:G:H2'	1:A:831:U:O4'	2.13	0.49
2:B:47:THR:HG23	2:B:202:PRO:HG2	1.95	0.49
1:A:1144:G:H21	1:A:1146:A:H61	1.60	0.48
1:A:1320:C:H42	19:S:36:ARG:HE	1.61	0.48
1:A:266:G:H5''	1:A:267:C:H5	1.77	0.48
7:G:66:VAL:HA	7:G:69:VAL:HG23	1.93	0.48
13:M:23:TYR:CD1	13:M:67:GLU:HA	2.48	0.48
20:T:56:MET:HE2	20:T:88:VAL:HG21	1.95	0.48
1:A:766:A:H2'	1:A:767:A:O4'	2.12	0.48
12:L:70:ILE:HG12	12:L:100:ILE:HD13	1.95	0.48
3:C:139:GLN:HA	3:C:142:MET:HB2	1.93	0.48
1:A:881:G:P	12:L:12:ARG:HH22	2.35	0.48
1:A:1124:G:H1'	10:J:38:ILE:HG21	1.95	0.48
1:A:1373:G:OP1	7:G:36:LYS:HB2	2.13	0.48
9:I:20:ARG:HG2	9:I:21:PRO:O	2.13	0.48
1:A:1069:C:H4'	1:A:1192:C:O2	2.13	0.48
1:A:420:U:N3	1:A:422:C:N3	2.61	0.48
1:A:346:G:H2'	1:A:347:G:O4'	2.14	0.48
12:L:42:THR:HB	12:L:52:LEU:HD12	1.94	0.48
1:A:1165:C:C2	1:A:1171:G:N2	2.81	0.48
1:A:1004:A:C2	1:A:1037:C:N4	2.82	0.48
2:B:77:ALA:HB1	2:B:211:ILE:HG21	1.94	0.48
1:A:9:G:H2'	1:A:10:A:C8	2.48	0.48
3:C:132:ARG:O	3:C:136:GLN:HB2	2.13	0.48
1:A:1013:G:HO2'	1:A:1014:A:H8	1.58	0.48
1:A:189(A):C:H42	1:A:189(J):G:H1	1.60	0.48
1:A:512:U:H2'	1:A:513:C:H6	1.79	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:D:120:LEU:HB3	4:D:126:ILE:HD11	1.94	0.48
1:A:390:C:H2'	1:A:391:G:C8	2.49	0.48
1:A:1071:C:H5''	5:E:49:PRO:HG2	1.94	0.48
1:A:1086:U:H4'	1:A:1389:C:H5''	1.94	0.48
1:A:684:A:H2'	1:A:685:G:C8	2.47	0.48
1:A:625:G:C6	1:A:626:U:C4	3.01	0.48
2:B:37:ASN:O	2:B:39:ILE:HD12	2.13	0.48
8:H:37:ARG:HE	8:H:37:ARG:HB3	1.50	0.48
1:A:859:A:H2'	1:A:860:A:O4'	2.13	0.48
1:A:560:U:OP2	25:A:1919:HOH:O	2.20	0.48
1:A:1508:G:P	25:A:2029:HOH:O	2.71	0.48
3:C:111:LEU:HD23	3:C:141:VAL:HG13	1.94	0.48
17:Q:76:LEU:HD21	17:Q:79:SER:H	1.79	0.48
1:A:1256:A:H5'	1:A:1258:G:O4'	2.13	0.48
1:A:626:U:C2	1:A:627:G:C8	3.02	0.48
6:F:19:LEU:HD11	6:F:59:TYR:CZ	2.49	0.48
1:A:1446:U:H4'	1:A:1447:A:C2	2.49	0.48
2:B:42:ILE:HD12	2:B:203:GLY:HA2	1.96	0.48
1:A:1460:A:H8	1:A:1460:A:O5'	1.95	0.48
1:A:990:C:N4	1:A:991:U:O4	2.47	0.48
1:A:1023:G:C2'	1:A:1024:G:H5'	2.43	0.48
7:G:88:PRO:O	7:G:89:MET:HG3	2.13	0.48
1:A:1245:A:N6	1:A:1292:U:H3	2.10	0.48
17:Q:31:LEU:HD23	17:Q:32:TYR:CZ	2.48	0.48
8:H:111:ILE:HD12	8:H:111:ILE:H	1.78	0.48
1:A:1210:C:H1'	1:A:1214:C:C2	2.49	0.48
9:I:65:VAL:HG13	9:I:73:GLN:NE2	2.28	0.48
1:A:1003:G:H1	1:A:1037:C:N4	2.12	0.48
10:J:9:ARG:O	10:J:95:GLU:N	2.28	0.48
2:B:97:TRP:CZ3	2:B:99:GLY:HA2	2.49	0.48
11:K:33:THR:HA	11:K:40:ILE:HG12	1.95	0.48
1:A:1427:U:H2'	1:A:1428:A:C8	2.49	0.48
1:A:636:U:H2'	1:A:637:G:H8	1.78	0.48
2:B:102:LEU:HB3	2:B:180:LEU:HD12	1.96	0.48
1:A:1251:A:H61	1:A:1354:C:HO2'	1.55	0.48
1:A:1508:G:H2'	1:A:1509:C:C6	2.49	0.48
16:P:28:ARG:HG2	16:P:29:ASP:OD2	2.13	0.48
1:A:1085:U:C2	1:A:1094:G:O6	2.67	0.48
1:A:921:U:O2	5:E:19:MET:HB2	2.14	0.48
1:A:38:G:H22	1:A:397:A:H5''	1.78	0.48
4:D:101:LEU:HD23	4:D:102:ASP:N	2.29	0.48
1:A:962:C:H2'	1:A:963:G:O4'	2.13	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:968:A:H8	1:A:968:A:OP1	1.97	0.48
7:G:32:ARG:HD3	7:G:32:ARG:HA	1.50	0.48
3:C:7:PRO:O	3:C:11:ARG:NH1	2.47	0.48
1:A:1149:C:H2'	1:A:1150:U:C6	2.49	0.48
1:A:300:A:O2'	1:A:564:C:N3	2.38	0.48
10:J:62:HIS:N	10:J:62:HIS:CD2	2.81	0.48
1:A:1276:G:H2'	1:A:1277:C:O4'	2.13	0.48
11:K:92:GLU:HB3	11:K:96:ARG:HH12	1.77	0.48
2:B:117:GLU:O	2:B:120:ALA:HB3	2.14	0.48
1:A:989:C:C4	1:A:990:C:C4	3.02	0.48
1:A:1236:A:O2'	1:A:1304:G:H4'	2.13	0.48
1:A:1251:A:N3	1:A:1369:C:O2'	2.34	0.48
20:T:25:ARG:O	20:T:29:LYS:HG3	2.14	0.48
1:A:1360:A:C6	14:N:18:VAL:HG11	2.49	0.48
3:C:175:LEU:HD23	3:C:201:TYR:HE2	1.79	0.48
1:A:324:G:OP2	25:A:1978:HOH:O	2.20	0.48
12:L:32:PHE:HB3	12:L:84:LEU:HD11	1.95	0.48
1:A:1516:G:N1	1:A:1519:A:OP2	2.45	0.48
8:H:20:TYR:HA	8:H:65:TYR:CE2	2.49	0.48
1:A:671:G:H2'	1:A:672:U:C6	2.48	0.48
1:A:1442(A):G:H3'	1:A:1442(B):A:H5''	1.96	0.47
1:A:673:G:H5''	6:F:87:ARG:CZ	2.44	0.47
1:A:1296:C:H5''	1:A:1302:U:C4	2.49	0.47
16:P:28:ARG:NH1	16:P:29:ASP:OD2	2.46	0.47
1:A:176:C:H2'	1:A:177:C:C6	2.49	0.47
3:C:134:ILE:HD11	3:C:153:VAL:HG23	1.95	0.47
4:D:108:LEU:HD12	4:D:174:LEU:HD13	1.96	0.47
1:A:57:G:H2'	1:A:58:C:C6	2.49	0.47
1:A:458:C:H2'	1:A:460:G:C8	2.49	0.47
16:P:4:ILE:HB	16:P:66:PRO:HB3	1.94	0.47
1:A:1442(A):G:H2'	1:A:1442(B):A:O4'	2.14	0.47
1:A:1089:G:N1	1:A:1096:C:N4	2.39	0.47
13:M:85:GLY:HA3	13:M:86:CYS:HA	1.32	0.47
13:M:92:HIS:CE1	13:M:98:VAL:HG21	2.49	0.47
1:A:149:A:O2'	1:A:150:C:C6	2.67	0.47
10:J:44:VAL:HG22	10:J:66:ARG:HD3	1.95	0.47
1:A:375:U:C2	1:A:376:G:C8	3.01	0.47
1:A:545:C:OP2	4:D:62:GLN:NE2	2.46	0.47
1:A:309:G:H2'	1:A:310:G:H8	1.79	0.47
1:A:401:C:OP1	4:D:73:ARG:NH2	2.47	0.47
1:A:1319:A:H5'	19:S:4:SER:HA	1.96	0.47
7:G:133:GLY:HA2	7:G:136:LYS:CB	2.44	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:940:C:N3	1:A:1343:G:N2	2.60	0.47
1:A:1157:A:C5	1:A:1181:G:C2	3.03	0.47
3:C:136:GLN:HB2	3:C:136:GLN:HE21	1.50	0.47
1:A:1017:G:H2'	1:A:1018:C:C6	2.49	0.47
1:A:564:C:O2'	8:H:91:ARG:NH2	2.34	0.47
1:A:806:C:H2'	1:A:807:A:C8	2.50	0.47
1:A:717:C:H4'	11:K:117:ASN:HB3	1.95	0.47
5:E:110:LEU:HD13	5:E:118:ILE:HG21	1.95	0.47
7:G:80:VAL:HG23	7:G:83:ALA:O	2.14	0.47
1:A:965:A:OP1	1:A:1198:G:H5''	2.14	0.47
13:M:97:PRO:HB2	13:M:103:THR:HG22	1.95	0.47
1:A:604:G:C5	1:A:605:U:C5	3.02	0.47
1:A:475:G:H2'	1:A:476:G:H8	1.78	0.47
20:T:86:ARG:CZ	20:T:86:ARG:HB3	2.43	0.47
1:A:616:G:N2	1:A:624:C:O2	2.42	0.47
2:B:70:PHE:CD2	2:B:163:PHE:HB3	2.50	0.47
1:A:263:A:OP2	20:T:79:ARG:NH1	2.47	0.47
16:P:71:ARG:O	16:P:75:ARG:N	2.47	0.47
1:A:930:C:H2'	1:A:931:C:H6	1.79	0.47
7:G:127:ALA:HB1	7:G:135:VAL:HG13	1.96	0.47
4:D:14:ARG:HA	4:D:39:PRO:HB3	1.97	0.47
7:G:42:ILE:CA	7:G:45:ASP:HB2	2.41	0.47
1:A:73:G:C6	1:A:97:G:C6	3.02	0.47
2:B:61:LEU:HD21	2:B:160:ASP:HB2	1.97	0.47
7:G:108:ALA:O	7:G:119:ARG:HB3	2.14	0.47
1:A:767:A:H2'	1:A:768:A:O4'	2.14	0.47
18:R:32:ARG:HA	18:R:69:THR:HG21	1.96	0.47
1:A:491:G:H2'	1:A:492:G:O4'	2.15	0.47
1:A:1441:G:C2	1:A:1459:C:C5	3.02	0.47
1:A:1458:G:N2	1:A:1459:C:O4'	2.47	0.47
9:I:9:ARG:HD2	9:I:104:ARG:HH21	1.78	0.47
25:A:1972:HOH:O	16:P:13:HIS:CD2	2.67	0.47
1:A:59:A:H5''	1:A:60:A:C5'	2.45	0.47
1:A:920:U:H2'	1:A:921:U:H6	1.78	0.47
1:A:113:G:N3	1:A:353:A:O2'	2.37	0.47
22:X:3:LEU:HD21	22:X:24:PHE:HB2	1.96	0.47
6:F:45:LEU:HD11	6:F:57:GLN:OE1	2.14	0.47
2:B:226:ARG:HG3	2:B:227:GLY:H	1.80	0.47
1:A:1225:A:N3	1:A:1225:A:H2'	2.30	0.47
1:A:1023:G:H3'	1:A:1024:G:C8	2.49	0.47
1:A:1053:G:N7	1:A:1200:C:H5''	2.30	0.47
1:A:946:A:C2	1:A:1236:A:C2	3.02	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:179:LYS:HA	8:H:72:PRO:HG3	1.96	0.47
7:G:71:PRO:HA	7:G:138:LYS:NZ	2.30	0.47
3:C:182:ILE:HG23	3:C:202:ILE:C	2.34	0.47
1:A:709:G:C4	1:A:710:G:C8	3.02	0.47
5:E:8:GLU:HB2	5:E:34:VAL:HG23	1.96	0.47
1:A:1063:C:H3'	1:A:1064:G:H2'	1.96	0.47
13:M:60:VAL:HG13	13:M:64:TRP:CZ3	2.50	0.47
2:B:142:LEU:HG	2:B:146:GLN:HE21	1.80	0.47
1:A:505:G:C6	1:A:535:A:C2	3.03	0.47
1:A:819:A:H4'	1:A:820:U:OP2	2.13	0.47
6:F:99:ALA:HB3	18:R:29:PHE:CE1	2.49	0.47
1:A:109:A:C6	1:A:326:G:C6	3.03	0.47
1:A:973:G:C3'	1:A:974:A:H5''	2.37	0.47
9:I:10:ARG:O	9:I:72:GLY:HA2	2.15	0.47
2:B:171:ALA:HA	2:B:174:VAL:HB	1.96	0.47
19:S:12:ASP:O	19:S:14:HIS:N	2.40	0.47
1:A:1133:G:H2'	1:A:1134:G:C8	2.50	0.47
6:F:97:PHE:O	18:R:31:LEU:HD23	2.15	0.47
1:A:555:C:H2'	1:A:556:C:H6	1.79	0.47
11:K:32:ILE:HG12	11:K:32:ILE:H	1.57	0.47
5:E:78:HIS:HA	8:H:105:ARG:HG3	1.95	0.47
1:A:1229:A:H2'	1:A:1230:C:C6	2.50	0.47
10:J:49:VAL:CG2	14:N:41:ARG:HB2	2.43	0.47
1:A:964:A:O5'	1:A:964:A:H8	1.98	0.47
1:A:9:G:H2'	1:A:10:A:H8	1.79	0.47
1:A:1299:A:C4	1:A:1301:U:H1'	2.50	0.47
1:A:77:G:O6	1:A:78:G:C2	2.68	0.47
4:D:159:ARG:O	4:D:162:LEU:N	2.47	0.47
10:J:45:ARG:N	10:J:65:LEU:O	2.33	0.47
1:A:130:A:O2'	1:A:131:C:O5'	2.32	0.47
4:D:121:VAL:HA	4:D:126:ILE:HG12	1.95	0.47
9:I:105:ASP:HB2	9:I:107:ARG:HD3	1.97	0.47
15:O:74:ASP:OD1	15:O:76:GLU:HB2	2.15	0.47
1:A:949:A:C6	1:A:950:U:C4	3.03	0.47
10:J:50:ILE:CA	10:J:60:ARG:HG2	2.32	0.47
1:A:1395:C:O2'	1:A:1401:G:O2'	2.13	0.47
14:N:4:LYS:HA	14:N:7:ILE:HG12	1.96	0.47
14:N:18:VAL:O	14:N:18:VAL:HG12	2.15	0.47
1:A:56:U:H2'	1:A:57:G:H8	1.80	0.47
1:A:232:G:H1'	1:A:262:A:N1	2.30	0.47
13:M:16:ASP:HB3	13:M:34:LEU:HD11	1.97	0.47
6:F:25:ILE:CD1	6:F:82:ARG:HE	2.28	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1441:G:N3	1:A:1459:C:H5	2.13	0.46
1:A:1401:G:C2	1:A:1402:C:H1'	2.50	0.46
3:C:19:GLU:HA	3:C:54:ARG:HH12	1.80	0.46
7:G:69:VAL:HG21	7:G:104:LEU:CD1	2.40	0.46
1:A:1323:G:H4'	1:A:1363:C:C2	2.50	0.46
1:A:350:G:O2'	1:A:351:G:H5'	2.15	0.46
1:A:600:C:H2'	1:A:601:C:C6	2.50	0.46
6:F:44:GLY:HA2	6:F:59:TYR:CZ	2.50	0.46
1:A:956:U:H4'	19:S:82:GLY:O	2.15	0.46
2:B:59:GLU:O	2:B:63:MET:HG2	2.15	0.46
8:H:25:ASP:HA	8:H:59:LEU:O	2.15	0.46
2:B:233:SER:OG	2:B:234:PRO:HD2	2.15	0.46
17:Q:55:ASP:HA	17:Q:79:SER:HA	1.97	0.46
11:K:84:VAL:CG1	11:K:91:ARG:HD2	2.44	0.46
7:G:119:ARG:HB2	7:G:119:ARG:HE	1.45	0.46
1:A:105:G:H2'	1:A:106:C:C6	2.51	0.46
1:A:1349:A:H2'	1:A:1350:A:C8	2.39	0.46
1:A:1006:C:H42	1:A:1024:G:N2	1.93	0.46
1:A:1307:U:H2'	1:A:1308:U:C6	2.50	0.46
1:A:1240:U:C5'	1:A:1241:G:H8	2.29	0.46
1:A:1297:C:C3'	1:A:1298:C:H5'	2.44	0.46
1:A:1157:A:C6	1:A:1180:A:C5	3.03	0.46
1:A:413:G:N7	4:D:35:ARG:NH2	2.63	0.46
4:D:36:ARG:HB3	4:D:38:TYR:CZ	2.51	0.46
19:S:36:ARG:HB3	19:S:72:GLY:HA3	1.97	0.46
1:A:1106:G:H5''	3:C:172:ARG:CD	2.44	0.46
1:A:707:C:O2'	1:A:708:C:H5'	2.16	0.46
3:C:147:LYS:O	3:C:203:PHE:HD2	1.97	0.46
1:A:1016:A:H1'	1:A:1218:C:H1'	1.97	0.46
7:G:44:TYR:HA	7:G:47:CYS:HB2	1.97	0.46
1:A:11:G:C6	1:A:12:U:C4	3.03	0.46
11:K:99:GLN:HG3	11:K:105:VAL:HG11	1.97	0.46
1:A:1441:G:H5'	1:A:1442:G:OP1	2.15	0.46
1:A:953:G:C6	1:A:1228:C:N3	2.82	0.46
1:A:1501:C:N4	1:A:1504:G:C2	2.84	0.46
3:C:32:LEU:CD1	3:C:59:ARG:HD2	2.44	0.46
1:A:1264:C:O2'	1:A:1265:G:H5'	2.15	0.46
1:A:191:G:H21	20:T:103:GLY:HA2	1.81	0.46
1:A:1349:A:C2	1:A:1374:A:C5	3.02	0.46
1:A:1300:G:HO2'	1:A:1301:U:P	2.38	0.46
6:F:61:LEU:HD23	6:F:63:TYR:OH	2.16	0.46
4:D:173:TRP:HB2	4:D:187:ARG:O	2.15	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:324:G:N2	1:A:327:A:C8	2.84	0.46
1:A:922:G:H1'	5:E:19:MET:HB2	1.98	0.46
20:T:77:ALA:O	20:T:81:LYS:HG3	2.15	0.46
22:X:53:THR:HG23	22:X:62:HIS:ND1	2.30	0.46
1:A:270:A:H2'	1:A:271:C:C6	2.51	0.46
7:G:96:GLN:HB3	7:G:96:GLN:HE21	1.49	0.46
1:A:949:A:H1'	1:A:1364:U:C2	2.49	0.46
1:A:1170:A:H5''	1:A:1171:G:OP2	2.16	0.46
1:A:940:C:H1'	1:A:1374:A:C2	2.49	0.46
1:A:1206:G:C4	1:A:1207:G:C8	3.04	0.46
2:B:55:PHE:HA	2:B:58:ILE:HD12	1.98	0.46
1:A:96:U:O2'	1:A:97:G:H8	1.99	0.46
20:T:12:ALA:O	20:T:15:ARG:HB2	2.15	0.46
1:A:1499:A:O2'	1:A:1520:G:H5'	2.15	0.46
9:I:27:THR:HB	9:I:61:ALA:O	2.15	0.46
22:X:63:ALA:HB3	22:X:81:LEU:HD23	1.97	0.46
1:A:1443:G:O6	1:A:1444:C:C4	2.69	0.46
3:C:110:ASN:O	3:C:141:VAL:HG22	2.15	0.46
1:A:604:G:H2'	1:A:605:U:O4'	2.16	0.46
1:A:1246:C:H2'	1:A:1247:U:H6	1.81	0.46
1:A:651:C:H2'	1:A:652:U:C6	2.50	0.46
1:A:403:C:O2'	4:D:122:ARG:NH1	2.49	0.46
20:T:43:LEU:HA	20:T:43:LEU:HD23	1.71	0.46
3:C:137:ALA:CA	3:C:140:ARG:HD3	2.41	0.46
1:A:192:U:O3'	20:T:57:ARG:HD2	2.16	0.46
4:D:119:GLN:HG2	4:D:123:HIS:CD2	2.50	0.46
2:B:134:GLU:O	2:B:137:ARG:HG3	2.16	0.46
8:H:113:SER:O	8:H:131:GLY:HA3	2.16	0.46
10:J:11:PHE:HA	10:J:66:ARG:O	2.15	0.46
1:A:1266:G:C8	1:A:1266:G:OP2	2.69	0.46
4:D:88:VAL:HA	5:E:97:GLY:HA2	1.98	0.46
5:E:137:GLU:O	5:E:141:GLN:HB2	2.15	0.46
1:A:854:G:H3'	1:A:871:U:O4	2.16	0.46
9:I:13:ALA:HB3	9:I:72:GLY:C	2.37	0.46
1:A:1030(D):A:N6	1:A:1031:G:H21	2.14	0.46
1:A:1297:C:H5''	1:A:1299:A:N7	2.30	0.46
17:Q:79:SER:OG	17:Q:80:GLY:N	2.48	0.46
5:E:75:THR:HG23	5:E:76:ILE:O	2.16	0.46
1:A:1111:A:H61	3:C:177:THR:HA	1.79	0.46
9:I:17:VAL:CG2	9:I:80:GLY:HA3	2.46	0.46
7:G:111:ARG:HH12	7:G:122:HIS:HB2	1.80	0.46
1:A:539:A:H2'	1:A:540:G:C8	2.51	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:155:LEU:HD11	2:B:159:PRO:HD3	1.97	0.46
2:B:110:GLN:O	2:B:114:ARG:HB2	2.16	0.46
10:J:8:LEU:CD1	10:J:20:ALA:HB2	2.41	0.46
2:B:171:ALA:O	2:B:175:ARG:N	2.39	0.46
9:I:6:GLY:O	9:I:17:VAL:HB	2.16	0.46
1:A:614:A:H2'	1:A:615:C:H6	1.80	0.46
1:A:763:G:H2'	1:A:764:C:C6	2.50	0.46
1:A:262:A:C6	1:A:263:A:C6	3.04	0.46
1:A:636:U:H2'	1:A:637:G:C8	2.51	0.46
20:T:59:ALA:O	20:T:62:LEU:N	2.49	0.46
3:C:37:GLN:NE2	14:N:52:GLN:OE1	2.49	0.46
1:A:1342:C:H1'	9:I:124:GLN:OE1	2.17	0.45
21:U:3:LYS:HG2	21:U:10:ARG:CG	2.45	0.45
1:A:1010:G:N2	1:A:1020:U:H1'	2.31	0.45
7:G:73:MET:HG3	7:G:89:MET:O	2.15	0.45
11:K:67:ASP:OD2	11:K:71:LYS:HE3	2.16	0.45
7:G:61:VAL:O	7:G:64:GLN:HB3	2.16	0.45
8:H:97:VAL:HG21	8:H:128:GLY:HA2	1.99	0.45
4:D:91:SER:O	4:D:95:GLY:N	2.38	0.45
6:F:91:VAL:HG12	6:F:92:LYS:O	2.16	0.45
9:I:110:GLU:OE1	9:I:120:ARG:NH2	2.49	0.45
1:A:560:U:H4'	1:A:561:U:H5''	1.98	0.45
1:A:1251:A:H1'	1:A:1369:C:O2'	2.17	0.45
1:A:1283:G:H2'	1:A:1284:C:C6	2.51	0.45
1:A:1106:G:O3'	3:C:172:ARG:HD2	2.15	0.45
3:C:18:TRP:HE1	14:N:56:VAL:H	1.64	0.45
13:M:23:TYR:HB3	13:M:67:GLU:CD	2.37	0.45
4:D:107:ARG:NE	4:D:173:TRP:HZ2	2.14	0.45
2:B:135:GLN:O	2:B:139:LYS:N	2.42	0.45
1:A:624:C:H2'	1:A:625:G:C8	2.51	0.45
4:D:62:GLN:HB3	4:D:66:ARG:HD2	1.98	0.45
16:P:75:ARG:HA	16:P:80:PHE:CD1	2.52	0.45
1:A:189:G:H2'	1:A:189(A):C:C6	2.51	0.45
1:A:1124:G:C5	1:A:1127:G:N2	2.83	0.45
1:A:1346:A:C1'	1:A:1347:G:H5''	2.47	0.45
1:A:1022:G:H2'	1:A:1023:G:C1'	2.47	0.45
1:A:1030:C:C5	1:A:1032:G:N2	2.84	0.45
1:A:958:A:N6	1:A:959:A:C6	2.84	0.45
1:A:1173:G:H2'	1:A:1174:G:C8	2.44	0.45
1:A:1134:G:H2'	1:A:1135:U:H5'	1.99	0.45
10:J:45:ARG:HD3	14:N:36:PHE:CE1	2.51	0.45
10:J:10:GLY:O	10:J:68:HIS:N	2.34	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
15:O:61:GLY:O	15:O:65:ARG:HG3	2.17	0.45
1:A:1201:A:H1'	1:A:1202:G:OP2	2.17	0.45
1:A:580:U:H2'	1:A:581:G:O4'	2.15	0.45
1:A:1308:U:OP1	13:M:110:ARG:HD2	2.17	0.45
13:M:87:TYR:CD1	19:S:76:PRO:HB3	2.51	0.45
4:D:173:TRP:CG	4:D:189:PRO:HG3	2.51	0.45
1:A:1190:G:H5''	3:C:3:ASN:O	2.17	0.45
2:B:21:ARG:HE	2:B:21:ARG:H	1.64	0.45
1:A:403:C:H2'	1:A:404:U:H6	1.80	0.45
11:K:46:GLY:HA2	11:K:50:TYR:O	2.16	0.45
1:A:990:C:H2'	1:A:991:U:C6	2.51	0.45
13:M:40:ASN:HA	13:M:41:PRO:HD2	1.85	0.45
1:A:1399:C:C2	1:A:1502:A:N6	2.85	0.45
21:U:10:ARG:HE	21:U:10:ARG:CA	2.27	0.45
1:A:677:U:H2'	1:A:678:U:C6	2.51	0.45
1:A:1029:C:N4	1:A:1030(A):G:H22	2.15	0.45
1:A:1287:A:H61	1:A:1370:G:H21	1.65	0.45
1:A:957:U:O2	1:A:959:A:C8	2.69	0.45
1:A:706:A:N3	11:K:31:THR:HG21	2.32	0.45
16:P:43:LYS:HD3	16:P:48:TRP:CZ3	2.50	0.45
1:A:627:G:H2'	1:A:628:G:C8	2.50	0.45
1:A:460:G:H1'	1:A:472:A:H61	1.81	0.45
1:A:458:C:H2'	1:A:460:G:H8	1.81	0.45
1:A:516:U:C4	1:A:517:G:C6	3.04	0.45
21:U:9:ARG:O	21:U:13:ILE:HG13	2.16	0.45
1:A:667:G:H4'	15:O:51:HIS:CE1	2.51	0.45
5:E:144:THR:O	5:E:148:VAL:HG23	2.17	0.45
12:L:85:ILE:HD13	12:L:85:ILE:HA	1.74	0.45
1:A:953:G:C4	1:A:1229:A:C2	3.05	0.45
1:A:1147:C:H2'	1:A:1148:U:H6	1.81	0.45
4:D:108:LEU:HB3	4:D:110:PHE:CE1	2.52	0.45
7:G:113:GLU:CB	7:G:118:VAL:HB	2.45	0.45
3:C:68:VAL:HG12	3:C:70:VAL:HG23	1.99	0.45
1:A:5:U:H5''	1:A:6:G:C8	2.52	0.45
4:D:24:GLU:O	4:D:27:TYR:HD1	1.98	0.45
1:A:1418:A:H5''	1:A:1419:G:OP2	2.16	0.45
5:E:36:ASP:OD2	5:E:38:GLN:N	2.43	0.45
1:A:1159:U:H5	1:A:1172:C:H5	1.65	0.45
10:J:15:THR:O	10:J:19:SER:OG	2.34	0.45
1:A:1399:C:C2	1:A:1401:G:C5	3.04	0.45
1:A:1254:C:H5	10:J:43:ARG:CZ	2.29	0.45
5:E:75:THR:HA	5:E:115:VAL:HG13	1.97	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
14:N:26:ARG:HB3	14:N:26:ARG:HE	1.51	0.45
4:D:194:LEU:HB3	4:D:196:LEU:HD11	1.97	0.45
5:E:7:GLU:OE2	5:E:37:ARG:NH2	2.45	0.45
20:T:36:LEU:HD12	20:T:55:ILE:HG23	1.98	0.45
1:A:1092:A:OP1	1:A:1092:A:H8	2.00	0.45
1:A:1457:G:C2	1:A:1458:G:C8	3.05	0.45
1:A:1124:G:O2'	10:J:38:ILE:HD13	2.17	0.45
1:A:675:A:H2'	1:A:676:A:C8	2.52	0.45
2:B:51:LEU:HD23	2:B:55:PHE:HE2	1.82	0.45
1:A:9:G:C2	1:A:26:A:N1	2.84	0.45
1:A:1252:A:H61	1:A:1285:A:N6	2.15	0.45
9:I:114:TYR:N	9:I:114:TYR:HD2	2.13	0.45
9:I:11:LYS:O	9:I:12:GLU:HB3	2.17	0.45
1:A:391:G:C6	1:A:392:G:C5	3.05	0.45
1:A:872:A:C8	1:A:874:G:C8	3.05	0.45
1:A:375:U:C4	1:A:376:G:N7	2.84	0.45
12:L:113:ARG:NH2	25:L:201:HOH:O	2.50	0.45
1:A:1221:G:H1'	19:S:53:ASN:O	2.17	0.45
2:B:44:LEU:HA	2:B:47:THR:OG1	2.17	0.45
12:L:11:VAL:HG22	17:Q:29:HIS:CD2	2.52	0.45
1:A:510:A:H5''	1:A:511:C:OP2	2.17	0.45
1:A:949:A:N6	1:A:1232:U:N3	2.40	0.45
9:I:13:ALA:HB3	9:I:72:GLY:HA3	1.99	0.45
1:A:1079:G:C2	1:A:1080:A:C6	3.05	0.45
19:S:20:LEU:HD21	19:S:43:GLU:HG2	1.99	0.45
1:A:1299:A:C5	1:A:1301:U:H1'	2.51	0.45
1:A:1360:A:C5	14:N:18:VAL:HG11	2.51	0.45
1:A:1323:G:OP2	1:A:1323:G:H8	1.99	0.45
19:S:7:LYS:HA	19:S:7:LYS:HD3	1.77	0.45
3:C:12:LEU:HB3	3:C:18:TRP:CH2	2.52	0.45
13:M:74:VAL:O	13:M:78:ILE:HG12	2.17	0.45
1:A:142:G:N3	1:A:143:A:C8	2.85	0.45
1:A:194:C:C2'	1:A:195:A:H5''	2.47	0.45
2:B:70:PHE:HB2	2:B:92:TYR:HB3	1.98	0.45
1:A:546:G:OP1	4:D:73:ARG:HG2	2.17	0.45
1:A:1107:C:C4	1:A:1108:G:C8	3.04	0.45
13:M:108:ARG:O	13:M:112:GLY:N	2.50	0.45
1:A:1230:C:H2'	1:A:1231:G:H8	1.82	0.45
1:A:1169:A:H2'	1:A:1170:A:C8	2.52	0.45
1:A:939:G:N2	1:A:1344:C:N3	2.56	0.45
1:A:16:A:N3	1:A:1080:A:O2'	2.45	0.45
1:A:1237:C:C2	1:A:1337:G:N2	2.83	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1224:G:N1	1:A:1322:C:O4'	2.50	0.45
1:A:148:G:N2	1:A:175:C:C2	2.85	0.45
5:E:55:VAL:O	5:E:58:ALA:HB3	2.17	0.45
1:A:276:G:O3'	17:Q:68:ARG:NH1	2.50	0.45
1:A:1469:G:H2'	1:A:1470:G:H8	1.81	0.45
20:T:36:LEU:HD13	20:T:36:LEU:HA	1.68	0.45
1:A:724:G:C2	1:A:725:G:C8	3.05	0.45
15:O:4:THR:H	15:O:7:GLU:HB2	1.81	0.45
1:A:991:U:C4	1:A:1212:U:H1'	2.53	0.44
1:A:1164:G:H1	1:A:1171:G:H22	1.65	0.44
1:A:1344:C:H5''	9:I:120:ARG:HG2	1.99	0.44
1:A:1003:G:H3'	1:A:1004:A:H4'	1.98	0.44
1:A:966:G:C2	1:A:967:C:C2	3.05	0.44
1:A:9:G:OP1	5:E:122:GLU:HB2	2.17	0.44
1:A:1366:C:H2'	1:A:1367:C:C6	2.53	0.44
1:A:984:C:H2'	1:A:985:C:O4'	2.18	0.44
1:A:156:G:C6	1:A:166:G:C6	3.05	0.44
7:G:73:MET:CG	7:G:145:ALA:HB1	2.42	0.44
14:N:23:ARG:HG3	14:N:24:CYS:O	2.17	0.44
1:A:1002:G:O6	1:A:1038:C:N3	2.50	0.44
10:J:61:GLU:OE2	14:N:49:HIS:NE2	2.50	0.44
18:R:30:ASP:HB3	18:R:33:ASP:HB2	1.98	0.44
2:B:21:ARG:O	2:B:23:ARG:N	2.47	0.44
4:D:64:LEU:HD12	4:D:68:TYR:HE1	1.82	0.44
17:Q:58:GLU:OE1	17:Q:75:ARG:NH2	2.50	0.44
5:E:84:PHE:CE1	5:E:133:TYR:HB3	2.52	0.44
22:X:77:LEU:HD23	22:X:77:LEU:HA	1.81	0.44
1:A:690:G:H2'	1:A:691:G:O4'	2.17	0.44
1:A:838:G:C2'	1:A:839:U:H5''	2.47	0.44
7:G:26:PHE:CD2	7:G:30:ILE:HD11	2.52	0.44
1:A:369:C:O2'	1:A:370:C:H5'	2.17	0.44
1:A:1157:A:C2	1:A:1181:G:N3	2.86	0.44
7:G:18:TYR:HE1	7:G:58:PRO:HB2	1.81	0.44
3:C:50:ALA:HB1	3:C:70:VAL:HG11	1.98	0.44
1:A:609:A:H5'	16:P:18:ARG:NH2	2.32	0.44
22:X:81:LEU:HA	22:X:84:GLN:HB2	1.98	0.44
1:A:1429:C:H2'	1:A:1430:C:C6	2.53	0.44
1:A:1096:C:O2'	1:A:1097:C:H5'	2.17	0.44
10:J:50:ILE:HD13	14:N:41:ARG:HH11	1.82	0.44
9:I:13:ALA:HB2	9:I:68:GLY:N	2.33	0.44
1:A:1367:C:N4	1:A:1368:G:O6	2.50	0.44
2:B:178:ARG:HH22	8:H:68:ARG:NH2	2.13	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1361:G:O5'	1:A:1361:G:H8	2.01	0.44
1:A:152:A:N6	1:A:169:C:N3	2.65	0.44
13:M:23:TYR:HB3	13:M:67:GLU:OE1	2.17	0.44
10:J:48:THR:HG23	10:J:62:HIS:HB3	1.98	0.44
2:B:24:TRP:CZ3	2:B:29:ALA:HB2	2.51	0.44
2:B:143:GLU:O	2:B:146:GLN:HB2	2.17	0.44
1:A:1041:A:H2'	1:A:1042:G:O4'	2.17	0.44
1:A:1128:C:H1'	1:A:1146:A:N6	2.32	0.44
9:I:74:ILE:HG22	9:I:75:ASP:OD2	2.17	0.44
1:A:1003:G:C2	1:A:1004:A:H1'	2.52	0.44
1:A:782:A:O3'	1:A:1515:C:H4'	2.17	0.44
1:A:1026:G:N3	1:A:1026:G:H2'	2.31	0.44
7:G:137:LYS:HA	7:G:140:ASP:OD2	2.17	0.44
7:G:70:LYS:HA	7:G:71:PRO:HD2	1.74	0.44
5:E:32:VAL:HB	5:E:58:ALA:HB1	1.99	0.44
9:I:17:VAL:HG11	9:I:81:ILE:CA	2.47	0.44
7:G:53:LYS:HE2	7:G:53:LYS:HB3	1.54	0.44
1:A:1459:C:P	1:A:1460:A:OP2	2.75	0.44
1:A:1225:A:H5'	1:A:1226:C:OP2	2.17	0.44
1:A:1299:A:C8	1:A:1301:U:H1'	2.52	0.44
1:A:1155:G:H2'	1:A:1156:G:H8	1.81	0.44
3:C:153:VAL:HG12	3:C:196:LEU:HD12	2.00	0.44
1:A:1001(A):G:H2'	1:A:1002:G:C8	2.52	0.44
2:B:141:GLU:O	2:B:145:LEU:HB2	2.17	0.44
19:S:81:ARG:NH1	19:S:81:ARG:HB2	2.31	0.44
1:A:142:G:H1	1:A:221:C:H42	1.64	0.44
7:G:62:PHE:HD1	7:G:124:LEU:HD21	1.82	0.44
1:A:989:C:N4	1:A:1216:G:N1	2.28	0.44
13:M:10:PRO:HG2	13:M:45:VAL:HG21	1.98	0.44
1:A:1372:U:C4	1:A:1373:G:C6	3.05	0.44
1:A:1296:C:H4'	1:A:1302:U:C4	2.53	0.44
1:A:1250:A:C2	1:A:1370:G:H1'	2.53	0.44
1:A:427:U:P	4:D:13:ARG:HH22	2.40	0.44
1:A:958:A:N6	1:A:959:A:N1	2.66	0.44
1:A:982:U:H4'	1:A:983:A:O5'	2.17	0.44
19:S:12:ASP:C	19:S:14:HIS:H	2.17	0.44
10:J:51:ARG:NH2	10:J:61:GLU:HB3	2.33	0.44
1:A:346:G:N2	1:A:347:G:C8	2.86	0.44
3:C:71:ALA:HA	3:C:106:VAL:N	2.32	0.44
12:L:82:VAL:HG23	12:L:106:ASP:OD2	2.17	0.44
1:A:317:G:C6	1:A:318:G:C5	3.06	0.44
1:A:1459:C:H6	1:A:1459:C:H3'	1.83	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
9:I:73:GLN:O	9:I:76:ALA:HB3	2.18	0.44
1:A:1006:C:C2	1:A:1023:G:N1	2.86	0.44
20:T:21:LYS:O	20:T:25:ARG:HG3	2.17	0.44
1:A:657:G:H2'	1:A:658:G:H8	1.82	0.44
2:B:197:VAL:HG12	2:B:198:ASP:H	1.82	0.44
1:A:1323:G:N2	1:A:1361:G:O2'	2.51	0.44
5:E:76:ILE:HD11	5:E:142:LEU:HD11	2.00	0.44
4:D:31:CYS:O	4:D:31:CYS:SG	2.76	0.44
1:A:35:G:C2	1:A:550:G:N3	2.85	0.44
1:A:120:A:H2'	1:A:121:C:H4'	1.98	0.44
10:J:96:ILE:H	10:J:96:ILE:HG13	1.61	0.44
1:A:1442(A):G:H2'	1:A:1442(B):A:H5''	2.00	0.44
1:A:560:U:H4'	1:A:561:U:C5'	2.47	0.44
1:A:1117:G:H5''	1:A:1117:G:C8	2.53	0.44
1:A:979:C:O2	14:N:19:ARG:HG2	2.18	0.44
1:A:1112:C:H42	3:C:178:LEU:HD23	1.83	0.44
5:E:71:LEU:HD23	5:E:115:VAL:HG22	1.99	0.44
20:T:74:LYS:HB2	20:T:75:ASN:H	1.47	0.44
1:A:189(B):C:H2'	1:A:189(C):C:O4'	2.18	0.44
1:A:35:G:H2'	1:A:36:C:H6	1.81	0.44
1:A:1065:U:H6	1:A:1190:G:H21	1.64	0.44
1:A:328:C:H4'	1:A:329:A:H5'	1.99	0.44
1:A:687:A:H4'	11:K:47:VAL:HG13	2.00	0.44
10:J:7:LYS:N	10:J:97:GLU:O	2.48	0.44
10:J:55:LYS:O	10:J:56:HIS:CG	2.71	0.44
5:E:127:ASN:HA	5:E:128:PRO:HD3	1.80	0.44
1:A:1030(C):G:C5	1:A:1030(D):A:N7	2.86	0.44
1:A:1358:U:C5	1:A:1359:C:C4	3.06	0.44
1:A:148:G:C2	1:A:175:C:C2	3.06	0.44
1:A:614:A:H2'	1:A:615:C:C6	2.53	0.44
1:A:129(A):G:O2'	1:A:189(F):U:OP1	2.33	0.44
1:A:35:G:H22	1:A:550:G:H1'	1.83	0.44
15:O:88:ARG:HD2	15:O:88:ARG:HA	1.83	0.44
6:F:25:ILE:HD12	6:F:82:ARG:HE	1.83	0.44
1:A:269:C:H2'	1:A:270:A:C8	2.52	0.44
15:O:55:GLY:O	15:O:59:MET:HG3	2.18	0.44
1:A:991:U:N3	1:A:1212:U:H1'	2.32	0.43
1:A:959:A:H61	19:S:78:ARG:CA	2.29	0.43
3:C:15:THR:HG22	3:C:16:ARG:N	2.33	0.43
3:C:134:ILE:CG2	3:C:151:VAL:HB	2.46	0.43
4:D:12:CYS:SG	4:D:19:LEU:O	2.76	0.43
2:B:70:PHE:H	2:B:92:TYR:HA	1.82	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:516:U:O4	1:A:517:G:N1	2.51	0.43
1:A:1087:G:N2	1:A:1099:G:H1'	2.33	0.43
1:A:283:C:H2'	1:A:284:G:O4'	2.18	0.43
7:G:22:LEU:HA	7:G:22:LEU:HD12	1.78	0.43
15:O:43:LEU:O	15:O:44:LYS:C	2.57	0.43
1:A:713:G:H2'	1:A:714:G:C8	2.52	0.43
1:A:559:A:N3	1:A:559:A:H5'	2.32	0.43
1:A:957:U:H4'	19:S:79:THR:HG23	2.00	0.43
1:A:994:A:O2'	14:N:8:GLU:HG2	2.18	0.43
15:O:78:TYR:O	15:O:82:ILE:HG12	2.18	0.43
5:E:32:VAL:O	5:E:43:LEU:HD12	2.18	0.43
1:A:1014:A:H2'	1:A:1015:A:N9	2.33	0.43
1:A:1246:C:H2'	1:A:1247:U:C6	2.53	0.43
1:A:599:C:H4'	8:H:130:GLY:C	2.38	0.43
6:F:67:MET:HE3	6:F:75:LEU:HD22	1.99	0.43
8:H:36:LEU:O	8:H:45:ILE:HD11	2.18	0.43
1:A:1193:G:C5	1:A:1194:U:C5	3.06	0.43
16:P:14:ASN:OD1	16:P:16:HIS:CE1	2.71	0.43
1:A:674:G:H2'	1:A:675:A:H8	1.83	0.43
2:B:55:PHE:CG	2:B:58:ILE:HD12	2.52	0.43
1:A:1367:C:H5''	9:I:114:TYR:CB	2.48	0.43
17:Q:10:VAL:HG13	17:Q:19:VAL:HB	2.00	0.43
12:L:86:ARG:HB2	12:L:101:VAL:HG22	2.00	0.43
18:R:33:ASP:O	18:R:40:LEU:HD11	2.18	0.43
1:A:1410:G:C4	1:A:1491:G:N2	2.87	0.43
1:A:582:U:OP1	15:O:64:ARG:NH1	2.51	0.43
1:A:883:C:O2'	1:A:884:U:H5'	2.18	0.43
2:B:86:GLU:C	2:B:89:GLY:H	2.22	0.43
1:A:256:U:H2'	1:A:257:G:C8	2.53	0.43
12:L:60:LEU:HB3	12:L:62:SER:H	1.83	0.43
1:A:1457:G:C6	1:A:1458:G:C6	3.06	0.43
1:A:1443:G:O6	1:A:1459:C:C1'	2.66	0.43
1:A:1210:C:H5''	1:A:1211:U:C6	2.54	0.43
13:M:14:ARG:NH1	13:M:41:PRO:HB2	2.32	0.43
1:A:1379:G:H2'	1:A:1380:U:H5'	2.00	0.43
1:A:946:A:N1	1:A:1236:A:C2	2.87	0.43
1:A:18:C:H4'	1:A:1078:U:O2	2.18	0.43
1:A:1321:C:H3'	1:A:1322:C:H2'	2.00	0.43
1:A:79:G:N2	1:A:91:C:C2	2.87	0.43
1:A:1362:C:O2'	1:A:1363:C:H5'	2.17	0.43
1:A:1149:C:O2'	1:A:1150:U:H5'	2.18	0.43
7:G:115:ARG:O	7:G:118:VAL:HG23	2.18	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1270:C:H2'	1:A:1271:G:C8	2.52	0.43
2:B:158:LEU:HA	2:B:159:PRO:HD3	1.92	0.43
13:M:58:GLU:O	13:M:61:GLU:HB2	2.19	0.43
3:C:21:ARG:O	3:C:58:GLU:HG3	2.18	0.43
1:A:1348:U:H2'	1:A:1349:A:C8	2.53	0.43
1:A:965:A:H4'	1:A:966:G:O5'	2.18	0.43
2:B:28:PHE:CD2	2:B:194:PRO:HG3	2.51	0.43
1:A:1357:A:C8	1:A:1358:U:C5	3.07	0.43
1:A:164:U:H2'	1:A:165:C:C6	2.54	0.43
17:Q:13:ASP:CG	17:Q:14:LYS:N	2.71	0.43
1:A:650:G:O2'	1:A:651:C:H5'	2.18	0.43
1:A:397:A:N3	1:A:397:A:H3'	2.34	0.43
1:A:277:C:OP1	17:Q:68:ARG:NH2	2.48	0.43
1:A:384:G:H2'	1:A:385:C:H6	1.82	0.43
1:A:445:G:H2'	1:A:445:G:N3	2.33	0.43
1:A:949:A:OP1	13:M:101:GLN:HB3	2.19	0.43
8:H:88:LYS:HB3	8:H:89:PRO:HD2	2.01	0.43
7:G:31:MET:HG3	7:G:35:LYS:O	2.18	0.43
2:B:80:ILE:HG12	2:B:211:ILE:HG22	2.01	0.43
1:A:1295:G:H2'	1:A:1296:C:H5'	2.01	0.43
1:A:370:C:H2'	1:A:371:G:C8	2.53	0.43
9:I:28:VAL:O	9:I:31:GLN:HG2	2.18	0.43
19:S:36:ARG:HG2	19:S:51:VAL:HG12	2.00	0.43
13:M:70:LEU:O	13:M:74:VAL:HG23	2.18	0.43
1:A:142:G:C4	1:A:143:A:C8	3.07	0.43
16:P:38:TYR:N	16:P:38:TYR:CD2	2.86	0.43
1:A:189(F):U:C5	17:Q:72:ARG:NH2	2.86	0.43
1:A:65:U:H6	1:A:65:U:H5'	1.83	0.43
1:A:527:G:O2'	1:A:535:A:N1	2.46	0.43
5:E:30:ALA:O	5:E:45:PHE:HD1	2.01	0.43
1:A:441:A:H3'	1:A:442:C:C6	2.54	0.43
9:I:18:PHE:HD1	9:I:62:TYR:HD2	1.66	0.43
8:H:4:ASP:HA	8:H:5:PRO:HD3	1.91	0.43
1:A:1350:A:N1	1:A:1372:U:O2	2.51	0.43
1:A:1005:A:N7	1:A:1024:G:O2'	2.52	0.43
1:A:1299:A:H2'	1:A:1299:A:N3	2.33	0.43
1:A:1178:G:N2	1:A:1181:G:N7	2.65	0.43
8:H:29:SER:HB3	8:H:32:LYS:CG	2.43	0.43
3:C:67:THR:HG22	3:C:69:HIS:CE1	2.53	0.43
1:A:267:C:OP2	17:Q:67:LYS:HD2	2.19	0.43
1:A:1013:G:O2'	1:A:1014:A:C8	2.69	0.43
1:A:187:C:H2'	1:A:188:C:C6	2.54	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1137:C:C5'	1:A:1138:G:C6	3.01	0.43
8:H:8:ASP:O	8:H:12:ARG:N	2.43	0.43
1:A:614:A:C6	1:A:627:G:N1	2.87	0.43
1:A:35:G:C6	1:A:550:G:C2	3.07	0.43
3:C:53:ALA:CB	3:C:112:SER:HB2	2.48	0.43
6:F:10:LEU:HB2	6:F:59:TYR:HB3	2.00	0.43
1:A:929:G:C6	1:A:930:C:C4	3.07	0.43
5:E:7:GLU:HG2	5:E:112:LEU:HD22	2.01	0.43
4:D:106:TYR:CD2	4:D:106:TYR:C	2.90	0.43
13:M:15:VAL:HG13	13:M:43:THR:O	2.19	0.43
1:A:941:G:N2	9:I:124:GLN:HE22	2.15	0.43
19:S:16:LEU:CB	19:S:20:LEU:HD12	2.49	0.43
4:D:155:LEU:HD23	4:D:156:GLU:N	2.33	0.43
1:A:1112:C:N4	3:C:178:LEU:HD23	2.33	0.43
1:A:352:C:H2'	1:A:352:C:O2	2.18	0.43
1:A:652:U:O4	1:A:752:G:O2'	2.33	0.43
17:Q:45:HIS:CE1	17:Q:47:PRO:HG3	2.54	0.43
1:A:1415:G:C6	1:A:1486:G:C6	3.06	0.43
1:A:741:G:H2'	1:A:742:G:C8	2.53	0.43
9:I:9:ARG:HG3	9:I:14:VAL:HG22	2.01	0.43
1:A:1003:G:O2'	1:A:1024:G:N2	2.52	0.43
1:A:984:C:H2'	1:A:985:C:C6	2.53	0.43
1:A:1026:G:H3'	1:A:1027:C:C5'	2.49	0.43
3:C:19:GLU:HB3	3:C:40:ARG:NH2	2.34	0.43
1:A:604:G:C6	1:A:605:U:C4	3.07	0.43
17:Q:19:VAL:HG23	17:Q:44:ALA:HB3	2.01	0.43
13:M:64:TRP:HB2	13:M:66:LEU:HD23	2.00	0.43
6:F:95:GLU:HA	6:F:96:PRO:HD3	1.90	0.43
1:A:1265:G:O2'	1:A:1266:G:H5'	2.18	0.43
1:A:292:G:C5	1:A:293:G:H1'	2.53	0.43
5:E:41:VAL:O	5:E:67:VAL:HG12	2.17	0.43
8:H:14:ARG:O	8:H:18:ARG:HD3	2.19	0.43
5:E:126:ARG:HA	5:E:131:ILE:HD11	2.00	0.43
1:A:1238:A:C8	1:A:1239:A:C8	3.07	0.43
1:A:1010:G:C4	1:A:1011:G:C8	3.07	0.43
1:A:1070:U:H2'	1:A:1071:C:H6	1.84	0.43
3:C:13:GLY:HA3	14:N:57:ARG:NH2	2.30	0.43
1:A:902:G:H2'	1:A:903:G:H8	1.84	0.43
10:J:39:PRO:HG3	10:J:70:ARG:HH21	1.84	0.43
1:A:1013:G:N2	1:A:1017:G:C6	2.87	0.43
1:A:1279:A:O2'	1:A:1282:C:N4	2.52	0.43
13:M:16:ASP:HB3	13:M:34:LEU:CD1	2.48	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:D:177:ASP:CG	4:D:180:GLY:HA3	2.39	0.43
10:J:55:LYS:HG2	10:J:55:LYS:O	2.17	0.42
1:A:1288:A:C6	1:A:1371:G:H1'	2.54	0.42
1:A:1234:C:C4	1:A:1235:U:C4	3.07	0.42
13:M:97:PRO:HG3	13:M:110:ARG:HB3	2.00	0.42
1:A:1283:G:N2	1:A:1284:C:C2	2.87	0.42
1:A:1050:G:N1	1:A:1208:C:O2	2.40	0.42
1:A:235:C:H2'	1:A:236:G:H8	1.84	0.42
3:C:12:LEU:HD22	3:C:18:TRP:CE3	2.53	0.42
11:K:41:THR:HG22	11:K:42:TRP:N	2.34	0.42
3:C:113:ALA:HB1	3:C:200:ALA:HB3	2.01	0.42
2:B:14:GLY:HA3	2:B:16:HIS:HE1	1.84	0.42
5:E:8:GLU:CB	5:E:34:VAL:HG23	2.49	0.42
1:A:565:U:OP2	1:A:566:G:O2'	2.30	0.42
22:X:30:TYR:N	22:X:30:TYR:CD2	2.86	0.42
1:A:1350:A:C6	1:A:1351:U:C4	3.07	0.42
7:G:26:PHE:CE2	7:G:30:ILE:HD11	2.54	0.42
1:A:1055:A:C8	1:A:1206:G:C2	3.07	0.42
1:A:1055:A:N6	1:A:1206:G:N7	2.68	0.42
1:A:373:A:H2'	1:A:374:A:H8	1.84	0.42
1:A:151:A:C2	1:A:152:A:H1'	2.54	0.42
1:A:429:U:H3'	4:D:22:LYS:HZ1	1.84	0.42
4:D:111:ALA:HB1	4:D:116:GLN:OE1	2.19	0.42
1:A:132:C:H2'	1:A:133:U:O4'	2.19	0.42
20:T:74:LYS:HE2	20:T:74:LYS:HB3	1.84	0.42
9:I:27:THR:CG2	9:I:30:GLY:H	2.33	0.42
1:A:1093:A:C2	1:A:1095:U:H5'	2.54	0.42
16:P:22:THR:HA	16:P:33:ILE:HG12	2.01	0.42
1:A:1378:C:OP2	7:G:2:ALA:HB2	2.19	0.42
1:A:1263:C:N3	1:A:1272:G:O6	2.51	0.42
1:A:1198:G:H2'	1:A:1199:U:C6	2.55	0.42
10:J:9:ARG:HG2	10:J:69:ASN:CG	2.39	0.42
1:A:1250:A:N1	1:A:1251:A:C2	2.87	0.42
1:A:1321:C:H5''	1:A:1322:C:H2'	2.01	0.42
12:L:114:LYS:O	12:L:117:ARG:HG3	2.20	0.42
15:O:57:LEU:O	15:O:60:VAL:N	2.52	0.42
2:B:132:LYS:O	2:B:135:GLN:HG2	2.19	0.42
17:Q:66:SER:HB3	17:Q:69:LYS:HD3	2.00	0.42
1:A:1192:C:C6	1:A:1192:C:H3'	2.54	0.42
4:D:100:ARG:NH1	4:D:137:SER:HA	2.35	0.42
1:A:1345:U:C5	1:A:1377:A:C2	3.08	0.42
2:B:32:ILE:HD11	2:B:40:HIS:HB3	2.00	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1251:A:N6	1:A:1285:A:C6	2.85	0.42
1:A:1366:C:OP1	9:I:117:HIS:ND1	2.52	0.42
1:A:1157:A:OP1	1:A:1158:C:C5	2.72	0.42
1:A:748:C:O5'	1:A:748:C:H6	2.03	0.42
3:C:11:ARG:HB2	3:C:11:ARG:NH1	2.31	0.42
1:A:1150:U:O2'	10:J:39:PRO:HB2	2.19	0.42
4:D:18:LYS:HD2	4:D:33:MET:HB2	2.02	0.42
2:B:78:GLN:C	2:B:94:ASN:HD21	2.22	0.42
1:A:827:U:H5''	1:A:828:A:OP2	2.19	0.42
1:A:624:C:H2'	1:A:625:G:H8	1.85	0.42
1:A:512:U:H2'	1:A:513:C:C6	2.53	0.42
22:X:31:PHE:CG	22:X:85:LEU:HB3	2.54	0.42
5:E:89:ILE:HD13	5:E:90:VAL:N	2.34	0.42
2:B:52:GLU:HG2	2:B:56:ARG:NH1	2.35	0.42
10:J:50:ILE:N	10:J:50:ILE:HD12	2.31	0.42
13:M:15:VAL:O	13:M:18:ALA:HB3	2.19	0.42
1:A:1003:G:H2'	1:A:1004:A:H4'	2.01	0.42
1:A:1306:A:H62	1:A:1331:G:N2	2.17	0.42
4:D:158:ILE:O	4:D:162:LEU:HD12	2.19	0.42
1:A:1105:A:N1	1:A:1106:G:C5	2.87	0.42
3:C:12:LEU:O	14:N:57:ARG:NH1	2.52	0.42
4:D:112:VAL:HG22	4:D:116:GLN:OE1	2.19	0.42
9:I:46:ALA:CB	9:I:77:ILE:HB	2.48	0.42
1:A:617:G:C2	1:A:618:C:C5	3.08	0.42
1:A:1203:C:P	14:N:3:ARG:HH12	2.42	0.42
1:A:384:G:H2'	1:A:385:C:C6	2.54	0.42
1:A:1057:G:H2'	1:A:1058:G:H8	1.85	0.42
2:B:114:ARG:HD2	2:B:114:ARG:O	2.19	0.42
17:Q:29:HIS:HB3	17:Q:33:GLY:N	2.34	0.42
1:A:1459:C:H2'	1:A:1460:A:C8	2.55	0.42
1:A:1166:G:N2	1:A:1169:A:H3'	2.35	0.42
1:A:1160:G:O6	1:A:1181:G:C6	2.73	0.42
1:A:170:U:O2'	1:A:171:A:H5'	2.20	0.42
3:C:179:ARG:HG3	3:C:206:GLU:OE1	2.20	0.42
1:A:1460:A:H2'	1:A:1461:G:O4'	2.19	0.42
1:A:1128:C:H1'	1:A:1146:A:N1	2.35	0.42
1:A:1309:G:C6	1:A:1329:A:N6	2.87	0.42
1:A:1286:A:H2	21:U:22:ARG:NH2	2.09	0.42
1:A:235:C:H2'	1:A:236:G:C8	2.55	0.42
7:G:43:PHE:O	7:G:43:PHE:CD1	2.73	0.42
1:A:1151:A:C4	1:A:1152:A:C8	3.08	0.42
1:A:1001(A):G:N2	1:A:1040:U:C2	2.88	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:331:G:O4'	25:A:1865:HOH:O	2.21	0.42
1:A:472:A:H4'	16:P:80:PHE:O	2.20	0.42
17:Q:86:GLU:O	17:Q:90:ILE:HG13	2.18	0.42
1:A:439:A:C4	1:A:496:A:C2	3.08	0.42
6:F:68:PRO:HG2	6:F:71:ARG:HD2	2.01	0.42
16:P:23:ASP:OD1	16:P:25:ARG:HG3	2.20	0.42
7:G:31:MET:O	7:G:32:ARG:NH1	2.53	0.42
1:A:1379:G:N7	7:G:2:ALA:N	2.68	0.42
1:A:1306:A:H1'	1:A:1332:A:N3	2.35	0.42
1:A:1309:G:OP1	13:M:92:HIS:CE1	2.73	0.42
1:A:1309:G:O3'	13:M:77:ASN:HB3	2.20	0.42
5:E:43:LEU:HD21	5:E:132:ALA:HB1	2.01	0.42
3:C:30:ARG:HG3	3:C:31:HIS:HD2	1.85	0.42
3:C:31:HIS:CD2	3:C:31:HIS:H	2.36	0.42
1:A:1521:G:H2'	1:A:1522:U:H6	1.85	0.42
1:A:646:U:H2'	1:A:647:C:C6	2.55	0.42
1:A:1201:A:H4'	1:A:1202:G:O5'	2.19	0.42
1:A:622:A:C8	1:A:623:C:C5	3.07	0.42
11:K:120:ARG:HA	11:K:121:PRO:HD3	1.85	0.42
10:J:35:SER:HB3	10:J:73:ASP:HB3	2.01	0.42
2:B:172:ILE:H	2:B:172:ILE:HG13	1.43	0.42
1:A:1348:U:H4'	9:I:120:ARG:HD2	2.02	0.42
1:A:1375:A:H4'	7:G:29:LYS:HZ3	1.85	0.42
1:A:1378:C:H6	1:A:1378:C:O5'	2.02	0.42
1:A:1003:G:C2	1:A:1004:A:O2'	2.70	0.42
1:A:560:U:H4'	1:A:561:U:O5'	2.18	0.42
1:A:1357:A:C5	1:A:1358:U:C4	3.08	0.42
1:A:1070:U:O2	1:A:1106:G:C2	2.72	0.42
14:N:25:VAL:N	14:N:39:LEU:HD23	2.34	0.42
4:D:108:LEU:HB3	4:D:110:PHE:HE1	1.84	0.42
5:E:10:MET:HG2	5:E:13:ILE:HD11	2.02	0.42
1:A:1496:C:H2'	1:A:1497:G:O4'	2.20	0.42
1:A:1191:A:H8	1:A:1191:A:O5'	2.03	0.42
19:S:53:ASN:ND2	19:S:77:THR:O	2.49	0.42
20:T:38:LYS:O	20:T:41:ILE:HG13	2.19	0.42
1:A:45:U:H2'	1:A:46:G:C8	2.55	0.42
15:O:50:HIS:O	15:O:53:HIS:HB3	2.19	0.42
2:B:216:SER:O	2:B:219:VAL:N	2.53	0.42
1:A:1123:A:H2'	1:A:1124:G:O4'	2.19	0.42
1:A:1262:C:N4	1:A:1273:G:N1	2.39	0.42
1:A:1084:G:C5	1:A:1085:U:C4	3.07	0.42
1:A:1074:G:C4	1:A:1102:A:C2	3.08	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
15:O:56:LEU:O	15:O:60:VAL:HG23	2.20	0.42
1:A:683:G:C6	1:A:684:A:C5	3.08	0.42
1:A:1338:G:H2'	1:A:1339:A:O4'	2.19	0.42
8:H:25:ASP:HB2	8:H:58:TYR:CD2	2.55	0.42
1:A:909:A:H2'	1:A:910:C:O4'	2.20	0.42
1:A:1048:G:O4'	1:A:1215:G:H5''	2.20	0.41
1:A:1124:G:H1'	10:J:38:ILE:CG2	2.50	0.41
9:I:9:ARG:N	9:I:76:ALA:HA	2.35	0.41
3:C:136:GLN:CG	3:C:140:ARG:HD2	2.50	0.41
1:A:1071:C:H5''	5:E:49:PRO:CG	2.50	0.41
1:A:706:A:C5	1:A:707:C:C5	3.08	0.41
1:A:1325:C:H4'	21:U:17:THR:HG21	2.02	0.41
1:A:611:A:N6	1:A:629:G:H1	2.16	0.41
15:O:43:LEU:HA	15:O:43:LEU:HD23	1.86	0.41
16:P:6:LEU:HG	16:P:17:TYR:HB3	2.01	0.41
7:G:63:LYS:HA	7:G:67:GLU:OE2	2.20	0.41
1:A:1442:G:N7	1:A:1442(A):G:O6	2.53	0.41
1:A:877:C:H5''	8:H:88:LYS:HD3	2.02	0.41
1:A:1288:A:H1'	1:A:1353:G:H4'	2.01	0.41
1:A:17:U:O2'	1:A:1079:G:N3	2.49	0.41
1:A:1116:C:H2'	1:A:1117:G:O4'	2.20	0.41
3:C:148:GLY:HA3	3:C:172:ARG:O	2.20	0.41
1:A:1313:U:OP1	19:S:7:LYS:NZ	2.53	0.41
3:C:12:LEU:HA	3:C:16:ARG:O	2.20	0.41
1:A:101:A:C6	1:A:102:G:N7	2.88	0.41
2:B:70:PHE:HB2	2:B:92:TYR:CB	2.50	0.41
1:A:1445:C:H2'	1:A:1446:U:H5'	2.02	0.41
1:A:1095:U:P	1:A:1108:G:H22	2.42	0.41
1:A:445:G:H3'	1:A:446:G:H8	1.85	0.41
1:A:792:A:H4'	1:A:793:U:H5''	2.02	0.41
14:N:13:THR:HG21	14:N:20:ALA:HB2	2.02	0.41
1:A:585:G:N3	1:A:879:C:H4'	2.36	0.41
1:A:417:C:H6	1:A:417:C:O5'	2.03	0.41
4:D:97:LEU:HD23	4:D:97:LEU:HA	1.86	0.41
13:M:111:LYS:HB3	13:M:111:LYS:HE2	1.60	0.41
1:A:961:U:OP2	1:A:1223:C:O2'	2.12	0.41
1:A:990:C:C4	1:A:991:U:O4	2.73	0.41
1:A:1308:U:O2'	1:A:1309:G:H5'	2.20	0.41
1:A:1305:G:C8	21:U:5:ASP:HA	2.53	0.41
2:B:48:MET:HA	2:B:51:LEU:HD12	2.03	0.41
1:A:1050:G:C6	1:A:1208:C:N3	2.87	0.41
1:A:748:C:H4'	1:A:749:C:O5'	2.20	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:165:C:H2'	1:A:166:G:H8	1.86	0.41
1:A:484:G:O2'	1:A:485:G:P	2.78	0.41
20:T:53:LEU:HA	20:T:56:MET:HG2	2.03	0.41
1:A:1063:C:H6	1:A:1063:C:OP2	2.04	0.41
1:A:684:A:C6	1:A:685:G:C6	3.08	0.41
1:A:1339:A:C5	1:A:1340:A:H1'	2.55	0.41
4:D:61:LYS:HE3	4:D:62:GLN:OE1	2.20	0.41
5:E:137:GLU:HA	5:E:140:ARG:HB3	2.02	0.41
1:A:1431:C:H2'	1:A:1432:G:O4'	2.20	0.41
3:C:51:GLY:O	3:C:52:LEU:HD22	2.20	0.41
8:H:87:SER:HB2	8:H:93:VAL:HB	2.01	0.41
2:B:165:VAL:O	2:B:187:LEU:HB3	2.21	0.41
1:A:1368:G:O2'	1:A:1369:C:H5'	2.20	0.41
1:A:1083:U:C5	1:A:1084:G:C6	3.08	0.41
1:A:994:A:C2	14:N:4:LYS:HD3	2.52	0.41
1:A:509:A:H3'	1:A:509:A:C8	2.55	0.41
1:A:618:C:H5'	1:A:619:U:H5''	2.03	0.41
1:A:409:G:OP1	4:D:25:ARG:N	2.35	0.41
8:H:86:ILE:HG21	8:H:133:LEU:HD13	2.01	0.41
1:A:721:G:H4'	1:A:722:A:O4'	2.20	0.41
9:I:82:ALA:HB2	9:I:101:PHE:HB3	2.02	0.41
1:A:1442:G:C8	1:A:1442(A):G:C5	3.09	0.41
8:H:4:ASP:HB2	8:H:89:PRO:HG3	2.03	0.41
1:A:936:C:H3'	1:A:937:A:H8	1.85	0.41
1:A:1003:G:C3'	1:A:1004:A:H4'	2.51	0.41
1:A:1030:C:H2'	1:A:1030(A):G:H5'	2.00	0.41
3:C:35:GLU:OE2	3:C:59:ARG:NH2	2.53	0.41
14:N:23:ARG:HG3	14:N:24:CYS:N	2.34	0.41
3:C:18:TRP:NE1	14:N:55:GLY:N	2.69	0.41
13:M:23:TYR:HE1	13:M:71:ARG:HG2	1.85	0.41
17:Q:91:ARG:HB2	17:Q:91:ARG:HE	1.55	0.41
1:A:766:A:H2	1:A:1525:G:N3	2.19	0.41
1:A:130:A:C8	17:Q:63:ARG:HG3	2.56	0.41
17:Q:63:ARG:HA	17:Q:64:PRO:HD3	1.89	0.41
16:P:20:VAL:HG21	16:P:32:TYR:CG	2.54	0.41
2:B:110:GLN:HG3	2:B:110:GLN:H	1.49	0.41
1:A:1416:G:H2'	1:A:1417:G:O4'	2.20	0.41
1:A:1437:C:H2'	1:A:1438:G:C8	2.56	0.41
10:J:57:LYS:O	10:J:60:ARG:HG3	2.21	0.41
1:A:1176:A:C6	1:A:1177:G:O6	2.73	0.41
4:D:173:TRP:CD1	4:D:174:LEU:HG	2.56	0.41
20:T:53:LEU:HD12	20:T:99:LEU:O	2.20	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:102:G:C4	1:A:103:C:C5	3.09	0.41
1:A:832:C:O2'	1:A:833:U:P	2.79	0.41
12:L:27:LEU:C	12:L:29:GLY:H	2.24	0.41
16:P:45:THR:O	16:P:48:TRP:HB3	2.21	0.41
1:A:1265:G:N2	1:A:1271:G:N3	2.69	0.41
2:B:24:TRP:CZ2	2:B:26:PRO:HB3	2.55	0.41
4:D:63:LYS:O	4:D:67:ILE:HG13	2.21	0.41
3:C:130:VAL:HA	3:C:133:ALA:HB3	2.02	0.41
1:A:124:G:H2'	1:A:125:U:O4'	2.20	0.41
12:L:36:VAL:O	12:L:58:VAL:HG13	2.20	0.41
8:H:75:ARG:HA	8:H:76:PRO:HD2	1.68	0.41
1:A:1004:A:N3	1:A:1037:C:N3	2.69	0.41
2:B:55:PHE:HA	2:B:58:ILE:CG1	2.51	0.41
7:G:69:VAL:HG11	7:G:104:LEU:HB2	2.02	0.41
19:S:62:ILE:HD12	19:S:62:ILE:H	1.86	0.41
1:A:67:C:H2'	1:A:68:G:C8	2.55	0.41
1:A:734:G:C5	1:A:735:C:C4	3.09	0.41
1:A:1014:A:H5'	19:S:14:HIS:CD2	2.56	0.41
10:J:61:GLU:OE2	14:N:45:ARG:HG2	2.20	0.41
10:J:63:PHE:CD1	14:N:58:LYS:HA	2.51	0.41
1:A:855:G:C6	1:A:856:C:C4	3.08	0.41
1:A:627:G:O2'	1:A:628:G:H5'	2.21	0.41
1:A:737:A:H2'	1:A:738:C:H6	1.84	0.41
13:M:53:VAL:HA	13:M:56:LEU:HD12	2.03	0.41
1:A:189(J):G:H2'	1:A:189(K):U:C6	2.55	0.41
1:A:881:G:H2'	1:A:882:C:O4'	2.19	0.41
1:A:317:G:C6	1:A:318:G:N7	2.89	0.41
8:H:86:ILE:CB	8:H:133:LEU:HD22	2.51	0.41
1:A:1443:G:H1	1:A:1459:C:H2'	1.86	0.41
1:A:1098:C:C5'	1:A:1169:A:H1'	2.49	0.41
1:A:954:G:N1	1:A:1226:C:C2	2.88	0.41
1:A:560:U:H6	1:A:560:U:H2'	1.61	0.41
1:A:1368:G:OP2	9:I:112:LYS:HG3	2.21	0.41
1:A:997:U:N3	1:A:1044:A:C2	2.89	0.41
5:E:100:VAL:O	5:E:107:ARG:NH2	2.53	0.41
1:A:22:G:H2'	1:A:23:C:C6	2.56	0.41
3:C:57:ILE:HG23	3:C:66:VAL:HA	2.03	0.41
3:C:66:VAL:O	3:C:102:ASN:HB3	2.21	0.41
11:K:34:ASP:HB3	11:K:40:ILE:HD11	2.03	0.41
1:A:269:C:H2'	1:A:270:A:H8	1.84	0.41
1:A:329:A:C2	1:A:332:G:C8	3.09	0.41
16:P:6:LEU:HG	16:P:17:TYR:CB	2.50	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
12:L:46:LYS:H	12:L:46:LYS:HG2	1.69	0.41
1:A:1442(A):G:C2'	1:A:1442(B):A:H5''	2.50	0.41
1:A:1442(A):G:H3'	1:A:1442(B):A:C5'	2.51	0.41
8:H:87:SER:HB2	8:H:93:VAL:H	1.86	0.41
1:A:1126:U:H2'	1:A:1126:U:O2	2.21	0.41
1:A:1380:U:H5	7:G:3:ARG:HA	1.85	0.41
1:A:1308:U:H5'	13:M:110:ARG:NH1	2.36	0.41
10:J:9:ARG:HG2	10:J:69:ASN:ND2	2.36	0.41
1:A:373:A:C2	1:A:374:A:C8	3.09	0.41
1:A:1154:G:C2	1:A:1155:G:C5	3.09	0.41
3:C:136:GLN:HG2	3:C:140:ARG:HD2	2.01	0.41
3:C:19:GLU:HA	3:C:54:ARG:NH1	2.36	0.41
9:I:44:VAL:HA	9:I:45:ALA:HA	1.58	0.41
1:A:657:G:C2	1:A:750:G:C5	3.09	0.41
1:A:1072:G:O6	1:A:1102:A:N6	2.53	0.41
14:N:23:ARG:HH11	14:N:30:ALA:HB2	1.85	0.41
15:O:21:ASP:OD2	15:O:24:SER:HB3	2.20	0.41
3:C:12:LEU:HD11	14:N:51:GLY:HA2	2.03	0.41
3:C:121:ALA:HB2	3:C:198:VAL:HG21	2.03	0.41
10:J:39:PRO:HG3	10:J:70:ARG:HE	1.85	0.41
21:U:18:TYR:CG	21:U:24:ARG:HG3	2.55	0.41
1:A:584:G:OP1	17:Q:91:ARG:NH2	2.54	0.41
13:M:60:VAL:HG13	13:M:64:TRP:HZ3	1.86	0.41
1:A:626:U:H4'	16:P:38:TYR:CZ	2.56	0.41
7:G:62:PHE:HA	7:G:124:LEU:CD2	2.50	0.41
6:F:55:ASP:HA	6:F:56:PRO:HD2	1.78	0.41
1:A:575:G:O2'	1:A:821:G:H5'	2.21	0.41
10:J:62:HIS:HD2	10:J:62:HIS:H	1.68	0.41
1:A:499:A:H4'	1:A:500:G:H5'	2.02	0.41
1:A:1065:U:O2'	1:A:1066:C:OP2	2.27	0.41
12:L:6:THR:O	12:L:9:GLN:HB2	2.20	0.41
8:H:48:TYR:HA	8:H:60:ARG:O	2.20	0.41
1:A:420:U:HO2'	1:A:421:U:H6	1.67	0.41
2:B:180:LEU:HD23	2:B:180:LEU:HA	1.79	0.41
1:A:968:A:C8	1:A:1062:U:H4'	2.55	0.41
10:J:15:THR:HG22	10:J:91:PRO:HB2	2.03	0.41
16:P:9:PHE:HB2	16:P:16:HIS:O	2.21	0.41
8:H:30:ARG:O	8:H:34:GLU:HB2	2.20	0.41
22:X:79:ASP:O	22:X:82:ALA:HB3	2.21	0.41
2:B:111:ARG:HD3	2:B:111:ARG:HA	1.52	0.41
4:D:146:ILE:N	4:D:146:ILE:HD12	2.36	0.41
22:X:78:ILE:HA	22:X:78:ILE:HD13	1.83	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:M:19:LEU:HA	13:M:22:ILE:CD1	2.51	0.41
13:M:25:ILE:HG23	13:M:29:ARG:CB	2.51	0.41
9:I:109:VAL:HG22	9:I:110:GLU:H	1.86	0.41
1:A:436:C:O2'	1:A:437:U:P	2.79	0.41
1:A:437:U:C4	1:A:438:G:C6	3.09	0.41
1:A:148:G:C2	1:A:149:A:N7	2.88	0.41
3:C:150:LYS:O	3:C:201:TYR:N	2.54	0.41
1:A:1268:A:O2'	1:A:1326:C:H4'	2.21	0.41
1:A:1292:U:O2'	1:A:1293:G:H5'	2.20	0.41
1:A:836:G:C6	1:A:851:G:C6	3.09	0.41
2:B:74:LYS:H	2:B:74:LYS:HG2	1.58	0.41
3:C:184:TYR:HA	3:C:200:ALA:O	2.21	0.41
1:A:685:G:C2	1:A:686:U:C4	3.09	0.41
1:A:627:G:N3	1:A:628:G:C8	2.88	0.41
9:I:9:ARG:HA	9:I:14:VAL:HA	2.03	0.40
1:A:1204:A:H5''	1:A:1205:U:OP2	2.21	0.40
1:A:1206:G:C2'	1:A:1207:G:H5'	2.51	0.40
3:C:54:ARG:HB3	3:C:69:HIS:CD2	2.57	0.40
1:A:1318:A:H4'	19:S:10:PHE:CD2	2.56	0.40
2:B:94:ASN:HB3	2:B:95:GLN:NE2	2.36	0.40
1:A:628:G:O2'	1:A:629:G:H5'	2.21	0.40
2:B:25:ASN:HA	2:B:26:PRO:HD2	1.93	0.40
1:A:1091:U:C2	1:A:1095:U:C4	3.09	0.40
1:A:1095:U:OP2	1:A:1108:G:N1	2.50	0.40
1:A:145:G:C6	1:A:146:G:C5	3.09	0.40
8:H:134:ILE:HG22	8:H:135:CYS:SG	2.61	0.40
19:S:35:SER:HA	19:S:37:ARG:HG2	2.03	0.40
17:Q:99:SER:C	17:Q:100:LYS:HD3	2.41	0.40
1:A:489:C:C4	1:A:490:G:N7	2.89	0.40
1:A:115:G:H4'	1:A:116:A:O5'	2.19	0.40
1:A:875:C:H5''	1:A:876:G:OP2	2.21	0.40
1:A:693:G:H2'	1:A:694:A:C8	2.56	0.40
1:A:1089:G:C6	1:A:1090:U:C4	3.09	0.40
1:A:1308:U:H5'	13:M:110:ARG:CZ	2.51	0.40
1:A:1287:A:N6	1:A:1370:G:H21	2.18	0.40
1:A:959:A:H2'	1:A:960:U:H4'	2.02	0.40
1:A:78:G:H1	1:A:91:C:H42	1.68	0.40
1:A:997:U:O5'	1:A:997:U:H6	2.04	0.40
1:A:918:A:H2'	1:A:919:A:O4'	2.21	0.40
5:E:102:ALA:O	5:E:107:ARG:NH1	2.54	0.40
10:J:45:ARG:HD3	10:J:65:LEU:HD23	2.02	0.40
1:A:377:G:H2'	1:A:378:G:H8	1.82	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:B:70:PHE:HE2	2:B:163:PHE:HD2	1.69	0.40
1:A:536:C:H2'	1:A:537:G:C8	2.56	0.40
16:P:39:TYR:CG	16:P:73:LEU:HD13	2.56	0.40
1:A:333:G:H4'	20:T:16:HIS:CE1	2.56	0.40
1:A:318:G:H2'	1:A:319:G:H8	1.85	0.40
20:T:89:ARG:HH22	20:T:104:LEU:H	1.67	0.40
1:A:620:C:H2'	1:A:621:A:O4'	2.21	0.40
8:H:38:ILE:HG13	8:H:118:VAL:HG12	2.03	0.40
1:A:1392:G:N2	1:A:1502:A:H8	2.19	0.40
13:M:86:CYS:SG	13:M:88:ARG:HG2	2.62	0.40
1:A:1296:C:H4'	1:A:1302:U:C5	2.56	0.40
1:A:1300:G:O2'	1:A:1301:U:O5'	2.33	0.40
1:A:1300:G:O6	1:A:1334:G:H3'	2.21	0.40
1:A:1250:A:N1	1:A:1251:A:N1	2.70	0.40
4:D:18:LYS:HG3	4:D:31:CYS:SG	2.60	0.40
1:A:1265:G:N2	1:A:1271:G:C4	2.90	0.40
1:A:1270:C:H6	1:A:1270:C:O5'	2.05	0.40
11:K:34:ASP:OD2	11:K:38:ASN:N	2.54	0.40
1:A:665:A:H2'	1:A:725:G:N2	2.36	0.40
1:A:1429:C:H2'	1:A:1430:C:H6	1.86	0.40
3:C:52:LEU:HD23	3:C:52:LEU:O	2.21	0.40
1:A:127:G:O2'	17:Q:2:PRO:O	2.39	0.40
18:R:53:ARG:HE	18:R:59:SER:C	2.25	0.40
1:A:729:A:H2'	1:A:730:G:H8	1.87	0.40
1:A:1442(A):G:C3'	1:A:1442(B):A:H5''	2.51	0.40
7:G:38:LEU:O	7:G:42:ILE:HG12	2.22	0.40
1:A:1072:G:C2	1:A:1104:G:C2	3.10	0.40
1:A:68:G:N2	1:A:152:A:O2'	2.55	0.40
1:A:1175:G:C2	1:A:1176:A:C4	3.10	0.40
1:A:1256:A:H5''	1:A:1257:U:OP1	2.21	0.40
17:Q:13:ASP:HB3	17:Q:19:VAL:HG12	2.03	0.40
1:A:35:G:N3	12:L:118:SER:HB2	2.37	0.40
1:A:1446:U:H4'	1:A:1447:A:C6	2.56	0.40
9:I:52:ALA:HB2	9:I:101:PHE:CE1	2.56	0.40
1:A:794:A:H2'	1:A:795:C:O4'	2.21	0.40
9:I:66:ARG:C	9:I:73:GLN:HE21	2.25	0.40
1:A:1346:A:H4'	1:A:1347:G:OP1	2.21	0.40
1:A:1262:C:H2'	1:A:1263:C:C6	2.56	0.40
1:A:947:G:O2'	1:A:1306:A:H4'	2.21	0.40
2:B:205:ASP:C	2:B:211:ILE:HD11	2.42	0.40
2:B:80:ILE:HG21	2:B:208:ILE:CG2	2.51	0.40
10:J:40:LEU:HG	10:J:69:ASN:O	2.21	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1336:C:H4'	1:A:1337:G:O4'	2.22	0.40
1:A:1313:U:H3	1:A:1324:A:H61	1.69	0.40
1:A:126:G:OP1	1:A:605:U:O2'	2.39	0.40
2:B:14:GLY:HA3	2:B:16:HIS:CE1	2.56	0.40
1:A:35:G:O2'	12:L:121:GLY:HA2	2.21	0.40
1:A:105:G:H2'	1:A:106:C:H6	1.87	0.40
1:A:319:G:C2	1:A:320:C:C2	3.10	0.40
8:H:112:LEU:HB3	8:H:133:LEU:HA	2.03	0.40
2:B:100:GLY:HA3	2:B:104:ASN:HB3	2.03	0.40
22:X:68:GLN:O	22:X:72:ALA:HB3	2.22	0.40
13:M:105:THR:OG1	13:M:106:ASN:N	2.52	0.40
16:P:40:ASP:HA	16:P:41:PRO:HD2	1.93	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	227/256 (89%)	197 (87%)	29 (13%)	1 (0%)	43	84
3	C	204/239 (85%)	177 (87%)	27 (13%)	0	100	100
4	D	206/209 (99%)	190 (92%)	16 (8%)	0	100	100
5	E	146/162 (90%)	135 (92%)	10 (7%)	1 (1%)	30	76
6	F	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
7	G	153/156 (98%)	132 (86%)	20 (13%)	1 (1%)	30	76
8	H	136/138 (99%)	131 (96%)	5 (4%)	0	100	100
9	I	123/128 (96%)	111 (90%)	11 (9%)	1 (1%)	27	74
10	J	94/105 (90%)	76 (81%)	16 (17%)	2 (2%)	11	48
11	K	112/129 (87%)	106 (95%)	6 (5%)	0	100	100
12	L	120/132 (91%)	109 (91%)	10 (8%)	1 (1%)	27	74
13	M	112/126 (89%)	87 (78%)	21 (19%)	4 (4%)	5	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
14	N	58/61 (95%)	52 (90%)	6 (10%)	0	100	100
15	O	86/89 (97%)	75 (87%)	9 (10%)	2 (2%)	10	45
16	P	80/88 (91%)	74 (92%)	5 (6%)	1 (1%)	18	60
17	Q	97/105 (92%)	89 (92%)	8 (8%)	0	100	100
18	R	66/88 (75%)	63 (96%)	3 (4%)	0	100	100
19	S	79/93 (85%)	65 (82%)	13 (16%)	1 (1%)	18	60
20	T	95/106 (90%)	84 (88%)	8 (8%)	3 (3%)	6	35
21	U	21/27 (78%)	20 (95%)	1 (5%)	0	100	100
22	X	93/101 (92%)	84 (90%)	9 (10%)	0	100	100
All	All	2406/2639 (91%)	2153 (90%)	235 (10%)	18 (1%)	30	76

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
20	T	100	ILE
12	L	28	LYS
16	P	79	VAL
9	I	102	LEU
10	J	80	LYS
13	M	88	ARG
15	O	75	PRO
2	B	150	SER
15	O	76	GLU
7	G	100	ALA
10	J	41	PRO
13	M	87	TYR
5	E	21	ALA
20	T	71	THR
19	S	45	VAL
13	M	10	PRO
13	M	7	VAL
20	T	98	PRO

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	177/220 (80%)	133 (75%)	44 (25%)	1	3
3	C	114/188 (61%)	92 (81%)	22 (19%)	2	8
4	D	141/181 (78%)	119 (84%)	22 (16%)	4	14
5	E	108/123 (88%)	87 (81%)	21 (19%)	2	8
6	F	76/90 (84%)	58 (76%)	18 (24%)	1	4
7	G	103/127 (81%)	68 (66%)	35 (34%)	0	0
8	H	103/119 (87%)	83 (81%)	20 (19%)	2	8
9	I	62/99 (63%)	47 (76%)	15 (24%)	1	4
10	J	53/92 (58%)	39 (74%)	14 (26%)	1	2
11	K	81/99 (82%)	70 (86%)	11 (14%)	5	21
12	L	91/109 (84%)	81 (89%)	10 (11%)	9	34
13	M	64/101 (63%)	49 (77%)	15 (23%)	1	5
14	N	46/50 (92%)	32 (70%)	14 (30%)	0	1
15	O	77/80 (96%)	68 (88%)	9 (12%)	8	29
16	P	63/74 (85%)	44 (70%)	19 (30%)	0	1
17	Q	94/97 (97%)	81 (86%)	13 (14%)	5	21
18	R	49/77 (64%)	44 (90%)	5 (10%)	11	37
19	S	43/80 (54%)	32 (74%)	11 (26%)	1	2
20	T	65/82 (79%)	55 (85%)	10 (15%)	4	15
21	U	18/22 (82%)	11 (61%)	7 (39%)	0	0
22	X	38/87 (44%)	29 (76%)	9 (24%)	1	4
All	All	1666/2197 (76%)	1322 (79%)	344 (21%)	2	8

All (344) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	15	VAL
2	B	17	PHE
2	B	21	ARG
2	B	24	TRP
2	B	47	THR
2	B	51	LEU
2	B	67	THR
2	B	69	LEU
2	B	74	LYS
2	B	80	ILE

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Mol	Chain	Res	Type
2	B	82	ARG
2	B	86	GLU
2	B	87	ARG
2	B	93	VAL
2	B	94	ASN
2	B	110	GLN
2	B	113	HIS
2	B	114	ARG
2	B	117	GLU
2	B	121	LEU
2	B	124	SER
2	B	133	LYS
2	B	137	ARG
2	B	139	LYS
2	B	140	HIS
2	B	150	SER
2	B	153	ARG
2	B	157	ARG
2	B	160	ASP
2	B	163	PHE
2	B	170	GLU
2	B	185	ILE
2	B	187	LEU
2	B	191	ASP
2	B	197	VAL
2	B	200	ILE
2	B	205	ASP
2	B	208	ILE
2	B	209	ARG
2	B	210	SER
2	B	212	GLN
2	B	221	LEU
2	B	230	VAL
2	B	233	SER
3	C	4	LYS
3	C	11	ARG
3	C	26	LYS
3	C	30	ARG
3	C	31	HIS
3	C	32	LEU
3	C	36	ASP
3	C	47	LEU

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Mol	Chain	Res	Type
3	C	49	SER
3	C	52	LEU
3	C	56	ASP
3	C	59	ARG
3	C	104	GLN
3	C	136	GLN
3	C	143	GLU
3	C	154	SER
3	C	175	LEU
3	C	176	HIS
3	C	183	ASP
3	C	188	LEU
3	C	195	VAL
3	C	202	ILE
4	D	11	LEU
4	D	12	CYS
4	D	13	ARG
4	D	20	TYR
4	D	36	ARG
4	D	52	SER
4	D	53	ASP
4	D	57	ARG
4	D	70	ILE
4	D	76	ARG
4	D	83	SER
4	D	106	TYR
4	D	113	SER
4	D	119	GLN
4	D	122	ARG
4	D	127	THR
4	D	129	ASN
4	D	135	LEU
4	D	138	TYR
4	D	158	ILE
4	D	170	VAL
4	D	193	ASP
5	E	11	ILE
5	E	12	LEU
5	E	14	ARG
5	E	16	THR
5	E	41	VAL
5	E	51	VAL

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Mol	Chain	Res	Type
5	E	60	TYR
5	E	63	ARG
5	E	65	ASN
5	E	76	ILE
5	E	78	HIS
5	E	79	GLU
5	E	83	GLU
5	E	84	PHE
5	E	87	SER
5	E	89	ILE
5	E	91	LEU
5	E	98	THR
5	E	107	ARG
5	E	147	ASP
5	E	152	ARG
6	F	7	ASN
6	F	22	GLU
6	F	36	ARG
6	F	40	VAL
6	F	45	LEU
6	F	48	LEU
6	F	57	GLN
6	F	63	TYR
6	F	69	GLU
6	F	70	ASP
6	F	72	VAL
6	F	73	ASN
6	F	74	ASP
6	F	75	LEU
6	F	89	MET
6	F	94	GLN
6	F	98	LEU
6	F	100	ASN
7	G	3	ARG
7	G	6	ARG
7	G	12	LEU
7	G	17	VAL
7	G	20	ASP
7	G	23	VAL
7	G	24	THR
7	G	26	PHE
7	G	32	ARG

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Mol	Chain	Res	Type
7	G	33	ASP
7	G	36	LYS
7	G	44	TYR
7	G	47	CYS
7	G	56	GLN
7	G	61	VAL
7	G	62	PHE
7	G	67	GLU
7	G	73	MET
7	G	75	VAL
7	G	80	VAL
7	G	90	GLU
7	G	96	GLN
7	G	111	ARG
7	G	113	GLU
7	G	118	VAL
7	G	119	ARG
7	G	120	ILE
7	G	125	MET
7	G	126	ASP
7	G	135	VAL
7	G	142	GLU
7	G	143	ARG
7	G	148	ASN
7	G	153	HIS
7	G	155	ARG
8	H	2	LEU
8	H	21	LYS
8	H	25	ASP
8	H	37	ARG
8	H	49	GLU
8	H	52	ASP
8	H	54	ASP
8	H	60	ARG
8	H	63	LEU
8	H	77	GLU
8	H	78	GLN
8	H	83	ILE
8	H	84	ARG
8	H	85	ARG
8	H	91	ARG
8	H	95	VAL

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Mol	Chain	Res	Type
8	H	109	ILE
8	H	119	LEU
8	H	120	THR
8	H	127	LEU
9	I	5	TYR
9	I	11	LYS
9	I	62	TYR
9	I	63	ILE
9	I	64	THR
9	I	65	VAL
9	I	66	ARG
9	I	74	ILE
9	I	75	ASP
9	I	77	ILE
9	I	88	TYR
9	I	104	ARG
9	I	107	ARG
9	I	108	VAL
9	I	114	TYR
10	J	12	ASP
10	J	21	GLN
10	J	33	GLN
10	J	38	ILE
10	J	42	THR
10	J	45	ARG
10	J	49	VAL
10	J	55	LYS
10	J	62	HIS
10	J	64	GLU
10	J	73	ASP
10	J	94	VAL
10	J	96	ILE
10	J	100	THR
11	K	14	VAL
11	K	16	SER
11	K	29	ILE
11	K	30	VAL
11	K	32	ILE
11	K	47	VAL
11	K	81	ASP
11	K	96	ARG
11	K	103	LEU

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Mol	Chain	Res	Type
11	K	109	VAL
11	K	117	ASN
12	L	33	ARG
12	L	44	THR
12	L	52	LEU
12	L	53	ARG
12	L	60	LEU
12	L	66	VAL
12	L	82	VAL
12	L	97	ARG
12	L	115	LYS
12	L	119	LYS
13	M	3	ARG
13	M	19	LEU
13	M	34	LEU
13	M	45	VAL
13	M	47	ASP
13	M	55	ARG
13	M	56	LEU
13	M	61	GLU
13	M	65	LYS
13	M	66	LEU
13	M	67	GLU
13	M	70	LEU
13	M	71	ARG
13	M	88	ARG
13	M	105	THR
14	N	3	ARG
14	N	6	LEU
14	N	7	ILE
14	N	8	GLU
14	N	13	THR
14	N	17	LYS
14	N	24	CYS
14	N	25	VAL
14	N	32	SER
14	N	33	VAL
14	N	39	LEU
14	N	42	ILE
14	N	45	ARG
14	N	53	LEU
15	O	3	ILE

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Mol	Chain	Res	Type
15	O	4	THR
15	O	13	GLN
15	O	24	SER
15	O	26	GLU
15	O	39	LEU
15	O	66	LEU
15	O	72	ARG
15	O	87	ILE
16	P	1	MET
16	P	2	VAL
16	P	6	LEU
16	P	11	SER
16	P	21	VAL
16	P	22	THR
16	P	25	ARG
16	P	26	ARG
16	P	27	LYS
16	P	29	ASP
16	P	36	ILE
16	P	38	TYR
16	P	43	LYS
16	P	45	THR
16	P	62	VAL
16	P	65	GLN
16	P	67	THR
16	P	69	THR
16	P	76	GLN
17	Q	11	VAL
17	Q	34	LYS
17	Q	43	LEU
17	Q	45	HIS
17	Q	50	LYS
17	Q	57	VAL
17	Q	59	ILE
17	Q	65	ILE
17	Q	72	ARG
17	Q	74	LEU
17	Q	86	GLU
17	Q	96	GLU
17	Q	100	LYS
18	R	35	ARG
18	R	36	ASN

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Mol	Chain	Res	Type
18	R	76	LEU
18	R	79	LEU
18	R	85	LEU
19	S	44	MET
19	S	47	HIS
19	S	51	VAL
19	S	61	TYR
19	S	62	ILE
19	S	66	MET
19	S	67	VAL
19	S	69	HIS
19	S	78	ARG
19	S	79	THR
19	S	81	ARG
20	T	10	LEU
20	T	13	LEU
20	T	36	LEU
20	T	39	LYS
20	T	62	LEU
20	T	71	THR
20	T	72	LEU
20	T	73	HIS
20	T	74	LYS
20	T	84	LEU
21	U	6	ARG
21	U	7	ARG
21	U	9	ARG
21	U	10	ARG
21	U	12	LYS
21	U	13	ILE
21	U	17	THR
22	X	4	ASN
22	X	6	THR
22	X	31	PHE
22	X	54	LEU
22	X	62	HIS
22	X	64	SER
22	X	66	GLU
22	X	77	LEU
22	X	93	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	94	ASN
2	B	110	GLN
2	B	140	HIS
2	B	146	GLN
2	B	212	GLN
3	C	31	HIS
3	C	37	GLN
3	C	69	HIS
3	C	136	GLN
5	E	65	ASN
5	E	78	HIS
5	E	130	ASN
6	F	64	GLN
6	F	73	ASN
6	F	94	GLN
7	G	96	GLN
7	G	148	ASN
9	I	3	GLN
10	J	68	HIS
13	M	77	ASN
14	N	52	GLN
16	P	16	HIS
16	P	65	GLN
17	Q	45	HIS
18	R	36	ASN
19	S	83	HIS
22	X	94	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1495/1522 (98%)	396 (26%)	34 (2%)

All (396) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	5	U
1	A	6	G
1	A	7	G
1	A	9	G
1	A	32	A
1	A	39	G

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Mol	Chain	Res	Type
1	A	47	C
1	A	48	C
1	A	50	A
1	A	51	A
1	A	53	A
1	A	60	A
1	A	61	G
1	A	62	U
1	A	65	U
1	A	66	G
1	A	67	C
1	A	77	G
1	A	78	G
1	A	79	G
1	A	91	C
1	A	93	G
1	A	96	U
1	A	97	G
1	A	115	G
1	A	116	A
1	A	121	C
1	A	131	C
1	A	142	G
1	A	150	C
1	A	163	C
1	A	173	U
1	A	182	U
1	A	189(G)	G
1	A	189(H)	G
1	A	195	A
1	A	197	A
1	A	201	C
1	A	203	U
1	A	204	U
1	A	216	G
1	A	227	G
1	A	243	A
1	A	244	U
1	A	247	G
1	A	251	G
1	A	266	G
1	A	267	C

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Mol	Chain	Res	Type
1	A	289	G
1	A	321	A
1	A	328	C
1	A	332	G
1	A	342	C
1	A	343	U
1	A	344	A
1	A	345	C
1	A	351	G
1	A	352	C
1	A	353	A
1	A	354	G
1	A	365	U
1	A	367	U
1	A	372	C
1	A	373	A
1	A	388	G
1	A	392	G
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	414	A
1	A	422	C
1	A	423	G
1	A	424	G
1	A	429	U
1	A	430	A
1	A	435	C
1	A	437	U
1	A	439	A
1	A	442	C
1	A	445	G
1	A	452	A
1	A	457	C
1	A	461	A
1	A	484	G
1	A	485	G
1	A	493	G
1	A	496	A

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Mol	Chain	Res	Type
1	A	498	U
1	A	505	G
1	A	509	A
1	A	510	A
1	A	511	C
1	A	518	C
1	A	520	A
1	A	521	G
1	A	524	G
1	A	525	C
1	A	527	G
1	A	531	U
1	A	532	A
1	A	533	A
1	A	547	A
1	A	559	A
1	A	560	U
1	A	561	U
1	A	562	C
1	A	563	A
1	A	564	C
1	A	570	G
1	A	572	A
1	A	573	A
1	A	575	G
1	A	576	G
1	A	577	G
1	A	588	G
1	A	596	C
1	A	607	A
1	A	618	C
1	A	623	C
1	A	629	G
1	A	630	G
1	A	631	G
1	A	632	A
1	A	633	G
1	A	634	C
1	A	653	A
1	A	661	G
1	A	665	A
1	A	666	G

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Mol	Chain	Res	Type
1	A	680	C
1	A	687	A
1	A	688	G
1	A	690	G
1	A	724	G
1	A	731	G
1	A	749	C
1	A	755	G
1	A	766	A
1	A	774	G
1	A	777	A
1	A	786	G
1	A	787	A
1	A	793	U
1	A	794	A
1	A	796	C
1	A	802	A
1	A	816	A
1	A	817	C
1	A	818	G
1	A	821	G
1	A	827	U
1	A	828	A
1	A	833	U
1	A	836	G
1	A	839	U
1	A	840	C
1	A	841	U
1	A	848	C
1	A	859	A
1	A	870	U
1	A	873	A
1	A	875	C
1	A	876	G
1	A	902	G
1	A	914	A
1	A	926	G
1	A	927	G
1	A	932	C
1	A	933	G
1	A	934	C
1	A	935	A

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Mol	Chain	Res	Type
1	A	936	C
1	A	937	A
1	A	940	C
1	A	942	G
1	A	945	G
1	A	950	U
1	A	953	G
1	A	954	G
1	A	958	A
1	A	960	U
1	A	961	U
1	A	964	A
1	A	966	G
1	A	969	A
1	A	971	G
1	A	972	C
1	A	974	A
1	A	975	A
1	A	976	G
1	A	977	A
1	A	978	A
1	A	982	U
1	A	984	C
1	A	985	C
1	A	989	C
1	A	990	C
1	A	991	U
1	A	992	U
1	A	993	G
1	A	996	A
1	A	1001(A)	G
1	A	1004	A
1	A	1005	A
1	A	1006	C
1	A	1009	G
1	A	1012	U
1	A	1016	A
1	A	1019	C
1	A	1023	G
1	A	1024	G
1	A	1026	G
1	A	1027	C

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Mol	Chain	Res	Type
1	A	1028	C
1	A	1029	C
1	A	1030	C
1	A	1031	G
1	A	1035	A
1	A	1036	G
1	A	1037	C
1	A	1039	C
1	A	1042	G
1	A	1043	C
1	A	1044	A
1	A	1045	C
1	A	1046	A
1	A	1053	G
1	A	1054	C
1	A	1055	A
1	A	1063	C
1	A	1064	G
1	A	1065	U
1	A	1066	C
1	A	1068	G
1	A	1081	G
1	A	1084	G
1	A	1085	U
1	A	1086	U
1	A	1088	G
1	A	1089	G
1	A	1094	G
1	A	1096	C
1	A	1101	A
1	A	1107	C
1	A	1109	C
1	A	1112	C
1	A	1114	C
1	A	1115	C
1	A	1117	G
1	A	1118	C
1	A	1119	C
1	A	1124	G
1	A	1125	U
1	A	1126	U
1	A	1127	G

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Mol	Chain	Res	Type
1	A	1129	C
1	A	1131	G
1	A	1134	G
1	A	1136	U
1	A	1137	C
1	A	1138	G
1	A	1139	G
1	A	1140	C
1	A	1144	G
1	A	1145	C
1	A	1149	C
1	A	1150	U
1	A	1151	A
1	A	1152	A
1	A	1155	G
1	A	1159	U
1	A	1160	G
1	A	1161	C
1	A	1162	C
1	A	1166	G
1	A	1170	A
1	A	1182	G
1	A	1183	A
1	A	1184	G
1	A	1185	G
1	A	1186	G
1	A	1187	G
1	A	1188	A
1	A	1190	G
1	A	1196	U
1	A	1197	G
1	A	1201	A
1	A	1202	G
1	A	1206	G
1	A	1207	G
1	A	1210	C
1	A	1211	U
1	A	1212	U
1	A	1213	A
1	A	1214	C
1	A	1220	G
1	A	1224	G

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Mol	Chain	Res	Type
1	A	1225	A
1	A	1226	C
1	A	1227	A
1	A	1228	C
1	A	1233	G
1	A	1236	A
1	A	1238	A
1	A	1240	U
1	A	1241	G
1	A	1242	C
1	A	1244	C
1	A	1245	A
1	A	1250	A
1	A	1252	A
1	A	1256	A
1	A	1257	U
1	A	1258	G
1	A	1260	C
1	A	1264	C
1	A	1265	G
1	A	1266	G
1	A	1267	C
1	A	1270	C
1	A	1271	G
1	A	1272	G
1	A	1275	A
1	A	1278	U
1	A	1279	A
1	A	1280	A
1	A	1282	C
1	A	1284	C
1	A	1286	A
1	A	1287	A
1	A	1288	A
1	A	1293	G
1	A	1294	G
1	A	1295	G
1	A	1297	C
1	A	1298	C
1	A	1299	A
1	A	1300	G
1	A	1301	U

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Mol	Chain	Res	Type
1	A	1302	U
1	A	1304	G
1	A	1305	G
1	A	1307	U
1	A	1319	A
1	A	1322	C
1	A	1323	G
1	A	1331	G
1	A	1333	A
1	A	1335	C
1	A	1336	C
1	A	1338	G
1	A	1346	A
1	A	1347	G
1	A	1348	U
1	A	1357	A
1	A	1359	C
1	A	1362	C
1	A	1363	C
1	A	1363(A)	A
1	A	1364	U
1	A	1369	C
1	A	1372	U
1	A	1373	G
1	A	1379	G
1	A	1381	U
1	A	1394	A
1	A	1397	C
1	A	1398	A
1	A	1401	G
1	A	1419	G
1	A	1441	G
1	A	1442	G
1	A	1442(B)	A
1	A	1446	U
1	A	1447	A
1	A	1452	C
1	A	1456	G
1	A	1457	G
1	A	1459	C
1	A	1460	A
1	A	1487	G

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Mol	Chain	Res	Type
1	A	1492	A
1	A	1493	A
1	A	1494	G
1	A	1495	U
1	A	1497	G
1	A	1504	G
1	A	1505	G
1	A	1506	U
1	A	1517	G
1	A	1520	G
1	A	1529	G
1	A	1530	G

All (34) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	60	A
1	A	115	G
1	A	173	U
1	A	243	A
1	A	266	G
1	A	344	A
1	A	428	G
1	A	429	U
1	A	484	G
1	A	495	A
1	A	509	A
1	A	560	U
1	A	561	U
1	A	687	A
1	A	748	C
1	A	793	U
1	A	913	A
1	A	991	U
1	A	992	U
1	A	1064	G
1	A	1065	U
1	A	1067	A
1	A	1201	A
1	A	1211	U
1	A	1227	A
1	A	1256	A

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Mol	Chain	Res	Type
1	A	1280	A
1	A	1285	A
1	A	1299	A
1	A	1300	G
1	A	1346	A
1	A	1442	G
1	A	1493	A
1	A	1504	G

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 172 ligands modelled in this entry, 172 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.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	1497/1522 (98%)	0.29	71 (4%) 30 4	50, 96, 158, 171	0
2	B	229/256 (89%)	0.24	7 (3%) 47 7	92, 116, 136, 149	0
3	C	206/239 (86%)	0.22	8 (3%) 37 5	94, 120, 143, 158	0
4	D	208/209 (99%)	0.28	17 (8%) 12 2	76, 93, 114, 124	0
5	E	148/162 (91%)	-0.06	1 (0%) 84 32	69, 88, 104, 127	0
6	F	100/101 (99%)	-0.06	2 (2%) 62 12	70, 86, 103, 117	0
7	G	155/156 (99%)	0.55	15 (9%) 8 2	122, 137, 149, 159	0
8	H	138/138 (100%)	0.36	6 (4%) 34 5	71, 92, 103, 113	0
9	I	125/128 (97%)	0.93	24 (19%) 2 0	115, 139, 152, 163	0
10	J	96/105 (91%)	0.52	8 (8%) 11 2	108, 134, 150, 160	0
11	K	114/129 (88%)	0.14	3 (2%) 53 8	63, 89, 107, 126	0
12	L	122/132 (92%)	0.28	6 (4%) 28 4	63, 77, 96, 109	0
13	M	114/126 (90%)	0.98	18 (15%) 3 1	116, 140, 151, 160	0
14	N	60/61 (98%)	1.09	11 (18%) 2 0	103, 122, 134, 139	0
15	O	88/89 (98%)	0.28	4 (4%) 32 5	63, 85, 105, 111	0
16	P	82/88 (93%)	0.39	2 (2%) 56 9	73, 85, 105, 117	0
17	Q	99/105 (94%)	0.16	1 (1%) 79 23	69, 83, 101, 108	0
18	R	68/88 (77%)	0.03	0 100 100	75, 85, 105, 117	0
19	S	81/93 (87%)	0.81	12 (14%) 3 1	114, 140, 150, 153	0
20	T	97/106 (91%)	0.63	11 (11%) 6 1	72, 86, 105, 115	0
21	U	23/27 (85%)	3.74	18 (78%) 0 0	129, 137, 148, 150	0
22	X	95/101 (94%)	0.57	10 (10%) 7 1	88, 106, 129, 145	0
All	All	3945/4161 (94%)	0.37	255 (6%) 18 3	50, 101, 152, 171	0

All (255) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
13	M	86	CYS	16.4
21	U	24	ARG	10.1
21	U	16	GLY	9.2
13	M	87	TYR	8.8
19	S	74	PHE	8.3
19	S	75	ALA	8.1
13	M	85	GLY	7.8
19	S	76	PRO	7.1
13	M	89	GLY	7.0
13	M	90	LEU	6.8
7	G	10	ARG	6.6
13	M	93	ARG	6.5
21	U	17	THR	6.5
21	U	23	PRO	6.4
13	M	88	ARG	6.4
22	X	1	MET	6.2
13	M	84	ILE	6.1
14	N	58	LYS	6.0
13	M	81	LEU	5.9
9	I	105	ASP	5.9
9	I	30	GLY	5.8
7	G	5	ARG	5.8
10	J	99	LYS	5.5
1	A	1149	C	5.4
1	A	1019	C	5.4
1	A	1030(B)	C	5.3
9	I	35	GLU	5.2
19	S	69	HIS	5.1
1	A	1148	U	5.0
1	A	1363	C	4.9
7	G	11	GLN	4.9
9	I	42	ARG	4.8
13	M	94	ARG	4.7
10	J	100	THR	4.7
1	A	1285	A	4.7
1	A	1286	A	4.6
1	A	1018	C	4.5
7	G	13	GLN	4.5
3	C	164	ARG	4.5
21	U	3	LYS	4.5
21	U	15	ARG	4.4
21	U	18	TYR	4.3

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Mol	Chain	Res	Type	RSRZ
1	A	1367	C	4.3
21	U	4	GLY	4.3
1	A	1224	G	4.3
1	A	1368	G	4.3
14	N	57	ARG	4.2
19	S	72	GLY	4.2
1	A	1310	G	4.2
9	I	43	ALA	4.1
21	U	6	ARG	4.1
9	I	44	VAL	4.0
19	S	73	GLU	4.0
9	I	106	ALA	4.0
7	G	8	GLU	3.9
1	A	1324	A	3.9
13	M	91	ARG	3.8
1	A	1066	C	3.8
20	T	9	ASN	3.8
4	D	2	GLY	3.7
12	L	64	TYR	3.6
9	I	115	GLY	3.5
7	G	4	ARG	3.5
1	A	1322	C	3.5
4	D	47	ARG	3.5
4	D	73	ARG	3.5
9	I	123	PRO	3.4
1	A	1363(A)	A	3.4
1	A	1260	C	3.4
1	A	1321	C	3.4
9	I	31	GLN	3.4
3	C	17	ASP	3.4
10	J	58	ASP	3.4
8	H	70	GLN	3.4
13	M	82	MET	3.3
1	A	1117	G	3.3
7	G	29	LYS	3.3
21	U	14	TRP	3.3
1	A	1320	C	3.3
4	D	48	ALA	3.3
19	S	36	ARG	3.3
4	D	67	ILE	3.3
20	T	73	HIS	3.3
1	A	1249	C	3.3

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Mol	Chain	Res	Type	RSRZ
14	N	59	ALA	3.2
7	G	41	ARG	3.2
7	G	12	LEU	3.2
22	X	2	GLN	3.2
9	I	41	VAL	3.1
14	N	51	GLY	3.1
10	J	62	HIS	3.1
1	A	1183	A	3.1
20	T	66	ALA	3.0
9	I	116	LYS	3.0
4	D	68	TYR	3.0
15	O	47	LYS	3.0
13	M	72	ALA	3.0
1	A	575	G	3.0
9	I	110	GLU	3.0
21	U	21	TYR	3.0
2	B	150	SER	3.0
1	A	1362	C	3.0
12	L	63	GLY	3.0
21	U	7	ARG	3.0
1	A	111	G	3.0
11	K	119	CYS	3.0
1	A	1040	U	2.9
4	D	46	LYS	2.9
1	A	135	C	2.9
1	A	1115	C	2.9
12	L	18	VAL	2.9
9	I	114	TYR	2.9
19	S	77	THR	2.9
8	H	84	ARG	2.9
22	X	61	ILE	2.8
13	M	100	GLY	2.8
1	A	1394	A	2.8
9	I	126	SER	2.8
10	J	60	ARG	2.8
20	T	13	LEU	2.8
1	A	1325	C	2.8
7	G	2	ALA	2.8
1	A	940	C	2.7
22	X	89	LYS	2.7
4	D	21	LEU	2.7
9	I	66	ARG	2.7

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Mol	Chain	Res	Type	RSRZ
12	L	19	ARG	2.7
21	U	12	LYS	2.7
11	K	86	GLY	2.7
7	G	9	VAL	2.7
1	A	1257	U	2.7
1	A	1007	C	2.7
12	L	26	ALA	2.7
2	B	149	LEU	2.6
1	A	1196	U	2.6
7	G	7	ALA	2.6
1	A	1364	U	2.6
7	G	112	PRO	2.6
3	C	165	THR	2.6
13	M	101	GLN	2.6
1	A	934	C	2.5
21	U	22	ARG	2.5
10	J	61	GLU	2.5
9	I	74	ILE	2.5
6	F	65	VAL	2.5
9	I	111	ARG	2.5
1	A	32	A	2.5
21	U	2	GLY	2.5
20	T	29	LYS	2.5
14	N	12	ARG	2.5
19	S	80	TYR	2.5
4	D	6	GLY	2.5
1	A	1186	G	2.5
2	B	93	VAL	2.5
5	E	23	GLY	2.5
15	O	68	ARG	2.5
1	A	853	G	2.5
4	D	3	ARG	2.5
2	B	113	HIS	2.5
1	A	267	C	2.4
1	A	1284	C	2.4
22	X	72	ALA	2.4
14	N	50	LYS	2.4
19	S	70	LYS	2.4
20	T	14	LYS	2.4
1	A	1098	C	2.4
4	D	5	ILE	2.4
14	N	13	THR	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	325	A	2.4
1	A	876	G	2.4
7	G	28	ASN	2.4
11	K	91	ARG	2.4
1	A	1194	U	2.4
9	I	62	TYR	2.4
1	A	58	C	2.4
21	U	11	GLY	2.4
10	J	98	ILE	2.4
3	C	16	ARG	2.4
4	D	45	GLN	2.4
22	X	88	HIS	2.4
14	N	38	GLY	2.3
2	B	134	GLU	2.3
2	B	146	GLN	2.3
2	B	91	PRO	2.3
9	I	117	HIS	2.3
20	T	71	THR	2.3
1	A	994	A	2.3
21	U	5	ASP	2.3
19	S	71	LEU	2.3
1	A	1116	C	2.3
1	A	1262	C	2.3
20	T	8	ARG	2.3
14	N	30	ALA	2.3
21	U	13	ILE	2.3
22	X	60	GLU	2.3
1	A	1147	C	2.3
1	A	331	G	2.2
4	D	66	ARG	2.2
14	N	4	LYS	2.2
4	D	69	GLY	2.2
9	I	34	ASN	2.2
22	X	91	LYS	2.2
4	D	4	TYR	2.2
12	L	17	LYS	2.2
1	A	46	G	2.2
20	T	77	ALA	2.2
20	T	70	SER	2.2
1	A	1188	A	2.2
1	A	970	C	2.2
15	O	71	GLN	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	1252	A	2.2
1	A	61	G	2.2
8	H	136	GLU	2.2
1	A	1193	G	2.2
20	T	69	GLY	2.2
1	A	1323	G	2.2
4	D	196	LEU	2.2
3	C	166	GLU	2.1
13	M	92	HIS	2.1
15	O	59	MET	2.1
13	M	83	ASP	2.1
16	P	35	LYS	2.1
1	A	31	G	2.1
14	N	35	ARG	2.1
19	S	81	ARG	2.1
6	F	92	LYS	2.1
16	P	1	MET	2.1
3	C	131	ARG	2.1
22	X	62	HIS	2.1
1	A	105	G	2.1
1	A	1371	G	2.1
8	H	82	HIS	2.1
10	J	66	ARG	2.1
1	A	1045	C	2.1
13	M	71	ARG	2.1
17	Q	68	ARG	2.1
1	A	48	C	2.1
3	C	188	LEU	2.1
9	I	122	ALA	2.1
7	G	32	ARG	2.1
8	H	1	MET	2.1
4	D	20	TYR	2.1
22	X	44	GLU	2.1
1	A	1154	G	2.0
1	A	106	C	2.0
3	C	100	ALA	2.0
1	A	1374	A	2.0
1	A	1526	G	2.0
1	A	612	C	2.0
1	A	422	C	2.0
1	A	1220	G	2.0
1	A	1385	G	2.0

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Mol	Chain	Res	Type	RSRZ
9	I	98	PRO	2.0
9	I	124	GLN	2.0
8	H	81	HIS	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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	RSR	LLDF	B-factors(Å ²)	Q<0.9
24	ZN	N	101	1/1	0.04	-	107,107,107,107	0
23	MG	A	1631	1/1	0.82	-	48,48,48,48	0
23	MG	A	1629	1/1	0.13	-	87,87,87,87	0
23	MG	A	1757	1/1	0.18	-	71,71,71,71	0
23	MG	A	1690	1/1	0.24	-	64,64,64,64	0
23	MG	A	1709	1/1	0.53	-	103,103,103,103	0
23	MG	A	1738	1/1	0.14	-	69,69,69,69	0
23	MG	A	1693	1/1	0.87	-	59,59,59,59	0
23	MG	A	1739	1/1	0.10	-	70,70,70,70	0
23	MG	A	1747	1/1	0.12	-	83,83,83,83	0
23	MG	A	1706	1/1	0.13	-	56,56,56,56	0
23	MG	A	1633	1/1	2.26	-	77,77,77,77	0
23	MG	A	1678	1/1	0.18	-	55,55,55,55	0
23	MG	A	1740	1/1	0.12	-	89,89,89,89	0
23	MG	A	1668	1/1	0.29	-	87,87,87,87	0
23	MG	A	1704	1/1	0.27	-	72,72,72,72	0
23	MG	A	1694	1/1	0.21	-	62,62,62,62	0
23	MG	A	1713	1/1	0.20	-	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
23	MG	A	1654	1/1	0.23	-	65,65,65,65	0
23	MG	A	1612	1/1	0.10	-	65,65,65,65	0
23	MG	A	1697	1/1	0.62	-	57,57,57,57	0
23	MG	A	1746	1/1	0.15	-	61,61,61,61	0
23	MG	A	1642	1/1	0.40	-	87,87,87,87	0
23	MG	A	1767	1/1	0.18	-	156,156,156,156	0
23	MG	A	1608	1/1	0.61	-	93,93,93,93	0
23	MG	A	1733	1/1	0.25	-	62,62,62,62	0
23	MG	A	1744	1/1	0.55	-	79,79,79,79	0
23	MG	A	1639	1/1	0.21	-	76,76,76,76	0
23	MG	A	1765	1/1	0.17	-	87,87,87,87	0
23	MG	A	1677	1/1	0.31	-	64,64,64,64	0
23	MG	A	1646	1/1	0.18	-	59,59,59,59	0
23	MG	A	1685	1/1	0.21	-	71,71,71,71	0
23	MG	A	1736	1/1	0.38	-	82,82,82,82	0
23	MG	A	1681	1/1	0.28	-	82,82,82,82	0
23	MG	A	1725	1/1	0.14	-	71,71,71,71	0
23	MG	A	1670	1/1	0.85	-	73,73,73,73	0
23	MG	A	1634	1/1	0.41	-	64,64,64,64	0
23	MG	A	1623	1/1	0.52	-	43,43,43,43	0
23	MG	A	1742	1/1	0.11	-	87,87,87,87	0
23	MG	A	1619	1/1	0.12	-	50,50,50,50	0
23	MG	A	1657	1/1	2.06	-	61,61,61,61	0
23	MG	A	1756	1/1	0.45	-	120,120,120,120	0
23	MG	A	1711	1/1	0.06	-	80,80,80,80	0
23	MG	A	1720	1/1	0.19	-	110,110,110,110	0
23	MG	A	1603	1/1	1.26	-	56,56,56,56	0
23	MG	A	1674	1/1	0.13	-	74,74,74,74	0
23	MG	A	1734	1/1	0.17	-	74,74,74,74	0
23	MG	A	1659	1/1	0.13	-	48,48,48,48	0
23	MG	A	1727	1/1	0.18	-	49,49,49,49	0
23	MG	A	1699	1/1	1.63	-	48,48,48,48	0
23	MG	A	1679	1/1	0.77	-	59,59,59,59	0
23	MG	A	1761	1/1	0.21	-	80,80,80,80	0
24	ZN	D	301	1/1	0.05	-	71,71,71,71	0
23	MG	A	1601	1/1	0.29	-	45,45,45,45	0
23	MG	A	1643	1/1	0.35	-	70,70,70,70	0
23	MG	A	1606	1/1	0.52	-	59,59,59,59	0
23	MG	A	1696	1/1	0.38	-	61,61,61,61	0
23	MG	A	1705	1/1	0.09	-	64,64,64,64	0
23	MG	A	1762	1/1	0.35	-	80,80,80,80	0
23	MG	A	1718	1/1	0.14	-	103,103,103,103	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
23	MG	A	1766	1/1	0.12	-	65,65,65,65	0
23	MG	A	1723	1/1	0.06	-	89,89,89,89	0
23	MG	A	1641	1/1	0.67	-	52,52,52,52	0
23	MG	A	1630	1/1	1.62	-	72,72,72,72	0
23	MG	A	1760	1/1	0.36	-	129,129,129,129	0
23	MG	A	1624	1/1	0.34	-	63,63,63,63	0
23	MG	A	1662	1/1	0.91	-	75,75,75,75	0
23	MG	A	1745	1/1	0.28	-	113,113,113,113	0
23	MG	A	1702	1/1	1.13	-	83,83,83,83	0
23	MG	A	1701	1/1	0.87	-	46,46,46,46	0
23	MG	A	1614	1/1	0.53	-	85,85,85,85	0
23	MG	A	1689	1/1	0.36	-	61,61,61,61	0
23	MG	A	1648	1/1	0.63	-	60,60,60,60	0
23	MG	A	1687	1/1	0.40	-	62,62,62,62	0
23	MG	A	1617	1/1	0.10	-	87,87,87,87	0
23	MG	A	1660	1/1	0.40	-	70,70,70,70	0
23	MG	A	1651	1/1	0.47	-	46,46,46,46	0
23	MG	A	1715	1/1	0.21	-	87,87,87,87	0
23	MG	A	1620	1/1	0.25	-	58,58,58,58	0
23	MG	A	1611	1/1	0.18	-	43,43,43,43	0
23	MG	Q	201	1/1	0.50	-	62,62,62,62	0
23	MG	A	1628	1/1	0.22	-	75,75,75,75	0
23	MG	A	1656	1/1	0.33	-	86,86,86,86	0
23	MG	A	1691	1/1	0.69	-	51,51,51,51	0
23	MG	A	1683	1/1	0.37	-	100,100,100,100	0
23	MG	A	1609	1/1	0.14	-	70,70,70,70	0
23	MG	A	1764	1/1	0.40	-	69,69,69,69	0
23	MG	A	1649	1/1	1.19	-	66,66,66,66	0
23	MG	A	1755	1/1	0.10	-	61,61,61,61	0
23	MG	A	1675	1/1	0.29	-	61,61,61,61	0
23	MG	A	1632	1/1	0.75	-	69,69,69,69	0
23	MG	A	1652	1/1	0.32	-	76,76,76,76	0
23	MG	A	1613	1/1	0.52	-	66,66,66,66	0
23	MG	A	1673	1/1	0.82	-	57,57,57,57	0
23	MG	A	1664	1/1	0.20	-	80,80,80,80	0
23	MG	A	1708	1/1	0.33	-	96,96,96,96	0
23	MG	A	1625	1/1	1.32	-	63,63,63,63	0
23	MG	A	1751	1/1	0.16	-	95,95,95,95	0
23	MG	A	1640	1/1	0.46	-	82,82,82,82	0
23	MG	A	1732	1/1	0.18	-	81,81,81,81	0
23	MG	A	1663	1/1	0.46	-	64,64,64,64	0
23	MG	A	1627	1/1	0.29	-	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
23	MG	A	1658	1/1	0.20	-	58,58,58,58	0
23	MG	A	1698	1/1	0.51	-	47,47,47,47	0
23	MG	A	1665	1/1	0.68	-	84,84,84,84	0
23	MG	A	1729	1/1	0.27	-	52,52,52,52	0
23	MG	A	1688	1/1	0.63	-	54,54,54,54	0
23	MG	A	1647	1/1	0.38	-	86,86,86,86	0
23	MG	A	1737	1/1	0.09	-	66,66,66,66	0
23	MG	A	1644	1/1	0.67	-	53,53,53,53	0
23	MG	A	1667	1/1	0.37	-	77,77,77,77	0
23	MG	A	1669	1/1	1.09	-	76,76,76,76	0
23	MG	A	1682	1/1	0.17	-	58,58,58,58	0
23	MG	A	1750	1/1	0.08	-	88,88,88,88	0
23	MG	A	1749	1/1	0.69	-	97,97,97,97	0
23	MG	A	1638	1/1	0.27	-	52,52,52,52	0
23	MG	A	1636	1/1	1.12	-	59,59,59,59	0
23	MG	A	1758	1/1	0.34	-	86,86,86,86	0
23	MG	A	1763	1/1	0.18	-	84,84,84,84	0
23	MG	A	1716	1/1	0.41	-	73,73,73,73	0
23	MG	A	1602	1/1	0.44	-	62,62,62,62	0
23	MG	A	1700	1/1	0.58	-	69,69,69,69	0
23	MG	A	1661	1/1	0.51	-	67,67,67,67	0
23	MG	A	1676	1/1	0.49	-	73,73,73,73	0
23	MG	A	1714	1/1	0.19	-	103,103,103,103	0
23	MG	A	1752	1/1	0.11	-	58,58,58,58	0
23	MG	A	1759	1/1	0.81	-	74,74,74,74	0
23	MG	A	1653	1/1	0.25	-	57,57,57,57	0
23	MG	A	1607	1/1	0.23	-	50,50,50,50	0
23	MG	A	1712	1/1	0.19	-	63,63,63,63	0
23	MG	A	1724	1/1	0.11	-	64,64,64,64	0
23	MG	A	1695	1/1	0.57	-	50,50,50,50	0
23	MG	A	1728	1/1	0.09	-	65,65,65,65	0
23	MG	A	1655	1/1	0.42	-	98,98,98,98	0
23	MG	A	1726	1/1	0.18	-	55,55,55,55	0
23	MG	A	1710	1/1	0.23	-	94,94,94,94	0
23	MG	A	1692	1/1	0.29	-	86,86,86,86	0
23	MG	A	1721	1/1	0.07	-	83,83,83,83	0
23	MG	A	1626	1/1	0.57	-	62,62,62,62	0
23	MG	A	1615	1/1	0.37	-	65,65,65,65	0
23	MG	A	1686	1/1	0.13	-	61,61,61,61	0
23	MG	A	1722	1/1	0.08	-	54,54,54,54	0
23	MG	E	201	1/1	1.14	-	77,77,77,77	0
23	MG	A	1672	1/1	0.40	-	66,66,66,66	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
23	MG	A	1735	1/1	0.20	-	110,110,110,110	0
23	MG	A	1707	1/1	0.17	-	92,92,92,92	0
23	MG	A	1741	1/1	0.28	-	112,112,112,112	0
23	MG	A	1666	1/1	0.29	-	64,64,64,64	0
23	MG	A	1621	1/1	0.41	-	64,64,64,64	0
23	MG	A	1730	1/1	0.35	-	46,46,46,46	0
23	MG	A	1610	1/1	0.52	-	60,60,60,60	0
23	MG	A	1622	1/1	0.23	-	47,47,47,47	0
23	MG	A	1719	1/1	0.22	-	102,102,102,102	0
23	MG	A	1604	1/1	0.56	-	81,81,81,81	0
23	MG	A	1768	1/1	0.25	-	77,77,77,77	0
23	MG	A	1743	1/1	0.23	-	68,68,68,68	0
23	MG	A	1684	1/1	0.46	-	91,91,91,91	0
23	MG	A	1754	1/1	0.15	-	78,78,78,78	0
23	MG	A	1616	1/1	0.28	-	58,58,58,58	0
23	MG	A	1618	1/1	1.29	-	64,64,64,64	0
23	MG	A	1703	1/1	0.23	-	70,70,70,70	0
23	MG	A	1748	1/1	0.22	-	116,116,116,116	0
23	MG	A	1635	1/1	0.31	-	60,60,60,60	0
23	MG	A	1753	1/1	0.19	-	61,61,61,61	0
23	MG	A	1717	1/1	0.10	-	87,87,87,87	0
23	MG	A	1645	1/1	0.77	-	60,60,60,60	0
23	MG	A	1605	1/1	0.68	-	67,67,67,67	0
23	MG	A	1680	1/1	0.80	-	78,78,78,78	0
23	MG	A	1650	1/1	0.21	-	60,60,60,60	0
23	MG	A	1637	1/1	0.61	-	73,73,73,73	0
23	MG	A	1671	1/1	0.81	-	49,49,49,49	0
23	MG	A	1731	1/1	0.08	-	60,60,60,60	0

6.5 Other polymers ⓘ

There are no such residues in this entry.