Full wwPDB X-ray Structure Validation Report ⓘ

Jun 15, 2024 – 11:33 PM EDT

PDB ID	:	2F4V
Title	:	30S ribosome + designer antibiotic
Authors	:	Murray, J.B.; Meroueh, S.O.; Russell, R.J.; Lentzen, G.; Haddad, J.; Mobashery, S.
Deposited on	:	2005-11-24
Resolution	:	3.80 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

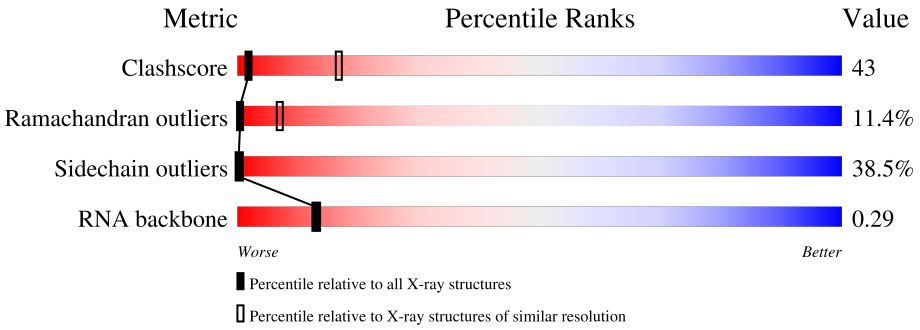
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.80 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))
Clashscore	141614	1288 (4.00-3.60)
Ramachandran outliers	138981	1243 (4.00-3.60)
Sidechain outliers	138945	1237 (4.00-3.60)
RNA backbone	3102	1036 (4.60-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	1511	11% 37% 36% 17%
2	Z	4	100%
3	B	256	20% 45% 24% • 7%
4	C	239	20% 37% 24% 5% 14%
5	D	209	21% 45% 28% 5%
6	E	162	20% 40% 31% • 7%

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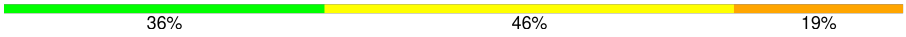
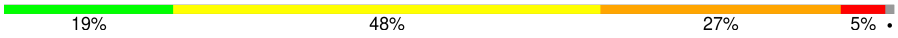
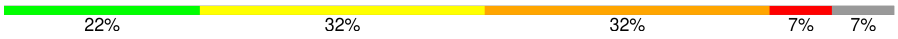
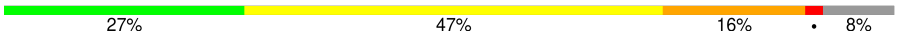
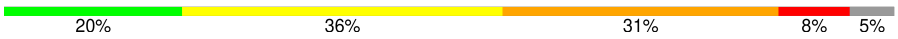
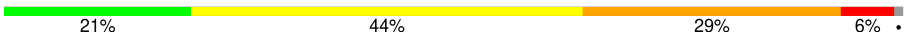
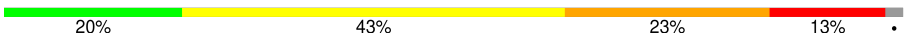
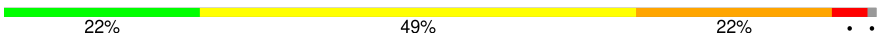
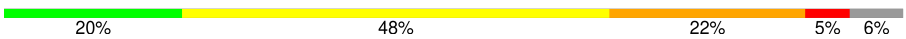
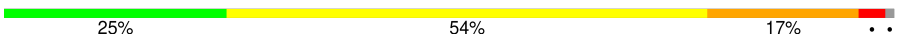
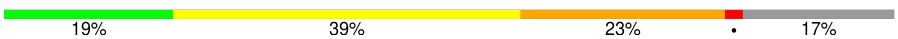
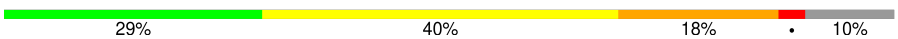
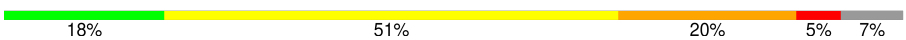
Mol	Chain	Length	Quality of chain
7	F	101	
8	G	156	
9	H	138	
10	I	128	
11	J	105	
12	K	129	
13	L	132	
14	M	126	
15	N	61	
16	O	89	
17	P	88	
18	Q	105	
19	R	88	
20	S	93	
21	T	106	

2 Entry composition

There are 26 unique types of molecules in this entry. The entry contains 51728 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1507	Total	C	N	O	P	22	0	0
			32391	14418	6002	10465	1506			

- Molecule 2 is a RNA chain called 5'-R(P*UP*UP*CP*U)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	Z	4	Total	C	N	O	P	0	0	0
			80	36	9	31	4			

- Molecule 3 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	B	237	Total	C	N	O	S	0	0	0
			1923	1226	344	348	5			

- Molecule 4 is a protein called 30S ribosomal protein S3.

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

- Molecule 5 is a protein called 30S ribosomal protein S4.

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

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	199	GLN	ASN	CONFLICT	UNP P80373
D	201	ASN	GLN	CONFLICT	UNP P80373

- Molecule 6 is a protein called 30S ribosomal protein S5.

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

- Molecule 7 is a protein called 30S ribosomal protein S6.

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

- Molecule 8 is a protein called 30S ribosomal protein S7.

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

- Molecule 9 is a protein called 30S ribosomal protein S8.

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

- Molecule 10 is a protein called 30S ribosomal protein S9.

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

- Molecule 11 is a protein called 30S ribosomal protein S10.

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

- Molecule 12 is a protein called 30S ribosomal protein S11.

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

- Molecule 13 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	L	125	Total	C	N	O	S	0	0	0
			975	614	196	164	1			

- Molecule 14 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	M	125	Total	C	N	O	S	0	0	0
			997	617	207	171	2			

- Molecule 15 is a protein called 30S ribosomal protein S14.

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

- Molecule 16 is a protein called 30S ribosomal protein S15.

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

- Molecule 17 is a protein called 30S ribosomal protein S16.

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

- Molecule 18 is a protein called 30S ribosomal protein S17.

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

- Molecule 19 is a protein called 30S ribosomal protein S18.

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

- Molecule 20 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	S	84	Total	C	N	O	S	0	0	0
			674	430	126	116	2			

- Molecule 21 is a protein called 30S ribosomal protein S20.

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

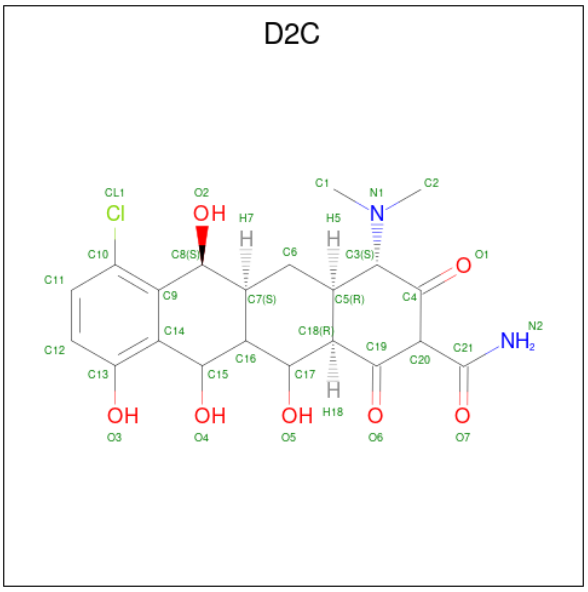
- Molecule 22 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
22	A	98	Total	Mg	0	0
			98	98		
22	Z	1	Total	Mg	0	0
			1	1		
22	D	1	Total	Mg	0	0
			1	1		
22	M	1	Total	Mg	0	0
			1	1		

- Molecule 23 is POTASSIUM ION (three-letter code: K) (formula: K).

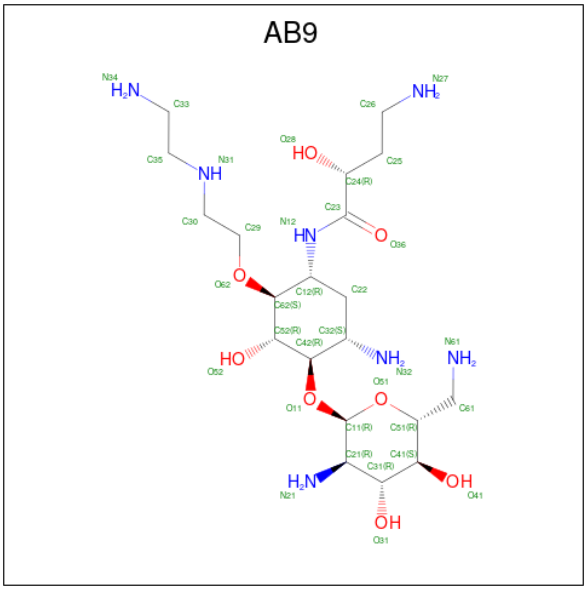
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
23	A	12	Total	K	0	0
			12	12		

- Molecule 24 is (2S,4S,4AR,5AS,6S,11R,11AS,12R,12AR)-7-CHLORO-4-(DIMETHYLAMINO)-6,10,11,12-TETRAHYDROXY-1,3-DIOXO-1,2,3,4,4A,5,5A,6,11,11A,12,12A-DODECAHYDROTETRACENE-2-CARBOXAMIDE (three-letter code: D2C) (formula: $C_{21}H_{25}ClN_2O_7$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
24	A	1	Total	C	Cl	N	O	0	0
			31	21	1	2	7		

- Molecule 25 is (2R)-4-AMINO-N-{(1R,2S,3R,4R,5S)-5-AMINO-2-{2-[(2-AMINOETHYL)AMINO]ETHOXY}-4-[(2,6-DIAMINO-2,6-DIDEOXY-ALPHA-D-GLUCOPYRANOSYL)OXY]-3-HYDROXYCYCLOHEXYL}-2-HYDROXYBUTANAMIDE (three-letter code: AB9) (formula: $C_{20}H_{43}N_7O_8$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
25	A	1	Total	C	N	O	0	0
			35	20	7	8		

- Molecule 26 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

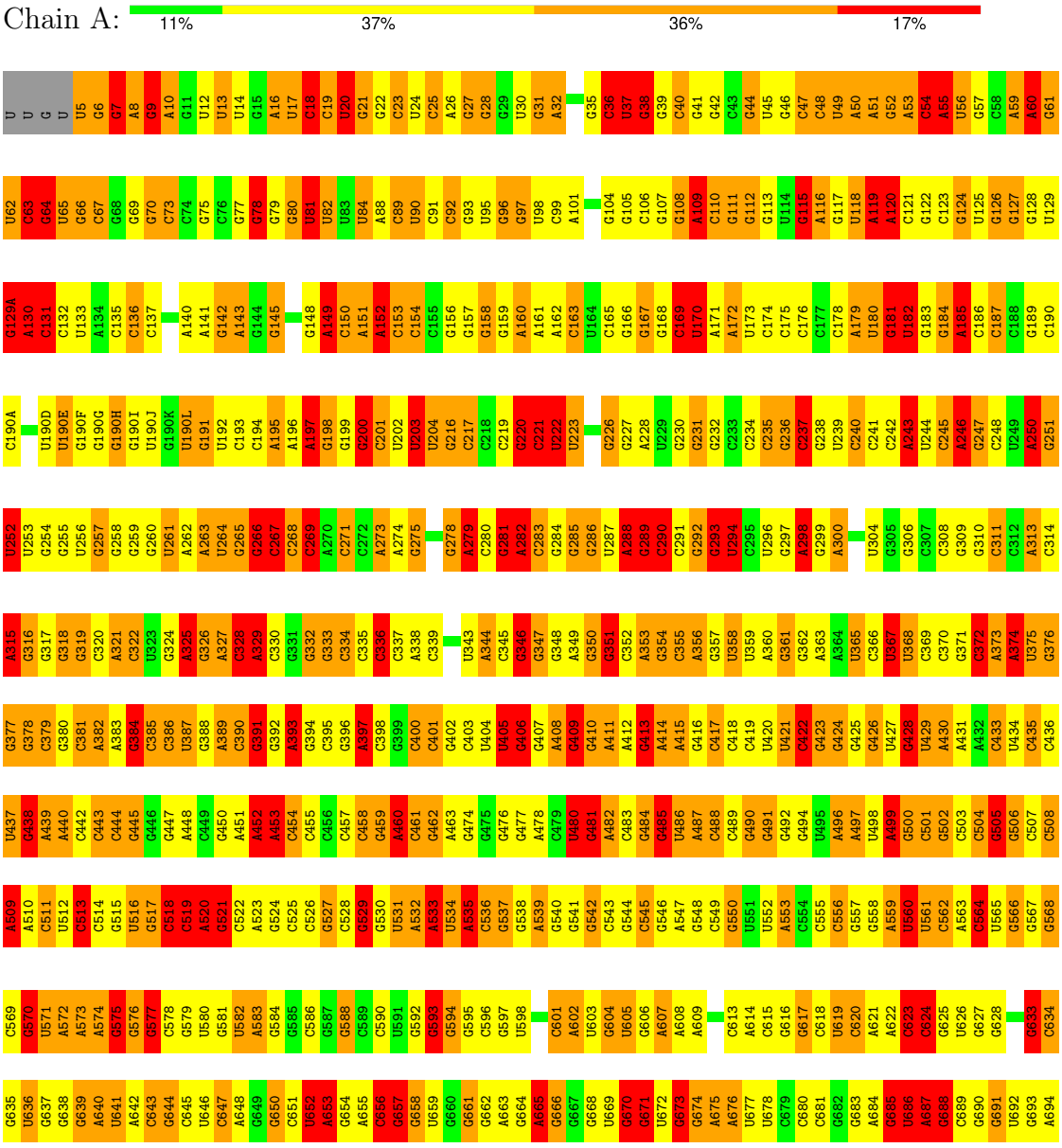
3 Residue-property plots (i)

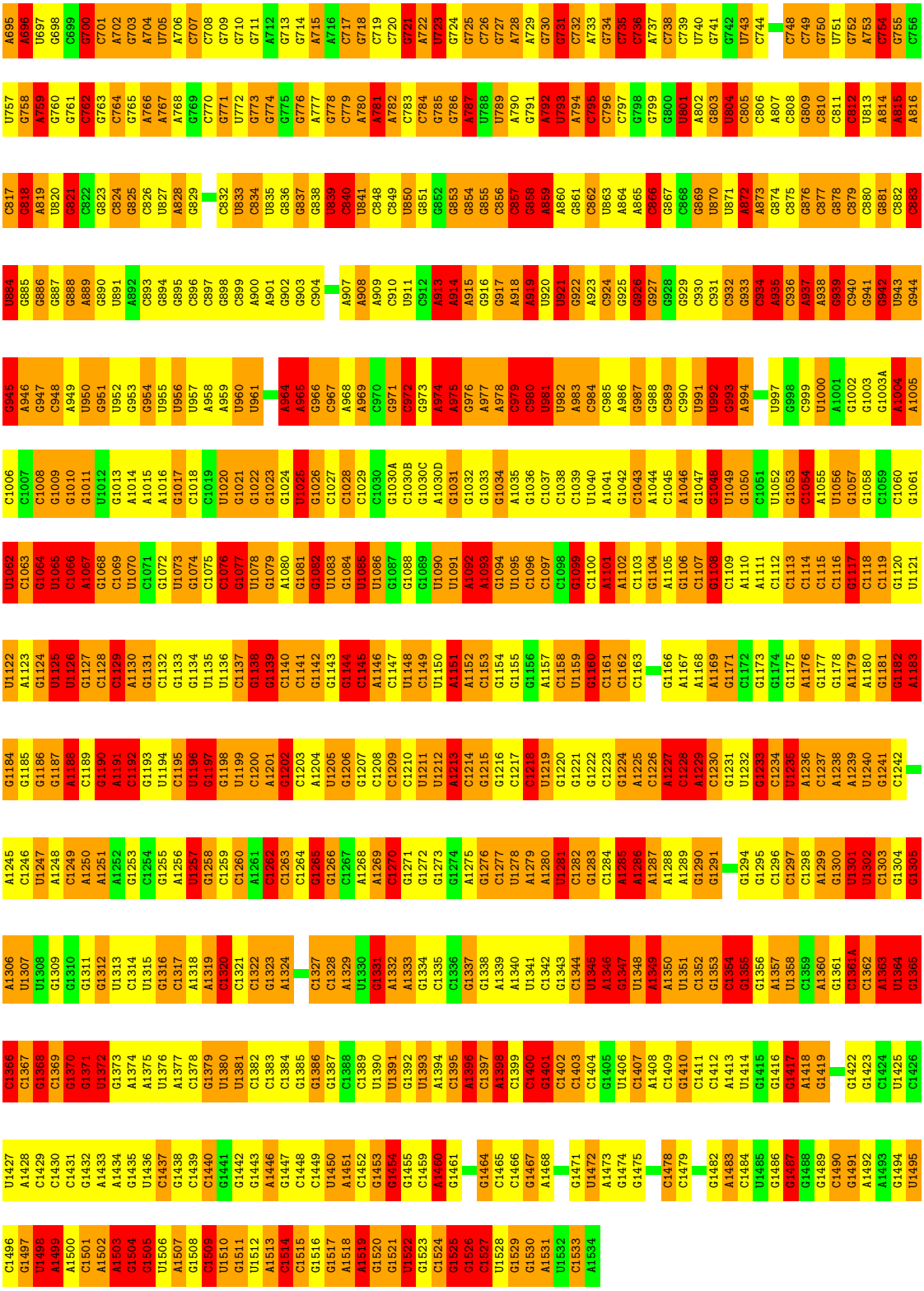
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS was not executed.

- Molecule 1: 16S ribosomal RNA

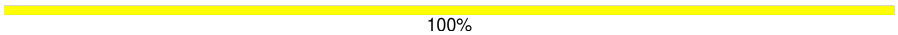
Chain A:





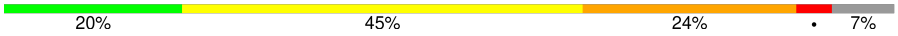
• Molecule 2: 5'-R(P*UP*UP*CP*U)-3'

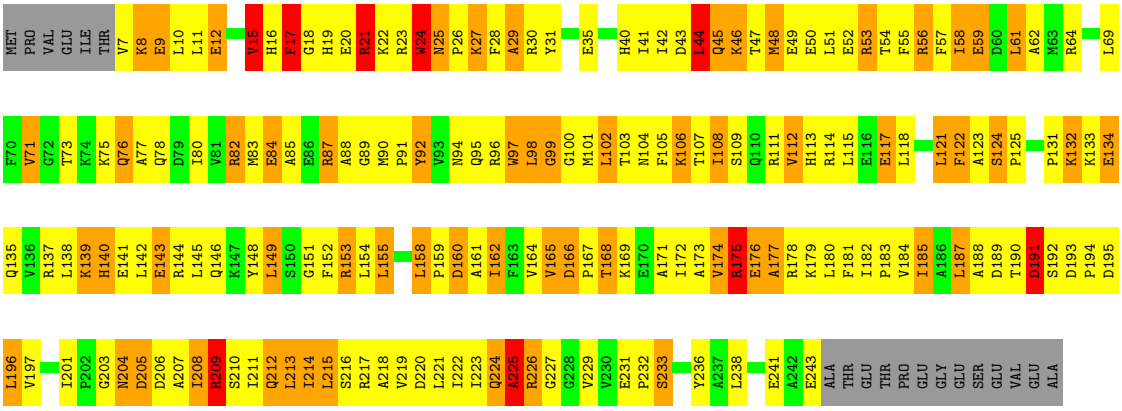
Chain Z:



• Molecule 3: 30S ribosomal protein S2

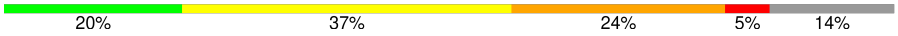
Chain B:

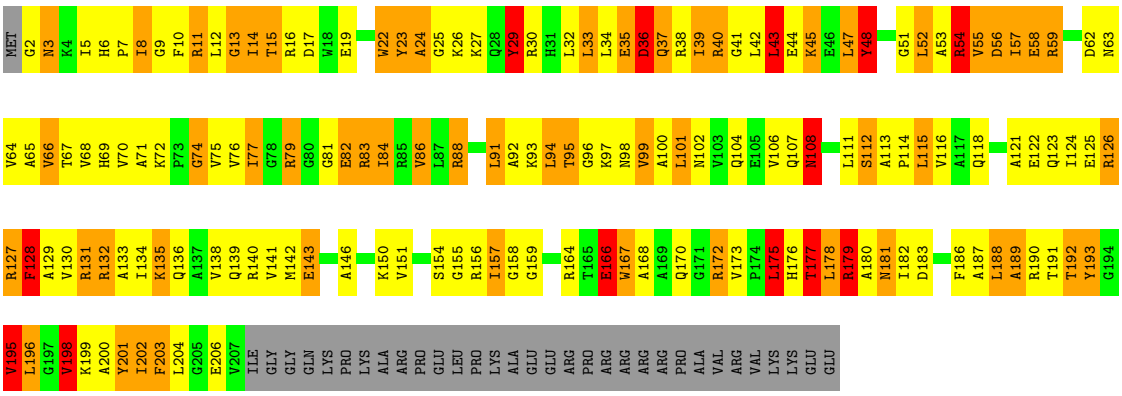




• Molecule 4: 30S ribosomal protein S3

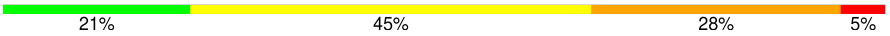
Chain C:

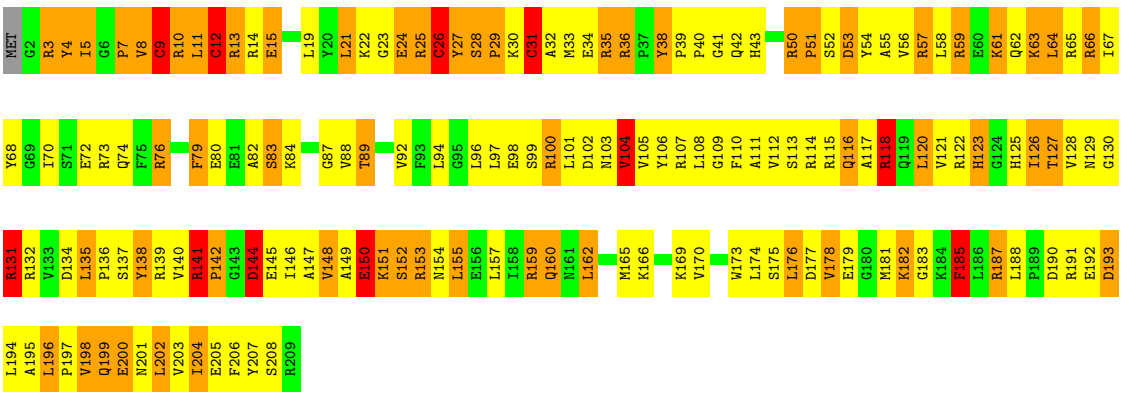




• Molecule 5: 30S ribosomal protein S4

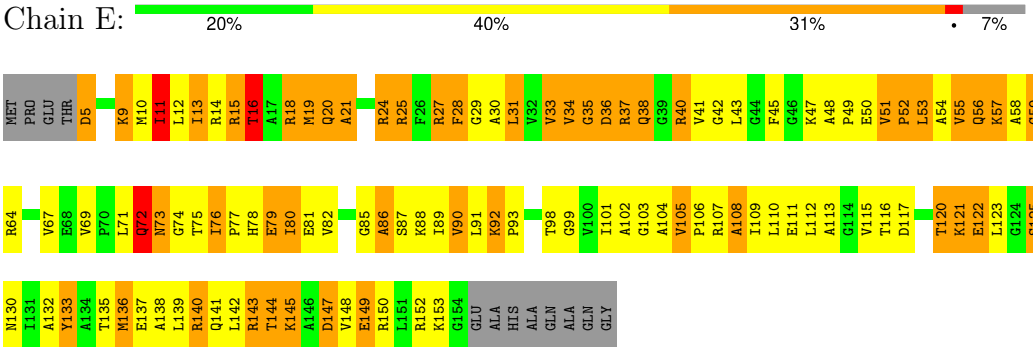
Chain D:





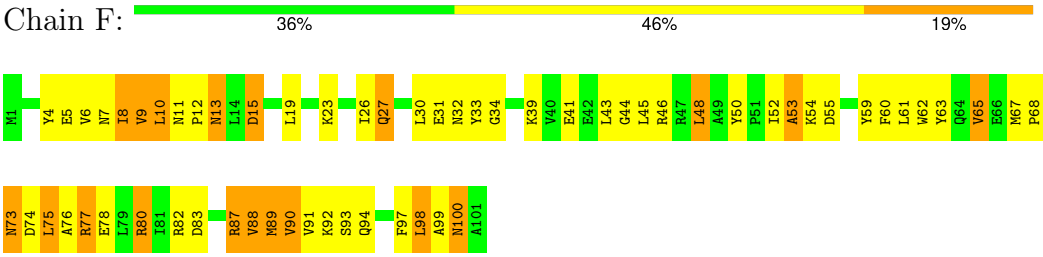
• Molecule 6: 30S ribosomal protein S5

Chain E:



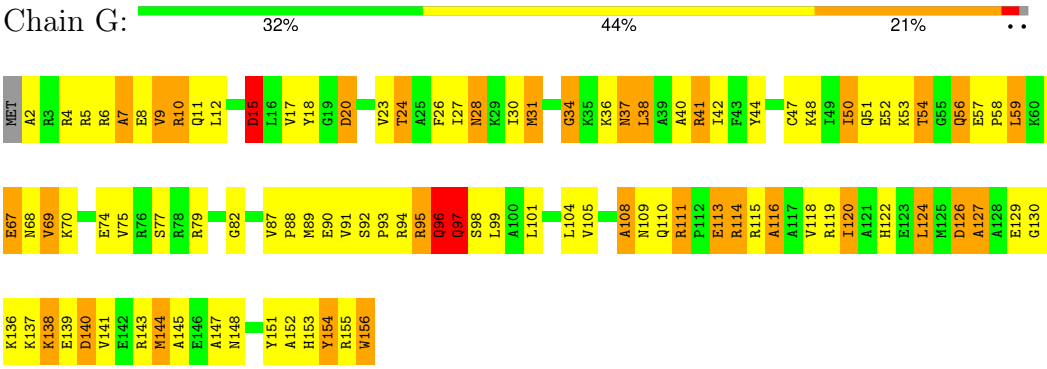
• Molecule 7: 30S ribosomal protein S6

Chain F:



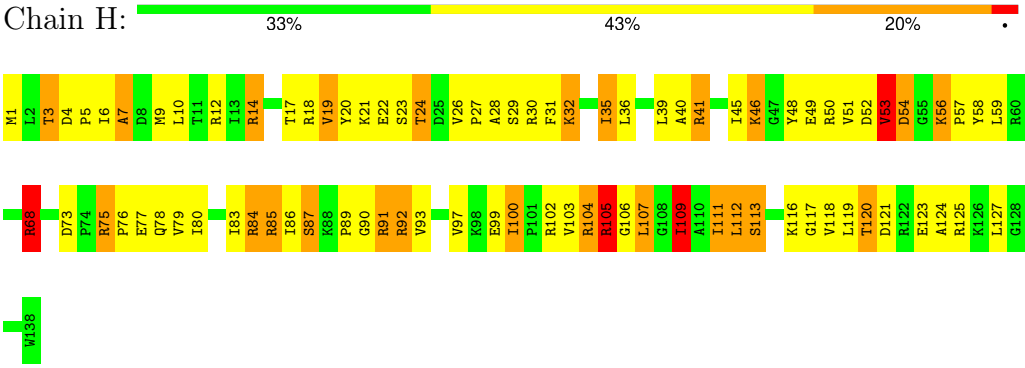
• Molecule 8: 30S ribosomal protein S7

Chain G:



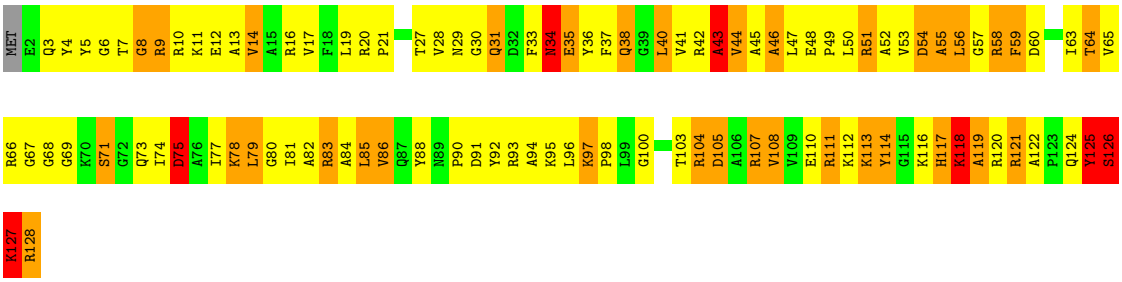
• Molecule 9: 30S ribosomal protein S8

Chain H:



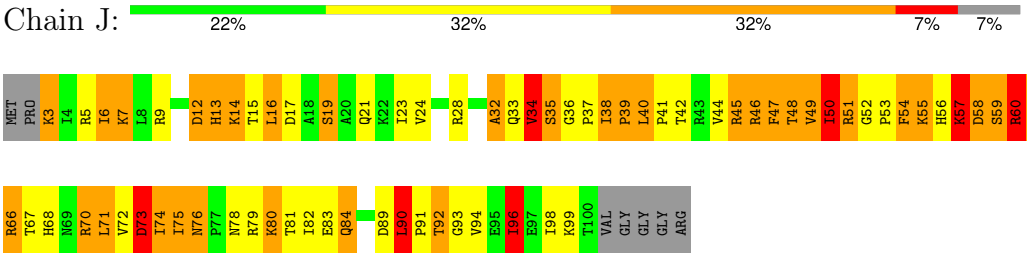
• Molecule 10: 30S ribosomal protein S9

Chain I:



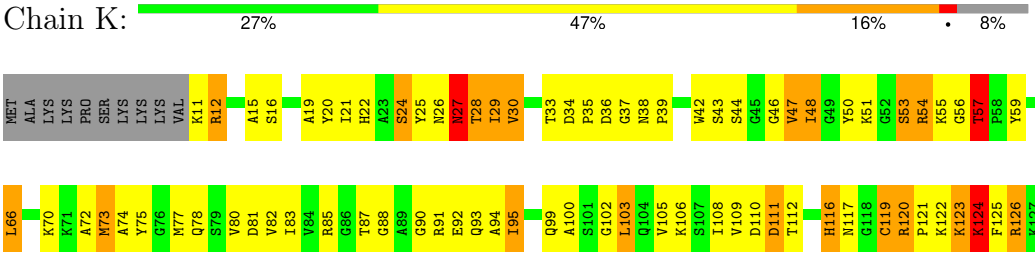
• Molecule 11: 30S ribosomal protein S10

Chain J:



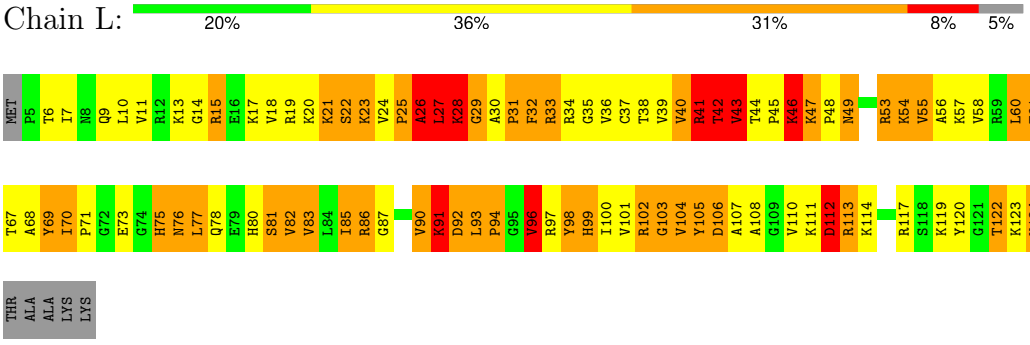
• Molecule 12: 30S ribosomal protein S11

Chain K:



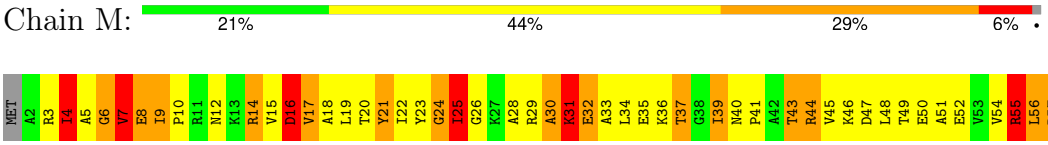
• Molecule 13: 30S ribosomal protein S12

Chain L:



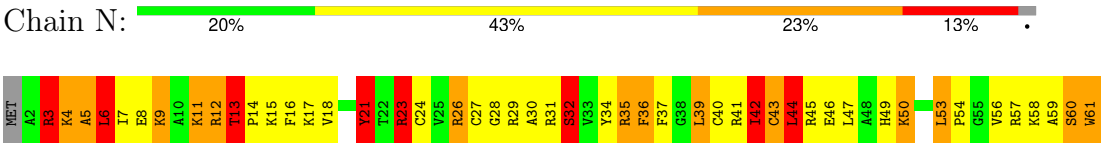
• Molecule 14: 30S ribosomal protein S13

Chain M:



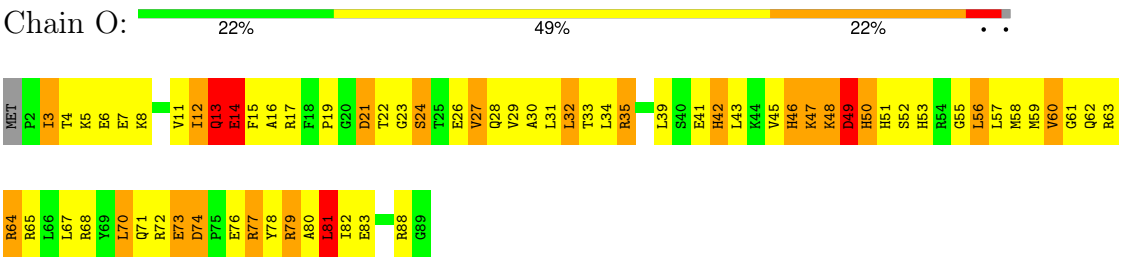
• Molecule 15: 30S ribosomal protein S14

Chain N:



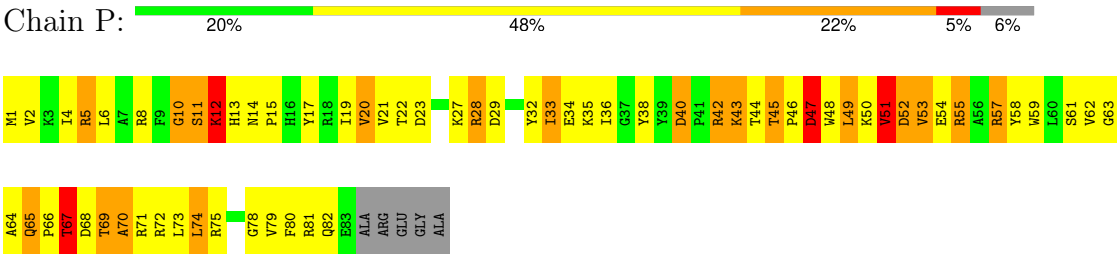
• Molecule 16: 30S ribosomal protein S15

Chain O:



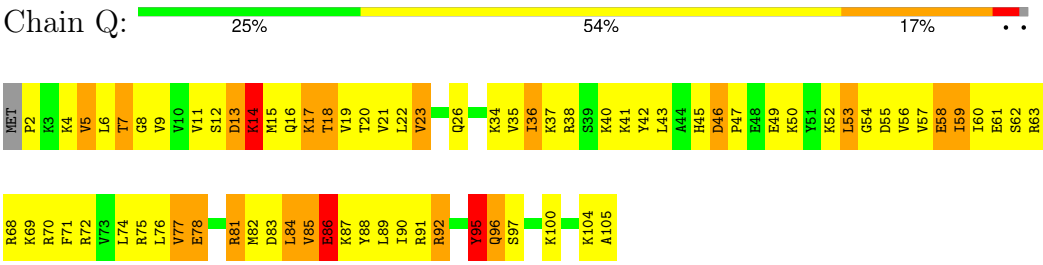
• Molecule 17: 30S ribosomal protein S16

Chain P:



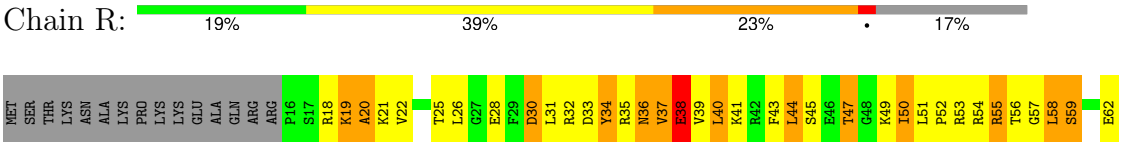
• Molecule 18: 30S ribosomal protein S17

Chain Q:



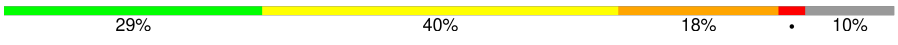
• Molecule 19: 30S ribosomal protein S18

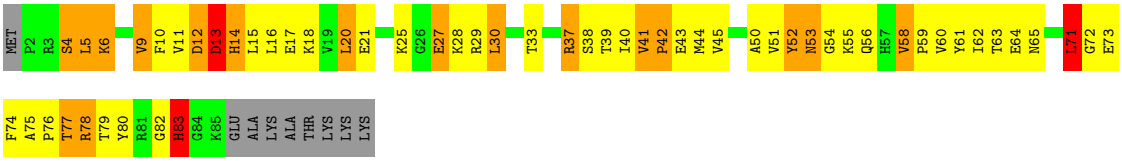
Chain R:



• Molecule 20: 30S ribosomal protein S19

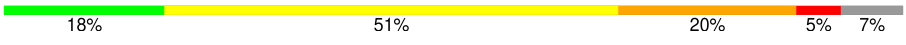
Chain S:

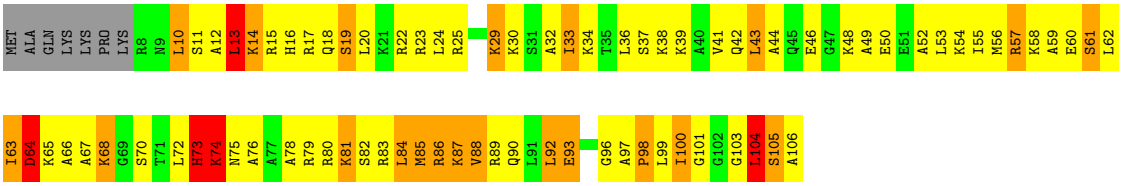




• Molecule 21: 30S ribosomal protein S20

Chain T:





4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	403.32Å 403.32Å 176.69Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 3.80	Depositor
% Data completeness (in resolution range)	97.2 (30.00-3.80)	Depositor
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.259 , 0.315	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	51728	wwPDB-VP
Average B, all atoms (Å^2)	84.0	wwPDB-VP

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, AB9, K, ZN, D2C

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	1.70	440/36247 (1.2%)	1.64	607/56545 (1.1%)
2	Z	2.01	1/87 (1.1%)	1.60	0/132
3	B	0.84	1/1958 (0.1%)	0.69	5/2640 (0.2%)
4	C	0.91	1/1636 (0.1%)	0.66	3/2205 (0.1%)
5	D	0.81	1/1733 (0.1%)	0.66	5/2318 (0.2%)
6	E	1.14	1/1162 (0.1%)	0.75	3/1564 (0.2%)
7	F	0.73	0/856	0.65	2/1154 (0.2%)
8	G	0.89	1/1276 (0.1%)	0.64	4/1709 (0.2%)
9	H	1.18	1/1136 (0.1%)	0.80	2/1527 (0.1%)
10	I	0.79	0/1029	0.67	5/1378 (0.4%)
11	J	0.81	1/805 (0.1%)	0.75	3/1082 (0.3%)
12	K	0.99	0/900	0.73	2/1213 (0.2%)
13	L	0.87	0/991	0.67	3/1327 (0.2%)
14	M	0.87	1/1008 (0.1%)	0.69	3/1347 (0.2%)
15	N	0.86	0/501	0.63	0/664
16	O	0.88	0/745	0.67	3/992 (0.3%)
17	P	1.16	1/716 (0.1%)	0.82	2/963 (0.2%)
18	Q	1.01	0/870	0.71	3/1159 (0.3%)
19	R	0.92	0/603	0.72	1/799 (0.1%)
20	S	0.70	0/689	0.66	2/926 (0.2%)
21	T	1.07	0/764	0.68	0/1006
All	All	1.47	450/55712 (0.8%)	1.41	658/82650 (0.8%)

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
3	B	0	2
4	C	0	6

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Mol	Chain	#Chirality outliers	#Planarity outliers
5	D	0	6
6	E	0	5
7	F	0	1
9	H	0	5
10	I	0	4
11	J	0	6
12	K	0	5
13	L	0	8
14	M	0	4
15	N	0	8
17	P	0	4
18	Q	0	1
20	S	0	5
21	T	0	4
All	All	0	74

All (450) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1169	A	O3'-P	35.46	2.03	1.61
1	A	1227	A	N9-C4	-13.10	1.29	1.37
1	A	1346	A	C3'-O3'	11.14	1.57	1.42
1	A	1224	G	C3'-O3'	10.61	1.57	1.42
1	A	1129	C	C1'-N1	10.46	1.64	1.48
1	A	279	A	N9-C4	-10.23	1.31	1.37
1	A	1125	U	C3'-O3'	10.21	1.56	1.42
1	A	766	A	N9-C4	-9.68	1.32	1.37
1	A	975	A	N9-C4	-9.63	1.32	1.37
1	A	533	A	C3'-O3'	9.56	1.55	1.42
1	A	1064	G	N9-C4	-8.93	1.30	1.38
1	A	1192	C	C1'-N1	8.92	1.62	1.48
1	A	573	A	N7-C5	-8.91	1.33	1.39
1	A	1502	A	N9-C4	-8.88	1.32	1.37
1	A	723	U	C1'-N1	8.86	1.62	1.48
1	A	1199	U	C1'-N1	8.68	1.61	1.48
1	A	1397	C	C1'-N1	8.45	1.61	1.48
1	A	1509	C	C3'-O3'	-8.40	1.30	1.42
1	A	1073	U	C1'-N1	8.36	1.61	1.48
1	A	817	C	N1-C6	-8.35	1.32	1.37
1	A	1101	A	N9-C4	8.30	1.42	1.37
1	A	386	C	C3'-O3'	-8.26	1.30	1.42
1	A	1533	C	C1'-N1	8.23	1.61	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1281	U	C3'-O3'	8.17	1.53	1.42
1	A	1159	U	C1'-N1	8.15	1.60	1.48
1	A	60	A	C3'-O3'	8.14	1.53	1.42
1	A	115	G	C3'-O3'	8.07	1.53	1.42
1	A	812	C	C3'-O3'	8.01	1.53	1.42
1	A	458	C	C1'-N1	7.97	1.60	1.48
1	A	866	C	N3-C4	-7.93	1.28	1.33
1	A	687	A	C3'-O3'	7.93	1.53	1.42
2	Z	3	U	C1'-N1	7.93	1.60	1.48
1	A	401	C	C1'-N1	7.91	1.60	1.48
1	A	665	A	N9-C4	-7.89	1.33	1.37
1	A	1398	A	C3'-O3'	-7.85	1.31	1.42
1	A	1239	A	N9-C4	-7.69	1.33	1.37
1	A	919	A	C5-C4	-7.57	1.33	1.38
1	A	1281	U	C1'-N1	7.57	1.60	1.48
4	C	22	TRP	CB-CG	-7.55	1.36	1.50
1	A	82	U	C1'-N1	7.50	1.59	1.48
1	A	553	A	C3'-O3'	-7.47	1.31	1.42
1	A	1302	U	C3'-O3'	7.44	1.52	1.42
1	A	246	A	N9-C4	-7.42	1.33	1.37
1	A	181	G	C3'-O3'	7.41	1.52	1.42
1	A	5	U	N1-C2	7.40	1.45	1.38
1	A	1502	A	C5-C6	-7.39	1.34	1.41
1	A	1361(A)	C	C1'-N1	7.37	1.59	1.48
1	A	753	A	C6-N1	-7.32	1.30	1.35
1	A	1367	C	N1-C2	7.26	1.47	1.40
1	A	532	A	N9-C4	7.26	1.42	1.37
1	A	119	A	C3'-O3'	7.24	1.52	1.42
1	A	371	G	C3'-O3'	-7.19	1.32	1.42
1	A	1397	C	N1-C2	7.18	1.47	1.40
1	A	981	U	C2-N3	7.17	1.42	1.37
1	A	940	C	C3'-O3'	-7.10	1.32	1.42
1	A	279	A	N7-C5	-7.07	1.35	1.39
1	A	727	G	N7-C5	-7.06	1.35	1.39
1	A	766	A	C5-C6	-7.04	1.34	1.41
1	A	372	C	C3'-O3'	6.96	1.51	1.42
1	A	7	G	C1'-N9	-6.96	1.37	1.46
1	A	886	G	N9-C4	-6.95	1.32	1.38
1	A	859	A	N7-C5	-6.93	1.35	1.39
1	A	81	U	C1'-N1	6.92	1.59	1.48
1	A	298	A	N3-C4	-6.92	1.30	1.34
1	A	1117	G	O5'-C5'	-6.90	1.31	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	753	A	C6-N6	-6.90	1.28	1.33
1	A	921	U	C3'-O3'	-6.90	1.32	1.42
1	A	257	G	N9-C4	6.86	1.43	1.38
1	A	1369	C	C3'-O3'	-6.84	1.32	1.42
1	A	1275	A	N9-C4	6.83	1.42	1.37
1	A	378	G	C3'-O3'	-6.83	1.32	1.42
1	A	743	U	P-O5'	6.80	1.66	1.59
1	A	374	A	C3'-O3'	-6.76	1.32	1.42
1	A	520	A	N9-C4	6.73	1.41	1.37
1	A	377	G	N9-C4	6.73	1.43	1.38
1	A	1265	G	N9-C4	6.73	1.43	1.38
1	A	1073	U	C2-N3	6.72	1.42	1.37
1	A	389	A	N7-C5	-6.72	1.35	1.39
1	A	5	U	C3'-O3'	6.71	1.51	1.42
1	A	801	U	C4-O4	-6.71	1.18	1.23
1	A	421	U	C3'-O3'	6.71	1.51	1.42
1	A	1257	U	C1'-N1	6.71	1.58	1.48
1	A	613	C	C1'-N1	6.69	1.58	1.48
1	A	1126	U	P-O5'	6.69	1.66	1.59
1	A	393	A	C3'-O3'	-6.66	1.32	1.42
1	A	1074	G	C3'-O3'	-6.64	1.32	1.42
1	A	200	G	N1-C2	6.62	1.43	1.37
1	A	915	A	N7-C5	-6.59	1.35	1.39
1	A	1067	A	N9-C4	6.59	1.41	1.37
1	A	1126	U	C1'-N1	6.56	1.58	1.48
1	A	61	G	N7-C5	-6.55	1.35	1.39
1	A	1324	A	N7-C5	-6.54	1.35	1.39
1	A	1495	U	C1'-N1	6.53	1.58	1.48
1	A	1149	C	C3'-O3'	-6.53	1.33	1.42
1	A	334	C	C1'-N1	6.52	1.58	1.48
1	A	1090	U	C1'-N1	6.50	1.58	1.48
1	A	61	G	N3-C4	-6.49	1.30	1.35
1	A	1114	C	C1'-N1	6.47	1.58	1.48
1	A	1363	A	N9-C4	6.45	1.41	1.37
1	A	688	G	N9-C4	-6.45	1.32	1.38
1	A	766	A	N7-C5	-6.44	1.35	1.39
1	A	1085	U	C3'-O3'	6.44	1.51	1.42
1	A	574	A	C5-C6	-6.43	1.35	1.41
1	A	574	A	N7-C5	-6.41	1.35	1.39
1	A	1188	A	N9-C4	-6.41	1.34	1.37
1	A	149	A	C3'-O3'	-6.40	1.33	1.42
1	A	172	A	N7-C5	-6.39	1.35	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	351	G	C3'-O3'	6.39	1.51	1.42
1	A	460	A	N9-C4	6.39	1.41	1.37
1	A	1504	G	O5'-C5'	-6.39	1.32	1.42
1	A	440	A	N9-C4	6.38	1.41	1.37
1	A	828	A	N9-C4	-6.38	1.34	1.37
1	A	1514	C	C3'-O3'	-6.36	1.33	1.42
1	A	232	G	C3'-O3'	-6.35	1.33	1.42
1	A	688	G	N7-C5	-6.35	1.35	1.39
1	A	1135	U	C1'-N1	6.35	1.58	1.48
1	A	7	G	N9-C4	-6.34	1.32	1.38
1	A	1082	G	O5'-C5'	-6.34	1.32	1.42
1	A	1350	A	N3-C4	-6.34	1.31	1.34
1	A	595	G	C6-N1	-6.34	1.35	1.39
1	A	170	U	C3'-O3'	-6.33	1.33	1.42
1	A	294	U	C2-N3	-6.32	1.33	1.37
1	A	1101	A	C3'-O3'	6.32	1.50	1.42
1	A	5	U	C1'-N1	6.32	1.58	1.48
1	A	1235	U	C1'-N1	6.31	1.58	1.48
1	A	696	A	N7-C5	-6.31	1.35	1.39
1	A	700	G	C6-O6	6.30	1.29	1.24
1	A	688	G	C8-N7	-6.29	1.27	1.30
1	A	773	G	N9-C4	6.29	1.43	1.38
1	A	975	A	N3-C4	-6.29	1.31	1.34
1	A	1465	C	C1'-N1	6.28	1.58	1.48
1	A	782	A	N7-C5	-6.27	1.35	1.39
1	A	190(H)	G	P-O5'	6.27	1.66	1.59
1	A	1433	A	C3'-O3'	-6.25	1.33	1.42
9	H	105	ARG	NE-CZ	6.24	1.41	1.33
1	A	61	G	C5-C6	-6.24	1.36	1.42
1	A	1229	A	C3'-O3'	-6.24	1.33	1.42
1	A	518	C	C1'-N1	6.22	1.58	1.48
1	A	63	C	O5'-C5'	-6.21	1.32	1.42
1	A	279	A	N3-C4	-6.21	1.31	1.34
1	A	1521	G	C6-N1	-6.21	1.35	1.39
1	A	27	G	C6-N1	-6.20	1.35	1.39
1	A	281	G	C3'-O3'	6.19	1.50	1.42
1	A	240	C	C3'-O3'	-6.18	1.33	1.42
1	A	1064	G	N3-C4	-6.18	1.31	1.35
1	A	1188	A	N3-C4	-6.17	1.31	1.34
1	A	635	G	N3-C4	-6.17	1.31	1.35
1	A	935	A	N9-C4	-6.16	1.34	1.37
1	A	1434	A	N7-C5	-6.16	1.35	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	9	G	C5-C6	-6.15	1.36	1.42
1	A	1138	G	C3'-O3'	6.15	1.50	1.42
1	A	967	C	N1-C2	6.15	1.46	1.40
1	A	1347	G	N7-C5	-6.14	1.35	1.39
1	A	1195	C	C1'-N1	6.13	1.57	1.48
1	A	1510	U	C3'-O3'	-6.12	1.33	1.42
1	A	1380	U	C3'-O3'	6.12	1.50	1.42
1	A	701	C	C3'-O3'	6.11	1.50	1.42
1	A	1499	A	N9-C4	-6.10	1.34	1.37
1	A	81	U	O5'-C5'	6.10	1.54	1.44
1	A	821	G	C5-C4	-6.09	1.34	1.38
1	A	135	C	N1-C6	6.08	1.40	1.37
1	A	1182	G	C3'-O3'	6.06	1.50	1.42
1	A	222	U	C3'-O3'	-6.06	1.33	1.42
1	A	571	U	C1'-N1	6.06	1.57	1.48
1	A	53	A	C6-N1	-6.03	1.31	1.35
1	A	53	A	N7-C5	-6.03	1.35	1.39
14	M	7	VAL	CA-CB	6.02	1.67	1.54
1	A	375	U	C3'-O3'	-6.02	1.33	1.42
1	A	190	C	C3'-O3'	6.01	1.50	1.42
1	A	1370	G	C6-O6	6.01	1.29	1.24
1	A	385	C	C3'-O3'	-6.01	1.33	1.42
1	A	759	A	N9-C4	-6.00	1.34	1.37
1	A	700	G	C6-N1	6.00	1.43	1.39
1	A	919	A	N9-C4	-6.00	1.34	1.37
1	A	1125	U	P-O5'	5.99	1.65	1.59
1	A	1063	C	C3'-O3'	-5.99	1.33	1.42
1	A	163	C	C1'-N1	5.97	1.57	1.48
1	A	1079	G	C6-O6	5.96	1.29	1.24
6	E	28	PHE	CB-CG	-5.96	1.41	1.51
1	A	527	G	P-O5'	5.96	1.65	1.59
1	A	1299	A	N9-C4	-5.95	1.34	1.37
1	A	898	G	N9-C4	-5.94	1.33	1.38
1	A	1237	C	C1'-N1	5.93	1.57	1.48
1	A	572	A	N7-C5	-5.92	1.35	1.39
1	A	438	G	C3'-O3'	5.92	1.50	1.42
1	A	787	A	N9-C4	-5.92	1.34	1.37
1	A	27	G	N7-C5	-5.91	1.35	1.39
1	A	1129	C	N1-C2	5.90	1.46	1.40
1	A	440	A	N3-C4	5.90	1.38	1.34
1	A	1397	C	N1-C6	5.90	1.40	1.37
1	A	841	U	C1'-N1	5.88	1.57	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	409	G	P-O5'	5.88	1.65	1.59
1	A	644	G	C3'-O3'	-5.88	1.33	1.42
1	A	781	A	N3-C4	5.88	1.38	1.34
1	A	676	A	C3'-O3'	-5.87	1.33	1.42
1	A	9	G	N7-C5	-5.86	1.35	1.39
1	A	5	U	O3'-P	5.86	1.68	1.61
1	A	730	G	C3'-O3'	-5.86	1.33	1.42
1	A	946	A	C6-N1	-5.86	1.31	1.35
1	A	152	A	C5-C6	5.84	1.46	1.41
1	A	377	G	N3-C4	5.84	1.39	1.35
1	A	728	A	N9-C4	-5.84	1.34	1.37
1	A	325	A	N3-C4	-5.84	1.31	1.34
1	A	604	G	N7-C5	-5.84	1.35	1.39
1	A	49	U	C5'-C4'	5.83	1.58	1.51
1	A	266	G	C5-C6	-5.82	1.36	1.42
1	A	867	G	N9-C4	5.82	1.42	1.38
1	A	78	G	C6-N1	-5.81	1.35	1.39
1	A	1064	G	C2-N3	-5.81	1.28	1.32
1	A	1503	A	N3-C4	5.80	1.38	1.34
1	A	993	G	C3'-O3'	5.80	1.50	1.42
1	A	1067	A	C3'-O3'	5.80	1.50	1.42
1	A	815	A	O3'-P	-5.79	1.54	1.61
1	A	1467	G	C2-N3	5.79	1.37	1.32
1	A	566	G	C6-N1	-5.78	1.35	1.39
1	A	748	C	C3'-O3'	5.77	1.50	1.42
1	A	381	C	C1'-N1	5.77	1.57	1.48
1	A	1401	G	C6-N1	-5.77	1.35	1.39
1	A	484	G	C3'-O3'	5.77	1.50	1.42
1	A	1364	U	C3'-O3'	5.76	1.50	1.42
1	A	1247	U	C1'-N1	5.76	1.57	1.48
1	A	1531	A	N9-C4	5.76	1.41	1.37
1	A	181	G	N9-C4	5.75	1.42	1.38
1	A	782	A	C5-C6	-5.75	1.35	1.41
1	A	104	G	C2-N3	5.75	1.37	1.32
1	A	61	G	C6-N1	-5.75	1.35	1.39
1	A	1396	A	N9-C4	-5.75	1.34	1.37
1	A	310	G	N7-C5	-5.73	1.35	1.39
1	A	539	A	N9-C4	5.73	1.41	1.37
1	A	832	C	C1'-N1	5.72	1.57	1.48
1	A	823	G	C6-N1	-5.70	1.35	1.39
1	A	1092	A	N9-C4	5.69	1.41	1.37
1	A	731	G	C3'-O3'	-5.69	1.34	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	729	A	N3-C4	-5.68	1.31	1.34
1	A	814	A	N9-C4	-5.68	1.34	1.37
1	A	1249	C	C1'-N1	5.68	1.57	1.48
1	A	129(A)	G	C3'-O3'	5.66	1.50	1.42
1	A	930	C	N3-C4	-5.66	1.29	1.33
1	A	1079	G	N7-C5	-5.66	1.35	1.39
1	A	883	C	N3-C4	5.65	1.38	1.33
1	A	1062	U	C3'-O3'	-5.65	1.34	1.42
1	A	282	A	C6-N1	-5.64	1.31	1.35
1	A	50	A	N3-C4	5.64	1.38	1.34
1	A	62	U	N1-C2	5.64	1.43	1.38
1	A	409	G	O5'-C5'	5.64	1.53	1.44
1	A	920	U	C3'-O3'	-5.63	1.34	1.42
1	A	786	G	N7-C5	-5.63	1.35	1.39
1	A	513	C	C1'-N1	5.63	1.57	1.48
1	A	81	U	C5'-C4'	5.62	1.58	1.51
1	A	1467	G	N9-C4	5.61	1.42	1.38
1	A	1367	C	C4'-C3'	-5.60	1.47	1.52
1	A	266	G	N9-C4	-5.60	1.33	1.38
1	A	358	U	C1'-N1	5.60	1.57	1.48
1	A	653	A	N7-C5	-5.59	1.35	1.39
1	A	1129	C	O5'-C5'	5.59	1.53	1.44
1	A	973	G	N9-C4	-5.59	1.33	1.38
1	A	1460	A	C3'-O3'	-5.58	1.34	1.42
1	A	1125	U	O5'-C5'	5.58	1.53	1.44
1	A	173	U	C3'-O3'	5.57	1.50	1.42
1	A	727	G	C5-C4	-5.57	1.34	1.38
1	A	1398	A	N7-C5	-5.56	1.35	1.39
1	A	21	G	N7-C5	-5.56	1.35	1.39
1	A	633	G	C5-C6	-5.56	1.36	1.42
1	A	634	C	C3'-O3'	-5.56	1.34	1.42
1	A	279	A	C3'-O3'	5.56	1.50	1.42
1	A	666	G	C3'-O3'	-5.56	1.34	1.42
1	A	1083	U	C3'-O3'	5.56	1.50	1.42
1	A	1504	G	C3'-O3'	5.55	1.50	1.42
1	A	1065	U	C3'-O3'	5.55	1.50	1.42
1	A	739	C	C1'-N1	5.54	1.57	1.48
1	A	73	C	C1'-N1	5.54	1.57	1.48
1	A	887	G	N9-C4	-5.54	1.33	1.38
1	A	1119	C	C1'-N1	5.54	1.57	1.48
1	A	1125	U	O3'-P	5.54	1.67	1.61
1	A	109	A	N7-C5	-5.53	1.35	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	947	G	C3'-O3'	-5.53	1.34	1.42
1	A	738	C	O5'-C5'	-5.53	1.34	1.42
1	A	872	A	O3'-P	-5.53	1.54	1.61
1	A	1355	G	N9-C4	5.53	1.42	1.38
1	A	367	U	C3'-O3'	5.52	1.49	1.42
1	A	553	A	C6-N1	-5.52	1.31	1.35
1	A	1303	C	N1-C6	-5.52	1.33	1.37
1	A	489	C	C1'-N1	5.51	1.57	1.48
1	A	1079	G	C3'-O3'	-5.51	1.34	1.42
1	A	1018	C	C1'-N1	5.51	1.57	1.48
1	A	1526	G	N1-C2	-5.51	1.33	1.37
1	A	313	A	N9-C4	-5.51	1.34	1.37
1	A	382	A	C6-N1	-5.50	1.31	1.35
1	A	306	G	N3-C4	5.50	1.39	1.35
1	A	376	G	C3'-O3'	-5.50	1.34	1.42
1	A	556	C	C3'-O3'	-5.50	1.34	1.42
1	A	893	C	C1'-N1	5.48	1.56	1.48
1	A	397	A	C3'-O3'	5.48	1.49	1.42
1	A	293	G	N3-C4	-5.47	1.31	1.35
1	A	279	A	C5-C6	-5.45	1.36	1.41
1	A	857	C	C3'-O3'	-5.45	1.34	1.42
1	A	499	A	N9-C4	5.45	1.41	1.37
1	A	893	C	N1-C2	5.45	1.45	1.40
1	A	929	G	N7-C5	-5.45	1.35	1.39
1	A	635	G	C2-N3	-5.45	1.28	1.32
1	A	118	U	C3'-O3'	-5.45	1.34	1.42
1	A	1070	U	C3'-O3'	5.43	1.49	1.42
1	A	723	U	N1-C2	5.42	1.43	1.38
1	A	1278	U	C1'-N1	5.42	1.56	1.48
1	A	361	G	P-O5'	5.41	1.65	1.59
1	A	230	G	C6-O6	5.41	1.29	1.24
1	A	1233	G	C6-O6	5.40	1.29	1.24
1	A	533	A	C6-N1	-5.38	1.31	1.35
1	A	406	G	C6-N1	5.38	1.43	1.39
1	A	453	A	N9-C4	-5.37	1.34	1.37
1	A	901	A	N7-C5	-5.37	1.36	1.39
1	A	1367	C	C1'-N1	5.37	1.56	1.48
1	A	999	C	C1'-N1	5.36	1.56	1.48
1	A	924	C	C1'-N1	5.36	1.56	1.48
1	A	1196	U	C3'-O3'	5.36	1.49	1.42
1	A	1320	C	C3'-O3'	5.36	1.49	1.42
1	A	1063	C	C1'-N1	5.36	1.56	1.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1354	C	P-O5'	5.35	1.65	1.59
1	A	1054	C	N1-C2	5.35	1.45	1.40
1	A	839	U	C1'-N1	5.34	1.56	1.48
1	A	273	A	C3'-O3'	5.33	1.49	1.42
1	A	653	A	N9-C4	-5.33	1.34	1.37
1	A	982	U	C1'-N1	5.32	1.56	1.48
1	A	941	G	N7-C5	-5.32	1.36	1.39
1	A	203	U	C1'-N1	5.31	1.56	1.48
1	A	267	C	N1-C6	-5.31	1.33	1.37
1	A	780	A	C5-C6	-5.31	1.36	1.41
1	A	1361(A)	C	N1-C2	5.30	1.45	1.40
1	A	773	G	C3'-O3'	-5.30	1.34	1.42
11	J	57	LYS	CD-CE	5.30	1.64	1.51
1	A	560	U	C3'-O3'	5.30	1.49	1.42
1	A	588	G	N7-C5	-5.30	1.36	1.39
1	A	290	C	N3-C4	-5.29	1.30	1.33
1	A	696	A	C5-C6	-5.29	1.36	1.41
1	A	979	C	C3'-O3'	5.29	1.49	1.42
1	A	1277	C	C1'-N1	5.29	1.56	1.48
1	A	1366	C	C3'-O3'	-5.29	1.34	1.42
1	A	956	U	C1'-N1	-5.28	1.39	1.46
1	A	603	U	P-O5'	5.28	1.65	1.59
1	A	1020	U	C1'-N1	5.28	1.56	1.48
1	A	804	U	C1'-N1	5.28	1.56	1.48
1	A	735	C	C3'-O3'	-5.26	1.34	1.42
1	A	1211	U	C3'-O3'	5.25	1.49	1.42
1	A	405	U	C1'-N1	5.25	1.56	1.48
1	A	1393	U	C4'-C3'	-5.25	1.47	1.52
1	A	444	C	C1'-N1	5.25	1.56	1.48
1	A	1285	A	N9-C4	5.25	1.41	1.37
1	A	1368	G	N3-C4	5.24	1.39	1.35
1	A	294	U	N3-C4	-5.24	1.33	1.38
1	A	1066	C	P-O5'	5.24	1.65	1.59
1	A	1093	A	N7-C5	-5.24	1.36	1.39
1	A	914	A	O5'-C5'	-5.24	1.34	1.42
1	A	577	G	C1'-N9	-5.23	1.39	1.46
1	A	1333	A	C5-C4	-5.23	1.35	1.38
1	A	1183	A	C3'-O3'	5.23	1.49	1.42
1	A	1514	C	C1'-N1	5.23	1.56	1.48
8	G	5	ARG	CG-CD	5.23	1.65	1.51
1	A	1372	U	C1'-N1	5.23	1.56	1.48
1	A	246	A	C2'-C1'	-5.23	1.47	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	32	A	N9-C4	5.22	1.41	1.37
1	A	491	G	P-O5'	5.22	1.65	1.59
1	A	197	A	C6-N1	-5.22	1.31	1.35
1	A	825	G	N9-C8	-5.22	1.34	1.37
1	A	78	G	N1-C2	-5.22	1.33	1.37
1	A	834	C	C3'-O3'	-5.22	1.34	1.42
1	A	336	C	C1'-N1	5.21	1.56	1.48
1	A	1129	C	C3'-O3'	5.20	1.49	1.42
5	D	145	GLU	CG-CD	5.20	1.59	1.51
1	A	727	G	N9-C8	-5.20	1.34	1.37
1	A	501	C	C3'-O3'	-5.19	1.34	1.42
1	A	237	C	C1'-N1	5.18	1.56	1.48
1	A	904	C	N3-C4	-5.18	1.30	1.33
1	A	730	G	C3'-C2'	-5.18	1.47	1.52
1	A	304	U	C1'-N1	5.18	1.56	1.48
1	A	1270	C	C5'-C4'	5.17	1.57	1.51
1	A	828	A	N3-C4	-5.17	1.31	1.34
1	A	754	C	N1-C6	-5.17	1.34	1.37
1	A	1501	C	C3'-O3'	-5.17	1.34	1.42
1	A	1533	C	N1-C2	5.17	1.45	1.40
1	A	624	C	C3'-O3'	-5.16	1.34	1.42
1	A	1514	C	C4-N4	-5.16	1.29	1.33
1	A	1197	G	C4'-C3'	-5.16	1.47	1.52
1	A	325	A	N9-C4	-5.15	1.34	1.37
1	A	51	A	N7-C5	-5.15	1.36	1.39
1	A	1093	A	C5-C6	-5.15	1.36	1.41
1	A	124	G	N3-C4	-5.15	1.31	1.35
1	A	862	C	N1-C6	-5.15	1.34	1.37
1	A	243	A	C6-N1	-5.15	1.31	1.35
1	A	771	G	C8-N7	-5.15	1.27	1.30
1	A	704	A	N7-C5	-5.14	1.36	1.39
1	A	391	G	C3'-O3'	-5.14	1.34	1.42
1	A	558	G	N7-C5	-5.14	1.36	1.39
1	A	704	A	C6-N1	-5.14	1.31	1.35
1	A	239	U	C1'-N1	5.13	1.56	1.48
1	A	673	G	C4'-C3'	-5.13	1.47	1.52
1	A	920	U	C4'-C3'	-5.13	1.47	1.52
1	A	1511	G	C3'-O3'	-5.13	1.34	1.42
1	A	602	A	N7-C5	-5.13	1.36	1.39
1	A	920	U	C4-C5	5.13	1.48	1.43
1	A	5	U	C2-N3	5.13	1.41	1.37
1	A	282	A	N3-C4	-5.13	1.31	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	221	C	N3-C4	5.12	1.37	1.33
1	A	293	G	C6-N1	-5.12	1.35	1.39
1	A	974	A	P-O5'	5.12	1.64	1.59
1	A	686	U	C1'-N1	-5.12	1.39	1.46
1	A	721	G	C3'-O3'	5.11	1.49	1.42
1	A	257	G	P-O5'	5.11	1.64	1.59
1	A	732	C	N3-C4	-5.11	1.30	1.33
1	A	753	A	N7-C5	-5.11	1.36	1.39
1	A	1283	G	C3'-O3'	5.11	1.49	1.42
1	A	182	U	C1'-N1	5.10	1.56	1.48
1	A	313	A	N3-C4	-5.10	1.31	1.34
1	A	919	A	N9-C8	-5.10	1.33	1.37
1	A	190(F)	G	C2'-C1'	-5.09	1.47	1.53
1	A	136	C	N1-C6	-5.08	1.34	1.37
1	A	727	G	C5-C6	-5.08	1.37	1.42
1	A	778	G	N7-C5	-5.08	1.36	1.39
1	A	588	G	C6-N1	5.08	1.43	1.39
1	A	1084	G	C3'-O3'	5.07	1.49	1.42
1	A	319	G	C2-N3	5.07	1.36	1.32
1	A	328	C	O5'-C5'	-5.07	1.34	1.42
1	A	265	G	N9-C4	-5.07	1.33	1.38
1	A	866	C	C1'-N1	5.07	1.56	1.48
1	A	884	U	C3'-O3'	-5.06	1.35	1.42
1	A	20	U	C1'-N1	-5.06	1.39	1.46
3	B	205	ASP	CB-CG	5.06	1.62	1.51
1	A	1266	G	C5-C4	5.05	1.41	1.38
1	A	235	C	N1-C6	-5.05	1.34	1.37
1	A	53	A	N3-C4	-5.05	1.31	1.34
1	A	460	A	C3'-O3'	5.04	1.49	1.42
1	A	553	A	C4'-C3'	-5.04	1.47	1.52
1	A	300	A	N7-C5	-5.04	1.36	1.39
1	A	562	C	C4-C5	5.04	1.47	1.43
1	A	315	A	C3'-O3'	5.04	1.49	1.42
1	A	930	C	N1-C6	-5.04	1.34	1.37
1	A	1228	C	C3'-O3'	-5.03	1.35	1.42
1	A	140	A	P-O5'	5.03	1.64	1.59
1	A	401	C	N3-C4	5.03	1.37	1.33
17	P	38	TYR	CD2-CE2	5.03	1.46	1.39
1	A	1179	A	N9-C4	-5.02	1.34	1.37
1	A	1390	U	C1'-N1	5.02	1.56	1.48
1	A	1056	U	C3'-O3'	-5.02	1.35	1.42
1	A	557	G	C5-C4	-5.02	1.34	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	840	C	C3'-O3'	5.02	1.49	1.42
1	A	23	C	N1-C6	-5.01	1.34	1.37
1	A	131	C	N3-C4	-5.01	1.30	1.33
1	A	790	A	C5-C4	5.01	1.42	1.38
1	A	1239	A	C5-C4	-5.01	1.35	1.38
1	A	855	G	C3'-O3'	-5.01	1.35	1.42
1	A	382	A	N7-C5	-5.01	1.36	1.39

All (658) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1169	A	P-O3'-C3'	29.86	155.53	119.70
1	A	1525	G	C4'-C3'-C2'	-12.91	89.69	102.60
1	A	1346	A	P-O3'-C3'	11.99	134.09	119.70
1	A	1345	U	C1'-O4'-C4'	-11.81	100.45	109.90
1	A	1025	U	C1'-O4'-C4'	-11.60	100.62	109.90
1	A	1224	G	P-O3'-C3'	10.79	132.65	119.70
1	A	1183	A	C1'-O4'-C4'	-10.54	101.47	109.90
1	A	1529	G	C1'-O4'-C4'	-10.54	101.47	109.90
1	A	964	A	O4'-C1'-N9	-10.38	99.90	108.20
1	A	1380	U	P-O3'-C3'	10.22	131.96	119.70
1	A	1099	G	O4'-C1'-N9	10.20	116.36	108.20
1	A	686	U	C3'-C2'-C1'	-9.68	93.76	101.50
1	A	686	U	C1'-O4'-C4'	-9.65	102.18	109.90
1	A	1169	A	O3'-P-O5'	-9.65	85.67	104.00
1	A	566	G	O4'-C1'-N9	-9.47	100.62	108.20
1	A	980	C	C1'-O4'-C4'	-9.37	102.41	109.90
1	A	501	C	P-O3'-C3'	-9.28	108.56	119.70
1	A	115	G	P-O3'-C3'	9.25	130.80	119.70
1	A	1317	C	C1'-O4'-C4'	-9.23	102.52	109.90
1	A	1358	U	O4'-C1'-N1	9.22	115.58	108.20
1	A	1151	A	C1'-O4'-C4'	-9.21	102.53	109.90
1	A	290	C	P-O3'-C3'	-9.08	108.80	119.70
1	A	872	A	C1'-O4'-C4'	-9.08	102.64	109.90
1	A	1504	G	P-O3'-C3'	9.06	130.57	119.70
1	A	1125	U	P-O3'-C3'	9.01	130.51	119.70
1	A	533	A	P-O3'-C3'	8.97	130.47	119.70
1	A	48	C	P-O3'-C3'	8.92	130.40	119.70
1	A	328	C	P-O3'-C3'	8.92	130.40	119.70
1	A	173	U	C3'-C2'-C1'	-8.86	94.41	101.50
1	A	942	G	O4'-C1'-N9	8.82	115.26	108.20
1	A	1196	U	O4'-C1'-N1	8.82	115.26	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	197	A	P-O3'-C3'	8.81	130.27	119.70
1	A	1347	G	P-O3'-C3'	8.79	130.25	119.70
1	A	246	A	C1'-O4'-C4'	-8.77	102.89	109.90
1	A	1085	U	P-O3'-C3'	8.75	130.20	119.70
1	A	730	G	C4'-C3'-C2'	-8.73	93.87	102.60
1	A	1090	U	O4'-C1'-N1	8.69	115.16	108.20
1	A	266	G	P-O3'-C3'	8.63	130.06	119.70
1	A	1169	A	OP1-P-O3'	8.55	124.01	105.20
1	A	1522	U	C4'-C3'-C2'	-8.50	94.10	102.60
1	A	129(A)	G	O4'-C1'-N9	-8.48	101.42	108.20
1	A	1397	C	O4'-C1'-N1	8.42	114.93	108.20
1	A	279	A	P-O3'-C3'	8.38	129.76	119.70
1	A	1524	C	C4'-C3'-C2'	-8.32	94.28	102.60
1	A	702	A	C1'-O4'-C4'	-8.29	103.27	109.90
1	A	1306	A	O4'-C1'-N9	8.28	114.83	108.20
1	A	1067	A	O4'-C1'-N9	-8.26	101.59	108.20
1	A	656	C	C4'-C3'-C2'	-8.20	94.40	102.60
1	A	1065	U	C1'-O4'-C4'	-8.20	103.34	109.90
1	A	266	G	O4'-C1'-N9	-8.20	101.64	108.20
1	A	452	A	C3'-C2'-C1'	-8.11	95.02	101.50
1	A	1190	G	P-O3'-C3'	8.10	129.41	119.70
1	A	243	A	P-O3'-C3'	8.08	129.40	119.70
1	A	913	A	P-O3'-C3'	8.04	129.35	119.70
1	A	601	C	P-O3'-C3'	-7.99	110.11	119.70
1	A	1519	A	O4'-C1'-N9	7.98	114.59	108.20
1	A	687	A	P-O3'-C3'	7.97	129.27	119.70
1	A	288	A	C4'-C3'-C2'	-7.95	94.66	102.60
1	A	608	A	P-O3'-C3'	-7.93	110.18	119.70
1	A	387	U	O4'-C1'-N1	7.93	114.54	108.20
1	A	967	C	N1-C2-O2	7.93	123.66	118.90
1	A	405	U	P-O3'-C3'	7.92	129.20	119.70
1	A	1525	G	C1'-O4'-C4'	-7.88	103.60	109.90
1	A	529	G	C4'-C3'-C2'	-7.82	94.78	102.60
1	A	484	G	O4'-C1'-N9	-7.80	101.96	108.20
1	A	1054	C	O4'-C1'-N1	7.79	114.43	108.20
1	A	1067	A	P-O3'-C3'	7.77	129.03	119.70
1	A	1065	U	P-O3'-C3'	7.76	129.02	119.70
1	A	786	G	C8-N9-C4	-7.75	103.30	106.40
1	A	1531	A	O4'-C1'-N9	7.75	114.40	108.20
1	A	1301	U	P-O3'-C3'	7.73	128.98	119.70
1	A	60	A	P-O3'-C3'	7.71	128.95	119.70
1	A	575	G	P-O3'-C3'	7.68	128.92	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	863	U	O4'-C1'-N1	7.66	114.33	108.20
1	A	49	U	C5'-C4'-O4'	7.62	118.24	109.10
1	A	388	G	O4'-C1'-N9	-7.60	102.12	108.20
1	A	686	U	O4'-C1'-N1	7.58	114.27	108.20
1	A	315	A	C4'-C3'-C2'	-7.57	95.03	102.60
1	A	936	C	O4'-C1'-N1	-7.57	102.15	108.20
1	A	509	A	C3'-C2'-C1'	-7.56	95.45	101.50
1	A	346	G	C1'-O4'-C4'	-7.55	103.86	109.90
1	A	758	G	O4'-C1'-N9	7.55	114.24	108.20
1	A	812	C	P-O3'-C3'	7.54	128.75	119.70
1	A	793	U	C1'-O4'-C4'	-7.54	103.87	109.90
1	A	1025	U	O4'-C1'-N1	7.48	114.18	108.20
1	A	1050	G	C4'-C3'-C2'	-7.46	95.14	102.60
1	A	814	A	N9-C1'-C2'	-7.44	103.82	112.00
1	A	1235	U	C3'-C2'-C1'	-7.43	95.56	101.50
1	A	1365	G	O4'-C1'-N9	7.38	114.11	108.20
1	A	1214	C	C1'-O4'-C4'	-7.37	104.00	109.90
1	A	1498	U	P-O3'-C3'	7.37	128.54	119.70
1	A	1364	U	P-O3'-C3'	7.36	128.53	119.70
1	A	934	C	C1'-O4'-C4'	-7.34	104.03	109.90
1	A	739	C	C3'-C2'-C1'	-7.31	95.65	101.50
1	A	804	U	O4'-C1'-N1	7.29	114.03	108.20
1	A	81	U	O4'-C1'-N1	7.28	114.02	108.20
1	A	1192	C	C6-N1-C2	-7.26	117.40	120.30
1	A	1079	G	C8-N9-C4	-7.26	103.50	106.40
1	A	384	G	O4'-C1'-N9	7.24	113.99	108.20
9	H	52	ASP	CB-CG-OD2	7.22	124.80	118.30
1	A	559	A	C1'-O4'-C4'	-7.22	104.12	109.90
1	A	760	G	P-O3'-C3'	-7.20	111.06	119.70
1	A	108	G	O4'-C1'-N9	7.18	113.94	108.20
1	A	281	G	P-O3'-C3'	7.17	128.31	119.70
1	A	1331	G	O4'-C1'-N9	7.15	113.92	108.20
1	A	1380	U	C2'-C3'-O3'	7.14	125.20	109.50
1	A	1064	G	N3-C4-N9	-7.11	121.73	126.00
1	A	519	C	C1'-O4'-C4'	-7.10	104.22	109.90
1	A	898	G	C4'-C3'-C2'	-7.09	95.51	102.60
1	A	1317	C	O4'-C1'-N1	7.09	113.87	108.20
1	A	115	G	C2'-C3'-O3'	7.09	125.10	109.50
1	A	930	C	O4'-C4'-C3'	-7.07	96.93	104.00
1	A	965	A	P-O3'-C3'	7.07	128.18	119.70
1	A	6	G	C5'-C4'-O4'	7.03	117.53	109.10
1	A	1302	U	O4'-C1'-N1	-7.02	102.58	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	129	U	O4'-C1'-N1	7.01	113.81	108.20
1	A	279	A	N9-C1'-C2'	-6.98	104.32	112.00
1	A	1144	G	C3'-C2'-C1'	-6.98	95.92	101.50
1	A	382	A	O4'-C1'-N9	6.97	113.77	108.20
1	A	855	G	O4'-C1'-N9	6.95	113.76	108.20
1	A	1114	C	C3'-C2'-C1'	-6.95	95.94	101.50
1	A	781	A	C4'-C3'-C2'	-6.93	95.67	102.60
1	A	25	C	P-O3'-C3'	-6.92	111.40	119.70
1	A	609	A	O4'-C1'-N9	-6.90	102.68	108.20
1	A	1505	G	O4'-C1'-N9	6.89	113.71	108.20
1	A	641	U	O4'-C1'-N1	6.88	113.70	108.20
1	A	941	G	C8-N9-C4	-6.87	103.65	106.40
1	A	829	G	O4'-C1'-N9	-6.87	102.71	108.20
1	A	484	G	P-O3'-C3'	6.86	127.92	119.70
1	A	1510	U	C1'-O4'-C4'	-6.86	104.42	109.90
1	A	343	U	O4'-C1'-N1	6.85	113.68	108.20
9	H	54	ASP	CB-CG-OD2	6.83	124.45	118.30
1	A	878	G	P-O3'-C3'	-6.81	111.53	119.70
1	A	1515	C	N3-C4-N4	6.81	122.77	118.00
1	A	169	C	C1'-O4'-C4'	-6.81	104.45	109.90
1	A	1190	G	C8-N9-C4	-6.80	103.68	106.40
1	A	1107	C	C3'-C2'-C1'	-6.79	96.06	101.50
1	A	108	G	O4'-C4'-C3'	-6.79	97.21	104.00
1	A	119	A	P-O3'-C3'	6.78	127.84	119.70
1	A	1355	G	C8-N9-C4	-6.78	103.69	106.40
1	A	409	G	O4'-C1'-N9	6.77	113.62	108.20
1	A	5	U	O4'-C1'-N1	6.77	113.62	108.20
1	A	1502	A	C5-N7-C8	-6.77	100.52	103.90
1	A	130	A	P-O5'-C5'	-6.77	110.07	120.90
1	A	332	G	P-O3'-C3'	6.77	127.82	119.70
1	A	1139	G	C1'-O4'-C4'	-6.75	104.50	109.90
1	A	222	U	O4'-C4'-C3'	-6.75	97.25	104.00
1	A	1126	U	O4'-C1'-N1	6.75	113.60	108.20
1	A	1108	G	C4'-C3'-C2'	-6.74	95.86	102.60
1	A	1129	C	O4'-C1'-N1	6.73	113.58	108.20
1	A	1265	G	C8-N9-C4	-6.71	103.72	106.40
1	A	570	G	C8-N9-C4	-6.71	103.72	106.40
1	A	1302	U	P-O3'-C3'	6.71	127.75	119.70
1	A	907	A	O4'-C1'-N9	6.71	113.56	108.20
1	A	1073	U	O4'-C1'-N1	6.70	113.56	108.20
1	A	1190	G	O4'-C1'-C2'	-6.70	99.10	105.80
4	C	17	ASP	CB-CG-OD2	6.69	124.32	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	108	G	C1'-O4'-C4'	-6.68	104.56	109.90
1	A	950	U	P-O3'-C3'	-6.67	111.70	119.70
1	A	481	G	O4'-C1'-N9	6.66	113.53	108.20
1	A	21	G	C6-C5-N7	-6.64	126.41	130.40
1	A	1522	U	N3-C2-O2	-6.64	117.55	122.20
1	A	926	G	N9-C1'-C2'	-6.63	104.71	112.00
1	A	889	A	C3'-C2'-C1'	-6.62	96.21	101.50
1	A	652	U	O4'-C1'-N1	-6.61	102.91	108.20
1	A	947	G	P-O3'-C3'	-6.61	111.77	119.70
1	A	7	G	O4'-C1'-N9	-6.59	102.93	108.20
1	A	279	A	C2-N3-C4	-6.59	107.31	110.60
1	A	409	G	C3'-C2'-C1'	6.58	106.76	101.50
1	A	586	C	O4'-C1'-N1	6.57	113.46	108.20
1	A	217	C	C3'-C2'-C1'	-6.56	96.25	101.50
1	A	158	G	C8-N9-C4	-6.56	103.78	106.40
1	A	924	C	O4'-C1'-N1	6.56	113.45	108.20
1	A	879	C	C4'-C3'-C2'	-6.55	96.05	102.60
1	A	64	G	P-O3'-C3'	6.53	127.54	119.70
1	A	1101	A	P-O3'-C3'	6.52	127.53	119.70
1	A	243	A	C1'-O4'-C4'	-6.51	104.69	109.90
1	A	605	U	O4'-C1'-N1	6.50	113.40	108.20
1	A	531	U	C1'-O4'-C4'	-6.49	104.71	109.90
1	A	1446	A	C1'-O4'-C4'	-6.49	104.71	109.90
1	A	1247	U	C3'-C2'-C1'	-6.49	96.31	101.50
1	A	560	U	P-O3'-C3'	6.47	127.47	119.70
1	A	115	G	O4'-C1'-N9	-6.46	103.03	108.20
1	A	743	U	N1-C1'-C2'	-6.46	104.90	112.00
1	A	866	C	O4'-C1'-N1	6.44	113.35	108.20
1	A	1072	G	N9-C1'-C2'	-6.43	104.92	112.00
1	A	671	G	O4'-C1'-N9	6.43	113.34	108.20
1	A	542	G	C4'-C3'-C2'	-6.43	96.17	102.60
1	A	594	G	O4'-C1'-N9	6.42	113.33	108.20
1	A	1527	C	P-O3'-C3'	6.41	127.39	119.70
1	A	252	U	C1'-O4'-C4'	-6.40	104.78	109.90
1	A	1502	A	C4-C5-N7	6.38	113.89	110.70
1	A	1227	A	N9-C1'-C2'	-6.37	104.99	112.00
1	A	1345	U	O4'-C1'-N1	6.37	113.29	108.20
1	A	108	G	C4'-C3'-C2'	-6.35	96.25	102.60
1	A	604	G	C8-N9-C4	-6.35	103.86	106.40
1	A	1065	U	C5'-C4'-O4'	6.34	116.71	109.10
1	A	993	G	N9-C1'-C2'	6.34	122.24	114.00
1	A	1349	A	P-O3'-C3'	-6.34	112.10	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	372	C	C5'-C4'-O4'	6.33	116.70	109.10
1	A	90	U	C3'-C2'-C1'	-6.33	96.44	101.50
1	A	965	A	C4'-C3'-C2'	6.33	108.93	102.60
1	A	1183	A	P-O3'-C3'	6.33	127.30	119.70
17	P	40	ASP	CB-CG-OD2	6.33	123.99	118.30
1	A	408	A	C4'-C3'-C2'	-6.32	96.28	102.60
1	A	1305	G	P-O3'-C3'	6.31	127.28	119.70
1	A	521	G	O4'-C1'-N9	-6.31	103.16	108.20
1	A	818	G	C4'-C3'-C2'	-6.30	96.30	102.60
1	A	1397	C	N1-C2-O2	6.30	122.68	118.90
16	O	21	ASP	CB-CG-OD2	6.30	123.97	118.30
1	A	246	A	O4'-C1'-N9	6.29	113.23	108.20
1	A	1192	C	O4'-C1'-N1	6.29	113.23	108.20
1	A	1115	C	N1-C1'-C2'	-6.29	105.08	112.00
1	A	1526	G	C4'-C3'-C2'	-6.28	96.32	102.60
1	A	1380	U	O4'-C1'-N1	-6.28	103.17	108.20
1	A	1054	C	C2-N1-C1'	6.28	125.70	118.80
1	A	696	A	N1-C6-N6	6.27	122.36	118.60
1	A	104	G	N3-C4-N9	6.27	129.76	126.00
1	A	1502	A	N1-C6-N6	6.27	122.36	118.60
1	A	644	G	N9-C1'-C2'	-6.26	105.11	112.00
1	A	1099	G	N3-C4-N9	-6.25	122.25	126.00
1	A	159	G	C3'-C2'-C1'	-6.25	96.50	101.50
1	A	438	G	P-O3'-C3'	6.25	127.20	119.70
1	A	137	C	O4'-C1'-N1	6.24	113.19	108.20
1	A	488	C	C3'-C2'-C1'	-6.23	96.51	101.50
1	A	1525	G	C5'-C4'-O4'	6.22	116.57	109.10
1	A	795	C	O4'-C1'-N1	-6.22	103.23	108.20
1	A	992	U	P-O3'-C3'	6.21	127.16	119.70
1	A	939	G	C5'-C4'-O4'	6.21	116.55	109.10
1	A	1116	C	N1-C1'-C2'	-6.20	105.19	112.00
1	A	1004	A	O4'-C1'-N9	6.19	113.15	108.20
1	A	1504	G	C5'-C4'-O4'	-6.18	101.68	109.10
6	E	147	ASP	CB-CG-OD2	6.18	123.86	118.30
1	A	695	A	O4'-C1'-N9	6.18	113.14	108.20
1	A	1281	U	P-O3'-C3'	6.17	127.11	119.70
1	A	889	A	O4'-C1'-N9	6.17	113.13	108.20
7	F	15	ASP	CB-CG-OD2	6.16	123.84	118.30
1	A	1294	G	N1-C6-O6	6.15	123.59	119.90
1	A	489	C	C3'-C2'-C1'	-6.14	96.59	101.50
1	A	647	C	N1-C1'-C2'	-6.14	105.25	112.00
1	A	422	C	O4'-C1'-N1	6.14	113.11	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	257	G	N3-C4-N9	6.14	129.68	126.00
1	A	1395	C	O4'-C1'-N1	-6.14	103.29	108.20
1	A	129(A)	G	C5'-C4'-O4'	-6.13	101.74	109.10
1	A	867	G	C5-C6-O6	-6.13	124.92	128.60
1	A	674	G	P-O3'-C3'	-6.11	112.37	119.70
1	A	5	U	C3'-C2'-C1'	6.11	106.39	101.50
1	A	1052	U	O4'-C1'-N1	6.10	113.08	108.20
1	A	26	A	O4'-C1'-N9	-6.09	103.32	108.20
1	A	944	G	C4'-C3'-C2'	-6.09	96.51	102.60
1	A	945	G	O4'-C1'-N9	-6.09	103.33	108.20
1	A	736	C	C1'-O4'-C4'	-6.09	105.03	109.90
1	A	951	G	O4'-C1'-N9	6.08	113.07	108.20
1	A	770	C	O5'-P-OP2	-6.08	100.23	105.70
1	A	315	A	C3'-C2'-C1'	-6.06	96.65	101.50
1	A	292	G	C4'-C3'-C2'	-6.05	96.55	102.60
1	A	1048	G	C4'-C3'-C2'	-6.05	96.55	102.60
1	A	381	C	O4'-C1'-N1	6.03	113.03	108.20
1	A	1196	U	C1'-O4'-C4'	-6.03	105.08	109.90
1	A	897	C	O4'-C1'-N1	6.02	113.02	108.20
1	A	558	G	C8-N9-C4	-6.02	103.99	106.40
1	A	1093	A	P-O3'-C3'	6.02	126.92	119.70
1	A	875	C	C4'-C3'-C2'	-6.02	96.58	102.60
1	A	857	C	P-O3'-C3'	-6.01	112.49	119.70
1	A	1387	G	O4'-C1'-N9	-6.01	103.39	108.20
1	A	149	A	P-O3'-C3'	-6.00	112.50	119.70
1	A	16	A	N9-C1'-C2'	-6.00	105.40	112.00
1	A	38	G	O4'-C1'-N9	6.00	113.00	108.20
1	A	1526	G	C1'-O4'-C4'	-5.99	105.11	109.90
1	A	216	G	C1'-O4'-C4'	-5.98	105.11	109.90
7	F	83	ASP	CB-CG-OD2	5.98	123.68	118.30
1	A	278	G	O4'-C1'-N9	5.98	112.98	108.20
1	A	261	U	P-O3'-C3'	-5.97	112.53	119.70
1	A	7	G	P-O3'-C3'	5.97	126.86	119.70
1	A	1346	A	C1'-O4'-C4'	-5.97	105.12	109.90
1	A	1239	A	C3'-C2'-C1'	-5.96	96.73	101.50
1	A	220	G	N3-C4-C5	-5.95	125.63	128.60
1	A	112	G	C4'-C3'-C2'	-5.94	96.66	102.60
1	A	867	G	N3-C4-N9	5.94	129.56	126.00
1	A	372	C	C1'-O4'-C4'	-5.93	105.16	109.90
3	B	191	ASP	CB-CG-OD2	5.93	123.64	118.30
5	D	134	ASP	CB-CG-OD2	5.93	123.63	118.30
1	A	1077	G	C6-C5-N7	-5.92	126.84	130.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	824	C	C4'-C3'-C2'	-5.92	96.68	102.60
1	A	142	G	C4'-C3'-C2'	-5.91	96.69	102.60
1	A	372	C	P-O3'-C3'	5.91	126.79	119.70
1	A	860	A	N9-C1'-C2'	-5.91	105.50	112.00
1	A	911	U	C1'-O4'-C4'	-5.91	105.18	109.90
1	A	1067	A	C2-N3-C4	5.90	113.55	110.60
1	A	1175	G	C3'-C2'-C1'	-5.90	96.78	101.50
1	A	1067	A	C5-C6-N1	5.89	120.65	117.70
1	A	670	G	N9-C1'-C2'	-5.89	105.52	112.00
1	A	947	G	O4'-C1'-N9	-5.89	103.49	108.20
1	A	676	A	P-O3'-C3'	-5.89	112.63	119.70
1	A	1213	A	C1'-O4'-C4'	-5.89	105.19	109.90
1	A	717	C	C2-N1-C1'	5.89	125.28	118.80
1	A	271	C	O4'-C1'-N1	5.88	112.91	108.20
1	A	1126	U	C3'-C2'-C1'	5.88	106.20	101.50
1	A	859	A	N9-C1'-C2'	-5.88	105.53	112.00
1	A	1008	C	C3'-C2'-C1'	-5.88	96.80	101.50
1	A	127	G	N9-C1'-C2'	-5.87	105.54	112.00
1	A	576	G	C5'-C4'-O4'	5.87	116.14	109.10
1	A	1525	G	P-O3'-C3'	5.87	126.74	119.70
1	A	890	G	C3'-C2'-C1'	-5.86	96.81	101.50
1	A	458	C	O4'-C1'-N1	5.86	112.89	108.20
1	A	1331	G	O4'-C1'-C2'	-5.86	99.94	105.80
1	A	993	G	P-O3'-C3'	5.85	126.72	119.70
1	A	1446	A	C3'-C2'-C1'	-5.85	96.82	101.50
1	A	234	C	N3-C4-C5	5.85	124.24	121.90
1	A	967	C	N3-C2-O2	-5.84	117.81	121.90
1	A	220	G	C8-N9-C4	-5.84	104.07	106.40
1	A	265	G	O4'-C1'-N9	5.84	112.87	108.20
1	A	1190	G	N7-C8-N9	5.84	116.02	113.10
1	A	661	G	C8-N9-C4	-5.83	104.07	106.40
8	G	140	ASP	CB-CG-OD2	5.83	123.55	118.30
1	A	1030(A)	G	C8-N9-C4	-5.83	104.07	106.40
1	A	265	G	C4'-C3'-C2'	-5.82	96.78	102.60
1	A	379	C	O4'-C1'-N1	5.82	112.86	108.20
1	A	914	A	C4'-C3'-C2'	-5.82	96.78	102.60
1	A	1398	A	N1-C6-N6	5.81	122.08	118.60
1	A	47	C	C3'-C2'-C1'	-5.80	96.86	101.50
19	R	30	ASP	CB-CG-OD2	5.80	123.52	118.30
4	C	62	ASP	CB-CG-OD2	5.80	123.52	118.30
1	A	130	A	P-O3'-C3'	5.79	126.65	119.70
1	A	770	C	C4'-C3'-C2'	-5.79	96.81	102.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	725	G	C5-C6-O6	-5.78	125.13	128.60
1	A	577	G	N9-C1'-C2'	-5.78	105.64	112.00
1	A	1339	A	O4'-C1'-N9	5.78	112.82	108.20
3	B	166	ASP	CB-CG-OD2	5.78	123.50	118.30
1	A	1081	G	N9-C1'-C2'	-5.77	105.65	112.00
1	A	1329	A	C3'-C2'-C1'	-5.77	96.89	101.50
1	A	1346	A	C4'-C3'-O3'	5.77	124.53	113.00
6	E	5	ASP	CB-CG-OD2	5.76	123.48	118.30
1	A	421	U	P-O3'-C3'	5.76	126.61	119.70
1	A	318	G	N9-C1'-C2'	-5.75	105.67	112.00
1	A	685	G	O4'-C1'-N9	5.75	112.80	108.20
1	A	37	U	C3'-C2'-C1'	-5.75	96.90	101.50
1	A	1372	U	O4'-C1'-N1	5.74	112.79	108.20
1	A	486	U	O4'-C1'-N1	5.73	112.79	108.20
1	A	623	C	N3-C4-C5	5.73	124.19	121.90
1	A	643	C	P-O3'-C3'	-5.73	112.82	119.70
1	A	184	G	P-O3'-C3'	-5.72	112.83	119.70
1	A	1467	G	N3-C4-C5	-5.72	125.74	128.60
1	A	1074	G	C6-C5-N7	-5.72	126.97	130.40
1	A	911	U	O4'-C4'-C3'	-5.71	98.29	104.00
1	A	1283	G	C4'-C3'-C2'	-5.71	96.89	102.60
5	D	193	ASP	CB-CG-OD2	5.71	123.44	118.30
1	A	440	A	O4'-C1'-N9	5.71	112.77	108.20
1	A	250	A	P-O3'-C3'	5.70	126.54	119.70
1	A	50	A	O4'-C1'-N9	5.70	112.76	108.20
1	A	711	G	O4'-C1'-N9	5.70	112.76	108.20
1	A	1283	G	C8-N9-C4	-5.70	104.12	106.40
1	A	980	C	O4'-C1'-N1	5.70	112.76	108.20
1	A	1346	A	C3'-C2'-C1'	-5.70	96.94	101.50
1	A	1108	G	O4'-C1'-N9	5.69	112.75	108.20
1	A	635	G	N1-C6-O6	5.69	123.31	119.90
1	A	1446	A	O4'-C1'-N9	5.69	112.75	108.20
10	I	91	ASP	CB-CG-OD2	5.68	123.42	118.30
14	M	83	ASP	CB-CG-OD2	5.68	123.41	118.30
1	A	942	G	C8-N9-C4	-5.68	104.13	106.40
1	A	1224	G	O4'-C1'-N9	5.68	112.74	108.20
1	A	786	G	O4'-C1'-N9	5.68	112.74	108.20
1	A	9	G	C4-C5-N7	5.67	113.07	110.80
1	A	1050	G	C3'-C2'-C1'	-5.67	96.96	101.50
1	A	228	A	O4'-C1'-N9	5.67	112.74	108.20
1	A	604	G	C5'-C4'-O4'	5.67	115.90	109.10
1	A	624	C	N1-C1'-C2'	-5.67	105.76	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	575	G	C6-C5-N7	-5.66	127.00	130.40
1	A	16	A	O4'-C1'-N9	-5.65	103.68	108.20
1	A	980	C	C5'-C4'-O4'	5.65	115.88	109.10
1	A	835	U	N1-C1'-C2'	-5.65	105.78	112.00
1	A	18	C	N3-C4-C5	5.65	124.16	121.90
13	L	112	ASP	CB-CG-OD2	5.64	123.38	118.30
12	K	111	ASP	CB-CG-OD2	5.63	123.37	118.30
1	A	1054	C	N1-C2-O2	5.63	122.28	118.90
1	A	64	G	O4'-C1'-N9	5.63	112.70	108.20
1	A	1294	G	C5-C6-O6	-5.63	125.22	128.60
1	A	239	U	O4'-C1'-N1	5.62	112.70	108.20
1	A	570	G	P-O3'-C3'	5.62	126.44	119.70
1	A	9	G	C6-C5-N7	-5.62	127.03	130.40
1	A	1266	G	C8-N9-C4	-5.61	104.16	106.40
1	A	678	U	C4'-C3'-C2'	-5.60	97.00	102.60
1	A	568	G	C4'-C3'-C2'	-5.60	97.00	102.60
1	A	750	G	C8-N9-C4	-5.59	104.16	106.40
1	A	1021	G	C3'-C2'-C1'	-5.59	97.03	101.50
1	A	329	A	C3'-C2'-C1'	5.59	105.97	101.50
16	O	74	ASP	CB-CG-OD2	5.58	123.32	118.30
1	A	371	G	C8-N9-C4	-5.58	104.17	106.40
1	A	485	G	C1'-O4'-C4'	-5.58	105.44	109.90
1	A	562	C	O4'-C1'-N1	5.58	112.66	108.20
10	I	75	ASP	CB-CG-OD2	5.57	123.32	118.30
1	A	657	G	N9-C1'-C2'	-5.57	105.88	112.00
1	A	691	G	C4-C5-C6	5.57	122.14	118.80
1	A	564	C	OP1-P-OP2	5.56	127.94	119.60
1	A	62	U	N1-C2-O2	5.56	126.69	122.80
1	A	1195	C	C6-N1-C2	-5.56	118.08	120.30
1	A	31	G	P-O3'-C3'	5.56	126.37	119.70
1	A	332	G	C8-N9-C4	-5.55	104.18	106.40
4	C	183	ASP	CB-CG-OD2	5.55	123.30	118.30
1	A	773	G	C8-N9-C4	-5.55	104.18	106.40
1	A	1043	C	C1'-O4'-C4'	-5.55	105.46	109.90
1	A	944	G	N9-C1'-C2'	5.54	121.21	114.00
1	A	1286	A	C4'-C3'-C2'	-5.54	97.06	102.60
1	A	428	G	P-O3'-C3'	5.54	126.35	119.70
1	A	1294	G	C8-N9-C4	-5.54	104.19	106.40
1	A	1527	C	O5'-P-OP2	-5.54	100.72	105.70
1	A	971	G	C1'-O4'-C4'	-5.53	105.47	109.90
17	P	47	ASP	CB-CG-OD2	5.53	123.28	118.30
1	A	80	G	O4'-C1'-N9	-5.53	103.78	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1451	A	P-O3'-C3'	5.53	126.33	119.70
1	A	55	A	N9-C1'-C2'	-5.52	105.93	112.00
1	A	792	A	P-O3'-C3'	5.51	126.32	119.70
5	D	144	ASP	CB-CG-OD2	5.51	123.26	118.30
1	A	1202	G	C4-C5-N7	-5.51	108.60	110.80
14	M	47	ASP	CB-CG-OD2	5.50	123.25	118.30
1	A	27	G	C8-N9-C4	-5.50	104.20	106.40
1	A	577	G	C8-N9-C4	5.50	108.60	106.40
1	A	124	G	N9-C1'-C2'	-5.50	105.95	112.00
1	A	145	G	C8-N9-C4	-5.50	104.20	106.40
1	A	937	A	C3'-C2'-C1'	-5.49	97.11	101.50
1	A	997	U	C4'-C3'-C2'	-5.49	97.11	102.60
1	A	190(H)	G	C4'-C3'-C2'	-5.49	97.11	102.60
1	A	377	G	N3-C4-N9	5.47	129.28	126.00
1	A	790	A	N1-C6-N6	5.46	121.88	118.60
1	A	652	U	C3'-C2'-C1'	-5.46	97.13	101.50
1	A	1371	G	C5'-C4'-O4'	5.46	115.65	109.10
1	A	1144	G	C8-N9-C4	-5.46	104.22	106.40
1	A	1391	U	N1-C1'-C2'	-5.45	106.00	112.00
1	A	7	G	N9-C1'-C2'	-5.45	106.01	112.00
1	A	190(D)	U	C1'-O4'-C4'	-5.45	105.54	109.90
1	A	286	G	C1'-O4'-C4'	-5.45	105.54	109.90
1	A	944	G	C8-N9-C4	-5.44	104.22	106.40
1	A	1235	U	P-O3'-C3'	5.44	126.23	119.70
1	A	10	A	C4'-C3'-C2'	-5.44	97.16	102.60
1	A	1513	A	N9-C1'-C2'	-5.44	106.01	112.00
1	A	1331	G	C1'-O4'-C4'	-5.44	105.55	109.90
1	A	1397	C	C2-N1-C1'	5.44	124.78	118.80
1	A	529	G	C3'-C2'-C1'	-5.43	97.15	101.50
14	M	16	ASP	CB-CG-OD2	5.43	123.19	118.30
1	A	1178	G	C8-N9-C4	-5.43	104.23	106.40
1	A	701	C	P-O3'-C3'	5.43	126.21	119.70
1	A	776	G	O3'-P-O5'	-5.42	93.70	104.00
1	A	1367	C	C3'-C2'-C1'	5.42	105.84	101.50
1	A	19	C	P-O3'-C3'	5.41	126.19	119.70
1	A	105	G	C4'-C3'-C2'	-5.41	97.19	102.60
1	A	656	C	C3'-C2'-C1'	-5.41	97.17	101.50
1	A	273	A	O4'-C1'-N9	5.41	112.52	108.20
1	A	356	A	C4'-C3'-C2'	-5.40	97.20	102.60
1	A	1239	A	C8-N9-C4	5.40	107.96	105.80
1	A	332	G	O4'-C1'-N9	5.40	112.52	108.20
1	A	867	G	C4'-C3'-C2'	-5.40	97.20	102.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	12	U	N3-C4-O4	5.39	123.17	119.40
1	A	1091	U	C4'-C3'-C2'	-5.39	97.21	102.60
1	A	269	C	C6-N1-C2	5.39	122.45	120.30
1	A	1525	G	C3'-C2'-C1'	-5.38	97.19	101.50
11	J	89	ASP	CB-CG-OD2	5.38	123.15	118.30
3	B	160	ASP	CB-CG-OD2	5.38	123.14	118.30
1	A	180	U	C5'-C4'-O4'	5.38	115.55	109.10
1	A	1504	G	OP2-P-O3'	5.38	117.03	105.20
1	A	1521	G	N9-C4-C5	5.38	107.55	105.40
1	A	405	U	C2'-C3'-O3'	5.38	122.30	113.70
1	A	1190	G	N9-C1'-C2'	5.38	120.99	114.00
1	A	1305	G	C8-N9-C4	-5.38	104.25	106.40
1	A	1487	G	N1-C6-O6	5.38	123.13	119.90
1	A	232	G	O4'-C1'-N9	-5.37	103.90	108.20
1	A	24	U	N1-C1'-C2'	-5.37	106.09	112.00
1	A	968	A	N1-C6-N6	5.37	121.82	118.60
1	A	1352	C	C3'-C2'-C1'	5.36	105.79	101.50
1	A	853	G	N1-C6-O6	5.36	123.12	119.90
1	A	774	G	C8-N9-C4	-5.35	104.26	106.40
1	A	926	G	C3'-C2'-C1'	5.35	105.78	101.50
1	A	1213	A	C3'-C2'-C1'	-5.35	97.22	101.50
1	A	566	G	N9-C1'-C2'	5.34	120.95	114.00
1	A	480	U	O4'-C1'-N1	5.34	112.47	108.20
1	A	322	C	N3-C4-C5	5.34	124.03	121.90
1	A	858	G	C6-C5-N7	-5.34	127.20	130.40
1	A	1450	U	O4'-C1'-N1	5.33	112.47	108.20
1	A	922	G	C5'-C4'-O4'	5.33	115.50	109.10
1	A	942	G	C1'-O4'-C4'	-5.33	105.64	109.90
1	A	1073	U	N3-C4-O4	5.33	123.13	119.40
1	A	1190	G	C4'-C3'-C2'	-5.33	97.27	102.60
1	A	922	G	C6-C5-N7	-5.33	127.20	130.40
1	A	1064	G	N3-C2-N2	-5.33	116.17	119.90
11	J	12	ASP	CB-CG-OD2	5.33	123.09	118.30
1	A	185	A	C3'-C2'-C1'	-5.32	97.24	101.50
1	A	535	A	C1'-O4'-C4'	-5.32	105.64	109.90
1	A	811	C	O4'-C1'-N1	-5.32	103.94	108.20
1	A	929	G	C6-C5-N7	-5.32	127.21	130.40
1	A	366	C	C2-N1-C1'	5.32	124.65	118.80
1	A	509	A	P-O3'-C3'	5.32	126.08	119.70
1	A	1000	U	C3'-C2'-C1'	-5.32	97.25	101.50
1	A	1349	A	O4'-C1'-N9	5.32	112.45	108.20
1	A	1054	C	C6-N1-C1'	-5.31	114.43	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	460	A	C3'-C2'-C1'	5.31	105.75	101.50
1	A	1069	C	N3-C4-C5	-5.30	119.78	121.90
1	A	1448	C	P-O3'-C3'	-5.30	113.33	119.70
16	O	49	ASP	CB-CG-OD2	5.30	123.07	118.30
1	A	292	G	N1-C6-O6	5.30	123.08	119.90
11	J	58	ASP	CB-CG-OD2	5.30	123.07	118.30
1	A	656	C	P-O3'-C3'	5.29	126.05	119.70
1	A	1487	G	C5-C6-O6	-5.29	125.42	128.60
1	A	371	G	C5'-C4'-O4'	5.28	115.44	109.10
1	A	850	U	C3'-C2'-C1'	-5.28	97.27	101.50
1	A	28	G	N1-C6-O6	5.28	123.07	119.90
1	A	858	G	C5-C6-O6	-5.28	125.43	128.60
1	A	1091	U	O4'-C1'-N1	5.28	112.42	108.20
1	A	1227	A	C5-N7-C8	-5.28	101.26	103.90
20	S	12	ASP	CB-CG-OD2	5.28	123.05	118.30
1	A	104	G	O4'-C1'-N9	-5.28	103.98	108.20
8	G	15	ASP	CB-CG-OD2	5.28	123.05	118.30
1	A	120	A	P-O3'-C3'	-5.27	113.37	119.70
1	A	568	G	N9-C1'-C2'	5.27	120.86	114.00
1	A	1104	G	O4'-C1'-N9	5.27	112.42	108.20
1	A	1307	U	P-O3'-C3'	-5.27	113.38	119.70
6	E	36	ASP	CB-CG-OD2	5.27	123.04	118.30
1	A	516	U	O4'-C1'-N1	5.27	112.42	108.20
1	A	1067	A	N3-C4-C5	-5.27	123.11	126.80
1	A	1064	G	N9-C4-C5	5.27	107.51	105.40
8	G	126	ASP	CB-CG-OD2	5.26	123.04	118.30
10	I	60	ASP	CB-CG-OD2	5.26	123.04	118.30
1	A	972	C	C4'-C3'-C2'	-5.26	97.34	102.60
1	A	266	G	N9-C1'-C2'	5.26	120.84	114.00
1	A	876	G	N9-C1'-C2'	-5.26	106.22	112.00
1	A	1357	A	O4'-C1'-N9	5.26	112.41	108.20
1	A	911	U	C4'-C3'-C2'	-5.26	97.34	102.60
1	A	1013	G	O4'-C1'-N9	5.26	112.41	108.20
10	I	54	ASP	CB-CG-OD2	5.25	123.03	118.30
5	D	177	ASP	CB-CG-OD2	5.25	123.03	118.30
1	A	1248	A	C5'-C4'-O4'	5.25	115.40	109.10
1	A	1249	C	C6-N1-C2	-5.25	118.20	120.30
1	A	588	G	N1-C6-O6	5.24	123.05	119.90
1	A	1509	C	O3'-P-O5'	-5.24	94.04	104.00
1	A	639	G	N1-C6-O6	5.24	123.04	119.90
1	A	1498	U	C4'-C3'-C2'	5.24	107.84	102.60
1	A	1181	G	N9-C1'-C2'	5.23	120.80	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
18	Q	13	ASP	CB-CG-OD2	5.23	123.01	118.30
1	A	930	C	C3'-C2'-C1'	-5.23	97.32	101.50
1	A	257	G	N3-C4-C5	-5.22	125.99	128.60
1	A	1533	C	C3'-C2'-C1'	5.22	105.68	101.50
1	A	252	U	C5'-C4'-O4'	5.22	115.36	109.10
1	A	505	G	O4'-C1'-N9	-5.22	104.02	108.20
1	A	979	C	O4'-C1'-N1	5.22	112.37	108.20
1	A	773	G	N3-C4-C5	-5.21	125.99	128.60
1	A	1145	C	P-O3'-C3'	5.21	125.95	119.70
1	A	484	G	N9-C1'-C2'	5.21	120.77	114.00
1	A	1417	G	C3'-C2'-C1'	5.21	105.67	101.50
1	A	49	U	O4'-C1'-N1	5.20	112.36	108.20
1	A	644	G	C5-C6-O6	-5.20	125.48	128.60
12	K	36	ASP	CB-CG-OD2	5.20	122.98	118.30
1	A	859	A	C3'-C2'-C1'	5.20	105.66	101.50
1	A	1091	U	C1'-O4'-C4'	-5.20	105.74	109.90
1	A	1129	C	C6-N1-C2	-5.20	118.22	120.30
1	A	1218	C	C1'-O4'-C4'	-5.20	105.74	109.90
18	Q	46	ASP	CB-CG-OD2	5.20	122.98	118.30
1	A	1371	G	C8-N9-C4	-5.19	104.32	106.40
1	A	1434	A	N9-C1'-C2'	-5.19	106.29	112.00
1	A	1529	G	C5'-C4'-O4'	5.19	115.33	109.10
1	A	408	A	C3'-C2'-C1'	-5.19	97.35	101.50
1	A	674	G	O4'-C1'-N9	5.18	112.35	108.20
1	A	1062	U	O4'-C1'-N1	5.18	112.34	108.20
1	A	1159	U	O4'-C1'-N1	5.18	112.34	108.20
1	A	1454	G	C3'-C2'-C1'	-5.18	97.36	101.50
1	A	1230	C	O4'-C1'-N1	5.18	112.34	108.20
1	A	973	G	N3-C4-N9	-5.17	122.90	126.00
1	A	1079	G	C5-C6-N1	-5.17	108.91	111.50
1	A	131	C	N3-C2-O2	-5.17	118.28	121.90
1	A	1191	A	P-O3'-C3'	5.17	125.90	119.70
1	A	1331	G	C8-N9-C4	-5.17	104.33	106.40
1	A	1119	C	C3'-C2'-C1'	-5.16	97.37	101.50
1	A	1076	C	P-O3'-C3'	5.16	125.89	119.70
1	A	1202	G	O4'-C1'-N9	5.16	112.33	108.20
1	A	1297	C	C1'-O4'-C4'	-5.16	105.78	109.90
1	A	1248	A	C4'-C3'-C2'	-5.15	97.45	102.60
1	A	279	A	C5-N7-C8	-5.15	101.33	103.90
1	A	691	G	O4'-C1'-N9	-5.15	104.08	108.20
1	A	721	G	C3'-C2'-C1'	5.14	105.61	101.50
1	A	1389	C	C3'-C2'-C1'	-5.14	97.39	101.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1365	G	C8-N9-C4	-5.14	104.34	106.40
3	B	205	ASP	CB-CG-OD2	5.14	122.92	118.30
1	A	351	G	P-O3'-C3'	5.14	125.86	119.70
1	A	372	C	N1-C2-O2	5.13	121.98	118.90
1	A	750	G	N3-C4-C5	-5.13	126.03	128.60
1	A	1099	G	N9-C4-C5	5.12	107.45	105.40
1	A	1277	C	O4'-C1'-N1	5.12	112.30	108.20
1	A	1175	G	O4'-C1'-N9	5.12	112.30	108.20
1	A	1262	C	O4'-C1'-N1	5.12	112.29	108.20
1	A	593	G	C8-N9-C4	-5.12	104.35	106.40
1	A	1531	A	C8-N9-C4	-5.11	103.76	105.80
1	A	1358	U	C1'-O4'-C4'	-5.11	105.81	109.90
1	A	1515	C	N3-C4-C5	-5.11	119.86	121.90
1	A	1299	A	O4'-C1'-N9	-5.11	104.11	108.20
1	A	762	C	P-O3'-C3'	-5.11	113.57	119.70
1	A	1093	A	N1-C6-N6	5.11	121.66	118.60
1	A	816	A	O4'-C1'-N9	-5.10	104.12	108.20
1	A	658	G	O4'-C1'-N9	-5.10	104.12	108.20
18	Q	55	ASP	CB-CG-OD2	5.10	122.89	118.30
1	A	401	C	C4'-C3'-C2'	-5.09	97.51	102.60
1	A	815	A	P-O3'-C3'	-5.09	113.59	119.70
1	A	855	G	O4'-C4'-C3'	-5.09	98.91	104.00
1	A	1464	G	P-O3'-C3'	-5.09	113.59	119.70
1	A	311	C	C3'-C2'-C1'	-5.09	97.43	101.50
1	A	191	G	C3'-C2'-C1'	-5.09	97.43	101.50
1	A	1367	C	N1-C2-O2	5.09	121.95	118.90
13	L	106	ASP	CB-CG-OD2	5.09	122.88	118.30
1	A	733	A	C3'-C2'-C1'	-5.09	97.43	101.50
1	A	1502	A	C3'-C2'-C1'	-5.09	97.43	101.50
1	A	1079	G	N7-C8-N9	5.08	115.64	113.10
1	A	619	U	C5'-C4'-C3'	-5.08	107.87	116.00
1	A	623	C	N1-C1'-C2'	-5.07	106.42	112.00
1	A	1518	A	P-O3'-C3'	5.07	125.79	119.70
1	A	289	G	O4'-C1'-N9	5.07	112.26	108.20
1	A	1375	A	C5'-C4'-O4'	5.07	115.18	109.10
1	A	801	U	N3-C4-C5	5.07	117.64	114.60
13	L	92	ASP	CB-CG-OD2	5.07	122.86	118.30
5	D	53	ASP	CB-CG-OD2	5.07	122.86	118.30
1	A	366	C	N1-C2-O2	5.06	121.94	118.90
1	A	832	C	O4'-C1'-N1	5.06	112.25	108.20
1	A	918	A	O4'-C1'-N9	-5.06	104.15	108.20
1	A	1302	U	N1-C1'-C2'	5.06	120.58	114.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1346	A	C8-N9-C4	5.06	107.82	105.80
1	A	780	A	N9-C1'-C2'	-5.06	106.44	112.00
1	A	1249	C	C5-C6-N1	5.06	123.53	121.00
1	A	1351	U	P-O3'-C3'	-5.06	113.63	119.70
1	A	1361(A)	C	O4'-C1'-N1	5.05	112.24	108.20
1	A	142	G	N3-C4-C5	-5.05	126.08	128.60
1	A	248	C	C4'-C3'-C2'	-5.05	97.55	102.60
3	B	195	ASP	CB-CG-OD2	5.05	122.84	118.30
1	A	54	C	C4'-C3'-C2'	-5.05	97.55	102.60
1	A	796	C	C4'-C3'-C2'	-5.05	97.55	102.60
10	I	105	ASP	CB-CG-OD2	5.04	122.84	118.30
20	S	13	ASP	CB-CG-OD2	5.04	122.84	118.30
1	A	1387	G	P-O3'-C3'	-5.04	113.65	119.70
1	A	781	A	N9-C1'-C2'	-5.04	106.46	112.00
1	A	1341	U	P-O3'-C3'	-5.04	113.66	119.70
1	A	944	G	P-O3'-C3'	5.03	125.74	119.70
1	A	1276	G	C8-N9-C4	-5.03	104.39	106.40
1	A	1160	G	O4'-C1'-N9	5.03	112.23	108.20
1	A	733	A	C1'-O4'-C4'	-5.03	105.88	109.90
1	A	727	G	C5-C6-O6	-5.03	125.58	128.60
1	A	1115	C	O4'-C1'-N1	5.03	112.22	108.20
1	A	559	A	C3'-C2'-C1'	-5.03	97.48	101.50
1	A	319	G	N3-C4-C5	-5.03	126.09	128.60
1	A	858	G	C5'-C4'-O4'	5.03	115.13	109.10
1	A	907	A	N1-C6-N6	-5.02	115.59	118.60
1	A	89	C	C5'-C4'-O4'	5.02	115.12	109.10
1	A	604	G	C6-C5-N7	-5.02	127.39	130.40
1	A	36	C	C3'-C2'-C1'	-5.01	97.49	101.50
1	A	223	U	C4'-C3'-C2'	-5.01	97.58	102.60
1	A	982	U	N1-C1'-C2'	5.01	120.52	114.00
1	A	413	G	C3'-C2'-C1'	-5.01	97.49	101.50
1	A	1400	C	P-O3'-C3'	5.01	125.72	119.70
1	A	143	A	C8-N9-C4	5.01	107.81	105.80
1	A	1205	U	C4'-C3'-C2'	-5.01	97.59	102.60
1	A	656	C	C1'-O4'-C4'	-5.00	105.90	109.90
1	A	1383	C	P-O3'-C3'	-5.00	113.70	119.70
8	G	20	ASP	CB-CG-OD2	5.00	122.80	118.30
1	A	619	U	C3'-C2'-C1'	5.00	105.50	101.50
1	A	1300	G	C3'-C2'-C1'	-5.00	97.50	101.50

There are no chirality outliers.

All (74) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	B	133	LYS	Peptide
3	B	225	ALA	Peptide
4	C	13	GLY	Peptide
4	C	166	GLU	Peptide
4	C	167	TRP	Peptide
4	C	177	THR	Peptide
4	C	178	LEU	Peptide
4	C	48	TYR	Peptide
5	D	11	LEU	Peptide
5	D	185	PHE	Peptide
5	D	195	ALA	Peptide
5	D	208	SER	Peptide
5	D	28	SER	Peptide
5	D	31	CYS	Peptide
6	E	14	ARG	Peptide
6	E	20	GLN	Peptide
6	E	35	GLY	Peptide
6	E	85	GLY	Peptide
6	E	86	ALA	Peptide
7	F	13	ASN	Peptide
9	H	109	ILE	Peptide
9	H	135	CYS	Peptide
9	H	27	PRO	Peptide
9	H	53	VAL	Peptide
9	H	90	GLY	Peptide
10	I	117	HIS	Peptide
10	I	125	TYR	Peptide
10	I	127	LYS	Peptide
10	I	43	ALA	Peptide
11	J	47	PHE	Peptide
11	J	49	VAL	Peptide
11	J	52	GLY	Peptide
11	J	57	LYS	Peptide
11	J	90	LEU	Peptide
11	J	96	ILE	Peptide
12	K	116	HIS	Peptide
12	K	126	ARG	Peptide
12	K	27	ASN	Peptide
12	K	48	ILE	Peptide
12	K	88	GLY	Peptide
13	L	25	PRO	Peptide
13	L	26	ALA	Peptide
13	L	43	VAL	Peptide

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Mol	Chain	Res	Type	Group
13	L	46	LYS	Peptide
13	L	66	VAL	Peptide
13	L	77	LEU	Peptide
13	L	80	HIS	Peptide
13	L	94	PRO	Peptide
14	M	107	ALA	Peptide
14	M	112	GLY	Peptide
14	M	8	GLU	Peptide
14	M	97	PRO	Peptide
15	N	11	LYS	Peptide
15	N	21	TYR	Peptide
15	N	30	ALA	Peptide
15	N	32	SER	Peptide
15	N	42	ILE	Peptide
15	N	6	LEU	Peptide
15	N	8	GLU	Peptide
15	N	9	LYS	Peptide
17	P	15	PRO	Peptide
17	P	63	GLY	Peptide
17	P	64	ALA	Peptide
17	P	70	ALA	Peptide
18	Q	17	LYS	Peptide
20	S	37	ARG	Peptide
20	S	4	SER	Peptide
20	S	53	ASN	Peptide
20	S	71	LEU	Peptide
20	S	83	HIS	Peptide
21	T	10	LEU	Peptide
21	T	12	ALA	Peptide
21	T	48	LYS	Peptide
21	T	73	HIS	Peptide

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32391	0	16359	1894	0
2	Z	80	0	42	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	1923	0	1968	218	0
4	C	1612	0	1677	175	0
5	D	1703	0	1763	198	0
6	E	1146	0	1207	161	0
7	F	843	0	857	58	0
8	G	1257	0	1296	105	0
9	H	1116	0	1177	93	0
10	I	1011	0	1043	122	0
11	J	792	0	835	125	0
12	K	885	0	904	80	0
13	L	975	0	1062	129	0
14	M	997	0	1072	111	0
15	N	492	0	530	84	0
16	O	734	0	771	70	0
17	P	700	0	720	72	0
18	Q	857	0	930	70	0
19	R	597	0	668	68	0
20	S	674	0	699	56	0
21	T	762	0	859	97	0
22	A	98	0	0	0	0
22	D	1	0	0	0	0
22	M	1	0	0	0	0
22	Z	1	0	0	0	0
23	A	12	0	0	0	0
24	A	31	0	19	4	0
25	A	35	0	43	1	0
26	D	1	0	0	0	0
26	N	1	0	0	0	0
All	All	51728	0	36501	3715	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 43.

All (3715) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:89:MET:CE	8:G:89:MET:SD	2.02	1.45
1:A:492:G:H3'	1:A:494:G:OP2	1.29	1.32
6:E:80:ILE:CD1	6:E:91:LEU:HB2	1.62	1.29
1:A:70:G:H3'	1:A:73:C:P	1.72	1.27
15:N:40:CYS:O	15:N:43:CYS:HB2	1.23	1.27

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:O:33:THR:HG23	16:O:63:ARG:NH1	1.51	1.23
1:A:1249:C:O2'	10:I:73:GLN:NE2	1.71	1.22
3:B:162:ILE:O	3:B:185:ILE:HD12	1.42	1.20
4:C:7:PRO:O	4:C:11:ARG:HG2	1.40	1.20
1:A:1491:G:H5'	1:A:1491:G:C8	1.77	1.19
10:I:114:TYR:HD1	11:J:60:ARG:HB2	1.00	1.17
3:B:100:GLY:HA2	3:B:176:GLU:OE2	1.41	1.17
1:A:1169:A:O3'	1:A:1171:G:P	2.03	1.16
21:T:104:LEU:H	21:T:104:LEU:CD2	1.52	1.16
1:A:948:C:OP1	14:M:109:THR:HG22	1.42	1.15
4:C:5:ILE:HD13	4:C:10:PHE:HB2	1.26	1.15
10:I:114:TYR:CD1	11:J:60:ARG:HB2	1.80	1.15
11:J:90:LEU:HB3	11:J:91:PRO:HD3	1.21	1.15
13:L:97:ARG:HB2	13:L:98:TYR:CE1	1.79	1.15
1:A:444:C:H2'	1:A:445:G:H8	1.12	1.14
1:A:1497:G:H2'	1:A:1498:U:H5'	1.27	1.14
21:T:104:LEU:N	21:T:104:LEU:HD23	1.48	1.14
1:A:99:C:H3'	1:A:101:A:P	1.89	1.12
1:A:975:A:H5'	1:A:975:A:H8	1.12	1.12
1:A:1168:A:H2'	1:A:1169:A:C8	1.85	1.12
6:E:51:VAL:HB	6:E:52:PRO:HD3	1.32	1.12
8:G:120:ILE:CD1	8:G:120:ILE:H	1.58	1.11
1:A:373:A:H5'	1:A:373:A:H8	1.14	1.10
1:A:1314:C:OP2	20:S:6:LYS:HG2	1.49	1.10
5:D:26:CYS:HA	5:D:31:CYS:HB2	1.27	1.10
19:R:79:LEU:HD23	19:R:80:PRO:HD2	1.27	1.09
6:E:80:ILE:HD11	6:E:91:LEU:HB2	1.17	1.09
5:D:62:GLN:NE2	5:D:65:ARG:HH12	1.49	1.09
17:P:28:ARG:HG2	17:P:28:ARG:HH11	1.06	1.08
1:A:492:G:H3'	1:A:494:G:P	1.93	1.08
8:G:120:ILE:H	8:G:120:ILE:HD12	0.92	1.07
14:M:34:LEU:HD13	14:M:41:PRO:HA	1.36	1.07
1:A:392:G:H2'	1:A:393:A:C8	1.90	1.07
1:A:93:G:H3'	1:A:95:U:P	1.95	1.07
16:O:16:ALA:HB1	16:O:21:ASP:HB3	1.09	1.06
1:A:1399:C:H4'	1:A:1400:C:H5"	1.35	1.06
3:B:77:ALA:HB2	3:B:211:ILE:HD13	1.34	1.06
1:A:1182:G:H4'	1:A:1183:A:O5'	1.54	1.06
3:B:114:ARG:HH11	3:B:118:LEU:HD11	1.21	1.05
1:A:1400:C:H3'	1:A:1401:G:H5'	1.34	1.04
8:G:23:VAL:HG12	8:G:27:ILE:HD11	1.39	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:T:86:ARG:HH11	21:T:86:ARG:HG3	1.17	1.04
1:A:376:G:H5"	17:P:5:ARG:HG3	1.40	1.04
1:A:538:G:H2'	1:A:539:A:H8	1.20	1.04
21:T:73:HIS:O	21:T:74:LYS:HG2	1.55	1.04
8:G:120:ILE:HD12	8:G:120:ILE:N	1.69	1.03
14:M:96:LEU:HB3	14:M:97:PRO:HD2	1.35	1.03
16:O:16:ALA:CB	16:O:21:ASP:HB3	1.86	1.03
1:A:1250:A:H4'	10:I:68:GLY:H	0.89	1.02
14:M:49:THR:HB	14:M:52:GLU:HG3	1.36	1.02
1:A:350:G:H5'	1:A:350:G:H8	1.25	1.02
6:E:79:GLU:HB3	6:E:92:LYS:HG3	1.40	1.02
1:A:984:C:H2'	1:A:985:C:H6	1.23	1.02
1:A:1168:A:H2'	1:A:1169:A:H8	1.26	1.01
1:A:1250:A:H4'	10:I:68:GLY:N	1.74	1.01
6:E:51:VAL:HB	6:E:52:PRO:CD	1.90	1.01
1:A:1249:C:HO2'	10:I:73:GLN:NE2	1.50	1.00
13:L:6:THR:OG1	13:L:9:GLN:HG3	1.61	1.00
5:D:62:GLN:NE2	5:D:65:ARG:NH1	2.07	1.00
6:E:48:ALA:HB1	6:E:49:PRO:HD2	1.40	1.00
3:B:114:ARG:NH1	3:B:118:LEU:HD11	1.77	0.99
1:A:1077:G:N2	1:A:1080:A:OP2	1.96	0.99
1:A:1347:G:H22	1:A:1373:G:H2'	1.23	0.99
3:B:9:GLU:HG3	3:B:217:ARG:NH1	1.79	0.98
1:A:353:A:H5'	1:A:353:A:C8	1.96	0.98
1:A:444:C:H2'	1:A:445:G:C8	1.98	0.98
1:A:838:G:H2'	1:A:839:U:H5"	1.43	0.98
5:D:19:LEU:HD21	5:D:67:ILE:HG12	1.46	0.98
1:A:1497:G:C2'	1:A:1498:U:H5'	1.94	0.98
4:C:131:ARG:HG3	4:C:135:LYS:HE2	1.45	0.98
1:A:373:A:H5'	1:A:373:A:C8	1.98	0.98
12:K:54:ARG:O	12:K:57:THR:CG2	2.12	0.98
1:A:1060:C:O2'	1:A:1061:G:H5'	1.63	0.97
1:A:975:A:H5'	1:A:975:A:C8	1.98	0.97
1:A:1103:C:OP1	3:B:96:ARG:NH2	1.98	0.97
1:A:795:C:H5"	1:A:796:C:OP2	1.65	0.97
1:A:1263:C:H42	1:A:1272:G:H1	1.07	0.97
4:C:23:TYR:O	4:C:24:ALA:O	1.80	0.97
1:A:954:G:H21	1:A:1227:A:H62	1.12	0.97
19:R:78:LEU:HD12	19:R:78:LEU:N	1.77	0.97
1:A:353:A:C5'	1:A:353:A:H8	1.77	0.96
1:A:721:G:H4'	1:A:722:A:O5'	1.62	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:463:A:O3'	1:A:474:G:OP2	1.83	0.96
11:J:49:VAL:HA	11:J:50:ILE:HD12	1.48	0.96
6:E:80:ILE:HD11	6:E:91:LEU:CB	1.96	0.95
18:Q:66:SER:OG	18:Q:69:LYS:HB2	1.64	0.95
3:B:91:PRO:HG2	3:B:155:LEU:HD23	1.43	0.95
6:E:103:GLY:O	6:E:106:PRO:HD2	1.65	0.95
5:D:111:ALA:HB1	5:D:116:GLN:OE1	1.66	0.95
1:A:1356:G:H2'	1:A:1357:A:C8	2.01	0.95
3:B:118:LEU:HB3	3:B:142:LEU:HD12	1.48	0.95
1:A:152:A:N6	1:A:170:U:O2	2.01	0.94
1:A:1028:C:N4	1:A:1034:G:H1	1.63	0.94
1:A:1194:U:H2'	1:A:1195:C:H6	1.31	0.94
1:A:1435:G:H2'	1:A:1436:U:C6	2.02	0.94
1:A:382:A:H2'	1:A:383:A:H8	1.33	0.94
1:A:1152:A:H5'	11:J:13:HIS:HD2	1.32	0.93
1:A:154:C:O2	1:A:167:G:N2	1.99	0.93
14:M:78:ILE:HG22	14:M:79:LYS:H	1.34	0.93
3:B:44:LEU:HA	3:B:47:THR:OG1	1.68	0.93
1:A:382:A:H2'	1:A:383:A:C8	2.03	0.93
11:J:12:ASP:HB3	11:J:15:THR:HG22	1.51	0.93
1:A:1152:A:H5'	11:J:13:HIS:CD2	2.03	0.93
1:A:1391:U:H2'	1:A:1392:G:C8	2.04	0.93
1:A:1250:A:C4'	10:I:68:GLY:H	1.81	0.93
5:D:57:ARG:NH2	5:D:205:GLU:OE2	2.01	0.92
1:A:392:G:H2'	1:A:393:A:H8	1.20	0.92
10:I:125:TYR:H	10:I:125:TYR:HD2	1.07	0.92
1:A:538:G:H2'	1:A:539:A:C8	2.04	0.92
1:A:1010:G:H22	1:A:1020:U:H1'	1.34	0.92
1:A:1209:C:O2	1:A:1209:C:H2'	1.68	0.92
5:D:141:ARG:HB3	5:D:142:PRO:CD	1.99	0.92
12:K:19:ALA:HB2	12:K:80:VAL:HG11	1.52	0.92
21:T:73:HIS:C	21:T:74:LYS:HG2	1.89	0.92
1:A:1347:G:N2	1:A:1373:G:H2'	1.84	0.92
1:A:1364:U:O2'	1:A:1365:G:H5'	1.70	0.92
4:C:71:ALA:HA	4:C:106:VAL:HB	1.52	0.92
10:I:114:TYR:HD1	11:J:60:ARG:CB	1.82	0.92
1:A:797:C:OP1	12:K:124:LYS:HE2	1.69	0.91
14:M:90:LEU:HD23	14:M:93:ARG:HH12	1.32	0.91
1:A:536:C:H2'	1:A:537:G:C8	2.05	0.91
1:A:1343:G:H2'	1:A:1344:C:C6	2.05	0.91
12:K:43:SER:HA	12:K:47:VAL:HG21	1.49	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:420:U:H1'	1:A:424:G:N2	1.85	0.91
14:M:17:VAL:O	14:M:20:THR:HB	1.70	0.91
16:O:33:THR:HG23	16:O:63:ARG:HH11	1.17	0.91
1:A:436:C:H2'	1:A:437:U:H6	1.35	0.91
15:N:40:CYS:O	15:N:43:CYS:CB	2.16	0.91
1:A:669:U:H2'	1:A:670:G:C8	2.05	0.91
1:A:1028:C:H42	1:A:1034:G:H1	0.91	0.91
13:L:102:ARG:HH12	13:L:110:VAL:HA	1.34	0.91
18:Q:86:GLU:O	18:Q:90:ILE:HG13	1.68	0.91
1:A:1203:C:H2'	1:A:1204:A:O4'	1.69	0.91
5:D:61:LYS:CE	5:D:62:GLN:HE21	1.83	0.91
11:J:90:LEU:CB	11:J:91:PRO:HD3	2.00	0.91
13:L:97:ARG:HB2	13:L:98:TYR:CD1	2.05	0.91
17:P:19:ILE:HG22	17:P:36:ILE:HG13	1.52	0.91
1:A:447:G:H2'	1:A:485:G:H22	1.32	0.91
11:J:90:LEU:HB3	11:J:91:PRO:CD	2.00	0.91
11:J:56:HIS:O	11:J:58:ASP:N	2.02	0.90
1:A:500:G:N2	1:A:546:G:H1'	1.85	0.90
1:A:1491:G:C8	1:A:1491:G:C5'	2.54	0.90
13:L:81:SER:O	13:L:106:ASP:HB2	1.70	0.90
1:A:989:C:HO2'	1:A:1017:G:HO2'	1.17	0.90
4:C:126:ARG:O	4:C:127:ARG:HB2	1.70	0.90
16:O:16:ALA:HB1	16:O:21:ASP:CB	2.00	0.90
1:A:1356:G:H2'	1:A:1357:A:H8	1.33	0.90
1:A:707:C:H4'	12:K:20:TYR:CD2	2.05	0.90
1:A:1003(A):G:H2'	1:A:1004:A:H4'	1.53	0.89
1:A:1491:G:H5'	1:A:1491:G:H8	1.34	0.89
10:I:8:GLY:HA2	10:I:79:LEU:HB3	1.53	0.89
1:A:1047:G:C2'	1:A:1048:G:H5'	2.01	0.89
1:A:622:A:N7	1:A:623:C:C6	2.40	0.89
4:C:7:PRO:O	4:C:11:ARG:CG	2.20	0.89
5:D:62:GLN:HE22	5:D:65:ARG:NH1	1.65	0.89
5:D:117:ALA:O	5:D:121:VAL:HG23	1.72	0.89
1:A:581:G:N2	1:A:759:A:OP2	2.05	0.89
1:A:792:A:H4'	1:A:793:U:H5"	1.52	0.89
1:A:1305:G:HO2'	1:A:1306:A:H8	0.94	0.89
4:C:6:HIS:NE2	4:C:8:ILE:HB	1.88	0.89
12:K:54:ARG:O	12:K:57:THR:HG23	1.72	0.89
1:A:519:C:H2'	1:A:520:A:C8	2.08	0.89
4:C:11:ARG:NH1	4:C:178:LEU:HA	1.88	0.89
1:A:353:A:C8	1:A:353:A:C5'	2.55	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:539:A:H2'	1:A:540:G:H8	1.37	0.88
1:A:1455:G:O3'	1:A:1459:C:P	2.31	0.88
17:P:67:THR:HG22	17:P:68:ASP:N	1.88	0.88
1:A:328:C:O2	1:A:328:C:H2'	1.72	0.88
3:B:101:MET:HA	3:B:108:ILE:HD12	1.56	0.88
17:P:57:ARG:HG3	17:P:57:ARG:HH11	1.35	0.88
1:A:1315:U:OP2	20:S:6:LYS:NZ	2.06	0.88
4:C:54:ARG:O	4:C:55:VAL:HG23	1.73	0.88
3:B:84:GLU:HG3	3:B:219:VAL:HG21	1.55	0.88
5:D:63:LYS:HD3	5:D:198:VAL:HG23	1.53	0.88
1:A:492:G:C3'	1:A:494:G:P	2.61	0.88
10:I:48:GLU:N	10:I:49:PRO:HD2	1.89	0.88
14:M:81:LEU:H	14:M:81:LEU:CD2	1.86	0.88
21:T:104:LEU:H	21:T:104:LEU:HD23	0.73	0.87
1:A:350:G:H8	1:A:350:G:C5'	1.86	0.87
1:A:407:G:O2'	5:D:116:GLN:HG2	1.74	0.87
5:D:64:LEU:HD11	5:D:97:LEU:CD1	2.04	0.87
6:E:135:THR:O	6:E:138:ALA:HB3	1.74	0.87
11:J:37:PRO:HA	11:J:72:VAL:HG22	1.54	0.87
11:J:47:PHE:HD2	15:N:34:TYR:CE2	1.93	0.87
1:A:992:U:OP2	1:A:992:U:H6	1.58	0.87
4:C:8:ILE:HG22	4:C:9:GLY:N	1.89	0.87
4:C:11:ARG:HH12	4:C:178:LEU:HA	1.37	0.87
13:L:86:ARG:HH11	13:L:86:ARG:HG2	1.38	0.87
16:O:70:LEU:HD12	16:O:78:TYR:HB2	1.55	0.87
18:Q:12:SER:HB3	18:Q:20:THR:OG1	1.75	0.86
1:A:1323:G:H2'	1:A:1324:A:C8	2.10	0.86
13:L:75:HIS:CD2	13:L:77:LEU:H	1.93	0.86
1:A:1194:U:H2'	1:A:1195:C:C6	2.10	0.86
1:A:1400:C:H3'	1:A:1401:G:C5'	2.04	0.86
13:L:98:TYR:CD1	13:L:98:TYR:N	2.43	0.86
15:N:26:ARG:NH2	15:N:47:LEU:HD21	1.89	0.86
17:P:28:ARG:HG2	17:P:28:ARG:NH1	1.86	0.86
1:A:1366:C:H2'	1:A:1367:C:H6	1.40	0.86
8:G:38:LEU:O	8:G:42:ILE:HG13	1.75	0.86
17:P:67:THR:CG2	17:P:68:ASP:N	2.38	0.86
1:A:1152:A:C5'	11:J:13:HIS:HD2	1.88	0.86
1:A:1250:A:H2'	1:A:1251:A:C8	2.10	0.86
1:A:376:G:H2'	1:A:377:G:H8	1.37	0.86
1:A:1047:G:H2'	1:A:1048:G:H5'	1.56	0.86
7:F:80:ARG:HG3	7:F:88:VAL:HG21	1.56	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1366:C:H2'	1:A:1367:C:C6	2.11	0.86
4:C:112:SER:O	4:C:115:LEU:HD12	1.75	0.86
14:M:45:VAL:O	14:M:48:LEU:HB2	1.74	0.86
1:A:335:C:H2'	1:A:336:C:H6	1.40	0.86
4:C:8:ILE:HG22	4:C:9:GLY:H	1.39	0.86
21:T:67:ALA:O	21:T:73:HIS:CE1	2.28	0.86
1:A:1195:C:H3'	1:A:1196:U:H5"	1.57	0.86
1:A:1502:A:H2	1:A:1505:G:H1	1.22	0.85
8:G:111:ARG:NH1	8:G:122:HIS:HB3	1.90	0.85
1:A:99:C:C3'	1:A:101:A:P	2.63	0.85
15:N:12:ARG:C	15:N:14:PRO:HD3	1.95	0.85
1:A:1057:G:H2'	1:A:1058:G:C8	2.11	0.85
1:A:1091:U:O2	1:A:1093:A:H8	1.58	0.85
6:E:59:GLY:O	6:E:62:ALA:HB3	1.77	0.85
1:A:353:A:H5'	1:A:353:A:H8	1.36	0.85
1:A:560:U:H5'	1:A:566:G:N2	1.92	0.85
8:G:116:ALA:HA	8:G:119:ARG:NH2	1.91	0.85
1:A:254:G:OP1	18:Q:67:LYS:O	1.94	0.85
3:B:61:LEU:HD11	3:B:160:ASP:HB2	1.58	0.85
19:R:86:VAL:O	19:R:87:ARG:HB2	1.77	0.85
21:T:86:ARG:HG3	21:T:86:ARG:NH1	1.83	0.85
3:B:87:ARG:NH1	3:B:233:SER:HB3	1.92	0.85
1:A:393:A:H2'	1:A:394:G:H8	1.42	0.85
1:A:979:C:C5	1:A:980:C:C6	2.65	0.85
1:A:1369:C:H2'	1:A:1370:G:C8	2.12	0.85
6:E:36:ASP:O	6:E:37:ARG:HB2	1.75	0.85
1:A:1286:A:H8	1:A:1287:A:H4'	1.42	0.84
1:A:984:C:H2'	1:A:985:C:C6	2.12	0.84
19:R:76:LEU:HB2	19:R:78:LEU:CD1	2.07	0.84
21:T:13:LEU:HD22	21:T:14:LYS:N	1.91	0.84
1:A:1221:G:O3'	20:S:77:THR:HG21	1.76	0.84
12:K:123:LYS:O	12:K:125:PHE:N	2.10	0.84
1:A:539:A:H2'	1:A:540:G:C8	2.12	0.84
9:H:97:VAL:HA	9:H:100:ILE:HD12	1.60	0.84
1:A:518:C:H5"	1:A:519:C:C6	2.13	0.84
1:A:707:C:H5"	12:K:20:TYR:HD2	1.42	0.84
1:A:1490:C:C3'	1:A:1491:G:H5"	2.07	0.84
1:A:359:U:H2'	1:A:360:A:H8	1.43	0.84
1:A:644:G:C5	1:A:645:C:C5	2.66	0.84
1:A:503:C:H2'	1:A:504:C:H5'	1.60	0.84
1:A:804:U:H5"	1:A:805:C:OP2	1.77	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1491:G:C5'	1:A:1491:G:H8	1.89	0.83
13:L:27:LEU:O	13:L:29:GLY:N	2.10	0.83
14:M:78:ILE:CG2	14:M:79:LYS:H	1.91	0.83
9:H:9:MET:HG3	9:H:26:VAL:HG11	1.61	0.83
16:O:26:GLU:HA	16:O:81:LEU:HD11	1.60	0.83
1:A:350:G:H5'	1:A:350:G:C8	2.14	0.83
3:B:26:PRO:O	3:B:29:ALA:HB2	1.79	0.83
6:E:13:ILE:H	6:E:13:ILE:HD12	1.43	0.83
6:E:80:ILE:HD12	6:E:80:ILE:H	1.42	0.83
12:K:80:VAL:HG21	12:K:103:LEU:HD13	1.58	0.83
1:A:670:G:H1	1:A:736:C:H42	1.23	0.83
1:A:1154:G:H2'	1:A:1155:G:H8	1.44	0.83
8:G:26:PHE:CE2	8:G:30:ILE:HD11	2.12	0.83
1:A:923:A:H1'	1:A:1398:A:C2	2.14	0.83
3:B:184:VAL:HG12	3:B:197:VAL:HG13	1.58	0.83
14:M:37:THR:HG21	14:M:55:ARG:O	1.79	0.83
20:S:42:PRO:O	20:S:45:VAL:HG23	1.78	0.82
1:A:459:G:H5"	1:A:460:A:OP2	1.79	0.82
8:G:15:ASP:OD1	8:G:18:TYR:N	2.11	0.82
10:I:47:LEU:C	10:I:49:PRO:HD2	1.99	0.82
13:L:75:HIS:CD2	13:L:76:ASN:N	2.47	0.82
18:Q:58:GLU:O	18:Q:59:ILE:HD13	1.78	0.82
1:A:260:G:OP2	21:T:83:ARG:NH1	2.12	0.82
1:A:1053:G:N7	1:A:1200:C:H5"	1.95	0.82
1:A:1285:A:OP1	1:A:1285:A:C8	2.33	0.82
1:A:1179:A:O3'	10:I:103:THR:HG23	1.80	0.82
10:I:125:TYR:HD2	10:I:125:TYR:N	1.76	0.82
11:J:62:HIS:HB3	15:N:59:ALA:HB3	1.61	0.82
1:A:1091:U:O2	1:A:1093:A:C8	2.32	0.82
13:L:86:ARG:HH22	13:L:99:HIS:CD2	1.97	0.82
1:A:35:G:H2'	1:A:36:C:C6	2.15	0.82
6:E:80:ILE:CD1	6:E:91:LEU:CB	2.53	0.81
1:A:480:U:H2'	1:A:481:G:OP2	1.81	0.81
1:A:1298:C:H4'	1:A:1299:A:O4'	1.79	0.81
1:A:965:A:H4'	1:A:966:G:O5'	1.81	0.81
1:A:496:A:H4'	1:A:497:A:OP1	1.80	0.81
1:A:21:G:H2'	1:A:22:G:C8	2.16	0.81
1:A:1226:C:H2'	14:M:103:THR:OG1	1.80	0.81
1:A:1270:C:HO2'	1:A:1313:U:HO2'	1.22	0.81
6:E:30:ALA:O	6:E:45:PHE:HD1	1.62	0.81
6:E:107:ARG:HG2	6:E:111:GLU:HG3	1.61	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:111:ARG:HH12	8:G:122:HIS:HB3	1.45	0.81
4:C:129:ALA:HB3	4:C:132:ARG:HB2	1.61	0.81
14:M:78:ILE:CG2	14:M:79:LYS:N	2.43	0.81
1:A:1255:G:H2'	1:A:1279:A:N6	1.96	0.81
1:A:1403:C:O2	1:A:1403:C:H2'	1.79	0.81
13:L:28:LYS:C	13:L:30:ALA:H	1.84	0.81
1:A:337:C:H2'	1:A:338:A:H8	1.46	0.81
1:A:850:U:H3'	1:A:850:U:H6	1.46	0.80
1:A:129(A):G:O2'	1:A:190(E):U:H2'	1.81	0.80
1:A:254:G:H2'	1:A:255:G:H8	1.44	0.80
3:B:98:LEU:O	3:B:100:GLY:N	2.15	0.80
5:D:13:ARG:HD3	5:D:38:TYR:O	1.81	0.80
15:N:53:LEU:HD12	15:N:56:VAL:HG21	1.63	0.80
4:C:52:LEU:N	4:C:52:LEU:HD23	1.96	0.80
19:R:66:LEU:O	19:R:69:THR:N	2.14	0.80
1:A:1361(A):C:H2'	1:A:1362:C:H5"	1.62	0.80
3:B:25:ASN:HD22	3:B:25:ASN:C	1.84	0.80
3:B:111:ARG:HB3	3:B:149:LEU:HD11	1.62	0.80
6:E:116:THR:HG23	6:E:117:ASP:OD2	1.81	0.80
13:L:98:TYR:N	13:L:98:TYR:HD1	1.78	0.80
1:A:579:G:H5'	1:A:728:A:H1'	1.62	0.80
1:A:1111:A:N1	4:C:177:THR:OG1	2.14	0.80
4:C:118:GLN:O	4:C:121:ALA:HB3	1.82	0.80
13:L:87:GLY:H	13:L:98:TYR:HB3	1.46	0.80
8:G:56:GLN:HE21	8:G:56:GLN:H	1.29	0.80
1:A:37:U:O2'	1:A:500:G:H4'	1.81	0.79
1:A:93:G:C3'	1:A:95:U:P	2.69	0.79
1:A:262:A:C6	1:A:263:A:C6	2.70	0.79
1:A:384:G:H2'	1:A:385:C:C6	2.18	0.79
11:J:61:GLU:OE1	15:N:45:ARG:HD2	1.82	0.79
13:L:45:PRO:HG3	13:L:53:ARG:HD2	1.63	0.79
14:M:78:ILE:O	14:M:81:LEU:HD23	1.81	0.79
1:A:838:G:C2'	1:A:839:U:H5"	2.12	0.79
1:A:1255:G:H2'	1:A:1279:A:H62	1.47	0.79
7:F:9:VAL:HG23	7:F:87:ARG:HB2	1.63	0.79
1:A:653:A:OP1	9:H:56:LYS:HE2	1.83	0.79
4:C:52:LEU:HD23	4:C:52:LEU:H	1.44	0.79
1:A:954:G:H21	1:A:1227:A:N6	1.79	0.79
5:D:8:VAL:C	5:D:10:ARG:H	1.82	0.79
1:A:378:G:C2	1:A:386:C:O2	2.35	0.79
1:A:707:C:H4'	12:K:20:TYR:CE2	2.17	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:162:ILE:O	3:B:185:ILE:CD1	2.28	0.79
1:A:1314:C:N4	20:S:4:SER:OG	2.15	0.79
4:C:8:ILE:CG2	4:C:9:GLY:N	2.46	0.79
4:C:131:ARG:HG3	4:C:135:LYS:CE	2.11	0.79
1:A:1201:A:H4'	1:A:1202:G:O5'	1.83	0.79
21:T:74:LYS:HG3	21:T:75:ASN:H	1.48	0.79
1:A:436:C:H2'	1:A:437:U:C6	2.17	0.79
1:A:379:C:O2'	1:A:380:G:H5'	1.82	0.78
1:A:658:G:C2	1:A:749:C:N3	2.51	0.78
1:A:1360:A:H2'	1:A:1361:G:O4'	1.81	0.78
3:B:92:TYR:CD1	3:B:151:GLY:HA3	2.18	0.78
16:O:3:ILE:HG21	16:O:34:LEU:HD11	1.63	0.78
18:Q:90:ILE:C	18:Q:92:ARG:H	1.86	0.78
1:A:450:G:OP1	17:P:43:LYS:NZ	2.17	0.78
1:A:946:A:H2'	1:A:947:G:C8	2.18	0.78
1:A:1060:C:C5	4:C:2:GLY:HA2	2.18	0.78
1:A:1131:G:H22	1:A:1143:G:H21	1.30	0.78
1:A:1435:G:H2'	1:A:1436:U:H6	1.44	0.78
7:F:80:ARG:CG	7:F:88:VAL:HG21	2.13	0.78
9:H:112:LEU:N	9:H:112:LEU:CD2	2.45	0.78
1:A:463:A:C3'	1:A:474:G:OP2	2.30	0.78
5:D:162:LEU:HD21	5:D:178:VAL:HG12	1.63	0.78
6:E:80:ILE:CG2	9:H:104:ARG:HH22	1.96	0.78
11:J:63:PHE:HE1	15:N:45:ARG:HG3	1.49	0.78
1:A:263:A:O2'	1:A:264:U:H5'	1.83	0.78
1:A:422:C:O2	1:A:423:G:N2	2.16	0.78
1:A:1103:C:H5'	3:B:98:LEU:HD23	1.64	0.78
1:A:706:A:H5"	1:A:707:C:OP2	1.84	0.78
1:A:1235:U:C6	1:A:1235:U:H3'	2.19	0.78
5:D:128:VAL:HG12	5:D:129:ASN:ND2	1.98	0.78
6:E:137:GLU:O	6:E:141:GLN:HG3	1.84	0.78
1:A:106:C:H2'	1:A:107:G:H8	1.49	0.78
1:A:199:G:H2'	1:A:200:G:H5'	1.66	0.78
6:E:98:THR:HB	6:E:117:ASP:HB3	1.66	0.78
8:G:69:VAL:HG21	8:G:104:LEU:HD21	1.64	0.78
11:J:63:PHE:CE1	15:N:45:ARG:HG3	2.17	0.78
13:L:47:LYS:HB3	13:L:48:PRO:HD3	1.65	0.78
1:A:676:A:H2'	1:A:677:U:C6	2.19	0.78
1:A:736:C:OP1	19:R:68:LYS:HE2	1.83	0.78
1:A:1285:A:OP1	1:A:1285:A:H8	1.66	0.78
3:B:180:LEU:O	3:B:181:PHE:HB2	1.83	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:219:VAL:HA	3:B:222:ILE:HD12	1.66	0.78
4:C:166:GLU:HA	4:C:166:GLU:OE2	1.83	0.78
11:J:49:VAL:O	11:J:60:ARG:O	2.02	0.78
13:L:97:ARG:HB2	13:L:98:TYR:HE1	1.47	0.78
1:A:409:G:H2'	1:A:410:G:C8	2.19	0.78
1:A:818:G:C3'	1:A:819:A:H5'	2.14	0.78
13:L:55:VAL:HG12	13:L:56:ALA:N	1.97	0.78
1:A:252:U:H2'	1:A:253:U:C6	2.19	0.78
5:D:62:GLN:HE22	5:D:65:ARG:HH12	1.19	0.78
1:A:783:C:H2'	1:A:784:C:H5'	1.66	0.77
1:A:854:G:H3'	1:A:871:U:O4	1.82	0.77
12:K:30:VAL:HG21	12:K:65:ALA:HA	1.66	0.77
13:L:81:SER:O	13:L:106:ASP:CB	2.32	0.77
1:A:10:A:OP2	6:E:126:ARG:HG3	1.82	0.77
11:J:48:THR:HG22	11:J:62:HIS:NE2	1.99	0.77
11:J:76:ASN:HB3	11:J:78:ASN:ND2	1.98	0.77
1:A:826:C:H2'	1:A:827:U:H6	1.50	0.77
6:E:15:ARG:HH11	6:E:15:ARG:CG	1.97	0.77
1:A:622:A:N7	1:A:623:C:C5	2.53	0.77
1:A:850:U:H3'	1:A:850:U:C6	2.18	0.77
19:R:78:LEU:N	19:R:78:LEU:CD1	2.47	0.77
1:A:190(L):U:O2	21:T:105:SER:HB2	1.82	0.77
1:A:1455:G:HO3'	1:A:1459:C:P	2.07	0.77
3:B:187:LEU:HD23	3:B:201:ILE:CG2	2.14	0.77
1:A:949:A:C2	1:A:1233:G:N3	2.53	0.77
13:L:86:ARG:HG2	13:L:86:ARG:NH1	1.95	0.77
14:M:90:LEU:HD23	14:M:93:ARG:NH1	1.99	0.77
1:A:1454:G:O2'	1:A:1455:G:H5'	1.85	0.77
3:B:26:PRO:O	3:B:29:ALA:CB	2.32	0.77
21:T:86:ARG:HH11	21:T:86:ARG:CG	1.96	0.77
1:A:1523:G:H2'	1:A:1524:C:H6	1.50	0.77
4:C:187:ALA:O	4:C:198:VAL:HG23	1.84	0.77
1:A:447:G:H2'	1:A:485:G:N2	2.00	0.77
19:R:78:LEU:HD12	19:R:78:LEU:H	1.49	0.77
1:A:942:G:N3	1:A:943:U:C6	2.52	0.76
10:I:128:ARG:O	10:I:128:ARG:HG2	1.83	0.76
1:A:362:G:N2	1:A:365:U:OP2	2.17	0.76
1:A:437:U:HO2'	5:D:125:HIS:HE2	0.78	0.76
3:B:118:LEU:HB3	3:B:142:LEU:CD1	2.15	0.76
4:C:33:LEU:HD11	15:N:53:LEU:HB3	1.67	0.76
5:D:64:LEU:HD23	5:D:198:VAL:HG11	1.65	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:438:G:H4'	1:A:439:A:OP1	1.85	0.76
5:D:83:SER:HA	5:D:89:THR:HG23	1.68	0.76
1:A:1112:C:O2	4:C:179:ARG:HB2	1.86	0.76
4:C:155:GLY:HA3	4:C:196:LEU:HB3	1.67	0.76
20:S:72:GLY:C	20:S:74:PHE:H	1.88	0.76
4:C:178:LEU:O	4:C:179:ARG:HB2	1.86	0.76
6:E:72:GLN:O	6:E:73:ASN:HB3	1.86	0.76
1:A:401:C:C6	1:A:401:C:H3'	2.21	0.76
5:D:128:VAL:HG12	5:D:129:ASN:HD22	1.49	0.76
1:A:1511:G:H2'	1:A:1512:U:O4'	1.85	0.76
6:E:144:THR:H	6:E:147:ASP:HB2	1.50	0.76
1:A:1063:C:H3'	1:A:1064:G:H2'	1.68	0.75
5:D:61:LYS:HE2	5:D:62:GLN:HE21	1.49	0.75
1:A:942:G:C4	1:A:943:U:C5	2.74	0.75
5:D:83:SER:HA	5:D:89:THR:CG2	2.15	0.75
6:E:36:ASP:OD1	6:E:37:ARG:N	2.19	0.75
5:D:11:LEU:C	5:D:13:ARG:N	2.38	0.75
13:L:31:PRO:HB2	13:L:32:PHE:CD2	2.22	0.75
14:M:113:PRO:O	14:M:115:LYS:NZ	2.18	0.75
1:A:254:G:H2'	1:A:255:G:C8	2.21	0.75
1:A:1281:U:H5'	1:A:1282:C:H5	1.51	0.75
7:F:100:ASN:O	19:R:28:GLU:HB3	1.87	0.75
17:P:57:ARG:HG3	17:P:57:ARG:NH1	1.98	0.75
1:A:1443:G:H4'	1:A:1446:A:P	2.26	0.75
10:I:125:TYR:N	10:I:125:TYR:CD2	2.49	0.75
5:D:67:ILE:HG22	5:D:68:TYR:CD1	2.21	0.75
6:E:74:GLY:HA3	6:E:116:THR:HG22	1.67	0.75
18:Q:66:SER:O	18:Q:70:ARG:NH1	2.20	0.75
5:D:63:LYS:CD	5:D:198:VAL:HG23	2.17	0.75
16:O:46:HIS:C	16:O:48:LYS:H	1.90	0.75
1:A:359:U:H2'	1:A:360:A:C8	2.21	0.75
4:C:10:PHE:CE2	4:C:178:LEU:HD13	2.22	0.75
6:E:80:ILE:HG22	9:H:104:ARG:HH22	1.50	0.75
9:H:59:LEU:O	9:H:61:VAL:HG23	1.87	0.75
4:C:191:THR:HG22	4:C:192:THR:H	1.52	0.75
9:H:112:LEU:N	9:H:112:LEU:HD23	2.01	0.75
15:N:26:ARG:HH22	15:N:47:LEU:HD21	1.50	0.75
1:A:1221:G:O4'	20:S:54:GLY:HA3	1.87	0.74
7:F:76:ALA:O	7:F:78:GLU:N	2.20	0.74
13:L:75:HIS:HD2	13:L:77:LEU:H	1.33	0.74
15:N:36:PHE:O	15:N:36:PHE:CD1	2.40	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:540:G:H2'	1:A:541:G:O4'	1.87	0.74
1:A:948:C:H42	1:A:1233:G:H1	1.33	0.74
1:A:987:G:H1	1:A:1218:C:H42	1.35	0.74
3:B:225:ALA:O	3:B:226:ARG:HB2	1.86	0.74
4:C:129:ALA:HB3	4:C:132:ARG:CB	2.16	0.74
5:D:5:ILE:HG22	5:D:5:ILE:O	1.86	0.74
9:H:112:LEU:HD23	9:H:112:LEU:H	1.51	0.74
1:A:767:A:H2'	1:A:768:A:C8	2.21	0.74
1:A:959:A:H3'	1:A:960:U:H5"	1.69	0.74
5:D:41:GLY:O	5:D:43:HIS:N	2.19	0.74
14:M:81:LEU:H	14:M:81:LEU:HD22	1.51	0.74
5:D:21:LEU:HD11	5:D:26:CYS:SG	2.28	0.74
6:E:33:VAL:HA	6:E:42:GLY:O	1.87	0.74
1:A:1240:U:H4'	8:G:38:LEU:HD11	1.68	0.74
1:A:1499:A:C2'	1:A:1500:A:H5'	2.18	0.74
1:A:1116:C:H2'	1:A:1117:G:H5"	1.69	0.74
1:A:1124:G:O2'	1:A:1145:C:N4	2.21	0.74
15:N:23:ARG:HD3	15:N:29:ARG:O	1.88	0.74
1:A:1112:C:O2	4:C:179:ARG:CB	2.35	0.74
19:R:76:LEU:HB2	19:R:78:LEU:HD11	1.70	0.74
1:A:707:C:H5"	12:K:20:TYR:CD2	2.23	0.74
1:A:1526:G:C2'	1:A:1527:C:H5'	2.17	0.74
4:C:107:GLN:O	4:C:108:ASN:HB3	1.86	0.74
5:D:150:GLU:HA	5:D:153:ARG:HB2	1.70	0.74
1:A:376:G:H2'	1:A:377:G:C8	2.22	0.73
1:A:570:G:N3	1:A:571:U:C5	2.56	0.73
4:C:29:TYR:OH	15:N:54:PRO:HD2	1.86	0.73
9:H:73:ASP:OD2	9:H:75:ARG:NE	2.20	0.73
1:A:976:G:H4'	1:A:977:A:OP1	1.86	0.73
3:B:178:ARG:HH22	9:H:68:ARG:NH2	1.85	0.73
15:N:41:ARG:HG3	15:N:42:ILE:H	1.53	0.73
1:A:959:A:C2	1:A:1222:G:O4'	2.40	0.73
6:E:15:ARG:HH11	6:E:15:ARG:HG2	1.52	0.73
13:L:86:ARG:NH2	13:L:99:HIS:CD2	2.56	0.73
1:A:335:C:H2'	1:A:336:C:C6	2.23	0.73
6:E:34:VAL:HG23	6:E:42:GLY:HA3	1.68	0.73
9:H:111:ILE:HG22	9:H:134:ILE:HB	1.70	0.73
1:A:1276:G:O5'	1:A:1276:G:H8	1.71	0.73
1:A:1296:C:H4'	1:A:1302:U:H5	1.51	0.73
5:D:21:LEU:HD12	5:D:22:LYS:H	1.53	0.73
1:A:35:G:H2'	1:A:36:C:H6	1.52	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:515:G:C5	1:A:516:U:C5	2.77	0.73
1:A:564:C:O2	1:A:564:C:H2'	1.88	0.73
1:A:833:U:O2	1:A:854:G:C2	2.42	0.73
10:I:128:ARG:O	10:I:128:ARG:CG	2.36	0.73
17:P:21:VAL:HG21	17:P:59:TRP:CD1	2.24	0.73
1:A:97:G:H5"	1:A:98:U:OP2	1.89	0.73
1:A:481:G:O2'	1:A:483:C:N4	2.21	0.73
1:A:731:G:OP1	1:A:766:A:H1'	1.89	0.73
4:C:195:VAL:O	4:C:196:LEU:HD23	1.87	0.73
5:D:25:ARG:C	5:D:27:TYR:H	1.92	0.73
16:O:78:TYR:CE1	16:O:82:ILE:HD11	2.24	0.73
1:A:503:C:C2'	1:A:504:C:H5'	2.18	0.73
4:C:150:LYS:HG2	4:C:151:VAL:N	2.04	0.73
6:E:81:GLU:HG3	6:E:90:VAL:HG13	1.69	0.73
1:A:622:A:C8	1:A:623:C:C6	2.77	0.73
1:A:1305:G:H2'	1:A:1331:G:N2	2.03	0.73
1:A:1343:G:H4'	10:I:122:ALA:HB3	1.71	0.73
3:B:55:PHE:HA	3:B:58:ILE:HG13	1.71	0.73
5:D:79:PHE:O	5:D:82:ALA:N	2.22	0.73
1:A:401:C:H3'	1:A:401:C:H6	1.54	0.73
1:A:839:U:O2	1:A:839:U:H2'	1.87	0.72
1:A:84:U:H3'	1:A:88:A:P	2.29	0.72
15:N:40:CYS:C	15:N:43:CYS:HB2	2.08	0.72
17:P:67:THR:CG2	17:P:68:ASP:H	2.00	0.72
1:A:854:G:C2	1:A:855:G:C8	2.77	0.72
4:C:91:LEU:HD11	4:C:99:VAL:HG22	1.70	0.72
21:T:64:ASP:O	21:T:67:ALA:HB3	1.89	0.72
1:A:377:G:C2	1:A:387:U:O2	2.43	0.72
1:A:1228:C:OP1	14:M:115:LYS:HG2	1.89	0.72
4:C:6:HIS:HD2	4:C:8:ILE:H	1.37	0.72
11:J:15:THR:O	11:J:19:SER:HB3	1.89	0.72
14:M:49:THR:HG22	14:M:51:ALA:H	1.53	0.72
15:N:41:ARG:HG3	15:N:42:ILE:N	2.04	0.72
1:A:509:A:C8	1:A:509:A:H3'	2.24	0.72
1:A:794:A:H2'	1:A:795:C:H6	1.55	0.72
17:P:5:ARG:HG2	17:P:6:LEU:N	2.04	0.72
17:P:50:LYS:C	17:P:51:VAL:HG22	2.09	0.72
20:S:71:LEU:HD22	20:S:72:GLY:H	1.55	0.72
1:A:266:G:C5'	1:A:266:G:C8	2.72	0.72
1:A:794:A:H2'	1:A:795:C:C6	2.25	0.72
4:C:55:VAL:O	4:C:55:VAL:HG12	1.88	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:119:LEU:HB3	9:H:123:GLU:HB3	1.70	0.72
1:A:157:G:C2	1:A:158:G:C8	2.77	0.72
1:A:356:A:H2'	1:A:357:G:H5'	1.71	0.72
1:A:458:C:C2	1:A:459:G:C8	2.78	0.72
11:J:76:ASN:HB3	11:J:78:ASN:HD21	1.54	0.72
14:M:96:LEU:HB3	14:M:97:PRO:CD	2.17	0.72
15:N:37:PHE:HE2	15:N:53:LEU:HD13	1.55	0.72
5:D:26:CYS:HA	5:D:31:CYS:CB	2.16	0.72
6:E:139:LEU:O	6:E:141:GLN:N	2.21	0.72
6:E:152:ARG:O	9:H:64:LYS:NZ	2.23	0.72
1:A:353:A:H8	1:A:353:A:H5"	1.55	0.71
1:A:1346:A:C8	1:A:1348:U:C2	2.78	0.71
3:B:187:LEU:HD23	3:B:201:ILE:HG22	1.72	0.71
1:A:99:C:H2'	1:A:101:A:C8	2.26	0.71
1:A:602:A:C2	1:A:637:G:C2	2.78	0.71
3:B:208:ILE:HA	3:B:211:ILE:HD12	1.72	0.71
19:R:59:SER:HB3	19:R:62:GLU:OE1	1.90	0.71
1:A:625:G:H2'	1:A:626:U:C6	2.25	0.71
6:E:27:ARG:HG3	6:E:28:PHE:N	2.04	0.71
1:A:185:A:H5"	1:A:186:C:OP2	1.90	0.71
1:A:350:G:C5'	1:A:350:G:C8	2.71	0.71
1:A:639:G:C2'	1:A:640:A:H5'	2.21	0.71
1:A:1064:G:H5'	1:A:1066:C:O4'	1.91	0.71
1:A:526:C:OP2	13:L:91:LYS:NZ	2.17	0.71
1:A:1113:C:H42	1:A:1187:G:H1	1.36	0.71
1:A:1264:C:H2'	1:A:1265:G:H8	1.54	0.71
1:A:1286:A:C8	1:A:1287:A:H4'	2.25	0.71
10:I:9:ARG:HG3	10:I:14:VAL:HG12	1.70	0.71
18:Q:95:TYR:O	18:Q:97:SER:N	2.24	0.71
1:A:90:U:H3'	1:A:90:U:C6	2.26	0.71
1:A:977:A:O2'	1:A:978:A:H5"	1.89	0.71
1:A:1234:C:C2'	1:A:1235:U:H5'	2.20	0.71
1:A:1314:C:OP2	20:S:6:LYS:CG	2.34	0.71
1:A:5:U:O2	1:A:5:U:H2'	1.90	0.71
1:A:882:C:O2'	1:A:883:C:H5'	1.90	0.71
1:A:922:G:N3	1:A:1396:A:C2	2.58	0.71
1:A:1361:G:C2'	1:A:1361(A):C:H5'	2.21	0.71
10:I:43:ALA:O	10:I:45:ALA:N	2.23	0.71
11:J:5:ARG:HA	11:J:73:ASP:OD1	1.91	0.71
1:A:480:U:C2'	1:A:481:G:OP2	2.37	0.71
6:E:142:LEU:O	6:E:143:ARG:HG2	1.91	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:102:ARG:NH1	13:L:110:VAL:HA	2.04	0.71
19:R:33:ASP:O	19:R:35:ARG:N	2.22	0.71
1:A:707:C:C5'	12:K:20:TYR:HD2	2.04	0.71
1:A:931:C:O2	1:A:1386:G:N2	2.18	0.71
1:A:1235:U:H2'	1:A:1236:A:O5'	1.90	0.71
7:F:62:TRP:C	7:F:63:TYR:HD2	1.94	0.71
1:A:734:G:H2'	1:A:735:C:C6	2.26	0.71
1:A:922:G:N2	1:A:1396:A:C4	2.59	0.71
15:N:12:ARG:O	15:N:14:PRO:HD3	1.90	0.71
7:F:50:TYR:HE1	19:R:77:GLY:HA2	1.56	0.70
18:Q:4:LYS:H	18:Q:61:GLU:HB2	1.56	0.70
20:S:72:GLY:O	20:S:74:PHE:N	2.24	0.70
21:T:49:ALA:O	21:T:53:LEU:HD12	1.90	0.70
1:A:18:C:O2'	1:A:19:C:H5'	1.91	0.70
1:A:872:A:O2'	1:A:873:A:H3'	1.91	0.70
1:A:1454:G:C2'	1:A:1455:G:H5'	2.20	0.70
21:T:75:ASN:O	21:T:78:ALA:N	2.24	0.70
1:A:1364:U:O2'	1:A:1365:G:C5'	2.38	0.70
14:M:34:LEU:CD1	14:M:41:PRO:HA	2.18	0.70
1:A:111:G:H5"	1:A:112:G:OP2	1.91	0.70
1:A:247:G:O6	1:A:278:G:C6	2.44	0.70
1:A:1009:G:N3	1:A:1009:G:H2'	2.07	0.70
11:J:16:LEU:HD22	11:J:94:VAL:HG13	1.74	0.70
1:A:1126:U:C2	1:A:1127:G:N7	2.60	0.70
1:A:1379:G:O6	8:G:2:ALA:HB3	1.91	0.70
15:N:21:TYR:HE2	15:N:23:ARG:NE	1.90	0.70
4:C:180:ALA:HB1	4:C:182:ILE:CD1	2.22	0.70
13:L:43:VAL:HG13	13:L:44:THR:H	1.57	0.70
14:M:49:THR:CB	14:M:52:GLU:HG3	2.16	0.70
20:S:53:ASN:HB2	20:S:56:GLN:H	1.55	0.70
1:A:266:G:C8	1:A:266:G:H5"	2.27	0.70
3:B:12:GLU:OE1	3:B:12:GLU:HA	1.89	0.70
7:F:62:TRP:O	7:F:63:TYR:HD2	1.75	0.70
14:M:5:ALA:HB3	14:M:8:GLU:HB2	1.72	0.70
1:A:88:A:H2'	1:A:89:C:O4'	1.91	0.70
1:A:90:U:H3'	1:A:90:U:H6	1.56	0.70
1:A:358:U:H2'	1:A:359:U:C6	2.27	0.70
1:A:1064:G:H4'	1:A:1065:U:H5'	1.73	0.70
1:A:1102:A:H2'	1:A:1103:C:C6	2.26	0.70
1:A:1258:G:OP2	1:A:1258:G:H8	1.74	0.70
11:J:16:LEU:HD12	11:J:70:ARG:HG3	1.74	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:492:G:O3'	1:A:494:G:P	2.50	0.70
1:A:781:A:C5	1:A:802:A:C2	2.79	0.70
1:A:1264:C:H2'	1:A:1265:G:C8	2.27	0.70
15:N:24:CYS:HB3	15:N:28:GLY:N	2.07	0.70
1:A:518:C:H5"	1:A:519:C:H6	1.55	0.69
1:A:1126:U:OP2	1:A:1281:U:O2	2.10	0.69
1:A:1281:U:H5'	1:A:1282:C:C5	2.27	0.69
5:D:11:LEU:C	5:D:13:ARG:H	1.96	0.69
1:A:437:U:O2'	5:D:125:HIS:NE2	2.08	0.69
1:A:568:G:H2'	1:A:569:C:H5'	1.73	0.69
1:A:976:G:C4'	1:A:977:A:OP1	2.40	0.69
9:H:10:LEU:HB3	9:H:83:ILE:HD11	1.74	0.69
1:A:657:G:H2'	1:A:658:G:H8	1.57	0.69
4:C:39:ILE:O	4:C:43:LEU:HB2	1.92	0.69
8:G:116:ALA:O	8:G:120:ILE:HD13	1.92	0.69
1:A:451:A:O5'	1:A:451:A:H8	1.75	0.69
1:A:838:G:H1	1:A:848:C:H42	1.41	0.69
1:A:914:A:C2	1:A:915:A:C4	2.81	0.69
1:A:1139:G:H4'	1:A:1140:C:H5"	1.73	0.69
4:C:6:HIS:CD2	4:C:8:ILE:H	2.10	0.69
10:I:111:ARG:HH11	10:I:111:ARG:CG	2.06	0.69
20:S:78:ARG:H	20:S:78:ARG:HD2	1.57	0.69
9:H:30:ARG:HG2	9:H:30:ARG:HH11	1.56	0.69
1:A:63:C:H5'	1:A:64:G:OP2	1.93	0.69
1:A:674:G:H2'	1:A:675:A:H8	1.58	0.69
1:A:880:C:H2'	1:A:881:G:H8	1.56	0.69
1:A:1158:C:C5	1:A:1160:G:H1'	2.27	0.69
3:B:182:ILE:HG23	3:B:183:PRO:HD2	1.75	0.69
5:D:204:ILE:HG22	5:D:205:GLU:N	2.07	0.69
8:G:91:VAL:HG12	8:G:96:GLN:NE2	2.08	0.69
17:P:74:LEU:O	17:P:79:VAL:HG23	1.91	0.69
3:B:9:GLU:HG3	3:B:217:ARG:HH12	1.55	0.69
5:D:149:ALA:O	5:D:151:LYS:N	2.25	0.69
11:J:38:ILE:HB	11:J:71:LEU:HB3	1.73	0.69
13:L:27:LEU:C	13:L:29:GLY:H	1.91	0.69
17:P:74:LEU:HD13	17:P:79:VAL:HG11	1.75	0.69
18:Q:40:LYS:HD3	18:Q:42:TYR:CZ	2.28	0.69
1:A:501:C:H2'	1:A:502:G:H8	1.56	0.69
1:A:1040:U:H2'	1:A:1041:A:C8	2.28	0.69
1:A:1157:A:H4'	1:A:1158:C:O5'	1.93	0.69
3:B:88:ALA:O	3:B:90:MET:N	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:102:LEU:N	3:B:102:LEU:CD1	2.55	0.69
4:C:35:GLU:HG2	4:C:59:ARG:HH12	1.58	0.69
13:L:32:PHE:HB3	13:L:85:ILE:O	1.93	0.69
18:Q:75:ARG:HH12	18:Q:77:VAL:HG13	1.56	0.69
1:A:149:A:C2	1:A:150:C:C2	2.80	0.69
1:A:736:C:H2'	1:A:737:A:C8	2.28	0.69
1:A:1226:C:H4'	1:A:1227:A:OP1	1.91	0.69
10:I:113:LYS:N	10:I:113:LYS:HD2	2.08	0.69
1:A:200:G:C5'	1:A:200:G:H8	2.06	0.69
1:A:680:C:H42	1:A:710:G:H1	1.40	0.69
4:C:180:ALA:HB1	4:C:182:ILE:HD11	1.75	0.69
1:A:45:U:H3	1:A:396:G:H1	1.41	0.68
8:G:67:GLU:HG3	8:G:67:GLU:O	1.92	0.68
20:S:83:HIS:N	20:S:83:HIS:CD2	2.61	0.68
1:A:250:A:H4'	1:A:251:G:O5'	1.93	0.68
1:A:1502:A:H2	1:A:1505:G:N1	1.89	0.68
11:J:46:ARG:HG2	11:J:46:ARG:NH1	2.08	0.68
12:K:24:SER:C	12:K:26:ASN:H	1.97	0.68
1:A:337:C:H2'	1:A:338:A:C8	2.28	0.68
1:A:1152:A:C4'	11:J:13:HIS:HD2	2.06	0.68
1:A:1227:A:H2'	1:A:1228:C:O5'	1.92	0.68
1:A:1347:G:H3'	10:I:108:VAL:O	1.94	0.68
1:A:1508:G:H2'	1:A:1509:C:C6	2.28	0.68
3:B:101:MET:HG2	3:B:108:ILE:HD12	1.74	0.68
5:D:64:LEU:HD21	5:D:94:LEU:HD21	1.75	0.68
6:E:71:LEU:HD21	6:E:115:VAL:HG22	1.75	0.68
8:G:155:ARG:O	8:G:156:TRP:HB2	1.92	0.68
1:A:463:A:H3'	1:A:474:G:OP2	1.93	0.68
1:A:502:G:H2'	1:A:503:C:C6	2.28	0.68
1:A:979:C:H5	1:A:980:C:C5	2.11	0.68
1:A:1231:G:H2'	1:A:1232:U:C6	2.27	0.68
4:C:5:ILE:HD13	4:C:10:PHE:CB	2.15	0.68
6:E:18:ARG:NH2	6:E:25:ARG:HG2	2.08	0.68
21:T:65:LYS:O	21:T:68:LYS:HB2	1.93	0.68
1:A:1154:G:H2'	1:A:1155:G:C8	2.27	0.68
16:O:78:TYR:CZ	16:O:82:ILE:HD11	2.28	0.68
1:A:1350:A:C6	1:A:1351:U:N3	2.62	0.68
5:D:23:GLY:O	5:D:27:TYR:HB2	1.94	0.68
13:L:102:ARG:NH2	13:L:108:ALA:O	2.27	0.68
1:A:116:A:H2'	1:A:117:G:C8	2.29	0.68
1:A:491:G:C4	1:A:492:G:C8	2.82	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:536:C:H2'	1:A:537:G:H8	1.57	0.68
1:A:1138:G:N2	1:A:1140:C:O2	2.26	0.68
1:A:1235:U:H3'	1:A:1235:U:H6	1.57	0.68
16:O:26:GLU:OE1	16:O:77:ARG:HD2	1.93	0.68
21:T:79:ARG:HE	21:T:83:ARG:HH22	1.39	0.68
1:A:706:A:H1'	12:K:29:ILE:HD11	1.75	0.68
1:A:1066:C:H2'	1:A:1067:A:H5'	1.75	0.68
1:A:1526:G:O2'	1:A:1527:C:H5'	1.94	0.68
3:B:84:GLU:HG3	3:B:219:VAL:CG2	2.24	0.68
5:D:64:LEU:HD11	5:D:97:LEU:HD13	1.74	0.68
1:A:960:U:H1'	1:A:1223:C:H5'	1.76	0.68
1:A:1010:G:H2'	1:A:1011:G:C8	2.29	0.68
1:A:1314:C:N3	1:A:1315:U:C5	2.62	0.68
7:F:50:TYR:HE1	19:R:77:GLY:CA	2.07	0.68
15:N:21:TYR:HE2	15:N:23:ARG:HE	1.41	0.68
1:A:575:G:OP1	1:A:575:G:H4'	1.94	0.68
1:A:657:G:H4'	16:O:28:GLN:HG2	1.76	0.68
10:I:95:LYS:O	10:I:96:LEU:HD12	1.93	0.68
8:G:23:VAL:O	8:G:27:ILE:HG13	1.93	0.67
10:I:114:TYR:CE1	11:J:59:SER:O	2.47	0.67
1:A:1048:G:H5"	15:N:3:ARG:HG3	1.74	0.67
1:A:1197:G:H5"	24:A:1636:D2C:O5	1.92	0.67
1:A:1288:A:C5	1:A:1289:A:N7	2.62	0.67
8:G:26:PHE:O	8:G:30:ILE:HD12	1.95	0.67
1:A:1015:A:H2'	1:A:1016:A:C8	2.29	0.67
1:A:1342:C:O3'	10:I:125:TYR:HE2	1.75	0.67
1:A:1377:A:H3'	1:A:1377:A:C8	2.28	0.67
1:A:376:G:N3	1:A:389:A:C2	2.62	0.67
6:E:72:GLN:O	6:E:73:ASN:CB	2.42	0.67
6:E:74:GLY:CA	6:E:116:THR:HG22	2.24	0.67
14:M:30:ALA:O	14:M:33:ALA:N	2.27	0.67
1:A:439:A:N6	1:A:497:A:H1'	2.08	0.67
1:A:767:A:H2'	1:A:768:A:H8	1.58	0.67
1:A:914:A:N1	1:A:915:A:C4	2.62	0.67
5:D:15:GLU:HG2	5:D:63:LYS:HG3	1.77	0.67
19:R:50:ILE:HG12	19:R:70:ILE:HD13	1.76	0.67
1:A:95:U:H2'	1:A:96:G:C8	2.30	0.67
1:A:1055:A:C8	1:A:1206:G:N2	2.63	0.67
6:E:80:ILE:HD13	6:E:91:LEU:HB2	1.71	0.67
11:J:12:ASP:HB3	11:J:15:THR:CG2	2.24	0.67
12:K:54:ARG:O	12:K:57:THR:HG22	1.94	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:R:78:LEU:CD1	19:R:78:LEU:H	2.07	0.67
1:A:976:G:H8	1:A:1358:U:HO2'	1.42	0.67
1:A:1130:A:OP2	1:A:1131:G:OP2	2.13	0.67
19:R:67:ALA:O	19:R:71:LYS:HG3	1.94	0.67
1:A:1229:A:C2	1:A:1230:C:C5	2.83	0.67
1:A:1455:G:H3'	1:A:1459:C:OP2	1.95	0.67
5:D:9:CYS:HA	5:D:12:CYS:HB2	1.77	0.67
8:G:15:ASP:OD2	8:G:44:TYR:OH	2.13	0.67
10:I:50:LEU:HB3	10:I:55:ALA:HB3	1.76	0.67
15:N:24:CYS:HB3	15:N:28:GLY:CA	2.25	0.67
1:A:418:C:O2	1:A:425:G:N2	2.23	0.67
1:A:1228:C:H6	1:A:1228:C:H5"	1.58	0.67
1:A:1285:A:H4'	1:A:1286:A:O5'	1.95	0.67
3:B:42:ILE:HD12	3:B:203:GLY:HA2	1.77	0.67
10:I:8:GLY:CA	10:I:79:LEU:HB3	2.23	0.67
10:I:71:SER:HA	10:I:74:ILE:HD12	1.76	0.67
21:T:56:MET:HE3	21:T:104:LEU:HD21	1.75	0.67
21:T:73:HIS:O	21:T:74:LYS:CG	2.40	0.67
1:A:639:G:H2'	1:A:640:A:H5'	1.76	0.67
1:A:707:C:H2'	1:A:708:C:C6	2.30	0.67
1:A:707:C:O3'	12:K:20:TYR:HE2	1.78	0.67
1:A:1525:G:C8	1:A:1525:G:H3'	2.29	0.67
4:C:66:VAL:O	4:C:68:VAL:N	2.28	0.67
19:R:55:ARG:HB3	19:R:55:ARG:CZ	2.25	0.67
1:A:275:G:H5"	1:A:275:G:C8	2.29	0.66
4:C:129:ALA:CB	4:C:132:ARG:HB2	2.25	0.66
7:F:7:ASN:O	7:F:88:VAL:HA	1.96	0.66
10:I:34:ASN:HD22	10:I:34:ASN:H	1.42	0.66
13:L:117:ARG:HG2	13:L:122:THR:O	1.96	0.66
1:A:109:A:C4	1:A:327:A:C2	2.83	0.66
1:A:854:G:N1	1:A:855:G:N7	2.43	0.66
1:A:923:A:C1'	1:A:1398:A:C2	2.78	0.66
3:B:97:TRP:HZ2	3:B:102:LEU:HD13	1.60	0.66
4:C:91:LEU:HD21	4:C:99:VAL:HG13	1.77	0.66
19:R:66:LEU:HG	19:R:70:ILE:CD1	2.24	0.66
1:A:358:U:H2'	1:A:359:U:H6	1.59	0.66
1:A:1227:A:OP1	20:S:80:TYR:OH	2.10	0.66
1:A:1403:C:O2	1:A:1403:C:C2'	2.42	0.66
11:J:47:PHE:HD2	15:N:34:TYR:HE2	1.39	0.66
1:A:976:G:C5'	1:A:977:A:OP1	2.44	0.66
5:D:141:ARG:HB3	5:D:142:PRO:HD2	1.76	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:53:ARG:NH1	13:L:92:ASP:OD2	2.28	0.66
1:A:1152:A:C5'	11:J:13:HIS:CD2	2.72	0.66
1:A:1187:G:H2'	1:A:1188:A:H8	1.61	0.66
3:B:48:MET:HA	3:B:51:LEU:HD12	1.78	0.66
1:A:1081:G:OP1	6:E:16:THR:OG1	2.14	0.66
3:B:161:ALA:HB1	3:B:185:ILE:HD11	1.75	0.66
13:L:28:LYS:O	13:L:30:ALA:N	2.29	0.66
1:A:499:A:C4'	1:A:500:G:H5'	2.26	0.66
1:A:803:G:C5	1:A:804:U:C5	2.84	0.66
1:A:923:A:H1'	1:A:1398:A:N3	2.10	0.66
4:C:139:GLN:O	4:C:143:GLU:N	2.28	0.66
6:E:67:VAL:HG13	6:E:67:VAL:O	1.95	0.66
11:J:56:HIS:C	11:J:58:ASP:H	1.97	0.66
1:A:459:G:H3'	1:A:460:A:H5'	1.78	0.66
3:B:87:ARG:HH21	3:B:219:VAL:HB	1.61	0.66
3:B:167:PRO:HG3	3:B:188:ALA:HB2	1.78	0.66
13:L:111:LYS:O	13:L:112:ASP:HB2	1.96	0.66
21:T:56:MET:CE	21:T:104:LEU:HD21	2.26	0.66
1:A:91:C:H2'	1:A:92:C:H6	1.59	0.66
1:A:676:A:H2'	1:A:677:U:H6	1.59	0.66
1:A:1015:A:H2'	1:A:1016:A:H8	1.60	0.66
1:A:1047:G:H8	1:A:1047:G:O5'	1.77	0.66
1:A:1055:A:N7	1:A:1206:G:N1	2.44	0.66
1:A:836:G:C6	1:A:851:G:C6	2.84	0.66
4:C:6:HIS:NE2	4:C:8:ILE:CB	2.59	0.66
5:D:79:PHE:CD1	5:D:207:TYR:HD1	2.14	0.66
6:E:51:VAL:O	6:E:54:ALA:HB3	1.96	0.66
1:A:448:A:C5	1:A:487:A:C2	2.84	0.65
13:L:41:ARG:HD2	13:L:42:THR:H	1.61	0.65
1:A:95:U:H2'	1:A:96:G:H8	1.61	0.65
1:A:942:G:H2'	1:A:943:U:C6	2.31	0.65
1:A:1189:C:H5"	1:A:1190:G:OP2	1.95	0.65
3:B:182:ILE:CG2	3:B:183:PRO:HD2	2.26	0.65
1:A:1003(A):G:H2'	1:A:1004:A:C4'	2.24	0.65
1:A:1288:A:N7	1:A:1289:A:N7	2.43	0.65
1:A:1366:C:C2	1:A:1367:C:C5	2.84	0.65
10:I:82:ALA:O	10:I:86:VAL:HG23	1.96	0.65
12:K:33:THR:CG2	12:K:37:GLY:HA2	2.26	0.65
1:A:715:A:H8	1:A:715:A:O5'	1.80	0.65
3:B:176:GLU:O	3:B:177:ALA:C	2.35	0.65
1:A:948:C:OP1	14:M:109:THR:CG2	2.34	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:987:G:O5'	1:A:987:G:H8	1.79	0.65
1:A:1314:C:C2	1:A:1315:U:C5	2.84	0.65
1:A:1347:G:O2'	1:A:1348:U:OP2	2.14	0.65
3:B:117:GLU:O	3:B:121:LEU:HB2	1.97	0.65
6:E:80:ILE:HG23	9:H:104:ARG:NH2	2.10	0.65
1:A:1381:U:C4	1:A:1382:C:C5	2.85	0.65
4:C:15:THR:HG21	4:C:179:ARG:HA	1.78	0.65
8:G:92:SER:HB2	8:G:93:PRO:HD2	1.78	0.65
9:H:119:LEU:HD13	9:H:124:ALA:HA	1.76	0.65
10:I:28:VAL:HA	10:I:63:ILE:O	1.97	0.65
10:I:50:LEU:HD11	10:I:81:ILE:HG21	1.78	0.65
19:R:66:LEU:HG	19:R:70:ILE:HD12	1.77	0.65
1:A:291:C:O2'	1:A:292:G:H5'	1.96	0.65
1:A:382:A:C2	1:A:383:A:C4	2.84	0.65
1:A:1392:G:H2'	1:A:1393:U:H6	1.62	0.65
5:D:149:ALA:C	5:D:151:LYS:H	2.00	0.65
6:E:34:VAL:HG22	6:E:62:ALA:HB1	1.78	0.65
17:P:28:ARG:HH11	17:P:28:ARG:CG	1.96	0.65
1:A:983:A:H3'	1:A:983:A:N3	2.11	0.65
1:A:1350:A:C2	1:A:1351:U:O2	2.50	0.65
1:A:1438:G:H2'	1:A:1439:C:C6	2.31	0.65
8:G:15:ASP:HB3	8:G:20:ASP:H	1.61	0.65
17:P:57:ARG:HH11	17:P:57:ARG:CG	2.07	0.65
21:T:13:LEU:C	21:T:13:LEU:CD2	2.66	0.65
21:T:43:LEU:HD12	21:T:52:ALA:HA	1.78	0.65
1:A:861:G:H2'	1:A:862:C:H6	1.62	0.65
1:A:1158:C:H5	1:A:1160:G:H1'	1.61	0.65
1:A:1182:G:C4'	1:A:1183:A:O5'	2.37	0.65
4:C:191:THR:HG21	4:C:193:TYR:CZ	2.32	0.65
21:T:13:LEU:HD22	21:T:13:LEU:C	2.16	0.65
1:A:62:U:H2'	1:A:63:C:C6	2.32	0.65
1:A:200:G:H2'	1:A:201:C:O4'	1.97	0.65
3:B:25:ASN:HD21	3:B:27:LYS:HB2	1.60	0.65
3:B:111:ARG:CB	3:B:149:LEU:HD11	2.27	0.65
3:B:217:ARG:O	3:B:220:ASP:HB2	1.96	0.65
4:C:91:LEU:HD23	4:C:92:ALA:N	2.11	0.65
13:L:67:THR:HG23	13:L:67:THR:O	1.97	0.65
1:A:1056:U:O2'	1:A:1057:G:H5'	1.97	0.64
5:D:21:LEU:CD1	5:D:22:LYS:H	2.10	0.64
9:H:19:VAL:HG23	9:H:19:VAL:O	1.96	0.64
1:A:62:U:H2'	1:A:63:C:H6	1.61	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:669:U:H2'	1:A:670:G:H8	1.56	0.64
1:A:753:A:H4'	1:A:754:C:O5'	1.97	0.64
7:F:44:GLY:HA2	7:F:60:PHE:H	1.63	0.64
20:S:41:VAL:HG12	20:S:42:PRO:HD2	1.78	0.64
21:T:82:SER:O	21:T:86:ARG:HB2	1.97	0.64
1:A:373:A:C8	1:A:373:A:C5'	2.78	0.64
1:A:623:C:O2	1:A:623:C:H2'	1.98	0.64
1:A:1399:C:H4'	1:A:1400:C:C5'	2.21	0.64
3:B:17:PHE:HD1	3:B:18:GLY:H	1.44	0.64
7:F:9:VAL:CG2	7:F:87:ARG:HB2	2.26	0.64
9:H:103:VAL:HG21	9:H:109:ILE:C	2.18	0.64
20:S:72:GLY:O	20:S:74:PHE:HD1	1.79	0.64
1:A:522:C:OP2	13:L:69:TYR:OH	2.12	0.64
1:A:1063:C:OP2	1:A:1064:G:O2'	2.14	0.64
1:A:1187:G:H2'	1:A:1188:A:C8	2.33	0.64
6:E:90:VAL:O	6:E:120:THR:HA	1.97	0.64
6:E:103:GLY:O	6:E:106:PRO:CD	2.43	0.64
11:J:46:ARG:HG2	11:J:46:ARG:HH11	1.61	0.64
15:N:32:SER:HB2	15:N:41:ARG:HB3	1.78	0.64
1:A:779:C:H2'	1:A:780:A:O4'	1.96	0.64
1:A:864:A:H2'	1:A:865:A:C8	2.31	0.64
1:A:1074:G:O2'	3:B:103:THR:HG22	1.96	0.64
1:A:1169:A:HO3'	1:A:1171:G:P	2.19	0.64
1:A:1316:G:O2'	1:A:1318:A:N7	2.26	0.64
8:G:23:VAL:HG12	8:G:27:ILE:CD1	2.23	0.64
11:J:16:LEU:CD2	11:J:94:VAL:HG13	2.28	0.64
15:N:36:PHE:O	15:N:36:PHE:HD1	1.79	0.64
16:O:76:GLU:O	16:O:78:TYR:N	2.31	0.64
1:A:705:U:H3'	1:A:706:A:H8	1.63	0.64
1:A:1092:A:C5'	1:A:1092:A:H8	2.10	0.64
1:A:1100:C:O5'	1:A:1100:C:H6	1.80	0.64
1:A:1161:C:H2'	1:A:1162:C:C6	2.33	0.64
13:L:6:THR:HG1	13:L:9:GLN:HG3	1.61	0.64
19:R:79:LEU:HD23	19:R:80:PRO:CD	2.15	0.64
1:A:109:A:C6	1:A:326:G:C6	2.86	0.64
1:A:895:G:H2'	1:A:896:C:H6	1.62	0.64
1:A:960:U:H5'	1:A:960:U:O2	1.97	0.64
1:A:1119:C:H3'	1:A:1119:C:C6	2.33	0.64
3:B:101:MET:CA	3:B:108:ILE:HD12	2.27	0.64
6:E:51:VAL:CB	6:E:52:PRO:CD	2.69	0.64
14:M:22:ILE:HB	14:M:25:ILE:HD12	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1055:A:C8	1:A:1206:G:C2	2.85	0.64
1:A:1066:C:O2'	1:A:1067:A:H5"	1.98	0.64
3:B:102:LEU:HD13	3:B:102:LEU:H	1.62	0.64
5:D:79:PHE:CD1	5:D:207:TYR:CD1	2.86	0.64
14:M:40:ASN:ND2	14:M:41:PRO:HD2	2.12	0.64
20:S:39:THR:HG22	20:S:40:ILE:H	1.61	0.64
1:A:113:G:H1	1:A:314:C:H42	1.44	0.64
1:A:390:C:H2'	1:A:391:G:C8	2.33	0.64
1:A:401:C:OP2	5:D:73:ARG:NH2	2.31	0.64
1:A:750:G:N3	16:O:23:GLY:HA3	2.13	0.64
1:A:1328:C:H2'	1:A:1329:A:O4'	1.97	0.64
1:A:1499:A:H2'	1:A:1500:A:H5'	1.78	0.64
12:K:34:ASP:HB2	12:K:35:PRO:CD	2.28	0.64
20:S:39:THR:HG22	20:S:40:ILE:N	2.13	0.64
1:A:409:G:H2'	1:A:410:G:H8	1.62	0.63
1:A:528:C:H41	13:L:49:ASN:HD21	1.44	0.63
1:A:942:G:N3	1:A:943:U:C5	2.66	0.63
1:A:1438:G:H2'	1:A:1439:C:H6	1.63	0.63
1:A:1513:A:H2'	1:A:1514:C:C6	2.33	0.63
6:E:19:MET:CE	6:E:24:ARG:HH11	2.11	0.63
1:A:55:A:H2'	1:A:56:U:C6	2.32	0.63
1:A:253:U:H2'	1:A:254:G:C8	2.33	0.63
1:A:522:C:H2'	1:A:523:A:O4'	1.99	0.63
1:A:529:G:H3'	1:A:529:G:C8	2.33	0.63
1:A:580:U:H4'	16:O:57:LEU:HD23	1.80	0.63
1:A:942:G:H2'	1:A:943:U:H6	1.63	0.63
1:A:1234:C:H2'	1:A:1235:U:H5'	1.80	0.63
3:B:114:ARG:HD3	3:B:141:GLU:OE1	1.99	0.63
3:B:218:ALA:O	3:B:222:ILE:HG13	1.98	0.63
8:G:116:ALA:O	8:G:120:ILE:CD1	2.46	0.63
1:A:176:C:H2'	1:A:176:C:O2	1.98	0.63
1:A:384:G:H2'	1:A:385:C:H6	1.60	0.63
1:A:656:C:H3'	1:A:656:C:C6	2.33	0.63
4:C:11:ARG:HB2	4:C:15:THR:OG1	1.98	0.63
4:C:123:GLN:NE2	4:C:140:ARG:HH22	1.96	0.63
5:D:8:VAL:C	5:D:10:ARG:N	2.52	0.63
16:O:56:LEU:HD23	16:O:57:LEU:N	2.13	0.63
21:T:33:ILE:O	21:T:34:LYS:C	2.36	0.63
1:A:1103:C:C5'	3:B:98:LEU:CD2	2.76	0.63
6:E:80:ILE:HD12	6:E:80:ILE:N	2.09	0.63
1:A:1367:C:O2	1:A:1368:G:C8	2.52	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:88:ARG:HG2	4:C:91:LEU:HD22	1.81	0.63
8:G:18:TYR:CD2	8:G:59:LEU:HD13	2.33	0.63
1:A:549:C:H2'	1:A:550:G:H8	1.64	0.63
1:A:818:G:H3'	1:A:819:A:H5'	1.78	0.63
1:A:858:G:O2'	1:A:859:A:H5'	1.99	0.63
1:A:985:C:O2	1:A:985:C:H2'	1.99	0.63
6:E:13:ILE:HD12	6:E:13:ILE:N	2.10	0.63
1:A:355:C:H5"	1:A:389:A:OP2	1.99	0.63
1:A:879:C:O2'	1:A:880:C:H5'	1.98	0.63
14:M:89:GLY:O	14:M:92:HIS:N	2.23	0.63
16:O:78:TYR:O	16:O:80:ALA:N	2.32	0.63
1:A:826:C:H2'	1:A:827:U:C6	2.32	0.63
1:A:1459:C:H2'	1:A:1460:A:H8	1.64	0.63
3:B:25:ASN:ND2	3:B:27:LYS:HB2	2.13	0.63
3:B:118:LEU:CB	3:B:142:LEU:HD12	2.24	0.63
13:L:31:PRO:HB2	13:L:32:PHE:CE2	2.33	0.63
18:Q:40:LYS:HD3	18:Q:42:TYR:OH	1.98	0.63
1:A:839:U:H5'	1:A:840:C:H5	1.64	0.63
1:A:1068:G:N7	1:A:1094:G:C8	2.67	0.63
1:A:1391:U:H2'	1:A:1392:G:H8	1.60	0.63
4:C:188:LEU:O	4:C:189:ALA:CB	2.46	0.63
6:E:48:ALA:CB	6:E:49:PRO:HD2	2.23	0.63
7:F:76:ALA:C	7:F:78:GLU:H	1.99	0.63
17:P:67:THR:HG23	17:P:68:ASP:H	1.62	0.63
20:S:78:ARG:CG	20:S:78:ARG:HH11	2.12	0.63
1:A:497:A:N3	1:A:497:A:H2'	2.14	0.62
1:A:1305:G:H2'	1:A:1331:G:H22	1.63	0.62
3:B:25:ASN:ND2	3:B:27:LYS:H	1.97	0.62
8:G:68:ASN:O	8:G:138:LYS:HE2	1.99	0.62
1:A:1235:U:C2'	1:A:1236:A:O5'	2.46	0.62
1:A:1263:C:O2	1:A:1263:C:H2'	1.97	0.62
1:A:1526:G:H2'	1:A:1527:C:H5'	1.81	0.62
10:I:33:PHE:C	10:I:35:GLU:H	2.03	0.62
15:N:4:LYS:C	15:N:6:LEU:H	2.01	0.62
1:A:1067:A:O2'	1:A:1093:A:O3'	2.14	0.62
1:A:1406:U:H2'	1:A:1407:C:H6	1.63	0.62
4:C:123:GLN:HE22	4:C:140:ARG:HH22	1.45	0.62
21:T:87:LYS:O	21:T:88:VAL:C	2.38	0.62
1:A:734:G:H2'	1:A:735:C:H6	1.63	0.62
1:A:781:A:H2'	1:A:781:A:N3	2.14	0.62
1:A:1053:G:O2'	1:A:1054:C:OP2	2.18	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1247:U:C6	1:A:1247:U:H3'	2.35	0.62
1:A:1503:A:C8	1:A:1531:A:N3	2.68	0.62
5:D:21:LEU:CD1	5:D:26:CYS:SG	2.87	0.62
17:P:34:GLU:OE1	17:P:55:ARG:NH1	2.31	0.62
20:S:9:VAL:HG12	20:S:10:PHE:H	1.63	0.62
1:A:235:C:O2'	1:A:236:G:H5'	1.98	0.62
1:A:268:C:H2'	1:A:269:C:H6	1.64	0.62
1:A:1399:C:C4'	1:A:1400:C:H5"	2.22	0.62
5:D:10:ARG:O	5:D:10:ARG:HG2	1.99	0.62
8:G:23:VAL:CG1	8:G:27:ILE:HD11	2.24	0.62
10:I:9:ARG:HG3	10:I:14:VAL:CG1	2.28	0.62
1:A:245:C:O2	1:A:283:C:N3	2.32	0.62
1:A:644:G:C6	1:A:645:C:C5	2.87	0.62
9:H:103:VAL:O	9:H:104:ARG:HB2	1.98	0.62
14:M:81:LEU:CD2	14:M:81:LEU:N	2.57	0.62
1:A:1055:A:C2	1:A:1056:U:H1'	2.34	0.62
1:A:1279:A:H4'	1:A:1280:A:OP1	1.99	0.62
1:A:1305:G:C8	1:A:1305:G:OP2	2.53	0.62
5:D:32:ALA:O	5:D:36:ARG:N	2.32	0.62
11:J:47:PHE:CD2	15:N:34:TYR:CE2	2.83	0.62
14:M:81:LEU:H	14:M:81:LEU:HD23	1.64	0.62
17:P:51:VAL:O	17:P:52:ASP:C	2.37	0.62
1:A:42:G:C2	1:A:401:C:O2	2.53	0.62
1:A:983:A:OP1	15:N:3:ARG:NH2	2.33	0.62
1:A:1229:A:C2	1:A:1230:C:C4	2.88	0.62
5:D:7:PRO:O	5:D:10:ARG:HB3	1.98	0.62
5:D:138:TYR:C	5:D:138:TYR:CD2	2.73	0.62
13:L:40:VAL:O	13:L:40:VAL:HG12	1.99	0.62
18:Q:9:VAL:HG21	18:Q:84:LEU:HD13	1.80	0.62
1:A:314:C:H2'	1:A:315:A:H5'	1.82	0.62
1:A:670:G:H1	1:A:736:C:N4	1.96	0.62
1:A:1167:A:H8	1:A:1167:A:O5'	1.83	0.62
6:E:137:GLU:HG2	6:E:140:ARG:HH11	1.65	0.62
8:G:108:ALA:O	8:G:110:GLN:N	2.32	0.62
9:H:117:GLY:O	9:H:119:LEU:HG	1.99	0.62
10:I:111:ARG:HH11	10:I:111:ARG:HG3	1.64	0.62
12:K:33:THR:OG1	12:K:38:ASN:C	2.38	0.62
12:K:33:THR:HG21	12:K:37:GLY:HA2	1.81	0.62
16:O:4:THR:N	16:O:7:GLU:OE2	2.27	0.62
19:R:39:VAL:HG13	19:R:40:LEU:HD23	1.80	0.62
1:A:925:G:H1	1:A:1391:U:H3	1.46	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:25:ASN:HD22	3:B:27:LYS:H	1.47	0.62
13:L:75:HIS:HD2	13:L:77:LEU:N	1.98	0.62
14:M:81:LEU:HA	14:M:84:ILE:HG12	1.81	0.62
15:N:37:PHE:CE2	15:N:53:LEU:HD13	2.33	0.62
17:P:6:LEU:HD23	17:P:17:TYR:CG	2.34	0.62
21:T:89:ARG:HH22	21:T:106:ALA:HB2	1.65	0.62
1:A:256:U:O2'	1:A:257:G:H5'	2.00	0.61
1:A:499:A:H4'	1:A:500:G:H5'	1.82	0.61
1:A:653:A:H2'	1:A:653:A:N3	2.15	0.61
1:A:662:G:O2'	1:A:836:G:H5"	2.00	0.61
6:E:27:ARG:HG3	6:E:28:PHE:H	1.62	0.61
21:T:74:LYS:CG	21:T:75:ASN:H	2.06	0.61
1:A:299:G:H2'	1:A:300:A:C8	2.35	0.61
1:A:975:A:C8	1:A:975:A:C5'	2.80	0.61
1:A:1249:C:C6	1:A:1249:C:H3'	2.35	0.61
7:F:50:TYR:CE1	19:R:77:GLY:HA3	2.35	0.61
13:L:28:LYS:C	13:L:30:ALA:N	2.52	0.61
14:M:5:ALA:O	14:M:6:GLY:C	2.37	0.61
17:P:57:ARG:NH1	17:P:79:VAL:O	2.33	0.61
18:Q:83:ASP:OD1	18:Q:84:LEU:N	2.33	0.61
18:Q:90:ILE:C	18:Q:92:ARG:N	2.53	0.61
1:A:96:G:H5"	1:A:97:G:OP2	2.00	0.61
1:A:149:A:C2	1:A:150:C:N3	2.68	0.61
1:A:1377:A:C8	1:A:1377:A:C3'	2.83	0.61
1:A:1508:G:H2'	1:A:1509:C:H6	1.65	0.61
5:D:149:ALA:C	5:D:151:LYS:N	2.53	0.61
18:Q:95:TYR:C	18:Q:97:SER:H	2.03	0.61
1:A:1057:G:C5	1:A:1204:A:C2	2.88	0.61
1:A:1147:C:H4'	10:I:5:TYR:CE1	2.35	0.61
1:A:1316:G:N1	1:A:1319:A:OP2	2.31	0.61
1:A:1455:G:C3'	1:A:1459:C:OP2	2.48	0.61
1:A:1521:G:C2	1:A:1522:U:C2	2.89	0.61
13:L:22:SER:OG	13:L:23:LYS:N	2.34	0.61
14:M:32:GLU:O	14:M:35:GLU:HB3	2.00	0.61
1:A:988:G:N2	1:A:1218:C:C2	2.68	0.61
3:B:16:HIS:HB2	3:B:210:SER:HB3	1.83	0.61
3:B:100:GLY:CA	3:B:176:GLU:OE2	2.33	0.61
15:N:27:CYS:SG	15:N:29:ARG:HG3	2.41	0.61
19:R:36:ASN:HB3	19:R:39:VAL:HG12	1.80	0.61
1:A:262:A:C6	1:A:263:A:N6	2.69	0.61
1:A:689:C:P	12:K:46:GLY:HA3	2.41	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1092:A:H8	1:A:1092:A:O5'	1.83	0.61
10:I:79:LEU:HD23	10:I:83:ARG:HD2	1.82	0.61
12:K:33:THR:HG1	12:K:38:ASN:C	2.02	0.61
19:R:87:ARG:HB3	19:R:87:ARG:HH11	1.64	0.61
1:A:193:C:H1'	21:T:60:GLU:OE1	2.00	0.61
1:A:657:G:H2'	1:A:658:G:C8	2.36	0.61
1:A:666:G:H5'	1:A:726:C:H1'	1.83	0.61
1:A:801:U:O2'	1:A:802:A:H5'	2.01	0.61
1:A:979:C:C5	1:A:980:C:C5	2.86	0.61
1:A:1103:C:H5"	3:B:98:LEU:HD21	1.81	0.61
1:A:1142:G:H2'	1:A:1142:G:N3	2.14	0.61
1:A:1345:U:C2	1:A:1377:A:N1	2.69	0.61
3:B:51:LEU:O	3:B:55:PHE:HD1	1.84	0.61
3:B:223:ILE:HD12	3:B:226:ARG:HH11	1.64	0.61
11:J:49:VAL:CA	11:J:50:ILE:HD12	2.28	0.61
1:A:298:A:H5"	1:A:299:G:OP2	2.00	0.61
1:A:677:U:H3	1:A:713:G:H22	1.48	0.61
1:A:1161:C:H2'	1:A:1162:C:C5	2.35	0.61
1:A:1429:C:H42	1:A:1471:G:H1	1.48	0.61
1:A:1496:C:N4	25:A:1637:AB9:O28	2.33	0.61
6:E:80:ILE:CG2	9:H:104:ARG:NH2	2.62	0.61
10:I:48:GLU:N	10:I:49:PRO:CD	2.63	0.61
10:I:86:VAL:HG13	10:I:92:TYR:HB2	1.81	0.61
19:R:19:LYS:O	19:R:20:ALA:CB	2.48	0.61
1:A:325:A:H2'	1:A:326:G:C8	2.36	0.61
1:A:501:C:H2'	1:A:502:G:C8	2.35	0.61
1:A:502:G:H2'	1:A:503:C:H6	1.65	0.61
1:A:850:U:C6	1:A:850:U:C3'	2.82	0.61
1:A:977:A:H2'	1:A:978:A:C5'	2.30	0.61
1:A:1372:U:H2'	1:A:1373:G:O4'	2.00	0.61
1:A:1495:U:C2	1:A:1496:C:C5	2.88	0.61
6:E:139:LEU:C	6:E:141:GLN:H	2.02	0.61
1:A:148:G:H2'	1:A:149:A:H8	1.66	0.61
1:A:614:A:C2	1:A:627:G:C2	2.88	0.61
1:A:818:G:O2'	1:A:819:A:C5'	2.49	0.61
1:A:854:G:C6	1:A:855:G:N7	2.69	0.61
1:A:1075:C:C2'	1:A:1076:C:H5'	2.30	0.61
1:A:1203:C:O5'	1:A:1203:C:H6	1.83	0.61
1:A:1208:C:C4	1:A:1209:C:H5	2.19	0.61
5:D:67:ILE:HG22	5:D:68:TYR:HD1	1.65	0.61
13:L:39:VAL:O	13:L:41:ARG:N	2.32	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Q:82:MET:HA	18:Q:85:VAL:HG23	1.82	0.61
1:A:264:U:H4'	18:Q:63:ARG:HD3	1.83	0.60
1:A:394:G:H2'	1:A:395:C:H6	1.66	0.60
1:A:659:U:OP2	16:O:8:LYS:HE2	2.01	0.60
1:A:803:G:H8	1:A:803:G:O5'	1.84	0.60
1:A:1113:C:N4	1:A:1187:G:H1	1.97	0.60
1:A:1160:G:H2'	1:A:1161:C:O5'	2.00	0.60
1:A:1333:A:H2'	1:A:1334:G:O4'	2.01	0.60
1:A:1495:U:H2'	1:A:1496:C:H6	1.65	0.60
10:I:57:GLY:O	10:I:58:ARG:CG	2.49	0.60
13:L:55:VAL:CG1	13:L:56:ALA:N	2.63	0.60
1:A:256:U:C2'	1:A:257:G:H5'	2.31	0.60
1:A:459:G:H3'	1:A:460:A:C5'	2.31	0.60
1:A:507:C:H2'	1:A:508:C:C5	2.36	0.60
1:A:537:G:H2'	1:A:538:G:H8	1.65	0.60
1:A:549:C:H2'	1:A:550:G:C8	2.35	0.60
1:A:620:C:H2'	1:A:621:A:O4'	2.00	0.60
1:A:803:G:H2'	1:A:804:U:O4'	2.00	0.60
1:A:922:G:C2	1:A:1396:A:C2	2.89	0.60
1:A:1361(A):C:C2'	1:A:1362:C:H5"	2.31	0.60
1:A:1525:G:OP2	12:K:120:ARG:NH2	2.34	0.60
3:B:28:PHE:O	3:B:30:ARG:N	2.35	0.60
4:C:128:PHE:HE2	4:C:132:ARG:HH11	1.48	0.60
6:E:141:GLN:O	6:E:143:ARG:NH1	2.34	0.60
8:G:66:VAL:HG12	8:G:67:GLU:N	2.15	0.60
10:I:118:LYS:O	10:I:119:ALA:HB3	2.01	0.60
11:J:47:PHE:CD2	15:N:34:TYR:HE2	2.19	0.60
1:A:357:G:H2'	1:A:358:U:H6	1.66	0.60
1:A:308:C:H2'	1:A:309:G:H8	1.65	0.60
1:A:627:G:H2'	1:A:628:G:H8	1.65	0.60
1:A:1151:A:O2'	1:A:1152:A:O5'	2.17	0.60
1:A:1343:G:H2'	1:A:1344:C:H6	1.61	0.60
2:Z:4:U:H2'	2:Z:5:C:C6	2.36	0.60
16:O:3:ILE:HG21	16:O:34:LEU:CD1	2.32	0.60
16:O:39:LEU:CD1	16:O:56:LEU:HB2	2.31	0.60
17:P:75:ARG:O	17:P:78:GLY:N	2.28	0.60
21:T:63:ILE:O	21:T:65:LYS:N	2.35	0.60
1:A:410:G:H5'	5:D:30:LYS:NZ	2.16	0.60
1:A:959:A:N1	1:A:1222:G:C4'	2.65	0.60
1:A:964:A:H5"	1:A:965:A:OP2	2.01	0.60
1:A:1116:C:C2'	1:A:1117:G:H5"	2.31	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1498:U:O2'	1:A:1499:A:OP2	2.18	0.60
3:B:168:THR:HG21	3:B:191:ASP:O	2.02	0.60
5:D:5:ILE:O	5:D:5:ILE:CG2	2.49	0.60
10:I:50:LEU:CD1	10:I:81:ILE:HG21	2.32	0.60
16:O:32:LEU:HD12	16:O:63:ARG:HB2	1.81	0.60
1:A:865:A:O2'	1:A:866:C:H5'	2.01	0.60
4:C:111:LEU:HD21	4:C:146:ALA:H	1.66	0.60
6:E:102:ALA:HB2	6:E:120:THR:OG1	2.01	0.60
8:G:137:LYS:HA	8:G:140:ASP:HB2	1.84	0.60
1:A:190(L):U:C2	21:T:105:SER:HB2	2.37	0.60
1:A:1262:C:O2'	1:A:1263:C:O5'	2.19	0.60
1:A:1296:C:H4'	1:A:1302:U:C5	2.36	0.60
1:A:1497:G:C2'	1:A:1498:U:C5'	2.74	0.60
5:D:92:VAL:HG12	5:D:96:LEU:HD13	1.83	0.60
6:E:91:LEU:HD23	6:E:120:THR:HG23	1.84	0.60
8:G:120:ILE:O	8:G:124:LEU:HD12	2.01	0.60
11:J:79:ARG:HD3	11:J:82:ILE:HD12	1.82	0.60
1:A:543:C:O2'	1:A:544:G:H5'	2.01	0.60
1:A:789:U:O2	1:A:791:G:C8	2.54	0.60
1:A:807:A:H2'	1:A:808:C:C6	2.37	0.60
1:A:945:G:C2	1:A:946:A:C8	2.89	0.60
1:A:1262:C:O2'	1:A:1263:C:H6	1.85	0.60
1:A:1392:G:N2	1:A:1502:A:H8	2.00	0.60
3:B:77:ALA:CB	3:B:211:ILE:HD13	2.21	0.60
3:B:114:ARG:HH11	3:B:118:LEU:CD1	2.04	0.60
4:C:113:ALA:N	4:C:114:PRO:CD	2.64	0.60
6:E:15:ARG:CG	6:E:15:ARG:NH1	2.59	0.60
1:A:393:A:N3	1:A:394:G:C8	2.70	0.60
1:A:491:G:H2'	1:A:492:G:O4'	2.01	0.60
1:A:737:A:H1'	7:F:73:ASN:ND2	2.17	0.60
1:A:981:U:H5"	1:A:982:U:O5'	2.01	0.60
1:A:1101:A:H4'	1:A:1102:A:O5'	2.01	0.60
1:A:1230:C:O2'	1:A:1231:G:H5'	2.02	0.60
4:C:113:ALA:N	4:C:114:PRO:HD3	2.17	0.60
14:M:19:LEU:O	14:M:22:ILE:HD12	2.01	0.60
1:A:181:G:H4'	1:A:182:U:H5'	1.84	0.60
1:A:201:C:N4	1:A:203:U:C2	2.70	0.60
1:A:322:C:H4'	21:T:23:ARG:HD2	1.83	0.60
1:A:882:C:C2'	1:A:883:C:H5'	2.32	0.60
1:A:916:G:H2'	1:A:917:G:H8	1.66	0.60
1:A:932:C:H6	1:A:932:C:H5"	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1229:A:H2'	1:A:1230:C:C6	2.37	0.60
3:B:75:LYS:HA	3:B:78:GLN:HB2	1.83	0.60
3:B:97:TRP:CZ2	3:B:102:LEU:HD13	2.36	0.60
13:L:75:HIS:HD2	13:L:76:ASN:N	1.96	0.60
1:A:283:C:C2	1:A:284:G:C8	2.90	0.59
1:A:818:G:O2'	1:A:819:A:H5'	2.01	0.59
1:A:1225:A:H2'	1:A:1225:A:N3	2.16	0.59
9:H:104:ARG:O	9:H:106:GLY:N	2.35	0.59
10:I:50:LEU:HD11	10:I:81:ILE:CG2	2.32	0.59
1:A:52:G:O2'	1:A:53:A:H5'	2.01	0.59
1:A:200:G:C5'	1:A:200:G:C8	2.85	0.59
1:A:1179:A:H2'	1:A:1180:A:O4'	2.02	0.59
4:C:6:HIS:CD2	4:C:6:HIS:C	2.73	0.59
12:K:73:MET:CE	12:K:102:GLY:HA3	2.32	0.59
13:L:81:SER:O	13:L:106:ASP:CG	2.39	0.59
1:A:136:C:H42	1:A:227:G:H1	1.50	0.59
1:A:390:C:H2'	1:A:391:G:H8	1.66	0.59
1:A:543:C:C2'	1:A:544:G:H5'	2.32	0.59
1:A:1068:G:N3	1:A:1191:A:C2	2.70	0.59
1:A:1282:C:O2	1:A:1282:C:H2'	2.02	0.59
1:A:1507:A:H2'	1:A:1508:G:C8	2.36	0.59
4:C:35:GLU:OE1	4:C:95:THR:HG21	2.01	0.59
4:C:52:LEU:N	4:C:52:LEU:CD2	2.63	0.59
5:D:11:LEU:HA	5:D:14:ARG:H	1.67	0.59
6:E:76:ILE:HG22	6:E:93:PRO:HG3	1.84	0.59
8:G:47:CYS:O	8:G:50:ILE:HG22	2.03	0.59
15:N:24:CYS:HB3	15:N:28:GLY:H	1.65	0.59
1:A:22:G:H2'	1:A:23:C:C6	2.37	0.59
1:A:192:U:H4'	21:T:103:GLY:H	1.66	0.59
1:A:286:G:C5	1:A:287:U:C5	2.90	0.59
1:A:314:C:C2'	1:A:315:A:H5'	2.31	0.59
1:A:878:G:H5'	9:H:89:PRO:HG2	1.84	0.59
1:A:1377:A:H3'	1:A:1377:A:H8	1.64	0.59
6:E:48:ALA:HB1	6:E:49:PRO:CD	2.25	0.59
8:G:24:THR:O	8:G:28:ASN:ND2	2.36	0.59
9:H:6:ILE:O	9:H:7:ALA:C	2.41	0.59
13:L:45:PRO:HG3	13:L:53:ARG:CD	2.32	0.59
15:N:6:LEU:HD23	15:N:21:TYR:OH	2.02	0.59
1:A:938:A:H1'	1:A:1376:U:O2'	2.02	0.59
1:A:977:A:C2'	1:A:978:A:C5'	2.80	0.59
1:A:1121:U:H2'	1:A:1122:U:C6	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1513:A:N1	1:A:1523:G:C6	2.70	0.59
5:D:8:VAL:O	5:D:10:ARG:N	2.36	0.59
6:E:19:MET:HE2	6:E:24:ARG:HH11	1.68	0.59
9:H:85:ARG:HD3	9:H:87:SER:O	2.01	0.59
19:R:33:ASP:C	19:R:35:ARG:H	2.06	0.59
20:S:62:ILE:HG23	20:S:62:ILE:O	2.02	0.59
1:A:181:G:H4'	1:A:182:U:C5'	2.32	0.59
1:A:362:G:C8	1:A:362:G:H3'	2.37	0.59
1:A:448:A:C4	1:A:487:A:C2	2.90	0.59
1:A:1152:A:O3'	11:J:13:HIS:NE2	2.36	0.59
1:A:1158:C:C5	1:A:1160:G:C1'	2.84	0.59
1:A:1316:G:H4'	15:N:18:VAL:HG11	1.84	0.59
7:F:8:ILE:HD12	7:F:61:LEU:HB3	1.85	0.59
1:A:836:G:C5	1:A:851:G:C6	2.91	0.59
1:A:1366:C:H5"	1:A:1367:C:OP2	2.03	0.59
5:D:64:LEU:O	5:D:64:LEU:HD13	2.03	0.59
6:E:11:ILE:CG1	6:E:31:LEU:HB3	2.33	0.59
10:I:34:ASN:H	10:I:34:ASN:ND2	2.00	0.59
11:J:50:ILE:H	11:J:60:ARG:HD2	1.66	0.59
12:K:24:SER:O	12:K:26:ASN:N	2.36	0.59
1:A:570:G:C4	1:A:571:U:C5	2.91	0.59
1:A:972:C:O2'	11:J:57:LYS:HB3	2.02	0.59
1:A:1157:A:O4'	1:A:1158:C:O2	2.20	0.59
1:A:1495:U:H2'	1:A:1496:C:C6	2.38	0.59
11:J:45:ARG:O	11:J:64:GLU:HA	2.02	0.59
12:K:119:CYS:O	12:K:121:PRO:HD3	2.02	0.59
14:M:87:TYR:HA	14:M:90:LEU:HD12	1.85	0.59
16:O:74:ASP:O	16:O:76:GLU:N	2.36	0.59
1:A:253:U:H2'	1:A:254:G:H8	1.68	0.59
1:A:1258:G:OP2	1:A:1258:G:C8	2.56	0.59
1:A:1259:C:O2'	1:A:1284:C:H1'	2.02	0.59
1:A:1490:C:C2'	1:A:1491:G:H5"	2.32	0.59
5:D:99:SER:O	5:D:140:VAL:HG23	2.02	0.59
11:J:7:LYS:HG3	11:J:71:LEU:CD2	2.33	0.59
18:Q:85:VAL:O	18:Q:86:GLU:C	2.41	0.59
1:A:45:U:H2'	1:A:46:G:C8	2.37	0.59
1:A:300:A:H8	1:A:300:A:O5'	1.85	0.59
1:A:410:G:H5'	5:D:30:LYS:HZ2	1.67	0.59
1:A:767:A:H2'	1:A:768:A:O4'	2.03	0.59
1:A:806:C:O2'	1:A:807:A:H5'	2.03	0.59
1:A:1455:G:O3'	1:A:1459:C:OP2	2.19	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:193:ASP:HB3	3:B:196:LEU:HD11	1.85	0.59
8:G:124:LEU:O	8:G:127:ALA:HB3	2.02	0.59
10:I:111:ARG:HG3	10:I:111:ARG:NH1	2.17	0.59
1:A:356:A:C2'	1:A:357:G:H5'	2.32	0.58
1:A:394:G:H2'	1:A:395:C:C6	2.38	0.58
1:A:583:A:H5"	1:A:584:G:OP2	2.02	0.58
1:A:1055:A:C2	1:A:1056:U:C1'	2.85	0.58
1:A:1057:G:H2'	1:A:1058:G:H8	1.66	0.58
20:S:11:VAL:HG12	20:S:12:ASP:O	2.03	0.58
1:A:65:U:C5	1:A:381:C:C4	2.91	0.58
1:A:883:C:C2'	1:A:884:U:O5'	2.51	0.58
1:A:1063:C:H2'	1:A:1064:G:C8	2.37	0.58
1:A:1490:C:H5"	1:A:1491:G:OP2	2.03	0.58
1:A:1523:G:C5	1:A:1524:C:C5	2.91	0.58
3:B:92:TYR:CE1	3:B:151:GLY:HA3	2.38	0.58
5:D:63:LYS:HE2	5:D:197:PRO:O	2.04	0.58
6:E:30:ALA:O	6:E:45:PHE:CD1	2.51	0.58
14:M:78:ILE:HG23	14:M:79:LYS:N	2.17	0.58
17:P:21:VAL:HG21	17:P:59:TRP:NE1	2.19	0.58
18:Q:62:SER:OG	18:Q:72:ARG:HG3	2.03	0.58
1:A:1251:A:H4'	10:I:12:GLU:OE1	2.03	0.58
1:A:1266:G:H21	1:A:1270:C:H42	1.50	0.58
4:C:141:VAL:O	4:C:146:ALA:HB2	2.03	0.58
5:D:170:VAL:CG2	5:D:174:LEU:HB2	2.34	0.58
9:H:30:ARG:HG2	9:H:30:ARG:NH1	2.16	0.58
1:A:577:G:H1'	1:A:816:A:N3	2.18	0.58
1:A:604:G:C5	1:A:605:U:C5	2.91	0.58
1:A:1078:U:H5"	1:A:1079:G:OP2	2.04	0.58
5:D:22:LYS:O	5:D:26:CYS:HB2	2.03	0.58
6:E:34:VAL:CG2	6:E:62:ALA:HB1	2.33	0.58
14:M:91:ARG:O	14:M:95:GLY:N	2.32	0.58
14:M:91:ARG:NH1	14:M:96:LEU:HD13	2.19	0.58
1:A:1304:G:H1'	1:A:1333:A:H61	1.67	0.58
1:A:1361:G:H2'	1:A:1361(A):C:H5'	1.84	0.58
1:A:1507:A:H2'	1:A:1508:G:H8	1.69	0.58
4:C:191:THR:HG22	4:C:192:THR:N	2.16	0.58
7:F:50:TYR:CE1	19:R:77:GLY:CA	2.86	0.58
18:Q:13:ASP:C	18:Q:15:MET:H	2.07	0.58
1:A:411:A:C8	1:A:413:G:C8	2.92	0.58
1:A:533:A:C5	1:A:536:C:C4	2.92	0.58
1:A:948:C:N3	1:A:1233:G:N2	2.44	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:72:LYS:O	4:C:74:GLY:N	2.37	0.58
4:C:126:ARG:O	4:C:127:ARG:CB	2.44	0.58
1:A:407:G:O2'	5:D:116:GLN:CG	2.49	0.58
1:A:580:U:H2'	1:A:581:G:O4'	2.03	0.58
1:A:730:G:N2	1:A:765:G:H5"	2.19	0.58
1:A:1152:A:OP1	11:J:68:HIS:CE1	2.57	0.58
1:A:1255:G:C2'	1:A:1279:A:N6	2.67	0.58
7:F:6:VAL:HG12	7:F:7:ASN:N	2.19	0.58
10:I:13:ALA:HB2	10:I:67:GLY:O	2.02	0.58
12:K:80:VAL:CG2	12:K:103:LEU:HD13	2.33	0.58
14:M:96:LEU:CB	14:M:97:PRO:HD2	2.21	0.58
16:O:13:GLN:O	16:O:15:PHE:N	2.37	0.58
6:E:105:VAL:CG1	6:E:132:ALA:HB2	2.33	0.58
12:K:128:ALA:O	12:K:129:SER:HB2	2.03	0.58
14:M:105:THR:O	14:M:107:ALA:N	2.37	0.58
17:P:4:ILE:HA	17:P:20:VAL:O	2.04	0.58
1:A:376:G:C2	1:A:389:A:N1	2.72	0.58
1:A:378:G:H2'	1:A:379:C:C6	2.39	0.58
1:A:492:G:HO3'	1:A:494:G:P	2.25	0.58
1:A:1299:A:C5	1:A:1301:U:O2	2.57	0.58
3:B:102:LEU:CD1	3:B:102:LEU:H	2.16	0.58
5:D:21:LEU:O	5:D:113:SER:HB2	2.04	0.58
5:D:103:ASN:O	5:D:105:VAL:N	2.37	0.58
5:D:104:VAL:CG2	5:D:185:PHE:HD1	2.17	0.58
1:A:437:U:H2'	5:D:123:HIS:HD2	1.69	0.58
1:A:877:C:O2'	9:H:3:THR:HB	2.04	0.58
1:A:981:U:O5'	1:A:981:U:H6	1.87	0.58
3:B:219:VAL:HA	3:B:222:ILE:CD1	2.34	0.58
4:C:6:HIS:NE2	4:C:8:ILE:CG2	2.67	0.58
5:D:61:LYS:CE	5:D:62:GLN:NE2	2.62	0.58
11:J:47:PHE:HD2	15:N:34:TYR:CD2	2.21	0.58
13:L:53:ARG:HD3	13:L:93:LEU:HD21	1.85	0.58
1:A:401:C:C6	1:A:401:C:C3'	2.86	0.57
1:A:883:C:H2'	1:A:884:U:O5'	2.03	0.57
1:A:960:U:O2	1:A:960:U:H2'	2.04	0.57
1:A:1103:C:H5'	3:B:98:LEU:CD2	2.34	0.57
1:A:1141:C:O2'	1:A:1142:G:O4'	2.20	0.57
1:A:1189:C:P	11:J:51:ARG:HH22	2.27	0.57
1:A:1402:C:O2	1:A:1500:A:N1	2.37	0.57
4:C:193:TYR:HE1	4:C:196:LEU:HD21	1.68	0.57
5:D:62:GLN:O	5:D:66:ARG:HB2	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:43:VAL:HG22	13:L:44:THR:HG23	1.86	0.57
21:T:41:VAL:O	21:T:43:LEU:N	2.36	0.57
21:T:56:MET:O	21:T:59:ALA:HB3	2.04	0.57
1:A:685:G:N2	1:A:686:U:C4	2.72	0.57
1:A:1259:C:O2	1:A:1283:G:H1'	2.03	0.57
1:A:1366:C:O2'	11:J:60:ARG:NH2	2.37	0.57
6:E:20:GLN:O	6:E:21:ALA:C	2.42	0.57
14:M:90:LEU:O	14:M:93:ARG:N	2.37	0.57
16:O:33:THR:CG2	16:O:63:ARG:NH1	2.47	0.57
1:A:99:C:O3'	1:A:101:A:P	2.63	0.57
1:A:390:C:O3'	17:P:28:ARG:NH2	2.37	0.57
1:A:1103:C:C5'	3:B:98:LEU:HD23	2.33	0.57
1:A:1435:G:H2'	1:A:1436:U:C5	2.38	0.57
4:C:68:VAL:HG12	4:C:70:VAL:CG2	2.34	0.57
11:J:46:ARG:HH12	11:J:64:GLU:HB3	1.69	0.57
16:O:76:GLU:O	16:O:77:ARG:C	2.42	0.57
19:R:45:SER:HB2	19:R:49:LYS:HB2	1.85	0.57
1:A:42:G:H1	1:A:400:C:H42	1.52	0.57
1:A:743:U:H2'	1:A:744:C:C6	2.39	0.57
1:A:913:A:O2'	1:A:914:A:OP2	2.22	0.57
1:A:1316:G:N2	1:A:1318:A:H3'	2.19	0.57
1:A:1392:G:H2'	1:A:1393:U:C6	2.39	0.57
1:A:781:A:H5'	1:A:782:A:OP2	2.05	0.57
4:C:173:VAL:O	4:C:173:VAL:HG12	2.05	0.57
6:E:142:LEU:C	6:E:143:ARG:HG2	2.25	0.57
16:O:33:THR:HG23	16:O:63:ARG:HH12	1.60	0.57
1:A:175:C:C2	1:A:176:C:C6	2.92	0.57
1:A:1145:C:H4'	1:A:1146:A:O5'	2.04	0.57
1:A:1157:A:O4'	1:A:1158:C:C2	2.58	0.57
1:A:1365:G:C5	1:A:1366:C:C4	2.92	0.57
6:E:89:ILE:HD12	6:E:121:LYS:O	2.05	0.57
1:A:653:A:H5"	9:H:56:LYS:HD3	1.85	0.57
1:A:1060:C:O2'	1:A:1061:G:C5'	2.45	0.57
1:A:1232:U:H2'	1:A:1233:G:H8	1.70	0.57
6:E:11:ILE:HG13	6:E:31:LEU:HD13	1.87	0.57
9:H:17:THR:HB	9:H:78:GLN:HE22	1.70	0.57
1:A:93:G:H3'	1:A:95:U:OP2	2.04	0.57
1:A:254:G:H4'	18:Q:18:THR:HG21	1.86	0.57
1:A:564:C:O2	1:A:564:C:C2'	2.48	0.57
1:A:1518:A:H2'	1:A:1519:A:C8	2.40	0.57
3:B:208:ILE:O	3:B:210:SER:N	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:56:ASP:N	4:C:56:ASP:OD1	2.37	0.57
5:D:199:GLN:HA	5:D:199:GLN:NE2	2.19	0.57
8:G:120:ILE:CD1	8:G:120:ILE:N	2.36	0.57
1:A:17:U:H1'	1:A:1080:A:H1'	1.87	0.57
1:A:157:G:N3	1:A:158:G:C8	2.73	0.57
1:A:315:A:H2'	1:A:315:A:O5'	2.05	0.57
1:A:627:G:H2'	1:A:628:G:C8	2.39	0.57
1:A:1153:C:P	11:J:13:HIS:HE2	2.28	0.57
1:A:1195:C:H3'	1:A:1196:U:C5'	2.31	0.57
1:A:1231:G:H2'	1:A:1232:U:H6	1.67	0.57
1:A:1259:C:H42	1:A:1276:G:H1	1.52	0.57
1:A:1349:A:H2'	1:A:1350:A:C8	2.40	0.57
4:C:8:ILE:HG12	4:C:16:ARG:HG2	1.87	0.57
11:J:38:ILE:HB	11:J:72:VAL:H	1.69	0.57
16:O:29:VAL:HG11	16:O:67:LEU:HD21	1.87	0.57
17:P:50:LYS:C	17:P:51:VAL:CG2	2.73	0.57
1:A:153:C:H42	1:A:168:G:H1	1.53	0.57
1:A:313:A:H2'	1:A:314:C:C6	2.39	0.57
1:A:338:A:C2	1:A:339:C:C2	2.93	0.57
1:A:448:A:C6	1:A:487:A:N3	2.73	0.57
1:A:506:G:C6	1:A:507:C:C4	2.93	0.57
1:A:1099:G:H2'	1:A:1100:C:C6	2.40	0.57
3:B:180:LEU:HB2	3:B:182:ILE:HD12	1.87	0.57
3:B:225:ALA:O	3:B:226:ARG:CB	2.53	0.57
5:D:108:LEU:HG	5:D:174:LEU:HD22	1.87	0.57
6:E:137:GLU:HG2	6:E:140:ARG:NH1	2.20	0.57
13:L:55:VAL:HG12	13:L:56:ALA:H	1.68	0.57
19:R:58:LEU:HD13	19:R:62:GLU:HB2	1.87	0.57
1:A:369:C:N3	1:A:370:C:C5	2.73	0.56
1:A:520:A:H5"	1:A:521:G:OP2	2.05	0.56
1:A:1010:G:N1	1:A:1020:U:O2	2.38	0.56
4:C:173:VAL:O	4:C:175:LEU:N	2.34	0.56
11:J:76:ASN:CB	11:J:78:ASN:ND2	2.67	0.56
17:P:6:LEU:HD23	17:P:17:TYR:CD2	2.39	0.56
1:A:124:G:H2'	1:A:125:U:C6	2.39	0.56
1:A:397:A:H3'	1:A:397:A:N3	2.20	0.56
1:A:705:U:H5"	1:A:706:A:OP2	2.05	0.56
1:A:814:A:N7	1:A:816:A:C4	2.73	0.56
1:A:914:A:C2	1:A:915:A:N9	2.73	0.56
1:A:941:G:N1	1:A:942:G:C8	2.73	0.56
3:B:162:ILE:C	3:B:185:ILE:HD12	2.24	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:162:LEU:CD2	5:D:178:VAL:HG12	2.32	0.56
20:S:78:ARG:HH11	20:S:78:ARG:HB3	1.70	0.56
1:A:119:A:H5"	1:A:120:A:H5'	1.86	0.56
1:A:524:G:H2'	1:A:525:C:C6	2.40	0.56
1:A:736:C:H2'	1:A:737:A:H8	1.68	0.56
1:A:946:A:C2	1:A:947:G:C5	2.93	0.56
1:A:961:U:OP1	1:A:1223:C:O2'	2.23	0.56
1:A:1184:G:O2'	1:A:1185:G:H5'	2.05	0.56
1:A:1323:G:H2'	1:A:1324:A:H8	1.65	0.56
1:A:1348:U:C2	1:A:1349:A:C8	2.93	0.56
3:B:78:GLN:O	3:B:94:ASN:OD1	2.24	0.56
5:D:26:CYS:CA	5:D:31:CYS:HB2	2.17	0.56
6:E:77:PRO:HB2	6:E:78:HIS:HD2	1.71	0.56
15:N:26:ARG:HH22	15:N:47:LEU:CD2	2.18	0.56
20:S:78:ARG:HH11	20:S:78:ARG:CB	2.18	0.56
1:A:243:A:C2	1:A:246:A:C8	2.93	0.56
1:A:455:C:H42	1:A:477:G:H1	1.52	0.56
1:A:533:A:O2'	1:A:534:U:H5"	2.05	0.56
1:A:1066:C:C2'	1:A:1067:A:H5'	2.35	0.56
1:A:1305:G:OP2	1:A:1305:G:H8	1.87	0.56
5:D:199:GLN:HG3	5:D:202:LEU:HB2	1.86	0.56
9:H:56:LYS:O	9:H:58:TYR:HD1	1.88	0.56
1:A:166:G:H2'	1:A:167:G:O5'	2.06	0.56
1:A:328:C:H4'	1:A:329:A:C5'	2.35	0.56
1:A:502:G:C2	1:A:503:C:C2	2.93	0.56
1:A:570:G:C2	1:A:571:U:C5	2.94	0.56
1:A:959:A:N1	1:A:1222:G:H4'	2.19	0.56
1:A:1511:G:C6	1:A:1512:U:N3	2.74	0.56
3:B:213:LEU:O	3:B:217:ARG:HG2	2.05	0.56
4:C:131:ARG:O	4:C:132:ARG:C	2.43	0.56
10:I:6:GLY:N	10:I:84:ALA:HB2	2.20	0.56
1:A:279:A:OP2	18:Q:95:TYR:OH	2.22	0.56
1:A:1348:U:H6	1:A:1348:U:H5'	1.71	0.56
5:D:150:GLU:HA	5:D:153:ARG:CB	2.34	0.56
7:F:99:ALA:O	7:F:100:ASN:HB2	2.04	0.56
8:G:15:ASP:CG	8:G:17:VAL:H	2.09	0.56
18:Q:5:VAL:HA	18:Q:59:ILE:O	2.05	0.56
1:A:426:G:H2'	1:A:427:U:O4'	2.06	0.56
1:A:865:A:C2'	1:A:866:C:H5'	2.35	0.56
1:A:1025:U:OP1	1:A:1025:U:H4'	2.03	0.56
1:A:1139:G:H4'	1:A:1140:C:C5'	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1206:G:C4	1:A:1207:G:C8	2.94	0.56
3:B:212:GLN:O	3:B:213:LEU:C	2.43	0.56
3:B:223:ILE:HG23	3:B:224:GLN:N	2.20	0.56
17:P:78:GLY:C	17:P:80:PHE:H	2.09	0.56
21:T:14:LYS:O	21:T:17:ARG:HB2	2.06	0.56
1:A:55:A:H2'	1:A:56:U:H6	1.70	0.56
1:A:168:G:O2'	1:A:169:C:H5'	2.05	0.56
1:A:696:A:O5'	1:A:696:A:H8	1.89	0.56
1:A:1190:G:O2'	1:A:1191:A:O5'	2.17	0.56
1:A:1499:A:O2'	1:A:1500:A:H5'	2.06	0.56
3:B:85:ALA:O	3:B:88:ALA:O	2.23	0.56
3:B:97:TRP:HH2	3:B:176:GLU:CD	2.09	0.56
5:D:13:ARG:CD	5:D:38:TYR:O	2.51	0.56
1:A:665:A:H2'	1:A:732:C:O2	2.06	0.56
1:A:858:G:N2	1:A:870:U:OP2	2.35	0.56
1:A:949:A:H1'	1:A:1364:U:H3	1.70	0.56
1:A:1017:G:H8	1:A:1017:G:O5'	1.89	0.56
4:C:39:ILE:C	4:C:41:GLY:H	2.09	0.56
9:H:14:ARG:HB3	9:H:14:ARG:NH1	2.20	0.56
14:M:8:GLU:C	14:M:9:ILE:HG13	2.25	0.56
1:A:40:C:H5"	1:A:41:G:OP2	2.06	0.56
1:A:200:G:H5'	1:A:200:G:C8	2.41	0.56
1:A:690:G:H2'	1:A:691:G:O4'	2.05	0.56
1:A:1148:U:OP1	10:I:7:THR:HG21	2.06	0.56
1:A:1235:U:C6	1:A:1235:U:C3'	2.87	0.56
3:B:44:LEU:O	3:B:47:THR:HB	2.05	0.56
21:T:29:LYS:O	21:T:32:ALA:HB3	2.06	0.56
1:A:148:G:N3	1:A:149:A:C8	2.75	0.55
1:A:160:A:C6	1:A:346:G:O6	2.60	0.55
1:A:267:C:C2'	1:A:268:C:H5'	2.36	0.55
1:A:408:A:H3'	1:A:408:A:C8	2.41	0.55
1:A:1218:C:H2'	1:A:1219:U:C6	2.40	0.55
5:D:206:PHE:CD1	5:D:206:PHE:O	2.59	0.55
6:E:35:GLY:N	6:E:112:LEU:HD13	2.21	0.55
7:F:97:PHE:CB	19:R:32:ARG:HH21	2.19	0.55
1:A:193:C:C2	1:A:194:C:C5	2.93	0.55
1:A:375:U:H2'	1:A:376:G:C8	2.41	0.55
1:A:646:U:H2'	1:A:647:C:C6	2.41	0.55
1:A:1103:C:H5"	3:B:98:LEU:CD2	2.36	0.55
3:B:104:ASN:OD1	3:B:107:THR:OG1	2.24	0.55
5:D:120:LEU:HD23	5:D:125:HIS:HB2	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:13:ILE:CD1	6:E:13:ILE:O	2.54	0.55
8:G:115:ARG:HB3	8:G:118:VAL:HG23	1.86	0.55
9:H:20:TYR:HD1	9:H:65:TYR:CE2	2.24	0.55
9:H:86:ILE:HG21	9:H:133:LEU:HB3	1.88	0.55
16:O:78:TYR:O	16:O:79:ARG:C	2.44	0.55
18:Q:74:LEU:HD23	18:Q:74:LEU:C	2.26	0.55
1:A:60:A:H5'	1:A:60:A:C8	2.41	0.55
1:A:252:U:H2'	1:A:253:U:C5	2.41	0.55
1:A:346:G:H2'	1:A:347:G:O4'	2.06	0.55
1:A:500:G:H22	1:A:546:G:H1'	1.66	0.55
1:A:706:A:C5	1:A:707:C:C5	2.94	0.55
1:A:1350:A:C2	1:A:1351:U:C2	2.93	0.55
5:D:65:ARG:O	5:D:66:ARG:C	2.43	0.55
11:J:63:PHE:HD2	15:N:57:ARG:O	1.90	0.55
18:Q:58:GLU:C	18:Q:59:ILE:HD13	2.27	0.55
1:A:281:G:O2'	1:A:282:A:OP2	2.18	0.55
1:A:761:G:H2'	1:A:762:C:C6	2.42	0.55
1:A:836:G:C6	1:A:851:G:C5	2.95	0.55
1:A:959:A:C3'	1:A:960:U:H5"	2.37	0.55
1:A:1088:G:H8	1:A:1088:G:O5'	1.89	0.55
1:A:1229:A:H2'	1:A:1230:C:H6	1.72	0.55
1:A:1240:U:H3	8:G:30:ILE:CG2	2.19	0.55
1:A:1346:A:O4'	1:A:1348:U:C6	2.59	0.55
1:A:1385:G:H2'	1:A:1386:G:O4'	2.06	0.55
3:B:166:ASP:OD1	3:B:205:ASP:HB2	2.05	0.55
8:G:37:ASN:HD21	10:I:41:VAL:HG23	1.70	0.55
11:J:78:ASN:O	11:J:80:LYS:N	2.39	0.55
14:M:122:LYS:O	14:M:123:ALA:HB2	2.06	0.55
18:Q:9:VAL:O	18:Q:11:VAL:HG13	2.05	0.55
18:Q:59:ILE:HG23	18:Q:71:PHE:HB3	1.89	0.55
1:A:590:C:OP1	9:H:30:ARG:N	2.36	0.55
1:A:668:G:O2'	16:O:46:HIS:HB3	2.07	0.55
1:A:937:A:H5"	1:A:938:A:OP2	2.07	0.55
1:A:1269:A:N1	1:A:1312:G:O2'	2.35	0.55
7:F:5:GLU:HG2	7:F:62:TRP:CZ2	2.41	0.55
7:F:62:TRP:C	7:F:63:TYR:CD2	2.77	0.55
13:L:35:GLY:O	13:L:83:VAL:HG12	2.07	0.55
13:L:102:ARG:HH11	13:L:110:VAL:HG22	1.72	0.55
14:M:10:PRO:HB2	14:M:18:ALA:HB1	1.88	0.55
19:R:59:SER:HB3	19:R:62:GLU:CD	2.26	0.55
1:A:434:U:H2'	1:A:435:C:C6	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:58:ALA:O	6:E:59:GLY:C	2.45	0.55
10:I:46:ALA:HB2	10:I:74:ILE:HG23	1.89	0.55
13:L:87:GLY:N	13:L:98:TYR:HB3	2.17	0.55
1:A:200:G:C8	1:A:200:G:H3'	2.41	0.55
1:A:261:U:O2	1:A:263:A:C8	2.60	0.55
1:A:949:A:C2	1:A:1233:G:C4	2.94	0.55
1:A:1352:C:H2'	1:A:1353:G:C8	2.41	0.55
4:C:14:ILE:O	4:C:14:ILE:HG22	2.06	0.55
6:E:47:LYS:O	6:E:48:ALA:HB2	2.07	0.55
8:G:108:ALA:C	8:G:110:GLN:H	2.09	0.55
10:I:7:THR:O	10:I:7:THR:HG22	2.06	0.55
11:J:61:GLU:HG2	11:J:62:HIS:H	1.71	0.55
1:A:200:G:C8	1:A:200:G:C3'	2.89	0.55
1:A:1124:G:H21	1:A:1126:U:H3	1.53	0.55
3:B:51:LEU:HD23	3:B:55:PHE:CE1	2.42	0.55
5:D:64:LEU:HD11	5:D:97:LEU:HD11	1.85	0.55
5:D:190:ASP:O	5:D:193:ASP:N	2.40	0.55
12:K:123:LYS:C	12:K:125:PHE:H	2.10	0.55
18:Q:12:SER:HB3	18:Q:20:THR:CB	2.37	0.55
1:A:181:G:N1	1:A:195:A:C8	2.75	0.55
1:A:636:U:H5"	1:A:637:G:OP2	2.07	0.55
1:A:668:G:H8	1:A:668:G:O5'	1.90	0.55
1:A:755:G:H1'	9:H:1:MET:HE3	1.89	0.55
1:A:1472:U:O5'	1:A:1472:U:H6	1.90	0.55
3:B:30:ARG:HG3	3:B:31:TYR:CD2	2.42	0.55
3:B:105:PHE:C	3:B:105:PHE:CD2	2.78	0.55
10:I:41:VAL:O	10:I:44:VAL:HG21	2.07	0.55
15:N:29:ARG:HB2	15:N:40:CYS:HB3	1.89	0.55
1:A:552:U:H2'	1:A:553:A:O4'	2.07	0.55
1:A:645:C:H2'	1:A:645:C:O2	2.05	0.55
1:A:915:A:N7	1:A:916:G:C8	2.75	0.55
1:A:1521:G:N1	1:A:1522:U:C2	2.75	0.55
12:K:53:SER:O	12:K:55:LYS:N	2.40	0.55
21:T:74:LYS:CG	21:T:75:ASN:N	2.70	0.55
1:A:79:G:H2'	1:A:79:G:N3	2.22	0.54
1:A:570:G:C2	1:A:571:U:C4	2.95	0.54
1:A:977:A:O2'	1:A:978:A:C5'	2.54	0.54
1:A:1107:C:H3'	1:A:1107:C:C6	2.41	0.54
1:A:1443:G:O5'	1:A:1443:G:H8	1.90	0.54
3:B:82:ARG:HA	3:B:92:TYR:CD2	2.42	0.54
3:B:173:ALA:O	3:B:176:GLU:HB2	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:174:VAL:O	3:B:176:GLU:N	2.40	0.54
5:D:127:THR:HG23	5:D:147:ALA:HB3	1.88	0.54
8:G:37:ASN:ND2	10:I:41:VAL:HG23	2.21	0.54
9:H:6:ILE:O	9:H:10:LEU:HG	2.06	0.54
4:C:156:ARG:N	4:C:196:LEU:HD22	2.22	0.54
7:F:63:TYR:O	7:F:65:VAL:HG13	2.07	0.54
9:H:86:ILE:HG22	9:H:87:SER:N	2.21	0.54
9:H:104:ARG:O	9:H:105:ARG:C	2.45	0.54
11:J:16:LEU:HD22	11:J:94:VAL:CG1	2.37	0.54
11:J:51:ARG:HG2	15:N:45:ARG:NH1	2.23	0.54
13:L:41:ARG:HD2	13:L:42:THR:O	2.07	0.54
21:T:41:VAL:O	21:T:44:ALA:N	2.40	0.54
1:A:296:U:O2'	1:A:297:G:H5'	2.07	0.54
1:A:437:U:H2'	1:A:437:U:O2	2.07	0.54
1:A:658:G:H2'	1:A:659:U:C6	2.42	0.54
1:A:922:G:C6	1:A:923:A:C6	2.96	0.54
1:A:1053:G:HO2'	1:A:1054:C:P	2.30	0.54
1:A:1055:A:N7	1:A:1206:G:C2	2.75	0.54
1:A:1112:C:O2	4:C:179:ARG:HB3	2.07	0.54
1:A:1129:C:P	1:A:1130:A:H8	2.30	0.54
6:E:91:LEU:HD23	6:E:120:THR:CG2	2.37	0.54
9:H:63:LEU:HD22	9:H:63:LEU:H	1.72	0.54
11:J:50:ILE:N	11:J:60:ARG:HA	2.23	0.54
14:M:15:VAL:HG23	14:M:41:PRO:O	2.08	0.54
1:A:247:G:C6	1:A:278:G:C2	2.96	0.54
1:A:260:G:H2'	1:A:261:U:C6	2.42	0.54
1:A:353:A:C2'	1:A:354:G:OP2	2.55	0.54
1:A:602:A:N3	1:A:637:G:C2	2.76	0.54
1:A:776:G:N2	1:A:802:A:OP2	2.31	0.54
1:A:978:A:O2'	1:A:1322:C:N3	2.33	0.54
1:A:992:U:OP2	1:A:992:U:C6	2.49	0.54
1:A:1092:A:C5'	1:A:1092:A:C8	2.90	0.54
3:B:25:ASN:C	3:B:25:ASN:ND2	2.56	0.54
5:D:59:ARG:NE	5:D:59:ARG:HA	2.22	0.54
7:F:48:LEU:HD13	7:F:52:ILE:HD12	1.89	0.54
8:G:56:GLN:HE21	8:G:56:GLN:N	2.01	0.54
14:M:81:LEU:HD23	14:M:81:LEU:N	2.20	0.54
1:A:977:A:C2'	1:A:978:A:H5"	2.37	0.54
1:A:1525:G:C8	1:A:1525:G:C3'	2.90	0.54
1:A:1530:G:H4'	1:A:1530:G:OP1	2.07	0.54
3:B:187:LEU:CD2	3:B:201:ILE:HG22	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:11:ILE:HG12	6:E:31:LEU:HB3	1.89	0.54
11:J:53:PRO:HA	15:N:41:ARG:HH21	1.72	0.54
13:L:61:THR:C	13:L:63:GLY:H	2.10	0.54
21:T:33:ILE:HD12	21:T:33:ILE:H	1.72	0.54
1:A:292:G:H8	1:A:292:G:O5'	1.91	0.54
1:A:486:U:H2'	1:A:486:U:O2	2.07	0.54
1:A:705:U:H3'	1:A:706:A:C8	2.43	0.54
1:A:707:C:C4'	12:K:20:TYR:CD2	2.86	0.54
1:A:976:G:H5'	1:A:977:A:OP1	2.06	0.54
1:A:990:C:N3	1:A:1216:G:C2	2.75	0.54
1:A:1150:U:O2	1:A:1150:U:H2'	2.07	0.54
1:A:1227:A:C2'	1:A:1228:C:O5'	2.56	0.54
3:B:16:HIS:CD2	3:B:204:ASN:HB2	2.42	0.54
6:E:79:GLU:O	9:H:104:ARG:NH1	2.41	0.54
7:F:9:VAL:HG13	7:F:60:PHE:CD2	2.43	0.54
10:I:8:GLY:HA2	10:I:79:LEU:HD22	1.90	0.54
1:A:255:G:H2'	1:A:256:U:C6	2.42	0.54
1:A:357:G:C2	1:A:358:U:C4	2.96	0.54
1:A:1228:C:H2'	1:A:1229:A:H8	1.73	0.54
1:A:1237:C:O2	1:A:1334:G:O2'	2.24	0.54
4:C:35:GLU:O	4:C:36:ASP:C	2.46	0.54
7:F:94:GLN:HB2	19:R:32:ARG:HD3	1.89	0.54
11:J:38:ILE:HG22	11:J:71:LEU:HB2	1.88	0.54
13:L:76:ASN:HD21	13:L:107:ALA:HA	1.73	0.54
14:M:19:LEU:O	14:M:22:ILE:CD1	2.56	0.54
14:M:73:GLU:O	14:M:76:ALA:HB3	2.07	0.54
17:P:43:LYS:HB3	17:P:48:TRP:CG	2.43	0.54
18:Q:83:ASP:O	18:Q:86:GLU:HB2	2.07	0.54
5:D:36:ARG:HB2	5:D:38:TYR:CE1	2.42	0.54
10:I:97:LYS:O	10:I:100:GLY:N	2.41	0.54
13:L:27:LEU:C	13:L:29:GLY:N	2.57	0.54
20:S:5:LEU:O	20:S:6:LYS:CB	2.55	0.54
1:A:941:G:C2	1:A:942:G:C8	2.95	0.54
3:B:132:LYS:HA	3:B:135:GLN:HB2	1.89	0.54
4:C:122:GLU:O	4:C:125:GLU:N	2.39	0.54
6:E:75:THR:HG23	6:E:76:ILE:N	2.22	0.54
1:A:193:C:H2'	1:A:194:C:H6	1.71	0.54
1:A:395:C:O2	1:A:395:C:H2'	2.06	0.54
1:A:663:A:H2'	1:A:664:G:O4'	2.08	0.54
1:A:691:G:C8	1:A:691:G:H3'	2.43	0.54
1:A:740:U:H6	1:A:740:U:H5"	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:854:G:N1	1:A:855:G:C8	2.76	0.54
1:A:939:G:C6	1:A:940:C:N4	2.76	0.54
1:A:1055:A:C6	1:A:1056:U:C6	2.96	0.54
1:A:1230:C:O2	1:A:1230:C:H2'	2.07	0.54
1:A:1366:C:C2'	1:A:1367:C:C6	2.90	0.54
1:A:1496:C:H2'	1:A:1497:G:C8	2.43	0.54
3:B:215:LEU:O	3:B:218:ALA:HB3	2.08	0.54
7:F:8:ILE:HB	7:F:61:LEU:HB2	1.90	0.54
10:I:19:LEU:HD22	10:I:59:PHE:CD2	2.42	0.54
13:L:45:PRO:HB3	13:L:92:ASP:HB3	1.90	0.54
1:A:20:U:H1'	1:A:916:G:N2	2.22	0.53
1:A:369:C:C2	1:A:370:C:C5	2.96	0.53
1:A:440:A:O3'	1:A:442:C:P	2.65	0.53
1:A:444:C:N3	1:A:491:G:C2	2.76	0.53
1:A:622:A:C8	1:A:623:C:C5	2.96	0.53
1:A:795:C:C5'	1:A:796:C:OP2	2.48	0.53
1:A:869:G:H5"	1:A:870:U:OP1	2.07	0.53
1:A:1236:A:H4'	1:A:1304:G:H4'	1.90	0.53
1:A:1255:G:H3'	1:A:1279:A:H61	1.72	0.53
1:A:1306:A:C4	1:A:1307:U:C6	2.96	0.53
1:A:1413:A:H2	1:A:1487:G:H22	1.56	0.53
1:A:1473:A:H2'	1:A:1474:G:O4'	2.08	0.53
4:C:131:ARG:O	4:C:134:ILE:HD12	2.07	0.53
11:J:39:PRO:HA	11:J:70:ARG:NH2	2.23	0.53
18:Q:53:LEU:HG	18:Q:54:GLY:N	2.23	0.53
1:A:14:U:O2	1:A:17:U:H5	1.90	0.53
1:A:275:G:H5"	1:A:275:G:H8	1.71	0.53
1:A:515:G:C4	1:A:516:U:C6	2.96	0.53
1:A:570:G:H1'	1:A:820:U:C4	2.44	0.53
1:A:751:U:H1'	16:O:23:GLY:O	2.07	0.53
1:A:958:A:C6	20:S:55:LYS:HB2	2.42	0.53
1:A:1186:G:H5"	1:A:1187:G:OP2	2.08	0.53
1:A:1205:U:H1'	4:C:195:VAL:HG22	1.89	0.53
1:A:1213:A:C2	1:A:1215:G:C8	2.96	0.53
3:B:24:TRP:CD1	3:B:24:TRP:C	2.82	0.53
3:B:166:ASP:CG	3:B:205:ASP:HB2	2.29	0.53
19:R:58:LEU:HD13	19:R:62:GLU:CB	2.38	0.53
21:T:74:LYS:HG3	21:T:75:ASN:N	2.21	0.53
1:A:90:U:C6	1:A:90:U:C3'	2.91	0.53
1:A:376:G:C2	1:A:389:A:C2	2.96	0.53
1:A:726:C:H2'	1:A:727:G:H8	1.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1202:G:H8	1:A:1202:G:OP1	1.91	0.53
1:A:1208:C:H2'	1:A:1209:C:H6	1.73	0.53
5:D:116:GLN:O	5:D:120:LEU:HB2	2.08	0.53
6:E:41:VAL:HG22	6:E:113:ALA:HA	1.91	0.53
14:M:16:ASP:N	14:M:16:ASP:OD1	2.40	0.53
1:A:1347:G:C5	10:I:107:ARG:NH1	2.76	0.53
6:E:80:ILE:HA	9:H:104:ARG:HH12	1.74	0.53
8:G:56:GLN:H	8:G:56:GLN:NE2	2.02	0.53
10:I:3:GLN:HG3	10:I:20:ARG:HE	1.73	0.53
14:M:15:VAL:O	14:M:19:LEU:HG	2.09	0.53
14:M:30:ALA:O	14:M:32:GLU:N	2.42	0.53
17:P:10:GLY:HA3	17:P:14:ASN:O	2.09	0.53
19:R:43:PHE:C	19:R:51:LEU:HD12	2.28	0.53
20:S:51:VAL:HG23	20:S:60:VAL:HG23	1.90	0.53
1:A:1075:C:H2'	1:A:1076:C:H5'	1.89	0.53
7:F:6:VAL:HB	7:F:63:TYR:HB2	1.89	0.53
7:F:87:ARG:HD2	19:R:76:LEU:HA	1.91	0.53
9:H:87:SER:HB2	9:H:133:LEU:O	2.08	0.53
9:H:116:LYS:HD2	9:H:129:VAL:HG21	1.89	0.53
1:A:408:A:H5'	5:D:116:GLN:HG3	1.90	0.53
1:A:426:G:OP1	5:D:38:TYR:OH	2.22	0.53
1:A:652:U:C5	1:A:752:G:C4	2.97	0.53
1:A:880:C:H2'	1:A:881:G:C8	2.41	0.53
1:A:1345:U:C4	1:A:1377:A:C2	2.97	0.53
1:A:1523:G:H2'	1:A:1524:C:C6	2.37	0.53
4:C:180:ALA:CB	4:C:182:ILE:CD1	2.86	0.53
5:D:120:LEU:HD22	5:D:126:ILE:HD11	1.90	0.53
8:G:41:ARG:O	8:G:44:TYR:N	2.41	0.53
9:H:103:VAL:HG21	9:H:109:ILE:O	2.08	0.53
11:J:12:ASP:OD2	11:J:15:THR:N	2.36	0.53
12:K:44:SER:H	12:K:47:VAL:HB	1.74	0.53
13:L:43:VAL:HG13	13:L:44:THR:N	2.20	0.53
1:A:427:U:H4'	1:A:541:G:H5"	1.89	0.53
1:A:1075:C:H5'	3:B:103:THR:HG21	1.90	0.53
1:A:1152:A:P	11:J:68:HIS:CE1	3.02	0.53
1:A:1216:G:C2	1:A:1217:C:C4	2.97	0.53
3:B:71:VAL:O	3:B:165:VAL:HG22	2.09	0.53
4:C:101:LEU:HD23	4:C:102:ASN:H	1.72	0.53
6:E:91:LEU:CD2	6:E:120:THR:HG23	2.39	0.53
8:G:91:VAL:HG12	8:G:96:GLN:HE21	1.73	0.53
1:A:378:G:C6	1:A:379:C:N4	2.77	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:781:A:C4	1:A:802:A:C2	2.96	0.53
1:A:899:C:O5'	1:A:899:C:H6	1.91	0.53
1:A:1151:A:H5'	11:J:41:PRO:HA	1.90	0.53
1:A:1152:A:H4'	11:J:13:HIS:HD2	1.73	0.53
1:A:1288:A:N3	1:A:1353:G:H1'	2.23	0.53
5:D:25:ARG:C	5:D:27:TYR:N	2.62	0.53
5:D:59:ARG:HA	5:D:59:ARG:HE	1.73	0.53
5:D:79:PHE:O	5:D:80:GLU:C	2.46	0.53
6:E:59:GLY:O	6:E:62:ALA:CB	2.54	0.53
8:G:120:ILE:HG22	8:G:124:LEU:HD12	1.91	0.53
9:H:29:SER:HB3	9:H:32:LYS:HB2	1.90	0.53
9:H:87:SER:HA	9:H:93:VAL:HG23	1.89	0.53
10:I:64:THR:HG23	10:I:65:VAL:N	2.24	0.53
14:M:23:TYR:HB2	14:M:67:GLU:OE2	2.09	0.53
1:A:19:C:H2'	1:A:20:U:H6	1.73	0.53
1:A:1003(A):G:C2'	1:A:1004:A:H4'	2.32	0.53
1:A:1063:C:H2'	1:A:1064:G:H8	1.74	0.53
1:A:1096:C:C4	1:A:1097:C:C5	2.97	0.53
3:B:51:LEU:HD23	3:B:55:PHE:HE1	1.72	0.53
4:C:3:ASN:ND2	4:C:3:ASN:H	2.06	0.53
5:D:67:ILE:CG2	5:D:68:TYR:CD1	2.91	0.53
5:D:128:VAL:O	5:D:129:ASN:HB2	2.08	0.53
6:E:91:LEU:CD2	6:E:120:THR:CG2	2.86	0.53
6:E:139:LEU:C	6:E:141:GLN:N	2.59	0.53
8:G:28:ASN:ND2	8:G:28:ASN:H	2.06	0.53
17:P:21:VAL:HG12	17:P:33:ILE:HD12	1.90	0.53
1:A:414:A:H2'	1:A:415:A:O4'	2.09	0.53
1:A:642:A:N3	9:H:113:SER:OG	2.41	0.53
1:A:1003(A):G:N2	1:A:1039:C:C2	2.77	0.53
1:A:1056:U:O2	1:A:1057:G:C8	2.62	0.53
3:B:167:PRO:HG2	3:B:192:SER:HB2	1.90	0.53
8:G:92:SER:O	8:G:93:PRO:C	2.48	0.53
13:L:61:THR:O	13:L:63:GLY:N	2.42	0.53
1:A:66:G:C6	1:A:67:C:C5	2.98	0.52
1:A:915:A:H2'	1:A:916:G:H5'	1.91	0.52
1:A:959:A:C2	1:A:1222:G:C4'	2.92	0.52
5:D:24:GLU:O	5:D:27:TYR:HB3	2.09	0.52
5:D:58:LEU:HD23	5:D:58:LEU:C	2.29	0.52
6:E:13:ILE:HA	6:E:29:GLY:O	2.08	0.52
7:F:53:ALA:C	7:F:54:LYS:HG2	2.28	0.52
10:I:111:ARG:HH11	10:I:111:ARG:CB	2.21	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:J:49:VAL:HG13	15:N:41:ARG:HD2	1.90	0.52
12:K:19:ALA:CB	12:K:80:VAL:HG11	2.30	0.52
20:S:52:TYR:CD1	20:S:56:GLN:O	2.62	0.52
1:A:19:C:C2	1:A:20:U:C6	2.98	0.52
1:A:453:A:C2	1:A:454:C:C2	2.96	0.52
1:A:826:C:C2	1:A:827:U:C5	2.97	0.52
1:A:1266:G:N2	1:A:1270:C:H42	2.07	0.52
1:A:1346:A:C8	1:A:1348:U:N3	2.78	0.52
3:B:101:MET:CG	3:B:108:ILE:HD12	2.38	0.52
3:B:189:ASP:OD1	3:B:205:ASP:HB3	2.09	0.52
5:D:138:TYR:C	5:D:138:TYR:HD2	2.12	0.52
9:H:14:ARG:HH11	9:H:14:ARG:CG	2.21	0.52
11:J:12:ASP:OD1	11:J:13:HIS:N	2.43	0.52
1:A:171:A:H2'	1:A:172:A:O4'	2.09	0.52
1:A:247:G:H4'	1:A:247:G:OP1	2.09	0.52
1:A:933:G:H5"	1:A:934:C:OP2	2.10	0.52
1:A:1438:G:C2	1:A:1464:G:C2	2.97	0.52
3:B:101:MET:HG2	3:B:108:ILE:CD1	2.38	0.52
8:G:96:GLN:O	8:G:97:GLN:C	2.47	0.52
8:G:105:VAL:O	8:G:108:ALA:HB3	2.09	0.52
17:P:4:ILE:O	17:P:5:ARG:HB3	2.08	0.52
1:A:78:G:N2	1:A:79:G:H1'	2.24	0.52
1:A:152:A:C6	1:A:170:U:O2	2.63	0.52
1:A:451:A:O5'	1:A:451:A:C8	2.60	0.52
1:A:837:G:C2	1:A:850:U:O2	2.62	0.52
1:A:865:A:H2'	1:A:866:C:C6	2.44	0.52
1:A:924:C:H5'	1:A:1399:C:OP2	2.10	0.52
1:A:1394:A:C5	1:A:1501:C:H4'	2.44	0.52
4:C:131:ARG:HG3	4:C:135:LYS:NZ	2.24	0.52
4:C:199:LYS:HB3	4:C:201:TYR:HE1	1.75	0.52
5:D:199:GLN:CA	5:D:199:GLN:HE21	2.22	0.52
10:I:50:LEU:HD23	10:I:56:LEU:H	1.74	0.52
12:K:73:MET:HE3	12:K:102:GLY:HA3	1.92	0.52
13:L:86:ARG:HH11	13:L:86:ARG:CG	2.12	0.52
21:T:72:LEU:HB3	21:T:76:ALA:HB3	1.90	0.52
1:A:166:G:C2	1:A:167:G:C8	2.98	0.52
1:A:166:G:C2'	1:A:167:G:O5'	2.58	0.52
1:A:374:A:C5	1:A:375:U:C5	2.98	0.52
1:A:393:A:C2	1:A:394:G:C8	2.97	0.52
1:A:640:A:C2'	1:A:641:U:H5'	2.39	0.52
1:A:1149:C:H5"	1:A:1150:U:OP2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:83:ARG:HG2	4:C:86:VAL:HG12	1.91	0.52
9:H:31:PHE:O	9:H:32:LYS:C	2.48	0.52
14:M:10:PRO:HB3	14:M:21:TYR:HD1	1.74	0.52
14:M:109:THR:HG23	14:M:110:ARG:N	2.24	0.52
15:N:53:LEU:CD1	15:N:56:VAL:HG21	2.38	0.52
19:R:55:ARG:HB3	19:R:55:ARG:NH1	2.25	0.52
20:S:52:TYR:HA	20:S:56:GLN:O	2.10	0.52
1:A:53:A:H61	1:A:358:U:H3	1.58	0.52
1:A:223:U:H5'	21:T:68:LYS:NZ	2.25	0.52
1:A:255:G:O2'	1:A:256:U:H5'	2.09	0.52
1:A:818:G:N2	1:A:820:U:C2	2.77	0.52
1:A:1096:C:N3	1:A:1097:C:C5	2.78	0.52
1:A:1144:G:C8	1:A:1144:G:H3'	2.44	0.52
1:A:1502:A:C2'	1:A:1502:A:N3	2.72	0.52
6:E:30:ALA:O	6:E:45:PHE:HA	2.09	0.52
11:J:32:ALA:HB2	11:J:76:ASN:HD22	1.75	0.52
15:N:24:CYS:CB	15:N:29:ARG:H	2.23	0.52
1:A:116:A:H2'	1:A:117:G:H8	1.75	0.52
1:A:256:U:H2'	1:A:257:G:H5'	1.91	0.52
1:A:978:A:C4	1:A:1319:A:C2	2.97	0.52
1:A:1010:G:H2'	1:A:1011:G:H8	1.72	0.52
1:A:1123:A:O3'	11:J:36:GLY:HA3	2.09	0.52
1:A:1129:C:H4'	1:A:1130:A:OP2	2.09	0.52
1:A:1402:C:H2'	1:A:1403:C:H6	1.75	0.52
3:B:106:LYS:O	3:B:109:SER:OG	2.28	0.52
10:I:11:LYS:N	10:I:104:ARG:HH21	2.08	0.52
10:I:114:TYR:CE1	11:J:60:ARG:HB2	2.42	0.52
19:R:37:VAL:O	19:R:39:VAL:N	2.43	0.52
1:A:819:A:H4'	1:A:820:U:OP2	2.10	0.52
1:A:1095:U:H2'	1:A:1096:C:C6	2.45	0.52
1:A:1430:C:C2	1:A:1471:G:N2	2.78	0.52
3:B:102:LEU:N	3:B:102:LEU:HD12	2.24	0.52
1:A:403:C:H2'	1:A:404:U:H6	1.74	0.52
1:A:781:A:C8	1:A:802:A:C2	2.98	0.52
1:A:1107:C:C4	1:A:1108:G:C8	2.98	0.52
1:A:1366:C:C2'	1:A:1367:C:H6	2.16	0.52
3:B:102:LEU:HB2	3:B:176:GLU:OE1	2.10	0.52
3:B:180:LEU:HB2	3:B:182:ILE:CD1	2.39	0.52
5:D:199:GLN:HE21	5:D:199:GLN:C	2.13	0.52
6:E:15:ARG:O	6:E:16:THR:C	2.48	0.52
10:I:118:LYS:O	10:I:119:ALA:CB	2.58	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:25:PRO:C	13:L:27:LEU:N	2.63	0.52
13:L:53:ARG:HD3	13:L:93:LEU:CD2	2.39	0.52
18:Q:7:THR:O	18:Q:23:VAL:HG23	2.10	0.52
18:Q:78:GLU:OE1	18:Q:81:ARG:HD3	2.09	0.52
21:T:41:VAL:C	21:T:43:LEU:N	2.63	0.52
1:A:397:A:C6	1:A:548:G:N7	2.78	0.52
1:A:437:U:H3	1:A:496:A:H62	1.58	0.52
1:A:664:G:H22	1:A:741:G:H1	1.57	0.52
4:C:131:ARG:CG	4:C:135:LYS:NZ	2.73	0.52
6:E:144:THR:O	6:E:147:ASP:N	2.43	0.52
13:L:56:ALA:HB2	13:L:70:ILE:HD11	1.92	0.52
14:M:5:ALA:CB	14:M:22:ILE:HG21	2.40	0.52
1:A:54:C:H42	1:A:357:G:H1	1.58	0.51
1:A:937:A:N6	1:A:1345:U:O4	2.43	0.51
2:Z:4:U:H2'	2:Z:5:C:H6	1.75	0.51
3:B:76:GLN:NE2	3:B:207:ALA:H	2.07	0.51
8:G:27:ILE:CG2	8:G:40:ALA:HA	2.40	0.51
14:M:49:THR:C	14:M:51:ALA:H	2.13	0.51
5:D:3:ARG:HG2	5:D:118:ARG:CZ	2.40	0.51
11:J:3:LYS:N	11:J:75:ILE:HA	2.25	0.51
18:Q:62:SER:CB	18:Q:72:ARG:HG3	2.40	0.51
1:A:590:C:N3	1:A:650:G:C2	2.78	0.51
1:A:691:G:O2'	1:A:797:C:H4'	2.10	0.51
1:A:786:G:C2	1:A:797:C:C2	2.99	0.51
1:A:989:C:O2'	1:A:990:C:H5'	2.11	0.51
1:A:1137:C:H4'	1:A:1138:G:N2	2.26	0.51
1:A:1247:U:H3'	1:A:1247:U:H6	1.76	0.51
3:B:167:PRO:HG3	3:B:188:ALA:CB	2.40	0.51
6:E:144:THR:O	6:E:145:LYS:C	2.47	0.51
9:H:24:THR:HG22	9:H:63:LEU:HD21	1.91	0.51
11:J:7:LYS:O	11:J:96:ILE:HA	2.11	0.51
17:P:74:LEU:N	17:P:74:LEU:HD23	2.24	0.51
20:S:71:LEU:HD22	20:S:72:GLY:N	2.24	0.51
1:A:69:G:H2'	1:A:70:G:H8	1.76	0.51
1:A:615:C:C6	1:A:615:C:H3'	2.45	0.51
1:A:714:G:H2'	1:A:715:A:C8	2.45	0.51
1:A:1056:U:O2	1:A:1056:U:H2'	2.10	0.51
1:A:1192:C:H2'	1:A:1193:G:O4'	2.09	0.51
1:A:1435:G:C4	1:A:1436:U:C5	2.98	0.51
3:B:44:LEU:O	3:B:47:THR:CB	2.58	0.51
4:C:19:GLU:HB3	4:C:40:ARG:HH22	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:41:ARG:HB2	9:H:41:ARG:CZ	2.40	0.51
9:H:104:ARG:C	9:H:106:GLY:N	2.63	0.51
9:H:121:ASP:O	9:H:125:ARG:HB2	2.11	0.51
12:K:122:LYS:O	12:K:123:LYS:C	2.48	0.51
16:O:46:HIS:C	16:O:48:LYS:N	2.58	0.51
20:S:5:LEU:O	20:S:6:LYS:HB2	2.09	0.51
21:T:75:ASN:O	21:T:76:ALA:C	2.47	0.51
1:A:9:G:OP2	6:E:121:LYS:NZ	2.38	0.51
1:A:115:G:H1'	1:A:116:A:N7	2.25	0.51
1:A:362:G:OP1	13:L:61:THR:HG22	2.10	0.51
1:A:416:G:H2'	1:A:417:C:O4'	2.10	0.51
1:A:533:A:O2'	1:A:535:A:OP2	2.27	0.51
1:A:592:G:C2	1:A:648:A:C2	2.98	0.51
1:A:656:C:C6	1:A:656:C:C3'	2.94	0.51
4:C:53:ALA:O	4:C:54:ARG:HB2	2.09	0.51
6:E:51:VAL:O	6:E:54:ALA:N	2.38	0.51
9:H:4:ASP:OD2	9:H:85:ARG:NH1	2.44	0.51
10:I:47:LEU:C	10:I:49:PRO:CD	2.74	0.51
11:J:44:VAL:HG22	11:J:66:ARG:HB3	1.93	0.51
13:L:93:LEU:O	13:L:96:VAL:CG2	2.58	0.51
20:S:83:HIS:N	20:S:83:HIS:HD2	2.07	0.51
1:A:141:A:H1'	1:A:182:U:O2	2.11	0.51
1:A:223:U:H5'	21:T:68:LYS:HZ1	1.75	0.51
1:A:437:U:H5'	5:D:155:LEU:HD11	1.91	0.51
1:A:488:C:O5'	1:A:488:C:H6	1.93	0.51
1:A:1208:C:N3	1:A:1209:C:C5	2.79	0.51
15:N:32:SER:CB	15:N:41:ARG:HB3	2.40	0.51
16:O:74:ASP:C	16:O:76:GLU:H	2.13	0.51
19:R:47:THR:HG22	19:R:83:GLU:O	2.11	0.51
1:A:511:C:C4	1:A:512:U:O4	2.63	0.51
1:A:965:A:C2	1:A:969:A:C2	2.98	0.51
1:A:972:C:H4'	11:J:57:LYS:HB3	1.93	0.51
1:A:1184:G:H2'	1:A:1185:G:H8	1.75	0.51
1:A:1229:A:N3	1:A:1230:C:C5	2.79	0.51
4:C:23:TYR:HD2	11:J:94:VAL:N	2.09	0.51
5:D:41:GLY:C	5:D:43:HIS:H	2.14	0.51
9:H:56:LYS:O	9:H:58:TYR:CD1	2.64	0.51
10:I:4:TYR:CD1	10:I:88:TYR:HB2	2.46	0.51
12:K:33:THR:OG1	12:K:37:GLY:C	2.49	0.51
14:M:22:ILE:HB	14:M:25:ILE:CD1	2.40	0.51
14:M:108:ARG:O	14:M:109:THR:C	2.48	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:O:77:ARG:O	16:O:80:ALA:HB3	2.11	0.51
1:A:328:C:O2	1:A:328:C:C2'	2.46	0.51
1:A:644:G:C5	1:A:645:C:C6	2.98	0.51
1:A:864:A:H3'	1:A:865:A:H8	1.76	0.51
1:A:925:G:O4'	1:A:1502:A:C5	2.64	0.51
1:A:1073:U:H3	1:A:1102:A:H61	1.58	0.51
1:A:1160:G:C2'	1:A:1161:C:O5'	2.57	0.51
1:A:1400:C:C3'	1:A:1401:G:C5'	2.82	0.51
3:B:139:LYS:O	3:B:143:GLU:HB2	2.11	0.51
5:D:32:ALA:C	5:D:34:GLU:N	2.64	0.51
10:I:21:PRO:HA	10:I:59:PHE:HA	1.92	0.51
21:T:34:LYS:HB3	21:T:38:LYS:NZ	2.26	0.51
1:A:404:U:O2'	1:A:405:U:H5'	2.11	0.51
1:A:428:G:C2	1:A:430:A:N6	2.79	0.51
1:A:922:G:H4'	6:E:20:GLN:HA	1.93	0.51
1:A:1014:A:H3'	1:A:1015:A:C8	2.45	0.51
1:A:1449:C:O2	1:A:1449:C:H2'	2.09	0.51
3:B:211:ILE:O	3:B:215:LEU:HB2	2.11	0.51
3:B:223:ILE:HG23	3:B:224:GLN:H	1.74	0.51
5:D:24:GLU:O	5:D:27:TYR:CB	2.59	0.51
10:I:79:LEU:O	10:I:80:GLY:C	2.49	0.51
13:L:35:GLY:HA3	13:L:58:VAL:HG11	1.93	0.51
14:M:14:ARG:HG2	14:M:14:ARG:HH11	1.76	0.51
1:A:570:G:O6	1:A:873:A:C2	2.64	0.51
4:C:22:TRP:N	4:C:22:TRP:CD1	2.71	0.51
8:G:135:VAL:O	8:G:139:GLU:HG3	2.10	0.51
12:K:24:SER:C	12:K:26:ASN:N	2.62	0.51
14:M:17:VAL:O	14:M:20:THR:CB	2.51	0.51
14:M:23:TYR:HB3	14:M:67:GLU:H	1.74	0.51
15:N:4:LYS:C	15:N:6:LEU:N	2.62	0.51
17:P:5:ARG:CG	17:P:6:LEU:N	2.73	0.51
1:A:109:A:C6	1:A:327:A:C6	2.99	0.50
1:A:174:C:O2'	1:A:175:C:H5'	2.11	0.50
1:A:273:A:N6	1:A:274:A:C6	2.79	0.50
1:A:321:A:C2	1:A:333:G:C2	2.98	0.50
1:A:783:C:C2'	1:A:784:C:H5'	2.40	0.50
1:A:976:G:H2'	1:A:1361(A):C:H42	1.74	0.50
7:F:44:GLY:HA2	7:F:60:PHE:N	2.25	0.50
13:L:55:VAL:CG1	13:L:56:ALA:H	2.23	0.50
16:O:35:ARG:HB3	16:O:59:MET:HE3	1.93	0.50
17:P:21:VAL:CG1	17:P:33:ILE:HD12	2.40	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:167:G:H2'	1:A:168:G:H8	1.76	0.50
1:A:640:A:H2'	1:A:641:U:H5'	1.92	0.50
1:A:803:G:C6	1:A:804:U:C4	2.99	0.50
1:A:1237:C:H4'	1:A:1334:G:N2	2.25	0.50
1:A:1286:A:H2'	1:A:1287:A:H4'	1.92	0.50
1:A:1346:A:C5	8:G:10:ARG:NH2	2.79	0.50
1:A:1355:G:C2'	1:A:1356:G:H5'	2.40	0.50
1:A:1371:G:OP1	10:I:11:LYS:O	2.28	0.50
1:A:1428:A:H2'	1:A:1429:C:C6	2.46	0.50
3:B:178:ARG:HH22	9:H:68:ARG:HH21	1.57	0.50
3:B:208:ILE:O	3:B:209:ARG:C	2.49	0.50
16:O:78:TYR:C	16:O:80:ALA:N	2.64	0.50
1:A:1066:C:C2'	1:A:1067:A:C5'	2.90	0.50
1:A:1227:A:C2	20:S:83:HIS:HB2	2.46	0.50
1:A:1365:G:C5	1:A:1366:C:C5	2.99	0.50
1:A:1406:U:H2'	1:A:1407:C:C6	2.45	0.50
1:A:1507:A:H5"	1:A:1507:A:H8	1.76	0.50
5:D:62:GLN:O	5:D:66:ARG:HD3	2.11	0.50
6:E:13:ILE:O	6:E:13:ILE:HD13	2.11	0.50
13:L:69:TYR:C	13:L:69:TYR:CD2	2.85	0.50
1:A:382:A:N3	1:A:383:A:C8	2.79	0.50
1:A:429:U:C4	1:A:431:A:N6	2.76	0.50
1:A:505:G:H5"	1:A:506:G:OP2	2.11	0.50
1:A:509:A:C8	1:A:509:A:C3'	2.93	0.50
1:A:793:U:O4	1:A:1517:G:H5"	2.12	0.50
1:A:976:G:N7	1:A:1358:U:C2	2.79	0.50
1:A:1118:C:H1'	1:A:1179:A:C4	2.47	0.50
3:B:112:VAL:HG12	3:B:153:ARG:HG2	1.91	0.50
20:S:17:GLU:O	20:S:21:GLU:HB2	2.12	0.50
1:A:20:U:O2	1:A:20:U:H2'	2.12	0.50
1:A:644:G:C4	1:A:645:C:C6	2.99	0.50
1:A:762:C:O5'	1:A:762:C:H6	1.94	0.50
1:A:977:A:H2'	1:A:978:A:H5'	1.93	0.50
1:A:1048:G:C8	1:A:1048:G:H3'	2.46	0.50
6:E:28:PHE:O	6:E:47:LYS:HA	2.11	0.50
18:Q:4:LYS:H	18:Q:61:GLU:CB	2.21	0.50
1:A:37:U:N3	1:A:38:G:C8	2.80	0.50
1:A:463:A:O3'	1:A:474:G:P	2.68	0.50
1:A:512:U:H2'	1:A:513:C:C6	2.46	0.50
1:A:1125:U:H3	11:J:5:ARG:HE	1.59	0.50
6:E:67:VAL:O	6:E:67:VAL:CG1	2.58	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:75:HIS:CD2	13:L:76:ASN:H	2.27	0.50
19:R:36:ASN:O	19:R:39:VAL:HG12	2.12	0.50
1:A:109:A:H3'	1:A:110:C:H5'	1.93	0.50
1:A:362:G:C8	1:A:362:G:C3'	2.94	0.50
1:A:426:G:P	5:D:36:ARG:HH21	2.33	0.50
1:A:992:U:H4'	1:A:993:G:O5'	2.11	0.50
1:A:1249:C:C6	1:A:1249:C:C3'	2.94	0.50
4:C:115:LEU:O	4:C:118:GLN:N	2.44	0.50
6:E:33:VAL:HG11	6:E:109:ILE:HG12	1.93	0.50
8:G:26:PHE:CD2	8:G:30:ILE:HD11	2.47	0.50
14:M:14:ARG:HB3	14:M:16:ASP:OD1	2.12	0.50
14:M:109:THR:HG23	14:M:110:ARG:H	1.76	0.50
20:S:72:GLY:C	20:S:74:PHE:N	2.54	0.50
1:A:437:U:H3'	1:A:438:G:H8	1.76	0.50
1:A:888:G:H8	1:A:888:G:O5'	1.93	0.50
1:A:1065:U:C5	1:A:1190:G:C4	3.00	0.50
1:A:1513:A:C6	1:A:1523:G:C6	3.00	0.50
3:B:102:LEU:O	3:B:105:PHE:HB2	2.12	0.50
4:C:19:GLU:HB3	4:C:40:ARG:NH2	2.27	0.50
4:C:123:GLN:HE22	4:C:140:ARG:NH2	2.08	0.50
5:D:199:GLN:NE2	5:D:199:GLN:CA	2.75	0.50
6:E:101:ILE:O	6:E:120:THR:OG1	2.28	0.50
6:E:107:ARG:O	6:E:109:ILE:N	2.45	0.50
11:J:32:ALA:HB2	11:J:76:ASN:ND2	2.27	0.50
13:L:102:ARG:NH1	13:L:110:VAL:CA	2.74	0.50
16:O:39:LEU:HD13	16:O:56:LEU:HB2	1.93	0.50
1:A:664:G:H1	1:A:741:G:H1	1.59	0.50
1:A:986:A:C2	1:A:1220:G:C2	3.00	0.50
1:A:1168:A:C6	1:A:1169:A:C6	3.00	0.50
1:A:1342:C:O2'	10:I:124:GLN:HB2	2.12	0.50
1:A:1368:G:C2	1:A:1369:C:C6	2.99	0.50
6:E:148:VAL:HG21	9:H:107:LEU:HD13	1.94	0.50
7:F:33:TYR:HD2	7:F:71:ARG:HD2	1.76	0.50
11:J:17:ASP:O	11:J:21:GLN:HB2	2.12	0.50
13:L:35:GLY:HA3	13:L:58:VAL:CG1	2.42	0.50
19:R:66:LEU:O	19:R:67:ALA:C	2.50	0.50
1:A:18:C:C2'	1:A:19:C:H5'	2.42	0.49
1:A:129(A):G:H4'	1:A:130:A:OP2	2.12	0.49
1:A:358:U:C2	1:A:359:U:C5	2.99	0.49
1:A:374:A:H5"	1:A:375:U:OP2	2.12	0.49
1:A:983:A:HO2'	1:A:1049:U:HO2'	1.57	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1053:G:C4	1:A:1199:U:C5	3.00	0.49
3:B:185:ILE:HD12	3:B:185:ILE:H	1.77	0.49
4:C:54:ARG:O	4:C:55:VAL:CG2	2.55	0.49
7:F:26:ILE:HG21	7:F:63:TYR:HE1	1.76	0.49
11:J:12:ASP:CG	11:J:14:LYS:H	2.15	0.49
15:N:24:CYS:HB3	15:N:29:ARG:H	1.77	0.49
18:Q:82:MET:HA	18:Q:85:VAL:CG2	2.42	0.49
1:A:13:U:O2	1:A:914:A:H3'	2.11	0.49
1:A:84:U:H5"	1:A:88:A:OP2	2.12	0.49
1:A:109:A:N6	1:A:326:G:C6	2.80	0.49
1:A:167:G:H2'	1:A:168:G:C8	2.48	0.49
1:A:288:A:C2'	1:A:289:G:O5'	2.61	0.49
1:A:357:G:H2'	1:A:358:U:C6	2.47	0.49
1:A:363:A:OP1	13:L:61:THR:OG1	2.19	0.49
1:A:577:G:H1'	1:A:816:A:C2	2.46	0.49
1:A:673:G:H5"	1:A:674:G:OP2	2.11	0.49
1:A:691:G:C8	1:A:691:G:C3'	2.94	0.49
1:A:738:C:OP2	7:F:92:LYS:HE2	2.12	0.49
1:A:1226:C:C4	14:M:104:ARG:HG3	2.47	0.49
1:A:1378:C:H3'	1:A:1379:G:H5"	1.93	0.49
1:A:1413:A:C2	1:A:1414:U:C2	3.01	0.49
1:A:1502:A:H5'	1:A:1504:G:N7	2.27	0.49
5:D:159:ARG:O	5:D:160:GLN:C	2.50	0.49
12:K:22:HIS:HA	12:K:85:ARG:O	2.11	0.49
20:S:9:VAL:HG12	20:S:10:PHE:N	2.26	0.49
1:A:69:G:H2'	1:A:70:G:C8	2.47	0.49
1:A:502:G:C6	1:A:544:G:N1	2.80	0.49
1:A:546:G:OP1	5:D:73:ARG:HB2	2.11	0.49
1:A:577:G:H1'	1:A:816:A:C4	2.48	0.49
1:A:942:G:C2	1:A:943:U:C6	3.00	0.49
1:A:977:A:H2'	1:A:978:A:H5"	1.93	0.49
1:A:1082:G:H5"	1:A:1083:U:OP2	2.13	0.49
1:A:1120:G:N2	1:A:1153:C:O2	2.43	0.49
1:A:1226:C:N4	14:M:104:ARG:HG3	2.27	0.49
1:A:1372:U:O2'	1:A:1373:G:H5'	2.12	0.49
1:A:1437:C:H2'	1:A:1438:G:C8	2.47	0.49
3:B:77:ALA:HB2	3:B:211:ILE:CD1	2.24	0.49
4:C:141:VAL:HG11	4:C:202:ILE:HG12	1.94	0.49
5:D:55:ALA:O	5:D:59:ARG:HG2	2.12	0.49
6:E:15:ARG:O	6:E:16:THR:O	2.30	0.49
10:I:33:PHE:CE1	10:I:37:PHE:CE1	3.01	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:R:32:ARG:O	19:R:34:TYR:N	2.44	0.49
1:A:529:G:C8	1:A:529:G:C3'	2.94	0.49
1:A:651:C:C2'	1:A:652:U:H5'	2.42	0.49
1:A:957:U:O2	1:A:960:U:C2	2.65	0.49
1:A:1068:G:N7	1:A:1094:G:H8	2.09	0.49
1:A:1102:A:H1'	3:B:99:GLY:HA3	1.94	0.49
1:A:1201:A:HO2'	1:A:1202:G:P	2.34	0.49
4:C:39:ILE:C	4:C:41:GLY:N	2.65	0.49
5:D:152:SER:O	5:D:155:LEU:HB2	2.11	0.49
12:K:82:VAL:CG1	12:K:83:ILE:N	2.75	0.49
12:K:94:ALA:O	12:K:95:ILE:C	2.51	0.49
13:L:67:THR:O	13:L:67:THR:CG2	2.60	0.49
16:O:60:VAL:HG12	16:O:61:GLY:N	2.27	0.49
17:P:75:ARG:HA	17:P:80:PHE:HD1	1.76	0.49
1:A:287:U:O2'	1:A:288:A:H5'	2.12	0.49
1:A:292:G:C3'	1:A:292:G:C8	2.95	0.49
1:A:357:G:C2	1:A:358:U:C5	3.00	0.49
1:A:939:G:P	8:G:95:ARG:HH12	2.36	0.49
1:A:959:A:H5"	1:A:960:U:OP2	2.13	0.49
1:A:991:U:C6	1:A:1212:U:C2	3.01	0.49
1:A:1003(A):G:C4	1:A:1004:A:H1'	2.47	0.49
1:A:1119:C:C6	1:A:1119:C:C3'	2.94	0.49
1:A:1121:U:H2'	1:A:1122:U:H6	1.75	0.49
1:A:1144:G:H2'	1:A:1145:C:H5'	1.95	0.49
1:A:1240:U:N3	8:G:30:ILE:HG23	2.27	0.49
1:A:1395:C:H6	1:A:1395:C:O5'	1.95	0.49
1:A:1402:C:H2'	1:A:1403:C:C6	2.47	0.49
1:A:1502:A:N3	1:A:1502:A:H2'	2.28	0.49
3:B:71:VAL:HG23	3:B:164:VAL:HA	1.94	0.49
7:F:80:ARG:CG	7:F:88:VAL:CG2	2.89	0.49
10:I:4:TYR:CG	10:I:88:TYR:HB2	2.48	0.49
13:L:104:VAL:O	13:L:105:TYR:HB2	2.13	0.49
17:P:11:SER:O	17:P:14:ASN:N	2.36	0.49
1:A:251:G:H4'	1:A:252:U:O5'	2.12	0.49
1:A:268:C:H2'	1:A:269:C:C6	2.44	0.49
1:A:429:U:O4	1:A:431:A:N6	2.46	0.49
1:A:946:A:N1	1:A:947:G:C6	2.81	0.49
1:A:969:A:H61	14:M:126:LYS:CB	2.25	0.49
1:A:982:U:H4'	1:A:983:A:O5'	2.12	0.49
1:A:1348:U:H4'	10:I:120:ARG:HG3	1.93	0.49
3:B:166:ASP:OD1	3:B:205:ASP:CB	2.61	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:42:LEU:O	4:C:43:LEU:C	2.50	0.49
5:D:88:VAL:O	5:D:92:VAL:HG23	2.12	0.49
14:M:30:ALA:O	14:M:31:LYS:C	2.48	0.49
1:A:575:G:HO2'	1:A:821:G:H5'	1.77	0.49
1:A:709:G:H2'	1:A:710:G:H8	1.77	0.49
1:A:945:G:C8	1:A:1337:G:H1'	2.48	0.49
1:A:1069:C:O3'	6:E:25:ARG:NH2	2.45	0.49
1:A:1131:G:H22	1:A:1143:G:N2	2.04	0.49
1:A:1142:G:H5"	1:A:1143:G:OP2	2.11	0.49
5:D:30:LYS:HA	5:D:35:ARG:HE	1.78	0.49
5:D:141:ARG:HB3	5:D:142:PRO:HD3	1.90	0.49
14:M:22:ILE:HG22	14:M:23:TYR:N	2.27	0.49
17:P:43:LYS:HA	17:P:48:TRP:CB	2.41	0.49
17:P:78:GLY:C	17:P:80:PHE:N	2.64	0.49
19:R:86:VAL:O	19:R:87:ARG:CB	2.56	0.49
1:A:192:U:C4'	21:T:103:GLY:H	2.26	0.49
1:A:617:G:O6	1:A:623:C:N4	2.44	0.49
1:A:722:A:H5"	1:A:722:A:N3	2.27	0.49
1:A:812:C:OP1	1:A:903:G:H1'	2.13	0.49
1:A:1097:C:O2	1:A:1097:C:H2'	2.12	0.49
1:A:1191:A:O2'	1:A:1192:C:H5'	2.13	0.49
1:A:1370:G:H2'	1:A:1371:G:H8	1.78	0.49
4:C:115:LEU:O	4:C:116:VAL:C	2.50	0.49
5:D:150:GLU:CA	5:D:153:ARG:HB2	2.40	0.49
8:G:137:LYS:O	8:G:141:VAL:HG23	2.13	0.49
9:H:89:PRO:HA	9:H:92:ARG:NH1	2.28	0.49
11:J:76:ASN:CB	11:J:78:ASN:HD21	2.22	0.49
12:K:70:LYS:O	12:K:73:MET:HB2	2.13	0.49
12:K:123:LYS:C	12:K:125:PHE:N	2.66	0.49
16:O:13:GLN:O	16:O:14:GLU:C	2.51	0.49
21:T:92:LEU:O	21:T:93:GLU:C	2.51	0.49
1:A:149:A:C2	1:A:150:C:C4	3.01	0.49
1:A:656:C:H2'	1:A:657:G:O5'	2.13	0.49
1:A:1247:U:O2	1:A:1291:G:C2	2.65	0.49
1:A:1291:G:H4'	10:I:38:GLN:O	2.12	0.49
1:A:1365:G:C6	1:A:1366:C:C4	3.00	0.49
1:A:1422:G:H8	1:A:1422:G:O5'	1.96	0.49
7:F:7:ASN:HA	7:F:61:LEU:O	2.12	0.49
8:G:67:GLU:HA	8:G:70:LYS:HE3	1.95	0.49
9:H:4:ASP:O	9:H:7:ALA:HB3	2.13	0.49
12:K:82:VAL:HG12	12:K:108:ILE:HG23	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:M:39:ILE:HG21	14:M:48:LEU:HD21	1.95	0.49
18:Q:75:ARG:HH11	18:Q:75:ARG:HG3	1.77	0.49
21:T:54:LYS:HA	21:T:57:ARG:HH12	1.78	0.49
1:A:107:G:N2	1:A:108:G:H1'	2.28	0.49
1:A:129(A):G:C2	1:A:190(E):U:H5"	2.47	0.49
1:A:570:G:C6	1:A:873:A:C2	3.00	0.49
1:A:623:C:C2	1:A:624:C:C6	3.01	0.49
1:A:1010:G:N2	1:A:1020:U:H1'	2.16	0.49
1:A:1081:G:P	6:E:16:THR:OG1	2.71	0.49
1:A:1104:G:H4'	3:B:111:ARG:NH2	2.28	0.49
1:A:1142:G:C2	1:A:1143:G:H1'	2.47	0.49
1:A:1209:C:O2	1:A:1209:C:C2'	2.45	0.49
1:A:1239:A:C4	1:A:1298:C:N4	2.81	0.49
1:A:1250:A:N6	1:A:1354:C:O4'	2.38	0.49
1:A:1523:G:C4	1:A:1524:C:C5	3.00	0.49
24:A:1636:D2C:H11A	24:A:1636:D2C:H18	1.95	0.49
3:B:59:GLU:O	3:B:62:ALA:HB3	2.13	0.49
3:B:109:SER:O	3:B:112:VAL:HG23	2.13	0.49
4:C:35:GLU:O	4:C:37:GLN:N	2.46	0.49
5:D:120:LEU:HD22	5:D:126:ILE:CD1	2.43	0.49
13:L:6:THR:O	13:L:7:ILE:C	2.50	0.49
13:L:86:ARG:NH2	13:L:99:HIS:HD2	2.07	0.49
13:L:98:TYR:HD1	13:L:98:TYR:H	1.59	0.49
1:A:290:C:C5	1:A:291:C:H5	2.31	0.48
1:A:1184:G:H8	1:A:1184:G:O5'	1.95	0.48
1:A:1394:A:N7	1:A:1501:C:H4'	2.28	0.48
1:A:1399:C:C2	1:A:1401:G:C5	3.01	0.48
1:A:1486:G:H2'	1:A:1487:G:O4'	2.12	0.48
5:D:196:LEU:HD23	5:D:197:PRO:HD2	1.95	0.48
6:E:102:ALA:HB1	6:E:106:PRO:HG2	1.94	0.48
7:F:5:GLU:O	7:F:90:VAL:HA	2.13	0.48
18:Q:75:ARG:NH1	18:Q:77:VAL:HG13	2.26	0.48
1:A:1065:U:H4'	1:A:1066:C:H5'	1.95	0.48
1:A:1074:G:C6	1:A:1075:C:C4	3.01	0.48
1:A:1167:A:O5'	1:A:1167:A:C8	2.63	0.48
4:C:95:THR:HG22	4:C:97:LYS:HE3	1.94	0.48
6:E:86:ALA:O	6:E:125:SER:N	2.43	0.48
11:J:61:GLU:HG2	11:J:62:HIS:N	2.28	0.48
14:M:49:THR:C	14:M:51:ALA:N	2.67	0.48
16:O:11:VAL:O	16:O:12:ILE:C	2.51	0.48
1:A:53:A:C6	1:A:54:C:C2	3.02	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:264:U:H3'	1:A:264:U:C6	2.49	0.48
1:A:601:C:C2	1:A:638:G:N2	2.81	0.48
1:A:1249:C:O5'	1:A:1249:C:H6	1.96	0.48
1:A:1333:A:H2'	1:A:1334:G:H8	1.78	0.48
1:A:1377:A:C2'	1:A:1378:C:OP2	2.61	0.48
1:A:1513:A:H2'	1:A:1514:C:H6	1.77	0.48
3:B:107:THR:C	3:B:109:SER:N	2.67	0.48
4:C:172:ARG:HB2	4:C:203:PHE:CE2	2.49	0.48
6:E:107:ARG:C	6:E:109:ILE:H	2.17	0.48
10:I:10:ARG:HG3	10:I:11:LYS:HB2	1.94	0.48
15:N:44:LEU:C	15:N:44:LEU:HD12	2.33	0.48
18:Q:22:LEU:HD13	18:Q:41:LYS:HG2	1.95	0.48
21:T:72:LEU:HB3	21:T:76:ALA:CB	2.43	0.48
1:A:200:G:C8	1:A:200:G:C4'	2.97	0.48
1:A:252:U:H2'	1:A:253:U:H6	1.73	0.48
1:A:255:G:O6	1:A:266:G:O6	2.32	0.48
1:A:420:U:O2	1:A:424:G:C2	2.67	0.48
1:A:991:U:C5	1:A:1212:U:H1'	2.49	0.48
1:A:1208:C:C2	1:A:1209:C:C6	3.01	0.48
3:B:58:ILE:O	3:B:59:GLU:C	2.51	0.48
3:B:92:TYR:CD1	3:B:92:TYR:C	2.86	0.48
5:D:79:PHE:HD2	5:D:79:PHE:C	2.16	0.48
6:E:60:TYR:CD2	6:E:60:TYR:C	2.87	0.48
14:M:5:ALA:CB	14:M:22:ILE:HG12	2.43	0.48
14:M:48:LEU:HD22	14:M:52:GLU:HB2	1.95	0.48
17:P:52:ASP:C	17:P:52:ASP:OD2	2.51	0.48
1:A:1279:A:O2'	1:A:1281:U:OP2	2.22	0.48
1:A:1432:G:C8	1:A:1432:G:H3'	2.49	0.48
24:A:1636:D2C:O5	24:A:1636:D2C:O4	2.31	0.48
5:D:148:VAL:CG2	5:D:181:MET:HB3	2.43	0.48
16:O:39:LEU:HD12	16:O:56:LEU:HB2	1.95	0.48
17:P:11:SER:O	17:P:12:LYS:C	2.52	0.48
21:T:78:ALA:O	21:T:79:ARG:C	2.51	0.48
1:A:106:C:O2'	1:A:107:G:H5'	2.14	0.48
1:A:176:C:O2	1:A:176:C:C2'	2.62	0.48
1:A:354:G:C6	1:A:355:C:C4	3.02	0.48
1:A:771:G:O2'	1:A:772:U:H5'	2.14	0.48
1:A:858:G:H8	1:A:858:G:O5'	1.97	0.48
1:A:976:G:C8	1:A:1358:U:O2	2.67	0.48
1:A:1081:G:P	6:E:16:THR:HG1	2.36	0.48
1:A:1117:G:O3'	10:I:104:ARG:HD2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1166:G:C8	1:A:1166:G:H3'	2.48	0.48
1:A:1240:U:H1'	8:G:38:LEU:HD21	1.95	0.48
1:A:1381:U:C2	1:A:1382:C:C6	3.02	0.48
4:C:6:HIS:CD2	4:C:8:ILE:N	2.79	0.48
5:D:61:LYS:HE2	5:D:62:GLN:NE2	2.25	0.48
10:I:45:ALA:C	10:I:47:LEU:H	2.17	0.48
11:J:38:ILE:CB	11:J:71:LEU:HB3	2.42	0.48
15:N:21:TYR:C	15:N:21:TYR:CD2	2.87	0.48
21:T:63:ILE:O	21:T:66:ALA:N	2.45	0.48
1:A:157:G:C6	1:A:158:G:N7	2.82	0.48
1:A:506:G:C5	1:A:507:C:C4	3.02	0.48
1:A:570:G:H2'	1:A:571:U:C6	2.49	0.48
1:A:647:C:N4	1:A:648:A:N6	2.62	0.48
1:A:1086:U:H3	1:A:1099:G:H22	1.60	0.48
1:A:1163:C:H42	1:A:1173:G:H1	1.60	0.48
1:A:1241:G:C6	1:A:1242:C:N4	2.81	0.48
1:A:1345:U:C2	1:A:1377:A:C2	3.02	0.48
1:A:1348:U:C6	1:A:1348:U:C5'	2.97	0.48
1:A:1363:A:C4	1:A:1365:G:C6	3.02	0.48
1:A:1453:G:N2	1:A:1454:G:C5	2.81	0.48
5:D:105:VAL:HG13	5:D:110:PHE:HB2	1.95	0.48
6:E:99:GLY:O	6:E:117:ASP:HA	2.13	0.48
7:F:98:LEU:HB3	19:R:30:ASP:HA	1.96	0.48
10:I:65:VAL:HG22	10:I:66:ARG:N	2.29	0.48
10:I:97:LYS:N	10:I:98:PRO:HD2	2.27	0.48
13:L:90:VAL:O	13:L:92:ASP:N	2.46	0.48
13:L:100:ILE:HG22	13:L:101:VAL:N	2.28	0.48
1:A:128:G:H5'	18:Q:2:PRO:HA	1.94	0.48
1:A:132:C:O2'	1:A:133:U:H5'	2.14	0.48
1:A:581:G:O6	1:A:758:G:C8	2.67	0.48
1:A:652:U:O4	1:A:752:G:O2'	2.21	0.48
1:A:1128:C:N3	1:A:1144:G:N2	2.62	0.48
1:A:1208:C:C2	1:A:1209:C:C5	3.02	0.48
1:A:1216:G:H5"	15:N:5:ALA:HB2	1.95	0.48
1:A:1283:G:H2'	1:A:1284:C:O4'	2.14	0.48
24:A:1636:D2C:H5	24:A:1636:D2C:H13	1.51	0.48
3:B:92:TYR:CE1	3:B:151:GLY:CA	2.97	0.48
3:B:134:GLU:O	3:B:138:LEU:HG	2.14	0.48
3:B:145:LEU:O	3:B:149:LEU:HB2	2.14	0.48
6:E:82:VAL:HG12	6:E:89:ILE:HG22	1.95	0.48
8:G:92:SER:CB	8:G:93:PRO:HD2	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:108:ALA:O	8:G:111:ARG:N	2.42	0.48
10:I:11:LYS:H	10:I:104:ARG:HH21	1.62	0.48
10:I:49:PRO:HB3	10:I:82:ALA:HB2	1.95	0.48
11:J:38:ILE:CG2	11:J:71:LEU:CB	2.92	0.48
11:J:46:ARG:HH11	11:J:46:ARG:CG	2.24	0.48
21:T:29:LYS:O	21:T:33:ILE:HD12	2.14	0.48
1:A:142:G:O2'	1:A:195:A:N6	2.47	0.48
1:A:153:C:N4	1:A:168:G:H1	2.11	0.48
1:A:286:G:C6	1:A:287:U:C4	3.01	0.48
1:A:786:G:C6	1:A:787:A:C5	3.02	0.48
1:A:1097:C:O2'	1:A:1168:A:N3	2.44	0.48
1:A:1106:G:O2'	1:A:1107:C:H5'	2.14	0.48
3:B:24:TRP:CD1	3:B:25:ASN:N	2.82	0.48
3:B:54:THR:O	3:B:57:PHE:HB3	2.13	0.48
4:C:55:VAL:O	4:C:55:VAL:CG1	2.59	0.48
5:D:79:PHE:C	5:D:79:PHE:CD2	2.86	0.48
8:G:91:VAL:CG1	8:G:96:GLN:HE21	2.27	0.48
10:I:82:ALA:O	10:I:86:VAL:CG2	2.60	0.48
14:M:74:VAL:C	14:M:76:ALA:H	2.16	0.48
1:A:197:A:H4'	1:A:198:G:O5'	2.13	0.48
1:A:512:U:H2'	1:A:513:C:H6	1.79	0.48
1:A:1003(A):G:C2	1:A:1004:A:H1'	2.49	0.48
1:A:1416:G:H2'	1:A:1417:G:H5'	1.95	0.48
10:I:86:VAL:HG12	10:I:90:PRO:HA	1.96	0.48
10:I:93:ARG:O	10:I:94:ALA:C	2.51	0.48
11:J:24:VAL:HG21	11:J:37:PRO:HD3	1.94	0.48
14:M:98:VAL:C	14:M:100:GLY:H	2.17	0.48
16:O:28:GLN:O	16:O:30:ALA:N	2.46	0.48
1:A:252:U:C4	1:A:253:U:O4	2.67	0.47
1:A:319:G:N2	1:A:334:C:O2	2.40	0.47
1:A:838:G:H1	1:A:848:C:N4	2.08	0.47
1:A:1101:A:C4'	1:A:1102:A:O5'	2.62	0.47
6:E:108:ALA:HA	6:E:111:GLU:HB2	1.96	0.47
11:J:81:THR:O	11:J:84:GLN:N	2.35	0.47
12:K:16:SER:O	12:K:35:PRO:HG3	2.14	0.47
19:R:33:ASP:C	19:R:35:ARG:N	2.65	0.47
20:S:78:ARG:HD2	20:S:78:ARG:N	2.26	0.47
21:T:84:LEU:O	21:T:87:LYS:N	2.47	0.47
1:A:285:G:H2'	1:A:285:G:N3	2.29	0.47
1:A:404:U:H2'	1:A:405:U:H6	1.79	0.47
1:A:420:U:H1'	1:A:424:G:H22	1.71	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:477:G:C2	1:A:478:A:C5	3.02	0.47
1:A:719:C:H42	19:R:74:ARG:HH12	1.61	0.47
1:A:950:U:C5	14:M:102:ARG:NH1	2.82	0.47
1:A:1060:C:O2	1:A:1198:G:C2	2.67	0.47
1:A:1095:U:P	1:A:1108:G:H1	2.37	0.47
1:A:1288:A:C8	1:A:1289:A:C8	3.02	0.47
1:A:1443:G:H5'	1:A:1446:A:H3'	1.94	0.47
1:A:1525:G:P	12:K:120:ARG:HH21	2.37	0.47
3:B:105:PHE:O	3:B:106:LYS:C	2.52	0.47
4:C:11:ARG:HH12	4:C:178:LEU:CA	2.17	0.47
5:D:30:LYS:HD3	5:D:35:ARG:HH21	1.78	0.47
7:F:44:GLY:HA3	7:F:59:TYR:CE1	2.49	0.47
8:G:154:TYR:N	8:G:154:TYR:CD2	2.82	0.47
9:H:40:ALA:O	9:H:41:ARG:C	2.50	0.47
20:S:52:TYR:HD1	20:S:56:GLN:O	1.97	0.47
1:A:78:G:C2	1:A:79:G:C8	3.02	0.47
1:A:935:A:C2'	1:A:936:C:O5'	2.61	0.47
1:A:964:A:O2'	11:J:55:LYS:HD2	2.14	0.47
1:A:1148:U:H2'	1:A:1149:C:O4'	2.13	0.47
4:C:58:GLU:HG2	11:J:92:THR:CB	2.45	0.47
4:C:201:TYR:C	4:C:202:ILE:HG13	2.33	0.47
5:D:190:ASP:O	5:D:191:ARG:C	2.52	0.47
6:E:11:ILE:HG13	6:E:31:LEU:HB3	1.96	0.47
7:F:67:MET:HB2	7:F:68:PRO:CD	2.44	0.47
8:G:154:TYR:N	8:G:154:TYR:HD2	2.12	0.47
10:I:113:LYS:N	10:I:113:LYS:CD	2.77	0.47
19:R:66:LEU:HG	19:R:70:ILE:HD11	1.96	0.47
1:A:235:C:H5'	18:Q:70:ARG:HD3	1.96	0.47
1:A:392:G:C2	1:A:393:A:C5	3.02	0.47
1:A:568:G:C2'	1:A:569:C:H5'	2.42	0.47
1:A:582:U:H5"	16:O:64:ARG:HH22	1.78	0.47
1:A:640:A:C6	1:A:641:U:C4	3.02	0.47
1:A:726:C:H2'	1:A:727:G:C8	2.49	0.47
1:A:978:A:C6	1:A:1318:A:C6	3.03	0.47
1:A:1053:G:O2'	1:A:1054:C:P	2.72	0.47
1:A:1112:C:N3	4:C:178:LEU:HB3	2.29	0.47
1:A:1114:C:H1'	15:N:60:SER:HB3	1.97	0.47
1:A:1197:G:C2'	1:A:1198:G:H5'	2.44	0.47
3:B:52:GLU:O	3:B:54:THR:N	2.48	0.47
4:C:10:PHE:CZ	4:C:178:LEU:HD13	2.50	0.47
12:K:33:THR:HG23	12:K:37:GLY:HA2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:N:54:PRO:C	15:N:56:VAL:H	2.18	0.47
16:O:52:SER:O	16:O:53:HIS:C	2.52	0.47
21:T:13:LEU:O	21:T:15:ARG:N	2.47	0.47
1:A:160:A:H1'	1:A:344:A:N7	2.29	0.47
1:A:237:C:H5"	1:A:238:G:OP2	2.15	0.47
1:A:1205:U:H1'	4:C:195:VAL:CG2	2.44	0.47
1:A:1345:U:N3	1:A:1377:A:C2	2.82	0.47
14:M:96:LEU:O	14:M:110:ARG:NH1	2.44	0.47
17:P:75:ARG:HA	17:P:80:PHE:CD1	2.49	0.47
18:Q:67:LYS:O	18:Q:68:ARG:HB2	2.14	0.47
1:A:52:G:C2'	1:A:53:A:H5'	2.45	0.47
1:A:809:G:C6	1:A:810:C:C5	3.03	0.47
1:A:836:G:H2'	1:A:837:G:H8	1.80	0.47
1:A:840:C:O5'	1:A:840:C:H6	1.98	0.47
1:A:914:A:C2	1:A:915:A:C1'	2.98	0.47
1:A:939:G:C6	1:A:940:C:C4	3.02	0.47
1:A:1066:C:O2'	1:A:1067:A:C5'	2.61	0.47
1:A:1121:U:O2'	1:A:1122:U:O5'	2.28	0.47
4:C:6:HIS:HD2	4:C:8:ILE:N	2.07	0.47
4:C:113:ALA:O	4:C:116:VAL:N	2.48	0.47
5:D:29:PRO:O	5:D:30:LYS:HG2	2.15	0.47
8:G:24:THR:HA	8:G:27:ILE:HD12	1.97	0.47
9:H:14:ARG:NH1	9:H:14:ARG:CB	2.78	0.47
10:I:114:TYR:HE1	11:J:59:SER:O	1.96	0.47
11:J:6:ILE:HD11	11:J:73:ASP:H	1.79	0.47
12:K:46:GLY:O	12:K:47:VAL:C	2.53	0.47
1:A:130:A:O2'	1:A:131:C:O5'	2.24	0.47
1:A:150:C:C2'	1:A:151:A:O5'	2.63	0.47
1:A:193:C:H2'	1:A:194:C:C6	2.49	0.47
1:A:226:G:C2	1:A:227:G:C8	3.02	0.47
1:A:247:G:C6	1:A:278:G:N1	2.82	0.47
1:A:313:A:H2'	1:A:314:C:H6	1.79	0.47
1:A:354:G:H2'	1:A:354:G:N3	2.29	0.47
1:A:393:A:H2'	1:A:394:G:C8	2.34	0.47
1:A:408:A:C6	1:A:409:G:N7	2.82	0.47
1:A:675:A:H1'	12:K:116:HIS:CD2	2.50	0.47
1:A:718:G:N7	1:A:719:C:C5	2.83	0.47
1:A:754:C:O2	1:A:754:C:H3'	2.14	0.47
1:A:862:C:O2	1:A:862:C:H2'	2.14	0.47
1:A:895:G:H2'	1:A:896:C:C6	2.48	0.47
1:A:951:G:H2'	1:A:952:U:O4'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1103:C:P	3:B:96:ARG:HH22	2.38	0.47
1:A:1131:G:H2'	1:A:1132:C:C6	2.50	0.47
1:A:1238:A:C4	1:A:1303:C:O2'	2.66	0.47
1:A:1262:C:O2'	1:A:1263:C:O4'	2.32	0.47
1:A:1366:C:C4	1:A:1367:C:N4	2.83	0.47
1:A:1454:G:H2'	1:A:1455:G:H5'	1.96	0.47
3:B:15:VAL:HG12	3:B:209:ARG:HB3	1.97	0.47
3:B:171:ALA:O	3:B:175:ARG:HB2	2.15	0.47
4:C:68:VAL:HG12	4:C:70:VAL:HG23	1.97	0.47
4:C:139:GLN:O	4:C:142:MET:N	2.48	0.47
4:C:182:ILE:HA	4:C:202:ILE:O	2.15	0.47
5:D:141:ARG:CB	5:D:142:PRO:CD	2.77	0.47
5:D:199:GLN:HA	5:D:199:GLN:HE21	1.79	0.47
12:K:62:GLN:O	12:K:63:LEU:C	2.52	0.47
13:L:40:VAL:HG21	13:L:77:LEU:C	2.35	0.47
13:L:77:LEU:HD21	13:L:107:ALA:N	2.30	0.47
13:L:97:ARG:C	13:L:98:TYR:CD1	2.86	0.47
14:M:84:ILE:HD11	14:M:86:CYS:HB2	1.96	0.47
17:P:66:PRO:C	17:P:67:THR:O	2.51	0.47
19:R:22:VAL:O	19:R:22:VAL:HG12	2.14	0.47
1:A:1113:C:OP2	1:A:1113:C:H6	1.98	0.47
1:A:1208:C:N3	1:A:1209:C:H5	2.11	0.47
1:A:1346:A:C4	8:G:10:ARG:NH2	2.83	0.47
6:E:50:GLU:O	6:E:51:VAL:C	2.52	0.47
6:E:55:VAL:O	6:E:58:ALA:HB3	2.15	0.47
9:H:28:ALA:HA	9:H:59:LEU:HD12	1.97	0.47
10:I:33:PHE:C	10:I:35:GLU:N	2.68	0.47
13:L:75:HIS:HD2	13:L:76:ASN:H	1.61	0.47
13:L:93:LEU:HD12	13:L:96:VAL:HG21	1.96	0.47
16:O:28:GLN:C	16:O:30:ALA:N	2.68	0.47
17:P:43:LYS:HA	17:P:48:TRP:HB3	1.96	0.47
21:T:44:ALA:O	21:T:46:GLU:N	2.47	0.47
1:A:243:A:C2	1:A:245:C:C2	3.03	0.47
1:A:604:G:C6	1:A:605:U:C4	3.02	0.47
1:A:765:G:N2	1:A:812:C:HO2'	2.13	0.47
5:D:83:SER:HA	5:D:89:THR:HG21	1.94	0.47
8:G:88:PRO:HG2	8:G:152:ALA:HB2	1.97	0.47
8:G:141:VAL:O	8:G:144:MET:N	2.47	0.47
9:H:48:TYR:CD1	9:H:48:TYR:C	2.88	0.47
9:H:64:LYS:HG2	9:H:79:VAL:HG21	1.97	0.47
10:I:114:TYR:CD2	10:I:114:TYR:N	2.82	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:P:49:LEU:HD11	17:P:73:LEU:HB3	1.96	0.47
1:A:262:A:N1	1:A:263:A:C6	2.83	0.47
1:A:437:U:HO2'	5:D:125:HIS:CE1	2.26	0.47
1:A:504:C:C2	1:A:542:G:N2	2.83	0.47
1:A:616:G:C2	1:A:617:G:N7	2.83	0.47
1:A:850:U:H6	1:A:850:U:C3'	2.21	0.47
1:A:864:A:H3'	1:A:865:A:C8	2.49	0.47
1:A:988:G:N2	1:A:1218:C:O2	2.48	0.47
1:A:994:A:H61	1:A:1046:A:H2	1.62	0.47
5:D:31:CYS:O	5:D:33:MET:N	2.45	0.47
5:D:87:GLY:O	5:D:88:VAL:C	2.54	0.47
6:E:129:ILE:H	6:E:129:ILE:HD12	1.80	0.47
11:J:47:PHE:CD2	15:N:34:TYR:CD2	3.01	0.47
12:K:27:ASN:O	12:K:56:GLY:HA2	2.14	0.47
18:Q:16:GLN:O	18:Q:18:THR:OG1	2.18	0.47
1:A:488:C:H3'	1:A:488:C:C6	2.49	0.46
1:A:491:G:C5	1:A:492:G:N7	2.83	0.46
1:A:818:G:C2'	1:A:819:A:H5'	2.44	0.46
1:A:838:G:C3'	1:A:839:U:H5"	2.45	0.46
1:A:925:G:C2	1:A:927:G:C8	3.03	0.46
1:A:932:C:H42	1:A:1385:G:H1	1.61	0.46
1:A:955:U:H2'	1:A:956:U:C6	2.49	0.46
1:A:1014:A:H2'	1:A:1015:A:C8	2.50	0.46
3:B:182:ILE:CG2	3:B:183:PRO:CD	2.92	0.46
4:C:45:LYS:HE2	4:C:45:LYS:HB3	1.64	0.46
4:C:139:GLN:O	4:C:140:ARG:C	2.53	0.46
5:D:104:VAL:HG23	5:D:185:PHE:HD1	1.80	0.46
10:I:30:GLY:C	10:I:31:GLN:HG2	2.35	0.46
10:I:36:TYR:CD2	10:I:37:PHE:CE2	3.02	0.46
10:I:81:ILE:O	10:I:85:LEU:HD12	2.15	0.46
11:J:47:PHE:N	11:J:63:PHE:O	2.48	0.46
14:M:79:LYS:O	14:M:83:ASP:HB2	2.15	0.46
14:M:82:MET:O	14:M:93:ARG:NH2	2.47	0.46
1:A:231:G:H2'	1:A:231:G:N3	2.28	0.46
1:A:290:C:C4	1:A:291:C:C5	3.03	0.46
1:A:413:G:N2	1:A:428:G:O2'	2.49	0.46
1:A:434:U:H2'	1:A:435:C:C1'	2.46	0.46
1:A:451:A:C5	1:A:481:G:C6	3.04	0.46
1:A:564:C:C4	1:A:565:U:C4	3.02	0.46
1:A:794:A:C4	1:A:795:C:C5	3.03	0.46
1:A:921:U:O2	6:E:19:MET:HB2	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1003:G:N2	1:A:1039:C:N3	2.63	0.46
3:B:180:LEU:CB	3:B:182:ILE:HD12	2.45	0.46
5:D:57:ARG:HE	5:D:205:GLU:HB3	1.81	0.46
5:D:101:LEU:C	5:D:103:ASN:N	2.68	0.46
8:G:6:ARG:O	8:G:7:ALA:O	2.33	0.46
10:I:50:LEU:CD1	10:I:81:ILE:CG2	2.92	0.46
21:T:41:VAL:C	21:T:43:LEU:H	2.18	0.46
1:A:165:C:H2'	1:A:166:G:H8	1.79	0.46
1:A:200:G:C2'	1:A:201:C:O5'	2.63	0.46
1:A:427:U:O2'	1:A:541:G:OP1	2.33	0.46
1:A:588:G:C8	1:A:753:A:C2	3.03	0.46
1:A:597:G:C4	1:A:644:G:C2	3.03	0.46
1:A:978:A:H1'	1:A:1322:C:O2	2.15	0.46
1:A:1057:G:O2'	1:A:1058:G:H5'	2.16	0.46
1:A:1102:A:H2'	1:A:1103:C:H6	1.75	0.46
1:A:1232:U:H2'	1:A:1233:G:C8	2.50	0.46
5:D:128:VAL:HG22	5:D:146:ILE:HG13	1.97	0.46
7:F:30:LEU:HD23	7:F:75:LEU:HD11	1.97	0.46
7:F:97:PHE:HB3	19:R:32:ARG:HH21	1.79	0.46
8:G:95:ARG:HG3	8:G:99:LEU:HD12	1.96	0.46
11:J:38:ILE:CG2	11:J:71:LEU:HB3	2.45	0.46
13:L:100:ILE:CG2	13:L:101:VAL:N	2.78	0.46
14:M:8:GLU:HA	14:M:9:ILE:HG13	1.98	0.46
21:T:97:ALA:HB1	21:T:98:PRO:HD3	1.97	0.46
1:A:106:C:C2	1:A:107:G:C8	3.04	0.46
1:A:264:U:C6	1:A:264:U:C3'	2.99	0.46
1:A:855:G:H2'	1:A:856:C:C6	2.51	0.46
1:A:880:C:C3'	1:A:880:C:C6	2.99	0.46
1:A:1003:G:C8	1:A:1003:G:O5'	2.68	0.46
1:A:1490:C:H2'	1:A:1491:G:H5"	1.98	0.46
3:B:108:ILE:HG22	3:B:152:PHE:CE2	2.51	0.46
3:B:111:ARG:HB3	3:B:149:LEU:CD1	2.37	0.46
4:C:122:GLU:HA	4:C:125:GLU:HB2	1.97	0.46
5:D:4:TYR:O	5:D:5:ILE:HB	2.14	0.46
8:G:61:VAL:O	8:G:62:PHE:C	2.54	0.46
8:G:119:ARG:O	8:G:120:ILE:C	2.54	0.46
9:H:119:LEU:HD13	9:H:124:ALA:CA	2.45	0.46
11:J:64:GLU:H	11:J:64:GLU:HG3	1.60	0.46
14:M:102:ARG:NH1	14:M:105:THR:OG1	2.49	0.46
17:P:6:LEU:HD23	17:P:17:TYR:CB	2.45	0.46
1:A:157:G:C4	1:A:158:G:C8	3.03	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:382:A:C2	1:A:383:A:C5	3.04	0.46
1:A:394:G:H2'	1:A:394:G:N3	2.30	0.46
1:A:537:G:H2'	1:A:538:G:C8	2.47	0.46
1:A:696:A:H2'	1:A:697:U:O4'	2.16	0.46
1:A:1065:U:H5	1:A:1190:G:C4	2.34	0.46
1:A:1090:U:H2'	1:A:1091:U:H6	1.80	0.46
1:A:1152:A:C4'	11:J:13:HIS:CD2	2.95	0.46
1:A:1154:G:N3	1:A:1155:G:C8	2.84	0.46
1:A:1250:A:C6	1:A:1287:A:C2	3.03	0.46
4:C:193:TYR:CE1	4:C:196:LEU:HD21	2.49	0.46
5:D:103:ASN:C	5:D:105:VAL:N	2.69	0.46
6:E:71:LEU:HD21	6:E:115:VAL:CG2	2.43	0.46
6:E:105:VAL:HG11	6:E:132:ALA:HB2	1.97	0.46
8:G:111:ARG:NH1	8:G:122:HIS:CB	2.73	0.46
9:H:104:ARG:C	9:H:106:GLY:H	2.19	0.46
17:P:74:LEU:HD13	17:P:79:VAL:HG21	1.96	0.46
18:Q:86:GLU:O	18:Q:89:LEU:HB2	2.15	0.46
19:R:73:ALA:O	19:R:74:ARG:C	2.53	0.46
20:S:78:ARG:HH11	20:S:78:ARG:HG3	1.80	0.46
1:A:46:G:C2	1:A:396:G:C2	3.03	0.46
1:A:193:C:C1'	21:T:60:GLU:OE1	2.64	0.46
1:A:664:G:H22	1:A:741:G:H22	1.63	0.46
1:A:1240:U:C4'	8:G:38:LEU:HD11	2.42	0.46
1:A:1347:G:C8	10:I:107:ARG:HB3	2.51	0.46
1:A:1367:C:C2	1:A:1368:G:C8	3.03	0.46
3:B:55:PHE:HA	3:B:58:ILE:CG1	2.43	0.46
6:E:9:LYS:HB3	6:E:33:VAL:HG23	1.96	0.46
6:E:15:ARG:NH1	6:E:15:ARG:HG3	2.28	0.46
6:E:41:VAL:O	6:E:67:VAL:HG12	2.16	0.46
12:K:90:GLY:O	12:K:91:ARG:C	2.52	0.46
14:M:89:GLY:O	14:M:90:LEU:C	2.54	0.46
14:M:107:ALA:CB	14:M:111:LYS:HG3	2.46	0.46
20:S:80:TYR:CZ	20:S:82:GLY:HA2	2.50	0.46
1:A:113:G:H1	1:A:314:C:N4	2.12	0.46
1:A:266:G:H5'	1:A:266:G:H8	1.81	0.46
1:A:320:C:HO2'	1:A:321:A:C4'	2.29	0.46
1:A:738:C:OP1	7:F:92:LYS:HD3	2.16	0.46
1:A:879:C:C2'	1:A:880:C:H5'	2.45	0.46
1:A:976:G:O2'	1:A:977:A:H5'	2.15	0.46
1:A:1003:G:O5'	1:A:1003:G:H8	1.98	0.46
1:A:1271:G:H5'	1:A:1314:C:H5"	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1500:A:C2'	1:A:1501:C:H5'	2.45	0.46
3:B:112:VAL:HG11	3:B:153:ARG:HA	1.97	0.46
5:D:185:PHE:C	5:D:185:PHE:CD2	2.89	0.46
11:J:23:ILE:O	11:J:23:ILE:CG2	2.63	0.46
14:M:14:ARG:HG2	14:M:14:ARG:NH1	2.29	0.46
14:M:122:LYS:O	14:M:123:ALA:CB	2.63	0.46
20:S:78:ARG:HG3	20:S:78:ARG:NH1	2.31	0.46
1:A:392:G:C4	1:A:393:A:N7	2.83	0.46
1:A:507:C:H2'	1:A:508:C:H5	1.81	0.46
1:A:691:G:H8	1:A:691:G:O5'	1.98	0.46
1:A:838:G:N2	1:A:849:C:C2	2.84	0.46
1:A:956:U:C2	1:A:1225:A:C2	3.04	0.46
1:A:980:C:H3'	1:A:981:U:C6	2.51	0.46
1:A:1121:U:O4	1:A:1152:A:N1	2.49	0.46
1:A:1314:C:C2	1:A:1315:U:C6	3.04	0.46
5:D:103:ASN:C	5:D:105:VAL:H	2.19	0.46
5:D:141:ARG:CB	5:D:142:PRO:HD3	2.46	0.46
15:N:23:ARG:HD3	15:N:23:ARG:HA	1.51	0.46
16:O:27:VAL:O	16:O:30:ALA:HB3	2.15	0.46
17:P:22:THR:HG23	17:P:23:ASP:O	2.16	0.46
18:Q:68:ARG:N	18:Q:70:ARG:HH12	2.14	0.46
1:A:575:G:C5	1:A:881:G:C2	3.04	0.46
1:A:731:G:OP1	1:A:766:A:C1'	2.59	0.46
1:A:791:G:C6	1:A:792:A:N7	2.84	0.46
1:A:946:A:C2	1:A:1236:A:C2	3.04	0.46
1:A:959:A:H2	1:A:1222:G:O4'	1.94	0.46
1:A:1381:U:N3	1:A:1382:C:C5	2.83	0.46
1:A:1507:A:H8	1:A:1507:A:C5'	2.29	0.46
3:B:87:ARG:CZ	3:B:233:SER:HB3	2.45	0.46
3:B:158:LEU:HD23	3:B:159:PRO:HD2	1.97	0.46
4:C:122:GLU:O	4:C:123:GLN:C	2.53	0.46
5:D:52:SER:O	5:D:55:ALA:N	2.48	0.46
6:E:51:VAL:O	6:E:54:ALA:CB	2.62	0.46
8:G:50:ILE:HG21	8:G:58:PRO:HA	1.98	0.46
13:L:46:LYS:CG	13:L:47:LYS:H	2.29	0.46
13:L:102:ARG:HH12	13:L:110:VAL:CA	2.18	0.46
14:M:29:ARG:HD3	14:M:64:TRP:CE2	2.51	0.46
19:R:66:LEU:HD12	19:R:66:LEU:HA	1.75	0.46
20:S:78:ARG:CG	20:S:78:ARG:NH1	2.76	0.46
20:S:83:HIS:CD2	20:S:83:HIS:H	2.34	0.46
1:A:91:C:H2'	1:A:92:C:O5'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:175:C:N3	1:A:176:C:C5	2.84	0.46
1:A:223:U:H5"	21:T:68:LYS:HZ2	1.80	0.46
1:A:259:G:H2'	1:A:260:G:O4'	2.15	0.46
1:A:519:C:H2'	1:A:520:A:H8	1.69	0.46
1:A:625:G:C6	1:A:626:U:C4	3.04	0.46
1:A:722:A:O2'	1:A:723:U:C2	2.69	0.46
1:A:941:G:C6	1:A:942:G:N7	2.84	0.46
1:A:959:A:C2	1:A:1222:G:C1'	2.99	0.46
1:A:1112:C:N3	4:C:178:LEU:N	2.63	0.46
1:A:1240:U:H3	8:G:30:ILE:HG22	1.81	0.46
1:A:1306:A:C5	1:A:1307:U:C5	3.03	0.46
4:C:167:TRP:O	4:C:168:ALA:HB2	2.16	0.46
6:E:69:VAL:O	6:E:69:VAL:HG12	2.16	0.46
7:F:7:ASN:HD21	19:R:34:TYR:HE1	1.62	0.46
9:H:14:ARG:HH11	9:H:14:ARG:HG2	1.81	0.46
10:I:50:LEU:O	10:I:52:ALA:N	2.48	0.46
13:L:10:LEU:HD23	13:L:10:LEU:HA	1.70	0.46
20:S:17:GLU:HA	20:S:20:LEU:HD23	1.98	0.46
1:A:64:G:H4'	1:A:65:U:O5'	2.15	0.45
1:A:160:A:C5	1:A:346:G:O6	2.69	0.45
1:A:257:G:H8	1:A:257:G:O5'	1.99	0.45
1:A:266:G:C5'	1:A:266:G:H8	2.26	0.45
1:A:367:U:O2	1:A:369:C:C6	2.69	0.45
1:A:444:C:C2'	1:A:445:G:H8	2.03	0.45
1:A:639:G:O2'	1:A:640:A:H5'	2.17	0.45
1:A:643:C:C3'	1:A:643:C:C6	2.99	0.45
1:A:705:U:O2	1:A:705:U:H2'	2.16	0.45
1:A:1030(D):A:H5"	1:A:1031:G:OP2	2.16	0.45
1:A:1105:A:H2'	1:A:1106:G:H8	1.80	0.45
1:A:1125:U:O4	11:J:5:ARG:HG3	2.15	0.45
1:A:1265:G:C4	1:A:1271:G:N2	2.84	0.45
10:I:19:LEU:HD23	10:I:19:LEU:HA	1.79	0.45
12:K:73:MET:HE1	12:K:102:GLY:HA3	1.99	0.45
17:P:19:ILE:CG2	17:P:36:ILE:HG13	2.35	0.45
1:A:106:C:H2'	1:A:107:G:C8	2.39	0.45
1:A:127:G:HO2'	18:Q:2:PRO:N	2.15	0.45
1:A:256:U:H2'	1:A:257:G:C5'	2.46	0.45
1:A:292:G:C8	1:A:292:G:H3'	2.51	0.45
1:A:623:C:O2	1:A:623:C:C2'	2.60	0.45
1:A:749:C:H2'	1:A:750:G:H8	1.80	0.45
1:A:914:A:N1	1:A:915:A:N3	2.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:926:G:H22	2:Z:4:U:P	2.38	0.45
1:A:1153:C:H2'	1:A:1154:G:O4'	2.16	0.45
1:A:1228:C:H2'	1:A:1229:A:C8	2.51	0.45
1:A:1295:G:O2'	1:A:1302:U:O4	2.23	0.45
1:A:1296:C:C4'	1:A:1302:U:C5	2.98	0.45
1:A:1327:C:O2'	1:A:1328:C:H5'	2.17	0.45
1:A:1459:C:H2'	1:A:1460:A:C8	2.47	0.45
1:A:1510:U:O2	1:A:1510:U:H2'	2.16	0.45
3:B:162:ILE:CG2	3:B:184:VAL:HG22	2.46	0.45
5:D:54:TYR:O	5:D:55:ALA:C	2.54	0.45
6:E:107:ARG:O	6:E:110:LEU:N	2.49	0.45
10:I:45:ALA:C	10:I:47:LEU:N	2.69	0.45
12:K:73:MET:C	12:K:75:TYR:H	2.20	0.45
14:M:44:ARG:O	14:M:45:VAL:C	2.54	0.45
15:N:21:TYR:CE2	15:N:23:ARG:NE	2.73	0.45
17:P:4:ILE:O	17:P:66:PRO:HA	2.16	0.45
19:R:87:ARG:HH11	19:R:87:ARG:CB	2.29	0.45
1:A:504:C:C2	1:A:542:G:C2	3.04	0.45
1:A:521:G:OP2	13:L:54:LYS:NZ	2.34	0.45
1:A:781:A:C2	1:A:1514:C:H1'	2.51	0.45
1:A:803:G:C4	1:A:804:U:C6	3.04	0.45
1:A:880:C:H3'	1:A:880:C:H6	1.81	0.45
1:A:922:G:H2'	1:A:923:A:O4'	2.16	0.45
1:A:1123:A:C2	1:A:1151:A:N1	2.84	0.45
1:A:1185:G:H2'	1:A:1186:G:H8	1.82	0.45
1:A:1350:A:H8	1:A:1350:A:O5'	2.00	0.45
3:B:178:ARG:C	3:B:180:LEU:N	2.69	0.45
10:I:79:LEU:O	10:I:82:ALA:N	2.49	0.45
15:N:4:LYS:O	15:N:6:LEU:N	2.49	0.45
18:Q:22:LEU:HD12	18:Q:22:LEU:HA	1.57	0.45
1:A:157:G:N1	1:A:158:G:N7	2.64	0.45
1:A:184:G:H2'	1:A:185:A:C8	2.51	0.45
1:A:417:C:H5"	1:A:418:C:OP2	2.17	0.45
1:A:462:G:C2	1:A:463:A:C4	3.04	0.45
1:A:513:C:H5"	1:A:514:C:OP2	2.17	0.45
1:A:515:G:C6	1:A:516:U:C5	3.05	0.45
1:A:615:C:C6	1:A:615:C:C3'	3.00	0.45
1:A:672:U:H4'	7:F:80:ARG:NH1	2.30	0.45
1:A:935:A:H2'	1:A:936:C:O5'	2.17	0.45
1:A:1152:A:O3'	11:J:13:HIS:CD2	2.69	0.45
1:A:1240:U:N3	8:G:30:ILE:CG2	2.79	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1393:U:O2'	1:A:1501:C:O2'	2.34	0.45
3:B:100:GLY:O	3:B:104:ASN:N	2.49	0.45
3:B:219:VAL:O	3:B:220:ASP:C	2.55	0.45
4:C:178:LEU:O	4:C:178:LEU:HG	2.16	0.45
8:G:26:PHE:HA	8:G:101:LEU:HD22	1.97	0.45
10:I:71:SER:CA	10:I:74:ILE:HD12	2.44	0.45
1:A:59:A:H2'	1:A:59:A:N3	2.31	0.45
1:A:125:U:H2'	1:A:126:G:C8	2.51	0.45
1:A:160:A:H2'	1:A:161:A:O4'	2.15	0.45
1:A:299:G:H8	1:A:299:G:O5'	2.00	0.45
1:A:414:A:C2	1:A:415:A:C4	3.05	0.45
1:A:618:C:N3	1:A:622:A:N6	2.65	0.45
1:A:818:G:O2'	1:A:819:A:H5"	2.16	0.45
1:A:1061:G:C6	1:A:1062:U:N3	2.85	0.45
1:A:1107:C:C6	1:A:1107:C:C3'	2.99	0.45
1:A:1460:A:C2	1:A:1461:G:H1'	2.52	0.45
7:F:89:MET:HE2	19:R:76:LEU:HD21	1.99	0.45
1:A:41:G:H2'	1:A:42:G:C8	2.52	0.45
1:A:44:G:N2	1:A:45:U:H1'	2.31	0.45
1:A:293:G:C6	1:A:294:U:C4	3.04	0.45
1:A:372:C:H4'	1:A:373:A:O5'	2.16	0.45
1:A:1074:G:O3'	3:B:103:THR:CG2	2.64	0.45
1:A:1123:A:N3	11:J:39:PRO:HG3	2.32	0.45
1:A:1419:G:O6	1:A:1482:G:N2	2.49	0.45
3:B:19:HIS:HB2	3:B:204:ASN:CG	2.37	0.45
3:B:71:VAL:O	3:B:165:VAL:CG2	2.64	0.45
3:B:174:VAL:C	3:B:176:GLU:N	2.70	0.45
4:C:186:PHE:CE1	4:C:187:ALA:O	2.70	0.45
8:G:31:MET:SD	8:G:34:GLY:HA2	2.57	0.45
10:I:77:ILE:HG23	10:I:81:ILE:CD1	2.46	0.45
10:I:120:ARG:O	10:I:121:ARG:C	2.55	0.45
12:K:111:ASP:O	12:K:112:THR:C	2.55	0.45
14:M:15:VAL:HB	14:M:34:LEU:HD11	1.99	0.45
21:T:56:MET:HE2	21:T:88:VAL:HG11	1.98	0.45
1:A:42:G:H1	1:A:400:C:N4	2.14	0.45
1:A:781:A:N7	1:A:802:A:C2	2.85	0.45
1:A:880:C:C6	1:A:880:C:H3'	2.51	0.45
1:A:894:G:H2'	1:A:895:G:H8	1.80	0.45
1:A:1167:A:C6	1:A:1168:A:C6	3.04	0.45
1:A:1229:A:H5"	1:A:1230:C:OP2	2.17	0.45
1:A:1298:C:H2'	8:G:114:ARG:NH1	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:105:PHE:O	3:B:107:THR:N	2.50	0.45
4:C:22:TRP:CH2	4:C:32:LEU:O	2.70	0.45
4:C:57:ILE:CG2	4:C:58:GLU:N	2.79	0.45
4:C:138:VAL:O	4:C:142:MET:N	2.46	0.45
7:F:30:LEU:O	7:F:34:GLY:N	2.50	0.45
8:G:6:ARG:O	8:G:6:ARG:HG2	2.16	0.45
8:G:108:ALA:C	8:G:110:GLN:N	2.69	0.45
12:K:53:SER:C	12:K:55:LYS:H	2.19	0.45
13:L:75:HIS:CD2	13:L:77:LEU:N	2.72	0.45
14:M:49:THR:HG22	14:M:51:ALA:N	2.27	0.45
16:O:3:ILE:CG2	16:O:34:LEU:HD11	2.40	0.45
18:Q:60:ILE:C	18:Q:71:PHE:HD1	2.20	0.45
1:A:56:U:H2'	1:A:57:G:C8	2.52	0.45
1:A:109:A:C3'	1:A:110:C:H5'	2.47	0.45
1:A:122:G:N2	1:A:123:C:H1'	2.32	0.45
1:A:408:A:C8	1:A:408:A:C3'	2.99	0.45
1:A:560:U:C5'	1:A:566:G:N2	2.73	0.45
1:A:684:A:H2'	1:A:685:G:O5'	2.15	0.45
1:A:989:C:O2	1:A:1217:C:N3	2.50	0.45
5:D:111:ALA:HB1	5:D:116:GLN:HB3	1.99	0.45
9:H:9:MET:HG3	9:H:26:VAL:HG21	1.99	0.45
14:M:8:GLU:CA	14:M:9:ILE:HG13	2.46	0.45
18:Q:45:HIS:HA	18:Q:69:LYS:CE	2.47	0.45
21:T:67:ALA:O	21:T:73:HIS:ND1	2.47	0.45
1:A:505:G:C6	1:A:506:G:O6	2.70	0.45
1:A:878:G:H1'	9:H:3:THR:HG21	1.98	0.45
1:A:943:U:C2	1:A:944:G:C8	3.05	0.45
1:A:955:U:H2'	1:A:956:U:H6	1.82	0.45
1:A:991:U:H3	1:A:1215:G:H1	1.64	0.45
1:A:1057:G:C4	1:A:1204:A:C2	3.04	0.45
1:A:1365:G:H2'	1:A:1366:C:C6	2.52	0.45
1:A:1365:G:H2'	1:A:1366:C:H6	1.82	0.45
3:B:9:GLU:HG3	3:B:217:ARG:CZ	2.44	0.45
3:B:187:LEU:HA	3:B:201:ILE:HB	1.98	0.45
8:G:115:ARG:HB3	8:G:118:VAL:CG2	2.47	0.45
13:L:10:LEU:HD21	13:L:15:ARG:HD3	1.99	0.45
14:M:74:VAL:O	14:M:76:ALA:N	2.50	0.45
15:N:36:PHE:CD1	15:N:36:PHE:C	2.90	0.45
15:N:36:PHE:CD1	15:N:37:PHE:CE1	3.05	0.45
18:Q:56:VAL:HG12	18:Q:77:VAL:HG23	1.99	0.45
1:A:129(A):G:N2	1:A:190(E):U:H5"	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:160:A:C6	1:A:161:A:C2	3.05	0.45
1:A:247:G:C5	1:A:278:G:C2	3.05	0.45
1:A:324:G:H8	1:A:324:G:O5'	2.00	0.45
1:A:491:G:H2'	1:A:492:G:H8	1.82	0.45
1:A:720:C:O5'	1:A:720:C:H6	2.00	0.45
1:A:1047:G:C3'	1:A:1048:G:H5'	2.42	0.45
1:A:1416:G:C6	1:A:1417:G:C5	3.05	0.45
3:B:71:VAL:HG23	3:B:164:VAL:HG13	1.97	0.45
3:B:162:ILE:HG22	3:B:184:VAL:HA	1.99	0.45
3:B:178:ARG:C	3:B:180:LEU:H	2.19	0.45
4:C:88:ARG:HG2	4:C:91:LEU:CD2	2.47	0.45
5:D:165:MET:HG2	5:D:176:LEU:HD21	1.98	0.45
8:G:66:VAL:CG1	8:G:67:GLU:N	2.80	0.45
10:I:6:GLY:HA3	10:I:83:ARG:HB3	1.98	0.45
10:I:47:LEU:CA	10:I:49:PRO:HD2	2.46	0.45
19:R:36:ASN:O	19:R:37:VAL:C	2.53	0.45
20:S:40:ILE:HG12	20:S:62:ILE:HD11	1.99	0.45
21:T:60:GLU:O	21:T:61:SER:C	2.54	0.45
21:T:89:ARG:HH12	21:T:106:ALA:HB2	1.82	0.45
1:A:38:G:H22	1:A:397:A:H5"	1.82	0.44
1:A:373:A:H2'	1:A:374:A:H8	1.82	0.44
1:A:615:C:H3'	1:A:615:C:H6	1.82	0.44
1:A:925:G:C6	1:A:927:G:N7	2.85	0.44
1:A:975:A:H4'	1:A:976:G:O5'	2.16	0.44
1:A:1060:C:C2	1:A:1198:G:C2	3.06	0.44
1:A:1092:A:C8	1:A:1092:A:H5'	2.52	0.44
1:A:1105:A:H2'	1:A:1106:G:C8	2.52	0.44
1:A:1119:C:H3'	1:A:1119:C:H6	1.79	0.44
1:A:1303:C:O2	1:A:1303:C:H2'	2.15	0.44
1:A:1453:G:H2'	1:A:1454:G:O4'	2.17	0.44
1:A:1511:G:C6	1:A:1512:U:C2	3.05	0.44
3:B:167:PRO:HG2	3:B:192:SER:CB	2.47	0.44
5:D:106:TYR:CD2	5:D:106:TYR:C	2.90	0.44
13:L:43:VAL:HG12	13:L:55:VAL:HG21	1.98	0.44
14:M:52:GLU:O	14:M:56:LEU:HB2	2.17	0.44
16:O:24:SER:HB3	16:O:27:VAL:H	1.81	0.44
16:O:49:ASP:O	16:O:51:HIS:N	2.49	0.44
1:A:689:C:H4'	1:A:705:U:O2'	2.18	0.44
3:B:19:HIS:HB2	3:B:204:ASN:OD1	2.17	0.44
3:B:91:PRO:HG2	3:B:155:LEU:CD2	2.32	0.44
4:C:6:HIS:HD2	4:C:6:HIS:C	2.19	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:3:ARG:HA	5:D:3:ARG:HD3	1.58	0.44
15:N:12:ARG:H	15:N:12:ARG:HG3	1.53	0.44
1:A:285:G:C2	1:A:286:G:C8	3.06	0.44
1:A:543:C:H2'	1:A:544:G:H5'	2.00	0.44
1:A:1186:G:C2	1:A:1187:G:C8	3.06	0.44
1:A:1247:U:C6	1:A:1247:U:C3'	2.99	0.44
1:A:1265:G:H5"	1:A:1266:G:OP2	2.17	0.44
1:A:1333:A:H2'	1:A:1334:G:C8	2.53	0.44
1:A:1401:G:OP2	2:Z:6:U:H3'	2.17	0.44
3:B:162:ILE:HG21	3:B:184:VAL:HG22	1.98	0.44
3:B:223:ILE:CG2	3:B:224:GLN:H	2.31	0.44
4:C:29:TYR:CE2	4:C:33:LEU:HD12	2.52	0.44
5:D:64:LEU:CD1	5:D:97:LEU:HD11	2.47	0.44
6:E:148:VAL:O	6:E:149:GLU:C	2.55	0.44
12:K:42:TRP:CZ3	12:K:47:VAL:HG23	2.53	0.44
15:N:24:CYS:SG	15:N:27:CYS:SG	3.15	0.44
19:R:22:VAL:HB	19:R:56:THR:HA	1.99	0.44
19:R:76:LEU:HD12	19:R:78:LEU:HD13	2.00	0.44
1:A:291:C:O2	1:A:291:C:H2'	2.16	0.44
1:A:392:G:C6	1:A:393:A:N6	2.85	0.44
1:A:443:C:H2'	1:A:444:C:C6	2.52	0.44
1:A:452:A:H1'	1:A:453:A:C8	2.51	0.44
1:A:797:C:OP1	12:K:124:LYS:HG3	2.17	0.44
1:A:942:G:C6	1:A:1342:C:C4	3.05	0.44
1:A:976:G:H8	1:A:1358:U:O2'	1.97	0.44
1:A:1229:A:C4	1:A:1230:C:C5	3.06	0.44
1:A:1365:G:C6	1:A:1366:C:N3	2.85	0.44
1:A:1443:G:C4'	1:A:1446:A:P	3.01	0.44
4:C:128:PHE:HE2	4:C:132:ARG:NH1	2.15	0.44
4:C:188:LEU:O	4:C:189:ALA:HB3	2.16	0.44
5:D:97:LEU:O	5:D:100:ARG:HB2	2.17	0.44
9:H:58:TYR:O	9:H:59:LEU:HG	2.18	0.44
9:H:112:LEU:N	9:H:112:LEU:HD22	2.32	0.44
11:J:56:HIS:O	11:J:59:SER:OG	2.35	0.44
12:K:33:THR:OG1	12:K:38:ASN:N	2.50	0.44
13:L:71:PRO:HG2	13:L:102:ARG:HG3	2.00	0.44
14:M:14:ARG:NH1	14:M:16:ASP:OD2	2.51	0.44
14:M:19:LEU:HB3	14:M:25:ILE:HG21	1.99	0.44
18:Q:19:VAL:HG23	18:Q:21:VAL:HG23	2.00	0.44
19:R:74:ARG:HD3	19:R:80:PRO:O	2.17	0.44
1:A:186:C:C2	1:A:187:C:C5	3.05	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:243:A:N7	1:A:281:G:C2	2.85	0.44
1:A:348:G:H2'	1:A:349:A:H8	1.83	0.44
1:A:707:C:C4'	12:K:20:TYR:HD2	2.29	0.44
1:A:784:C:H3'	1:A:784:C:C6	2.53	0.44
1:A:939:G:H2'	1:A:940:C:C6	2.51	0.44
1:A:1115:C:O2'	1:A:1116:C:H5'	2.16	0.44
1:A:1435:G:C6	1:A:1436:U:O4	2.70	0.44
1:A:1454:G:O5'	1:A:1454:G:H8	2.01	0.44
3:B:12:GLU:HG3	3:B:213:LEU:HD13	2.00	0.44
3:B:15:VAL:HG13	3:B:209:ARG:HH11	1.81	0.44
3:B:92:TYR:C	3:B:92:TYR:HD1	2.21	0.44
4:C:15:THR:HG21	4:C:179:ARG:CA	2.45	0.44
4:C:22:TRP:HH2	4:C:32:LEU:O	2.00	0.44
6:E:126:ARG:HD3	6:E:126:ARG:HA	1.53	0.44
8:G:67:GLU:O	8:G:67:GLU:CG	2.62	0.44
10:I:111:ARG:NH1	15:N:61:TRP:OXT	2.50	0.44
13:L:71:PRO:HB2	13:L:120:TYR:HE2	1.82	0.44
16:O:74:ASP:C	16:O:76:GLU:N	2.69	0.44
17:P:42:ARG:NH1	17:P:42:ARG:HB3	2.32	0.44
18:Q:8:GLY:O	18:Q:56:VAL:HA	2.18	0.44
21:T:19:SER:O	21:T:20:LEU:C	2.56	0.44
21:T:73:HIS:C	21:T:74:LYS:CG	2.66	0.44
1:A:267:C:H2'	1:A:268:C:H5'	1.98	0.44
1:A:285:G:N2	1:A:286:G:H1'	2.33	0.44
1:A:290:C:H2'	1:A:291:C:O4'	2.18	0.44
1:A:426:G:OP1	5:D:36:ARG:NH2	2.34	0.44
1:A:560:U:H5'	1:A:566:G:H21	1.75	0.44
1:A:668:G:H4'	16:O:48:LYS:HB3	1.99	0.44
1:A:950:U:O5'	1:A:950:U:H6	2.01	0.44
1:A:1114:C:C4	1:A:1115:C:H5	2.36	0.44
1:A:1130:A:N3	1:A:1130:A:H2'	2.33	0.44
1:A:1208:C:H2'	1:A:1209:C:C6	2.53	0.44
1:A:1355:G:H2'	1:A:1356:G:H5'	1.99	0.44
3:B:44:LEU:H	3:B:44:LEU:HG	1.40	0.44
3:B:122:PHE:O	3:B:125:PRO:HD2	2.17	0.44
5:D:38:TYR:HB2	5:D:39:PRO:HD2	2.00	0.44
5:D:111:ALA:HB2	5:D:120:LEU:CD1	2.47	0.44
6:E:143:ARG:HH11	6:E:143:ARG:CG	2.31	0.44
11:J:35:SER:OG	11:J:73:ASP:O	2.33	0.44
15:N:47:LEU:O	15:N:50:LYS:N	2.51	0.44
17:P:28:ARG:HG3	17:P:29:ASP:OD2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:P:58:TYR:O	17:P:61:SER:N	2.50	0.44
17:P:65:GLN:HA	17:P:66:PRO:HD2	1.63	0.44
1:A:290:C:C5	1:A:291:C:C5	3.06	0.44
1:A:355:C:H2'	1:A:356:A:O4'	2.18	0.44
1:A:606:G:H5"	1:A:607:A:H5'	1.98	0.44
1:A:686:U:O4	1:A:703:G:O2'	2.29	0.44
1:A:789:U:O2	1:A:791:G:N7	2.51	0.44
1:A:858:G:H1	1:A:869:G:H3'	1.82	0.44
1:A:1061:G:C6	1:A:1197:G:C6	3.06	0.44
1:A:1064:G:C2	1:A:1066:C:N4	2.86	0.44
1:A:1126:U:P	1:A:1281:U:O2	2.76	0.44
1:A:1240:U:H3	8:G:30:ILE:HG23	1.82	0.44
1:A:1287:A:C6	1:A:1288:A:C6	3.06	0.44
1:A:1324:A:H1'	1:A:1361(A):C:H4'	2.00	0.44
1:A:1525:G:H2'	1:A:1526:G:O5'	2.16	0.44
3:B:46:LYS:O	3:B:47:THR:C	2.56	0.44
5:D:11:LEU:O	5:D:12:CYS:C	2.56	0.44
5:D:67:ILE:CG2	5:D:68:TYR:HD1	2.27	0.44
6:E:19:MET:HE1	6:E:24:ARG:HH11	1.81	0.44
6:E:138:ALA:O	6:E:141:GLN:HB2	2.18	0.44
8:G:127:ALA:O	8:G:130:GLY:N	2.51	0.44
9:H:4:ASP:HA	9:H:5:PRO:HD2	1.90	0.44
13:L:85:ILE:HG23	13:L:86:ARG:N	2.33	0.44
14:M:20:THR:O	14:M:22:ILE:N	2.51	0.44
17:P:21:VAL:O	17:P:32:TYR:HB2	2.17	0.44
17:P:53:VAL:O	17:P:54:GLU:C	2.56	0.44
18:Q:11:VAL:HB	18:Q:88:TYR:CD2	2.52	0.44
1:A:19:C:C2	1:A:20:U:C5	3.06	0.44
1:A:349:A:H2'	1:A:350:G:H5"	2.00	0.44
1:A:454:C:H5"	1:A:455:C:OP2	2.17	0.44
1:A:781:A:C4	1:A:802:A:H2	2.36	0.44
1:A:913:A:H1'	1:A:914:A:O4'	2.17	0.44
1:A:1056:U:O4	1:A:1200:C:N3	2.51	0.44
1:A:1246:C:H42	1:A:1291:G:H1	1.65	0.44
3:B:118:LEU:CD2	3:B:142:LEU:HB2	2.47	0.44
3:B:139:LYS:HB2	3:B:139:LYS:HE3	1.85	0.44
4:C:133:ALA:O	4:C:136:GLN:N	2.51	0.44
6:E:102:ALA:CB	6:E:120:THR:OG1	2.65	0.44
13:L:97:ARG:CB	13:L:98:TYR:CD1	2.91	0.44
16:O:42:HIS:CD2	16:O:42:HIS:C	2.91	0.44
18:Q:36:ILE:H	18:Q:36:ILE:HG13	1.46	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:106:C:O2	1:A:379:C:H4'	2.18	0.44
1:A:157:G:C2	1:A:158:G:N7	2.86	0.44
1:A:199:G:H2'	1:A:200:G:C5'	2.43	0.44
1:A:564:C:H5"	1:A:565:U:OP2	2.17	0.44
1:A:592:G:C2'	1:A:593:G:H5'	2.47	0.44
1:A:643:C:C6	1:A:643:C:H3'	2.52	0.44
1:A:784:C:C6	1:A:784:C:C3'	3.00	0.44
1:A:922:G:N2	1:A:1396:A:C5	2.86	0.44
1:A:1096:C:C2	1:A:1097:C:C5	3.06	0.44
1:A:1185:G:N3	1:A:1186:G:C8	2.86	0.44
1:A:1281:U:H3'	1:A:1281:U:H6	1.83	0.44
5:D:11:LEU:O	5:D:13:ARG:N	2.51	0.44
5:D:130:GLY:O	5:D:131:ARG:C	2.55	0.44
6:E:92:LYS:HA	6:E:93:PRO:HD3	1.82	0.44
8:G:115:ARG:O	8:G:116:ALA:C	2.56	0.44
15:N:60:SER:O	15:N:61:TRP:HB3	2.18	0.44
17:P:74:LEU:O	17:P:79:VAL:CG2	2.65	0.44
20:S:58:VAL:HG12	20:S:59:PRO:HD2	2.00	0.44
1:A:286:G:C5	1:A:287:U:C4	3.05	0.43
1:A:288:A:H2'	1:A:289:G:H4'	1.99	0.43
1:A:622:A:C8	1:A:622:A:H3'	2.53	0.43
1:A:642:A:C2'	1:A:643:C:H5'	2.48	0.43
1:A:766:A:C8	1:A:814:A:C6	3.06	0.43
1:A:881:G:C2	1:A:882:C:C2	3.06	0.43
1:A:949:A:H1'	1:A:1364:U:N3	2.31	0.43
1:A:969:A:H61	14:M:126:LYS:HB2	1.83	0.43
1:A:1144:G:H8	1:A:1144:G:O5'	2.01	0.43
1:A:1363:A:H1'	1:A:1365:G:N7	2.33	0.43
1:A:1399:C:C2	1:A:1502:A:N6	2.86	0.43
1:A:1437:C:H2'	1:A:1438:G:H8	1.83	0.43
5:D:109:GLY:O	5:D:111:ALA:N	2.51	0.43
6:E:89:ILE:HD12	6:E:89:ILE:HA	1.77	0.43
9:H:48:TYR:O	9:H:48:TYR:CG	2.71	0.43
9:H:91:ARG:HG3	13:L:7:ILE:HG13	1.98	0.43
12:K:29:ILE:HB	12:K:44:SER:HB2	2.00	0.43
13:L:77:LEU:HD11	13:L:107:ALA:HB2	2.00	0.43
16:O:33:THR:CG2	16:O:63:ARG:HH11	2.07	0.43
17:P:42:ARG:HB3	17:P:42:ARG:HH11	1.82	0.43
18:Q:63:ARG:HA	18:Q:64:PRO:HD2	1.72	0.43
18:Q:90:ILE:O	18:Q:92:ARG:N	2.51	0.43
1:A:194:C:O2'	21:T:68:LYS:HD3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:351:G:O5'	1:A:351:G:H8	2.01	0.43
1:A:686:U:C2	1:A:687:A:N7	2.86	0.43
1:A:688:G:C6	1:A:700:G:C2	3.06	0.43
1:A:778:G:H8	1:A:778:G:O5'	2.01	0.43
1:A:990:C:C4	1:A:1216:G:N2	2.86	0.43
1:A:1197:G:H2'	1:A:1198:G:H5'	2.00	0.43
4:C:8:ILE:O	4:C:12:LEU:N	2.51	0.43
4:C:40:ARG:O	4:C:44:GLU:HB2	2.18	0.43
5:D:64:LEU:CD2	5:D:198:VAL:HG11	2.41	0.43
5:D:76:ARG:O	5:D:79:PHE:HB3	2.17	0.43
5:D:120:LEU:CD2	5:D:126:ILE:HD11	2.48	0.43
5:D:126:ILE:HD13	5:D:126:ILE:N	2.33	0.43
6:E:107:ARG:C	6:E:109:ILE:N	2.71	0.43
10:I:40:LEU:C	10:I:42:ARG:H	2.21	0.43
10:I:126:SER:HB2	10:I:127:LYS:H	1.57	0.43
12:K:62:GLN:CG	12:K:63:LEU:N	2.82	0.43
13:L:40:VAL:HG21	13:L:78:GLN:N	2.33	0.43
14:M:15:VAL:HG22	14:M:43:THR:O	2.17	0.43
14:M:24:GLY:O	14:M:25:ILE:C	2.56	0.43
14:M:117:VAL:HG12	14:M:118:ALA:H	1.82	0.43
1:A:143:A:C2	1:A:221:C:O2	2.71	0.43
1:A:219:C:C4	1:A:220:G:C8	3.07	0.43
1:A:477:G:H5"	1:A:478:A:P	2.59	0.43
1:A:568:G:C6	1:A:569:C:N4	2.86	0.43
1:A:991:U:H6	1:A:1212:U:C2	2.36	0.43
3:B:73:THR:HG23	3:B:95:GLN:O	2.18	0.43
4:C:94:LEU:HD12	4:C:95:THR:OG1	2.17	0.43
4:C:159:GLY:HA2	4:C:193:TYR:CD2	2.53	0.43
9:H:30:ARG:O	9:H:31:PHE:C	2.56	0.43
12:K:123:LYS:O	12:K:124:LYS:C	2.56	0.43
13:L:93:LEU:O	13:L:96:VAL:HG23	2.17	0.43
15:N:24:CYS:HB3	15:N:28:GLY:HA2	2.00	0.43
16:O:52:SER:O	16:O:55:GLY:N	2.51	0.43
1:A:784:C:H2'	1:A:785:G:O4'	2.18	0.43
1:A:1281:U:H3'	1:A:1281:U:C6	2.53	0.43
1:A:1483:A:H2'	1:A:1484:C:O4'	2.17	0.43
3:B:124:SER:H	3:B:125:PRO:CD	2.31	0.43
3:B:193:ASP:HA	3:B:194:PRO:HD2	1.88	0.43
4:C:32:LEU:O	4:C:35:GLU:HB3	2.18	0.43
5:D:113:SER:OG	5:D:116:GLN:HB2	2.18	0.43
6:E:34:VAL:HG23	6:E:42:GLY:CA	2.44	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:82:VAL:O	6:E:88:LYS:HA	2.18	0.43
11:J:9:ARG:O	11:J:9:ARG:CG	2.65	0.43
12:K:59:TYR:O	12:K:62:GLN:HB3	2.19	0.43
14:M:26:GLY:O	14:M:28:ALA:N	2.41	0.43
1:A:189:G:H1	1:A:190(J):U:H3	1.66	0.43
1:A:316:G:N2	1:A:338:A:C4	2.86	0.43
1:A:436:C:C2	1:A:437:U:C5	3.06	0.43
1:A:560:U:H4'	1:A:561:U:H5"	2.00	0.43
1:A:674:G:N2	1:A:717:C:O2	2.51	0.43
1:A:994:A:N7	1:A:1216:G:H4'	2.33	0.43
1:A:1056:U:O4	1:A:1200:C:C2	2.71	0.43
1:A:1085:U:H5'	1:A:1094:G:N2	2.34	0.43
1:A:1504:G:O2'	1:A:1505:G:OP2	2.32	0.43
3:B:134:GLU:HA	3:B:137:ARG:HB3	1.99	0.43
3:B:223:ILE:CG2	3:B:224:GLN:N	2.82	0.43
4:C:6:HIS:HD2	4:C:7:PRO:N	2.16	0.43
4:C:57:ILE:HG23	4:C:58:GLU:N	2.34	0.43
4:C:141:VAL:O	4:C:146:ALA:CB	2.66	0.43
5:D:8:VAL:HB	5:D:21:LEU:HD22	2.00	0.43
8:G:111:ARG:HB3	8:G:113:GLU:HG2	2.01	0.43
11:J:38:ILE:HG22	11:J:71:LEU:CB	2.49	0.43
13:L:47:LYS:HB3	13:L:48:PRO:CD	2.44	0.43
13:L:101:VAL:O	13:L:103:GLY:N	2.51	0.43
15:N:24:CYS:HB3	15:N:29:ARG:N	2.34	0.43
16:O:48:LYS:O	16:O:50:HIS:N	2.44	0.43
18:Q:13:ASP:O	18:Q:15:MET:N	2.51	0.43
18:Q:18:THR:HG23	18:Q:69:LYS:HE3	2.00	0.43
18:Q:56:VAL:O	18:Q:77:VAL:HG23	2.18	0.43
21:T:63:ILE:C	21:T:65:LYS:N	2.69	0.43
21:T:65:LYS:O	21:T:68:LYS:N	2.40	0.43
1:A:70:G:H5"	1:A:73:C:P	2.59	0.43
1:A:166:G:N3	1:A:167:G:C8	2.87	0.43
1:A:262:A:N6	1:A:263:A:N6	2.67	0.43
1:A:337:C:C2	1:A:338:A:N7	2.87	0.43
1:A:642:A:C6	1:A:643:C:N3	2.87	0.43
1:A:824:C:C3'	1:A:824:C:C6	3.01	0.43
1:A:941:G:C6	1:A:942:G:C8	3.07	0.43
1:A:992:U:OP2	1:A:992:U:O4'	2.37	0.43
1:A:1185:G:C2	1:A:1186:G:C8	3.06	0.43
1:A:1490:C:H3'	1:A:1491:G:H5"	1.95	0.43
1:A:1512:U:H2'	1:A:1513:A:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:178:ARG:HH22	9:H:68:ARG:HH22	1.64	0.43
5:D:68:TYR:OH	5:D:98:GLU:OE1	2.17	0.43
9:H:53:VAL:O	9:H:53:VAL:CG1	2.67	0.43
10:I:75:ASP:O	10:I:78:LYS:HB3	2.19	0.43
10:I:92:TYR:O	10:I:96:LEU:HB2	2.19	0.43
11:J:19:SER:HB2	11:J:91:PRO:CD	2.48	0.43
12:K:64:ALA:O	12:K:65:ALA:C	2.55	0.43
17:P:20:VAL:HG13	17:P:21:VAL:O	2.19	0.43
17:P:67:THR:HB	17:P:70:ALA:HB2	2.01	0.43
20:S:51:VAL:O	20:S:58:VAL:HG23	2.18	0.43
21:T:22:ARG:O	21:T:25:ARG:N	2.52	0.43
1:A:13:U:C5	1:A:916:G:O6	2.72	0.43
1:A:80:G:H2'	1:A:81:U:H5'	2.01	0.43
1:A:223:U:C5'	21:T:68:LYS:HZ2	2.32	0.43
1:A:463:A:P	17:P:75:ARG:HH12	2.41	0.43
1:A:506:G:C6	1:A:507:C:N4	2.87	0.43
1:A:625:G:C6	1:A:626:U:O4	2.72	0.43
1:A:647:C:H42	1:A:648:A:N6	2.17	0.43
1:A:942:G:C2	1:A:943:U:C5	3.07	0.43
1:A:953:G:H2'	1:A:954:G:O4'	2.19	0.43
1:A:1206:G:C6	1:A:1207:G:C5	3.07	0.43
1:A:1309:G:C6	1:A:1329:A:C2	3.06	0.43
1:A:1343:G:C6	1:A:1344:C:N4	2.87	0.43
1:A:1478:C:O5'	1:A:1478:C:H6	2.01	0.43
4:C:76:VAL:O	4:C:83:ARG:HD2	2.18	0.43
9:H:35:ILE:H	9:H:35:ILE:HG13	1.44	0.43
10:I:17:VAL:HG11	10:I:81:ILE:HA	2.00	0.43
11:J:90:LEU:CB	11:J:91:PRO:CD	2.76	0.43
12:K:72:ALA:HB1	12:K:77:MET:HG3	1.99	0.43
13:L:46:LYS:HD2	13:L:47:LYS:H	1.84	0.43
14:M:5:ALA:HB2	14:M:22:ILE:HG12	2.01	0.43
21:T:14:LYS:HG2	21:T:18:GLN:HE22	1.82	0.43
1:A:368:U:O2'	1:A:369:C:P	2.76	0.43
1:A:380:G:C2	1:A:384:G:C6	3.06	0.43
1:A:451:A:C6	1:A:481:G:C5	3.07	0.43
1:A:1183:A:O2'	1:A:1184:G:OP1	2.29	0.43
1:A:1410:G:C2'	1:A:1411:C:O5'	2.67	0.43
1:A:1471:G:H8	1:A:1471:G:O5'	2.02	0.43
3:B:103:THR:HA	3:B:180:LEU:HD11	2.00	0.43
4:C:77:ILE:HA	4:C:84:ILE:HG22	2.00	0.43
5:D:104:VAL:HG23	5:D:185:PHE:CD1	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:9:LYS:O	6:E:33:VAL:N	2.39	0.43
8:G:153:HIS:CE1	8:G:154:TYR:HE2	2.36	0.43
10:I:33:PHE:CE1	10:I:37:PHE:HE1	2.37	0.43
20:S:5:LEU:O	20:S:6:LYS:HG3	2.18	0.43
1:A:118:U:C5	1:A:288:A:C6	3.07	0.43
1:A:132:C:C2'	1:A:133:U:H5'	2.49	0.43
1:A:193:C:O2	1:A:194:C:C6	2.72	0.43
1:A:289:G:C6	1:A:290:C:N4	2.87	0.43
1:A:313:A:H2'	1:A:314:C:O4'	2.18	0.43
1:A:362:G:O3'	13:L:33:ARG:NH1	2.52	0.43
1:A:376:G:C4	1:A:389:A:C2	3.07	0.43
1:A:378:G:C6	1:A:379:C:C4	3.06	0.43
1:A:487:A:H2'	1:A:488:C:O4'	2.18	0.43
1:A:540:G:C2'	1:A:541:G:O4'	2.64	0.43
1:A:578:C:H2'	1:A:579:G:O4'	2.19	0.43
1:A:689:C:OP1	12:K:44:SER:OG	2.25	0.43
1:A:987:G:H1	1:A:1218:C:N4	2.10	0.43
1:A:1114:C:O5'	1:A:1114:C:H6	2.01	0.43
1:A:1187:G:C2	1:A:1188:A:C4	3.07	0.43
1:A:1348:U:H6	1:A:1348:U:C5'	2.31	0.43
1:A:1515:C:H2'	1:A:1516:G:C8	2.54	0.43
4:C:64:VAL:HG12	4:C:65:ALA:H	1.84	0.43
5:D:64:LEU:HD21	5:D:94:LEU:CD2	2.48	0.43
6:E:55:VAL:O	6:E:56:GLN:C	2.56	0.43
6:E:79:GLU:O	9:H:104:ARG:CZ	2.67	0.43
6:E:130:ASN:HA	6:E:133:TYR:HB2	2.00	0.43
7:F:11:ASN:HA	7:F:12:PRO:HD2	1.78	0.43
13:L:68:ALA:HB3	13:L:100:ILE:HD11	2.00	0.43
16:O:76:GLU:C	16:O:78:TYR:N	2.72	0.43
17:P:67:THR:HG22	17:P:69:THR:N	2.34	0.43
17:P:74:LEU:CD1	17:P:79:VAL:HG11	2.46	0.43
21:T:68:LYS:HD2	21:T:68:LYS:HA	1.72	0.43
21:T:93:GLU:O	21:T:96:GLY:N	2.43	0.43
1:A:21:G:C2	1:A:22:G:C6	3.07	0.43
1:A:136:C:O2'	17:P:65:GLN:OE1	2.35	0.43
1:A:504:C:N3	1:A:542:G:C2	2.86	0.43
1:A:984:C:C2	1:A:985:C:C5	3.07	0.43
1:A:1005:A:C4	1:A:1026:G:N2	2.86	0.43
1:A:1255:G:C3'	1:A:1279:A:H61	2.31	0.43
1:A:1418:A:N6	1:A:1419:G:C2	2.87	0.43
1:A:1509:C:C5'	1:A:1510:U:OP2	2.67	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:66:VAL:O	4:C:66:VAL:HG12	2.19	0.43
5:D:61:LYS:NZ	5:D:62:GLN:NE2	2.67	0.43
9:H:75:ARG:HA	9:H:76:PRO:HD3	1.92	0.43
11:J:60:ARG:HD2	11:J:60:ARG:HA	1.74	0.43
14:M:91:ARG:O	14:M:95:GLY:CA	2.66	0.43
14:M:125:ARG:HD2	14:M:126:LYS:H	1.84	0.43
1:A:192:U:C4	1:A:193:C:C5	3.07	0.42
1:A:376:G:C2	1:A:389:A:C6	3.07	0.42
1:A:426:G:P	5:D:36:ARG:NH2	2.92	0.42
1:A:459:G:C6	1:A:461:C:OP2	2.72	0.42
1:A:767:A:O2'	1:A:768:A:H5'	2.19	0.42
1:A:919:A:O2'	1:A:1080:A:N1	2.48	0.42
1:A:1092:A:H8	1:A:1092:A:H5'	1.84	0.42
1:A:1162:C:O2	1:A:1162:C:H2'	2.17	0.42
3:B:215:LEU:HD23	3:B:215:LEU:HA	1.93	0.42
4:C:36:ASP:HB3	4:C:40:ARG:NH1	2.34	0.42
6:E:18:ARG:HE	6:E:25:ARG:HB3	1.84	0.42
7:F:97:PHE:HB2	19:R:32:ARG:HH21	1.82	0.42
8:G:151:TYR:OH	12:K:54:ARG:HD3	2.18	0.42
12:K:34:ASP:HB2	12:K:35:PRO:HD2	1.99	0.42
12:K:53:SER:C	12:K:55:LYS:N	2.73	0.42
13:L:75:HIS:CG	13:L:76:ASN:N	2.86	0.42
16:O:3:ILE:HA	16:O:7:GLU:OE2	2.19	0.42
1:A:374:A:C6	1:A:375:U:C4	3.08	0.42
1:A:1114:C:H1'	15:N:60:SER:CB	2.49	0.42
1:A:1151:A:H5"	11:J:42:THR:OG1	2.19	0.42
1:A:1320:C:H2'	1:A:1321:C:O4'	2.19	0.42
1:A:1431:C:H2'	1:A:1432:G:H5'	2.00	0.42
3:B:15:VAL:CG1	3:B:209:ARG:HH11	2.31	0.42
3:B:214:ILE:O	3:B:215:LEU:C	2.56	0.42
4:C:6:HIS:CD2	4:C:8:ILE:HB	2.53	0.42
8:G:74:GLU:HA	8:G:141:VAL:HG12	2.01	0.42
12:K:99:GLN:HA	12:K:105:VAL:HG21	2.01	0.42
12:K:103:LEU:H	12:K:103:LEU:HG	1.58	0.42
13:L:124:LYS:HA	13:L:125:PRO:HD3	1.83	0.42
16:O:78:TYR:O	16:O:82:ILE:HD12	2.18	0.42
18:Q:17:LYS:HB3	18:Q:46:ASP:O	2.19	0.42
1:A:694:A:N6	1:A:787:A:O2'	2.49	0.42
1:A:853:G:C2'	1:A:854:G:O5'	2.67	0.42
1:A:922:G:H2'	1:A:923:A:C8	2.54	0.42
1:A:1151:A:HO2'	1:A:1152:A:P	2.43	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1250:A:H8	1:A:1250:A:H5"	1.83	0.42
1:A:1377:A:H2'	1:A:1378:C:OP2	2.18	0.42
3:B:16:HIS:CE1	3:B:203:GLY:HA3	2.54	0.42
6:E:129:ILE:HD12	6:E:129:ILE:N	2.34	0.42
8:G:62:PHE:C	8:G:62:PHE:CD2	2.93	0.42
13:L:86:ARG:O	13:L:86:ARG:HG3	2.18	0.42
16:O:78:TYR:CD1	16:O:82:ILE:HD11	2.55	0.42
18:Q:14:LYS:H	18:Q:14:LYS:HG3	1.55	0.42
18:Q:20:THR:HG23	18:Q:43:LEU:CD2	2.49	0.42
19:R:58:LEU:HD23	19:R:58:LEU:HA	1.78	0.42
20:S:14:HIS:O	20:S:18:LYS:HB2	2.20	0.42
1:A:178:C:C2'	1:A:179:A:O5'	2.68	0.42
1:A:708:C:OP1	12:K:85:ARG:NH2	2.49	0.42
1:A:990:C:C4	1:A:1216:G:C2	3.07	0.42
1:A:1202:G:C4	15:N:42:ILE:HD12	2.54	0.42
1:A:1206:G:C5	1:A:1207:G:N7	2.87	0.42
1:A:1288:A:H2	1:A:1370:G:H21	1.66	0.42
1:A:1289:A:H5'	1:A:1290:G:OP2	2.18	0.42
1:A:1401:G:C2	1:A:1402:C:H1'	2.54	0.42
1:A:1479:C:O5'	1:A:1479:C:H6	2.01	0.42
3:B:24:TRP:CG	3:B:25:ASN:N	2.87	0.42
3:B:52:GLU:O	3:B:53:ARG:C	2.58	0.42
5:D:64:LEU:O	5:D:67:ILE:HB	2.20	0.42
6:E:36:ASP:OD1	6:E:36:ASP:C	2.58	0.42
10:I:77:ILE:HG22	10:I:78:LYS:N	2.33	0.42
16:O:27:VAL:O	16:O:31:LEU:HD12	2.19	0.42
17:P:42:ARG:H	17:P:42:ARG:HG2	1.49	0.42
18:Q:58:GLU:HG3	18:Q:75:ARG:HG2	2.01	0.42
19:R:69:THR:O	19:R:70:ILE:C	2.56	0.42
21:T:63:ILE:O	21:T:64:ASP:C	2.56	0.42
1:A:5:U:O2	1:A:5:U:C2'	2.64	0.42
1:A:579:G:N2	1:A:763:G:C4	2.87	0.42
1:A:642:A:H2'	1:A:643:C:H5'	2.02	0.42
1:A:1064:G:N2	1:A:1190:G:H2'	2.35	0.42
1:A:1099:G:C5	1:A:1100:C:C4	3.07	0.42
1:A:1241:G:H2'	1:A:1242:C:C6	2.55	0.42
1:A:1309:G:C5	1:A:1329:A:C2	3.07	0.42
1:A:1368:G:C2'	1:A:1369:C:H5'	2.49	0.42
1:A:1425:U:H3	1:A:1475:G:H1	1.67	0.42
3:B:52:GLU:C	3:B:54:THR:N	2.71	0.42
3:B:84:GLU:CG	3:B:216:SER:HA	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:187:LEU:HD13	3:B:204:ASN:O	2.19	0.42
3:B:189:ASP:HB3	3:B:205:ASP:H	1.84	0.42
6:E:105:VAL:HG12	6:E:132:ALA:HB2	2.01	0.42
9:H:46:LYS:HG3	9:H:64:LYS:HB2	2.00	0.42
9:H:84:ARG:HB3	9:H:84:ARG:HH11	1.84	0.42
10:I:43:ALA:O	10:I:46:ALA:N	2.51	0.42
13:L:61:THR:C	13:L:63:GLY:N	2.73	0.42
13:L:69:TYR:HE2	13:L:71:PRO:HA	1.82	0.42
14:M:74:VAL:C	14:M:76:ALA:N	2.72	0.42
16:O:35:ARG:HB3	16:O:59:MET:CE	2.50	0.42
20:S:13:ASP:HA	20:S:16:LEU:HB3	2.02	0.42
1:A:282:A:C4	1:A:283:C:C6	3.07	0.42
1:A:286:G:C4	1:A:287:U:C6	3.07	0.42
1:A:709:G:C4	1:A:710:G:C8	3.08	0.42
1:A:1111:A:H2'	1:A:1112:C:O5'	2.20	0.42
1:A:1132:C:H2'	1:A:1133:G:H8	1.84	0.42
1:A:1257:U:H4'	1:A:1258:G:OP2	2.19	0.42
1:A:1266:G:H21	1:A:1270:C:N4	2.16	0.42
1:A:1439:C:O2	1:A:1439:C:H2'	2.20	0.42
3:B:21:ARG:H	3:B:21:ARG:HG3	1.66	0.42
3:B:85:ALA:CB	3:B:92:TYR:HB3	2.49	0.42
5:D:25:ARG:HE	5:D:30:LYS:HB3	1.84	0.42
7:F:7:ASN:HB2	7:F:89:MET:HB3	2.02	0.42
7:F:27:GLN:O	7:F:31:GLU:HG2	2.18	0.42
8:G:138:LYS:C	8:G:140:ASP:H	2.23	0.42
21:T:81:LYS:HB3	21:T:81:LYS:HE2	1.48	0.42
1:A:223:U:C5'	21:T:68:LYS:NZ	2.83	0.42
1:A:404:U:H2'	1:A:405:U:C6	2.54	0.42
1:A:824:C:C6	1:A:824:C:H3'	2.54	0.42
1:A:1005:A:H1'	1:A:1036:G:H22	1.83	0.42
1:A:1022:G:H2'	1:A:1023:G:C8	2.55	0.42
1:A:1454:G:H2'	1:A:1455:G:H8	1.84	0.42
1:A:1455:G:C3'	1:A:1459:C:P	3.08	0.42
3:B:108:ILE:O	3:B:108:ILE:CG2	2.68	0.42
3:B:166:ASP:HA	3:B:167:PRO:HD2	1.95	0.42
4:C:66:VAL:HG12	4:C:68:VAL:HG23	2.01	0.42
4:C:86:VAL:O	4:C:86:VAL:HG13	2.18	0.42
4:C:172:ARG:H	4:C:172:ARG:HG2	1.52	0.42
5:D:173:TRP:HB2	5:D:187:ARG:O	2.19	0.42
6:E:52:PRO:C	6:E:54:ALA:N	2.72	0.42
9:H:35:ILE:O	9:H:36:LEU:C	2.58	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:57:GLY:O	10:I:58:ARG:HG2	2.19	0.42
18:Q:60:ILE:HG13	18:Q:61:GLU:N	2.34	0.42
1:A:150:C:H2'	1:A:151:A:O5'	2.18	0.42
1:A:199:G:C2'	1:A:200:G:H5'	2.45	0.42
1:A:395:C:O2	1:A:395:C:C2'	2.66	0.42
1:A:529:G:O2'	1:A:533:A:C6	2.72	0.42
1:A:582:U:O2	1:A:582:U:H2'	2.19	0.42
1:A:597:G:N7	1:A:598:U:C5	2.88	0.42
1:A:1056:U:O2	1:A:1056:U:C2'	2.67	0.42
1:A:1233:G:N2	1:A:1234:C:C2	2.87	0.42
1:A:1260:C:O5'	1:A:1284:C:H4'	2.20	0.42
1:A:1368:G:O2'	1:A:1369:C:H5'	2.19	0.42
1:A:1525:G:H2'	1:A:1526:G:C5'	2.49	0.42
3:B:28:PHE:O	3:B:29:ALA:C	2.57	0.42
3:B:114:ARG:NH1	3:B:118:LEU:CD1	2.67	0.42
9:H:10:LEU:HB3	9:H:83:ILE:CD1	2.45	0.42
13:L:15:ARG:HD2	13:L:15:ARG:HA	1.90	0.42
14:M:18:ALA:O	14:M:21:TYR:N	2.40	0.42
14:M:57:ARG:O	14:M:61:GLU:HB2	2.19	0.42
15:N:46:GLU:O	15:N:49:HIS:HB2	2.20	0.42
20:S:80:TYR:OH	20:S:82:GLY:HA2	2.19	0.42
1:A:255:G:H1'	18:Q:16:GLN:NE2	2.35	0.42
1:A:482:A:H2'	1:A:483:C:O4'	2.19	0.42
1:A:978:A:C5	1:A:1319:A:C2	3.08	0.42
1:A:991:U:C6	1:A:1212:U:O2	2.72	0.42
1:A:1152:A:OP1	11:J:68:HIS:ND1	2.53	0.42
4:C:35:GLU:HB3	4:C:36:ASP:H	1.70	0.42
4:C:36:ASP:OD2	4:C:36:ASP:N	2.37	0.42
5:D:13:ARG:HB3	5:D:40:PRO:HD3	2.02	0.42
5:D:79:PHE:CE1	5:D:207:TYR:CD1	3.07	0.42
6:E:71:LEU:CD2	6:E:115:VAL:HG22	2.48	0.42
11:J:56:HIS:O	11:J:57:LYS:C	2.55	0.42
13:L:119:LYS:O	13:L:120:TYR:HB2	2.20	0.42
20:S:14:HIS:ND1	20:S:14:HIS:N	2.68	0.42
21:T:70:SER:O	21:T:70:SER:OG	2.30	0.42
21:T:74:LYS:HB2	21:T:74:LYS:HE3	1.92	0.42
21:T:88:VAL:O	21:T:90:GLN:N	2.53	0.42
1:A:131:C:H2'	1:A:132:C:C6	2.54	0.42
1:A:193:C:O3'	21:T:61:SER:HB2	2.20	0.42
1:A:690:G:N2	1:A:698:G:C6	2.88	0.42
1:A:864:A:C6	1:A:865:A:C6	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:896:C:O2	1:A:896:C:H2'	2.20	0.42
1:A:918:A:H2'	1:A:919:A:C8	2.55	0.42
1:A:1124:G:C2'	1:A:1145:C:H41	2.33	0.42
1:A:1141:C:C2	1:A:1142:G:C8	3.07	0.42
1:A:1230:C:O2	1:A:1230:C:C2'	2.68	0.42
1:A:1237:C:C4'	1:A:1334:G:H21	2.32	0.42
1:A:1510:U:O2	1:A:1510:U:C2'	2.62	0.42
3:B:138:LEU:C	3:B:140:HIS:N	2.73	0.42
4:C:157:ILE:O	4:C:158:GLY:C	2.58	0.42
4:C:191:THR:HG21	4:C:193:TYR:CE1	2.55	0.42
6:E:87:SER:OG	6:E:130:ASN:HB2	2.20	0.42
7:F:4:TYR:HA	7:F:91:VAL:O	2.19	0.42
8:G:87:VAL:HA	8:G:88:PRO:HD3	1.80	0.42
8:G:145:ALA:C	8:G:147:ALA:H	2.22	0.42
11:J:46:ARG:NH1	11:J:64:GLU:HB3	2.32	0.42
11:J:56:HIS:C	11:J:58:ASP:N	2.58	0.42
13:L:10:LEU:O	13:L:14:GLY:HA2	2.20	0.42
13:L:55:VAL:O	13:L:70:ILE:HD12	2.20	0.42
21:T:54:LYS:HA	21:T:57:ARG:NH1	2.34	0.42
1:A:130:A:H5'	18:Q:63:ARG:HE	1.85	0.41
1:A:354:G:N1	1:A:355:C:C4	2.88	0.41
1:A:516:U:C4	1:A:517:G:C6	3.08	0.41
1:A:674:G:OP1	7:F:87:ARG:NH2	2.53	0.41
1:A:761:G:H2'	1:A:762:C:H6	1.83	0.41
1:A:861:G:C4	1:A:862:C:C6	3.08	0.41
1:A:949:A:N1	1:A:1233:G:C4	2.88	0.41
1:A:989:C:HO2'	1:A:990:C:H5'	1.84	0.41
1:A:1124:G:H2'	1:A:1145:C:C5	2.54	0.41
1:A:1152:A:H4'	11:J:13:HIS:CD2	2.54	0.41
1:A:1233:G:C8	1:A:1233:G:H5"	2.55	0.41
1:A:1368:G:H5"	10:I:112:LYS:O	2.20	0.41
3:B:43:ASP:O	3:B:45:GLN:N	2.53	0.41
5:D:98:GLU:OE2	5:D:107:ARG:NE	2.44	0.41
5:D:121:VAL:HA	5:D:126:ILE:HG12	2.00	0.41
9:H:99:GLU:O	9:H:100:ILE:C	2.58	0.41
11:J:79:ARG:HH11	11:J:82:ILE:HD12	1.84	0.41
12:K:50:TYR:CD2	12:K:54:ARG:HB2	2.55	0.41
16:O:33:THR:OG1	16:O:63:ARG:HD2	2.19	0.41
21:T:104:LEU:CD2	21:T:104:LEU:N	2.26	0.41
1:A:45:U:O2	1:A:396:G:N2	2.41	0.41
1:A:109:A:H4'	1:A:110:C:OP2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:433:C:H2'	1:A:434:U:C6	2.56	0.41
1:A:490:G:O2'	1:A:491:G:H5'	2.20	0.41
1:A:512:U:C3'	1:A:512:U:C6	3.03	0.41
1:A:545:C:H2'	1:A:546:G:O4'	2.20	0.41
1:A:705:U:C4	1:A:706:A:C5	3.08	0.41
1:A:1014:A:C3'	1:A:1015:A:C8	3.03	0.41
1:A:1084:G:C5	1:A:1085:U:C4	3.07	0.41
1:A:1161:C:H2'	1:A:1162:C:H6	1.80	0.41
1:A:1277:C:HO2'	1:A:1279:A:H8	1.60	0.41
3:B:207:ALA:O	3:B:208:ILE:C	2.58	0.41
4:C:58:GLU:HG2	11:J:92:THR:HB	2.02	0.41
5:D:14:ARG:HD3	5:D:14:ARG:C	2.40	0.41
5:D:50:ARG:O	5:D:51:PRO:C	2.59	0.41
5:D:144:ASP:N	5:D:144:ASP:OD1	2.53	0.41
6:E:127:ASN:OD1	6:E:129:ILE:HB	2.21	0.41
7:F:69:GLU:HA	7:F:72:VAL:HG23	2.02	0.41
8:G:113:GLU:HG2	8:G:113:GLU:H	1.64	0.41
11:J:9:ARG:O	11:J:9:ARG:HG3	2.18	0.41
17:P:33:ILE:H	17:P:33:ILE:HG13	1.62	0.41
18:Q:26:GLN:HE21	18:Q:37:LYS:HE2	1.85	0.41
20:S:39:THR:CG2	20:S:40:ILE:N	2.83	0.41
1:A:117:G:H8	1:A:117:G:O5'	2.02	0.41
1:A:1004:A:H5"	1:A:1025:U:C4	2.55	0.41
1:A:1131:G:O6	1:A:1139:G:O6	2.38	0.41
1:A:1358:U:OP1	15:N:35:ARG:HB2	2.20	0.41
1:A:1412:C:C2	1:A:1489:G:N2	2.88	0.41
5:D:152:SER:O	5:D:154:ASN:N	2.54	0.41
11:J:9:ARG:HB3	11:J:9:ARG:NH1	2.35	0.41
11:J:67:THR:O	11:J:67:THR:HG22	2.21	0.41
13:L:23:LYS:C	13:L:24:VAL:CG2	2.88	0.41
13:L:24:VAL:O	13:L:26:ALA:N	2.54	0.41
14:M:22:ILE:CB	14:M:25:ILE:HD12	2.48	0.41
16:O:39:LEU:HA	16:O:39:LEU:HD23	1.73	0.41
16:O:73:GLU:OE2	16:O:73:GLU:HA	2.14	0.41
19:R:44:LEU:N	19:R:51:LEU:HD12	2.34	0.41
1:A:62:U:C2	1:A:63:C:C5	3.09	0.41
1:A:149:A:H2	1:A:150:C:C2	2.35	0.41
1:A:192:U:H2'	1:A:193:C:H6	1.85	0.41
1:A:204:U:H4'	1:A:216:G:P	2.61	0.41
1:A:262:A:N1	1:A:263:A:N1	2.67	0.41
1:A:411:A:C2	1:A:413:G:H1'	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:418:C:H2'	1:A:419:C:C6	2.55	0.41
1:A:426:G:C2	1:A:427:U:C2	3.08	0.41
1:A:512:U:C6	1:A:512:U:H3'	2.56	0.41
1:A:563:A:HO2'	1:A:566:G:HO2'	1.44	0.41
1:A:622:A:C8	1:A:622:A:C3'	3.04	0.41
1:A:940:C:H2'	1:A:941:G:C8	2.55	0.41
1:A:1125:U:O4	11:J:73:ASP:OD2	2.38	0.41
1:A:1521:G:C2'	1:A:1522:U:O5'	2.68	0.41
3:B:50:GLU:O	3:B:51:LEU:C	2.58	0.41
3:B:118:LEU:HD22	3:B:142:LEU:HB2	2.01	0.41
4:C:6:HIS:NE2	4:C:8:ILE:HG22	2.35	0.41
4:C:131:ARG:HG2	4:C:135:LYS:NZ	2.36	0.41
5:D:68:TYR:CE2	5:D:97:LEU:HB3	2.56	0.41
8:G:120:ILE:HG22	8:G:124:LEU:CD1	2.51	0.41
10:I:46:ALA:HA	10:I:78:LYS:HB2	2.03	0.41
10:I:46:ALA:HB1	10:I:77:ILE:CG2	2.51	0.41
15:N:21:TYR:CD2	15:N:21:TYR:O	2.73	0.41
16:O:58:MET:O	16:O:62:GLN:N	2.44	0.41
19:R:37:VAL:O	19:R:38:GLU:C	2.58	0.41
21:T:29:LYS:O	21:T:33:ILE:CD1	2.69	0.41
21:T:39:LYS:HG2	21:T:55:ILE:HD12	2.03	0.41
21:T:84:LEU:HD23	21:T:84:LEU:HA	1.87	0.41
1:A:253:U:C2	1:A:254:G:C8	3.08	0.41
1:A:457:C:C4	1:A:458:C:C5	3.09	0.41
1:A:625:G:H2'	1:A:626:U:H6	1.82	0.41
1:A:633:G:H5"	1:A:634:C:OP2	2.20	0.41
1:A:1227:A:C3'	1:A:1227:A:C8	3.04	0.41
1:A:1240:U:OP1	8:G:119:ARG:NH2	2.48	0.41
1:A:1299:A:C5	1:A:1301:U:C2	3.08	0.41
1:A:1346:A:H61	1:A:1374:A:H3'	1.85	0.41
1:A:1347:G:C2	1:A:1373:G:C4	3.08	0.41
1:A:1500:A:H2'	1:A:1501:C:H5'	2.02	0.41
4:C:38:ARG:O	4:C:41:GLY:HA3	2.20	0.41
4:C:79:ARG:O	4:C:82:GLU:HG2	2.21	0.41
5:D:57:ARG:HA	5:D:202:LEU:HD23	2.02	0.41
7:F:10:LEU:HD12	7:F:59:TYR:HB3	2.03	0.41
13:L:93:LEU:N	13:L:93:LEU:HD23	2.35	0.41
14:M:4:ILE:HB	14:M:5:ALA:H	1.53	0.41
18:Q:104:LYS:HG3	18:Q:105:ALA:N	2.36	0.41
1:A:7:G:H5'	1:A:298:A:O4'	2.21	0.41
1:A:91:C:C2'	1:A:92:C:O5'	2.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:142:G:N3	1:A:196:A:H2	2.18	0.41
1:A:267:C:O2'	1:A:268:C:H5'	2.20	0.41
1:A:373:A:C2	1:A:482:A:C6	3.08	0.41
1:A:407:G:C6	1:A:408:A:C6	3.08	0.41
1:A:568:G:N3	1:A:574:A:H2	2.19	0.41
1:A:645:C:O2	1:A:645:C:C2'	2.69	0.41
1:A:757:U:H2'	1:A:758:G:O4'	2.19	0.41
1:A:856:C:H5"	1:A:857:C:OP2	2.21	0.41
1:A:908:A:C2'	1:A:909:A:H5'	2.51	0.41
1:A:951:G:C6	1:A:952:U:C5	3.09	0.41
1:A:974:A:H8	1:A:974:A:OP1	2.03	0.41
1:A:1131:G:N2	1:A:1143:G:H21	2.07	0.41
1:A:1332:A:C2	1:A:1333:A:C4	3.08	0.41
4:C:42:LEU:O	4:C:44:GLU:N	2.54	0.41
5:D:135:LEU:HA	5:D:136:PRO:HD3	1.95	0.41
6:E:52:PRO:O	6:E:54:ALA:N	2.54	0.41
8:G:127:ALA:O	8:G:129:GLU:N	2.54	0.41
9:H:56:LYS:HA	9:H:57:PRO:HD2	1.85	0.41
19:R:51:LEU:HA	19:R:52:PRO:HD3	1.84	0.41
20:S:75:ALA:HA	20:S:76:PRO:HD3	1.90	0.41
1:A:36:C:C4	1:A:37:U:C5	3.09	0.41
1:A:333:G:H2'	1:A:334:C:C6	2.56	0.41
1:A:440:A:H5"	1:A:442:C:C5	2.56	0.41
1:A:496:A:C4'	1:A:497:A:OP1	2.58	0.41
1:A:503:C:C2'	1:A:504:C:C5'	2.95	0.41
1:A:692:U:O2	1:A:694:A:C8	2.74	0.41
1:A:749:C:OP2	1:A:750:G:OP2	2.39	0.41
1:A:1103:C:H2'	1:A:1104:G:O4'	2.21	0.41
1:A:1114:C:C4	1:A:1115:C:C5	3.09	0.41
1:A:1176:A:H2'	1:A:1177:G:O4'	2.21	0.41
1:A:1314:C:C4	1:A:1315:U:C5	3.09	0.41
1:A:1371:G:O3'	10:I:69:GLY:HA3	2.20	0.41
3:B:12:GLU:HG3	3:B:213:LEU:CD1	2.51	0.41
3:B:103:THR:HB	3:B:176:GLU:OE2	2.20	0.41
3:B:222:ILE:HG13	3:B:222:ILE:H	1.71	0.41
4:C:47:LEU:O	4:C:48:TYR:C	2.58	0.41
5:D:109:GLY:O	5:D:110:PHE:C	2.59	0.41
6:E:89:ILE:HD13	6:E:122:GLU:HG3	2.01	0.41
6:E:127:ASN:HA	6:E:128:PRO:HD3	1.76	0.41
6:E:136:MET:C	6:E:138:ALA:N	2.74	0.41
8:G:54:THR:HB	8:G:56:GLN:NE2	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:J:63:PHE:CZ	15:N:45:ARG:HG3	2.56	0.41
12:K:110:ASP:HB2	19:R:88:LYS:HG3	2.02	0.41
16:O:6:GLU:O	16:O:7:GLU:C	2.57	0.41
17:P:45:THR:C	17:P:47:ASP:H	2.23	0.41
18:Q:13:ASP:C	18:Q:15:MET:N	2.73	0.41
20:S:77:THR:HB	20:S:78:ARG:HD2	2.02	0.41
1:A:8:A:N6	5:D:205:GLU:O	2.54	0.41
1:A:19:C:H2'	1:A:20:U:O5'	2.21	0.41
1:A:77:G:H2'	1:A:78:G:H8	1.86	0.41
1:A:190(A):C:O5'	1:A:190(A):C:H6	2.04	0.41
1:A:191:G:H1'	21:T:105:SER:HB3	2.02	0.41
1:A:282:A:C5	1:A:283:C:C5	3.08	0.41
1:A:351:G:O5'	1:A:351:G:C8	2.74	0.41
1:A:406:G:H1'	1:A:496:A:N1	2.36	0.41
1:A:477:G:H5"	1:A:478:A:OP2	2.21	0.41
1:A:592:G:C6	1:A:593:G:N7	2.89	0.41
1:A:633:G:C6	1:A:634:C:C4	3.09	0.41
1:A:885:G:C2	1:A:913:A:N1	2.89	0.41
1:A:945:G:C6	1:A:1337:G:C5	3.08	0.41
1:A:1107:C:N4	1:A:1108:G:N7	2.69	0.41
1:A:1117:G:H4'	10:I:104:ARG:NH1	2.36	0.41
1:A:1349:A:C6	1:A:1374:A:C8	3.08	0.41
1:A:1432:G:C8	1:A:1432:G:C3'	3.03	0.41
4:C:23:TYR:HB3	11:J:93:GLY:C	2.40	0.41
4:C:64:VAL:HG12	4:C:65:ALA:N	2.35	0.41
4:C:133:ALA:O	4:C:134:ILE:C	2.59	0.41
4:C:181:ASN:C	4:C:182:ILE:HG13	2.40	0.41
5:D:94:LEU:HD23	5:D:97:LEU:HD12	2.02	0.41
6:E:54:ALA:O	6:E:57:LYS:N	2.53	0.41
8:G:31:MET:HE3	8:G:34:GLY:HA2	2.02	0.41
11:J:33:GLN:C	11:J:34:VAL:HG23	2.41	0.41
12:K:33:THR:HG23	12:K:34:ASP:O	2.20	0.41
13:L:60:LEU:HD13	13:L:60:LEU:HA	1.92	0.41
14:M:4:ILE:H	14:M:4:ILE:HG13	1.56	0.41
15:N:24:CYS:SG	15:N:39:LEU:HA	2.61	0.41
15:N:39:LEU:HB2	15:N:43:CYS:HB3	2.03	0.41
21:T:50:GLU:HB2	21:T:100:ILE:HD13	2.03	0.41
1:A:152:A:H3'	1:A:153:C:H6	1.86	0.41
1:A:165:C:H2'	1:A:166:G:C8	2.55	0.41
1:A:361:G:O6	1:A:362:G:N1	2.54	0.41
1:A:444:C:N4	1:A:491:G:H1	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:481:G:HO2'	1:A:483:C:N4	2.19	0.41
1:A:506:G:O6	1:A:507:C:N4	2.53	0.41
1:A:575:G:O2'	1:A:821:G:H5'	2.20	0.41
1:A:671:G:N3	1:A:671:G:H2'	2.35	0.41
1:A:707:C:C5'	12:K:20:TYR:CD2	2.90	0.41
1:A:913:A:HO2'	1:A:914:A:P	2.43	0.41
1:A:981:U:H5'	15:N:21:TYR:CE1	2.55	0.41
1:A:1181:G:H4'	1:A:1182:G:OP1	2.21	0.41
1:A:1255:G:C6	1:A:1279:A:C8	3.09	0.41
1:A:1266:G:H3'	1:A:1266:G:C8	2.54	0.41
1:A:1440:C:O2	1:A:1440:C:H2'	2.20	0.41
1:A:1454:G:C2	1:A:1455:G:C5	3.09	0.41
1:A:1459:C:C2	1:A:1460:A:C8	3.09	0.41
3:B:108:ILE:HG22	3:B:108:ILE:O	2.21	0.41
3:B:196:LEU:H	3:B:196:LEU:HG	1.74	0.41
6:E:112:LEU:HD23	6:E:112:LEU:HA	1.67	0.41
7:F:97:PHE:HB3	19:R:32:ARG:NH2	2.36	0.41
9:H:10:LEU:CB	9:H:83:ILE:HD11	2.47	0.41
9:H:36:LEU:HA	9:H:39:LEU:HD23	2.02	0.41
9:H:120:THR:HG23	9:H:123:GLU:CD	2.40	0.41
13:L:7:ILE:O	13:L:11:VAL:HG23	2.20	0.41
13:L:32:PHE:CD2	13:L:32:PHE:N	2.89	0.41
13:L:102:ARG:NH1	13:L:110:VAL:HG22	2.34	0.41
15:N:11:LYS:HG2	15:N:13:THR:HB	2.02	0.41
15:N:44:LEU:C	15:N:44:LEU:CD1	2.89	0.41
16:O:63:ARG:O	16:O:64:ARG:C	2.58	0.41
17:P:70:ALA:C	17:P:72:ARG:N	2.74	0.41
17:P:74:LEU:HD22	17:P:74:LEU:HA	1.44	0.41
19:R:22:VAL:O	19:R:22:VAL:CG1	2.69	0.41
20:S:50:ALA:HA	20:S:58:VAL:O	2.21	0.41
21:T:13:LEU:CD2	21:T:14:LYS:N	2.72	0.41
21:T:13:LEU:O	21:T:14:LYS:C	2.58	0.41
21:T:16:HIS:O	21:T:17:ARG:C	2.59	0.41
21:T:33:ILE:HD12	21:T:33:ILE:N	2.34	0.41
21:T:44:ALA:C	21:T:46:GLU:N	2.73	0.41
21:T:56:MET:HE1	21:T:104:LEU:HD21	2.00	0.41
1:A:28:G:O2'	1:A:296:U:H5"	2.21	0.41
1:A:160:A:N6	1:A:161:A:C2	2.89	0.41
1:A:191:G:C1'	21:T:105:SER:HB3	2.51	0.41
1:A:247:G:C6	1:A:278:G:C6	3.08	0.41
1:A:375:U:H2'	1:A:376:G:H8	1.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:401:C:H2'	1:A:402:G:C8	2.56	0.41
1:A:833:U:H2'	1:A:834:C:C6	2.56	0.41
1:A:836:G:N1	1:A:851:G:C5	2.89	0.41
1:A:949:A:C2	1:A:1233:G:C2	3.07	0.41
5:D:59:ARG:NE	5:D:59:ARG:CA	2.82	0.41
6:E:34:VAL:O	6:E:42:GLY:N	2.42	0.41
8:G:37:ASN:O	8:G:38:LEU:C	2.60	0.41
10:I:4:TYR:CE1	10:I:88:TYR:HB2	2.57	0.41
12:K:63:LEU:O	12:K:66:LEU:N	2.54	0.41
13:L:76:ASN:ND2	13:L:106:ASP:O	2.54	0.41
16:O:31:LEU:O	16:O:34:LEU:HB3	2.20	0.41
1:A:93:G:O3'	1:A:95:U:P	2.78	0.40
1:A:175:C:O5'	1:A:175:C:H6	2.04	0.40
1:A:287:U:H2'	1:A:288:A:O5'	2.21	0.40
1:A:354:G:C6	1:A:355:C:N4	2.89	0.40
1:A:486:U:O2	1:A:486:U:C2'	2.69	0.40
1:A:730:G:N3	1:A:765:G:H4'	2.37	0.40
1:A:945:G:C6	1:A:1337:G:C4	3.09	0.40
1:A:1048:G:C8	1:A:1048:G:C3'	3.04	0.40
1:A:1088:G:O5'	1:A:1088:G:C8	2.73	0.40
1:A:1126:U:H2'	1:A:1127:G:N7	2.36	0.40
1:A:1221:G:C6	1:A:1222:G:N7	2.89	0.40
1:A:1357:A:C6	1:A:1358:U:C4	3.09	0.40
1:A:1361:G:C3'	1:A:1361(A):C:H5'	2.50	0.40
1:A:1520:G:H2'	1:A:1521:G:H8	1.85	0.40
3:B:96:ARG:O	3:B:98:LEU:HD12	2.21	0.40
4:C:52:LEU:C	4:C:54:ARG:H	2.23	0.40
5:D:200:GLU:HA	5:D:203:VAL:HG23	2.02	0.40
10:I:114:TYR:C	10:I:116:LYS:H	2.24	0.40
11:J:6:ILE:O	11:J:71:LEU:O	2.39	0.40
12:K:82:VAL:HG13	12:K:83:ILE:N	2.35	0.40
13:L:75:HIS:CD2	13:L:75:HIS:C	2.95	0.40
13:L:117:ARG:NH2	13:L:124:LYS:HD3	2.36	0.40
14:M:62:ASN:HD22	14:M:62:ASN:HA	1.74	0.40
15:N:42:ILE:HB	15:N:43:CYS:H	1.75	0.40
1:A:190(H):G:H2'	1:A:190(I):G:O5'	2.21	0.40
1:A:262:A:H2'	1:A:263:A:C8	2.56	0.40
1:A:401:C:H6	1:A:401:C:C3'	2.26	0.40
1:A:815:A:O2'	1:A:1527:C:O4'	2.39	0.40
1:A:818:G:C3'	1:A:819:A:C5'	2.91	0.40
1:A:1055:A:C6	1:A:1056:U:C5	3.09	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1335:C:H2'	1:A:1335:C:O5'	2.21	0.40
1:A:1509:C:H5'	1:A:1510:U:OP2	2.20	0.40
4:C:131:ARG:CG	4:C:135:LYS:HZ1	2.34	0.40
4:C:180:ALA:HB1	4:C:182:ILE:CG1	2.51	0.40
5:D:140:VAL:HG11	5:D:146:ILE:HD11	2.03	0.40
6:E:11:ILE:HG12	6:E:11:ILE:H	1.48	0.40
6:E:36:ASP:OD2	6:E:40:ARG:HB2	2.21	0.40
7:F:7:ASN:HB2	7:F:89:MET:O	2.22	0.40
11:J:6:ILE:HD12	11:J:71:LEU:O	2.22	0.40
13:L:93:LEU:HA	13:L:94:PRO:HD3	1.82	0.40
17:P:40:ASP:OD2	17:P:42:ARG:HG2	2.21	0.40
17:P:43:LYS:HB3	17:P:48:TRP:CD1	2.56	0.40
19:R:56:THR:O	19:R:57:GLY:C	2.59	0.40
1:A:378:G:C2	1:A:386:C:C2	3.07	0.40
1:A:477:G:C2	1:A:478:A:N7	2.90	0.40
1:A:536:C:C2	1:A:537:G:N7	2.90	0.40
1:A:764:C:N4	1:A:765:G:C6	2.89	0.40
1:A:802:A:C8	1:A:802:A:H3'	2.57	0.40
1:A:1057:G:C5	1:A:1204:A:N1	2.89	0.40
1:A:1332:A:C2	1:A:1333:A:C5	3.09	0.40
1:A:1347:G:C4	10:I:107:ARG:NH1	2.89	0.40
3:B:174:VAL:C	3:B:176:GLU:H	2.24	0.40
5:D:97:LEU:HD23	5:D:97:LEU:HA	1.75	0.40
5:D:182:LYS:HB3	5:D:183:GLY:H	1.52	0.40
6:E:91:LEU:HD21	6:E:120:THR:CG2	2.50	0.40
6:E:128:PRO:O	6:E:129:ILE:C	2.60	0.40
11:J:74:ILE:H	11:J:74:ILE:HG13	1.57	0.40
13:L:21:LYS:HA	13:L:21:LYS:HD2	1.80	0.40
14:M:5:ALA:HB2	14:M:22:ILE:HG21	2.03	0.40
15:N:9:LYS:C	15:N:11:LYS:N	2.75	0.40
15:N:23:ARG:CD	15:N:29:ARG:O	2.62	0.40
16:O:6:GLU:HG2	16:O:7:GLU:H	1.85	0.40
1:A:241:C:O2'	1:A:242:C:H5'	2.22	0.40
1:A:440:A:C3'	1:A:442:C:P	3.09	0.40
1:A:518:C:OP2	1:A:530:G:H4'	2.21	0.40
1:A:658:G:N2	1:A:749:C:N3	2.68	0.40
1:A:671:G:C2	1:A:672:U:H1'	2.55	0.40
1:A:684:A:C2	12:K:39:PRO:HG2	2.57	0.40
1:A:918:A:H2'	1:A:919:A:O4'	2.21	0.40
1:A:1120:G:C2	1:A:1121:U:C4	3.10	0.40
1:A:1120:G:O5'	1:A:1120:G:H8	2.05	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1466:C:H2'	1:A:1467:G:H5'	2.03	0.40
1:A:1503:A:OP1	1:A:1531:A:O2'	2.39	0.40
5:D:125:HIS:C	5:D:126:ILE:HD13	2.41	0.40
6:E:52:PRO:O	6:E:53:LEU:C	2.60	0.40
7:F:26:ILE:HG21	7:F:63:TYR:CE1	2.55	0.40
9:H:92:ARG:HD2	9:H:92:ARG:HA	1.78	0.40
13:L:55:VAL:O	13:L:70:ILE:CD1	2.70	0.40
15:N:43:CYS:O	15:N:44:LEU:C	2.60	0.40
18:Q:75:ARG:HG3	18:Q:75:ARG:NH1	2.36	0.40
1:A:27:G:H2'	1:A:28:G:H8	1.86	0.40
1:A:142:G:C2	1:A:222:U:C2	3.10	0.40
1:A:179:A:H5"	1:A:180:U:OP2	2.21	0.40
1:A:420:U:C2	1:A:424:G:N1	2.89	0.40
1:A:422:C:O2'	1:A:423:G:P	2.79	0.40
1:A:987:G:O5'	1:A:987:G:C8	2.68	0.40
5:D:61:LYS:HE3	5:D:62:GLN:HE21	1.77	0.40
5:D:101:LEU:C	5:D:103:ASN:H	2.25	0.40
9:H:85:ARG:CD	9:H:87:SER:O	2.67	0.40
15:N:14:PRO:O	15:N:15:LYS:C	2.59	0.40
15:N:61:TRP:N	15:N:61:TRP:CE3	2.90	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
3	B	235/256 (92%)	153 (65%)	48 (20%)	34 (14%)	0 4
4	C	204/239 (85%)	120 (59%)	51 (25%)	33 (16%)	0 3
5	D	206/209 (99%)	145 (70%)	37 (18%)	24 (12%)	0 6
6	E	148/162 (91%)	110 (74%)	24 (16%)	14 (10%)	0 11

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
7	F	99/101 (98%)	76 (77%)	17 (17%)	6 (6%)	1 20
8	G	153/156 (98%)	103 (67%)	36 (24%)	14 (9%)	1 12
9	H	136/138 (99%)	103 (76%)	26 (19%)	7 (5%)	2 23
10	I	125/128 (98%)	79 (63%)	33 (26%)	13 (10%)	0 9
11	J	96/105 (91%)	63 (66%)	20 (21%)	13 (14%)	0 4
12	K	117/129 (91%)	79 (68%)	25 (21%)	13 (11%)	0 7
13	L	123/132 (93%)	76 (62%)	29 (24%)	18 (15%)	0 4
14	M	123/126 (98%)	75 (61%)	31 (25%)	17 (14%)	0 4
15	N	58/61 (95%)	43 (74%)	8 (14%)	7 (12%)	0 6
16	O	86/89 (97%)	56 (65%)	22 (26%)	8 (9%)	0 11
17	P	81/88 (92%)	55 (68%)	17 (21%)	9 (11%)	0 7
18	Q	102/105 (97%)	73 (72%)	21 (21%)	8 (8%)	1 15
19	R	71/88 (81%)	50 (70%)	14 (20%)	7 (10%)	0 10
20	S	82/93 (88%)	58 (71%)	17 (21%)	7 (8%)	1 12
21	T	97/106 (92%)	60 (62%)	21 (22%)	16 (16%)	0 3
All	All	2342/2511 (93%)	1577 (67%)	497 (21%)	268 (11%)	0 7

All (268) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	B	17	PHE
3	B	29	ALA
3	B	99	GLY
3	B	106	LYS
3	B	131	PRO
3	B	134	GLU
3	B	175	ARG
3	B	209	ARG
3	B	226	ARG
4	C	24	ALA
4	C	35	GLU
4	C	43	LEU
4	C	54	ARG
4	C	55	VAL
4	C	67	THR
4	C	127	ARG
4	C	132	ARG

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Mol	Chain	Res	Type
4	C	179	ARG
4	C	189	ALA
5	D	9	CYS
5	D	12	CYS
5	D	29	PRO
5	D	104	VAL
5	D	141	ARG
5	D	153	ARG
5	D	160	GLN
6	E	16	THR
6	E	37	ARG
6	E	38	GLN
6	E	72	GLN
6	E	73	ASN
7	F	77	ARG
7	F	100	ASN
8	G	7	ALA
8	G	108	ALA
9	H	105	ARG
10	I	43	ALA
10	I	44	VAL
10	I	55	ALA
10	I	58	ARG
10	I	118	LYS
10	I	119	ALA
11	J	32	ALA
11	J	34	VAL
11	J	50	ILE
11	J	54	PHE
11	J	57	LYS
12	K	100	ALA
12	K	124	LYS
13	L	27	LEU
13	L	28	LYS
13	L	40	VAL
13	L	41	ARG
13	L	96	VAL
14	M	4	ILE
14	M	7	VAL
14	M	106	ASN
14	M	123	ALA
15	N	3	ARG

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Mol	Chain	Res	Type
15	N	42	ILE
15	N	43	CYS
17	P	51	VAL
17	P	52	ASP
17	P	67	THR
17	P	71	ARG
18	Q	14	LYS
18	Q	95	TYR
19	R	20	ALA
19	R	37	VAL
19	R	74	ARG
19	R	87	ARG
20	S	6	LYS
20	S	9	VAL
21	T	14	LYS
21	T	73	HIS
21	T	92	LEU
3	B	44	LEU
3	B	89	GLY
3	B	177	ALA
3	B	191	ASP
3	B	204	ASN
3	B	208	ILE
3	B	212	GLN
3	B	225	ALA
4	C	13	GLY
4	C	74	GLY
4	C	96	GLY
4	C	98	ASN
4	C	100	ALA
4	C	128	PHE
4	C	181	ASN
4	C	195	VAL
4	C	206	GLU
5	D	26	CYS
5	D	42	GLN
5	D	118	ARG
5	D	150	GLU
5	D	176	LEU
6	E	59	GLY
6	E	108	ALA
6	E	140	ARG

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Mol	Chain	Res	Type
7	F	27	GLN
7	F	45	LEU
8	G	134	ALA
9	H	7	ALA
9	H	54	ASP
10	I	8	GLY
10	I	46	ALA
11	J	73	ASP
12	K	47	VAL
12	K	95	ILE
12	K	117	ASN
13	L	26	ALA
13	L	42	THR
13	L	91	LYS
13	L	103	GLY
13	L	112	ASP
14	M	30	ALA
14	M	31	LYS
14	M	55	ARG
15	N	13	THR
15	N	23	ARG
16	O	47	LYS
16	O	77	ARG
16	O	81	LEU
17	P	13	HIS
18	Q	49	GLU
20	S	27	GLU
20	S	73	GLU
21	T	13	LEU
21	T	88	VAL
21	T	93	GLU
3	B	59	GLU
3	B	123	ALA
3	B	124	SER
3	B	232	PRO
4	C	47	LEU
4	C	200	ALA
5	D	7	PRO
5	D	63	LYS
5	D	102	ASP
5	D	131	ARG
5	D	142	PRO

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Mol	Chain	Res	Type
6	E	21	ALA
6	E	56	GLN
7	F	13	ASN
7	F	53	ALA
8	G	82	GLY
8	G	97	GLN
8	G	109	ASN
9	H	23	SER
9	H	68	ARG
10	I	34	ASN
11	J	39	PRO
11	J	60	ARG
12	K	12	ARG
12	K	25	TYR
12	K	74	ALA
13	L	29	GLY
13	L	31	PRO
13	L	62	SER
13	L	105	TYR
13	L	113	ARG
14	M	6	GLY
14	M	50	GLU
14	M	90	LEU
14	M	99	ARG
14	M	109	THR
15	N	5	ALA
15	N	44	LEU
16	O	79	ARG
17	P	46	PRO
18	Q	91	ARG
18	Q	96	GLN
19	R	38	GLU
19	R	67	ALA
20	S	77	THR
21	T	42	GLN
21	T	64	ASP
21	T	84	LEU
21	T	85	MET
21	T	104	LEU
3	B	20	GLU
3	B	21	ARG
3	B	24	TRP

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Mol	Chain	Res	Type
3	B	139	LYS
3	B	227	GLY
4	C	25	GLY
4	C	29	TYR
4	C	40	ARG
4	C	108	ASN
4	C	198	VAL
5	D	5	ILE
5	D	31	CYS
5	D	51	PRO
5	D	159	ARG
5	D	182	LYS
6	E	11	ILE
8	G	59	LEU
8	G	116	ALA
10	I	51	ARG
10	I	126	SER
11	J	40	LEU
11	J	55	LYS
12	K	28	THR
13	L	82	VAL
14	M	21	TYR
16	O	14	GLU
16	O	49	ASP
17	P	69	THR
18	Q	18	THR
19	R	34	TYR
20	S	30	LEU
21	T	74	LYS
3	B	41	ILE
3	B	56	ARG
3	B	122	PHE
3	B	143	GLU
4	C	36	ASP
5	D	4	TYR
6	E	104	ALA
6	E	136	MET
8	G	41	ARG
8	G	96	GLN
8	G	127	ALA
10	I	56	LEU
10	I	71	SER

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Mol	Chain	Res	Type
11	J	61	GLU
11	J	90	LEU
12	K	126	ARG
14	M	79	LYS
14	M	80	ARG
16	O	13	GLN
17	P	10	GLY
21	T	63	ILE
3	B	8	LYS
4	C	51	GLY
4	C	175	LEU
9	H	80	ILE
12	K	15	ALA
13	L	43	VAL
17	P	12	LYS
18	Q	86	GLU
4	C	39	ILE
8	G	9	VAL
13	L	55	VAL
14	M	25	ILE
16	O	19	PRO
18	Q	47	PRO
20	S	42	PRO
21	T	98	PRO
3	B	174	VAL
3	B	214	ILE
4	C	14	ILE
4	C	66	VAL
5	D	56	VAL
8	G	111	ARG
12	K	57	THR
12	K	120	ARG
4	C	81	GLY
8	G	34	GLY
9	H	100	ILE
21	T	33	ILE
6	E	51	VAL
11	J	76	ASN
14	M	24	GLY
3	B	15	VAL
21	T	101	GLY

5.3.2 Protein sidechains (i)

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	
3	B	204/220 (93%)	125 (61%)	79 (39%)	0	0
4	C	160/188 (85%)	90 (56%)	70 (44%)	0	0
5	D	180/181 (99%)	105 (58%)	75 (42%)	0	0
6	E	115/123 (94%)	70 (61%)	45 (39%)	0	0
7	F	90/90 (100%)	63 (70%)	27 (30%)	0	2
8	G	126/127 (99%)	80 (64%)	46 (36%)	0	0
9	H	119/119 (100%)	78 (66%)	41 (34%)	0	1
10	I	98/99 (99%)	61 (62%)	37 (38%)	0	0
11	J	87/92 (95%)	51 (59%)	36 (41%)	0	0
12	K	90/99 (91%)	62 (69%)	28 (31%)	0	2
13	L	104/109 (95%)	53 (51%)	51 (49%)	0	0
14	M	100/101 (99%)	59 (59%)	41 (41%)	0	0
15	N	49/50 (98%)	26 (53%)	23 (47%)	0	0
16	O	79/80 (99%)	48 (61%)	31 (39%)	0	0
17	P	72/74 (97%)	45 (62%)	27 (38%)	0	0
18	Q	96/97 (99%)	69 (72%)	27 (28%)	0	3
19	R	64/77 (83%)	37 (58%)	27 (42%)	0	0
20	S	73/80 (91%)	47 (64%)	26 (36%)	0	1
21	T	76/82 (93%)	50 (66%)	26 (34%)	0	1
All	All	1982/2088 (95%)	1219 (62%)	763 (38%)	0	0

All (763) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	B	7	VAL
3	B	8	LYS
3	B	9	GLU
3	B	10	LEU

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Mol	Chain	Res	Type
3	B	11	LEU
3	B	12	GLU
3	B	15	VAL
3	B	17	PHE
3	B	21	ARG
3	B	22	LYS
3	B	23	ARG
3	B	24	TRP
3	B	25	ASN
3	B	27	LYS
3	B	35	GLU
3	B	40	HIS
3	B	44	LEU
3	B	45	GLN
3	B	46	LYS
3	B	48	MET
3	B	49	GLU
3	B	53	ARG
3	B	56	ARG
3	B	58	ILE
3	B	61	LEU
3	B	64	ARG
3	B	69	LEU
3	B	71	VAL
3	B	76	GLN
3	B	80	ILE
3	B	82	ARG
3	B	83	MET
3	B	84	GLU
3	B	87	ARG
3	B	92	TYR
3	B	97	TRP
3	B	98	LEU
3	B	102	LEU
3	B	108	ILE
3	B	112	VAL
3	B	113	HIS
3	B	115	LEU
3	B	117	GLU
3	B	121	LEU
3	B	132	LYS
3	B	140	HIS

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Mol	Chain	Res	Type
3	B	144	ARG
3	B	146	GLN
3	B	148	TYR
3	B	149	LEU
3	B	153	ARG
3	B	154	LEU
3	B	155	LEU
3	B	158	LEU
3	B	162	ILE
3	B	165	VAL
3	B	168	THR
3	B	169	LYS
3	B	172	ILE
3	B	175	ARG
3	B	176	GLU
3	B	179	LYS
3	B	185	ILE
3	B	187	LEU
3	B	190	THR
3	B	196	LEU
3	B	206	ASP
3	B	209	ARG
3	B	213	LEU
3	B	215	LEU
3	B	221	LEU
3	B	224	GLN
3	B	229	VAL
3	B	231	GLU
3	B	233	SER
3	B	236	TYR
3	B	238	LEU
3	B	241	GLU
3	B	243	GLU
4	C	3	ASN
4	C	8	ILE
4	C	11	ARG
4	C	15	THR
4	C	23	TYR
4	C	26	LYS
4	C	27	LYS
4	C	29	TYR
4	C	30	ARG

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Mol	Chain	Res	Type
4	C	33	LEU
4	C	34	LEU
4	C	36	ASP
4	C	37	GLN
4	C	43	LEU
4	C	45	LYS
4	C	48	TYR
4	C	52	LEU
4	C	54	ARG
4	C	56	ASP
4	C	57	ILE
4	C	58	GLU
4	C	59	ARG
4	C	63	ASN
4	C	69	HIS
4	C	75	VAL
4	C	77	ILE
4	C	79	ARG
4	C	82	GLU
4	C	83	ARG
4	C	84	ILE
4	C	86	VAL
4	C	88	ARG
4	C	91	LEU
4	C	93	LYS
4	C	94	LEU
4	C	95	THR
4	C	99	VAL
4	C	101	LEU
4	C	104	GLN
4	C	108	ASN
4	C	112	SER
4	C	115	LEU
4	C	124	ILE
4	C	126	ARG
4	C	128	PHE
4	C	130	VAL
4	C	131	ARG
4	C	135	LYS
4	C	143	GLU
4	C	154	SER
4	C	157	ILE

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Mol	Chain	Res	Type
4	C	164	ARG
4	C	166	GLU
4	C	170	GLN
4	C	172	ARG
4	C	175	LEU
4	C	176	HIS
4	C	177	THR
4	C	179	ARG
4	C	188	LEU
4	C	190	ARG
4	C	192	THR
4	C	193	TYR
4	C	195	VAL
4	C	196	LEU
4	C	198	VAL
4	C	201	TYR
4	C	202	ILE
4	C	203	PHE
4	C	204	LEU
5	D	3	ARG
5	D	8	VAL
5	D	9	CYS
5	D	10	ARG
5	D	12	CYS
5	D	13	ARG
5	D	15	GLU
5	D	21	LEU
5	D	24	GLU
5	D	25	ARG
5	D	26	CYS
5	D	27	TYR
5	D	28	SER
5	D	35	ARG
5	D	36	ARG
5	D	38	TYR
5	D	50	ARG
5	D	53	ASP
5	D	57	ARG
5	D	59	ARG
5	D	61	LYS
5	D	64	LEU
5	D	66	ARG

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Mol	Chain	Res	Type
5	D	70	ILE
5	D	72	GLU
5	D	74	GLN
5	D	76	ARG
5	D	79	PHE
5	D	83	SER
5	D	84	LYS
5	D	89	THR
5	D	100	ARG
5	D	104	VAL
5	D	112	VAL
5	D	114	ARG
5	D	115	ARG
5	D	116	GLN
5	D	118	ARG
5	D	120	LEU
5	D	122	ARG
5	D	123	HIS
5	D	126	ILE
5	D	127	THR
5	D	131	ARG
5	D	132	ARG
5	D	135	LEU
5	D	137	SER
5	D	138	TYR
5	D	139	ARG
5	D	141	ARG
5	D	144	ASP
5	D	148	VAL
5	D	150	GLU
5	D	151	LYS
5	D	152	SER
5	D	155	LEU
5	D	157	LEU
5	D	162	LEU
5	D	166	LYS
5	D	169	LYS
5	D	175	SER
5	D	178	VAL
5	D	179	GLU
5	D	185	PHE
5	D	187	ARG

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Mol	Chain	Res	Type
5	D	188	LEU
5	D	192	GLU
5	D	194	LEU
5	D	196	LEU
5	D	198	VAL
5	D	199	GLN
5	D	200	GLU
5	D	201	ASN
5	D	202	LEU
5	D	204	ILE
6	E	5	ASP
6	E	9	LYS
6	E	10	MET
6	E	11	ILE
6	E	12	LEU
6	E	13	ILE
6	E	15	ARG
6	E	16	THR
6	E	18	ARG
6	E	19	MET
6	E	24	ARG
6	E	25	ARG
6	E	27	ARG
6	E	31	LEU
6	E	33	VAL
6	E	34	VAL
6	E	38	GLN
6	E	40	ARG
6	E	43	LEU
6	E	52	PRO
6	E	53	LEU
6	E	55	VAL
6	E	57	LYS
6	E	60	TYR
6	E	64	ARG
6	E	72	GLN
6	E	76	ILE
6	E	79	GLU
6	E	80	ILE
6	E	90	VAL
6	E	92	LYS
6	E	105	VAL

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Mol	Chain	Res	Type
6	E	120	THR
6	E	121	LYS
6	E	122	GLU
6	E	123	LEU
6	E	125	SER
6	E	126	ARG
6	E	133	TYR
6	E	143	ARG
6	E	144	THR
6	E	145	LYS
6	E	149	GLU
6	E	150	ARG
6	E	153	LYS
7	F	8	ILE
7	F	9	VAL
7	F	10	LEU
7	F	15	ASP
7	F	19	LEU
7	F	23	LYS
7	F	32	ASN
7	F	39	LYS
7	F	41	GLU
7	F	43	LEU
7	F	46	ARG
7	F	48	LEU
7	F	55	ASP
7	F	65	VAL
7	F	70	ASP
7	F	73	ASN
7	F	74	ASP
7	F	75	LEU
7	F	77	ARG
7	F	80	ARG
7	F	82	ARG
7	F	87	ARG
7	F	88	VAL
7	F	89	MET
7	F	90	VAL
7	F	93	SER
7	F	98	LEU
8	G	4	ARG
8	G	8	GLU

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Mol	Chain	Res	Type
8	G	9	VAL
8	G	10	ARG
8	G	11	GLN
8	G	12	LEU
8	G	15	ASP
8	G	24	THR
8	G	28	ASN
8	G	31	MET
8	G	36	LYS
8	G	37	ASN
8	G	38	LEU
8	G	48	LYS
8	G	50	ILE
8	G	51	GLN
8	G	52	GLU
8	G	53	LYS
8	G	54	THR
8	G	56	GLN
8	G	57	GLU
8	G	67	GLU
8	G	69	VAL
8	G	75	VAL
8	G	77	SER
8	G	79	ARG
8	G	90	GLU
8	G	94	ARG
8	G	95	ARG
8	G	96	GLN
8	G	97	GLN
8	G	98	SER
8	G	113	GLU
8	G	114	ARG
8	G	120	ILE
8	G	124	LEU
8	G	126	ASP
8	G	131	LYS
8	G	135	VAL
8	G	136	LYS
8	G	138	LYS
8	G	143	ARG
8	G	144	MET
8	G	148	ASN

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Mol	Chain	Res	Type
8	G	154	TYR
8	G	156	TRP
9	H	3	THR
9	H	12	ARG
9	H	14	ARG
9	H	18	ARG
9	H	19	VAL
9	H	21	LYS
9	H	22	GLU
9	H	24	THR
9	H	32	LYS
9	H	35	ILE
9	H	41	ARG
9	H	45	ILE
9	H	46	LYS
9	H	49	GLU
9	H	50	ARG
9	H	51	VAL
9	H	53	VAL
9	H	56	LYS
9	H	63	LEU
9	H	64	LYS
9	H	68	ARG
9	H	75	ARG
9	H	77	GLU
9	H	84	ARG
9	H	85	ARG
9	H	87	SER
9	H	91	ARG
9	H	92	ARG
9	H	102	ARG
9	H	104	ARG
9	H	105	ARG
9	H	107	LEU
9	H	109	ILE
9	H	111	ILE
9	H	112	LEU
9	H	113	SER
9	H	118	VAL
9	H	120	THR
9	H	127	LEU
9	H	129	VAL

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Mol	Chain	Res	Type
9	H	133	LEU
10	I	9	ARG
10	I	14	VAL
10	I	16	ARG
10	I	27	THR
10	I	29	ASN
10	I	31	GLN
10	I	34	ASN
10	I	35	GLU
10	I	38	GLN
10	I	40	LEU
10	I	51	ARG
10	I	53	VAL
10	I	54	ASP
10	I	59	PHE
10	I	64	THR
10	I	75	ASP
10	I	78	LYS
10	I	79	LEU
10	I	83	ARG
10	I	85	LEU
10	I	86	VAL
10	I	97	LYS
10	I	104	ARG
10	I	105	ASP
10	I	107	ARG
10	I	108	VAL
10	I	110	GLU
10	I	111	ARG
10	I	113	LYS
10	I	114	TYR
10	I	117	HIS
10	I	118	LYS
10	I	121	ARG
10	I	125	TYR
10	I	126	SER
10	I	127	LYS
10	I	128	ARG
11	J	3	LYS
11	J	6	ILE
11	J	7	LYS
11	J	13	HIS

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Mol	Chain	Res	Type
11	J	14	LYS
11	J	16	LEU
11	J	19	SER
11	J	28	ARG
11	J	34	VAL
11	J	35	SER
11	J	38	ILE
11	J	40	LEU
11	J	45	ARG
11	J	46	ARG
11	J	48	THR
11	J	50	ILE
11	J	51	ARG
11	J	54	PHE
11	J	57	LYS
11	J	59	SER
11	J	60	ARG
11	J	64	GLU
11	J	65	LEU
11	J	66	ARG
11	J	70	ARG
11	J	71	LEU
11	J	73	ASP
11	J	74	ILE
11	J	75	ILE
11	J	80	LYS
11	J	83	GLU
11	J	84	GLN
11	J	92	THR
11	J	96	ILE
11	J	98	ILE
11	J	99	LYS
12	K	11	LYS
12	K	12	ARG
12	K	21	ILE
12	K	24	SER
12	K	27	ASN
12	K	28	THR
12	K	29	ILE
12	K	30	VAL
12	K	48	ILE
12	K	51	LYS

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Mol	Chain	Res	Type
12	K	53	SER
12	K	54	ARG
12	K	57	THR
12	K	62	GLN
12	K	66	LEU
12	K	73	MET
12	K	78	GLN
12	K	81	ASP
12	K	87	THR
12	K	92	GLU
12	K	93	GLN
12	K	103	LEU
12	K	106	LYS
12	K	109	VAL
12	K	119	CYS
12	K	123	LYS
12	K	124	LYS
12	K	129	SER
13	L	13	LYS
13	L	15	ARG
13	L	17	LYS
13	L	18	VAL
13	L	19	ARG
13	L	20	LYS
13	L	21	LYS
13	L	22	SER
13	L	23	LYS
13	L	27	LEU
13	L	28	LYS
13	L	32	PHE
13	L	33	ARG
13	L	34	ARG
13	L	36	VAL
13	L	37	CYS
13	L	38	THR
13	L	41	ARG
13	L	42	THR
13	L	43	VAL
13	L	46	LYS
13	L	47	LYS
13	L	49	ASN
13	L	53	ARG

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Mol	Chain	Res	Type
13	L	54	LYS
13	L	57	LYS
13	L	60	LEU
13	L	61	THR
13	L	69	TYR
13	L	70	ILE
13	L	73	GLU
13	L	75	HIS
13	L	76	ASN
13	L	81	SER
13	L	82	VAL
13	L	83	VAL
13	L	85	ILE
13	L	86	ARG
13	L	90	VAL
13	L	91	LYS
13	L	93	LEU
13	L	96	VAL
13	L	98	TYR
13	L	99	HIS
13	L	102	ARG
13	L	104	VAL
13	L	113	ARG
13	L	114	LYS
13	L	122	THR
13	L	123	LYS
13	L	124	LYS
14	M	3	ARG
14	M	4	ILE
14	M	7	VAL
14	M	9	ILE
14	M	12	ASN
14	M	14	ARG
14	M	16	ASP
14	M	17	VAL
14	M	25	ILE
14	M	31	LYS
14	M	32	GLU
14	M	36	LYS
14	M	37	THR
14	M	39	ILE
14	M	43	THR

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Mol	Chain	Res	Type
14	M	44	ARG
14	M	46	LYS
14	M	54	VAL
14	M	55	ARG
14	M	56	LEU
14	M	57	ARG
14	M	62	ASN
14	M	67	GLU
14	M	70	LEU
14	M	78	ILE
14	M	81	LEU
14	M	83	ASP
14	M	91	ARG
14	M	94	ARG
14	M	99	ARG
14	M	102	ARG
14	M	105	THR
14	M	106	ASN
14	M	108	ARG
14	M	110	ARG
14	M	111	LYS
14	M	115	LYS
14	M	120	LYS
14	M	121	LYS
14	M	122	LYS
14	M	125	ARG
15	N	3	ARG
15	N	4	LYS
15	N	6	LEU
15	N	7	ILE
15	N	12	ARG
15	N	13	THR
15	N	16	PHE
15	N	17	LYS
15	N	21	TYR
15	N	23	ARG
15	N	26	ARG
15	N	31	ARG
15	N	32	SER
15	N	35	ARG
15	N	36	PHE
15	N	39	LEU

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Mol	Chain	Res	Type
15	N	42	ILE
15	N	44	LEU
15	N	50	LYS
15	N	53	LEU
15	N	58	LYS
15	N	60	SER
15	N	61	TRP
16	O	3	ILE
16	O	5	LYS
16	O	12	ILE
16	O	13	GLN
16	O	14	GLU
16	O	17	ARG
16	O	22	THR
16	O	24	SER
16	O	27	VAL
16	O	32	LEU
16	O	35	ARG
16	O	41	GLU
16	O	42	HIS
16	O	43	LEU
16	O	45	VAL
16	O	46	HIS
16	O	47	LYS
16	O	48	LYS
16	O	50	HIS
16	O	56	LEU
16	O	60	VAL
16	O	64	ARG
16	O	65	ARG
16	O	68	ARG
16	O	70	LEU
16	O	71	GLN
16	O	72	ARG
16	O	73	GLU
16	O	81	LEU
16	O	83	GLU
16	O	88	ARG
17	P	1	MET
17	P	2	VAL
17	P	5	ARG
17	P	8	ARG

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Mol	Chain	Res	Type
17	P	11	SER
17	P	12	LYS
17	P	20	VAL
17	P	27	LYS
17	P	28	ARG
17	P	33	ILE
17	P	35	LYS
17	P	42	ARG
17	P	43	LYS
17	P	44	THR
17	P	45	THR
17	P	47	ASP
17	P	49	LEU
17	P	51	VAL
17	P	53	VAL
17	P	55	ARG
17	P	57	ARG
17	P	62	VAL
17	P	65	GLN
17	P	67	THR
17	P	74	LEU
17	P	81	ARG
17	P	82	GLN
18	Q	5	VAL
18	Q	6	LEU
18	Q	7	THR
18	Q	14	LYS
18	Q	23	VAL
18	Q	34	LYS
18	Q	35	VAL
18	Q	36	ILE
18	Q	38	ARG
18	Q	50	LYS
18	Q	52	LYS
18	Q	53	LEU
18	Q	57	VAL
18	Q	58	GLU
18	Q	59	ILE
18	Q	76	LEU
18	Q	77	VAL
18	Q	78	GLU
18	Q	81	ARG

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Mol	Chain	Res	Type
18	Q	84	LEU
18	Q	85	VAL
18	Q	86	GLU
18	Q	87	LYS
18	Q	92	ARG
18	Q	95	TYR
18	Q	96	GLN
18	Q	100	LYS
19	R	18	ARG
19	R	19	LYS
19	R	21	LYS
19	R	25	THR
19	R	26	LEU
19	R	31	LEU
19	R	36	ASN
19	R	38	GLU
19	R	40	LEU
19	R	41	LYS
19	R	44	LEU
19	R	47	THR
19	R	50	ILE
19	R	53	ARG
19	R	54	ARG
19	R	55	ARG
19	R	58	LEU
19	R	59	SER
19	R	69	THR
19	R	75	ILE
19	R	76	LEU
19	R	78	LEU
19	R	82	THR
19	R	84	LYS
19	R	86	VAL
19	R	87	ARG
19	R	88	LYS
20	S	5	LEU
20	S	13	ASP
20	S	14	HIS
20	S	15	LEU
20	S	20	LEU
20	S	25	LYS
20	S	27	GLU

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Mol	Chain	Res	Type
20	S	28	LYS
20	S	29	ARG
20	S	30	LEU
20	S	33	THR
20	S	37	ARG
20	S	38	SER
20	S	41	VAL
20	S	43	GLU
20	S	44	MET
20	S	52	TYR
20	S	58	VAL
20	S	61	TYR
20	S	63	THR
20	S	64	GLU
20	S	65	ASN
20	S	71	LEU
20	S	78	ARG
20	S	79	THR
20	S	83	HIS
21	T	10	LEU
21	T	11	SER
21	T	13	LEU
21	T	19	SER
21	T	24	LEU
21	T	29	LYS
21	T	30	LYS
21	T	36	LEU
21	T	37	SER
21	T	43	LEU
21	T	57	ARG
21	T	58	LYS
21	T	61	SER
21	T	62	LEU
21	T	64	ASP
21	T	68	LYS
21	T	74	LYS
21	T	80	ARG
21	T	81	LYS
21	T	85	MET
21	T	86	ARG
21	T	87	LYS
21	T	99	LEU

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Mol	Chain	Res	Type
21	T	100	ILE
21	T	104	LEU
21	T	105	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (38) such sidechains are listed below:

Mol	Chain	Res	Type
3	B	25	ASN
3	B	94	ASN
3	B	135	GLN
3	B	212	GLN
4	C	3	ASN
4	C	6	HIS
4	C	123	GLN
4	C	176	HIS
5	D	62	GLN
5	D	123	HIS
5	D	129	ASN
5	D	199	GLN
7	F	73	ASN
8	G	37	ASN
8	G	56	GLN
8	G	96	GLN
8	G	106	GLN
8	G	148	ASN
9	H	78	GLN
10	I	34	ASN
10	I	73	GLN
11	J	68	HIS
11	J	76	ASN
11	J	78	ASN
12	K	27	ASN
13	L	49	ASN
13	L	75	HIS
13	L	76	ASN
13	L	99	HIS
14	M	40	ASN
14	M	62	ASN
16	O	37	ASN
18	Q	16	GLN
18	Q	96	GLN
20	S	53	ASN

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Mol	Chain	Res	Type
20	S	65	ASN
21	T	18	GLN
21	T	73	HIS

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1494/1511 (98%)	656 (43%)	162 (10%)
2	Z	3/4 (75%)	0	0
All	All	1497/1515 (98%)	656 (43%)	162 (10%)

All (656) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	6	G
1	A	8	A
1	A	9	G
1	A	13	U
1	A	16	A
1	A	17	U
1	A	18	C
1	A	20	U
1	A	25	C
1	A	31	G
1	A	32	A
1	A	36	C
1	A	37	U
1	A	38	G
1	A	39	G
1	A	40	C
1	A	44	G
1	A	47	C
1	A	48	C
1	A	49	U
1	A	50	A
1	A	51	A
1	A	52	G
1	A	54	C
1	A	55	A
1	A	56	U
1	A	59	A

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Mol	Chain	Res	Type
1	A	60	A
1	A	61	G
1	A	63	C
1	A	64	G
1	A	65	U
1	A	66	G
1	A	67	C
1	A	70	G
1	A	75	G
1	A	78	G
1	A	81	U
1	A	82	U
1	A	84	U
1	A	92	C
1	A	96	G
1	A	97	G
1	A	109	A
1	A	110	C
1	A	111	G
1	A	116	A
1	A	120	A
1	A	121	C
1	A	126	G
1	A	129(A)	G
1	A	130	A
1	A	131	C
1	A	145	G
1	A	149	A
1	A	150	C
1	A	152	A
1	A	153	C
1	A	154	C
1	A	156	G
1	A	160	A
1	A	162	A
1	A	163	C
1	A	167	G
1	A	169	C
1	A	170	U
1	A	179	A
1	A	182	U
1	A	183	G

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Mol	Chain	Res	Type
1	A	185	A
1	A	187	C
1	A	190(E)	U
1	A	190(G)	G
1	A	190(L)	U
1	A	195	A
1	A	197	A
1	A	198	G
1	A	200	G
1	A	201	C
1	A	202	U
1	A	203	U
1	A	204	U
1	A	217	C
1	A	220	G
1	A	221	C
1	A	222	U
1	A	226	G
1	A	231	G
1	A	236	G
1	A	237	C
1	A	240	C
1	A	244	U
1	A	245	C
1	A	246	A
1	A	247	G
1	A	250	A
1	A	251	G
1	A	252	U
1	A	258	G
1	A	263	A
1	A	264	U
1	A	265	G
1	A	266	G
1	A	267	C
1	A	268	C
1	A	269	C
1	A	271	C
1	A	275	G
1	A	279	A
1	A	280	C
1	A	281	G

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Mol	Chain	Res	Type
1	A	282	A
1	A	283	C
1	A	285	G
1	A	288	A
1	A	289	G
1	A	290	C
1	A	293	G
1	A	294	U
1	A	298	A
1	A	311	C
1	A	315	A
1	A	316	G
1	A	317	G
1	A	318	G
1	A	321	A
1	A	325	A
1	A	326	G
1	A	327	A
1	A	328	C
1	A	329	A
1	A	330	C
1	A	332	G
1	A	333	G
1	A	336	C
1	A	344	A
1	A	345	C
1	A	346	G
1	A	347	G
1	A	350	G
1	A	351	G
1	A	352	C
1	A	353	A
1	A	354	G
1	A	355	C
1	A	365	U
1	A	367	U
1	A	368	U
1	A	372	C
1	A	373	A
1	A	374	A
1	A	384	G
1	A	390	C

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Mol	Chain	Res	Type
1	A	391	G
1	A	393	A
1	A	397	A
1	A	398	C
1	A	400	C
1	A	406	G
1	A	409	G
1	A	410	G
1	A	411	A
1	A	412	A
1	A	413	G
1	A	414	A
1	A	415	A
1	A	417	C
1	A	421	U
1	A	422	C
1	A	423	G
1	A	424	G
1	A	426	G
1	A	429	U
1	A	430	A
1	A	433	C
1	A	435	C
1	A	437	U
1	A	439	A
1	A	443	C
1	A	445	G
1	A	452	A
1	A	453	A
1	A	454	C
1	A	459	G
1	A	460	A
1	A	461	C
1	A	462	G
1	A	476	G
1	A	480	U
1	A	481	G
1	A	482	A
1	A	484	G
1	A	485	G
1	A	487	A
1	A	490	G

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Mol	Chain	Res	Type
1	A	496	A
1	A	497	A
1	A	498	U
1	A	500	G
1	A	502	G
1	A	504	C
1	A	505	G
1	A	506	G
1	A	508	C
1	A	509	A
1	A	510	A
1	A	511	C
1	A	513	C
1	A	517	G
1	A	518	C
1	A	519	C
1	A	520	A
1	A	521	G
1	A	527	G
1	A	529	G
1	A	531	U
1	A	532	A
1	A	533	A
1	A	534	U
1	A	535	A
1	A	536	C
1	A	537	G
1	A	545	C
1	A	547	A
1	A	550	G
1	A	555	C
1	A	556	C
1	A	559	A
1	A	560	U
1	A	561	U
1	A	562	C
1	A	564	C
1	A	567	G
1	A	570	G
1	A	572	A
1	A	573	A
1	A	575	G

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Mol	Chain	Res	Type
1	A	576	G
1	A	577	G
1	A	582	U
1	A	583	A
1	A	593	G
1	A	594	G
1	A	596	C
1	A	607	A
1	A	617	G
1	A	620	C
1	A	623	C
1	A	624	C
1	A	633	G
1	A	636	U
1	A	640	A
1	A	653	A
1	A	654	G
1	A	655	A
1	A	657	G
1	A	661	G
1	A	665	A
1	A	670	G
1	A	671	G
1	A	673	G
1	A	675	A
1	A	681	C
1	A	683	G
1	A	685	G
1	A	686	U
1	A	688	G
1	A	693	G
1	A	695	A
1	A	696	A
1	A	700	G
1	A	701	C
1	A	702	A
1	A	703	G
1	A	704	A
1	A	705	U
1	A	707	C
1	A	715	A
1	A	718	G

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Mol	Chain	Res	Type
1	A	721	G
1	A	722	A
1	A	723	U
1	A	724	G
1	A	725	G
1	A	726	C
1	A	731	G
1	A	734	G
1	A	735	C
1	A	736	C
1	A	748	C
1	A	749	C
1	A	752	G
1	A	754	C
1	A	755	G
1	A	759	A
1	A	762	C
1	A	764	C
1	A	767	A
1	A	773	G
1	A	774	G
1	A	777	A
1	A	779	C
1	A	781	A
1	A	784	C
1	A	785	G
1	A	787	A
1	A	789	U
1	A	792	A
1	A	793	U
1	A	794	A
1	A	795	C
1	A	799	G
1	A	801	U
1	A	803	G
1	A	804	U
1	A	805	C
1	A	809	G
1	A	810	C
1	A	813	U
1	A	815	A
1	A	817	C

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Mol	Chain	Res	Type
1	A	818	G
1	A	819	A
1	A	821	G
1	A	825	G
1	A	828	A
1	A	833	U
1	A	837	G
1	A	839	U
1	A	840	C
1	A	841	U
1	A	854	G
1	A	856	C
1	A	857	C
1	A	858	G
1	A	859	A
1	A	866	C
1	A	869	G
1	A	870	U
1	A	872	A
1	A	873	A
1	A	874	G
1	A	876	G
1	A	877	C
1	A	881	G
1	A	883	C
1	A	884	U
1	A	886	G
1	A	888	G
1	A	889	A
1	A	891	U
1	A	900	A
1	A	902	G
1	A	908	A
1	A	910	C
1	A	913	A
1	A	914	A
1	A	917	G
1	A	919	A
1	A	921	U
1	A	926	G
1	A	927	G
1	A	932	C

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Mol	Chain	Res	Type
1	A	933	G
1	A	934	C
1	A	935	A
1	A	937	A
1	A	938	A
1	A	939	G
1	A	942	G
1	A	943	U
1	A	945	G
1	A	948	C
1	A	954	G
1	A	960	U
1	A	961	U
1	A	964	A
1	A	965	A
1	A	966	G
1	A	967	C
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	979	C
1	A	981	U
1	A	983	A
1	A	984	C
1	A	987	G
1	A	989	C
1	A	991	U
1	A	992	U
1	A	993	G
1	A	994	A
1	A	1000	U
1	A	1002	G
1	A	1004	A
1	A	1005	A
1	A	1006	C
1	A	1008	C
1	A	1009	G

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Mol	Chain	Res	Type
1	A	1010	G
1	A	1011	G
1	A	1017	G
1	A	1021	G
1	A	1022	G
1	A	1023	G
1	A	1024	G
1	A	1025	U
1	A	1026	G
1	A	1027	C
1	A	1028	C
1	A	1029	C
1	A	1030(B)	C
1	A	1030(C)	G
1	A	1031	G
1	A	1032	G
1	A	1033	G
1	A	1034	G
1	A	1035	A
1	A	1037	C
1	A	1038	C
1	A	1042	G
1	A	1043	C
1	A	1044	A
1	A	1045	C
1	A	1046	A
1	A	1048	G
1	A	1049	U
1	A	1050	G
1	A	1053	G
1	A	1054	C
1	A	1057	G
1	A	1062	U
1	A	1064	G
1	A	1065	U
1	A	1066	C
1	A	1067	A
1	A	1068	G
1	A	1070	U
1	A	1076	C
1	A	1077	G
1	A	1078	U

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Mol	Chain	Res	Type
1	A	1082	G
1	A	1085	U
1	A	1086	U
1	A	1092	A
1	A	1093	A
1	A	1094	G
1	A	1095	U
1	A	1096	C
1	A	1097	C
1	A	1099	G
1	A	1101	A
1	A	1102	A
1	A	1106	G
1	A	1108	G
1	A	1109	C
1	A	1110	A
1	A	1113	C
1	A	1117	G
1	A	1118	C
1	A	1122	U
1	A	1124	G
1	A	1125	U
1	A	1126	U
1	A	1127	G
1	A	1128	C
1	A	1129	C
1	A	1130	A
1	A	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	1141	C
1	A	1142	G
1	A	1144	G
1	A	1145	C
1	A	1146	A
1	A	1148	U
1	A	1151	A
1	A	1152	A

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Mol	Chain	Res	Type
1	A	1153	C
1	A	1158	C
1	A	1159	U
1	A	1160	G
1	A	1161	C
1	A	1162	C
1	A	1171	G
1	A	1176	A
1	A	1182	G
1	A	1183	A
1	A	1184	G
1	A	1186	G
1	A	1187	G
1	A	1188	A
1	A	1190	G
1	A	1191	A
1	A	1192	C
1	A	1196	U
1	A	1197	G
1	A	1198	G
1	A	1200	C
1	A	1201	A
1	A	1202	G
1	A	1206	G
1	A	1209	C
1	A	1210	C
1	A	1211	U
1	A	1212	U
1	A	1213	A
1	A	1214	C
1	A	1215	G
1	A	1218	C
1	A	1219	U
1	A	1224	G
1	A	1225	A
1	A	1226	C
1	A	1227	A
1	A	1228	C
1	A	1229	A
1	A	1233	G
1	A	1234	C
1	A	1235	U

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Mol	Chain	Res	Type
1	A	1236	A
1	A	1238	A
1	A	1240	U
1	A	1241	G
1	A	1245	A
1	A	1250	A
1	A	1251	A
1	A	1253	G
1	A	1256	A
1	A	1257	U
1	A	1258	G
1	A	1260	C
1	A	1263	C
1	A	1265	G
1	A	1268	A
1	A	1269	A
1	A	1270	C
1	A	1273	G
1	A	1278	U
1	A	1279	A
1	A	1280	A
1	A	1281	U
1	A	1282	C
1	A	1286	A
1	A	1287	A
1	A	1290	G
1	A	1291	G
1	A	1297	C
1	A	1300	G
1	A	1302	U
1	A	1305	G
1	A	1311	G
1	A	1312	G
1	A	1316	G
1	A	1317	C
1	A	1320	C
1	A	1322	C
1	A	1323	G
1	A	1327	C
1	A	1328	C
1	A	1332	A
1	A	1337	G

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Mol	Chain	Res	Type
1	A	1338	G
1	A	1340	A
1	A	1344	C
1	A	1345	U
1	A	1346	A
1	A	1347	G
1	A	1348	U
1	A	1349	A
1	A	1353	G
1	A	1354	C
1	A	1355	G
1	A	1360	A
1	A	1361(A)	C
1	A	1362	C
1	A	1363	A
1	A	1364	U
1	A	1365	G
1	A	1366	C
1	A	1368	G
1	A	1370	G
1	A	1371	G
1	A	1372	U
1	A	1379	G
1	A	1380	U
1	A	1381	U
1	A	1384	C
1	A	1386	G
1	A	1396	A
1	A	1397	C
1	A	1398	A
1	A	1400	C
1	A	1401	G
1	A	1402	C
1	A	1403	C
1	A	1404	C
1	A	1407	C
1	A	1408	A
1	A	1409	C
1	A	1410	G
1	A	1418	A
1	A	1419	G
1	A	1423	G

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Mol	Chain	Res	Type
1	A	1427	U
1	A	1437	C
1	A	1440	C
1	A	1442	G
1	A	1447	G
1	A	1450	U
1	A	1451	A
1	A	1452	C
1	A	1453	G
1	A	1454	G
1	A	1460	A
1	A	1468	A
1	A	1472	U
1	A	1478	C
1	A	1483	A
1	A	1487	G
1	A	1490	C
1	A	1491	G
1	A	1492	A
1	A	1494	G
1	A	1497	G
1	A	1498	U
1	A	1499	A
1	A	1503	A
1	A	1504	G
1	A	1505	G
1	A	1506	U
1	A	1507	A
1	A	1509	C
1	A	1514	C
1	A	1517	G
1	A	1519	A
1	A	1520	G
1	A	1522	U
1	A	1525	G
1	A	1526	G
1	A	1527	C
1	A	1528	U
1	A	1529	G
1	A	1530	G
1	A	1533	C

All (162) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	7	G
1	A	30	U
1	A	48	C
1	A	51	A
1	A	60	A
1	A	64	G
1	A	115	G
1	A	119	A
1	A	129(A)	G
1	A	151	A
1	A	181	G
1	A	197	A
1	A	202	U
1	A	203	U
1	A	243	A
1	A	244	U
1	A	246	A
1	A	250	A
1	A	251	G
1	A	266	G
1	A	275	G
1	A	279	A
1	A	281	G
1	A	288	A
1	A	293	G
1	A	315	A
1	A	328	C
1	A	329	A
1	A	345	C
1	A	350	G
1	A	351	G
1	A	353	A
1	A	367	U
1	A	372	C
1	A	373	A
1	A	405	U
1	A	409	G
1	A	410	G
1	A	412	A
1	A	421	U
1	A	428	G
1	A	429	U
1	A	438	G

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Mol	Chain	Res	Type
1	A	453	A
1	A	460	A
1	A	461	C
1	A	481	G
1	A	484	G
1	A	485	G
1	A	496	A
1	A	497	A
1	A	499	A
1	A	504	C
1	A	509	A
1	A	518	C
1	A	531	U
1	A	533	A
1	A	535	A
1	A	536	C
1	A	559	A
1	A	560	U
1	A	575	G
1	A	576	G
1	A	619	U
1	A	650	G
1	A	652	U
1	A	653	A
1	A	656	C
1	A	687	A
1	A	701	C
1	A	702	A
1	A	703	G
1	A	721	G
1	A	722	A
1	A	734	G
1	A	793	U
1	A	812	C
1	A	817	C
1	A	818	G
1	A	872	A
1	A	873	A
1	A	913	A
1	A	934	C
1	A	960	U
1	A	965	A

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Mol	Chain	Res	Type
1	A	971	G
1	A	974	A
1	A	975	A
1	A	976	G
1	A	980	C
1	A	992	U
1	A	993	G
1	A	1024	G
1	A	1027	C
1	A	1049	U
1	A	1053	G
1	A	1064	G
1	A	1065	U
1	A	1066	C
1	A	1067	A
1	A	1085	U
1	A	1092	A
1	A	1101	A
1	A	1108	G
1	A	1117	G
1	A	1124	G
1	A	1126	U
1	A	1129	C
1	A	1139	G
1	A	1145	C
1	A	1151	A
1	A	1159	U
1	A	1182	G
1	A	1187	G
1	A	1190	G
1	A	1192	C
1	A	1196	U
1	A	1200	C
1	A	1201	A
1	A	1212	U
1	A	1213	A
1	A	1214	C
1	A	1224	G
1	A	1225	A
1	A	1233	G
1	A	1235	U
1	A	1240	U

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Mol	Chain	Res	Type
1	A	1256	A
1	A	1257	U
1	A	1262	C
1	A	1263	C
1	A	1278	U
1	A	1279	A
1	A	1280	A
1	A	1281	U
1	A	1285	A
1	A	1297	C
1	A	1301	U
1	A	1317	C
1	A	1319	A
1	A	1320	C
1	A	1322	C
1	A	1331	G
1	A	1337	G
1	A	1345	U
1	A	1346	A
1	A	1347	G
1	A	1348	U
1	A	1364	U
1	A	1380	U
1	A	1396	A
1	A	1417	G
1	A	1451	A
1	A	1491	G
1	A	1498	U
1	A	1504	G
1	A	1505	G
1	A	1506	U
1	A	1507	A
1	A	1509	C
1	A	1525	G
1	A	1529	G

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 117 ligands modelled in this entry, 115 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
25	AB9	A	1637	-	35,36,36	2.20	3 (8%)	43,49,49	1.65	3 (6%)
24	D2C	A	1636	22	31,34,34	4.34	11 (35%)	37,54,54	2.47	16 (43%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
25	AB9	A	1637	-	-	11/24/64/64	0/2/2/2
24	D2C	A	1636	22	-	6/6/64/64	0/4/4/4

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	A	1636	D2C	C16-C15	-15.94	1.40	1.53
24	A	1636	D2C	C16-C17	-12.35	1.37	1.53
25	A	1637	AB9	O36-C23	10.63	1.43	1.23
24	A	1636	D2C	C18-C5	-7.06	1.44	1.54
24	A	1636	D2C	C14-C15	-6.64	1.43	1.52
25	A	1637	AB9	C23-N12	6.25	1.47	1.34
24	A	1636	D2C	C20-C21	4.37	1.62	1.53
25	A	1637	AB9	C24-C23	2.77	1.55	1.52
24	A	1636	D2C	O2-C8	2.76	1.48	1.42
24	A	1636	D2C	C6-C5	-2.57	1.49	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	A	1636	D2C	O5-C17	-2.48	1.36	1.43
24	A	1636	D2C	C9-C8	2.21	1.54	1.52
24	A	1636	D2C	C21-N2	2.03	1.37	1.32
24	A	1636	D2C	O4-C15	-2.02	1.38	1.42

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
25	A	1637	AB9	O36-C23-N12	-7.27	109.94	122.96
25	A	1637	AB9	O36-C23-C24	-6.29	111.32	120.61
24	A	1636	D2C	O5-C17-C18	5.18	121.55	109.80
24	A	1636	D2C	O4-C15-C14	5.09	122.53	110.56
24	A	1636	D2C	C18-C17-C16	4.88	118.55	110.45
24	A	1636	D2C	C7-C16-C17	4.55	121.75	111.30
24	A	1636	D2C	C7-C16-C15	4.07	118.89	110.87
24	A	1636	D2C	O4-C15-C16	3.83	118.30	110.83
24	A	1636	D2C	O6-C19-C18	-3.77	115.72	122.57
24	A	1636	D2C	C3-C4-C20	3.74	121.89	113.71
24	A	1636	D2C	O5-C17-C16	3.43	119.43	111.25
24	A	1636	D2C	C7-C6-C5	-2.79	105.77	110.23
24	A	1636	D2C	O1-C4-C20	-2.73	118.14	121.97
25	A	1637	AB9	O51-C51-C61	2.67	111.20	106.07
24	A	1636	D2C	C2-N1-C3	-2.66	108.04	114.10
24	A	1636	D2C	C11-C10-C9	-2.42	119.17	122.38
24	A	1636	D2C	C6-C5-C3	2.29	117.12	113.54
24	A	1636	D2C	C1-N1-C3	-2.09	109.35	114.10
24	A	1636	D2C	C5-C18-C19	2.02	116.77	109.64

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
24	A	1636	D2C	C4-C3-N1-C1
24	A	1636	D2C	C5-C3-N1-C1
24	A	1636	D2C	C4-C3-N1-C2
24	A	1636	D2C	C4-C20-C21-O7
24	A	1636	D2C	C19-C20-C21-O7
25	A	1637	AB9	N12-C23-C24-C25
25	A	1637	AB9	N12-C23-C24-O28
25	A	1637	AB9	O28-C24-C25-C26
25	A	1637	AB9	N34-C33-C35-N31
25	A	1637	AB9	C41-C51-C61-N61

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Mol	Chain	Res	Type	Atoms
25	A	1637	AB9	O51-C51-C61-N61
25	A	1637	AB9	O36-C23-N12-C12
25	A	1637	AB9	C29-C30-N31-C35
25	A	1637	AB9	C23-C24-C25-C26
24	A	1636	D2C	C5-C3-N1-C2
25	A	1637	AB9	C33-C35-N31-C30
25	A	1637	AB9	O62-C29-C30-N31

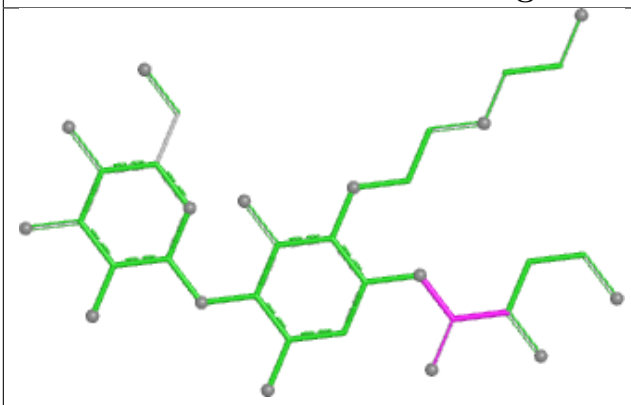
There are no ring outliers.

2 monomers are involved in 5 short contacts:

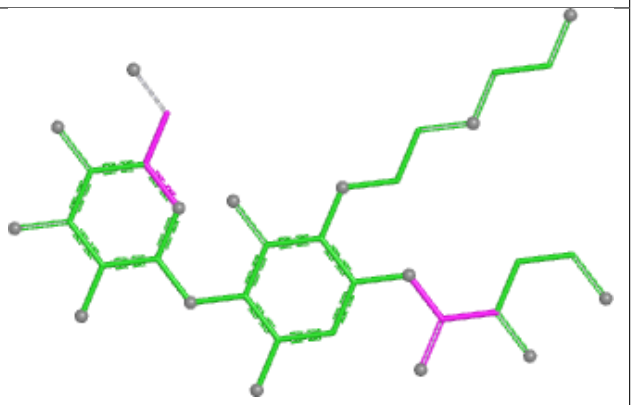
Mol	Chain	Res	Type	Clashes	Symm-Clashes
25	A	1637	AB9	1	0
24	A	1636	D2C	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

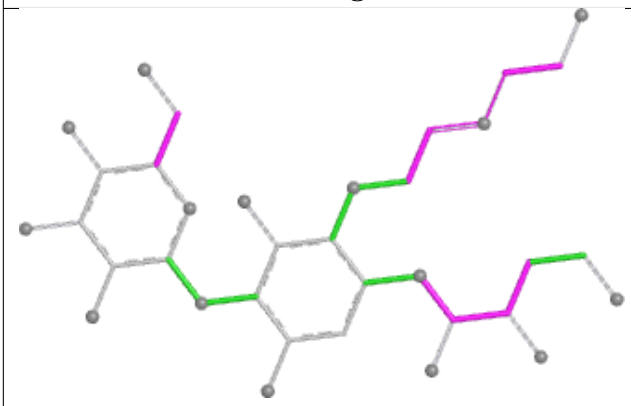
Ligand AB9 A 1637



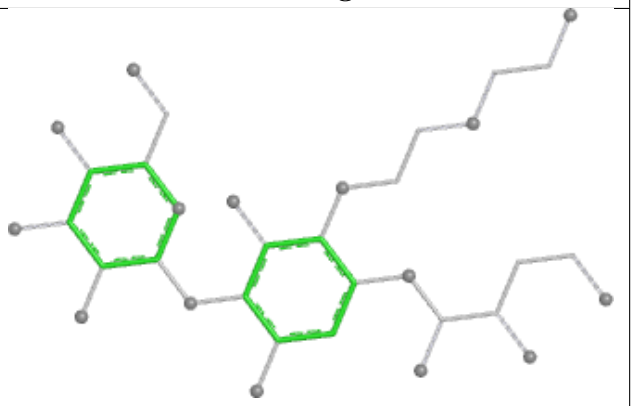
Bond lengths



Bond angles

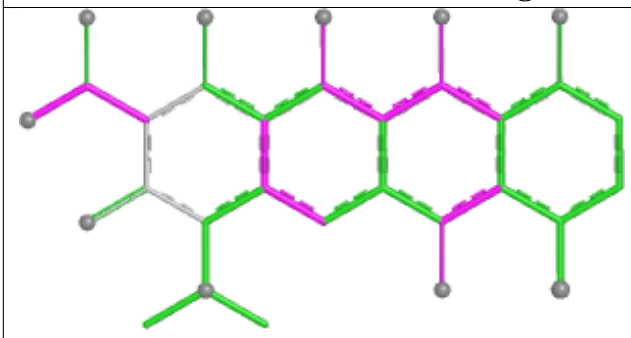


Torsions

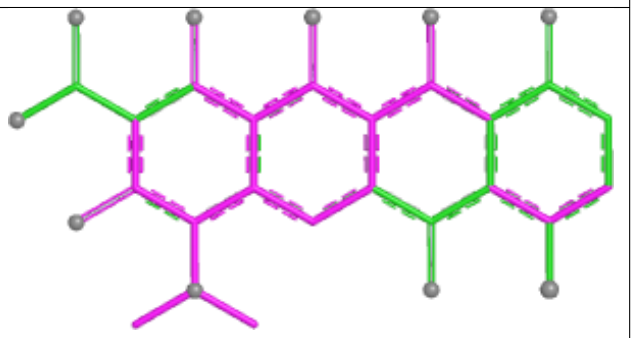


Rings

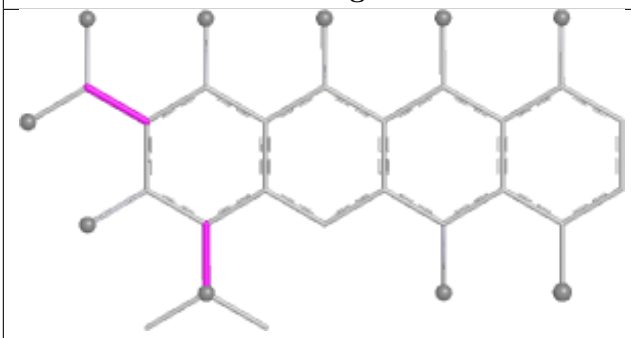
Ligand D2C A 1636



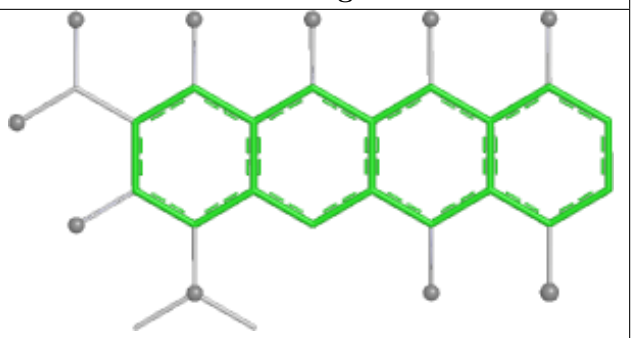
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	13

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	841:U	O3'	848:C	P	5.02
1	A	84:U	O3'	88:A	P	3.79
1	A	1533:C	O3'	1534:A	P	3.45
1	A	70:G	O3'	73:C	P	3.36
1	A	204:U	O3'	216:G	P	3.36
1	A	1443:G	O3'	1446:A	P	2.95
1	A	93:G	O3'	95:U	P	2.78
1	A	463:A	O3'	474:G	P	2.68
1	A	440:A	O3'	442:C	P	2.65
1	A	99:C	O3'	101:A	P	2.63
1	A	492:G	O3'	494:G	P	2.50
1	A	1455:G	O3'	1459:C	P	2.31
1	A	1169:A	O3'	1171:G	P	2.03

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.