



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 06:25 am GMT

PDB ID : 4DR7  
Title : Crystal structure of the *Thermus thermophilus* (HB8) 30S ribosomal subunit with codon, crystallographically disordered near-cognate transfer RNA anti-codon stem-loop mismatched at the second codon position, and streptomycin bound  
Authors : Demirci, H.; Murphy IV, F.; Murphy, E.; Gregory, S.T.; Dahlberg, A.E.; Jogl, G.  
Deposited on : 2012-02-16  
Resolution : 3.75 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

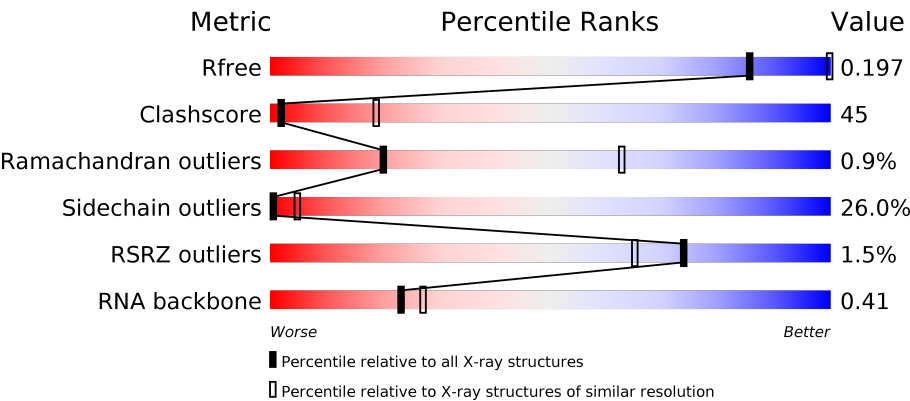
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.75 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R <sub>free</sub>	100719	1423 (4.02-3.50)
Clashscore	112137	1087 (4.00-3.52)
Ramachandran outliers	110173	1047 (4.00-3.52)
Sidechain outliers	110143	1041 (4.00-3.52)
RSRZ outliers	101464	1011 (4.00-3.52)
RNA backbone	2435	1014 (4.62-2.90)

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

Mol	Chain	Length	Quality of chain
1	A	1522	<div><div></div><div>13%43%34%10%.</div></div>
2	B	256	<div><div>%</div><div>26%49%17%8%</div></div>
3	C	239	<div><div>2%</div><div>22%50%15%13%</div></div>
4	D	209	<div><div>2%</div><div>29%52%18%.</div></div>

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Mol	Chain	Length	Quality of chain
5	E	162	
6	F	101	
7	G	156	
8	H	138	
9	I	128	
10	J	105	
11	K	129	
12	L	135	
13	M	126	
14	N	61	
15	O	89	
16	P	88	
17	Q	105	
18	R	88	
19	S	93	
20	T	106	
21	U	27	
22	V	4	
23	W	11	
24	a	8	
25	b	3	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	2MG	A	1207	-	-	X	-
1	5MC	A	1407	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	UR3	A	1498	-	-	X	-
1	MA6	A	1518[A]	-	-	X	-
1	MA6	A	1518[B]	-	-	X	-
1	MA6	A	1519[A]	-	-	X	-
1	MA6	A	1519[B]	-	-	X	-
26	MG	A	1621	-	-	-	X
26	MG	A	1637	-	-	-	X
26	MG	A	1655	-	-	-	X
26	MG	A	1656	-	-	-	X
26	MG	A	1659	-	-	-	X
26	MG	A	1665	-	-	-	X
26	MG	A	1670	-	-	-	X
26	MG	A	1701	-	-	-	X
26	MG	A	1708	-	-	-	X
26	MG	A	1709	-	-	-	X
26	MG	A	1715	-	-	-	X
26	MG	A	1721	-	-	-	X
26	MG	A	1723	-	-	-	X
26	MG	A	1728	-	-	-	X
26	MG	A	1732	-	-	-	X
26	MG	A	1733	-	-	-	X
26	MG	A	1740	-	-	-	X
26	MG	A	1741	-	-	-	X
26	MG	A	1743	-	-	-	X
26	MG	A	1759	-	-	-	X
26	MG	A	1761	-	-	-	X
26	MG	A	1763	-	-	-	X
26	MG	A	1764	-	-	-	X
26	MG	A	1768	-	-	-	X
26	MG	A	1784	-	-	-	X
26	MG	A	1804	-	-	-	X
26	MG	A	1812	-	-	-	X
26	MG	A	1834	-	-	-	X
26	MG	A	1869	-	-	-	X
26	MG	A	1870	-	-	-	X
26	MG	A	1888	-	-	-	X
26	MG	A	1900	-	-	-	X
26	MG	A	1904	-	-	-	X
26	MG	E	201	-	-	-	X
26	MG	E	204	-	-	-	X
26	MG	N	102	-	-	-	X
26	MG	Q	201	-	-	-	X

## 2 Entry composition

There are 29 unique types of molecules in this entry. The entry contains 53659 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1513	Total	C	N	O	P	0	8	0
			32707	14570	6056	10561	1520			

There are 2 discrepancies between the modelled and reference sequences:

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

- Molecule 2 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	236	Total	C	N	O	S	0	0	1
			1896	1211	337	343	5			

- Molecule 3 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	207	Total	C	N	O	S	0	0	1
			1613	1016	315	281	1			

- Molecule 4 is a protein called 30S ribosomal protein S4.

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

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	151	Total	C	N	O	S	0	0	1
			1147	724	218	201	4			

- Molecule 6 is a protein called 30S ribosomal protein S6.

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

- Molecule 7 is a protein called 30S ribosomal protein S7.

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

- Molecule 8 is a protein called 30S ribosomal protein S8.

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

- Molecule 9 is a protein called 30S ribosomal protein S9.

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

- Molecule 10 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	J	99	Total	C	N	O	S	0	0	1
			793	498	157	137	1			

- Molecule 11 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	K	117	Total	C	N	O	S	0	0	0
			873	543	166	161	3			

- Molecule 12 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	L	125	Total	C	N	O	S	0	0	1
			973	612	196	163	2			

- Molecule 13 is a protein called 30S ribosomal protein S13.

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

- Molecule 14 is a protein called 30S ribosomal protein S14.

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

- Molecule 15 is a protein called 30S ribosomal protein S15.

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

- Molecule 16 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	P	84	Total	C	N	O	S	0	0	1
			701	443	140	117	1			

- Molecule 17 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
17	Q	100	Total	C	N	O	S	0	0	0
			834	534	156	142	2			

There is a discrepancy between the modelled and reference sequences:

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

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	R	71	Total	C	N	O		0	0	0
			585	373	116	96				

- Molecule 19 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	S	81	Total	C	N	O	S	0	0	1
			648	414	120	112	2			

- Molecule 20 is a protein called 30S ribosomal protein S20.

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

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	U	25	Total	C	N	O	0	0	1
			209	128	51	30			

- Molecule 22 is a RNA chain called 5'-R(\*UP\*UP\*UP\*U)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
22	V	4	Total	C	N	O	P	0	0	0
			77	36	8	30	3			

- Molecule 23 is a RNA chain called 5'-R(\*GP\*CP\*CP\*UP\*GP\*GP\*AP\*AP\*AP\*GP\*(PSU))-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
23	W	11	Total	C	N	O	P	0	0	0
			235	106	45	74	10			

- Molecule 24 is a RNA chain called 5'-R(P\*UP\*GP\*GP\*AP\*AP\*AP\*GP\*(PSU))-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
24	a	8	Total	C	N	O	P	0	0	0
			175	78	34	55	8			

- Molecule 25 is a RNA chain called 5'-R(P\*UP\*UP\*U)-3'.

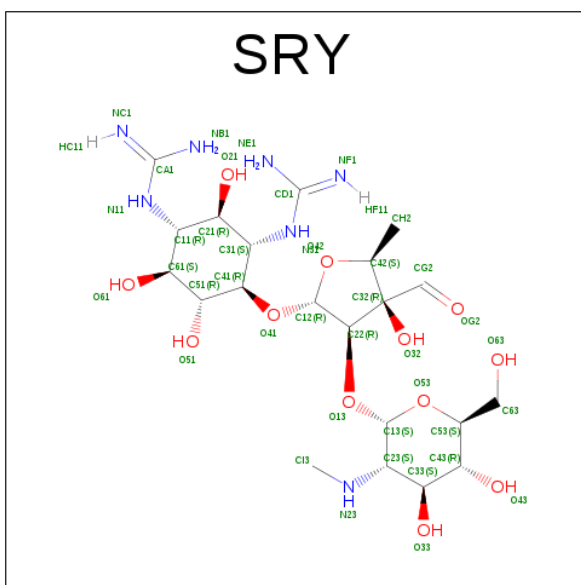
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
25	b	3	Total	C	N	O	P	0	0	0
			60	27	6	24	3			

- Molecule 26 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
26	P	3	Total 3 Mg 3	0	0
26	G	1	Total 1 Mg 1	0	0
26	J	1	Total 1 Mg 1	0	0
26	Q	1	Total 1 Mg 1	0	0
26	D	3	Total 3 Mg 3	0	0
26	E	4	Total 4 Mg 4	0	0
26	H	1	Total 1 Mg 1	0	0
26	A	326	Total 326 Mg 326	0	0
26	N	1	Total 1 Mg 1	0	0
26	S	2	Total 2 Mg 2	0	0
26	F	1	Total 1 Mg 1	0	0

- Molecule 27 is STREPTOMYCIN (three-letter code: SRY) (formula:  $C_{21}H_{39}N_7O_{12}$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
27	A	1	Total	C	N	O	0	0
			40	21	7	12		

- Molecule 28 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

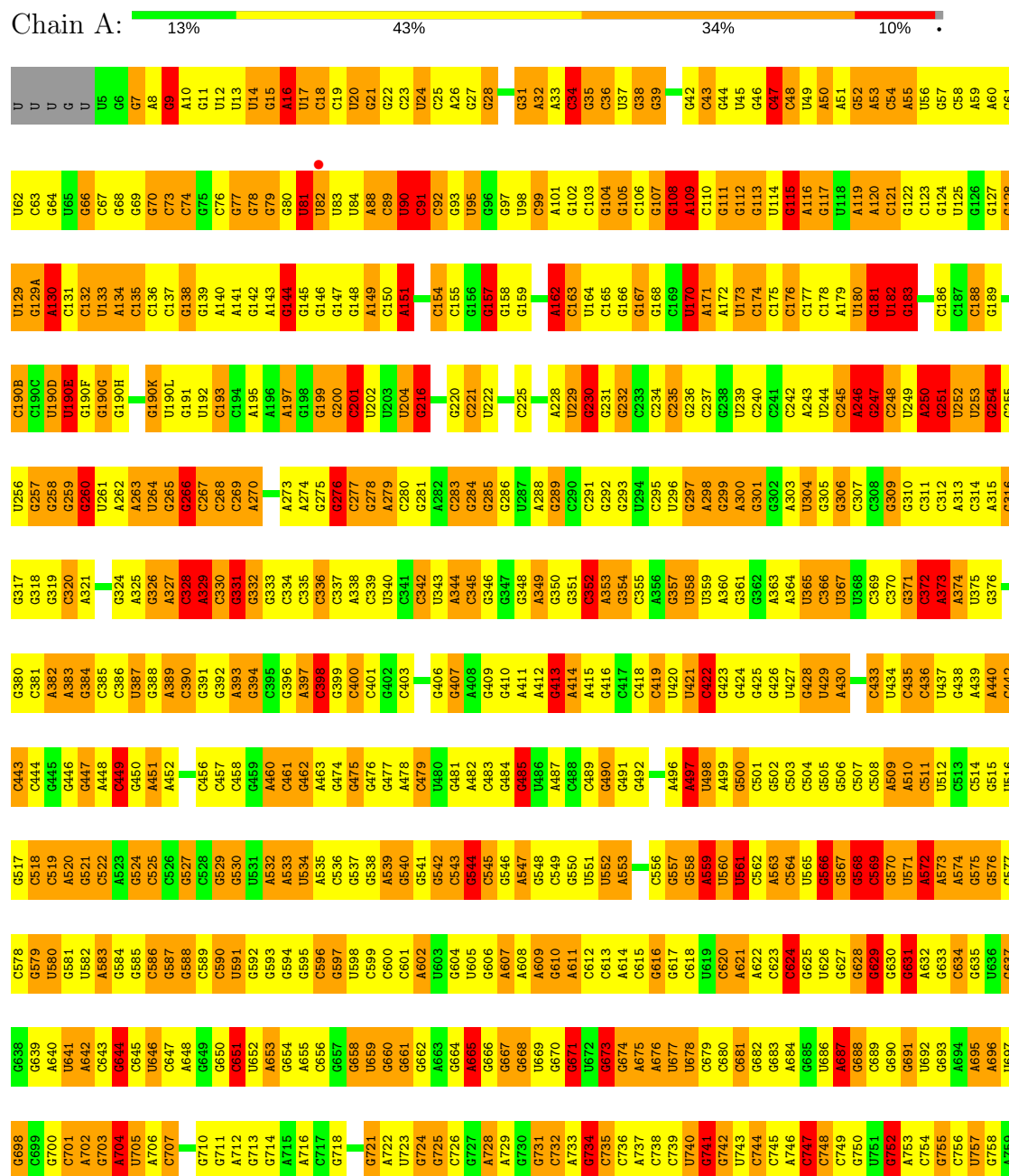
- Molecule 29 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
29	A	866	Total	O	0	0
			866	866		
29	C	1	Total	O	0	0
			1	1		
29	D	7	Total	O	0	0
			7	7		
29	E	5	Total	O	0	0
			5	5		
29	L	1	Total	O	0	0
			1	1		
29	N	1	Total	O	0	0
			1	1		
29	P	1	Total	O	0	0
			1	1		
29	Q	2	Total	O	0	0
			2	2		
29	T	3	Total	O	0	0
			3	3		
29	U	4	Total	O	0	0
			4	4		
29	W	1	Total	O	0	0
			1	1		

### 3 Residue-property plots

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

#### • Molecule 1: 16S rRNA

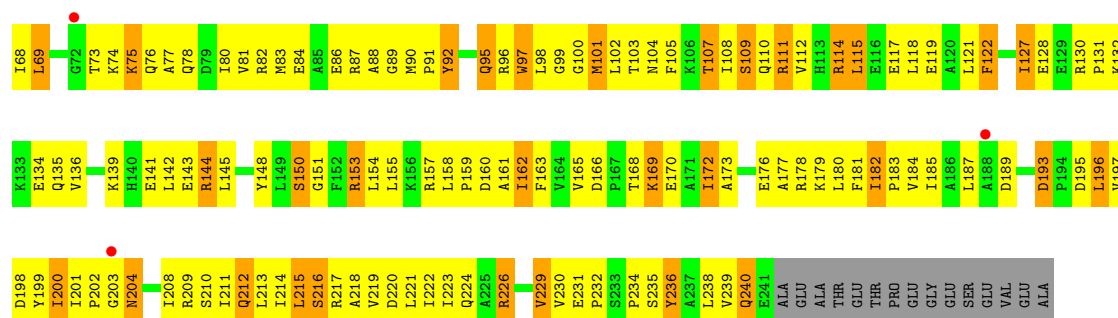


U1510	G1442	A1375	G1316	A1250	C1189	U1125	G1064	C1008	A949	G888	C822	G760
G1511	G1443	U1376	C1317	A1251	G1199	U1126	U1065	G1009	U950	A889	G823	G761
U1512	A1446	A1377	A1318	A1252	G1191	G1127	C1066	G1010	G951	G890	G824	C762
A1513	G1447	C1378	A1319	G1253	C1192	C1128	A1067	G1011	U952	U891	G825	G763
C1514	C1448	G1379	C1320	G1254	G1193	C1129	G1068	U1012	G953	A892	C826	C764
C1515	C1449	U1380	C1321	G1255	U1194	C1130	C1069	G1013	G954	C893	U827	
G1516	U1450	U1381	C1322	A1256	C1195	G1131	U1070	A1014	U955	G894	A828	A766
G1517	A1451	C1382	G1323	U1257	U1196	C1132	C1071	A1015	U956	G895	A829	A767
A1518	C1452		A1324	G1258	G1197	C1133	G1072	A1016	U957	C896	G830	A768
A1519	G1385		C1325	C1259	U1198	G1134	U1073	G1017	A958	C897	U831	G769
G1520	G1453		C1326	C1259	U1199	U1135	G1074	C1018	A959	G898	C832	C770
G1521	G1454		C1327	C1263	C1200	U1136	G1075	C1019	U960	C899	U833	
U1522	G1455		C1328	C1264	A1201	C1137	C1076	U1020	U961	A900	C834	G771
G1523	G1459	A1460	A1329		G1202	G1138	G1077	G1021	C962	A901	U835	
G1524			U1330	C1267	C1203	U1139	U1078	G1022	G963	A902	U836	G774
G1525	C1465		G1331	A1268	A1204	C1140	G1079	G1023	A964	G903	G837	A777
G1526	G1466		A1332	A1269	U1205	C1141	A1080	G1024	A965	C904	G838	G778
C1527	G1467		A1333	C1270	G1206	G1142	U1081	U1025	G966	U905	U839	C779
U1528	A1468	A1394	G1334	G1271	G1207	G1143	G1082	G1026	C967	G906	C840	A780
G1529	G1469	C1395	C1335	G1272	C1208	G1144	U1083	G1027	A968	A907	U841	A781
G1530	G1470	A1396	C1336	G1273	C1209	C1145	G1084	C1028	U969	A908	C848	A782
A1531	G1471	C1397	G1337		C1210	A1146	U1085	C1029	C970	A909	C849	C783
C1532	U1472	A1398	G1338	G1276	U1211	C1147	U1086	C1030	G971	U910	U850	C784
C1533	G1473	C1399	A1339	C1277	U1212	U1148	G1087	G1030A	C972	U911	G851	G785
G1534	A1474	C1400	A1340	U1278	A1213	C1149	G1088	C1030B	G973	C912	G852	G786
A1535	C1475	G1401	U1341	A1279	C1214	U1150	G1089	G1030C	A974	A913	G853	A787
A1536	G1476	C1402	C1342	U1280	G1215	A1151	U1090	A1030D	A975	A914	G854	U788
U1537	C1477	C1403	G1343	U1281	A1152	U1091	U1091	G1031	G976	U789	G855	U789
C1538	G1478	G1404	C1344	C1282	C1153	A1092	U1092	G1032	A977	A915	C856	A790
C1539	C1479	C1405	U1345	G1283		A1093	A1093	G1033	A978	C857	C857	G791
U1540	U1480	U1406	A1346		U1219	G1094	U1095	G1034	C979	A919	G858	A792
PSU	U1481	C1407	U1347	A1286	G1221	C1158	U1096	A1035	C980	U920	A859	U793
U	G1482	A1408	U1348	A1287	G1222	U1159	C1096	G1036	U981	U921	A860	A794
C	A1483	C1409	A1349	A1288	C1223	G1160	C1097	C1037	U982	G922	G861	C795
U	C1484	G1410	A1350	A1289	G1224	C1161	C1098	C1038	A983	A923	C862	C796
		C1411	U1351	G1290	A1225	G1162	G1099	C1039	C984	C924	U863	C797
		C1412	C1352	G1291	G1226	C1163	C1100	U1040	C985	G925	A864	G798
		A1413	G1353	U1292	A1227	G1164	A1101	A1041	A986	G926	A865	G799
	G1487	U1414	C1354	U1293	C1228	C1165	A1102	G1042	G987	G927	C866	G800
	G1488	G1415	G1355	G1294	A1229	G1166	C1103	C1043	G988	G928	G867	U801
	G1489	G1416	G1356	G1295	C1230	A1167	C1104	A1044	C989	C929	C868	A802
	C1490	G1417	A1357	C1296	G1231	A1168		C1045	C990	C930	G869	G803
	G1491	A1418	U1358	C1297	U1232	A1169		U1052	U991	C931	U870	U804
	A1492	G1419	C1359	C1298	G1233	G1171	C1113	U1053	U992	C932	U871	C805
	A1493	C1420	A1360	A1299	C1234	C1172	C1114	G1054	G993	G933	A872	C806
	G1494		G1361	G1300	U1235	G1173	C1115	A1055	A994	C934	A873	A807
	U1495		C1362	U1301	A1236	G1174	C1116	U1056	A995	C935	G874	C808
	G1496		U1363	U1302	C1237	G1175	C1117	C1057	A996	C936	C875	G809
	G1497	C1424	A1364	G1303	A1238	C1178	C1118	G1058	U997	A937	G876	C810
	U1498	U1425	U1365	G1304	U1239	A1179	C1119	U1059	G998	A938	C877	C811
	A1499	C1426	U1366	G1305	G1241	A1180	C1120	A1060	C999	C940	G878	C812
	C1501		C1367	U1306	G1242	G1181	C1121	G1061	U1000	G941	C879	U813
	A1502		G1368	U1307	C1243	G1182	C1122	U1062	A1001	G942	C880	A814
	G1503		C1369		C1244	U1183	C1123	G1063	G1002	U943	C881	A815
	G1504		G1370	G1310	A1245	G1184	C1124	C1059	G1003	G944	C882	A816
	A1505		G1371	G1311	C1246	G1185	U1121	U1060	G1004	G945	C883	C817
	U1506		C1372	G1312	U1247	G1186	U1122	G1060	A1004	G946	U884	G818
	G1507		G1373	U1313	G1248	G1187	U1123	G1061	A1005	G947	G885	A819
	U1508		A1374	U1315	C1249	A1188	G1124	U1062	C1006	G948	G886	U820
	C1509							C1063	C1007		G887	G821

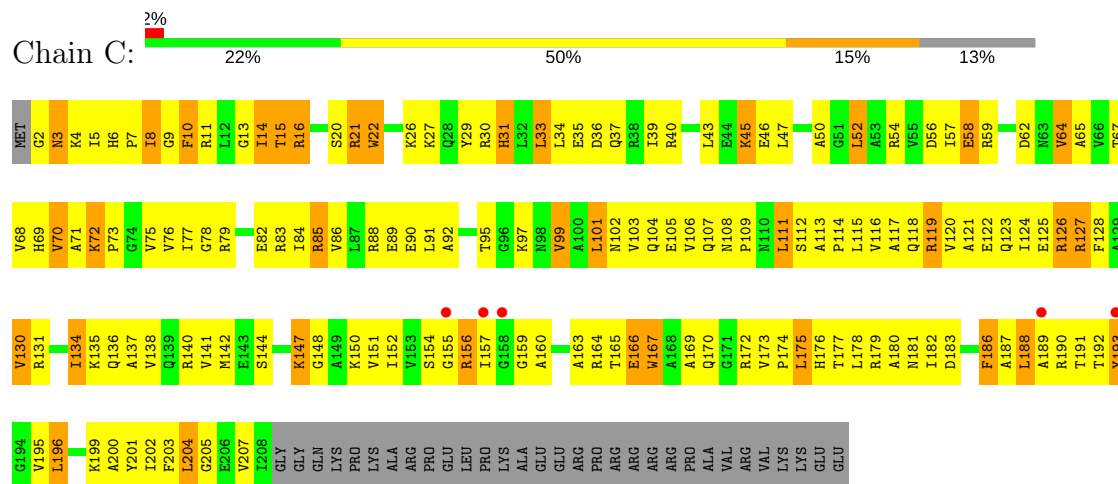
• Molecule 2: 30S ribosomal protein S2



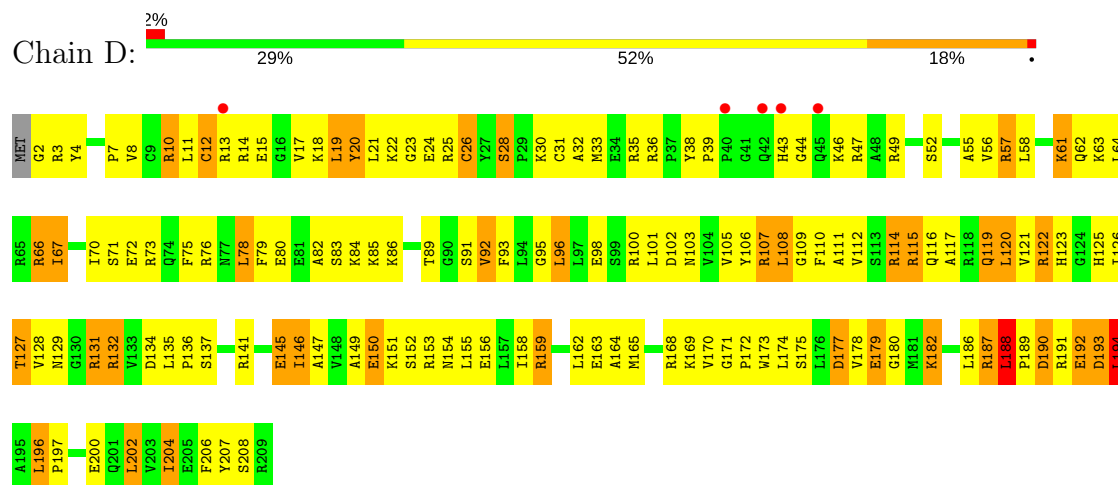
MET	G14	A13	G13	A12	C11	U11	G10	C10	A9	G8	C8	G7
PRO	G14	U13	C13	A12	G11	U11	U10	G10	U9	A8	G8	C7
VAL	A14	A13	A13	A12	G11	G11	C10	G10	G9	G9	G8	C7
GLU	G14	C13	A13	G12	C11	C11	A10	G10	U9	U9	G8	C7
ILE	C14	G13	C13	G12	G11	C11	G10	U10	G9	A8	C8	C7
	C14	U13	C13	G12	U11	C11	C10	G10	G9	C8	U8	
T6	U14	U13	C13	A12	C11	G11	U10	A10	U9	G8	A8	A7
V7	A14	C13		U12	U11	C11	C10	A10	U9	G8	A8	A7
K8	C14		A13	G12	G11	C11	G10	A10	U9	C8	G8	A7
E9	G14		C13	C12	U11	G11	U10	G10	A9	C8	U8	C7
L10	G14		C13	C12	U11	U11	G10	C10	A9	G8	C8	C7
L11	G14		C13	C12	C12	U11	G10	C10	U9	C8	U8	
	G14	A14	C13	C12	A12	C11	U10	A10	U9	A8	C8	A7
G14			A13		G12	G11	U10	G10	C9	A8	U8	
V15			U13	C12	C12	U11	U10	G10	A9	A8	U8	G7
H16	C14		G13	A12	A12	C11	G10	G10	A9	G8	C8	A7
F17	G14		A13	A12	U12	C11	A10	G10	A9	C8	G8	A7
G18	G14		A13	C12	G12	G11	U10	U10	G9	U8	U8	C7
H19	G14	A13	G13	G12	G12	G11	G10	G10	A9	G8	C8	A7
E20		C13	C13	G12	C12	G11	U10	G10	A9	A8	C8	A7
R21	G14	A13	C13	G12	C12	C11	G10	C10	U9	A8	C8	A7
K22	G14	C13	G13		C12	A11	U10	C10	C9	A8	C8	C7
G23	U14	A13	G13	G12	U12	C11	U10	C10	G9	U8	U8	C7
W24	G14	C13	A13	A12	U12	U11	G10	U10	A9	A8	C8	A7
N25	A14	C13	A13	U12	A12	C11	G10	C10	A9	A8	C8	A7
P26	G14	G14	U13	A12	C12	U11	U10	C10	A9	A8	C8	A7
K27	G14	C13	C13	U12	G12	A11	U10	A10	A9	A8	C8	U7
F28	C14	C13	G13	U12	A12	U11	U10	G10	C9	U8	G8	U7
R29	G14	G14	C13	C12	C12	U11	U10	C10	A9	A8	C8	A7
A30	C14	C13	U13	G12		A11	U10	C10	A9	A8	C8	A7
R30	C14	C13	A13		U12	G11	U10	C10	A9	A8	C8	A7
Y31	U14	U14	A13		U12	G11	U10	C10	A9	A8	C8	A7
I32	U14	C13	U13	A12	G12	C11	U10	A10	C9	U8	A8	U7
Y33	G14	A13	U13	A12	G12	U11	C10	G10	A9	A8	C8	A7
A34	A14	C13	A13	A12	C12	G11	C10	C10	A9	A8	C8	A7
E35	C14	G14	A13	A12	G12	C11	C10	C10	A9	A8	C8	A7
R36		C13	U13	G12	A12	G11	G10	C10	A9	A8	C8	A7
		C13	C13	G12	G12	C11	C10	U10	C9	A8	C8	A7
I39	G14		G13	U12	A12	G11	A10	A10	A9	G8	A8	G7
H40	G14	U14	C13	U12	C12	C11	A10	G10	G9	G8	C8	G7
I41	G14	G14	G13	G12	A12	G11	C10	C10	A9	G8	C8	U7
I42	G14	G14	G13	G12	C12	A11	C10	A10	C9	C8	G8	A7
D43	C14	G14	A13	G12	G12	A11		C10	C9	C8	G8	A7
L44	G14	A14	U13	C12	U12	A11		U10	U9	C8	U8	U7
K45	A14	G14	C13	C12	G12	G11	C11	U10	U9	C8	U8	C7
K46												
T47												
M48												
R38												
R56												
F57												
D60												
L61												
A62												
M63												
R64												
G65												
G66												
T67												



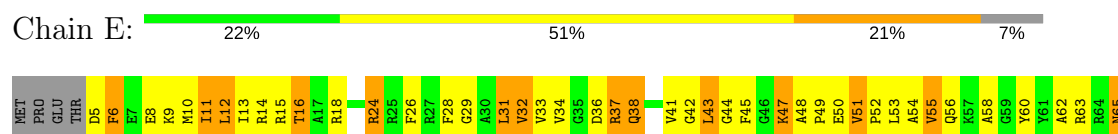
• Molecule 3: 30S ribosomal protein S3

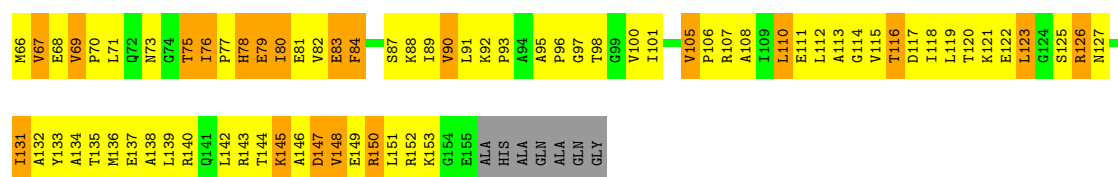


• Molecule 4: 30S ribosomal protein S4

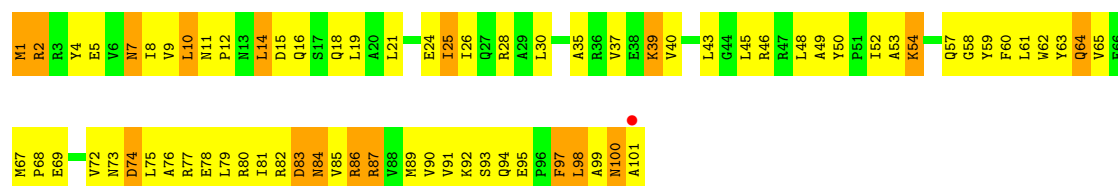


• Molecule 5: 30S ribosomal protein S5

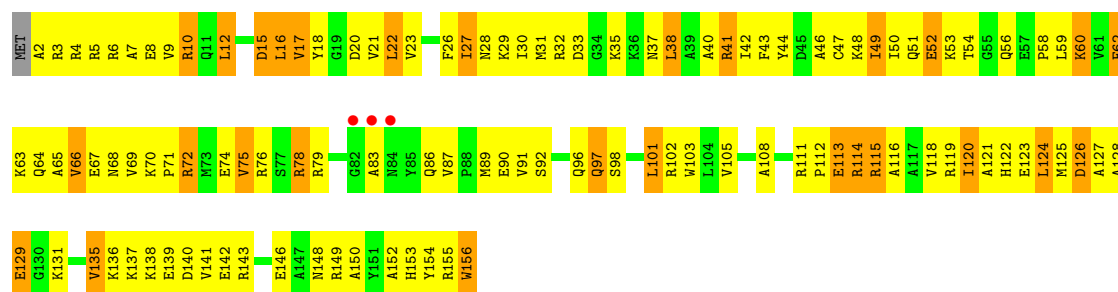




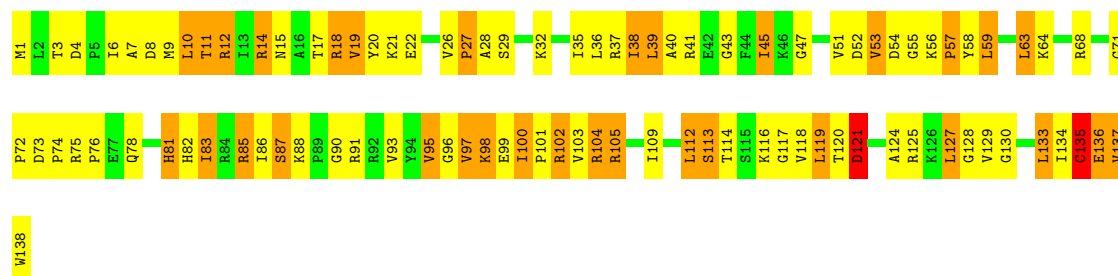
• Molecule 6: 30S ribosomal protein S6



• Molecule 7: 30S ribosomal protein S7

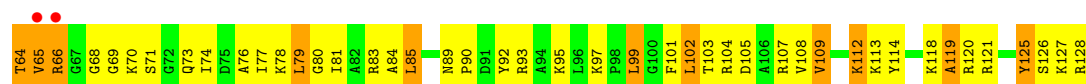


• Molecule 8: 30S ribosomal protein S8

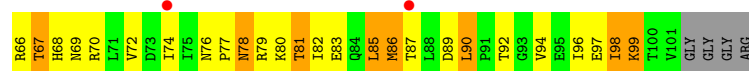


• Molecule 9: 30S ribosomal protein S9

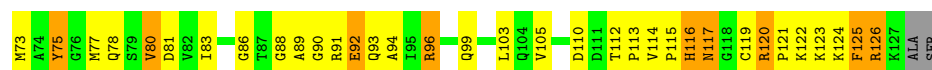




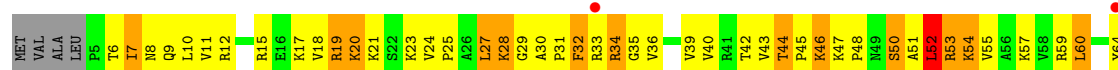
• Molecule 10: 30S ribosomal protein S10



• Molecule 11: 30S ribosomal protein S11



• Molecule 12: 30S ribosomal protein S12

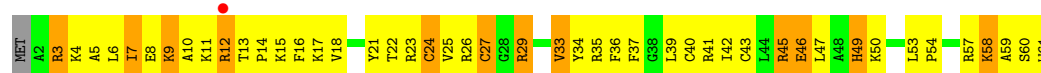


• Molecule 13: 30S ribosomal protein S13

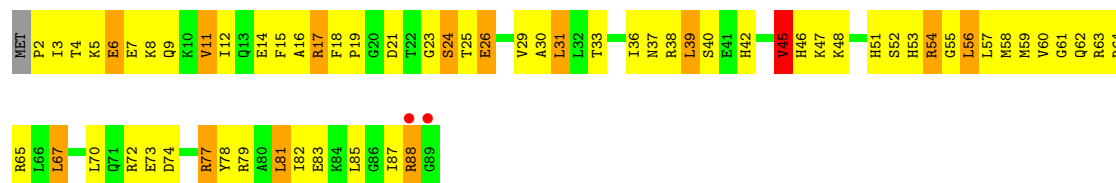


• Molecule 14: 30S ribosomal protein S14

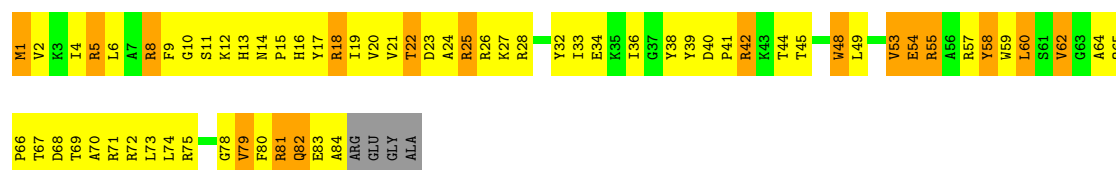




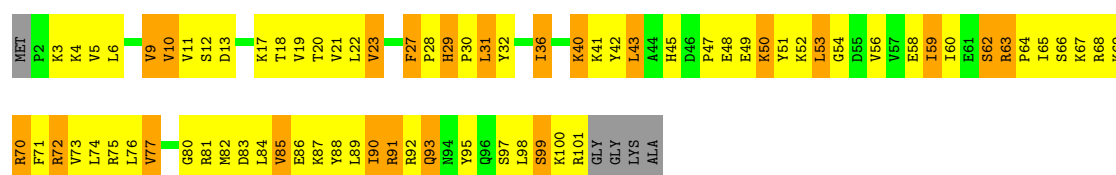
• Molecule 15: 30S ribosomal protein S15



• Molecule 16: 30S ribosomal protein S16



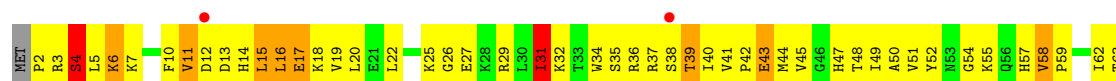
• Molecule 17: 30S ribosomal protein S17



• Molecule 18: 30S ribosomal protein S18



• Molecule 19: 30S ribosomal protein S19

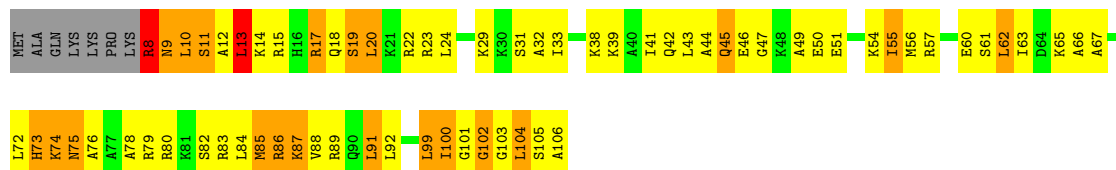






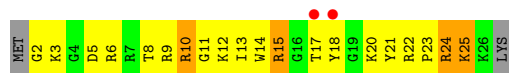
- Molecule 20: 30S ribosomal protein S20

Chain T: 29% 43% 19% 7%



- Molecule 21: 30S ribosomal protein THX

Chain U: 7% 19% 59% 15% 7%



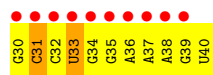
- Molecule 22: 5'-R(\*UP\*UP\*UP\*U)-3'

Chain V: 100% 50% 50%



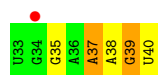
- Molecule 23: 5'-R(\*GP\*CP\*CP\*UP\*GP\*GP\*AP\*AP\*AP\*GP\*(PSU))-3'

Chain W: 91% 82% 18%



- Molecule 24: 5'-R(P\*UP\*GP\*GP\*AP\*AP\*AP\*GP\*(PSU))-3'

Chain a: 13% 38% 38% 25%



- Molecule 25: 5'-R(P\*UP\*UP\*U)-3'

Chain b: 67% 33%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	402.49Å 402.49Å 174.79Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.91 – 3.75 49.65 – 3.75	Depositor EDS
% Data completeness (in resolution range)	99.9 (48.91-3.75) 100.0 (49.65-3.75)	Depositor EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.41 (at 3.77Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_978)	Depositor
R, $R_{free}$	0.148 , 0.201 0.144 , 0.197	Depositor DCC
$R_{free}$ test set	7300 reflections (5.00%)	DCC
Wilson B-factor (Å <sup>2</sup> )	130.7	Xtriage
Anisotropy	0.226	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.25 , 102.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	53659	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	146.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.65% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

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

## 5 Model quality

### 5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	1.21	135/36234 (0.4%)	1.90	1769/56547 (3.1%)
2	B	0.74	0/1931	0.93	2/2607 (0.1%)
3	C	0.62	0/1637	0.83	0/2207
4	D	0.73	1/1733 (0.1%)	0.93	4/2318 (0.2%)
5	E	1.04	1/1163 (0.1%)	1.17	3/1566 (0.2%)
6	F	0.65	0/856	0.86	0/1154
7	G	0.68	0/1276	0.87	0/1709
8	H	1.11	2/1136 (0.2%)	1.18	4/1527 (0.3%)
9	I	0.65	0/1029	0.88	2/1379 (0.1%)
10	J	0.71	1/806 (0.1%)	0.95	2/1084 (0.2%)
11	K	0.76	0/888	0.97	0/1198
12	L	0.90	0/978	1.08	3/1308 (0.2%)
13	M	0.68	0/947	0.94	0/1270
14	N	0.68	0/501	0.85	1/664 (0.2%)
15	O	0.86	0/745	1.02	3/992 (0.3%)
16	P	0.93	0/717	1.08	3/965 (0.3%)
17	Q	1.08	1/847 (0.1%)	1.25	4/1131 (0.4%)
18	R	0.76	0/590	1.00	1/782 (0.1%)
19	S	0.57	0/662	0.77	0/892
20	T	0.87	0/765	1.18	4/1007 (0.4%)
21	U	0.69	0/213	0.87	0/279
22	V	0.53	0/84	0.98	0/128
23	W	0.62	0/241	0.92	0/375
24	a	0.85	0/174	1.89	10/270 (3.7%)
25	b	0.76	0/65	1.31	2/98 (2.0%)
All	All	1.08	141/56218 (0.3%)	1.66	1817/83457 (2.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	3
3	C	0	2
4	D	0	1
8	H	0	2
9	I	0	1
10	J	0	2
12	L	0	2
16	P	0	1
19	S	0	1
20	T	0	2
21	U	0	1
All	All	0	18

All (141) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	828	A	N9-C4	-10.24	1.31	1.37
1	A	1513	A	N9-C4	-9.49	1.32	1.37
1	A	266	G	N7-C5	-9.34	1.33	1.39
1	A	573	A	N7-C5	-9.28	1.33	1.39
8	H	135	CYS	CB-SG	-9.04	1.66	1.82
1	A	1227	A	N9-C4	-8.41	1.32	1.37
1	A	1502	A	N3-C4	-8.37	1.29	1.34
1	A	860	A	N3-C4	-8.21	1.29	1.34
1	A	1502	A	N9-C4	-8.06	1.33	1.37
1	A	788	U	C2-N3	7.67	1.43	1.37
1	A	151	A	N9-C4	-7.36	1.33	1.37
1	A	868	C	N1-C6	-7.28	1.32	1.37
1	A	1509	C	N3-C4	-7.25	1.28	1.33
1	A	814	A	N9-C4	-7.15	1.33	1.37
1	A	1066	C	N1-C6	-7.12	1.32	1.37
1	A	787	A	N9-C4	-6.99	1.33	1.37
1	A	109	A	N9-C4	-6.97	1.33	1.37
1	A	130	A	N9-C4	-6.87	1.33	1.37
1	A	563	A	N3-C4	-6.87	1.30	1.34
1	A	366	C	N1-C2	6.81	1.47	1.40
1	A	1502	A	C5-C6	-6.80	1.34	1.41
1	A	1079	G	N7-C5	-6.78	1.35	1.39
1	A	920	U	C4-O4	6.69	1.28	1.23
1	A	868	C	C4-C5	-6.67	1.37	1.43
1	A	1080	A	N3-C4	-6.54	1.30	1.34
1	A	1525	G	C6-N1	-6.52	1.34	1.39
1	A	266	G	C5-C6	-6.52	1.35	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	882	C	N3-C4	-6.52	1.29	1.33
1	A	926	G	N9-C4	6.47	1.43	1.38
1	A	691	G	N7-C5	-6.45	1.35	1.39
1	A	298	A	N3-C4	-6.38	1.31	1.34
1	A	767	A	N3-C4	-6.38	1.31	1.34
1	A	26	A	N9-C4	-6.38	1.34	1.37
1	A	1076	C	N1-C6	-6.37	1.33	1.37
1	A	279	A	N9-C4	-6.36	1.34	1.37
1	A	780	A	N9-C4	-6.34	1.34	1.37
1	A	828	A	N7-C5	-6.34	1.35	1.39
1	A	798	G	C5-C4	-6.32	1.33	1.38
1	A	600	C	N1-C6	-6.28	1.33	1.37
1	A	858	G	C6-O6	6.28	1.29	1.24
1	A	26	A	N3-C4	-6.27	1.31	1.34
1	A	574	A	C5-C4	-6.22	1.34	1.38
1	A	1500	A	C6-N1	-6.16	1.31	1.35
1	A	892	A	N9-C4	-6.00	1.34	1.37
1	A	1487	G	N3-C4	-5.98	1.31	1.35
1	A	572	A	C5-C4	-5.97	1.34	1.38
1	A	938	A	N9-C4	-5.97	1.34	1.37
1	A	144	G	N1-C2	5.91	1.42	1.37
1	A	1340	A	N9-C4	-5.88	1.34	1.37
1	A	1239	A	N9-C4	-5.86	1.34	1.37
1	A	1513	A	N3-C4	-5.85	1.31	1.34
1	A	1500	A	N3-C4	-5.85	1.31	1.34
17	Q	9	VAL	CA-CB	-5.85	1.42	1.54
1	A	722	A	C5-C6	-5.84	1.35	1.41
1	A	242	C	N1-C6	-5.82	1.33	1.37
1	A	1528	U	C3'-O3'	5.81	1.50	1.42
1	A	934	C	C2-O2	5.79	1.29	1.24
1	A	644	G	N1-C2	-5.79	1.33	1.37
1	A	913	A	C3'-O3'	5.76	1.50	1.42
1	A	266	G	C3'-C2'	5.75	1.59	1.52
1	A	817	C	N1-C6	-5.75	1.33	1.37
1	A	1487	G	N7-C5	-5.75	1.35	1.39
1	A	1527	C	C4-C5	-5.73	1.38	1.43
1	A	1064	G	N3-C4	-5.73	1.31	1.35
1	A	807	A	N3-C4	-5.72	1.31	1.34
1	A	567	G	C5-C4	-5.71	1.34	1.38
1	A	572	A	C6-N1	-5.69	1.31	1.35
1	A	246	A	C5-C4	-5.67	1.34	1.38
4	D	12	CYS	CB-SG	5.67	1.91	1.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	569	C	N3-C4	-5.67	1.29	1.33
8	H	137	VAL	CB-CG2	-5.65	1.41	1.52
1	A	325	A	N3-C4	-5.62	1.31	1.34
1	A	698	G	N7-C5	-5.60	1.35	1.39
1	A	868	C	N3-C4	-5.57	1.30	1.33
1	A	1103	C	N1-C6	-5.57	1.33	1.37
1	A	863	U	N1-C2	-5.55	1.33	1.38
1	A	926	G	C5-C6	5.53	1.47	1.42
1	A	609	A	N9-C4	-5.52	1.34	1.37
1	A	298	A	N9-C4	-5.52	1.34	1.37
1	A	320	C	N1-C6	-5.50	1.33	1.37
1	A	915	A	N7-C5	-5.50	1.35	1.39
1	A	566	G	N7-C5	-5.47	1.35	1.39
1	A	577	G	N9-C4	-5.46	1.33	1.38
1	A	144	G	C5-C4	5.46	1.42	1.38
1	A	602	A	N3-C4	-5.46	1.31	1.34
1	A	1377	A	N9-C4	-5.43	1.34	1.37
1	A	107	G	C5-C6	-5.42	1.36	1.42
1	A	601	C	N1-C6	-5.42	1.33	1.37
1	A	1078	U	C4-O4	-5.42	1.19	1.23
1	A	642	A	N9-C4	-5.41	1.34	1.37
1	A	1530	G	C2-N3	-5.41	1.28	1.32
1	A	599	C	N1-C6	-5.41	1.33	1.37
1	A	81	U	N1-C2	5.40	1.43	1.38
1	A	611	A	N9-C4	-5.39	1.34	1.37
1	A	858	G	N3-C4	-5.36	1.31	1.35
1	A	1507	A	C6-N1	-5.34	1.31	1.35
1	A	881	G	N9-C8	-5.33	1.34	1.37
1	A	655	A	N9-C4	-5.33	1.34	1.37
1	A	1487	G	N9-C8	-5.31	1.34	1.37
1	A	1514	C	N3-C4	-5.29	1.30	1.33
5	E	90	VAL	CB-CG1	-5.29	1.41	1.52
1	A	574	A	C6-N1	-5.27	1.31	1.35
1	A	1512	U	C4-O4	5.26	1.27	1.23
1	A	1350	A	N7-C5	-5.25	1.36	1.39
1	A	926	G	C5-C4	5.23	1.42	1.38
1	A	1507	A	N3-C4	-5.22	1.31	1.34
1	A	1513	A	C5-C4	-5.22	1.35	1.38
1	A	266	G	C2-N3	5.22	1.36	1.32
1	A	811	C	N1-C6	-5.22	1.34	1.37
1	A	1502	A	N7-C5	-5.20	1.36	1.39
1	A	704	A	N3-C4	-5.19	1.31	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	162	A	N9-C4	5.18	1.41	1.37
1	A	327	A	C5-C6	-5.18	1.36	1.41
1	A	1053	G	N7-C5	5.15	1.42	1.39
1	A	574	A	N3-C4	-5.15	1.31	1.34
1	A	1080	A	C6-N1	-5.12	1.31	1.35
1	A	1375	A	C6-N6	-5.12	1.29	1.33
1	A	134	A	N3-C4	-5.12	1.31	1.34
1	A	1084	G	C5-C6	5.12	1.47	1.42
1	A	855	G	N3-C4	-5.12	1.31	1.35
1	A	819	A	N3-C4	-5.11	1.31	1.34
1	A	813	U	N1-C6	-5.10	1.33	1.38
1	A	325	A	N9-C4	-5.09	1.34	1.37
1	A	828	A	N3-C4	-5.08	1.31	1.34
1	A	853	G	N7-C5	-5.08	1.36	1.39
1	A	117	G	N1-C2	5.07	1.41	1.37
1	A	640	A	N3-C4	-5.05	1.31	1.34
1	A	823	G	N3-C4	-5.05	1.31	1.35
1	A	117	G	C5-C4	5.05	1.41	1.38
1	A	781	A	N7-C5	-5.05	1.36	1.39
1	A	926	G	C2-N3	5.04	1.36	1.32
1	A	741	G	N9-C4	-5.04	1.33	1.38
1	A	120	A	C6-N1	-5.02	1.32	1.35
1	A	568	G	P-O5'	-5.01	1.54	1.59
1	A	1488	G	N9-C8	-5.01	1.34	1.37
1	A	1350	A	C5-C6	-5.01	1.36	1.41
1	A	239	U	C4-O4	-5.00	1.19	1.23
1	A	640	A	C6-N1	-5.00	1.32	1.35
1	A	74	C	N1-C6	5.00	1.40	1.37
1	A	654	G	C6-N1	-5.00	1.36	1.39
10	J	57	LYS	CB-CG	5.00	1.66	1.52

All (1817) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	266	G	C6-C5-N7	-19.86	118.48	130.40
1	A	366	C	N1-C2-O2	17.84	129.60	118.90
1	A	117	G	N1-C6-O6	15.21	129.03	119.90
1	A	1200	C	C2-N1-C1'	15.12	135.43	118.80
1	A	573	A	C8-N9-C4	-15.02	99.79	105.80
1	A	266	G	N1-C6-O6	14.91	128.85	119.90
1	A	1403	C	N3-C2-O2	14.11	131.78	121.90
1	A	1200	C	N1-C2-O2	14.05	127.33	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	858	G	C5-C6-N1	-13.71	104.64	111.50
1	A	366	C	N3-C2-O2	-13.36	112.55	121.90
1	A	1524	C	N3-C4-C5	-13.31	116.58	121.90
1	A	266	G	C5-C6-O6	-12.74	120.95	128.60
1	A	117	G	N9-C4-C5	-12.34	100.46	105.40
1	A	266	G	C4-C5-C6	12.10	126.06	118.80
1	A	1524	C	C6-N1-C2	-12.09	115.46	120.30
1	A	1092	A	N1-C6-N6	12.09	125.85	118.60
1	A	863	U	C2-N1-C1'	-12.03	103.27	117.70
1	A	1403	C	N1-C2-O2	-11.95	111.73	118.90
1	A	366	C	C2-N1-C1'	11.95	131.94	118.80
1	A	481	G	N1-C6-O6	11.95	127.07	119.90
1	A	1281	U	C5-C4-O4	11.94	133.06	125.90
1	A	624	C	C6-N1-C2	11.88	125.05	120.30
1	A	117	G	C6-C5-N7	-11.85	123.29	130.40
1	A	117	G	C2-N3-C4	-11.83	105.98	111.90
1	A	104	G	N1-C6-O6	11.73	126.94	119.90
1	A	144	G	N1-C6-O6	11.73	126.94	119.90
1	A	762	C	C6-N1-C2	11.70	124.98	120.30
1	A	579	G	N1-C6-O6	11.67	126.90	119.90
1	A	266	G	C4-C5-N7	11.64	115.45	110.80
1	A	873	A	C8-N9-C4	-11.51	101.20	105.80
1	A	1200	C	C5-C6-N1	11.48	126.74	121.00
1	A	1234	C	C6-N1-C2	11.42	124.87	120.30
1	A	1084	G	N3-C4-C5	-11.26	122.97	128.60
1	A	1079	G	C8-N9-C4	-11.20	101.92	106.40
1	A	1200	C	C6-N1-C1'	-11.19	107.38	120.80
1	A	586	C	C6-N1-C2	11.14	124.76	120.30
1	A	570	G	N3-C4-C5	-10.99	123.11	128.60
1	A	283	C	C2-N1-C1'	10.97	130.87	118.80
1	A	295	C	C6-N1-C2	10.96	124.68	120.30
1	A	117	G	C8-N9-C1'	-10.95	112.77	127.00
1	A	634	C	C6-N1-C2	-10.87	115.95	120.30
1	A	1084	G	C4-C5-N7	-10.80	106.48	110.80
1	A	788	U	N3-C4-O4	10.76	126.93	119.40
1	A	920	U	N3-C4-C5	-10.65	108.21	114.60
1	A	572	A	N1-C6-N6	-10.62	112.23	118.60
1	A	863	U	C5-C4-O4	10.58	132.25	125.90
1	A	868	C	N1-C2-O2	-10.58	112.55	118.90
1	A	732	C	N3-C4-C5	10.56	126.12	121.90
1	A	144	G	C5-C6-N1	-10.54	106.23	111.50
1	A	266	G	N7-C8-N9	10.54	118.37	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	572	A	C5-C6-N1	10.33	122.86	117.70
1	A	824	C	C6-N1-C2	10.31	124.42	120.30
1	A	449	C	C6-N1-C2	-10.25	116.20	120.30
1	A	572	A	N9-C4-C5	10.25	109.90	105.80
1	A	1502	A	C2-N3-C4	-10.24	105.48	110.60
1	A	248	C	C5-C6-N1	-10.22	115.89	121.00
1	A	644	G	C4-C5-N7	10.20	114.88	110.80
1	A	873	A	C2-N3-C4	10.20	115.70	110.60
1	A	863	U	C6-N1-C1'	10.18	135.45	121.20
1	A	248	C	C6-N1-C2	10.17	124.37	120.30
1	A	884	U	C5-C6-N1	-10.15	117.62	122.70
1	A	820	U	N1-C2-N3	10.05	120.93	114.90
1	A	1329	A	N1-C6-N6	10.02	124.61	118.60
1	A	860	A	C8-N9-C4	-10.00	101.80	105.80
1	A	703	G	C4-C5-N7	-9.97	106.81	110.80
1	A	176	C	C6-N1-C2	9.96	124.28	120.30
1	A	559	A	C6-N1-C2	-9.95	112.63	118.60
1	A	856	C	N1-C2-O2	-9.94	112.94	118.90
1	A	283	C	C5-C6-N1	9.94	125.97	121.00
1	A	1190	G	C4-N9-C1'	9.93	139.41	126.50
1	A	691	G	C8-N9-C4	-9.92	102.43	106.40
1	A	90	U	C5-C4-O4	9.90	131.84	125.90
1	A	117	G	C5-C6-N1	-9.90	106.55	111.50
1	A	770	C	C5-C6-N1	-9.90	116.05	121.00
1	A	648	A	C8-N9-C4	9.89	109.76	105.80
1	A	859	A	N1-C6-N6	9.89	124.53	118.60
1	A	266	G	C4-N9-C1'	9.87	139.33	126.50
1	A	729	A	N1-C6-N6	9.86	124.51	118.60
1	A	1530	G	N3-C4-C5	9.81	133.50	128.60
1	A	920	U	C5-C4-O4	9.76	131.75	125.90
1	A	866	C	C6-N1-C2	-9.75	116.40	120.30
1	A	1370	G	C8-N9-C4	-9.75	102.50	106.40
1	A	635	G	C2-N3-C4	-9.75	107.03	111.90
1	A	1381	U	N1-C2-O2	9.74	129.62	122.80
1	A	864	A	N1-C6-N6	-9.70	112.78	118.60
1	A	563	A	C8-N9-C4	-9.67	101.93	105.80
1	A	722	A	N1-C6-N6	9.67	124.40	118.60
1	A	825	G	C8-N9-C4	9.67	110.27	106.40
1	A	117	G	C8-N9-C4	9.66	110.26	106.40
1	A	1524	C	N1-C2-O2	-9.61	113.14	118.90
1	A	266	G	N3-C4-N9	9.58	131.75	126.00
1	A	146	G	N1-C6-O6	9.57	125.64	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	529	G	C4-C5-C6	9.54	124.52	118.80
1	A	139	G	C5-C6-N1	-9.53	106.74	111.50
1	A	232	G	C6-C5-N7	-9.51	124.69	130.40
1	A	1335	C	C6-N1-C2	9.51	124.10	120.30
1	A	563	A	N9-C4-C5	9.49	109.59	105.80
1	A	366	C	C6-N1-C1'	-9.48	109.43	120.80
1	A	1232	U	N1-C2-O2	-9.47	116.17	122.80
1	A	1066	C	C6-N1-C1'	-9.47	109.44	120.80
1	A	874	G	N1-C6-O6	9.47	125.58	119.90
1	A	703	G	C5-C6-O6	9.44	134.26	128.60
1	A	1528	U	C2-N1-C1'	9.43	129.02	117.70
1	A	91	C	C2-N1-C1'	9.43	129.17	118.80
1	A	481	G	C6-C5-N7	-9.43	124.75	130.40
1	A	266	G	C5-N7-C8	-9.42	99.59	104.30
1	A	768	A	C8-N9-C4	9.41	109.57	105.80
1	A	283	C	N1-C2-O2	9.40	124.54	118.90
1	A	328	C	N3-C4-N4	-9.38	111.44	118.00
1	A	732	C	C2-N3-C4	-9.36	115.22	119.90
1	A	621	A	C8-N9-C4	-9.32	102.07	105.80
1	A	815	A	C8-N9-C4	9.31	109.53	105.80
1	A	867	G	N1-C6-O6	9.31	125.49	119.90
1	A	1514	C	N1-C2-O2	-9.31	113.31	118.90
1	A	648	A	N7-C8-N9	-9.31	109.15	113.80
1	A	867	G	C8-N9-C1'	-9.30	114.90	127.00
1	A	698	G	C4-N9-C1'	9.29	138.58	126.50
1	A	795	C	N3-C2-O2	9.25	128.38	121.90
1	A	721	G	C6-C5-N7	-9.24	124.86	130.40
1	A	864	A	C5-C6-N6	9.21	131.07	123.70
1	A	90	U	N3-C4-O4	-9.20	112.96	119.40
1	A	1239	A	C8-N9-C4	9.20	109.48	105.80
1	A	529	G	N1-C6-O6	9.17	125.40	119.90
1	A	269	C	C5-C6-N1	-9.13	116.43	121.00
1	A	860	A	N9-C4-C5	9.13	109.45	105.80
1	A	722	A	C2-N3-C4	-9.10	106.05	110.60
1	A	1507	A	N1-C6-N6	-9.09	113.15	118.60
1	A	1200	C	C6-N1-C2	-9.08	116.67	120.30
1	A	559	A	C8-N9-C4	-9.08	102.17	105.80
1	A	644	G	C6-C5-N7	-9.06	124.96	130.40
1	A	577	G	C2-N3-C4	-9.06	107.37	111.90
1	A	940	C	C6-N1-C2	9.04	123.92	120.30
1	A	283	C	C2-N3-C4	9.02	124.41	119.90
1	A	818	G	N1-C6-O6	9.02	125.31	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	729	A	C5-N7-C8	-9.02	99.39	103.90
1	A	1381	U	N3-C2-O2	-9.00	115.90	122.20
1	A	635	G	C6-C5-N7	-8.99	125.00	130.40
1	A	481	G	C5-C6-N1	-8.98	107.01	111.50
1	A	1108	G	N3-C4-C5	-8.98	124.11	128.60
1	A	623	C	C6-N1-C2	8.97	123.89	120.30
1	A	1392	G	C6-C5-N7	-8.97	125.02	130.40
1	A	1107	C	C6-N1-C2	-8.96	116.72	120.30
1	A	881	G	C8-N9-C4	8.93	109.97	106.40
1	A	635	G	C5-C6-N1	-8.92	107.04	111.50
1	A	788	U	N3-C2-O2	8.91	128.44	122.20
1	A	975	A	N1-C6-N6	8.86	123.92	118.60
1	A	232	G	N1-C6-O6	8.86	125.22	119.90
1	A	284	G	N1-C6-O6	8.86	125.22	119.90
1	A	1186	G	N3-C4-C5	8.86	133.03	128.60
1	A	1068	G	C8-N9-C4	-8.84	102.86	106.40
1	A	1392	G	N1-C6-O6	8.83	125.20	119.90
1	A	91	C	C6-N1-C2	-8.82	116.77	120.30
1	A	783	C	C6-N1-C2	8.80	123.82	120.30
1	A	885	G	C2-N3-C4	-8.80	107.50	111.90
1	A	570	G	C8-N9-C4	-8.78	102.89	106.40
1	A	1524	C	C4-C5-C6	8.78	121.79	117.40
1	A	909	A	C5-C6-N6	-8.77	116.69	123.70
1	A	651	C	C6-N1-C2	8.73	123.79	120.30
1	A	698	G	C6-C5-N7	-8.73	125.16	130.40
1	A	529	G	C4-N9-C1'	8.73	137.85	126.50
1	A	621	A	N7-C8-N9	8.73	118.17	113.80
1	A	144	G	C2-N3-C4	-8.72	107.54	111.90
1	A	1053	G	C8-N9-C4	8.72	109.89	106.40
1	A	244	U	N1-C2-O2	8.72	128.90	122.80
1	A	91	C	N1-C2-O2	8.71	124.13	118.90
1	A	926	G	N3-C4-C5	-8.71	124.25	128.60
1	A	700	G	C4-C5-N7	8.70	114.28	110.80
1	A	700	G	N3-C4-N9	8.69	131.22	126.00
1	A	1066	C	C6-N1-C2	8.69	123.78	120.30
1	A	259	G	N1-C2-N3	8.68	129.11	123.90
1	A	1228	C	N1-C2-O2	8.68	124.11	118.90
1	A	741	G	N3-C4-N9	-8.68	120.80	126.00
1	A	814	A	C2-N3-C4	-8.67	106.27	110.60
1	A	1186	G	C2-N3-C4	-8.66	107.57	111.90
1	A	529	G	C8-N9-C1'	-8.64	115.77	127.00
1	A	50	A	C8-N9-C4	8.61	109.24	105.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	579	G	C5-C6-O6	-8.61	123.44	128.60
1	A	277	C	C6-N1-C2	8.60	123.74	120.30
1	A	1468	A	C8-N9-C4	8.59	109.24	105.80
1	A	795	C	N1-C2-O2	-8.58	113.75	118.90
1	A	1388	C	N3-C2-O2	8.55	127.89	121.90
1	A	266	G	C8-N9-C4	-8.55	102.98	106.40
1	A	868	C	C6-N1-C2	-8.55	116.88	120.30
1	A	618	C	C2-N1-C1'	-8.54	109.41	118.80
1	A	971	G	N1-C6-O6	8.53	125.02	119.90
1	A	909	A	N1-C6-N6	8.53	123.72	118.60
1	A	573	A	C4-C5-C6	8.52	121.26	117.00
1	A	1202	G	N1-C6-O6	-8.52	114.79	119.90
1	A	735	C	C6-N1-C2	8.52	123.71	120.30
1	A	858	G	N1-C6-O6	8.51	125.00	119.90
1	A	525	C	C6-N1-C2	8.50	123.70	120.30
1	A	127	G	C8-N9-C4	8.47	109.79	106.40
1	A	928	G	N1-C6-O6	8.47	124.98	119.90
1	A	232	G	C4-C5-N7	8.46	114.18	110.80
1	A	283	C	C6-N1-C2	-8.46	116.92	120.30
1	A	884	U	C4-C5-C6	8.46	124.77	119.70
1	A	1200	C	N3-C2-O2	-8.45	115.98	121.90
1	A	650	G	C8-N9-C4	8.45	109.78	106.40
1	A	780	A	C8-N9-C4	8.44	109.17	105.80
1	A	1080	A	N1-C6-N6	-8.43	113.54	118.60
1	A	382	A	C8-N9-C4	-8.42	102.43	105.80
1	A	656	C	C6-N1-C2	8.41	123.67	120.30
1	A	268	C	N1-C2-O2	8.40	123.94	118.90
1	A	519	C	N1-C2-O2	8.39	123.94	118.90
1	A	182	U	N3-C2-O2	-8.39	116.33	122.20
1	A	1083	U	N3-C2-O2	8.38	128.07	122.20
1	A	701	C	N1-C2-O2	8.37	123.92	118.90
1	A	721	G	N3-C4-N9	8.37	131.02	126.00
1	A	788	U	C5-C6-N1	8.37	126.88	122.70
1	A	872	A	C2-N3-C4	-8.36	106.42	110.60
1	A	572	A	C8-N9-C4	-8.36	102.46	105.80
1	A	874	G	C8-N9-C4	8.35	109.74	106.40
1	A	1527	C	C5-C4-N4	-8.34	114.36	120.20
1	A	111	G	N3-C4-N9	-8.34	121.00	126.00
1	A	763	G	C8-N9-C4	8.33	109.73	106.40
1	A	1202	G	C5-C6-O6	8.32	133.59	128.60
1	A	573	A	N7-C8-N9	8.32	117.96	113.80
1	A	1058	G	C8-N9-C4	8.31	109.72	106.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	716	A	N1-C6-N6	-8.29	113.63	118.60
1	A	8	A	C8-N9-C4	-8.28	102.49	105.80
1	A	175	C	C6-N1-C2	8.26	123.60	120.30
1	A	634	C	N3-C4-C5	-8.26	118.60	121.90
1	A	440	A	C2-N3-C4	-8.23	106.48	110.60
1	A	721	G	C4-C5-C6	8.23	123.74	118.80
1	A	810	C	N3-C4-N4	8.23	123.76	118.00
1	A	259	G	N1-C2-N2	-8.22	108.80	116.20
1	A	874	G	N9-C4-C5	-8.22	102.11	105.40
1	A	914	A	C8-N9-C4	-8.20	102.52	105.80
1	A	398	C	C6-N1-C2	8.19	123.58	120.30
1	A	559	A	N3-C4-C5	-8.18	121.08	126.80
1	A	814	A	N1-C2-N3	8.18	133.39	129.30
1	A	871	U	N1-C2-O2	8.18	128.53	122.80
1	A	1365	G	C8-N9-C4	-8.18	103.13	106.40
1	A	1054	C	N1-C2-O2	8.18	123.81	118.90
1	A	965	A	C8-N9-C4	8.17	109.07	105.80
1	A	721	G	C4-N9-C1'	8.16	137.11	126.50
1	A	132	C	C2-N3-C4	-8.15	115.82	119.90
1	A	283	C	N3-C4-C5	-8.14	118.64	121.90
1	A	867	G	C6-C5-N7	-8.12	125.53	130.40
1	A	1390	U	N3-C4-C5	-8.11	109.73	114.60
1	A	829	G	C8-N9-C4	8.11	109.64	106.40
1	A	1186	G	C5-C6-N1	-8.10	107.45	111.50
1	A	1392	G	C5-C6-N1	-8.10	107.45	111.50
1	A	266	G	C8-N9-C1'	-8.09	116.48	127.00
1	A	864	A	N9-C4-C5	8.08	109.03	105.80
1	A	1502	A	C5-N7-C8	-8.07	99.86	103.90
1	A	1512	U	N3-C4-C5	-8.07	109.76	114.60
1	A	873	A	C5-C6-N1	8.07	121.73	117.70
1	A	1190	G	N7-C8-N9	8.06	117.13	113.10
1	A	1530	G	N3-C4-N9	-8.05	121.17	126.00
1	A	816	A	N1-C6-N6	-8.05	113.77	118.60
1	A	1186	G	N3-C4-N9	-8.05	121.17	126.00
1	A	1452	C	N1-C2-O2	8.04	123.72	118.90
1	A	659	U	C5-C6-N1	-8.03	118.68	122.70
1	A	278	G	C4-C5-N7	-8.02	107.59	110.80
1	A	1083	U	C5-C4-O4	-8.02	121.09	125.90
1	A	32	A	C6-N1-C2	-8.01	113.80	118.60
1	A	1500	A	N1-C6-N6	-8.00	113.80	118.60
1	A	288	A	C2-N3-C4	-8.00	106.60	110.60
1	A	867	G	C4-N9-C1'	7.99	136.89	126.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1227	A	N1-C6-N6	7.99	123.39	118.60
1	A	788	U	N3-C4-C5	-7.99	109.81	114.60
1	A	481	G	C4-C5-C6	7.98	123.59	118.80
1	A	1279	A	C8-N9-C4	-7.98	102.61	105.80
1	A	91	C	N3-C2-O2	-7.97	116.32	121.90
1	A	940	C	C5-C6-N1	-7.97	117.02	121.00
1	A	807	A	N1-C2-N3	7.96	133.28	129.30
1	A	1092	A	N9-C4-C5	-7.96	102.62	105.80
1	A	1190	G	C8-N9-C1'	-7.96	116.66	127.00
1	A	479	C	N3-C4-C5	-7.95	118.72	121.90
1	A	820	U	N1-C2-O2	-7.95	117.23	122.80
1	A	885	G	N3-C4-C5	7.94	132.57	128.60
1	A	944	G	C5-C6-O6	7.94	133.36	128.60
1	A	1488	G	C8-N9-C4	7.94	109.58	106.40
1	A	265	G	N1-C2-N2	-7.93	109.06	116.20
1	A	1507	A	N9-C4-C5	7.93	108.97	105.80
1	A	1235	U	N1-C2-N3	7.93	119.66	114.90
1	A	704	A	C8-N9-C4	-7.93	102.63	105.80
1	A	609	A	C2-N3-C4	-7.92	106.64	110.60
1	A	815	A	N7-C8-N9	-7.92	109.84	113.80
1	A	853	G	C6-C5-N7	-7.92	125.65	130.40
1	A	1322	C	C2-N1-C1'	7.92	127.51	118.80
1	A	674	G	C8-N9-C4	7.92	109.57	106.40
1	A	970	C	N1-C2-O2	7.92	123.65	118.90
1	A	43	C	C6-N1-C2	7.91	123.47	120.30
1	A	299	G	N1-C6-O6	7.91	124.65	119.90
1	A	1528	U	C6-N1-C1'	-7.91	110.13	121.20
1	A	732	C	C5-C6-N1	-7.91	117.05	121.00
1	A	628	G	N3-C4-N9	7.91	130.74	126.00
1	A	721	G	C8-N9-C1'	-7.90	116.73	127.00
1	A	1064	G	N9-C4-C5	7.90	108.56	105.40
1	A	232	G	N9-C4-C5	-7.88	102.25	105.40
1	A	117	G	C4-N9-C1'	7.88	136.74	126.50
9	I	39	GLY	N-CA-C	-7.88	93.41	113.10
1	A	729	A	C5-C6-N6	-7.87	117.40	123.70
1	A	874	G	C5-C6-O6	-7.87	123.88	128.60
1	A	117	G	C4-C5-C6	7.87	123.52	118.80
1	A	852	G	N1-C6-O6	7.85	124.61	119.90
1	A	104	G	C6-C5-N7	-7.85	125.69	130.40
1	A	1344	C	C6-N1-C2	7.85	123.44	120.30
1	A	1493[A]	A	C5-N7-C8	-7.84	99.98	103.90
1	A	1493[B]	A	C5-N7-C8	-7.84	99.98	103.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1488	G	N7-C8-N9	-7.84	109.18	113.10
1	A	559	A	C5-C6-N1	7.84	121.62	117.70
1	A	813	U	C2-N1-C1'	7.84	127.10	117.70
24	a	39	G	N1-C6-O6	7.83	124.60	119.90
1	A	487	A	C8-N9-C4	7.83	108.93	105.80
1	A	522	C	C5-C6-N1	-7.83	117.09	121.00
20	T	20	LEU	CA-CB-CG	-7.83	97.30	115.30
1	A	266	G	N3-C4-C5	-7.82	124.69	128.60
1	A	1222	G	C5-C6-N1	-7.81	107.60	111.50
1	A	635	G	N1-C6-O6	7.80	124.58	119.90
1	A	858	G	C4-C5-C6	7.79	123.47	118.80
1	A	529	G	C5-C6-N1	-7.78	107.61	111.50
1	A	819	A	C4-C5-C6	7.78	120.89	117.00
1	A	596	C	C6-N1-C2	7.77	123.41	120.30
1	A	963	G	N1-C6-O6	7.75	124.55	119.90
1	A	135	C	N3-C4-C5	-7.75	118.80	121.90
1	A	383	A	N1-C6-N6	-7.74	113.96	118.60
1	A	580	U	N3-C4-C5	-7.74	109.96	114.60
1	A	570	G	C4-N9-C1'	7.74	136.56	126.50
1	A	400	C	N3-C4-C5	7.73	124.99	121.90
1	A	918	A	N1-C2-N3	7.73	133.16	129.30
1	A	1528	U	P-O3'-C3'	7.73	128.97	119.70
1	A	1092	A	C6-C5-N7	-7.72	126.89	132.30
1	A	190(G)	G	C5-C6-N1	-7.71	107.65	111.50
1	A	1414	U	N3-C2-O2	-7.71	116.81	122.20
1	A	1074	G	C5-C6-N1	-7.71	107.65	111.50
1	A	867	G	N3-C4-N9	7.70	130.62	126.00
1	A	522	C	C2-N1-C1'	-7.70	110.33	118.80
1	A	783	C	N3-C4-C5	7.69	124.98	121.90
1	A	1277	C	C6-N1-C2	-7.69	117.22	120.30
1	A	1099	G	N9-C4-C5	7.69	108.47	105.40
1	A	109	A	C2-N3-C4	-7.68	106.76	110.60
1	A	753	A	N9-C4-C5	7.68	108.87	105.80
1	A	813	U	C5-C4-O4	-7.67	121.30	125.90
1	A	1394	A	C5-C6-N6	-7.67	117.56	123.70
1	A	570	G	C2-N3-C4	7.67	115.74	111.90
1	A	128	G	N1-C6-O6	7.66	124.49	119.90
1	A	805	C	N3-C4-C5	7.66	124.96	121.90
1	A	770	C	C6-N1-C2	7.66	123.36	120.30
1	A	1108	G	C8-N9-C4	-7.66	103.34	106.40
1	A	783	C	N3-C4-N4	-7.65	112.64	118.00
1	A	55	A	N1-C6-N6	-7.63	114.02	118.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	21	G	C8-N9-C4	7.62	109.45	106.40
1	A	700	G	C6-C5-N7	-7.61	125.83	130.40
1	A	779	C	N1-C2-O2	-7.61	114.34	118.90
1	A	1230	C	N3-C4-N4	7.61	123.32	118.00
1	A	946	A	C6-N1-C2	-7.60	114.04	118.60
1	A	1390	U	N1-C2-N3	7.60	119.46	114.90
1	A	529	G	C6-C5-N7	-7.60	125.84	130.40
1	A	591	U	C5-C6-N1	-7.60	118.90	122.70
1	A	1496	C	N3-C4-C5	-7.60	118.86	121.90
1	A	697	U	C5-C6-N1	-7.59	118.90	122.70
1	A	1525	G	N1-C6-O6	-7.59	115.34	119.90
1	A	722	A	C6-C5-N7	-7.59	126.99	132.30
1	A	1353	G	N3-C4-C5	-7.59	124.81	128.60
1	A	1240	U	C5-C4-O4	7.58	130.45	125.90
1	A	1053	G	N7-C8-N9	-7.58	109.31	113.10
1	A	242	C	C4-C5-C6	7.58	121.19	117.40
1	A	326	G	C5-C6-N1	-7.57	107.72	111.50
1	A	858	G	N3-C2-N2	-7.57	114.60	119.90
1	A	32	A	C4-N9-C1'	7.57	139.92	126.30
1	A	572	A	C2-N3-C4	7.57	114.38	110.60
1	A	782	A	C8-N9-C4	-7.56	102.78	105.80
1	A	618	C	N3-C2-O2	7.56	127.19	121.90
1	A	297	G	N3-C4-C5	-7.55	124.82	128.60
1	A	1190	G	C8-N9-C4	-7.54	103.38	106.40
1	A	1403	C	N3-C4-N4	7.53	123.27	118.00
1	A	981	U	N3-C4-O4	7.52	124.67	119.40
1	A	1525	G	C5-C6-N1	7.52	115.26	111.50
1	A	579	G	C4-C5-N7	7.52	113.81	110.80
1	A	782	A	N9-C4-C5	7.52	108.81	105.80
1	A	400	C	N1-C2-O2	7.52	123.41	118.90
1	A	693	G	N1-C6-O6	7.52	124.41	119.90
1	A	1487	G	N3-C4-C5	-7.51	124.84	128.60
1	A	667	G	C2-N3-C4	-7.51	108.15	111.90
1	A	784	C	N3-C2-O2	-7.51	116.65	121.90
1	A	107	G	C4-C5-N7	7.49	113.80	110.80
1	A	928	G	C5-C6-O6	-7.49	124.10	128.60
1	A	1084	G	C5-N7-C8	7.49	108.05	104.30
1	A	1202	G	C4-C5-N7	-7.49	107.80	110.80
1	A	874	G	C8-N9-C1'	-7.49	117.26	127.00
1	A	698	G	C8-N9-C1'	-7.48	117.27	127.00
1	A	16	A	C8-N9-C4	7.48	108.79	105.80
1	A	1055	A	N1-C6-N6	-7.48	114.11	118.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	36	C	C6-N1-C2	-7.47	117.31	120.30
1	A	648	A	C5-N7-C8	7.46	107.63	103.90
1	A	27	G	C5-C6-O6	-7.46	124.13	128.60
1	A	893	C	N1-C2-O2	7.45	123.37	118.90
1	A	230	G	C8-N9-C1'	-7.45	117.32	127.00
1	A	859	A	C5-C6-N6	-7.44	117.75	123.70
1	A	881	G	C8-N9-C1'	-7.44	117.33	127.00
1	A	332	G	C5-C6-O6	-7.43	124.14	128.60
1	A	1281	U	N3-C4-O4	-7.42	114.20	119.40
1	A	781	A	C8-N9-C4	-7.42	102.83	105.80
1	A	923	A	C2-N3-C4	-7.42	106.89	110.60
1	A	920	U	C4-C5-C6	7.42	124.15	119.70
1	A	382	A	N9-C4-C5	7.40	108.76	105.80
1	A	628	G	N3-C4-C5	-7.40	124.90	128.60
1	A	637	G	C5-C6-N1	-7.39	107.80	111.50
1	A	698	G	N3-C4-C5	-7.39	124.91	128.60
1	A	1232	U	N3-C2-O2	7.38	127.37	122.20
1	A	760	G	C8-N9-C1'	-7.36	117.43	127.00
1	A	573	A	N9-C4-C5	7.36	108.75	105.80
1	A	1305	G	C5-C6-N1	-7.36	107.82	111.50
1	A	328	C	C5-C4-N4	7.36	125.35	120.20
1	A	1092	A	C5-C6-N6	-7.36	117.81	123.70
1	A	852	G	C5-C6-N1	-7.35	107.82	111.50
1	A	134	A	N1-C2-N3	7.33	132.97	129.30
1	A	745	C	C6-N1-C2	7.33	123.23	120.30
1	A	1094	G	C4-C5-N7	7.33	113.73	110.80
1	A	816	A	C5-C6-N6	7.33	129.56	123.70
1	A	946	A	N1-C6-N6	-7.32	114.21	118.60
1	A	436	C	C6-N1-C2	7.32	123.23	120.30
1	A	1068	G	N7-C8-N9	7.32	116.76	113.10
1	A	1199	U	N3-C2-O2	-7.31	117.08	122.20
1	A	251	G	N1-C2-N2	-7.31	109.62	116.20
1	A	447	G	N3-C4-N9	7.31	130.38	126.00
1	A	1370	G	N7-C8-N9	7.30	116.75	113.10
1	A	1084	G	N1-C6-O6	-7.30	115.52	119.90
1	A	635	G	N1-C2-N3	7.29	128.28	123.90
1	A	1092	A	C4-C5-N7	7.29	114.34	110.70
1	A	139	G	N1-C6-O6	7.29	124.27	119.90
1	A	38	G	N3-C4-N9	-7.28	121.63	126.00
1	A	1193	G	C5-C6-N1	-7.28	107.86	111.50
1	A	27	G	C8-N9-C4	-7.28	103.49	106.40
1	A	1080	A	N9-C4-C5	7.28	108.71	105.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	312	C	N3-C4-C5	7.27	124.81	121.90
1	A	823	G	C2-N3-C4	-7.27	108.26	111.90
1	A	1353	G	C8-N9-C4	-7.27	103.49	106.40
1	A	787	A	C5-N7-C8	-7.27	100.27	103.90
1	A	597	G	N3-C4-N9	7.26	130.36	126.00
1	A	1301	U	C6-N1-C2	-7.26	116.64	121.00
1	A	250	A	C5-C6-N1	-7.25	114.08	117.70
1	A	1205	U	N3-C2-O2	-7.24	117.13	122.20
1	A	1447	G	N1-C6-O6	7.24	124.25	119.90
1	A	1350	A	C5-N7-C8	-7.24	100.28	103.90
1	A	830	G	C2-N3-C4	-7.23	108.28	111.90
1	A	1143	G	N1-C6-O6	7.22	124.23	119.90
1	A	7	G	N9-C4-C5	-7.22	102.51	105.40
15	O	67	LEU	CA-CB-CG	-7.22	98.70	115.30
1	A	635	G	C4-C5-C6	7.20	123.12	118.80
1	A	577	G	N3-C4-C5	7.19	132.20	128.60
1	A	867	G	C4-C5-C6	7.19	123.11	118.80
1	A	1403	C	C6-N1-C2	7.19	123.18	120.30
1	A	254	G	C2-N3-C4	-7.19	108.31	111.90
1	A	451	A	C2-N3-C4	-7.19	107.00	110.60
1	A	586	C	C2-N1-C1'	-7.19	110.89	118.80
1	A	929	G	N1-C6-O6	7.18	124.21	119.90
1	A	1231	G	C8-N9-C1'	-7.18	117.66	127.00
1	A	868	C	N3-C4-C5	-7.18	119.03	121.90
1	A	32	A	C8-N9-C1'	-7.18	114.78	127.70
1	A	1530	G	C8-N9-C4	7.18	109.27	106.40
1	A	760	G	C6-C5-N7	-7.17	126.10	130.40
1	A	854	G	N1-C2-N2	-7.17	109.75	116.20
1	A	722	A	C4-C5-N7	7.16	114.28	110.70
1	A	197	A	N1-C6-N6	-7.16	114.30	118.60
1	A	1338	G	C5-C6-O6	7.16	132.90	128.60
1	A	109	A	N3-C4-N9	-7.16	121.67	127.40
1	A	522	C	C6-N1-C2	7.16	123.16	120.30
1	A	703	G	N9-C4-C5	7.16	108.26	105.40
1	A	732	C	C6-N1-C2	7.16	123.16	120.30
1	A	283	C	C6-N1-C1'	-7.15	112.22	120.80
1	A	20	U	C5-C6-N1	-7.15	119.12	122.70
1	A	783	C	C2-N1-C1'	-7.14	110.94	118.80
1	A	1399	C	C5-C4-N4	-7.14	115.20	120.20
1	A	183	G	C8-N9-C4	-7.14	103.54	106.40
1	A	583	A	N1-C6-N6	7.14	122.89	118.60
24	a	38	A	C5-C6-N1	-7.13	114.13	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	318	G	N1-C6-O6	7.13	124.18	119.90
1	A	718	G	N1-C6-O6	7.12	124.17	119.90
1	A	1230	C	C5-C4-N4	-7.11	115.22	120.20
1	A	813	U	N3-C4-O4	7.11	124.37	119.40
1	A	1227	A	C5-N7-C8	-7.10	100.35	103.90
1	A	365	U	C2-N1-C1'	7.10	126.22	117.70
1	A	1230	C	N3-C2-O2	7.10	126.87	121.90
1	A	50	A	N1-C2-N3	-7.10	125.75	129.30
1	A	1375	A	C5-C6-N1	7.10	121.25	117.70
1	A	729	A	C4-C5-N7	7.09	114.25	110.70
1	A	1310	G	C8-N9-C1'	-7.09	117.78	127.00
1	A	1276	G	N1-C6-O6	7.09	124.15	119.90
1	A	68	G	C8-N9-C4	7.08	109.23	106.40
1	A	91	C	C5-C6-N1	7.08	124.54	121.00
1	A	371	G	N1-C6-O6	-7.08	115.65	119.90
1	A	934	C	N1-C2-N3	-7.08	114.25	119.20
1	A	828	A	C2-N3-C4	-7.08	107.06	110.60
1	A	701	C	N3-C2-O2	-7.07	116.95	121.90
1	A	8	A	N9-C4-C5	7.07	108.63	105.80
1	A	856	C	N3-C4-C5	-7.07	119.07	121.90
1	A	698	G	N3-C4-N9	7.07	130.24	126.00
1	A	1190	G	C6-C5-N7	-7.07	126.16	130.40
1	A	120	A	N1-C6-N6	-7.06	114.36	118.60
1	A	895	G	C8-N9-C4	-7.06	103.58	106.40
1	A	945	G	C5-C6-N1	7.06	115.03	111.50
1	A	36	C	N3-C2-O2	-7.06	116.96	121.90
1	A	1388	C	C6-N1-C2	7.06	123.12	120.30
1	A	1507	A	C8-N9-C4	-7.05	102.98	105.80
1	A	365	U	N3-C4-O4	7.05	124.34	119.40
1	A	259	G	C2-N3-C4	-7.05	108.38	111.90
1	A	912	C	N3-C4-C5	7.05	124.72	121.90
1	A	1061	G	C2-N3-C4	-7.04	108.38	111.90
1	A	1380	U	N3-C2-O2	-7.04	117.27	122.20
1	A	269	C	C2-N3-C4	-7.04	116.38	119.90
1	A	1341	U	C5-C4-O4	7.04	130.12	125.90
1	A	799	G	N1-C6-O6	7.03	124.12	119.90
1	A	700	G	C5-C6-O6	-7.03	124.38	128.60
1	A	621	A	C5-N7-C8	-7.02	100.39	103.90
1	A	975	A	C4-C5-N7	7.01	114.21	110.70
1	A	681	C	C6-N1-C2	-7.01	117.50	120.30
1	A	190(G)	G	N1-C6-O6	7.01	124.11	119.90
1	A	104	G	C5-C6-N1	-7.01	108.00	111.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	7	G	C8-N9-C4	7.01	109.20	106.40
1	A	1322	C	N3-C4-C5	-7.01	119.10	121.90
1	A	250	A	C2-N3-C4	-7.00	107.10	110.60
1	A	1061	G	C5-C6-N1	-7.00	108.00	111.50
1	A	181	G	C4-N9-C1'	6.99	135.59	126.50
1	A	774	G	N1-C6-O6	6.99	124.09	119.90
1	A	940	C	C2-N3-C4	-6.99	116.41	119.90
1	A	552	U	C2-N3-C4	-6.98	122.81	127.00
1	A	1438	G	N1-C6-O6	6.98	124.09	119.90
1	A	1047	G	C8-N9-C4	6.98	109.19	106.40
1	A	117	G	C5-C6-O6	-6.98	124.41	128.60
1	A	316	G	N1-C6-O6	-6.98	115.71	119.90
1	A	329	A	C2-N3-C4	-6.98	107.11	110.60
1	A	1399	C	N3-C4-N4	6.97	122.88	118.00
1	A	674	G	N9-C4-C5	-6.97	102.61	105.40
1	A	278	G	N9-C4-C5	6.96	108.19	105.40
1	A	590	C	C6-N1-C2	6.96	123.09	120.30
1	A	817	C	C6-N1-C1'	-6.96	112.44	120.80
1	A	753	A	N1-C6-N6	-6.96	114.42	118.60
1	A	1403	C	C5-C4-N4	-6.96	115.33	120.20
1	A	552	U	N3-C2-O2	-6.96	117.33	122.20
1	A	854	G	C8-N9-C1'	-6.96	117.95	127.00
1	A	127	G	N1-C6-O6	6.96	124.07	119.90
1	A	447	G	C8-N9-C1'	-6.95	117.96	127.00
1	A	580	U	C5-C4-O4	6.95	130.07	125.90
1	A	722	A	C5-N7-C8	-6.95	100.42	103.90
1	A	1493[A]	A	N7-C8-N9	6.95	117.28	113.80
1	A	1493[B]	A	N7-C8-N9	6.95	117.28	113.80
1	A	27	G	C4-C5-N7	6.95	113.58	110.80
4	D	202	LEU	CA-CB-CG	-6.94	99.34	115.30
1	A	703	G	N1-C6-O6	-6.94	115.74	119.90
1	A	1421	G	C8-N9-C4	-6.94	103.62	106.40
1	A	686	U	C5-C4-O4	6.93	130.06	125.90
1	A	235	C	C6-N1-C2	6.93	123.07	120.30
1	A	946	A	C8-N9-C4	-6.93	103.03	105.80
1	A	1373	G	N9-C4-C5	6.93	108.17	105.40
1	A	295	C	C5-C6-N1	-6.92	117.54	121.00
1	A	755	G	C5-C6-O6	-6.92	124.45	128.60
10	J	58	ASP	CB-CG-OD2	-6.92	112.08	118.30
1	A	182	U	N1-C2-O2	6.91	127.64	122.80
1	A	824	C	N3-C4-C5	6.91	124.66	121.90
1	A	549	C	C6-N1-C2	6.91	123.06	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	863	U	N3-C4-O4	-6.91	114.57	119.40
1	A	260	G	C5-C6-N1	-6.90	108.05	111.50
1	A	1442	G	C8-N9-C1'	-6.89	118.04	127.00
1	A	1525	G	N9-C4-C5	6.89	108.16	105.40
1	A	635	G	C8-N9-C1'	-6.89	118.04	127.00
1	A	1228	C	C2-N1-C1'	6.89	126.38	118.80
1	A	246	A	C2-N3-C4	6.88	114.04	110.60
1	A	975	A	C5-N7-C8	-6.88	100.46	103.90
1	A	1530	G	N7-C8-N9	-6.88	109.66	113.10
1	A	487	A	N7-C8-N9	-6.88	110.36	113.80
1	A	113	G	N1-C6-O6	6.87	124.02	119.90
1	A	758	G	C2-N3-C4	-6.87	108.46	111.90
1	A	1066	C	N1-C2-O2	6.86	123.02	118.90
1	A	919	A	N1-C6-N6	6.86	122.71	118.60
1	A	1323	G	C2-N3-C4	-6.86	108.47	111.90
1	A	167	G	C5-C6-N1	6.85	114.92	111.50
1	A	90	U	C2-N1-C1'	-6.85	109.48	117.70
1	A	700	G	N3-C2-N2	6.85	124.69	119.90
1	A	830	G	N1-C2-N3	6.85	128.01	123.90
1	A	787	A	C2-N3-C4	-6.85	107.18	110.60
1	A	1336	C	N3-C4-C5	-6.84	119.16	121.90
1	A	357	G	C4-C5-N7	-6.84	108.06	110.80
1	A	741	G	C4-N9-C1'	-6.84	117.61	126.50
1	A	852	G	C2-N3-C4	-6.84	108.48	111.90
24	a	39	G	C5-C6-O6	-6.84	124.50	128.60
1	A	729	A	C6-C5-N7	-6.83	127.52	132.30
1	A	884	U	N3-C2-O2	-6.83	117.42	122.20
1	A	1202	G	N3-C4-C5	-6.83	125.19	128.60
1	A	874	G	C6-C5-N7	-6.83	126.31	130.40
1	A	857	C	C6-N1-C2	6.82	123.03	120.30
1	A	881	G	N9-C4-C5	-6.82	102.67	105.40
1	A	104	G	C2-N3-C4	-6.82	108.49	111.90
1	A	188	C	N3-C4-C5	-6.82	119.17	121.90
1	A	1178	G	C8-N9-C4	-6.81	103.68	106.40
1	A	398	C	N3-C4-C5	6.81	124.62	121.90
1	A	1200	C	C2-N3-C4	6.80	123.30	119.90
1	A	1337	G	C5-C6-N1	-6.80	108.10	111.50
1	A	1338	G	N1-C6-O6	-6.79	115.83	119.90
1	A	193	C	C5-C6-N1	-6.78	117.61	121.00
25	b	3	U	N1-C2-O2	6.78	127.55	122.80
1	A	644	G	N3-C2-N2	6.78	124.64	119.90
1	A	1292	U	N3-C2-O2	6.78	126.94	122.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	a	39	G	N9-C4-C5	-6.78	102.69	105.40
1	A	947	G	C4-C5-N7	6.77	113.51	110.80
1	A	788	U	N1-C2-O2	-6.77	118.06	122.80
1	A	1310	G	N3-C4-N9	6.77	130.06	126.00
1	A	1343	G	C6-C5-N7	-6.77	126.34	130.40
1	A	1447	G	C4-C5-N7	6.77	113.51	110.80
1	A	677	U	N1-C2-N3	6.76	118.96	114.90
1	A	168	G	C5-C6-N1	-6.76	108.12	111.50
1	A	765	G	N1-C6-O6	6.75	123.95	119.90
1	A	285	G	N3-C4-C5	6.75	131.98	128.60
1	A	706	A	C2-N3-C4	-6.75	107.22	110.60
1	A	1195	C	N3-C4-N4	6.75	122.72	118.00
1	A	1249	C	C6-N1-C2	-6.75	117.60	120.30
1	A	133	U	C5-C4-O4	6.75	129.95	125.90
1	A	1202	G	N9-C4-C5	6.75	108.10	105.40
1	A	677	U	N3-C2-O2	-6.74	117.48	122.20
1	A	973	G	C8-N9-C4	6.74	109.10	106.40
1	A	1054	C	C2-N3-C4	6.74	123.27	119.90
1	A	32	A	N3-C4-C5	-6.73	122.09	126.80
1	A	563	A	N1-C6-N6	-6.73	114.56	118.60
1	A	27	G	C5-N7-C8	-6.73	100.94	104.30
1	A	1338	G	N9-C4-C5	6.72	108.09	105.40
1	A	383	A	N9-C4-C5	6.72	108.49	105.80
1	A	1329	A	C5-C6-N6	-6.71	118.33	123.70
1	A	400	C	N3-C4-N4	-6.71	113.30	118.00
1	A	662	G	N1-C6-O6	6.71	123.92	119.90
17	Q	63	ARG	NE-CZ-NH1	-6.71	116.95	120.30
1	A	73	C	C5-C6-N1	6.70	124.35	121.00
1	A	644	G	N1-C2-N2	-6.70	110.17	116.20
1	A	964	A	C8-N9-C4	-6.70	103.12	105.80
1	A	1066	C	N1-C2-N3	-6.70	114.51	119.20
1	A	623	C	C5-C6-N1	-6.70	117.65	121.00
1	A	157	G	N1-C6-O6	6.69	123.92	119.90
1	A	615	C	C6-N1-C2	-6.69	117.62	120.30
1	A	824	C	C5-C6-N1	-6.68	117.66	121.00
1	A	1442	G	C4-N9-C1'	6.68	135.18	126.50
1	A	762	C	N3-C4-C5	6.68	124.57	121.90
1	A	64	G	N1-C6-O6	6.67	123.91	119.90
1	A	885	G	N1-C6-O6	6.67	123.90	119.90
1	A	275	G	N9-C4-C5	-6.67	102.73	105.40
24	a	39	G	C4-C5-N7	6.67	113.47	110.80
1	A	1447	G	C5-C6-O6	-6.67	124.60	128.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	27	G	N7-C8-N9	6.66	116.43	113.10
1	A	747	C	C6-N1-C2	6.66	122.96	120.30
1	A	975	A	N9-C4-C5	-6.66	103.14	105.80
1	A	285	G	C2-N3-C4	-6.66	108.57	111.90
1	A	586	C	C5-C6-N1	-6.66	117.67	121.00
1	A	687	A	P-O3'-C3'	6.66	127.69	119.70
1	A	1077	G	C6-C5-N7	-6.66	126.41	130.40
1	A	28	G	N9-C4-C5	6.65	108.06	105.40
1	A	1405	G	N3-C4-C5	6.65	131.93	128.60
1	A	729	A	N7-C8-N9	6.65	117.12	113.80
1	A	16	A	C2-N3-C4	-6.64	107.28	110.60
1	A	1234	C	N1-C2-N3	-6.64	114.55	119.20
1	A	14	U	C6-N1-C2	-6.64	117.02	121.00
1	A	275	G	C8-N9-C1'	-6.64	118.37	127.00
1	A	795	C	N3-C4-C5	-6.64	119.24	121.90
1	A	782	A	N1-C2-N3	6.64	132.62	129.30
1	A	18	C	C6-N1-C2	6.64	122.95	120.30
1	A	109	A	N9-C4-C5	6.64	108.45	105.80
1	A	828	A	C5-N7-C8	-6.64	100.58	103.90
1	A	1282	C	C6-N1-C2	-6.63	117.65	120.30
1	A	171	A	N1-C6-N6	-6.62	114.63	118.60
1	A	873	A	N7-C8-N9	6.62	117.11	113.80
1	A	247	G	C8-N9-C4	6.62	109.05	106.40
1	A	873	A	N3-C4-C5	-6.62	122.17	126.80
1	A	117	G	N1-C2-N3	6.61	127.87	123.90
1	A	529	G	N3-C4-N9	6.61	129.97	126.00
1	A	1483	A	N1-C6-N6	-6.61	114.63	118.60
17	Q	9	VAL	CB-CA-C	-6.61	98.85	111.40
1	A	275	G	C8-N9-C4	6.60	109.04	106.40
1	A	47	C	N3-C4-C5	6.59	124.54	121.90
1	A	700	G	N9-C4-C5	-6.59	102.76	105.40
1	A	1073	U	C5-C6-N1	-6.59	119.41	122.70
1	A	1107	C	C5-C6-N1	6.59	124.29	121.00
1	A	818	G	N3-C2-N2	-6.58	115.29	119.90
1	A	1226	C	C6-N1-C2	6.58	122.93	120.30
1	A	529	G	N3-C4-C5	-6.58	125.31	128.60
1	A	934	C	N1-C2-O2	6.58	122.85	118.90
1	A	784	C	C6-N1-C2	-6.58	117.67	120.30
1	A	824	C	C2-N1-C1'	-6.57	111.57	118.80
1	A	130	A	C2-N3-C4	-6.57	107.31	110.60
1	A	620	C	N1-C2-O2	6.57	122.84	118.90
1	A	1322	C	N3-C4-N4	6.57	122.60	118.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	111	G	N1-C2-N2	6.57	122.11	116.20
1	A	1079	G	N7-C8-N9	6.57	116.38	113.10
1	A	449	C	N3-C4-N4	6.56	122.59	118.00
1	A	543	C	C6-N1-C2	-6.56	117.67	120.30
1	A	644	G	C5-N7-C8	-6.56	101.02	104.30
1	A	7	G	N3-C4-N9	6.56	129.94	126.00
1	A	818	G	C5-C6-N1	-6.56	108.22	111.50
1	A	559	A	N1-C2-N3	6.56	132.58	129.30
1	A	563	A	C2-N3-C4	6.56	113.88	110.60
1	A	1227	A	C4-C5-N7	6.56	113.98	110.70
1	A	1227	A	C2-N3-C4	-6.56	107.32	110.60
1	A	521	G	N1-C6-O6	-6.56	115.97	119.90
1	A	784	C	N3-C4-C5	-6.56	119.28	121.90
1	A	1524	C	N3-C4-N4	6.55	122.59	118.00
1	A	734	G	N1-C6-O6	6.55	123.83	119.90
1	A	365	U	C5-C4-O4	-6.55	121.97	125.90
1	A	251	G	N3-C4-N9	6.55	129.93	126.00
1	A	676	A	C8-N9-C4	6.55	108.42	105.80
1	A	525	C	N3-C2-O2	6.55	126.48	121.90
1	A	1094	G	N9-C4-C5	-6.55	102.78	105.40
1	A	170	U	C5-C6-N1	-6.54	119.43	122.70
1	A	265	G	C2-N3-C4	-6.54	108.63	111.90
1	A	1033	G	C8-N9-C4	-6.54	103.78	106.40
1	A	1414	U	C5-C6-N1	-6.54	119.43	122.70
1	A	403	C	C5-C6-N1	-6.54	117.73	121.00
1	A	1500	A	N9-C4-C5	6.54	108.42	105.80
1	A	620	C	C6-N1-C2	6.53	122.91	120.30
1	A	854	G	C6-C5-N7	-6.53	126.48	130.40
1	A	1249	C	N3-C4-C5	-6.53	119.29	121.90
1	A	1341	U	C2-N1-C1'	-6.53	109.86	117.70
1	A	372	C	C6-N1-C1'	-6.53	112.97	120.80
1	A	1058	G	N7-C8-N9	-6.53	109.84	113.10
1	A	971	G	C5-C6-N1	-6.52	108.24	111.50
1	A	32	A	N3-C4-N9	6.52	132.62	127.40
1	A	770	C	C2-N3-C4	-6.52	116.64	119.90
1	A	742	G	N3-C4-N9	-6.52	122.09	126.00
1	A	859	A	N9-C4-C5	-6.51	103.19	105.80
1	A	1060	C	C2-N1-C1'	6.51	125.97	118.80
1	A	745	C	N3-C4-C5	6.51	124.50	121.90
1	A	1502	A	C4-C5-N7	6.51	113.96	110.70
1	A	885	G	C5-C6-N1	-6.51	108.25	111.50
1	A	365	U	C6-N1-C1'	-6.51	112.09	121.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	151	A	C5-N7-C8	-6.51	100.65	103.90
1	A	651	C	N3-C2-O2	6.51	126.45	121.90
1	A	889	A	N1-C2-N3	6.50	132.55	129.30
1	A	918	A	C6-N1-C2	-6.50	114.70	118.60
1	A	698	G	C4-C5-C6	6.50	122.70	118.80
1	A	229	U	N1-C2-O2	-6.50	118.25	122.80
1	A	1084	G	C6-N1-C2	-6.49	121.20	125.10
1	A	1051	C	N3-C4-C5	-6.49	119.30	121.90
1	A	1390	U	C4-C5-C6	6.48	123.59	119.70
1	A	963	G	C5-C6-N1	-6.48	108.26	111.50
1	A	268	C	C6-N1-C2	6.48	122.89	120.30
1	A	1053	G	C5-N7-C8	6.47	107.54	104.30
1	A	534	U	N3-C2-O2	6.47	126.73	122.20
1	A	760	G	C4-N9-C1'	6.47	134.91	126.50
1	A	111	G	N3-C4-C5	6.46	131.83	128.60
1	A	774	G	N9-C4-C5	-6.46	102.81	105.40
1	A	13	U	N3-C4-O4	6.46	123.92	119.40
1	A	181	G	N3-C4-C5	-6.46	125.37	128.60
1	A	276	G	N1-C6-O6	-6.46	116.03	119.90
1	A	1341	U	N3-C4-O4	-6.46	114.88	119.40
1	A	725	G	C5-C6-N1	6.45	114.73	111.50
1	A	693	G	C5-C6-O6	-6.45	124.73	128.60
1	A	1301	U	N3-C4-C5	-6.45	110.73	114.60
1	A	597	G	N1-C2-N2	-6.44	110.40	116.20
1	A	108	G	N1-C6-O6	6.44	123.76	119.90
1	A	258	G	N1-C6-O6	6.44	123.76	119.90
1	A	644	G	C4-N9-C1'	6.43	134.87	126.50
1	A	77	G	N3-C4-N9	6.43	129.86	126.00
1	A	761	G	C2-N3-C4	-6.43	108.69	111.90
1	A	867	G	N9-C4-C5	-6.42	102.83	105.40
1	A	867	G	N1-C2-N3	6.42	127.75	123.90
1	A	654	G	N1-C2-N2	-6.42	110.42	116.20
1	A	798	G	N1-C2-N2	6.42	121.98	116.20
1	A	825	G	N7-C8-N9	-6.42	109.89	113.10
1	A	561	U	N3-C4-O4	6.42	123.89	119.40
1	A	789	U	C5-C6-N1	6.42	125.91	122.70
1	A	248	C	C2-N3-C4	-6.41	116.69	119.90
1	A	1350	A	C8-N9-C4	-6.41	103.23	105.80
1	A	204	U	C2-N1-C1'	6.41	125.39	117.70
1	A	522	C	N3-C4-N4	-6.41	113.51	118.00
1	A	15	G	N1-C6-O6	6.41	123.74	119.90
1	A	1199	U	C6-N1-C2	-6.40	117.16	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1390	U	C6-N1-C2	-6.40	117.16	121.00
1	A	92	C	C6-N1-C1'	-6.39	113.13	120.80
1	A	1433	A	N1-C2-N3	6.39	132.50	129.30
1	A	635	G	N9-C4-C5	-6.39	102.84	105.40
1	A	807	A	N7-C8-N9	-6.39	110.61	113.80
1	A	1092	A	C5-N7-C8	-6.39	100.71	103.90
1	A	868	C	N3-C4-N4	6.39	122.47	118.00
1	A	870	U	C5-C6-N1	-6.38	119.51	122.70
1	A	721	G	N1-C2-N2	-6.38	110.46	116.20
1	A	1183	A	N1-C6-N6	6.38	122.43	118.60
1	A	390	C	N3-C4-N4	6.38	122.47	118.00
1	A	1099	G	C4-C5-N7	-6.38	108.25	110.80
1	A	32	A	C4-C5-C6	6.38	120.19	117.00
1	A	90	U	C6-N1-C1'	6.38	130.13	121.20
1	A	679	C	N1-C2-O2	-6.38	115.07	118.90
1	A	297	G	C8-N9-C4	-6.38	103.85	106.40
1	A	866	C	N1-C2-N3	6.37	123.66	119.20
1	A	1340	A	C2-N3-C4	-6.37	107.42	110.60
1	A	123	C	N3-C4-C5	-6.37	119.35	121.90
1	A	928	G	C6-C5-N7	-6.37	126.58	130.40
1	A	9	G	C4-C5-N7	6.36	113.34	110.80
1	A	129	U	N1-C2-N3	6.36	118.72	114.90
1	A	618	C	C6-N1-C2	6.36	122.84	120.30
1	A	946	A	N9-C4-C5	6.36	108.34	105.80
1	A	1073	U	C6-N1-C2	6.36	124.82	121.00
1	A	1107	C	N3-C4-C5	-6.36	119.36	121.90
1	A	447	G	N9-C4-C5	-6.36	102.86	105.40
1	A	77	G	C4-C5-N7	6.36	113.34	110.80
1	A	524	G	C5-C6-N1	-6.36	108.32	111.50
1	A	789	U	C6-N1-C2	-6.35	117.19	121.00
1	A	902	G	C8-N9-C4	6.35	108.94	106.40
1	A	639	G	C5-C6-O6	-6.35	124.79	128.60
1	A	269	C	C4-C5-C6	6.34	120.57	117.40
1	A	703	G	C5-N7-C8	6.34	107.47	104.30
1	A	230	G	C4-N9-C1'	6.34	134.74	126.50
1	A	1237	C	C4-C5-C6	6.33	120.57	117.40
1	A	960	U	N1-C2-O2	6.33	127.23	122.80
1	A	28	G	C4-C5-N7	-6.33	108.27	110.80
1	A	671	G	C5-C6-N1	-6.33	108.34	111.50
1	A	839	U	N1-C2-O2	6.33	127.23	122.80
1	A	579	G	C5-N7-C8	-6.32	101.14	104.30
1	A	874	G	C4-C5-N7	6.32	113.33	110.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	194	LEU	CA-CB-CG	6.32	129.84	115.30
1	A	721	G	C5-C6-N1	-6.32	108.34	111.50
9	I	47	LEU	CA-CB-CG	-6.32	100.77	115.30
1	A	924	C	N3-C2-O2	6.32	126.32	121.90
1	A	407	G	C2-N3-C4	-6.31	108.75	111.90
1	A	962	C	C6-N1-C2	6.31	122.82	120.30
1	A	616	G	C5-C6-N1	-6.31	108.35	111.50
1	A	741	G	N3-C4-C5	6.31	131.75	128.60
1	A	154	C	C5-C4-N4	-6.30	115.79	120.20
1	A	830	G	N1-C6-O6	6.30	123.68	119.90
1	A	881	G	N3-C4-N9	6.30	129.78	126.00
1	A	1487	G	C8-N9-C4	-6.30	103.88	106.40
1	A	1497	G	N3-C4-N9	6.29	129.78	126.00
1	A	372	C	C6-N1-C2	6.29	122.82	120.30
1	A	428	G	C8-N9-C4	-6.29	103.88	106.40
1	A	91	C	N3-C4-N4	6.29	122.40	118.00
1	A	342	C	C6-N1-C2	-6.29	117.79	120.30
1	A	1279	A	N7-C8-N9	6.29	116.94	113.80
1	A	1205	U	C2-N1-C1'	6.28	125.24	117.70
1	A	597	G	C6-C5-N7	-6.28	126.63	130.40
1	A	1530	G	C5-C6-N1	-6.28	108.36	111.50
1	A	77	G	N9-C4-C5	-6.28	102.89	105.40
1	A	557	G	N9-C4-C5	6.28	107.91	105.40
1	A	810	C	C5-C4-N4	-6.28	115.81	120.20
1	A	1389	C	C6-N1-C2	6.28	122.81	120.30
1	A	1350	A	N7-C8-N9	6.27	116.94	113.80
1	A	250	A	C8-N9-C4	6.27	108.31	105.80
1	A	297	G	C4-N9-C1'	6.27	134.65	126.50
1	A	721	G	N3-C4-C5	-6.27	125.46	128.60
1	A	774	G	C4-C5-N7	6.27	113.31	110.80
1	A	1074	G	C2-N3-C4	-6.27	108.77	111.90
1	A	1362	C	C6-N1-C2	-6.27	117.79	120.30
1	A	91	C	C5-C4-N4	-6.26	115.81	120.20
1	A	691	G	N7-C8-N9	6.26	116.23	113.10
1	A	788	U	C2-N3-C4	6.26	130.76	127.00
1	A	927	G	N1-C6-O6	6.26	123.66	119.90
1	A	285	G	C5-C6-N1	-6.26	108.37	111.50
1	A	246	A	N1-C2-N3	-6.26	126.17	129.30
1	A	1342	C	N1-C2-O2	-6.26	115.15	118.90
1	A	125	U	N1-C2-N3	6.25	118.65	114.90
1	A	1531	A	N7-C8-N9	6.25	116.92	113.80
1	A	637	G	N1-C6-O6	6.25	123.65	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	92	C	C2-N1-C1'	6.24	125.67	118.80
1	A	795	C	C6-N1-C2	6.24	122.80	120.30
1	A	252	U	C5-C6-N1	-6.24	119.58	122.70
1	A	1327	C	C4-C5-C6	6.24	120.52	117.40
1	A	32	A	C5-C6-N6	-6.23	118.71	123.70
1	A	947	G	N9-C4-C5	-6.23	102.91	105.40
1	A	1068	G	N3-C4-C5	-6.23	125.49	128.60
1	A	1281	U	N1-C2-N3	6.23	118.64	114.90
1	A	981	U	C5-C6-N1	6.22	125.81	122.70
1	A	665	A	C5-N7-C8	-6.22	100.79	103.90
1	A	969	A	N1-C6-N6	6.22	122.33	118.60
1	A	1310	G	C4-N9-C1'	6.22	134.59	126.50
1	A	598	U	N1-C2-O2	-6.22	118.45	122.80
1	A	260	G	N1-C2-N3	6.22	127.63	123.90
1	A	928	G	C4-C5-N7	6.21	113.28	110.80
1	A	1329	A	C6-C5-N7	-6.21	127.95	132.30
1	A	162	A	C8-N9-C4	-6.21	103.32	105.80
1	A	1157	A	C5-C6-N6	6.21	128.67	123.70
1	A	1228	C	C6-N1-C1'	-6.21	113.35	120.80
1	A	1338	G	C4-C5-N7	-6.21	108.32	110.80
1	A	199	G	C2-N3-C4	-6.20	108.80	111.90
1	A	828	A	N1-C6-N6	6.20	122.32	118.60
1	A	1178	G	N9-C4-C5	6.20	107.88	105.40
1	A	1512	U	C4-C5-C6	6.19	123.42	119.70
1	A	201	C	C2-N1-C1'	6.19	125.61	118.80
1	A	1157	A	N1-C6-N6	-6.19	114.89	118.60
1	A	232	G	C5-N7-C8	-6.18	101.21	104.30
1	A	400	C	N3-C2-O2	-6.18	117.57	121.90
1	A	7	G	C8-N9-C1'	-6.18	118.97	127.00
1	A	242	C	C5-C6-N1	-6.18	117.91	121.00
1	A	246	A	N7-C8-N9	-6.18	110.71	113.80
1	A	50	A	C4-C5-C6	-6.18	113.91	117.00
1	A	640	A	N1-C2-N3	6.17	132.39	129.30
1	A	884	U	N1-C2-O2	6.17	127.12	122.80
1	A	558	G	C4-C5-N7	6.16	113.27	110.80
1	A	887	G	N1-C2-N3	6.16	127.60	123.90
1	A	1066	C	C2-N1-C1'	6.16	125.58	118.80
1	A	859	A	C8-N9-C4	6.16	108.27	105.80
1	A	862	C	N3-C4-C5	6.16	124.36	121.90
1	A	673	G	C5-C6-O6	-6.16	124.90	128.60
1	A	1209	C	C6-N1-C2	-6.16	117.84	120.30
1	A	912	C	C4-C5-C6	-6.15	114.32	117.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	190(E)	U	C2-N3-C4	-6.15	123.31	127.00
1	A	1064	G	N3-C2-N2	-6.15	115.59	119.90
1	A	1231	G	N3-C4-N9	6.15	129.69	126.00
24	a	39	G	C8-N9-C4	6.15	108.86	106.40
1	A	284	G	C6-C5-N7	-6.15	126.71	130.40
1	A	1235	U	N1-C2-O2	-6.15	118.50	122.80
1	A	898	G	N1-C2-N3	6.14	127.59	123.90
1	A	848	C	C5-C6-N1	6.14	124.07	121.00
1	A	1442	G	N3-C4-C5	-6.14	125.53	128.60
1	A	285	G	N1-C6-O6	6.14	123.58	119.90
1	A	897	C	N3-C4-C5	6.13	124.35	121.90
1	A	1103	C	C5-C6-N1	-6.13	117.93	121.00
1	A	1487	G	N9-C4-C5	6.13	107.85	105.40
1	A	109	A	C8-N9-C4	-6.13	103.35	105.80
1	A	181	G	C4-C5-C6	6.13	122.48	118.80
1	A	755	G	N1-C6-O6	6.13	123.58	119.90
1	A	900	A	C2-N3-C4	-6.13	107.54	110.60
1	A	257	G	C8-N9-C4	6.12	108.85	106.40
1	A	1493[A]	A	C3'-C2'-C1'	-6.12	96.60	101.50
1	A	1493[B]	A	C3'-C2'-C1'	-6.12	96.60	101.50
1	A	265	G	N9-C4-C5	-6.12	102.95	105.40
1	A	926	G	N3-C4-N9	6.12	129.67	126.00
1	A	970	C	N3-C2-O2	-6.12	117.62	121.90
1	A	1391	U	C5-C6-N1	-6.12	119.64	122.70
1	A	1500	A	C6-N1-C2	-6.12	114.93	118.60
1	A	524	G	N1-C6-O6	6.11	123.57	119.90
1	A	35	G	N1-C6-O6	6.11	123.56	119.90
1	A	1253	G	C6-C5-N7	-6.11	126.74	130.40
1	A	1300	G	N9-C4-C5	6.10	107.84	105.40
1	A	1487	G	C6-N1-C2	-6.10	121.44	125.10
1	A	540	G	N1-C6-O6	6.10	123.56	119.90
1	A	230	G	N1-C2-N2	-6.10	110.71	116.20
1	A	373	A	C5-C6-N6	6.10	128.58	123.70
1	A	1058	G	C6-C5-N7	6.10	134.06	130.40
1	A	1483	A	C5-N7-C8	6.09	106.95	103.90
1	A	782	A	N1-C6-N6	-6.09	114.94	118.60
1	A	130	A	C5-N7-C8	-6.09	100.86	103.90
1	A	976	G	C2-N3-C4	-6.09	108.86	111.90
1	A	910	C	C2-N3-C4	-6.08	116.86	119.90
1	A	1531	A	C5-C6-N6	-6.08	118.83	123.70
1	A	144	G	C6-C5-N7	-6.08	126.75	130.40
1	A	335	C	C5-C6-N1	-6.08	117.96	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	277	C	N3-C4-C5	6.07	124.33	121.90
1	A	768	A	N7-C8-N9	-6.07	110.77	113.80
8	H	38	ILE	CB-CA-C	-6.07	99.46	111.60
1	A	115	G	C5-C6-N1	6.07	114.53	111.50
1	A	654	G	N1-C2-N3	6.07	127.54	123.90
1	A	174	C	C5-C4-N4	-6.06	115.95	120.20
1	A	733	A	C2-N3-C4	-6.06	107.57	110.60
1	A	833	U	N3-C2-O2	-6.05	117.96	122.20
1	A	812	C	C6-N1-C2	-6.05	117.88	120.30
1	A	1488	G	C5-N7-C8	6.05	107.32	104.30
1	A	127	G	N3-C4-C5	6.04	131.62	128.60
1	A	741	G	C4-C5-N7	-6.04	108.38	110.80
1	A	631	G	C4-N9-C1'	6.04	134.35	126.50
1	A	586	C	N3-C4-C5	6.03	124.31	121.90
1	A	1502	A	C6-C5-N7	-6.03	128.08	132.30
1	A	1237	C	N3-C4-C5	-6.03	119.49	121.90
1	A	742	G	N1-C2-N2	6.03	121.63	116.20
1	A	1079	G	N9-C4-C5	6.03	107.81	105.40
1	A	263	A	N1-C6-N6	-6.03	114.98	118.60
1	A	78	G	N1-C6-O6	6.03	123.52	119.90
1	A	1029	C	C6-N1-C2	-6.03	117.89	120.30
8	H	12	ARG	NE-CZ-NH1	-6.03	117.29	120.30
1	A	300	A	C4-C5-C6	6.02	120.01	117.00
1	A	868	C	N3-C2-O2	6.02	126.12	121.90
1	A	260	G	C4-C5-C6	6.02	122.41	118.80
1	A	363	A	C2-N3-C4	-6.02	107.59	110.60
1	A	1487	G	C4-N9-C1'	6.02	134.32	126.50
1	A	572	A	C6-N1-C2	-6.01	114.99	118.60
1	A	1505	G	N3-C2-N2	-6.01	115.69	119.90
1	A	1399	C	C6-N1-C2	-6.00	117.90	120.30
1	A	447	G	C6-C5-N7	-6.00	126.80	130.40
1	A	570	G	N9-C4-C5	6.00	107.80	105.40
1	A	1497	G	C8-N9-C1'	-6.00	119.20	127.00
1	A	852	G	C8-N9-C4	6.00	108.80	106.40
1	A	1337	G	N1-C6-O6	5.99	123.50	119.90
1	A	854	G	C2-N3-C4	-5.99	108.91	111.90
1	A	873	A	N9-C4-C5	5.99	108.19	105.80
1	A	1084	G	C5-C6-O6	5.98	132.19	128.60
1	A	79	G	N7-C8-N9	5.98	116.09	113.10
1	A	145	G	N1-C6-O6	5.97	123.48	119.90
1	A	21	G	N3-C4-N9	5.97	129.58	126.00
1	A	607	A	C5-C6-N1	-5.97	114.71	117.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	893	C	C2-N3-C4	5.97	122.89	119.90
1	A	896	C	C6-N1-C2	-5.97	117.91	120.30
1	A	1491	G	N3-C2-N2	-5.97	115.72	119.90
1	A	374	A	C8-N9-C4	5.97	108.19	105.80
1	A	1074	G	C4-C5-C6	5.97	122.38	118.80
1	A	1530	G	N3-C2-N2	-5.97	115.72	119.90
1	A	1325	C	C6-N1-C2	-5.97	117.91	120.30
1	A	1353	G	C2-N3-C4	5.96	114.88	111.90
1	A	117	G	C4-C5-N7	5.96	113.19	110.80
1	A	944	G	N1-C6-O6	-5.96	116.32	119.90
1	A	259	G	C4-C5-C6	5.96	122.38	118.80
1	A	786	G	N1-C6-O6	5.96	123.47	119.90
1	A	1531	A	C8-N9-C4	-5.96	103.42	105.80
1	A	768	A	N1-C6-N6	5.96	122.17	118.60
1	A	774	G	C5-C6-O6	-5.95	125.03	128.60
1	A	856	C	C4-C5-C6	5.95	120.38	117.40
1	A	1094	G	C6-C5-N7	-5.95	126.83	130.40
1	A	349	A	N1-C6-N6	-5.95	115.03	118.60
1	A	651	C	N3-C4-C5	5.95	124.28	121.90
1	A	712	A	N1-C2-N3	5.95	132.27	129.30
1	A	767	A	N9-C4-C5	5.95	108.18	105.80
1	A	946	A	C5-C6-N1	5.95	120.67	117.70
1	A	1531	A	C5-N7-C8	-5.95	100.93	103.90
1	A	38	G	C8-N9-C1'	5.94	134.72	127.00
1	A	170	U	N1-C2-O2	-5.94	118.64	122.80
1	A	1089	G	C8-N9-C4	-5.94	104.03	106.40
1	A	1439	C	N3-C4-C5	-5.94	119.53	121.90
1	A	1307	U	N1-C2-O2	5.94	126.95	122.80
17	Q	31	LEU	CA-CB-CG	-5.94	101.65	115.30
1	A	15	G	N9-C4-C5	-5.93	103.03	105.40
1	A	250	A	N1-C6-N6	5.93	122.16	118.60
1	A	654	G	C2-N3-C4	-5.93	108.93	111.90
1	A	853	G	N3-C4-N9	5.93	129.56	126.00
1	A	807	A	C8-N9-C4	5.93	108.17	105.80
8	H	135	CYS	CA-CB-SG	-5.93	103.32	114.00
1	A	1234	C	N3-C4-C5	5.93	124.27	121.90
1	A	265	G	C6-C5-N7	-5.93	126.84	130.40
1	A	898	G	C2-N3-C4	-5.93	108.94	111.90
1	A	190(K)	G	C8-N9-C4	5.92	108.77	106.40
1	A	542	G	N1-C6-O6	-5.92	116.35	119.90
1	A	774	G	C6-C5-N7	-5.92	126.85	130.40
1	A	791	G	C5-C6-N1	-5.92	108.54	111.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	718	G	C5-C6-O6	-5.92	125.05	128.60
1	A	920	U	N1-C2-N3	5.92	118.45	114.90
1	A	618	C	N3-C4-N4	-5.92	113.86	118.00
1	A	674	G	C2-N3-C4	-5.92	108.94	111.90
1	A	1529	G	N3-C2-N2	-5.91	115.76	119.90
1	A	711	G	C2-N3-C4	-5.91	108.94	111.90
1	A	1084	G	N1-C2-N3	5.91	127.45	123.90
1	A	136	C	C6-N1-C2	-5.91	117.94	120.30
1	A	931	C	C5-C6-N1	-5.91	118.05	121.00
1	A	1335	C	N1-C2-N3	-5.91	115.06	119.20
1	A	1507	A	N1-C2-N3	5.91	132.25	129.30
1	A	38	G	C4-N9-C1'	-5.91	118.82	126.50
1	A	144	G	N3-C2-N2	-5.91	115.77	119.90
1	A	553	A	C8-N9-C4	5.91	108.16	105.80
1	A	1300	G	C4-C5-N7	-5.91	108.44	110.80
1	A	328	C	P-O3'-C3'	5.90	126.78	119.70
1	A	317	G	C2-N3-C4	-5.90	108.95	111.90
1	A	1529	G	N1-C2-N3	5.90	127.44	123.90
1	A	1530	G	N1-C2-N2	5.90	121.51	116.20
24	a	37	A	C2-N3-C4	-5.90	107.65	110.60
2	B	7	VAL	N-CA-C	5.90	126.93	111.00
1	A	447	G	C4-N9-C1'	5.90	134.17	126.50
1	A	610	G	N1-C6-O6	-5.90	116.36	119.90
1	A	799	G	C4-C5-N7	5.90	113.16	110.80
1	A	1301	U	N3-C4-O4	5.90	123.53	119.40
1	A	924	C	N3-C4-C5	-5.89	119.54	121.90
1	A	104	G	C5-C6-O6	-5.89	125.06	128.60
1	A	854	G	C4-N9-C1'	5.89	134.15	126.50
1	A	1214	C	C2-N1-C1'	5.88	125.27	118.80
24	a	37	A	C5-C6-N1	-5.88	114.76	117.70
1	A	1099	G	C8-N9-C4	-5.88	104.05	106.40
8	H	136	GLU	N-CA-C	-5.88	95.13	111.00
1	A	284	G	C2-N3-C4	-5.88	108.96	111.90
1	A	686	U	C5-C6-N1	-5.88	119.76	122.70
1	A	1534	C	N1-C2-O2	5.88	122.42	118.90
1	A	1530	G	C4-N9-C1'	-5.87	118.86	126.50
1	A	650	G	N1-C6-O6	5.87	123.42	119.90
1	A	963	G	C6-C5-N7	-5.87	126.88	130.40
1	A	1253	G	N1-C6-O6	5.87	123.42	119.90
1	A	1467	G	C8-N9-C4	-5.87	104.05	106.40
1	A	90	U	N3-C2-O2	-5.87	118.09	122.20
1	A	1502	A	N3-C4-C5	5.87	130.91	126.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	122	G	N1-C6-O6	5.86	123.42	119.90
1	A	400	C	C6-N1-C2	5.86	122.65	120.30
1	A	53	A	C6-N1-C2	-5.86	115.08	118.60
1	A	449	C	C2-N1-C1'	5.86	125.25	118.80
1	A	599	C	C2-N3-C4	-5.86	116.97	119.90
1	A	875	C	C2-N3-C4	-5.86	116.97	119.90
1	A	552	U	N3-C4-O4	-5.86	115.30	119.40
1	A	880	C	C6-N1-C2	5.85	122.64	120.30
1	A	1062	U	C5-C4-O4	5.85	129.41	125.90
1	A	1452	C	C6-N1-C2	5.85	122.64	120.30
1	A	658	G	N1-C2-N3	5.85	127.41	123.90
1	A	1310	G	N1-C2-N2	-5.85	110.93	116.20
1	A	1064	G	C6-N1-C2	-5.85	121.59	125.10
1	A	251	G	N3-C4-C5	-5.85	125.68	128.60
1	A	1414	U	C4-C5-C6	5.85	123.21	119.70
1	A	607	A	C6-N1-C2	5.84	122.11	118.60
1	A	1108	G	C4-N9-C1'	5.84	134.10	126.50
1	A	1527	C	N3-C4-N4	5.84	122.09	118.00
1	A	579	G	C6-C5-N7	-5.84	126.89	130.40
1	A	975	A	C6-N1-C2	5.84	122.10	118.60
1	A	796	C	C4-C5-C6	5.84	120.32	117.40
1	A	481	G	C4-N9-C1'	5.84	134.09	126.50
1	A	741	G	C6-C5-N7	5.84	133.90	130.40
1	A	1335	C	C5-C4-N4	-5.84	116.11	120.20
1	A	1483	A	C2-N3-C4	5.84	113.52	110.60
20	T	13	LEU	CB-CA-C	-5.84	99.11	110.20
1	A	1438	G	C8-N9-C4	5.83	108.73	106.40
1	A	1523	G	N3-C2-N2	-5.83	115.82	119.90
1	A	1487	G	C4-C5-C6	5.83	122.30	118.80
1	A	1190	G	C4-C5-C6	5.82	122.30	118.80
1	A	864	A	C4-C5-N7	-5.82	107.79	110.70
1	A	656	C	N3-C4-C5	5.82	124.23	121.90
1	A	852	G	N9-C4-C5	-5.82	103.07	105.40
1	A	190(G)	G	C4-C5-C6	5.82	122.29	118.80
1	A	679	C	C5-C6-N1	-5.82	118.09	121.00
1	A	1249	C	C5-C6-N1	5.82	123.91	121.00
1	A	1482	G	C8-N9-C1'	-5.82	119.44	127.00
1	A	1510	U	N1-C2-O2	5.82	126.87	122.80
1	A	129	U	C5-C4-O4	5.82	129.39	125.90
1	A	865	A	C5-C6-N1	5.82	120.61	117.70
1	A	344	A	N7-C8-N9	5.81	116.71	113.80
1	A	693	G	C6-C5-N7	-5.81	126.91	130.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	127	G	N9-C4-C5	-5.81	103.08	105.40
1	A	854	G	N1-C2-N3	5.81	127.39	123.90
1	A	297	G	C5-C6-O6	5.80	132.08	128.60
1	A	707	C	C2-N1-C1'	-5.80	112.42	118.80
1	A	38	G	N3-C4-C5	5.80	131.50	128.60
1	A	235	C	C5-C6-N1	-5.80	118.10	121.00
1	A	242	C	C6-N1-C2	5.80	122.62	120.30
1	A	259	G	C5-C6-N1	-5.80	108.60	111.50
1	A	565	U	C6-N1-C2	5.80	124.48	121.00
1	A	676	A	N7-C8-N9	-5.80	110.90	113.80
1	A	925	G	N3-C4-C5	-5.80	125.70	128.60
1	A	860	A	N1-C2-N3	5.79	132.20	129.30
1	A	1200	C	N3-C4-N4	5.79	122.06	118.00
1	A	142	G	N3-C4-C5	-5.79	125.70	128.60
1	A	251	G	C8-N9-C1'	-5.79	119.47	127.00
1	A	1303	C	N3-C4-N4	-5.79	113.95	118.00
1	A	925	G	N3-C4-N9	5.79	129.47	126.00
1	A	519	C	C6-N1-C2	5.78	122.61	120.30
1	A	944	G	N9-C4-C5	5.78	107.71	105.40
1	A	1281	U	C6-N1-C1'	5.78	129.29	121.20
1	A	597	G	C8-N9-C1'	-5.78	119.49	127.00
1	A	760	G	C4-C5-C6	5.78	122.27	118.80
1	A	258	G	C2-N3-C4	-5.78	109.01	111.90
1	A	332	G	C4-C5-N7	5.78	113.11	110.80
1	A	566	G	N3-C4-N9	5.78	129.47	126.00
1	A	552	U	N1-C2-N3	5.77	118.36	114.90
1	A	644	G	N7-C8-N9	5.77	115.99	113.10
1	A	831	U	C5-C4-O4	5.77	129.36	125.90
1	A	629	G	N3-C4-C5	-5.77	125.72	128.60
1	A	716	A	C5-C6-N1	5.77	120.58	117.70
1	A	779	C	C2-N3-C4	-5.77	117.02	119.90
1	A	945	G	C4-C5-C6	-5.77	115.34	118.80
1	A	1153	C	C6-N1-C2	5.77	122.61	120.30
1	A	910	C	C5-C6-N1	-5.76	118.12	121.00
1	A	180	U	C5-C4-O4	-5.76	122.44	125.90
1	A	259	G	C8-N9-C4	-5.76	104.10	106.40
1	A	68	G	N7-C8-N9	-5.76	110.22	113.10
1	A	752	G	N1-C6-O6	5.76	123.35	119.90
1	A	1231	G	C4-N9-C1'	5.75	133.98	126.50
1	A	73	C	C2-N3-C4	5.75	122.78	119.90
1	A	618	C	C6-N1-C1'	5.75	127.70	120.80
1	A	414	A	N1-C2-N3	5.75	132.17	129.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	799	G	C5-C6-O6	-5.74	125.15	128.60
1	A	1227	A	N3-C4-C5	5.74	130.82	126.80
1	A	15	G	C8-N9-C4	5.74	108.70	106.40
1	A	1129	C	C5-C6-N1	5.74	123.87	121.00
1	A	130	A	N1-C6-N6	5.74	122.04	118.60
1	A	181	G	C8-N9-C1'	-5.74	119.54	127.00
1	A	292	G	N1-C6-O6	5.74	123.34	119.90
1	A	725	G	C5-C6-O6	-5.73	125.16	128.60
1	A	251	G	N3-C2-N2	5.73	123.91	119.90
1	A	1373	G	C8-N9-C4	-5.73	104.11	106.40
1	A	265	G	C8-N9-C1'	-5.73	119.55	127.00
1	A	637	G	C8-N9-C1'	-5.73	119.55	127.00
1	A	1055	A	C2-N3-C4	5.73	113.46	110.60
1	A	50	A	N7-C8-N9	-5.73	110.94	113.80
1	A	911	U	C2-N1-C1'	-5.73	110.83	117.70
1	A	635	G	N1-C2-N2	-5.72	111.05	116.20
1	A	875	C	C5-C6-N1	-5.72	118.14	121.00
1	A	905	U	C4-C5-C6	5.72	123.13	119.70
1	A	154	C	C6-N1-C1'	-5.72	113.94	120.80
1	A	558	G	C6-C5-N7	-5.72	126.97	130.40
1	A	693	G	N9-C4-C5	-5.72	103.11	105.40
1	A	745	C	C2-N3-C4	-5.72	117.04	119.90
1	A	326	G	N3-C4-N9	-5.72	122.57	126.00
1	A	21	G	C8-N9-C1'	-5.71	119.57	127.00
1	A	125	U	N3-C2-O2	-5.71	118.20	122.20
1	A	32	A	C6-C5-N7	-5.71	128.30	132.30
1	A	373	A	N1-C6-N6	-5.71	115.17	118.60
1	A	674	G	N1-C6-O6	5.71	123.32	119.90
1	A	698	G	C8-N9-C4	-5.71	104.12	106.40
1	A	1221	G	C5-C6-N1	-5.71	108.65	111.50
1	A	1531	A	C4-C5-N7	5.71	113.55	110.70
1	A	711	G	C5-N7-C8	-5.70	101.45	104.30
1	A	540	G	C5-C6-O6	-5.70	125.18	128.60
1	A	127	G	C5-C6-O6	-5.70	125.18	128.60
1	A	704	A	N7-C8-N9	5.70	116.65	113.80
1	A	963	G	N7-C8-N9	5.70	115.95	113.10
1	A	631	G	N7-C8-N9	5.70	115.95	113.10
1	A	779	C	C6-N1-C2	5.70	122.58	120.30
1	A	407	G	N3-C4-C5	5.70	131.45	128.60
1	A	1134	G	C8-N9-C4	-5.70	104.12	106.40
1	A	144	G	N3-C4-C5	5.70	131.45	128.60
1	A	232	G	C8-N9-C1'	-5.70	119.59	127.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	677	U	C6-N1-C2	-5.69	117.58	121.00
1	A	920	U	C6-N1-C2	-5.69	117.58	121.00
1	A	240	C	C6-N1-C2	5.69	122.58	120.30
1	A	279	A	C2-N3-C4	-5.69	107.75	110.60
1	A	1415	G	C8-N9-C4	5.69	108.68	106.40
1	A	1062	U	C6-N1-C2	-5.69	117.59	121.00
1	A	673	G	C4-C5-N7	5.68	113.07	110.80
1	A	856	C	N1-C2-N3	5.68	123.18	119.20
1	A	440	A	N1-C2-N3	5.68	132.14	129.30
1	A	1092	A	C8-N9-C1'	-5.68	117.48	127.70
1	A	91	C	C6-N1-C1'	-5.67	113.99	120.80
1	A	1084	G	N9-C4-C5	5.67	107.67	105.40
1	A	1329	A	N9-C4-C5	-5.67	103.53	105.80
1	A	1504	G	N3-C4-N9	5.67	129.40	126.00
1	A	753	A	C4-C5-N7	-5.67	107.86	110.70
1	A	858	G	C4-C5-N7	-5.67	108.53	110.80
1	A	1364	U	C6-N1-C2	5.67	124.40	121.00
1	A	1310	G	C6-C5-N7	-5.66	127.00	130.40
1	A	1381	U	C2-N1-C1'	5.66	124.50	117.70
1	A	204	U	C5-C6-N1	5.66	125.53	122.70
1	A	121	C	C6-N1-C2	5.66	122.56	120.30
1	A	1074	G	N1-C6-O6	5.66	123.30	119.90
15	O	77	ARG	NE-CZ-NH2	5.66	123.13	120.30
1	A	1388	C	N1-C2-O2	-5.66	115.51	118.90
1	A	597	G	C4-N9-C1'	5.66	133.85	126.50
1	A	1074	G	C6-C5-N7	-5.66	127.01	130.40
1	A	1524	C	N1-C2-N3	5.66	123.16	119.20
1	A	1058	G	C4-C5-N7	-5.65	108.54	110.80
1	A	637	G	C6-C5-N7	-5.65	127.01	130.40
1	A	971	G	C2-N3-C4	-5.65	109.08	111.90
1	A	1143	G	C4-C5-N7	5.65	113.06	110.80
1	A	830	G	N3-C2-N2	-5.65	115.95	119.90
1	A	21	G	N9-C4-C5	-5.65	103.14	105.40
1	A	330	C	N1-C2-O2	-5.65	115.51	118.90
1	A	1394	A	C5-C6-N1	5.64	120.52	117.70
1	A	1433	A	C6-N1-C2	-5.64	115.21	118.60
5	E	63	ARG	NE-CZ-NH2	-5.64	117.48	120.30
1	A	1442	G	N3-C4-N9	5.64	129.38	126.00
1	A	1505	G	C4-C5-N7	-5.64	108.55	110.80
1	A	902	G	N7-C8-N9	-5.64	110.28	113.10
1	A	1120	G	N3-C4-C5	-5.64	125.78	128.60
1	A	1286	A	C8-N9-C4	-5.63	103.55	105.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1438	G	C5-C6-O6	-5.63	125.22	128.60
1	A	111	G	C8-N9-C1'	5.63	134.32	127.00
1	A	393	A	C2-N3-C4	-5.62	107.79	110.60
1	A	1190	G	N3-C4-C5	-5.62	125.79	128.60
1	A	125	U	C4-C5-C6	5.62	123.07	119.70
1	A	435	C	N3-C4-C5	-5.62	119.65	121.90
1	A	933	G	C6-C5-N7	-5.62	127.03	130.40
1	A	1301	U	N1-C2-N3	5.62	118.27	114.90
1	A	1527	C	C2-N1-C1'	5.62	124.98	118.80
1	A	383	A	C8-N9-C4	-5.62	103.55	105.80
1	A	497	A	N1-C6-N6	-5.62	115.23	118.60
1	A	656	C	C5-C4-N4	-5.62	116.27	120.20
1	A	216	G	N1-C6-O6	-5.62	116.53	119.90
1	A	1077	G	C4-C5-C6	5.61	122.17	118.80
1	A	162	A	N1-C6-N6	-5.61	115.23	118.60
1	A	816	A	N7-C8-N9	-5.61	111.00	113.80
1	A	1531	A	C5-C6-N1	5.61	120.50	117.70
1	A	270	A	N1-C6-N6	5.61	121.96	118.60
1	A	190(G)	G	C6-C5-N7	-5.60	127.04	130.40
1	A	787	A	N7-C8-N9	5.60	116.60	113.80
1	A	588	G	C8-N9-C4	5.60	108.64	106.40
1	A	816	A	N3-C4-N9	-5.60	122.92	127.40
1	A	559	A	N7-C8-N9	5.60	116.60	113.80
1	A	1220	G	N1-C6-O6	5.60	123.26	119.90
1	A	1392	G	C4-C5-N7	5.60	113.04	110.80
1	A	21	G	N7-C8-N9	-5.59	110.30	113.10
1	A	120	A	N7-C8-N9	-5.59	111.00	113.80
1	A	1392	G	C4-N9-C1'	5.59	133.77	126.50
1	A	1343	G	C4-C5-N7	5.59	113.04	110.80
1	A	204	U	C6-N1-C1'	-5.59	113.38	121.20
24	a	39	G	N3-C4-C5	5.59	131.40	128.60
1	A	38	G	C5-C6-N1	-5.59	108.71	111.50
1	A	831	U	N3-C2-O2	-5.59	118.29	122.20
1	A	122	G	C2-N3-C4	-5.59	109.11	111.90
1	A	497	A	C4-C5-N7	-5.59	107.91	110.70
1	A	675	A	C2-N3-C4	-5.59	107.81	110.60
1	A	767	A	N1-C6-N6	-5.58	115.25	118.60
1	A	113	G	C6-C5-N7	-5.58	127.05	130.40
1	A	146	G	C5-C6-O6	-5.58	125.25	128.60
1	A	741	G	C8-N9-C1'	5.58	134.26	127.00
1	A	1186	G	N1-C6-O6	5.58	123.25	119.90
1	A	634	C	C5-C4-N4	5.58	124.11	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	297	G	C4-C5-C6	5.58	122.15	118.80
1	A	190(B)	C	C6-N1-C2	-5.58	118.07	120.30
17	Q	99	SER	N-CA-C	5.58	126.06	111.00
1	A	1075	C	C6-N1-C2	5.57	122.53	120.30
1	A	761	G	C6-C5-N7	-5.57	127.06	130.40
1	A	644	G	N3-C4-N9	5.57	129.34	126.00
1	A	696	A	N1-C6-N6	5.57	121.94	118.60
1	A	1112	C	N3-C2-O2	-5.57	118.00	121.90
1	A	79	G	C8-N9-C4	-5.56	104.17	106.40
1	A	265	G	N1-C2-N3	5.56	127.24	123.90
1	A	1253	G	C8-N9-C4	-5.56	104.18	106.40
1	A	332	G	N3-C2-N2	-5.56	116.01	119.90
1	A	373	A	N1-C2-N3	5.56	132.08	129.30
1	A	1425	U	C5-C4-O4	5.56	129.23	125.90
1	A	252	U	C4-C5-C6	5.55	123.03	119.70
1	A	1068	G	C6-C5-N7	-5.55	127.07	130.40
1	A	863	U	N1-C2-O2	-5.55	118.92	122.80
1	A	931	C	C2-N3-C4	-5.55	117.12	119.90
1	A	201	C	N1-C2-O2	5.55	122.23	118.90
1	A	52	G	N1-C2-N2	-5.55	111.21	116.20
1	A	55	A	C6-N1-C2	-5.55	115.27	118.60
1	A	580	U	C4-C5-C6	5.55	123.03	119.70
1	A	1500	A	C8-N9-C4	-5.54	103.58	105.80
1	A	389	A	C4-C5-C6	5.54	119.77	117.00
1	A	577	G	C8-N9-C4	5.54	108.62	106.40
1	A	811	C	C6-N1-C1'	-5.54	114.15	120.80
1	A	881	G	N7-C8-N9	-5.54	110.33	113.10
20	T	13	LEU	CB-CG-CD1	5.54	120.42	111.00
1	A	1415	G	C8-N9-C1'	-5.54	119.80	127.00
1	A	747	C	N1-C2-O2	-5.54	115.58	118.90
1	A	1322	C	C6-N1-C2	-5.54	118.08	120.30
1	A	9	G	N9-C4-C5	-5.54	103.19	105.40
1	A	422	C	N1-C2-N3	-5.54	115.32	119.20
1	A	1322	C	C6-N1-C1'	-5.54	114.16	120.80
1	A	232	G	N3-C4-N9	5.54	129.32	126.00
1	A	893	C	N1-C2-N3	-5.54	115.33	119.20
1	A	190(B)	C	C5-C6-N1	5.53	123.77	121.00
1	A	650	G	N7-C8-N9	-5.53	110.33	113.10
1	A	811	C	C5-C4-N4	-5.53	116.33	120.20
1	A	1293	G	N3-C4-N9	-5.53	122.68	126.00
1	A	924	C	C2-N3-C4	5.53	122.67	119.90
1	A	1529	G	C4-N9-C1'	5.53	133.69	126.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	451	A	N1-C2-N3	5.53	132.06	129.30
1	A	926	G	C4-C5-N7	-5.53	108.59	110.80
1	A	829	G	N9-C4-C5	-5.53	103.19	105.40
1	A	1157	A	N9-C4-C5	5.53	108.01	105.80
1	A	27	G	N1-C6-O6	5.53	123.22	119.90
1	A	135	C	C2-N1-C1'	-5.53	112.72	118.80
1	A	889	A	C8-N9-C4	-5.53	103.59	105.80
1	A	1394	A	N1-C6-N6	5.53	121.92	118.60
1	A	1084	G	N3-C4-N9	5.52	129.31	126.00
1	A	628	G	C4-N9-C1'	5.52	133.68	126.50
1	A	283	C	N3-C4-N4	5.52	121.86	118.00
1	A	357	G	C5-C6-O6	5.52	131.91	128.60
1	A	650	G	C2-N3-C4	-5.52	109.14	111.90
1	A	711	G	C8-N9-C4	-5.52	104.19	106.40
1	A	864	A	C8-N9-C4	-5.52	103.59	105.80
1	A	867	G	C5-C6-N1	-5.51	108.74	111.50
1	A	245	C	C5-C4-N4	-5.51	116.34	120.20
1	A	761	G	N1-C2-N3	5.51	127.21	123.90
1	A	962	C	N3-C4-C5	5.51	124.10	121.90
1	A	969	A	C6-C5-N7	-5.51	128.44	132.30
1	A	281	G	C4-C5-N7	5.51	113.00	110.80
1	A	778	G	N1-C2-N3	-5.51	120.60	123.90
1	A	1249	C	N3-C4-N4	5.51	121.85	118.00
1	A	142	G	C5-C6-N1	5.50	114.25	111.50
1	A	767	A	C5-C6-N6	5.50	128.10	123.70
1	A	1280	A	N9-C4-C5	5.50	108.00	105.80
1	A	117	G	N3-C4-N9	5.50	129.30	126.00
16	P	58	TYR	CB-CA-C	-5.50	99.40	110.40
1	A	145	G	C5-C6-N1	-5.50	108.75	111.50
1	A	973	G	N7-C8-N9	-5.50	110.35	113.10
1	A	264	U	C5-C4-O4	5.50	129.20	125.90
1	A	1392	G	C8-N9-C1'	-5.49	119.86	127.00
1	A	1140	C	C6-N1-C2	-5.49	118.10	120.30
1	A	107	G	N1-C6-O6	5.49	123.19	119.90
1	A	583	A	C8-N9-C4	5.49	108.00	105.80
1	A	583	A	C2-N3-C4	-5.49	107.85	110.60
1	A	175	C	C5-C6-N1	-5.49	118.26	121.00
1	A	1083	U	C6-N1-C2	5.49	124.29	121.00
1	A	372	C	N3-C4-N4	5.49	121.84	118.00
1	A	1322	C	C5-C6-N1	5.49	123.74	121.00
1	A	976	G	N3-C4-N9	-5.49	122.71	126.00
1	A	1417	G	N3-C4-C5	-5.49	125.86	128.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	675	A	C5-C6-N6	5.48	128.09	123.70
1	A	77	G	C5-C6-O6	-5.48	125.31	128.60
1	A	279	A	N1-C2-N3	5.48	132.04	129.30
1	A	301	G	C4-N9-C1'	5.48	133.62	126.50
1	A	20	U	C4-C5-C6	5.48	122.99	119.70
1	A	1373	G	C4-C5-N7	-5.48	108.61	110.80
1	A	1083	U	N3-C4-O4	5.47	123.23	119.40
1	A	73	C	N3-C2-O2	5.47	125.73	121.90
1	A	1235	U	C6-N1-C2	-5.47	117.72	121.00
1	A	1374	A	C8-N9-C4	-5.47	103.61	105.80
1	A	570	G	C6-N1-C2	-5.47	121.82	125.10
1	A	686	U	C4-C5-C6	5.47	122.98	119.70
1	A	260	G	C2-N3-C4	-5.47	109.17	111.90
1	A	678	U	C5-C4-O4	-5.47	122.62	125.90
1	A	132	C	C5-C6-N1	-5.46	118.27	121.00
1	A	1199	U	N1-C2-N3	5.46	118.18	114.90
1	A	300	A	C8-N9-C4	-5.46	103.61	105.80
1	A	745	C	C5-C6-N1	-5.46	118.27	121.00
1	A	816	A	C2-N3-C4	-5.46	107.87	110.60
1	A	860	A	C4-C5-C6	5.46	119.73	117.00
1	A	335	C	C6-N1-C2	5.46	122.48	120.30
1	A	734	G	N7-C8-N9	5.46	115.83	113.10
1	A	59	A	C5-C6-N1	5.46	120.43	117.70
1	A	419	C	C6-N1-C2	5.45	122.48	120.30
1	A	1368	G	N3-C4-C5	-5.45	125.87	128.60
1	A	174	C	C2-N1-C1'	5.45	124.80	118.80
1	A	180	U	C6-N1-C1'	-5.45	113.57	121.20
1	A	366	C	C6-N1-C2	-5.45	118.12	120.30
1	A	853	G	C4-N9-C1'	5.45	133.59	126.50
4	D	12	CYS	CA-CB-SG	5.45	123.81	114.00
1	A	34	C	N1-C2-O2	-5.45	115.63	118.90
1	A	43	C	C5-C6-N1	-5.45	118.28	121.00
1	A	1434	A	C8-N9-C4	5.45	107.98	105.80
1	A	32	A	N1-C6-N6	5.45	121.87	118.60
1	A	232	G	C4-N9-C1'	5.45	133.58	126.50
1	A	280	C	N3-C4-N4	-5.45	114.19	118.00
1	A	1098	C	C6-N1-C2	5.45	122.48	120.30
1	A	1240	U	N3-C2-O2	-5.45	118.39	122.20
1	A	1354	C	C6-N1-C2	-5.45	118.12	120.30
1	A	1494	G	N3-C4-N9	5.45	129.27	126.00
1	A	70	G	N3-C4-C5	5.45	131.32	128.60
1	A	394	G	C5-C6-O6	5.44	131.87	128.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	953	G	N9-C4-C5	-5.44	103.22	105.40
1	A	1323	G	C5-C6-N1	-5.44	108.78	111.50
1	A	1506	U	C5-C4-O4	-5.44	122.64	125.90
1	A	26	A	N1-C2-N3	5.44	132.02	129.30
1	A	265	G	N3-C2-N2	5.43	123.70	119.90
1	A	1055	A	N9-C4-C5	5.43	107.97	105.80
1	A	1527	C	C6-N1-C1'	-5.43	114.28	120.80
1	A	111	G	N3-C2-N2	-5.43	116.10	119.90
1	A	1493[A]	A	C4-C5-N7	5.43	113.41	110.70
1	A	1493[B]	A	C4-C5-N7	5.43	113.41	110.70
1	A	552	U	N3-C4-C5	5.43	117.86	114.60
1	A	250	A	N9-C4-C5	-5.42	103.63	105.80
1	A	278	G	C5-C6-O6	5.42	131.85	128.60
1	A	1502	A	N3-C4-N9	-5.42	123.06	127.40
1	A	608	A	C2-N3-C4	-5.42	107.89	110.60
1	A	648	A	C6-N1-C2	-5.42	115.35	118.60
1	A	724	G	N1-C6-O6	5.42	123.15	119.90
1	A	924	C	N1-C2-O2	-5.42	115.65	118.90
1	A	120	A	C5-N7-C8	5.42	106.61	103.90
1	A	317	G	N3-C4-C5	5.42	131.31	128.60
1	A	628	G	C8-N9-C1'	-5.42	119.96	127.00
1	A	675	A	C5-C6-N1	-5.42	114.99	117.70
1	A	230	G	N3-C4-N9	5.42	129.25	126.00
1	A	530	G	N1-C6-O6	-5.42	116.65	119.90
1	A	1343	G	N7-C8-N9	5.42	115.81	113.10
1	A	1405	G	N3-C4-N9	-5.42	122.75	126.00
1	A	107	G	C6-C5-N7	-5.42	127.15	130.40
18	R	76	LEU	CA-CB-CG	-5.41	102.85	115.30
1	A	259	G	C4-N9-C1'	5.41	133.53	126.50
1	A	874	G	C2-N3-C4	-5.41	109.19	111.90
1	A	881	G	N1-C6-O6	5.41	123.15	119.90
1	A	400	C	C5-C6-N1	-5.41	118.30	121.00
1	A	671	G	N1-C6-O6	5.41	123.14	119.90
1	A	1125	U	N3-C2-O2	5.41	125.99	122.20
1	A	107	G	N9-C4-C5	-5.41	103.24	105.40
1	A	283	C	N3-C2-O2	-5.41	118.12	121.90
1	A	817	C	C2-N1-C1'	5.41	124.75	118.80
1	A	589	C	C2-N3-C4	-5.40	117.20	119.90
1	A	1242	C	N3-C4-C5	5.40	124.06	121.90
1	A	304	U	C5-C6-N1	-5.40	120.00	122.70
1	A	16	A	N7-C8-N9	-5.39	111.10	113.80
1	A	124	G	N1-C2-N3	5.39	127.14	123.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1202	G	C8-N9-C4	-5.39	104.24	106.40
1	A	641	U	N1-C2-N3	5.38	118.13	114.90
1	A	826	C	N3-C4-N4	5.38	121.77	118.00
1	A	20	U	C2-N3-C4	-5.38	123.77	127.00
1	A	1143	G	C5-C6-O6	-5.38	125.37	128.60
1	A	1276	G	C6-C5-N7	-5.38	127.17	130.40
1	A	1395	C	N1-C2-O2	-5.38	115.67	118.90
1	A	1413	A	N1-C2-N3	5.38	131.99	129.30
1	A	1231	G	N9-C4-C5	-5.38	103.25	105.40
16	P	60	LEU	CA-CB-CG	-5.38	102.93	115.30
1	A	631	G	C8-N9-C4	-5.37	104.25	106.40
1	A	1375	A	N1-C6-N6	-5.37	115.38	118.60
1	A	197	A	C5-C6-N6	5.37	128.00	123.70
1	A	264	U	N1-C2-N3	5.37	118.12	114.90
1	A	413	G	C4-C5-N7	-5.37	108.65	110.80
1	A	490	G	C5-C6-O6	-5.37	125.38	128.60
5	E	69	VAL	CB-CA-C	-5.37	101.20	111.40
1	A	931	C	N3-C4-C5	5.37	124.05	121.90
1	A	1023	G	N3-C4-C5	-5.37	125.92	128.60
1	A	1332	A	C5-C6-N6	5.37	127.99	123.70
1	A	1053	G	C4-C5-N7	-5.37	108.65	110.80
1	A	1108	G	N3-C4-N9	5.37	129.22	126.00
1	A	92	C	C5-C4-N4	-5.36	116.44	120.20
1	A	279	A	C4-C5-C6	5.36	119.68	117.00
1	A	497	A	N9-C4-C5	5.36	107.95	105.80
1	A	1054	C	C5-C6-N1	5.36	123.68	121.00
1	A	1206	G	C5-C6-N1	-5.36	108.82	111.50
1	A	1350	A	C4-C5-N7	5.36	113.38	110.70
1	A	566	G	C6-C5-N7	-5.36	127.19	130.40
1	A	200	G	C5-C6-N1	-5.36	108.82	111.50
1	A	800	G	C4-N9-C1'	5.36	133.46	126.50
1	A	854	G	N9-C4-C5	-5.35	103.26	105.40
1	A	524	G	N3-C2-N2	-5.35	116.15	119.90
1	A	779	C	C5-C6-N1	-5.35	118.32	121.00
1	A	1304	G	C8-N9-C4	-5.35	104.26	106.40
1	A	1338	G	N1-C2-N3	5.35	127.11	123.90
1	A	1460	A	N1-C6-N6	5.35	121.81	118.60
1	A	10	A	N1-C2-N3	5.35	131.97	129.30
1	A	358	U	N1-C2-N3	5.35	118.11	114.90
1	A	1165	C	C6-N1-C2	-5.35	118.16	120.30
1	A	1399	C	N1-C2-O2	-5.35	115.69	118.90
1	A	204	U	N1-C2-N3	-5.35	111.69	114.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	934	C	C2-N3-C4	5.35	122.57	119.90
1	A	1125	U	C5-C4-O4	-5.35	122.69	125.90
1	A	1080	A	C5-C6-N6	5.35	127.98	123.70
1	A	558	G	N1-C6-O6	5.34	123.11	119.90
4	D	188	LEU	CB-CG-CD1	5.34	120.08	111.00
1	A	77	G	C6-C5-N7	-5.34	127.19	130.40
1	A	277	C	C5-C6-N1	-5.34	118.33	121.00
1	A	291	C	N3-C4-C5	5.34	124.04	121.90
1	A	1068	G	C4-N9-C1'	5.34	133.44	126.50
1	A	1433	A	N1-C6-N6	-5.34	115.39	118.60
1	A	786	G	C5-C6-N1	-5.34	108.83	111.50
1	A	1530	G	N1-C6-O6	5.34	123.10	119.90
1	A	483	C	C2-N1-C1'	-5.34	112.93	118.80
1	A	644	G	C8-N9-C1'	-5.34	120.06	127.00
1	A	1246	C	C2-N1-C1'	-5.34	112.93	118.80
1	A	55	A	C5-C6-N1	5.33	120.37	117.70
1	A	281	G	C5-N7-C8	-5.33	101.64	104.30
1	A	767	A	C4-C5-N7	-5.33	108.03	110.70
1	A	871	U	N3-C2-O2	-5.33	118.47	122.20
1	A	1167	A	C8-N9-C4	-5.33	103.67	105.80
20	T	102	GLY	N-CA-C	-5.33	99.78	113.10
1	A	635	G	C4-N9-C1'	5.33	133.43	126.50
1	A	557	G	C4-C5-N7	-5.33	108.67	110.80
1	A	351	G	N1-C2-N3	5.32	127.09	123.90
1	A	403	C	C4-C5-C6	5.32	120.06	117.40
1	A	288	A	N1-C6-N6	5.32	121.79	118.60
1	A	1055	A	C5-C6-N1	5.32	120.36	117.70
1	A	1286	A	N7-C8-N9	5.32	116.46	113.80
1	A	780	A	N7-C8-N9	-5.32	111.14	113.80
1	A	1092	A	C4-N9-C1'	5.32	135.87	126.30
1	A	317	G	N1-C6-O6	5.31	123.09	119.90
1	A	1324	A	C8-N9-C4	-5.31	103.67	105.80
1	A	423	G	N3-C4-N9	5.31	129.19	126.00
1	A	479	C	C2-N3-C4	5.31	122.55	119.90
1	A	876	G	C5-N7-C8	-5.31	101.64	104.30
1	A	1480	G	C5-C6-N1	-5.31	108.84	111.50
1	A	980	C	C5-C4-N4	-5.31	116.48	120.20
1	A	936	C	C5-C6-N1	-5.30	118.35	121.00
1	A	1481	U	C5-C4-O4	5.30	129.08	125.90
2	B	25	ASN	C-N-CD	5.30	139.54	128.40
1	A	17	U	N1-C2-N3	5.30	118.08	114.90
1	A	70	G	N1-C6-O6	5.29	123.08	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	783	C	C5-C6-N1	-5.29	118.35	121.00
1	A	895	G	N7-C8-N9	5.29	115.75	113.10
1	A	963	G	C8-N9-C4	-5.29	104.28	106.40
1	A	1415	G	N9-C4-C5	-5.29	103.28	105.40
1	A	607	A	N1-C6-N6	5.29	121.77	118.60
1	A	69	G	C8-N9-C4	5.29	108.52	106.40
1	A	389	A	N1-C2-N3	5.29	131.94	129.30
1	A	732	C	N3-C2-O2	-5.29	118.20	121.90
1	A	752	G	C8-N9-C4	5.29	108.52	106.40
1	A	822	C	C2-N3-C4	-5.29	117.26	119.90
1	A	947	G	C6-C5-N7	-5.29	127.23	130.40
1	A	1091	U	N3-C4-C5	-5.29	111.43	114.60
1	A	534	U	C6-N1-C2	5.29	124.17	121.00
1	A	820	U	C6-N1-C1'	5.29	128.60	121.20
1	A	947	G	N3-C2-N2	5.29	123.60	119.90
1	A	705	U	C5-C6-N1	-5.28	120.06	122.70
1	A	1295	G	C8-N9-C4	-5.28	104.29	106.40
1	A	861	G	C5-C6-N1	5.28	114.14	111.50
1	A	920	U	C6-N1-C1'	5.28	128.59	121.20
1	A	1201	A	N3-C4-C5	-5.28	123.11	126.80
1	A	259	G	C6-C5-N7	-5.27	127.24	130.40
14	N	10	ALA	N-CA-C	-5.27	96.76	111.00
1	A	577	G	N1-C2-N3	5.27	127.06	123.90
1	A	721	G	N3-C2-N2	5.27	123.59	119.90
1	A	1350	A	C6-C5-N7	-5.27	128.61	132.30
1	A	820	U	C2-N3-C4	-5.27	123.84	127.00
1	A	934	C	C6-N1-C2	5.27	122.41	120.30
1	A	827	U	C2-N1-C1'	5.27	124.02	117.70
1	A	54	C	C2-N3-C4	-5.26	117.27	119.90
1	A	635	G	C8-N9-C4	5.26	108.51	106.40
1	A	644	G	N9-C4-C5	-5.26	103.29	105.40
1	A	800	G	C6-C5-N7	-5.26	127.24	130.40
1	A	819	A	N1-C2-N3	5.26	131.93	129.30
12	L	66	VAL	CB-CA-C	-5.26	101.40	111.40
1	A	919	A	C5-C6-N6	-5.26	119.49	123.70
1	A	1077	G	N1-C2-N2	-5.26	111.46	116.20
1	A	1380	U	C5-C4-O4	5.26	129.06	125.90
10	J	58	ASP	CB-CG-OD1	5.26	123.03	118.30
1	A	1033	G	N9-C4-C5	5.26	107.50	105.40
1	A	1281	U	N3-C2-O2	-5.26	118.52	122.20
1	A	221	C	C5-C6-N1	-5.25	118.37	121.00
1	A	565	U	N1-C2-N3	-5.25	111.75	114.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	964	A	C2-N3-C4	-5.25	107.97	110.60
1	A	1505	G	N9-C4-C5	5.25	107.50	105.40
1	A	1512	U	N1-C2-N3	5.25	118.05	114.90
1	A	1487	G	N3-C2-N2	-5.25	116.22	119.90
1	A	1494	G	C6-C5-N7	-5.25	127.25	130.40
1	A	248	C	C4-C5-C6	5.25	120.03	117.40
1	A	1249	C	C2-N1-C1'	5.25	124.58	118.80
1	A	112	G	C8-N9-C4	5.25	108.50	106.40
1	A	119	A	N1-C6-N6	5.25	121.75	118.60
1	A	244	U	N1-C2-N3	-5.24	111.75	114.90
1	A	1058	G	N3-C4-C5	5.24	131.22	128.60
15	O	45	VAL	CB-CA-C	-5.24	101.44	111.40
1	A	573	A	C6-C5-N7	-5.24	128.63	132.30
1	A	1392	G	C4-C5-C6	5.24	121.94	118.80
1	A	711	G	N7-C8-N9	5.24	115.72	113.10
1	A	740	U	C5-C6-N1	-5.24	120.08	122.70
1	A	1099	G	N3-C4-N9	-5.24	122.86	126.00
1	A	440	A	C5-C6-N1	-5.23	115.08	117.70
1	A	1200	C	C5-C4-N4	-5.23	116.54	120.20
1	A	801	U	N3-C4-C5	5.23	117.74	114.60
1	A	831	U	N1-C2-N3	5.23	118.04	114.90
1	A	946	A	N1-C2-N3	5.23	131.92	129.30
1	A	149	A	N1-C6-N6	-5.23	115.46	118.60
1	A	650	G	N3-C2-N2	-5.23	116.24	119.90
1	A	668	G	C8-N9-C4	5.23	108.49	106.40
1	A	489	C	C6-N1-C2	5.23	122.39	120.30
1	A	1497	G	N3-C4-C5	-5.22	125.99	128.60
1	A	309	G	C4-C5-N7	5.22	112.89	110.80
1	A	544	G	N3-C4-C5	-5.22	125.99	128.60
1	A	816	A	N3-C4-C5	5.22	130.46	126.80
1	A	122	G	N3-C4-C5	5.22	131.21	128.60
1	A	352	C	N1-C2-O2	-5.22	115.77	118.90
1	A	965	A	N9-C4-C5	-5.22	103.71	105.80
1	A	1096	C	C6-N1-C2	-5.22	118.21	120.30
1	A	975	A	C2-N3-C4	-5.22	107.99	110.60
1	A	1305	G	C4-C5-C6	5.22	121.93	118.80
1	A	641	U	C2-N3-C4	-5.21	123.87	127.00
1	A	1027	C	N3-C4-C5	-5.21	119.81	121.90
1	A	1525	G	C6-N1-C2	-5.21	121.97	125.10
1	A	744	C	C5-C6-N1	-5.21	118.39	121.00
1	A	823	G	N1-C2-N3	5.21	127.03	123.90
1	A	190(E)	U	N1-C2-N3	5.21	118.03	114.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	931	C	N3-C4-N4	-5.21	114.35	118.00
1	A	1507	A	C5-C6-N6	5.21	127.87	123.70
1	A	1134	G	N9-C4-C5	5.21	107.48	105.40
1	A	331	G	C8-N9-C1'	-5.21	120.23	127.00
1	A	1484	C	N1-C2-O2	-5.21	115.78	118.90
1	A	15	G	C4-C5-N7	5.20	112.88	110.80
1	A	781	A	N7-C8-N9	5.20	116.40	113.80
1	A	781	A	C4-C5-C6	5.20	119.60	117.00
1	A	782	A	C5-C6-N6	5.20	127.86	123.70
1	A	953	G	N1-C6-O6	5.20	123.02	119.90
1	A	1421	G	N7-C8-N9	5.20	115.70	113.10
1	A	900	A	N1-C2-N3	5.20	131.90	129.30
1	A	679	C	C6-N1-C2	5.20	122.38	120.30
1	A	964	A	N7-C8-N9	5.19	116.40	113.80
1	A	436	C	C2-N1-C1'	-5.19	113.09	118.80
1	A	830	G	C5-C6-N1	-5.19	108.90	111.50
1	A	1049	U	C2-N1-C1'	5.19	123.93	117.70
12	L	17	LYS	CD-CE-NZ	5.19	123.64	111.70
1	A	25	C	C6-N1-C2	5.19	122.38	120.30
1	A	104	G	C4-C5-C6	5.19	121.91	118.80
1	A	481	G	C8-N9-C1'	-5.19	120.25	127.00
1	A	1108	G	C4-C5-C6	5.19	121.91	118.80
1	A	540	G	C4-C5-N7	5.19	112.88	110.80
1	A	804	U	C4-C5-C6	5.19	122.81	119.70
1	A	1037	C	C6-N1-C2	-5.18	118.23	120.30
1	A	882	C	N1-C2-N3	5.18	122.83	119.20
5	E	63	ARG	NE-CZ-NH1	5.18	122.89	120.30
1	A	760	G	N9-C4-C5	-5.18	103.33	105.40
1	A	497	A	C5-C6-N6	5.18	127.84	123.70
1	A	1322	C	C2-N3-C4	5.18	122.49	119.90
1	A	1293	G	N3-C4-C5	5.18	131.19	128.60
1	A	1272	G	N3-C4-C5	-5.18	126.01	128.60
1	A	232	G	C5-C6-N1	-5.17	108.91	111.50
1	A	691	G	C6-C5-N7	-5.17	127.30	130.40
1	A	311	C	C5-C6-N1	-5.17	118.42	121.00
1	A	969	A	C5-N7-C8	-5.17	101.31	103.90
1	A	1030(C)	G	C8-N9-C4	-5.17	104.33	106.40
1	A	816	A	C6-C5-N7	5.17	135.92	132.30
1	A	558	G	C5-N7-C8	-5.17	101.72	104.30
1	A	811	C	C2-N3-C4	-5.17	117.32	119.90
1	A	816	A	C8-N9-C4	5.17	107.87	105.80
1	A	134	A	C2-N3-C4	-5.16	108.02	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	299	G	C5-C6-O6	-5.16	125.50	128.60
1	A	190(H)	G	C4-C5-N7	-5.16	108.74	110.80
1	A	648	A	C4-C5-N7	-5.16	108.12	110.70
1	A	1253	G	C4-N9-C1'	5.16	133.21	126.50
1	A	700	G	N3-C4-C5	-5.16	126.02	128.60
1	A	1493[A]	A	N1-C6-N6	5.16	121.69	118.60
1	A	1493[B]	A	N1-C6-N6	5.16	121.69	118.60
1	A	824	C	C2-N3-C4	-5.16	117.32	119.90
1	A	190(B)	C	C2-N1-C1'	5.16	124.47	118.80
1	A	667	G	N3-C4-C5	5.16	131.18	128.60
1	A	566	G	N3-C4-C5	-5.15	126.02	128.60
1	A	280	C	C5-C6-N1	-5.15	118.42	121.00
1	A	701	C	N3-C4-N4	-5.15	114.39	118.00
1	A	705	U	N1-C2-N3	5.15	117.99	114.90
1	A	976	G	N3-C2-N2	-5.15	116.30	119.90
1	A	1390	U	C5-C4-O4	5.15	128.99	125.90
1	A	97	G	C8-N9-C4	-5.15	104.34	106.40
1	A	596	C	N3-C2-O2	5.15	125.50	121.90
1	A	193	C	C6-N1-C2	5.15	122.36	120.30
1	A	1052	U	C6-N1-C2	-5.14	117.91	121.00
1	A	596	C	C2-N1-C1'	-5.14	113.14	118.80
1	A	220	G	N1-C6-O6	5.14	122.98	119.90
1	A	306	G	N3-C4-C5	5.14	131.17	128.60
1	A	785	G	C8-N9-C4	5.14	108.46	106.40
1	A	1377	A	N1-C6-N6	-5.14	115.52	118.60
1	A	1395	C	C5-C4-N4	5.14	123.80	120.20
1	A	612	C	C5-C6-N1	-5.14	118.43	121.00
1	A	1484	C	N3-C2-O2	5.14	125.50	121.90
1	A	109	A	C5-C6-N6	5.13	127.81	123.70
1	A	357	G	N9-C4-C5	5.13	107.45	105.40
1	A	246	A	C8-N9-C4	5.13	107.85	105.80
1	A	881	G	C6-C5-N7	-5.13	127.32	130.40
1	A	558	G	C5-C6-O6	-5.13	125.52	128.60
1	A	796	C	C5-C6-N1	-5.13	118.44	121.00
1	A	1186	G	N3-C2-N2	-5.13	116.31	119.90
1	A	618	C	C5-C4-N4	5.13	123.79	120.20
1	A	120	A	C5-C6-N6	5.13	127.80	123.70
1	A	435	C	C6-N1-C2	-5.13	118.25	120.30
1	A	805	C	C4-C5-C6	-5.13	114.84	117.40
12	L	52	LEU	CA-CB-CG	5.13	127.09	115.30
1	A	683	G	C8-N9-C4	-5.12	104.35	106.40
1	A	390	C	N3-C4-C5	-5.12	119.85	121.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	758	G	N1-C2-N3	5.12	126.97	123.90
1	A	1030(C)	G	N3-C4-C5	-5.12	126.04	128.60
1	A	1365	G	N9-C4-C5	5.12	107.45	105.40
1	A	201	C	C6-N1-C1'	-5.12	114.65	120.80
1	A	539	A	C2-N3-C4	5.12	113.16	110.60
1	A	570	G	N3-C4-N9	5.12	129.07	126.00
1	A	812	C	N3-C2-O2	-5.12	118.31	121.90
1	A	889	A	C4-C5-C6	5.12	119.56	117.00
1	A	1332	A	C8-N9-C4	-5.12	103.75	105.80
1	A	1077	G	N1-C2-N3	5.12	126.97	123.90
1	A	828	A	C6-C5-N7	-5.12	128.72	132.30
1	A	109	A	N1-C2-N3	5.12	131.86	129.30
1	A	1139	G	N3-C4-C5	-5.12	126.04	128.60
1	A	317	G	C4-C5-N7	5.11	112.84	110.80
1	A	621	A	C6-C5-N7	-5.11	128.72	132.30
1	A	910	C	N1-C2-N3	5.11	122.78	119.20
1	A	919	A	C4-C5-N7	5.11	113.26	110.70
1	A	1370	G	C4-N9-C1'	5.11	133.14	126.50
1	A	47	C	C6-N1-C2	5.11	122.34	120.30
1	A	316	G	C6-C5-N7	5.11	133.46	130.40
1	A	803	G	N1-C2-N2	-5.11	111.60	116.20
1	A	823	G	C6-C5-N7	-5.11	127.33	130.40
1	A	10	A	N1-C6-N6	-5.11	115.54	118.60
1	A	530	G	N3-C2-N2	5.11	123.47	119.90
1	A	120	A	C4-C5-N7	-5.10	108.15	110.70
1	A	266	G	N9-C4-C5	-5.10	103.36	105.40
1	A	284	G	C5-C6-N1	-5.10	108.95	111.50
1	A	521	G	C6-C5-N7	5.10	133.46	130.40
1	A	660	G	N9-C4-C5	-5.10	103.36	105.40
1	A	1344	C	C5-C6-N1	-5.10	118.45	121.00
1	A	181	G	N3-C4-N9	5.10	129.06	126.00
1	A	66	G	C2-N3-C4	-5.10	109.35	111.90
1	A	485	G	C5-C6-N1	-5.10	108.95	111.50
1	A	741	G	N9-C4-C5	5.10	107.44	105.40
1	A	1341	U	C6-N1-C1'	5.10	128.34	121.20
1	A	757	U	N1-C2-O2	-5.10	119.23	122.80
1	A	253	U	N1-C2-O2	-5.09	119.23	122.80
1	A	930	C	C2-N3-C4	-5.09	117.35	119.90
1	A	1084	G	C4-C5-C6	5.09	121.86	118.80
1	A	1504	G	N9-C4-C5	-5.09	103.36	105.40
1	A	190(F)	G	C4-C5-N7	-5.09	108.76	110.80
1	A	259	G	N7-C8-N9	5.09	115.64	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	570	G	C8-N9-C1'	-5.09	120.39	127.00
1	A	1078	U	C4-C5-C6	-5.09	116.65	119.70
1	A	1222	G	N1-C6-O6	5.09	122.95	119.90
1	A	796	C	N3-C4-C5	-5.09	119.86	121.90
1	A	306	G	N1-C6-O6	5.09	122.95	119.90
1	A	853	G	N7-C8-N9	5.09	115.64	113.10
1	A	909	A	C4-C5-N7	5.09	113.24	110.70
1	A	1277	C	N3-C2-O2	-5.09	118.34	121.90
1	A	1012	U	C6-N1-C2	-5.08	117.95	121.00
1	A	947	G	N1-C2-N2	-5.08	111.62	116.20
1	A	1310	G	N9-C4-C5	-5.08	103.37	105.40
24	a	37	A	N1-C2-N3	5.08	131.84	129.30
1	A	336	C	N3-C4-N4	5.08	121.56	118.00
1	A	903	G	N9-C4-C5	5.08	107.43	105.40
1	A	1195	C	C5-C4-N4	-5.08	116.64	120.20
1	A	1236	A	C5-C6-N6	-5.08	119.64	123.70
1	A	393	A	N1-C6-N6	5.08	121.65	118.60
1	A	814	A	C8-N9-C4	5.07	107.83	105.80
1	A	597	G	N1-C2-N3	5.07	126.94	123.90
1	A	933	G	C4-C5-N7	5.07	112.83	110.80
1	A	977	A	N3-C4-C5	-5.07	123.25	126.80
1	A	1405	G	C4-N9-C1'	-5.07	119.91	126.50
1	A	1494	G	C4-C5-N7	5.07	112.83	110.80
1	A	92	C	N1-C2-O2	5.07	121.94	118.90
1	A	344	A	C5-N7-C8	-5.07	101.37	103.90
1	A	183	G	N7-C8-N9	5.06	115.63	113.10
1	A	544	G	C4-N9-C1'	5.06	133.08	126.50
1	A	579	G	N3-C4-C5	5.06	131.13	128.60
1	A	190(D)	U	N3-C2-O2	-5.06	118.66	122.20
1	A	292	G	C8-N9-C4	5.06	108.42	106.40
1	A	794	A	N1-C2-N3	-5.06	126.77	129.30
1	A	795	C	C2-N1-C1'	-5.06	113.23	118.80
1	A	1127	G	N1-C6-O6	-5.06	116.86	119.90
1	A	858	G	C4-N9-C1'	5.06	133.08	126.50
1	A	886	G	C5-C6-N1	-5.06	108.97	111.50
1	A	433	C	N3-C2-O2	-5.05	118.36	121.90
1	A	50	A	C6-N1-C2	5.05	121.63	118.60
1	A	149	A	N1-C2-N3	5.05	131.83	129.30
1	A	642	A	N1-C2-N3	5.05	131.83	129.30
1	A	600	C	C4-C5-C6	5.05	119.92	117.40
1	A	658	G	N1-C2-N2	-5.05	111.66	116.20
1	A	1356	G	C8-N9-C4	-5.05	104.38	106.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	24	U	C2-N3-C4	-5.05	123.97	127.00
1	A	903	G	N1-C6-O6	-5.05	116.87	119.90
1	A	1324	A	N1-C6-N6	5.05	121.63	118.60
1	A	403	C	C2-N1-C1'	-5.04	113.25	118.80
1	A	1232	U	C2-N3-C4	-5.04	123.97	127.00
1	A	16	A	C5-C6-N1	-5.04	115.18	117.70
1	A	288	A	N3-C4-C5	5.04	130.33	126.80
1	A	447	G	N3-C2-N2	5.04	123.43	119.90
1	A	910	C	C4-C5-C6	5.04	119.92	117.40
1	A	1279	A	C4-C5-C6	5.04	119.52	117.00
1	A	637	G	C4-N9-C1'	5.04	133.05	126.50
1	A	1434	A	C5-C6-N6	-5.04	119.67	123.70
1	A	1476	G	C8-N9-C4	-5.04	104.38	106.40
1	A	521	G	C4-C5-N7	-5.03	108.79	110.80
1	A	964	A	N9-C4-C5	5.03	107.81	105.80
25	b	3	U	N3-C2-O2	-5.03	118.68	122.20
1	A	64	G	C6-C5-N7	-5.03	127.38	130.40
1	A	646	U	C5-C4-O4	5.03	128.92	125.90
1	A	330	C	N3-C4-C5	-5.03	119.89	121.90
1	A	800	G	N1-C6-O6	5.03	122.92	119.90
1	A	899	C	C2-N1-C1'	5.03	124.33	118.80
1	A	250	A	C6-N1-C2	5.03	121.62	118.60
1	A	558	G	C8-N9-C4	-5.03	104.39	106.40
1	A	1488	G	C4-C5-N7	-5.03	108.79	110.80
1	A	142	G	C2-N3-C4	5.03	114.41	111.90
1	A	826	C	C2-N1-C1'	5.03	124.33	118.80
1	A	135	C	C6-N1-C1'	5.02	126.83	120.80
1	A	1055	A	C4-C5-N7	-5.02	108.19	110.70
1	A	828	A	C4-C5-N7	5.02	113.21	110.70
1	A	1099	G	N3-C2-N2	-5.02	116.39	119.90
1	A	1303	C	N3-C4-C5	5.02	123.91	121.90
1	A	712	A	C2-N3-C4	-5.02	108.09	110.60
1	A	651	C	N1-C2-O2	-5.02	115.89	118.90
1	A	859	A	N3-C4-N9	5.02	131.41	127.40
1	A	357	G	N1-C6-O6	-5.02	116.89	119.90
1	A	21	G	N3-C2-N2	5.01	123.41	119.90
16	P	5	ARG	NE-CZ-NH2	-5.01	117.79	120.30
1	A	276	G	C5-C6-O6	5.01	131.60	128.60
1	A	611	A	N1-C6-N6	5.01	121.61	118.60
1	A	786	G	N3-C4-C5	5.01	131.10	128.60
1	A	125	U	C5-C6-N1	-5.01	120.20	122.70
1	A	673	G	N1-C6-O6	5.01	122.90	119.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1303	C	C6-N1-C2	5.00	122.30	120.30
1	A	266	G	P-O3'-C3'	5.00	125.70	119.70
1	A	1179	A	N1-C6-N6	-5.00	115.60	118.60

There are no chirality outliers.

All (18) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	14	GLY	Peptide
2	B	75	LYS	Peptide
2	B	89	GLY	Peptide
3	C	166	GLU	Peptide
3	C	2	GLY	Peptide
4	D	154	ASN	Peptide
8	H	27	PRO	Peptide
8	H	90	GLY	Peptide
9	I	38	GLN	Peptide
10	J	61	GLU	Peptide
10	J	85	LEU	Peptide
12	L	46	LYS	Peptide
12	L	91	LYS	Peptide
16	P	82	GLN	Peptide
19	S	4	SER	Peptide
20	T	12	ALA	Peptide
20	T	8	ARG	Peptide
21	U	24	ARG	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	32707	0	16542	1874	1
2	B	1896	0	1936	217	0
3	C	1613	0	1677	201	0
4	D	1703	0	1763	203	0
5	E	1147	0	1207	135	1
6	F	843	0	857	87	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	G	1257	0	1296	146	0
8	H	1116	0	1177	118	0
9	I	1010	0	1037	144	0
10	J	793	0	835	125	0
11	K	873	0	894	76	0
12	L	973	0	1058	109	0
13	M	937	0	995	134	0
14	N	492	0	529	85	0
15	O	734	0	771	101	0
16	P	701	0	720	73	0
17	Q	834	0	906	115	0
18	R	585	0	657	80	0
19	S	648	0	673	83	0
20	T	763	0	861	101	0
21	U	209	0	221	43	0
22	V	77	0	42	1	0
23	W	235	0	121	34	0
24	a	175	0	87	0	0
25	b	60	0	31	0	0
26	A	326	0	0	0	0
26	D	3	0	0	0	0
26	E	4	0	0	0	0
26	F	1	0	0	0	0
26	G	1	0	0	0	0
26	H	1	0	0	0	0
26	J	1	0	0	0	0
26	N	1	0	0	0	0
26	P	3	0	0	0	0
26	Q	1	0	0	0	0
26	S	2	0	0	0	0
27	A	40	0	38	14	0
28	D	1	0	0	0	0
28	N	1	0	0	0	0
29	A	866	0	0	97	0
29	C	1	0	0	0	0
29	D	7	0	0	1	0
29	E	5	0	0	0	0
29	L	1	0	0	0	0
29	N	1	0	0	0	0
29	P	1	0	0	0	0
29	Q	2	0	0	0	0
29	T	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
29	U	4	0	0	0	0
29	W	1	0	0	0	0
All	All	53659	0	36931	3978	2

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 45.

All (3978) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:451:A:O2'	29:A:2729:HOH:O	1.59	1.20
12:L:70:ILE:HG21	12:L:75:HIS:HD2	1.13	1.14
15:O:88:ARG:HE	15:O:88:ARG:HA	1.10	1.12
1:A:266:G:H5'	1:A:266:G:C8	1.83	1.12
21:U:10:ARG:CB	21:U:10:ARG:HH11	1.62	1.12
7:G:12:LEU:HD12	7:G:12:LEU:H	1.08	1.11
1:A:1054:C:H3'	1:A:1054:C:O2	1.48	1.11
10:J:55:LYS:HG2	10:J:56:HIS:H	0.99	1.11
10:J:30:SER:HB2	10:J:80:LYS:HB2	1.32	1.11
1:A:692:U:OP1	11:K:124:LYS:NZ	1.82	1.10
9:I:50:LEU:HD11	9:I:81:ILE:HG21	1.20	1.10
6:F:14:LEU:HD13	6:F:18:GLN:HB3	1.33	1.10
1:A:1493[A]:A:H8	1:A:1493[A]:A:H3'	1.10	1.10
2:B:88:ALA:HB2	2:B:219:VAL:HG13	1.33	1.10
2:B:25:ASN:ND2	2:B:193:ASP:HB2	1.67	1.09
1:A:538:G:H5''	12:L:114:LYS:HB2	1.35	1.08
1:A:266:G:O2'	1:A:267:C:OP2	1.72	1.08
1:A:1493[A]:A:H3'	1:A:1493[A]:A:C8	1.86	1.07
4:D:36:ARG:HB3	4:D:38:TYR:CE2	1.87	1.07
12:L:127:GLU:CG	12:L:128:ALA:H	1.62	1.07
14:N:27:CYS:SG	14:N:29:ARG:HB2	1.94	1.07
20:T:57:ARG:HH21	20:T:100:ILE:HD13	1.19	1.07
1:A:328:C:O2'	1:A:329:A:OP2	1.72	1.06
12:L:127:GLU:HG3	12:L:128:ALA:H	0.93	1.06
5:E:126:ARG:HG2	5:E:126:ARG:HH11	1.16	1.06
7:G:50:ILE:HG21	7:G:58:PRO:HA	1.34	1.06
7:G:5:ARG:HG3	7:G:7:ALA:H	1.17	1.06
1:A:328:C:O2	1:A:328:C:H2'	1.55	1.06
2:B:75:LYS:HA	2:B:78:GLN:HG3	1.37	1.06
10:J:82:ILE:HA	10:J:85:LEU:HB2	1.14	1.06
8:H:102:ARG:H	8:H:102:ARG:HD2	1.17	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:17:ARG:HH11	15:O:17:ARG:HG3	1.14	1.05
12:L:127:GLU:HG3	12:L:128:ALA:N	1.70	1.05
20:T:49:ALA:HB3	20:T:99:LEU:HD21	1.38	1.04
1:A:89:C:H5	1:A:90:U:N3	1.54	1.04
1:A:543:C:C2'	1:A:544:G:H5'	1.87	1.04
1:A:61:G:O2'	29:A:2002:HOH:O	1.76	1.04
4:D:32:ALA:HA	4:D:35:ARG:HB2	1.39	1.04
6:F:12:PRO:HG3	6:F:58:GLY:HA2	1.33	1.03
1:A:1443:G:H4'	1:A:1446:A:H5'	1.41	1.03
1:A:107:G:H2'	1:A:108:G:H5''	1.40	1.03
21:U:10:ARG:HB2	21:U:10:ARG:HH11	1.21	1.03
1:A:89:C:C5	1:A:90:U:N3	2.25	1.02
1:A:858:G:O2'	1:A:859:A:H5'	1.59	1.02
1:A:1402:4OC:HM22	1:A:1403:C:H5'	1.37	1.02
6:F:50:TYR:CE1	18:R:77:GLY:HA2	1.95	1.02
1:A:1026:G:H2'	1:A:1027:C:H5''	1.42	1.01
7:G:152:ALA:O	7:G:155:ARG:NH1	1.93	1.01
18:R:87:ARG:HH21	18:R:87:ARG:HG3	1.22	1.01
1:A:1498:UR3:H4'	1:A:1519[A]:MA6:C2	1.91	1.01
10:J:86:MET:HG3	10:J:87:THR:H	1.26	1.00
1:A:103:C:OP1	20:T:17:ARG:NH1	1.93	1.00
1:A:1148:U:H2'	1:A:1149:C:O4'	1.61	1.00
1:A:1347:G:H3'	9:I:108:VAL:O	1.59	1.00
17:Q:100:LYS:HB2	17:Q:101:ARG:HH11	1.21	1.00
18:R:37:VAL:O	18:R:40:LEU:N	1.92	1.00
4:D:150:GLU:OE2	4:D:150:GLU:N	1.92	1.00
11:K:15:ALA:HA	11:K:77:MET:HA	1.43	1.00
1:A:1497:G:C2'	1:A:1498:UR3:H5'	1.91	1.00
1:A:9:G:OP1	5:E:122:GLU:HG3	1.60	0.99
1:A:1328:C:OP1	21:U:20:LYS:NZ	1.96	0.99
13:M:16:ASP:OD2	13:M:17:VAL:N	1.95	0.99
1:A:710:G:H5''	6:F:54:LYS:HE3	1.43	0.99
1:A:746:A:H2'	1:A:747:C:H5'	1.44	0.99
1:A:1049:U:H4'	1:A:1050:G:O5'	1.60	0.98
1:A:1316:G:N2	1:A:1319:A:OP2	1.96	0.98
1:A:571:U:H5''	1:A:572:A:OP2	1.63	0.98
4:D:18:LYS:HE3	4:D:20:TYR:HE2	1.29	0.98
1:A:1404:5MC:H1'	1:A:1499:A:C2	1.99	0.98
1:A:1399:C:H4'	1:A:1400:5MC:H5''	1.46	0.98
7:G:16:LEU:H	7:G:16:LEU:HD22	1.29	0.98
1:A:1026:G:O2'	1:A:1027:C:OP1	1.80	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:A:1928:SRY:HI32	27:A:1928:SRY:H22	1.46	0.97
1:A:867:G:H2'	1:A:868:C:H5'	1.44	0.97
2:B:231:GLU:HB3	2:B:232:PRO:HD2	1.45	0.97
1:A:1435:G:H2'	1:A:1436:U:C6	1.99	0.97
18:R:26:LEU:HD11	18:R:42:ARG:HD3	1.45	0.97
10:J:55:LYS:HG2	10:J:56:HIS:N	1.79	0.96
9:I:9:ARG:HB2	9:I:13:ALA:O	1.63	0.96
7:G:120:ILE:HD13	7:G:120:ILE:N	1.78	0.96
12:L:27:LEU:HG	12:L:28:LYS:H	1.30	0.96
1:A:1532:U:H2'	1:A:1533:C:C6	2.01	0.96
12:L:70:ILE:HG21	12:L:75:HIS:CD2	2.00	0.96
1:A:644:G:H5'	1:A:644:G:H8	1.28	0.95
1:A:914:A:P	27:A:1928:SRY:HI33	2.06	0.95
1:A:1305:G:OP2	21:U:2:GLY:N	1.99	0.95
9:I:108:VAL:HG12	9:I:109:VAL:H	1.31	0.95
6:F:50:TYR:HE1	18:R:77:GLY:HA2	1.30	0.94
1:A:1299:A:C5	1:A:1301:U:O2	2.20	0.94
1:A:792:A:H4'	1:A:793:U:OP1	1.65	0.94
23:W:31:C:N4	23:W:39:G:H1	1.63	0.94
1:A:1068:G:P	29:A:2218:HOH:O	2.25	0.94
1:A:372:C:O2'	29:A:2721:HOH:O	1.84	0.94
1:A:1104:G:O5'	2:B:111:ARG:HD2	1.67	0.94
1:A:707:C:H4'	11:K:20:TYR:CD1	2.01	0.94
1:A:746:A:C2'	1:A:747:C:H5'	1.96	0.94
10:J:30:SER:CB	10:J:80:LYS:HB2	1.98	0.94
6:F:87:ARG:HG3	6:F:87:ARG:HH11	1.33	0.94
1:A:1064:G:H22	1:A:1190:G:H2'	1.31	0.93
10:J:44:VAL:HG13	10:J:66:ARG:HD3	1.50	0.93
13:M:49:THR:HG22	13:M:51:ALA:H	1.32	0.93
15:O:5:LYS:HA	15:O:5:LYS:NZ	1.83	0.93
3:C:188:LEU:HD11	3:C:195:VAL:HG13	1.51	0.93
13:M:49:THR:HB	13:M:52:GLU:HG3	1.50	0.93
8:H:54:ASP:OD2	8:H:55:GLY:N	2.02	0.93
9:I:8:GLY:HA3	9:I:79:LEU:HB3	1.49	0.93
17:Q:40:LYS:HD2	17:Q:42:TYR:CE1	2.04	0.93
1:A:1064:G:N2	1:A:1190:G:H2'	1.84	0.93
12:L:20:LYS:HE2	12:L:20:LYS:H	1.34	0.92
1:A:499:A:H4'	1:A:500:G:OP1	1.66	0.92
1:A:1412:C:H2'	1:A:1413:A:C8	2.05	0.92
2:B:97:TRP:HZ2	2:B:102:LEU:HD13	1.34	0.92
1:A:229:U:C2'	1:A:230:G:H5'	2.00	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:37:ARG:HG2	5:E:37:ARG:HH11	1.32	0.92
4:D:22:LYS:HB2	4:D:26:CYS:SG	2.10	0.92
4:D:36:ARG:HB3	4:D:38:TYR:HE2	1.30	0.92
15:O:79:ARG:HH11	15:O:79:ARG:HG3	1.35	0.92
4:D:83:SER:HA	4:D:89:THR:HG23	1.52	0.91
18:R:87:ARG:CG	18:R:87:ARG:HH21	1.82	0.91
11:K:120:ARG:HG2	11:K:120:ARG:HH11	1.34	0.91
8:H:102:ARG:N	8:H:102:ARG:HD2	1.85	0.91
1:A:1392:G:C2'	1:A:1393:U:H5'	1.99	0.91
1:A:279:A:OP2	17:Q:95:TYR:OH	1.86	0.91
1:A:867:G:C2'	1:A:868:C:H5'	2.01	0.91
13:M:34:LEU:HD13	13:M:41:PRO:HA	1.52	0.91
1:A:1035:A:H2'	1:A:1036:G:H8	1.34	0.91
1:A:1392:G:H2'	1:A:1393:U:H5'	1.49	0.91
1:A:1381:U:C5	1:A:1382:C:C5	2.58	0.91
5:E:106:PRO:O	5:E:110:LEU:HD12	1.71	0.91
15:O:88:ARG:NE	15:O:88:ARG:HA	1.85	0.91
1:A:1497:G:H2'	1:A:1498:UR3:H5'	1.54	0.90
12:L:47:LYS:N	12:L:48:PRO:HD2	1.85	0.90
10:J:55:LYS:CG	10:J:56:HIS:H	1.78	0.90
15:O:33:THR:HG23	15:O:63:ARG:HH12	1.35	0.89
2:B:92:TYR:CD1	2:B:151:GLY:HA3	2.07	0.89
3:C:127:ARG:HA	3:C:127:ARG:NE	1.85	0.89
12:L:76:ASN:O	12:L:77:LEU:HD23	1.72	0.89
1:A:991:U:O2'	1:A:992:U:O5'	1.90	0.89
2:B:74:LYS:HE3	2:B:166:ASP:HB2	1.54	0.89
3:C:91:LEU:HD21	3:C:99:VAL:HG22	1.54	0.89
15:O:16:ALA:HB1	15:O:21:ASP:HB3	1.53	0.89
1:A:1538:C:H2'	1:A:1539:C:O4'	1.73	0.89
16:P:67:THR:HG22	16:P:68:ASP:H	1.36	0.89
1:A:192:U:H1'	20:T:103:GLY:HA2	1.55	0.89
10:J:25:GLU:HA	10:J:28:ARG:HB2	1.55	0.89
1:A:1442:G:C6	1:A:1446:A:N6	2.41	0.88
1:A:791:G:H2'	1:A:792:A:H5'	1.55	0.88
1:A:1056:U:H5'	3:C:163:ALA:HB2	1.55	0.88
1:A:484:G:O2'	1:A:485:G:OP2	1.90	0.88
1:A:500:G:C5	1:A:546:G:N2	2.42	0.88
10:J:48:THR:HA	10:J:62:HIS:HB3	1.54	0.88
1:A:1047:G:C2'	1:A:1048:G:H5'	2.04	0.88
1:A:1400:5MC:H3'	1:A:1401:G:H5'	1.55	0.88
7:G:38:LEU:O	7:G:42:ILE:HG13	1.71	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:604:G:H2'	1:A:605:U:H5'	1.54	0.88
15:O:88:ARG:CA	15:O:88:ARG:HE	1.83	0.88
1:A:543:C:H2'	1:A:544:G:H5'	1.52	0.88
12:L:117:ARG:O	12:L:120:TYR:N	2.06	0.88
13:M:10:PRO:HB2	13:M:18:ALA:HB1	1.52	0.88
2:B:236:TYR:O	2:B:239:VAL:HG23	1.73	0.88
1:A:1493[A]:A:H2	23:W:36:A:HO2'	1.19	0.88
7:G:18:TYR:OH	7:G:58:PRO:HG2	1.74	0.87
1:A:1136:U:H5''	1:A:1137:C:OP2	1.74	0.87
1:A:353:A:OP1	29:A:2224:HOH:O	1.91	0.87
9:I:8:GLY:HA2	9:I:79:LEU:HD13	1.55	0.87
1:A:1047:G:H5''	14:N:4:LYS:HD3	1.56	0.87
16:P:1:MET:O	16:P:1:MET:HG2	1.75	0.87
1:A:1035:A:H2'	1:A:1036:G:C8	2.09	0.87
15:O:25:THR:O	15:O:29:VAL:HG23	1.75	0.87
16:P:74:LEU:HB3	16:P:79:VAL:HG21	1.54	0.87
1:A:839:U:O2	1:A:839:U:H2'	1.72	0.87
1:A:1256:A:H4'	1:A:1257:U:O5'	1.74	0.86
1:A:974:A:OP2	14:N:41:ARG:NH1	2.09	0.86
1:A:176:C:O2'	1:A:177:C:H5'	1.75	0.86
10:J:82:ILE:HA	10:J:85:LEU:CB	2.05	0.86
20:T:61:SER:OG	20:T:65:LYS:HD2	1.73	0.86
1:A:1381:U:H5	1:A:1382:C:C5	1.92	0.86
13:M:39:ILE:HG22	13:M:40:ASN:O	1.76	0.86
1:A:1493[A]:A:C8	1:A:1493[A]:A:C3'	2.59	0.86
5:E:51:VAL:HG23	5:E:52:PRO:HD3	1.57	0.86
6:F:98:LEU:H	6:F:98:LEU:HD13	1.41	0.85
1:A:1412:C:H2'	1:A:1413:A:H8	1.39	0.85
8:H:112:LEU:N	8:H:112:LEU:HD23	1.91	0.85
10:J:40:LEU:HB2	10:J:69:ASN:HB2	1.58	0.85
13:M:19:LEU:O	13:M:22:ILE:HG12	1.76	0.85
1:A:1004:A:H5''	29:A:2325:HOH:O	1.75	0.85
1:A:284:G:H2'	1:A:285:G:H8	1.41	0.85
1:A:54:C:C4	1:A:352:C:C5	2.65	0.85
13:M:108:ARG:NH2	13:M:114:ARG:HA	1.92	0.85
1:A:1068:G:OP2	1:A:1068:G:H8	1.59	0.85
1:A:1225:A:H5'	1:A:1226:C:OP2	1.77	0.85
1:A:328:C:C2'	1:A:328:C:O2	2.22	0.85
4:D:150:GLU:HA	4:D:153:ARG:HG3	1.56	0.85
1:A:192:U:C1'	20:T:103:GLY:HA2	2.05	0.85
4:D:192:GLU:N	4:D:192:GLU:OE2	2.10	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:981:U:H5'	14:N:21:TYR:CE1	2.12	0.85
1:A:393:A:C2	1:A:394:G:C8	2.64	0.85
1:A:821:G:H4'	29:A:2105:HOH:O	1.74	0.84
12:L:27:LEU:C	12:L:29:GLY:H	1.81	0.84
3:C:123:GLN:O	3:C:128:PHE:HB2	1.77	0.84
3:C:16:ARG:HG2	3:C:16:ARG:HH11	1.40	0.84
3:C:58:GLU:H	3:C:65:ALA:HB3	1.43	0.84
19:S:15:LEU:O	19:S:19:VAL:HG12	1.77	0.84
20:T:57:ARG:NH2	20:T:100:ILE:HD13	1.93	0.84
1:A:54:C:C4	1:A:352:C:H5	1.96	0.84
2:B:61:LEU:HD13	2:B:66:GLY:HA3	1.60	0.84
11:K:33:THR:HG22	11:K:39:PRO:HA	1.58	0.84
1:A:304:U:O4	29:A:2495:HOH:O	1.94	0.84
17:Q:10:VAL:HG11	17:Q:52:LYS:O	1.77	0.84
1:A:114:U:O2'	1:A:115:G:H5'	1.78	0.83
1:A:509:A:O2'	1:A:510:A:OP1	1.93	0.83
4:D:189:PRO:HB2	4:D:194:LEU:HD21	1.59	0.83
1:A:604:G:C2'	1:A:605:U:H5'	2.07	0.83
1:A:1321:C:H4'	13:M:87:TYR:HE2	1.42	0.83
4:D:98:GLU:OE2	4:D:107:ARG:HD3	1.77	0.83
10:J:34:VAL:HG13	10:J:74:ILE:HG22	1.59	0.83
5:E:90:VAL:O	5:E:91:LEU:HD23	1.77	0.83
1:A:1212:U:H1'	1:A:1213:A:OP2	1.78	0.83
2:B:170:GLU:OE2	2:B:170:GLU:HA	1.79	0.83
16:P:67:THR:HG22	16:P:68:ASP:N	1.91	0.83
18:R:38:GLU:OE2	18:R:38:GLU:N	2.12	0.83
1:A:1281:U:H4'	1:A:1282:C:OP2	1.76	0.83
1:A:1300:G:O2'	1:A:1301:U:P	2.37	0.83
8:H:112:LEU:HD23	8:H:112:LEU:H	1.44	0.83
1:A:448:A:O2'	1:A:449:C:H5'	1.79	0.83
15:O:45:VAL:HB	15:O:46:HIS:ND1	1.92	0.83
19:S:18:LYS:HG2	19:S:31:ILE:HD11	1.59	0.83
4:D:70:ILE:HG22	4:D:71:SER:O	1.79	0.82
10:J:47:PHE:CZ	14:N:37:PHE:HE1	1.97	0.82
2:B:82:ARG:HA	2:B:92:TYR:CE2	2.14	0.82
9:I:32:ASP:OD1	9:I:33:PHE:N	2.12	0.82
1:A:1435:G:H2'	1:A:1436:U:H6	1.40	0.82
2:B:130:ARG:NH1	2:B:134:GLU:OE1	2.12	0.82
1:A:1057:G:H5''	3:C:154:SER:HB2	1.61	0.82
19:S:17:GLU:HA	19:S:20:LEU:HD12	1.60	0.82
23:W:31:C:H42	23:W:39:G:H1	0.84	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:120:VAL:O	3:C:124:ILE:HG13	1.80	0.82
1:A:1399:C:O2	1:A:1401:G:C5	2.32	0.82
9:I:17:VAL:HG13	9:I:63:ILE:HD11	1.62	0.82
15:O:26:GLU:OE2	15:O:77:ARG:NH1	2.12	0.82
1:A:512:U:O2	1:A:540:G:N2	2.13	0.81
5:E:144:THR:O	5:E:148:VAL:CG2	2.28	0.81
1:A:1532:U:C4	1:A:1533:C:N4	2.48	0.81
19:S:10:PHE:O	19:S:39:THR:OG1	1.98	0.81
1:A:107:G:C2'	1:A:108:G:H5''	2.09	0.81
1:A:1314:C:OP2	19:S:6:LYS:HD3	1.80	0.81
4:D:173:TRP:O	4:D:174:LEU:HD23	1.80	0.81
1:A:1054:C:C3'	1:A:1054:C:O2	2.28	0.81
1:A:839:U:H5'	1:A:840:C:H5	1.44	0.81
2:B:131:PRO:O	2:B:134:GLU:HB3	1.80	0.81
1:A:1152:A:OP1	10:J:68:HIS:ND1	2.14	0.81
1:A:117:G:OP2	29:A:2018:HOH:O	1.98	0.81
1:A:138:G:H8	1:A:138:G:H5'	1.45	0.81
17:Q:100:LYS:HB2	17:Q:101:ARG:NH1	1.96	0.81
17:Q:40:LYS:HG2	17:Q:41:LYS:N	1.93	0.81
21:U:10:ARG:CG	21:U:10:ARG:HH11	1.94	0.81
1:A:1532:U:H2'	1:A:1533:C:H6	1.46	0.81
1:A:1399:C:C6	1:A:1502:A:N6	2.48	0.81
7:G:5:ARG:HG3	7:G:7:ALA:N	1.96	0.81
19:S:18:LYS:O	19:S:22:LEU:HG	1.81	0.81
4:D:120:LEU:HD22	4:D:126:ILE:HD11	1.61	0.80
4:D:19:LEU:HD23	4:D:19:LEU:H	1.45	0.80
1:A:673:G:H2'	1:A:674:G:C8	2.15	0.80
1:A:392:G:H2'	1:A:393:A:H8	1.46	0.80
1:A:1300:G:O2'	1:A:1301:U:O5'	1.99	0.80
1:A:303:A:N6	29:A:2495:HOH:O	2.15	0.80
1:A:1057:G:H5''	3:C:154:SER:CB	2.12	0.80
1:A:141:A:H1'	1:A:182:U:O2	1.82	0.80
1:A:415:A:H2'	1:A:416:G:H8	1.44	0.80
1:A:539:A:H2'	1:A:540:G:C8	2.17	0.80
1:A:250:A:H4'	1:A:251:G:O5'	1.82	0.80
1:A:628:G:C2'	1:A:629:G:H5'	2.12	0.80
1:A:984:C:H42	1:A:1221:G:H1	1.28	0.80
1:A:1412:C:OP1	12:L:57:LYS:NZ	2.15	0.80
1:A:1496:C:H2'	1:A:1497:G:C8	2.16	0.80
1:A:853:G:C2'	1:A:854:G:H5'	2.12	0.80
10:J:16:LEU:HD21	10:J:70:ARG:HG3	1.63	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1356:G:H2'	1:A:1357:A:C8	2.17	0.80
4:D:18:LYS:HE3	4:D:20:TYR:CE2	2.17	0.80
1:A:89:C:H5	1:A:90:U:C4	2.00	0.80
1:A:1054:C:O2	23:W:34:G:H5'	1.81	0.80
13:M:19:LEU:O	13:M:22:ILE:CG1	2.30	0.79
18:R:43:PHE:C	18:R:44:LEU:HD23	2.02	0.79
2:B:87:ARG:HD2	2:B:88:ALA:H	1.47	0.79
13:M:84:ILE:HD12	13:M:86:CYS:HB2	1.64	0.79
1:A:512:U:OP1	4:D:46:LYS:NZ	2.15	0.79
7:G:74:GLU:HG2	7:G:91:VAL:HG22	1.63	0.79
17:Q:29:HIS:CE1	17:Q:32:TYR:H	2.01	0.79
19:S:80:TYR:CE1	19:S:81:ARG:HG2	2.16	0.79
1:A:114:U:C2'	1:A:115:G:H5'	2.13	0.79
1:A:1101:A:H4'	1:A:1102:A:O5'	1.82	0.79
1:A:624:C:H5''	29:A:2767:HOH:O	1.82	0.79
4:D:100:ARG:NH1	4:D:137:SER:HA	1.97	0.79
15:O:5:LYS:HA	15:O:5:LYS:HZ2	1.43	0.79
7:G:120:ILE:HD13	7:G:120:ILE:H	1.48	0.79
8:H:55:GLY:HA3	8:H:56:LYS:HE3	1.63	0.79
15:O:9:GLN:OE1	15:O:9:GLN:HA	1.81	0.79
1:A:1515[B]:C:N4	1:A:1520[B]:G:O6	2.14	0.79
1:A:229:U:H2'	1:A:230:G:H5'	1.62	0.79
1:A:777:A:OP1	29:A:2536:HOH:O	2.00	0.79
1:A:89:C:H5	1:A:90:U:H3	1.16	0.79
1:A:542:G:OP1	4:D:10:ARG:NH2	2.16	0.79
9:I:50:LEU:CD1	9:I:81:ILE:HG21	2.08	0.79
20:T:50:GLU:CA	20:T:99:LEU:HD11	2.13	0.79
1:A:1272:G:N7	29:A:2695:HOH:O	2.16	0.78
1:A:924:C:O2'	1:A:1399:C:H6	1.65	0.78
1:A:1346:A:C4	7:G:10:ARG:NH1	2.51	0.78
1:A:527:7MG:OP2	27:A:1928:SRV:O32	2.01	0.78
2:B:87:ARG:HE	2:B:219:VAL:HG11	1.48	0.78
8:H:10:LEU:HD23	8:H:10:LEU:N	1.97	0.78
9:I:43:ALA:HA	9:I:74:ILE:HD12	1.63	0.78
9:I:69:GLY:O	9:I:73:GLN:HG3	1.83	0.78
9:I:90:PRO:O	9:I:93:ARG:HG3	1.82	0.78
20:T:67:ALA:O	20:T:73:HIS:ND1	2.16	0.78
3:C:86:VAL:O	3:C:89:GLU:HB3	1.82	0.78
1:A:1033:G:H2'	1:A:1034:G:H5'	1.66	0.78
1:A:643:C:H2'	1:A:644:G:H5''	1.65	0.78
4:D:61:LYS:HD2	4:D:62:GLN:N	1.97	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:85:LEU:HD23	15:O:85:LEU:N	1.97	0.78
1:A:352:C:O2'	1:A:354:G:OP1	2.02	0.78
4:D:159:ARG:HG2	4:D:159:ARG:HH11	1.48	0.78
5:E:126:ARG:CG	5:E:126:ARG:HH11	1.97	0.78
5:E:24:ARG:HG2	5:E:24:ARG:HH11	1.47	0.78
8:H:4:ASP:OD2	8:H:85:ARG:NE	2.15	0.78
1:A:1147:C:H4'	9:I:5:TYR:HE2	1.47	0.78
1:A:76:C:O2'	1:A:77:G:H5'	1.83	0.78
5:E:48:ALA:HB1	5:E:49:PRO:HD2	1.65	0.78
20:T:10:LEU:CD2	20:T:13:LEU:H	1.96	0.78
1:A:1400:5MC:H3'	1:A:1401:G:C5'	2.14	0.78
1:A:597:G:H1	1:A:643:C:H42	1.29	0.78
1:A:965:A:C2	1:A:969:A:C2	2.72	0.78
1:A:1347:G:O2'	1:A:1348:U:P	2.41	0.78
5:E:144:THR:HG22	5:E:145:LYS:H	1.49	0.78
9:I:31:GLN:NE2	9:I:36:TYR:HD1	1.81	0.78
1:A:1157:A:H4'	1:A:1158:C:O5'	1.83	0.77
1:A:643:C:C2'	1:A:644:G:H5''	2.14	0.77
7:G:97:GLN:O	7:G:101:LEU:HD12	1.84	0.77
1:A:768:A:OP2	29:A:2052:HOH:O	2.02	0.77
3:C:46:GLU:HB3	3:C:47:LEU:HD12	1.66	0.77
4:D:15:GLU:HG3	4:D:63:LYS:HD3	1.65	0.77
6:F:48:LEU:CD1	6:F:52:ILE:HG13	2.14	0.77
9:I:121:ARG:HH11	9:I:121:ARG:HG3	1.48	0.77
21:U:10:ARG:NH1	21:U:10:ARG:CB	2.45	0.77
15:O:74:ASP:OD2	15:O:77:ARG:HG2	1.84	0.77
20:T:54:LYS:HG2	20:T:55:ILE:HD12	1.65	0.77
3:C:179:ARG:HD2	3:C:207:VAL:HG22	1.65	0.77
1:A:1534:C:N3	1:A:1535:A:C2	2.53	0.77
2:B:36:ARG:HG3	2:B:41:ILE:HD11	1.66	0.77
4:D:119:GLN:HG3	4:D:123:HIS:HD1	1.49	0.77
4:D:208:SER:HA	29:D:404:HOH:O	1.85	0.77
9:I:108:VAL:HG12	9:I:109:VAL:N	1.99	0.77
10:J:29:ARG:N	10:J:29:ARG:HD2	2.00	0.77
19:S:80:TYR:CD1	19:S:81:ARG:N	2.53	0.77
18:R:47:THR:HG22	18:R:48:GLY:H	1.50	0.77
3:C:116:VAL:O	3:C:120:VAL:HG23	1.85	0.77
1:A:673:G:H5''	6:F:87:ARG:NH1	2.00	0.77
13:M:11:ARG:HG3	13:M:12:ASN:N	1.99	0.77
1:A:201:C:H42	1:A:216:G:H1	1.32	0.77
1:A:89:C:C2'	1:A:90:U:O5'	2.33	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1026:G:H2'	1:A:1027:C:O2	1.84	0.76
12:L:53:ARG:HD2	12:L:93:LEU:HD21	1.65	0.76
1:A:1245:A:C2	1:A:1293:G:C2	2.74	0.76
27:A:1928:SRY:HI32	27:A:1928:SRY:C22	2.16	0.76
2:B:219:VAL:HA	2:B:222:ILE:HG12	1.66	0.76
4:D:32:ALA:O	4:D:36:ARG:N	2.17	0.76
5:E:8:GLU:HB3	5:E:34:VAL:HG12	1.65	0.76
13:M:51:ALA:O	13:M:54:VAL:HG12	1.85	0.76
1:A:1047:G:N7	29:A:2425:HOH:O	2.19	0.76
1:A:1498:UR3:H4'	1:A:1519[A]:MA6:H2	1.67	0.76
14:N:26:ARG:HD3	14:N:47:LEU:HD11	1.66	0.76
15:O:33:THR:HG23	15:O:63:ARG:NH1	1.99	0.76
1:A:137:C:C2'	1:A:138:G:H5''	2.15	0.76
2:B:240:GLN:O	2:B:240:GLN:HG2	1.84	0.76
6:F:12:PRO:CG	6:F:58:GLY:HA2	2.14	0.76
6:F:7:ASN:HD21	18:R:34:TYR:HE1	1.32	0.76
1:A:247:G:OP2	17:Q:100:LYS:HG2	1.85	0.76
3:C:155:GLY:O	3:C:196:LEU:HD22	1.85	0.76
11:K:48:ILE:HG22	11:K:49:GLY:H	1.48	0.76
1:A:628:G:O2'	1:A:629:G:H5'	1.86	0.76
7:G:64:GLN:O	7:G:68:ASN:ND2	2.18	0.76
2:B:6:THR:HB	2:B:48:MET:HE3	1.67	0.76
1:A:1268:A:OP1	29:A:2314:HOH:O	2.02	0.76
1:A:284:G:H2'	1:A:285:G:C8	2.21	0.76
1:A:677:U:H3	1:A:713:G:H22	1.32	0.76
3:C:11:ARG:NH1	3:C:177:THR:O	2.19	0.76
1:A:438:G:H4'	4:D:123:HIS:HD2	1.51	0.76
5:E:144:THR:HG22	5:E:145:LYS:N	2.01	0.76
10:J:42:THR:HG23	10:J:67:THR:O	1.85	0.76
1:A:1314:C:C5	19:S:6:LYS:HE2	2.21	0.76
1:A:1504:G:OP1	1:A:1507:A:H4'	1.86	0.76
1:A:543:C:O2'	1:A:544:G:H5'	1.85	0.76
2:B:16:HIS:CD2	2:B:17:PHE:HD2	2.04	0.76
18:R:26:LEU:HD11	18:R:42:ARG:CD	2.16	0.76
3:C:180:ALA:HB1	3:C:182:ILE:HG13	1.68	0.75
1:A:438:G:H4'	4:D:123:HIS:CD2	2.21	0.75
1:A:1034:G:H2'	1:A:1035:A:C8	2.22	0.75
1:A:1343:G:H1'	9:I:121:ARG:HH12	1.51	0.75
1:A:1407:5MC:C2'	1:A:1408:A:H5'	2.17	0.75
1:A:461:C:OP2	29:A:2254:HOH:O	2.04	0.75
9:I:53:VAL:HG21	9:I:85:LEU:HD11	1.66	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1003(A):G:N2	1:A:1038:C:O2	2.19	0.75
1:A:1408:A:H2'	1:A:1409:C:H6	1.49	0.75
1:A:463:A:H2'	1:A:474:G:H8	1.50	0.75
1:A:731:G:OP1	1:A:766:A:H1'	1.87	0.75
1:A:827:U:H5''	1:A:828:A:OP2	1.85	0.75
10:J:76:ASN:C	10:J:78:ASN:H	1.88	0.75
20:T:51:GLU:O	20:T:55:ILE:HD13	1.85	0.75
1:A:1225:A:H2'	1:A:1225:A:N3	2.00	0.75
10:J:76:ASN:O	10:J:78:ASN:N	2.19	0.75
12:L:117:ARG:O	12:L:119:LYS:N	2.20	0.75
15:O:8:LYS:O	15:O:11:VAL:HG13	1.86	0.75
1:A:73:C:N4	1:A:74:C:N4	2.34	0.75
1:A:853:G:H2'	1:A:854:G:H5'	1.68	0.75
15:O:70:LEU:CD2	15:O:78:TYR:HB2	2.15	0.75
1:A:1006:C:H42	1:A:1023:G:H1	1.34	0.75
1:A:1256:A:N6	1:A:1277:C:C5	2.54	0.75
4:D:173:TRP:HB3	4:D:187:ARG:HH21	1.52	0.75
5:E:122:GLU:OE1	5:E:131:ILE:HG13	1.86	0.75
7:G:90:GLU:HA	7:G:90:GLU:OE1	1.87	0.75
13:M:37:THR:O	13:M:55:ARG:HD2	1.86	0.75
1:A:1005:A:N7	1:A:1026:G:N1	2.30	0.75
1:A:1010:G:N2	1:A:1020:U:H1'	2.02	0.75
7:G:103:TRP:CE2	7:G:137:LYS:HG2	2.21	0.75
1:A:1054:C:OP1	1:A:1197:G:OP2	2.04	0.75
2:B:97:TRP:CE3	2:B:98:LEU:O	2.40	0.75
6:F:87:ARG:NH1	6:F:87:ARG:HG3	2.01	0.75
11:K:18:ARG:NH1	11:K:35:PRO:O	2.19	0.75
5:E:13:ILE:HG22	5:E:14:ARG:N	2.02	0.74
5:E:76:ILE:HG22	5:E:93:PRO:HG3	1.67	0.74
10:J:28:ARG:HB3	10:J:29:ARG:HH11	1.52	0.74
21:U:10:ARG:NH1	21:U:10:ARG:HB2	2.00	0.74
1:A:229:U:O2'	1:A:230:G:H5'	1.87	0.74
1:A:39:G:H2'	1:A:39:G:N3	2.81	0.74
1:A:427:U:OP1	4:D:13:ARG:NH2	2.20	0.74
15:O:17:ARG:NH1	15:O:17:ARG:HG3	1.91	0.74
15:O:15:PHE:CE2	15:O:85:LEU:HD21	2.21	0.74
20:T:44:ALA:HA	20:T:92:LEU:HD21	1.68	0.74
1:A:839:U:H5'	1:A:840:C:C5	2.23	0.74
4:D:8:VAL:O	4:D:11:LEU:N	2.17	0.74
1:A:1212:U:H4'	1:A:1213:A:O5'	1.84	0.74
9:I:48:GLU:HB3	9:I:101:PHE:CZ	2.23	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:644:G:H5'	1:A:644:G:C8	2.18	0.74
1:A:474:G:H4'	16:P:81:ARG:HH21	1.51	0.74
20:T:82:SER:O	20:T:86:ARG:HG3	1.87	0.74
3:C:137:ALA:O	3:C:141:VAL:HG23	1.87	0.74
1:A:503:C:OP2	12:L:116:SER:HB3	1.87	0.74
23:W:39:G:N2	23:W:40:PSU:O4	2.21	0.74
1:A:1404:5MC:H1'	1:A:1499:A:H2	1.52	0.74
1:A:297:G:N7	29:A:2519:HOH:O	2.19	0.74
1:A:348:G:N7	29:A:2636:HOH:O	2.21	0.74
1:A:440:A:H5'	1:A:442:C:OP2	1.88	0.74
1:A:583:A:OP2	29:A:2103:HOH:O	2.05	0.74
1:A:620:C:C2	4:D:135:LEU:HD22	2.22	0.74
10:J:78:ASN:OD1	10:J:79:ARG:NH1	2.21	0.74
1:A:331:G:OP2	29:A:2266:HOH:O	2.06	0.74
1:A:413:G:O2'	1:A:428:G:N2	2.20	0.74
1:A:1090:U:H2'	1:A:1091:U:H6	1.53	0.74
1:A:949:A:C2	1:A:1233:G:N3	2.56	0.74
4:D:52:SER:O	4:D:56:VAL:HG23	1.88	0.74
20:T:10:LEU:HD21	20:T:13:LEU:H	1.53	0.74
2:B:212:GLN:O	2:B:216:SER:HB3	1.88	0.73
2:B:75:LYS:HA	2:B:78:GLN:CG	2.16	0.73
7:G:17:VAL:HG12	7:G:18:TYR:N	2.01	0.73
14:N:9:LYS:HD2	14:N:9:LYS:O	1.88	0.73
1:A:289:G:OP2	29:A:2015:HOH:O	2.04	0.73
13:M:87:TYR:CE1	13:M:91:ARG:HD3	2.23	0.73
2:B:97:TRP:CZ2	2:B:102:LEU:HD13	2.22	0.73
6:F:101:ALA:HA	18:R:28:GLU:HB2	1.71	0.73
6:F:25:ILE:HD12	6:F:82:ARG:HH11	1.53	0.73
1:A:1133:G:N2	1:A:1141:C:N3	2.36	0.73
1:A:182:U:H5	1:A:183:G:C4	2.06	0.73
10:J:63:PHE:HA	14:N:59:ALA:CB	2.18	0.73
17:Q:81:ARG:HE	17:Q:84:LEU:HD11	1.52	0.73
17:Q:23:VAL:HG21	17:Q:42:TYR:CD1	2.23	0.73
20:T:10:LEU:HD21	20:T:13:LEU:N	2.04	0.73
1:A:52:G:O6	29:A:2441:HOH:O	2.06	0.73
9:I:89:ASN:HB3	9:I:92:TYR:CD1	2.23	0.73
15:O:15:PHE:CD2	15:O:30:ALA:HB2	2.23	0.73
1:A:939:G:H5'	7:G:102:ARG:NH2	2.04	0.73
1:A:1226:C:H4'	1:A:1227:A:OP1	1.88	0.73
1:A:1286:A:H2	21:U:22:ARG:NH2	1.86	0.73
1:A:243:A:C2	1:A:246:A:C8	2.76	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:103:THR:N	2:B:176:GLU:OE1	2.20	0.73
1:A:1518[B]:MA6:N6	1:A:1519[B]:MA6:H103	2.04	0.73
1:A:1321:C:H4'	13:M:87:TYR:CE2	2.23	0.73
20:T:13:LEU:HD12	20:T:14:LYS:HA	1.71	0.73
1:A:1408:A:H2'	1:A:1409:C:C6	2.24	0.72
1:A:1510:U:H2'	1:A:1511:G:C8	2.23	0.72
2:B:44:LEU:H	2:B:44:LEU:HD22	1.53	0.72
15:O:15:PHE:CZ	15:O:85:LEU:HD21	2.24	0.72
1:A:1193:G:H2'	1:A:1194:U:H6	1.54	0.72
1:A:1407:5MC:H2'	1:A:1408:A:H5'	1.71	0.72
1:A:444:C:H42	1:A:490:G:H1	1.37	0.72
3:C:130:VAL:HG11	3:C:157:ILE:HG22	1.70	0.72
1:A:157:G:H5''	1:A:158:G:OP2	1.90	0.72
1:A:500:G:C6	1:A:501:C:N4	2.58	0.72
6:F:74:ASP:N	6:F:74:ASP:OD2	2.19	0.72
9:I:118:LYS:O	9:I:120:ARG:N	2.20	0.72
20:T:45:GLN:HA	20:T:91:LEU:CD2	2.19	0.72
1:A:421:U:OP2	1:A:422:C:N4	2.22	0.72
6:F:82:ARG:HB2	6:F:85:VAL:HG23	1.72	0.72
1:A:977:A:H2'	1:A:978:A:H5'	1.69	0.72
1:A:1403:C:O2'	1:A:1404:5MC:H5'	1.89	0.72
1:A:9:G:OP2	5:E:121:LYS:NZ	2.20	0.72
5:E:144:THR:O	5:E:148:VAL:HG23	1.89	0.72
13:M:19:LEU:O	13:M:22:ILE:HD11	1.89	0.72
1:A:345:C:OP2	1:A:345:C:H6	1.71	0.72
1:A:427:U:OP2	1:A:428:G:O2'	2.07	0.72
19:S:69:HIS:HB3	19:S:73:GLU:OE1	1.88	0.72
1:A:1329:A:OP1	13:M:29:ARG:HG3	1.89	0.72
1:A:1537:U:H2'	1:A:1538:C:C6	2.25	0.72
3:C:150:LYS:HG3	3:C:169:ALA:CB	2.18	0.72
1:A:107:G:H2'	1:A:108:G:C5'	2.20	0.72
1:A:1385:G:N7	29:A:2670:HOH:O	2.23	0.72
1:A:928:G:O2'	1:A:1533:C:OP1	2.08	0.72
1:A:1536:C:H5	1:A:1537:U:C4	2.08	0.72
1:A:914:A:O5'	27:A:1928:SRV:HI33	1.88	0.72
3:C:195:VAL:C	3:C:196:LEU:HD23	2.11	0.72
4:D:22:LYS:CB	4:D:26:CYS:SG	2.78	0.72
13:M:19:LEU:O	13:M:22:ILE:CD1	2.37	0.72
18:R:47:THR:HG22	18:R:48:GLY:N	2.05	0.72
1:A:1347:G:O2'	1:A:1348:U:OP2	2.08	0.71
1:A:1402:4OC:CM2	1:A:1403:C:H5'	2.15	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1493[A]:A:O2'	1:A:1494:G:OP1	2.04	0.71
1:A:616:G:H1'	1:A:625:G:N2	2.05	0.71
3:C:174:PRO:O	3:C:177:THR:N	2.23	0.71
8:H:95:VAL:HG12	8:H:99:GLU:HB2	1.72	0.71
10:J:16:LEU:HD21	10:J:70:ARG:CG	2.20	0.71
16:P:22:THR:HA	16:P:33:ILE:HD12	1.71	0.71
17:Q:51:TYR:CD1	17:Q:73:VAL:HG11	2.25	0.71
18:R:44:LEU:HD23	18:R:44:LEU:N	2.04	0.71
1:A:1361(A):C:O2'	1:A:1362:C:O5'	2.05	0.71
1:A:179:A:H2'	1:A:180:U:H6	1.55	0.71
1:A:266:G:HO2'	1:A:267:C:P	2.12	0.71
1:A:273:A:H2'	1:A:274:A:H5'	1.71	0.71
1:A:791:G:C2'	1:A:792:A:H5'	2.20	0.71
2:B:97:TRP:CZ3	2:B:98:LEU:O	2.43	0.71
10:J:41:PRO:O	10:J:69:ASN:ND2	2.23	0.71
3:C:151:VAL:C	3:C:152:ILE:HD12	2.10	0.71
1:A:532:A:N6	1:A:1207:2MG:H5'	2.06	0.71
1:A:538:G:H5''	12:L:114:LYS:CB	2.17	0.71
17:Q:81:ARG:HE	17:Q:84:LEU:CD1	2.03	0.71
1:A:1366:C:H2'	1:A:1367:C:C6	2.25	0.71
1:A:1131:G:OP2	1:A:1131:G:H8	1.72	0.71
1:A:447:G:H2'	1:A:485:G:N2	2.05	0.71
1:A:835:U:O4	29:A:2788:HOH:O	2.06	0.71
1:A:893:C:O2'	1:A:894:G:H5'	1.90	0.71
1:A:89:C:O2'	1:A:90:U:P	2.49	0.71
1:A:1518[B]:MA6:H93	1:A:1519[B]:MA6:N1	2.05	0.71
1:A:382:A:O2'	1:A:383:A:H5'	1.90	0.71
1:A:1498:UR3:H4'	1:A:1519[A]:MA6:N1	2.04	0.71
1:A:415:A:H2'	1:A:416:G:C8	2.25	0.71
1:A:446:G:H2'	1:A:447:G:H5'	1.72	0.71
7:G:46:ALA:O	7:G:50:ILE:HG12	1.91	0.71
1:A:352:C:H6	1:A:352:C:H3'	1.55	0.71
1:A:951:G:OP2	13:M:102:ARG:NH2	2.24	0.71
11:K:40:ILE:HG23	11:K:75:TYR:CD1	2.25	0.71
2:B:102:LEU:N	2:B:102:LEU:HD12	2.06	0.71
3:C:10:PHE:CE1	3:C:178:LEU:HD11	2.26	0.71
1:A:77:G:C4	1:A:93:G:N2	2.59	0.70
6:F:12:PRO:HG3	6:F:58:GLY:CA	2.17	0.70
10:J:81:THR:HG22	10:J:82:ILE:HG13	1.73	0.70
1:A:537:G:H2'	1:A:538:G:H8	1.55	0.70
15:O:14:GLU:HG3	15:O:15:PHE:HD1	1.55	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:204:U:H4'	1:A:216:G:O5'	1.90	0.70
4:D:63:LYS:O	4:D:67:ILE:HD12	1.91	0.70
8:H:27:PRO:HA	8:H:58:TYR:CD2	2.27	0.70
10:J:50:ILE:HG13	10:J:60:ARG:HG2	1.72	0.70
12:L:27:LEU:C	12:L:29:GLY:N	2.45	0.70
1:A:782:A:OP1	29:A:2280:HOH:O	2.09	0.70
7:G:46:ALA:HA	7:G:49:ILE:HD12	1.74	0.70
12:L:20:LYS:CE	12:L:20:LYS:H	2.05	0.70
1:A:104:G:H2'	1:A:105:G:H5''	1.72	0.70
3:C:147:LYS:CE	3:C:205:GLY:H	2.04	0.70
5:E:81:GLU:OE2	5:E:88:LYS:HD3	1.92	0.70
8:H:82:HIS:ND1	8:H:138:TRP:NE1	2.38	0.70
14:N:22:THR:HG23	14:N:33:VAL:HG21	1.72	0.70
10:J:62:HIS:O	14:N:59:ALA:HB3	1.90	0.70
1:A:1110:A:OP2	29:A:2142:HOH:O	2.09	0.70
1:A:1534:C:C4	1:A:1535:A:N1	2.59	0.70
2:B:82:ARG:HA	2:B:92:TYR:CD2	2.27	0.70
8:H:118:VAL:C	8:H:119:LEU:HD23	2.12	0.70
17:Q:11:VAL:HG11	17:Q:88:TYR:CD2	2.26	0.70
1:A:1270:C:OP2	21:U:24:ARG:NH2	2.25	0.70
7:G:97:GLN:HG3	7:G:98:SER:N	2.07	0.70
19:S:39:THR:O	19:S:41:VAL:HG13	1.92	0.70
1:A:689:C:C2'	1:A:690:G:H5'	2.21	0.70
2:B:238:LEU:HD23	2:B:238:LEU:O	1.91	0.70
5:E:11:ILE:HG22	5:E:31:LEU:HB3	1.73	0.70
1:A:266:G:C8	1:A:266:G:C5'	2.69	0.70
1:A:298:A:N6	29:A:2215:HOH:O	2.25	0.70
7:G:12:LEU:HD12	7:G:12:LEU:N	1.93	0.70
1:A:22:G:H2'	1:A:23:C:H6	1.57	0.70
1:A:918:A:H2'	1:A:919:A:C8	2.27	0.70
6:F:10:LEU:CD1	6:F:59:TYR:HB3	2.21	0.70
12:L:127:GLU:CG	12:L:128:ALA:N	2.40	0.70
7:G:50:ILE:CG2	7:G:58:PRO:HA	2.16	0.69
8:H:73:ASP:OD2	8:H:75:ARG:HG3	1.92	0.69
27:A:1928:SRY:O61	12:L:46:LYS:HD2	1.92	0.69
15:O:21:ASP:OD1	15:O:24:SER:HB3	1.92	0.69
16:P:15:PRO:HD2	16:P:42:ARG:HD3	1.74	0.69
1:A:1300:G:HO2'	1:A:1301:U:P	2.14	0.69
1:A:1533:C:O2'	1:A:1534:C:OP1	2.09	0.69
2:B:25:ASN:HD21	2:B:193:ASP:HB2	1.51	0.69
4:D:146:ILE:N	4:D:146:ILE:CD1	2.56	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:27:LEU:HG	12:L:28:LYS:N	2.06	0.69
13:M:8:GLU:OE2	13:M:22:ILE:HA	1.92	0.69
14:N:13:THR:N	14:N:14:PRO:HD3	2.06	0.69
17:Q:51:TYR:CE1	17:Q:73:VAL:HG11	2.27	0.69
1:A:88:A:N7	1:A:89:C:N4	2.39	0.69
1:A:707:C:H4'	11:K:20:TYR:CE1	2.27	0.69
1:A:1130:A:OP1	1:A:1131:G:OP2	2.11	0.69
1:A:1213:A:H4'	1:A:1214:C:OP1	1.92	0.69
1:A:1454:G:N7	29:A:2825:HOH:O	2.25	0.69
1:A:21:G:H2'	1:A:22:G:C8	2.27	0.69
1:A:463:A:H2'	1:A:474:G:C8	2.27	0.69
1:A:606:G:N1	29:A:2550:HOH:O	2.25	0.69
1:A:1286:A:C2	21:U:22:ARG:NH2	2.60	0.69
1:A:1206:G:C6	1:A:1207:2MG:C5	2.81	0.69
1:A:1518[B]:MA6:H93	1:A:1519[B]:MA6:C6	2.22	0.69
1:A:1527:C:O2'	1:A:1528:U:H5'	1.92	0.69
4:D:4:TYR:O	4:D:4:TYR:CD2	2.45	0.69
1:A:316:G:O2'	29:A:2463:HOH:O	2.10	0.69
2:B:84:GLU:HB3	2:B:219:VAL:HG21	1.75	0.69
5:E:37:ARG:NH1	5:E:37:ARG:HG2	2.03	0.69
7:G:16:LEU:H	7:G:16:LEU:CD2	2.04	0.69
12:L:34:ARG:HB2	12:L:105:TYR:HE1	1.57	0.69
10:J:47:PHE:HB3	14:N:34:TYR:HE2	1.58	0.69
19:S:31:ILE:O	19:S:50:ALA:HB3	1.91	0.69
20:T:45:GLN:HA	20:T:91:LEU:HD22	1.74	0.69
3:C:62:ASP:O	3:C:97:LYS:HG2	1.92	0.69
1:A:1395:C:O2'	1:A:1396:A:H5'	1.91	0.69
1:A:924:C:O2'	1:A:1399:C:C6	2.41	0.69
3:C:58:GLU:HB2	10:J:92:THR:HG21	1.75	0.69
6:F:7:ASN:ND2	18:R:34:TYR:HE1	1.91	0.69
1:A:620:C:H2'	1:A:621:A:O4'	1.93	0.69
5:E:48:ALA:HB1	5:E:49:PRO:CD	2.22	0.69
1:A:1003:G:C2	1:A:1003(A):G:C6	2.81	0.69
1:A:1057:G:C4	1:A:1204:A:C2	2.81	0.69
9:I:28:VAL:O	9:I:31:GLN:N	2.25	0.69
10:J:51:ARG:HG3	10:J:59:SER:O	1.92	0.69
14:N:15:LYS:O	14:N:16:PHE:CD2	2.46	0.69
15:O:70:LEU:HD22	15:O:78:TYR:HB2	1.72	0.69
1:A:1047:G:O2'	1:A:1048:G:H5'	1.93	0.69
1:A:119:A:OP2	29:A:2559:HOH:O	2.11	0.69
1:A:79:G:C2	1:A:80:G:C8	2.81	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:814:A:H2'	1:A:816:A:C5'	2.23	0.69
2:B:47:THR:HA	2:B:202:PRO:HG2	1.75	0.69
1:A:1062:U:H2'	1:A:1063:C:C6	2.28	0.68
1:A:117:G:OP2	29:A:2016:HOH:O	2.11	0.68
1:A:1419:G:C6	1:A:1420:C:C4	2.81	0.68
9:I:19:LEU:HB3	9:I:59:PHE:CE2	2.28	0.68
1:A:1249:C:O2'	9:I:73:GLN:NE2	2.27	0.68
20:T:50:GLU:N	20:T:99:LEU:HD11	2.08	0.68
1:A:1501:C:N4	1:A:1504:G:N3	2.42	0.68
6:F:95:GLU:O	18:R:32:ARG:NH1	2.27	0.68
7:G:148:ASN:O	7:G:150:ALA:N	2.25	0.68
8:H:121:ASP:HB2	8:H:125:ARG:NH2	2.08	0.68
18:R:59:SER:H	18:R:62:GLU:HB2	1.58	0.68
23:W:37:A:N1	23:W:38:A:C2	2.61	0.68
9:I:5:TYR:HD1	9:I:6:GLY:N	1.91	0.68
1:A:1033:G:C2'	1:A:1034:G:H5'	2.23	0.68
7:G:120:ILE:HG22	7:G:124:LEU:HD11	1.74	0.68
10:J:63:PHE:HB2	14:N:57:ARG:O	1.93	0.68
1:A:1066:C:H2'	1:A:1067:A:H5'	1.76	0.68
1:A:1279:A:H4'	1:A:1280:A:OP1	1.93	0.68
1:A:1369:C:H2'	1:A:1370:G:C8	2.28	0.68
1:A:392:G:H2'	1:A:393:A:C8	2.29	0.68
1:A:357:G:N7	29:A:2433:HOH:O	2.27	0.68
6:F:100:ASN:OD1	18:R:23:LYS:HE3	1.93	0.68
1:A:1067:A:O3'	29:A:2218:HOH:O	2.11	0.68
5:E:24:ARG:CG	5:E:24:ARG:HH11	2.07	0.68
10:J:9:ARG:CZ	10:J:9:ARG:HB3	2.23	0.68
16:P:58:TYR:CE1	16:P:62:VAL:HG11	2.28	0.68
21:U:13:ILE:HG22	21:U:22:ARG:CZ	2.24	0.68
1:A:1436:U:H2'	1:A:1437:C:H6	1.59	0.68
1:A:828:A:H4'	1:A:828:A:OP1	1.94	0.68
9:I:15:ALA:HB1	9:I:77:ILE:HD12	1.76	0.68
17:Q:29:HIS:CE1	17:Q:31:LEU:H	2.11	0.68
1:A:1311:G:N7	19:S:2:PRO:HA	2.08	0.68
19:S:19:VAL:HG23	19:S:47:HIS:ND1	2.09	0.68
3:C:112:SER:O	3:C:115:LEU:HB2	1.93	0.68
3:C:85:ARG:HG2	3:C:86:VAL:N	2.09	0.68
9:I:55:ALA:HA	9:I:58:HIS:HB2	1.75	0.68
1:A:704:A:H5''	1:A:705:U:OP2	1.94	0.68
1:A:865:A:C2'	1:A:866:C:H5'	2.24	0.68
3:C:155:GLY:HA2	3:C:164:ARG:O	1.93	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:79:PHE:O	4:D:82:ALA:N	2.27	0.68
14:N:24:CYS:HB2	14:N:29:ARG:HB3	1.76	0.68
15:O:14:GLU:CG	15:O:15:PHE:HD1	2.07	0.68
1:A:1003:G:N2	1:A:1039:C:C2	2.61	0.67
2:B:92:TYR:HD1	2:B:151:GLY:HA3	1.59	0.67
9:I:11:LYS:O	9:I:12:GLU:HB2	1.93	0.67
10:J:28:ARG:HB3	10:J:29:ARG:HD2	1.76	0.67
11:K:33:THR:HG22	11:K:39:PRO:CA	2.24	0.67
4:D:206:PHE:CD2	4:D:207:TYR:CE2	2.81	0.67
1:A:1086:U:H3	1:A:1099:G:H22	1.42	0.67
1:A:358:U:H2'	1:A:359:U:C6	2.29	0.67
5:E:131:ILE:HG22	5:E:132:ALA:N	2.09	0.67
5:E:75:THR:HG23	5:E:76:ILE:N	2.08	0.67
12:L:6:THR:OG1	12:L:9:GLN:HG3	1.92	0.67
17:Q:53:LEU:HD11	17:Q:85:VAL:HG11	1.76	0.67
1:A:1014:A:N7	1:A:1015:A:C6	2.63	0.67
1:A:1060:C:H1'	1:A:1198:G:N2	2.10	0.67
1:A:975:A:H8	1:A:975:A:H5'	1.60	0.67
7:G:129:GLU:OE2	7:G:131:LYS:HE2	1.95	0.67
7:G:69:VAL:O	7:G:69:VAL:HG12	1.93	0.67
1:A:1347:G:C2'	1:A:1348:U:OP2	2.41	0.67
1:A:1497:G:O2'	1:A:1498:UR3:H5'	1.94	0.67
1:A:556:C:H2'	1:A:557:G:O4'	1.95	0.67
8:H:57:PRO:O	8:H:57:PRO:HG2	1.95	0.67
13:M:87:TYR:HE1	13:M:91:ARG:HD3	1.59	0.67
17:Q:59:ILE:HG22	17:Q:71:PHE:CD1	2.29	0.67
1:A:1342:C:H2'	1:A:1343:G:C8	2.29	0.67
1:A:109:A:C6	1:A:326:G:C6	2.83	0.67
1:A:785:G:C2'	1:A:786:G:H5'	2.24	0.67
1:A:814:A:H2'	1:A:816:A:H5'	1.77	0.67
1:A:975:A:H8	1:A:975:A:C5'	2.07	0.67
2:B:219:VAL:HA	2:B:222:ILE:CG1	2.24	0.67
8:H:86:ILE:HG21	8:H:133:LEU:HD13	1.77	0.67
10:J:48:THR:CA	10:J:62:HIS:HB3	2.25	0.67
11:K:120:ARG:HG2	11:K:120:ARG:NH1	2.08	0.67
15:O:4:THR:HG22	15:O:5:LYS:N	2.09	0.67
16:P:12:LYS:O	16:P:13:HIS:HB2	1.95	0.67
2:B:61:LEU:CD1	2:B:66:GLY:HA3	2.24	0.67
1:A:1310:G:O6	19:S:2:PRO:HG3	1.94	0.67
1:A:170:U:O2'	1:A:171:A:H5'	1.95	0.67
1:A:606:G:O6	29:A:2549:HOH:O	2.11	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:804:U:H5''	1:A:805:C:OP2	1.94	0.67
1:A:966:M2G:HM22	1:A:967:5MC:C2	2.30	0.67
1:A:995:C:O2	14:N:4:LYS:NZ	2.23	0.67
3:C:85:ARG:HG3	3:C:85:ARG:HH11	1.59	0.67
8:H:20:TYR:CE1	8:H:76:PRO:HD2	2.29	0.67
10:J:29:ARG:H	10:J:29:ARG:HD2	1.60	0.67
1:A:1125:U:O2'	1:A:1126:U:OP2	2.13	0.67
1:A:1443:G:C4'	1:A:1446:A:H5'	2.23	0.67
1:A:182:U:OP1	29:A:2183:HOH:O	2.11	0.67
1:A:509:A:H3'	1:A:509:A:C8	2.30	0.67
20:T:55:ILE:H	20:T:55:ILE:CD1	2.08	0.67
1:A:103:C:P	20:T:17:ARG:HH12	2.17	0.67
1:A:1299:A:C6	1:A:1301:U:O2	2.48	0.67
1:A:665:A:N3	1:A:732:C:H2'	2.10	0.67
17:Q:4:LYS:CG	17:Q:6:LEU:HD21	2.25	0.67
1:A:112:G:O2'	1:A:113:G:H5'	1.96	0.66
1:A:22:G:H2'	1:A:23:C:C6	2.30	0.66
2:B:36:ARG:HG3	2:B:41:ILE:CD1	2.24	0.66
1:A:407:G:OP1	4:D:115:ARG:NH2	2.28	0.66
4:D:15:GLU:CG	4:D:63:LYS:HD3	2.25	0.66
10:J:86:MET:HG3	10:J:87:THR:N	2.05	0.66
16:P:10:GLY:HA3	16:P:14:ASN:O	1.94	0.66
17:Q:51:TYR:CE1	17:Q:73:VAL:CG1	2.78	0.66
20:T:44:ALA:O	20:T:47:GLY:N	2.28	0.66
1:A:661:G:H8	1:A:661:G:H5''	1.58	0.66
3:C:182:ILE:HG23	3:C:202:ILE:O	1.95	0.66
5:E:105:VAL:HB	5:E:106:PRO:HD3	1.75	0.66
9:I:46:ALA:HB1	9:I:77:ILE:CG2	2.25	0.66
12:L:45:PRO:HB3	12:L:93:LEU:HD23	1.77	0.66
13:M:16:ASP:O	13:M:19:LEU:N	2.28	0.66
20:T:29:LYS:O	20:T:32:ALA:HB3	1.95	0.66
1:A:643:C:H2'	1:A:644:G:C5'	2.24	0.66
15:O:4:THR:HG22	15:O:5:LYS:H	1.60	0.66
15:O:70:LEU:HD23	15:O:70:LEU:C	2.16	0.66
1:A:1015:A:N6	1:A:1016:A:C6	2.63	0.66
1:A:1078:U:H5''	1:A:1079:G:OP2	1.94	0.66
1:A:1490:C:H5''	27:A:1928:SRV:NC1	2.11	0.66
1:A:349:A:C2'	1:A:350:G:H5'	2.26	0.66
3:C:58:GLU:CB	10:J:92:THR:HG21	2.24	0.66
12:L:93:LEU:O	12:L:96:VAL:HG23	1.95	0.66
13:M:4:ILE:HG22	13:M:5:ALA:N	2.11	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:62:VAL:O	16:P:62:VAL:HG23	1.95	0.66
21:U:18:TYR:CE1	21:U:24:ARG:HG3	2.31	0.66
1:A:174:C:OP1	29:A:2211:HOH:O	2.14	0.66
1:A:179:A:H2'	1:A:180:U:C6	2.31	0.66
1:A:458:C:OP2	29:A:2257:HOH:O	2.13	0.66
1:A:509:A:O3'	29:A:2165:HOH:O	2.14	0.66
1:A:783:C:H42	1:A:799:G:H1	1.43	0.66
1:A:1011:G:C2'	1:A:1012:U:H5'	2.25	0.66
1:A:273:A:C2'	1:A:274:A:H5'	2.25	0.66
1:A:443:C:H42	1:A:491:G:H1	1.41	0.66
1:A:501:C:H2'	1:A:502:G:H8	1.61	0.66
1:A:946:A:H2'	1:A:947:G:C8	2.30	0.66
2:B:162:ILE:O	2:B:185:ILE:HD12	1.94	0.66
3:C:186:PHE:CD2	3:C:187:ALA:N	2.64	0.66
1:A:137:C:O2'	1:A:138:G:H5''	1.96	0.66
1:A:192:U:O4'	20:T:103:GLY:HA2	1.96	0.66
5:E:13:ILE:CG2	5:E:14:ARG:N	2.59	0.66
18:R:87:ARG:NH2	18:R:87:ARG:HG3	1.97	0.66
20:T:50:GLU:HA	20:T:99:LEU:HD11	1.77	0.66
1:A:1026:G:C2'	1:A:1027:C:H5''	2.23	0.66
1:A:1054:C:C2	23:W:34:G:H5'	2.30	0.66
1:A:1342:C:H2'	1:A:1343:G:H8	1.61	0.66
1:A:687:A:H4'	1:A:688:G:O5'	1.95	0.66
6:F:97:PHE:C	6:F:97:PHE:HD2	1.99	0.66
1:A:1532:U:H2'	1:A:1533:C:C5	2.31	0.66
1:A:944:G:OP1	29:A:2285:HOH:O	2.14	0.66
2:B:139:LYS:O	2:B:143:GLU:HG3	1.95	0.66
2:B:80:ILE:HD11	2:B:208:ILE:HG23	1.77	0.66
4:D:135:LEU:O	4:D:135:LEU:HD12	1.96	0.66
5:E:51:VAL:HG23	5:E:52:PRO:CD	2.26	0.66
10:J:80:LYS:HA	10:J:83:GLU:HB2	1.76	0.66
1:A:390:C:H4'	16:P:28:ARG:HH21	1.61	0.66
1:A:1480:G:H2'	1:A:1481:U:C6	2.31	0.65
1:A:89:C:HO2'	1:A:90:U:P	2.19	0.65
10:J:63:PHE:HA	14:N:59:ALA:HB2	1.77	0.65
1:A:1256:A:H8	1:A:1258:G:C2	2.15	0.65
1:A:76:C:C2'	1:A:77:G:H5'	2.27	0.65
5:E:79:GLU:HA	5:E:91:LEU:O	1.95	0.65
18:R:39:VAL:HG13	18:R:40:LEU:N	2.11	0.65
1:A:1030(A):G:H2'	1:A:1030(B):C:H5''	1.77	0.65
5:E:51:VAL:CG2	5:E:52:PRO:HD3	2.27	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:12:LEU:CD1	7:G:12:LEU:H	1.88	0.65
11:K:117:ASN:N	11:K:117:ASN:OD1	2.26	0.65
1:A:1197:G:OP1	29:A:2229:HOH:O	2.14	0.65
1:A:1480:G:H2'	1:A:1481:U:H6	1.61	0.65
1:A:545:C:H2'	1:A:545:C:O2	1.95	0.65
1:A:838:G:C3'	1:A:839:U:H5''	2.27	0.65
3:C:131:ARG:O	3:C:134:ILE:HG12	1.97	0.65
6:F:26:ILE:O	6:F:30:LEU:HD12	1.96	0.65
7:G:22:LEU:HD21	7:G:66:VAL:HG21	1.77	0.65
9:I:6:GLY:HA3	9:I:83:ARG:HB2	1.79	0.65
14:N:21:TYR:HE2	14:N:23:ARG:HE	1.44	0.65
20:T:49:ALA:HB3	20:T:99:LEU:CD2	2.21	0.65
1:A:1065:U:H5''	1:A:1190:G:N2	2.12	0.65
1:A:1407:5MC:C4	1:A:1408:A:N7	2.64	0.65
1:A:1425:U:H2'	1:A:1426:C:H6	1.60	0.65
7:G:27:ILE:HD11	7:G:40:ALA:HA	1.77	0.65
9:I:5:TYR:CD1	9:I:6:GLY:N	2.64	0.65
17:Q:11:VAL:HG11	17:Q:88:TYR:CE2	2.32	0.65
20:T:56:MET:CE	20:T:85:MET:HG3	2.26	0.65
20:T:73:HIS:O	20:T:76:ALA:HB3	1.96	0.65
1:A:474:G:H4'	16:P:81:ARG:NH2	2.11	0.65
1:A:793:U:H4'	1:A:794:A:OP2	1.97	0.65
2:B:161:ALA:HA	2:B:183:PRO:HD2	1.78	0.65
4:D:175:SER:OG	4:D:186:LEU:HD21	1.96	0.65
4:D:191:ARG:HD2	4:D:200:GLU:OE2	1.97	0.65
9:I:108:VAL:CG1	9:I:109:VAL:H	2.05	0.65
13:M:59:TYR:O	13:M:59:TYR:HD2	1.79	0.65
1:A:179:A:O2'	1:A:180:U:H5'	1.96	0.65
1:A:977:A:C2'	1:A:978:A:H5'	2.26	0.65
3:C:67:THR:HA	3:C:102:ASN:HB2	1.77	0.65
3:C:16:ARG:HG2	3:C:16:ARG:NH1	2.11	0.65
4:D:204:ILE:CD1	4:D:204:ILE:N	2.60	0.65
13:M:96:LEU:HD23	13:M:96:LEU:N	2.11	0.65
1:A:1200:C:O2	1:A:1205:U:N3	2.19	0.65
1:A:1294:G:N7	29:A:2265:HOH:O	2.30	0.65
1:A:913:A:O3'	27:A:1928:SRY:CI3	2.45	0.65
1:A:204:U:O2	1:A:204:U:H2'	1.97	0.65
1:A:91:C:H2'	1:A:92:C:C6	2.32	0.65
6:F:60:PHE:CZ	18:R:78:LEU:HD21	2.31	0.65
1:A:1222:G:OP2	1:A:1322:C:N4	2.30	0.65
1:A:436:C:H2'	1:A:437:U:C6	2.31	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:661:G:N7	29:A:2819:HOH:O	2.30	0.65
1:A:89:C:H2'	1:A:90:U:O5'	1.97	0.65
5:E:142:LEU:C	5:E:143:ARG:HG2	2.16	0.65
1:A:838:G:H3'	1:A:839:U:H5''	1.79	0.65
2:B:87:ARG:HD2	2:B:88:ALA:N	2.12	0.65
4:D:190:ASP:HB2	4:D:193:ASP:OD2	1.97	0.65
11:K:34:ASP:HB2	11:K:35:PRO:HD2	1.79	0.65
19:S:48:THR:C	19:S:49:ILE:HD13	2.17	0.65
20:T:55:ILE:N	20:T:55:ILE:CD1	2.61	0.65
1:A:1047:G:H2'	1:A:1048:G:H5'	1.77	0.64
1:A:411:A:C2	1:A:413:G:H1'	2.32	0.64
7:G:50:ILE:HG21	7:G:58:PRO:CA	2.20	0.64
1:A:393:A:O2'	1:A:394:G:H5'	1.97	0.64
3:C:5:ILE:HD12	3:C:5:ILE:C	2.18	0.64
7:G:71:PRO:O	7:G:96:GLN:NE2	2.24	0.64
11:K:27:ASN:OD1	11:K:28:THR:N	2.30	0.64
17:Q:29:HIS:CG	17:Q:30:PRO:HD2	2.33	0.64
2:B:84:GLU:OE1	2:B:216:SER:HA	1.97	0.64
1:A:1129:C:OP1	9:I:62:TYR:OH	2.15	0.64
1:A:976:G:OP2	1:A:1358:U:O2'	2.15	0.64
1:A:150:C:H2'	1:A:151:A:O5'	1.97	0.64
1:A:1536:C:H5	1:A:1537:U:N3	1.94	0.64
1:A:16:A:C2'	1:A:17:U:H5'	2.27	0.64
4:D:180:GLY:O	4:D:182:LYS:HG2	1.98	0.64
5:E:11:ILE:HG22	5:E:12:LEU:N	2.10	0.64
9:I:97:LYS:HA	9:I:102:LEU:HD11	1.78	0.64
15:O:14:GLU:CG	15:O:15:PHE:CD1	2.80	0.64
16:P:21:VAL:O	16:P:33:ILE:HB	1.96	0.64
17:Q:5:VAL:HG22	17:Q:60:ILE:HD12	1.79	0.64
20:T:99:LEU:HD12	20:T:100:ILE:N	2.12	0.64
20:T:13:LEU:HD12	20:T:14:LYS:CA	2.27	0.64
1:A:1201:A:H4'	1:A:1202:G:O5'	1.97	0.64
2:B:201:ILE:O	2:B:203:GLY:N	2.31	0.64
6:F:97:PHE:C	6:F:97:PHE:CD2	2.70	0.64
1:A:514:C:O2'	1:A:515:G:H5'	1.97	0.64
3:C:131:ARG:NH1	5:E:50:GLU:OE1	2.31	0.64
4:D:189:PRO:HB2	4:D:194:LEU:CD2	2.25	0.64
18:R:61:LYS:O	18:R:65:ILE:HD12	1.97	0.64
1:A:1132:C:H2'	1:A:1133:G:H5'	1.79	0.64
4:D:119:GLN:HG3	4:D:123:HIS:ND1	2.11	0.64
10:J:16:LEU:CD2	10:J:70:ARG:HG3	2.28	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:92:GLU:HB3	11:K:96:ARG:HH22	1.63	0.64
2:B:103:THR:HG23	2:B:176:GLU:OE1	1.98	0.64
4:D:131:ARG:NH1	4:D:131:ARG:HB2	2.13	0.64
4:D:146:ILE:N	4:D:146:ILE:HD12	2.12	0.64
6:F:67:MET:HB2	6:F:68:PRO:HD2	1.80	0.64
13:M:15:VAL:HG21	13:M:48:LEU:HD21	1.77	0.64
4:D:117:ALA:O	4:D:121:VAL:HG23	1.98	0.64
6:F:10:LEU:HD12	6:F:59:TYR:HB3	1.79	0.64
16:P:8:ARG:HB2	16:P:28:ARG:NH1	2.13	0.64
20:T:55:ILE:N	20:T:55:ILE:HD12	2.13	0.64
1:A:580:U:OP2	29:A:2740:HOH:O	2.15	0.64
1:A:689:C:O2'	1:A:690:G:H5'	1.98	0.64
3:C:47:LEU:CD2	3:C:68:VAL:HG11	2.28	0.64
4:D:32:ALA:HA	4:D:35:ARG:CB	2.22	0.64
1:A:1330:U:OP1	13:M:23:TYR:O	2.16	0.63
2:B:157:ARG:HG3	2:B:158:LEU:N	2.13	0.63
6:F:8:ILE:HD13	6:F:26:ILE:HD12	1.80	0.63
1:A:1303:C:O2	1:A:1303:C:H2'	1.97	0.63
1:A:1366:C:H2'	1:A:1367:C:H6	1.63	0.63
1:A:627:G:O2'	1:A:628:G:H5'	1.98	0.63
3:C:62:ASP:HA	3:C:97:LYS:NZ	2.12	0.63
1:A:1081:G:OP1	5:E:16:THR:OG1	2.16	0.63
10:J:25:GLU:HG2	10:J:28:ARG:HD2	1.79	0.63
17:Q:29:HIS:HB2	17:Q:36:ILE:CD1	2.29	0.63
17:Q:74:LEU:HD22	17:Q:75:ARG:HG2	1.78	0.63
1:A:1020:U:H2'	1:A:1021:G:H8	1.62	0.63
1:A:1256:A:C8	1:A:1258:G:N1	2.66	0.63
1:A:1372:U:OP1	9:I:71:SER:HB3	1.99	0.63
1:A:1493[B]:A:H2'	1:A:1494:G:N7	2.13	0.63
1:A:1518[B]:MA6:C10	1:A:1519[B]:MA6:H103	2.28	0.63
1:A:15:G:H4'	5:E:24:ARG:NH2	2.12	0.63
1:A:539:A:H2'	1:A:540:G:H8	1.63	0.63
1:A:943:U:C2'	1:A:944:G:H5'	2.28	0.63
1:A:959:A:H3'	1:A:960:U:H5''	1.81	0.63
2:B:119:GLU:HG3	2:B:142:LEU:HD11	1.79	0.63
8:H:97:VAL:HG12	8:H:98:LYS:N	2.13	0.63
16:P:58:TYR:CD1	16:P:58:TYR:C	2.72	0.63
6:F:99:ALA:HB1	18:R:23:LYS:HZ3	1.64	0.63
1:A:166:G:C2'	1:A:167:G:H5'	2.29	0.63
1:A:790:A:C8	1:A:791:G:N7	2.67	0.63
3:C:119:ARG:O	3:C:122:GLU:HB2	1.97	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:136:GLN:O	3:C:140:ARG:HG3	1.98	0.63
9:I:17:VAL:HG13	9:I:63:ILE:CD1	2.28	0.63
10:J:77:PRO:HA	10:J:81:THR:OG1	1.98	0.63
15:O:79:ARG:NH1	15:O:79:ARG:HG3	2.07	0.63
1:A:1068:G:C8	1:A:1068:G:OP2	2.48	0.63
1:A:1305:G:N2	1:A:1331:G:H1'	2.12	0.63
1:A:943:U:H2'	1:A:944:G:H5'	1.80	0.63
2:B:218:ALA:O	2:B:222:ILE:HG12	1.98	0.63
2:B:69:LEU:HD23	2:B:91:PRO:O	1.99	0.63
19:S:19:VAL:HG23	19:S:47:HIS:CE1	2.33	0.63
19:S:34:TRP:CZ2	19:S:57:HIS:HE1	2.16	0.63
1:A:112:G:C2'	1:A:113:G:H5'	2.29	0.63
1:A:54:C:N3	1:A:352:C:C5	2.67	0.63
1:A:500:G:C6	1:A:546:G:N2	2.66	0.63
1:A:627:G:O6	29:A:2664:HOH:O	2.14	0.63
1:A:785:G:H2'	1:A:786:G:H5'	1.79	0.63
3:C:14:ILE:HD13	3:C:14:ILE:N	2.13	0.63
3:C:150:LYS:HG3	3:C:169:ALA:HB2	1.80	0.63
3:C:16:ARG:NH2	3:C:183:ASP:OD2	2.32	0.63
4:D:164:ALA:O	4:D:168:ARG:HD2	1.99	0.63
1:A:1343:G:H1'	9:I:121:ARG:NH1	2.13	0.63
7:G:16:LEU:HD11	9:I:45:ALA:HB2	1.80	0.63
18:R:50:ILE:HD11	18:R:70:ILE:HG21	1.78	0.63
20:T:41:ILE:HD12	20:T:41:ILE:N	2.14	0.63
1:A:1291:G:H2'	1:A:1292:U:C6	2.34	0.63
1:A:266:G:H5'	1:A:266:G:H8	1.57	0.63
1:A:616:G:O2'	1:A:617:G:H5'	1.98	0.63
3:C:10:PHE:O	3:C:10:PHE:HD1	1.82	0.63
8:H:28:ALA:HA	8:H:59:LEU:HD11	1.80	0.63
2:B:179:LYS:HA	8:H:72:PRO:HD3	1.80	0.63
10:J:30:SER:HB2	10:J:80:LYS:CB	2.21	0.63
18:R:74:ARG:HB3	18:R:81:PHE:CE1	2.34	0.63
20:T:13:LEU:HD12	20:T:14:LYS:N	2.14	0.63
20:T:61:SER:O	20:T:62:LEU:C	2.37	0.63
1:A:1125:U:O2'	1:A:1126:U:P	2.57	0.63
1:A:1125:U:H3'	1:A:1126:U:H5	1.62	0.63
1:A:1130:A:OP1	1:A:1131:G:P	2.56	0.63
1:A:1204:A:OP2	29:A:2248:HOH:O	2.15	0.63
1:A:1281:U:C4'	1:A:1282:C:OP2	2.47	0.63
3:C:119:ARG:HH11	3:C:119:ARG:HG3	1.63	0.63
4:D:79:PHE:HD2	4:D:80:GLU:N	1.96	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:59:TYR:CD2	13:M:59:TYR:C	2.69	0.63
19:S:36:ARG:NH2	19:S:75:ALA:O	2.32	0.63
1:A:235:C:N4	29:A:2113:HOH:O	2.31	0.63
3:C:119:ARG:HH11	3:C:119:ARG:CG	2.11	0.63
3:C:188:LEU:HD11	3:C:195:VAL:CG1	2.28	0.63
1:A:1001:A:H2'	1:A:1002:G:C8	2.34	0.62
1:A:1003:G:N1	1:A:1003(A):G:O6	2.31	0.62
1:A:1314:C:OP2	19:S:6:LYS:CD	2.46	0.62
1:A:837:G:C2	1:A:850:U:O2	2.51	0.62
9:I:121:ARG:HH11	9:I:121:ARG:CG	2.10	0.62
12:L:84:LEU:O	12:L:101:VAL:HG23	1.99	0.62
15:O:14:GLU:HG2	15:O:15:PHE:CE1	2.34	0.62
1:A:1126:U:OP2	1:A:1281:U:H1'	1.99	0.62
3:C:191:THR:OG1	3:C:193:TYR:CE1	2.49	0.62
20:T:67:ALA:HA	20:T:73:HIS:H	1.65	0.62
1:A:1026:G:C8	1:A:1027:C:N3	2.68	0.62
1:A:1057:G:C5	1:A:1204:A:C2	2.87	0.62
6:F:62:TRP:CH2	6:F:64:GLN:HB2	2.35	0.62
7:G:120:ILE:HG22	7:G:124:LEU:CD1	2.29	0.62
19:S:15:LEU:HD13	19:S:16:LEU:N	2.15	0.62
1:A:1160:G:O6	1:A:1181:G:O6	2.16	0.62
1:A:1328:C:OP1	21:U:21:TYR:OH	2.13	0.62
1:A:352:C:C6	1:A:352:C:H3'	2.35	0.62
1:A:750:G:N3	15:O:23:GLY:HA3	2.14	0.62
2:B:180:LEU:O	2:B:181:PHE:HB2	1.98	0.62
7:G:17:VAL:CG1	7:G:18:TYR:N	2.62	0.62
8:H:127:LEU:O	8:H:127:LEU:HD23	1.99	0.62
23:W:37:A:N6	23:W:38:A:N1	2.47	0.62
1:A:1124:G:N7	1:A:1145:C:O2'	2.28	0.62
1:A:1316:G:H2'	1:A:1317:C:H5''	1.81	0.62
1:A:1425:U:H2'	1:A:1426:C:C6	2.34	0.62
16:P:26:ARG:HG3	16:P:27:LYS:N	2.13	0.62
1:A:99:C:H2'	1:A:101:A:C8	2.35	0.62
1:A:1519[A]:MA6:H3'	1:A:1520[A]:G:C5'	2.29	0.62
1:A:330:C:H2'	1:A:331:G:H5'	1.81	0.62
1:A:506:G:C5	1:A:507:C:C5	2.87	0.62
2:B:87:ARG:HE	2:B:219:VAL:CG1	2.11	0.62
7:G:120:ILE:N	7:G:120:ILE:CD1	2.52	0.62
8:H:28:ALA:HA	8:H:59:LEU:CD1	2.29	0.62
9:I:112:LYS:HA	9:I:119:ALA:HB2	1.80	0.62
13:M:16:ASP:O	13:M:19:LEU:HB2	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:13:LEU:HD12	20:T:13:LEU:C	2.20	0.62
1:A:35:G:C6	1:A:36:C:N4	2.68	0.62
3:C:33:LEU:HD21	14:N:53:LEU:HD22	1.82	0.62
4:D:31:CYS:SG	4:D:31:CYS:O	2.57	0.62
6:F:14:LEU:CD1	6:F:18:GLN:HB3	2.22	0.62
16:P:74:LEU:O	16:P:79:VAL:HG23	1.99	0.62
16:P:8:ARG:HB2	16:P:28:ARG:HH11	1.64	0.62
17:Q:54:GLY:O	17:Q:80:GLY:HA2	1.99	0.62
18:R:26:LEU:N	18:R:26:LEU:HD13	2.13	0.62
20:T:83:ARG:O	20:T:87:LYS:HD2	2.00	0.62
1:A:544:G:C5	1:A:545:C:C5	2.88	0.62
1:A:975:A:H4'	1:A:976:G:H5''	1.81	0.62
4:D:150:GLU:OE1	4:D:151:LYS:HG3	2.00	0.62
8:H:113:SER:HB3	8:H:134:ILE:HD11	1.80	0.62
15:O:14:GLU:HG2	15:O:15:PHE:CD1	2.35	0.62
20:T:104:LEU:N	20:T:104:LEU:HD23	2.15	0.62
1:A:1052:U:H2'	1:A:1055:A:OP1	2.00	0.62
1:A:1368:G:H2'	1:A:1369:C:H5'	1.82	0.62
1:A:415:A:C4	1:A:416:G:C8	2.88	0.62
1:A:414:A:C2	1:A:415:A:N9	2.68	0.62
1:A:551:U:H2'	1:A:552:U:C6	2.35	0.62
1:A:592:G:O2'	1:A:593:G:H5'	2.00	0.62
1:A:922:G:H5''	1:A:922:G:H8	1.64	0.62
9:I:11:LYS:HG3	9:I:11:LYS:O	2.00	0.62
9:I:125:TYR:CD2	9:I:125:TYR:N	2.67	0.62
20:T:44:ALA:HB1	20:T:91:LEU:HB3	1.82	0.62
1:A:349:A:O2'	1:A:350:G:H5'	2.00	0.61
1:A:501:C:H2'	1:A:502:G:C8	2.34	0.61
1:A:88:A:C5	1:A:89:C:N3	2.68	0.61
2:B:193:ASP:C	2:B:193:ASP:OD1	2.38	0.61
2:B:74:LYS:HE3	2:B:166:ASP:CB	2.28	0.61
3:C:204:LEU:N	3:C:204:LEU:HD23	2.15	0.61
4:D:14:ARG:HD3	4:D:14:ARG:O	2.00	0.61
5:E:90:VAL:C	5:E:91:LEU:HD23	2.21	0.61
11:K:125:PHE:N	11:K:125:PHE:CD2	2.68	0.61
1:A:1338:G:H2'	1:A:1339:A:C8	2.35	0.61
1:A:1406:U:C5	1:A:1407:5MC:HM52	2.35	0.61
1:A:986:A:C2	1:A:1220:G:C2	2.88	0.61
20:T:41:ILE:HD12	20:T:41:ILE:H	1.64	0.61
1:A:130:A:H5'	17:Q:63:ARG:HE	1.66	0.61
1:A:1385:G:C5	29:A:2670:HOH:O	2.52	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1536:C:C5	1:A:1537:U:C2	2.87	0.61
1:A:200:G:H2'	1:A:201:C:O4'	2.00	0.61
2:B:92:TYR:HE1	2:B:150:SER:HG	1.48	0.61
3:C:156:ARG:H	3:C:163:ALA:HA	1.65	0.61
4:D:24:GLU:O	4:D:25:ARG:HB3	1.98	0.61
4:D:38:TYR:H	4:D:38:TYR:HD2	1.48	0.61
5:E:126:ARG:HG2	5:E:126:ARG:NH1	1.97	0.61
6:F:83:ASP:OD1	6:F:83:ASP:N	2.32	0.61
7:G:135:VAL:O	7:G:139:GLU:HG3	2.00	0.61
8:H:104:ARG:CZ	8:H:138:TRP:CZ2	2.82	0.61
11:K:29:ILE:HG22	11:K:43:SER:O	2.00	0.61
1:A:1194:U:O2	1:A:1194:U:H2'	2.00	0.61
1:A:16:A:H2'	1:A:17:U:H5'	1.81	0.61
1:A:188:C:C2'	1:A:189:G:H5'	2.30	0.61
1:A:353:A:H8	1:A:353:A:C5'	2.12	0.61
1:A:358:U:H2'	1:A:359:U:H6	1.66	0.61
1:A:544:G:C6	1:A:545:C:C5	2.89	0.61
1:A:642:A:H2'	1:A:643:C:C6	2.35	0.61
1:A:831:U:H2'	1:A:832:C:H6	1.65	0.61
1:A:892:A:C2	1:A:907:A:C4	2.89	0.61
1:A:983:A:N3	1:A:983:A:H3'	2.15	0.61
2:B:178:ARG:HD2	2:B:196:LEU:O	2.00	0.61
5:E:110:LEU:O	5:E:115:VAL:HB	2.01	0.61
11:K:16:SER:O	11:K:35:PRO:HD3	2.00	0.61
12:L:30:ALA:HB1	12:L:31:PRO:HD2	1.82	0.61
12:L:86:ARG:HG3	12:L:86:ARG:HH11	1.66	0.61
17:Q:53:LEU:HD12	17:Q:54:GLY:N	2.14	0.61
1:A:914:A:P	27:A:1928:SRV:CI3	2.87	0.61
1:A:442:C:H2'	1:A:443:C:H5'	1.81	0.61
1:A:865:A:O2'	1:A:866:C:H5'	1.99	0.61
2:B:8:LYS:C	2:B:10:LEU:H	2.02	0.61
2:B:160:ASP:O	2:B:161:ALA:HB2	2.00	0.61
7:G:51:GLN:O	7:G:52:GLU:HG2	2.00	0.61
13:M:37:THR:CG2	13:M:39:ILE:HD13	2.31	0.61
18:R:36:ASN:OD1	18:R:39:VAL:HG12	2.00	0.61
1:A:137:C:H2'	1:A:138:G:C5'	2.30	0.61
1:A:1482:G:N1	29:A:2362:HOH:O	2.16	0.61
1:A:190(D):U:O2'	1:A:190(E):U:H5'	2.01	0.61
1:A:248:C:C2'	1:A:249:U:H5'	2.31	0.61
1:A:304:U:C4	29:A:2495:HOH:O	2.48	0.61
1:A:414:A:H2'	1:A:414:A:N3	2.15	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:544:G:C4	1:A:545:C:C6	2.89	0.61
1:A:767:A:H2'	1:A:768:A:O4'	2.01	0.61
1:A:829:G:O2'	1:A:830:G:H5'	2.00	0.61
1:A:923:A:O5'	1:A:923:A:H8	1.82	0.61
2:B:172:ILE:H	2:B:172:ILE:HD13	1.64	0.61
4:D:23:GLY:HA2	4:D:112:VAL:O	2.00	0.61
7:G:21:VAL:HG23	7:G:22:LEU:H	1.65	0.61
1:A:1348:U:H4'	9:I:120:ARG:HD2	1.81	0.61
1:A:191:G:N3	20:T:103:GLY:O	2.34	0.61
20:T:22:ARG:O	20:T:23:ARG:C	2.38	0.61
1:A:778:G:H8	1:A:778:G:O5'	1.83	0.61
2:B:178:ARG:NH1	2:B:198:ASP:OD1	2.33	0.61
1:A:289:G:P	29:A:2015:HOH:O	2.57	0.61
1:A:448:A:C2'	1:A:449:C:H5'	2.30	0.61
1:A:53:A:C6	1:A:54:C:C5	2.89	0.61
1:A:1103:C:H5'	2:B:98:LEU:HD12	1.82	0.61
14:N:15:LYS:O	14:N:16:PHE:CG	2.53	0.61
17:Q:29:HIS:C	17:Q:29:HIS:ND1	2.54	0.61
23:W:32:C:O2'	23:W:33:U:O4'	2.17	0.61
1:A:109:A:H3'	1:A:110:C:H5'	1.83	0.61
1:A:114:U:H2'	1:A:115:G:H5'	1.82	0.61
1:A:1399:C:O2	1:A:1401:G:C4	2.54	0.61
2:B:157:ARG:HG3	2:B:158:LEU:O	2.01	0.61
2:B:88:ALA:HB2	2:B:219:VAL:CG1	2.21	0.61
4:D:159:ARG:CG	4:D:159:ARG:HH11	2.14	0.61
9:I:89:ASN:HB3	9:I:92:TYR:CE1	2.35	0.61
12:L:7:ILE:HG22	12:L:8:ASN:N	2.16	0.61
1:A:1035:A:N6	1:A:1036:G:O6	2.33	0.61
1:A:182:U:C5	1:A:183:G:N9	2.69	0.61
8:H:112:LEU:N	8:H:112:LEU:CD2	2.64	0.61
9:I:37:PHE:CD2	9:I:74:ILE:HD11	2.36	0.61
10:J:27:ALA:CB	10:J:74:ILE:HD12	2.31	0.61
2:B:15:VAL:O	2:B:42:ILE:HD12	2.01	0.60
4:D:131:ARG:HB2	4:D:131:ARG:HH11	1.66	0.60
7:G:54:THR:HG22	7:G:56:GLN:HB2	1.83	0.60
8:H:97:VAL:O	8:H:100:ILE:HG12	2.01	0.60
9:I:31:GLN:NE2	9:I:36:TYR:CD1	2.66	0.60
17:Q:83:ASP:OD1	17:Q:84:LEU:N	2.34	0.60
1:A:1015:A:C6	1:A:1016:A:C6	2.89	0.60
1:A:259:G:O2'	1:A:260:G:H5'	2.01	0.60
4:D:170:VAL:HG22	4:D:171:GLY:N	2.16	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:118:VAL:O	8:H:119:LEU:HD23	2.01	0.60
17:Q:40:LYS:CD	17:Q:42:TYR:CE1	2.83	0.60
1:A:109:A:H2'	1:A:326:G:N2	2.16	0.60
1:A:1279:A:C4'	1:A:1280:A:OP1	2.50	0.60
1:A:1454:G:O6	29:A:2826:HOH:O	2.16	0.60
1:A:386:C:O2'	29:A:2002:HOH:O	2.15	0.60
1:A:633:G:H2'	1:A:634:C:C6	2.35	0.60
1:A:644:G:C5	1:A:645:C:C5	2.89	0.60
1:A:783:C:O2'	1:A:784:C:H5'	2.01	0.60
3:C:8:ILE:HG22	3:C:9:GLY:N	2.16	0.60
3:C:91:LEU:HD23	3:C:92:ALA:N	2.16	0.60
7:G:37:ASN:ND2	7:G:41:ARG:HH21	1.98	0.60
15:O:7:GLU:O	15:O:11:VAL:HG12	2.01	0.60
1:A:1027:C:C5	1:A:1035:A:N1	2.69	0.60
2:B:19:HIS:O	2:B:39:ILE:HG13	2.01	0.60
9:I:46:ALA:HB1	9:I:77:ILE:HG22	1.83	0.60
7:G:153:HIS:NE2	11:K:57:THR:HG22	2.16	0.60
1:A:1251:A:H2'	1:A:1252:A:O4'	2.02	0.60
1:A:14:U:O2	1:A:16:A:C8	2.54	0.60
1:A:182:U:C5	1:A:183:G:H1'	2.35	0.60
1:A:130:A:H1'	1:A:263:A:O2'	2.01	0.60
1:A:446:G:H2'	1:A:447:G:C5'	2.32	0.60
5:E:41:VAL:HG13	5:E:113:ALA:HA	1.83	0.60
14:N:12:ARG:HH11	14:N:12:ARG:H	1.48	0.60
1:A:1500:A:OP2	1:A:1505:G:OP1	2.19	0.60
1:A:328:C:HO2'	1:A:329:A:P	2.16	0.60
1:A:44:G:N2	1:A:399:G:C4	2.70	0.60
1:A:875:C:O2'	8:H:14:ARG:NH1	2.35	0.60
1:A:972:C:OP1	10:J:57:LYS:HD2	2.02	0.60
2:B:185:ILE:H	2:B:185:ILE:HD12	1.66	0.60
2:B:231:GLU:HB3	2:B:232:PRO:CD	2.28	0.60
3:C:148:GLY:HA3	3:C:172:ARG:O	2.01	0.60
5:E:50:GLU:HG3	5:E:52:PRO:HD2	1.83	0.60
9:I:9:ARG:HA	9:I:76:ALA:CB	2.31	0.60
1:A:1126:U:C4	1:A:1127:G:C2	2.89	0.60
1:A:740:U:O2'	1:A:741:G:H5'	2.01	0.60
2:B:240:GLN:O	2:B:240:GLN:CG	2.50	0.60
4:D:79:PHE:C	4:D:79:PHE:CD2	2.75	0.60
7:G:38:LEU:HD12	7:G:42:ILE:HD11	1.83	0.60
8:H:38:ILE:HG22	8:H:38:ILE:O	2.02	0.60
14:N:29:ARG:HG2	14:N:40:CYS:CB	2.31	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1066:C:C2'	1:A:1067:A:H5'	2.31	0.60
3:C:14:ILE:O	3:C:16:ARG:N	2.35	0.60
7:G:26:PHE:HD1	7:G:101:LEU:HD23	1.66	0.60
13:M:99:ARG:HB2	13:M:101:GLN:HE22	1.66	0.60
20:T:56:MET:HE3	20:T:85:MET:HG3	1.84	0.60
1:A:1004:A:N7	1:A:1037:C:N3	2.49	0.60
1:A:1234:C:H1'	1:A:1364:U:O2	2.00	0.60
1:A:1518[A]:MA6:H93	1:A:1519[A]:MA6:H103	1.82	0.60
1:A:276:G:OP1	17:Q:12:SER:OG	2.14	0.60
1:A:476:G:H2'	1:A:477:G:H8	1.66	0.60
2:B:100:GLY:HA2	2:B:176:GLU:OE2	2.01	0.60
2:B:20:GLU:HA	2:B:39:ILE:CD1	2.31	0.60
10:J:63:PHE:CD1	10:J:63:PHE:N	2.68	0.60
17:Q:23:VAL:HG21	17:Q:42:TYR:HD1	1.64	0.60
18:R:87:ARG:HH21	18:R:87:ARG:CB	2.13	0.60
23:W:37:A:C6	23:W:38:A:C2	2.89	0.60
1:A:254:G:OP1	17:Q:67:LYS:O	2.20	0.60
1:A:543:C:H2'	1:A:544:G:C5'	2.30	0.60
1:A:710:G:H5''	6:F:54:LYS:CE	2.27	0.60
1:A:868:C:H2'	1:A:869:G:C5'	2.31	0.60
7:G:65:ALA:HB2	7:G:128:ALA:HB2	1.83	0.60
7:G:5:ARG:NH2	7:G:8:GLU:HG2	2.17	0.60
11:K:73:MET:HG3	11:K:103:LEU:HD21	1.83	0.60
11:K:48:ILE:HD13	11:K:48:ILE:N	2.15	0.60
1:A:1060:C:O2	1:A:1198:G:C2	2.55	0.59
1:A:1118:C:H1'	1:A:1179:A:C4	2.37	0.59
1:A:1494:G:O2'	1:A:1495:U:H5'	2.02	0.59
1:A:1503:A:C4	1:A:1531:A:C2	2.90	0.59
1:A:524:G:H2'	1:A:525:C:C6	2.37	0.59
4:D:13:ARG:HD2	4:D:38:TYR:O	2.02	0.59
12:L:90:VAL:HG12	12:L:90:VAL:O	2.02	0.59
13:M:78:ILE:O	13:M:81:LEU:N	2.34	0.59
15:O:60:VAL:HG12	15:O:61:GLY:N	2.17	0.59
19:S:34:TRP:CZ2	19:S:57:HIS:CE1	2.90	0.59
19:S:80:TYR:CZ	19:S:81:ARG:HG2	2.36	0.59
1:A:1027:C:O4'	1:A:1027:C:O2	2.17	0.59
1:A:1060:C:C2	1:A:1198:G:N1	2.70	0.59
1:A:182:U:C5	1:A:183:G:C1'	2.85	0.59
6:F:98:LEU:HD13	6:F:98:LEU:N	2.15	0.59
8:H:26:VAL:HG22	8:H:27:PRO:HD2	1.84	0.59
13:M:73:GLU:O	13:M:77:ASN:HB2	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:51:VAL:CG2	19:S:58:VAL:HG23	2.33	0.59
19:S:64:GLU:O	19:S:67:VAL:HG23	2.02	0.59
1:A:149:A:O2'	1:A:150:C:H5'	2.03	0.59
1:A:667:G:H4'	15:O:51:HIS:CE1	2.38	0.59
1:A:89:C:O2'	1:A:90:U:O5'	2.19	0.59
3:C:84:ILE:HG23	3:C:88:ARG:HH12	1.67	0.59
4:D:206:PHE:CE2	4:D:207:TYR:HE2	2.20	0.59
7:G:52:GLU:N	7:G:52:GLU:OE1	2.35	0.59
7:G:74:GLU:HG2	7:G:91:VAL:CG2	2.32	0.59
17:Q:29:HIS:ND1	17:Q:30:PRO:HD2	2.17	0.59
18:R:58:LEU:HD12	18:R:62:GLU:HB3	1.85	0.59
20:T:99:LEU:HD12	20:T:100:ILE:H	1.65	0.59
1:A:1026:G:N7	1:A:1027:C:N3	2.50	0.59
1:A:1130:A:P	1:A:1131:G:OP2	2.60	0.59
1:A:17:U:H2'	1:A:18:C:C6	2.37	0.59
1:A:399:G:OP1	29:A:2086:HOH:O	2.17	0.59
4:D:18:LYS:HB3	4:D:33:MET:HG3	1.84	0.59
1:A:939:G:H5'	7:G:102:ARG:HH22	1.67	0.59
1:A:1399:C:O2	1:A:1401:G:C8	2.55	0.59
1:A:380:G:N7	29:A:2680:HOH:O	2.35	0.59
1:A:848:C:O5'	1:A:848:C:H6	1.86	0.59
4:D:127:THR:HG23	4:D:147:ALA:O	2.03	0.59
5:E:121:LYS:HG2	5:E:123:LEU:HD21	1.84	0.59
5:E:36:ASP:CG	5:E:38:GLN:HB2	2.23	0.59
5:E:80:ILE:O	5:E:80:ILE:HG23	2.03	0.59
6:F:12:PRO:HG2	6:F:57:GLN:O	2.01	0.59
6:F:74:ASP:O	6:F:77:ARG:HB3	2.02	0.59
1:A:1124:G:O4'	10:J:38:ILE:HD11	2.02	0.59
16:P:82:GLN:O	16:P:84:ALA:N	2.35	0.59
1:A:1124:G:H2'	1:A:1145:C:H5	1.68	0.59
1:A:504:C:OP1	29:A:2163:HOH:O	2.17	0.59
1:A:868:C:H2'	1:A:869:G:O5'	2.02	0.59
4:D:128:VAL:HG12	4:D:129:ASN:ND2	2.18	0.59
4:D:172:PRO:HD2	4:D:173:TRP:CZ3	2.37	0.59
5:E:33:VAL:HG12	5:E:34:VAL:N	2.16	0.59
13:M:70:LEU:O	13:M:74:VAL:HG22	2.03	0.59
20:T:61:SER:HG	20:T:65:LYS:HD2	1.65	0.59
1:A:138:G:C8	1:A:138:G:H5'	2.34	0.59
3:C:6:HIS:CD2	3:C:7:PRO:HD2	2.38	0.59
9:I:2:GLU:O	9:I:20:ARG:HG2	2.02	0.59
11:K:47:VAL:HG12	11:K:48:ILE:HD13	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:29:HIS:HB2	17:Q:36:ILE:HD12	1.84	0.59
1:A:1291:G:H4'	9:I:39:GLY:CA	2.32	0.59
1:A:1527:C:C2'	1:A:1528:U:H5'	2.32	0.59
1:A:747:C:H2'	1:A:748:C:O5'	2.03	0.59
1:A:960:U:H4'	1:A:961:U:C5'	2.32	0.59
6:F:5:GLU:OE1	18:R:34:TYR:OH	2.15	0.59
19:S:22:LEU:O	19:S:26:GLY:O	2.21	0.59
1:A:1190:G:H8	1:A:1190:G:C5'	2.16	0.59
1:A:180:U:H2'	1:A:181:G:H5'	1.85	0.59
1:A:500:G:C6	1:A:501:C:C4	2.91	0.59
1:A:644:G:H8	1:A:644:G:C5'	2.09	0.59
1:A:994:A:C2	1:A:995:C:C6	2.90	0.59
2:B:105:PHE:O	2:B:109:SER:OG	2.20	0.59
3:C:203:PHE:C	3:C:204:LEU:HD23	2.23	0.59
10:J:24:VAL:HG22	10:J:28:ARG:HH12	1.68	0.59
19:S:25:LYS:HG3	19:S:26:GLY:H	1.67	0.59
1:A:1010:G:H22	1:A:1020:U:H1'	1.67	0.59
1:A:1126:U:O4	1:A:1127:G:N2	2.35	0.59
1:A:1151:A:HO2'	1:A:1152:A:H8	1.49	0.59
1:A:1256:A:N6	1:A:1277:C:C6	2.71	0.59
1:A:1499:A:H5'	1:A:1519[A]:MA6:N1	2.18	0.59
1:A:433:C:C2	1:A:434:U:H5	2.21	0.59
1:A:510:A:H5''	1:A:511:C:P	2.43	0.59
8:H:87:SER:HA	8:H:93:VAL:HG23	1.84	0.59
10:J:44:VAL:HG13	10:J:66:ARG:CD	2.29	0.59
11:K:119:CYS:O	11:K:121:PRO:HD3	2.02	0.59
11:K:45:GLY:HA3	11:K:55:LYS:HB3	1.84	0.59
1:A:1493[A]:A:H2	23:W:36:A:O2'	1.83	0.58
1:A:923:A:O4'	1:A:1398:A:C2	2.56	0.58
5:E:15:ARG:NH1	5:E:26:PHE:CE2	2.71	0.58
9:I:102:LEU:HD12	9:I:102:LEU:H	1.68	0.58
17:Q:45:HIS:HE2	17:Q:47:PRO:HB3	1.67	0.58
19:S:12:ASP:O	19:S:15:LEU:CD1	2.51	0.58
1:A:1332:A:C2	1:A:1333:A:C4	2.91	0.58
1:A:529:G:C8	1:A:529:G:H3'	2.37	0.58
1:A:790:A:H2'	1:A:791:G:C8	2.38	0.58
1:A:893:C:C2'	1:A:894:G:H5'	2.32	0.58
9:I:39:GLY:O	9:I:40:LEU:HD22	2.03	0.58
11:K:125:PHE:N	11:K:125:PHE:HD2	2.02	0.58
1:A:128:G:H4'	17:Q:3:LYS:HG3	1.84	0.58
18:R:82:THR:HG23	18:R:83:GLU:N	2.17	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1018:C:O5'	1:A:1018:C:H6	1.86	0.58
1:A:364:A:H2'	1:A:365:U:O2	2.03	0.58
5:E:152:ARG:HB3	8:H:43:GLY:HA3	1.83	0.58
9:I:14:VAL:HG23	9:I:66:ARG:O	2.03	0.58
14:N:37:PHE:HB3	14:N:39:LEU:HD12	1.85	0.58
19:S:51:VAL:O	19:S:51:VAL:HG23	2.04	0.58
1:A:11:G:O6	29:A:2647:HOH:O	2.16	0.58
1:A:327:A:HO2'	1:A:328:C:H6	1.51	0.58
1:A:345:C:OP2	1:A:345:C:C6	2.56	0.58
1:A:625:G:H4'	16:P:16:HIS:CD2	2.37	0.58
1:A:737:A:H2'	1:A:738:C:C6	2.37	0.58
1:A:864:A:H2'	1:A:865:A:C8	2.37	0.58
3:C:186:PHE:CD2	3:C:186:PHE:C	2.76	0.58
8:H:53:VAL:HG12	8:H:58:TYR:CE1	2.38	0.58
9:I:55:ALA:O	9:I:56:LEU:C	2.42	0.58
12:L:113:ARG:NH1	12:L:116:SER:H	2.00	0.58
13:M:37:THR:HG23	13:M:39:ILE:CD1	2.33	0.58
1:A:101:A:H2'	1:A:102:G:H8	1.68	0.58
1:A:1329:A:C2'	1:A:1330:U:H5'	2.34	0.58
1:A:1371:G:C5	1:A:1372:U:C5	2.90	0.58
4:D:100:ARG:HH12	4:D:137:SER:HA	1.68	0.58
4:D:152:SER:O	4:D:155:LEU:HB2	2.04	0.58
1:A:1147:C:O2	9:I:16:ARG:NH2	2.37	0.58
15:O:62:GLN:O	15:O:63:ARG:C	2.39	0.58
18:R:44:LEU:HD13	18:R:48:GLY:O	2.03	0.58
1:A:1003:G:N1	1:A:1003(A):G:C6	2.71	0.58
1:A:1035:A:C6	1:A:1036:G:O6	2.57	0.58
1:A:1405:G:C2'	1:A:1406:U:H5'	2.33	0.58
1:A:1424:C:C4	1:A:1425:U:C5	2.91	0.58
1:A:820:U:H4'	1:A:821:G:OP2	2.03	0.58
8:H:103:VAL:HG21	8:H:109:ILE:C	2.24	0.58
13:M:59:TYR:HD2	13:M:59:TYR:C	2.07	0.58
13:M:86:CYS:SG	13:M:87:TYR:N	2.77	0.58
1:A:1329:A:O2'	1:A:1330:U:H5'	2.03	0.58
1:A:358:U:O2'	1:A:359:U:H5'	2.04	0.58
1:A:741:G:H5''	15:O:39:LEU:CD1	2.33	0.58
12:L:70:ILE:CG2	12:L:75:HIS:HD2	2.02	0.58
19:S:44:MET:HB2	19:S:62:ILE:HD13	1.86	0.58
1:A:1054:C:O2'	1:A:1055:A:O5'	2.22	0.58
1:A:1124:G:O2'	1:A:1145:C:N4	2.36	0.58
1:A:1347:G:N2	1:A:1373:G:H2'	2.18	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:162:A:H5''	1:A:163:C:OP2	2.03	0.58
2:B:25:ASN:ND2	2:B:193:ASP:CB	2.55	0.58
4:D:106:TYR:O	4:D:109:GLY:N	2.29	0.58
1:A:409:G:OP1	4:D:24:GLU:O	2.21	0.58
11:K:11:LYS:N	11:K:75:TYR:HE2	2.01	0.58
17:Q:4:LYS:HG2	17:Q:6:LEU:HD21	1.85	0.58
21:U:10:ARG:NH1	21:U:10:ARG:CG	2.59	0.58
1:A:1501:C:C4	1:A:1504:G:C4	2.92	0.58
1:A:1502:A:H2'	1:A:1504:G:N7	2.19	0.58
1:A:386:C:C2'	1:A:387:U:H5'	2.34	0.58
3:C:151:VAL:O	3:C:167:TRP:O	2.20	0.58
4:D:25:ARG:NH2	4:D:30:LYS:HD3	2.19	0.58
5:E:24:ARG:HG2	5:E:24:ARG:NH1	2.18	0.58
6:F:87:ARG:CG	6:F:87:ARG:HH11	2.14	0.58
10:J:24:VAL:HG22	10:J:28:ARG:NH1	2.19	0.58
13:M:4:ILE:HD13	13:M:57:ARG:HB2	1.85	0.58
16:P:23:ASP:OD1	16:P:25:ARG:HG3	2.02	0.58
1:A:1095:U:H2'	1:A:1096:C:O4'	2.03	0.58
1:A:1206:G:H2'	1:A:1207:2MG:O4'	2.04	0.58
1:A:984:C:N4	1:A:1221:G:H1	2.01	0.58
1:A:1250:A:C2	1:A:1287:A:C2	2.91	0.58
1:A:1418:A:H2'	1:A:1419:G:O4'	2.04	0.58
1:A:150:C:C2'	1:A:151:A:O5'	2.51	0.58
2:B:165:VAL:HG12	2:B:166:ASP:N	2.18	0.58
3:C:82:GLU:HG3	3:C:83:ARG:H	1.69	0.58
10:J:49:VAL:HA	10:J:50:ILE:HD12	1.84	0.58
17:Q:40:LYS:HD2	17:Q:42:TYR:CZ	2.38	0.58
1:A:419:C:C2'	1:A:420:U:H5'	2.34	0.57
1:A:966:M2G:HM22	1:A:967:5MC:O2	2.04	0.57
2:B:97:TRP:CE2	2:B:101:MET:HG3	2.39	0.57
2:B:107:THR:O	2:B:110:GLN:HB2	2.04	0.57
1:A:137:C:H2'	1:A:138:G:H5''	1.84	0.57
1:A:1501:C:N4	1:A:1504:G:C2	2.72	0.57
1:A:409:G:N2	1:A:434:U:C5	2.72	0.57
1:A:540:G:C6	1:A:541:G:C5	2.92	0.57
1:A:633:G:H2'	1:A:634:C:H6	1.68	0.57
1:A:909:A:C8	1:A:910:C:C6	2.91	0.57
9:I:55:ALA:HB1	9:I:59:PHE:HB2	1.85	0.57
1:A:1004:A:H2'	1:A:1005:A:H5'	1.86	0.57
1:A:581:G:O2'	1:A:582:U:H5'	2.04	0.57
1:A:734:G:O5'	1:A:734:G:H8	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:993:G:N3	1:A:993:G:H2'	2.19	0.57
3:C:10:PHE:C	3:C:10:PHE:HD1	2.07	0.57
3:C:118:GLN:O	3:C:122:GLU:HG3	2.04	0.57
5:E:116:THR:HB	5:E:117:ASP:OD2	2.04	0.57
7:G:16:LEU:CD1	9:I:45:ALA:HB2	2.34	0.57
10:J:50:ILE:HD12	10:J:50:ILE:N	2.19	0.57
1:A:1193:G:C2	1:A:1194:U:C5	2.92	0.57
1:A:53:A:N6	1:A:54:C:C4	2.73	0.57
1:A:691:G:H2'	1:A:692:U:C6	2.40	0.57
4:D:150:GLU:CD	4:D:150:GLU:N	2.57	0.57
21:U:8:THR:HG22	21:U:9:ARG:H	1.68	0.57
1:A:1063:C:H2'	1:A:1064:G:C8	2.39	0.57
1:A:1189:C:H5''	1:A:1190:G:OP2	2.04	0.57
1:A:1419:G:O6	1:A:1420:C:N4	2.38	0.57
4:D:187:ARG:CG	4:D:188:LEU:HD12	2.35	0.57
5:E:9:LYS:NZ	5:E:111:GLU:OE1	2.38	0.57
13:M:74:VAL:HG23	13:M:75:ALA:H	1.69	0.57
14:N:4:LYS:O	14:N:7:ILE:HG12	2.05	0.57
1:A:134:A:N6	16:P:25:ARG:HH21	2.02	0.57
20:T:39:LYS:O	20:T:43:LEU:HG	2.04	0.57
1:A:1277:C:H1'	1:A:1282:C:H1'	1.86	0.57
27:A:1928:SRV:OG2	12:L:91:LYS:NZ	2.27	0.57
1:A:293:G:C4	1:A:305:G:N2	2.72	0.57
1:A:510:A:H5''	1:A:511:C:OP2	2.04	0.57
9:I:26:VAL:HG12	9:I:61:ALA:HB3	1.85	0.57
12:L:92:OTD:N	12:L:92:OTD:OD1	2.36	0.57
17:Q:58:GLU:O	17:Q:59:ILE:HD13	2.02	0.57
17:Q:81:ARG:HG3	17:Q:84:LEU:HD12	1.87	0.57
1:A:1055:A:C2	1:A:1056:U:H1'	2.40	0.57
1:A:54:C:O2'	1:A:55:A:H5'	2.03	0.57
3:C:10:PHE:CD1	3:C:10:PHE:C	2.77	0.57
9:I:31:GLN:HE22	9:I:36:TYR:HD1	1.50	0.57
19:S:15:LEU:H	19:S:15:LEU:HD12	1.70	0.57
1:A:1241:G:H2'	1:A:1242:C:H6	1.70	0.57
1:A:315:A:OP1	29:A:2576:HOH:O	2.17	0.57
1:A:54:C:N3	1:A:352:C:H5	2.02	0.57
3:C:33:LEU:O	3:C:37:GLN:HG2	2.04	0.57
5:E:11:ILE:HD11	5:E:105:VAL:HA	1.87	0.57
13:M:87:TYR:HE1	13:M:91:ARG:CD	2.18	0.57
17:Q:18:THR:CG2	17:Q:69:LYS:HD3	2.35	0.57
18:R:43:PHE:CD2	18:R:66:LEU:HD21	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:954:G:H21	1:A:1227:A:H62	1.51	0.57
1:A:1494:G:N3	1:A:1495:U:C6	2.73	0.57
1:A:1533:C:O2'	1:A:1534:C:P	2.63	0.57
1:A:174:C:O5'	1:A:174:C:H6	1.86	0.57
1:A:540:G:C4	1:A:541:G:C8	2.92	0.57
1:A:975:A:C8	1:A:975:A:C5'	2.87	0.57
2:B:170:GLU:O	2:B:173:ALA:N	2.38	0.57
2:B:88:ALA:CB	2:B:219:VAL:HG13	2.22	0.57
4:D:79:PHE:CD2	4:D:80:GLU:N	2.73	0.57
5:E:65:ASN:O	5:E:65:ASN:ND2	2.38	0.57
12:L:28:LYS:HE3	12:L:33:ARG:NH2	2.19	0.57
13:M:40:ASN:OD1	13:M:41:PRO:HD2	2.04	0.57
13:M:87:TYR:CD1	13:M:87:TYR:C	2.77	0.57
17:Q:74:LEU:HD23	17:Q:74:LEU:C	2.25	0.57
20:T:63:ILE:O	20:T:66:ALA:HB3	2.04	0.57
1:A:1279:A:H5''	1:A:1280:A:OP1	2.05	0.57
1:A:264:U:H2'	1:A:265:G:H5'	1.87	0.57
8:H:17:THR:O	8:H:78:GLN:NE2	2.38	0.57
9:I:125:TYR:HD2	9:I:125:TYR:N	2.03	0.57
11:K:80:VAL:HG13	11:K:81:ASP:N	2.20	0.57
12:L:53:ARG:NH1	12:L:92:OTD:OD2	2.38	0.57
16:P:18:ARG:O	16:P:20:VAL:HG23	2.05	0.57
3:C:50:ALA:O	3:C:71:ALA:HB3	2.04	0.56
4:D:114:ARG:HG3	4:D:114:ARG:HH11	1.70	0.56
5:E:117:ASP:OD2	5:E:117:ASP:N	2.37	0.56
5:E:79:GLU:HB3	5:E:92:LYS:HG2	1.87	0.56
10:J:82:ILE:HG22	10:J:82:ILE:O	2.05	0.56
13:M:4:ILE:CG2	13:M:5:ALA:N	2.68	0.56
13:M:87:TYR:O	13:M:90:LEU:N	2.38	0.56
10:J:49:VAL:HG23	14:N:41:ARG:HB2	1.86	0.56
16:P:23:ASP:OD1	16:P:24:ALA:N	2.39	0.56
1:A:1126:U:O4	1:A:1127:G:C2	2.58	0.56
1:A:1507:A:C8	1:A:1530:G:N2	2.73	0.56
1:A:502:G:H2'	1:A:503:C:O4'	2.05	0.56
1:A:994:A:C2	1:A:995:C:C5	2.92	0.56
3:C:174:PRO:O	3:C:176:HIS:N	2.38	0.56
5:E:96:PRO:HA	5:E:117:ASP:OD1	2.05	0.56
7:G:136:LYS:HD2	7:G:140:ASP:OD1	2.04	0.56
8:H:114:THR:HG21	8:H:129:VAL:CG2	2.35	0.56
9:I:105:ASP:OD2	9:I:107:ARG:HG3	2.04	0.56
10:J:48:THR:HA	10:J:62:HIS:CB	2.31	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:41:ILE:O	20:T:44:ALA:HB3	2.04	0.56
1:A:1054:C:N3	23:W:34:G:C5'	2.68	0.56
1:A:1004:A:N6	1:A:1037:C:H42	2.04	0.56
1:A:1126:U:H2'	1:A:1127:G:O5'	2.06	0.56
1:A:1124:G:O2'	1:A:1145:C:C5	2.58	0.56
1:A:537:G:H2'	1:A:538:G:C8	2.37	0.56
1:A:667:G:H4'	15:O:51:HIS:ND1	2.19	0.56
1:A:695:A:H2'	1:A:696:A:C8	2.41	0.56
3:C:134:ILE:O	3:C:138:VAL:HG23	2.05	0.56
4:D:206:PHE:HD2	4:D:207:TYR:CE2	2.22	0.56
13:M:44:ARG:HB3	13:M:46:LYS:HG3	1.86	0.56
21:U:8:THR:HG22	21:U:9:ARG:N	2.20	0.56
1:A:854:G:N2	1:A:855:G:C4	2.74	0.56
1:A:910:C:OP2	12:L:21:LYS:NZ	2.38	0.56
7:G:27:ILE:CD1	7:G:40:ALA:HA	2.36	0.56
8:H:29:SER:OG	8:H:32:LYS:HG3	2.06	0.56
11:K:124:LYS:C	11:K:125:PHE:HD2	2.09	0.56
13:M:87:TYR:CE1	13:M:91:ARG:CD	2.88	0.56
13:M:87:TYR:O	13:M:90:LEU:HB2	2.06	0.56
17:Q:101:ARG:HD3	17:Q:101:ARG:H	1.70	0.56
19:S:62:ILE:HA	19:S:66:MET:CE	2.35	0.56
1:A:106:C:C2'	1:A:107:G:H5'	2.34	0.56
1:A:1092:A:H8	1:A:1092:A:C5'	2.18	0.56
1:A:1053:G:HO2'	1:A:1199:U:H5	1.54	0.56
1:A:1534:C:C2	1:A:1535:A:C2	2.93	0.56
1:A:344:A:H5''	1:A:345:C:H5	1.70	0.56
1:A:945:G:N1	1:A:1337:G:C2	2.73	0.56
1:A:830:G:O3'	2:B:22:LYS:HB3	2.05	0.56
2:B:36:ARG:CG	2:B:41:ILE:HD11	2.35	0.56
1:A:1124:G:H5'	10:J:35:SER:O	2.05	0.56
10:J:69:ASN:O	10:J:70:ARG:HD3	2.04	0.56
12:L:11:VAL:HG22	17:Q:29:HIS:CD2	2.40	0.56
21:U:18:TYR:HD1	21:U:24:ARG:CZ	2.18	0.56
1:A:1125:U:H3'	1:A:1126:U:C5	2.40	0.56
1:A:1499:A:OP1	1:A:1519[A]:MA6:N1	2.38	0.56
1:A:564:C:H5'	17:Q:32:TYR:CE2	2.41	0.56
1:A:83:U:H5	1:A:84:U:C5	2.24	0.56
2:B:97:TRP:CH2	2:B:176:GLU:OE2	2.58	0.56
6:F:4:TYR:CZ	6:F:72:VAL:HG21	2.41	0.56
9:I:118:LYS:C	9:I:120:ARG:H	2.08	0.56
19:S:41:VAL:HB	19:S:42:PRO:HD2	1.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1250:A:C2	1:A:1287:A:N1	2.74	0.56
1:A:1360:A:H2'	1:A:1361:G:O5'	2.06	0.56
1:A:337:C:H2'	1:A:338:A:C8	2.41	0.56
1:A:831:U:H2'	1:A:832:C:C6	2.41	0.56
4:D:196:LEU:HD23	4:D:196:LEU:N	2.21	0.56
16:P:57:ARG:O	16:P:58:TYR:C	2.40	0.56
1:A:1014:A:N7	1:A:1015:A:N6	2.54	0.56
1:A:1065:U:O2'	1:A:1066:C:OP2	2.19	0.56
1:A:1395:C:C2'	1:A:1396:A:H5'	2.35	0.56
1:A:1400:5MC:OP1	1:A:1400:5MC:HM51	2.06	0.56
1:A:1536:C:H6	1:A:1536:C:H3'	1.69	0.56
1:A:28:G:O2'	1:A:296:U:OP1	2.20	0.56
1:A:427:U:C4	1:A:428:G:C6	2.94	0.56
1:A:827:U:O2	1:A:827:U:H2'	2.05	0.56
3:C:8:ILE:HG12	3:C:16:ARG:HG3	1.88	0.56
4:D:173:TRP:CD1	4:D:189:PRO:HD3	2.41	0.56
11:K:122:LYS:O	11:K:124:LYS:N	2.39	0.56
1:A:1128:C:O2'	1:A:1130:A:C8	2.58	0.56
1:A:476:G:H2'	1:A:477:G:C8	2.40	0.56
1:A:908:A:C2	1:A:909:A:C4	2.94	0.56
3:C:105:GLU:HG2	3:C:106:VAL:N	2.21	0.56
4:D:19:LEU:HD12	4:D:67:ILE:HG13	1.86	0.56
8:H:102:ARG:H	8:H:102:ARG:CD	2.01	0.56
8:H:36:LEU:HA	8:H:39:LEU:HD23	1.88	0.56
12:L:27:LEU:CG	12:L:28:LYS:H	2.05	0.56
16:P:21:VAL:HG12	16:P:21:VAL:O	2.05	0.56
17:Q:86:GLU:O	17:Q:90:ILE:HG12	2.05	0.56
1:A:1082:G:C2'	1:A:1083:U:H5'	2.35	0.56
1:A:1407:5MC:C2	1:A:1408:A:C8	2.94	0.56
2:B:170:GLU:O	2:B:173:ALA:HB3	2.06	0.56
3:C:59:ARG:HG2	3:C:64:VAL:HG13	1.88	0.56
1:A:559:A:OP1	5:E:126:ARG:NH2	2.39	0.56
9:I:5:TYR:HD1	9:I:6:GLY:H	1.54	0.56
10:J:55:LYS:CG	10:J:56:HIS:N	2.51	0.56
1:A:1316:G:H4'	14:N:18:VAL:HG11	1.86	0.56
15:O:12:ILE:C	15:O:14:GLU:N	2.57	0.56
1:A:1096:C:H2'	1:A:1097:C:H6	1.71	0.56
1:A:188:C:O2'	1:A:189:G:H5'	2.06	0.56
1:A:273:A:N6	1:A:274:A:C6	2.73	0.56
3:C:147:LYS:HE3	3:C:205:GLY:H	1.69	0.56
4:D:18:LYS:CE	4:D:20:TYR:HE2	2.11	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:137:GLU:HG2	5:E:140:ARG:HH11	1.71	0.56
5:E:76:ILE:HG12	5:E:118:ILE:CD1	2.36	0.56
12:L:127:GLU:HG3	12:L:128:ALA:O	2.05	0.56
18:R:37:VAL:O	18:R:39:VAL:N	2.39	0.56
23:W:32:C:HO2'	23:W:33:U:H6	1.54	0.56
1:A:137:C:C2'	1:A:138:G:C5'	2.84	0.55
1:A:176:C:HO2'	1:A:177:C:H5'	1.71	0.55
1:A:353:A:H5'	1:A:353:A:H8	1.70	0.55
1:A:500:G:O6	1:A:501:C:N4	2.39	0.55
2:B:141:GLU:O	2:B:144:ARG:HG3	2.06	0.55
4:D:172:PRO:HG2	4:D:173:TRP:HE3	1.71	0.55
8:H:124:ALA:O	8:H:128:GLY:N	2.38	0.55
9:I:27:THR:OG1	9:I:28:VAL:N	2.39	0.55
10:J:61:GLU:O	10:J:61:GLU:HG2	2.06	0.55
12:L:34:ARG:HB2	12:L:105:TYR:CE1	2.41	0.55
12:L:24:VAL:HG13	12:L:98:TYR:HE2	1.71	0.55
1:A:190(E):U:C5	17:Q:72:ARG:NH2	2.74	0.55
1:A:1126:U:H6	1:A:1126:U:OP1	1.89	0.55
1:A:1248:A:H2'	1:A:1249:C:H5'	1.87	0.55
1:A:1399:C:O2	1:A:1401:G:N7	2.38	0.55
1:A:1436:U:C2	1:A:1437:C:C6	2.93	0.55
1:A:21:G:P	29:A:2044:HOH:O	2.65	0.55
1:A:264:U:C2'	1:A:265:G:H5'	2.37	0.55
1:A:446:G:C2'	1:A:447:G:H5'	2.36	0.55
1:A:462:G:H5'	1:A:463:A:OP2	2.07	0.55
3:C:8:ILE:CG2	3:C:9:GLY:N	2.70	0.55
5:E:11:ILE:CG2	5:E:12:LEU:N	2.68	0.55
1:A:939:G:H5'	7:G:102:ARG:CZ	2.36	0.55
7:G:66:VAL:HG12	7:G:67:GLU:N	2.21	0.55
8:H:36:LEU:O	8:H:37:ARG:C	2.44	0.55
9:I:10:ARG:HG3	9:I:11:LYS:HG2	1.89	0.55
14:N:12:ARG:HH11	14:N:12:ARG:N	2.04	0.55
19:S:13:ASP:O	19:S:16:LEU:HB3	2.06	0.55
13:M:99:ARG:NH2	19:S:2:PRO:CG	2.70	0.55
1:A:1360:A:C2'	1:A:1361:G:O5'	2.54	0.55
1:A:1408:A:O2'	1:A:1409:C:H5'	2.07	0.55
1:A:1536:C:C5	1:A:1537:U:N3	2.74	0.55
1:A:414:A:C2	1:A:415:A:C4	2.93	0.55
1:A:506:G:C2'	1:A:507:C:H5'	2.36	0.55
1:A:569:C:H5''	1:A:570:G:OP1	2.07	0.55
1:A:89:C:C5	1:A:90:U:C4	2.84	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:27:THR:CG2	9:I:62:TYR:HA	2.37	0.55
10:J:48:THR:CB	10:J:62:HIS:HB3	2.36	0.55
20:T:10:LEU:CD2	20:T:13:LEU:N	2.64	0.55
1:A:1029:C:C2'	1:A:1030:C:H5'	2.37	0.55
1:A:1027:C:O2'	1:A:1034:G:N2	2.40	0.55
1:A:1195:C:H5''	1:A:1196:U:O5'	2.06	0.55
1:A:829:G:C2'	1:A:830:G:H5'	2.35	0.55
2:B:8:LYS:C	2:B:10:LEU:N	2.58	0.55
1:A:547:A:OP2	4:D:2:GLY:CA	2.55	0.55
5:E:69:VAL:HG12	5:E:70:PRO:N	2.20	0.55
7:G:75:VAL:O	7:G:75:VAL:HG22	2.06	0.55
8:H:28:ALA:HB2	8:H:58:TYR:CA	2.36	0.55
9:I:128:ARG:OXT	9:I:128:ARG:HG2	2.06	0.55
12:L:83:VAL:HG12	12:L:107:ALA:HB2	1.88	0.55
13:M:23:TYR:CE2	13:M:70:LEU:HD13	2.42	0.55
20:T:84:LEU:O	20:T:84:LEU:HD23	2.07	0.55
1:A:1006:C:N4	1:A:1023:G:H1	2.02	0.55
1:A:1015:A:H2'	1:A:1016:A:O4'	2.05	0.55
1:A:1124:G:HO2'	1:A:1145:C:N4	2.03	0.55
1:A:255:G:O6	1:A:266:G:O6	2.25	0.55
1:A:337:C:H2'	1:A:338:A:H8	1.71	0.55
1:A:922:G:N3	1:A:1398:A:H2	2.05	0.55
4:D:196:LEU:HD23	4:D:196:LEU:H	1.72	0.55
5:E:76:ILE:HG12	5:E:118:ILE:HD12	1.88	0.55
7:G:121:ALA:O	7:G:125:MET:HG3	2.07	0.55
9:I:63:ILE:HG22	9:I:63:ILE:O	2.06	0.55
1:A:1139:G:N2	1:A:1143:G:N2	2.54	0.55
1:A:1417:G:O2'	1:A:1418:A:H5'	2.06	0.55
1:A:1448:C:H2'	1:A:1449:C:H6	1.71	0.55
1:A:261:U:O2	1:A:263:A:C8	2.60	0.55
1:A:668:G:O2'	1:A:669:U:H5'	2.07	0.55
1:A:838:G:N2	1:A:849:C:C2	2.75	0.55
2:B:7:VAL:O	2:B:10:LEU:HB2	2.06	0.55
1:A:933:G:OP2	7:G:3:ARG:HB3	2.07	0.55
8:H:57:PRO:CG	8:H:57:PRO:O	2.53	0.55
12:L:60:LEU:HB2	12:L:64:TYR:O	2.06	0.55
1:A:1114:C:H1'	14:N:60:SER:OG	2.05	0.55
23:W:35:G:H2'	23:W:36:A:H8	1.70	0.55
1:A:1028:C:N3	1:A:1034:G:C2	2.75	0.55
1:A:36:C:C2'	1:A:37:U:H5'	2.37	0.55
1:A:822:C:C2'	1:A:823:G:H5'	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:54:ARG:NH1	3:C:56:ASP:OD1	2.27	0.55
4:D:170:VAL:HG22	4:D:171:GLY:H	1.71	0.55
7:G:108:ALA:O	7:G:119:ARG:HB3	2.07	0.55
8:H:20:TYR:CZ	8:H:76:PRO:HD2	2.41	0.55
10:J:4:ILE:HG22	10:J:77:PRO:HD3	1.87	0.55
23:W:39:G:C2	23:W:40:PSU:N3	2.74	0.55
1:A:1415:G:C2'	1:A:1416:G:H5'	2.36	0.55
1:A:961:U:C2'	1:A:962:C:H5'	2.36	0.55
1:A:998:G:H2'	1:A:999:C:C6	2.41	0.55
5:E:67:VAL:HG21	5:E:140:ARG:HB3	1.89	0.55
13:M:27:LYS:CE	21:U:21:TYR:HE2	2.20	0.55
13:M:37:THR:HG23	13:M:39:ILE:HD13	1.88	0.55
19:S:63:THR:OG1	19:S:66:MET:HG3	2.07	0.55
1:A:1005:A:C8	1:A:1026:G:N1	2.73	0.55
1:A:1027:C:C5	1:A:1035:A:C2	2.95	0.55
1:A:1206:G:C6	1:A:1207:2MG:C6	2.94	0.55
1:A:545:C:O2	1:A:546:G:O4'	2.25	0.55
2:B:101:MET:HB2	2:B:102:LEU:HD12	1.89	0.55
2:B:56:ARG:HB2	2:B:56:ARG:NH1	2.22	0.55
3:C:5:ILE:CD1	3:C:10:PHE:HB2	2.37	0.55
3:C:59:ARG:NH1	3:C:97:LYS:HE2	2.22	0.55
8:H:4:ASP:HB3	8:H:7:ALA:HB3	1.88	0.55
1:A:278:G:C6	17:Q:95:TYR:HD2	2.25	0.55
1:A:1011:G:H2'	1:A:1012:U:H5'	1.87	0.55
1:A:107:G:C3'	1:A:108:G:H5''	2.36	0.55
1:A:357:G:C2	1:A:358:U:C5	2.95	0.55
1:A:597:G:N2	1:A:643:C:N3	2.40	0.55
4:D:204:ILE:HD13	4:D:204:ILE:H	1.73	0.55
1:A:1117:G:H5''	9:I:104:ARG:NH2	2.22	0.55
16:P:19:ILE:HG22	16:P:36:ILE:HG13	1.87	0.55
1:A:1160:G:O6	1:A:1181:G:C6	2.60	0.54
1:A:1190:G:H5''	1:A:1190:G:C8	2.42	0.54
1:A:192:U:H1'	20:T:103:GLY:CA	2.34	0.54
1:A:421:U:O4'	1:A:421:U:O2	2.25	0.54
3:C:76:VAL:HG23	3:C:77:ILE:N	2.22	0.54
7:G:113:GLU:HB2	7:G:119:ARG:HG2	1.89	0.54
9:I:16:ARG:HD3	9:I:64:THR:HG22	1.89	0.54
9:I:64:THR:O	9:I:64:THR:HG22	2.07	0.54
10:J:38:ILE:HG23	10:J:39:PRO:HD2	1.88	0.54
12:L:76:ASN:CG	12:L:76:ASN:O	2.45	0.54
14:N:39:LEU:HD22	14:N:43:CYS:HB3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:45:SER:OG	18:R:46:GLU:N	2.38	0.54
19:S:11:VAL:CG1	19:S:16:LEU:HD22	2.37	0.54
1:A:1030(A):G:C4	1:A:1030(C):G:OP2	2.60	0.54
1:A:1319:A:OP1	19:S:5:LEU:HD22	2.08	0.54
1:A:132:C:O2'	1:A:133:U:H5'	2.08	0.54
1:A:1500:A:P	1:A:1505:G:OP1	2.65	0.54
1:A:389:A:C5	1:A:390:C:H1'	2.42	0.54
1:A:860:A:OP2	29:A:2124:HOH:O	2.18	0.54
2:B:212:GLN:HE21	2:B:235:SER:HB3	1.72	0.54
3:C:130:VAL:O	3:C:134:ILE:CD1	2.56	0.54
3:C:20:SER:HA	3:C:57:ILE:O	2.07	0.54
4:D:72:GLU:O	4:D:75:PHE:HB3	2.07	0.54
6:F:98:LEU:H	6:F:98:LEU:CD1	2.17	0.54
1:A:1346:A:C5	7:G:10:ARG:NH1	2.75	0.54
12:L:78:GLN:N	12:L:81:SER:OG	2.29	0.54
1:A:1122:U:H2'	1:A:1123:A:H5'	1.89	0.54
1:A:1381:U:C6	1:A:1382:C:C5	2.96	0.54
1:A:178:C:C2'	1:A:179:A:H5'	2.38	0.54
1:A:529:G:C8	1:A:529:G:C3'	2.89	0.54
1:A:568:G:N2	1:A:883:C:C2	2.75	0.54
1:A:676:A:O2'	1:A:677:U:H5'	2.06	0.54
1:A:839:U:C5'	1:A:840:C:H5	2.18	0.54
3:C:36:ASP:O	3:C:39:ILE:HB	2.07	0.54
9:I:23:ASN:OD1	9:I:25:LYS:HE3	2.07	0.54
9:I:46:ALA:HB2	9:I:74:ILE:HG23	1.89	0.54
11:K:91:ARG:O	11:K:94:ALA:N	2.35	0.54
2:B:172:ILE:HG12	2:B:173:ALA:N	2.22	0.54
8:H:10:LEU:HD22	8:H:83:ILE:HD11	1.90	0.54
9:I:99:LEU:N	9:I:99:LEU:HD22	2.22	0.54
17:Q:23:VAL:CG2	17:Q:42:TYR:HD1	2.21	0.54
1:A:1108:G:O6	29:A:2136:HOH:O	2.16	0.54
1:A:1122:U:C2'	1:A:1123:A:H5'	2.38	0.54
1:A:22:G:C6	1:A:23:C:C4	2.96	0.54
1:A:22:G:C5	1:A:23:C:C5	2.96	0.54
1:A:448:A:H2'	1:A:449:C:H6	1.73	0.54
1:A:998:G:H2'	1:A:999:C:H6	1.73	0.54
4:D:63:LYS:NZ	4:D:197:PRO:O	2.40	0.54
6:F:53:ALA:C	6:F:54:LYS:HG2	2.28	0.54
7:G:51:GLN:HA	7:G:54:THR:O	2.07	0.54
8:H:86:ILE:HG22	8:H:87:SER:N	2.22	0.54
19:S:42:PRO:O	19:S:45:VAL:HG23	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:6:ARG:HG3	21:U:15:ARG:NH1	2.22	0.54
1:A:1197:G:H2'	1:A:1198:G:H5''	1.90	0.54
1:A:1533:C:H2'	1:A:1534:C:C6	2.42	0.54
1:A:380:G:C8	29:A:2680:HOH:O	2.54	0.54
1:A:53:A:C6	1:A:54:C:C4	2.96	0.54
2:B:74:LYS:C	2:B:76:GLN:H	2.10	0.54
4:D:21:LEU:HD21	4:D:66:ARG:O	2.07	0.54
3:C:13:GLY:HA2	14:N:57:ARG:HH12	1.72	0.54
15:O:15:PHE:HE2	15:O:85:LEU:HD21	1.72	0.54
19:S:80:TYR:HD1	19:S:81:ARG:H	1.51	0.54
20:T:10:LEU:HD23	20:T:13:LEU:H	1.68	0.54
20:T:88:VAL:HG12	20:T:89:ARG:N	2.21	0.54
1:A:1005:A:H2'	1:A:1005:A:N3	2.23	0.54
1:A:1256:A:C8	1:A:1258:G:C2	2.94	0.54
1:A:1498:UR3:C4'	1:A:1519[A]:MA6:H2	2.37	0.54
1:A:39:G:H1	1:A:1532:U:H3	88.34	0.54
1:A:98:U:C2'	1:A:99:C:H5'	2.37	0.54
1:A:991:U:O2'	1:A:992:U:P	2.66	0.54
2:B:97:TRP:CZ2	2:B:101:MET:HB2	2.43	0.54
6:F:48:LEU:HG	6:F:57:GLN:HA	1.88	0.54
6:F:48:LEU:HD13	6:F:52:ILE:HG13	1.89	0.54
8:H:4:ASP:OD1	8:H:6:ILE:N	2.40	0.54
9:I:33:PHE:CE2	9:I:47:LEU:HD11	2.41	0.54
17:Q:12:SER:HB3	17:Q:20:THR:OG1	2.07	0.54
17:Q:90:ILE:O	17:Q:91:ARG:C	2.46	0.54
19:S:19:VAL:HG23	19:S:47:HIS:HD1	1.71	0.54
20:T:82:SER:O	20:T:83:ARG:C	2.44	0.54
1:A:119:A:P	29:A:2559:HOH:O	2.64	0.54
1:A:1279:A:C5'	1:A:1280:A:OP1	2.56	0.54
1:A:257:G:C2	1:A:270:A:C2	2.94	0.54
1:A:259:G:H2'	1:A:260:G:O5'	2.08	0.54
1:A:895:G:H2'	1:A:896:C:H6	1.73	0.54
1:A:89:C:C6	1:A:90:U:N3	2.75	0.54
2:B:92:TYR:CE1	2:B:151:GLY:HA3	2.42	0.54
3:C:3:ASN:N	3:C:3:ASN:OD1	2.40	0.54
5:E:107:ARG:O	5:E:108:ALA:C	2.46	0.54
12:L:59:ARG:HG3	12:L:65:GLU:OE2	2.08	0.54
17:Q:45:HIS:NE2	17:Q:47:PRO:HB3	2.22	0.54
17:Q:81:ARG:NE	17:Q:84:LEU:CD1	2.71	0.54
1:A:1055:A:C8	1:A:1206:G:N2	2.76	0.54
1:A:500:G:C6	1:A:546:G:C2	2.96	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:156:ARG:NH1	3:C:193:TYR:HB2	2.23	0.54
3:C:6:HIS:HD2	3:C:7:PRO:HD2	1.70	0.54
4:D:58:LEU:C	4:D:58:LEU:HD23	2.27	0.54
7:G:54:THR:CG2	7:G:56:GLN:HB2	2.38	0.54
10:J:79:ARG:HD2	10:J:79:ARG:H	1.73	0.54
14:N:9:LYS:O	14:N:11:LYS:N	2.40	0.54
19:S:41:VAL:HG22	19:S:44:MET:HG3	1.89	0.54
1:A:1018:C:H2'	1:A:1019:C:C6	2.43	0.54
1:A:610:G:H2'	1:A:611:A:H5'	1.89	0.54
1:A:91:C:H2'	1:A:92:C:H6	1.70	0.54
4:D:57:ARG:HG3	4:D:202:LEU:HD22	1.89	0.54
5:E:11:ILE:CG2	5:E:31:LEU:HB3	2.37	0.54
10:J:79:ARG:H	10:J:79:ARG:CD	2.21	0.54
13:M:37:THR:OG1	13:M:55:ARG:HG2	2.08	0.54
1:A:1004:A:C5'	29:A:2327:HOH:O	2.55	0.53
1:A:1054:C:N3	23:W:34:G:H5'	2.21	0.53
1:A:1190:G:C8	1:A:1190:G:C5'	2.91	0.53
1:A:1206:G:C4	1:A:1207:2MG:C8	2.96	0.53
1:A:1505:G:H5'	1:A:1506:U:OP1	2.08	0.53
1:A:384:G:H2'	1:A:385:C:C6	2.42	0.53
1:A:725:G:C2'	1:A:726:C:H5'	2.38	0.53
1:A:579:G:H5'	1:A:728:A:H1'	1.90	0.53
1:A:769:G:C2'	1:A:770:C:H5'	2.38	0.53
2:B:114:ARG:O	2:B:117:GLU:HB3	2.08	0.53
3:C:46:GLU:HG3	3:C:83:ARG:HH21	1.71	0.53
6:F:62:TRP:C	6:F:63:TYR:HD2	2.11	0.53
1:A:671:G:H5'	6:F:77:ARG:NH2	2.23	0.53
6:F:98:LEU:N	6:F:98:LEU:CD1	2.71	0.53
14:N:46:GLU:O	14:N:49:HIS:HB2	2.08	0.53
17:Q:48:GLU:O	17:Q:49:GLU:HB2	2.08	0.53
18:R:50:ILE:HG12	18:R:70:ILE:HD13	1.89	0.53
19:S:31:ILE:O	19:S:50:ALA:CB	2.56	0.53
20:T:45:GLN:HA	20:T:91:LEU:HD21	1.90	0.53
1:A:1006:C:O2'	1:A:1007:C:H5'	2.08	0.53
1:A:1236:A:H4'	1:A:1304:G:H4'	1.91	0.53
1:A:1278:U:O2	1:A:1278:U:H2'	2.07	0.53
1:A:1502:A:N3	1:A:1502:A:C2'	2.70	0.53
1:A:602:A:C2	1:A:637:G:C2	2.96	0.53
1:A:689:C:H2'	1:A:690:G:H5'	1.89	0.53
1:A:691:G:H2'	1:A:692:U:H6	1.73	0.53
1:A:865:A:H8	1:A:865:A:O5'	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:890:G:O2'	1:A:906:G:O6	2.16	0.53
1:A:947:G:H2'	1:A:948:C:O4'	2.08	0.53
3:C:150:LYS:HA	3:C:169:ALA:HB2	1.90	0.53
4:D:83:SER:CA	4:D:89:THR:HG23	2.32	0.53
7:G:69:VAL:HA	7:G:138:LYS:HD3	1.89	0.53
9:I:15:ALA:CB	9:I:77:ILE:HD12	2.37	0.53
17:Q:59:ILE:CG2	17:Q:71:PHE:CD1	2.90	0.53
19:S:41:VAL:HG23	19:S:43:GLU:OE2	2.07	0.53
1:A:1054:C:N4	23:W:34:G:C8	2.76	0.53
1:A:154:C:C2'	1:A:155:C:H5'	2.38	0.53
1:A:256:U:O2'	1:A:257:G:H5'	2.07	0.53
1:A:34:C:H1'	12:L:32:PHE:CZ	2.43	0.53
1:A:778:G:H2'	1:A:779:C:O4'	2.08	0.53
1:A:784:C:H2'	1:A:785:G:O5'	2.08	0.53
1:A:858:G:O2'	1:A:859:A:C5'	2.44	0.53
4:D:43:HIS:HA	4:D:46:LYS:HG3	1.90	0.53
5:E:8:GLU:CB	5:E:34:VAL:HG12	2.38	0.53
7:G:27:ILE:HG22	7:G:28:ASN:N	2.24	0.53
11:K:56:GLY:O	11:K:57:THR:C	2.45	0.53
12:L:55:VAL:N	12:L:70:ILE:HD12	2.23	0.53
20:T:84:LEU:HD23	20:T:84:LEU:C	2.29	0.53
1:A:1371:G:O3'	9:I:69:GLY:HA3	2.09	0.53
1:A:594:G:H2'	1:A:595:G:H5'	1.90	0.53
1:A:664:G:OP1	18:R:64:ARG:HD2	2.09	0.53
1:A:688:G:H2'	1:A:689:C:C6	2.43	0.53
3:C:113:ALA:N	3:C:114:PRO:HD2	2.24	0.53
4:D:105:VAL:HG13	4:D:110:PHE:HB2	1.91	0.53
7:G:115:ARG:HG3	7:G:118:VAL:HG23	1.90	0.53
8:H:9:MET:SD	8:H:36:LEU:HD21	2.48	0.53
12:L:19:ARG:HA	12:L:20:LYS:NZ	2.23	0.53
17:Q:81:ARG:O	17:Q:81:ARG:HG3	2.08	0.53
18:R:38:GLU:CD	18:R:38:GLU:H	2.11	0.53
21:U:18:TYR:CD1	21:U:24:ARG:HG3	2.44	0.53
1:A:1055:A:C8	1:A:1206:G:C2	2.96	0.53
1:A:1413:A:C2	1:A:1414:U:C2	2.97	0.53
1:A:229:U:O2'	16:P:23:ASP:HB2	2.09	0.53
2:B:30:ARG:HD2	2:B:31:TYR:CE1	2.43	0.53
7:G:59:LEU:HD23	7:G:60:LYS:HE3	1.91	0.53
7:G:62:PHE:C	7:G:62:PHE:CD1	2.79	0.53
7:G:78:ARG:HD2	7:G:156:TRP:CB	2.38	0.53
9:I:48:GLU:HB3	9:I:101:PHE:CE1	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:22:VAL:HG23	18:R:56:THR:HA	1.91	0.53
1:A:1026:G:C8	1:A:1027:C:C2	2.96	0.53
1:A:1472:U:H2'	1:A:1473:A:O5'	2.09	0.53
1:A:144:G:H1	1:A:178:C:H42	1.57	0.53
1:A:182:U:C5	1:A:183:G:C4	2.94	0.53
1:A:392:G:N3	1:A:393:A:C8	2.77	0.53
1:A:98:U:O2'	1:A:99:C:H5'	2.09	0.53
4:D:147:ALA:CB	4:D:182:LYS:HB3	2.39	0.53
5:E:51:VAL:O	5:E:54:ALA:HB3	2.09	0.53
10:J:29:ARG:CD	10:J:29:ARG:H	2.16	0.53
1:A:1321:C:C4'	13:M:87:TYR:HE2	2.18	0.53
14:N:26:ARG:HD3	14:N:47:LEU:CD1	2.39	0.53
17:Q:11:VAL:HG13	17:Q:85:VAL:HG12	1.91	0.53
6:F:99:ALA:HB1	18:R:23:LYS:NZ	2.23	0.53
23:W:35:G:N3	23:W:36:A:C8	2.76	0.53
1:A:1212:U:C1'	1:A:1213:A:OP2	2.52	0.53
1:A:1369:C:H2'	1:A:1370:G:H8	1.73	0.53
1:A:443:C:N4	1:A:491:G:H1	2.06	0.53
1:A:89:C:O2'	1:A:90:U:OP1	2.23	0.53
2:B:122:PHE:CE1	2:B:127:ILE:HD12	2.44	0.53
7:G:5:ARG:CZ	7:G:8:GLU:HG2	2.37	0.53
13:M:15:VAL:O	13:M:19:LEU:HG	2.08	0.53
1:A:1026:G:C8	1:A:1027:C:O2	2.62	0.53
1:A:532:A:H61	1:A:1207:2MG:H5'	1.74	0.53
1:A:1303:C:N4	1:A:1304:G:C6	2.77	0.53
1:A:1407:5MC:N3	1:A:1408:A:C8	2.77	0.53
1:A:560:U:H5'	1:A:566:G:N2	2.24	0.53
1:A:922:G:C6	1:A:923:A:C6	2.97	0.53
2:B:100:GLY:CA	2:B:176:GLU:OE2	2.55	0.53
6:F:49:ALA:HB3	6:F:50:TYR:HD1	1.74	0.53
8:H:54:ASP:CG	8:H:55:GLY:H	2.00	0.53
10:J:49:VAL:O	10:J:61:GLU:N	2.36	0.53
11:K:48:ILE:HG22	11:K:49:GLY:N	2.22	0.53
12:L:50:SER:O	12:L:51:ALA:HB2	2.09	0.53
12:L:79:GLU:HG2	12:L:80:HIS:NE2	2.23	0.53
20:T:74:LYS:HB2	20:T:76:ALA:H	1.74	0.53
1:A:1035:A:C4	1:A:1036:G:N7	2.76	0.53
1:A:1077:G:N2	1:A:1081:G:C4	2.77	0.53
1:A:1090:U:H2'	1:A:1091:U:C6	2.38	0.53
1:A:1131:G:C8	1:A:1131:G:OP2	2.59	0.53
1:A:456:C:H2'	1:A:457:C:C6	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:984:C:N3	1:A:1221:G:N2	2.47	0.53
4:D:150:GLU:O	4:D:153:ARG:N	2.34	0.53
6:F:2:ARG:HE	6:F:69:GLU:HG2	1.74	0.53
7:G:37:ASN:HD22	7:G:41:ARG:HH21	1.57	0.53
8:H:28:ALA:HB2	8:H:58:TYR:HA	1.90	0.53
9:I:53:VAL:HG21	9:I:85:LEU:CD1	2.35	0.53
10:J:65:LEU:HD12	10:J:66:ARG:N	2.24	0.53
10:J:47:PHE:HD2	14:N:34:TYR:CD2	2.27	0.53
16:P:15:PRO:HB2	16:P:41:PRO:HG2	1.91	0.53
1:A:1314:C:O2'	1:A:1315:U:H5'	2.08	0.53
1:A:1349:A:OP1	9:I:118:LYS:HG3	2.08	0.53
1:A:781:A:C5	1:A:802:A:C2	2.97	0.53
2:B:239:VAL:HG12	2:B:239:VAL:O	2.09	0.53
6:F:67:MET:HB2	6:F:68:PRO:CD	2.38	0.53
7:G:139:GLU:HB3	7:G:143:ARG:HH22	1.73	0.53
1:A:1130:A:H5''	9:I:62:TYR:CE2	2.43	0.53
9:I:8:GLY:CA	9:I:79:LEU:HB3	2.30	0.53
10:J:61:GLU:CG	10:J:61:GLU:O	2.57	0.53
11:K:14:VAL:O	11:K:15:ALA:HB3	2.08	0.53
11:K:92:GLU:HB3	11:K:96:ARG:NH2	2.24	0.53
15:O:14:GLU:HG3	15:O:15:PHE:CD1	2.38	0.53
17:Q:40:LYS:HG2	17:Q:41:LYS:H	1.73	0.53
18:R:50:ILE:HD11	18:R:70:ILE:CG2	2.38	0.53
20:T:105:SER:O	20:T:106:ALA:OXT	2.27	0.53
1:A:1058:G:H2'	1:A:1059:C:C6	2.43	0.52
1:A:178:C:H2'	1:A:179:A:H5'	1.92	0.52
1:A:375:U:C4	1:A:376:G:N7	2.77	0.52
1:A:437:U:OP2	29:A:2795:HOH:O	2.19	0.52
1:A:783:C:C2'	1:A:784:C:H5'	2.39	0.52
5:E:11:ILE:HG21	5:E:31:LEU:HD13	1.90	0.52
8:H:19:VAL:O	8:H:19:VAL:HG23	2.09	0.52
11:K:40:ILE:CG2	11:K:75:TYR:CD1	2.92	0.52
14:N:26:ARG:CD	14:N:47:LEU:HD11	2.36	0.52
1:A:1003(A):G:N1	1:A:1038:C:N3	2.46	0.52
1:A:1130:A:H5''	9:I:62:TYR:HE2	1.74	0.52
1:A:1320:C:C2'	1:A:1321:C:H5'	2.40	0.52
1:A:164:U:H2'	1:A:165:C:C6	2.43	0.52
1:A:514:C:H2'	1:A:515:G:H8	1.73	0.52
1:A:56:U:H2'	1:A:57:G:C8	2.43	0.52
2:B:212:GLN:NE2	2:B:235:SER:HB2	2.23	0.52
2:B:26:PRO:O	2:B:29:ALA:HB2	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1057:G:H5''	3:C:154:SER:OG	2.08	0.52
6:F:10:LEU:HD12	6:F:10:LEU:H	1.73	0.52
6:F:78:GLU:O	6:F:81:ILE:HG12	2.10	0.52
5:E:152:ARG:O	8:H:64:LYS:NZ	2.42	0.52
11:K:120:ARG:CG	11:K:120:ARG:NH1	2.72	0.52
18:R:47:THR:HA	18:R:83:GLU:HB2	1.90	0.52
19:S:38:SER:HB3	19:S:71:LEU:HD12	1.91	0.52
1:A:1054:C:N4	23:W:34:G:OP1	2.41	0.52
1:A:1005:A:OP2	1:A:1006:C:C5	2.62	0.52
1:A:1517[B]:G:O6	1:A:1518[B]:MA6:H103	2.09	0.52
1:A:35:G:C5	1:A:36:C:C5	2.97	0.52
1:A:509:A:H3'	1:A:509:A:H8	1.70	0.52
1:A:520:A:H61	1:A:529:G:H1'	1.74	0.52
1:A:661:G:C8	1:A:661:G:H5''	2.42	0.52
2:B:97:TRP:HH2	2:B:176:GLU:CD	2.13	0.52
4:D:155:LEU:CD2	4:D:156:GLU:H	2.22	0.52
7:G:46:ALA:HB1	7:G:121:ALA:HB2	1.90	0.52
12:L:75:HIS:HB3	12:L:102:ARG:NH1	2.24	0.52
12:L:54:LYS:HD3	12:L:54:LYS:N	2.25	0.52
13:M:23:TYR:CD2	13:M:70:LEU:HD13	2.44	0.52
1:A:1054:C:C4	23:W:34:G:OP1	2.63	0.52
1:A:1056:U:H5'	3:C:163:ALA:CB	2.34	0.52
1:A:1186:G:N2	1:A:1187:G:H1'	2.25	0.52
1:A:1350:A:C5	1:A:1351:U:C5	2.97	0.52
1:A:1391:U:H2'	1:A:1392:G:H8	1.74	0.52
1:A:1519[A]:MA6:H2'	1:A:1520[A]:G:H5'	1.90	0.52
1:A:1537:U:H6	1:A:1537:U:O5'	1.93	0.52
1:A:93:G:C2'	1:A:95:U:H5'	2.40	0.52
2:B:204:ASN:OD1	2:B:204:ASN:C	2.47	0.52
2:B:92:TYR:O	2:B:92:TYR:HD1	1.92	0.52
4:D:2:GLY:O	4:D:3:ARG:HB3	2.08	0.52
10:J:44:VAL:CG1	10:J:66:ARG:HD3	2.32	0.52
16:P:67:THR:CG2	16:P:68:ASP:N	2.63	0.52
17:Q:50:LYS:HE3	17:Q:51:TYR:CE2	2.44	0.52
19:S:11:VAL:HG11	19:S:16:LEU:HD22	1.91	0.52
1:A:1069:C:O2'	1:A:1192:C:H1'	2.10	0.52
1:A:1085:U:C6	1:A:1094:G:N1	2.78	0.52
1:A:259:G:C2'	1:A:260:G:O5'	2.58	0.52
1:A:442:C:C2'	1:A:443:C:H5'	2.39	0.52
1:A:461:C:H4'	1:A:462:G:OP2	2.09	0.52
1:A:746:A:O2'	1:A:747:C:H5'	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:837:G:N2	1:A:850:U:O2	2.42	0.52
2:B:184:VAL:HG12	2:B:197:VAL:HG13	1.90	0.52
2:B:212:GLN:NE2	2:B:235:SER:CB	2.72	0.52
3:C:77:ILE:HG13	3:C:103:VAL:HG21	1.92	0.52
5:E:92:LYS:O	5:E:118:ILE:HG13	2.09	0.52
6:F:48:LEU:HD11	6:F:52:ILE:HG13	1.87	0.52
7:G:75:VAL:HG21	7:G:86:GLN:HB3	1.90	0.52
9:I:27:THR:OG1	9:I:31:GLN:O	2.19	0.52
11:K:33:THR:HG21	11:K:37:GLY:O	2.10	0.52
1:A:995:C:H1'	14:N:4:LYS:HE2	1.90	0.52
1:A:735:C:H1'	18:R:75:ILE:HD11	1.92	0.52
19:S:49:ILE:N	19:S:49:ILE:HD13	2.24	0.52
1:A:1439:C:OP1	20:T:38:LYS:HE2	2.10	0.52
1:A:1392:G:N2	1:A:1502:A:H8	2.08	0.52
1:A:171:A:P	29:A:2844:HOH:O	2.68	0.52
1:A:182:U:H5	1:A:183:G:N9	2.05	0.52
1:A:191:G:O2'	20:T:101:GLY:O	2.28	0.52
1:A:506:G:H2'	1:A:507:C:H5'	1.92	0.52
1:A:969:A:H2'	1:A:970:C:H5'	1.90	0.52
2:B:47:THR:HG23	2:B:202:PRO:O	2.09	0.52
3:C:62:ASP:HA	3:C:97:LYS:HZ1	1.74	0.52
13:M:71:ARG:HA	13:M:74:VAL:CG2	2.40	0.52
16:P:9:PHE:HB2	16:P:16:HIS:O	2.10	0.52
19:S:51:VAL:HG23	19:S:58:VAL:HG23	1.91	0.52
21:U:18:TYR:HD2	21:U:22:ARG:HD3	1.73	0.52
1:A:1054:C:H2'	1:A:1055:A:H5''	1.92	0.52
1:A:1190:G:O2'	1:A:1191:A:O5'	2.27	0.52
1:A:1241:G:H2'	1:A:1242:C:C6	2.45	0.52
1:A:532:A:N1	1:A:1207:2MG:H4'	2.25	0.52
1:A:740:U:H4'	15:O:42:HIS:CD2	2.45	0.52
4:D:111:ALA:HB1	4:D:116:GLN:HG2	1.91	0.52
5:E:88:LYS:HB3	5:E:123:LEU:HB2	1.92	0.52
7:G:89:MET:SD	7:G:156:TRP:CZ3	3.03	0.52
9:I:118:LYS:HG3	9:I:118:LYS:O	2.09	0.52
18:R:87:ARG:HB2	18:R:87:ARG:NH2	2.25	0.52
1:A:1067:A:O2'	1:A:1093:A:O2'	2.07	0.52
1:A:1396:A:H4'	1:A:1397:C:H5''	1.90	0.52
1:A:1494:G:C2	1:A:1495:U:C6	2.98	0.52
1:A:35:G:C4	1:A:36:C:C5	2.98	0.52
4:D:32:ALA:C	4:D:35:ARG:H	2.13	0.52
8:H:10:LEU:HD11	8:H:135:CYS:HB3	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:15:LEU:HD12	19:S:15:LEU:N	2.25	0.52
1:A:1147:C:H4'	9:I:5:TYR:CE2	2.38	0.52
1:A:1288:A:N6	1:A:1289:A:N6	2.57	0.52
1:A:414:A:C2	1:A:415:A:C8	2.98	0.52
1:A:512:U:O2	1:A:540:G:C2	2.62	0.52
1:A:909:A:C8	1:A:910:C:C5	2.98	0.52
1:A:92:C:H2'	1:A:93:G:C8	2.44	0.52
4:D:173:TRP:C	4:D:174:LEU:HD23	2.30	0.52
6:F:14:LEU:HD12	6:F:19:LEU:HA	1.91	0.52
12:L:79:GLU:HG2	12:L:80:HIS:CE1	2.45	0.52
1:A:1110:A:H8	1:A:1110:A:O5'	1.92	0.52
1:A:1124:G:C8	1:A:1145:C:C6	2.98	0.52
1:A:132:C:C2'	1:A:133:U:H5'	2.40	0.52
1:A:504:C:C2	1:A:542:G:N2	2.78	0.52
1:A:568:G:H5''	1:A:568:G:H8	1.75	0.52
9:I:17:VAL:HG22	9:I:63:ILE:HD11	1.92	0.52
10:J:48:THR:HG23	10:J:62:HIS:HB3	1.91	0.52
10:J:6:ILE:CD1	10:J:98:ILE:HG23	2.40	0.52
18:R:22:VAL:CG2	18:R:56:THR:HA	2.39	0.52
1:A:1003:G:H2'	1:A:1003(A):G:C8	2.45	0.51
1:A:1009:G:N2	1:A:1010:G:C4	2.78	0.51
1:A:630:G:H8	1:A:630:G:OP2	1.92	0.51
3:C:34:LEU:HD12	3:C:34:LEU:O	2.10	0.51
5:E:55:VAL:O	5:E:56:GLN:C	2.47	0.51
7:G:22:LEU:CD2	7:G:66:VAL:HG21	2.38	0.51
9:I:27:THR:HG22	9:I:62:TYR:HA	1.92	0.51
10:J:7:LYS:HE2	10:J:9:ARG:HH21	1.73	0.51
12:L:10:LEU:HD11	12:L:15:ARG:HE	1.75	0.51
13:M:22:ILE:HG13	13:M:25:ILE:HD12	1.91	0.51
1:A:1031:G:N2	1:A:1032:G:C4	2.78	0.51
1:A:1206:G:C5	1:A:1207:2MG:N7	2.78	0.51
1:A:428:G:H1'	1:A:429:U:OP2	2.10	0.51
1:A:1103:C:OP1	2:B:96:ARG:NH1	2.43	0.51
3:C:78:GLY:HA3	3:C:83:ARG:HB3	1.92	0.51
7:G:54:THR:HG22	7:G:56:GLN:CB	2.40	0.51
10:J:32:ALA:HB2	10:J:76:ASN:OD1	2.10	0.51
12:L:75:HIS:HB3	12:L:102:ARG:HH12	1.75	0.51
16:P:67:THR:CG2	16:P:68:ASP:H	2.15	0.51
13:M:99:ARG:NH2	19:S:2:PRO:HG2	2.24	0.51
1:A:1009:G:H2'	1:A:1009:G:N3	2.25	0.51
1:A:1103:C:C5'	2:B:98:LEU:HD12	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:328:C:C2'	1:A:329:A:OP2	2.58	0.51
1:A:36:C:H2'	1:A:37:U:H5'	1.93	0.51
1:A:747:C:C2'	1:A:748:C:O5'	2.58	0.51
1:A:770:C:O2'	1:A:771:G:H5'	2.10	0.51
1:A:840:C:H5'	1:A:848:C:O2	2.11	0.51
1:A:924:C:H5'	1:A:1399:C:OP2	2.09	0.51
1:A:975:A:C8	1:A:975:A:H5'	2.43	0.51
1:A:988:G:C2	1:A:1218:C:O2	2.64	0.51
10:J:47:PHE:CD2	14:N:34:TYR:CD2	2.99	0.51
13:M:22:ILE:HD13	13:M:22:ILE:N	2.25	0.51
13:M:36:LYS:HB2	13:M:59:TYR:HE1	1.75	0.51
3:C:13:GLY:HA2	14:N:57:ARG:NH1	2.25	0.51
16:P:58:TYR:O	16:P:62:VAL:HG13	2.11	0.51
1:A:1061:G:C6	1:A:1062:U:N3	2.78	0.51
1:A:1407:5MC:N3	1:A:1408:A:N7	2.58	0.51
1:A:1519[B]:MA6:H93	1:A:1520[B]:G:H21	1.75	0.51
1:A:509:A:HO2'	1:A:510:A:P	2.25	0.51
1:A:688:G:H2'	1:A:689:C:H6	1.75	0.51
2:B:219:VAL:CA	2:B:222:ILE:HG12	2.39	0.51
4:D:78:LEU:HD21	4:D:96:LEU:HB3	1.92	0.51
4:D:82:ALA:HB2	4:D:96:LEU:HD22	1.92	0.51
6:F:14:LEU:HD21	6:F:84:ASN:OD1	2.10	0.51
7:G:21:VAL:HG23	7:G:22:LEU:N	2.26	0.51
7:G:26:PHE:CE2	7:G:30:ILE:HD11	2.46	0.51
11:K:122:LYS:O	11:K:123:LYS:C	2.47	0.51
13:M:23:TYR:CE2	13:M:71:ARG:HG3	2.45	0.51
18:R:39:VAL:HG13	18:R:40:LEU:H	1.75	0.51
1:A:1162:C:O2'	1:A:1163:C:H5'	2.10	0.51
1:A:1168:A:H2'	1:A:1169:A:C8	2.45	0.51
1:A:1441:G:H5''	1:A:1442:G:O5'	2.10	0.51
1:A:1482:G:O5'	1:A:1482:G:H8	1.94	0.51
3:C:84:ILE:HG12	3:C:88:ARG:HH22	1.75	0.51
1:A:1368:G:C2'	1:A:1369:C:H5'	2.41	0.51
1:A:1408:A:C4	1:A:1409:C:C5	2.99	0.51
1:A:658:G:C2	1:A:749:C:N3	2.79	0.51
4:D:145:GLU:C	4:D:146:ILE:HD12	2.31	0.51
7:G:111:ARG:HD3	7:G:113:GLU:HG3	1.93	0.51
1:A:1152:A:OP1	10:J:68:HIS:CE1	2.63	0.51
15:O:39:LEU:HD23	15:O:39:LEU:O	2.11	0.51
1:A:1267:C:O2'	21:U:20:LYS:HG3	2.11	0.51
23:W:35:G:C4	23:W:36:A:N7	2.79	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1203:C:H2'	1:A:1204:A:O4'	2.11	0.51
1:A:509:A:C8	1:A:509:A:C3'	2.92	0.51
1:A:849:C:H2'	1:A:850:U:H5'	1.92	0.51
1:A:865:A:H2'	1:A:866:C:C6	2.45	0.51
13:M:48:LEU:HB3	13:M:53:VAL:HG23	1.91	0.51
1:A:1060:C:OP1	14:N:45:ARG:NH2	2.44	0.51
15:O:11:VAL:HG22	15:O:12:ILE:HD13	1.92	0.51
1:A:1055:A:N7	1:A:1206:G:C2	2.79	0.51
1:A:1148:U:C4	1:A:1149:C:C2	2.99	0.51
1:A:1163:C:C2	1:A:1174:G:N2	2.79	0.51
1:A:429:U:O2	1:A:430:A:C8	2.64	0.51
4:D:18:LYS:CB	4:D:33:MET:HG3	2.40	0.51
5:E:150:ARG:HG2	5:E:151:LEU:HD23	1.92	0.51
1:A:1351:U:H5'	7:G:33:ASP:OD1	2.10	0.51
7:G:38:LEU:O	7:G:42:ILE:CG1	2.52	0.51
8:H:83:ILE:HB	8:H:137:VAL:HG22	1.93	0.51
1:A:1020:U:H2'	1:A:1021:G:C8	2.42	0.51
1:A:1098:C:H2'	1:A:1099:G:O4'	2.10	0.51
1:A:1126:U:O4	1:A:1127:G:N1	2.44	0.51
1:A:1518[A]:MA6:C9	1:A:1519[A]:MA6:H103	2.41	0.51
1:A:1534:C:C4	1:A:1535:A:C2	2.99	0.51
1:A:22:G:C4	1:A:23:C:C5	2.99	0.51
1:A:433:C:H2'	1:A:434:U:H6	1.75	0.51
1:A:31:G:N2	1:A:48:C:OP1	2.34	0.51
1:A:676:A:H8	1:A:676:A:O5'	1.94	0.51
1:A:814:A:H2'	1:A:816:A:H5''	1.93	0.51
1:A:983:A:H2	1:A:984:C:C6	2.29	0.51
2:B:83:MET:SD	2:B:234:PRO:O	2.69	0.51
2:B:8:LYS:O	2:B:11:LEU:HD13	2.11	0.51
10:J:50:ILE:HA	10:J:60:ARG:HA	1.92	0.51
14:N:22:THR:O	14:N:23:ARG:HG3	2.10	0.51
1:A:191:G:N2	20:T:103:GLY:O	2.43	0.51
23:W:39:G:C2	23:W:40:PSU:O4	2.64	0.51
1:A:1048:G:C6	1:A:1210:C:N4	2.79	0.51
1:A:1088:G:C2'	1:A:1089:G:H5'	2.41	0.51
1:A:1173:G:H2'	1:A:1174:G:C8	2.45	0.51
1:A:1328:C:H2'	1:A:1329:A:H8	1.76	0.51
1:A:1494:G:C2'	1:A:1495:U:H5'	2.41	0.51
1:A:266:G:H5''	1:A:268:C:H41	1.76	0.51
1:A:352:C:C3'	1:A:352:C:C6	2.94	0.51
1:A:922:G:C2	1:A:1396:A:C6	2.98	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:61:LYS:CD	4:D:61:LYS:C	2.79	0.51
9:I:121:ARG:NH1	9:I:121:ARG:CG	2.69	0.51
10:J:21:GLN:HA	10:J:24:VAL:HG12	1.93	0.51
12:L:90:VAL:CG1	12:L:93:LEU:HG	2.41	0.51
3:C:29:TYR:OH	14:N:54:PRO:O	2.29	0.51
10:J:63:PHE:HB3	14:N:58:LYS:HA	1.93	0.51
1:A:134:A:N6	16:P:25:ARG:NH2	2.59	0.51
17:Q:63:ARG:HG2	17:Q:64:PRO:HD2	1.93	0.51
1:A:1243:C:H5''	21:U:8:THR:HG23	1.91	0.51
1:A:1081:G:P	5:E:16:THR:HG1	2.34	0.50
1:A:1172:C:O2'	1:A:1173:G:H5'	2.11	0.50
1:A:1499:A:H5'	1:A:1519[A]:MA6:C2	2.42	0.50
1:A:162:A:H3'	1:A:163:C:O4'	2.11	0.50
1:A:297:G:N2	1:A:300:A:OP2	2.37	0.50
1:A:475:G:O6	29:A:2600:HOH:O	2.20	0.50
1:A:581:G:O3'	15:O:64:ARG:NH2	2.39	0.50
1:A:658:G:H2'	1:A:659:U:C6	2.46	0.50
1:A:797:C:O2'	1:A:798:G:H5'	2.10	0.50
1:A:981:U:H5'	14:N:21:TYR:CZ	2.45	0.50
4:D:92:VAL:O	4:D:93:PHE:C	2.47	0.50
10:J:47:PHE:CZ	14:N:37:PHE:CE1	2.88	0.50
19:S:47:HIS:O	19:S:62:ILE:HG22	2.10	0.50
1:A:1375:A:C5	1:A:1376:U:C5	2.99	0.50
1:A:1470:G:O2'	1:A:1471:G:H5'	2.11	0.50
1:A:928:G:C2	1:A:1390:U:O2	2.65	0.50
2:B:100:GLY:O	2:B:101:MET:C	2.49	0.50
9:I:95:LYS:HD2	9:I:95:LYS:H	1.76	0.50
17:Q:40:LYS:CD	17:Q:42:TYR:CZ	2.94	0.50
20:T:50:GLU:HA	20:T:99:LEU:CD1	2.39	0.50
1:A:1110:A:N7	29:A:2140:HOH:O	2.35	0.50
1:A:1305:G:OP1	21:U:2:GLY:HA3	2.11	0.50
1:A:973:G:H2'	1:A:974:A:OP1	2.11	0.50
1:A:976:G:C8	1:A:1358:U:C2	2.99	0.50
10:J:63:PHE:HA	14:N:59:ALA:H	1.76	0.50
17:Q:5:VAL:C	17:Q:6:LEU:HD23	2.32	0.50
1:A:1052:U:C2'	1:A:1055:A:OP1	2.59	0.50
1:A:1179:A:H2'	1:A:1180:A:O4'	2.11	0.50
1:A:1349:A:C2	1:A:1374:A:C4	3.00	0.50
1:A:1493[B]:A:H2'	1:A:1494:G:C8	2.46	0.50
1:A:849:C:C2'	1:A:850:U:H5'	2.41	0.50
2:B:57:PHE:CG	2:B:199:TYR:CE1	2.99	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:80:ILE:HD12	2:B:208:ILE:HD12	1.94	0.50
3:C:33:LEU:HD21	14:N:53:LEU:CD2	2.41	0.50
3:C:58:GLU:O	3:C:65:ALA:HB2	2.11	0.50
5:E:147:ASP:O	5:E:150:ARG:HB3	2.12	0.50
7:G:143:ARG:NH2	7:G:143:ARG:HB2	2.27	0.50
8:H:18:ARG:NH2	8:H:81:HIS:O	2.45	0.50
10:J:24:VAL:HG23	10:J:34:VAL:HG11	1.94	0.50
12:L:90:VAL:HG11	12:L:93:LEU:HD12	1.93	0.50
13:M:4:ILE:HG22	13:M:5:ALA:HB2	1.93	0.50
14:N:15:LYS:HG2	14:N:15:LYS:O	2.11	0.50
21:U:13:ILE:HA	21:U:22:ARG:NH1	2.26	0.50
1:A:1438:G:C6	1:A:1439:C:C4	2.99	0.50
1:A:1517[A]:G:C6	1:A:1518[A]:MA6:C5	2.95	0.50
1:A:411:A:H3'	1:A:411:A:H8	1.77	0.50
5:E:10:MET:HA	5:E:32:VAL:HG23	1.93	0.50
9:I:48:GLU:HB3	9:I:101:PHE:HZ	1.74	0.50
12:L:55:VAL:CG1	12:L:67:THR:OG1	2.59	0.50
17:Q:59:ILE:HG23	17:Q:71:PHE:HB3	1.94	0.50
18:R:37:VAL:O	18:R:38:GLU:C	2.49	0.50
1:A:1515[A]:C:H42	1:A:1520[A]:G:H1	1.59	0.50
1:A:193:C:O3'	20:T:61:SER:HB2	2.11	0.50
1:A:228:A:H2'	1:A:229:U:C6	2.46	0.50
1:A:725:G:O2'	1:A:726:C:H5'	2.12	0.50
1:A:736:C:H2'	1:A:737:A:C8	2.47	0.50
1:A:738:C:OP1	6:F:92:LYS:HD3	2.11	0.50
1:A:768:A:C5	1:A:769:G:C8	2.99	0.50
1:A:83:U:C5	1:A:84:U:C6	3.00	0.50
2:B:102:LEU:O	2:B:105:PHE:HB2	2.11	0.50
2:B:213:LEU:HB3	2:B:214:ILE:HD12	1.94	0.50
3:C:39:ILE:HG21	3:C:57:ILE:HD11	1.94	0.50
1:A:1251:A:H4'	9:I:12:GLU:OE2	2.12	0.50
9:I:19:LEU:HB3	9:I:59:PHE:CD2	2.47	0.50
1:A:1123:A:C2	10:J:39:PRO:HG3	2.47	0.50
10:J:78:ASN:CG	10:J:79:ARG:HH11	2.14	0.50
12:L:35:GLY:HA3	12:L:60:LEU:HD13	1.94	0.50
12:L:39:VAL:HG12	12:L:40:VAL:N	2.27	0.50
1:A:324:G:OP1	20:T:22:ARG:HD3	2.11	0.50
1:A:201:C:N4	1:A:216:G:H1	2.04	0.50
1:A:491:G:C4	1:A:492:G:C8	3.00	0.50
1:A:53:A:OP2	29:A:2222:HOH:O	2.19	0.50
1:A:802:A:C2'	1:A:803:G:H5'	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:939:G:H2'	1:A:940:C:C6	2.46	0.50
2:B:97:TRP:CZ3	2:B:176:GLU:OE2	2.65	0.50
2:B:211:ILE:O	2:B:215:LEU:HB2	2.11	0.50
3:C:178:LEU:C	3:C:180:ALA:H	2.14	0.50
8:H:59:LEU:HD12	8:H:59:LEU:N	2.26	0.50
14:N:13:THR:N	14:N:14:PRO:CD	2.75	0.50
15:O:88:ARG:NE	15:O:88:ARG:CA	2.57	0.50
23:W:35:G:C4	23:W:36:A:C8	2.99	0.50
1:A:1248:A:C2'	1:A:1249:C:H5'	2.42	0.50
1:A:1492[B]:A:H2'	1:A:1492[B]:A:N3	2.27	0.50
1:A:478:A:O2'	1:A:479:C:H5'	2.12	0.50
1:A:690:G:H2'	1:A:691:G:O4'	2.12	0.50
1:A:834:C:O2'	1:A:835:U:H5'	2.12	0.50
2:B:158:LEU:HB3	2:B:159:PRO:HD2	1.94	0.50
5:E:77:PRO:O	5:E:78:HIS:HB3	2.11	0.50
8:H:20:TYR:CE1	8:H:76:PRO:HG2	2.46	0.50
11:K:20:TYR:CD2	11:K:83:ILE:HB	2.47	0.50
13:M:63:THR:HG23	13:M:64:TRP:N	2.27	0.50
1:A:740:U:H4'	15:O:42:HIS:HD2	1.77	0.50
21:U:23:PRO:C	21:U:25:LYS:H	2.15	0.50
21:U:5:ASP:HB3	21:U:8:THR:OG1	2.12	0.50
1:A:1115:C:H6	1:A:1115:C:O5'	1.95	0.50
1:A:264:U:H2'	1:A:265:G:C5'	2.42	0.50
2:B:101:MET:C	2:B:102:LEU:HD12	2.31	0.50
3:C:157:ILE:C	3:C:159:GLY:H	2.15	0.50
7:G:48:LYS:O	7:G:52:GLU:OE2	2.30	0.50
9:I:36:TYR:HE2	9:I:73:GLN:OE1	1.93	0.50
13:M:4:ILE:O	13:M:6:GLY:O	2.30	0.50
17:Q:53:LEU:CD1	17:Q:54:GLY:N	2.74	0.50
20:T:56:MET:HE1	20:T:85:MET:HG3	1.92	0.50
1:A:1057:G:C5'	3:C:154:SER:OG	2.60	0.49
1:A:1072:G:H2'	1:A:1073:U:C6	2.46	0.49
1:A:1126:U:C2'	1:A:1127:G:O5'	2.59	0.49
1:A:1352:C:H2'	1:A:1353:G:O4'	2.12	0.49
1:A:1368:G:OP2	9:I:114:TYR:N	2.45	0.49
1:A:1434:A:H2'	1:A:1435:G:O4'	2.11	0.49
1:A:172:A:O2'	1:A:173:U:H5'	2.12	0.49
1:A:586:C:C2'	1:A:587:G:H5'	2.41	0.49
1:A:664:G:H22	1:A:741:G:H1	1.60	0.49
2:B:195:ASP:O	8:H:68:ARG:NH2	2.45	0.49
4:D:127:THR:HA	4:D:132:ARG:HA	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:180:GLY:O	4:D:182:LYS:CG	2.60	0.49
7:G:101:LEU:O	7:G:105:VAL:HG23	2.11	0.49
1:A:1123:A:H2	10:J:39:PRO:HG3	1.77	0.49
11:K:12:ARG:O	11:K:12:ARG:HG2	2.10	0.49
15:O:39:LEU:O	15:O:42:HIS:HB3	2.12	0.49
18:R:73:ALA:HB3	18:R:79:LEU:HD12	1.94	0.49
1:A:1031:G:C2	1:A:1032:G:C5	3.00	0.49
1:A:990:C:H42	1:A:1215:G:H1	1.61	0.49
1:A:130:A:H1'	1:A:263:A:HO2'	1.76	0.49
1:A:1518[B]:MA6:H93	1:A:1519[B]:MA6:N6	2.27	0.49
1:A:440:A:C5'	1:A:442:C:OP2	2.58	0.49
1:A:540:G:C5	1:A:541:G:N7	2.80	0.49
1:A:866:C:H2'	1:A:867:G:O4'	2.13	0.49
13:M:33:ALA:O	13:M:37:THR:HG22	2.12	0.49
17:Q:58:GLU:C	17:Q:59:ILE:HD13	2.33	0.49
23:W:30:G:H2'	23:W:30:G:N3	2.27	0.49
1:A:1090:U:C2	1:A:1091:U:C6	3.00	0.49
1:A:250:A:H1'	1:A:251:G:OP2	2.12	0.49
1:A:357:G:O2'	1:A:358:U:H5'	2.12	0.49
1:A:37:U:H2'	1:A:38:G:O4'	2.12	0.49
1:A:426:G:O2'	1:A:427:U:H5'	2.12	0.49
1:A:91:C:H2'	1:A:92:C:C5	2.47	0.49
3:C:76:VAL:HG21	3:C:103:VAL:HG13	1.94	0.49
3:C:130:VAL:O	3:C:134:ILE:HD11	2.12	0.49
4:D:19:LEU:CD2	4:D:19:LEU:H	2.21	0.49
4:D:64:LEU:HA	4:D:67:ILE:HD12	1.92	0.49
7:G:72:ARG:NH1	7:G:142:GLU:OE2	2.46	0.49
8:H:85:ARG:HD2	8:H:87:SER:O	2.12	0.49
1:A:676:A:H5''	11:K:113:PRO:HB3	1.93	0.49
11:K:43:SER:OG	11:K:44:SER:N	2.45	0.49
12:L:82:VAL:HG23	12:L:106:ASP:OD1	2.13	0.49
15:O:36:ILE:HG22	15:O:37:ASN:N	2.26	0.49
1:A:1326:C:OP2	21:U:6:ARG:HD3	2.12	0.49
1:A:1026:G:C2'	1:A:1027:C:OP1	2.60	0.49
1:A:106:C:H2'	1:A:107:G:H5'	1.93	0.49
1:A:1300:G:C6	1:A:1335:C:C5	3.01	0.49
1:A:922:G:O2'	1:A:1398:A:N1	2.37	0.49
1:A:1425:U:C2	1:A:1426:C:C5	3.00	0.49
1:A:1441:G:O2'	1:A:1442:G:N2	2.45	0.49
1:A:166:G:H2'	1:A:167:G:H5'	1.94	0.49
1:A:19:C:O2'	1:A:20:U:H5'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:45:U:H2'	1:A:46:G:C8	2.47	0.49
1:A:491:G:N3	1:A:492:G:C8	2.80	0.49
1:A:854:G:N1	1:A:855:G:C5	2.80	0.49
12:L:42:THR:HA	12:L:53:ARG:O	2.13	0.49
16:P:40:ASP:HB3	16:P:48:TRP:CB	2.42	0.49
17:Q:6:LEU:HB3	17:Q:23:VAL:HG11	1.94	0.49
20:T:55:ILE:HD13	20:T:55:ILE:H	1.77	0.49
20:T:44:ALA:HB3	20:T:91:LEU:HD13	1.95	0.49
1:A:1112:C:O2	3:C:179:ARG:HG3	2.12	0.49
1:A:116:A:H3'	29:A:2018:HOH:O	2.12	0.49
1:A:1305:G:P	21:U:2:GLY:HA3	2.52	0.49
1:A:811:C:O2'	1:A:901:A:N1	2.45	0.49
2:B:28:PHE:CD2	2:B:28:PHE:O	2.66	0.49
1:A:1321:C:C5'	13:M:87:TYR:HE2	2.25	0.49
15:O:56:LEU:CD1	15:O:56:LEU:C	2.80	0.49
17:Q:62:SER:CB	17:Q:72:ARG:HD3	2.42	0.49
17:Q:82:MET:O	17:Q:85:VAL:HG23	2.12	0.49
19:S:35:SER:OG	19:S:38:SER:HB2	2.13	0.49
20:T:10:LEU:HG	20:T:11:SER:N	2.27	0.49
1:A:1166:G:C2	1:A:1171:G:C6	3.01	0.49
1:A:1193:G:N3	1:A:1194:U:C6	2.80	0.49
1:A:1197:G:C2'	1:A:1198:G:H5''	2.42	0.49
1:A:1501:C:C5	1:A:1504:G:C4	3.00	0.49
1:A:1532:U:C6	1:A:1533:C:H5	2.30	0.49
1:A:544:G:C2	1:A:545:C:C6	3.00	0.49
1:A:653:A:OP1	8:H:56:LYS:HE2	2.13	0.49
1:A:836:G:C6	1:A:851:G:C5	3.00	0.49
3:C:22:TRP:CG	3:C:59:ARG:HD2	2.48	0.49
3:C:92:ALA:O	3:C:95:THR:O	2.30	0.49
5:E:42:GLY:HA2	5:E:136:MET:CE	2.43	0.49
13:M:22:ILE:HG13	13:M:25:ILE:CD1	2.43	0.49
1:A:1090:U:C2	1:A:1091:U:C5	3.00	0.49
1:A:1507:A:C5	1:A:1530:G:C2	3.00	0.49
1:A:47:C:C6	1:A:365:U:H2'	2.48	0.49
1:A:741:G:H5''	15:O:39:LEU:HD12	1.95	0.49
1:A:741:G:H2'	1:A:742:G:O4'	2.13	0.49
1:A:89:C:O2'	1:A:90:U:C5'	2.61	0.49
3:C:47:LEU:N	3:C:47:LEU:HD12	2.26	0.49
4:D:194:LEU:HB3	4:D:196:LEU:HD21	1.94	0.49
4:D:43:HIS:ND1	4:D:46:LYS:HE2	2.28	0.49
5:E:10:MET:SD	5:E:13:ILE:HG13	2.53	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:86:ILE:HG21	8:H:133:LEU:HB3	1.95	0.49
9:I:113:LYS:H	9:I:119:ALA:HA	1.77	0.49
17:Q:53:LEU:CD1	17:Q:85:VAL:HG11	2.43	0.49
1:A:1047:G:C5	29:A:2425:HOH:O	2.63	0.49
1:A:1067:A:H1'	1:A:1068:G:OP2	2.13	0.49
1:A:1082:G:H2'	1:A:1083:U:H5'	1.93	0.49
1:A:110:C:H2'	1:A:111:G:O4'	2.13	0.49
1:A:1057:G:C4	1:A:1204:A:H2	2.28	0.49
1:A:949:A:C2	1:A:1233:G:C4	3.01	0.49
1:A:1233:G:N2	1:A:1234:C:C2	2.81	0.49
1:A:1361(A):C:C2'	1:A:1362:C:O5'	2.60	0.49
1:A:137:C:H2'	1:A:138:G:H5'	1.94	0.49
1:A:1419:G:C6	1:A:1420:C:N4	2.81	0.49
1:A:355:C:H5'	1:A:389:A:OP2	2.13	0.49
1:A:443:C:C4	1:A:444:C:C5	3.01	0.49
1:A:490:G:C6	1:A:491:G:N7	2.81	0.49
1:A:630:G:H5'	1:A:631:G:OP2	2.13	0.49
2:B:144:ARG:NH1	2:B:148:TYR:HE1	2.10	0.49
16:P:2:VAL:O	16:P:64:ALA:HA	2.13	0.49
17:Q:68:ARG:H	17:Q:70:ARG:NH1	2.10	0.49
19:S:62:ILE:HA	19:S:66:MET:SD	2.52	0.49
20:T:10:LEU:HD23	20:T:13:LEU:HB3	1.95	0.49
1:A:1128:C:H5'	9:I:16:ARG:NH2	2.28	0.49
1:A:278:G:OP2	17:Q:41:LYS:NZ	2.44	0.49
2:B:238:LEU:CD2	2:B:238:LEU:O	2.60	0.49
3:C:88:ARG:HB2	3:C:101:LEU:HD22	1.95	0.49
4:D:39:PRO:O	4:D:44:GLY:HA3	2.12	0.49
6:F:25:ILE:HD12	6:F:82:ARG:NH1	2.26	0.49
7:G:123:GLU:O	7:G:126:ASP:N	2.46	0.49
7:G:20:ASP:OD2	7:G:63:LYS:NZ	2.46	0.49
13:M:65:LYS:C	13:M:66:LEU:HD23	2.33	0.49
20:T:44:ALA:O	20:T:45:GLN:C	2.50	0.49
1:A:1202:G:H2'	1:A:1203:C:H5'	1.94	0.49
1:A:1352:C:H2'	1:A:1353:G:C8	2.48	0.49
1:A:349:A:H2'	1:A:350:G:H5'	1.95	0.49
1:A:507:C:OP2	1:A:508:C:O2'	2.25	0.49
1:A:945:G:N3	1:A:945:G:H2'	2.28	0.49
1:A:1055:A:O2'	3:C:156:ARG:NH2	2.46	0.49
4:D:187:ARG:HG2	4:D:188:LEU:N	2.27	0.49
1:A:19:C:P	5:E:127:ASN:HD22	2.35	0.49
5:E:32:VAL:HG12	5:E:58:ALA:HB1	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:84:PHE:HB3	5:E:134:ALA:HB2	1.95	0.49
5:E:95:ALA:O	5:E:98:THR:OG1	2.17	0.49
13:M:11:ARG:HG3	13:M:12:ASN:H	1.74	0.49
15:O:70:LEU:HD23	15:O:78:TYR:HB2	1.95	0.49
17:Q:65:ILE:CG2	17:Q:69:LYS:HE3	2.43	0.49
20:T:13:LEU:C	20:T:13:LEU:CD1	2.80	0.49
1:A:1071:C:O2'	1:A:1072:G:H5'	2.12	0.48
1:A:1330:U:H2'	1:A:1331:G:H5'	1.93	0.48
1:A:1357:A:H5''	1:A:1358:U:OP2	2.13	0.48
1:A:1385:G:H2'	1:A:1386:G:O4'	2.12	0.48
1:A:154:C:O2'	1:A:155:C:H5'	2.13	0.48
1:A:610:G:C2'	1:A:611:A:H5'	2.43	0.48
1:A:77:G:O2'	1:A:78:G:H5'	2.13	0.48
1:A:79:G:N3	1:A:80:G:C8	2.81	0.48
1:A:954:G:N2	1:A:1227:A:H62	2.11	0.48
2:B:220:ASP:O	2:B:223:ILE:HG13	2.13	0.48
3:C:121:ALA:HA	3:C:124:ILE:HD12	1.94	0.48
4:D:206:PHE:CE2	4:D:207:TYR:CE2	3.01	0.48
4:D:61:LYS:NZ	4:D:72:GLU:OE2	2.44	0.48
5:E:34:VAL:HG22	5:E:62:ALA:HB1	1.95	0.48
7:G:47:CYS:HA	7:G:50:ILE:HG12	1.95	0.48
17:Q:60:ILE:O	17:Q:60:ILE:HG23	2.12	0.48
1:A:1124:G:H2'	1:A:1145:C:C5	2.46	0.48
1:A:1248:A:C6	1:A:1249:C:C4	3.01	0.48
1:A:1520[A]:G:H2'	1:A:1521:G:H8	1.78	0.48
1:A:56:U:H2'	1:A:57:G:H8	1.78	0.48
1:A:807:A:H2'	1:A:808:C:C6	2.49	0.48
1:A:834:C:N4	29:A:2788:HOH:O	2.45	0.48
1:A:83:U:C5	1:A:84:U:C5	3.01	0.48
1:A:570:G:C6	1:A:873:A:C2	3.01	0.48
2:B:168:THR:O	2:B:169:LYS:C	2.51	0.48
2:B:16:HIS:HD2	2:B:17:PHE:N	2.11	0.48
2:B:224:GLN:HG3	2:B:229:VAL:HG22	1.94	0.48
3:C:35:GLU:O	3:C:36:ASP:C	2.51	0.48
3:C:45:LYS:HA	3:C:45:LYS:HE3	1.95	0.48
3:C:64:VAL:CG2	3:C:99:VAL:HB	2.43	0.48
6:F:62:TRP:CE2	18:R:35:ARG:NH2	2.81	0.48
8:H:97:VAL:HG23	8:H:129:VAL:C	2.33	0.48
1:A:1350:A:OP1	9:I:121:ARG:HD2	2.12	0.48
14:N:11:LYS:HE3	14:N:13:THR:OG1	2.12	0.48
15:O:4:THR:CG2	15:O:5:LYS:H	2.26	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:U:5:ASP:O	21:U:11:GLY:HA3	2.12	0.48
1:A:254:G:C2	1:A:273:A:C2	3.01	0.48
1:A:429:U:H1'	1:A:430:A:H5''	1.95	0.48
1:A:777:A:H2'	1:A:777:A:N3	2.28	0.48
1:A:994:A:H2'	1:A:994:A:N3	2.28	0.48
3:C:82:GLU:HG3	3:C:83:ARG:N	2.28	0.48
5:E:142:LEU:O	5:E:143:ARG:HG2	2.13	0.48
7:G:43:PHE:O	7:G:46:ALA:HB3	2.13	0.48
8:H:82:HIS:HD1	8:H:138:TRP:HE1	1.57	0.48
9:I:36:TYR:HD2	9:I:37:PHE:CE1	2.31	0.48
14:N:23:ARG:HG2	14:N:29:ARG:O	2.13	0.48
1:A:1060:C:O2'	1:A:1061:G:H5'	2.13	0.48
1:A:1229:A:C2	1:A:1230:C:C4	3.02	0.48
1:A:1347:G:H1'	1:A:1348:U:H5	1.78	0.48
1:A:923:A:C1'	1:A:1398:A:C2	2.96	0.48
1:A:1399:C:C2	1:A:1401:G:C4	3.02	0.48
1:A:418:C:H2'	1:A:419:C:C6	2.48	0.48
1:A:421:U:H4'	1:A:422:C:OP2	2.14	0.48
2:B:212:GLN:O	2:B:213:LEU:C	2.51	0.48
3:C:152:ILE:HD12	3:C:152:ILE:N	2.27	0.48
3:C:175:LEU:HD21	3:C:201:TYR:CE2	2.49	0.48
3:C:50:ALA:HA	3:C:72:LYS:HG3	1.94	0.48
3:C:86:VAL:O	3:C:89:GLU:CB	2.57	0.48
8:H:38:ILE:HD13	8:H:41:ARG:NH2	2.27	0.48
11:K:90:GLY:HA2	11:K:93:GLN:HB2	1.95	0.48
12:L:75:HIS:CB	12:L:102:ARG:HH12	2.26	0.48
16:P:8:ARG:CB	16:P:28:ARG:NH1	2.75	0.48
16:P:65:GLN:HA	16:P:65:GLN:OE1	2.13	0.48
17:Q:21:VAL:HG12	17:Q:22:LEU:N	2.28	0.48
17:Q:48:GLU:OE1	17:Q:50:LYS:HG3	2.13	0.48
17:Q:9:VAL:O	17:Q:11:VAL:HG23	2.14	0.48
20:T:18:GLN:O	20:T:19:SER:C	2.52	0.48
20:T:43:LEU:N	20:T:43:LEU:HD23	2.27	0.48
1:A:1248:A:N6	1:A:1249:C:N4	2.62	0.48
1:A:1397:C:H4'	1:A:1398:A:OP2	2.14	0.48
1:A:1392:G:H21	1:A:1502:A:H8	1.61	0.48
1:A:180:U:C2'	1:A:181:G:H5'	2.44	0.48
1:A:39:G:C2'	1:A:39:G:N3	3.30	0.48
1:A:426:G:OP1	4:D:38:TYR:OH	2.29	0.48
1:A:802:A:H2'	1:A:803:G:H5'	1.96	0.48
1:A:547:A:OP2	4:D:2:GLY:HA3	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:16:LEU:N	7:G:16:LEU:HD22	2.13	0.48
7:G:31:MET:HG3	7:G:32:ARG:N	2.28	0.48
12:L:117:ARG:O	12:L:118:SER:C	2.52	0.48
15:O:31:LEU:N	15:O:31:LEU:HD13	2.28	0.48
16:P:9:PHE:N	16:P:16:HIS:O	2.46	0.48
1:A:1238:A:H5'	1:A:1336:C:H41	1.78	0.48
1:A:926:G:C6	1:A:1505:G:C6	3.01	0.48
2:B:102:LEU:N	2:B:102:LEU:CD1	2.75	0.48
2:B:212:GLN:HE22	2:B:235:SER:HB2	1.79	0.48
2:B:83:MET:SD	2:B:238:LEU:HD12	2.53	0.48
3:C:126:ARG:NE	3:C:128:PHE:HD1	2.11	0.48
4:D:172:PRO:HD2	4:D:173:TRP:HZ3	1.78	0.48
7:G:26:PHE:CD1	7:G:101:LEU:HD23	2.48	0.48
12:L:24:VAL:HG13	12:L:98:TYR:CE2	2.48	0.48
1:A:1330:U:OP1	13:M:25:ILE:O	2.31	0.48
16:P:74:LEU:HB3	16:P:79:VAL:CG2	2.35	0.48
18:R:40:LEU:HB3	18:R:79:LEU:HD11	1.96	0.48
18:R:86:VAL:O	18:R:87:ARG:NH2	2.46	0.48
1:A:1143:G:H2'	1:A:1144:G:C8	2.47	0.48
1:A:1290:G:H2'	1:A:1291:G:C8	2.48	0.48
1:A:154:C:H6	1:A:154:C:O5'	1.97	0.48
27:A:1928:SRV:H12	27:A:1928:SRV:O53	2.13	0.48
1:A:228:A:H2'	1:A:229:U:H6	1.78	0.48
1:A:668:G:H1	1:A:738:C:H42	1.62	0.48
1:A:967:5MC:O2	1:A:967:5MC:H2'	2.13	0.48
2:B:122:PHE:HE2	2:B:139:LYS:HD2	1.78	0.48
2:B:24:TRP:CZ3	2:B:26:PRO:HA	2.49	0.48
6:F:76:ALA:HA	6:F:79:LEU:HD12	1.95	0.48
10:J:28:ARG:HB3	10:J:29:ARG:NH1	2.25	0.48
10:J:76:ASN:C	10:J:78:ASN:N	2.59	0.48
15:O:15:PHE:HZ	15:O:85:LEU:HD21	1.77	0.48
19:S:31:ILE:HG23	19:S:32:LYS:N	2.29	0.48
20:T:60:GLU:HA	20:T:63:ILE:HD12	1.96	0.48
20:T:56:MET:HE1	20:T:85:MET:CG	2.43	0.48
1:A:1228:C:OP1	13:M:115:LYS:HE2	2.13	0.48
1:A:1392:G:O2'	1:A:1393:U:H5'	2.14	0.48
1:A:109:A:C4	1:A:327:A:C2	3.01	0.48
1:A:333:G:O2'	1:A:334:C:H5'	2.13	0.48
1:A:840:C:H3'	1:A:840:C:OP2	2.13	0.48
1:A:945:G:O6	1:A:1236:A:N1	2.47	0.48
2:B:118:LEU:HB2	2:B:142:LEU:CD1	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:98:GLU:CD	4:D:103:ASN:HD21	2.17	0.48
5:E:105:VAL:HB	5:E:106:PRO:CD	2.43	0.48
7:G:116:ALA:O	7:G:119:ARG:N	2.47	0.48
8:H:14:ARG:CZ	8:H:14:ARG:CB	2.91	0.48
9:I:10:ARG:HD3	9:I:105:ASP:HB3	1.95	0.48
9:I:127:LYS:HG3	9:I:127:LYS:O	2.14	0.48
13:M:81:LEU:HD11	13:M:88:ARG:HH22	1.77	0.48
15:O:12:ILE:C	15:O:14:GLU:H	2.17	0.48
15:O:8:LYS:O	15:O:12:ILE:HG12	2.14	0.48
15:O:78:TYR:CE1	15:O:82:ILE:HD12	2.49	0.48
19:S:40:ILE:HG22	19:S:67:VAL:HG13	1.96	0.48
1:A:1133:G:N2	1:A:1141:C:C2	2.77	0.48
1:A:1391:U:H2'	1:A:1392:G:C8	2.48	0.48
8:H:40:ALA:O	8:H:41:ARG:C	2.52	0.48
9:I:17:VAL:CG2	9:I:80:GLY:HA3	2.44	0.48
9:I:46:ALA:HB1	9:I:77:ILE:HG21	1.96	0.48
10:J:79:ARG:HD2	10:J:79:ARG:N	2.29	0.48
12:L:57:LYS:HA	12:L:67:THR:HA	1.96	0.48
13:M:99:ARG:NH2	19:S:2:PRO:CD	2.77	0.48
1:A:754:C:P	15:O:72:ARG:HH12	2.37	0.48
1:A:1004:A:H5''	29:A:2327:HOH:O	2.13	0.48
1:A:1084:G:H5'	1:A:1102:A:OP2	2.14	0.48
1:A:1371:G:C6	1:A:1372:U:C4	3.01	0.48
1:A:1441:G:H4'	1:A:1442:G:C2	2.48	0.48
1:A:782:A:P	29:A:2280:HOH:O	2.71	0.48
1:A:961:U:O2'	1:A:962:C:H5'	2.13	0.48
4:D:187:ARG:HG3	4:D:188:LEU:HD12	1.94	0.48
5:E:97:GLY:N	5:E:117:ASP:OD1	2.47	0.48
7:G:111:ARG:CB	7:G:112:PRO:HD2	2.43	0.48
8:H:11:THR:O	8:H:12:ARG:C	2.53	0.48
1:A:1054:C:N3	23:W:34:G:O4'	2.47	0.48
1:A:1006:C:N3	1:A:1023:G:N2	2.56	0.47
1:A:1263:C:N4	1:A:1264:C:N4	2.62	0.47
1:A:794:A:C8	1:A:794:A:H3'	2.48	0.47
2:B:162:ILE:HD13	2:B:177:ALA:HB2	1.95	0.47
2:B:73:THR:HG23	2:B:95:GLN:O	2.14	0.47
5:E:87:SER:HB3	5:E:131:ILE:HD13	1.96	0.47
6:F:39:LYS:HE3	6:F:39:LYS:HB2	1.66	0.47
6:F:7:ASN:OD1	6:F:7:ASN:N	2.47	0.47
8:H:19:VAL:CG2	8:H:21:LYS:HD3	2.44	0.47
12:L:75:HIS:C	12:L:75:HIS:ND1	2.67	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:4:ILE:HG22	13:M:5:ALA:CB	2.44	0.47
15:O:18:PHE:HD1	15:O:19:PRO:O	1.97	0.47
15:O:70:LEU:HD22	15:O:78:TYR:CB	2.41	0.47
17:Q:4:LYS:HG3	17:Q:6:LEU:CD2	2.44	0.47
1:A:1015:A:N6	1:A:1016:A:N6	2.61	0.47
1:A:1204:A:N7	1:A:1205:U:C5	2.82	0.47
1:A:1048:G:O6	1:A:1210:C:N4	2.47	0.47
1:A:257:G:H8	1:A:257:G:O5'	1.97	0.47
1:A:277:C:C2'	1:A:278:G:H5'	2.44	0.47
1:A:373:A:H2'	1:A:374:A:H8	1.79	0.47
1:A:390:C:O3'	16:P:28:ARG:NH2	2.47	0.47
1:A:500:G:N7	1:A:546:G:N2	2.60	0.47
1:A:584:G:OP2	17:Q:87:LYS:NZ	2.31	0.47
1:A:877:C:O2'	1:A:878:G:H5'	2.13	0.47
1:A:924:C:C4'	1:A:1399:C:OP2	2.62	0.47
3:C:76:VAL:HG21	3:C:103:VAL:CG1	2.44	0.47
5:E:38:GLN:OE1	5:E:38:GLN:HA	2.14	0.47
5:E:5:ASP:CG	5:E:6:PHE:H	2.16	0.47
8:H:27:PRO:CA	8:H:58:TYR:CD2	2.96	0.47
10:J:47:PHE:HB3	14:N:34:TYR:CE2	2.44	0.47
12:L:110:VAL:O	12:L:122:THR:HG21	2.13	0.47
13:M:35:GLU:HG2	13:M:36:LYS:N	2.29	0.47
14:N:36:PHE:CD1	14:N:36:PHE:C	2.87	0.47
15:O:70:LEU:HD22	15:O:78:TYR:CA	2.44	0.47
18:R:87:ARG:CG	18:R:87:ARG:NH2	2.53	0.47
1:A:1162:C:N3	1:A:1175:G:C2	2.83	0.47
1:A:190(K):G:H2'	1:A:190(L):U:C6	2.48	0.47
2:B:121:LEU:HD23	2:B:121:LEU:C	2.35	0.47
8:H:137:VAL:O	8:H:138:TRP:HB3	2.14	0.47
10:J:54:PHE:C	10:J:54:PHE:CD2	2.87	0.47
13:M:20:THR:CG2	13:M:20:THR:O	2.62	0.47
1:A:1329:A:H5'	13:M:29:ARG:HD2	1.97	0.47
14:N:24:CYS:HB2	14:N:29:ARG:CB	2.43	0.47
1:A:1202:G:C2'	1:A:1203:C:H5'	2.44	0.47
1:A:1327:C:OP2	21:U:12:LYS:NZ	2.41	0.47
1:A:1329:A:P	13:M:29:ARG:HG3	2.55	0.47
1:A:116:A:H61	1:A:313:A:H1'	1.80	0.47
1:A:609:A:N6	29:A:2320:HOH:O	2.39	0.47
1:A:60:A:H4'	1:A:61:G:O5'	2.14	0.47
3:C:112:SER:O	3:C:116:VAL:HG23	2.15	0.47
3:C:52:LEU:HA	3:C:70:VAL:HA	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:69:VAL:CG1	5:E:71:LEU:HD23	2.44	0.47
8:H:101:PRO:HA	8:H:102:ARG:HH11	1.78	0.47
9:I:66:ARG:HE	9:I:66:ARG:HB3	1.38	0.47
10:J:25:GLU:HG2	10:J:28:ARG:CD	2.43	0.47
1:A:35:G:O2'	12:L:118:SER:O	2.20	0.47
16:P:8:ARG:C	16:P:9:PHE:HD2	2.17	0.47
17:Q:11:VAL:CG1	17:Q:88:TYR:CD2	2.94	0.47
17:Q:29:HIS:ND1	17:Q:30:PRO:CD	2.76	0.47
18:R:66:LEU:O	18:R:66:LEU:HD12	2.13	0.47
19:S:40:ILE:HG23	19:S:62:ILE:CD1	2.44	0.47
1:A:1381:U:C6	1:A:1382:C:C6	3.02	0.47
1:A:1402:4OC:HM22	1:A:1402:4OC:O3'	2.15	0.47
1:A:147:G:C2	1:A:148:G:C8	3.03	0.47
1:A:1498:UR3:C4'	1:A:1519[A]:MA6:C2	2.78	0.47
1:A:645:C:C2	1:A:646:U:C6	3.02	0.47
1:A:838:G:H3'	1:A:839:U:C5'	2.42	0.47
1:A:892:A:C2	1:A:907:A:C5	3.02	0.47
1:A:956:U:O2'	1:A:957:U:H5'	2.14	0.47
1:A:969:A:C2'	1:A:970:C:H5'	2.45	0.47
7:G:50:ILE:HB	7:G:58:PRO:HB3	1.97	0.47
12:L:113:ARG:HH11	12:L:116:SER:H	1.62	0.47
13:M:95:GLY:C	13:M:96:LEU:HD23	2.34	0.47
1:A:1520[A]:G:H2'	1:A:1521:G:C8	2.49	0.47
1:A:437:U:H5'	4:D:155:LEU:HD21	1.96	0.47
1:A:506:G:C6	1:A:507:C:C4	3.02	0.47
1:A:836:G:C6	1:A:851:G:C6	3.03	0.47
1:A:70:G:C2	1:A:99:C:O2	2.67	0.47
2:B:101:MET:HA	2:B:108:ILE:HD12	1.96	0.47
3:C:130:VAL:O	3:C:134:ILE:HG12	2.15	0.47
3:C:173:VAL:N	3:C:174:PRO:HD3	2.29	0.47
3:C:22:TRP:CD1	3:C:59:ARG:HD2	2.50	0.47
7:G:78:ARG:HD2	7:G:156:TRP:HB3	1.95	0.47
10:J:63:PHE:HA	14:N:59:ALA:HB3	1.95	0.47
13:M:99:ARG:C	13:M:101:GLN:HE22	2.17	0.47
16:P:40:ASP:OD1	16:P:44:THR:OG1	2.31	0.47
17:Q:47:PRO:HD2	17:Q:48:GLU:H	1.79	0.47
20:T:102:GLY:O	20:T:104:LEU:N	2.47	0.47
20:T:41:ILE:CD1	20:T:41:ILE:H	2.27	0.47
1:A:1148:U:C5	1:A:1149:C:C4	3.03	0.47
1:A:1286:A:H3'	1:A:1287:A:H5''	1.96	0.47
1:A:976:G:H5'	1:A:1358:U:O2'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1435:G:C4	1:A:1436:U:C5	3.03	0.47
1:A:1503:A:C5	1:A:1531:A:C2	3.02	0.47
1:A:19:C:H2'	1:A:20:U:H6	1.80	0.47
1:A:514:C:H2'	1:A:515:G:C8	2.48	0.47
1:A:78:G:C6	1:A:79:G:N7	2.83	0.47
1:A:811:C:H4'	1:A:900:A:N6	2.30	0.47
4:D:177:ASP:OD1	4:D:179:GLU:N	2.47	0.47
4:D:12:CYS:HA	4:D:19:LEU:CD2	2.44	0.47
9:I:48:GLU:N	9:I:49:PRO:CD	2.78	0.47
9:I:95:LYS:HD2	9:I:95:LYS:N	2.29	0.47
10:J:21:GLN:O	10:J:24:VAL:HG12	2.15	0.47
14:N:45:ARG:HH11	14:N:45:ARG:CG	2.28	0.47
18:R:36:ASN:CG	18:R:39:VAL:HG11	2.35	0.47
19:S:41:VAL:O	19:S:42:PRO:C	2.52	0.47
1:A:1027:C:O2	1:A:1027:C:H5''	2.13	0.47
1:A:1092:A:H8	1:A:1092:A:O5'	1.98	0.47
1:A:1060:C:C2	1:A:1198:G:C2	3.03	0.47
1:A:1351:U:O2'	1:A:1352:C:H5'	2.14	0.47
1:A:232:G:H1'	1:A:262:A:N1	2.29	0.47
1:A:284:G:N3	1:A:285:G:C8	2.82	0.47
1:A:77:G:C6	1:A:93:G:N1	2.83	0.47
3:C:117:ALA:HB2	3:C:200:ALA:HB2	1.96	0.47
3:C:26:LYS:NZ	3:C:26:LYS:HB2	2.29	0.47
4:D:70:ILE:HD11	4:D:100:ARG:NE	2.30	0.47
10:J:85:LEU:O	10:J:86:MET:HB3	2.15	0.47
13:M:27:LYS:HD2	13:M:28:ALA:N	2.30	0.47
13:M:54:VAL:HG13	13:M:55:ARG:N	2.30	0.47
13:M:90:LEU:HD23	13:M:90:LEU:HA	1.81	0.47
15:O:46:HIS:C	15:O:48:LYS:H	2.17	0.47
16:P:8:ARG:O	16:P:9:PHE:CD2	2.68	0.47
17:Q:66:SER:OG	17:Q:69:LYS:HG3	2.14	0.47
20:T:54:LYS:HG2	20:T:55:ILE:N	2.28	0.47
1:A:1035:A:C6	1:A:1036:G:C6	3.02	0.47
1:A:1073:U:O2	2:B:104:ASN:ND2	2.45	0.47
1:A:1163:C:C6	1:A:1163:C:H3'	2.49	0.47
1:A:1228:C:H4'	13:M:116:THR:HA	1.96	0.47
1:A:1405:G:H2'	1:A:1406:U:H5'	1.95	0.47
1:A:644:G:C6	1:A:645:C:C5	3.01	0.47
1:A:868:C:H2'	1:A:869:G:H5'	1.97	0.47
4:D:188:LEU:H	4:D:188:LEU:CD1	2.24	0.47
4:D:31:CYS:O	4:D:32:ALA:HB3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:103:TRP:NE1	7:G:137:LYS:HE2	2.30	0.47
7:G:153:HIS:CE1	7:G:154:TYR:CE2	3.03	0.47
11:K:57:THR:HG22	11:K:58:PRO:HD2	1.95	0.47
13:M:39:ILE:N	13:M:39:ILE:HD12	2.30	0.47
15:O:17:ARG:HA	15:O:17:ARG:HD2	1.78	0.47
20:T:75:ASN:O	20:T:76:ALA:C	2.53	0.47
1:A:1061:G:C2	1:A:1062:U:O2	2.67	0.47
1:A:1131:G:H2'	1:A:1132:C:C6	2.50	0.47
1:A:1288:A:H2'	1:A:1289:A:C8	2.50	0.47
1:A:129(A):G:N3	1:A:190(E):U:H5''	2.29	0.47
1:A:1360:A:O2'	1:A:1361:G:H5'	2.15	0.47
1:A:1360:A:HO2'	1:A:1361:G:P	2.38	0.47
1:A:1533:C:HO2'	1:A:1534:C:P	2.30	0.47
1:A:262:A:C6	1:A:263:A:C6	3.03	0.47
1:A:802:A:O2'	29:A:2374:HOH:O	2.20	0.47
1:A:826:C:C2	1:A:827:U:C5	3.02	0.47
3:C:175:LEU:HD12	3:C:175:LEU:H	1.80	0.47
4:D:111:ALA:HB2	4:D:120:LEU:HD12	1.95	0.47
7:G:123:GLU:O	7:G:124:LEU:C	2.53	0.47
1:A:875:C:H1'	8:H:15:ASN:HD21	1.80	0.47
12:L:19:ARG:HH12	12:L:21:LYS:HB3	1.79	0.47
15:O:11:VAL:O	15:O:14:GLU:HB3	2.15	0.47
18:R:45:SER:HB3	18:R:47:THR:O	2.15	0.47
1:A:1182:G:H4'	1:A:1183:A:O5'	2.14	0.47
1:A:1206:G:O6	1:A:1207:2MG:C6	2.68	0.47
1:A:1286:A:C8	1:A:1286:A:H3'	2.50	0.47
1:A:913:A:O3'	27:A:1928:SRV:HI33	2.10	0.47
1:A:248:C:H2'	1:A:249:U:H5'	1.95	0.47
1:A:401:C:H1'	1:A:622:A:H1'	1.97	0.47
3:C:121:ALA:HB1	3:C:189:ALA:HB2	1.95	0.47
4:D:145:GLU:O	4:D:145:GLU:HG3	2.13	0.47
7:G:69:VAL:HG22	7:G:135:VAL:HG22	1.96	0.47
7:G:47:CYS:HA	7:G:50:ILE:CG1	2.45	0.47
8:H:100:ILE:H	8:H:100:ILE:HG12	1.52	0.47
9:I:8:GLY:HA2	9:I:79:LEU:CD1	2.38	0.47
10:J:86:MET:CG	10:J:87:THR:H	2.09	0.47
10:J:99:LYS:HD2	10:J:99:LYS:N	2.30	0.47
17:Q:17:LYS:HG2	17:Q:47:PRO:HA	1.97	0.47
1:A:1054:C:N3	23:W:34:G:OP1	2.48	0.47
1:A:1181:G:C2	1:A:1182:G:N2	2.83	0.46
1:A:22:G:C6	1:A:23:C:N4	2.83	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:339:C:H2'	1:A:340:U:C6	2.51	0.46
1:A:353:A:C8	1:A:353:A:C5'	2.96	0.46
1:A:385:C:H2'	1:A:386:C:H6	1.81	0.46
1:A:819:A:H4'	1:A:820:U:OP2	2.15	0.46
1:A:925:G:H1'	1:A:1502:A:N9	2.30	0.46
1:A:77:G:N2	1:A:92:C:O2	2.48	0.46
2:B:208:ILE:HD13	2:B:211:ILE:HD12	1.96	0.46
2:B:97:TRP:HH2	2:B:176:GLU:OE2	1.98	0.46
4:D:107:ARG:HH11	4:D:114:ARG:NH2	2.13	0.46
4:D:196:LEU:HA	4:D:197:PRO:HD3	1.52	0.46
6:F:14:LEU:HD13	6:F:18:GLN:CB	2.24	0.46
9:I:64:THR:HG23	9:I:66:ARG:NH2	2.30	0.46
11:K:120:ARG:CZ	11:K:126:ARG:HE	2.28	0.46
13:M:17:VAL:HG12	13:M:18:ALA:N	2.30	0.46
15:O:55:GLY:O	15:O:59:MET:HG3	2.16	0.46
15:O:56:LEU:HD12	15:O:56:LEU:C	2.35	0.46
15:O:70:LEU:HD23	15:O:70:LEU:O	2.14	0.46
21:U:10:ARG:NH1	21:U:10:ARG:HG3	2.30	0.46
1:A:1258:G:O2'	1:A:1259:C:H5'	2.15	0.46
1:A:264:U:O2'	17:Q:63:ARG:HD3	2.15	0.46
1:A:743:U:H2'	1:A:744:C:H6	1.81	0.46
1:A:822:C:H2'	1:A:823:G:H5'	1.97	0.46
1:A:983:A:OP1	14:N:3:ARG:NH2	2.41	0.46
1:A:983:A:H5'	1:A:984:C:OP2	2.16	0.46
2:B:132:LYS:O	2:B:136:VAL:HG23	2.15	0.46
3:C:157:ILE:CD1	3:C:166:GLU:HG2	2.45	0.46
3:C:15:THR:HB	3:C:181:ASN:HA	1.97	0.46
7:G:126:ASP:OD2	7:G:131:LYS:HE3	2.15	0.46
10:J:4:ILE:HG23	10:J:74:ILE:O	2.15	0.46
12:L:90:VAL:O	12:L:91:LYS:C	2.53	0.46
16:P:48:TRP:CD1	16:P:48:TRP:N	2.81	0.46
1:A:1054:C:C3'	1:A:1054:C:C2	2.98	0.46
1:A:1064:G:H1'	1:A:1190:G:H21	1.81	0.46
1:A:116:A:H5''	29:A:2018:HOH:O	2.15	0.46
1:A:1290:G:H2'	1:A:1291:G:H8	1.81	0.46
1:A:1367:C:N3	1:A:1368:G:C8	2.84	0.46
1:A:1368:G:H5''	9:I:112:LYS:HB3	1.97	0.46
1:A:162:A:H1'	1:A:348:G:O2'	2.16	0.46
1:A:44:G:C2	1:A:399:G:C4	3.04	0.46
1:A:419:C:O2'	1:A:420:U:H5'	2.16	0.46
1:A:570:G:H2'	1:A:571:U:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:653:A:OP1	8:H:56:LYS:NZ	2.45	0.46
1:A:669:U:H2'	1:A:670:G:C8	2.51	0.46
1:A:81:U:C6	1:A:81:U:H3'	2.49	0.46
1:A:853:G:C2	1:A:854:G:C8	3.02	0.46
1:A:861:G:H8	1:A:861:G:O5'	1.98	0.46
1:A:918:A:OP2	29:A:2624:HOH:O	2.21	0.46
3:C:20:SER:HB3	3:C:57:ILE:HB	1.97	0.46
3:C:64:VAL:HG23	3:C:99:VAL:HB	1.95	0.46
6:F:15:ASP:OD2	6:F:18:GLN:HB2	2.15	0.46
8:H:4:ASP:HB3	8:H:7:ALA:CB	2.45	0.46
10:J:28:ARG:CB	10:J:29:ARG:HH11	2.25	0.46
11:K:20:TYR:O	11:K:30:VAL:HA	2.16	0.46
12:L:54:LYS:HB2	12:L:70:ILE:HB	1.97	0.46
12:L:90:VAL:HG11	12:L:93:LEU:CD1	2.46	0.46
1:A:11:G:H2'	1:A:12:U:O4'	2.15	0.46
1:A:1519[B]:MA6:C9	1:A:1520[B]:G:H21	2.29	0.46
1:A:1519[A]:MA6:H3'	1:A:1520[A]:G:H5'	1.98	0.46
1:A:285:G:C2	1:A:286:G:C8	3.03	0.46
1:A:382:A:H2'	1:A:383:A:C8	2.50	0.46
1:A:391:G:C6	1:A:392:G:C5	3.04	0.46
1:A:433:C:H2'	1:A:434:U:C6	2.50	0.46
1:A:544:G:H2'	1:A:545:C:O5'	2.14	0.46
1:A:547:A:OP2	4:D:2:GLY:HA2	2.15	0.46
1:A:575:G:C8	1:A:881:G:N2	2.83	0.46
2:B:121:LEU:HD23	2:B:121:LEU:O	2.15	0.46
3:C:119:ARG:NH1	3:C:119:ARG:CG	2.76	0.46
4:D:8:VAL:C	4:D:10:ARG:N	2.69	0.46
5:E:142:LEU:HA	5:E:142:LEU:HD23	1.62	0.46
8:H:96:GLY:H	8:H:99:GLU:CD	2.18	0.46
9:I:126:SER:C	9:I:128:ARG:H	2.18	0.46
1:A:553:A:O2'	12:L:29:GLY:O	2.31	0.46
12:L:30:ALA:CB	12:L:31:PRO:HD2	2.43	0.46
13:M:25:ILE:HG23	13:M:29:ARG:HB2	1.97	0.46
14:N:9:LYS:C	14:N:9:LYS:HD2	2.36	0.46
16:P:19:ILE:HG22	16:P:36:ILE:CG1	2.45	0.46
1:A:1109:C:OP2	3:C:176:HIS:ND1	2.48	0.46
1:A:1148:U:C5	1:A:1149:C:C5	3.03	0.46
1:A:1233:G:H2'	1:A:1234:C:C6	2.51	0.46
1:A:1393:U:C3'	1:A:1393:U:C6	2.99	0.46
1:A:438:G:O6	29:A:2233:HOH:O	2.17	0.46
1:A:491:G:C2	1:A:492:G:C4	3.04	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:92:C:H2'	1:A:93:G:H8	1.81	0.46
1:A:966:M2G:N7	1:A:967:5MC:HM52	2.30	0.46
2:B:107:THR:HG23	2:B:110:GLN:OE1	2.16	0.46
2:B:16:HIS:NE2	2:B:17:PHE:HD2	2.12	0.46
4:D:100:ARG:HH12	4:D:137:SER:HB3	1.81	0.46
7:G:74:GLU:HA	7:G:141:VAL:HG12	1.97	0.46
8:H:105:ARG:HD3	8:H:105:ARG:HA	1.73	0.46
10:J:12:ASP:OD2	10:J:12:ASP:O	2.33	0.46
13:M:2:ALA:O	13:M:10:PRO:HD2	2.15	0.46
1:A:1300:G:O2'	1:A:1301:U:OP2	2.34	0.46
1:A:610:G:H5'	29:A:2771:HOH:O	2.14	0.46
1:A:652:U:O4	1:A:752:G:O2'	2.29	0.46
2:B:185:ILE:N	2:B:185:ILE:HD12	2.29	0.46
2:B:97:TRP:HZ2	2:B:102:LEU:CD1	2.18	0.46
3:C:142:MET:HE3	3:C:142:MET:O	2.16	0.46
4:D:122:ARG:HA	4:D:134:ASP:O	2.15	0.46
7:G:150:ALA:HA	11:K:59:TYR:CD2	2.51	0.46
8:H:54:ASP:CG	8:H:55:GLY:N	2.61	0.46
10:J:9:ARG:HB3	10:J:9:ARG:NH1	2.31	0.46
1:A:1148:U:C6	1:A:1149:C:C6	3.04	0.46
1:A:1370:G:C2	1:A:1371:G:C8	3.04	0.46
1:A:1407:5MC:H2'	1:A:1408:A:C5'	2.43	0.46
1:A:164:U:H2'	1:A:165:C:H6	1.81	0.46
1:A:643:C:C2'	1:A:644:G:C5'	2.87	0.46
1:A:666:G:H5'	1:A:726:C:H1'	1.98	0.46
1:A:668:G:C2'	1:A:669:U:H5'	2.46	0.46
1:A:89:C:C6	1:A:90:U:C2	3.03	0.46
1:A:961:U:H2'	1:A:962:C:C5'	2.45	0.46
7:G:111:ARG:HD3	7:G:113:GLU:CG	2.45	0.46
7:G:64:GLN:HA	7:G:64:GLN:OE1	2.15	0.46
11:K:11:LYS:N	11:K:75:TYR:CE2	2.82	0.46
13:M:59:TYR:CE2	13:M:63:THR:HG21	2.50	0.46
15:O:55:GLY:HA2	15:O:58:MET:HE2	1.97	0.46
18:R:39:VAL:CG1	18:R:40:LEU:N	2.79	0.46
1:A:1314:C:OP2	19:S:6:LYS:HG2	2.15	0.46
1:A:1502:A:C2	1:A:1504:G:C2	3.04	0.46
1:A:1519[B]:MA6:C9	1:A:1520[B]:G:N2	2.79	0.46
1:A:344:A:C5'	1:A:345:C:H5	2.27	0.46
1:A:460:A:C6	1:A:462:G:C6	3.04	0.46
1:A:499:A:C4'	1:A:500:G:OP1	2.49	0.46
1:A:538:G:C2	1:A:539:A:C4	3.04	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:923:A:H1'	1:A:1398:A:N3	2.30	0.46
2:B:115:LEU:HD21	2:B:153:ARG:NH1	2.31	0.46
4:D:107:ARG:NH1	4:D:114:ARG:NH2	2.64	0.46
5:E:84:PHE:CE1	5:E:133:TYR:HB3	2.50	0.46
5:E:84:PHE:CB	5:E:134:ALA:HB2	2.46	0.46
6:F:45:LEU:HB3	6:F:59:TYR:HD1	1.81	0.46
11:K:30:VAL:HG21	11:K:65:ALA:HA	1.97	0.46
16:P:21:VAL:HG21	16:P:59:TRP:CD1	2.51	0.46
1:A:1015:A:C5	1:A:1016:A:C5	3.04	0.46
1:A:1413:A:H2'	1:A:1414:U:O4'	2.15	0.46
1:A:1511:G:H2'	1:A:1512:U:O4'	2.16	0.46
1:A:1518[B]:MA6:H102	1:A:1519[B]:MA6:H103	1.98	0.46
1:A:411:A:C8	1:A:411:A:H3'	2.51	0.46
1:A:630:G:C5'	1:A:631:G:OP2	2.64	0.46
1:A:66:G:C2	1:A:67:C:C6	3.03	0.46
1:A:920:U:H2'	1:A:921:U:C6	2.51	0.46
1:A:923:A:C2'	1:A:924:C:H5'	2.45	0.46
4:D:127:THR:HG22	4:D:149:ALA:HB2	1.97	0.46
5:E:45:PHE:CE2	5:E:47:LYS:HE3	2.51	0.46
9:I:103:THR:HG22	9:I:104:ARG:O	2.15	0.46
10:J:46:ARG:HH11	10:J:46:ARG:HG3	1.80	0.46
16:P:6:LEU:HD23	16:P:17:TYR:CG	2.51	0.46
19:S:51:VAL:O	19:S:51:VAL:CG2	2.64	0.46
1:A:978:A:O2'	1:A:1322:C:O2	2.27	0.46
1:A:1454:G:C5	29:A:2825:HOH:O	2.65	0.46
1:A:166:G:O2'	1:A:167:G:H5'	2.15	0.46
1:A:336:C:N4	29:A:2573:HOH:O	2.49	0.46
1:A:342:C:H2'	1:A:343:U:H5'	1.98	0.46
1:A:407:G:C5'	4:D:3:ARG:HH12	2.29	0.46
1:A:510:A:P	29:A:2165:HOH:O	2.74	0.46
1:A:511:C:O2'	1:A:534:U:H1'	2.16	0.46
1:A:803:G:C6	1:A:804:U:C4	3.04	0.46
3:C:113:ALA:O	3:C:116:VAL:N	2.50	0.46
3:C:178:LEU:HA	3:C:178:LEU:HD13	1.78	0.46
3:C:39:ILE:HG22	3:C:40:ARG:N	2.31	0.46
4:D:52:SER:O	4:D:55:ALA:HB3	2.16	0.46
9:I:17:VAL:CG1	9:I:63:ILE:HD11	2.40	0.46
9:I:77:ILE:O	9:I:78:LYS:C	2.54	0.46
9:I:17:VAL:HG21	9:I:80:GLY:HA3	1.98	0.46
11:K:116:HIS:N	11:K:116:HIS:ND1	2.62	0.46
12:L:27:LEU:CG	12:L:28:LYS:N	2.75	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:65:LYS:HE3	13:M:65:LYS:HB2	1.68	0.46
18:R:36:ASN:OD1	18:R:39:VAL:CG1	2.64	0.46
1:A:1032:G:H2'	1:A:1033:G:H8	1.82	0.45
1:A:1125:U:C3'	1:A:1126:U:H5	2.28	0.45
1:A:1304:G:C6	1:A:1305:G:N1	2.83	0.45
1:A:1379:G:C6	1:A:1380:U:C5	3.04	0.45
1:A:182:U:P	29:A:2183:HOH:O	2.73	0.45
1:A:515:G:C6	1:A:516:PSU:C2	3.04	0.45
1:A:76:C:H2'	1:A:77:G:H8	1.82	0.45
3:C:5:ILE:HD11	3:C:10:PHE:CD2	2.51	0.45
4:D:120:LEU:HD23	4:D:125:HIS:HB2	1.98	0.45
4:D:172:PRO:HG2	4:D:173:TRP:CE3	2.51	0.45
4:D:196:LEU:CD2	4:D:196:LEU:H	2.29	0.45
1:A:642:A:C4	8:H:114:THR:O	2.70	0.45
8:H:9:MET:O	8:H:10:LEU:C	2.54	0.45
9:I:15:ALA:HA	9:I:65:VAL:HG13	1.98	0.45
12:L:44:THR:HA	12:L:45:PRO:HD3	1.76	0.45
13:M:40:ASN:HD22	13:M:43:THR:HG23	1.81	0.45
16:P:34:GLU:OE2	16:P:55:ARG:HD2	2.15	0.45
20:T:57:ARG:HD3	20:T:102:GLY:CA	2.45	0.45
1:A:1068:G:O4'	1:A:1068:G:OP2	2.33	0.45
1:A:109:A:C3'	1:A:110:C:H5'	2.46	0.45
1:A:1151:A:O2'	1:A:1152:A:H8	1.99	0.45
1:A:1178:G:N2	1:A:1180:A:H3'	2.31	0.45
1:A:1190:G:HO2'	1:A:1191:A:P	2.39	0.45
1:A:1290:G:C6	1:A:1291:G:C6	3.04	0.45
1:A:1315:U:H2'	1:A:1316:G:O4'	2.16	0.45
1:A:1368:G:H2'	1:A:1369:C:C5'	2.46	0.45
1:A:1425:U:H3	1:A:1475:G:H1	1.64	0.45
1:A:179:A:C2'	1:A:180:U:H5'	2.46	0.45
1:A:373:A:C2	1:A:482:A:C6	3.04	0.45
1:A:386:C:H2'	1:A:387:U:H5'	1.97	0.45
1:A:642:A:H2'	1:A:643:C:H6	1.76	0.45
1:A:792:A:C4'	1:A:793:U:OP1	2.48	0.45
1:A:89:C:C5	1:A:90:U:C2	3.03	0.45
4:D:155:LEU:HD22	4:D:156:GLU:H	1.80	0.45
4:D:159:ARG:CG	4:D:159:ARG:NH1	2.77	0.45
4:D:31:CYS:C	4:D:33:MET:H	2.19	0.45
8:H:4:ASP:CG	8:H:7:ALA:H	2.20	0.45
12:L:46:LYS:C	12:L:48:PRO:HD2	2.36	0.45
15:O:46:HIS:C	15:O:48:LYS:N	2.70	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:5:LYS:HA	15:O:5:LYS:HZ3	1.72	0.45
1:A:1502:A:H2'	1:A:1504:G:C8	2.51	0.45
1:A:1503:A:C4	1:A:1531:A:N3	2.85	0.45
1:A:566:G:H4'	1:A:567:G:OP1	2.16	0.45
1:A:575:G:H4'	1:A:576:G:OP1	2.16	0.45
1:A:631:G:H2'	1:A:632:A:C8	2.51	0.45
1:A:853:G:O2'	1:A:854:G:H5'	2.17	0.45
2:B:200:ILE:HG23	2:B:201:ILE:N	2.29	0.45
3:C:152:ILE:HB	3:C:199:LYS:HB2	1.98	0.45
3:C:27:LYS:HA	3:C:30:ARG:HH12	1.81	0.45
1:A:437:U:C5'	4:D:155:LEU:HD21	2.46	0.45
4:D:188:LEU:H	4:D:188:LEU:HD12	1.81	0.45
4:D:61:LYS:CD	4:D:62:GLN:N	2.75	0.45
7:G:148:ASN:C	7:G:150:ALA:N	2.66	0.45
8:H:20:TYR:HE1	8:H:76:PRO:HG2	1.81	0.45
10:J:47:PHE:HD2	14:N:34:TYR:CE2	2.34	0.45
11:K:58:PRO:O	11:K:61:ALA:HB3	2.16	0.45
12:L:11:VAL:HG12	12:L:12:ARG:N	2.31	0.45
13:M:66:LEU:O	13:M:69:GLU:HG2	2.16	0.45
15:O:4:THR:CG2	15:O:5:LYS:N	2.76	0.45
15:O:61:GLY:O	15:O:65:ARG:HD2	2.17	0.45
15:O:78:TYR:CZ	15:O:82:ILE:HD12	2.51	0.45
17:Q:59:ILE:HA	17:Q:59:ILE:HD12	1.59	0.45
17:Q:18:THR:HG23	17:Q:69:LYS:HD3	1.99	0.45
18:R:53:ARG:HG3	18:R:63:GLN:NE2	2.31	0.45
1:A:101:A:N3	1:A:102:G:C8	2.85	0.45
1:A:1084:G:N2	29:A:2128:HOH:O	2.50	0.45
1:A:1319:A:H4'	1:A:1320:C:OP1	2.16	0.45
1:A:1400:5MC:O5'	1:A:1400:5MC:H6	2.00	0.45
1:A:1415:G:C6	1:A:1486:G:C6	3.04	0.45
1:A:1519[A]:MA6:C3'	1:A:1520[A]:G:H5'	2.47	0.45
1:A:1518[A]:MA6:H2'	1:A:1519[A]:MA6:H8	1.98	0.45
1:A:411:A:N3	1:A:413:G:H1'	2.32	0.45
1:A:557:G:H5''	1:A:558:G:OP2	2.16	0.45
1:A:626:U:H2'	1:A:627:G:C8	2.51	0.45
1:A:933:G:OP1	7:G:4:ARG:HG3	2.17	0.45
2:B:77:ALA:O	2:B:81:VAL:HG23	2.16	0.45
3:C:199:LYS:HB3	3:C:201:TYR:HE1	1.80	0.45
4:D:149:ALA:O	4:D:152:SER:HB2	2.15	0.45
4:D:38:TYR:N	4:D:38:TYR:CD2	2.84	0.45
5:E:144:THR:HB	5:E:146:ALA:HB3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:37:PHE:HB3	9:I:43:ALA:HB2	1.99	0.45
12:L:7:ILE:O	12:L:8:ASN:C	2.55	0.45
13:M:74:VAL:HG23	13:M:75:ALA:N	2.31	0.45
14:N:27:CYS:SG	14:N:29:ARG:CB	2.86	0.45
16:P:67:THR:HB	16:P:70:ALA:H	1.80	0.45
17:Q:81:ARG:O	17:Q:81:ARG:CG	2.65	0.45
19:S:10:PHE:CD2	19:S:10:PHE:C	2.89	0.45
1:A:1003(A):G:N1	1:A:1004:A:H1'	2.32	0.45
1:A:1005:A:C8	1:A:1026:G:O6	2.70	0.45
1:A:1233:G:C2	1:A:1234:C:C4	3.05	0.45
1:A:1286:A:H3'	1:A:1286:A:H8	1.81	0.45
1:A:1288:A:C6	1:A:1289:A:C6	3.04	0.45
1:A:590:C:O2'	1:A:591:U:H5'	2.16	0.45
1:A:77:G:C2	1:A:93:G:C2	3.05	0.45
2:B:223:ILE:HD13	2:B:230:VAL:HG23	1.99	0.45
1:A:1112:C:C2	3:C:178:LEU:HB2	2.51	0.45
4:D:119:GLN:HG3	4:D:123:HIS:CE1	2.51	0.45
4:D:177:ASP:OD1	4:D:177:ASP:C	2.54	0.45
4:D:70:ILE:CG2	4:D:71:SER:O	2.59	0.45
6:F:97:PHE:HD2	6:F:98:LEU:N	2.14	0.45
7:G:148:ASN:O	7:G:149:ARG:C	2.55	0.45
9:I:32:ASP:CG	9:I:33:PHE:N	2.69	0.45
11:K:116:HIS:C	11:K:117:ASN:OD1	2.54	0.45
7:G:150:ALA:HA	11:K:59:TYR:HD2	1.82	0.45
13:M:77:ASN:O	13:M:80:ARG:HB3	2.16	0.45
13:M:91:ARG:HH21	13:M:96:LEU:CB	2.30	0.45
14:N:12:ARG:NH1	14:N:12:ARG:H	2.13	0.45
14:N:14:PRO:O	14:N:15:LYS:CB	2.64	0.45
15:O:17:ARG:HD3	15:O:26:GLU:OE2	2.16	0.45
18:R:56:THR:HB	18:R:58:LEU:HD23	1.97	0.45
20:T:31:SER:O	20:T:32:ALA:C	2.55	0.45
20:T:73:HIS:HB3	20:T:74:LYS:HG2	1.99	0.45
1:A:1003(A):G:C6	1:A:1004:A:H1'	2.51	0.45
1:A:1250:A:C6	1:A:1251:A:N1	2.84	0.45
1:A:1393:U:C6	1:A:1393:U:H3'	2.52	0.45
1:A:147:G:O2'	1:A:148:G:H5'	2.17	0.45
1:A:1494:G:C2	1:A:1495:U:C5	3.05	0.45
1:A:434:U:H2'	1:A:434:U:O2	2.14	0.45
1:A:646:U:H2'	1:A:647:C:C6	2.51	0.45
1:A:770:C:C2'	1:A:771:G:H5'	2.47	0.45
1:A:769:G:H2'	1:A:770:C:H5'	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:90:U:O2'	1:A:91:C:O5'	2.33	0.45
4:D:102:ASP:OD1	4:D:102:ASP:N	2.48	0.45
4:D:92:VAL:O	4:D:95:GLY:N	2.49	0.45
5:E:112:LEU:C	5:E:114:GLY:N	2.70	0.45
14:N:27:CYS:HB3	14:N:43:CYS:SG	2.57	0.45
14:N:41:ARG:HG3	14:N:42:ILE:N	2.32	0.45
17:Q:47:PRO:CD	17:Q:48:GLU:H	2.30	0.45
18:R:25:THR:OG1	18:R:26:LEU:HD13	2.16	0.45
1:A:129:U:O3'	1:A:129(A):G:H3'	2.16	0.45
1:A:1514:C:N4	1:A:1515[B]:C:H41	2.15	0.45
1:A:507:C:H3'	1:A:508:C:H2'	1.98	0.45
1:A:651:C:O2'	1:A:652:U:H5'	2.17	0.45
2:B:231:GLU:CB	2:B:232:PRO:HD2	2.30	0.45
1:A:1112:C:H1'	3:C:179:ARG:HH11	1.82	0.45
6:F:61:LEU:HB3	6:F:63:TYR:HE2	1.81	0.45
10:J:63:PHE:HD1	10:J:63:PHE:H	1.60	0.45
11:K:20:TYR:HD2	11:K:83:ILE:HB	1.80	0.45
13:M:97:PRO:HB3	13:M:101:GLN:OE1	2.16	0.45
17:Q:43:LEU:HA	17:Q:43:LEU:HD23	1.27	0.45
20:T:79:ARG:HD2	20:T:83:ARG:HH12	1.82	0.45
20:T:8:ARG:HG3	20:T:9:ASN:HB3	1.99	0.45
1:A:1054:C:O2'	1:A:1056:U:OP2	2.32	0.45
1:A:1157:A:C4	1:A:1181:G:C2	3.05	0.45
1:A:1166:G:N2	1:A:1171:G:C6	2.85	0.45
1:A:1162:C:C2	1:A:1175:G:C2	3.05	0.45
1:A:1194:U:H5''	1:A:1195:C:OP2	2.17	0.45
1:A:1277:C:C1'	1:A:1282:C:H1'	2.46	0.45
1:A:1345:U:P	29:A:2503:HOH:O	2.74	0.45
1:A:1451:A:O5'	1:A:1451:A:H8	2.00	0.45
1:A:613:C:O2'	1:A:614:A:H5'	2.15	0.45
1:A:946:A:H2'	1:A:947:G:H8	1.79	0.45
2:B:226:ARG:H	2:B:226:ARG:HG2	1.43	0.45
5:E:83:GLU:O	5:E:83:GLU:CG	2.65	0.45
7:G:8:GLU:HG3	7:G:8:GLU:O	2.17	0.45
9:I:89:ASN:O	9:I:92:TYR:HB2	2.16	0.45
11:K:124:LYS:HE3	11:K:125:PHE:HE2	1.82	0.45
12:L:68:ALA:HB1	12:L:100:ILE:HD12	1.99	0.45
13:M:7:VAL:O	13:M:9:ILE:CD1	2.65	0.45
19:S:52:TYR:CE2	19:S:54:GLY:CA	3.00	0.45
1:A:1090:U:N3	1:A:1091:U:C5	2.84	0.45
1:A:1059:C:N3	1:A:1198:G:O6	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1420:C:H2'	1:A:1421:G:H8	1.81	0.45
1:A:1442:G:N1	1:A:1446:A:N6	2.63	0.45
1:A:186:C:H5'	20:T:78:ALA:HB1	1.98	0.45
1:A:283:C:C2	1:A:284:G:C8	3.04	0.45
1:A:438:G:N2	1:A:496:A:C8	2.85	0.45
1:A:533:A:OP1	29:A:2170:HOH:O	2.21	0.45
1:A:582:U:H5''	15:O:64:ARG:HH21	1.82	0.45
2:B:197:VAL:HG11	2:B:200:ILE:HG13	1.99	0.45
2:B:53:ARG:HA	2:B:56:ARG:HH12	1.80	0.45
3:C:46:GLU:HB3	3:C:47:LEU:CD1	2.42	0.45
3:C:84:ILE:CG2	3:C:85:ARG:N	2.80	0.45
3:C:90:GLU:H	3:C:90:GLU:HG3	1.57	0.45
4:D:204:ILE:N	4:D:204:ILE:HD12	2.32	0.45
7:G:120:ILE:H	7:G:120:ILE:CD1	2.16	0.45
7:G:69:VAL:O	7:G:69:VAL:CG1	2.63	0.45
11:K:14:VAL:HG12	11:K:15:ALA:N	2.32	0.45
17:Q:10:VAL:CG2	17:Q:19:VAL:HB	2.47	0.45
17:Q:27:PHE:CZ	17:Q:36:ILE:HD11	2.52	0.45
18:R:56:THR:HB	18:R:58:LEU:CD2	2.47	0.45
1:A:1015:A:N3	1:A:1218:C:O2'	2.50	0.45
1:A:1029:C:H2'	1:A:1030:C:H5'	1.98	0.45
1:A:1110:A:C8	29:A:2140:HOH:O	2.69	0.45
1:A:1248:A:C6	1:A:1249:C:N4	2.85	0.45
1:A:503:C:OP2	12:L:116:SER:CB	2.63	0.45
1:A:677:U:C2'	1:A:678:U:H5'	2.47	0.45
1:A:713:G:N2	1:A:714:G:C2	2.85	0.45
1:A:741:G:H5''	15:O:39:LEU:HD11	1.98	0.45
1:A:895:G:C5	1:A:896:C:C5	3.05	0.45
2:B:196:LEU:H	2:B:196:LEU:HG	1.28	0.45
2:B:68:ILE:O	2:B:90:MET:HB3	2.16	0.45
4:D:63:LYS:O	4:D:67:ILE:CD1	2.63	0.45
11:K:114:VAL:HG22	11:K:115:PRO:O	2.17	0.45
11:K:34:ASP:HB2	11:K:35:PRO:CD	2.45	0.45
11:K:72:ALA:HB1	11:K:77:MET:HE2	1.98	0.45
16:P:53:VAL:O	16:P:54:GLU:C	2.53	0.45
1:A:1003(A):G:N1	1:A:1038:C:C2	2.77	0.44
1:A:1130:A:OP2	1:A:1130:A:H3'	2.17	0.44
1:A:1201:A:H4'	1:A:1202:G:C5'	2.46	0.44
1:A:1303:C:C2'	1:A:1303:C:O2	2.56	0.44
1:A:1313:U:H5	19:S:4:SER:HB2	1.81	0.44
1:A:1314:C:OP2	19:S:6:LYS:CG	2.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:306:G:H2'	1:A:307:C:H6	1.82	0.44
1:A:355:C:C5'	1:A:389:A:OP2	2.65	0.44
1:A:44:G:H2'	1:A:45:U:O4'	2.17	0.44
2:B:224:GLN:OE1	2:B:229:VAL:HG22	2.16	0.44
2:B:57:PHE:CD1	2:B:199:TYR:CE1	3.05	0.44
3:C:5:ILE:C	3:C:5:ILE:CD1	2.85	0.44
4:D:177:ASP:CG	4:D:180:GLY:H	2.18	0.44
5:E:37:ARG:HA	5:E:114:GLY:CA	2.47	0.44
7:G:103:TRP:HE1	7:G:137:LYS:HE2	1.82	0.44
8:H:56:LYS:HB3	8:H:57:PRO:HD2	2.00	0.44
13:M:10:PRO:HB3	13:M:18:ALA:O	2.17	0.44
17:Q:10:VAL:O	17:Q:10:VAL:CG1	2.65	0.44
1:A:1053:G:C4'	1:A:1054:C:H5'	2.47	0.44
1:A:1052:U:O4	1:A:1200:C:C2	2.70	0.44
1:A:1507:A:C4	1:A:1530:G:C2	3.05	0.44
1:A:400:C:N4	1:A:401:C:N4	2.65	0.44
1:A:42:G:C2	1:A:43:C:C2	3.05	0.44
1:A:55:A:C2	1:A:56:U:H1'	2.51	0.44
1:A:784:C:C2'	1:A:785:G:O5'	2.65	0.44
3:C:131:ARG:C	3:C:134:ILE:HG12	2.36	0.44
5:E:98:THR:HB	5:E:117:ASP:HB3	1.98	0.44
8:H:104:ARG:HD2	8:H:138:TRP:CD2	2.53	0.44
9:I:28:VAL:HA	9:I:63:ILE:HG22	1.99	0.44
11:K:86:GLY:H	11:K:112:THR:HG23	1.81	0.44
13:M:22:ILE:H	13:M:22:ILE:HD13	1.82	0.44
13:M:52:GLU:O	13:M:53:VAL:C	2.54	0.44
16:P:20:VAL:HG13	16:P:32:TYR:HD2	1.82	0.44
16:P:4:ILE:HG12	16:P:21:VAL:HG22	1.99	0.44
19:S:41:VAL:CG2	19:S:43:GLU:OE2	2.65	0.44
1:A:1054:C:N3	23:W:34:G:P	2.91	0.44
23:W:36:A:N3	23:W:36:A:H2'	2.33	0.44
23:W:39:G:N2	23:W:40:PSU:C4	2.86	0.44
1:A:1055:A:N1	1:A:1056:U:H1'	2.32	0.44
1:A:1291:G:O5'	1:A:1291:G:H8	2.00	0.44
2:B:97:TRP:CH2	2:B:176:GLU:CD	2.90	0.44
7:G:113:GLU:O	7:G:119:ARG:HD3	2.17	0.44
7:G:40:ALA:O	7:G:41:ARG:C	2.53	0.44
7:G:59:LEU:O	7:G:62:PHE:HB3	2.17	0.44
13:M:115:LYS:HB2	13:M:115:LYS:HE2	1.72	0.44
13:M:19:LEU:HA	13:M:19:LEU:HD23	1.48	0.44
14:N:24:CYS:SG	14:N:40:CYS:N	2.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:56:VAL:O	17:Q:76:LEU:HD12	2.17	0.44
20:T:42:GLN:OE1	20:T:42:GLN:HA	2.17	0.44
1:A:1014:A:C5	1:A:1015:A:C6	3.06	0.44
1:A:1297:C:HO2'	1:A:1298:C:P	2.39	0.44
1:A:1347:G:H2'	1:A:1348:U:OP2	2.15	0.44
1:A:1403:C:O2'	1:A:1404:5MC:C5'	2.61	0.44
1:A:1488:G:H2'	1:A:1489:G:H8	1.83	0.44
1:A:229:U:H2'	1:A:230:G:C5'	2.41	0.44
1:A:256:U:C2'	1:A:257:G:H5'	2.48	0.44
1:A:514:C:C2'	1:A:515:G:H5'	2.47	0.44
1:A:616:G:C2'	1:A:617:G:H5'	2.47	0.44
1:A:629:G:H2'	1:A:630:G:O4'	2.17	0.44
1:A:681:C:C2	1:A:682:G:C8	3.06	0.44
1:A:925:G:C1'	1:A:1502:A:C8	3.01	0.44
2:B:139:LYS:HA	2:B:139:LYS:HD2	1.72	0.44
2:B:76:GLN:O	2:B:208:ILE:HD11	2.16	0.44
3:C:69:HIS:HA	3:C:104:GLN:O	2.17	0.44
5:E:148:VAL:O	5:E:152:ARG:HG3	2.18	0.44
8:H:4:ASP:OD2	8:H:85:ARG:CZ	2.64	0.44
10:J:19:SER:HA	10:J:22:LYS:HB3	1.99	0.44
11:K:54:ARG:O	11:K:57:THR:OG1	2.35	0.44
11:K:88:GLY:O	11:K:89:ALA:C	2.56	0.44
16:P:57:ARG:HD3	16:P:79:VAL:O	2.18	0.44
16:P:6:LEU:HD23	16:P:17:TYR:CB	2.47	0.44
18:R:47:THR:CG2	18:R:48:GLY:N	2.76	0.44
1:A:1126:U:H6	1:A:1126:U:P	2.40	0.44
1:A:1126:U:H3	1:A:1127:G:N2	2.15	0.44
1:A:1227:A:H2'	1:A:1228:C:O5'	2.18	0.44
1:A:1347:G:C6	9:I:107:ARG:NH1	2.85	0.44
1:A:1394:A:C6	1:A:1501:C:H4'	2.53	0.44
1:A:1518[A]:MA6:N6	1:A:1519[A]:MA6:H103	2.33	0.44
1:A:1519[B]:MA6:H93	1:A:1520[B]:G:N2	2.32	0.44
1:A:176:C:C2'	1:A:177:C:H5'	2.46	0.44
1:A:440:A:C8	1:A:442:C:C6	3.05	0.44
1:A:448:A:C4	1:A:449:C:C5	3.05	0.44
1:A:444:C:N4	1:A:490:G:H1	2.12	0.44
1:A:778:G:H2'	1:A:779:C:C5'	2.48	0.44
1:A:815:A:O2'	1:A:1527:C:H1'	2.18	0.44
1:A:862:C:H5''	29:A:2609:HOH:O	2.16	0.44
1:A:868:C:C2'	1:A:869:G:O5'	2.63	0.44
1:A:942:G:H2'	1:A:942:G:N3	2.31	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:190:ASP:O	4:D:194:LEU:HD23	2.17	0.44
5:E:36:ASP:OD2	5:E:38:GLN:HB2	2.18	0.44
8:H:10:LEU:HA	8:H:10:LEU:HD22	1.52	0.44
9:I:64:THR:HG23	9:I:66:ARG:CZ	2.47	0.44
9:I:97:LYS:HD2	9:I:97:LYS:O	2.18	0.44
10:J:33:GLN:C	10:J:34:VAL:HG23	2.38	0.44
13:M:67:GLU:HB3	13:M:68:GLY:H	1.20	0.44
1:A:1027:C:H5	1:A:1035:A:C2	2.36	0.44
1:A:1088:G:H2'	1:A:1089:G:H5'	2.00	0.44
1:A:108:G:N3	1:A:108:G:H5'	2.33	0.44
1:A:532:A:H61	1:A:1207:2MG:C5'	2.30	0.44
1:A:1245:A:C2	1:A:1293:G:N3	2.86	0.44
1:A:1350:A:C4	1:A:1351:U:C6	3.06	0.44
1:A:1437:C:O2	1:A:1437:C:H2'	2.17	0.44
1:A:155:C:C2	1:A:167:G:C2	3.06	0.44
1:A:540:G:H2'	1:A:541:G:O4'	2.18	0.44
1:A:630:G:H3'	1:A:631:G:H5''	1.99	0.44
1:A:73:C:N4	1:A:74:C:H41	2.15	0.44
3:C:7:PRO:CB	3:C:11:ARG:HH21	2.30	0.44
4:D:158:ILE:HA	4:D:158:ILE:HD13	1.88	0.44
5:E:135:THR:O	5:E:136:MET:C	2.52	0.44
6:F:91:VAL:HG12	6:F:92:LYS:O	2.17	0.44
1:A:1346:A:N3	7:G:10:ARG:NH1	2.66	0.44
8:H:102:ARG:CD	8:H:102:ARG:N	2.64	0.44
9:I:40:LEU:HD13	9:I:40:LEU:HA	1.56	0.44
10:J:50:ILE:CD1	10:J:50:ILE:N	2.80	0.44
10:J:85:LEU:HB3	10:J:86:MET:H	1.61	0.44
18:R:76:LEU:HD23	18:R:76:LEU:HA	1.38	0.44
1:A:1113:C:H6	1:A:1113:C:O5'	2.01	0.44
1:A:1347:G:O2'	1:A:1348:U:O5'	2.36	0.44
1:A:154:C:H2'	1:A:155:C:H5'	1.99	0.44
1:A:54:C:C2	1:A:352:C:H5	2.36	0.44
1:A:428:G:C1'	1:A:429:U:OP2	2.65	0.44
1:A:433:C:C2	1:A:434:U:C5	3.02	0.44
1:A:521:G:O2'	1:A:522:C:H5'	2.17	0.44
1:A:595:G:C2	1:A:641:U:C2	3.05	0.44
1:A:77:G:H2'	1:A:78:G:O5'	2.18	0.44
4:D:114:ARG:HG3	4:D:114:ARG:NH1	2.33	0.44
4:D:62:GLN:HB3	4:D:66:ARG:NH1	2.32	0.44
5:E:90:VAL:O	5:E:120:THR:HA	2.17	0.44
5:E:84:PHE:C	5:E:84:PHE:CD2	2.90	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:15:ASP:OD2	7:G:44:TYR:OH	2.35	0.44
2:B:178:ARG:O	8:H:71:GLY:HA2	2.18	0.44
8:H:87:SER:C	8:H:88:LYS:HG3	2.38	0.44
9:I:49:PRO:HG3	9:I:101:PHE:HD1	1.82	0.44
15:O:53:HIS:O	15:O:54:ARG:C	2.54	0.44
1:A:1112:C:N3	3:C:178:LEU:HB2	2.32	0.44
1:A:960:U:H1'	1:A:1223:C:H5'	1.99	0.44
1:A:1516[A]:G:H2'	1:A:1518[A]:MA6:OP2	2.17	0.44
1:A:1527:C:H2'	1:A:1528:U:H5'	1.98	0.44
1:A:21:G:H2'	1:A:22:G:H8	1.78	0.44
1:A:277:C:O2'	1:A:278:G:H5'	2.18	0.44
1:A:510:A:H1'	1:A:543:C:O4'	2.18	0.44
1:A:653:A:OP1	8:H:56:LYS:CE	2.66	0.44
1:A:710:G:N7	29:A:2472:HOH:O	2.36	0.44
2:B:30:ARG:HD2	2:B:31:TYR:CZ	2.53	0.44
4:D:101:LEU:O	4:D:101:LEU:HG	2.17	0.44
13:M:108:ARG:HH21	13:M:114:ARG:HA	1.81	0.44
16:P:60:LEU:HD23	16:P:60:LEU:HA	1.34	0.44
1:A:1003(A):G:C2	1:A:1004:A:H1'	2.53	0.44
1:A:1271:G:H2'	1:A:1272:G:H8	1.83	0.44
1:A:236:G:H2'	1:A:237:C:O4'	2.18	0.44
1:A:594:G:C2'	1:A:595:G:H5'	2.47	0.44
1:A:886:G:H1	1:A:911:U:H3	1.66	0.44
1:A:89:C:O2'	1:A:90:U:H5'	2.17	0.44
2:B:168:THR:HG22	2:B:169:LYS:N	2.33	0.44
2:B:231:GLU:O	2:B:232:PRO:C	2.55	0.44
2:B:92:TYR:CE1	2:B:151:GLY:CA	3.00	0.44
3:C:73:PRO:HD3	3:C:105:GLU:HB2	1.99	0.44
5:E:42:GLY:HA2	5:E:136:MET:HE1	2.00	0.44
5:E:43:LEU:HD12	5:E:43:LEU:O	2.18	0.44
5:E:51:VAL:CB	5:E:52:PRO:HD3	2.48	0.44
8:H:116:LYS:HD2	8:H:129:VAL:HG11	2.00	0.44
9:I:9:ARG:HA	9:I:76:ALA:HB1	2.00	0.44
13:M:68:GLY:C	13:M:70:LEU:N	2.70	0.44
14:N:5:ALA:O	14:N:8:GLU:HG3	2.18	0.44
16:P:1:MET:O	16:P:2:VAL:C	2.56	0.44
16:P:4:ILE:HB	16:P:66:PRO:HA	1.99	0.44
18:R:61:LYS:O	18:R:62:GLU:C	2.54	0.44
19:S:52:TYR:CE1	19:S:55:LYS:C	2.91	0.44
20:T:92:LEU:HD23	20:T:92:LEU:N	2.33	0.44
1:A:1124:G:C2'	1:A:1145:C:C5	3.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:956:U:C2	1:A:1225:A:C2	3.06	0.43
1:A:1401:G:C5	1:A:1402:4OC:C5	3.01	0.43
1:A:1436:U:H2'	1:A:1437:C:C6	2.47	0.43
1:A:102:G:O2'	1:A:151:A:N3	2.39	0.43
1:A:285:G:O6	29:A:2039:HOH:O	2.20	0.43
3:C:34:LEU:HD13	14:N:25:VAL:CG2	2.48	0.43
4:D:70:ILE:HD13	4:D:70:ILE:HA	1.79	0.43
5:E:33:VAL:CG1	5:E:34:VAL:N	2.80	0.43
8:H:36:LEU:HG	8:H:36:LEU:H	1.65	0.43
1:A:1250:A:H4'	9:I:68:GLY:N	2.33	0.43
10:J:99:LYS:H	10:J:99:LYS:HD2	1.83	0.43
13:M:27:LYS:C	13:M:27:LYS:HD2	2.38	0.43
10:J:47:PHE:CD2	14:N:34:TYR:HD2	2.36	0.43
18:R:36:ASN:O	18:R:40:LEU:HG	2.18	0.43
21:U:21:TYR:N	21:U:21:TYR:CD1	2.86	0.43
1:A:1004:A:N6	1:A:1037:C:N4	2.66	0.43
1:A:1071:C:H42	1:A:1104:G:H1	1.66	0.43
1:A:1255:G:C2	1:A:1283:G:C2	3.06	0.43
1:A:1465:C:C5	1:A:1466:C:C5	3.06	0.43
1:A:1537:U:H2'	1:A:1538:C:N1	2.33	0.43
1:A:81:U:C5'	1:A:82:U:OP2	2.66	0.43
2:B:114:ARG:NE	2:B:118:LEU:HD21	2.33	0.43
3:C:114:PRO:O	3:C:118:GLN:HG3	2.18	0.43
5:E:89:ILE:HD12	5:E:90:VAL:H	1.82	0.43
8:H:20:TYR:CE1	8:H:76:PRO:CD	3.00	0.43
8:H:63:LEU:HA	8:H:63:LEU:HD13	1.53	0.43
9:I:37:PHE:CE2	9:I:74:ILE:HD11	2.52	0.43
12:L:39:VAL:HG23	12:L:57:LYS:HB3	1.99	0.43
14:N:29:ARG:HG2	14:N:40:CYS:HB3	2.00	0.43
16:P:4:ILE:O	16:P:66:PRO:HA	2.18	0.43
18:R:38:GLU:CD	18:R:38:GLU:N	2.71	0.43
20:T:10:LEU:O	20:T:10:LEU:HD23	2.18	0.43
1:A:1242:C:H4'	1:A:1304:G:OP1	2.17	0.43
1:A:1342:C:O2'	1:A:1343:G:H5'	2.18	0.43
1:A:134:A:H2'	1:A:135:C:O4'	2.18	0.43
1:A:1502:A:H2	1:A:1505:G:H1	1.66	0.43
2:B:98:LEU:HB2	2:B:101:MET:SD	2.59	0.43
3:C:62:ASP:HA	3:C:97:LYS:HZ2	1.82	0.43
6:F:90:VAL:HG12	6:F:91:VAL:N	2.33	0.43
13:M:99:ARG:CB	13:M:101:GLN:HE22	2.31	0.43
19:S:44:MET:HB2	19:S:62:ILE:CD1	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1163:C:C6	1:A:1163:C:C3'	3.02	0.43
1:A:1225:A:C5'	1:A:1226:C:OP2	2.58	0.43
1:A:1332:A:C2	1:A:1333:A:N9	2.86	0.43
1:A:1407:5MC:O2'	1:A:1408:A:H5'	2.18	0.43
1:A:537:G:C2	1:A:538:G:C5	3.06	0.43
1:A:644:G:C8	1:A:644:G:C4'	3.02	0.43
1:A:707:C:H4'	11:K:20:TYR:HD1	1.74	0.43
1:A:949:A:N1	1:A:1233:G:C4	2.86	0.43
4:D:61:LYS:HD2	4:D:61:LYS:C	2.38	0.43
5:E:84:PHE:C	5:E:84:PHE:HD2	2.22	0.43
7:G:51:GLN:HB2	7:G:52:GLU:OE1	2.18	0.43
8:H:127:LEU:CD2	8:H:127:LEU:O	2.65	0.43
8:H:45:ILE:HG13	8:H:47:GLY:N	2.34	0.43
1:A:1148:U:O3'	9:I:14:VAL:HG11	2.19	0.43
10:J:4:ILE:HD12	10:J:5:ARG:N	2.32	0.43
11:K:19:ALA:HA	11:K:32:ILE:HD13	2.00	0.43
12:L:33:ARG:C	12:L:84:LEU:HD12	2.38	0.43
13:M:63:THR:HG23	13:M:64:TRP:H	1.84	0.43
13:M:78:ILE:O	13:M:81:LEU:HB2	2.19	0.43
13:M:99:ARG:HB2	13:M:101:GLN:NE2	2.32	0.43
3:C:37:GLN:OE1	14:N:47:LEU:CD2	2.66	0.43
15:O:82:ILE:HG22	15:O:83:GLU:N	2.34	0.43
18:R:43:PHE:HE2	18:R:58:LEU:HD21	1.83	0.43
11:K:110:ASP:N	18:R:85:LEU:O	2.39	0.43
1:A:986:A:O2'	19:S:55:LYS:O	2.35	0.43
20:T:44:ALA:O	20:T:46:GLU:N	2.51	0.43
1:A:1082:G:H2'	1:A:1083:U:C5'	2.49	0.43
1:A:1168:A:C6	1:A:1169:A:C6	3.07	0.43
1:A:1166:G:N2	1:A:1171:G:C5	2.86	0.43
1:A:1221:G:C4	1:A:1222:G:C8	3.06	0.43
1:A:1515[B]:C:C4	1:A:1520[B]:G:O6	2.69	0.43
1:A:1526:G:C2'	1:A:1527:C:H5'	2.48	0.43
1:A:231:G:C2	1:A:232:G:C8	3.06	0.43
1:A:353:A:H5'	1:A:353:A:C8	2.50	0.43
1:A:778:G:C6	1:A:779:C:N3	2.87	0.43
2:B:44:LEU:H	2:B:44:LEU:CD2	2.25	0.43
3:C:111:LEU:N	3:C:111:LEU:HD23	2.33	0.43
3:C:78:GLY:HA3	3:C:83:ARG:CB	2.48	0.43
4:D:58:LEU:C	4:D:58:LEU:CD2	2.86	0.43
6:F:35:ALA:CB	6:F:67:MET:HB3	2.49	0.43
7:G:127:ALA:C	7:G:129:GLU:N	2.71	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:9:MET:HG3	8:H:26:VAL:HG21	2.01	0.43
9:I:47:LEU:HD23	9:I:47:LEU:HA	1.59	0.43
10:J:97:GLU:HG2	10:J:99:LYS:HE2	2.01	0.43
15:O:36:ILE:HA	15:O:59:MET:CE	2.49	0.43
17:Q:4:LYS:HG3	17:Q:6:LEU:HD21	1.98	0.43
20:T:44:ALA:HA	20:T:92:LEU:CD2	2.43	0.43
1:A:1039:C:N3	1:A:1040:U:C4	2.86	0.43
1:A:1054:C:OP1	1:A:1197:G:P	2.76	0.43
1:A:1132:C:H3'	1:A:1132:C:C6	2.52	0.43
1:A:132:C:H2'	1:A:133:U:H5'	2.01	0.43
1:A:1351:U:C2'	1:A:1352:C:H5'	2.48	0.43
1:A:360:A:C6	1:A:361:G:C6	3.06	0.43
1:A:448:A:C2	1:A:449:C:C5	3.06	0.43
1:A:484:G:C2'	1:A:485:G:OP2	2.66	0.43
1:A:90:U:C2'	1:A:91:C:O5'	2.66	0.43
1:A:925:G:C2	1:A:927:G:C8	3.07	0.43
2:B:145:LEU:HD23	2:B:145:LEU:HA	1.85	0.43
2:B:155:LEU:HD22	2:B:157:ARG:O	2.19	0.43
4:D:173:TRP:H	4:D:173:TRP:HE3	1.64	0.43
5:E:13:ILE:HA	5:E:29:GLY:O	2.19	0.43
3:C:135:LYS:NZ	5:E:50:GLU:HG2	2.34	0.43
7:G:54:THR:HG22	7:G:56:GLN:H	1.84	0.43
9:I:126:SER:O	9:I:128:ARG:N	2.52	0.43
10:J:40:LEU:CB	10:J:69:ASN:HB2	2.39	0.43
11:K:89:ALA:O	11:K:90:GLY:C	2.56	0.43
20:T:99:LEU:CD1	20:T:100:ILE:H	2.32	0.43
20:T:41:ILE:CD1	20:T:41:ILE:N	2.82	0.43
1:A:1501:C:C4	1:A:1504:G:C2	3.07	0.43
1:A:1517[B]:G:H2'	1:A:1518[B]:MA6:H8	2.00	0.43
1:A:1521:G:C2	1:A:1522:U:C2	3.07	0.43
1:A:236:G:C6	1:A:237:C:C2	3.06	0.43
1:A:397:A:C6	1:A:548:G:C8	3.07	0.43
1:A:443:C:N3	1:A:491:G:N2	2.58	0.43
1:A:77:G:N2	1:A:78:G:C4	2.86	0.43
1:A:909:A:H2'	1:A:910:C:O4'	2.18	0.43
2:B:223:ILE:HD13	2:B:230:VAL:CG2	2.49	0.43
4:D:24:GLU:O	4:D:25:ARG:CB	2.67	0.43
4:D:78:LEU:HD23	4:D:78:LEU:HA	1.81	0.43
5:E:121:LYS:CG	5:E:123:LEU:CD2	2.96	0.43
5:E:139:LEU:HD23	5:E:139:LEU:HA	1.62	0.43
5:E:76:ILE:HA	5:E:77:PRO:HD3	1.89	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1032:G:C4	1:A:1033:G:C8	3.06	0.43
1:A:1048:G:H5''	14:N:3:ARG:HG3	2.01	0.43
1:A:1053:G:O3'	1:A:1054:C:H4'	2.18	0.43
1:A:1056:U:H2'	1:A:1057:G:H8	1.84	0.43
1:A:1126:U:C4	1:A:1127:G:N2	2.87	0.43
1:A:1480:G:C4	1:A:1481:U:C5	3.07	0.43
1:A:234:C:H2'	1:A:235:C:H6	1.83	0.43
1:A:702:A:OP2	29:A:2798:HOH:O	2.21	0.43
1:A:78:G:C6	1:A:79:G:C8	3.06	0.43
1:A:848:C:H3'	1:A:848:C:C6	2.53	0.43
2:B:56:ARG:HB2	2:B:56:ARG:HH11	1.82	0.43
3:C:156:ARG:NE	3:C:160:ALA:O	2.51	0.43
4:D:28:SER:O	4:D:30:LYS:N	2.41	0.43
4:D:7:PRO:HG2	4:D:10:ARG:HD2	2.00	0.43
6:F:46:ARG:HB3	6:F:46:ARG:HE	1.59	0.43
7:G:65:ALA:HB2	7:G:128:ALA:CA	2.49	0.43
12:L:90:VAL:HG11	12:L:93:LEU:HG	1.99	0.43
10:J:45:ARG:HH11	14:N:36:PHE:HE2	1.65	0.43
1:A:988:G:N2	1:A:1218:C:O2	2.51	0.43
1:A:1287:A:C6	1:A:1288:A:C6	3.07	0.43
1:A:1478:C:H2'	1:A:1479:C:H6	1.84	0.43
1:A:1519[A]:MA6:C2'	1:A:1520[A]:G:H5'	2.49	0.43
1:A:46:G:C2	1:A:396:G:C2	3.06	0.43
1:A:680:C:H2'	1:A:681:C:H6	1.82	0.43
1:A:93:G:O2'	1:A:95:U:H5'	2.19	0.43
2:B:43:ASP:OD2	2:B:46:LYS:HB2	2.19	0.43
1:A:1298:C:OP2	7:G:114:ARG:NH2	2.51	0.43
8:H:20:TYR:CE1	8:H:76:PRO:CG	3.02	0.43
12:L:104:VAL:O	12:L:105:TYR:HB2	2.19	0.43
14:N:11:LYS:HG3	14:N:13:THR:OG1	2.19	0.43
14:N:12:ARG:C	14:N:14:PRO:HD3	2.39	0.43
3:C:33:LEU:HD11	14:N:53:LEU:HA	2.01	0.43
1:A:110:C:N4	1:A:111:G:C6	2.87	0.43
1:A:1135:U:N3	1:A:1137:C:O2	2.52	0.43
1:A:1326:C:P	21:U:6:ARG:HD3	2.59	0.43
1:A:1472:U:C2'	1:A:1473:A:O5'	2.67	0.43
1:A:266:G:C4'	1:A:266:G:C8	3.01	0.43
1:A:284:G:C4	1:A:285:G:C8	3.07	0.43
1:A:57:G:C2	1:A:58:C:C2	3.07	0.43
1:A:702:A:H3'	1:A:703:G:C5'	2.49	0.43
1:A:77:G:C2'	1:A:78:G:O5'	2.67	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:11:LEU:H	2:B:11:LEU:CD1	2.31	0.43
2:B:74:LYS:C	2:B:76:GLN:N	2.72	0.43
3:C:21:ARG:O	3:C:21:ARG:HG2	2.18	0.43
5:E:69:VAL:HG21	5:E:113:ALA:HB1	2.01	0.43
5:E:135:THR:O	5:E:138:ALA:HB3	2.18	0.43
6:F:97:PHE:HE1	18:R:61:LYS:HE2	1.84	0.43
8:H:36:LEU:HA	8:H:39:LEU:CD2	2.49	0.43
9:I:16:ARG:CD	9:I:64:THR:HG22	2.49	0.43
11:K:53:SER:O	11:K:55:LYS:N	2.51	0.43
12:L:93:LEU:O	12:L:94:PRO:C	2.56	0.43
13:M:94:ARG:HG2	13:M:94:ARG:H	1.54	0.43
3:C:6:HIS:HE1	14:N:50:LYS:HE2	1.83	0.43
15:O:26:GLU:OE1	15:O:77:ARG:HB2	2.18	0.43
15:O:78:TYR:CZ	15:O:82:ILE:CD1	3.01	0.43
18:R:78:LEU:CD2	18:R:78:LEU:N	2.79	0.43
18:R:78:LEU:HD23	18:R:78:LEU:N	2.34	0.43
19:S:15:LEU:HD13	19:S:16:LEU:H	1.82	0.43
20:T:60:GLU:O	20:T:63:ILE:HB	2.18	0.43
1:A:1126:U:C6	1:A:1126:U:OP1	2.71	0.42
1:A:976:G:N7	1:A:1358:U:N3	2.67	0.42
1:A:1501:C:C4	1:A:1504:G:N3	2.87	0.42
1:A:248:C:O2'	1:A:249:U:H5'	2.19	0.42
1:A:327:A:HO2'	1:A:328:C:C1'	2.31	0.42
1:A:54:C:C5	1:A:352:C:H5	2.35	0.42
1:A:497:A:H4'	1:A:498:U:OP2	2.19	0.42
1:A:81:U:C6	1:A:81:U:C3'	3.02	0.42
1:A:942:G:C2	1:A:943:U:C6	3.07	0.42
1:A:995:C:C2'	1:A:996:A:H5'	2.49	0.42
2:B:27:LYS:C	2:B:29:ALA:H	2.23	0.42
2:B:61:LEU:HD13	2:B:66:GLY:CA	2.41	0.42
3:C:156:ARG:HB3	3:C:196:LEU:HD21	2.01	0.42
3:C:84:ILE:HG12	3:C:88:ARG:NH2	2.32	0.42
4:D:150:GLU:C	4:D:152:SER:N	2.72	0.42
4:D:62:GLN:HA	4:D:62:GLN:OE1	2.19	0.42
5:E:148:VAL:HG23	5:E:148:VAL:H	1.31	0.42
7:G:113:GLU:HG2	7:G:113:GLU:H	1.32	0.42
10:J:6:ILE:O	10:J:72:VAL:HG23	2.19	0.42
10:J:90:LEU:HD22	10:J:90:LEU:N	2.34	0.42
11:K:124:LYS:HG2	11:K:125:PHE:CE2	2.55	0.42
11:K:57:THR:O	11:K:60:ALA:HB3	2.18	0.42
13:M:37:THR:HG23	13:M:39:ILE:HD12	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1053:G:C3'	1:A:1054:C:H5'	2.48	0.42
1:A:106:C:O2'	1:A:107:G:H5'	2.19	0.42
1:A:1126:U:N3	1:A:1127:G:C2	2.87	0.42
1:A:1190:G:O3'	3:C:3:ASN:HB2	2.19	0.42
1:A:1508:G:C5	1:A:1509:C:C5	3.07	0.42
1:A:397:A:H5'	1:A:398:C:OP1	2.19	0.42
1:A:826:C:H2'	1:A:827:U:H6	1.84	0.42
3:C:109:PRO:HA	3:C:115:LEU:HD12	2.01	0.42
5:E:43:LEU:O	5:E:65:ASN:ND2	2.52	0.42
6:F:14:LEU:HD22	6:F:14:LEU:HA	1.70	0.42
8:H:100:ILE:HA	8:H:101:PRO:HD2	1.57	0.42
11:K:58:PRO:HB2	11:K:93:GLN:HG3	2.01	0.42
12:L:100:ILE:HD12	12:L:100:ILE:N	2.34	0.42
1:A:134:A:H62	16:P:25:ARG:HH21	1.67	0.42
20:T:8:ARG:CG	20:T:9:ASN:HB3	2.50	0.42
23:W:37:A:C6	23:W:38:A:N1	2.87	0.42
1:A:1052:U:O2'	1:A:1055:A:OP1	2.38	0.42
1:A:1092:A:C4'	1:A:1092:A:C8	3.02	0.42
1:A:1193:G:C4	1:A:1194:U:C5	3.08	0.42
1:A:1297:C:O2'	1:A:1298:C:OP2	2.29	0.42
1:A:1321:C:C5'	13:M:87:TYR:CE2	3.02	0.42
1:A:1341:U:O2'	1:A:1342:C:H5'	2.19	0.42
1:A:1437:C:C2	1:A:1438:G:C8	3.07	0.42
1:A:1480:G:C5	1:A:1481:U:C5	3.07	0.42
1:A:245:C:C6	1:A:284:G:N2	2.87	0.42
1:A:731:G:O2'	1:A:732:C:H5'	2.19	0.42
1:A:792:A:C6	1:A:794:A:C2	3.07	0.42
2:B:172:ILE:H	2:B:172:ILE:CD1	2.32	0.42
2:B:6:THR:N	2:B:48:MET:HE1	2.35	0.42
3:C:16:ARG:CG	3:C:16:ARG:NH1	2.78	0.42
7:G:51:GLN:C	7:G:53:LYS:H	2.23	0.42
8:H:133:LEU:CD2	8:H:133:LEU:C	2.85	0.42
8:H:27:PRO:HB3	8:H:58:TYR:CE2	2.54	0.42
15:O:15:PHE:CD1	15:O:15:PHE:N	2.86	0.42
16:P:39:TYR:CG	16:P:73:LEU:HD11	2.54	0.42
17:Q:31:LEU:HA	17:Q:31:LEU:HD12	1.44	0.42
20:T:75:ASN:OD1	20:T:75:ASN:N	2.52	0.42
23:W:39:G:C2	23:W:40:PSU:C4	3.07	0.42
1:A:1026:G:HO2'	1:A:1027:C:P	2.23	0.42
1:A:1221:G:C6	1:A:1222:G:N7	2.87	0.42
1:A:1263:C:N4	1:A:1264:C:H41	2.17	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1367:C:C2	1:A:1368:G:C8	3.08	0.42
1:A:925:G:O4'	1:A:1502:A:C5	2.72	0.42
1:A:1503:A:H5'	1:A:1531:A:H1'	2.01	0.42
1:A:833:U:H2'	1:A:834:C:C6	2.53	0.42
1:A:903:G:H2'	1:A:904:C:H6	1.85	0.42
1:A:961:U:H2'	1:A:962:C:H5'	2.01	0.42
1:A:1104:G:P	2:B:111:ARG:HD2	2.60	0.42
2:B:36:ARG:CB	2:B:41:ILE:HD11	2.48	0.42
3:C:88:ARG:HB2	3:C:101:LEU:CD2	2.49	0.42
4:D:173:TRP:O	4:D:186:LEU:HG	2.19	0.42
4:D:192:GLU:CA	4:D:192:GLU:OE2	2.68	0.42
7:G:65:ALA:HB2	7:G:128:ALA:N	2.33	0.42
1:A:518:C:O3'	12:L:50:SER:HB3	2.19	0.42
12:L:52:LEU:O	12:L:54:LYS:NZ	2.41	0.42
14:N:8:GLU:OE2	14:N:11:LYS:HD3	2.20	0.42
15:O:56:LEU:HA	15:O:56:LEU:HD13	1.83	0.42
17:Q:11:VAL:CG1	17:Q:88:TYR:CE2	3.01	0.42
1:A:1072:G:C5	1:A:1073:U:C4	3.07	0.42
1:A:1077:G:N2	1:A:1081:G:C5	2.88	0.42
1:A:1115:C:C4	1:A:1116:C:C5	3.08	0.42
1:A:1225:A:H1'	19:S:78:ARG:HH11	1.83	0.42
1:A:1241:G:C4	1:A:1242:C:C5	3.07	0.42
1:A:1358:U:H5''	14:N:35:ARG:HG3	2.01	0.42
1:A:320:C:O2'	1:A:1435:G:H1'	2.20	0.42
1:A:1518[B]:MA6:C9	1:A:1519[B]:MA6:H103	2.49	0.42
1:A:157:G:H2'	1:A:157:G:N3	2.35	0.42
1:A:914:A:OP1	27:A:1928:SRV:HI33	2.19	0.42
1:A:366:C:H1'	1:A:394:G:H22	1.84	0.42
1:A:596:C:C2	1:A:644:G:N2	2.88	0.42
2:B:97:TRP:CZ2	2:B:101:MET:HG3	2.55	0.42
2:B:100:GLY:N	2:B:176:GLU:OE2	2.52	0.42
3:C:157:ILE:HD12	3:C:164:ARG:NH1	2.34	0.42
4:D:76:ARG:O	4:D:80:GLU:HG2	2.19	0.42
6:F:82:ARG:CB	6:F:85:VAL:HG23	2.46	0.42
1:A:1379:G:OP2	7:G:6:ARG:HG2	2.20	0.42
8:H:114:THR:OG1	8:H:117:GLY:O	2.34	0.42
8:H:121:ASP:O	8:H:124:ALA:N	2.49	0.42
14:N:60:SER:O	14:N:61:TRP:HB3	2.19	0.42
14:N:61:TRP:CD1	14:N:61:TRP:O	2.73	0.42
15:O:31:LEU:HA	15:O:31:LEU:HD12	1.56	0.42
15:O:2:PRO:O	15:O:3:ILE:HG13	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:79:ARG:CG	15:O:79:ARG:NH1	2.76	0.42
15:O:8:LYS:O	15:O:9:GLN:C	2.55	0.42
17:Q:90:ILE:HA	17:Q:93:GLN:HB3	2.00	0.42
18:R:58:LEU:CD2	18:R:58:LEU:N	2.82	0.42
20:T:99:LEU:O	20:T:101:GLY:N	2.52	0.42
21:U:10:ARG:HG3	21:U:10:ARG:HH11	1.79	0.42
1:A:1401:G:C5	1:A:1402:4OC:C6	3.03	0.42
1:A:448:A:N3	1:A:449:C:C6	2.87	0.42
1:A:665:A:H3'	1:A:725:G:H21	1.84	0.42
1:A:891:U:C2'	1:A:892:A:H5'	2.49	0.42
1:A:922:G:C5'	1:A:922:G:H8	2.32	0.42
4:D:100:ARG:NH2	4:D:136:PRO:HB2	2.35	0.42
4:D:147:ALA:HB2	4:D:182:LYS:HB3	2.00	0.42
4:D:191:ARG:HB3	4:D:192:GLU:OE2	2.20	0.42
4:D:64:LEU:CA	4:D:67:ILE:HD12	2.50	0.42
8:H:19:VAL:HG21	8:H:21:LYS:HD3	2.02	0.42
12:L:69:TYR:HE2	12:L:71:PRO:HA	1.83	0.42
16:P:17:TYR:HB2	16:P:39:TYR:HB3	2.02	0.42
1:A:376:G:H5''	16:P:5:ARG:HD2	2.01	0.42
19:S:44:MET:O	19:S:62:ILE:HG21	2.19	0.42
1:A:1004:A:O2'	1:A:1005:A:OP1	2.27	0.42
1:A:114:U:C2'	1:A:115:G:C5'	2.92	0.42
1:A:1255:G:O2'	1:A:1258:G:H1'	2.19	0.42
1:A:1493[B]:A:O2'	1:A:1494:G:C8	2.66	0.42
1:A:1505:G:C5'	1:A:1506:U:OP1	2.67	0.42
1:A:415:A:C5	1:A:416:G:C5	3.08	0.42
1:A:429:U:H4'	1:A:430:A:O5'	2.19	0.42
1:A:53:A:C5	1:A:54:C:C5	3.08	0.42
1:A:885:G:O2'	1:A:886:G:H5'	2.20	0.42
1:A:934:C:H5''	29:A:2502:HOH:O	2.20	0.42
2:B:115:LEU:HD21	2:B:153:ARG:HH12	1.85	0.42
2:B:154:LEU:HA	2:B:154:LEU:HD23	1.74	0.42
3:C:112:SER:HB3	3:C:115:LEU:HD12	2.01	0.42
3:C:82:GLU:CG	3:C:83:ARG:H	2.31	0.42
4:D:17:VAL:O	4:D:17:VAL:HG13	2.19	0.42
4:D:21:LEU:HD12	4:D:21:LEU:N	2.34	0.42
6:F:1:MET:HE2	6:F:1:MET:H1	1.84	0.42
8:H:39:LEU:HB3	8:H:45:ILE:HG23	2.01	0.42
10:J:19:SER:O	10:J:22:LYS:HB3	2.20	0.42
12:L:105:TYR:CD2	12:L:105:TYR:N	2.83	0.42
13:M:37:THR:HG21	13:M:39:ILE:HD13	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1053:G:H4'	1:A:1054:C:H5'	2.02	0.42
1:A:1130:A:C2	1:A:1146:A:H1'	2.54	0.42
1:A:425:G:C2'	1:A:426:G:H5'	2.48	0.42
1:A:49:U:O2'	1:A:50:A:H2'	2.20	0.42
3:C:173:VAL:O	3:C:175:LEU:HD12	2.19	0.42
4:D:8:VAL:O	4:D:10:ARG:N	2.53	0.42
4:D:188:LEU:HA	4:D:189:PRO:HD2	1.79	0.42
5:E:126:ARG:CG	5:E:126:ARG:NH1	2.65	0.42
9:I:22:GLY:O	9:I:57:GLY:O	2.38	0.42
13:M:16:ASP:O	13:M:17:VAL:C	2.58	0.42
13:M:21:TYR:N	13:M:21:TYR:CD1	2.87	0.42
13:M:54:VAL:CG1	13:M:55:ARG:N	2.83	0.42
15:O:15:PHE:HD1	15:O:15:PHE:N	2.17	0.42
19:S:58:VAL:HA	19:S:59:PRO:HD3	1.52	0.42
19:S:72:GLY:O	19:S:74:PHE:N	2.53	0.42
1:A:1040:U:O2'	1:A:1041:A:H5'	2.20	0.42
1:A:1051:C:H2'	1:A:1052:U:O5'	2.19	0.42
1:A:1086:U:O5'	1:A:1086:U:H6	2.02	0.42
1:A:1182:G:H2'	1:A:1182:G:H8	1.78	0.42
1:A:1250:A:N1	1:A:1287:A:C2	2.88	0.42
1:A:1368:G:H5'	9:I:112:LYS:O	2.19	0.42
1:A:1379:G:C6	1:A:1380:U:C4	3.07	0.42
1:A:1493[B]:A:C2'	1:A:1494:G:C8	3.03	0.42
1:A:24:U:OP1	12:L:23:LYS:HE2	2.20	0.42
1:A:309:G:O2'	1:A:310:G:H5'	2.20	0.42
1:A:407:G:H5''	4:D:3:ARG:NH1	2.35	0.42
1:A:442:C:H42	1:A:492:G:H1	1.68	0.42
1:A:496:A:H4'	1:A:497:A:OP1	2.18	0.42
1:A:505:G:C5	1:A:535:A:C2	3.08	0.42
1:A:397:A:C6	1:A:548:G:N7	2.88	0.42
1:A:605:U:H3'	1:A:605:U:C6	2.55	0.42
1:A:877:C:OP1	8:H:88:LYS:HE3	2.19	0.42
2:B:101:MET:HB2	2:B:102:LEU:CD1	2.49	0.42
3:C:115:LEU:HA	3:C:115:LEU:HD23	1.59	0.42
3:C:8:ILE:HG22	3:C:9:GLY:H	1.84	0.42
5:E:5:ASP:OD1	5:E:6:PHE:N	2.49	0.42
7:G:70:LYS:HB3	7:G:96:GLN:HG2	2.02	0.42
9:I:99:LEU:HD22	9:I:99:LEU:H	1.85	0.42
1:A:1199:U:H4'	10:J:54:PHE:CD1	2.55	0.42
12:L:71:PRO:HG2	12:L:102:ARG:HG3	2.01	0.42
13:M:22:ILE:H	13:M:22:ILE:CD1	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:S:34:TRP:CD1	19:S:52:TYR:HB3	2.54	0.42
21:U:12:LYS:HD3	21:U:17:THR:OG1	2.20	0.42
1:A:1172:C:O5'	1:A:1172:C:H6	2.03	0.42
1:A:1204:A:C5	1:A:1205:U:C6	3.08	0.42
1:A:1381:U:C5	1:A:1382:C:C6	3.08	0.42
1:A:154:C:C3'	1:A:154:C:C6	3.03	0.42
1:A:415:A:C5	1:A:416:G:N7	2.88	0.42
1:A:491:G:H2'	1:A:492:G:H8	1.85	0.42
1:A:924:C:C3'	1:A:924:C:C6	3.03	0.42
2:B:10:LEU:CD1	2:B:15:VAL:HG21	2.50	0.42
5:E:80:ILE:HA	8:H:104:ARG:NH2	2.35	0.42
6:F:10:LEU:HD12	6:F:10:LEU:N	2.35	0.42
6:F:35:ALA:HA	6:F:67:MET:HB3	2.02	0.42
7:G:5:ARG:NH1	7:G:8:GLU:HG2	2.34	0.42
8:H:52:ASP:HA	8:H:57:PRO:HA	2.02	0.42
15:O:52:SER:O	15:O:53:HIS:C	2.58	0.42
17:Q:20:THR:HA	17:Q:43:LEU:CD2	2.50	0.42
17:Q:18:THR:HG21	17:Q:69:LYS:HD3	2.01	0.42
17:Q:54:GLY:HA3	17:Q:82:MET:HG2	2.02	0.42
1:A:1032:G:H2'	1:A:1033:G:O4'	2.20	0.41
1:A:1111:A:O2'	1:A:1112:C:H5'	2.20	0.41
1:A:1190:G:H5'	3:C:4:LYS:H	1.85	0.41
1:A:1222:G:N2	1:A:1223:C:C2	2.88	0.41
1:A:1310:G:H2'	1:A:1311:G:O4'	2.20	0.41
1:A:1410:G:C4	1:A:1411:C:C5	3.08	0.41
1:A:1536:C:C6	1:A:1536:C:C3'	3.03	0.41
1:A:316:G:C5	29:A:2572:HOH:O	2.72	0.41
1:A:114:U:H1'	1:A:353:A:H1'	2.01	0.41
1:A:560:U:H4'	1:A:561:U:H5''	2.01	0.41
2:B:135:GLN:O	2:B:139:LYS:HB2	2.20	0.41
2:B:47:THR:HA	2:B:202:PRO:CG	2.46	0.41
3:C:120:VAL:HG12	3:C:124:ILE:HD11	2.02	0.41
4:D:83:SER:HA	4:D:89:THR:CG2	2.37	0.41
6:F:45:LEU:HA	6:F:59:TYR:HA	2.02	0.41
8:H:129:VAL:HG23	8:H:130:GLY:N	2.35	0.41
12:L:60:LEU:HA	12:L:60:LEU:HD13	1.33	0.41
13:M:49:THR:C	13:M:51:ALA:N	2.73	0.41
13:M:63:THR:CG2	13:M:64:TRP:H	2.32	0.41
14:N:7:ILE:N	14:N:7:ILE:HD13	2.35	0.41
16:P:38:TYR:O	16:P:49:LEU:HD12	2.19	0.41
16:P:66:PRO:HG2	16:P:71:ARG:NH1	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:78:LEU:HD22	18:R:78:LEU:HA	1.73	0.41
19:S:40:ILE:HG23	19:S:62:ILE:HD12	2.02	0.41
1:A:1030(A):G:N2	1:A:1030(D):A:OP2	2.53	0.41
1:A:1137:C:H4'	1:A:1138:G:O5'	2.19	0.41
1:A:1190:G:C8	1:A:1190:G:C4'	3.02	0.41
1:A:1241:G:OP1	7:G:35:LYS:NZ	2.53	0.41
1:A:1288:A:H2'	1:A:1289:A:H8	1.85	0.41
1:A:1376:U:OP1	7:G:98:SER:OG	2.25	0.41
1:A:1502:A:C2	1:A:1504:G:N3	2.88	0.41
1:A:1536:C:C6	1:A:1536:C:H3'	2.52	0.41
1:A:574:A:H5''	1:A:575:G:OP2	2.20	0.41
1:A:665:A:H3'	1:A:725:G:N2	2.36	0.41
1:A:78:G:C2	1:A:79:G:C8	3.08	0.41
1:A:79:G:N3	1:A:91:C:O2	2.54	0.41
1:A:973:G:C2'	1:A:974:A:OP1	2.68	0.41
3:C:78:GLY:CA	3:C:83:ARG:HB3	2.50	0.41
4:D:162:LEU:O	4:D:165:MET:HB2	2.20	0.41
4:D:19:LEU:CD1	4:D:67:ILE:HG13	2.50	0.41
5:E:69:VAL:HA	5:E:70:PRO:HD3	1.82	0.41
7:G:79:ARG:CB	7:G:83:ALA:O	2.68	0.41
8:H:100:ILE:HG21	8:H:112:LEU:HD11	2.02	0.41
9:I:33:PHE:HD1	9:I:33:PHE:HA	1.66	0.41
9:I:9:ARG:HA	9:I:76:ALA:HB2	2.00	0.41
13:M:70:LEU:HD23	13:M:70:LEU:HA	1.75	0.41
16:P:4:ILE:HG22	16:P:4:ILE:O	2.18	0.41
6:F:97:PHE:CE1	18:R:61:LYS:HE2	2.55	0.41
19:S:51:VAL:HG11	19:S:71:LEU:HD22	2.01	0.41
21:U:23:PRO:C	21:U:25:LYS:N	2.74	0.41
1:A:101:A:C2	1:A:102:G:C8	3.08	0.41
1:A:1052:U:O2	1:A:1207:2MG:N2	2.54	0.41
1:A:1128:C:O2'	1:A:1130:A:H8	2.02	0.41
1:A:140:A:O2'	1:A:141:A:H5'	2.20	0.41
1:A:243:A:C2	1:A:246:A:N7	2.88	0.41
1:A:268:C:H2'	1:A:269:C:H6	1.85	0.41
1:A:922:G:N3	1:A:1398:A:C2	2.86	0.41
1:A:937:A:N6	1:A:1345:U:O4	2.53	0.41
3:C:174:PRO:HB2	3:C:177:THR:HB	2.02	0.41
4:D:19:LEU:HD23	4:D:19:LEU:N	2.22	0.41
5:E:105:VAL:O	5:E:106:PRO:C	2.56	0.41
6:F:63:TYR:N	6:F:63:TYR:CD2	2.89	0.41
15:O:5:LYS:O	15:O:6:GLU:C	2.57	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:32:TYR:HA	17:Q:32:TYR:HD2	1.62	0.41
17:Q:76:LEU:HD12	17:Q:77:VAL:N	2.35	0.41
20:T:105:SER:O	20:T:106:ALA:C	2.58	0.41
22:V:1:U:N3	23:W:37:A:C2	2.88	0.41
1:A:1091:U:O2	1:A:1093:A:C8	2.74	0.41
1:A:1329:A:C5'	13:M:29:ARG:HD2	2.50	0.41
1:A:370:C:C2	1:A:371:G:C8	3.09	0.41
1:A:505:G:C6	1:A:535:A:C2	3.07	0.41
1:A:504:C:C2	1:A:542:G:C2	3.09	0.41
1:A:684:A:N3	11:K:39:PRO:HD2	2.36	0.41
1:A:850:U:H6	1:A:850:U:H3'	1.86	0.41
1:A:89:C:H5	1:A:90:U:O4	2.02	0.41
1:A:892:A:C6	1:A:907:A:C8	3.09	0.41
2:B:158:LEU:HB3	2:B:159:PRO:CD	2.50	0.41
2:B:208:ILE:HD13	2:B:208:ILE:HA	1.85	0.41
2:B:230:VAL:HG12	2:B:231:GLU:N	2.35	0.41
4:D:17:VAL:HG11	4:D:63:LYS:HD2	2.02	0.41
5:E:105:VAL:CB	5:E:106:PRO:HD3	2.49	0.41
5:E:131:ILE:HD13	5:E:131:ILE:HA	1.50	0.41
5:E:95:ALA:HB1	5:E:96:PRO:HD2	2.03	0.41
9:I:50:LEU:HD23	9:I:55:ALA:HB3	2.01	0.41
13:M:20:THR:O	13:M:20:THR:HG22	2.19	0.41
13:M:36:LYS:HD2	13:M:59:TYR:OH	2.20	0.41
15:O:12:ILE:O	15:O:14:GLU:N	2.53	0.41
15:O:21:ASP:OD1	15:O:24:SER:CB	2.66	0.41
17:Q:27:PHE:CE2	17:Q:36:ILE:HD11	2.55	0.41
17:Q:95:TYR:O	17:Q:97:SER:N	2.53	0.41
1:A:986:A:H1'	19:S:52:TYR:OH	2.19	0.41
1:A:1195:C:H5''	1:A:1196:U:P	2.61	0.41
1:A:1492[B]:A:C6	1:A:1493[B]:A:H1'	2.56	0.41
1:A:188:C:H2'	1:A:189:G:H5'	2.02	0.41
1:A:313:A:H2'	1:A:314:C:O4'	2.21	0.41
1:A:62:U:H2'	1:A:63:C:C6	2.56	0.41
1:A:739:C:N4	1:A:740:U:C4	2.89	0.41
1:A:777:A:N6	1:A:778:G:C2	2.89	0.41
1:A:794:A:N6	1:A:795:C:N4	2.68	0.41
1:A:88:A:N7	1:A:89:C:N3	2.68	0.41
2:B:16:HIS:HB3	2:B:44:LEU:HD11	2.02	0.41
3:C:26:LYS:HZ2	3:C:26:LYS:HB2	1.86	0.41
4:D:141:ARG:HB2	4:D:141:ARG:HE	1.48	0.41
4:D:22:LYS:HB3	4:D:26:CYS:SG	2.59	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:17:VAL:HG11	9:I:81:ILE:HA	2.01	0.41
10:J:8:LEU:HD21	10:J:96:ILE:HG23	2.02	0.41
27:A:1928:SRV:C61	12:L:46:LYS:HD2	2.51	0.41
16:P:20:VAL:CG1	16:P:21:VAL:N	2.78	0.41
17:Q:22:LEU:HD12	17:Q:23:VAL:N	2.36	0.41
1:A:247:G:OP2	17:Q:99:SER:HB2	2.20	0.41
18:R:59:SER:OG	18:R:62:GLU:HG3	2.21	0.41
13:M:27:LYS:HE2	21:U:21:TYR:HE2	1.84	0.41
1:A:1022:G:C2	1:A:1023:G:C8	3.08	0.41
1:A:1029:C:C4	1:A:1030:C:H5	2.39	0.41
1:A:1068:G:OP1	29:A:2218:HOH:O	2.20	0.41
1:A:21:G:C2	1:A:22:G:C6	3.09	0.41
1:A:22:G:C5	1:A:23:C:C4	3.09	0.41
1:A:328:C:OP1	1:A:328:C:H4'	2.19	0.41
1:A:536:C:OP2	29:A:2174:HOH:O	2.22	0.41
1:A:544:G:N3	1:A:545:C:C6	2.88	0.41
1:A:584:G:C2'	1:A:585:G:H5'	2.50	0.41
1:A:924:C:H3'	1:A:924:C:C6	2.55	0.41
2:B:215:LEU:O	2:B:219:VAL:HG23	2.21	0.41
5:E:31:LEU:HD23	5:E:44:GLY:O	2.21	0.41
7:G:23:VAL:HA	7:G:62:PHE:HE2	1.85	0.41
16:P:19:ILE:CG2	16:P:36:ILE:HG13	2.51	0.41
16:P:78:GLY:C	16:P:80:PHE:N	2.69	0.41
17:Q:101:ARG:HD3	17:Q:101:ARG:N	2.34	0.41
19:S:15:LEU:N	19:S:15:LEU:CD1	2.83	0.41
21:U:13:ILE:HG13	21:U:14:TRP:N	2.35	0.41
1:A:1042:G:C6	1:A:1043:C:C4	3.08	0.41
1:A:106:C:H2'	1:A:107:G:C5'	2.50	0.41
1:A:1121:U:O2'	1:A:1122:U:H5'	2.21	0.41
1:A:1124:G:C4'	10:J:38:ILE:HD11	2.50	0.41
1:A:1350:A:OP2	9:I:118:LYS:HD2	2.21	0.41
1:A:1377:A:O2'	7:G:2:ALA:HB3	2.21	0.41
1:A:1497:G:O2'	1:A:1518[A]:MA6:N1	2.53	0.41
1:A:357:G:C2	1:A:358:U:C6	3.09	0.41
1:A:491:G:C2	1:A:492:G:C8	3.08	0.41
1:A:552:U:H2'	1:A:553:A:C8	2.56	0.41
1:A:756:C:H2'	1:A:757:U:O4'	2.20	0.41
1:A:922:G:N3	1:A:1396:A:C2	2.89	0.41
2:B:102:LEU:HB2	2:B:176:GLU:OE1	2.20	0.41
2:B:20:GLU:HG2	2:B:39:ILE:HD11	2.02	0.41
4:D:150:GLU:O	4:D:152:SER:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:101:ILE:HD13	5:E:101:ILE:N	2.36	0.41
6:F:39:LYS:HG2	6:F:40:VAL:N	2.36	0.41
6:F:11:ASN:HD22	6:F:86:ARG:NH1	2.19	0.41
7:G:78:ARG:HD2	7:G:156:TRP:HB2	2.02	0.41
9:I:108:VAL:CG1	9:I:109:VAL:N	2.68	0.41
12:L:25:PRO:C	12:L:27:LEU:N	2.73	0.41
15:O:15:PHE:CE2	15:O:30:ALA:HB2	2.55	0.41
16:P:32:TYR:CD1	16:P:32:TYR:N	2.88	0.41
17:Q:89:LEU:O	17:Q:93:GLN:HB3	2.20	0.41
18:R:22:VAL:HG21	18:R:56:THR:HG22	2.02	0.41
21:U:10:ARG:HA	21:U:13:ILE:HG12	2.02	0.41
1:A:1006:C:H2'	1:A:1007:C:H6	1.85	0.41
1:A:1010:G:C2	1:A:1020:U:O2	2.74	0.41
1:A:112:G:H2'	1:A:113:G:H5'	2.02	0.41
1:A:1202:G:H1'	14:N:42:ILE:HD12	2.02	0.41
1:A:133:U:O5'	1:A:133:U:H6	2.03	0.41
1:A:148:G:N2	1:A:149:A:C4	2.89	0.41
2:B:16:HIS:NE2	2:B:17:PHE:CD2	2.89	0.41
2:B:24:TRP:CZ2	2:B:26:PRO:HB3	2.56	0.41
2:B:86:GLU:O	2:B:88:ALA:O	2.38	0.41
3:C:107:GLN:HG3	3:C:108:ASN:N	2.34	0.41
3:C:112:SER:OG	3:C:115:LEU:HB2	2.20	0.41
3:C:175:LEU:CD2	3:C:201:TYR:HE2	2.34	0.41
4:D:204:ILE:HD13	4:D:204:ILE:N	2.31	0.41
5:E:119:LEU:HD23	5:E:119:LEU:HA	1.56	0.41
5:E:76:ILE:HA	5:E:76:ILE:HD12	1.46	0.41
6:F:52:ILE:O	6:F:53:ALA:HB3	2.21	0.41
7:G:50:ILE:CB	7:G:58:PRO:HB3	2.50	0.41
8:H:11:THR:OG1	8:H:14:ARG:NH2	2.50	0.41
9:I:49:PRO:HD3	9:I:101:PHE:HE1	1.85	0.41
11:K:58:PRO:O	11:K:61:ALA:N	2.54	0.41
13:M:82:MET:HE2	13:M:82:MET:HB2	1.80	0.41
14:N:9:LYS:O	14:N:11:LYS:HB2	2.20	0.41
14:N:29:ARG:HG2	14:N:40:CYS:HB2	2.02	0.41
1:A:740:U:C4'	15:O:42:HIS:CD2	3.03	0.41
18:R:47:THR:CG2	18:R:48:GLY:H	2.27	0.41
18:R:87:ARG:NH2	18:R:87:ARG:CB	2.79	0.41
1:A:1038:C:O2'	1:A:1039:C:H5'	2.21	0.41
1:A:1343:G:H2'	1:A:1344:C:C6	2.56	0.41
1:A:1406:U:C6	1:A:1407:5MC:HM52	2.56	0.41
1:A:791:G:N2	1:A:1518[A]:MA6:C9	2.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:262:A:H5'	20:T:74:LYS:HD3	2.03	0.41
1:A:575:G:C6	1:A:821:G:N7	2.89	0.41
2:B:20:GLU:HA	2:B:39:ILE:HD11	2.01	0.41
2:B:216:SER:OG	2:B:217:ARG:N	2.53	0.41
3:C:6:HIS:CD2	3:C:6:HIS:C	2.94	0.41
3:C:85:ARG:CG	3:C:85:ARG:HH11	2.29	0.41
4:D:100:ARG:HH12	4:D:137:SER:CA	2.34	0.41
6:F:101:ALA:HA	18:R:28:GLU:CB	2.46	0.41
9:I:5:TYR:O	9:I:84:ALA:HA	2.21	0.41
12:L:68:ALA:HB3	12:L:100:ILE:HD11	2.03	0.41
12:L:117:ARG:C	12:L:119:LYS:N	2.70	0.41
13:M:49:THR:HB	13:M:52:GLU:CG	2.35	0.41
14:N:36:PHE:CD1	14:N:36:PHE:O	2.73	0.41
16:P:66:PRO:C	16:P:67:THR:O	2.59	0.41
17:Q:81:ARG:NE	17:Q:84:LEU:HD12	2.34	0.41
1:A:1063:C:H2'	1:A:1064:G:H8	1.83	0.41
1:A:392:G:C2	1:A:393:A:C8	3.09	0.41
1:A:500:G:C5	1:A:501:C:C4	3.09	0.41
1:A:652:U:O2'	1:A:752:G:N1	2.54	0.41
1:A:674:G:H5'	6:F:50:TYR:CE2	2.56	0.41
3:C:125:GLU:C	3:C:127:ARG:H	2.24	0.41
3:C:178:LEU:C	3:C:180:ALA:N	2.73	0.41
3:C:56:ASP:HB3	3:C:67:THR:HB	2.03	0.41
3:C:85:ARG:O	3:C:86:VAL:C	2.60	0.41
4:D:107:ARG:HH11	4:D:114:ARG:HH21	1.68	0.41
4:D:108:LEU:HD23	4:D:108:LEU:HA	1.73	0.41
4:D:64:LEU:HA	4:D:67:ILE:CD1	2.50	0.41
5:E:41:VAL:HG13	5:E:113:ALA:CA	2.49	0.41
5:E:28:PHE:O	5:E:47:LYS:HA	2.21	0.41
6:F:50:TYR:CD1	6:F:50:TYR:N	2.88	0.41
8:H:35:ILE:O	8:H:39:LEU:HD22	2.21	0.41
11:K:69:ALA:O	11:K:70:LYS:C	2.58	0.41
12:L:10:LEU:HD11	12:L:15:ARG:NE	2.35	0.41
15:O:26:GLU:HG3	15:O:81:LEU:HG	2.03	0.41
19:S:52:TYR:CE2	19:S:54:GLY:HA2	2.56	0.41
23:W:33:U:O2	23:W:33:U:H2'	2.21	0.41
1:A:1022:G:H2'	1:A:1022:G:N3	2.35	0.41
1:A:1038:C:C2	1:A:1039:C:C6	3.09	0.41
1:A:1190:G:O2'	1:A:1191:A:P	2.79	0.41
1:A:1330:U:C2'	1:A:1331:G:H5'	2.50	0.41
1:A:179:A:C4	1:A:180:U:C5	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:143:A:C2	1:A:221:C:O2	2.74	0.41
1:A:447:G:H2'	1:A:485:G:C2	2.54	0.41
1:A:474:G:C2	1:A:475:G:C8	3.09	0.41
1:A:442:C:N4	1:A:492:G:H1	2.19	0.41
1:A:16:A:C2	1:A:920:U:O2	2.74	0.41
1:A:1104:G:H4'	2:B:111:ARG:NE	2.36	0.41
3:C:182:ILE:HA	3:C:202:ILE:O	2.20	0.41
8:H:86:ILE:N	8:H:134:ILE:O	2.54	0.41
8:H:73:ASP:HA	8:H:74:PRO:HD2	1.73	0.41
11:K:120:ARG:NH2	11:K:126:ARG:NE	2.69	0.41
16:P:67:THR:N	16:P:70:ALA:HB3	2.35	0.41
17:Q:53:LEU:HA	17:Q:53:LEU:HD13	1.79	0.41
17:Q:86:GLU:O	17:Q:87:LYS:C	2.60	0.41
1:A:1318:A:H5'	19:S:10:PHE:CD1	2.56	0.41
1:A:1005:A:C8	1:A:1026:G:C6	3.10	0.40
1:A:1102:A:O2'	2:B:99:GLY:N	2.54	0.40
1:A:1404:5MC:C2	1:A:1499:A:N1	2.89	0.40
1:A:1415:G:H2'	1:A:1416:G:H5'	2.02	0.40
1:A:1418:A:H61	1:A:1482:G:H1'	1.86	0.40
1:A:411:A:C8	1:A:411:A:C3'	3.05	0.40
1:A:865:A:H1'	1:A:918:A:O2'	2.21	0.40
1:A:891:U:O2'	1:A:892:A:H5'	2.21	0.40
2:B:157:ARG:CG	2:B:158:LEU:N	2.83	0.40
2:B:183:PRO:HA	2:B:198:ASP:OD2	2.21	0.40
2:B:239:VAL:O	2:B:240:GLN:HB3	2.21	0.40
2:B:60:ASP:O	2:B:64:ARG:HB2	2.20	0.40
4:D:19:LEU:CD2	4:D:19:LEU:N	2.83	0.40
5:E:121:LYS:HG3	5:E:123:LEU:CD2	2.50	0.40
6:F:25:ILE:HD12	6:F:82:ARG:HD3	2.02	0.40
7:G:51:GLN:CB	7:G:52:GLU:OE1	2.69	0.40
7:G:75:VAL:CG2	7:G:86:GLN:HB3	2.51	0.40
9:I:118:LYS:HE2	9:I:118:LYS:HB3	1.90	0.40
10:J:7:LYS:HE2	10:J:9:ARG:NH2	2.35	0.40
12:L:113:ARG:NH2	12:L:120:TYR:CE1	2.89	0.40
12:L:19:ARG:HA	12:L:20:LYS:HZ3	1.86	0.40
13:M:106:ASN:HB3	13:M:107:ALA:H	1.50	0.40
14:N:11:LYS:C	14:N:13:THR:H	2.22	0.40
1:A:108:G:H2'	1:A:109:A:OP1	2.21	0.40
1:A:1124:G:N2	1:A:1127:G:H21	2.19	0.40
1:A:1390:U:H2'	1:A:1391:U:C6	2.57	0.40
1:A:149:A:H2'	1:A:150:C:C6	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1517[A]:G:H2'	1:A:1518[A]:MA6:H8	2.04	0.40
1:A:1518[A]:MA6:C2	1:A:1519[A]:MA6:C5	2.99	0.40
1:A:47:C:H6	1:A:365:U:H2'	1.86	0.40
1:A:367:U:O2	1:A:369:C:C6	2.73	0.40
1:A:427:U:O4	1:A:428:G:C6	2.74	0.40
1:A:919:A:O5'	1:A:919:A:H8	2.04	0.40
1:A:972:C:OP1	10:J:57:LYS:NZ	2.50	0.40
2:B:15:VAL:O	2:B:15:VAL:HG12	2.21	0.40
3:C:88:ARG:NH2	3:C:101:LEU:HD23	2.36	0.40
7:G:65:ALA:HA	7:G:128:ALA:HA	2.03	0.40
7:G:65:ALA:HB2	7:G:128:ALA:CB	2.50	0.40
11:K:38:ASN:HA	11:K:39:PRO:HD3	1.85	0.40
11:K:73:MET:HE3	11:K:73:MET:HB2	1.97	0.40
13:M:6:GLY:O	13:M:7:VAL:C	2.59	0.40
17:Q:63:ARG:HA	17:Q:64:PRO:HD3	1.90	0.40
17:Q:9:VAL:HG23	17:Q:9:VAL:H	1.70	0.40
19:S:3:ARG:HD3	19:S:3:ARG:HA	1.76	0.40
19:S:31:ILE:HG21	19:S:49:ILE:HD12	2.02	0.40
1:A:1305:G:P	21:U:2:GLY:N	2.94	0.40
1:A:1027:C:C6	1:A:1035:A:C2	3.10	0.40
1:A:1236:A:OP1	21:U:3:LYS:HG3	2.21	0.40
1:A:1440:C:H2'	1:A:1441:G:O4'	2.22	0.40
1:A:166:G:C6	1:A:167:G:N7	2.89	0.40
1:A:246:A:C4	1:A:279:A:N6	2.90	0.40
1:A:393:A:N3	1:A:394:G:C8	2.89	0.40
1:A:643:C:C3'	1:A:644:G:H5''	2.52	0.40
1:A:660:G:C2	1:A:746:A:C2	3.10	0.40
1:A:777:A:N3	1:A:777:A:C2'	2.85	0.40
1:A:79:G:N1	1:A:80:G:C5	2.89	0.40
1:A:848:C:C6	1:A:848:C:C3'	3.05	0.40
1:A:838:G:C2	1:A:849:C:C2	3.10	0.40
2:B:16:HIS:CD2	2:B:17:PHE:CD2	2.96	0.40
2:B:214:ILE:N	2:B:214:ILE:HD12	2.36	0.40
3:C:131:ARG:HH21	3:C:166:GLU:CD	2.25	0.40
5:E:112:LEU:C	5:E:114:GLY:H	2.25	0.40
7:G:111:ARG:HG2	7:G:112:PRO:HD2	2.03	0.40
8:H:120:THR:O	8:H:121:ASP:C	2.59	0.40
12:L:86:ARG:HG3	12:L:86:ARG:NH1	2.33	0.40
17:Q:27:PHE:HA	17:Q:28:PRO:HD3	1.84	0.40
23:W:32:C:O2'	23:W:33:U:H6	2.03	0.40
1:A:1032:G:H2'	1:A:1033:G:C8	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1027:C:H5	1:A:1035:A:N1	2.16	0.40
1:A:1133:G:H1	1:A:1141:C:N4	2.20	0.40
1:A:1158:C:C5	1:A:1160:G:C8	3.09	0.40
1:A:115:G:O2'	1:A:116:A:OP2	2.22	0.40
1:A:1244:C:C2	1:A:1294:G:N2	2.90	0.40
1:A:1425:U:O2	1:A:1426:C:C6	2.75	0.40
1:A:36:C:C2	1:A:37:U:C6	3.10	0.40
1:A:392:G:C4	1:A:393:A:C8	3.09	0.40
1:A:543:C:C2'	1:A:544:G:C5'	2.79	0.40
1:A:632:A:H5''	1:A:633:G:OP2	2.21	0.40
1:A:735:C:H1'	18:R:75:ILE:CD1	2.52	0.40
1:A:747:C:C6	1:A:747:C:C3'	3.04	0.40
1:A:977:A:C2'	1:A:978:A:C5'	2.98	0.40
2:B:109:SER:O	2:B:112:VAL:HB	2.21	0.40
2:B:130:ARG:HA	2:B:131:PRO:HD2	1.88	0.40
2:B:180:LEU:HB2	2:B:182:ILE:HG13	2.04	0.40
3:C:126:ARG:HE	3:C:128:PHE:HD1	1.68	0.40
5:E:12:LEU:HG	5:E:13:ILE:N	2.36	0.40
7:G:51:GLN:O	7:G:52:GLU:CG	2.69	0.40
7:G:5:ARG:HE	7:G:7:ALA:HA	1.86	0.40
12:L:45:PRO:HB3	12:L:93:LEU:CD2	2.49	0.40
13:M:23:TYR:CZ	13:M:71:ARG:HG3	2.57	0.40
13:M:91:ARG:HH21	13:M:96:LEU:HB2	1.86	0.40
15:O:16:ALA:CB	15:O:21:ASP:HB3	2.38	0.40
15:O:70:LEU:HD22	15:O:78:TYR:HA	2.02	0.40
19:S:62:ILE:HG13	19:S:66:MET:HE2	2.03	0.40
20:T:78:ALA:O	20:T:79:ARG:C	2.59	0.40
21:U:18:TYR:CD2	21:U:22:ARG:HD3	2.56	0.40
1:A:1234:C:C2'	1:A:1235:U:H5'	2.52	0.40
1:A:1372:U:H2'	1:A:1373:G:O4'	2.22	0.40
1:A:1378:C:O2	7:G:76:ARG:NH1	2.55	0.40
1:A:1502:A:H2	1:A:1505:G:N1	2.20	0.40
1:A:328:C:O2'	1:A:329:A:P	2.74	0.40
1:A:35:G:H2'	1:A:36:C:H6	1.87	0.40
1:A:442:C:C3'	1:A:443:C:H5'	2.51	0.40
1:A:490:G:C4	1:A:491:G:C8	3.10	0.40
1:A:503:C:H2'	1:A:504:C:C6	2.55	0.40
1:A:765:G:C6	1:A:812:C:C2	3.09	0.40
1:A:961:U:H2'	1:A:962:C:O4'	2.22	0.40
2:B:172:ILE:HD13	2:B:172:ILE:N	2.33	0.40
2:B:75:LYS:HG2	2:B:78:GLN:HG3	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:31:HIS:HA	3:C:34:LEU:HB3	2.04	0.40
3:C:47:LEU:O	3:C:50:ALA:N	2.49	0.40
6:F:73:ASN:O	6:F:74:ASP:C	2.59	0.40
8:H:14:ARG:CZ	8:H:14:ARG:HB2	2.50	0.40
9:I:70:LYS:O	9:I:74:ILE:HG12	2.21	0.40
10:J:11:PHE:HD2	10:J:11:PHE:HA	1.63	0.40
10:J:79:ARG:HB3	10:J:80:LYS:HE2	2.03	0.40
10:J:9:ARG:CB	10:J:9:ARG:NH1	2.85	0.40
12:L:113:ARG:CZ	12:L:120:TYR:HD1	2.35	0.40
13:M:63:THR:CG2	13:M:64:TRP:N	2.84	0.40
15:O:42:HIS:HE1	15:O:46:HIS:CD2	2.39	0.40

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:82:U:O2	1:A:1400:5MC:N4[3_545]	2.15	0.05
5:E:73:ASN:N	5:E:149:GLU:OE1[7_555]	2.18	0.02

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	234/256 (91%)	197 (84%)	34 (14%)	3 (1%)	14	56
3	C	205/239 (86%)	169 (82%)	35 (17%)	1 (0%)	32	74
4	D	206/209 (99%)	180 (87%)	25 (12%)	1 (0%)	32	74
5	E	149/162 (92%)	137 (92%)	11 (7%)	1 (1%)	25	68
6	F	99/101 (98%)	93 (94%)	6 (6%)	0	100	100
7	G	153/156 (98%)	132 (86%)	21 (14%)	0	100	100
8	H	136/138 (99%)	128 (94%)	7 (5%)	1 (1%)	25	68

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
9	I	125/128 (98%)	107 (86%)	17 (14%)	1 (1%)	22	65
10	J	97/105 (92%)	77 (79%)	17 (18%)	3 (3%)	5	40
11	K	115/129 (89%)	98 (85%)	17 (15%)	0	100	100
12	L	122/135 (90%)	110 (90%)	8 (7%)	4 (3%)	4	39
13	M	116/126 (92%)	99 (85%)	16 (14%)	1 (1%)	20	63
14	N	58/61 (95%)	50 (86%)	8 (14%)	0	100	100
15	O	86/89 (97%)	72 (84%)	14 (16%)	0	100	100
16	P	82/88 (93%)	74 (90%)	7 (8%)	1 (1%)	15	58
17	Q	98/105 (93%)	93 (95%)	5 (5%)	0	100	100
18	R	69/88 (78%)	60 (87%)	9 (13%)	0	100	100
19	S	79/93 (85%)	68 (86%)	9 (11%)	2 (2%)	6	44
20	T	97/106 (92%)	80 (82%)	16 (16%)	1 (1%)	18	61
21	U	23/27 (85%)	22 (96%)	1 (4%)	0	100	100
All	All	2349/2541 (92%)	2046 (87%)	283 (12%)	20 (1%)	20	63

All (20) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	15	THR
9	I	119	ALA
12	L	28	LYS
16	P	83	GLU
19	S	31	ILE
10	J	81	THR
10	J	86	MET
19	S	6	LYS
12	L	115	LYS
20	T	73	HIS
2	B	21	ARG
2	B	95	GLN
2	B	229	VAL
5	E	153	LYS
8	H	121	ASP
12	L	27	LEU
10	J	34	VAL
12	L	71	PRO
13	M	7	VAL
4	D	67	ILE

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	201/220 (91%)	151 (75%)	50 (25%)	1	6
3	C	160/188 (85%)	119 (74%)	41 (26%)	0	5
4	D	180/181 (99%)	134 (74%)	46 (26%)	0	5
5	E	115/123 (94%)	75 (65%)	40 (35%)	0	1
6	F	90/90 (100%)	60 (67%)	30 (33%)	0	2
7	G	126/127 (99%)	92 (73%)	34 (27%)	0	4
8	H	119/119 (100%)	83 (70%)	36 (30%)	0	3
9	I	98/99 (99%)	75 (76%)	23 (24%)	1	6
10	J	87/92 (95%)	70 (80%)	17 (20%)	1	12
11	K	89/99 (90%)	72 (81%)	17 (19%)	2	12
12	L	103/110 (94%)	80 (78%)	23 (22%)	1	8
13	M	94/101 (93%)	64 (68%)	30 (32%)	0	2
14	N	49/50 (98%)	35 (71%)	14 (29%)	0	3
15	O	79/80 (99%)	60 (76%)	19 (24%)	1	6
16	P	72/74 (97%)	54 (75%)	18 (25%)	1	6
17	Q	95/97 (98%)	74 (78%)	21 (22%)	1	8
18	R	62/77 (80%)	48 (77%)	14 (23%)	1	8
19	S	71/80 (89%)	55 (78%)	16 (22%)	1	8
20	T	76/82 (93%)	51 (67%)	25 (33%)	0	2
21	U	19/22 (86%)	16 (84%)	3 (16%)	3	21
All	All	1985/2111 (94%)	1468 (74%)	517 (26%)	0	5

All (517) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	10	LEU
2	B	11	LEU
2	B	16	HIS

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Mol	Chain	Res	Type
2	B	17	PHE
2	B	20	GLU
2	B	30	ARG
2	B	33	TYR
2	B	35	GLU
2	B	39	ILE
2	B	44	LEU
2	B	53	ARG
2	B	61	LEU
2	B	63	MET
2	B	64	ARG
2	B	67	THR
2	B	69	LEU
2	B	92	TYR
2	B	97	TRP
2	B	101	MET
2	B	107	THR
2	B	109	SER
2	B	111	ARG
2	B	114	ARG
2	B	115	LEU
2	B	122	PHE
2	B	127	ILE
2	B	128	GLU
2	B	144	ARG
2	B	150	SER
2	B	153	ARG
2	B	162	ILE
2	B	163	PHE
2	B	169	LYS
2	B	172	ILE
2	B	182	ILE
2	B	187	LEU
2	B	189	ASP
2	B	193	ASP
2	B	196	LEU
2	B	200	ILE
2	B	204	ASN
2	B	209	ARG
2	B	210	SER
2	B	212	GLN
2	B	215	LEU

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Mol	Chain	Res	Type
2	B	216	SER
2	B	221	LEU
2	B	226	ARG
2	B	236	TYR
2	B	240	GLN
3	C	3	ASN
3	C	8	ILE
3	C	10	PHE
3	C	14	ILE
3	C	16	ARG
3	C	21	ARG
3	C	22	TRP
3	C	31	HIS
3	C	33	LEU
3	C	43	LEU
3	C	45	LYS
3	C	52	LEU
3	C	58	GLU
3	C	64	VAL
3	C	70	VAL
3	C	72	LYS
3	C	75	VAL
3	C	79	ARG
3	C	85	ARG
3	C	99	VAL
3	C	101	LEU
3	C	111	LEU
3	C	119	ARG
3	C	126	ARG
3	C	127	ARG
3	C	130	VAL
3	C	134	ILE
3	C	144	SER
3	C	147	LYS
3	C	156	ARG
3	C	165	THR
3	C	167	TRP
3	C	170	GLN
3	C	175	LEU
3	C	186	PHE
3	C	188	LEU
3	C	190	ARG

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Mol	Chain	Res	Type
3	C	192	THR
3	C	193	TYR
3	C	196	LEU
3	C	204	LEU
4	D	10	ARG
4	D	19	LEU
4	D	20	TYR
4	D	26	CYS
4	D	28	SER
4	D	47	ARG
4	D	49	ARG
4	D	57	ARG
4	D	61	LYS
4	D	66	ARG
4	D	73	ARG
4	D	78	LEU
4	D	84	LYS
4	D	85	LYS
4	D	86	LYS
4	D	91	SER
4	D	92	VAL
4	D	96	LEU
4	D	107	ARG
4	D	108	LEU
4	D	114	ARG
4	D	115	ARG
4	D	119	GLN
4	D	120	LEU
4	D	122	ARG
4	D	127	THR
4	D	131	ARG
4	D	132	ARG
4	D	145	GLU
4	D	146	ILE
4	D	150	GLU
4	D	159	ARG
4	D	163	GLU
4	D	169	LYS
4	D	177	ASP
4	D	178	VAL
4	D	179	GLU
4	D	182	LYS

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Mol	Chain	Res	Type
4	D	187	ARG
4	D	188	LEU
4	D	190	ASP
4	D	192	GLU
4	D	193	ASP
4	D	194	LEU
4	D	196	LEU
4	D	204	ILE
5	E	6	PHE
5	E	11	ILE
5	E	12	LEU
5	E	16	THR
5	E	18	ARG
5	E	24	ARG
5	E	31	LEU
5	E	32	VAL
5	E	37	ARG
5	E	38	GLN
5	E	43	LEU
5	E	47	LYS
5	E	51	VAL
5	E	53	LEU
5	E	55	VAL
5	E	60	TYR
5	E	65	ASN
5	E	66	MET
5	E	67	VAL
5	E	68	GLU
5	E	75	THR
5	E	76	ILE
5	E	78	HIS
5	E	79	GLU
5	E	80	ILE
5	E	82	VAL
5	E	83	GLU
5	E	84	PHE
5	E	100	VAL
5	E	105	VAL
5	E	110	LEU
5	E	116	THR
5	E	123	LEU
5	E	125	SER

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Mol	Chain	Res	Type
5	E	126	ARG
5	E	131	ILE
5	E	145	LYS
5	E	147	ASP
5	E	148	VAL
5	E	150	ARG
6	F	1	MET
6	F	2	ARG
6	F	7	ASN
6	F	9	VAL
6	F	10	LEU
6	F	14	LEU
6	F	16	GLN
6	F	21	LEU
6	F	24	GLU
6	F	25	ILE
6	F	28	ARG
6	F	37	VAL
6	F	39	LYS
6	F	43	LEU
6	F	54	LYS
6	F	64	GLN
6	F	65	VAL
6	F	74	ASP
6	F	75	LEU
6	F	80	ARG
6	F	83	ASP
6	F	84	ASN
6	F	86	ARG
6	F	87	ARG
6	F	89	MET
6	F	93	SER
6	F	94	GLN
6	F	97	PHE
6	F	98	LEU
6	F	100	ASN
7	G	9	VAL
7	G	10	ARG
7	G	12	LEU
7	G	15	ASP
7	G	16	LEU
7	G	17	VAL

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Mol	Chain	Res	Type
7	G	22	LEU
7	G	27	ILE
7	G	29	LYS
7	G	38	LEU
7	G	41	ARG
7	G	49	ILE
7	G	52	GLU
7	G	60	LYS
7	G	62	PHE
7	G	66	VAL
7	G	72	ARG
7	G	75	VAL
7	G	78	ARG
7	G	87	VAL
7	G	92	SER
7	G	97	GLN
7	G	101	LEU
7	G	113	GLU
7	G	114	ARG
7	G	115	ARG
7	G	120	ILE
7	G	122	HIS
7	G	124	LEU
7	G	126	ASP
7	G	129	GLU
7	G	135	VAL
7	G	146	GLU
7	G	156	TRP
8	H	1	MET
8	H	3	THR
8	H	8	ASP
8	H	10	LEU
8	H	11	THR
8	H	14	ARG
8	H	18	ARG
8	H	19	VAL
8	H	22	GLU
8	H	39	LEU
8	H	45	ILE
8	H	51	VAL
8	H	53	VAL
8	H	57	PRO

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Mol	Chain	Res	Type
8	H	59	LEU
8	H	63	LEU
8	H	81	HIS
8	H	83	ILE
8	H	85	ARG
8	H	87	SER
8	H	91	ARG
8	H	95	VAL
8	H	97	VAL
8	H	98	LYS
8	H	100	ILE
8	H	102	ARG
8	H	104	ARG
8	H	105	ARG
8	H	112	LEU
8	H	113	SER
8	H	119	LEU
8	H	121	ASP
8	H	127	LEU
8	H	133	LEU
8	H	135	CYS
8	H	136	GLU
9	I	2	GLU
9	I	5	TYR
9	I	14	VAL
9	I	16	ARG
9	I	23	ASN
9	I	29	ASN
9	I	33	PHE
9	I	34	ASN
9	I	40	LEU
9	I	48	GLU
9	I	59	PHE
9	I	62	TYR
9	I	63	ILE
9	I	64	THR
9	I	65	VAL
9	I	66	ARG
9	I	79	LEU
9	I	85	LEU
9	I	99	LEU
9	I	102	LEU

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Mol	Chain	Res	Type
9	I	109	VAL
9	I	112	LYS
9	I	125	TYR
10	J	4	ILE
10	J	9	ARG
10	J	12	ASP
10	J	19	SER
10	J	28	ARG
10	J	29	ARG
10	J	33	GLN
10	J	44	VAL
10	J	62	HIS
10	J	63	PHE
10	J	67	THR
10	J	78	ASN
10	J	89	ASP
10	J	90	LEU
10	J	94	VAL
10	J	98	ILE
10	J	99	LYS
11	K	11	LYS
11	K	29	ILE
11	K	40	ILE
11	K	57	THR
11	K	70	LYS
11	K	75	TYR
11	K	78	GLN
11	K	80	VAL
11	K	92	GLU
11	K	96	ARG
11	K	99	GLN
11	K	105	VAL
11	K	116	HIS
11	K	117	ASN
11	K	120	ARG
11	K	125	PHE
11	K	126	ARG
12	L	7	ILE
12	L	18	VAL
12	L	19	ARG
12	L	20	LYS
12	L	32	PHE

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Mol	Chain	Res	Type
12	L	34	ARG
12	L	36	VAL
12	L	43	VAL
12	L	44	THR
12	L	50	SER
12	L	52	LEU
12	L	53	ARG
12	L	54	LYS
12	L	60	LEU
12	L	75	HIS
12	L	81	SER
12	L	82	VAL
12	L	98	TYR
12	L	101	VAL
12	L	113	ARG
12	L	116	SER
12	L	122	THR
12	L	127	GLU
13	M	7	VAL
13	M	11	ARG
13	M	14	ARG
13	M	17	VAL
13	M	22	ILE
13	M	27	LYS
13	M	32	GLU
13	M	44	ARG
13	M	46	LYS
13	M	48	LEU
13	M	50	GLU
13	M	52	GLU
13	M	55	ARG
13	M	56	LEU
13	M	57	ARG
13	M	58	GLU
13	M	59	TYR
13	M	64	TRP
13	M	67	GLU
13	M	69	GLU
13	M	70	LEU
13	M	74	VAL
13	M	81	LEU
13	M	84	ILE

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Mol	Chain	Res	Type
13	M	87	TYR
13	M	88	ARG
13	M	94	ARG
13	M	99	ARG
13	M	102	ARG
13	M	105	THR
14	N	3	ARG
14	N	6	LEU
14	N	7	ILE
14	N	9	LYS
14	N	12	ARG
14	N	17	LYS
14	N	24	CYS
14	N	27	CYS
14	N	29	ARG
14	N	33	VAL
14	N	45	ARG
14	N	46	GLU
14	N	49	HIS
14	N	58	LYS
15	O	6	GLU
15	O	11	VAL
15	O	17	ARG
15	O	24	SER
15	O	26	GLU
15	O	31	LEU
15	O	38	ARG
15	O	39	LEU
15	O	40	SER
15	O	45	VAL
15	O	47	LYS
15	O	54	ARG
15	O	56	LEU
15	O	57	LEU
15	O	67	LEU
15	O	73	GLU
15	O	81	LEU
15	O	87	ILE
15	O	88	ARG
16	P	1	MET
16	P	8	ARG
16	P	11	SER

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Mol	Chain	Res	Type
16	P	18	ARG
16	P	22	THR
16	P	25	ARG
16	P	42	ARG
16	P	45	THR
16	P	48	TRP
16	P	53	VAL
16	P	54	GLU
16	P	55	ARG
16	P	62	VAL
16	P	69	THR
16	P	72	ARG
16	P	75	ARG
16	P	79	VAL
16	P	81	ARG
17	Q	10	VAL
17	Q	13	ASP
17	Q	23	VAL
17	Q	27	PHE
17	Q	29	HIS
17	Q	36	ILE
17	Q	40	LYS
17	Q	43	LEU
17	Q	50	LYS
17	Q	53	LEU
17	Q	59	ILE
17	Q	62	SER
17	Q	70	ARG
17	Q	72	ARG
17	Q	77	VAL
17	Q	85	VAL
17	Q	90	ILE
17	Q	91	ARG
17	Q	92	ARG
17	Q	93	GLN
17	Q	98	LEU
18	R	18	ARG
18	R	26	LEU
18	R	31	LEU
18	R	38	GLU
18	R	42	ARG
18	R	44	LEU

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Mol	Chain	Res	Type
18	R	46	GLU
18	R	58	LEU
18	R	70	ILE
18	R	78	LEU
18	R	82	THR
18	R	86	VAL
18	R	87	ARG
18	R	88	LYS
19	S	4	SER
19	S	7	LYS
19	S	11	VAL
19	S	14	HIS
19	S	15	LEU
19	S	16	LEU
19	S	17	GLU
19	S	27	GLU
19	S	29	ARG
19	S	31	ILE
19	S	37	ARG
19	S	39	THR
19	S	43	GLU
19	S	58	VAL
19	S	64	GLU
19	S	71	LEU
20	T	8	ARG
20	T	9	ASN
20	T	10	LEU
20	T	11	SER
20	T	13	LEU
20	T	15	ARG
20	T	17	ARG
20	T	19	SER
20	T	20	LEU
20	T	24	LEU
20	T	33	ILE
20	T	45	GLN
20	T	55	ILE
20	T	62	LEU
20	T	72	LEU
20	T	74	LYS
20	T	75	ASN
20	T	80	ARG

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Mol	Chain	Res	Type
20	T	85	MET
20	T	86	ARG
20	T	87	LYS
20	T	91	LEU
20	T	99	LEU
20	T	100	ILE
20	T	104	LEU
21	U	10	ARG
21	U	15	ARG
21	U	25	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	212	GLN
3	C	6	HIS
4	D	125	HIS
5	E	65	ASN
7	G	37	ASN
9	I	73	GLN
12	L	75	HIS
13	M	101	GLN
15	O	42	HIS
16	P	16	HIS
19	S	23	ASN
19	S	57	HIS
20	T	9	ASN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1503/1522 (98%)	377 (25%)	0
22	V	3/4 (75%)	1 (33%)	0
23	W	10/11 (90%)	2 (20%)	0
24	a	7/8 (87%)	4 (57%)	0
25	b	2/3 (66%)	0	0
All	All	1525/1548 (98%)	384 (25%)	0

All (384) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	7	G
1	A	9	G
1	A	16	A
1	A	31	G
1	A	32	A
1	A	33	A
1	A	34	C
1	A	39	G
1	A	47	C
1	A	48	C
1	A	51	A
1	A	81	U
1	A	82	U
1	A	88	A
1	A	89	C
1	A	90	U
1	A	91	C
1	A	95	U
1	A	99	C
1	A	105	G
1	A	108	G
1	A	109	A
1	A	115	G
1	A	116	A
1	A	120	A
1	A	121	C
1	A	129(A)	G
1	A	130	A
1	A	131	C
1	A	138	G
1	A	144	G
1	A	151	A
1	A	157	G
1	A	159	G
1	A	162	A
1	A	163	C
1	A	170	U
1	A	173	U
1	A	181	G
1	A	182	U
1	A	183	G
1	A	190(B)	C
1	A	190(E)	U

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Mol	Chain	Res	Type
1	A	190(G)	G
1	A	195	A
1	A	197	A
1	A	199	G
1	A	201	C
1	A	202	U
1	A	216	G
1	A	222	U
1	A	225	C
1	A	230	G
1	A	246	A
1	A	247	G
1	A	250	A
1	A	251	G
1	A	252	U
1	A	253	U
1	A	254	G
1	A	258	G
1	A	260	G
1	A	266	G
1	A	267	C
1	A	276	G
1	A	289	G
1	A	299	G
1	A	301	G
1	A	319	G
1	A	321	A
1	A	328	C
1	A	329	A
1	A	331	G
1	A	332	G
1	A	345	C
1	A	346	G
1	A	352	C
1	A	353	A
1	A	354	G
1	A	367	U
1	A	372	C
1	A	373	A
1	A	381	C
1	A	384	G
1	A	387	U

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Mol	Chain	Res	Type
1	A	388	G
1	A	397	A
1	A	398	C
1	A	406	G
1	A	410	G
1	A	412	A
1	A	413	G
1	A	421	U
1	A	422	C
1	A	424	G
1	A	429	U
1	A	430	A
1	A	435	C
1	A	439	A
1	A	442	C
1	A	443	C
1	A	449	C
1	A	450	G
1	A	452	A
1	A	460	A
1	A	461	C
1	A	462	G
1	A	475	G
1	A	485	G
1	A	497	A
1	A	498	U
1	A	500	G
1	A	509	A
1	A	510	A
1	A	511	C
1	A	517	G
1	A	518	C
1	A	519	C
1	A	520	A
1	A	527	7MG
1	A	530	G
1	A	532	A
1	A	533	A
1	A	544	G
1	A	545	C
1	A	547	A
1	A	550	G

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Mol	Chain	Res	Type
1	A	559	A
1	A	560	U
1	A	561	U
1	A	562	C
1	A	563	A
1	A	564	C
1	A	566	G
1	A	568	G
1	A	569	C
1	A	571	U
1	A	572	A
1	A	573	A
1	A	575	G
1	A	576	G
1	A	578	C
1	A	587	G
1	A	588	G
1	A	607	A
1	A	624	C
1	A	629	G
1	A	631	G
1	A	644	G
1	A	651	C
1	A	653	A
1	A	661	G
1	A	665	A
1	A	671	G
1	A	673	G
1	A	675	A
1	A	687	A
1	A	688	G
1	A	695	A
1	A	698	G
1	A	701	C
1	A	702	A
1	A	704	A
1	A	721	G
1	A	723	U
1	A	724	G
1	A	728	A
1	A	731	G
1	A	734	G

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Mol	Chain	Res	Type
1	A	741	G
1	A	747	C
1	A	748	C
1	A	752	G
1	A	755	G
1	A	777	A
1	A	785	G
1	A	786	G
1	A	788	U
1	A	789	U
1	A	792	A
1	A	793	U
1	A	794	A
1	A	795	C
1	A	804	U
1	A	812	C
1	A	813	U
1	A	815	A
1	A	816	A
1	A	817	C
1	A	827	U
1	A	828	A
1	A	829	G
1	A	839	U
1	A	840	C
1	A	841	U
1	A	848	C
1	A	851	G
1	A	866	C
1	A	867	G
1	A	868	C
1	A	869	G
1	A	873	A
1	A	889	A
1	A	902	G
1	A	905	U
1	A	914	A
1	A	922	G
1	A	926	G
1	A	927	G
1	A	933	G
1	A	934	C

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Mol	Chain	Res	Type
1	A	935	A
1	A	944	G
1	A	950	U
1	A	954	G
1	A	961	U
1	A	966	M2G
1	A	967	5MC
1	A	968	A
1	A	969	A
1	A	971	G
1	A	974	A
1	A	975	A
1	A	976	G
1	A	977	A
1	A	978	A
1	A	984	C
1	A	985	C
1	A	992	U
1	A	993	G
1	A	1003(A)	G
1	A	1004	A
1	A	1005	A
1	A	1006	C
1	A	1021	G
1	A	1025	U
1	A	1026	G
1	A	1027	C
1	A	1028	C
1	A	1030(B)	C
1	A	1030(C)	G
1	A	1045	C
1	A	1048	G
1	A	1050	G
1	A	1052	U
1	A	1053	G
1	A	1054	C
1	A	1055	A
1	A	1064	G
1	A	1065	U
1	A	1066	C
1	A	1068	G
1	A	1078	U

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Mol	Chain	Res	Type
1	A	1079	G
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	1104	G
1	A	1111	A
1	A	1122	U
1	A	1124	G
1	A	1125	U
1	A	1126	U
1	A	1127	G
1	A	1129	C
1	A	1130	A
1	A	1131	G
1	A	1137	C
1	A	1138	G
1	A	1139	G
1	A	1141	C
1	A	1142	G
1	A	1143	G
1	A	1159	U
1	A	1162	C
1	A	1164	G
1	A	1171	G
1	A	1178	G
1	A	1181	G
1	A	1182	G
1	A	1183	A
1	A	1184	G
1	A	1190	G
1	A	1191	A
1	A	1193	G
1	A	1196	U
1	A	1198	G
1	A	1200	C
1	A	1201	A
1	A	1202	G
1	A	1206	G
1	A	1211	U
1	A	1212	U
1	A	1213	A
1	A	1214	C

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Mol	Chain	Res	Type
1	A	1215	G
1	A	1225	A
1	A	1226	C
1	A	1227	A
1	A	1235	U
1	A	1238	A
1	A	1245	A
1	A	1249	C
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	1270	C
1	A	1273	G
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	1288	A
1	A	1300	G
1	A	1301	U
1	A	1302	U
1	A	1303	C
1	A	1304	G
1	A	1305	G
1	A	1312	G
1	A	1313	U
1	A	1317	C
1	A	1318	A
1	A	1319	A
1	A	1320	C
1	A	1322	C
1	A	1328	C
1	A	1338	G
1	A	1348	U
1	A	1353	G
1	A	1356	G
1	A	1359	C

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Mol	Chain	Res	Type
1	A	1360	A
1	A	1361	G
1	A	1362	C
1	A	1363	A
1	A	1370	G
1	A	1379	G
1	A	1381	U
1	A	1382	C
1	A	1393	U
1	A	1394	A
1	A	1397	C
1	A	1398	A
1	A	1399	C
1	A	1400	5MC
1	A	1401	G
1	A	1406	U
1	A	1407	5MC
1	A	1414	U
1	A	1418	A
1	A	1419	G
1	A	1420	C
1	A	1442	G
1	A	1443	G
1	A	1447	G
1	A	1451	A
1	A	1455	G
1	A	1478	C
1	A	1487	G
1	A	1494	G
1	A	1497	G
1	A	1502	A
1	A	1504	G
1	A	1505	G
1	A	1506	U
1	A	1507	A
1	A	1526	G
1	A	1529	G
1	A	1530	G
1	A	1534	C
1	A	1538	C
22	V	2	U
23	W	31	C

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Mol	Chain	Res	Type
23	W	33	U
24	a	35	G
24	a	37	A
24	a	39	G
24	a	40	PSU

There are no RNA pucker outliers to report.

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z  > 2$	Counts	RMSZ	# $ Z  > 2$
1	2MG	A	1207	1	19,26,27	2.89	6 (31%)	20,38,41	2.34	2 (10%)
1	5MC	A	1400	1	15,22,23	1.56	3 (20%)	17,32,35	0.85	0
1	4OC	A	1402	1	16,23,24	1.79	5 (31%)	19,32,35	1.15	1 (5%)
1	5MC	A	1404	1	15,22,23	1.06	1 (6%)	17,32,35	1.17	2 (11%)
1	5MC	A	1407	1	15,22,23	1.94	2 (13%)	17,32,35	1.11	1 (5%)
1	UR3	A	1498	1	14,22,23	0.83	1 (7%)	16,32,35	1.06	1 (6%)
1	MA6	A	1518[A]	1	16,26,27	1.33	3 (18%)	18,38,41	1.03	2 (11%)
1	MA6	A	1518[B]	1	16,26,27	1.00	1 (6%)	18,38,41	1.00	2 (11%)
1	MA6	A	1519[A]	1	16,26,27	1.07	2 (12%)	18,38,41	1.21	2 (11%)
1	MA6	A	1519[B]	1	16,26,27	1.77	4 (25%)	18,38,41	1.02	2 (11%)
1	PSU	A	1540	1	16,21,22	1.13	1 (6%)	20,30,33	3.55	5 (25%)
1	PSU	A	516	1	16,21,22	1.41	2 (12%)	20,30,33	3.70	5 (25%)
1	7MG	A	527	1	20,26,27	3.43	8 (40%)	22,39,42	1.43	4 (18%)
1	M2G	A	966	1	20,27,28	1.40	4 (20%)	21,40,43	2.35	5 (23%)
1	5MC	A	967	1	15,22,23	0.96	0	17,32,35	0.98	1 (5%)
12	0TD	L	92	12	5,9,10	2.35	1 (20%)	3,11,13	3.06	2 (66%)
23	PSU	W	40	23	16,21,22	1.05	2 (12%)	20,30,33	3.65	7 (35%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
24	PSU	a	40	24,1	16,21,22	1.68	2 (12%)	20,30,33	3.87	6 (30%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	2MG	A	1207	1	-	0/5/27/28	0/3/3/3
1	5MC	A	1400	1	-	0/3/25/26	0/2/2/2
1	4OC	A	1402	1	-	0/7/29/30	0/2/2/2
1	5MC	A	1404	1	-	0/3/25/26	0/2/2/2
1	5MC	A	1407	1	-	0/3/25/26	0/2/2/2
1	UR3	A	1498	1	-	0/3/25/26	0/2/2/2
1	MA6	A	1518[A]	1	-	0/7/29/30	0/3/3/3
1	MA6	A	1518[B]	1	-	0/7/29/30	0/3/3/3
1	MA6	A	1519[A]	1	-	0/7/29/30	0/3/3/3
1	MA6	A	1519[B]	1	-	0/7/29/30	0/3/3/3
1	PSU	A	1540	1	-	0/7/25/26	0/2/2/2
1	PSU	A	516	1	-	0/7/25/26	0/2/2/2
1	7MG	A	527	1	-	0/7/37/38	0/3/3/3
1	M2G	A	966	1	-	0/7/29/30	0/3/3/3
1	5MC	A	967	1	-	0/3/25/26	0/2/2/2
12	0TD	L	92	12	-	0/2/12/14	0/0/0/0
23	PSU	W	40	23	-	0/7/25/26	0/2/2/2
24	PSU	a	40	24,1	-	0/7/25/26	0/2/2/2

All (48) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	527	7MG	C8-N9	-9.11	1.32	1.45
1	A	527	7MG	O5'-C5'	-4.20	1.38	1.44
1	A	527	7MG	CM7-N7	-2.82	1.41	1.46
1	A	1207	2MG	O5'-C5'	-2.64	1.41	1.44
1	A	527	7MG	C8-N7	-2.50	1.32	1.43
1	A	966	M2G	O5'-C5'	-2.48	1.41	1.44
1	A	1498	UR3	C6-N1	-2.26	1.32	1.35
1	A	1402	4OC	C4-N3	-2.23	1.30	1.34
1	A	1402	4OC	C4-N4	-2.15	1.31	1.36
1	A	1402	4OC	O5'-C5'	-2.14	1.41	1.44
23	W	40	PSU	C5-C1'	-2.11	1.50	1.52
1	A	1519[A]	MA6	C5-C4	2.02	1.45	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	527	7MG	C6-N1	2.05	1.36	1.33
1	A	966	M2G	C4-N3	2.25	1.39	1.35
1	A	1404	5MC	C5-C4	2.31	1.44	1.41
1	A	966	M2G	C2-N1	2.33	1.38	1.34
1	A	1207	2MG	C5-C4	2.38	1.45	1.40
1	A	1519[A]	MA6	C2-N1	2.42	1.38	1.33
1	A	1518[A]	MA6	C4-N3	2.46	1.39	1.35
1	A	1407	5MC	C2-N3	2.57	1.43	1.38
23	W	40	PSU	C4-N3	2.71	1.37	1.33
1	A	1518[B]	MA6	C2-N1	2.74	1.39	1.33
1	A	1519[B]	MA6	C4-N3	2.75	1.39	1.35
24	a	40	PSU	C4-N3	2.77	1.38	1.33
1	A	1402	4OC	CM4-N4	2.82	1.50	1.45
1	A	1518[A]	MA6	C2-N1	2.82	1.39	1.33
1	A	1400	5MC	C4-N4	2.85	1.41	1.34
1	A	516	PSU	C5-C1'	2.92	1.54	1.52
1	A	1518[A]	MA6	C5-C4	2.92	1.47	1.40
1	A	1519[B]	MA6	C5-C4	3.14	1.47	1.40
1	A	1400	5MC	C2-N3	3.22	1.44	1.38
1	A	1207	2MG	C2-N1	3.22	1.45	1.34
1	A	1400	5MC	C5-C4	3.25	1.46	1.41
1	A	1540	PSU	C4-N3	3.33	1.39	1.33
1	A	516	PSU	C4-N3	3.48	1.39	1.33
1	A	1519[B]	MA6	C2-N3	3.55	1.38	1.32
1	A	1207	2MG	C6-C5	3.61	1.48	1.41
1	A	966	M2G	C6-N1	3.99	1.40	1.33
1	A	1519[B]	MA6	C2-N1	4.22	1.41	1.33
1	A	1402	4OC	C2-N3	4.28	1.46	1.38
1	A	527	7MG	C4-N3	4.34	1.39	1.34
1	A	527	7MG	C2-N2	4.51	1.43	1.34
12	L	92	0TD	CA-C	4.76	1.56	1.50
24	a	40	PSU	C5-C1'	5.23	1.56	1.52
1	A	1407	5MC	C5-C4	6.28	1.50	1.41
1	A	1207	2MG	C6-N1	6.88	1.45	1.33
1	A	527	7MG	C6-C5	7.83	1.50	1.41
1	A	1207	2MG	C2-N2	8.07	1.41	1.34

All (50) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	a	40	PSU	N1-C2-N3	-13.74	118.52	128.40
1	A	516	PSU	N1-C2-N3	-12.80	119.19	128.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1540	PSU	N1-C2-N3	-12.57	119.36	128.40
23	W	40	PSU	N1-C2-N3	-11.42	120.19	128.40
1	A	1207	2MG	C5-C6-N1	-9.06	110.58	123.48
1	A	966	M2G	C5-C6-N1	-7.96	112.14	123.48
23	W	40	PSU	C5-C4-N3	-7.66	119.14	125.43
1	A	516	PSU	C5-C4-N3	-6.14	120.39	125.43
1	A	1540	PSU	C5-C4-N3	-5.72	120.74	125.43
12	L	92	0TD	CSB-SB-CB	-4.31	93.56	101.60
1	A	1402	4OC	CM4-N4-C4	-3.96	119.52	122.94
24	a	40	PSU	C5-C4-N3	-3.69	122.40	125.43
24	a	40	PSU	C5-C6-N1	-3.52	119.83	124.39
23	W	40	PSU	C5-C1'-C2'	-3.36	109.75	115.55
23	W	40	PSU	C5-C6-N1	-3.23	120.20	124.39
1	A	527	7MG	C5-C4-N3	-3.09	121.31	126.47
1	A	1407	5MC	N4-C4-N3	-3.03	112.52	117.00
23	W	40	PSU	O4'-C1'-C5	-2.64	105.84	109.93
1	A	966	M2G	C2-N3-C4	-2.49	112.27	115.11
12	L	92	0TD	C-CA-N	-2.41	105.00	109.86
1	A	966	M2G	N1-C2-N2	-2.39	114.69	117.16
1	A	1498	UR3	C5-C4-N3	-2.32	112.57	117.34
1	A	966	M2G	CM1-N2-C2	-2.14	119.30	121.34
1	A	1540	PSU	C5-C6-N1	-2.14	121.62	124.39
1	A	1404	5MC	CM5-C5-C6	2.02	122.70	118.67
1	A	527	7MG	C6-N1-C2	2.03	118.98	116.06
1	A	1518[B]	MA6	N3-C2-N1	2.08	130.67	128.86
1	A	1519[B]	MA6	C2-N1-C6	2.14	117.08	111.82
1	A	1519[A]	MA6	C2-N1-C6	2.18	117.16	111.82
1	A	1404	5MC	C5-C4-N3	2.21	124.79	121.22
1	A	1518[A]	MA6	C2-N1-C6	2.23	117.30	111.82
1	A	1519[B]	MA6	N3-C2-N1	2.25	130.81	128.86
1	A	1518[B]	MA6	C2-N1-C6	2.31	117.48	111.82
1	A	516	PSU	O4'-C1'-C2'	2.31	108.16	104.45
1	A	1519[A]	MA6	N3-C2-N1	2.41	130.96	128.86
1	A	1518[A]	MA6	N3-C2-N1	2.50	131.04	128.86
1	A	527	7MG	N3-C4-N9	2.50	130.18	126.98
1	A	967	5MC	CM5-C5-C6	2.76	124.18	118.67
1	A	527	7MG	C2-N3-C4	2.78	121.76	113.95
23	W	40	PSU	C6-N1-C2	3.11	120.33	115.36
1	A	516	PSU	C6-N1-C2	3.32	120.68	115.36
1	A	1540	PSU	C6-N1-C2	3.47	120.91	115.36
1	A	1207	2MG	C6-N1-C2	4.25	122.80	115.18
24	a	40	PSU	C5-C1'-C2'	4.71	123.66	115.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	a	40	PSU	C6-N1-C2	5.17	123.63	115.36
24	a	40	PSU	C4-N3-C2	5.36	119.85	115.16
1	A	966	M2G	C6-N1-C2	5.48	122.71	116.18
1	A	1540	PSU	C4-N3-C2	5.78	120.22	115.16
23	W	40	PSU	C4-N3-C2	5.82	120.25	115.16
1	A	516	PSU	C4-N3-C2	6.47	120.82	115.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

16 monomers are involved in 89 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1207	2MG	11	0
1	A	1400	5MC	5	1
1	A	1402	4OC	5	0
1	A	1404	5MC	5	0
1	A	1407	5MC	10	0
1	A	1498	UR3	8	0
1	A	1518[A]	MA6	10	0
1	A	1518[B]	MA6	9	0
1	A	1519[A]	MA6	18	0
1	A	1519[B]	MA6	11	0
1	A	516	PSU	1	0
1	A	527	7MG	1	0
1	A	966	M2G	3	0
1	A	967	5MC	4	0
12	L	92	0TD	2	0
23	W	40	PSU	5	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 347 ligands modelled in this entry, 346 are monoatomic - leaving 1 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	$\# Z  > 2$
27	SRY	A	1928	-	39,42,42	2.27	10 (25%)	45,63,63	2.62	16 (35%)

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
27	SRY	A	1928	-	-	0/20/87/87	0/3/3/3

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
27	A	1928	SRY	O53-C53	-3.58	1.35	1.44
27	A	1928	SRY	C23-N23	-3.06	1.42	1.47
27	A	1928	SRY	C11-N11	-2.49	1.41	1.45
27	A	1928	SRY	C21-C11	-2.38	1.48	1.53
27	A	1928	SRY	O51-C51	-2.08	1.38	1.43
27	A	1928	SRY	C21-C31	-2.02	1.49	1.53
27	A	1928	SRY	CA1-NB1	2.33	1.44	1.34
27	A	1928	SRY	CD1-NE1	2.49	1.45	1.34
27	A	1928	SRY	CA1-N11	5.72	1.43	1.33
27	A	1928	SRY	CD1-N31	9.25	1.49	1.33

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	A	1928	SRY	C43-C33-C23	-7.42	99.32	110.33
27	A	1928	SRY	C61-C11-N11	-6.32	98.51	110.61
27	A	1928	SRY	C12-O42-C42	-6.09	98.71	108.48
27	A	1928	SRY	C13-O13-C22	-5.35	106.79	116.29
27	A	1928	SRY	O51-C51-C61	-3.14	103.52	110.36
27	A	1928	SRY	O53-C53-C63	-2.57	100.26	106.41
27	A	1928	SRY	C63-C53-C43	-2.17	107.92	113.00
27	A	1928	SRY	O63-C63-C53	-2.11	104.24	111.34
27	A	1928	SRY	O51-C51-C41	2.09	114.63	109.87

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	A	1928	SRY	O43-C43-C33	2.43	115.64	110.36
27	A	1928	SRY	O21-C21-C31	3.01	115.72	109.61
27	A	1928	SRY	C51-C61-C11	3.19	115.05	110.33
27	A	1928	SRY	O32-C32-C22	3.51	119.76	111.57
27	A	1928	SRY	O53-C53-C43	3.91	116.86	109.66
27	A	1928	SRY	O41-C41-C51	4.07	116.99	107.19
27	A	1928	SRY	O53-C13-C23	4.15	119.15	110.65

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 14 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
27	A	1928	SRY	14	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	1500/1522 (98%)	-0.49	2 (0%) 95 94	80, 129, 232, 327	0
2	B	236/256 (92%)	-0.17	3 (1%) 77 69	62, 153, 220, 247	0
3	C	207/239 (86%)	-0.25	5 (2%) 59 49	94, 191, 226, 244	0
4	D	208/209 (99%)	-0.24	5 (2%) 59 49	105, 149, 198, 214	0
5	E	151/162 (93%)	-0.46	0 100 100	80, 114, 166, 193	0
6	F	101/101 (100%)	-0.49	1 (0%) 82 75	110, 150, 182, 226	0
7	G	155/156 (99%)	-0.41	3 (1%) 67 59	121, 160, 223, 238	0
8	H	138/138 (100%)	-0.45	0 100 100	75, 104, 138, 155	0
9	I	127/128 (99%)	0.08	3 (2%) 59 49	125, 184, 217, 240	0
10	J	99/105 (94%)	0.14	4 (4%) 39 31	81, 203, 272, 295	0
11	K	117/129 (90%)	-0.42	0 100 100	88, 130, 160, 167	0
12	L	124/135 (91%)	0.03	5 (4%) 39 31	97, 136, 168, 247	0
13	M	118/126 (93%)	0.05	5 (4%) 37 29	127, 158, 192, 211	0
14	N	60/61 (98%)	-0.21	1 (1%) 70 62	144, 169, 210, 246	0
15	O	88/89 (98%)	-0.01	2 (2%) 61 52	94, 127, 182, 225	0
16	P	84/88 (95%)	-0.24	0 100 100	96, 126, 164, 239	0
17	Q	100/105 (95%)	-0.34	0 100 100	83, 111, 150, 189	0
18	R	71/88 (80%)	-0.32	0 100 100	95, 132, 178, 229	0
19	S	81/93 (87%)	0.16	2 (2%) 58 47	84, 184, 228, 234	0
20	T	99/106 (93%)	-0.28	0 100 100	95, 126, 167, 212	0
21	U	25/27 (92%)	0.40	2 (8%) 13 11	77, 163, 192, 220	0
22	V	4/4 (100%)	3.92	4 (100%) 0 0	263, 267, 272, 275	0
23	W	10/11 (90%)	7.09	10 (100%) 0 0	234, 291, 345, 387	5 (50%)
24	a	7/8 (87%)	0.68	1 (14%) 3 4	200, 217, 290, 330	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
25	b	3/3 (100%)	1.04	0 100 100	172, 172, 206, 218	0
All	All	3913/4089 (95%)	-0.29	58 (1%) 74 65	62, 140, 222, 387	5 (0%)

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
23	W	32	C	13.3
23	W	31	C	8.8
23	W	33	U	8.1
1	A	1129	C	8.0
23	W	35	G	7.6
23	W	30	G	7.6
12	L	129	ALA	7.1
15	O	89	GLY	7.0
23	W	38	A	6.0
23	W	37	A	6.0
22	V	2	U	5.1
22	V	3	U	4.9
23	W	36	A	4.9
23	W	34	G	4.9
21	U	18	TYR	4.6
10	J	33	GLN	4.2
10	J	34	VAL	3.8
23	W	39	G	3.7
9	I	15	ALA	3.6
12	L	65	GLU	3.4
22	V	4	U	3.3
6	F	101	ALA	3.2
7	G	83	ALA	3.1
13	M	2	ALA	3.1
7	G	84	ASN	3.0
13	M	117	VAL	2.9
12	L	33	ARG	2.9
3	C	157	ILE	2.9
7	G	82	GLY	2.9
3	C	158	GLY	2.9
12	L	128	ALA	2.8
3	C	155	GLY	2.8
14	N	12	ARG	2.7
4	D	42	GLN	2.7
1	A	82	U	2.6
10	J	74	ILE	2.6

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Mol	Chain	Res	Type	RSRZ
4	D	13	ARG	2.5
19	S	38	SER	2.5
3	C	189	ALA	2.5
3	C	193	TYR	2.5
24	a	34	G	2.5
15	O	88	ARG	2.4
9	I	65	VAL	2.4
22	V	1	U	2.3
13	M	116	THR	2.3
13	M	15	VAL	2.3
10	J	87	THR	2.3
2	B	72	GLY	2.3
19	S	12	ASP	2.3
12	L	64	TYR	2.2
4	D	43	HIS	2.2
21	U	17	THR	2.2
9	I	66	ARG	2.1
13	M	5	ALA	2.1
2	B	188	ALA	2.0
4	D	45	GLN	2.0
4	D	40	PRO	2.0
2	B	203	GLY	2.0

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

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
1	5MC	A	967	21/22	0.97	0.12	-	117,131,145,146	0
1	5MC	A	1404	21/22	0.95	0.17	-	102,129,148,149	0
1	7MG	A	527	24/25	0.97	0.17	-	91,114,123,126	0
1	M2G	A	966	25/26	0.94	0.18	-	122,137,142,145	0
1	2MG	A	1207	24/25	0.96	0.15	-	154,167,200,202	0
1	UR3	A	1498	21/22	0.95	0.25	-	111,124,183,193	0
1	MA6	A	1518[A]	24/25	0.94	0.20	-	110,122,127,131	24
1	5MC	A	1407	21/22	0.96	0.11	-	127,152,158,162	0
12	0TD	L	92	10/11	0.99	0.22	-	113,121,127,289	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
23	PSU	W	40	20/21	0.68	0.33	-	291,301,325,326	0
1	PSU	A	516	20/21	0.96	0.10	-	123,147,168,168	0
1	4OC	A	1402	22/23	0.92	0.21	-	104,119,127,142	0
1	PSU	A	1540	20/21	0.71	0.35	-	253,269,289,293	0
1	MA6	A	1519[A]	24/25	0.96	0.30	-	100,115,125,126	24
1	MA6	A	1518[B]	24/25	0.94	0.20	-	107,122,137,148	24
1	MA6	A	1519[B]	24/25	0.96	0.30	-	101,116,129,130	24
24	PSU	a	40	20/21	0.81	0.32	-	208,236,258,262	0
1	5MC	A	1400	21/22	0.95	0.17	-	103,130,148,159	0

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
26	MG	A	1870	1/1	0.94	0.48	51.50	406,406,406,406	0
26	MG	A	1834	1/1	0.83	0.93	45.54	412,412,412,412	1
26	MG	A	1759	1/1	0.78	0.86	33.54	86,86,86,86	0
26	MG	A	1804	1/1	0.89	0.50	22.88	447,447,447,447	0
26	MG	A	1670	1/1	0.86	0.47	15.78	234,234,234,234	0
26	MG	A	1904	1/1	0.64	0.65	15.63	97,97,97,97	0
26	MG	A	1728	1/1	0.82	0.86	14.98	114,114,114,114	0
26	MG	A	1761	1/1	0.98	0.59	12.51	105,105,105,105	0
26	MG	N	102	1/1	0.79	0.54	11.89	107,107,107,107	0
26	MG	A	1740	1/1	0.84	0.56	10.67	93,93,93,93	0
26	MG	A	1812	1/1	0.94	0.73	10.31	444,444,444,444	0
26	MG	E	201	1/1	0.94	0.34	7.43	95,95,95,95	0
26	MG	A	1659	1/1	0.94	0.30	6.60	90,90,90,90	0
26	MG	A	1655	1/1	0.89	0.30	6.12	125,125,125,125	0
26	MG	A	1743	1/1	0.79	0.35	6.08	105,105,105,105	0
26	MG	A	1665	1/1	0.63	0.67	5.79	117,117,117,117	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
26	MG	A	1869	1/1	0.91	0.27	5.22	431,431,431,431	0
26	MG	A	1784	1/1	0.85	0.28	5.05	122,122,122,122	0
26	MG	A	1888	1/1	0.93	0.32	4.30	89,89,89,89	0
26	MG	A	1656	1/1	0.98	0.22	4.14	236,236,236,236	0
26	MG	A	1637	1/1	0.95	0.28	3.53	228,228,228,228	0
26	MG	A	1721	1/1	0.96	0.26	3.42	92,92,92,92	0
26	MG	A	1900	1/1	0.84	0.33	3.39	93,93,93,93	0
26	MG	Q	201	1/1	0.90	0.47	3.33	145,145,145,145	0
26	MG	A	1621	1/1	0.92	0.16	3.23	131,131,131,131	0
26	MG	A	1709	1/1	0.93	0.21	3.12	245,245,245,245	0
26	MG	A	1764	1/1	0.98	0.44	2.99	78,78,78,78	0
26	MG	A	1715	1/1	0.96	0.22	2.93	229,229,229,229	0
26	MG	A	1701	1/1	0.97	0.22	2.68	108,108,108,108	0
26	MG	A	1708	1/1	0.96	0.22	2.42	152,152,152,152	0
26	MG	A	1741	1/1	0.95	0.16	2.26	105,105,105,105	0
26	MG	A	1733	1/1	0.98	0.19	2.25	70,70,70,70	0
26	MG	A	1768	1/1	0.94	0.35	2.25	107,107,107,107	0
26	MG	A	1723	1/1	0.84	0.26	2.23	117,117,117,117	0
26	MG	E	204	1/1	0.80	0.26	2.11	128,128,128,128	0
26	MG	A	1763	1/1	0.92	0.29	2.02	120,120,120,120	0
26	MG	A	1732	1/1	0.88	0.20	2.02	100,100,100,100	0
26	MG	A	1650	1/1	0.94	0.20	1.96	151,151,151,151	0
26	MG	A	1757	1/1	0.93	0.21	1.66	88,88,88,88	0
26	MG	A	1895	1/1	0.91	0.19	1.55	106,106,106,106	0
26	MG	A	1796	1/1	0.90	0.22	1.36	416,416,416,416	0
26	MG	A	1720	1/1	0.89	0.25	1.30	74,74,74,74	0
28	ZN	D	301	1/1	0.98	0.29	0.49	138,138,138,138	0
26	MG	A	1608	1/1	0.98	0.21	0.23	73,73,73,73	0
26	MG	A	1750	1/1	0.98	0.19	0.20	74,74,74,74	0
26	MG	A	1646	1/1	0.93	0.17	0.19	136,136,136,136	0
26	MG	D	303	1/1	0.96	0.21	0.17	104,104,104,104	0
26	MG	A	1847	1/1	0.98	0.18	0.02	441,441,441,441	0
26	MG	A	1617	1/1	0.89	0.22	-0.04	85,85,85,85	0
26	MG	A	1859	1/1	0.99	0.16	-0.05	427,427,427,427	0
26	MG	A	1919	1/1	0.91	0.18	-0.06	78,78,78,78	0
26	MG	A	1746	1/1	0.94	0.16	-0.08	104,104,104,104	0
26	MG	A	1736	1/1	0.98	0.15	-0.25	123,123,123,123	0
26	MG	A	1702	1/1	0.95	0.13	-0.32	279,279,279,279	0
28	ZN	N	101	1/1	0.97	0.16	-0.33	164,164,164,164	0
26	MG	A	1920	1/1	0.91	0.07	-0.38	138,138,138,138	0
26	MG	A	1776	1/1	0.96	0.17	-0.49	96,96,96,96	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
26	MG	A	1697	1/1	0.87	0.18	-0.54	135,135,135,135	0
26	MG	A	1693	1/1	0.97	0.10	-0.76	108,108,108,108	0
26	MG	A	1616	1/1	0.98	0.17	-0.77	63,63,63,63	0
27	SRY	A	1928	40/40	0.96	0.15	-0.86	70,100,124,130	0
26	MG	A	1775	1/1	0.97	0.12	-0.86	79,79,79,79	0
26	MG	A	1689	1/1	0.97	0.14	-0.92	126,126,126,126	0
26	MG	A	1786	1/1	0.91	0.09	-1.10	109,109,109,109	0
26	MG	A	1662	1/1	0.98	0.12	-1.38	123,123,123,123	0
26	MG	A	1713	1/1	0.99	0.11	-1.42	211,211,211,211	0
26	MG	A	1703	1/1	0.99	0.14	-1.45	97,97,97,97	0
26	MG	A	1672	1/1	0.98	0.10	-1.48	166,166,166,166	0
26	MG	A	1731	1/1	0.95	0.18	-1.74	68,68,68,68	0
26	MG	A	1623	1/1	0.99	0.13	-1.97	67,67,67,67	0
26	MG	A	1607	1/1	0.99	0.11	-2.19	154,154,154,154	0
26	MG	A	1638	1/1	0.99	0.13	-2.52	86,86,86,86	0
26	MG	A	1631	1/1	0.96	0.09	-2.75	158,158,158,158	0
26	MG	A	1643	1/1	0.95	0.08	-2.77	71,71,71,71	0
26	MG	A	1827	1/1	0.99	0.08	-2.79	251,251,251,251	0
26	MG	A	1906	1/1	0.96	0.13	-3.03	64,64,64,64	0
26	MG	A	1690	1/1	0.98	0.07	-3.29	114,114,114,114	0
26	MG	A	1611	1/1	1.00	0.10	-4.21	113,113,113,113	0
26	MG	A	1705	1/1	0.96	0.13	-4.40	74,74,74,74	0
26	MG	A	1835	1/1	0.95	0.13	-	309,309,309,309	0
26	MG	E	203	1/1	0.96	0.12	-	101,101,101,101	0
26	MG	A	1667	1/1	0.98	0.18	-	119,119,119,119	0
26	MG	G	201	1/1	0.61	0.83	-	117,117,117,117	0
26	MG	A	1640	1/1	0.93	0.22	-	172,172,172,172	0
26	MG	A	1907	1/1	0.91	0.27	-	120,120,120,120	0
26	MG	A	1632	1/1	0.78	0.34	-	248,248,248,248	0
26	MG	A	1606	1/1	0.97	0.41	-	87,87,87,87	0
26	MG	A	1716	1/1	0.98	0.24	-	132,132,132,132	0
26	MG	A	1781	1/1	0.73	0.35	-	104,104,104,104	0
26	MG	A	1845	1/1	0.91	0.31	-	410,410,410,410	0
26	MG	A	1829	1/1	0.90	0.28	-	489,489,489,489	0
26	MG	A	1921	1/1	0.68	0.39	-	84,84,84,84	0
26	MG	A	1657	1/1	0.89	0.34	-	220,220,220,220	0
26	MG	A	1603	1/1	0.97	0.13	-	277,277,277,277	0
26	MG	A	1896	1/1	0.96	0.13	-	114,114,114,114	0
26	MG	A	1649	1/1	0.83	0.33	-	84,84,84,84	0
26	MG	A	1725	1/1	0.90	0.26	-	92,92,92,92	0
26	MG	A	1682	1/1	0.87	0.07	-	242,242,242,242	0
26	MG	A	1604	1/1	0.94	0.25	-	91,91,91,91	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
26	MG	A	1807	1/1	0.84	0.47	-	517,517,517,517	1
26	MG	A	1860	1/1	0.93	0.22	-	460,460,460,460	0
26	MG	A	1626	1/1	0.99	0.26	-	245,245,245,245	0
26	MG	A	1668	1/1	0.97	0.25	-	173,173,173,173	0
26	MG	A	1855	1/1	0.93	0.18	-	401,401,401,401	0
26	MG	A	1612	1/1	0.95	0.45	-	281,281,281,281	0
26	MG	A	1816	1/1	0.92	0.44	-	454,454,454,454	0
26	MG	A	1853	1/1	0.92	0.25	-	502,502,502,502	0
26	MG	A	1926	1/1	0.51	0.58	-	116,116,116,116	0
26	MG	A	1858	1/1	0.99	0.23	-	355,355,355,355	0
26	MG	A	1641	1/1	0.95	0.17	-	102,102,102,102	0
26	MG	A	1633	1/1	0.98	0.18	-	118,118,118,118	0
26	MG	A	1675	1/1	0.53	1.12	-	122,122,122,122	0
26	MG	A	1873	1/1	0.98	0.12	-	361,361,361,361	0
26	MG	A	1753	1/1	0.93	0.24	-	109,109,109,109	0
26	MG	A	1622	1/1	0.62	0.51	-	81,81,81,81	0
26	MG	H	201	1/1	0.82	0.33	-	67,67,67,67	0
26	MG	A	1609	1/1	0.92	0.07	-	157,157,157,157	0
26	MG	A	1780	1/1	0.96	0.33	-	119,119,119,119	0
26	MG	A	1910	1/1	0.10	0.29	-	120,120,120,120	0
26	MG	A	1914	1/1	0.68	1.02	-	99,99,99,99	0
26	MG	A	1771	1/1	0.96	0.57	-	102,102,102,102	0
26	MG	A	1918	1/1	0.92	0.20	-	75,75,75,75	0
26	MG	A	1848	1/1	0.93	0.21	-	407,407,407,407	0
26	MG	A	1676	1/1	0.90	0.28	-	158,158,158,158	0
26	MG	A	1801	1/1	0.95	0.20	-	464,464,464,464	0
26	MG	A	1838	1/1	0.88	0.56	-	538,538,538,538	0
26	MG	A	1688	1/1	0.91	0.41	-	186,186,186,186	0
26	MG	A	1824	1/1	0.94	0.26	-	503,503,503,503	0
26	MG	A	1788	1/1	0.90	0.10	-	285,285,285,285	0
26	MG	A	1864	1/1	0.94	0.20	-	393,393,393,393	0
26	MG	A	1878	1/1	0.89	0.20	-	346,346,346,346	0
26	MG	A	1779	1/1	0.83	0.32	-	102,102,102,102	0
26	MG	A	1830	1/1	0.97	0.27	-	480,480,480,480	0
26	MG	A	1729	1/1	0.59	0.55	-	101,101,101,101	0
26	MG	A	1791	1/1	0.96	0.19	-	283,283,283,283	0
26	MG	A	1844	1/1	0.92	0.09	-	420,420,420,420	0
26	MG	A	1739	1/1	0.91	0.17	-	78,78,78,78	0
26	MG	A	1917	1/1	0.63	0.86	-	128,128,128,128	0
26	MG	A	1880	1/1	0.76	0.49	-	508,508,508,508	0
26	MG	A	1745	1/1	0.89	0.48	-	92,92,92,92	0
26	MG	A	1644	1/1	0.87	0.37	-	127,127,127,127	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
26	MG	A	1724	1/1	0.75	0.54	-	117,117,117,117	0
26	MG	A	1911	1/1	0.99	0.12	-	100,100,100,100	0
26	MG	A	1862	1/1	0.96	0.35	-	268,268,268,268	0
26	MG	A	1680	1/1	0.95	0.23	-	214,214,214,214	0
26	MG	A	1634	1/1	0.97	0.08	-	107,107,107,107	0
26	MG	A	1679	1/1	0.81	0.18	-	369,369,369,369	0
26	MG	A	1698	1/1	0.97	0.18	-	124,124,124,124	0
26	MG	A	1666	1/1	0.98	0.08	-	149,149,149,149	0
26	MG	A	1852	1/1	0.80	0.33	-	450,450,450,450	0
26	MG	A	1794	1/1	0.42	0.27	-	518,518,518,518	0
26	MG	A	1828	1/1	0.97	0.13	-	432,432,432,432	0
26	MG	A	1923	1/1	0.78	0.77	-	86,86,86,86	0
26	MG	A	1727	1/1	0.88	0.65	-	84,84,84,84	0
26	MG	A	1822	1/1	0.95	0.12	-	293,293,293,293	0
26	MG	A	1819	1/1	0.85	0.52	-	493,493,493,493	0
26	MG	A	1793	1/1	0.76	0.27	-	483,483,483,483	0
26	MG	A	1774	1/1	0.73	0.41	-	109,109,109,109	0
26	MG	A	1890	1/1	0.90	0.18	-	112,112,112,112	0
26	MG	A	1814	1/1	0.87	0.18	-	440,440,440,440	0
26	MG	A	1803	1/1	0.98	0.20	-	345,345,345,345	0
26	MG	A	1755	1/1	0.94	0.50	-	74,74,74,74	0
26	MG	A	1815	1/1	0.91	0.23	-	506,506,506,506	0
26	MG	A	1671	1/1	0.92	0.24	-	96,96,96,96	0
26	MG	A	1636	1/1	0.84	0.41	-	88,88,88,88	0
26	MG	A	1898	1/1	0.82	0.63	-	89,89,89,89	0
26	MG	A	1887	1/1	0.79	0.55	-	102,102,102,102	0
26	MG	A	1837	1/1	0.83	0.24	-	469,469,469,469	0
26	MG	A	1823	1/1	0.93	0.11	-	422,422,422,422	0
26	MG	A	1658	1/1	0.96	0.18	-	115,115,115,115	0
26	MG	A	1885	1/1	0.96	0.08	-	84,84,84,84	0
26	MG	A	1642	1/1	0.94	0.28	-	78,78,78,78	0
26	MG	S	101	1/1	0.92	0.11	-	115,115,115,115	0
26	MG	A	1800	1/1	0.96	0.32	-	415,415,415,415	1
26	MG	A	1678	1/1	0.88	0.11	-	217,217,217,217	0
26	MG	A	1851	1/1	0.97	0.27	-	328,328,328,328	0
26	MG	A	1694	1/1	0.85	0.39	-	87,87,87,87	0
26	MG	A	1866	1/1	0.91	0.20	-	434,434,434,434	0
26	MG	A	1901	1/1	0.24	0.36	-	101,101,101,101	0
26	MG	A	1661	1/1	0.91	0.28	-	244,244,244,244	0
26	MG	A	1908	1/1	0.83	0.30	-	81,81,81,81	0
26	MG	A	1899	1/1	0.77	0.33	-	68,68,68,68	0
26	MG	A	1767	1/1	0.91	0.33	-	111,111,111,111	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
26	MG	A	1783	1/1	0.95	0.13	-	110,110,110,110	0
26	MG	A	1663	1/1	0.92	0.14	-	160,160,160,160	0
26	MG	A	1686	1/1	0.98	0.38	-	184,184,184,184	0
26	MG	A	1778	1/1	0.97	0.11	-	119,119,119,119	1
26	MG	J	201	1/1	0.94	0.42	-	109,109,109,109	0
26	MG	A	1839	1/1	0.91	0.05	-	467,467,467,467	0
26	MG	A	1712	1/1	0.94	0.20	-	170,170,170,170	0
26	MG	A	1808	1/1	0.62	0.44	-	498,498,498,498	0
26	MG	A	1639	1/1	0.88	0.19	-	87,87,87,87	0
26	MG	A	1710	1/1	0.97	0.13	-	253,253,253,253	0
26	MG	A	1630	1/1	0.96	0.26	-	158,158,158,158	0
26	MG	A	1876	1/1	0.87	0.48	-	463,463,463,463	1
26	MG	A	1700	1/1	0.80	0.37	-	302,302,302,302	0
26	MG	A	1881	1/1	0.88	0.13	-	414,414,414,414	0
26	MG	A	1696	1/1	0.96	0.32	-	263,263,263,263	0
26	MG	A	1717	1/1	0.89	0.22	-	152,152,152,152	0
26	MG	F	601	1/1	0.88	0.06	-	102,102,102,102	0
26	MG	A	1785	1/1	0.90	0.21	-	108,108,108,108	0
26	MG	A	1836	1/1	0.86	0.22	-	416,416,416,416	1
26	MG	A	1893	1/1	0.82	0.44	-	114,114,114,114	0
26	MG	A	1648	1/1	0.98	0.25	-	93,93,93,93	0
26	MG	P	101	1/1	0.80	0.32	-	58,58,58,58	0
26	MG	A	1699	1/1	0.75	0.07	-	414,414,414,414	0
26	MG	A	1818	1/1	0.98	0.09	-	189,189,189,189	0
26	MG	A	1738	1/1	1.00	0.05	-	68,68,68,68	0
26	MG	A	1748	1/1	0.91	0.14	-	110,110,110,110	0
26	MG	A	1865	1/1	0.83	0.39	-	457,457,457,457	0
26	MG	A	1897	1/1	0.84	0.43	-	114,114,114,114	0
26	MG	A	1916	1/1	0.75	0.19	-	119,119,119,119	0
26	MG	A	1654	1/1	0.98	0.09	-	161,161,161,161	0
26	MG	A	1773	1/1	0.92	0.10	-	103,103,103,103	0
26	MG	A	1787	1/1	0.96	0.24	-	496,496,496,496	0
26	MG	A	1820	1/1	0.94	0.22	-	373,373,373,373	0
26	MG	A	1894	1/1	0.79	0.21	-	94,94,94,94	0
26	MG	A	1868	1/1	0.96	0.44	-	380,380,380,380	0
26	MG	A	1737	1/1	0.88	0.69	-	89,89,89,89	0
26	MG	P	103	1/1	0.74	0.47	-	96,96,96,96	0
26	MG	A	1628	1/1	0.80	0.28	-	152,152,152,152	0
26	MG	A	1806	1/1	0.93	0.19	-	505,505,505,505	0
26	MG	A	1915	1/1	0.93	0.66	-	117,117,117,117	0
26	MG	A	1863	1/1	0.82	0.22	-	409,409,409,409	0
26	MG	A	1912	1/1	0.75	0.55	-	104,104,104,104	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
26	MG	A	1770	1/1	0.61	0.63	-	106,106,106,106	0
26	MG	A	1902	1/1	0.83	0.35	-	119,119,119,119	0
26	MG	A	1742	1/1	0.91	0.35	-	97,97,97,97	0
26	MG	A	1685	1/1	0.97	0.50	-	126,126,126,126	0
26	MG	A	1627	1/1	1.00	0.11	-	141,141,141,141	0
26	MG	A	1674	1/1	0.96	0.08	-	260,260,260,260	0
26	MG	A	1817	1/1	0.92	0.18	-	419,419,419,419	0
26	MG	A	1872	1/1	0.96	0.25	-	359,359,359,359	0
26	MG	A	1811	1/1	0.97	1.57	-	468,468,468,468	0
26	MG	A	1809	1/1	0.79	0.24	-	494,494,494,494	0
26	MG	A	1846	1/1	0.54	0.32	-	449,449,449,449	0
26	MG	E	202	1/1	0.91	0.12	-	124,124,124,124	0
26	MG	A	1605	1/1	0.98	0.09	-	254,254,254,254	0
26	MG	A	1886	1/1	-0.01	1.21	-	121,121,121,121	0
26	MG	A	1647	1/1	0.87	0.30	-	104,104,104,104	0
26	MG	A	1619	1/1	0.98	0.12	-	64,64,64,64	0
26	MG	A	1602	1/1	0.97	0.47	-	66,66,66,66	1
26	MG	A	1782	1/1	0.90	0.59	-	87,87,87,87	0
26	MG	A	1762	1/1	0.89	0.43	-	82,82,82,82	0
26	MG	A	1645	1/1	0.97	0.40	-	227,227,227,227	0
26	MG	D	304	1/1	0.35	0.54	-	455,455,455,455	0
26	MG	A	1620	1/1	0.96	0.21	-	166,166,166,166	0
26	MG	A	1730	1/1	0.64	0.72	-	97,97,97,97	0
26	MG	A	1610	1/1	0.99	0.23	-	81,81,81,81	0
26	MG	A	1925	1/1	0.82	0.15	-	114,114,114,114	0
26	MG	P	102	1/1	0.69	0.35	-	101,101,101,101	0
26	MG	A	1913	1/1	0.78	0.79	-	108,108,108,108	0
26	MG	A	1695	1/1	0.92	0.06	-	176,176,176,176	0
26	MG	A	1922	1/1	0.95	0.34	-	110,110,110,110	0
26	MG	A	1927	1/1	0.92	0.21	-	112,112,112,112	0
26	MG	A	1760	1/1	0.76	0.60	-	88,88,88,88	0
26	MG	A	1726	1/1	0.85	0.17	-	98,98,98,98	0
26	MG	A	1677	1/1	0.98	0.23	-	235,235,235,235	0
26	MG	A	1722	1/1	0.87	0.89	-	95,95,95,95	0
26	MG	A	1772	1/1	0.89	0.12	-	93,93,93,93	0
26	MG	A	1826	1/1	0.87	0.08	-	395,395,395,395	0
26	MG	A	1810	1/1	0.91	0.37	-	474,474,474,474	0
26	MG	A	1879	1/1	0.89	0.28	-	438,438,438,438	0
26	MG	A	1850	1/1	0.93	0.07	-	236,236,236,236	0
26	MG	A	1861	1/1	0.94	0.11	-	443,443,443,443	0
26	MG	A	1765	1/1	0.91	0.16	-	104,104,104,104	0
26	MG	A	1789	1/1	0.96	0.16	-	378,378,378,378	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
26	MG	A	1849	1/1	0.96	0.31	-	471,471,471,471	0
26	MG	A	1875	1/1	0.93	0.20	-	460,460,460,460	0
26	MG	A	1735	1/1	0.96	0.12	-	106,106,106,106	0
26	MG	A	1795	1/1	0.90	1.11	-	359,359,359,359	0
26	MG	A	1874	1/1	0.96	0.09	-	467,467,467,467	0
26	MG	A	1909	1/1	0.71	0.34	-	93,93,93,93	0
26	MG	A	1704	1/1	0.98	0.15	-	104,104,104,104	0
26	MG	A	1882	1/1	0.99	0.34	-	315,315,315,315	0
26	MG	A	1749	1/1	0.97	0.14	-	84,84,84,84	0
26	MG	A	1871	1/1	0.80	0.25	-	392,392,392,392	0
26	MG	A	1618	1/1	0.83	0.39	-	130,130,130,130	0
26	MG	A	1758	1/1	0.70	0.32	-	101,101,101,101	0
26	MG	A	1651	1/1	0.98	0.17	-	110,110,110,110	0
26	MG	A	1798	1/1	0.91	0.07	-	464,464,464,464	0
26	MG	A	1857	1/1	0.93	0.33	-	308,308,308,308	0
26	MG	A	1805	1/1	0.91	0.09	-	331,331,331,331	0
26	MG	A	1714	1/1	0.93	0.24	-	108,108,108,108	0
26	MG	A	1840	1/1	0.93	0.17	-	467,467,467,467	1
26	MG	A	1683	1/1	0.91	0.05	-	154,154,154,154	0
26	MG	A	1883	1/1	0.93	0.27	-	443,443,443,443	0
26	MG	A	1625	1/1	0.99	0.06	-	113,113,113,113	0
26	MG	A	1614	1/1	0.86	0.17	-	285,285,285,285	0
26	MG	A	1856	1/1	0.90	0.06	-	478,478,478,478	0
26	MG	A	1867	1/1	0.98	0.55	-	413,413,413,413	1
26	MG	A	1747	1/1	0.97	0.15	-	115,115,115,115	0
26	MG	S	102	1/1	0.96	0.13	-	106,106,106,106	0
26	MG	A	1707	1/1	0.85	0.36	-	135,135,135,135	0
26	MG	A	1718	1/1	0.93	0.24	-	326,326,326,326	0
26	MG	A	1832	1/1	0.98	0.08	-	278,278,278,278	0
26	MG	A	1669	1/1	0.97	0.09	-	123,123,123,123	0
26	MG	A	1877	1/1	0.77	0.43	-	456,456,456,456	1
26	MG	A	1684	1/1	0.83	0.13	-	109,109,109,109	0
26	MG	A	1924	1/1	0.96	0.11	-	131,131,131,131	0
26	MG	A	1635	1/1	0.99	0.14	-	74,74,74,74	0
26	MG	A	1613	1/1	0.92	0.15	-	202,202,202,202	0
26	MG	A	1744	1/1	0.72	0.32	-	82,82,82,82	0
26	MG	A	1792	1/1	0.92	0.17	-	415,415,415,415	0
26	MG	D	302	1/1	0.81	0.38	-	104,104,104,104	0
26	MG	A	1664	1/1	0.96	0.19	-	154,154,154,154	0
26	MG	A	1691	1/1	0.95	0.21	-	186,186,186,186	0
26	MG	A	1711	1/1	0.77	0.99	-	133,133,133,133	0
26	MG	A	1624	1/1	0.43	1.10	-	147,147,147,147	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
26	MG	A	1802	1/1	0.94	0.11	-	355,355,355,355	0
26	MG	A	1905	1/1	0.90	0.20	-	105,105,105,105	0
26	MG	A	1734	1/1	0.75	0.52	-	124,124,124,124	0
26	MG	A	1889	1/1	0.88	0.22	-	95,95,95,95	0
26	MG	A	1615	1/1	0.97	0.09	-	147,147,147,147	0
26	MG	A	1673	1/1	0.90	0.92	-	91,91,91,91	0
26	MG	A	1777	1/1	0.91	0.15	-	94,94,94,94	0
26	MG	A	1681	1/1	0.94	0.03	-	256,256,256,256	0
26	MG	A	1903	1/1	0.93	0.21	-	78,78,78,78	0
26	MG	A	1843	1/1	0.98	0.68	-	357,357,357,357	0
26	MG	A	1751	1/1	0.91	0.46	-	76,76,76,76	0
26	MG	A	1825	1/1	0.94	0.20	-	436,436,436,436	0
26	MG	A	1653	1/1	0.99	0.25	-	96,96,96,96	0
26	MG	A	1752	1/1	0.93	0.22	-	91,91,91,91	0
26	MG	A	1841	1/1	0.93	0.26	-	496,496,496,496	0
26	MG	A	1797	1/1	0.87	0.16	-	502,502,502,502	0
26	MG	A	1754	1/1	0.97	0.16	-	85,85,85,85	0
26	MG	A	1813	1/1	0.76	0.65	-	471,471,471,471	0
26	MG	A	1692	1/1	0.99	0.20	-	182,182,182,182	0
26	MG	A	1884	1/1	0.82	1.04	-	119,119,119,119	0
26	MG	A	1756	1/1	0.91	0.16	-	126,126,126,126	0
26	MG	A	1706	1/1	0.95	0.13	-	190,190,190,190	0
26	MG	A	1719	1/1	0.96	0.08	-	262,262,262,262	0
26	MG	A	1660	1/1	0.89	0.23	-	224,224,224,224	0
26	MG	A	1766	1/1	0.83	0.52	-	105,105,105,105	0
26	MG	A	1842	1/1	0.92	0.50	-	488,488,488,488	0
26	MG	A	1821	1/1	0.96	0.29	-	428,428,428,428	0
26	MG	A	1892	1/1	0.54	0.38	-	92,92,92,92	0
26	MG	A	1854	1/1	0.95	0.51	-	418,418,418,418	0
26	MG	A	1769	1/1	0.67	0.54	-	127,127,127,127	0
26	MG	A	1891	1/1	0.75	0.16	-	127,127,127,127	0
26	MG	A	1833	1/1	0.98	0.12	-	335,335,335,335	0
26	MG	A	1652	1/1	0.97	0.09	-	72,72,72,72	0
26	MG	A	1687	1/1	0.97	0.14	-	106,106,106,106	0
26	MG	A	1831	1/1	0.95	0.18	-	395,395,395,395	0
26	MG	A	1799	1/1	0.90	0.22	-	426,426,426,426	0
26	MG	A	1790	1/1	0.91	0.14	-	444,444,444,444	0
26	MG	A	1629	1/1	0.90	0.26	-	223,223,223,223	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.