



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 31, 2014 – 05:38 PM BST

PDB ID : 2QB9  
Title : Crystal structure of the bacterial ribosome from Escherichia coli in complex with gentamicin. This file contains the 30S subunit of the first 70S ribosome, with gentamicin bound. The entire crystal structure contains two 70S ribosomes and is described in remark 400.  
Authors : Borovinskaya, M.A.; Pai, R.D.; Zhang, W.; Schuwirth, B.-S.; Holton, J.M.; Hirokawa, G.; Kaji, H.; Kaji, A.; Cate, J.H.D.  
Deposited on : 2007-06-16  
Resolution : 3.54 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

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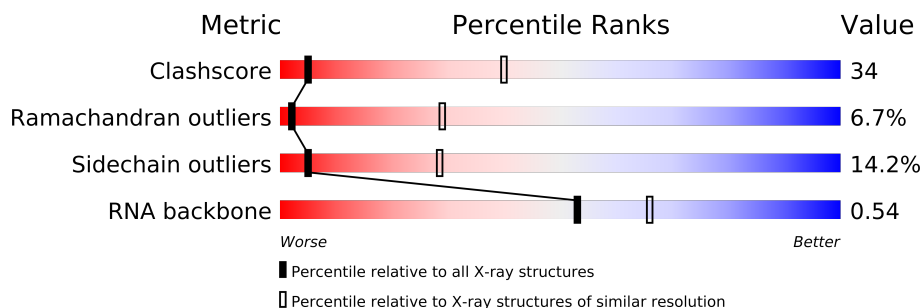
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : **NOT EXECUTED**  
Percentile statistics : 21963  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable23004

# 1 Overall quality at a glance

The reported resolution of this entry is 3.54 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	79885	1033 (3.70-3.38)
Ramachandran outliers	78287	1067 (3.72-3.36)
Sidechain outliers	78261	1067 (3.72-3.36)
RNA backbone	1838	1011 (4.30-2.76)

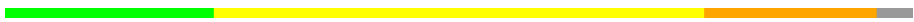
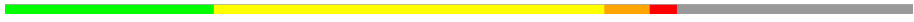
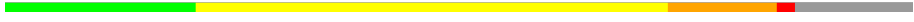

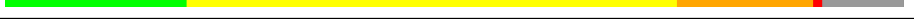

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	1542	
2	C	232	
3	D	205	
4	E	166	
5	F	135	
6	G	178	
7	H	129	
8	I	129	
9	J	103	
10	K	128	
11	L	123	
12	M	117	
13	N	100	
14	O	89	
15	P	82	

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Mol	Chain	Length	Quality of chain
16	Q	83	
17	R	74	
18	S	91	
19	T	86	
20	B	240	
21	U	70	

## 2 Entry composition

There are 24 unique types of molecules in this entry. The entry contains 51820 atoms, of which 0 are hydrogen and 0 are deuterium.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1530	Total	C	N	O	P	0	0	0
			32831	14642	6024	10635	1530			

- Molecule 2 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	206	Total	C	N	O	S	0	0	0
			1624	1028	305	288	3			

- Molecule 3 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	205	Total	C	N	O	S	0	0	0
			1643	1026	315	298	4			

- Molecule 4 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	E	150	Total	C	N	O	S	0	0	0
			1105	687	211	201	6			

- Molecule 5 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	F	100	Total	C	N	O	S	0	0	0
			817	515	148	148	6			

- Molecule 6 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	G	150	Total	C	N	O	S	0	0	0
			1174	730	226	214	4			

- Molecule 7 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	H	129	Total	C	N	O	S	0	0	0
			979	616	173	184	6			

- Molecule 8 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
8	I	127	Total	C	N	O	S	0	0	0
			1022	634	206	179	3			

- Molecule 9 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
9	J	98	Total	C	N	O	S	0	0	0
			786	493	150	142	1			

- Molecule 10 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
10	K	117	Total	C	N	O	S	0	0	0
			877	540	174	160	3			

- Molecule 11 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
11	L	123	Total	C	N	O	S	0	0	0
			955	590	196	165	4			

- Molecule 12 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
12	M	114	Total	C	N	O	S	0	0	0
			883	546	178	156	3			

- Molecule 13 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
13	N	96	Total	C	N	O	S	0	0	0
			774	483	160	128	3			

- Molecule 14 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	O	88	Total	C	N	O	S	0	0	0
			714	439	144	130	1			

- Molecule 15 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
15	P	82	Total	C	N	O	S	0	0	0
			649	406	128	114	1			

- Molecule 16 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
16	Q	80	Total	C	N	O	S	0	0	0
			648	411	121	113	3			

- Molecule 17 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
17	R	55	Total	C	N	O	0	0	0
			455	288	86	81			

- Molecule 18 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
18	S	79	Total	C	N	O	S	0	0	0
			637	408	120	107	2			

- Molecule 19 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
19	T	85	Total	C	N	O	S	0	0	0
			665	411	137	114	3			

- Molecule 20 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
20	B	218	Total	C	N	O	S	0	0	0
			1704	1081	305	311	7			

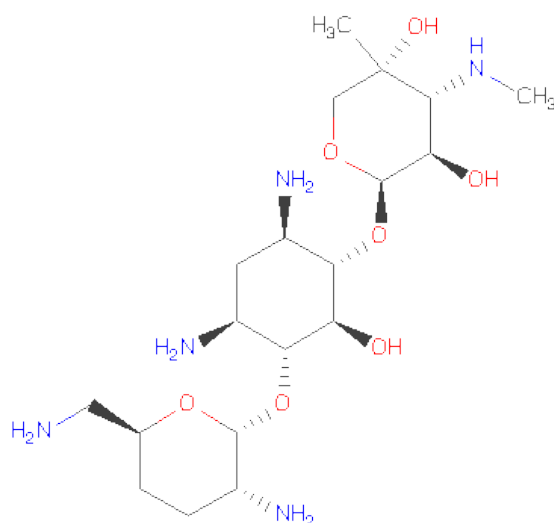
- Molecule 21 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	U	51	Total	C	N	O	S	0	0	0
			425	265	86	73	1			

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

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
22	A	60	Total	Mg	0	0
			60	60		

- Molecule 23 is (2R,3R,4R,5R)-2-((1S,2S,3R,4S,6R)-4,6-DIAMINO-3-((2R,3R,6S)-3-AMINO-O-6-(AMINOMETHYL)-TETRAHYDRO-2H-PYRAN-2-YLOXY)-2-HYDROXYCYCLOHEXYLOXY)-5-METHYL-4-(METHYLAMINO)-TETRAHYDRO-2H-PYRAN-3,5-DIOL (three-letter code: LLL) (formula: C<sub>19</sub>H<sub>39</sub>N<sub>5</sub>O<sub>7</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
23	A	1	Total	C	N	O	0	0
			31	19	5	7		
23	A	1	Total	C	N	O	0	0
			31	19	5	7		
23	A	1	Total	C	N	O	0	0
			31	19	5	7		

- Molecule 24 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
24	A	293	Total	O	0	0
			293	293		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
24	E	3	Total 3	O 3	0	0
24	L	2	Total 2	O 2	0	0
24	N	1	Total 1	O 1	0	0
24	T	1	Total 1	O 1	0	0



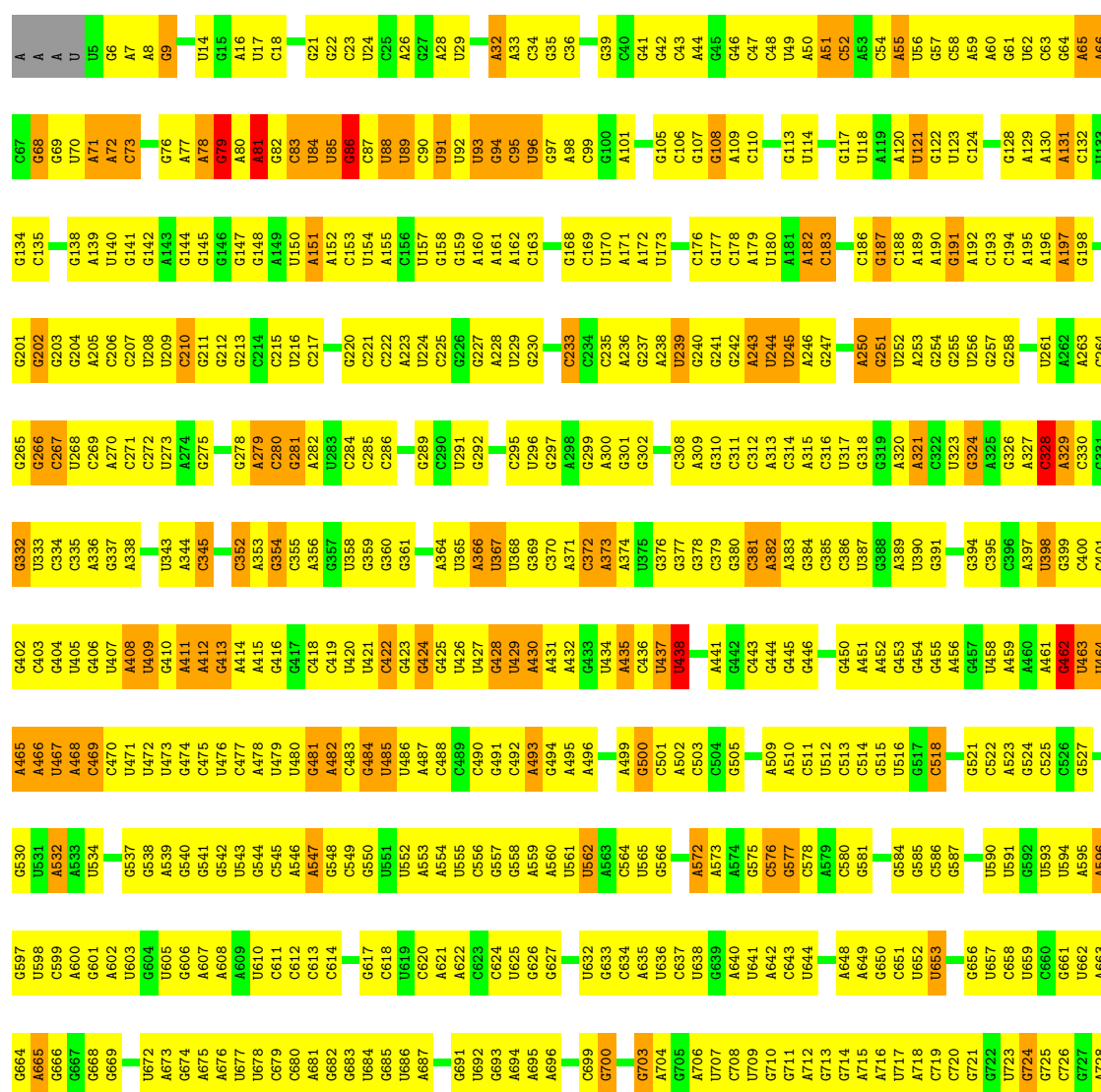
### 3 Residue-property plots

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

Note EDS was not executed.

#### • Molecule 1: 16S rRNA

Chain A:



A729	G809	G885	U960	A1021	G1084	A1152	A1219	C1284	G1347	U1425	C1501	G1	H68	A140
G730	C810	G886	U961	A1022	U1085	G1153	G1220	A1285	U1348	G1426	A1502	Q2	T69	A141
G731	C811	G889	G962	U1023	U1086	C1158	G1221	U1286	A1349	G1432	A1503	K3	A70	L142
G732	G812	G890	G963	U1024	U1090	U1159	G1222	U1287	A1350	G1433	G1504	V4	R71	L143
G733	U813	G895	A964	U1025	U1091	G1160	C1223	A1288	C1351	G1435	U1506	H5	P72	A144
G734	A814	G896	U965	U1026	U1092	U1161	U1224	A1289	C1352	U1436	U1507	G8	V75	A145
G735	A815	G898	G966	C1027	A1093	C1162	A1225	G1290	G1353	U1437	A1508	I9	I76	K146
G736	A816	C896	G967	C1028	A1094	C1163	C1226	U1291	G1356	G1438	C1509	R10	E81	G147
G737	C817	C897	A968	U1029	G1095	G1164	A1227	U1292	A1357	U1439	C1510	L11	K148	L148
G738	G818	C899	A969	U1030	U1096	U1165	C1228	G1293	U1358	U1440	U1511	G12	B82	V150
G739	A819	A900	G972	U1031	C1097	U1166	A1229	C1296	C1359	A1441	U1512	I13	V83	E151
U740	U820	G903	G973	G1032	C1098	A1167	C1230	G1297	C1362	A1446	U1513	Y14	K15	V152
G741	G821	U904	G974	G1033	G1099	U1168	C1231	U1298	A1363	U1447	G1514	K16	L86	S153
A747	U822	U905	A975	A1035	A1100	U1169	C1234	U1299	A1364	U1450	G1515	P17	R87	G154
G748	C823	U906	G976	A1036	A1101	A1170	U1235	G1300	U1365	U1456	U1516	W17	K88	L155
U751	A825	A907	A977	C1037	A1102	A1171	A1236	C1301	G1366	C1452	U1517	R18	V89	L156
G755	C826	A908	A978	C1038	A1103	C1172	C1237	C1302	C1367	G1453	A1518	S19	V90	A91
G756	U827	A909	C979	U1039	A1105	U1173	A1238	C1303	C1368	G1454	U1519	T20	A91	A162
G757	U828	C910	G980	U1040	G1106	G1174	A1239	G1304	U1369	G1455	C1520	W21	F28	R163
G763	G829	A914	U981	G1041	C1107	G1175	U1240	G1305	C1370	G1456	U1521	N24	A94	E165
G764	G833	G917	U982	A1042	G1108	A1176	G1241	G1306	G1371	U1457	U1522	T25	V96	E166
G765	U834	C984	A983	G1043	C1109	G1177	A1242	U1307	U1372	G1458	C1523	K26	P97	Y167
A766	U835	A918	C985	A1044	A1110	G1178	C1243	U1308	U1373	G1459	C1524	E27	A98	R168
A767	G836	A919	U986	C1045	A1111	A1179	G1244	G1309	G1374	C1460	U1525	F28	Q99	A169
A769	C839	U920	G987	A1046	A1112	A1180	C1245	G1310	A1374	G1461	G1526	F28	Q99	A169
G770	C840	U921	G988	G1047	U1118	G1181	A1246	A1311	U1381	G1462	U1527	N31	I100	R171
G771	C841	A922	U989	U1049	C1119	G1182	U1247	U1312	C1382	U1463	U1528	N31	N101	V172
A777	U842	A923	C990	G1050	C1120	G1183	C1249	U1313	C1383	U1464	G1529	S34	E104	L174
G778	U843	C924	U991	G1053	U1121	G1185	A1250	U1315	G1386	U1468	U1531	D35	V105	H175
G779	G844	G925	U992	A1054	U1122	G1186	A1251	G1316	C1387	A1469	U1532	V38	R106	R178
A780	G846	G926	G993	U1055	U1123	G1190	A1252	C1317	C1388	C1469	C1533	R39	K107	A179
A781	G847	G928	A994	A1056	U1125	A1191	G1253	U1318	C1389	U1470	A1534	Q40	P108	D180
A782	C848	U997	A996	G1057	U1126	C1192	A1254	A1319	U1390	U1471	C	Y41	L110	I181
C783	G849	C934	C998	C1058	G1127	A1196	A1255	C1320	C1391	U1472	C	L42	D111	D182
A784	C857	A935	C999	C1059	A1130	A1197	A1257	C1322	U1393	U1474	C	L46	A112	Y183
G785	G858	C936	A1000	U1060	G1131	G1198	G1258	G1323	A1394	U1477	U	A47	K113	N184
G786	G859	G945	U1007	G1061	C1132	U1199	C1259	U1324	C1397	U1478	U	K48	L114	T185
G787	U870	C940	C1001	U1062	G1133	U1200	A1261	U1330	A1398	C1479	U	A49	V115	A188
G791	G861	G941	G1002	C1063	U1134	U1201	C1262	U1331	C1400	A1480	U	S50	T120	H189
A792	A864	A1004	A1005	U1065	C1135	U1202	C1263	G1332	G1401	G1482	A1483	V51	Q122	T191
U793	A865	G946	A1006	C1066	C1136	C1203	A1269	A1332	C1404	A1484	C1483	R53	Q122	Y192
C795	A866	A946	U1007	G1068	U1138	U1204	G1270	A1333	C1405	U1485	C1484	I54	R126	G193
C796	G868	C948	U1009	U1069	C1139	G1206	A1271	G1334	U1406	U1486	U1485	V55	V127	G194
C797	U870	A949	U1010	C1071	G1140	G1207	G1272	U1335	U1407	G1487	G1486	I56	M128	V194
U798	U870	U950	C1011	U1072	G1141	C1208	C1273	C1336	C1409	G1488	G1487	E57	F129	G196
G802	G874	U952	A1012	G1073	G1142	C1209	A1274	G1337	A1410	G1489	G1488	R58	R130	V197
G803	U875	G953	G1013	U1074	G1143	U1211	G1276	G1338	C1411	U1490	A1491	P59	R131	K198
U804	A878	G954	A1014	G1077	A1144	U1212	C1277	A1340	C1412	U1491	A1492	A60	M132	V199
G805	G882	U955	G1015	U1078	A1146	A1213	G1278	U1341	U1418	U1495	A1496	S62	M133	W200
C806	U884	U956	A1016	G1079	C1147	C1214	G1279	U1342	A1418	C1496	C1495	I63	K134	I201
A807	C882	U957	U1017	G1079	U1148	G1215	A1280	G1343	G1423	U1497	U1496	R64	L135	F202
C808	U884	U958	G1018	A1081	C1149	A1216	C1281	U1344	G1424	U1497	U1496	R65	K203	K203
C809	U884	A959	A1019	A1081	C1217	A1150	C1282	U1345	G1423	U1497	U1496	T66	G204	G204
			G1020		A151	C1218	U1283	A1346	U1424			I67	M139	I206

• Molecule 2: 30S ribosomal protein S3

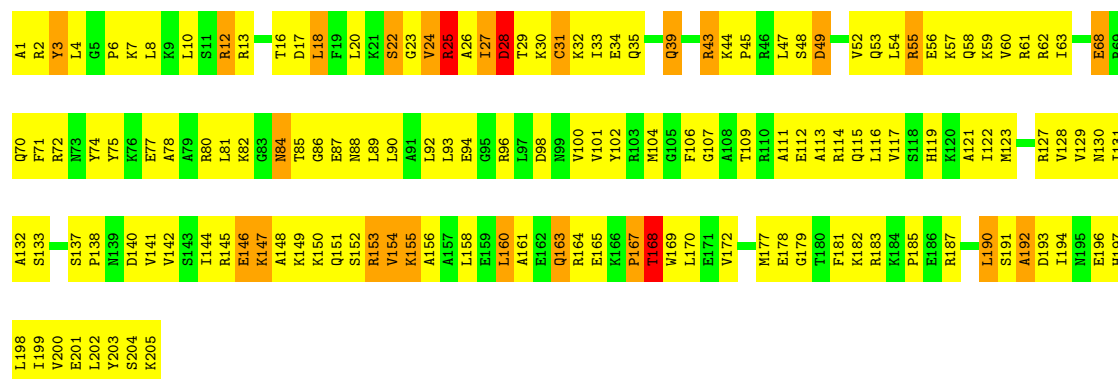
Chain C:



LEU  
GLY  
GLY  
MET  
ALA  
ALA  
VAL  
GLU  
GLN  
PRO  
GLU  
LYS  
PRO  
ALA  
ALA  
GLN  
PRO  
LYS  
LYS  
GLN  
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ARG  
LYS  
GLY  
ARG  
LYS

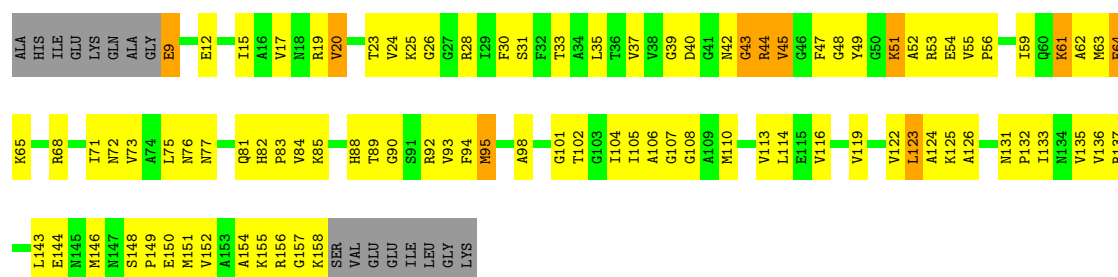
• Molecule 3: 30S ribosomal protein S4

Chain D:



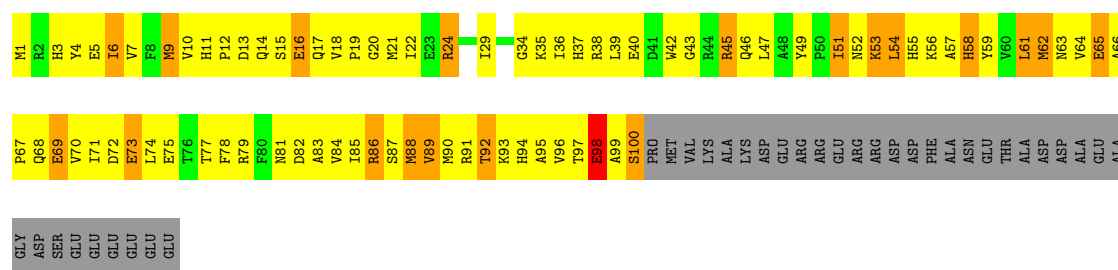
• Molecule 4: 30S ribosomal protein S5

Chain E:



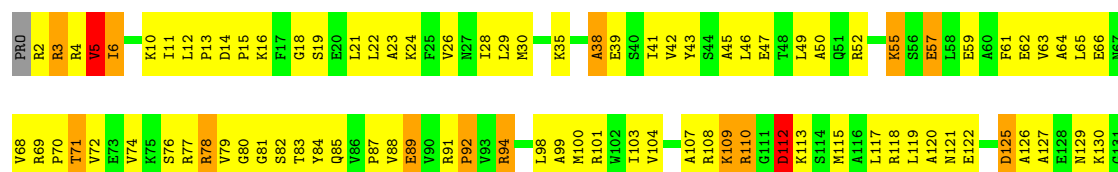
• Molecule 5: 30S ribosomal protein S6

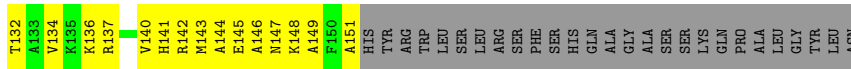
Chain F:



• Molecule 6: 30S ribosomal protein S7

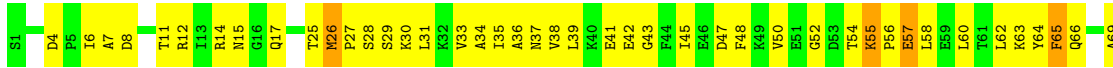
Chain G:





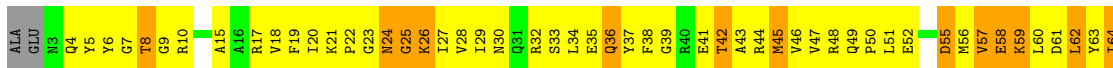
- Molecule 7: 30S ribosomal protein S8

Chain H: 



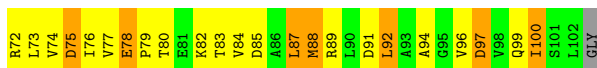
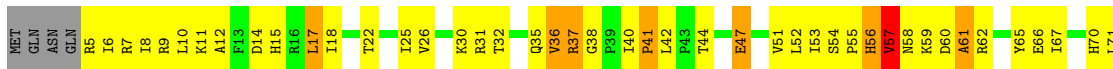
- Molecule 8: 30S ribosomal protein S9

Chain I:



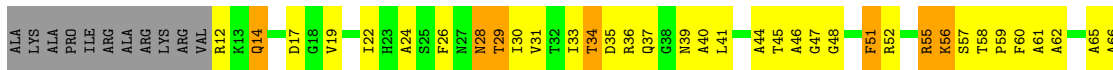
- Molecule 9: 30S ribosomal protein S10

Chain J: 



- Molecule 10: 30S ribosomal protein S11

Chain K:



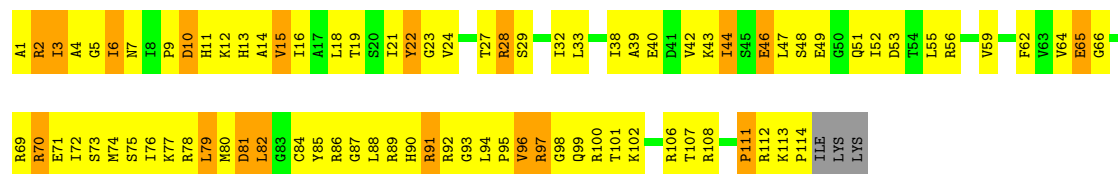
- Molecule 11: 30S ribosomal protein S12

Chain L:



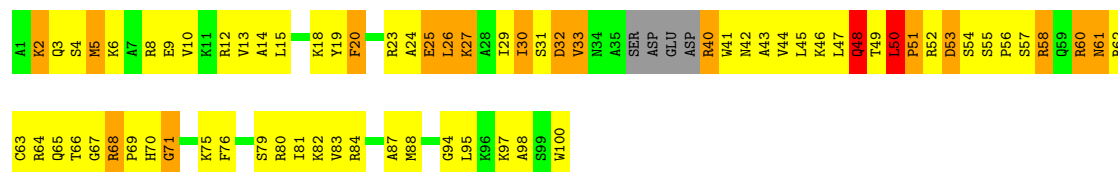
- Molecule 12: 30S ribosomal protein S13

Chain M: 



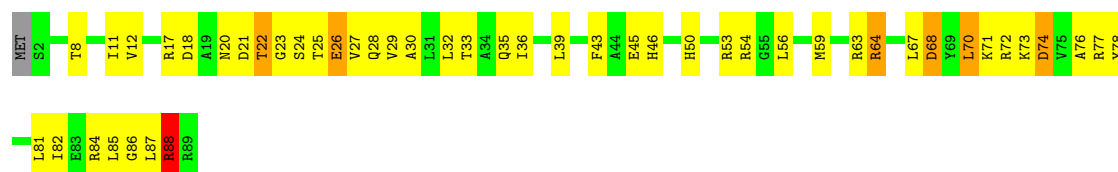
- Molecule 13: 30S ribosomal protein S14

Chain N: 



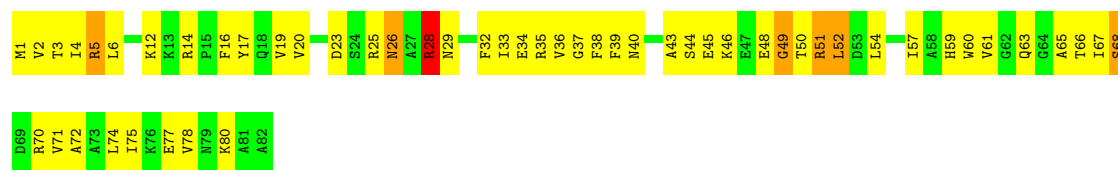
- Molecule 14: 30S ribosomal protein S15

Chain O: 



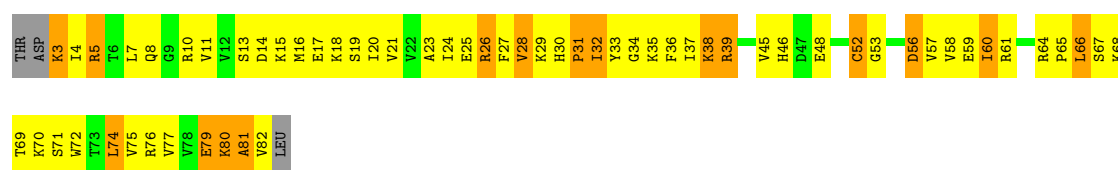
- Molecule 15: 30S ribosomal protein S16

Chain P: 



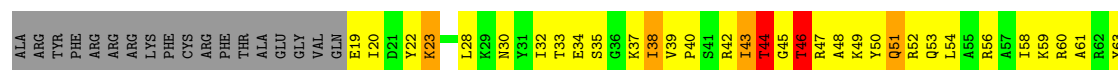
- Molecule 16: 30S ribosomal protein S17

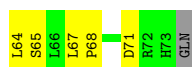
Chain Q: 



- Molecule 17: 30S ribosomal protein S18

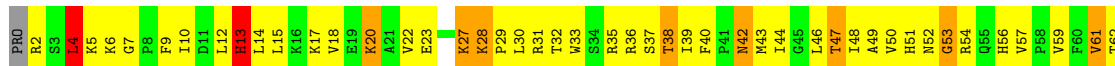
Chain R: 





- Molecule 18: 30S ribosomal protein S19

Chain S:



- Molecule 19: 30S ribosomal protein S20

Chain T:



- Molecule 20: 30S ribosomal protein S2

Chain B:



- Molecule 21: 30S ribosomal protein S21

Chain U:



## 4 Data and refinement statistics

EDS was not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	208.85Å 379.20Å 739.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	70.00 – 3.54	Depositor
% Data completeness (in resolution range)	88.8 (70.00-3.54)	Depositor
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.69 (at 3.58Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.281 , 0.320	Depositor
Wilson B-factor (Å <sup>2</sup> )	125.1	Xtriage
Anisotropy	0.234	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 627888 reflections (0.000%)	Xtriage
Total number of atoms	51820	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	84.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.39% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

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	0.26	2/36762 (0.0%)	0.76	22/57350 (0.0%)
2	C	0.23	0/1651	0.44	0/2225
3	D	0.23	0/1665	0.44	0/2227
4	E	0.23	0/1118	0.45	0/1504
5	F	0.24	0/835	0.44	0/1128
6	G	0.23	0/1187	0.45	0/1591
7	H	0.23	0/989	0.44	0/1326
8	I	0.24	0/1034	0.46	0/1375
9	J	0.22	0/796	0.48	0/1077
10	K	0.24	0/893	0.46	0/1205
11	L	0.22	0/969	0.48	0/1300
12	M	0.21	0/892	0.46	0/1193
13	N	0.24	0/785	0.45	0/1043
14	O	0.23	0/722	0.47	0/964
15	P	0.25	0/659	0.46	0/884
16	Q	0.24	0/657	0.46	0/881
17	R	0.23	0/462	0.46	0/621
18	S	0.25	0/652	0.46	0/877
19	T	0.24	0/671	0.39	0/888
20	B	0.25	0/1735	0.45	0/2338
21	U	0.26	0/430	0.47	0/570
All	All	0.25	2/55564 (0.0%)	0.68	22/82567 (0.0%)

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
1	A	0	15



All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1213	A	P-OP2	-8.66	1.34	1.49
1	A	495	A	N3-C4	-5.07	1.31	1.34

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1213	A	O5'-P-OP2	-28.32	76.72	110.70
1	A	1212	U	OP2-P-O3'	-9.32	84.69	105.20
1	A	366	A	C2'-C3'-O3'	8.50	128.21	109.50
1	A	1213	A	O5'-P-OP1	8.30	120.66	110.70
1	A	1212	U	OP1-P-O3'	8.23	123.30	105.20
1	A	765	G	N9-C1'-C2'	-7.58	103.67	112.00
1	A	1409	C	C5'-C4'-C3'	-6.55	105.52	116.00
1	A	1301	U	N1-C1'-C2'	5.74	121.45	114.00
1	A	438	U	N1-C1'-C2'	-5.68	105.75	112.00
1	A	1250	A	C5'-C4'-C3'	5.64	125.03	116.00
1	A	1432	G	N9-C1'-C2'	-5.61	105.83	112.00
1	A	576	C	C5'-C4'-C3'	5.57	124.91	116.00
1	A	79	G	C4'-C3'-O3'	5.55	124.11	113.00
1	A	81	A	C1'-O4'-C4'	-5.41	105.57	109.90
1	A	1490	U	C5'-C4'-C3'	-5.30	107.52	116.00
1	A	765	G	C4'-C3'-O3'	5.22	123.45	113.00
1	A	1212	U	O3'-P-O5'	5.21	113.89	104.00
1	A	345	C	C5'-C4'-C3'	-5.16	107.74	116.00
1	A	328	C	C2'-C3'-O3'	5.16	121.95	113.70
1	A	845	A	N9-C1'-C2'	-5.12	106.37	112.00
1	A	576	C	C5'-C4'-O4'	5.09	115.21	109.10
1	A	101	A	C5'-C4'-C3'	-5.07	107.89	116.00

There are no chirality outliers.

All (15) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1331	G	Sidechain
1	A	1432	G	Sidechain
1	A	1441	A	Sidechain
1	A	187	G	Sidechain
1	A	281	G	Sidechain
1	A	324	G	Sidechain
1	A	437	U	Sidechain
1	A	438	U	Sidechain

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Mol	Chain	Res	Type	Group
1	A	450	G	Sidechain
1	A	462	G	Sidechain
1	A	481	G	Sidechain
1	A	496	A	Sidechain
1	A	666	G	Sidechain
1	A	703	G	Sidechain
1	A	86	G	Sidechain

## 5.2 Close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	32831	0	16521	1235	0
2	C	1624	0	1699	150	0
3	D	1643	0	1710	174	0
4	E	1105	0	1148	94	0
5	F	817	0	808	97	0
6	G	1174	0	1230	105	0
7	H	979	0	1034	82	0
8	I	1022	0	1070	132	0
9	J	786	0	828	81	0
10	K	877	0	887	105	0
11	L	955	0	1019	95	0
12	M	883	0	944	105	0
13	N	774	0	827	108	0
14	O	714	0	734	41	0
15	P	649	0	666	65	0
16	Q	648	0	691	76	0
17	R	455	0	478	48	0
18	S	637	0	665	87	0
19	T	665	0	714	56	0
20	B	1704	0	1732	218	0
21	U	425	0	449	67	0
22	A	60	0	0	0	0
23	A	93	0	117	6	0
24	A	293	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	E	3	0	0	0	0
24	L	2	0	0	0	0
24	N	1	0	0	0	0
24	T	1	0	0	0	0
All	All	51820	0	35971	2933	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 34.

All (2933) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:N:63:CYS:HB3	13:N:67:GLY:H	1.16	1.06
5:F:3:HIS:HB2	5:F:92:THR:HA	1.31	1.05
20:B:33:ALA:HA	20:B:38:HIS:HA	1.38	1.05
8:I:51:LEU:HB3	8:I:56:MET:HG2	1.41	1.02
21:U:16:ARG:HE	21:U:16:ARG:HA	1.21	1.02
21:U:36:PHE:HB3	21:U:40:PRO:HD3	1.41	1.01
20:B:119:GLN:HA	20:B:124:THR:HB	1.40	0.99
12:M:71:GLU:HA	12:M:74:MET:HG2	1.42	0.99
3:D:116:LEU:HB3	3:D:122:ILE:HD11	1.40	0.99
1:A:664:G:H22	1:A:741:G:H1	1.07	0.99
20:B:46:VAL:HG13	20:B:47:PRO:HD3	1.45	0.98
2:C:76:ILE:HA	2:C:83:VAL:HG23	1.46	0.98
20:B:163:ILE:HG23	20:B:164:ASP:H	1.29	0.97
18:S:30:LEU:H	18:S:48:ILE:HA	1.30	0.97
1:A:1086:U:H3	1:A:1099:G:H22	1.02	0.97
10:K:31:VAL:HG21	10:K:66:ALA:HA	1.47	0.96
20:B:198:VAL:HG12	20:B:200:PRO:HD3	1.48	0.96
3:D:185:PRO:HB2	3:D:190:LEU:HB2	1.47	0.96
10:K:33:ILE:HB	10:K:73:VAL:HG11	1.49	0.95
9:J:9:ARG:HB2	9:J:99:GLN:HB2	1.44	0.95
3:D:84:ASN:HD22	4:E:101:GLY:HA2	1.33	0.94
10:K:91:GLY:HA2	10:K:94:SER:HB3	1.49	0.93
10:K:124:LYS:HA	21:U:34:ARG:HB3	1.50	0.93
20:B:202:ASN:HD22	20:B:204:ASP:H	1.16	0.93
8:I:25:GLY:HA3	8:I:57:VAL:HA	1.48	0.93
7:H:11:THR:HG22	7:H:14:ARG:HH12	1.34	0.93
1:A:532:A:H62	2:C:191:THR:HB	1.31	0.93
9:J:53:ILE:HG22	9:J:61:ALA:HB1	1.51	0.92
1:A:79:G:H2'	1:A:80:A:H8	1.34	0.92
3:D:160:LEU:HD13	3:D:160:LEU:H	1.35	0.90
4:E:106:ALA:HB1	4:E:110:MET:HB3	1.53	0.89

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:F:92:THR:HG22	5:F:94:HIS:H	1.38	0.89
5:F:62:MET:HG3	5:F:64:VAL:HG23	1.55	0.88
19:T:43:LYS:HE2	19:T:44:ALA:H	1.37	0.88
1:A:79:G:H2'	1:A:80:A:C8	2.08	0.88
1:A:68:G:H5'	1:A:171:A:H1'	1.54	0.87
10:K:86:LYS:HB3	10:K:112:VAL:HG23	1.55	0.87
18:S:18:VAL:HG21	18:S:43:MET:HG2	1.55	0.87
1:A:243:A:H4'	1:A:244:U:H5'	1.54	0.86
18:S:51:HIS:HA	18:S:56:HIS:HA	1.57	0.86
3:D:60:VAL:HB	3:D:194:ILE:HD11	1.58	0.85
2:C:126:ARG:HH22	2:C:190:THR:HG23	1.42	0.85
2:C:128:MET:HB2	2:C:131:ARG:HB2	1.56	0.85
1:A:522:C:H41	11:L:49:ARG:NH2	1.74	0.85
12:M:21:ILE:HB	12:M:24:VAL:HG22	1.58	0.85
19:T:60:GLN:HB3	19:T:65:LEU:HD23	1.59	0.84
10:K:110:THR:HG22	21:U:4:LYS:HA	1.58	0.84
1:A:1250:A:H4'	8:I:69:GLY:H	1.43	0.84
10:K:14:GLN:HA	10:K:77:GLY:HA3	1.59	0.84
1:A:981:U:H4'	13:N:60:ARG:HD2	1.59	0.84
8:I:55:ASP:HB2	8:I:59:LYS:HE3	1.60	0.84
16:Q:3:LYS:HZ3	16:Q:4:ILE:H	1.26	0.83
6:G:104:VAL:HG12	6:G:108:ARG:HD2	1.60	0.83
20:B:99:MET:HA	20:B:106:VAL:HG21	1.59	0.83
5:F:90:MET:HG2	17:R:60:ARG:HH21	1.44	0.83
1:A:120:A:H2'	1:A:121:U:H5''	1.59	0.83
9:J:17:LEU:HD22	9:J:96:VAL:HG13	1.58	0.83
15:P:28:ARG:HD2	15:P:29:ASN:H	1.43	0.83
1:A:617:G:H4'	15:P:46:LYS:HE2	1.60	0.82
6:G:130:LYS:H	6:G:134:VAL:HG21	1.42	0.82
10:K:22:ILE:HG21	10:K:95:THR:HG21	1.61	0.82
1:A:1412:C:H2'	1:A:1413:A:C8	2.13	0.82
20:B:184:ALA:HB3	20:B:195:VAL:HG21	1.61	0.82
20:B:65:LYS:HB2	20:B:158:ASP:H	1.43	0.81
6:G:115:MET:HA	6:G:118:ARG:HD2	1.62	0.81
1:A:1399:C:H4'	1:A:1400:C:H5''	1.62	0.81
2:C:190:THR:HG22	2:C:191:THR:H	1.45	0.81
6:G:78:ARG:HG2	6:G:83:THR:HG22	1.63	0.81
10:K:92:ARG:HH11	21:U:20:ARG:HH21	1.29	0.81
8:I:19:PHE:HB2	8:I:63:TYR:HB3	1.63	0.81
17:R:51:GLN:HA	17:R:51:GLN:HE21	1.44	0.81
18:S:31:ARG:HA	18:S:49:ALA:HB3	1.61	0.80
10:K:83:VAL:HB	10:K:109:ILE:HA	1.62	0.80

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
21:U:43:GLU:HG3	21:U:44:ARG:HH21	1.44	0.80
2:C:26:LYS:HG3	2:C:27:GLU:HG3	1.64	0.80
4:E:81:GLN:HG2	4:E:148:SER:HA	1.62	0.80
13:N:55:SER:HB2	13:N:58:ARG:HD2	1.62	0.80
18:S:30:LEU:HB2	18:S:48:ILE:HG23	1.64	0.80
1:A:1071:C:H2'	1:A:1072:G:H8	1.47	0.80
1:A:93:U:H5''	1:A:94:G:OP2	1.82	0.79
20:B:16:GLY:HA2	20:B:40:ILE:HG13	1.62	0.79
20:B:61:SER:HB2	20:B:62:ARG:HH11	1.48	0.79
15:P:54:LEU:HD22	15:P:80:LYS:HE2	1.64	0.79
10:K:28:ASN:HD21	10:K:47:GLY:H	1.30	0.79
2:C:70:ALA:HA	2:C:105:VAL:HG21	1.62	0.79
20:B:156:LEU:HD12	20:B:156:LEU:H	1.46	0.79
16:Q:56:ASP:HA	16:Q:81:ALA:HB2	1.62	0.79
13:N:26:LEU:HD23	13:N:27:LYS:H	1.46	0.79
13:N:30:ILE:HG21	13:N:44:VAL:HG21	1.63	0.79
13:N:63:CYS:HB3	13:N:67:GLY:N	1.97	0.79
19:T:4:LYS:HD2	19:T:5:SER:H	1.48	0.79
1:A:974:A:H4'	1:A:975:A:H5'	1.63	0.78
5:F:42:TRP:HE1	5:F:61:LEU:HD23	1.46	0.78
21:U:40:PRO:HA	21:U:44:ARG:HD2	1.63	0.78
18:S:10:ILE:HG22	18:S:38:THR:H	1.48	0.78
1:A:1296:C:H4'	1:A:1302:C:H41	1.49	0.78
3:D:10:LEU:HB3	3:D:62:ARG:HD3	1.64	0.78
8:I:34:LEU:HD21	8:I:48:ARG:HE	1.47	0.78
1:A:373:A:H1'	1:A:481:G:N3	1.99	0.78
10:K:88:PRO:HD3	21:U:28:LEU:HD11	1.66	0.77
1:A:1236:A:H4'	1:A:1304:G:H4'	1.65	0.77
10:K:52:ARG:HH12	10:K:56:LYS:HE3	1.49	0.77
1:A:17:U:H2'	1:A:18:C:C6	2.19	0.77
20:B:202:ASN:ND2	20:B:204:ASP:H	1.82	0.77
18:S:10:ILE:HB	18:S:14:LEU:HD11	1.67	0.77
10:K:80:ASN:N	10:K:80:ASN:HD22	1.82	0.77
18:S:10:ILE:HG22	18:S:37:SER:HB3	1.65	0.77
1:A:1323:G:H2'	1:A:1324:A:C8	2.20	0.77
1:A:600:A:H5''	7:H:88:LYS:HD2	1.66	0.77
12:M:79:LEU:HD13	12:M:86:ARG:HB3	1.65	0.77
1:A:817:C:H1'	1:A:819:A:H5'	1.67	0.76
1:A:781:A:H2'	1:A:782:A:H5'	1.67	0.76
15:P:61:VAL:HA	15:P:65:ALA:HB3	1.66	0.76
1:A:1239:A:H4'	1:A:1240:U:H5'	1.68	0.76
13:N:50:LEU:H	13:N:51:PRO:HD2	1.50	0.76

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
18:S:43:MET:HB2	18:S:61:VAL:HG11	1.67	0.76
20:B:60:ALA:HA	20:B:64:GLY:HA3	1.66	0.76
1:A:269:C:H2'	1:A:270:A:C8	2.20	0.76
1:A:1206:G:H4'	2:C:192:TYR:HA	1.68	0.76
2:C:182:ASP:HB2	2:C:203:LYS:HE2	1.68	0.76
1:A:204:G:H21	1:A:466:A:N6	1.84	0.76
20:B:61:SER:HB2	20:B:62:ARG:NH1	2.01	0.75
7:H:87:ARG:H	7:H:90:GLU:HB2	1.51	0.75
18:S:17:LYS:HB3	18:S:30:LEU:HD22	1.68	0.75
20:B:128:LEU:HD12	20:B:132:GLU:HB2	1.68	0.75
1:A:518:C:H2'	1:A:530:G:C8	2.21	0.75
2:C:137:VAL:HA	2:C:148:ILE:HD13	1.67	0.75
1:A:524:G:H2'	1:A:525:C:C6	2.22	0.75
1:A:1315:U:H5	18:S:5:LYS:HZ1	1.33	0.75
12:M:44:ILE:HD12	12:M:44:ILE:H	1.50	0.75
1:A:1328:C:H5''	12:M:27:THR:HG21	1.67	0.74
13:N:51:PRO:HB2	13:N:54:SER:HB3	1.69	0.74
1:A:239:U:OP1	1:A:239:U:H4'	1.87	0.74
3:D:197:HIS:O	3:D:200:VAL:HG22	1.87	0.74
6:G:149:ALA:HB2	10:K:55:ARG:NH1	2.01	0.74
1:A:1142:G:H2'	1:A:1143:G:O4'	1.86	0.74
1:A:662:U:O2'	1:A:836:G:H5''	1.87	0.74
5:F:88:MET:HG3	5:F:89:VAL:N	2.03	0.74
10:K:111:ASP:HB2	21:U:19:LYS:HE3	1.68	0.74
12:M:10:ASP:HA	12:M:44:ILE:HD13	1.69	0.74
13:N:68:ARG:HB3	13:N:68:ARG:HH11	1.52	0.74
9:J:12:ALA:HB2	9:J:96:VAL:HG12	1.69	0.74
11:L:35:ARG:NH1	11:L:36:VAL:HG22	2.03	0.74
1:A:522:C:H41	11:L:49:ARG:HH22	1.35	0.74
1:A:1009:U:H2'	1:A:1010:U:C6	2.22	0.74
19:T:61:ALA:HA	19:T:67:HIS:H	1.53	0.73
12:M:28:ARG:HH12	12:M:59:VAL:HA	1.53	0.73
1:A:1278:G:H4'	1:A:1279:G:H5'	1.70	0.73
12:M:14:ALA:HB2	12:M:42:VAL:HG23	1.69	0.73
1:A:1081:A:OP2	4:E:51:LYS:HE2	1.88	0.73
20:B:186:VAL:O	20:B:200:PRO:HA	1.88	0.73
1:A:328:C:H4'	1:A:329:A:H5''	1.69	0.73
2:C:149:LYS:HB3	2:C:200:TRP:HB2	1.71	0.73
3:D:77:GLU:HA	3:D:80:ARG:HG2	1.69	0.73
1:A:376:G:H5''	15:P:5:ARG:HB2	1.71	0.73
4:E:156:ARG:HA	4:E:158:LYS:HZ3	1.54	0.73
20:B:187:ASP:OD1	20:B:203:ASP:HB3	1.88	0.73

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:D:24:VAL:HG23	3:D:25:ARG:HD2	1.70	0.73
3:D:25:ARG:HD3	3:D:26:ALA:N	2.04	0.73
1:A:1343:G:H1'	8:I:122:ARG:HH12	1.54	0.73
20:B:79:VAL:HG12	20:B:90:PHE:HB2	1.70	0.73
2:C:48:LYS:H	2:C:48:LYS:HD3	1.53	0.72
1:A:505:G:H5'	1:A:534:U:H2'	1.70	0.72
5:F:42:TRP:NE1	5:F:61:LEU:HD23	2.03	0.72
1:A:484:G:H4'	1:A:485:U:O5'	1.88	0.72
16:Q:45:VAL:HG12	16:Q:46:HIS:H	1.54	0.72
17:R:22:TYR:HB2	17:R:61:ALA:HB2	1.70	0.72
2:C:19:SER:HB3	2:C:21:TRP:HE1	1.55	0.72
1:A:636:U:H2'	1:A:637:C:C6	2.25	0.72
11:L:120:ARG:HG2	11:L:121:PRO:HD2	1.72	0.72
5:F:88:MET:HG3	5:F:89:VAL:H	1.51	0.71
4:E:114:LEU:HD13	4:E:122:VAL:HG21	1.71	0.71
1:A:474:G:H2'	1:A:475:C:C6	2.25	0.71
1:A:473:U:H2'	1:A:474:G:C8	2.25	0.71
10:K:34:THR:HA	10:K:41:LEU:HG	1.71	0.71
1:A:264:C:H4'	16:Q:64:ARG:HD2	1.70	0.71
5:F:91:ARG:HG3	5:F:93:LYS:HE3	1.72	0.71
7:H:76:ARG:HG3	7:H:77:VAL:N	2.04	0.71
19:T:68:LYS:HA	19:T:68:LYS:HE2	1.71	0.71
1:A:451:A:H5'	15:P:70:ARG:HH22	1.56	0.71
10:K:105:ARG:HH21	21:U:10:PRO:HB3	1.55	0.71
1:A:1314:C:H3'	18:S:5:LYS:HZ2	1.55	0.71
1:A:1151:A:HO2'	1:A:1152:A:H8	1.35	0.71
1:A:1060:U:H4'	9:J:54:SER:HB2	1.71	0.71
20:B:128:LEU:HD13	20:B:129:THR:N	2.05	0.71
20:B:19:THR:HG23	20:B:20:ARG:H	1.53	0.71
4:E:28:ARG:HH12	4:E:30:PHE:HB3	1.55	0.71
11:L:56:LEU:HD12	11:L:60:PHE:HB2	1.73	0.71
9:J:53:ILE:CG2	9:J:61:ALA:HB1	2.20	0.71
1:A:523:A:H61	11:L:88:ASP:HB2	1.55	0.71
1:A:238:A:H2'	1:A:239:U:H5''	1.73	0.71
20:B:218:ALA:HA	20:B:221:ARG:HG2	1.71	0.70
3:D:24:VAL:HG23	3:D:25:ARG:H	1.56	0.70
6:G:23:ALA:O	6:G:26:VAL:HG22	1.91	0.70
1:A:237:G:H2'	1:A:238:A:H8	1.56	0.70
11:L:24:GLU:HB2	11:L:26:CYS:SG	2.31	0.70
1:A:999:C:H2'	1:A:1000:A:C8	2.27	0.70
8:I:41:GLU:H	8:I:44:ARG:NH1	1.88	0.70
3:D:153:ARG:HG3	3:D:154:VAL:H	1.57	0.70

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:F:36:ILE:HG13	5:F:64:VAL:HG22	1.73	0.70
6:G:110:ARG:HD2	6:G:122:GLU:HB2	1.73	0.70
2:C:122:GLN:HB3	2:C:127:VAL:HG21	1.74	0.70
3:D:96:ARG:HB3	3:D:98:ASP:OD2	1.90	0.70
20:B:185:ILE:HA	20:B:199:ILE:HB	1.72	0.70
1:A:1477:U:H2'	1:A:1478:U:C6	2.27	0.70
21:U:40:PRO:O	21:U:44:ARG:HB2	1.92	0.70
10:K:92:ARG:NH1	21:U:20:ARG:HH21	1.90	0.70
9:J:37:ARG:NE	9:J:37:ARG:HA	2.06	0.70
2:C:2:GLN:H	2:C:2:GLN:NE2	1.90	0.70
1:A:859:G:H2'	1:A:860:A:C8	2.26	0.70
1:A:1202:U:H1'	13:N:68:ARG:HD2	1.74	0.69
1:A:473:U:H2'	1:A:474:G:H8	1.57	0.69
1:A:993:G:H2'	1:A:995:C:H41	1.55	0.69
1:A:154:U:H2'	1:A:155:A:C8	2.28	0.69
4:E:89:THR:HG22	4:E:90:GLY:H	1.56	0.69
8:I:27:ILE:HB	8:I:34:LEU:HB2	1.72	0.69
1:A:1490:U:H5'	1:A:1491:G:OP2	1.92	0.69
7:H:113:ARG:NH2	7:H:114:ALA:HA	2.07	0.69
1:A:1086:U:H3	1:A:1099:G:N2	1.86	0.69
2:C:69:THR:HG21	2:C:75:VAL:HG21	1.74	0.69
1:A:842:U:H2'	1:A:843:U:O3'	1.92	0.69
4:E:158:LYS:HZ1	7:H:63:LYS:HD3	1.57	0.69
8:I:48:ARG:HA	8:I:51:LEU:HD12	1.74	0.69
20:B:120:SER:HA	20:B:125:PHE:CD1	2.27	0.69
6:G:145:GLU:HA	6:G:148:LYS:HB2	1.75	0.69
20:B:45:THR:HA	20:B:48:MET:HG3	1.73	0.69
5:F:5:GLU:HA	5:F:63:ASN:HA	1.75	0.69
9:J:12:ALA:HB3	9:J:18:ILE:HB	1.75	0.69
6:G:130:LYS:N	6:G:134:VAL:HG21	2.06	0.69
1:A:518:C:H2'	1:A:530:G:H8	1.58	0.69
2:C:61:LYS:HZ2	2:C:96:VAL:HG11	1.57	0.69
1:A:182:A:O2'	1:A:183:C:H3'	1.92	0.69
4:E:61:LYS:O	4:E:65:LYS:HG2	1.92	0.69
2:C:190:THR:HG22	2:C:191:THR:N	2.07	0.69
1:A:1007:U:H2'	1:A:1008:U:C6	2.28	0.69
15:P:6:LEU:HB3	15:P:17:TYR:HB3	1.73	0.69
12:M:106:ARG:HD3	12:M:111:PRO:HA	1.75	0.69
3:D:146:GLU:HA	3:D:149:LYS:HG2	1.73	0.68
1:A:1391:U:H2'	1:A:1392:G:C8	2.29	0.68
20:B:23:ASN:HD22	20:B:24:PRO:HD2	1.58	0.68
1:A:865:A:H5'	1:A:1078:U:O4	1.93	0.68

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:N:30:ILE:H	13:N:30:ILE:HD12	1.58	0.68
1:A:1296:C:H4'	1:A:1302:C:N4	2.08	0.68
6:G:12:LEU:HD22	6:G:13:PRO:HD2	1.73	0.68
3:D:28:ASP:HA	3:D:33:ILE:HG21	1.73	0.68
1:A:1218:C:H2'	1:A:1219:A:C8	2.28	0.68
4:E:95:MET:HA	4:E:124:ALA:HB2	1.75	0.68
20:B:202:ASN:HD22	20:B:204:ASP:N	1.90	0.68
1:A:384:G:H2'	1:A:385:C:C6	2.28	0.68
1:A:312:C:H2'	1:A:313:A:H8	1.59	0.68
21:U:16:ARG:NE	21:U:16:ARG:HA	2.04	0.68
1:A:1038:C:H2'	1:A:1039:G:C8	2.29	0.68
2:C:26:LYS:HG3	2:C:27:GLU:H	1.59	0.68
1:A:1250:A:H4'	8:I:69:GLY:N	2.09	0.68
1:A:560:A:H4'	1:A:561:U:H5''	1.76	0.68
21:U:34:ARG:HH21	21:U:36:PHE:HE2	1.42	0.68
1:A:90:C:H2'	1:A:91:U:C5	2.29	0.68
1:A:337:G:H2'	1:A:338:A:C8	2.29	0.68
1:A:1018:G:H2'	1:A:1019:A:H8	1.58	0.68
5:F:1:MET:SD	5:F:67:PRO:HD3	2.34	0.67
1:A:160:A:H2'	1:A:161:A:O4'	1.94	0.67
1:A:279:A:H5''	1:A:280:C:H3'	1.76	0.67
10:K:75:GLU:CD	10:K:75:GLU:H	1.95	0.67
13:N:14:ALA:HB1	13:N:18:LYS:HE3	1.75	0.67
1:A:1092:A:H5''	6:G:3:ARG:HH12	1.58	0.67
1:A:590:U:H2'	1:A:591:U:C6	2.29	0.67
20:B:221:ARG:HH11	20:B:221:ARG:HB3	1.59	0.67
15:P:57:ILE:O	15:P:61:VAL:HG23	1.94	0.67
1:A:1348:U:H4'	8:I:121:ARG:HG3	1.76	0.67
1:A:269:C:H2'	1:A:270:A:H8	1.58	0.67
1:A:658:C:H2'	1:A:659:U:H6	1.57	0.67
1:A:56:U:H2'	1:A:57:G:H8	1.58	0.67
2:C:31:ASN:HD22	2:C:58:ARG:HE	1.40	0.67
8:I:46:VAL:HA	8:I:49:GLN:HG3	1.77	0.67
4:E:33:THR:HG22	4:E:51:LYS:HB3	1.76	0.67
15:P:3:THR:HG22	15:P:66:THR:HB	1.77	0.67
19:T:69:ASN:H	19:T:69:ASN:ND2	1.92	0.67
19:T:56:ILE:O	19:T:60:GLN:HG2	1.93	0.67
1:A:973:G:H3'	1:A:974:A:H5''	1.77	0.67
1:A:157:U:O2'	1:A:158:G:H5'	1.94	0.67
3:D:22:SER:H	3:D:109:THR:HG22	1.60	0.67
11:L:17:LYS:HE3	11:L:17:LYS:N	2.09	0.67
3:D:94:GLU:HG2	3:D:190:LEU:HG	1.76	0.67

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:N:45:LEU:HD21	18:S:9:PHE:HB2	1.75	0.67
15:P:43:ALA:HA	15:P:46:LYS:HE3	1.76	0.67
3:D:71:PHE:HE1	3:D:89:LEU:HD21	1.59	0.67
16:Q:75:VAL:HG23	16:Q:76:ARG:H	1.58	0.67
13:N:12:ARG:HA	13:N:15:LEU:HD12	1.77	0.67
19:T:43:LYS:HE2	19:T:44:ALA:N	2.10	0.67
12:M:33:LEU:HB3	12:M:38:ILE:O	1.95	0.67
20:B:86:CYS:HB3	20:B:88:GLN:CD	2.14	0.67
1:A:190:A:H2'	1:A:191:G:O4'	1.95	0.67
8:I:64:ILE:H	8:I:64:ILE:HD12	1.60	0.66
12:M:18:LEU:HD23	12:M:24:VAL:HG21	1.77	0.66
3:D:25:ARG:NH1	3:D:30:LYS:HE3	2.10	0.66
2:C:59:PRO:HG2	2:C:62:SER:OG	1.94	0.66
8:I:50:PRO:HD3	8:I:79:ARG:HG3	1.77	0.66
5:F:90:MET:HG2	17:R:60:ARG:NH2	2.09	0.66
1:A:1316:G:N2	1:A:1318:A:H3'	2.08	0.66
10:K:51:PHE:CZ	10:K:61:ALA:HA	2.30	0.66
1:A:1238:A:H5'	1:A:1336:C:H41	1.60	0.66
6:G:64:ALA:HA	6:G:127:ALA:HA	1.74	0.66
1:A:539:A:H2'	1:A:540:G:C8	2.30	0.66
12:M:10:ASP:HB2	12:M:11:HIS:ND1	2.10	0.66
16:Q:8:GLN:HA	16:Q:59:GLU:HA	1.77	0.66
1:A:764:C:C2'	1:A:765:G:H5'	2.26	0.66
21:U:38:GLU:C	21:U:40:PRO:HD2	2.16	0.66
1:A:465:A:H2'	1:A:467:U:OP2	1.94	0.66
2:C:61:LYS:NZ	2:C:96:VAL:HG11	2.10	0.66
1:A:764:C:H2'	1:A:765:G:H5'	1.77	0.66
1:A:673:A:H2'	1:A:674:G:C8	2.30	0.66
10:K:91:GLY:O	10:K:95:THR:HG22	1.96	0.66
1:A:1343:G:H2'	1:A:1344:C:C6	2.31	0.66
1:A:1018:G:H2'	1:A:1019:A:C8	2.31	0.66
20:B:163:ILE:HG23	20:B:164:ASP:N	2.08	0.66
18:S:30:LEU:HD12	18:S:48:ILE:HG12	1.75	0.66
9:J:53:ILE:HG13	13:N:84:ARG:CZ	2.26	0.66
1:A:920:U:H2'	1:A:921:U:C6	2.31	0.66
1:A:140:U:H2'	1:A:141:G:H8	1.60	0.66
13:N:63:CYS:HB2	13:N:79:SER:HB3	1.76	0.66
1:A:68:G:H5'	1:A:171:A:C1'	2.24	0.66
11:L:51:VAL:HG12	11:L:52:CYS:H	1.59	0.66
8:I:71:ILE:HD12	8:I:71:ILE:H	1.59	0.66
21:U:24:LYS:HD2	21:U:25:ALA:H	1.60	0.66
1:A:382:A:H2'	1:A:383:A:C8	2.31	0.66

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:678:U:H2'	1:A:679:C:C6	2.31	0.66
20:B:22:TRP:HB3	20:B:38:HIS:NE2	2.09	0.66
11:L:35:ARG:HH12	11:L:36:VAL:HG22	1.59	0.66
1:A:922:G:H2'	1:A:923:A:C8	2.30	0.66
1:A:478:A:H2'	1:A:479:U:O4'	1.96	0.66
1:A:763:G:H2'	1:A:764:C:H6	1.59	0.66
1:A:699:C:H2'	1:A:700:G:H5''	1.76	0.66
8:I:83:THR:HA	8:I:86:LEU:HD22	1.76	0.66
21:U:42:THR:O	21:U:46:ARG:HG3	1.95	0.66
3:D:160:LEU:HD22	3:D:161:ALA:N	2.11	0.66
5:F:42:TRP:HB2	5:F:59:TYR:HB2	1.77	0.66
20:B:10:LYS:HB3	20:B:211:LEU:HD21	1.78	0.66
1:A:957:U:H4'	18:S:78:THR:HB	1.77	0.66
1:A:1390:U:H2'	1:A:1391:U:C6	2.30	0.65
1:A:950:U:H2'	1:A:951:G:H8	1.61	0.65
1:A:35:G:H2'	1:A:36:C:C6	2.31	0.65
20:B:162:VAL:HG13	20:B:184:ALA:HB2	1.79	0.65
16:Q:16:MET:CB	16:Q:19:SER:HB2	2.26	0.65
12:M:85:TYR:HA	12:M:88:LEU:HD12	1.78	0.65
7:H:37:ASN:O	7:H:41:GLU:HG2	1.96	0.65
20:B:187:ASP:HB3	20:B:201:GLY:O	1.96	0.65
1:A:312:C:H2'	1:A:313:A:C8	2.31	0.65
1:A:719:C:H1'	17:R:37:LYS:HB2	1.77	0.65
4:E:143:LEU:O	4:E:146:MET:HG2	1.97	0.65
1:A:1302:C:OP2	12:M:16:ILE:HD11	1.96	0.65
1:A:1479:C:H2'	1:A:1480:A:H8	1.62	0.65
13:N:46:LYS:HZ2	18:S:10:ILE:H	1.43	0.65
2:C:65:VAL:HG21	2:C:90:VAL:HG11	1.79	0.65
1:A:1162:C:H2'	1:A:1163:A:C8	2.31	0.65
1:A:1026:G:N3	1:A:1026:G:H2'	2.10	0.65
13:N:79:SER:HG	13:N:82:LYS:HG2	1.61	0.65
1:A:1144:G:N2	1:A:1146:A:H62	1.95	0.65
1:A:632:U:H5''	1:A:633:G:C8	2.31	0.65
1:A:499:A:H4'	1:A:500:G:OP1	1.95	0.65
3:D:81:LEU:HB2	3:D:88:ASN:ND2	2.11	0.65
1:A:41:G:H2'	1:A:42:G:C8	2.32	0.65
10:K:80:ASN:HB3	10:K:105:ARG:HB3	1.79	0.65
4:E:84:VAL:HG11	4:E:146:MET:HB3	1.79	0.65
2:C:70:ALA:HA	2:C:105:VAL:CG2	2.26	0.65
1:A:1513:A:H2'	1:A:1514:G:C8	2.32	0.65
1:A:1144:G:H21	1:A:1146:A:H62	1.43	0.65
1:A:129:A:H1'	1:A:130:A:C8	2.31	0.65

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:E:64:GLU:O	4:E:68:ARG:HG2	1.97	0.65
15:P:59:HIS:O	15:P:63:GLN:HG3	1.97	0.65
10:K:80:ASN:H	10:K:80:ASN:HD22	1.45	0.65
20:B:101:THR:HA	20:B:178:LEU:HD11	1.77	0.65
12:M:48:SER:HB2	12:M:51:GLN:HG3	1.79	0.65
12:M:92:ARG:HE	12:M:92:ARG:HA	1.61	0.65
1:A:97:G:H2'	1:A:98:A:O4'	1.97	0.65
5:F:97:THR:O	5:F:98:GLU:HB3	1.95	0.65
10:K:124:LYS:O	21:U:33:ARG:NE	2.27	0.65
5:F:9:MET:HB3	5:F:59:TYR:CD2	2.31	0.65
1:A:1389:C:H2'	1:A:1390:U:C6	2.32	0.65
6:G:52:ARG:HH22	6:G:121:ASN:ND2	1.95	0.65
15:P:38:PHE:HE2	15:P:51:ARG:HH11	1.45	0.65
1:A:108:G:C6	19:T:9:ARG:HG2	2.32	0.65
8:I:56:MET:C	8:I:58:GLU:H	2.00	0.64
12:M:90:HIS:HA	12:M:108:ARG:HH22	1.60	0.64
3:D:145:ARG:HB3	3:D:147:LYS:HD2	1.78	0.64
13:N:50:LEU:N	13:N:51:PRO:HD2	2.12	0.64
2:C:120:THR:HG22	2:C:188:ALA:HB2	1.79	0.64
1:A:909:A:H2'	1:A:910:C:O4'	1.96	0.64
12:M:78:ARG:O	12:M:82:LEU:HB2	1.97	0.64
4:E:152:VAL:HG21	7:H:98:LEU:HB3	1.78	0.64
13:N:27:LYS:HA	13:N:31:SER:HB2	1.78	0.64
12:M:47:LEU:HD22	12:M:51:GLN:HB3	1.79	0.64
1:A:237:G:H2'	1:A:238:A:C8	2.32	0.64
1:A:1226:C:H4'	1:A:1227:A:OP1	1.96	0.64
5:F:7:VAL:HG13	5:F:88:MET:HB3	1.80	0.64
1:A:1218:C:H2'	1:A:1219:A:H8	1.63	0.64
1:A:270:A:H2'	1:A:271:C:C6	2.32	0.64
4:E:156:ARG:HA	4:E:158:LYS:NZ	2.13	0.64
1:A:1238:A:H5'	1:A:1336:C:N4	2.13	0.64
3:D:138:PRO:HA	3:D:181:PHE:HD2	1.61	0.64
19:T:49:ALA:HA	19:T:52:GLU:OE2	1.97	0.64
20:B:94:ARG:HE	20:B:94:ARG:N	1.96	0.64
3:D:155:LYS:HA	3:D:158:LEU:HD13	1.78	0.64
11:L:41:PRO:HB3	11:L:49:ARG:NH1	2.13	0.64
20:B:63:LYS:HG2	20:B:224:ARG:HH22	1.62	0.64
1:A:859:G:H2'	1:A:860:A:H8	1.62	0.64
20:B:125:PHE:HD2	20:B:125:PHE:H	1.46	0.64
1:A:17:U:H2'	1:A:18:C:H6	1.60	0.64
16:Q:60:ILE:HG22	16:Q:74:LEU:HA	1.79	0.64
9:J:66:GLU:HB3	13:N:98:ALA:HB2	1.78	0.64

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:501:C:H2'	1:A:502:A:H8	1.62	0.64
20:B:172:ILE:HG22	20:B:176:ASN:HD21	1.61	0.64
2:C:13:ILE:HD13	2:C:13:ILE:H	1.63	0.64
1:A:961:U:H3	1:A:983:A:N6	1.95	0.64
6:G:108:ARG:HG2	6:G:115:MET:HE3	1.79	0.64
1:A:1343:G:H4'	8:I:123:ARG:O	1.97	0.64
12:M:90:HIS:HA	12:M:108:ARG:NH2	2.13	0.64
9:J:55:PRO:HA	13:N:80:ARG:NH2	2.12	0.64
1:A:268:U:H2'	1:A:269:C:C6	2.33	0.64
2:C:39:ARG:NH1	2:C:56:ILE:HD12	2.13	0.64
18:S:35:ARG:NH2	18:S:52:ASN:HA	2.13	0.64
1:A:982:U:H5''	13:N:5:MET:HE2	1.80	0.63
4:E:82:HIS:HB2	4:E:83:PRO:HD2	1.79	0.63
13:N:46:LYS:NZ	18:S:10:ILE:H	1.95	0.63
1:A:946:A:H2'	1:A:947:G:C8	2.33	0.63
12:M:53:ASP:HA	12:M:56:ARG:NH1	2.13	0.63
1:A:453:G:H2'	1:A:454:G:C8	2.33	0.63
2:C:13:ILE:O	2:C:14:VAL:HG22	1.98	0.63
1:A:882:C:O2'	1:A:883:C:H5'	1.97	0.63
18:S:5:LYS:C	18:S:6:LYS:HD2	2.18	0.63
20:B:107:ARG:HH21	20:B:111:LYS:HB2	1.63	0.63
8:I:48:ARG:O	8:I:52:GLU:HG2	1.98	0.63
5:F:29:ILE:HD13	5:F:64:VAL:HG21	1.81	0.63
1:A:454:G:H2'	1:A:455:G:H8	1.62	0.63
1:A:1170:A:H2'	1:A:1171:A:O4'	1.99	0.63
1:A:1171:A:H2'	1:A:1172:C:C6	2.33	0.63
20:B:160:LEU:HD23	20:B:182:VAL:HG22	1.80	0.63
2:C:134:LYS:HA	2:C:167:TYR:HE2	1.63	0.63
1:A:1060:U:H5''	9:J:53:ILE:HG12	1.80	0.63
2:C:140:ALA:HB3	2:C:148:ILE:HD12	1.80	0.63
1:A:662:U:H2'	1:A:663:A:C8	2.32	0.63
1:A:590:U:H2'	1:A:591:U:H6	1.62	0.63
1:A:552:U:H2'	1:A:553:A:C8	2.33	0.63
1:A:8:A:H5'	4:E:105:ILE:HG22	1.80	0.63
19:T:79:THR:O	19:T:82:ILE:HG13	1.98	0.63
1:A:1399:C:H4'	1:A:1400:C:C5'	2.28	0.63
2:C:113:LYS:HB2	2:C:184:ASN:OD1	1.97	0.63
2:C:57:GLU:HB2	2:C:64:ARG:HB2	1.78	0.63
1:A:1309:G:H1'	12:M:72:ILE:HD11	1.79	0.63
1:A:1186:G:H21	13:N:100:TRP:C	2.02	0.63
1:A:452:A:H2'	1:A:453:G:O4'	1.98	0.63
3:D:106:PHE:CG	3:D:144:ILE:HD11	2.34	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1273:C:H2'	1:A:1274:A:O4'	1.99	0.63
1:A:68:G:H2'	1:A:69:G:O4'	1.98	0.62
10:K:17:ASP:HB3	10:K:80:ASN:ND2	2.13	0.62
1:A:33:A:H2'	1:A:34:C:H6	1.63	0.62
1:A:176:C:H2'	1:A:177:G:N3	2.14	0.62
14:O:36:ILE:HD11	14:O:59:MET:HB2	1.80	0.62
8:I:44:ARG:O	8:I:47:VAL:HG22	1.98	0.62
1:A:1513:A:H2'	1:A:1514:G:H8	1.62	0.62
6:G:52:ARG:HH22	6:G:121:ASN:HD21	1.44	0.62
1:A:1168:U:H4'	1:A:1169:A:OP2	1.99	0.62
4:E:53:ARG:HE	4:E:54:GLU:HG2	1.62	0.62
13:N:40:ARG:HH11	18:S:6:LYS:HB2	1.62	0.62
3:D:25:ARG:HD3	3:D:26:ALA:H	1.64	0.62
4:E:28:ARG:NH1	4:E:30:PHE:HB3	2.14	0.62
6:G:19:SER:OG	6:G:22:LEU:HB2	1.99	0.62
8:I:32:ARG:HH11	8:I:37:TYR:HD1	1.47	0.62
21:U:36:PHE:O	21:U:39:LYS:HD2	1.98	0.62
3:D:77:GLU:OE1	3:D:80:ARG:HD3	2.00	0.62
16:Q:45:VAL:HG11	16:Q:60:ILE:HG21	1.80	0.62
1:A:636:U:H2'	1:A:637:C:H6	1.62	0.62
1:A:56:U:H2'	1:A:57:G:C8	2.34	0.62
1:A:1137:C:H1'	1:A:1138:G:N1	2.15	0.62
1:A:784:A:H2'	1:A:785:G:H8	1.63	0.62
5:F:81:ASN:HB3	5:F:84:VAL:HG12	1.81	0.62
1:A:179:A:H2'	1:A:180:U:O4'	1.99	0.62
1:A:492:C:H2'	1:A:493:A:N3	2.14	0.62
10:K:22:ILE:HD12	10:K:85:VAL:HG22	1.80	0.62
1:A:1226:C:H5''	12:M:101:THR:HB	1.81	0.62
1:A:33:A:H2'	1:A:34:C:C6	2.35	0.62
1:A:796:C:H4'	10:K:126:ARG:HH21	1.63	0.62
20:B:14:HIS:HB2	20:B:208:ALA:HB2	1.81	0.62
12:M:15:VAL:HG22	12:M:33:LEU:HD11	1.81	0.62
12:M:52:ILE:HD12	12:M:55:LEU:HD12	1.82	0.62
13:N:23:ARG:O	13:N:26:LEU:HD22	1.99	0.62
12:M:95:PRO:N	12:M:108:ARG:HG2	2.14	0.62
1:A:109:A:H4'	1:A:110:C:OP2	1.99	0.62
8:I:25:GLY:HA3	8:I:57:VAL:CA	2.28	0.62
12:M:71:GLU:CA	12:M:74:MET:HG2	2.24	0.62
7:H:11:THR:HA	7:H:14:ARG:NH1	2.14	0.62
11:L:49:ARG:HH12	11:L:88:ASP:CB	2.12	0.62
20:B:16:GLY:H	20:B:39:ILE:HG23	1.65	0.62
16:Q:45:VAL:HG12	16:Q:46:HIS:N	2.13	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:D:13:ARG:HG3	3:D:55:ARG:HH12	1.64	0.62
1:A:285:C:H2'	1:A:286:C:H6	1.65	0.62
20:B:218:ALA:O	20:B:222:GLU:HG2	2.00	0.62
1:A:371:A:O2'	1:A:372:C:H5'	1.99	0.62
16:Q:66:LEU:H	16:Q:66:LEU:HD12	1.64	0.62
1:A:285:C:H2'	1:A:286:C:C6	2.35	0.62
1:A:806:C:H2'	1:A:807:A:H8	1.64	0.62
1:A:1450:U:H2'	1:A:1452:C:C4	2.35	0.62
1:A:1053:G:H4'	1:A:1054:C:H5'	1.81	0.62
9:J:6:ILE:HB	9:J:76:ILE:HD11	1.81	0.62
8:I:9:GLY:HA2	8:I:80:HIS:CD2	2.35	0.62
1:A:1369:C:H2'	1:A:1370:G:C8	2.34	0.62
1:A:1132:C:H2'	1:A:1133:G:H8	1.63	0.62
19:T:38:ILE:HD11	19:T:82:ILE:HA	1.82	0.62
1:A:266:G:O2'	1:A:267:C:H3'	1.99	0.62
6:G:26:VAL:HG12	6:G:42:VAL:HG11	1.82	0.62
1:A:1137:C:H1'	1:A:1138:G:C2	2.35	0.62
8:I:94:ARG:HH11	8:I:94:ARG:HB3	1.65	0.62
1:A:1134:G:C2	1:A:1135:U:H1'	2.35	0.61
2:C:154:GLY:HA3	2:C:162:ALA:HB1	1.82	0.61
18:S:44:ILE:HA	18:S:61:VAL:HB	1.82	0.61
9:J:57:VAL:HG22	9:J:58:ASN:H	1.65	0.61
4:E:125:LYS:HD2	4:E:126:ALA:H	1.63	0.61
19:T:66:ILE:HG23	19:T:70:LYS:HB3	1.83	0.61
1:A:82:G:H1'	1:A:89:U:O4'	2.00	0.61
8:I:38:PHE:HZ	8:I:74:GLN:HB3	1.65	0.61
4:E:89:THR:HG22	4:E:90:GLY:N	2.16	0.61
1:A:430:A:OP1	3:D:8:LEU:HB2	2.01	0.61
1:A:21:G:H2'	1:A:22:G:C8	2.35	0.61
1:A:9:G:H5'	4:E:107:GLY:HA3	1.83	0.61
8:I:33:SER:HB3	8:I:36:GLN:HB2	1.83	0.61
21:U:16:ARG:NH1	21:U:19:LYS:HE2	2.15	0.61
1:A:131:A:H2'	1:A:132:C:C6	2.36	0.61
1:A:1071:C:H2'	1:A:1072:G:C8	2.32	0.61
1:A:204:G:H21	1:A:466:A:H62	1.48	0.61
15:P:3:THR:HB	15:P:66:THR:O	1.99	0.61
1:A:1173:U:H2'	1:A:1174:G:C8	2.35	0.61
6:G:21:LEU:HD23	6:G:21:LEU:H	1.65	0.61
1:A:1491:G:H5''	1:A:1492:A:OP2	2.00	0.61
3:D:28:ASP:HA	3:D:33:ILE:CG2	2.30	0.61
1:A:1301:U:H2'	1:A:1301:U:O2	1.99	0.61
14:O:8:THR:O	14:O:12:VAL:HG23	2.00	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:B:53:LEU:HD11	20:B:216:VAL:HG12	1.83	0.61
1:A:1250:A:H2'	1:A:1251:A:C8	2.36	0.61
20:B:86:CYS:HB2	20:B:221:ARG:NH1	2.14	0.61
7:H:113:ARG:HA	7:H:116:ARG:NH1	2.16	0.61
1:A:918:A:H2'	1:A:919:A:C8	2.36	0.61
6:G:46:LEU:O	6:G:57:GLU:HB3	2.01	0.61
1:A:501:C:H2'	1:A:502:A:C8	2.35	0.61
1:A:796:C:H4'	10:K:126:ARG:NH2	2.16	0.61
8:I:9:GLY:HA2	8:I:80:HIS:HD2	1.65	0.61
1:A:1367:C:H5'	9:J:62:ARG:NH1	2.16	0.61
1:A:211:G:H2'	1:A:212:G:O4'	2.00	0.61
1:A:272:C:H2'	1:A:273:U:H6	1.66	0.61
1:A:1032:G:H5''	1:A:1032:G:N3	2.14	0.61
19:T:4:LYS:HD2	19:T:5:SER:N	2.15	0.61
3:D:29:THR:HB	3:D:30:LYS:HD3	1.83	0.61
1:A:1320:C:N3	18:S:35:ARG:HD3	2.15	0.61
10:K:108:ASN:HD21	21:U:6:ARG:HD2	1.66	0.61
16:Q:79:GLU:HG3	16:Q:80:LYS:HZ2	1.66	0.61
14:O:70:LEU:HD11	14:O:77:ARG:HB2	1.82	0.61
16:Q:5:ARG:HE	16:Q:5:ARG:HA	1.66	0.61
8:I:15:ALA:O	8:I:66:VAL:HG23	2.01	0.60
1:A:335:C:H2'	1:A:336:A:H8	1.65	0.60
1:A:429:U:H3'	3:D:8:LEU:HD23	1.81	0.60
8:I:23:GLY:O	8:I:61:ASP:HB3	2.01	0.60
8:I:27:ILE:HG21	8:I:34:LEU:HD13	1.82	0.60
13:N:53:ASP:HA	13:N:58:ARG:HD3	1.83	0.60
1:A:958:A:H61	18:S:53:GLY:HA3	1.67	0.60
10:K:26:PHE:CE2	21:U:32:ARG:HD3	2.36	0.60
1:A:736:C:H2'	1:A:737:C:C6	2.36	0.60
1:A:1423:G:H2'	1:A:1424:U:C6	2.36	0.60
7:H:45:ILE:HG21	7:H:60:LEU:HD21	1.84	0.60
9:J:65:TYR:OH	13:N:84:ARG:HG3	2.00	0.60
1:A:241:G:O2'	1:A:242:G:H5'	2.02	0.60
1:A:1008:U:H2'	1:A:1009:U:H5''	1.82	0.60
1:A:41:G:H2'	1:A:42:G:H8	1.66	0.60
14:O:12:VAL:HG11	14:O:22:THR:HG22	1.82	0.60
16:Q:80:LYS:N	16:Q:80:LYS:HE3	2.16	0.60
12:M:22:TYR:HB3	12:M:69:ARG:CZ	2.30	0.60
1:A:620:C:N1	3:D:131:ILE:HD13	2.16	0.60
18:S:29:PRO:HA	18:S:47:THR:HB	1.81	0.60
5:F:29:ILE:HG21	5:F:64:VAL:HG11	1.83	0.60
19:T:66:ILE:HG13	19:T:70:LYS:HE3	1.83	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:G:110:ARG:CD	6:G:122:GLU:HB2	2.31	0.60
12:M:13:HIS:HB2	12:M:16:ILE:HG22	1.83	0.60
20:B:75:ALA:O	20:B:79:VAL:HG23	2.01	0.60
20:B:134:LEU:HA	20:B:137:THR:OG1	2.01	0.60
15:P:68:SER:OG	15:P:71:VAL:HG12	2.00	0.60
15:P:52:LEU:HD21	15:P:75:ILE:HG23	1.83	0.60
1:A:999:C:H2'	1:A:1000:A:H8	1.63	0.60
1:A:607:A:H2'	1:A:608:A:C8	2.36	0.60
20:B:118:THR:O	20:B:121:GLN:HB3	2.01	0.60
1:A:664:G:N2	1:A:741:G:H1	1.89	0.60
1:A:244:U:O4	1:A:906:A:H1'	2.00	0.60
2:C:149:LYS:HB2	2:C:168:ARG:HG3	1.84	0.60
1:A:1330:U:H2'	1:A:1331:G:H5'	1.83	0.60
2:C:142:ARG:HH21	2:C:143:LEU:HD11	1.66	0.60
12:M:22:TYR:HB2	12:M:65:GLU:HA	1.83	0.60
1:A:723:U:O4'	21:U:48:LYS:HD3	2.02	0.60
1:A:372:C:H4'	1:A:373:A:H5'	1.83	0.60
1:A:763:G:H2'	1:A:764:C:C6	2.37	0.60
1:A:1307:U:H2'	1:A:1308:U:C6	2.36	0.60
1:A:607:A:H2'	1:A:608:A:H8	1.66	0.60
18:S:66:VAL:HG23	18:S:67:GLY:H	1.67	0.60
9:J:26:VAL:HG13	9:J:36:VAL:HG11	1.83	0.60
1:A:677:U:H2'	1:A:678:U:C6	2.37	0.60
11:L:106:VAL:HG23	11:L:116:TYR:HB3	1.84	0.60
13:N:79:SER:OG	13:N:82:LYS:HG2	2.02	0.60
20:B:205:ALA:HB3	20:B:208:ALA:HB3	1.84	0.60
10:K:80:ASN:N	10:K:80:ASN:ND2	2.46	0.60
7:H:6:ILE:HB	7:H:76:ARG:NH1	2.16	0.60
2:C:31:ASN:ND2	2:C:58:ARG:HE	1.99	0.60
1:A:676:A:H1'	10:K:116:PRO:HB3	1.83	0.60
1:A:966:G:H21	8:I:129:ARG:HD3	1.67	0.60
20:B:93:HIS:CD2	20:B:145:ASN:HB3	2.37	0.60
1:A:390:U:H2'	1:A:391:G:C8	2.37	0.60
13:N:41:TRP:HD1	13:N:44:VAL:HG23	1.66	0.59
1:A:1237:C:H3'	1:A:1336:C:H41	1.66	0.59
1:A:1486:G:H2'	1:A:1487:G:O4'	2.01	0.59
15:P:25:ARG:H	15:P:25:ARG:HD3	1.67	0.59
3:D:185:PRO:HB2	3:D:190:LEU:CB	2.27	0.59
20:B:23:ASN:HD22	20:B:24:PRO:CD	2.14	0.59
1:A:812:G:H2'	1:A:812:G:N3	2.17	0.59
1:A:1186:G:H4'	8:I:111:GLU:OE1	2.02	0.59
14:O:35:GLN:O	14:O:39:LEU:HB2	2.02	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:I:23:GLY:O	8:I:25:GLY:N	2.35	0.59
10:K:22:ILE:HG12	10:K:31:VAL:HG12	1.85	0.59
10:K:34:THR:HB	10:K:40:ALA:HA	1.84	0.59
3:D:104:MET:SD	3:D:179:GLY:HA3	2.42	0.59
1:A:1030:U:H4'	1:A:1031:C:C4	2.37	0.59
9:J:22:THR:OG1	9:J:72:ARG:HG3	2.01	0.59
10:K:22:ILE:HD13	10:K:95:THR:CG2	2.32	0.59
1:A:16:A:O2'	1:A:17:U:H5'	2.02	0.59
18:S:69:LYS:O	18:S:72:GLU:HG2	2.03	0.59
1:A:1132:C:H2'	1:A:1133:G:C8	2.38	0.59
20:B:133:ALA:O	20:B:137:THR:HG23	2.02	0.59
1:A:1435:G:H2'	1:A:1436:U:C6	2.37	0.59
7:H:28:SER:OG	7:H:56:PRO:HB2	2.02	0.59
18:S:62:THR:HG22	18:S:63:ASP:H	1.68	0.59
20:B:60:ALA:O	20:B:224:ARG:HD2	2.02	0.59
3:D:146:GLU:HB3	3:D:149:LYS:HE3	1.85	0.59
9:J:51:VAL:HG23	13:N:80:ARG:HB2	1.84	0.59
1:A:806:C:H2'	1:A:807:A:C8	2.37	0.59
2:C:155:ARG:H	2:C:162:ALA:HA	1.67	0.59
18:S:39:ILE:HB	18:S:66:VAL:O	2.02	0.59
16:Q:3:LYS:HA	16:Q:3:LYS:HE2	1.83	0.59
6:G:107:ALA:O	6:G:118:ARG:HB3	2.02	0.59
16:Q:64:ARG:HG2	16:Q:65:PRO:HD2	1.85	0.59
7:H:124:ILE:HG22	7:H:125:ILE:N	2.17	0.59
20:B:168:GLU:O	20:B:172:ILE:HD12	2.03	0.59
1:A:1272:G:H2'	1:A:1273:C:C6	2.38	0.59
1:A:443:C:H2'	1:A:444:G:C8	2.37	0.59
1:A:358:U:H2'	1:A:359:G:C8	2.37	0.59
1:A:797:C:OP1	10:K:125:LYS:HG2	2.02	0.59
21:U:39:LYS:N	21:U:40:PRO:HD2	2.18	0.59
6:G:134:VAL:HB	6:G:137:ARG:HH21	1.68	0.59
1:A:93:U:H3'	1:A:94:G:H5''	1.83	0.59
1:A:1314:C:H3'	18:S:5:LYS:NZ	2.18	0.59
1:A:1317:C:H2'	1:A:1318:A:O4'	2.03	0.59
6:G:52:ARG:HH12	6:G:121:ASN:HD22	1.51	0.59
1:A:82:G:C6	1:A:88:U:O2	2.56	0.59
1:A:602:A:O2'	1:A:603:U:H5'	2.02	0.59
9:J:85:ASP:HA	9:J:88:MET:SD	2.42	0.59
20:B:27:LYS:HA	20:B:30:ILE:HD12	1.84	0.59
1:A:472:U:H2'	1:A:473:U:C6	2.38	0.59
1:A:193:C:H2'	1:A:194:C:C6	2.38	0.59
1:A:272:C:H2'	1:A:273:U:C6	2.37	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:H:94:VAL:HG23	7:H:101:ALA:HB2	1.83	0.59
1:A:1070:U:H2'	1:A:1071:C:C6	2.37	0.59
1:A:320:A:H2'	1:A:321:A:C8	2.38	0.59
1:A:1151:A:O2'	1:A:1152:A:H8	1.86	0.59
1:A:235:C:H2'	1:A:236:A:C8	2.38	0.59
20:B:14:HIS:HD2	20:B:202:ASN:H	1.51	0.59
19:T:85:LEU:HD23	19:T:86:ALA:H	1.67	0.59
1:A:1152:A:H2'	1:A:1153:G:H8	1.67	0.59
1:A:950:U:H2'	1:A:951:G:C8	2.38	0.59
16:Q:79:GLU:HG3	16:Q:80:LYS:NZ	2.16	0.59
1:A:434:U:H3'	1:A:435:A:H8	1.65	0.59
11:L:43:LYS:HE2	11:L:44:PRO:HD3	1.84	0.59
10:K:95:THR:HG23	10:K:96:ILE:H	1.68	0.58
6:G:100:MET:O	6:G:104:VAL:HG23	2.03	0.58
20:B:102:ASN:O	20:B:106:VAL:HG23	2.03	0.58
1:A:1278:G:H4'	1:A:1279:G:C5'	2.33	0.58
11:L:60:PHE:HB3	11:L:62:VAL:HG13	1.85	0.58
11:L:81:ILE:HG23	11:L:94:TYR:HB3	1.84	0.58
1:A:677:U:H2'	1:A:678:U:H6	1.67	0.58
1:A:429:U:H1'	1:A:430:A:H5''	1.85	0.58
14:O:43:PHE:CD1	14:O:56:LEU:HD22	2.38	0.58
11:L:85:ARG:HG3	11:L:86:VAL:N	2.18	0.58
15:P:28:ARG:CD	15:P:29:ASN:H	2.14	0.58
13:N:51:PRO:HG2	13:N:52:ARG:H	1.68	0.58
18:S:35:ARG:HB2	18:S:71:GLY:HA2	1.86	0.58
9:J:35:GLN:HG2	9:J:77:VAL:HB	1.85	0.58
1:A:148:G:N3	1:A:1446:A:H2	2.01	0.58
19:T:19:HIS:O	19:T:23:ARG:HG2	2.03	0.58
6:G:72:VAL:HA	6:G:89:GLU:HA	1.85	0.58
20:B:42:LEU:O	20:B:46:VAL:HG12	2.02	0.58
1:A:981:U:H2'	1:A:982:U:C5	2.38	0.58
1:A:1323:G:H2'	1:A:1324:A:H8	1.65	0.58
2:C:152:VAL:HB	2:C:156:LEU:HD21	1.83	0.58
10:K:19:VAL:HG12	10:K:82:GLU:HB2	1.85	0.58
8:I:94:ARG:HA	8:I:97:LEU:HG	1.85	0.58
10:K:45:THR:HG23	10:K:48:GLY:HA3	1.85	0.58
1:A:1034:G:H2'	1:A:1034:G:N3	2.19	0.58
8:I:25:GLY:HA2	8:I:60:LEU:O	2.04	0.58
20:B:65:LYS:HD3	20:B:89:PHE:CZ	2.38	0.58
4:E:148:SER:HB2	4:E:149:PRO:HD2	1.85	0.58
16:Q:16:MET:HB3	16:Q:19:SER:HB2	1.83	0.58
1:A:736:C:H2'	1:A:737:C:H6	1.69	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
16:Q:30:HIS:CE1	16:Q:32:ILE:HG22	2.38	0.58
1:A:207:C:H2'	1:A:208:U:O4'	2.04	0.58
10:K:80:ASN:H	10:K:80:ASN:ND2	2.01	0.58
1:A:412:A:H4'	1:A:413:G:OP1	2.04	0.58
1:A:1390:U:H2'	1:A:1391:U:H6	1.67	0.58
1:A:140:U:H2'	1:A:141:G:C8	2.39	0.58
1:A:1028:C:H2'	1:A:1029:U:O4'	2.04	0.58
19:T:79:THR:HG22	19:T:83:ASN:HD21	1.68	0.58
16:Q:60:ILE:HG12	16:Q:72:TRP:HE3	1.68	0.58
1:A:57:G:H2'	1:A:58:C:C6	2.38	0.58
1:A:1338:G:H2'	1:A:1339:A:C8	2.39	0.58
12:M:1:ALA:O	12:M:3:ILE:HG13	2.04	0.58
12:M:52:ILE:HG13	12:M:56:ARG:HH11	1.68	0.58
2:C:26:LYS:HG3	2:C:27:GLU:N	2.18	0.58
3:D:196:GLU:O	3:D:199:ILE:HG12	2.04	0.58
1:A:1219:A:H2'	1:A:1220:G:C8	2.39	0.58
14:O:29:VAL:HG11	14:O:67:LEU:HD21	1.85	0.58
9:J:42:LEU:HD11	9:J:73:LEU:HB2	1.86	0.58
1:A:493:A:H5'	1:A:494:G:OP2	2.03	0.58
1:A:207:C:H3'	1:A:208:U:C6	2.39	0.58
7:H:118:ALA:HB3	7:H:120:LEU:HD22	1.84	0.58
1:A:715:A:H2'	1:A:716:A:C8	2.38	0.58
1:A:1005:A:H2'	1:A:1006:G:O4'	2.04	0.58
8:I:34:LEU:HD21	8:I:48:ARG:NE	2.18	0.58
3:D:58:GLN:O	3:D:62:ARG:HG2	2.04	0.58
2:C:156:LEU:HD11	2:C:165:GLU:HB2	1.86	0.58
3:D:90:LEU:HD21	3:D:196:GLU:HB3	1.85	0.58
3:D:98:ASP:HB3	3:D:132:ALA:HB1	1.86	0.58
1:A:796:C:OP1	10:K:127:ARG:HB3	2.04	0.58
2:C:91:ALA:HB2	2:C:98:ALA:H	1.69	0.58
1:A:398:U:H2'	1:A:399:G:H8	1.67	0.58
1:A:596:A:H2'	1:A:597:G:H8	1.69	0.58
1:A:1085:U:H3'	1:A:1086:U:C5	2.39	0.57
1:A:1343:G:H2'	1:A:1344:C:H6	1.67	0.57
1:A:1319:A:H3'	18:S:2:ARG:HA	1.84	0.57
6:G:99:ALA:O	6:G:103:ILE:HG13	2.04	0.57
16:Q:25:GLU:HB3	16:Q:38:LYS:HD3	1.86	0.57
1:A:1347:G:N2	1:A:1373:G:H2'	2.19	0.57
3:D:71:PHE:CE1	3:D:89:LEU:HD21	2.38	0.57
1:A:376:G:H2'	1:A:377:G:H8	1.68	0.57
1:A:923:A:H2'	1:A:924:C:C6	2.39	0.57
1:A:384:G:H2'	1:A:385:C:H6	1.68	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:135:C:O2	15:P:1:MET:HB2	2.03	0.57
1:A:708:C:H2'	1:A:709:U:C6	2.39	0.57
8:I:20:ILE:HD13	8:I:85:ALA:HB3	1.87	0.57
19:T:70:LYS:HA	19:T:73:ARG:NH1	2.19	0.57
6:G:59:GLU:O	6:G:63:VAL:HG23	2.04	0.57
19:T:15:LYS:HA	19:T:18:LYS:HE3	1.86	0.57
5:F:93:LYS:O	5:F:94:HIS:HB2	2.04	0.57
3:D:153:ARG:HG3	3:D:154:VAL:N	2.18	0.57
5:F:40:GLU:OE1	5:F:100:SER:HB2	2.04	0.57
5:F:88:MET:HE1	17:R:60:ARG:HB3	1.86	0.57
19:T:53:MET:HA	19:T:56:ILE:HD12	1.86	0.57
4:E:43:GLY:C	4:E:44:ARG:HD3	2.24	0.57
4:E:104:ILE:HD11	4:E:114:LEU:HB2	1.86	0.57
9:J:8:ILE:HG13	9:J:100:ILE:HG22	1.85	0.57
3:D:78:ALA:O	3:D:85:THR:HA	2.04	0.57
12:M:87:GLY:HA2	12:M:90:HIS:HD2	1.68	0.57
20:B:172:ILE:HG22	20:B:176:ASN:ND2	2.19	0.57
10:K:37:GLN:HB2	10:K:39:ASN:HD22	1.69	0.57
5:F:92:THR:HG22	5:F:93:LYS:N	2.19	0.57
10:K:22:ILE:HD13	10:K:95:THR:HG21	1.85	0.57
13:N:20:PHE:CD1	13:N:24:ALA:HB2	2.39	0.57
1:A:93:U:C3'	1:A:94:G:H4'	2.34	0.57
2:C:42:LEU:O	2:C:46:LEU:HB2	2.04	0.57
15:P:67:ILE:HD11	15:P:71:VAL:HG22	1.85	0.57
1:A:793:U:O2	1:A:1516:G:H4'	2.04	0.57
3:D:138:PRO:HA	3:D:181:PHE:CD2	2.40	0.57
9:J:56:HIS:O	9:J:57:VAL:HG12	2.05	0.57
12:M:2:ARG:HB3	12:M:6:ILE:HA	1.85	0.57
17:R:34:GLU:H	17:R:34:GLU:CD	2.08	0.57
1:A:524:G:H2'	1:A:525:C:H6	1.68	0.57
3:D:89:LEU:HD13	3:D:199:ILE:HD11	1.85	0.57
1:A:32:A:H2'	1:A:33:A:C8	2.40	0.57
1:A:431:A:H2'	1:A:432:A:O4'	2.04	0.57
19:T:29:THR:HA	19:T:32:LYS:HE3	1.86	0.57
12:M:38:ILE:HG13	12:M:55:LEU:HD21	1.87	0.57
20:B:104:LYS:HG3	20:B:105:THR:N	2.20	0.57
1:A:93:U:O5'	1:A:93:U:H6	1.86	0.57
4:E:19:ARG:O	4:E:20:VAL:HB	2.04	0.57
1:A:813:U:H5''	1:A:816:A:N6	2.19	0.57
21:U:24:LYS:HD2	21:U:25:ALA:N	2.19	0.57
3:D:137:SER:HB3	3:D:138:PRO:HD2	1.86	0.57
1:A:605:U:H2'	1:A:606:G:H8	1.69	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
9:J:5:ARG:HG2	9:J:79:PRO:HD3	1.85	0.57
18:S:50:VAL:O	18:S:57:VAL:HG22	2.04	0.57
17:R:34:GLU:HB2	21:U:18:PHE:CZ	2.40	0.57
2:C:126:ARG:NH2	2:C:190:THR:HG23	2.17	0.57
5:F:66:ALA:HB1	5:F:67:PRO:HD2	1.87	0.57
1:A:633:G:H2'	1:A:634:C:C6	2.39	0.57
14:O:28:GLN:O	14:O:32:LEU:HD23	2.04	0.57
1:A:441:A:H61	1:A:493:A:N6	2.02	0.57
4:E:55:VAL:N	4:E:56:PRO:HD2	2.19	0.57
5:F:53:LYS:HZ3	5:F:53:LYS:H	1.53	0.57
7:H:25:THR:O	7:H:26:MET:HB3	2.05	0.57
17:R:34:GLU:HB2	21:U:18:PHE:HZ	1.68	0.57
1:A:1060:U:C4'	9:J:54:SER:HB2	2.35	0.57
19:T:53:MET:O	19:T:57:VAL:HG22	2.05	0.57
16:Q:8:GLN:HB3	16:Q:59:GLU:HB2	1.87	0.57
1:A:1078:U:H2'	1:A:1079:G:O4'	2.04	0.57
1:A:335:C:H2'	1:A:336:A:C8	2.40	0.57
1:A:188:C:H2'	1:A:189:A:O4'	2.05	0.57
2:C:63:ILE:HD11	2:C:94:ALA:CB	2.35	0.57
1:A:409:U:H2'	1:A:410:G:C8	2.39	0.57
1:A:1241:G:H2'	1:A:1242:G:H8	1.70	0.57
1:A:301:G:H2'	1:A:302:G:H8	1.70	0.57
18:S:27:LYS:HB3	18:S:27:LYS:NZ	2.20	0.57
20:B:195:VAL:HG12	20:B:197:PHE:H	1.70	0.56
3:D:117:VAL:O	3:D:130:ASN:HA	2.05	0.56
11:L:113:ARG:NH2	11:L:120:ARG:HA	2.20	0.56
8:I:28:VAL:HA	8:I:32:ARG:O	2.05	0.56
1:A:1288:A:N1	1:A:1371:G:H1'	2.20	0.56
14:O:73:LYS:O	14:O:74:ASP:HB2	2.05	0.56
1:A:625:U:H4'	15:P:16:PHE:CZ	2.40	0.56
14:O:24:SER:HB3	14:O:27:VAL:HG23	1.85	0.56
8:I:5:TYR:HD1	8:I:20:ILE:HG22	1.69	0.56
16:Q:11:VAL:HG23	16:Q:56:ASP:O	2.05	0.56
1:A:204:G:H2'	1:A:205:A:C8	2.39	0.56
3:D:31:CYS:O	3:D:32:LYS:HB2	2.05	0.56
7:H:124:ILE:HG22	7:H:125:ILE:H	1.68	0.56
4:E:64:GLU:HG3	4:E:65:LYS:N	2.18	0.56
1:A:1172:C:O2'	1:A:1173:U:H5'	2.05	0.56
20:B:8:MET:HA	20:B:11:ALA:HB3	1.86	0.56
2:C:202:PHE:HZ	2:C:205:GLU:HG2	1.70	0.56
19:T:2:ASN:ND2	19:T:3:ILE:HG13	2.20	0.56
13:N:68:ARG:HH12	13:N:70:HIS:HB2	1.70	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:B:22:TRP:HZ3	20:B:27:LYS:HB2	1.70	0.56
8:I:57:VAL:HB	8:I:58:GLU:OE2	2.06	0.56
19:T:50:PHE:O	19:T:53:MET:HG3	2.05	0.56
19:T:66:ILE:HG22	19:T:67:HIS:N	2.19	0.56
13:N:58:ARG:HH11	13:N:58:ARG:HB3	1.70	0.56
10:K:28:ASN:ND2	10:K:46:ALA:HB3	2.20	0.56
1:A:237:G:H5''	16:Q:26:ARG:NH2	2.21	0.56
1:A:1141:C:H2'	1:A:1142:G:H8	1.69	0.56
3:D:102:TYR:HE1	3:D:109:THR:HA	1.70	0.56
1:A:678:U:H2'	1:A:679:C:H6	1.70	0.56
1:A:1306:A:N6	1:A:1331:G:H1'	2.21	0.56
1:A:398:U:H2'	1:A:399:G:C8	2.41	0.56
6:G:24:LYS:O	6:G:28:ILE:HG12	2.05	0.56
1:A:825:A:H2'	1:A:826:C:H6	1.69	0.56
5:F:86:ARG:NH1	17:R:64:LEU:HD12	2.20	0.56
1:A:1254:A:H2'	1:A:1255:G:C8	2.40	0.56
1:A:275:G:H5'	16:Q:15:LYS:HD3	1.87	0.56
21:U:8:ASN:O	21:U:9:GLU:HB2	2.06	0.56
8:I:79:ARG:NH2	8:I:102:PHE:HA	2.21	0.56
15:P:46:LYS:C	15:P:48:GLU:H	2.08	0.56
4:E:44:ARG:HA	4:E:71:ILE:O	2.05	0.56
1:A:455:G:H2'	1:A:456:A:H8	1.71	0.56
1:A:182:A:HO2'	1:A:183:C:H3'	1.68	0.56
1:A:1171:A:H2'	1:A:1172:C:H6	1.70	0.56
1:A:552:U:H4'	11:L:82:ARG:HG2	1.87	0.56
3:D:53:GLN:HB3	3:D:202:LEU:HB2	1.88	0.56
3:D:2:ARG:HB3	3:D:114:ARG:NH2	2.21	0.56
9:J:10:LEU:O	9:J:71:LEU:HA	2.05	0.56
18:S:14:LEU:HD23	18:S:14:LEU:H	1.69	0.56
4:E:84:VAL:CG1	4:E:146:MET:HB3	2.34	0.56
3:D:18:LEU:HB3	3:D:63:ILE:HG12	1.87	0.56
20:B:61:SER:HA	20:B:223:GLY:O	2.05	0.56
1:A:1011:C:H2'	1:A:1012:A:C8	2.41	0.56
21:U:24:LYS:HZ3	21:U:25:ALA:H	1.54	0.56
15:P:50:THR:HG22	15:P:51:ARG:N	2.21	0.56
9:J:55:PRO:HA	13:N:80:ARG:HH21	1.69	0.56
1:A:1231:G:H5'	8:I:128:LYS:HE2	1.87	0.56
13:N:50:LEU:HG	13:N:51:PRO:HD3	1.87	0.56
1:A:770:C:O2'	1:A:771:G:H5'	2.06	0.56
3:D:149:LYS:HD3	3:D:177:MET:HG3	1.88	0.56
1:A:1432:G:H1'	1:A:1468:A:N6	2.21	0.56
1:A:1292:G:H2'	1:A:1293:C:C6	2.40	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:I:5:TYR:O	8:I:19:PHE:HA	2.05	0.56
5:F:46:GLN:HG3	5:F:47:LEU:H	1.71	0.56
18:S:14:LEU:O	18:S:18:VAL:HG12	2.05	0.56
1:A:408:A:OP1	3:D:111:ALA:HB3	2.06	0.56
13:N:71:GLY:O	13:N:79:SER:HA	2.06	0.56
3:D:116:LEU:O	3:D:121:ALA:HB3	2.06	0.56
1:A:436:C:O2'	1:A:437:U:H5'	2.06	0.56
1:A:1252:A:H2'	1:A:1253:G:O4'	2.05	0.56
11:L:82:ARG:HG2	11:L:82:ARG:HH11	1.69	0.56
7:H:110:MET:HG3	7:H:115:ALA:HB2	1.88	0.56
1:A:545:C:H5''	3:D:68:GLU:HG2	1.88	0.56
19:T:54:GLN:N	19:T:55:PRO:HD2	2.21	0.56
8:I:19:PHE:O	8:I:62:LEU:HA	2.06	0.56
18:S:43:MET:O	18:S:46:LEU:HB2	2.05	0.56
13:N:9:GLU:OE2	13:N:60:ARG:HG2	2.06	0.56
20:B:68:PHE:HA	20:B:161:PHE:O	2.06	0.56
17:R:38:ILE:HG22	17:R:58:ILE:HG21	1.87	0.56
1:A:1329:A:O2'	1:A:1330:U:H5'	2.06	0.56
5:F:53:LYS:NZ	5:F:53:LYS:H	2.03	0.56
8:I:43:ALA:O	8:I:46:VAL:HG22	2.06	0.55
8:I:51:LEU:CB	8:I:56:MET:HG2	2.26	0.55
8:I:82:ILE:O	8:I:86:LEU:HD13	2.06	0.55
10:K:110:THR:HA	21:U:19:LYS:NZ	2.22	0.55
1:A:1206:G:C4'	2:C:192:TYR:HA	2.35	0.55
4:E:156:ARG:HD2	7:H:42:GLU:O	2.06	0.55
1:A:843:U:H5'	1:A:844:G:N7	2.20	0.55
12:M:106:ARG:HA	12:M:106:ARG:HH11	1.71	0.55
1:A:923:A:H2'	1:A:924:C:H6	1.72	0.55
1:A:280:C:O2	16:Q:39:ARG:HG3	2.05	0.55
2:C:57:GLU:O	2:C:63:ILE:HA	2.05	0.55
11:L:5:GLN:HA	11:L:8:ARG:HH21	1.70	0.55
11:L:107:LYS:O	11:L:107:LYS:HD2	2.06	0.55
1:A:1283:U:H2'	1:A:1284:C:C6	2.41	0.55
21:U:16:ARG:CA	21:U:16:ARG:HE	2.04	0.55
18:S:29:PRO:HA	18:S:47:THR:O	2.06	0.55
3:D:160:LEU:H	3:D:160:LEU:CD1	2.15	0.55
13:N:5:MET:O	13:N:8:ARG:HB2	2.05	0.55
1:A:455:G:H2'	1:A:456:A:C8	2.41	0.55
7:H:113:ARG:HA	7:H:116:ARG:HH12	1.71	0.55
3:D:27:ILE:O	3:D:28:ASP:HB3	2.07	0.55
8:I:94:ARG:HB3	8:I:94:ARG:NH1	2.21	0.55
1:A:212:G:H2'	1:A:213:G:H8	1.71	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
16:Q:80:LYS:H	16:Q:80:LYS:HE3	1.70	0.55
11:L:98:ARG:HB2	11:L:116:TYR:HA	1.86	0.55
10:K:124:LYS:HA	21:U:34:ARG:CB	2.31	0.55
14:O:32:LEU:O	14:O:36:ILE:HG12	2.05	0.55
1:A:625:U:H4'	15:P:16:PHE:CE2	2.40	0.55
12:M:44:ILE:CD1	12:M:44:ILE:H	2.13	0.55
1:A:107:G:O6	19:T:9:ARG:HD3	2.07	0.55
18:S:65:MET:HG3	18:S:73:PHE:CZ	2.42	0.55
21:U:33:ARG:CZ	21:U:34:ARG:HG2	2.37	0.55
2:C:148:ILE:O	2:C:168:ARG:HG2	2.06	0.55
9:J:76:ILE:O	9:J:76:ILE:HD12	2.07	0.55
1:A:1391:U:H2'	1:A:1392:G:H8	1.69	0.55
14:O:81:LEU:HD23	14:O:85:LEU:HD13	1.87	0.55
7:H:101:ALA:HB3	7:H:112:ASP:HB3	1.88	0.55
1:A:1386:G:H2'	1:A:1387:G:H8	1.70	0.55
20:B:69:VAL:HB	20:B:162:VAL:HG23	1.89	0.55
1:A:132:C:H5"	19:T:68:LYS:NZ	2.21	0.55
20:B:65:LYS:HB2	20:B:158:ASP:N	2.19	0.55
1:A:412:A:H61	3:D:29:THR:CG2	2.20	0.55
1:A:1342:C:H2'	1:A:1343:G:C8	2.41	0.55
1:A:922:G:N3	1:A:1398:A:H2	2.05	0.55
1:A:1053:G:HO2'	1:A:1199:U:H5	1.55	0.55
1:A:939:G:H5"	6:G:101:ARG:NH2	2.22	0.55
1:A:1149:C:H2'	1:A:1150:A:C8	2.41	0.55
8:I:10:ARG:HB3	8:I:15:ALA:HA	1.88	0.55
2:C:76:ILE:HA	2:C:83:VAL:CG2	2.30	0.55
10:K:31:VAL:HG23	10:K:44:ALA:HB3	1.89	0.55
1:A:80:A:C5	1:A:81:A:H1'	2.41	0.55
5:F:29:ILE:HG23	5:F:66:ALA:HB2	1.88	0.55
12:M:78:ARG:NH2	18:S:64:GLU:HB2	2.22	0.55
15:P:48:GLU:HG3	15:P:49:GLY:H	1.71	0.55
1:A:270:A:H2'	1:A:271:C:H6	1.72	0.55
5:F:81:ASN:OD1	5:F:83:ALA:HB3	2.06	0.55
11:L:43:LYS:CE	11:L:44:PRO:HD3	2.37	0.55
1:A:300:A:H2'	1:A:301:G:O4'	2.07	0.55
1:A:1508:A:H2'	1:A:1509:C:C6	2.42	0.55
1:A:420:U:H2'	1:A:422:C:C5	2.42	0.55
11:L:31:GLY:HA3	11:L:54:VAL:CG1	2.37	0.55
1:A:1404:C:H2'	1:A:1405:G:C8	2.40	0.55
3:D:123:MET:HB2	3:D:128:VAL:HA	1.88	0.55
1:A:839:C:H2'	1:A:840:C:O4'	2.06	0.55
1:A:840:C:H3'	1:A:842:U:OP2	2.06	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:864:A:H2'	1:A:865:A:C8	2.41	0.55
1:A:195:A:H1'	1:A:222:C:O2'	2.07	0.55
2:C:14:VAL:HG11	2:C:178:ARG:HA	1.88	0.55
1:A:784:A:H2'	1:A:785:G:C8	2.42	0.55
1:A:409:U:OP1	3:D:23:GLY:HA3	2.06	0.55
1:A:833:G:H2'	1:A:834:U:C6	2.41	0.55
20:B:31:PHE:HB2	20:B:41:ASN:HA	1.89	0.55
1:A:975:A:H4'	1:A:976:G:O5'	2.07	0.55
3:D:93:LEU:O	3:D:96:ARG:HB2	2.07	0.55
12:M:92:ARG:NE	12:M:92:ARG:HA	2.22	0.55
1:A:1287:A:H2'	1:A:1288:A:C8	2.42	0.55
1:A:201:G:O2'	1:A:202:G:H5'	2.07	0.55
8:I:49:GLN:N	8:I:50:PRO:HD2	2.21	0.55
1:A:437:U:H2'	1:A:438:U:O4'	2.06	0.55
1:A:1080:A:OP1	4:E:49:TYR:HE2	1.90	0.55
7:H:28:SER:HB3	7:H:57:GLU:O	2.07	0.55
1:A:323:U:H2'	1:A:324:G:O4'	2.06	0.55
1:A:1527:U:O2'	1:A:1528:U:H5'	2.07	0.55
1:A:1219:A:H2'	1:A:1220:G:H8	1.72	0.54
15:P:67:ILE:HG13	15:P:71:VAL:HG13	1.88	0.54
12:M:2:ARG:HD3	12:M:2:ARG:H	1.71	0.54
1:A:1405:G:H21	1:A:1518:A:H1'	1.72	0.54
17:R:44:THR:HB	17:R:46:THR:HG22	1.89	0.54
2:C:179:ALA:HB3	2:C:181:ILE:HD11	1.87	0.54
6:G:74:VAL:HA	6:G:87:PRO:HA	1.88	0.54
12:M:78:ARG:HH12	18:S:64:GLU:HG2	1.71	0.54
12:M:15:VAL:O	12:M:19:THR:HG23	2.07	0.54
1:A:373:A:H2'	1:A:374:A:H8	1.72	0.54
8:I:7:GLY:HA3	8:I:81:GLY:O	2.08	0.54
20:B:148:GLY:O	20:B:151:LYS:HG2	2.07	0.54
6:G:77:ARG:HG3	6:G:79:VAL:HG23	1.88	0.54
5:F:79:ARG:HH21	5:F:87:SER:HB3	1.72	0.54
12:M:24:VAL:HG12	12:M:28:ARG:HD2	1.89	0.54
1:A:1101:A:N6	20:B:174:GLU:OE2	2.40	0.54
20:B:207:ARG:HH11	20:B:207:ARG:HA	1.72	0.54
1:A:8:A:H61	3:D:53:GLN:HE22	1.55	0.54
1:A:65:A:C2	1:A:381:C:H2'	2.43	0.54
20:B:51:GLU:O	20:B:55:GLU:HG2	2.08	0.54
2:C:72:PRO:O	2:C:76:ILE:HG12	2.08	0.54
20:B:204:ASP:O	20:B:209:VAL:HG13	2.07	0.54
5:F:29:ILE:HG22	5:F:34:GLY:HA3	1.88	0.54
21:U:28:LEU:HD23	21:U:29:ALA:N	2.22	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
19:T:4:LYS:HE3	19:T:6:ALA:H	1.73	0.54
1:A:1239:A:H4'	1:A:1240:U:C5'	2.36	0.54
16:Q:68:LYS:C	16:Q:70:LYS:H	2.11	0.54
1:A:1321:U:H2'	1:A:1322:C:C5	2.42	0.54
7:H:58:LEU:CD2	7:H:60:LEU:HB2	2.38	0.54
21:U:49:ALA:O	21:U:52:VAL:HG12	2.08	0.54
14:O:43:PHE:CE1	14:O:56:LEU:HD22	2.42	0.54
4:E:154:ALA:HB1	7:H:65:PHE:CZ	2.43	0.54
20:B:49:PHE:HA	20:B:212:TYR:OH	2.08	0.54
3:D:155:LYS:H	3:D:155:LYS:HD2	1.72	0.54
4:E:45:VAL:HG23	4:E:71:ILE:CG2	2.37	0.54
1:A:189:A:H2'	1:A:190:A:C8	2.43	0.54
14:O:8:THR:O	14:O:11:ILE:HG22	2.07	0.54
1:A:208:U:H2'	1:A:210:C:C4	2.42	0.54
1:A:1234:C:O2'	1:A:1235:U:H5'	2.07	0.54
1:A:1060:U:H2'	1:A:1061:G:H8	1.72	0.54
4:E:156:ARG:HB3	7:H:43:GLY:O	2.08	0.54
1:A:919:A:O2'	1:A:920:U:H5'	2.07	0.54
1:A:1221:G:H4'	18:S:52:ASN:O	2.07	0.54
9:J:52:LEU:HA	9:J:62:ARG:HA	1.90	0.54
1:A:709:U:H2'	1:A:710:G:C8	2.42	0.54
1:A:709:U:H2'	1:A:710:G:H8	1.71	0.54
1:A:1469:C:H2'	1:A:1470:U:O4'	2.08	0.54
1:A:1458:G:H5''	19:T:25:SER:HB2	1.89	0.54
19:T:27:MET:O	19:T:31:ILE:HG13	2.08	0.54
15:P:20:VAL:HG23	15:P:35:ARG:HA	1.90	0.54
7:H:8:ASP:OD1	7:H:12:ARG:HD2	2.06	0.54
5:F:16:GLU:CD	5:F:16:GLU:H	2.11	0.54
5:F:38:ARG:HB3	5:F:63:ASN:HB2	1.89	0.54
3:D:194:ILE:HG23	3:D:194:ILE:O	2.08	0.54
1:A:93:U:H3'	1:A:94:G:C5'	2.38	0.54
1:A:482:A:H2'	1:A:483:C:O4'	2.08	0.54
1:A:57:G:H2'	1:A:58:C:H6	1.72	0.54
1:A:502:A:H2'	1:A:503:C:H6	1.72	0.54
1:A:430:A:P	3:D:6:PRO:HA	2.47	0.54
10:K:70:ALA:C	10:K:72:ALA:H	2.11	0.54
8:I:21:LYS:HG2	8:I:22:PRO:HD2	1.90	0.54
1:A:369:G:O2'	1:A:370:C:H5'	2.08	0.54
20:B:128:LEU:HD12	20:B:132:GLU:CB	2.37	0.54
1:A:415:A:H3'	1:A:416:G:H8	1.71	0.54
6:G:72:VAL:HG12	6:G:89:GLU:HA	1.89	0.54
11:L:107:LYS:H	11:L:107:LYS:NZ	2.05	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
10:K:79:LYS:HB2	10:K:80:ASN:HD22	1.73	0.54
1:A:484:G:O4'	1:A:486:U:H5'	2.08	0.54
11:L:36:VAL:HA	11:L:52:CYS:HA	1.89	0.54
1:A:1477:U:H2'	1:A:1478:U:H6	1.72	0.54
1:A:91:U:H2'	1:A:92:U:O4'	2.07	0.54
1:A:36:C:H4'	11:L:118:VAL:O	2.08	0.54
1:A:1054:C:H1'	1:A:1196:A:C5	2.43	0.54
1:A:737:C:H2'	1:A:738:C:H6	1.72	0.54
16:Q:31:PRO:O	16:Q:32:ILE:HB	2.08	0.54
17:R:33:THR:HG22	17:R:39:VAL:HG12	1.89	0.54
1:A:85:U:H4'	1:A:86:G:H4'	1.90	0.54
1:A:242:G:H2'	1:A:243:A:H5''	1.88	0.54
19:T:57:VAL:HB	19:T:71:ALA:HB1	1.89	0.54
13:N:60:ARG:HG3	13:N:62:ARG:HG3	1.90	0.54
13:N:50:LEU:H	13:N:51:PRO:CD	2.21	0.54
1:A:159:G:H1	1:A:163:C:N4	2.06	0.54
1:A:1069:C:H4'	1:A:1192:C:O2	2.08	0.54
6:G:45:ALA:O	6:G:49:LEU:HD23	2.07	0.54
1:A:686:U:O4	1:A:703:G:H1'	2.07	0.54
1:A:868:C:H2'	1:A:869:G:O4'	2.08	0.54
19:T:38:ILE:HD11	19:T:82:ILE:HG22	1.89	0.53
1:A:1019:A:H2'	1:A:1020:G:C8	2.43	0.53
1:A:939:G:H5''	6:G:101:ARG:HH22	1.72	0.53
11:L:78:VAL:HG12	11:L:101:LEU:HD13	1.90	0.53
5:F:79:ARG:NH2	5:F:87:SER:HB3	2.23	0.53
11:L:38:THR:HG22	11:L:50:LYS:HG2	1.90	0.53
10:K:58:THR:HB	10:K:59:PRO:HD2	1.88	0.53
2:C:171:ARG:HB2	2:C:171:ARG:NH1	2.23	0.53
3:D:152:SER:HA	3:D:155:LYS:HD3	1.90	0.53
12:M:28:ARG:NH2	12:M:62:PHE:HB2	2.23	0.53
13:N:26:LEU:CD2	13:N:27:LYS:H	2.19	0.53
1:A:1316:G:H22	1:A:1318:A:H3'	1.71	0.53
1:A:412:A:H1'	1:A:413:G:C8	2.44	0.53
1:A:797:C:O2'	1:A:798:U:H5'	2.09	0.53
1:A:437:U:H5''	3:D:151:GLN:NE2	2.23	0.53
11:L:85:ARG:HA	11:L:93:ARG:HA	1.90	0.53
20:B:101:THR:HG22	20:B:174:GLU:OE1	2.08	0.53
16:Q:16:MET:HB2	16:Q:19:SER:HB2	1.90	0.53
4:E:37:VAL:HG11	4:E:113:VAL:HG12	1.88	0.53
4:E:52:ALA:HB2	4:E:61:LYS:HE2	1.90	0.53
1:A:1028:C:H3'	1:A:1029:U:H6	1.73	0.53
1:A:1508:A:H2'	1:A:1509:C:H6	1.72	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:G:76:SER:HA	6:G:84:TYR:O	2.07	0.53
13:N:68:ARG:HB3	13:N:68:ARG:NH1	2.21	0.53
20:B:46:VAL:HA	20:B:49:PHE:HD2	1.74	0.53
1:A:1127:G:H5'	1:A:1280:A:O2'	2.08	0.53
8:I:41:GLU:C	8:I:43:ALA:H	2.12	0.53
21:U:36:PHE:CB	21:U:40:PRO:HD3	2.27	0.53
18:S:62:THR:HB	18:S:64:GLU:OE1	2.08	0.53
20:B:62:ARG:HD2	20:B:62:ARG:H	1.72	0.53
1:A:632:U:H5''	1:A:633:G:H8	1.72	0.53
1:A:560:A:H5'	1:A:566:G:N2	2.23	0.53
1:A:1020:G:N3	1:A:1020:G:H2'	2.22	0.53
1:A:1244:G:H2'	1:A:1245:C:C6	2.43	0.53
19:T:67:HIS:CE1	19:T:68:LYS:HE3	2.44	0.53
2:C:149:LYS:HG3	2:C:168:ARG:HB2	1.90	0.53
1:A:1152:A:H2'	1:A:1153:G:C8	2.42	0.53
9:J:26:VAL:O	9:J:30:LYS:HG3	2.09	0.53
1:A:922:G:H4'	4:E:24:VAL:HA	1.90	0.53
1:A:658:C:H2'	1:A:659:U:C6	2.42	0.53
1:A:1226:C:H5''	12:M:101:THR:CB	2.37	0.53
6:G:71:THR:HG22	6:G:141:HIS:CE1	2.43	0.53
1:A:939:G:H5''	6:G:101:ARG:NH1	2.24	0.53
1:A:512:U:H2'	1:A:513:C:C6	2.43	0.53
1:A:814:A:H5'	1:A:1511:G:H4'	1.90	0.53
1:A:1524:C:H2'	1:A:1525:G:C8	2.44	0.53
17:R:52:ARG:HB3	17:R:56:ARG:NH2	2.24	0.53
6:G:113:LYS:HB2	6:G:117:LEU:HD12	1.91	0.53
1:A:80:A:C4	1:A:81:A:H1'	2.42	0.53
1:A:1313:U:OP2	18:S:5:LYS:HA	2.09	0.53
20:B:128:LEU:HD13	20:B:129:THR:H	1.73	0.53
6:G:145:GLU:CD	6:G:148:LYS:HD2	2.29	0.53
1:A:412:A:H1'	1:A:413:G:H8	1.72	0.53
2:C:61:LYS:O	2:C:96:VAL:HB	2.09	0.53
1:A:182:A:H1'	1:A:183:C:C5	2.43	0.53
1:A:216:U:H2'	1:A:217:C:C6	2.44	0.53
20:B:14:HIS:CD2	20:B:202:ASN:H	2.27	0.53
12:M:19:THR:HA	12:M:24:VAL:HG23	1.90	0.53
6:G:125:ASP:HB3	6:G:130:LYS:HB3	1.91	0.53
1:A:254:G:OP1	16:Q:68:LYS:O	2.26	0.53
16:Q:74:LEU:HD22	16:Q:75:VAL:N	2.24	0.53
7:H:103:VAL:HG22	7:H:124:ILE:HA	1.90	0.53
1:A:407:U:O2'	3:D:112:GLU:HG3	2.08	0.53
1:A:413:G:O6	3:D:32:LYS:HG3	2.09	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:674:G:H2'	1:A:675:A:H8	1.73	0.53
1:A:1035:A:H2'	1:A:1036:A:C8	2.43	0.53
1:A:1062:U:H2'	1:A:1063:C:C6	2.44	0.53
12:M:43:LYS:O	12:M:46:GLU:HG3	2.09	0.53
12:M:5:GLY:C	12:M:7:ASN:H	2.12	0.53
8:I:18:VAL:HG13	8:I:64:ILE:HG13	1.89	0.53
8:I:29:ILE:HA	8:I:64:ILE:HB	1.91	0.53
3:D:147:LYS:HD3	3:D:148:ALA:N	2.24	0.53
19:T:38:ILE:HD13	19:T:85:LEU:HD13	1.91	0.53
12:M:89:ARG:NH2	12:M:94:LEU:HD12	2.24	0.53
5:F:86:ARG:HD2	17:R:63:TYR:O	2.09	0.53
8:I:98:ARG:NE	8:I:103:VAL:HG21	2.24	0.53
2:C:106:ARG:H	2:C:106:ARG:HD2	1.73	0.53
3:D:59:LYS:HE3	3:D:194:ILE:HD12	1.91	0.53
11:L:49:ARG:HG2	11:L:89:LEU:HD21	1.90	0.53
13:N:50:LEU:N	13:N:51:PRO:CD	2.71	0.53
1:A:239:U:C5'	1:A:239:U:H6	2.22	0.53
7:H:6:ILE:HD11	7:H:31:LEU:HD23	1.89	0.53
1:A:1017:U:H2'	1:A:1018:G:C8	2.44	0.53
1:A:1308:U:OP2	12:M:97:ARG:HB2	2.09	0.53
20:B:121:GLN:NE2	20:B:122:ASP:H	2.07	0.53
1:A:229:U:H2'	1:A:230:G:C8	2.44	0.53
1:A:720:C:H5''	17:R:40:PRO:HA	1.91	0.53
8:I:23:GLY:H	8:I:61:ASP:H	1.55	0.52
20:B:119:GLN:C	20:B:125:PHE:HB3	2.29	0.52
4:E:81:GLN:NE2	4:E:149:PRO:HD3	2.24	0.52
1:A:860:A:H2'	1:A:861:G:O4'	2.09	0.52
2:C:91:ALA:CB	2:C:98:ALA:H	2.23	0.52
1:A:708:C:H2'	1:A:709:U:H6	1.72	0.52
1:A:824:G:O2'	1:A:825:A:H5'	2.09	0.52
1:A:470:C:H2'	1:A:471:U:C6	2.44	0.52
7:H:54:THR:HG23	7:H:55:LYS:HG2	1.90	0.52
15:P:36:VAL:O	15:P:36:VAL:HG13	2.09	0.52
5:F:51:ILE:HG23	5:F:51:ILE:O	2.09	0.52
20:B:20:ARG:HD2	20:B:37:VAL:HA	1.91	0.52
1:A:147:G:H2'	1:A:148:G:C8	2.43	0.52
10:K:30:ILE:HG22	10:K:45:THR:HA	1.91	0.52
1:A:201:G:O2'	1:A:469:C:H4'	2.09	0.52
20:B:45:THR:HG23	20:B:200:PRO:HG2	1.91	0.52
1:A:1314:C:H2'	1:A:1315:U:C6	2.44	0.52
8:I:117:LEU:HD22	8:I:123:ARG:HG2	1.90	0.52
1:A:1163:A:H2'	1:A:1164:G:H8	1.74	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1138:G:N3	1:A:1138:G:H3'	2.24	0.52
14:O:39:LEU:HD23	14:O:56:LEU:HD13	1.91	0.52
1:A:1463:U:H2'	1:A:1464:U:C6	2.45	0.52
1:A:1405:G:H1'	1:A:1518:A:O2'	2.09	0.52
1:A:766:A:H2	1:A:1525:G:N3	2.07	0.52
6:G:136:LYS:O	6:G:140:VAL:HG23	2.08	0.52
1:A:458:U:H2'	1:A:459:A:H8	1.75	0.52
5:F:67:PRO:O	5:F:70:VAL:HG22	2.09	0.52
1:A:522:C:H2'	1:A:523:A:O4'	2.09	0.52
1:A:1342:C:H2'	1:A:1343:G:H8	1.73	0.52
1:A:190:A:H8	1:A:190:A:O5'	1.92	0.52
1:A:141:G:H2'	1:A:142:G:O4'	2.09	0.52
10:K:126:ARG:HE	10:K:126:ARG:HA	1.73	0.52
1:A:624:C:H2'	1:A:625:U:H6	1.74	0.52
11:L:79:ILE:HD12	11:L:96:THR:HG22	1.91	0.52
1:A:215:C:H2'	1:A:216:U:C6	2.44	0.52
1:A:1148:U:H5'	8:I:6:TYR:OH	2.08	0.52
21:U:42:THR:HB	21:U:46:ARG:HH21	1.74	0.52
9:J:65:TYR:HB3	13:N:95:LEU:HD11	1.91	0.52
4:E:37:VAL:HA	4:E:47:PHE:HA	1.92	0.52
1:A:1121:U:O2'	1:A:1122:U:H5'	2.09	0.52
1:A:920:U:H2'	1:A:921:U:H6	1.73	0.52
1:A:337:G:H2'	1:A:338:A:H8	1.73	0.52
6:G:55:LYS:HB2	6:G:59:GLU:OE1	2.10	0.52
1:A:1221:G:O3'	18:S:76:THR:HG21	2.10	0.52
1:A:1308:U:H2'	1:A:1309:G:H8	1.74	0.52
8:I:56:MET:SD	8:I:57:VAL:N	2.82	0.52
21:U:40:PRO:HG2	21:U:41:THR:H	1.75	0.52
20:B:115:ASP:O	20:B:119:GLN:HG2	2.09	0.52
3:D:122:ILE:O	3:D:128:VAL:HG23	2.09	0.52
18:S:29:PRO:CA	18:S:47:THR:HB	2.40	0.52
1:A:171:A:H2'	1:A:172:A:C8	2.44	0.52
12:M:13:HIS:HB2	12:M:16:ILE:CG2	2.39	0.52
1:A:203:G:N2	1:A:205:A:H61	2.08	0.52
2:C:130:ARG:HA	2:C:133:MET:HE2	1.90	0.52
20:B:13:VAL:CG1	20:B:207:ARG:HG2	2.40	0.52
1:A:22:G:H2'	1:A:23:C:C6	2.44	0.52
1:A:718:A:H5'	10:K:118:ASN:CG	2.29	0.52
1:A:1437:A:H2'	1:A:1438:G:H8	1.74	0.52
10:K:12:ARG:N	10:K:76:TYR:HA	2.24	0.52
1:A:6:G:HO2'	1:A:7:A:H8	1.57	0.52
5:F:36:ILE:HD12	5:F:36:ILE:H	1.73	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:238:A:C2'	1:A:239:U:H5''	2.40	0.52
3:D:96:ARG:NH1	3:D:133:SER:HA	2.25	0.52
13:N:14:ALA:O	13:N:18:LYS:HG3	2.10	0.52
15:P:4:ILE:O	15:P:71:VAL:HG11	2.09	0.52
1:A:1210:C:H1'	1:A:1214:C:O2'	2.10	0.52
2:C:185:THR:HG22	2:C:198:LYS:HA	1.92	0.52
1:A:935:A:N6	6:G:2:ARG:HD2	2.24	0.52
12:M:3:ILE:HA	12:M:56:ARG:HG2	1.91	0.52
15:P:28:ARG:HD3	15:P:29:ASN:HD22	1.75	0.52
1:A:484:G:H4'	1:A:485:U:C5'	2.38	0.52
1:A:719:C:H2'	17:R:38:ILE:CD1	2.40	0.52
1:A:1053:G:N7	1:A:1200:C:H5''	2.25	0.52
1:A:235:C:H2'	1:A:236:A:H8	1.74	0.52
1:A:1028:C:H3'	1:A:1029:U:C6	2.45	0.52
8:I:98:ARG:HA	8:I:103:VAL:HG22	1.92	0.52
5:F:17:GLN:O	5:F:21:MET:HG3	2.10	0.52
1:A:26:A:H61	1:A:558:G:H1'	1.75	0.52
20:B:55:GLU:HG3	20:B:197:PHE:CZ	2.45	0.52
5:F:100:SER:HA	17:R:23:LYS:HD3	1.91	0.52
1:A:1250:A:O3'	8:I:68:GLY:HA2	2.09	0.52
6:G:125:ASP:OD2	6:G:130:LYS:HD2	2.10	0.52
20:B:86:CYS:HB2	20:B:221:ARG:HH12	1.74	0.52
1:A:465:A:O2'	1:A:466:A:H3'	2.09	0.52
1:A:467:U:O2	1:A:467:U:H2'	2.09	0.52
1:A:413:G:C6	3:D:32:LYS:HE2	2.45	0.52
20:B:79:VAL:O	20:B:83:ALA:HB3	2.10	0.52
1:A:586:C:O2'	1:A:878:A:H4'	2.10	0.52
20:B:142:LYS:HA	20:B:145:ASN:OD1	2.09	0.52
1:A:1297:G:H1'	1:A:1298:U:H5	1.75	0.52
12:M:73:SER:O	12:M:77:LYS:HB2	2.10	0.52
1:A:95:C:O2	1:A:95:C:H2'	2.09	0.52
10:K:95:THR:HG23	10:K:96:ILE:N	2.24	0.52
3:D:169:TRP:CE2	3:D:185:PRO:HB3	2.45	0.52
20:B:95:TRP:HZ2	20:B:100:LEU:HD13	1.75	0.52
2:C:134:LYS:HA	2:C:167:TYR:CE2	2.43	0.52
16:Q:32:ILE:HG23	16:Q:33:TYR:CD2	2.45	0.52
1:A:546:A:P	3:D:68:GLU:HB3	2.50	0.52
1:A:656:G:O2'	1:A:657:U:H5'	2.09	0.52
1:A:394:G:H2'	1:A:395:C:H6	1.75	0.52
20:B:18:GLN:HB2	20:B:188:THR:OG1	2.11	0.51
4:E:85:LYS:HE3	4:E:94:PHE:HB2	1.91	0.51
2:C:137:VAL:HA	2:C:148:ILE:CD1	2.39	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:C:110:LEU:HD22	2:C:145:ALA:HB2	1.92	0.51
1:A:413:G:N1	3:D:32:LYS:HE2	2.26	0.51
3:D:25:ARG:HH12	3:D:30:LYS:HE3	1.75	0.51
1:A:840:C:C2	1:A:842:U:H4'	2.44	0.51
1:A:956:U:O2'	1:A:957:U:H5'	2.11	0.51
1:A:965:U:OP1	1:A:1198:G:H5''	2.10	0.51
9:J:10:LEU:HD11	9:J:25:ILE:HD12	1.92	0.51
1:A:939:G:H5''	6:G:101:ARG:HH12	1.74	0.51
4:E:132:PRO:O	4:E:136:VAL:HG12	2.10	0.51
1:A:640:A:O2'	1:A:641:U:H5'	2.10	0.51
8:I:61:ASP:C	8:I:62:LEU:HD13	2.31	0.51
10:K:111:ASP:CB	21:U:19:LYS:HE3	2.38	0.51
1:A:328:C:H4'	1:A:329:A:C5'	2.40	0.51
1:A:1308:U:H3'	12:M:97:ARG:HH11	1.76	0.51
20:B:121:GLN:HE21	20:B:122:ASP:H	1.58	0.51
1:A:405:U:O4	3:D:1:ALA:HA	2.09	0.51
3:D:43:ARG:NH2	3:D:45:PRO:HA	2.25	0.51
7:H:17:GLN:HE21	7:H:62:LEU:HD23	1.74	0.51
1:A:1181:G:H1'	1:A:1182:G:C5	2.45	0.51
5:F:6:ILE:HD12	5:F:7:VAL:N	2.24	0.51
6:G:149:ALA:H	10:K:55:ARG:NH2	2.08	0.51
11:L:56:LEU:HD21	11:L:81:ILE:HG13	1.93	0.51
12:M:96:VAL:C	12:M:98:GLY:H	2.13	0.51
1:A:1034:G:H2'	1:A:1035:A:H5'	1.93	0.51
1:A:1091:U:H2'	1:A:1093:A:OP2	2.10	0.51
1:A:1014:A:H4'	18:S:13:HIS:CD2	2.45	0.51
13:N:47:LEU:C	13:N:49:THR:H	2.14	0.51
1:A:598:U:H2'	1:A:599:C:C6	2.46	0.51
3:D:22:SER:CB	3:D:109:THR:HG22	2.40	0.51
1:A:191:G:H2'	1:A:192:A:C8	2.45	0.51
20:B:13:VAL:HG11	20:B:207:ARG:HG2	1.92	0.51
1:A:301:G:H2'	1:A:302:G:C8	2.46	0.51
1:A:656:G:HO2'	1:A:657:U:H5'	1.76	0.51
1:A:487:A:H3'	1:A:488:C:H6	1.75	0.51
7:H:87:ARG:N	7:H:90:GLU:HB2	2.22	0.51
2:C:129:PHE:CE2	2:C:156:LEU:HD13	2.46	0.51
1:A:624:C:H2'	1:A:625:U:C6	2.45	0.51
1:A:1040:U:H2'	1:A:1041:G:C8	2.46	0.51
3:D:123:MET:HG3	3:D:127:ARG:N	2.25	0.51
3:D:158:LEU:H	3:D:158:LEU:HD12	1.75	0.51
19:T:43:LYS:HA	19:T:85:LEU:HD11	1.93	0.51
11:L:81:ILE:CG2	11:L:94:TYR:HB3	2.40	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:C:71:ARG:O	2:C:75:VAL:HG23	2.11	0.51
19:T:49:ALA:O	19:T:52:GLU:HG2	2.11	0.51
9:J:56:HIS:H	13:N:80:ARG:HH22	1.59	0.51
1:A:1262:C:N4	1:A:1273:C:H42	2.09	0.51
1:A:652:U:H1'	1:A:653:U:C5	2.45	0.51
20:B:138:ARG:HG3	20:B:141:GLU:OE1	2.10	0.51
8:I:62:LEU:HD23	8:I:64:ILE:HD11	1.92	0.51
12:M:44:ILE:HD12	12:M:44:ILE:N	2.21	0.51
6:G:145:GLU:OE2	6:G:148:LYS:HD2	2.11	0.51
7:H:77:VAL:HG23	7:H:126:CYS:HA	1.93	0.51
1:A:1248:A:H2	8:I:71:ILE:HD11	1.76	0.51
1:A:8:A:C5	3:D:205:LYS:HA	2.45	0.51
1:A:1307:U:H2'	1:A:1308:U:H6	1.76	0.51
1:A:1272:G:H2'	1:A:1273:C:H6	1.74	0.51
14:O:78:TYR:CZ	14:O:82:ILE:HD11	2.46	0.51
11:L:54:VAL:HG22	11:L:79:ILE:HD11	1.92	0.51
7:H:55:LYS:HZ2	7:H:55:LYS:HA	1.75	0.51
4:E:131:ASN:HD21	4:E:133:ILE:HB	1.75	0.51
3:D:43:ARG:HD2	3:D:44:LYS:H	1.75	0.51
4:E:39:GLY:HA3	4:E:116:VAL:HB	1.93	0.51
1:A:332:G:O2'	1:A:333:U:H5'	2.11	0.51
1:A:1521:C:H2'	1:A:1522:U:C6	2.46	0.51
3:D:155:LYS:HG2	3:D:156:ALA:N	2.25	0.51
13:N:9:GLU:O	13:N:13:VAL:HG23	2.11	0.51
20:B:102:ASN:OD1	20:B:105:THR:HB	2.11	0.51
1:A:1320:C:H41	18:S:36:ARG:HB3	1.76	0.51
18:S:35:ARG:HB2	18:S:71:GLY:CA	2.41	0.51
15:P:20:VAL:HG23	15:P:34:GLU:O	2.11	0.51
2:C:8:GLY:HA2	2:C:11:LEU:HG	1.93	0.51
3:D:29:THR:HG22	3:D:30:LYS:H	1.74	0.51
1:A:1343:G:C1'	8:I:122:ARG:HH12	2.23	0.51
7:H:76:ARG:HG3	7:H:77:VAL:H	1.72	0.51
1:A:35:G:H2'	1:A:36:C:H6	1.76	0.51
1:A:1366:C:H2'	1:A:1367:C:H6	1.76	0.51
1:A:1176:A:H2'	1:A:1177:G:O4'	2.11	0.51
20:B:46:VAL:HA	20:B:49:PHE:CD2	2.45	0.51
3:D:169:TRP:CD2	3:D:185:PRO:HB3	2.46	0.51
20:B:205:ALA:O	20:B:209:VAL:HG22	2.11	0.51
18:S:44:ILE:HD12	18:S:63:ASP:HA	1.93	0.51
16:Q:3:LYS:NZ	16:Q:4:ILE:H	2.02	0.51
1:A:1073:U:H2'	1:A:1074:G:H8	1.76	0.51
20:B:16:GLY:HA3	20:B:39:ILE:HA	1.93	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
20:B:63:LYS:HG2	20:B:224:ARG:NH2	2.25	0.51
1:A:978:A:H5'	1:A:1362:A:N6	2.26	0.51
16:Q:46:HIS:HB2	16:Q:70:LYS:HE2	1.92	0.51
12:M:90:HIS:CE1	12:M:96:VAL:HG21	2.46	0.51
1:A:737:C:H2'	1:A:738:C:C6	2.45	0.51
1:A:1521:C:H2'	1:A:1522:U:H6	1.76	0.51
19:T:66:ILE:HG21	19:T:71:ALA:HB2	1.93	0.50
1:A:1073:U:H2'	1:A:1074:G:C8	2.47	0.50
4:E:17:VAL:HG23	4:E:33:THR:O	2.10	0.50
1:A:728:A:H2'	1:A:729:A:C8	2.46	0.50
11:L:72:ASN:ND2	11:L:104:SER:HB3	2.26	0.50
2:C:76:ILE:HD13	2:C:83:VAL:HG21	1.92	0.50
5:F:61:LEU:HD12	5:F:63:ASN:OD1	2.11	0.50
12:M:52:ILE:HG13	12:M:56:ARG:NH1	2.25	0.50
2:C:148:ILE:HA	2:C:200:TRP:O	2.11	0.50
10:K:51:PHE:HZ	10:K:61:ALA:HA	1.73	0.50
11:L:20:VAL:HG23	11:L:20:VAL:O	2.12	0.50
1:A:1308:U:H2'	1:A:1309:G:C8	2.46	0.50
6:G:15:PRO:HG2	6:G:43:TYR:OH	2.11	0.50
12:M:23:GLY:HA3	12:M:64:VAL:HG12	1.93	0.50
3:D:145:ARG:HB3	3:D:147:LYS:CD	2.40	0.50
3:D:160:LEU:HA	3:D:163:GLN:HG3	1.94	0.50
1:A:1124:G:H3'	9:J:37:ARG:HH12	1.76	0.50
1:A:279:A:H5'	1:A:281:G:O4'	2.11	0.50
1:A:714:G:N2	1:A:777:A:H1'	2.26	0.50
1:A:621:A:H2'	1:A:622:A:C8	2.46	0.50
11:L:65:TYR:HB3	11:L:95:HIS:CD2	2.47	0.50
5:F:62:MET:HG3	5:F:64:VAL:CG2	2.36	0.50
5:F:100:SER:HA	17:R:23:LYS:CE	2.41	0.50
6:G:107:ALA:HA	6:G:110:ARG:HD2	1.93	0.50
20:B:95:TRP:CZ2	20:B:100:LEU:HD13	2.46	0.50
1:A:1123:U:O2'	1:A:1124:G:H5'	2.11	0.50
1:A:993:G:C2'	1:A:995:C:H41	2.24	0.50
7:H:113:ARG:HH21	7:H:114:ALA:HA	1.77	0.50
1:A:538:G:OP2	11:L:111:GLN:HB2	2.11	0.50
1:A:502:A:H2'	1:A:503:C:C6	2.46	0.50
11:L:106:VAL:CG2	11:L:116:TYR:HB3	2.40	0.50
1:A:72:A:H2'	1:A:73:C:C6	2.46	0.50
18:S:20:LYS:O	18:S:23:GLU:HG3	2.12	0.50
1:A:827:U:H2'	1:A:870:U:O4	2.11	0.50
1:A:1289:A:H3'	1:A:1290:G:H8	1.76	0.50
21:U:13:VAL:HG13	21:U:13:VAL:O	2.12	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
3:D:191:SER:O	3:D:192:ALA:HB2	2.10	0.50
5:F:71:ILE:HG13	5:F:72:ASP:N	2.24	0.50
15:P:54:LEU:HD21	15:P:75:ILE:HG23	1.93	0.50
1:A:815:A:H4'	1:A:817:C:C4	2.46	0.50
10:K:55:ARG:NH1	10:K:60:PHE:HD1	2.10	0.50
11:L:35:ARG:NH1	11:L:36:VAL:H	2.09	0.50
1:A:586:C:H5''	7:H:81:GLY:HA2	1.93	0.50
1:A:923:A:OP1	4:E:25:LYS:HB3	2.10	0.50
1:A:963:G:H21	9:J:56:HIS:CE1	2.30	0.50
6:G:14:ASP:HB3	6:G:18:GLY:N	2.27	0.50
1:A:1515:G:O2'	1:A:1516:G:H5'	2.11	0.50
11:L:54:VAL:CG2	11:L:79:ILE:HD11	2.41	0.50
1:A:343:U:O2'	1:A:344:A:H2'	2.11	0.50
1:A:1095:U:H2'	1:A:1096:C:C6	2.47	0.50
1:A:1021:A:H2'	1:A:1022:A:O4'	2.10	0.50
4:E:144:GLU:HG2	4:E:144:GLU:O	2.11	0.50
21:U:42:THR:CB	21:U:46:ARG:HH21	2.25	0.50
1:A:979:C:H1'	1:A:1317:C:H41	1.76	0.50
2:C:19:SER:HB3	2:C:21:TRP:NE1	2.25	0.50
1:A:813:U:H5''	1:A:816:A:H62	1.75	0.50
1:A:22:G:H4'	1:A:885:G:C8	2.46	0.50
1:A:833:G:H2'	1:A:834:U:H6	1.76	0.50
1:A:858:G:O6	1:A:869:G:H3'	2.12	0.50
1:A:653:U:C4	7:H:55:LYS:HE2	2.47	0.50
1:A:394:G:H2'	1:A:395:C:C6	2.46	0.50
1:A:610:U:O2	1:A:610:U:O4'	2.30	0.50
1:A:131:A:H2'	1:A:132:C:H6	1.75	0.50
6:G:134:VAL:HB	6:G:137:ARG:NH2	2.26	0.50
20:B:65:LYS:HA	20:B:89:PHE:HE1	1.76	0.50
20:B:221:ARG:HG3	20:B:222:GLU:OE1	2.12	0.50
20:B:86:CYS:HB3	20:B:88:GLN:NE2	2.26	0.50
1:A:1080:A:O3'	4:E:20:VAL:HG11	2.12	0.50
1:A:253:A:H2'	1:A:254:G:H8	1.76	0.50
19:T:67:HIS:ND1	19:T:68:LYS:HG2	2.26	0.50
1:A:1271:A:H5'	1:A:1314:C:H5''	1.94	0.50
1:A:91:U:H6	1:A:91:U:O5'	1.94	0.50
1:A:958:A:N6	18:S:53:GLY:HA3	2.27	0.50
1:A:1053:G:N7	1:A:1199:U:H3'	2.27	0.50
1:A:620:C:C2	3:D:131:ILE:HD13	2.47	0.50
11:L:98:ARG:HD2	11:L:103:CYS:SG	2.52	0.50
16:Q:30:HIS:ND1	16:Q:32:ILE:HG22	2.26	0.50
4:E:131:ASN:O	4:E:135:VAL:HG23	2.12	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
7:H:74:ILE:HG13	7:H:128:VAL:HG22	1.93	0.50
1:A:643:C:H2'	1:A:644:U:H6	1.76	0.50
1:A:572:A:N3	1:A:917:G:H1'	2.26	0.50
18:S:42:ASN:N	18:S:42:ASN:HD22	2.10	0.50
2:C:25:THR:HG23	13:N:75:LYS:HE2	1.94	0.50
20:B:165:ALA:HB3	20:B:186:VAL:HG12	1.93	0.50
20:B:119:GLN:NE2	20:B:124:THR:HG22	2.27	0.50
5:F:42:TRP:HE3	5:F:45:ARG:HH12	1.59	0.50
14:O:11:ILE:HD11	14:O:30:ALA:HB1	1.94	0.50
9:J:52:LEU:HD12	9:J:52:LEU:H	1.76	0.50
1:A:665:A:H4'	23:A:2358:LLL:H531	1.94	0.50
1:A:1424:U:H2'	1:A:1425:U:C6	2.47	0.50
1:A:26:A:N6	1:A:558:G:H1'	2.26	0.50
20:B:116:LEU:HB3	20:B:140:LEU:HD11	1.92	0.50
1:A:295:C:H2'	1:A:296:U:C6	2.47	0.50
20:B:20:ARG:HA	20:B:20:ARG:NE	2.27	0.49
5:F:61:LEU:HD12	5:F:62:MET:H	1.77	0.49
1:A:1049:U:H2'	13:N:2:LYS:HD3	1.92	0.49
6:G:146:ALA:C	10:K:55:ARG:HH21	2.15	0.49
1:A:221:C:O2'	1:A:222:C:H5'	2.12	0.49
1:A:908:A:O2'	1:A:909:A:H5'	2.12	0.49
10:K:108:ASN:ND2	21:U:6:ARG:HD2	2.27	0.49
1:A:669:G:O6	23:A:2358:LLL:H312	2.12	0.49
1:A:1033:G:C2	1:A:1034:G:H1'	2.46	0.49
1:A:1090:U:H2'	1:A:1091:U:C6	2.47	0.49
5:F:3:HIS:CG	5:F:92:THR:HG23	2.47	0.49
5:F:36:ILE:N	5:F:36:ILE:HD12	2.28	0.49
11:L:86:VAL:HG11	11:L:89:LEU:HD23	1.94	0.49
11:L:49:ARG:HH12	11:L:88:ASP:HB3	1.76	0.49
13:N:31:SER:HA	13:N:40:ARG:HA	1.93	0.49
1:A:204:G:N2	1:A:466:A:N6	2.56	0.49
10:K:51:PHE:HB2	10:K:55:ARG:HB3	1.94	0.49
1:A:1141:C:H2'	1:A:1142:G:C8	2.46	0.49
9:J:36:VAL:HG22	9:J:76:ILE:HG22	1.94	0.49
2:C:49:ALA:O	2:C:71:ARG:HB2	2.12	0.49
1:A:812:G:O2'	1:A:813:U:H6	1.94	0.49
2:C:188:ALA:HB3	2:C:195:ILE:HB	1.94	0.49
10:K:30:ILE:HG22	10:K:45:THR:CB	2.43	0.49
14:O:74:ASP:OD1	14:O:76:ALA:HB3	2.12	0.49
1:A:1458:G:H2'	1:A:1459:G:H8	1.77	0.49
1:A:1175:G:O2'	1:A:1176:A:H5'	2.12	0.49
1:A:987:G:O2'	1:A:988:G:H5'	2.12	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
5:F:3:HIS:N	5:F:3:HIS:CD2	2.79	0.49
6:G:134:VAL:CB	6:G:137:ARG:HH21	2.25	0.49
1:A:1001:C:H2'	1:A:1002:G:C8	2.46	0.49
2:C:46:LEU:HD12	2:C:75:VAL:HG22	1.94	0.49
1:A:921:U:H2'	1:A:922:G:C8	2.48	0.49
1:A:34:C:H2'	1:A:35:G:C8	2.47	0.49
1:A:1330:U:C2'	1:A:1331:G:H5'	2.41	0.49
15:P:23:ASP:O	15:P:26:ASN:HB2	2.12	0.49
1:A:642:A:H2'	1:A:643:C:H6	1.77	0.49
1:A:747:A:H2'	1:A:748:G:O4'	2.12	0.49
1:A:1472:U:H2'	1:A:1473:G:H8	1.77	0.49
1:A:1363:A:H2'	1:A:1363:A:N3	2.27	0.49
1:A:317:U:H2'	1:A:318:G:H8	1.76	0.49
21:U:44:ARG:HG3	21:U:44:ARG:HH11	1.77	0.49
1:A:1099:G:H2'	1:A:1100:C:O4'	2.12	0.49
1:A:373:A:C1'	1:A:481:G:H1'	2.42	0.49
1:A:482:A:C2	1:A:483:C:H1'	2.47	0.49
1:A:464:U:H3'	1:A:466:A:OP1	2.13	0.49
1:A:376:G:OP1	15:P:5:ARG:HB2	2.11	0.49
1:A:947:G:H2'	1:A:948:C:C6	2.47	0.49
1:A:1201:A:H8	1:A:1201:A:H5''	1.77	0.49
1:A:1005:A:N6	1:A:1024:G:H1'	2.27	0.49
11:L:79:ILE:C	11:L:101:LEU:HD12	2.33	0.49
12:M:76:ILE:O	12:M:80:MET:HG3	2.12	0.49
1:A:418:C:H2'	1:A:419:C:H6	1.76	0.49
1:A:1269:A:H2	1:A:1312:G:N3	2.10	0.49
20:B:44:LYS:O	20:B:47:PRO:HD2	2.13	0.49
12:M:33:LEU:HD22	12:M:38:ILE:HB	1.93	0.49
1:A:204:G:O5'	1:A:204:G:H8	1.95	0.49
2:C:51:VAL:HA	2:C:69:THR:HA	1.94	0.49
6:G:50:ALA:HA	6:G:55:LYS:O	2.12	0.49
1:A:1131:G:O2'	1:A:1132:C:H5'	2.12	0.49
1:A:1033:G:N3	1:A:1034:G:H1'	2.27	0.49
1:A:162:A:H2'	1:A:163:C:O4'	2.12	0.49
20:B:76:SER:HA	20:B:92:ASN:HB2	1.93	0.49
3:D:56:GLU:HG2	3:D:198:LEU:HB3	1.94	0.49
1:A:1057:G:H4'	2:C:196:GLY:H	1.77	0.49
1:A:555:U:H2'	1:A:556:C:C6	2.48	0.49
1:A:197:A:H4'	1:A:198:G:O5'	2.13	0.49
6:G:65:LEU:O	6:G:69:ARG:HG3	2.13	0.49
8:I:20:ILE:HA	8:I:62:LEU:HB3	1.93	0.49
21:U:34:ARG:HD3	21:U:39:LYS:HZ3	1.76	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:N:52:ARG:NH1	13:N:58:ARG:HH21	2.10	0.49
5:F:15:SER:HA	5:F:18:VAL:HG23	1.94	0.49
1:A:836:G:OP2	17:R:49:LYS:HE2	2.12	0.49
2:C:190:THR:CG2	2:C:191:THR:H	2.20	0.49
18:S:10:ILE:HG22	18:S:38:THR:N	2.20	0.49
13:N:6:LYS:O	13:N:10:VAL:HG23	2.13	0.49
1:A:254:G:H4'	16:Q:19:SER:OG	2.13	0.49
1:A:336:A:O2'	1:A:337:G:H5'	2.13	0.49
8:I:32:ARG:NH1	8:I:37:TYR:HA	2.28	0.49
1:A:555:U:H2'	1:A:556:C:H6	1.77	0.49
6:G:61:PHE:O	6:G:65:LEU:HD13	2.12	0.49
5:F:100:SER:HA	17:R:23:LYS:CD	2.43	0.49
1:A:370:C:H2'	1:A:371:A:H8	1.78	0.49
11:L:20:VAL:HB	11:L:94:TYR:CE1	2.48	0.49
1:A:1336:C:H4'	1:A:1337:G:O5'	2.12	0.49
9:J:56:HIS:H	13:N:80:ARG:NH2	2.10	0.49
1:A:1200:C:C3'	1:A:1201:A:H5'	2.43	0.49
1:A:1370:G:O2'	1:A:1371:G:H5'	2.13	0.49
15:P:74:LEU:O	15:P:78:VAL:HG12	2.13	0.49
1:A:556:C:O2'	1:A:557:G:H5'	2.12	0.49
1:A:712:A:O2'	1:A:713:G:H5'	2.13	0.49
4:E:98:ALA:HB2	4:E:123:LEU:HG	1.94	0.49
1:A:875:U:O2'	7:H:14:ARG:HD2	2.13	0.49
13:N:60:ARG:NE	13:N:69:PRO:HB3	2.28	0.49
1:A:204:G:C2	1:A:465:A:H1'	2.48	0.49
1:A:194:C:O2'	1:A:195:A:H5'	2.13	0.49
3:D:106:PHE:CD1	3:D:144:ILE:HD11	2.48	0.49
1:A:178:C:O2'	1:A:179:A:H5'	2.12	0.49
1:A:418:C:H2'	1:A:419:C:C6	2.47	0.49
1:A:562:U:H1'	11:L:11:ARG:HB3	1.93	0.49
1:A:1203:C:H4'	13:N:66:THR:HG22	1.95	0.49
1:A:896:C:O2'	1:A:897:C:H5'	2.12	0.49
1:A:614:C:OP1	3:D:82:LYS:HE2	2.13	0.49
3:D:16:THR:HG22	3:D:17:ASP:N	2.27	0.49
3:D:7:LYS:O	3:D:20:LEU:HD12	2.12	0.48
16:Q:3:LYS:NZ	16:Q:4:ILE:HD12	2.28	0.48
20:B:59:ILE:HD12	20:B:60:ALA:N	2.28	0.48
11:L:35:ARG:O	11:L:53:ARG:N	2.46	0.48
4:E:113:VAL:HG23	4:E:114:LEU:N	2.28	0.48
1:A:719:C:O2'	17:R:37:LYS:HB2	2.12	0.48
1:A:961:U:H3	1:A:983:A:H62	1.61	0.48
1:A:706:A:H4'	10:K:30:ILE:HD11	1.94	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:751:U:H4'	14:O:24:SER:HA	1.94	0.48
1:A:1298:U:H4'	1:A:1299:A:C4	2.48	0.48
1:A:547:A:H4'	1:A:548:G:O5'	2.13	0.48
1:A:105:G:H2'	1:A:106:C:C6	2.47	0.48
3:D:151:GLN:HB2	3:D:154:VAL:HG23	1.94	0.48
12:M:78:ARG:HB3	12:M:78:ARG:CZ	2.43	0.48
12:M:33:LEU:CD2	12:M:38:ILE:HB	2.43	0.48
4:E:44:ARG:HD2	4:E:72:ASN:ND2	2.27	0.48
1:A:250:A:H1'	1:A:252:U:C5	2.48	0.48
1:A:947:G:H4'	12:M:107:THR:OG1	2.14	0.48
1:A:1038:C:H2'	1:A:1039:G:H8	1.76	0.48
1:A:90:C:H2'	1:A:91:U:C6	2.47	0.48
6:G:63:VAL:HG12	6:G:127:ALA:HB1	1.95	0.48
1:A:98:A:O2'	1:A:99:C:H5'	2.13	0.48
1:A:958:A:P	18:S:54:ARG:HH22	2.35	0.48
3:D:13:ARG:CG	3:D:55:ARG:HH12	2.24	0.48
20:B:93:HIS:HD2	20:B:145:ASN:HB3	1.77	0.48
1:A:390:U:H2'	1:A:391:G:H8	1.76	0.48
1:A:208:U:H2'	1:A:210:C:C2	2.48	0.48
1:A:208:U:H2'	1:A:210:C:N3	2.27	0.48
1:A:834:U:H2'	1:A:835:U:C6	2.48	0.48
11:L:14:LYS:HG2	11:L:15:VAL:N	2.28	0.48
6:G:85:GLN:HA	6:G:85:GLN:OE1	2.12	0.48
20:B:26:MET:HE1	20:B:186:VAL:HG23	1.94	0.48
1:A:93:U:P	1:A:94:G:H5'	2.54	0.48
13:N:26:LEU:O	13:N:30:ILE:N	2.47	0.48
2:C:156:LEU:CD1	2:C:165:GLU:HB2	2.43	0.48
7:H:123:GLU:HG2	7:H:124:ILE:O	2.13	0.48
1:A:1319:A:H4'	1:A:1320:C:OP1	2.13	0.48
1:A:783:C:O2'	1:A:784:A:H5'	2.11	0.48
5:F:81:ASN:O	5:F:84:VAL:HG12	2.13	0.48
16:Q:57:VAL:HB	16:Q:79:GLU:HB3	1.95	0.48
20:B:130:LYS:N	20:B:130:LYS:HD2	2.28	0.48
8:I:126:PHE:O	8:I:128:LYS:N	2.47	0.48
2:C:67:ILE:HD12	2:C:100:ILE:HD11	1.95	0.48
1:A:1246:A:H2'	1:A:1247:U:O4'	2.13	0.48
9:J:87:LEU:H	9:J:87:LEU:HD22	1.77	0.48
6:G:109:LYS:HE2	6:G:109:LYS:HA	1.96	0.48
1:A:977:A:N6	1:A:1224:U:O5'	2.46	0.48
20:B:46:VAL:CG1	20:B:47:PRO:HD3	2.32	0.48
2:C:133:MET:O	2:C:137:VAL:HG23	2.13	0.48
1:A:279:A:C5'	1:A:280:C:H3'	2.43	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1162:C:H2'	1:A:1163:A:H8	1.75	0.48
1:A:1163:A:H2'	1:A:1164:G:C8	2.47	0.48
1:A:1319:A:OP2	18:S:4:LEU:HD21	2.14	0.48
1:A:1169:A:H2'	1:A:1170:A:C8	2.48	0.48
3:D:104:MET:SD	3:D:142:VAL:HB	2.53	0.48
1:A:420:U:H2'	1:A:422:C:C4	2.49	0.48
15:P:20:VAL:HG21	15:P:32:PHE:CD2	2.49	0.48
1:A:651:C:H2'	1:A:652:U:C6	2.49	0.48
1:A:986:U:H2'	1:A:987:G:O4'	2.12	0.48
1:A:510:A:N3	1:A:543:U:H1'	2.28	0.48
9:J:92:LEU:HD22	9:J:92:LEU:H	1.77	0.48
5:F:69:GLU:O	5:F:73:GLU:HG2	2.13	0.48
1:A:682:G:O2'	1:A:683:G:H5'	2.14	0.48
18:S:48:ILE:HB	18:S:59:VAL:CG2	2.43	0.48
1:A:532:A:H62	2:C:191:THR:CB	2.15	0.48
3:D:147:LYS:HZ3	3:D:147:LYS:HB2	1.79	0.48
5:F:47:LEU:HD21	5:F:57:ALA:HB3	1.94	0.48
13:N:46:LYS:HZ2	18:S:10:ILE:N	2.11	0.48
1:A:906:A:C2'	1:A:907:A:H5''	2.44	0.48
13:N:51:PRO:CB	13:N:54:SER:HB3	2.39	0.48
1:A:1270:G:H4'	1:A:1313:U:O2'	2.13	0.48
1:A:599:C:O2'	1:A:600:A:H5'	2.13	0.48
2:C:96:VAL:HB	2:C:97:PRO:HD2	1.96	0.48
1:A:22:G:H2'	1:A:23:C:H6	1.78	0.48
1:A:1432:G:H1'	1:A:1468:A:H61	1.79	0.48
1:A:791:G:C6	1:A:792:A:N7	2.82	0.48
6:G:68:VAL:CG2	6:G:126:ALA:HB1	2.43	0.48
10:K:106:ILE:HD11	10:K:109:ILE:CG1	2.43	0.48
1:A:663:A:H5''	17:R:49:LYS:HD2	1.96	0.48
18:S:5:LYS:O	18:S:6:LYS:HD2	2.13	0.48
16:Q:66:LEU:HD13	16:Q:70:LYS:HG2	1.95	0.48
1:A:846:G:H2'	1:A:847:G:C8	2.49	0.48
1:A:552:U:H5'	11:L:82:ARG:HH11	1.79	0.48
1:A:513:C:H2'	1:A:514:C:H6	1.78	0.48
13:N:79:SER:O	13:N:83:VAL:HG23	2.12	0.48
20:B:184:ALA:H	20:B:195:VAL:HG11	1.77	0.48
20:B:26:MET:O	20:B:30:ILE:HG13	2.14	0.48
10:K:83:VAL:HG21	10:K:109:ILE:HG12	1.95	0.48
1:A:437:U:H1'	3:D:115:GLN:NE2	2.29	0.48
1:A:373:A:H1'	1:A:481:G:H1'	1.95	0.48
15:P:61:VAL:CA	15:P:65:ALA:HB3	2.42	0.48
1:A:220:G:O2'	1:A:221:C:H5'	2.13	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:693:G:OP1	10:K:126:ARG:NH1	2.47	0.48
1:A:735:C:OP2	23:A:2358:LLL:H832	2.13	0.48
1:A:169:C:O2'	1:A:170:U:H5'	2.13	0.48
1:A:224:U:H2'	1:A:225:C:C6	2.48	0.48
20:B:20:ARG:CZ	20:B:20:ARG:HB3	2.43	0.48
1:A:1149:C:H2'	1:A:1150:A:H8	1.78	0.48
3:D:115:GLN:HG3	3:D:119:HIS:CE1	2.49	0.48
12:M:78:ARG:HH22	18:S:64:GLU:HB2	1.77	0.48
1:A:890:G:O2'	1:A:906:A:N6	2.46	0.48
20:B:128:LEU:HB3	20:B:132:GLU:HB3	1.95	0.48
20:B:83:ALA:HB3	20:B:90:PHE:HB3	1.95	0.48
1:A:252:U:H2'	1:A:253:A:C8	2.49	0.48
1:A:865:A:H2	1:A:918:A:H4'	1.79	0.48
1:A:490:C:H2'	1:A:491:G:C8	2.49	0.48
1:A:1299:A:H3'	1:A:1299:A:OP2	2.14	0.48
3:D:47:LEU:HD23	3:D:52:VAL:HA	1.96	0.48
8:I:30:ASN:ND2	8:I:65:THR:HA	2.28	0.48
5:F:3:HIS:CD2	5:F:65:GLU:HG3	2.48	0.48
10:K:86:LYS:HB2	10:K:113:THR:HA	1.95	0.48
12:M:53:ASP:HA	12:M:56:ARG:CZ	2.42	0.48
1:A:1080:A:OP1	4:E:51:LYS:HD3	2.13	0.48
2:C:148:ILE:HG12	2:C:149:LYS:N	2.29	0.48
9:J:6:ILE:O	9:J:75:ASP:HA	2.14	0.48
1:A:993:G:N3	1:A:993:G:H2'	2.29	0.48
4:E:61:LYS:HB2	4:E:65:LYS:HZ1	1.77	0.48
3:D:34:GLU:HG3	3:D:34:GLU:O	2.14	0.48
1:A:491:G:O2'	1:A:492:C:H5'	2.14	0.48
2:C:142:ARG:NH2	2:C:143:LEU:HD21	2.28	0.48
1:A:215:C:H2'	1:A:216:U:H6	1.79	0.48
1:A:333:U:H2'	1:A:334:C:C6	2.48	0.48
1:A:1520:C:H2'	1:A:1521:C:C6	2.48	0.48
1:A:426:U:H4'	3:D:39:GLN:HA	1.96	0.48
1:A:54:C:H2'	1:A:352:C:H41	1.78	0.48
20:B:17:HIS:CG	20:B:18:GLN:H	2.31	0.48
20:B:19:THR:HG23	20:B:20:ARG:N	2.27	0.48
8:I:56:MET:HG3	8:I:57:VAL:HG23	1.96	0.48
1:A:1060:U:H2'	1:A:1061:G:C8	2.48	0.48
5:F:46:GLN:HG3	5:F:47:LEU:N	2.29	0.48
6:G:26:VAL:HA	6:G:42:VAL:HG21	1.95	0.48
2:C:2:GLN:H	2:C:2:GLN:HE21	1.59	0.48
3:D:12:ARG:HA	3:D:33:ILE:HD12	1.96	0.48
20:B:151:LYS:HG3	20:B:152:ASP:N	2.29	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1159:U:O4'	1:A:1182:G:N2	2.47	0.48
1:A:895:G:H2'	1:A:896:C:C6	2.49	0.48
19:T:77:ASN:O	19:T:81:GLN:HG3	2.14	0.48
14:O:68:ASP:O	14:O:72:ARG:HG3	2.14	0.48
1:A:1108:G:H5'	2:C:175:HIS:ND1	2.28	0.48
1:A:1453:G:H2'	1:A:1454:G:O4'	2.14	0.48
21:U:43:GLU:HA	21:U:46:ARG:HD2	1.96	0.47
5:F:47:LEU:HD21	5:F:57:ALA:CB	2.44	0.47
11:L:85:ARG:HD2	11:L:93:ARG:HG3	1.96	0.47
16:Q:3:LYS:HZ3	16:Q:4:ILE:HD12	1.79	0.47
20:B:96:LEU:HB2	20:B:99:MET:CE	2.44	0.47
11:L:36:VAL:HG12	11:L:52:CYS:HB2	1.95	0.47
8:I:119:LYS:C	8:I:121:ARG:H	2.16	0.47
1:A:560:A:N1	1:A:566:G:H5'	2.29	0.47
3:D:22:SER:N	3:D:109:THR:HG22	2.29	0.47
8:I:71:ILE:N	8:I:71:ILE:HD12	2.28	0.47
6:G:71:THR:HG23	6:G:72:VAL:HG22	1.96	0.47
17:R:44:THR:C	17:R:46:THR:H	2.17	0.47
11:L:66:ILE:HD12	11:L:66:ILE:N	2.29	0.47
1:A:66:A:H5'	1:A:173:U:O4	2.14	0.47
8:I:42:THR:HA	8:I:45:MET:SD	2.53	0.47
1:A:1418:A:N6	1:A:1482:G:H1'	2.29	0.47
20:B:212:TYR:HA	20:B:215:ALA:HB3	1.94	0.47
20:B:18:GLN:O	20:B:37:VAL:HG23	2.14	0.47
1:A:438:U:H4'	3:D:119:HIS:HD2	1.79	0.47
20:B:96:LEU:HB2	20:B:99:MET:HE2	1.97	0.47
13:N:41:TRP:CD1	13:N:43:ALA:HB3	2.49	0.47
1:A:464:U:H2'	1:A:466:A:OP2	2.13	0.47
20:B:187:ASP:O	20:B:189:ASN:N	2.48	0.47
10:K:19:VAL:HG23	10:K:34:THR:HG23	1.94	0.47
1:A:58:C:O2'	1:A:59:A:H5'	2.13	0.47
1:A:955:U:H2'	1:A:956:U:O4'	2.14	0.47
1:A:1249:C:H4'	8:I:37:TYR:OH	2.14	0.47
1:A:389:A:N3	1:A:389:A:H2'	2.29	0.47
10:K:36:ARG:HH11	10:K:36:ARG:HG3	1.79	0.47
8:I:6:TYR:HB2	8:I:19:PHE:CE1	2.49	0.47
1:A:203:G:H1'	1:A:465:A:N6	2.29	0.47
1:A:412:A:H61	3:D:29:THR:HG22	1.80	0.47
1:A:254:G:O2'	1:A:255:G:H5'	2.14	0.47
1:A:1262:C:H2'	1:A:1263:C:O4'	2.14	0.47
1:A:1033:G:H2'	1:A:1034:G:O4'	2.14	0.47
2:C:171:ARG:HB2	2:C:171:ARG:HH11	1.79	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:653:U:C5	7:H:55:LYS:HE2	2.49	0.47
1:A:425:G:O2'	1:A:426:U:H5'	2.15	0.47
1:A:355:C:O2'	1:A:356:A:H5'	2.14	0.47
5:F:52:ASN:O	5:F:52:ASN:CG	2.52	0.47
5:F:29:ILE:HG21	5:F:64:VAL:CG1	2.45	0.47
20:B:104:LYS:HG3	20:B:105:THR:H	1.79	0.47
13:N:40:ARG:NH1	18:S:6:LYS:HB2	2.28	0.47
15:P:38:PHE:CE2	15:P:51:ARG:HD3	2.50	0.47
20:B:172:ILE:H	20:B:172:ILE:HD12	1.79	0.47
1:A:1366:C:H2'	1:A:1367:C:C6	2.48	0.47
1:A:605:U:H2'	1:A:606:G:C8	2.49	0.47
1:A:1462:C:H2'	1:A:1463:U:C6	2.49	0.47
1:A:802:A:H2'	1:A:803:G:O4'	2.14	0.47
13:N:97:LYS:HB3	13:N:97:LYS:NZ	2.29	0.47
20:B:212:TYR:O	20:B:216:VAL:HG22	2.14	0.47
8:I:49:GLN:C	8:I:51:LEU:H	2.16	0.47
1:A:69:G:H2'	1:A:70:U:C6	2.49	0.47
1:A:981:U:H4'	13:N:60:ARG:CD	2.36	0.47
1:A:1337:G:H5''	1:A:1338:G:OP1	2.14	0.47
1:A:715:A:H2'	1:A:716:A:H8	1.77	0.47
1:A:1373:G:H5''	6:G:35:LYS:HB2	1.97	0.47
1:A:1045:C:H2'	1:A:1046:A:O4'	2.15	0.47
1:A:692:U:O2	1:A:694:A:H5''	2.15	0.47
1:A:1532:U:N3	1:A:1534:A:H5''	2.29	0.47
5:F:49:TYR:CE1	17:R:65:SER:HA	2.50	0.47
1:A:60:A:H4'	1:A:61:G:O5'	2.15	0.47
5:F:3:HIS:ND1	5:F:95:ALA:HB2	2.30	0.47
8:I:22:PRO:HA	8:I:60:LEU:HB2	1.96	0.47
8:I:62:LEU:N	8:I:62:LEU:HD22	2.30	0.47
18:S:48:ILE:HB	18:S:59:VAL:HG21	1.96	0.47
3:D:60:VAL:HA	3:D:63:ILE:HD12	1.97	0.47
15:P:52:LEU:HD21	15:P:75:ILE:HG12	1.95	0.47
7:H:87:ARG:HG3	7:H:90:GLU:OE2	2.15	0.47
17:R:61:ALA:HB3	17:R:67:LEU:HD12	1.97	0.47
1:A:635:A:H2'	1:A:636:U:C6	2.48	0.47
1:A:154:U:H2'	1:A:155:A:H8	1.78	0.47
1:A:847:G:H2'	1:A:848:C:H6	1.79	0.47
15:P:71:VAL:HG13	15:P:72:ALA:N	2.29	0.47
16:Q:30:HIS:HD2	16:Q:37:ILE:HD11	1.80	0.47
1:A:512:U:O2'	1:A:513:C:H5'	2.15	0.47
9:J:67:ILE:HA	13:N:94:GLY:O	2.15	0.47
1:A:927:G:O2'	1:A:928:G:H5'	2.14	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:G:4:ARG:HE	6:G:6:ILE:HG23	1.80	0.47
1:A:1409:C:N4	1:A:1410:A:H62	2.12	0.47
8:I:38:PHE:HE1	8:I:78:ILE:HD12	1.80	0.47
21:U:3:ILE:HG23	21:U:18:PHE:CE2	2.49	0.47
2:C:126:ARG:HH22	2:C:190:THR:CG2	2.21	0.47
12:M:52:ILE:HA	12:M:55:LEU:HG	1.95	0.47
20:B:86:CYS:O	20:B:88:GLN:N	2.47	0.47
10:K:28:ASN:HD21	10:K:47:GLY:N	2.07	0.47
16:Q:17:GLU:O	16:Q:18:LYS:HB2	2.15	0.47
1:A:130:A:C8	16:Q:64:ARG:HG3	2.50	0.47
11:L:21:PRO:C	11:L:23:LEU:H	2.17	0.47
1:A:539:A:H2'	1:A:540:G:H8	1.79	0.47
21:U:24:LYS:CD	21:U:25:ALA:H	2.24	0.47
1:A:499:A:H1'	1:A:500:G:C8	2.48	0.47
1:A:207:C:H3'	1:A:208:U:C5	2.49	0.47
1:A:399:G:H2'	1:A:400:C:C6	2.50	0.47
1:A:766:A:H2'	1:A:767:A:O4'	2.15	0.47
1:A:1180:A:P	8:I:98:ARG:HH22	2.38	0.47
1:A:720:C:H6	1:A:720:C:O5'	1.96	0.47
1:A:642:A:C5	7:H:106:SER:HA	2.50	0.47
9:J:92:LEU:HD22	9:J:92:LEU:N	2.30	0.47
1:A:515:G:H2'	1:A:516:U:C6	2.50	0.47
1:A:960:U:O2'	1:A:1223:C:H4'	2.14	0.47
1:A:1332:A:H2'	1:A:1333:A:C8	2.50	0.47
9:J:80:THR:O	9:J:84:VAL:HG23	2.15	0.47
20:B:185:ILE:HG12	20:B:199:ILE:HG21	1.97	0.47
20:B:20:ARG:HE	20:B:38:HIS:CD2	2.32	0.47
1:A:78:A:H8	1:A:78:A:O5'	1.98	0.47
9:J:15:HIS:O	9:J:18:ILE:HG22	2.15	0.47
1:A:93:U:OP2	1:A:94:G:H5''	2.14	0.47
1:A:481:G:O2'	1:A:482:A:H8	1.98	0.47
2:C:182:ASP:HB3	2:C:201:ILE:HB	1.97	0.47
7:H:77:VAL:HG12	7:H:84:ILE:HD12	1.96	0.47
1:A:1248:A:C2	8:I:71:ILE:HD11	2.50	0.47
2:C:194:VAL:HG12	2:C:195:ILE:N	2.30	0.47
4:E:12:GLU:HB3	4:E:63:MET:CE	2.44	0.47
1:A:1484:C:H2'	1:A:1485:U:C6	2.50	0.47
13:N:48:GLN:O	13:N:51:PRO:HD2	2.14	0.47
1:A:370:C:O2'	1:A:371:A:H5'	2.15	0.47
1:A:253:A:H2'	1:A:254:G:C8	2.49	0.47
1:A:634:C:H2'	1:A:635:A:C8	2.50	0.47
9:J:40:ILE:HD12	9:J:73:LEU:HD12	1.97	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:843:U:H4'	1:A:843:U:OP2	2.13	0.47
3:D:33:ILE:HG13	3:D:34:GLU:N	2.30	0.47
3:D:88:ASN:O	3:D:92:LEU:HD23	2.15	0.47
1:A:1320:C:P	18:S:69:LYS:HZ2	2.38	0.47
1:A:825:A:H2'	1:A:826:C:C6	2.48	0.47
5:F:18:VAL:O	5:F:22:ILE:HG13	2.14	0.47
9:J:80:THR:HG22	9:J:82:LYS:HG2	1.97	0.47
1:A:810:C:O2'	1:A:811:C:H5'	2.15	0.47
1:A:364:A:H2'	1:A:365:U:O2	2.15	0.47
1:A:593:U:H2'	1:A:594:U:C6	2.50	0.47
14:O:50:HIS:O	14:O:53:ARG:HB3	2.15	0.47
3:D:169:TRP:HB2	3:D:183:ARG:O	2.15	0.47
3:D:182:LYS:NZ	3:D:182:LYS:HB3	2.30	0.47
20:B:14:HIS:CB	20:B:208:ALA:HB2	2.45	0.47
5:F:45:ARG:O	5:F:56:LYS:HA	2.15	0.47
4:E:81:GLN:H	4:E:146:MET:HE1	1.80	0.47
20:B:223:GLY:C	20:B:225:SER:H	2.17	0.47
13:N:26:LEU:HD12	13:N:44:VAL:HG13	1.96	0.47
1:A:818:G:C3'	1:A:819:A:H5''	2.45	0.47
1:A:1240:U:O4	6:G:29:LEU:HG	2.14	0.47
1:A:465:A:H2'	1:A:466:A:H3'	1.96	0.47
1:A:327:A:H1'	1:A:329:A:O4'	2.15	0.47
16:Q:66:LEU:O	16:Q:67:SER:HB2	2.15	0.47
1:A:1491:G:C5	23:A:2356:LLL:H21	2.50	0.47
2:C:35:ASP:OD1	2:C:58:ARG:HD2	2.15	0.47
1:A:191:G:H2'	1:A:192:A:H8	1.79	0.47
21:U:24:LYS:NZ	21:U:24:LYS:HB3	2.31	0.47
5:F:14:GLN:NE2	5:F:83:ALA:HB2	2.30	0.47
10:K:127:ARG:HG3	10:K:127:ARG:HH11	1.79	0.47
1:A:692:U:C2	1:A:694:A:H5''	2.50	0.47
2:C:111:ASP:OD2	2:C:114:LEU:HG	2.15	0.47
3:D:170:LEU:N	3:D:170:LEU:HD23	2.30	0.47
1:A:1098:C:H2'	1:A:1099:G:H8	1.79	0.46
10:K:33:ILE:HG12	10:K:69:CYS:SG	2.55	0.46
13:N:60:ARG:HE	13:N:62:ARG:HG2	1.79	0.46
1:A:121:U:H3'	1:A:121:U:OP1	2.14	0.46
1:A:1143:G:O2'	1:A:1144:G:H5'	2.16	0.46
11:L:34:THR:HG23	11:L:55:ARG:HB2	1.97	0.46
3:D:137:SER:HB2	3:D:140:ASP:OD2	2.15	0.46
5:F:12:PRO:C	5:F:14:GLN:H	2.18	0.46
1:A:807:A:H2'	1:A:808:C:C6	2.50	0.46
1:A:620:C:O2	3:D:131:ILE:HG21	2.15	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:C:10:ARG:CZ	2:C:181:ILE:HD13	2.45	0.46
1:A:224:U:H2'	1:A:225:C:H6	1.79	0.46
1:A:952:U:H2'	1:A:953:G:C8	2.51	0.46
1:A:113:G:H2'	1:A:114:U:C6	2.50	0.46
16:Q:82:VAL:HG13	16:Q:82:VAL:O	2.15	0.46
18:S:29:PRO:HB3	18:S:47:THR:HG22	1.96	0.46
10:K:55:ARG:HH12	10:K:60:PHE:HD1	1.61	0.46
1:A:1010:U:O2'	1:A:1011:C:H5'	2.15	0.46
1:A:265:G:H5'	16:Q:65:PRO:O	2.15	0.46
2:C:58:ARG:HA	2:C:62:SER:O	2.15	0.46
15:P:1:MET:HG3	15:P:3:THR:CG2	2.46	0.46
5:F:37:HIS:O	5:F:97:THR:HG23	2.16	0.46
1:A:429:U:H4'	1:A:430:A:O5'	2.15	0.46
14:O:26:GLU:HA	14:O:81:LEU:HD11	1.97	0.46
7:H:118:ALA:HB3	7:H:120:LEU:CD2	2.46	0.46
17:R:63:TYR:N	17:R:63:TYR:CD2	2.82	0.46
1:A:997:U:H2'	1:A:998:C:C6	2.50	0.46
7:H:47:ASP:CG	7:H:48:PHE:H	2.18	0.46
1:A:1118:U:H2'	1:A:1119:C:H6	1.81	0.46
20:B:224:ARG:HB3	20:B:224:ARG:NH1	2.30	0.46
20:B:86:CYS:SG	20:B:87:ASP:N	2.89	0.46
1:A:1317:C:OP1	13:N:56:PRO:HD2	2.15	0.46
1:A:1512:U:H2'	1:A:1513:A:H8	1.80	0.46
1:A:252:U:H2'	1:A:253:A:H8	1.79	0.46
20:B:107:ARG:HG3	20:B:108:GLN:N	2.29	0.46
1:A:1005:A:C2	1:A:1006:G:H1'	2.49	0.46
20:B:116:LEU:HB3	20:B:140:LEU:CD1	2.46	0.46
1:A:356:A:H1'	1:A:368:U:O2'	2.16	0.46
1:A:1456:A:H2'	1:A:1457:G:O4'	2.15	0.46
15:P:54:LEU:HD11	15:P:80:LYS:HA	1.97	0.46
2:C:112:ALA:CB	2:C:184:ASN:HB2	2.45	0.46
1:A:411:A:C4	1:A:413:G:H1'	2.50	0.46
1:A:255:G:H2'	1:A:256:U:C6	2.51	0.46
1:A:878:A:H5''	7:H:80:PRO:HG2	1.96	0.46
9:J:73:LEU:HD13	9:J:75:ASP:HB2	1.97	0.46
1:A:849:G:N7	23:A:2357:LLL:N61	2.63	0.46
1:A:947:G:H5''	12:M:106:ARG:HB2	1.97	0.46
1:A:812:G:OP1	1:A:812:G:H4'	2.15	0.46
1:A:679:C:H2'	1:A:680:C:C6	2.50	0.46
1:A:499:A:H4'	1:A:500:G:H5'	1.96	0.46
14:O:81:LEU:O	14:O:85:LEU:HD13	2.15	0.46
1:A:435:A:N3	1:A:435:A:H2'	2.29	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
15:P:20:VAL:HG21	15:P:32:PHE:CG	2.50	0.46
1:A:643:C:H2'	1:A:644:U:C6	2.50	0.46
1:A:1409:C:H3'	1:A:1410:A:H8	1.80	0.46
1:A:811:C:H4'	1:A:900:A:N6	2.30	0.46
1:A:113:G:O4'	1:A:354:G:H4'	2.15	0.46
20:B:209:VAL:HG23	20:B:210:THR:H	1.80	0.46
5:F:38:ARG:NH2	5:F:63:ASN:HD21	2.13	0.46
1:A:321:A:H5''	1:A:328:C:N4	2.31	0.46
1:A:1308:U:H3'	12:M:97:ARG:NH1	2.30	0.46
6:G:14:ASP:H	6:G:19:SER:H	1.63	0.46
15:P:23:ASP:CG	15:P:25:ARG:HE	2.19	0.46
7:H:94:VAL:CG2	7:H:101:ALA:HB2	2.44	0.46
1:A:1468:A:O2'	1:A:1469:C:H5'	2.16	0.46
1:A:834:U:H2'	1:A:835:U:H6	1.81	0.46
1:A:83:C:H1'	1:A:84:U:C6	2.50	0.46
1:A:173:U:H6	1:A:198:G:HO2'	1.64	0.46
21:U:40:PRO:O	21:U:42:THR:N	2.49	0.46
5:F:6:ILE:HG23	5:F:62:MET:HB3	1.98	0.46
6:G:78:ARG:HA	6:G:83:THR:HA	1.97	0.46
1:A:847:G:H2'	1:A:848:C:C6	2.51	0.46
1:A:883:C:O2'	1:A:884:U:H5'	2.15	0.46
8:I:9:GLY:CA	8:I:80:HIS:HB3	2.46	0.46
14:O:70:LEU:HD12	14:O:78:TYR:HB2	1.96	0.46
1:A:564:C:H1'	16:Q:32:ILE:O	2.15	0.46
1:A:1460:C:H2'	1:A:1461:G:C8	2.51	0.46
12:M:77:LYS:HG2	12:M:81:ASP:OD1	2.16	0.46
1:A:1203:C:H2'	1:A:1204:A:O4'	2.16	0.46
1:A:1042:A:H2'	1:A:1043:G:O4'	2.15	0.46
5:F:70:VAL:HG23	5:F:71:ILE:N	2.31	0.46
4:E:81:GLN:CD	4:E:149:PRO:HD3	2.36	0.46
13:N:30:ILE:HG21	13:N:44:VAL:CG2	2.40	0.46
1:A:769:G:O2'	1:A:770:C:H5'	2.16	0.46
1:A:465:A:C2'	1:A:466:A:H3'	2.46	0.46
3:D:22:SER:H	3:D:109:THR:CG2	2.28	0.46
20:B:122:ASP:HB3	20:B:123:GLY:H	1.61	0.46
1:A:1036:A:H2'	1:A:1037:C:O4'	2.16	0.46
7:H:17:GLN:NE2	7:H:62:LEU:HB3	2.29	0.46
5:F:18:VAL:N	5:F:19:PRO:HD2	2.30	0.46
1:A:1111:A:O2'	1:A:1112:C:H5'	2.15	0.46
20:B:19:THR:O	20:B:37:VAL:HA	2.15	0.46
18:S:62:THR:HG22	18:S:63:ASP:N	2.30	0.46
6:G:80:GLY:C	6:G:82:SER:H	2.19	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
4:E:37:VAL:HG12	4:E:47:PHE:CB	2.46	0.46
14:O:82:ILE:O	14:O:86:GLY:N	2.49	0.46
1:A:333:U:H2'	1:A:334:C:H6	1.80	0.46
1:A:972:C:P	9:J:59:LYS:HD3	2.56	0.46
1:A:1110:A:H3'	24:A:2560:HOH:O	2.16	0.46
1:A:403:C:O2'	1:A:404:G:H5'	2.16	0.46
1:A:1149:C:OP2	8:I:10:ARG:NH1	2.49	0.46
1:A:411:A:N9	1:A:413:G:H1'	2.31	0.46
1:A:1348:U:O3'	8:I:121:ARG:HG3	2.15	0.46
1:A:251:G:H4'	1:A:252:U:H5'	1.98	0.46
1:A:865:A:C2	1:A:918:A:H4'	2.51	0.46
2:C:13:ILE:N	2:C:13:ILE:HD13	2.30	0.46
6:G:21:LEU:HD23	6:G:21:LEU:N	2.31	0.46
4:E:136:VAL:HG13	4:E:137:ARG:N	2.31	0.46
8:I:42:THR:O	8:I:45:MET:HG2	2.15	0.46
6:G:91:ARG:CB	6:G:92:PRO:HD2	2.46	0.46
1:A:822:U:H2'	1:A:823:C:H6	1.81	0.46
20:B:47:PRO:O	20:B:51:GLU:HB2	2.16	0.46
8:I:20:ILE:HG23	8:I:60:LEU:HD12	1.97	0.46
13:N:26:LEU:HA	13:N:30:ILE:HD13	1.98	0.46
2:C:48:LYS:HD3	2:C:48:LYS:N	2.26	0.46
1:A:586:C:C2'	1:A:587:G:H5'	2.46	0.46
1:A:719:C:H2'	17:R:38:ILE:HD13	1.97	0.46
1:A:668:G:O2'	1:A:669:G:H5'	2.15	0.46
1:A:620:C:H2'	1:A:621:A:C8	2.51	0.46
1:A:1292:G:H2'	1:A:1293:C:H6	1.81	0.46
17:R:32:ILE:HG22	17:R:33:THR:O	2.16	0.46
1:A:711:G:O2'	1:A:712:A:H5'	2.16	0.46
6:G:94:ARG:NE	6:G:98:LEU:HD11	2.31	0.46
1:A:984:C:O2'	1:A:985:C:H5'	2.16	0.46
1:A:1190:G:OP1	2:C:3:LYS:HA	2.16	0.46
8:I:24:ASN:CG	8:I:25:GLY:N	2.69	0.45
3:D:18:LEU:H	3:D:18:LEU:HD22	1.79	0.45
12:M:38:ILE:HG13	12:M:55:LEU:CD2	2.46	0.45
10:K:17:ASP:HB3	10:K:80:ASN:CG	2.37	0.45
13:N:60:ARG:CZ	13:N:62:ARG:CZ	2.95	0.45
1:A:203:G:H21	1:A:205:A:H61	1.63	0.45
7:H:6:ILE:HD12	7:H:35:ILE:HD12	1.98	0.45
1:A:451:A:C5'	15:P:70:ARG:HH22	2.28	0.45
11:L:26:CYS:SG	11:L:29:LYS:HE2	2.56	0.45
1:A:1397:C:H4'	1:A:1398:A:OP2	2.15	0.45
1:A:922:G:H2'	1:A:923:A:H8	1.76	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:552:U:H2'	1:A:553:A:H8	1.79	0.45
1:A:1200:C:H3'	1:A:1201:A:H5'	1.98	0.45
11:L:31:GLY:O	11:L:78:VAL:HA	2.16	0.45
17:R:45:GLY:O	17:R:46:THR:C	2.54	0.45
1:A:1532:U:C2	1:A:1534:A:H5''	2.51	0.45
1:A:1047:G:H21	1:A:1215:G:C4'	2.28	0.45
1:A:1216:A:H5''	13:N:4:SER:CB	2.46	0.45
1:A:308:C:H2'	1:A:309:A:H8	1.80	0.45
1:A:49:U:O2'	1:A:50:A:H2'	2.17	0.45
1:A:1207:G:H2'	1:A:1208:C:C6	2.51	0.45
3:D:94:GLU:HG2	3:D:185:PRO:HG3	1.98	0.45
11:L:88:ASP:C	11:L:89:LEU:HD22	2.36	0.45
12:M:21:ILE:HB	12:M:24:VAL:CG2	2.39	0.45
1:A:781:A:H2'	1:A:782:A:C5'	2.43	0.45
3:D:29:THR:HG22	3:D:30:LYS:N	2.31	0.45
1:A:1173:U:H2'	1:A:1174:G:H8	1.79	0.45
9:J:77:VAL:HG12	9:J:78:GLU:HG3	1.99	0.45
1:A:1058:G:H2'	1:A:1059:C:C6	2.51	0.45
1:A:150:U:H2'	1:A:151:A:H8	1.82	0.45
6:G:142:ARG:HG3	6:G:142:ARG:HH11	1.81	0.45
8:I:56:MET:C	8:I:58:GLU:N	2.69	0.45
21:U:3:ILE:CG2	21:U:19:LYS:HD2	2.47	0.45
3:D:148:ALA:O	3:D:154:VAL:HG21	2.16	0.45
6:G:41:ILE:HG21	6:G:115:MET:HG3	1.99	0.45
1:A:1101:A:H4'	1:A:1102:A:O5'	2.17	0.45
16:Q:7:LEU:O	16:Q:60:ILE:HD13	2.16	0.45
1:A:1151:A:O4'	9:J:41:PRO:HB2	2.17	0.45
7:H:113:ARG:HE	7:H:113:ARG:C	2.19	0.45
11:L:107:LYS:C	11:L:109:ARG:H	2.20	0.45
1:A:202:G:H1'	1:A:468:A:H8	1.81	0.45
1:A:685:G:O2'	1:A:686:U:H5'	2.15	0.45
1:A:730:G:O2'	1:A:766:A:H5'	2.15	0.45
1:A:1472:U:H2'	1:A:1473:G:C8	2.51	0.45
1:A:426:U:H2'	1:A:427:U:C6	2.52	0.45
9:J:59:LYS:HG3	9:J:60:ASP:N	2.31	0.45
1:A:152:A:H3'	1:A:153:C:H6	1.80	0.45
1:A:386:C:C2'	1:A:387:U:H5'	2.47	0.45
10:K:110:THR:HA	21:U:19:LYS:HZ1	1.80	0.45
1:A:663:A:H2'	1:A:664:G:C8	2.50	0.45
10:K:77:GLY:C	10:K:79:LYS:HE3	2.36	0.45
9:J:17:LEU:HD22	9:J:96:VAL:CG1	2.37	0.45
12:M:44:ILE:O	12:M:47:LEU:HB2	2.16	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:377:G:H2'	1:A:378:G:H8	1.82	0.45
1:A:1198:G:H2'	1:A:1199:U:C6	2.52	0.45
7:H:94:VAL:HG21	7:H:100:ILE:O	2.16	0.45
1:A:1509:C:O2'	1:A:1510:C:H5'	2.16	0.45
3:D:75:TYR:CG	3:D:203:TYR:HD1	2.35	0.45
6:G:30:MET:HA	6:G:38:ALA:HB2	1.98	0.45
1:A:618:C:H1'	15:P:14:ARG:NH1	2.31	0.45
1:A:580:C:H2'	1:A:581:G:O4'	2.17	0.45
20:B:52:ALA:O	20:B:56:LEU:HD13	2.15	0.45
7:H:72:GLU:H	7:H:72:GLU:CD	2.19	0.45
13:N:10:VAL:O	13:N:13:VAL:HB	2.16	0.45
20:B:104:LYS:HB2	20:B:104:LYS:NZ	2.32	0.45
11:L:63:THR:O	11:L:94:TYR:HB2	2.16	0.45
1:A:1389:C:H2'	1:A:1390:U:H6	1.81	0.45
14:O:25:THR:CG2	14:O:70:LEU:HD23	2.47	0.45
11:L:3:VAL:CG1	16:Q:33:TYR:HB3	2.46	0.45
1:A:716:A:H2'	1:A:717:U:H6	1.81	0.45
3:D:52:VAL:HG12	3:D:198:LEU:HD21	1.99	0.45
12:M:24:VAL:HB	12:M:28:ARG:HB3	1.99	0.45
20:B:98:GLY:O	20:B:102:ASN:N	2.47	0.45
7:H:6:ILE:HD12	7:H:35:ILE:CD1	2.47	0.45
9:J:41:PRO:O	9:J:42:LEU:HB2	2.17	0.45
11:L:23:LEU:O	11:L:25:ALA:N	2.50	0.45
1:A:948:C:O2'	1:A:949:A:H5'	2.16	0.45
3:D:146:GLU:HA	3:D:149:LYS:CG	2.45	0.45
11:L:68:GLY:HA3	11:L:106:VAL:CG2	2.47	0.45
1:A:731:G:O2'	1:A:732:C:H5'	2.16	0.45
1:A:367:U:OP1	1:A:395:C:H1'	2.16	0.45
1:A:152:A:H2'	1:A:153:C:O4'	2.16	0.45
1:A:926:G:N2	1:A:1505:G:H2'	2.31	0.45
1:A:945:G:H21	1:A:1334:G:H4'	1.81	0.45
5:F:20:GLY:O	5:F:24:ARG:HD3	2.16	0.45
1:A:186:C:H2'	1:A:187:G:O4'	2.17	0.45
19:T:85:LEU:HD23	19:T:86:ALA:N	2.31	0.45
9:J:12:ALA:N	9:J:18:ILE:HD12	2.32	0.45
1:A:1313:U:H2'	1:A:1314:C:C6	2.52	0.45
1:A:769:G:H4'	1:A:1513:A:H4'	1.99	0.45
1:A:1000:A:H2'	1:A:1001:C:C6	2.51	0.45
1:A:844:G:C6	1:A:846:G:H1'	2.52	0.45
10:K:108:ASN:ND2	21:U:6:ARG:HB2	2.32	0.45
1:A:766:A:H61	1:A:1511:G:H1'	1.81	0.45
1:A:1180:A:OP1	8:I:104:THR:HG22	2.17	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:168:G:O2'	1:A:169:C:H5'	2.17	0.45
1:A:663:A:H2'	1:A:664:G:H8	1.82	0.45
1:A:874:G:O2'	1:A:875:U:H5'	2.16	0.45
12:M:14:ALA:HB1	12:M:33:LEU:HD21	1.98	0.45
1:A:1251:A:O2'	1:A:1252:A:H5'	2.17	0.45
4:E:81:GLN:H	4:E:146:MET:CE	2.29	0.45
1:A:947:G:H2'	1:A:948:C:H6	1.82	0.45
12:M:111:PRO:HG2	12:M:112:ARG:H	1.82	0.45
9:J:55:PRO:O	9:J:56:HIS:HB3	2.16	0.45
2:C:55:VAL:HG23	2:C:68:HIS:NE2	2.32	0.45
8:I:9:GLY:HA3	8:I:81:GLY:N	2.31	0.45
1:A:299:G:H2'	1:A:300:A:C8	2.52	0.45
6:G:39:GLU:HB3	6:G:43:TYR:CE2	2.51	0.45
1:A:996:A:H2'	1:A:997:U:C6	2.52	0.45
4:E:15:ILE:HB	4:E:35:LEU:O	2.17	0.45
4:E:9:GLU:O	4:E:40:ASP:HA	2.16	0.45
2:C:126:ARG:HH12	2:C:190:THR:CG2	2.30	0.45
3:D:59:LYS:HE3	3:D:194:ILE:CD1	2.46	0.45
13:N:9:GLU:HB2	13:N:62:ARG:CZ	2.46	0.45
13:N:30:ILE:O	13:N:40:ARG:HA	2.17	0.45
3:D:71:PHE:O	3:D:74:TYR:HB2	2.15	0.45
6:G:144:ALA:C	6:G:146:ALA:H	2.19	0.45
1:A:955:U:H1'	1:A:1227:A:H62	1.80	0.45
17:R:38:ILE:HD13	17:R:38:ILE:H	1.82	0.45
1:A:1095:U:H5''	1:A:1109:C:O2	2.17	0.45
1:A:1096:C:H2'	1:A:1097:C:C6	2.52	0.45
5:F:18:VAL:HG21	5:F:58:HIS:CD2	2.51	0.45
4:E:59:ILE:O	4:E:63:MET:HG2	2.16	0.45
1:A:113:G:H2'	1:A:114:U:H6	1.81	0.45
20:B:113:LEU:HD11	20:B:144:GLU:HG3	1.98	0.45
3:D:167:PRO:O	3:D:168:THR:HG23	2.17	0.45
20:B:44:LYS:C	20:B:47:PRO:HD2	2.36	0.45
5:F:38:ARG:HH21	5:F:63:ASN:HD21	1.64	0.45
19:T:65:LEU:HG	19:T:66:ILE:HD13	1.99	0.45
6:G:147:ASN:CA	10:K:55:ARG:HH21	2.30	0.45
8:I:118:ARG:O	8:I:118:ARG:HG2	2.16	0.45
1:A:1342:C:H5'	8:I:127:SER:HA	1.99	0.45
6:G:50:ALA:HB2	6:G:57:GLU:N	2.31	0.45
1:A:537:G:H2'	1:A:538:G:C8	2.52	0.45
15:P:74:LEU:HA	15:P:77:GLU:OE2	2.16	0.45
1:A:109:A:H2'	1:A:326:G:N2	2.32	0.45
10:K:35:ASP:OD2	10:K:39:ASN:HB2	2.17	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:C:181:ILE:HD12	2:C:181:ILE:N	2.31	0.45
2:C:185:THR:HA	2:C:197:VAL:O	2.17	0.45
7:H:17:GLN:OE1	7:H:69:ALA:HB1	2.16	0.45
1:A:642:A:H2'	1:A:643:C:C6	2.52	0.45
20:B:139:GLU:HG2	20:B:143:LEU:CD1	2.47	0.45
14:O:21:ASP:C	14:O:23:GLY:H	2.20	0.45
3:D:169:TRP:C	3:D:182:LYS:HB2	2.37	0.44
20:B:15:PHE:HD1	20:B:16:GLY:N	2.15	0.44
1:A:1314:C:H2'	1:A:1315:U:H6	1.82	0.44
1:A:818:G:O2'	1:A:819:A:H5''	2.17	0.44
2:C:2:GLN:HE21	2:C:2:GLN:CA	2.30	0.44
4:E:95:MET:HA	4:E:124:ALA:CB	2.44	0.44
1:A:90:C:H2'	1:A:91:U:H5	1.82	0.44
1:A:134:G:H2'	1:A:135:C:O4'	2.17	0.44
2:C:194:VAL:HG12	2:C:195:ILE:H	1.81	0.44
20:B:93:HIS:HB2	20:B:145:ASN:O	2.17	0.44
1:A:358:U:H2'	1:A:359:G:H8	1.79	0.44
1:A:72:A:H2'	1:A:73:C:H6	1.82	0.44
1:A:1488:G:O2'	1:A:1489:G:H5'	2.17	0.44
3:D:72:ARG:HG2	3:D:72:ARG:HH11	1.81	0.44
8:I:18:VAL:HG11	8:I:82:ILE:HG12	2.00	0.44
8:I:48:ARG:HB3	8:I:52:GLU:OE1	2.17	0.44
18:S:10:ILE:CG2	18:S:38:THR:H	2.23	0.44
2:C:131:ARG:HG3	2:C:135:ARG:CZ	2.48	0.44
12:M:3:ILE:HD12	12:M:9:PRO:HD2	1.98	0.44
1:A:586:C:H2'	1:A:587:G:H5'	1.99	0.44
13:N:80:ARG:HG3	13:N:81:ILE:N	2.32	0.44
1:A:601:G:H2'	1:A:602:A:C8	2.52	0.44
18:S:27:LYS:HG3	18:S:28:LYS:HD3	1.99	0.44
1:A:643:C:OP1	7:H:30:LYS:HD2	2.17	0.44
1:A:1409:C:N4	1:A:1410:A:N6	2.66	0.44
1:A:821:G:O2'	1:A:822:U:H5'	2.18	0.44
4:E:76:ASN:O	4:E:77:ASN:HB3	2.17	0.44
19:T:72:ALA:HA	19:T:75:LYS:HD3	2.00	0.44
1:A:1147:C:H4'	8:I:6:TYR:CE1	2.52	0.44
12:M:75:SER:O	12:M:78:ARG:HB2	2.18	0.44
20:B:87:ASP:CB	20:B:224:ARG:HE	2.30	0.44
3:D:199:ILE:HG13	3:D:200:VAL:N	2.32	0.44
2:C:59:PRO:HB3	9:J:94:ALA:HB2	1.98	0.44
1:A:1237:C:H3'	1:A:1238:A:H5'	2.00	0.44
11:L:33:CYS:HA	11:L:54:VAL:HA	2.00	0.44
7:H:17:GLN:CD	7:H:69:ALA:HB1	2.37	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:542:G:O2'	1:A:543:U:H5'	2.17	0.44
20:B:80:LYS:O	20:B:84:LEU:HB3	2.17	0.44
1:A:1258:G:O2'	1:A:1259:C:H5'	2.18	0.44
1:A:117:G:H2'	1:A:118:U:O4'	2.18	0.44
19:T:38:ILE:HG22	19:T:39:GLU:N	2.32	0.44
18:S:18:VAL:O	18:S:22:VAL:HG23	2.17	0.44
10:K:77:GLY:O	10:K:79:LYS:HE3	2.17	0.44
20:B:95:TRP:HZ2	20:B:100:LEU:HD22	1.83	0.44
4:E:73:VAL:HG11	4:E:143:LEU:HB3	2.00	0.44
13:N:52:ARG:HH11	13:N:58:ARG:HH21	1.62	0.44
13:N:30:ILE:HD12	13:N:30:ILE:N	2.29	0.44
2:C:130:ARG:HD2	2:C:133:MET:HE3	2.00	0.44
7:H:63:LYS:CD	7:H:70:VAL:HG21	2.47	0.44
4:E:37:VAL:HG12	4:E:47:PHE:HB3	1.99	0.44
6:G:64:ALA:HA	6:G:127:ALA:CA	2.45	0.44
2:C:38:VAL:HG23	2:C:39:ARG:N	2.33	0.44
6:G:14:ASP:CB	6:G:19:SER:H	2.31	0.44
1:A:430:A:OP2	3:D:6:PRO:HA	2.17	0.44
20:B:121:GLN:HB3	20:B:121:GLN:HE21	1.55	0.44
11:L:7:VAL:HG22	16:Q:33:TYR:HD1	1.82	0.44
1:A:201:G:H2'	1:A:202:G:C8	2.52	0.44
1:A:640:A:O2'	7:H:107:LYS:HE3	2.17	0.44
18:S:20:LYS:HD2	18:S:20:LYS:O	2.18	0.44
20:B:116:LEU:HB3	20:B:140:LEU:HG	2.00	0.44
1:A:105:G:H2'	1:A:106:C:H6	1.83	0.44
1:A:649:A:H2'	1:A:650:G:O4'	2.18	0.44
20:B:25:LYS:O	20:B:28:PRO:HD2	2.18	0.44
20:B:63:LYS:HA	20:B:224:ARG:CZ	2.47	0.44
9:J:7:ARG:O	9:J:100:ILE:HA	2.18	0.44
14:O:17:ARG:HG2	14:O:24:SER:HB2	1.99	0.44
5:F:86:ARG:CZ	17:R:63:TYR:HB3	2.48	0.44
4:E:136:VAL:HG13	4:E:137:ARG:H	1.81	0.44
3:D:56:GLU:HB2	3:D:198:LEU:HD23	1.99	0.44
9:J:44:THR:HG23	9:J:70:HIS:HA	2.00	0.44
4:E:151:MET:O	4:E:155:LYS:HG3	2.17	0.44
20:B:119:GLN:HE22	20:B:124:THR:HG22	1.83	0.44
12:M:70:ARG:HG3	12:M:74:MET:CE	2.48	0.44
1:A:1060:U:C5'	9:J:53:ILE:HG12	2.46	0.44
9:J:53:ILE:HG23	9:J:54:SER:N	2.33	0.44
1:A:16:A:O2'	4:E:20:VAL:HG13	2.18	0.44
2:C:122:GLN:O	2:C:127:VAL:HG22	2.17	0.44
2:C:2:GLN:N	2:C:2:GLN:NE2	2.63	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1392:G:O2'	1:A:1393:U:H5'	2.17	0.44
1:A:314:C:O2'	1:A:315:A:H5'	2.17	0.44
1:A:961:U:N3	1:A:983:A:N6	2.65	0.44
1:A:1053:G:C4'	1:A:1054:C:H5'	2.45	0.44
3:D:100:VAL:HG11	3:D:142:VAL:HG21	2.00	0.44
7:H:50:VAL:HG23	7:H:57:GLU:O	2.18	0.44
1:A:1283:U:H2'	1:A:1284:C:H6	1.80	0.44
5:F:73:GLU:HG2	5:F:73:GLU:H	1.51	0.44
2:C:111:ASP:O	2:C:115:VAL:HG23	2.16	0.44
2:C:5:HIS:ND1	13:N:88:MET:HB3	2.33	0.44
1:A:123:U:H2'	1:A:124:C:C6	2.53	0.44
10:K:115:ILE:O	10:K:115:ILE:HD12	2.16	0.44
8:I:35:GLU:O	8:I:39:GLY:HA3	2.18	0.44
8:I:66:VAL:HG22	8:I:67:LYS:N	2.33	0.44
3:D:151:GLN:N	3:D:155:LYS:NZ	2.66	0.44
13:N:2:LYS:HB3	13:N:5:MET:HB2	1.99	0.44
2:C:133:MET:HG2	2:C:150:VAL:CG1	2.48	0.44
1:A:238:A:C3'	1:A:239:U:H5''	2.48	0.44
1:A:313:A:O2'	1:A:314:C:H5'	2.18	0.44
1:A:560:A:H4'	1:A:561:U:C5'	2.46	0.44
16:Q:57:VAL:HB	16:Q:79:GLU:CB	2.47	0.44
10:K:30:ILE:O	10:K:30:ILE:HG13	2.17	0.44
4:E:88:HIS:CE1	4:E:137:ARG:HH11	2.35	0.44
1:A:541:G:O2'	3:D:39:GLN:HB3	2.17	0.44
3:D:164:ARG:HG3	3:D:165:GLU:N	2.33	0.44
13:N:68:ARG:HB2	13:N:79:SER:HB3	2.00	0.44
20:B:199:ILE:HD13	20:B:212:TYR:HE2	1.83	0.44
8:I:18:VAL:HG22	8:I:64:ILE:HG23	1.98	0.44
8:I:66:VAL:CG1	8:I:74:GLN:HG3	2.48	0.44
20:B:209:VAL:HG23	20:B:210:THR:N	2.33	0.44
15:P:40:ASN:OD1	15:P:43:ALA:N	2.51	0.44
6:G:129:ASN:HA	6:G:134:VAL:HG11	1.99	0.44
20:B:59:ILE:O	20:B:62:ARG:HD2	2.18	0.44
6:G:144:ALA:O	6:G:145:GLU:HB3	2.17	0.44
4:E:157:GLY:O	4:E:158:LYS:HB2	2.17	0.44
8:I:118:ARG:HB3	8:I:122:ARG:HG2	2.00	0.44
1:A:479:U:O2'	1:A:480:U:H5'	2.17	0.44
9:J:57:VAL:O	9:J:58:ASN:HB2	2.18	0.44
8:I:115:VAL:HG21	9:J:62:ARG:HB2	2.00	0.44
1:A:206:C:H2'	1:A:207:C:C6	2.53	0.44
20:B:8:MET:HG3	20:B:9:LEU:N	2.33	0.44
1:A:85:U:H4'	1:A:86:G:C4'	2.47	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
6:G:4:ARG:HG3	6:G:5:VAL:N	2.33	0.44
1:A:114:U:O4'	1:A:353:A:H1'	2.18	0.44
1:A:308:C:H2'	1:A:309:A:C8	2.53	0.44
1:A:611:C:H2'	1:A:612:C:H6	1.83	0.44
20:B:119:GLN:CA	20:B:124:THR:HB	2.29	0.44
1:A:663:A:C5'	17:R:49:LYS:HD2	2.48	0.44
5:F:9:MET:HB3	5:F:59:TYR:CE2	2.52	0.44
12:M:79:LEU:CD2	12:M:86:ARG:HE	2.30	0.44
2:C:140:ALA:CB	2:C:148:ILE:HD12	2.45	0.44
16:Q:68:LYS:O	16:Q:70:LYS:N	2.51	0.44
17:R:38:ILE:CG2	17:R:58:ILE:HG21	2.48	0.44
15:P:38:PHE:CD1	15:P:39:PHE:N	2.85	0.44
2:C:39:ARG:CZ	2:C:56:ILE:HD12	2.48	0.44
1:A:596:A:H2'	1:A:597:G:C8	2.53	0.44
6:G:49:LEU:HD21	6:G:120:ALA:O	2.17	0.44
1:A:245:U:H2'	1:A:246:A:H5'	2.00	0.44
16:Q:52:CYS:HB2	16:Q:58:VAL:HG11	1.98	0.44
1:A:903:G:H2'	1:A:904:U:C6	2.53	0.44
1:A:1281:C:H5'	1:A:1282:C:H5	1.83	0.44
20:B:212:TYR:O	20:B:216:VAL:HG13	2.17	0.43
8:I:6:TYR:HE2	8:I:17:ARG:HB3	1.84	0.43
8:I:4:GLN:HE21	8:I:21:LYS:NZ	2.16	0.43
1:A:78:A:H2'	1:A:79:G:C8	2.53	0.43
5:F:68:GLN:HA	5:F:71:ILE:HG12	2.00	0.43
12:M:14:ALA:O	12:M:18:LEU:HB2	2.18	0.43
12:M:56:ARG:O	12:M:59:VAL:HG12	2.18	0.43
13:N:50:LEU:CD2	13:N:51:PRO:HD3	2.48	0.43
13:N:49:THR:O	13:N:50:LEU:HB3	2.18	0.43
1:A:598:U:H4'	7:H:85:TYR:CG	2.53	0.43
3:D:78:ALA:HA	3:D:88:ASN:HB3	1.99	0.43
20:B:121:GLN:NE2	20:B:122:ASP:HB2	2.33	0.43
1:A:389:A:H3'	1:A:390:U:H6	1.83	0.43
6:G:49:LEU:HD21	6:G:120:ALA:HA	1.99	0.43
1:A:768:A:H5'	1:A:1524:C:H1'	1.99	0.43
7:H:107:LYS:HA	7:H:107:LYS:HD3	1.83	0.43
11:L:72:ASN:CG	11:L:104:SER:HB3	2.38	0.43
15:P:12:LYS:C	15:P:14:ARG:H	2.21	0.43
17:R:20:ILE:HG22	17:R:53:GLN:NE2	2.33	0.43
7:H:29:SER:O	7:H:33:VAL:HG23	2.18	0.43
2:C:172:VAL:O	2:C:174:LEU:HD12	2.18	0.43
19:T:48:LYS:HA	19:T:51:ASN:HD21	1.83	0.43
20:B:45:THR:CA	20:B:48:MET:HG3	2.45	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:N:20:PHE:CZ	13:N:51:PRO:HG3	2.53	0.43
20:B:159:ALA:HB1	20:B:183:PHE:HE1	1.83	0.43
1:A:1343:G:H1'	8:I:122:ARG:NH1	2.27	0.43
17:R:61:ALA:CB	17:R:67:LEU:HD12	2.48	0.43
1:A:633:G:H2'	1:A:634:C:H6	1.83	0.43
1:A:637:C:O2'	1:A:638:U:H5'	2.18	0.43
7:H:76:ARG:HG2	7:H:79:ARG:HB3	2.00	0.43
1:A:451:A:H4'	1:A:452:A:O4'	2.18	0.43
1:A:192:A:O2'	1:A:193:C:H5'	2.18	0.43
3:D:202:LEU:HD12	3:D:202:LEU:O	2.18	0.43
14:O:26:GLU:HG3	14:O:81:LEU:HD12	2.00	0.43
1:A:1425:U:O2'	1:A:1426:G:H5'	2.18	0.43
1:A:939:G:H5''	6:G:101:ARG:CZ	2.49	0.43
1:A:1438:G:O2'	1:A:1439:G:H5'	2.18	0.43
1:A:1332:A:H2'	1:A:1333:A:H8	1.82	0.43
1:A:1346:A:N1	1:A:1374:A:H5''	2.33	0.43
1:A:1394:A:C5	1:A:1501:C:H4'	2.52	0.43
20:B:163:ILE:CG2	20:B:164:ASP:H	2.13	0.43
13:N:76:PHE:CE2	13:N:95:LEU:HD22	2.54	0.43
13:N:50:LEU:CG	13:N:51:PRO:HD3	2.48	0.43
1:A:313:A:H2'	1:A:314:C:C6	2.53	0.43
1:A:812:G:O2'	1:A:813:U:C6	2.70	0.43
1:A:1309:G:H2'	1:A:1310:G:H8	1.84	0.43
1:A:402:G:H5'	1:A:621:A:H1'	2.00	0.43
1:A:208:U:H6	1:A:208:U:O5'	2.01	0.43
1:A:297:G:N2	1:A:299:G:H3'	2.34	0.43
11:L:78:VAL:O	11:L:102:ASP:HB2	2.19	0.43
1:A:731:G:OP1	1:A:766:A:H1'	2.18	0.43
1:A:1207:G:H2'	1:A:1208:C:H6	1.84	0.43
1:A:648:A:H2'	1:A:649:A:C8	2.54	0.43
1:A:144:G:H2'	1:A:145:G:O4'	2.18	0.43
2:C:109:GLU:OE1	2:C:139:ASN:HB3	2.19	0.43
12:M:29:SER:O	12:M:32:ILE:HG22	2.18	0.43
1:A:278:G:O4'	1:A:282:A:H1'	2.19	0.43
1:A:575:G:O2'	1:A:820:U:H5''	2.18	0.43
3:D:169:TRP:HB2	3:D:183:ARG:HD2	2.01	0.43
7:H:4:ASP:OD1	7:H:7:ALA:HB2	2.19	0.43
19:T:71:ALA:O	19:T:74:HIS:HB2	2.19	0.43
16:Q:56:ASP:CA	16:Q:81:ALA:HB2	2.41	0.43
2:C:129:PHE:CG	2:C:130:ARG:N	2.86	0.43
12:M:94:LEU:HB3	12:M:95:PRO:HD2	2.01	0.43
2:C:13:ILE:C	2:C:15:LYS:H	2.22	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:179:A:O2'	1:A:180:U:H5'	2.18	0.43
14:O:71:LYS:HB2	14:O:78:TYR:CG	2.53	0.43
1:A:1260:G:O5'	1:A:1284:C:H4'	2.18	0.43
1:A:1484:C:H2'	1:A:1485:U:H6	1.83	0.43
1:A:822:U:H2'	1:A:823:C:C6	2.53	0.43
2:C:54:ILE:HG23	2:C:54:ILE:O	2.18	0.43
3:D:48:SER:O	3:D:49:ASP:C	2.56	0.43
1:A:291:U:H2'	1:A:292:G:H8	1.82	0.43
1:A:661:G:H2'	1:A:662:U:C6	2.53	0.43
3:D:169:TRP:O	3:D:182:LYS:HB2	2.19	0.43
20:B:87:ASP:CG	20:B:224:ARG:HH21	2.21	0.43
20:B:57:ASN:HA	20:B:60:ALA:HB3	2.00	0.43
20:B:68:PHE:CE1	20:B:88:GLN:HB3	2.54	0.43
1:A:370:C:H2'	1:A:371:A:C8	2.53	0.43
2:C:180:ASP:OD1	2:C:203:LYS:HB2	2.19	0.43
1:A:128:G:H2'	1:A:129:A:C8	2.53	0.43
7:H:80:PRO:C	7:H:82:LEU:H	2.21	0.43
9:J:76:ILE:HG13	9:J:76:ILE:H	1.62	0.43
1:A:211:G:N3	1:A:211:G:H5''	2.34	0.43
1:A:1254:A:OP1	9:J:47:GLU:HG3	2.18	0.43
3:D:2:ARG:O	3:D:3:TYR:HB3	2.19	0.43
6:G:45:ALA:HB3	6:G:119:LEU:HD23	1.99	0.43
1:A:1178:G:H2'	1:A:1180:A:OP2	2.19	0.43
20:B:138:ARG:HA	20:B:141:GLU:HG3	1.99	0.43
1:A:687:A:C2	1:A:704:A:C5	3.05	0.43
1:A:1406:U:O4	1:A:1495:U:N3	2.52	0.43
16:Q:29:LYS:HG3	16:Q:34:GLY:HA2	1.99	0.43
1:A:1085:U:H3'	1:A:1086:U:C6	2.52	0.43
1:A:80:A:H2'	1:A:81:A:H4'	2.01	0.43
19:T:43:LYS:H	19:T:43:LYS:HD3	1.84	0.43
3:D:18:LEU:HB2	3:D:20:LEU:HD21	2.00	0.43
1:A:521:G:OP1	11:L:69:GLU:HA	2.18	0.43
9:J:15:HIS:HA	9:J:18:ILE:HG22	2.00	0.43
13:N:30:ILE:C	13:N:32:ASP:H	2.21	0.43
1:A:818:G:C2'	1:A:819:A:H5''	2.49	0.43
1:A:1124:G:H3'	9:J:37:ARG:NH1	2.32	0.43
1:A:1077:G:N2	1:A:1079:G:H3'	2.34	0.43
1:A:777:A:H2'	1:A:778:G:C8	2.53	0.43
1:A:34:C:H2'	1:A:35:G:H8	1.83	0.43
12:M:91:ARG:HG3	12:M:92:ARG:N	2.34	0.43
1:A:108:G:O4'	1:A:108:G:N3	2.52	0.43
1:A:502:A:H2'	1:A:503:C:O4'	2.18	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
14:O:32:LEU:HD12	14:O:59:MET:HB3	2.01	0.43
4:E:125:LYS:HD2	4:E:126:ALA:N	2.31	0.43
1:A:735:C:H2'	1:A:736:C:H6	1.83	0.43
21:U:48:LYS:HG3	21:U:49:ALA:N	2.32	0.43
11:L:68:GLY:HA3	11:L:106:VAL:HG22	2.01	0.43
16:Q:28:VAL:HG12	16:Q:37:ILE:O	2.19	0.43
12:M:4:ALA:C	12:M:6:ILE:H	2.22	0.43
2:C:146:LYS:HB2	2:C:202:PHE:CD2	2.53	0.43
11:L:107:LYS:HZ2	11:L:107:LYS:H	1.67	0.43
19:T:27:MET:CE	19:T:28:ARG:HG2	2.48	0.43
6:G:112:ASP:HB3	6:G:113:LYS:H	1.67	0.43
1:A:822:U:O2'	1:A:823:C:H5'	2.18	0.43
2:C:54:ILE:HG12	2:C:54:ILE:O	2.19	0.43
8:I:44:ARG:HG2	8:I:44:ARG:HH11	1.84	0.43
3:D:160:LEU:N	3:D:160:LEU:HD13	2.18	0.43
6:G:110:ARG:NE	6:G:122:GLU:HB2	2.34	0.43
13:N:29:ILE:HB	13:N:30:ILE:HD12	2.00	0.43
1:A:848:C:N4	23:A:2357:LLL:H612	2.33	0.43
1:A:337:G:O2'	1:A:338:A:H5'	2.19	0.43
16:Q:39:ARG:HG2	16:Q:39:ARG:HH11	1.83	0.43
1:A:735:C:H5'	17:R:59:LYS:HD3	2.01	0.43
10:K:117:HIS:O	10:K:118:ASN:HB2	2.19	0.43
1:A:824:G:H2'	1:A:825:A:H8	1.83	0.43
1:A:1260:G:OP1	1:A:1284:C:H4'	2.19	0.43
12:M:84:CYS:HB3	18:S:73:PHE:CE2	2.53	0.43
2:C:9:ILE:HG23	2:C:10:ARG:HG3	2.01	0.43
1:A:46:G:O2'	1:A:365:U:H1'	2.18	0.43
1:A:138:G:O2'	1:A:139:A:H5'	2.19	0.43
1:A:379:C:O2'	1:A:380:G:H5'	2.19	0.43
20:B:22:TRP:HB3	20:B:38:HIS:CE1	2.54	0.43
1:A:1070:U:H2'	1:A:1071:C:H6	1.79	0.43
1:A:251:G:N2	1:A:266:G:H1	2.16	0.43
1:A:255:G:H5'	16:Q:17:GLU:O	2.19	0.43
9:J:40:ILE:HD12	9:J:73:LEU:HB3	2.00	0.43
1:A:1120:C:H2'	1:A:1121:U:C6	2.54	0.43
4:E:89:THR:CG2	4:E:90:GLY:H	2.22	0.43
1:A:714:G:H21	1:A:777:A:H1'	1.83	0.43
15:P:50:THR:CG2	15:P:51:ARG:N	2.82	0.43
18:S:68:HIS:HB3	18:S:72:GLU:CD	2.39	0.43
20:B:69:VAL:O	20:B:163:ILE:HG22	2.19	0.43
20:B:185:ILE:HG23	20:B:199:ILE:O	2.19	0.43
1:A:663:A:O2'	1:A:664:G:H5'	2.19	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1098:C:H2'	1:A:1099:G:C8	2.53	0.43
5:F:5:GLU:HG3	5:F:63:ASN:OD1	2.19	0.43
12:M:15:VAL:HG22	12:M:33:LEU:CD1	2.48	0.43
12:M:53:ASP:HA	12:M:56:ARG:HH12	1.82	0.43
1:A:93:U:H3'	1:A:94:G:H4'	2.01	0.43
1:A:1358:U:H3'	1:A:1359:C:C6	2.53	0.43
3:D:54:LEU:O	3:D:58:GLN:HB2	2.18	0.43
11:L:34:THR:O	11:L:35:ARG:HB2	2.18	0.43
1:A:1008:U:C2'	1:A:1009:U:H5''	2.49	0.43
11:L:20:VAL:HB	11:L:94:TYR:HE1	1.83	0.43
1:A:676:A:H2'	1:A:677:U:C6	2.54	0.43
20:B:10:LYS:CB	20:B:211:LEU:HD21	2.48	0.43
12:M:93:GLY:O	12:M:108:ARG:HG3	2.18	0.43
1:A:693:G:P	10:K:126:ARG:HH12	2.41	0.43
1:A:716:A:N3	10:K:118:ASN:O	2.51	0.43
2:C:10:ARG:NH2	2:C:181:ILE:HD13	2.34	0.43
1:A:1056:U:O2'	1:A:1057:G:H5'	2.18	0.43
1:A:1332:A:H2'	1:A:1333:A:O4'	2.19	0.43
10:K:68:ARG:HH11	10:K:68:ARG:HG3	1.83	0.43
5:F:74:LEU:HG	5:F:78:PHE:CE1	2.54	0.43
20:B:35:ASN:HA	20:B:35:ASN:HD22	1.63	0.43
21:U:39:LYS:N	21:U:40:PRO:CD	2.81	0.43
12:M:3:ILE:HG12	12:M:52:ILE:HD11	2.01	0.43
20:B:59:ILE:HG13	20:B:59:ILE:H	1.61	0.43
20:B:64:GLY:O	20:B:66:ILE:HG12	2.19	0.43
1:A:1122:U:H2'	1:A:1123:U:C6	2.54	0.43
8:I:71:ILE:CD1	8:I:71:ILE:H	2.30	0.43
12:M:91:ARG:CZ	12:M:91:ARG:HB2	2.47	0.43
1:A:958:A:N1	18:S:53:GLY:C	2.73	0.43
2:C:155:ARG:H	2:C:162:ALA:CA	2.32	0.43
1:A:1424:U:H2'	1:A:1425:U:H6	1.84	0.43
15:P:26:ASN:HD22	15:P:26:ASN:HA	1.65	0.43
1:A:1461:G:H2'	1:A:1462:C:H6	1.82	0.43
1:A:1461:G:H2'	1:A:1462:C:O4'	2.18	0.43
1:A:1283:U:O2'	1:A:1284:C:H5'	2.19	0.43
20:B:41:ASN:ND2	20:B:43:GLU:HG3	2.33	0.43
1:A:229:U:H2'	1:A:230:G:H8	1.84	0.43
1:A:1521:C:O2'	1:A:1522:U:H5'	2.19	0.43
1:A:988:G:H2'	1:A:989:U:O4'	2.19	0.43
17:R:42:ARG:HG3	17:R:43:ILE:H	1.84	0.43
1:A:577:G:O2'	1:A:578:C:H5'	2.19	0.43
8:I:34:LEU:HD23	8:I:35:GLU:OE1	2.18	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
13:N:42:ASN:O	13:N:46:LYS:HG2	2.18	0.42
18:S:40:PHE:O	18:S:43:MET:HG3	2.19	0.42
19:T:61:ALA:HA	19:T:67:HIS:N	2.26	0.42
15:P:28:ARG:HD3	15:P:29:ASN:ND2	2.34	0.42
10:K:88:PRO:HA	10:K:92:ARG:HD2	1.99	0.42
1:A:598:U:H2'	1:A:599:C:H6	1.82	0.42
1:A:1512:U:H2'	1:A:1513:A:C8	2.53	0.42
1:A:1011:C:H2'	1:A:1012:A:H8	1.82	0.42
7:H:125:ILE:HG22	7:H:126:CYS:SG	2.59	0.42
1:A:452:A:H1'	15:P:70:ARG:NH1	2.32	0.42
14:O:36:ILE:HD13	14:O:59:MET:HE3	2.01	0.42
12:M:2:ARG:O	12:M:4:ALA:N	2.52	0.42
3:D:187:ARG:HH11	3:D:187:ARG:HG3	1.84	0.42
1:A:51:A:H4'	1:A:52:C:OP2	2.19	0.42
1:A:1207:G:O2'	1:A:1208:C:H5'	2.18	0.42
1:A:1356:G:H2'	1:A:1357:A:C8	2.53	0.42
17:R:19:GLU:HG3	17:R:54:LEU:HD12	2.00	0.42
11:L:80:LEU:HB3	11:L:97:VAL:CG2	2.49	0.42
2:C:126:ARG:HH12	2:C:190:THR:HG23	1.84	0.42
13:N:60:ARG:CZ	13:N:69:PRO:HB3	2.50	0.42
20:B:161:PHE:HD2	20:B:183:PHE:HB2	1.84	0.42
13:N:32:ASP:OD2	13:N:33:VAL:N	2.52	0.42
2:C:156:LEU:HG	2:C:163:ARG:O	2.18	0.42
16:Q:60:ILE:HA	16:Q:75:VAL:HG22	2.01	0.42
1:A:1000:A:H2'	1:A:1001:C:H6	1.84	0.42
1:A:845:A:N7	1:A:846:G:O4'	2.52	0.42
1:A:812:G:HO2'	1:A:813:U:H6	1.67	0.42
1:A:1319:A:OP1	18:S:4:LEU:HD11	2.19	0.42
20:B:107:ARG:HA	20:B:110:ILE:HD12	2.00	0.42
1:A:177:G:N3	1:A:177:G:O4'	2.51	0.42
1:A:23:C:O2'	1:A:24:U:H5'	2.20	0.42
5:F:86:ARG:HH11	17:R:64:LEU:HD12	1.83	0.42
2:C:53:ARG:HG2	2:C:54:ILE:H	1.83	0.42
1:A:1503:A:H8	1:A:1531:A:H1'	1.84	0.42
11:L:45:ASN:HD22	11:L:45:ASN:N	2.17	0.42
9:J:53:ILE:HG13	13:N:84:ARG:NE	2.34	0.42
13:N:46:LYS:NZ	18:S:9:PHE:HA	2.34	0.42
13:N:9:GLU:HB2	13:N:62:ARG:NE	2.34	0.42
20:B:16:GLY:HA2	20:B:40:ILE:CG1	2.41	0.42
4:E:33:THR:HG22	4:E:51:LYS:CB	2.45	0.42
9:J:8:ILE:HD12	9:J:75:ASP:HA	2.00	0.42
1:A:92:U:OP2	1:A:92:U:H6	2.02	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:674:G:O2'	1:A:675:A:H5'	2.19	0.42
1:A:212:G:H2'	1:A:213:G:C8	2.51	0.42
14:O:26:GLU:OE2	14:O:77:ARG:HD2	2.18	0.42
1:A:935:A:O2'	1:A:936:C:H5'	2.20	0.42
1:A:987:G:H2'	1:A:988:G:H8	1.84	0.42
1:A:648:A:O2'	1:A:649:A:H5'	2.20	0.42
5:F:72:ASP:HA	5:F:75:GLU:OE1	2.20	0.42
2:C:104:GLU:O	2:C:105:VAL:HG13	2.19	0.42
1:A:1315:U:H5	18:S:5:LYS:NZ	2.11	0.42
1:A:1130:A:H61	1:A:1144:G:H1'	1.84	0.42
14:O:12:VAL:CG1	14:O:22:THR:HG22	2.48	0.42
4:E:55:VAL:N	4:E:56:PRO:CD	2.82	0.42
1:A:681:A:H2'	1:A:682:G:C8	2.54	0.42
4:E:48:GLY:O	4:E:62:ALA:HB1	2.19	0.42
17:R:47:ARG:HD3	17:R:50:TYR:CZ	2.54	0.42
16:Q:27:PHE:HB3	16:Q:36:PHE:HB3	2.01	0.42
21:U:36:PHE:HA	21:U:36:PHE:HD2	1.73	0.42
3:D:115:GLN:HG3	3:D:119:HIS:ND1	2.35	0.42
1:A:437:U:H4'	3:D:153:ARG:NH1	2.35	0.42
13:N:50:LEU:HG	13:N:51:PRO:CD	2.48	0.42
1:A:975:A:O2'	1:A:1358:U:H1'	2.19	0.42
11:L:55:ARG:HH11	11:L:55:ARG:HG3	1.84	0.42
20:B:83:ALA:CB	20:B:90:PHE:HB3	2.50	0.42
1:A:190:A:C4	1:A:191:G:H1'	2.53	0.42
1:A:410:G:H2'	1:A:429:U:C5	2.54	0.42
14:O:26:GLU:HG3	14:O:81:LEU:CD1	2.50	0.42
1:A:443:C:H2'	1:A:444:G:H8	1.81	0.42
1:A:857:C:H2'	1:A:858:G:O4'	2.20	0.42
1:A:513:C:H2'	1:A:514:C:C6	2.53	0.42
1:A:295:C:H2'	1:A:296:U:H6	1.84	0.42
1:A:683:G:O2'	1:A:684:U:H5'	2.18	0.42
1:A:594:U:H2'	1:A:595:A:C8	2.54	0.42
1:A:626:G:H2'	1:A:627:G:H8	1.85	0.42
1:A:1125:U:O2'	1:A:1126:U:H2'	2.19	0.42
1:A:1225:A:N3	1:A:1225:A:H2'	2.35	0.42
14:O:45:GLU:O	14:O:46:HIS:HB2	2.20	0.42
20:B:185:ILE:HG12	20:B:199:ILE:CG2	2.49	0.42
10:K:122:PRO:HD2	21:U:35:GLU:HG2	2.01	0.42
10:K:125:LYS:O	21:U:33:ARG:NE	2.53	0.42
5:F:100:SER:HA	17:R:23:LYS:HE2	2.01	0.42
13:N:46:LYS:HZ3	18:S:9:PHE:HA	1.83	0.42
6:G:78:ARG:NH1	6:G:82:SER:N	2.68	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:782:A:H4'	1:A:1514:G:O2'	2.19	0.42
15:P:2:VAL:O	15:P:65:ALA:HA	2.19	0.42
3:D:197:HIS:O	3:D:201:GLU:HG3	2.20	0.42
1:A:413:G:H2'	1:A:428:G:H21	1.84	0.42
1:A:554:A:H5'	11:L:25:ALA:HB1	2.02	0.42
18:S:35:ARG:O	18:S:71:GLY:N	2.53	0.42
1:A:284:C:O2'	1:A:285:C:H5'	2.20	0.42
1:A:734:G:H2'	1:A:735:C:C6	2.55	0.42
1:A:734:G:H2'	1:A:735:C:H6	1.85	0.42
1:A:1347:G:H8	8:I:108:ARG:HB3	1.84	0.42
19:T:2:ASN:ND2	19:T:3:ILE:H	2.18	0.42
1:A:84:U:O2'	1:A:86:G:N2	2.52	0.42
1:A:1222:G:H2'	1:A:1223:C:H5'	2.02	0.42
9:J:80:THR:HB	9:J:83:THR:CB	2.50	0.42
9:J:82:LYS:HG3	9:J:83:THR:N	2.34	0.42
4:E:40:ASP:OD2	4:E:42:ASN:HB3	2.19	0.42
10:K:65:ALA:O	10:K:68:ARG:HB3	2.20	0.42
9:J:11:LYS:HB2	9:J:97:ASP:OD1	2.19	0.42
20:B:46:VAL:O	20:B:49:PHE:HB2	2.19	0.42
21:U:36:PHE:CD2	21:U:39:LYS:HD3	2.55	0.42
1:A:1251:A:H2'	1:A:1252:A:C8	2.55	0.42
20:B:65:LYS:HB3	20:B:157:PRO:HA	2.01	0.42
1:A:255:G:H2'	1:A:256:U:H6	1.84	0.42
20:B:10:LYS:O	20:B:13:VAL:HG23	2.20	0.42
14:O:84:ARG:C	14:O:85:LEU:HD12	2.40	0.42
1:A:1004:A:H2'	1:A:1005:A:O4'	2.20	0.42
1:A:1298:U:H2'	6:G:113:LYS:HZ1	1.85	0.42
4:E:131:ASN:ND2	4:E:133:ILE:HB	2.35	0.42
1:A:317:U:H2'	1:A:318:G:C8	2.53	0.42
16:Q:58:VAL:HG12	16:Q:77:VAL:HG13	2.00	0.42
10:K:24:ALA:HA	10:K:29:THR:CG2	2.50	0.42
18:S:47:THR:C	18:S:48:ILE:HG13	2.39	0.42
1:A:77:A:H2'	1:A:78:A:C8	2.54	0.42
12:M:52:ILE:CD1	12:M:55:LEU:HD12	2.47	0.42
1:A:483:C:H2'	1:A:484:G:N7	2.34	0.42
1:A:475:C:O2'	1:A:476:U:H5'	2.19	0.42
1:A:1001:C:H2'	1:A:1002:G:O4'	2.19	0.42
2:C:55:VAL:HG12	2:C:56:ILE:N	2.35	0.42
1:A:958:A:N6	1:A:959:A:N1	2.67	0.42
4:E:53:ARG:HH21	4:E:54:GLU:CG	2.33	0.42
1:A:1201:A:C8	1:A:1201:A:H5''	2.54	0.42
1:A:1291:U:H2'	1:A:1292:G:H8	1.84	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:I:45:MET:N	8:I:45:MET:SD	2.93	0.42
1:A:152:A:H3'	1:A:153:C:C6	2.55	0.42
1:A:626:G:H2'	1:A:627:G:C8	2.55	0.42
15:P:33:ILE:HG21	15:P:60:TRP:CZ2	2.55	0.42
14:O:33:THR:HG23	14:O:63:ARG:NH1	2.35	0.42
6:G:11:ILE:HD12	6:G:11:ILE:N	2.34	0.42
1:A:310:G:O2'	1:A:311:C:H5'	2.20	0.42
10:K:111:ASP:N	21:U:19:LYS:HE3	2.35	0.42
3:D:117:VAL:HA	3:D:122:ILE:HG12	2.01	0.42
12:M:52:ILE:HA	12:M:55:LEU:CD1	2.49	0.42
1:A:815:A:H4'	1:A:817:C:C5	2.55	0.42
7:H:63:LYS:HG2	7:H:64:TYR:N	2.34	0.42
2:C:166:TRP:HB3	2:C:167:TYR:H	1.62	0.42
3:D:43:ARG:HH21	3:D:45:PRO:HA	1.84	0.42
2:C:11:LEU:HD11	13:N:87:ALA:O	2.20	0.42
7:H:39:LEU:HD21	7:H:128:VAL:HG21	2.02	0.42
1:A:50:A:H1'	1:A:52:C:C6	2.55	0.42
20:B:139:GLU:HG2	20:B:143:LEU:HD12	2.02	0.42
3:D:172:VAL:HG23	3:D:178:GLU:O	2.19	0.42
21:U:40:PRO:C	21:U:42:THR:N	2.73	0.42
20:B:65:LYS:HD3	20:B:89:PHE:CE1	2.54	0.42
4:E:149:PRO:HA	7:H:98:LEU:HD22	2.02	0.42
1:A:373:A:OP2	1:A:373:A:H3'	2.19	0.42
1:A:203:G:N2	1:A:205:A:N6	2.68	0.42
1:A:828:U:H2'	1:A:829:G:O5'	2.20	0.42
3:D:12:ARG:HG2	3:D:33:ILE:HD12	2.02	0.42
1:A:1226:C:N4	12:M:102:LYS:HG3	2.35	0.42
1:A:549:C:H2'	1:A:550:G:C8	2.55	0.42
3:D:141:VAL:HA	3:D:179:GLY:O	2.20	0.42
5:F:43:GLY:HA2	5:F:58:HIS:CE1	2.55	0.42
1:A:1067:A:N1	1:A:1108:G:O2'	2.51	0.42
17:R:28:LEU:C	17:R:30:ASN:H	2.23	0.42
5:F:55:HIS:N	5:F:55:HIS:ND1	2.68	0.42
8:I:41:GLU:N	8:I:44:ARG:NH1	2.63	0.41
21:U:43:GLU:HA	21:U:46:ARG:CD	2.50	0.41
18:S:14:LEU:HG	18:S:15:LEU:N	2.34	0.41
19:T:57:VAL:HG23	19:T:58:ASP:N	2.34	0.41
12:M:12:LYS:HB3	12:M:13:HIS:H	1.49	0.41
20:B:79:VAL:CG1	20:B:90:PHE:HB2	2.46	0.41
2:C:2:GLN:N	2:C:2:GLN:HE21	2.17	0.41
1:A:222:C:H2'	1:A:223:A:H8	1.85	0.41
1:A:538:G:H2'	1:A:539:A:C8	2.55	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:C:34:SER:O	2:C:38:VAL:HG22	2.20	0.41
1:A:401:C:H2'	1:A:402:G:H8	1.84	0.41
20:B:148:GLY:C	20:B:150:ILE:H	2.23	0.41
1:A:543:U:O2'	1:A:544:G:H5'	2.20	0.41
1:A:1105:A:H2'	1:A:1106:G:H8	1.85	0.41
15:P:19:VAL:HB	15:P:37:GLY:O	2.19	0.41
16:Q:23:ALA:C	16:Q:24:ILE:HD12	2.41	0.41
11:L:48:LEU:O	11:L:49:ARG:C	2.58	0.41
11:L:85:ARG:HG3	11:L:86:VAL:H	1.83	0.41
13:N:61:ASN:O	13:N:62:ARG:HB2	2.20	0.41
6:G:110:ARG:HB3	6:G:110:ARG:HH11	1.85	0.41
21:U:20:ARG:HD2	21:U:20:ARG:N	2.35	0.41
3:D:90:LEU:HD21	3:D:196:GLU:CB	2.49	0.41
1:A:1008:U:H2'	1:A:1009:U:C5'	2.48	0.41
1:A:415:A:N1	1:A:428:G:O6	2.53	0.41
16:Q:17:GLU:C	16:Q:19:SER:H	2.23	0.41
1:A:476:U:H2'	1:A:477:C:O4'	2.20	0.41
2:C:61:LYS:HA	2:C:61:LYS:NZ	2.35	0.41
1:A:1161:C:O2'	1:A:1162:C:H5'	2.19	0.41
1:A:430:A:O2'	1:A:431:A:H5'	2.20	0.41
5:F:10:VAL:HG12	5:F:11:HIS:N	2.35	0.41
1:A:1352:C:H2'	1:A:1353:G:C8	2.55	0.41
7:H:34:ALA:O	7:H:38:VAL:HG23	2.20	0.41
11:L:122:LYS:HG3	11:L:123:ALA:H	1.85	0.41
20:B:213:LEU:O	20:B:216:VAL:HG22	2.19	0.41
21:U:42:THR:HB	21:U:46:ARG:HE	1.86	0.41
7:H:7:ALA:O	7:H:11:THR:HG23	2.21	0.41
3:D:160:LEU:HD22	3:D:161:ALA:H	1.83	0.41
5:F:6:ILE:HG13	5:F:62:MET:HB2	2.02	0.41
1:A:1072:G:N2	20:B:105:THR:HG21	2.35	0.41
17:R:51:GLN:HA	17:R:51:GLN:NE2	2.24	0.41
4:E:73:VAL:O	4:E:75:LEU:HG	2.19	0.41
20:B:221:ARG:HH11	20:B:221:ARG:CB	2.28	0.41
1:A:598:U:H4'	7:H:85:TYR:CD2	2.55	0.41
6:G:145:GLU:C	6:G:147:ASN:N	2.74	0.41
1:A:1278:G:OP1	1:A:1279:G:H5'	2.20	0.41
16:Q:68:LYS:C	16:Q:70:LYS:N	2.74	0.41
7:H:79:ARG:NH1	7:H:82:LEU:HB3	2.35	0.41
11:L:17:LYS:H	11:L:17:LYS:HE3	1.84	0.41
19:T:49:ALA:HA	19:T:52:GLU:CD	2.40	0.41
18:S:52:ASN:CG	18:S:53:GLY:N	2.73	0.41
1:A:1133:G:H2'	1:A:1134:G:O4'	2.19	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:L:3:VAL:O	11:L:7:VAL:HG23	2.21	0.41
1:A:1222:G:C2'	1:A:1223:C:H5'	2.49	0.41
20:B:126:ASP:C	20:B:127:LYS:HD2	2.40	0.41
1:A:724:G:O2'	1:A:725:G:H5'	2.20	0.41
1:A:62:U:H2'	1:A:63:C:C6	2.56	0.41
1:A:940:C:H2'	1:A:941:G:C8	2.55	0.41
21:U:33:ARG:HH12	21:U:34:ARG:NH1	2.19	0.41
1:A:521:G:O2'	1:A:522:C:H5'	2.20	0.41
1:A:522:C:O2'	1:A:523:A:H5'	2.19	0.41
16:Q:3:LYS:HG3	16:Q:4:ILE:N	2.35	0.41
20:B:68:PHE:N	20:B:68:PHE:CD1	2.89	0.41
13:N:29:ILE:O	13:N:32:ASP:HB3	2.21	0.41
1:A:376:G:H5''	15:P:5:ARG:CB	2.47	0.41
4:E:113:VAL:CG2	4:E:114:LEU:N	2.83	0.41
1:A:586:C:C5'	7:H:81:GLY:HA2	2.50	0.41
1:A:845:A:H5''	1:A:846:G:C8	2.56	0.41
10:K:75:GLU:CD	10:K:75:GLU:N	2.69	0.41
1:A:1300:G:H1'	1:A:1301:U:C5	2.55	0.41
5:F:54:LEU:HD22	5:F:54:LEU:N	2.35	0.41
18:S:27:LYS:HB3	18:S:27:LYS:HZ3	1.85	0.41
3:D:1:ALA:O	3:D:2:ARG:HG2	2.20	0.41
1:A:1230:C:H2'	1:A:1231:G:H8	1.84	0.41
1:A:1291:U:H2'	1:A:1292:G:C8	2.56	0.41
12:M:77:LYS:O	12:M:80:MET:HB2	2.21	0.41
4:E:132:PRO:HG2	4:E:133:ILE:H	1.84	0.41
9:J:91:ASP:C	9:J:92:LEU:HD13	2.41	0.41
1:A:55:A:OP2	1:A:352:C:N4	2.53	0.41
1:A:612:C:H2'	1:A:613:C:C6	2.55	0.41
11:L:28:GLN:HE21	11:L:28:GLN:HB3	1.57	0.41
8:I:26:LYS:H	8:I:61:ASP:CB	2.34	0.41
8:I:27:ILE:HD13	8:I:34:LEU:HD22	2.03	0.41
3:D:122:ILE:HG22	3:D:123:MET:H	1.86	0.41
4:E:93:VAL:HG11	4:E:110:MET:SD	2.61	0.41
12:M:33:LEU:HD13	12:M:39:ALA:O	2.20	0.41
1:A:1073:U:O2	20:B:102:ASN:ND2	2.52	0.41
20:B:57:ASN:OD1	20:B:58:LYS:N	2.53	0.41
16:Q:18:LYS:HG2	16:Q:48:GLU:O	2.21	0.41
1:A:586:C:O2'	1:A:587:G:H5'	2.21	0.41
4:E:61:LYS:HB2	4:E:65:LYS:NZ	2.36	0.41
4:E:61:LYS:NZ	4:E:61:LYS:HB3	2.35	0.41
1:A:195:A:H1'	1:A:222:C:HO2'	1.85	0.41
15:P:39:PHE:CE1	15:P:74:LEU:HD21	2.56	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:885:G:C2	1:A:886:G:C8	3.07	0.41
9:J:82:LYS:HG3	9:J:83:THR:H	1.85	0.41
20:B:162:VAL:CG1	20:B:184:ALA:HB2	2.47	0.41
8:I:74:GLN:HE21	8:I:74:GLN:N	2.18	0.41
4:E:93:VAL:HG12	4:E:94:PHE:N	2.35	0.41
1:A:1072:G:H2'	1:A:1073:U:C6	2.56	0.41
1:A:195:A:H2'	1:A:196:A:C8	2.55	0.41
1:A:674:G:H2'	1:A:675:A:C8	2.55	0.41
12:M:95:PRO:HB2	12:M:99:GLN:OE1	2.21	0.41
1:A:501:C:H1'	1:A:549:C:H1'	2.02	0.41
20:B:130:LYS:O	20:B:134:LEU:HG	2.20	0.41
9:J:35:GLN:HG2	9:J:78:GLU:OE1	2.21	0.41
5:F:53:LYS:N	5:F:53:LYS:NZ	2.68	0.41
1:A:545:C:O2'	1:A:546:A:H5'	2.20	0.41
1:A:720:C:C5'	17:R:40:PRO:HA	2.51	0.41
1:A:487:A:H3'	1:A:488:C:C6	2.54	0.41
6:G:11:ILE:H	6:G:11:ILE:HD12	1.85	0.41
1:A:725:G:O2'	1:A:726:C:H5'	2.21	0.41
8:I:84:ARG:O	8:I:87:MET:HB3	2.21	0.41
8:I:66:VAL:HG11	8:I:74:GLN:HG3	2.03	0.41
8:I:85:ALA:HA	8:I:88:GLU:OE2	2.21	0.41
10:K:62:ALA:CB	10:K:91:GLY:HA3	2.51	0.41
13:N:60:ARG:O	13:N:62:ARG:N	2.54	0.41
15:P:52:LEU:HD23	15:P:54:LEU:HG	2.02	0.41
1:A:1323:G:O2'	1:A:1362:A:O4'	2.39	0.41
1:A:238:A:H3'	1:A:239:U:H5''	2.02	0.41
6:G:149:ALA:HB2	10:K:55:ARG:CZ	2.48	0.41
1:A:585:G:H2'	1:A:586:C:H6	1.85	0.41
1:A:956:U:C2'	1:A:957:U:H5'	2.51	0.41
3:D:78:ALA:C	3:D:85:THR:HG23	2.41	0.41
18:S:52:ASN:HD22	18:S:76:THR:HA	1.84	0.41
1:A:1450:U:H2'	1:A:1452:C:C5	2.56	0.41
14:O:77:ARG:O	14:O:81:LEU:HB2	2.21	0.41
7:H:115:ALA:O	7:H:120:LEU:HD23	2.20	0.41
11:L:107:LYS:O	11:L:108:ASP:HB2	2.21	0.41
11:L:33:CYS:O	11:L:75:GLU:O	2.38	0.41
1:A:64:G:H4'	1:A:65:A:H3'	2.02	0.41
1:A:173:U:H5'	1:A:197:A:O4'	2.20	0.41
9:J:59:LYS:HE3	9:J:60:ASP:OD1	2.20	0.41
1:A:1058:G:H2'	1:A:1059:C:H6	1.85	0.41
1:A:1256:A:H4'	1:A:1258:G:C8	2.55	0.41
1:A:1346:A:H61	1:A:1374:A:H3'	1.86	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:291:U:H2'	1:A:292:G:C8	2.56	0.41
1:A:423:G:H2'	1:A:424:G:O4'	2.19	0.41
1:A:462:G:H2'	1:A:463:U:C6	2.55	0.41
20:B:26:MET:SD	20:B:192:PRO:HD3	2.61	0.41
8:I:48:ARG:O	8:I:51:LEU:HB2	2.20	0.41
8:I:6:TYR:OH	8:I:8:THR:HG22	2.21	0.41
1:A:1084:G:H2'	1:A:1085:U:C6	2.56	0.41
1:A:171:A:O2'	1:A:172:A:H5'	2.21	0.41
1:A:132:C:H5''	19:T:68:LYS:HZ3	1.84	0.41
4:E:43:GLY:HA2	4:E:75:LEU:CD1	2.50	0.41
4:E:19:ARG:HG3	4:E:31:SER:O	2.20	0.41
1:A:237:G:H5''	16:Q:26:ARG:HH21	1.83	0.41
3:D:29:THR:CB	3:D:30:LYS:HD3	2.48	0.41
11:L:113:ARG:HH21	11:L:120:ARG:HA	1.86	0.41
1:A:584:G:H2'	1:A:585:G:H8	1.86	0.41
4:E:24:VAL:HG23	4:E:26:GLY:H	1.86	0.41
1:A:1166:G:N1	1:A:1169:A:OP2	2.53	0.41
1:A:621:A:H2'	1:A:622:A:H8	1.84	0.41
17:R:63:TYR:HD2	17:R:63:TYR:N	2.18	0.41
1:A:512:U:H2'	1:A:513:C:H6	1.85	0.41
3:D:187:ARG:O	3:D:191:SER:HB3	2.21	0.41
1:A:1473:G:H2'	1:A:1474:U:C6	2.55	0.41
2:C:4:VAL:HG22	2:C:5:HIS:N	2.36	0.41
5:F:74:LEU:HD12	5:F:77:THR:OG1	2.21	0.41
16:Q:14:ASP:OD1	16:Q:53:GLY:HA2	2.20	0.41
10:K:81:LEU:N	10:K:81:LEU:HD23	2.36	0.41
8:I:24:ASN:O	8:I:60:LEU:N	2.53	0.41
10:K:106:ILE:HD11	10:K:109:ILE:HD11	2.02	0.41
10:K:106:ILE:HG12	10:K:107:THR:N	2.36	0.41
1:A:1085:U:H3'	1:A:1086:U:H5	1.82	0.41
10:K:85:VAL:O	10:K:112:VAL:N	2.54	0.41
5:F:4:TYR:CD2	5:F:71:ILE:HG21	2.56	0.41
18:S:10:ILE:CG2	18:S:37:SER:HB3	2.43	0.41
18:S:64:GLU:N	18:S:64:GLU:OE1	2.53	0.41
15:P:52:LEU:HD22	15:P:75:ILE:HA	2.03	0.41
13:N:56:PRO:HG2	13:N:57:SER:H	1.85	0.41
2:C:112:ALA:HB2	2:C:182:ASP:O	2.21	0.41
2:C:112:ALA:HB3	2:C:184:ASN:HB2	2.02	0.41
12:M:48:SER:CB	12:M:51:GLN:HG3	2.50	0.41
11:L:53:ARG:HG2	11:L:61:GLU:OE1	2.21	0.41
1:A:1349:A:OP1	8:I:121:ARG:HB2	2.20	0.41
16:Q:45:VAL:HG11	16:Q:60:ILE:CG2	2.49	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:255:G:H1'	16:Q:17:GLU:OE2	2.20	0.41
1:A:828:U:O2'	20:B:24:PRO:HB3	2.20	0.41
1:A:565:U:H3'	1:A:566:G:H2'	2.03	0.41
1:A:191:G:OP2	1:A:191:G:H8	2.03	0.41
6:G:63:VAL:CG1	6:G:127:ALA:HB1	2.51	0.41
6:G:63:VAL:HA	6:G:66:GLU:OE2	2.20	0.41
1:A:672:U:H2'	1:A:673:A:C8	2.56	0.41
1:A:71:A:H61	1:A:99:C:H1'	1.86	0.41
2:C:13:ILE:HG12	2:C:14:VAL:HG13	2.03	0.41
1:A:961:U:O2	1:A:983:A:N7	2.53	0.41
1:A:1320:C:H2'	1:A:1321:U:O4'	2.21	0.41
7:H:26:MET:HB2	7:H:27:PRO:HD2	2.02	0.41
1:A:834:U:OP1	17:R:48:ALA:HB2	2.20	0.41
6:G:140:VAL:O	6:G:143:MET:HB3	2.21	0.41
20:B:116:LEU:HB3	20:B:140:LEU:CG	2.51	0.41
20:B:76:SER:HA	20:B:92:ASN:CB	2.51	0.41
6:G:6:ILE:H	6:G:6:ILE:HG13	1.58	0.41
1:A:1118:U:H2'	1:A:1119:C:C6	2.55	0.41
1:A:1216:A:H2'	1:A:1217:C:H6	1.86	0.41
1:A:611:C:H2'	1:A:612:C:C6	2.56	0.41
1:A:227:G:H2'	1:A:228:A:C8	2.56	0.41
1:A:28:A:H2'	1:A:29:U:O4'	2.21	0.41
1:A:968:A:H3'	1:A:969:A:C5'	2.51	0.41
8:I:21:LYS:O	8:I:60:LEU:HB2	2.21	0.41
8:I:38:PHE:O	8:I:44:ARG:HD3	2.20	0.41
21:U:35:GLU:HB3	21:U:36:PHE:H	1.64	0.41
21:U:44:ARG:HG3	21:U:44:ARG:NH1	2.35	0.41
1:A:532:A:C8	2:C:192:TYR:HD2	2.39	0.41
3:D:150:LYS:HA	3:D:155:LYS:HZ1	1.86	0.41
5:F:9:MET:HB2	5:F:57:ALA:HB1	2.03	0.41
19:T:43:LYS:CA	19:T:85:LEU:HD11	2.51	0.41
20:B:95:TRP:HZ3	20:B:174:GLU:OE2	2.05	0.41
1:A:238:A:H2'	1:A:239:U:C5'	2.48	0.41
1:A:411:A:O2'	1:A:412:A:O4'	2.37	0.41
2:C:48:LYS:H	2:C:48:LYS:CD	2.29	0.41
9:J:41:PRO:HG2	9:J:42:LEU:H	1.85	0.41
3:D:34:GLU:CG	3:D:34:GLU:O	2.67	0.41
10:K:30:ILE:HG22	10:K:45:THR:CA	2.51	0.41
20:B:8:MET:O	20:B:9:LEU:C	2.59	0.41
11:L:107:LYS:HD2	11:L:107:LYS:C	2.41	0.41
7:H:65:PHE:CD2	7:H:66:GLN:HG3	2.56	0.41
1:A:83:C:H1'	1:A:84:U:H6	1.86	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
11:L:65:TYR:HB3	11:L:95:HIS:NE2	2.36	0.41
7:H:38:VAL:CG1	7:H:111:THR:HG22	2.51	0.41
14:O:87:LEU:O	14:O:88:ARG:C	2.59	0.41
1:A:1381:U:O2'	1:A:1382:C:H5'	2.21	0.41
5:F:35:LYS:HB2	5:F:35:LYS:HE3	1.91	0.41
1:A:841:C:O2	1:A:841:C:H2'	2.19	0.41
8:I:56:MET:O	8:I:57:VAL:HB	2.21	0.40
7:H:14:ARG:HG3	7:H:15:ASN:N	2.36	0.40
12:M:39:ALA:HB3	12:M:42:VAL:HG13	2.03	0.40
13:N:60:ARG:NH2	13:N:69:PRO:HB3	2.36	0.40
20:B:65:LYS:CB	20:B:157:PRO:HA	2.51	0.40
2:C:26:LYS:HE3	2:C:26:LYS:HB2	1.96	0.40
4:E:148:SER:OG	4:E:150:GLU:HG2	2.21	0.40
2:C:104:GLU:HB3	2:C:105:VAL:H	1.72	0.40
2:C:110:LEU:HD21	2:C:140:ALA:O	2.21	0.40
17:R:67:LEU:HD23	17:R:68:PRO:HD2	2.03	0.40
11:L:23:LEU:HG	11:L:24:GLU:N	2.36	0.40
1:A:1390:U:O2'	1:A:1391:U:H5'	2.20	0.40
1:A:658:C:O2'	1:A:659:U:H5'	2.21	0.40
1:A:955:U:H2'	1:A:956:U:H6	1.86	0.40
18:S:68:HIS:HB3	18:S:72:GLU:OE2	2.21	0.40
1:A:1309:G:H2'	1:A:1310:G:C8	2.56	0.40
2:C:154:GLY:O	2:C:155:ARG:HB2	2.20	0.40
7:H:36:ALA:O	7:H:45:ILE:HD11	2.21	0.40
3:D:129:VAL:HG12	3:D:131:ILE:H	1.86	0.40
15:P:4:ILE:HB	15:P:67:ILE:HD12	2.03	0.40
1:A:1234:C:H1'	1:A:1364:U:O2	2.20	0.40
1:A:814:A:C5'	1:A:1511:G:H4'	2.51	0.40
1:A:1096:C:H2'	1:A:1097:C:H6	1.86	0.40
1:A:562:U:H1'	11:L:11:ARG:HD2	2.03	0.40
1:A:228:A:O2'	15:P:60:TRP:HZ3	2.03	0.40
2:C:82:ASP:O	2:C:86:LEU:HG	2.20	0.40
1:A:445:G:H2'	1:A:446:G:O4'	2.21	0.40
1:A:360:G:O2'	1:A:361:G:H5'	2.21	0.40
14:O:64:ARG:NE	14:O:64:ARG:HA	2.36	0.40
10:K:109:ILE:HG22	21:U:16:ARG:HH12	1.85	0.40
3:D:158:LEU:HA	3:D:161:ALA:HB3	2.03	0.40
1:A:889:A:H61	1:A:907:A:H3'	1.85	0.40
11:L:41:PRO:HB3	11:L:49:ARG:HH11	1.86	0.40
19:T:67:HIS:CG	19:T:68:LYS:N	2.89	0.40
20:B:174:GLU:O	20:B:177:ASN:HB3	2.22	0.40
20:B:86:CYS:N	20:B:88:GLN:NE2	2.69	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
8:I:119:LYS:HB3	8:I:122:ARG:HB3	2.02	0.40
9:J:6:ILE:HB	9:J:76:ILE:CD1	2.49	0.40
1:A:678:U:H4'	1:A:778:G:OP1	2.21	0.40
1:A:429:U:C1'	1:A:430:A:H5''	2.50	0.40
1:A:1305:G:H2'	1:A:1331:G:N2	2.36	0.40
1:A:716:A:H2'	1:A:717:U:C6	2.55	0.40
1:A:1229:A:H2'	1:A:1230:C:C6	2.56	0.40
15:P:20:VAL:CG2	15:P:32:PHE:HB2	2.51	0.40
1:A:768:A:H4'	1:A:1523:G:N2	2.35	0.40
16:Q:82:VAL:HG22	16:Q:82:VAL:O	2.21	0.40
16:Q:34:GLY:O	16:Q:35:LYS:C	2.60	0.40
1:A:1503:A:C8	1:A:1531:A:N3	2.90	0.40
2:C:40:GLN:HG3	2:C:41:TYR:N	2.36	0.40
18:S:33:TRP:CE3	18:S:33:TRP:N	2.89	0.40
1:A:1149:C:O2'	1:A:1280:A:N1	2.53	0.40
8:I:56:MET:HA	8:I:59:LYS:HB2	2.02	0.40
8:I:5:TYR:HB3	8:I:88:GLU:CD	2.41	0.40
3:D:113:ALA:O	3:D:117:VAL:HG23	2.21	0.40
3:D:25:ARG:HH12	3:D:30:LYS:HG2	1.86	0.40
1:A:130:A:N1	1:A:233:C:H1'	2.36	0.40
1:A:778:G:O2'	1:A:779:C:H5'	2.21	0.40
2:C:64:ARG:O	2:C:65:VAL:C	2.59	0.40
3:D:101:VAL:HG13	3:D:106:PHE:HB2	2.01	0.40
1:A:738:C:H2'	1:A:739:C:H6	1.85	0.40
15:P:67:ILE:HG23	15:P:67:ILE:O	2.21	0.40
1:A:707:U:H2'	1:A:708:C:C6	2.56	0.40
1:A:728:A:O2'	1:A:729:A:H5'	2.21	0.40
11:L:65:TYR:C	11:L:66:ILE:HD12	2.42	0.40
1:A:1481:U:H2'	1:A:1482:G:C8	2.57	0.40
1:A:113:G:H1'	1:A:354:G:H5'	2.03	0.40
1:A:903:G:H2'	1:A:904:U:O4'	2.21	0.40
1:A:1015:G:H2'	1:A:1016:A:C8	2.56	0.40
1:A:1351:U:O2'	1:A:1352:C:H5'	2.22	0.40
8:I:87:MET:O	8:I:91:GLU:HG2	2.21	0.40
2:C:81:GLU:HG3	2:C:82:ASP:N	2.36	0.40
1:A:261:U:H2'	1:A:263:A:OP2	2.21	0.40
8:I:34:LEU:C	8:I:36:GLN:H	2.23	0.40
3:D:190:LEU:O	3:D:190:LEU:HD13	2.20	0.40
2:C:129:PHE:CD2	2:C:156:LEU:HD22	2.57	0.40
6:G:148:LYS:HE2	6:G:151:ALA:CB	2.50	0.40
16:Q:74:LEU:O	16:Q:74:LEU:HD13	2.22	0.40
16:Q:59:GLU:HG2	16:Q:75:VAL:CG2	2.51	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1092:A:H5''	6:G:3:ARG:NH1	2.30	0.40
1:A:96:U:H2'	1:A:97:G:H8	1.87	0.40
1:A:784:A:N6	1:A:799:G:C6	2.90	0.40
1:A:735:C:O2'	1:A:736:C:H5'	2.22	0.40
1:A:1330:U:H5''	12:M:22:TYR:O	2.21	0.40
1:A:1028:C:N3	1:A:1029:U:H1'	2.37	0.40
1:A:545:C:P	3:D:61:ARG:HH12	2.45	0.40
1:A:1260:G:P	1:A:1284:C:H4'	2.61	0.40
1:A:933:G:N7	6:G:2:ARG:NH1	2.69	0.40
1:A:803:G:H2'	1:A:804:U:C6	2.57	0.40
1:A:60:A:H8	1:A:60:A:P	2.44	0.40
1:A:43:C:H2'	1:A:44:A:O4'	2.21	0.40
10:K:57:SER:O	10:K:90:PRO:HG3	2.21	0.40
12:M:113:LYS:N	12:M:114:PRO:CD	2.84	0.40
20:B:42:LEU:HA	20:B:45:THR:HB	2.02	0.40
8:I:24:ASN:ND2	8:I:25:GLY:N	2.70	0.40
8:I:35:GLU:H	8:I:35:GLU:CD	2.25	0.40
18:S:30:LEU:N	18:S:48:ILE:HA	2.14	0.40
1:A:1098:C:O2'	1:A:1099:G:H5'	2.21	0.40
10:K:33:ILE:CB	10:K:73:VAL:HG11	2.36	0.40
5:F:40:GLU:HB2	5:F:61:LEU:HB2	2.04	0.40
20:B:101:THR:HG23	20:B:102:ASN:N	2.36	0.40
15:P:46:LYS:C	15:P:48:GLU:N	2.74	0.40
20:B:15:PHE:CD1	20:B:16:GLY:N	2.90	0.40
20:B:57:ASN:HB3	20:B:219:THR:O	2.22	0.40
13:N:23:ARG:C	13:N:25:GLU:H	2.25	0.40
13:N:25:GLU:HG2	13:N:25:GLU:H	1.63	0.40
1:A:454:G:O2'	1:A:455:G:H5'	2.21	0.40
2:C:46:LEU:O	2:C:49:ALA:HB3	2.22	0.40
1:A:840:C:N3	1:A:842:U:H4'	2.36	0.40
6:G:47:GLU:OE1	6:G:57:GLU:HG2	2.21	0.40
1:A:778:G:H2'	1:A:779:C:C6	2.57	0.40
1:A:36:C:O3'	11:L:119:LYS:HA	2.22	0.40
5:F:53:LYS:HB2	5:F:54:LEU:HD22	2.02	0.40
1:A:469:C:O2'	1:A:470:C:H5'	2.22	0.40
1:A:159:G:N1	1:A:163:C:N4	2.69	0.40
1:A:407:U:O3'	3:D:112:GLU:HB2	2.22	0.40
6:G:16:LYS:HB3	6:G:43:TYR:CE1	2.56	0.40
9:J:80:THR:HB	9:J:83:THR:HB	2.02	0.40
1:A:1530:G:H2'	1:A:1531:A:C8	2.56	0.40
1:A:841:C:C2'	1:A:841:C:O2	2.70	0.40
1:A:691:G:H1'	1:A:696:A:N6	2.35	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:1340:A:O2'	1:A:1341:U:H5'	2.21	0.40
16:Q:13:SER:HB3	16:Q:21:VAL:CG2	2.51	0.40
1:A:1275:A:H2'	1:A:1276:G:O4'	2.21	0.40
12:M:100:ARG:HG3	12:M:100:ARG:O	2.21	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone ⓘ

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	C	204/232 (88%)	157 (77%)	34 (17%)	13 (6%)	2	30
3	D	203/205 (99%)	144 (71%)	45 (22%)	14 (7%)	2	28
4	E	148/166 (89%)	114 (77%)	30 (20%)	4 (3%)	8	57
5	F	98/135 (73%)	71 (72%)	17 (17%)	10 (10%)	1	15
6	G	148/178 (83%)	117 (79%)	22 (15%)	9 (6%)	2	31
7	H	127/129 (98%)	99 (78%)	24 (19%)	4 (3%)	7	54
8	I	125/129 (97%)	88 (70%)	28 (22%)	9 (7%)	2	26
9	J	96/103 (93%)	71 (74%)	15 (16%)	10 (10%)	1	15
10	K	115/128 (90%)	83 (72%)	26 (23%)	6 (5%)	3	36
11	L	121/123 (98%)	79 (65%)	34 (28%)	8 (7%)	2	29
12	M	112/117 (96%)	76 (68%)	28 (25%)	8 (7%)	2	27
13	N	92/100 (92%)	61 (66%)	21 (23%)	10 (11%)	1	13
14	O	86/89 (97%)	63 (73%)	19 (22%)	4 (5%)	4	40
15	P	80/82 (98%)	57 (71%)	19 (24%)	4 (5%)	3	38
16	Q	78/83 (94%)	56 (72%)	16 (20%)	6 (8%)	1	24
17	R	53/74 (72%)	39 (74%)	11 (21%)	3 (6%)	3	34
18	S	77/91 (85%)	60 (78%)	11 (14%)	6 (8%)	1	23
19	T	83/86 (96%)	63 (76%)	15 (18%)	5 (6%)	2	32

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	B	216/240 (90%)	149 (69%)	52 (24%)	15 (7%)	2	28
21	U	49/70 (70%)	28 (57%)	14 (29%)	7 (14%)	0	7
All	All	2311/2560 (90%)	1675 (72%)	481 (21%)	155 (7%)	2	29

All (155) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	C	14	VAL
2	C	54	ILE
2	C	205	GLU
3	D	24	VAL
3	D	192	ALA
4	E	102	THR
5	F	92	THR
6	G	6	ILE
6	G	71	THR
8	I	8	THR
8	I	24	ASN
8	I	127	SER
9	J	57	VAL
9	J	61	ALA
10	K	126	ARG
11	L	13	ARG
11	L	121	PRO
11	L	122	LYS
12	M	6	ILE
12	M	111	PRO
13	N	50	LEU
14	O	74	ASP
15	P	28	ARG
16	Q	32	ILE
19	T	3	ILE
20	B	9	LEU
20	B	19	THR
20	B	22	TRP
20	B	94	ARG
20	B	188	THR
2	C	104	GLU
2	C	153	SER
2	C	180	ASP
3	D	154	VAL

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Mol	Chain	Res	Type
3	D	168	THR
4	E	20	VAL
4	E	108	GLY
5	F	54	LEU
5	F	85	ILE
5	F	98	GLU
6	G	88	VAL
8	I	42	THR
8	I	57	VAL
8	I	106	ASP
9	J	36	VAL
9	J	38	GLY
9	J	74	VAL
9	J	100	ILE
10	K	88	PRO
11	L	24	GLU
11	L	117	GLY
12	M	15	VAL
12	M	22	TYR
13	N	33	VAL
13	N	61	ASN
13	N	71	GLY
15	P	44	SER
15	P	52	LEU
17	R	44	THR
20	B	14	HIS
20	B	15	PHE
20	B	150	ILE
20	B	163	ILE
21	U	34	ARG
21	U	36	PHE
2	C	3	LYS
2	C	47	ALA
2	C	59	PRO
3	D	31	CYS
3	D	167	PRO
4	E	43	GLY
6	G	70	PRO
6	G	92	PRO
6	G	112	ASP
8	I	122	ARG
9	J	32	THR

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Mol	Chain	Res	Type
9	J	56	HIS
10	K	14	GLN
10	K	125	LYS
12	M	3	ILE
12	M	49	GLU
12	M	97	ARG
13	N	20	PHE
13	N	48	GLN
14	O	88	ARG
17	R	43	ILE
17	R	46	THR
18	S	4	LEU
18	S	7	GLY
18	S	53	GLY
18	S	63	ASP
20	B	18	GLN
20	B	121	GLN
20	B	205	ALA
21	U	35	GLU
21	U	41	THR
2	C	107	LYS
2	C	145	ALA
3	D	27	ILE
3	D	28	ASP
3	D	68	GLU
5	F	58	HIS
5	F	62	MET
5	F	89	VAL
7	H	52	GLY
7	H	65	PHE
7	H	82	LEU
8	I	55	ASP
9	J	75	ASP
10	K	71	ASP
11	L	15	VAL
11	L	23	LEU
11	L	42	LYS
13	N	30	ILE
15	P	49	GLY
16	Q	28	VAL
18	S	13	HIS
19	T	65	LEU

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Mol	Chain	Res	Type
19	T	67	HIS
21	U	9	GLU
3	D	3	TYR
3	D	22	SER
3	D	25	ARG
5	F	99	ALA
6	G	5	VAL
6	G	38	ALA
13	N	19	TYR
14	O	18	ASP
14	O	22	THR
16	Q	26	ARG
16	Q	69	THR
19	T	42	ASP
20	B	58	LYS
21	U	37	TYR
21	U	40	PRO
2	C	167	TYR
3	D	86	GLY
5	F	51	ILE
5	F	82	ASP
13	N	2	LYS
16	Q	81	ALA
19	T	41	GLY
20	B	200	PRO
2	C	100	ILE
8	I	25	GLY
9	J	41	PRO
12	M	66	GLY
13	N	51	PRO
10	K	119	GLY
3	D	107	GLY
20	B	70	GLY
6	G	81	GLY
7	H	26	MET
16	Q	31	PRO
18	S	61	VAL

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	C	170/189 (90%)	145 (85%)	25 (15%)	4	27
3	D	172/172 (100%)	148 (86%)	24 (14%)	5	29
4	E	113/125 (90%)	102 (90%)	11 (10%)	12	51
5	F	87/116 (75%)	70 (80%)	17 (20%)	2	12
6	G	123/146 (84%)	109 (89%)	14 (11%)	8	40
7	H	104/104 (100%)	97 (93%)	7 (7%)	23	71
8	I	105/106 (99%)	89 (85%)	16 (15%)	4	25
9	J	86/90 (96%)	74 (86%)	12 (14%)	5	29
10	K	90/98 (92%)	76 (84%)	14 (16%)	4	23
11	L	103/103 (100%)	92 (89%)	11 (11%)	10	45
12	M	92/95 (97%)	79 (86%)	13 (14%)	5	29
13	N	79/83 (95%)	64 (81%)	15 (19%)	2	13
14	O	76/77 (99%)	69 (91%)	7 (9%)	13	54
15	P	65/65 (100%)	59 (91%)	6 (9%)	13	54
16	Q	74/77 (96%)	59 (80%)	15 (20%)	2	10
17	R	48/64 (75%)	41 (85%)	7 (15%)	5	27
18	S	70/78 (90%)	56 (80%)	14 (20%)	2	11
19	T	65/65 (100%)	58 (89%)	7 (11%)	9	44
20	B	180/198 (91%)	149 (83%)	31 (17%)	3	18
21	U	44/60 (73%)	33 (75%)	11 (25%)	1	6
All	All	1946/2111 (92%)	1669 (86%)	277 (14%)	5	28

All (277) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	2	GLN
2	C	13	ILE
2	C	14	VAL
2	C	17	TRP
2	C	20	THR
2	C	24	ASN
2	C	27	GLU
2	C	28	PHE

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Mol	Chain	Res	Type
2	C	35	ASP
2	C	41	TYR
2	C	42	LEU
2	C	48	LYS
2	C	61	LYS
2	C	88	LYS
2	C	101	ASN
2	C	106	ARG
2	C	120	THR
2	C	138	GLN
2	C	163	ARG
2	C	166	TRP
2	C	168	ARG
2	C	171	ARG
2	C	184	ASN
2	C	192	TYR
2	C	206	ILE
3	D	4	LEU
3	D	12	ARG
3	D	18	LEU
3	D	25	ARG
3	D	28	ASP
3	D	35	GLN
3	D	39	GLN
3	D	43	ARG
3	D	49	ASP
3	D	55	ARG
3	D	57	LYS
3	D	70	GLN
3	D	84	ASN
3	D	87	GLU
3	D	146	GLU
3	D	147	LYS
3	D	153	ARG
3	D	155	LYS
3	D	160	LEU
3	D	163	GLN
3	D	168	THR
3	D	190	LEU
3	D	193	ASP
3	D	204	SER
4	E	9	GLU

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Mol	Chain	Res	Type
4	E	23	THR
4	E	44	ARG
4	E	45	VAL
4	E	51	LYS
4	E	61	LYS
4	E	64	GLU
4	E	92	ARG
4	E	95	MET
4	E	119	VAL
4	E	123	LEU
5	F	6	ILE
5	F	9	MET
5	F	13	ASP
5	F	16	GLU
5	F	24	ARG
5	F	39	LEU
5	F	45	ARG
5	F	53	LYS
5	F	61	LEU
5	F	65	GLU
5	F	69	GLU
5	F	73	GLU
5	F	86	ARG
5	F	88	MET
5	F	96	VAL
5	F	98	GLU
5	F	100	SER
6	G	3	ARG
6	G	5	VAL
6	G	10	LYS
6	G	55	LYS
6	G	57	GLU
6	G	62	GLU
6	G	78	ARG
6	G	89	GLU
6	G	94	ARG
6	G	109	LYS
6	G	110	ARG
6	G	112	ASP
6	G	125	ASP
6	G	132	THR
7	H	55	LYS

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Mol	Chain	Res	Type
7	H	57	GLU
7	H	72	GLU
7	H	76	ARG
7	H	79	ARG
7	H	111	THR
7	H	113	ARG
8	I	26	LYS
8	I	36	GLN
8	I	45	MET
8	I	58	GLU
8	I	59	LYS
8	I	62	LEU
8	I	64	ILE
8	I	67	LYS
8	I	74	GLN
8	I	87	MET
8	I	92	SER
8	I	93	LEU
8	I	109	GLN
8	I	122	ARG
8	I	123	ARG
8	I	129	ARG
9	J	14	ASP
9	J	17	LEU
9	J	31	ARG
9	J	37	ARG
9	J	47	GLU
9	J	57	VAL
9	J	78	GLU
9	J	87	LEU
9	J	88	MET
9	J	89	ARG
9	J	92	LEU
9	J	97	ASP
10	K	28	ASN
10	K	29	THR
10	K	34	THR
10	K	51	PHE
10	K	55	ARG
10	K	56	LYS
10	K	76	TYR
10	K	80	ASN

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Mol	Chain	Res	Type
10	K	82	GLU
10	K	84	MET
10	K	100	ASN
10	K	105	ARG
10	K	121	ARG
10	K	126	ARG
11	L	14	LYS
11	L	15	VAL
11	L	17	LYS
11	L	19	ASN
11	L	28	GLN
11	L	33	CYS
11	L	43	LYS
11	L	49	ARG
11	L	77	SER
11	L	95	HIS
11	L	107	LYS
12	M	2	ARG
12	M	10	ASP
12	M	28	ARG
12	M	40	GLU
12	M	44	ILE
12	M	46	GLU
12	M	65	GLU
12	M	70	ARG
12	M	79	LEU
12	M	81	ASP
12	M	82	LEU
12	M	91	ARG
12	M	96	VAL
13	N	3	GLN
13	N	5	MET
13	N	25	GLU
13	N	26	LEU
13	N	27	LYS
13	N	32	ASP
13	N	40	ARG
13	N	48	GLN
13	N	50	LEU
13	N	53	ASP
13	N	58	ARG
13	N	60	ARG

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Mol	Chain	Res	Type
13	N	64	ARG
13	N	65	GLN
13	N	68	ARG
14	O	20	ASN
14	O	26	GLU
14	O	54	ARG
14	O	64	ARG
14	O	68	ASP
14	O	70	LEU
14	O	88	ARG
15	P	5	ARG
15	P	26	ASN
15	P	28	ARG
15	P	45	GLU
15	P	51	ARG
15	P	68	SER
16	Q	3	LYS
16	Q	5	ARG
16	Q	10	ARG
16	Q	20	ILE
16	Q	38	LYS
16	Q	39	ARG
16	Q	52	CYS
16	Q	56	ASP
16	Q	60	ILE
16	Q	61	ARG
16	Q	66	LEU
16	Q	71	SER
16	Q	74	LEU
16	Q	79	GLU
16	Q	80	LYS
17	R	23	LYS
17	R	35	SER
17	R	38	ILE
17	R	44	THR
17	R	46	THR
17	R	51	GLN
17	R	71	ASP
18	S	4	LEU
18	S	12	LEU
18	S	13	HIS
18	S	20	LYS

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Mol	Chain	Res	Type
18	S	27	LYS
18	S	28	LYS
18	S	32	THR
18	S	38	THR
18	S	42	ASN
18	S	47	THR
18	S	64	GLU
18	S	66	VAL
18	S	77	ARG
18	S	80	ARG
19	T	3	ILE
19	T	4	LYS
19	T	43	LYS
19	T	53	MET
19	T	69	ASN
19	T	74	HIS
19	T	85	LEU
20	B	8	MET
20	B	23	ASN
20	B	27	LYS
20	B	35	ASN
20	B	38	HIS
20	B	43	GLU
20	B	46	VAL
20	B	48	MET
20	B	50	ASN
20	B	62	ARG
20	B	72	LYS
20	B	88	GLN
20	B	93	HIS
20	B	94	ARG
20	B	104	LYS
20	B	107	ARG
20	B	113	LEU
20	B	119	GLN
20	B	121	GLN
20	B	124	THR
20	B	125	PHE
20	B	127	LYS
20	B	135	MET
20	B	144	GLU
20	B	196	ASP

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Mol	Chain	Res	Type
20	B	202	ASN
20	B	210	THR
20	B	211	LEU
20	B	212	TYR
20	B	221	ARG
20	B	224	ARG
21	U	11	PHE
21	U	16	ARG
21	U	22	CYS
21	U	24	LYS
21	U	28	LEU
21	U	33	ARG
21	U	34	ARG
21	U	36	PHE
21	U	38	GLU
21	U	44	ARG
21	U	48	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (62) such sidechains are listed below:

Mol	Chain	Res	Type
2	C	2	GLN
2	C	31	ASN
2	C	139	ASN
3	D	35	GLN
3	D	39	GLN
3	D	53	GLN
3	D	70	GLN
3	D	84	ASN
3	D	135	GLN
3	D	151	GLN
3	D	163	GLN
4	E	42	ASN
4	E	131	ASN
5	F	46	GLN
5	F	68	GLN
6	G	67	ASN
6	G	121	ASN
7	H	3	GLN
7	H	37	ASN
7	H	117	GLN
8	I	4	GLN

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Mol	Chain	Res	Type
8	I	30	ASN
8	I	36	GLN
8	I	49	GLN
8	I	80	HIS
9	J	20	GLN
9	J	56	HIS
9	J	99	GLN
10	K	21	HIS
10	K	28	ASN
10	K	39	ASN
10	K	80	ASN
10	K	100	ASN
10	K	118	ASN
11	L	19	ASN
11	L	28	GLN
11	L	45	ASN
11	L	111	GLN
12	M	7	ASN
12	M	90	HIS
14	O	28	GLN
14	O	40	GLN
14	O	62	GLN
15	P	9	HIS
15	P	29	ASN
15	P	63	GLN
17	R	51	GLN
17	R	53	GLN
18	S	42	ASN
18	S	52	ASN
18	S	55	GLN
19	T	2	ASN
19	T	20	ASN
19	T	69	ASN
19	T	83	ASN
20	B	14	HIS
20	B	23	ASN
20	B	35	ASN
20	B	88	GLN
20	B	119	GLN
20	B	121	GLN
20	B	202	ASN

## 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1529/1542 (99%)	246 (16%)	21 (1%)

All (246) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	9	G
1	A	14	U
1	A	32	A
1	A	39	G
1	A	47	C
1	A	48	C
1	A	51	A
1	A	52	C
1	A	55	A
1	A	65	A
1	A	66	A
1	A	68	G
1	A	71	A
1	A	72	A
1	A	73	C
1	A	76	G
1	A	78	A
1	A	79	G
1	A	81	A
1	A	83	C
1	A	84	U
1	A	85	U
1	A	86	G
1	A	87	C
1	A	88	U
1	A	89	U
1	A	91	U
1	A	93	U
1	A	94	G
1	A	95	C
1	A	96	U
1	A	108	G
1	A	121	U
1	A	122	G
1	A	131	A
1	A	151	A

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Mol	Chain	Res	Type
1	A	182	A
1	A	183	C
1	A	191	G
1	A	197	A
1	A	202	G
1	A	209	U
1	A	210	C
1	A	233	C
1	A	239	U
1	A	240	G
1	A	243	A
1	A	244	U
1	A	245	U
1	A	247	G
1	A	250	A
1	A	251	G
1	A	257	G
1	A	258	G
1	A	266	G
1	A	267	C
1	A	280	C
1	A	289	G
1	A	316	C
1	A	321	A
1	A	328	C
1	A	329	A
1	A	330	C
1	A	332	G
1	A	345	C
1	A	352	C
1	A	354	G
1	A	367	U
1	A	373	A
1	A	381	C
1	A	382	A
1	A	397	A
1	A	398	U
1	A	406	G
1	A	408	A
1	A	409	U
1	A	411	A
1	A	412	A

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Mol	Chain	Res	Type
1	A	413	G
1	A	414	A
1	A	421	U
1	A	422	C
1	A	424	G
1	A	429	U
1	A	430	A
1	A	435	A
1	A	438	U
1	A	461	A
1	A	462	G
1	A	463	U
1	A	464	U
1	A	465	A
1	A	466	A
1	A	467	U
1	A	468	A
1	A	469	C
1	A	482	A
1	A	484	G
1	A	485	U
1	A	493	A
1	A	500	G
1	A	509	A
1	A	511	C
1	A	518	C
1	A	527	G
1	A	532	A
1	A	547	A
1	A	559	A
1	A	562	U
1	A	572	A
1	A	573	A
1	A	576	C
1	A	577	G
1	A	596	A
1	A	653	U
1	A	665	A
1	A	695	A
1	A	700	G
1	A	721	G
1	A	724	G

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Mol	Chain	Res	Type
1	A	731	G
1	A	733	G
1	A	747	A
1	A	748	G
1	A	755	G
1	A	777	A
1	A	781	A
1	A	782	A
1	A	787	A
1	A	793	U
1	A	794	A
1	A	812	G
1	A	813	U
1	A	815	A
1	A	817	C
1	A	818	G
1	A	819	A
1	A	821	G
1	A	828	U
1	A	829	G
1	A	841	C
1	A	842	U
1	A	843	U
1	A	844	G
1	A	846	G
1	A	847	G
1	A	907	A
1	A	914	A
1	A	926	G
1	A	927	G
1	A	934	C
1	A	935	A
1	A	960	U
1	A	961	U
1	A	966	G
1	A	969	A
1	A	974	A
1	A	975	A
1	A	976	G
1	A	977	A
1	A	991	U
1	A	992	U

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Mol	Chain	Res	Type
1	A	993	G
1	A	994	A
1	A	1004	A
1	A	1009	U
1	A	1020	G
1	A	1025	U
1	A	1026	G
1	A	1027	C
1	A	1028	C
1	A	1030	U
1	A	1031	C
1	A	1034	G
1	A	1035	A
1	A	1050	G
1	A	1053	G
1	A	1065	U
1	A	1066	C
1	A	1085	U
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	1136	C
1	A	1137	C
1	A	1138	G
1	A	1139	G
1	A	1158	C
1	A	1159	U
1	A	1168	U
1	A	1169	A
1	A	1181	G
1	A	1183	U
1	A	1184	G
1	A	1196	A
1	A	1197	A
1	A	1201	A
1	A	1202	U
1	A	1212	U
1	A	1213	A
1	A	1225	A
1	A	1226	C
1	A	1227	A
1	A	1240	U

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Mol	Chain	Res	Type
1	A	1241	G
1	A	1256	A
1	A	1257	A
1	A	1261	A
1	A	1278	G
1	A	1279	G
1	A	1280	A
1	A	1281	C
1	A	1286	U
1	A	1299	A
1	A	1300	G
1	A	1301	U
1	A	1305	G
1	A	1316	G
1	A	1317	C
1	A	1318	A
1	A	1319	A
1	A	1320	C
1	A	1323	G
1	A	1336	C
1	A	1364	U
1	A	1381	U
1	A	1398	A
1	A	1400	C
1	A	1401	G
1	A	1410	A
1	A	1432	G
1	A	1446	A
1	A	1452	C
1	A	1491	G
1	A	1492	A
1	A	1497	G
1	A	1503	A
1	A	1505	G
1	A	1506	U
1	A	1517	G
1	A	1519	A
1	A	1520	C
1	A	1529	G
1	A	1530	G
1	A	1533	C
1	A	1534	A

All (21) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	51	A
1	A	81	A
1	A	239	U
1	A	243	A
1	A	266	G
1	A	279	A
1	A	328	C
1	A	366	A
1	A	372	C
1	A	428	G
1	A	429	U
1	A	484	G
1	A	576	C
1	A	975	A
1	A	1049	U
1	A	1065	U
1	A	1168	U
1	A	1201	A
1	A	1226	C
1	A	1397	C
1	A	1451	U

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 63 ligands modelled in this entry, 60 are monoatomic - leaving 3 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$
23	LLL	A	2356	-	33,33,33	3.19	14 (42%)	49,49,49	1.51	6 (12%)
23	LLL	A	2357	-	33,33,33	3.21	15 (45%)	49,49,49	1.55	5 (10%)
23	LLL	A	2358	-	33,33,33	3.17	14 (42%)	49,49,49	1.60	6 (12%)

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
23	LLL	A	2356	-	-	0/12/65/65	0/3/3/3
23	LLL	A	2357	-	-	0/12/65/65	0/3/3/3
23	LLL	A	2358	-	-	0/12/65/65	0/3/3/3

All (43) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	A	2356	LLL	C22-C32	9.64	1.59	1.52
23	A	2358	LLL	C22-C32	9.41	1.59	1.52
23	A	2357	LLL	C22-C32	9.09	1.59	1.52
23	A	2357	LLL	C22-C12	7.59	1.58	1.52
23	A	2358	LLL	C22-C12	7.17	1.57	1.52
23	A	2356	LLL	C22-C12	7.15	1.57	1.52
23	A	2357	LLL	O53-C53	6.10	1.52	1.43
23	A	2356	LLL	O53-C53	6.00	1.52	1.43
23	A	2358	LLL	O53-C53	5.96	1.51	1.43
23	A	2358	LLL	C43-C33	4.99	1.63	1.54
23	A	2356	LLL	C43-C33	4.97	1.63	1.54
23	A	2358	LLL	C42-C32	4.87	1.60	1.52
23	A	2358	LLL	O53-C13	4.75	1.52	1.41
23	A	2357	LLL	C42-C32	4.70	1.59	1.52
23	A	2357	LLL	C43-C33	4.62	1.63	1.54
23	A	2357	LLL	O53-C13	4.61	1.51	1.41
23	A	2356	LLL	O53-C13	4.47	1.51	1.41
23	A	2356	LLL	C42-C32	4.37	1.59	1.52
23	A	2356	LLL	C53-C43	3.76	1.56	1.52
23	A	2356	LLL	C41-C51	3.66	1.60	1.51
23	A	2357	LLL	C53-C43	3.64	1.56	1.52
23	A	2357	LLL	O51-C11	3.58	1.51	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	A	2358	LLL	O51-C11	3.58	1.51	1.41
23	A	2357	LLL	C41-C51	3.49	1.60	1.51
23	A	2358	LLL	C41-C51	3.48	1.60	1.51
23	A	2356	LLL	O51-C11	3.16	1.49	1.41
23	A	2358	LLL	C23-C33	3.04	1.60	1.52
23	A	2357	LLL	C23-C33	2.90	1.60	1.52
23	A	2356	LLL	C23-C33	2.78	1.60	1.52
23	A	2358	LLL	C53-C43	2.72	1.55	1.52
23	A	2356	LLL	C52-C42	2.54	1.59	1.52
23	A	2357	LLL	C52-C42	2.48	1.59	1.52
23	A	2357	LLL	C31-C21	2.40	1.59	1.52
23	A	2358	LLL	C52-C42	2.38	1.59	1.52
23	A	2357	LLL	C52-C62	2.27	1.58	1.52
23	A	2356	LLL	C31-C21	2.23	1.58	1.52
23	A	2356	LLL	C62-C12	2.22	1.56	1.52
23	A	2357	LLL	O62-C13	2.21	1.47	1.41
23	A	2358	LLL	C31-C21	2.19	1.58	1.52
23	A	2358	LLL	O62-C13	2.10	1.47	1.41
23	A	2358	LLL	C52-C62	2.09	1.58	1.52
23	A	2356	LLL	C52-C62	2.09	1.58	1.52
23	A	2357	LLL	C62-C12	2.07	1.55	1.52

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	A	2357	LLL	C93-N33-C33	6.07	117.30	113.85
23	A	2358	LLL	C93-N33-C33	5.76	117.13	113.85
23	A	2356	LLL	C93-N33-C33	5.27	116.85	113.85
23	A	2358	LLL	C53-O53-C13	5.12	118.52	111.22
23	A	2357	LLL	C53-O53-C13	4.69	117.90	111.22
23	A	2356	LLL	C53-O53-C13	4.35	117.42	111.22
23	A	2358	LLL	C83-C43-C33	3.43	117.85	112.15
23	A	2357	LLL	C83-C43-C33	3.03	117.19	112.15
23	A	2356	LLL	C83-C43-C33	2.82	116.83	112.15
23	A	2356	LLL	C13-O62-C62	2.76	125.03	117.99
23	A	2357	LLL	O43-C43-C83	-2.72	102.07	108.08
23	A	2358	LLL	C13-O62-C62	2.71	124.91	117.99
23	A	2356	LLL	O43-C43-C83	-2.59	102.36	108.08
23	A	2357	LLL	C13-O62-C62	2.52	124.42	117.99
23	A	2358	LLL	O43-C43-C83	-2.48	102.61	108.08
23	A	2358	LLL	C11-O51-C51	2.09	115.31	113.19
23	A	2356	LLL	C11-O51-C51	2.09	115.31	113.19

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.



## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates ⓘ

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands ⓘ

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers ⓘ

EDS was not executed - this section will therefore be empty.