



Full wwPDB EM Validation Report ⓘ

Jun 18, 2026 – 09:49 am BST

PDB ID : 6SW9 / pdb_00006sw9
EMDB ID : EMD-10320
Title : IC2A model of cryo-EM structure of a full archaeal ribosomal translation initiation complex devoid of aIF1 in *P. abyssi*
Authors : Coureux, P.-D.; Mechulam, Y.; Schmitt, E.
Deposited on : 2019-09-20
Resolution : 4.20 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

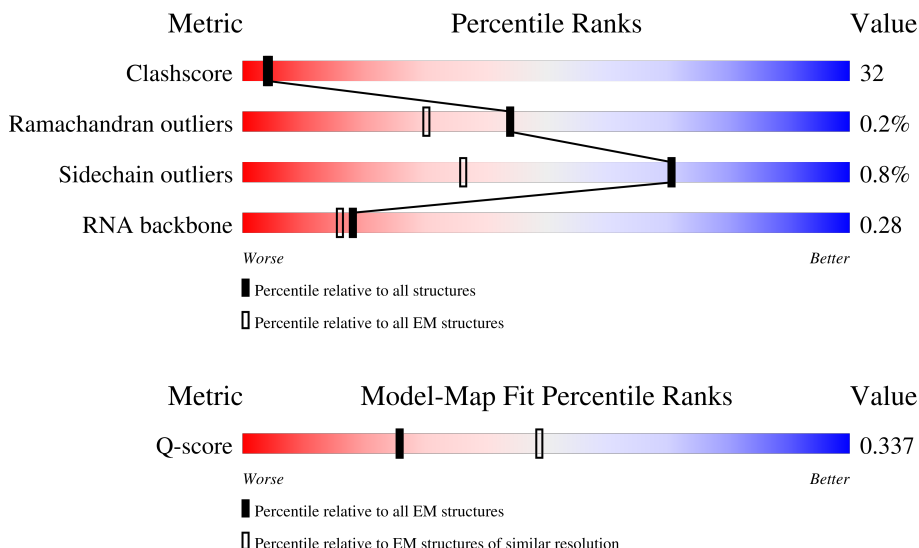
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 4.20 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.



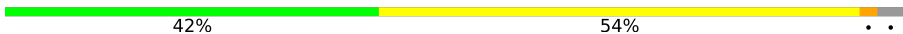
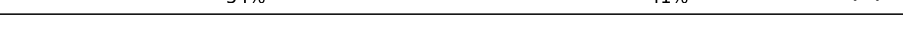
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	5410 (3.70 - 4.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	2	1497	
2	A	199	
3	B	202	

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Mol	Chain	Length	Quality of chain
4	C	63	
5	D	180	
6	E	243	
7	F	236	
8	G	125	
9	H	215	
10	I	130	
11	J	127	
12	K	135	
13	L	102	
14	M	137	
15	N	147	
16	O	148	
17	P	56	
18	Q	158	
19	R	113	
20	S	67	
21	T	132	
22	U	150	
23	V	99	
24	W	65	
25	X	71	
26	Y	51	
27	Z	210	
28	O	36	

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Mol	Chain	Length	Quality of chain
29	3	123	40% 59%
30	5	20	5% 60% 35%
31	4	76	53% 41%
32	6	113	40% 44% 16%
33	7	414	10% 36% 63%
34	8	129	71% 65% 35%
35	9	254	72% 65% 35%

2 Entry composition

There are 40 unique types of molecules in this entry. The entry contains 70661 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	1497	Total	C	N	O	P	0	0
			32291	14394	5959	10441	1497		

- Molecule 2 is a protein called 30S ribosomal protein S3Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	188	Total	C	N	O	S	0	0
			1533	995	268	266	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	196	Total	C	N	O	S	0	0
			1571	1017	269	281	4		

- Molecule 4 is a protein called Zn-ribbon RNA-binding protein involved in translation.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	61	Total	C	N	O	S	0	0
			482	304	85	85	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	175	Total	C	N	O	S	0	0
			1470	924	284	258	4		

- Molecule 6 is a protein called 30S ribosomal protein S4e.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	242	Total	C	N	O	S	0	0
			1983	1281	358	339	5		

- Molecule 7 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	229	Total	C	N	O	S	0	0
			1808	1147	334	320	7		

- Molecule 8 is a protein called 30S ribosomal protein S6e.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	124	Total	C	N	O	S	0	0
			977	621	178	176	2		

- Molecule 9 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	213	Total	C	N	O	S	0	0
			1720	1092	322	299	7		

- Molecule 10 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	I	129	Total	C	N	O	S	0	0
			1034	668	184	180	2		

- Molecule 11 is a protein called 30S ribosomal protein S8e.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	126	Total	C	N	O	S	0	0
			996	617	206	173			

- Molecule 12 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	134	Total	C	N	O	S	0	0
			1065	668	206	188	3		

- Molecule 13 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	101	Total	C	N	O	S	0	0
			817	507	158	148	4		

- Molecule 14 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	128	Total	C	N	O	S	0	0
			964	597	192	173	2		

- Molecule 15 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	146	Total	C	N	O	S	0	0
			1148	727	224	194	3		

- Molecule 16 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	O	138	Total	C	N	O	S	0	0
			1116	700	221	190	5		

- Molecule 17 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	55	Total	C	N	O	S	0	0
			455	288	95	67	5		

- Molecule 18 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Q	152	Total	C	N	O	S	0	0
			1262	804	240	214	4		

- Molecule 19 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	109	Total	C	N	O	S	0	0
			900	572	174	151	3		

- Molecule 20 is a protein called 30S ribosomal protein S17e.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	66	Total	C	N	O	S	0	0
			558	355	106	96	1		

- Molecule 21 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	125	Total	C	N	O	S	0	0
			1018	647	195	169	7		

- Molecule 22 is a protein called 30S ribosomal protein S19e.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	149	Total	C	N	O	S	0	0
			1223	790	221	212			

- Molecule 23 is a protein called 30S ribosomal protein S24e.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	94	Total	C	N	O	S	0	0
			790	516	125	146	3		

- Molecule 24 is a protein called 30S ribosomal protein S27e.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	63	Total	C	N	O	S	0	0
			481	303	93	80	5		

- Molecule 25 is a protein called 30S ribosomal protein S28e.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	X	67	Total	C	N	O	S	0	0
			536	327	111	98			

- Molecule 26 is a protein called 30S ribosomal protein S27ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Y	50	Total	C	N	O	S	0	0
			408	262	77	63	6		

- Molecule 27 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	197	Total	C	N	O	S	0	0
			1550	989	286	271	4		

- Molecule 28 is a protein called 50S ribosomal protein L41e.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	0	36	Total	C	N	O	S	0	0
			343	218	84	39	2		

- Molecule 29 is a protein called 50S ribosomal protein L7Ae.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	3	123	Total	C	N	O	S	0	0
			941	599	157	181	4		

- Molecule 30 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	5	20	Total	C	N	O	P	0	0
			430	192	78	140	20		

- Molecule 31 is a RNA chain called initiator Met-tRNA fMet from E. coli (A1U72 variant).

Mol	Chain	Residues	Atoms						AltConf	Trace
31	4	76	Total	C	N	O	P	S	0	0
			1622	724	291	530	76	1		

- Molecule 32 is a protein called Translation initiation factor 1A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	6	95	Total	C	N	O	S	0	0
			777	496	148	130	3		

- Molecule 33 is a protein called Translation initiation factor 2 subunit gamma.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	7	414	Total	C	N	O	S	0	0
			3213	2058	548	595	12		

- Molecule 34 is a protein called Translation initiation factor 2 subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	8	129	Total	C	N	O	S	0	0
			1032	659	171	192	10		

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
8	?	-	GLU	deletion	UNP Q97W59
8	?	-	LYS	deletion	UNP Q97W59
8	?	-	GLY	deletion	UNP Q97W59
8	?	-	ARG	deletion	UNP Q97W59
8	?	-	LYS	deletion	UNP Q97W59
8	?	-	GLU	deletion	UNP Q97W59
8	?	-	GLY	deletion	UNP Q97W59
8	?	-	THR	deletion	UNP Q97W59

- Molecule 35 is a protein called Translation initiation factor 2 subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	9	253	Total	C	N	O	S	0	0
			2025	1296	345	383	1		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
9	?	-	SER	deletion	UNP Q97Z79
9	?	-	LYS	deletion	UNP Q97Z79
9	?	-	TRP	deletion	UNP Q97Z79
9	?	-	VAL	deletion	UNP Q97Z79
9	?	-	LYS	deletion	UNP Q97Z79
9	?	-	LYS	deletion	UNP Q97Z79
9	?	-	HIS	deletion	UNP Q97Z79
9	?	-	ALA	deletion	UNP Q97Z79
9	?	-	GLU	deletion	UNP Q97Z79
9	?	-	GLU	deletion	UNP Q97Z79

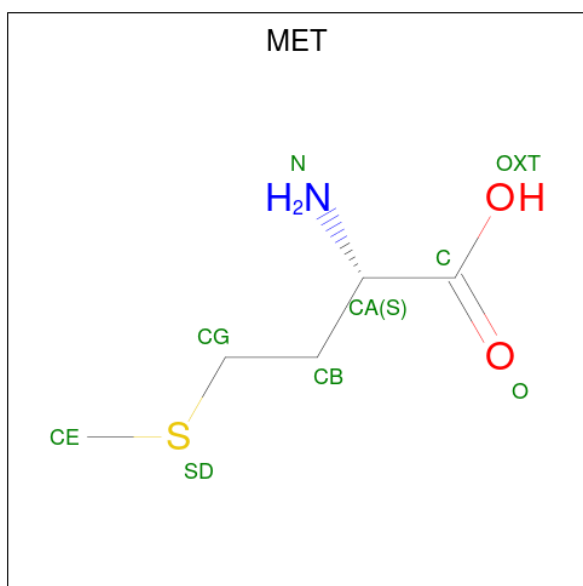
- Molecule 36 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
36	2	31	Total	Mg	0
			31	31	
36	5	1	Total	Mg	0
			1	1	
36	4	1	Total	Mg	0
			1	1	
36	7	1	Total	Mg	0
			1	1	

- Molecule 37 is ZINC ION (CCD ID: ZN) (formula: Zn).

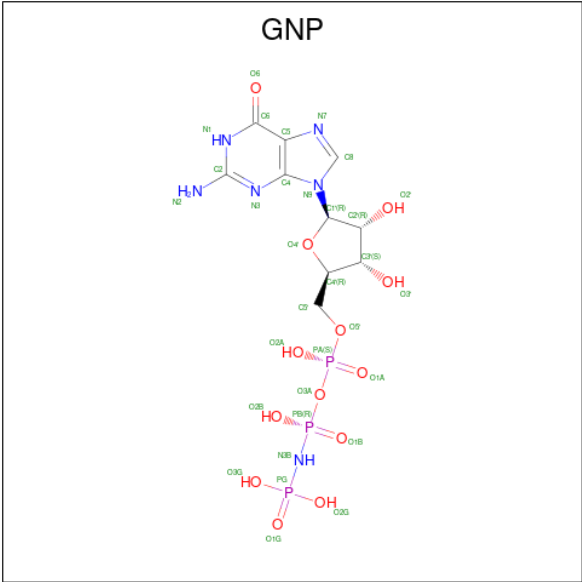
Mol	Chain	Residues	Atoms		AltConf
37	C	2	Total 2	Zn 2	0
37	F	1	Total 1	Zn 1	0
37	P	1	Total 1	Zn 1	0
37	R	1	Total 1	Zn 1	0
37	W	1	Total 1	Zn 1	0

- Molecule 38 is METHIONINE (CCD ID: MET) (formula: $C_5H_{11}NO_2S$).



Mol	Chain	Residues	Atoms					AltConf
38	7	1	Total 8	C 5	N 1	O 1	S 1	0

- Molecule 39 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (CCD ID: GNP) (formula: $C_{10}H_{17}N_6O_{13}P_3$).



Mol	Chain	Residues	Atoms					AltConf
39	7	1	Total	C	N	O	P	0
			32	10	6	13	3	

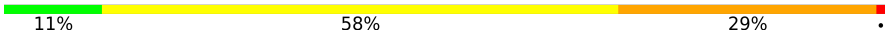
- Molecule 40 is water.

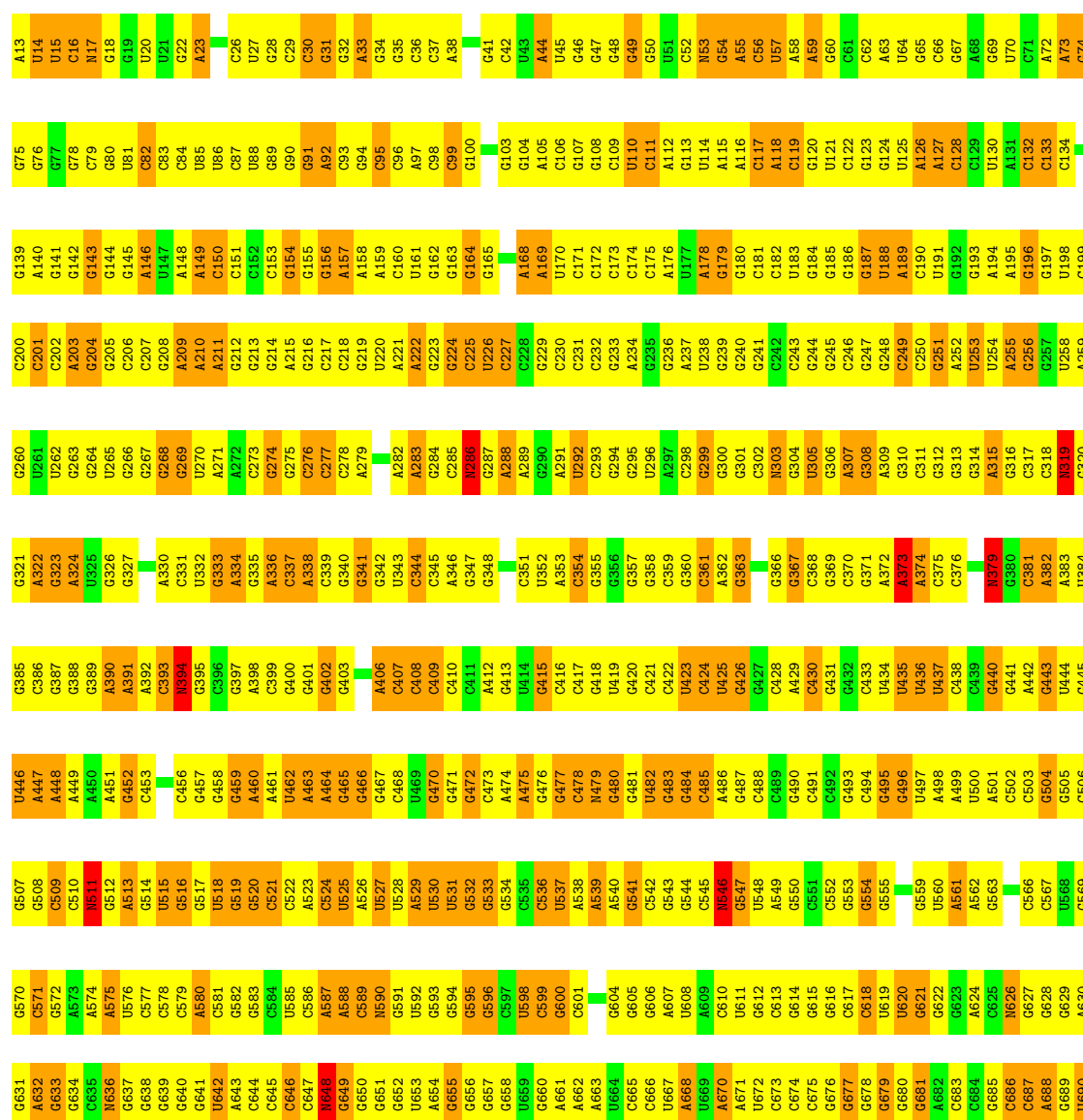
Mol	Chain	Residues	Atoms		AltConf
40	2	40	Total	O	0
			40	40	
40	K	1	Total	O	0
			1	1	
40	Q	1	Total	O	0
			1	1	

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: 16S ribosomal RNA

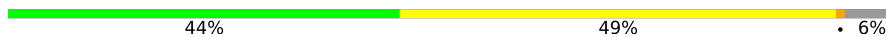
Chain 2: 



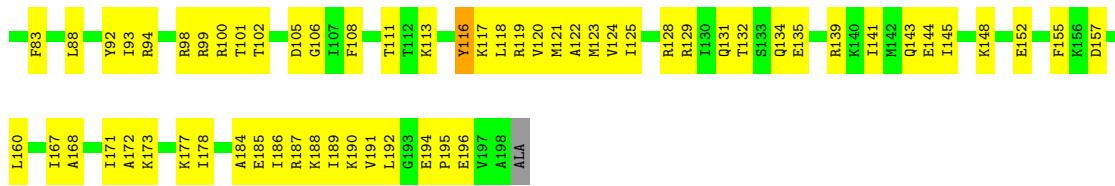
C1489	U1429	C1369	G1308	G1246	C1182	U1122	U1060	G1000	A940	C873	C813	G752	G691
C1430	C1430	A1370	C1309	G1247	C1123	G1061	G1061	A1001	A941	C874	A814	G753	G692
U1491	G1431	C1371	C1310	G1248	U1124	C1124	C1062	C1002	C942	C875	C815	G754	C693
A1492	C1432	A1372	G1311	G1249	G1125	G1063	G1063	C1003	C943	C876	C816	G755	G694
C1493	G1433	C1373	G1312	G1250	G1126	G1064	G1064	C1004	C944	C877	C817	G756	A1495
G1494	A1434	C1374	A1313	G1251	G1127	U1065	U1065	G1005	C945	A878	C818	G757	A696
C1495	C1435	G1375	G1314	U1252	A1187	G1127	U1066	G1006	C946	A879	C819	G758	G697
G1436	C1436	C1376	C1316	U1253	C1189	G1128	A1067	C1007	G947	A880	C820	G759	G698
U1497	A1437	C1377	C1317	A1254	C1190	G1129	A1068	C1008	G948	C881	C821	G760	C699
C1498	G1438	SHM1378	C1318	G1255	C1191	A1131	G1069	A1009	A949	U882	C822	G761	G700
A1499	C1439	G1379	U1319	C1257	C1192	G1132	A1070	G1010	A950	U883	G823	C762	G701
C1440	C1380	G1380	A1320	C1260	C1193	U1133	G1071	A1011	C951	A884	G824	C763	C702
C1381	C1381	G1321	G1321	U1260	G1194	G1134	C1072	G1012	C952	A885	U825	C764	U703
A1442	A1382	A1442	U1322	A1261	G1195	C1135	G1073	G1013	U953	A886	G826	C765	G704
C1443	A1443	C1383	A1323	A1262	G1196	C1136	A1074	A1014	C954	C887	C827	G767	G705
C1504	G1444	A1384	C1324	A1263	C1197	U1137	G1075	G1015	A955	C828	U828	G768	G706
G1445	C1445	C1385	C1325	G1264	U1198	G1138	C1078	G1016	C956	U891	G829	G769	U707
U1446	C1386	A1386	G1326	C1265	U1199	C1139	C1079	U1017	U957	U892	U830	G770	G708
C1447	A1387	G1387	G1327	C1266	C1200	G1140	G1080	G1018	G958	C893	A831	U771	G709
C1448	C1388	C1388	C1328	G1267	A1201	A1141	C1081	C1019	G959	C894	G832	C772	A710
G1449	A1389	C1389	G1329	C1268	U1202	G1142	G1082	U1020	C960	C895	G833	C773	A711
U1450	C1390	C1330	C1330	C1269	G1203	A1143	C1083	U1021	G961	C896	G834	U774	C712
G1451	G1391	A1391	G1331	C1270	C1204	A1144	C1084	G1022	G962	C897	G835	G775	G713
A1452	A1392	G1392	U1332	U1271	C1205	G1145	C1085	G1023	C963	C898	A836	G776	G714
G1453	G1393	C1393	C1333	C1272	C1206	C1146	C1086	G1024	G964	C903	C837	C777	G715
C1394	C1394	A1394	U1335	A1273	G1207	U1147	C1087	G1025	A965	C904	C838	U778	U716
G1455	G1455	G1395	U1335	G1274	C1208	G1148	A1088	C1026	C966	A904	U839	G779	C717
G1456	G1396	C1396	C1336	U1275	U1209	G1149	G1089	U1027	G967	C905	G840	U780	U718
G1457	G1397	A1397	U1337	U1276	A1210	A1150	U1090	U1028	G968	U906	U841	G781	G719
G1398	G1398	U1398	U1338	C1277	C1211	G1151	U1091	G1029	C969	A907	U842	G782	A720
A1458	C1399	C1399	C1339	G1278	A1212	G1152	G1092	U1030	A970	C908	A843	G783	C721
G1459	C1400	C1400	C1340	G1279	A1213	A1153	C1093	C1031	G971	A909	A844	G784	G722
A1461	U1401	A1401	C1341	A1280	U1214	A1154	C1094	A1032	C972	A910	G845	G785	G723
A1462	A1402	A1402	G1342	U1281	G1215	U1155	A1095	G1033	G973	C911	G846	U786	G724
G1463	G1403	G1403	C1343	G1282	G1216	G1156	G1096	C1034	U974	G912	C847	G787	G725
U1464	G1404	G1404	G1344	G1283	G1217	G1157	U1097	U1035	C975	C913	C848	G788	G726
C1465	U1405	G1405	G1345	C1284	C1218	G1158	C1098	C1036	A976	G914	G849	C789	A727
G1466	G1406	C1406	C1346	G1285	G1219	C1159	C1099	G1037	A977	U915	C850	G790	G728
U1467	A1407	G1407	G1347	G1286	G1220	C1100	C1100	U1038	G978	G916	U851	G791	C737
A1468	G1408	G1408	C1348	G1287	G1221	G1161	U1101	A1039	G979	C852	G853	G792	C738
A1469	A1409	A1409	A1349	C1288	G1162	C1162	C1102	C1040	C980	A918	C854	C793	A739
C1410	C1410	U1350	U1350	U1289	A1224	G1163	C1103	U1041	C981	C919	C854	U794	A733
A1471	C1411	C1351	A1351	G1290	C1229	G1164	C1104	G1042	A982	C923	U855	U795	A734
C1412	C1412	C1352	C1291	G1291	U1230	A1165	G1105	U1043	G983	G924	G856	G796	G735
G1413	G1413	C1353	A1292	A1293	G1231	G1166	C1106	A1045	G984	C985	G857	G797	G736
G1414	A1414	U1354	A1293	A1294	G1231	G1167	U1107	G1046	C985	G925	G858	U798	C737
U1415	U1415	C1355	C1355	G1294	C1232	G1168	C1108	G1045	U986	G926	G859	G799	C738
C1416	C1416	C1356	C1356	U1295	U1233	U1169	C1109	G1047	G987	U927	A860	U800	A739
U1417	U1417	C1357	C1357	C1296	G1234	A1170	G1110	C1048	A988	U928	C861	C801	G740
C1418	C1418	U1358	G1297	G1297	A1235	G1171	G1111	U1049	A989	U929	U862	G802	G741
U1479	C1419	G1359	G1298	G1298	C1236	G1172	G1112	G1050	G990	G931	A863	G803	G742
U1420	U1420	C1360	C1299	C1299	C1237	U1173	G1113	C1051	G991	A931	C864	G804	G743
A1421	U1421	C1361	C1300	C1300	C1238	C1174	G1114	C1052	U992	U932	G865	C805	A744
C1422	A1482	C1422	C1362	G1301	U1238	A1175	G1115	A1053	C993	U933	G866	G806	G745
G1483	G1483	G1423	C1363	C1302	G1240	A1176	A1116	C1054	U994	G934	C867	A807	C746
G1424	A1484	G1424	U1364	G1303	A1241	U1177	G1117	U1055	U995	G935	C868	G808	G747
A1425	G1485	A1425	U1365	U1304	A1242	A1178	G1118	U1056	G996	A936	G869	C809	A748
G1486	G1486	A1426	G1366	G1305	A1243	U1179	G1119	A1057	C997	U937	C870	U810	A749
A1487	A1487	G1427	C1367	A1306	G1244	G1180	A1120	A1058	C998	U938	A871	U811	C750
A1488	A1488	C1428	U1368	A1307	G1245	G1181	C1121	C1059	C999	C939	A872	C812	U751

• Molecule 2: 30S ribosomal protein S3Ae

Chain A:



NET	ALA	LYS	ARG	ARG	VAL	SER	ALA	ALA	K11	D12	K13	W14	K15	L16	K17	Q18	I22	Y23	A24	F27	V31	V32	V33	A38	D39	E42	K43	V44	L45	N46	R47	V48	V49	E50	V51	T52	L53	K54	D55	G58	D59	F60	H64	F69	Q70	G71	Y72	D73	V74	K75
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



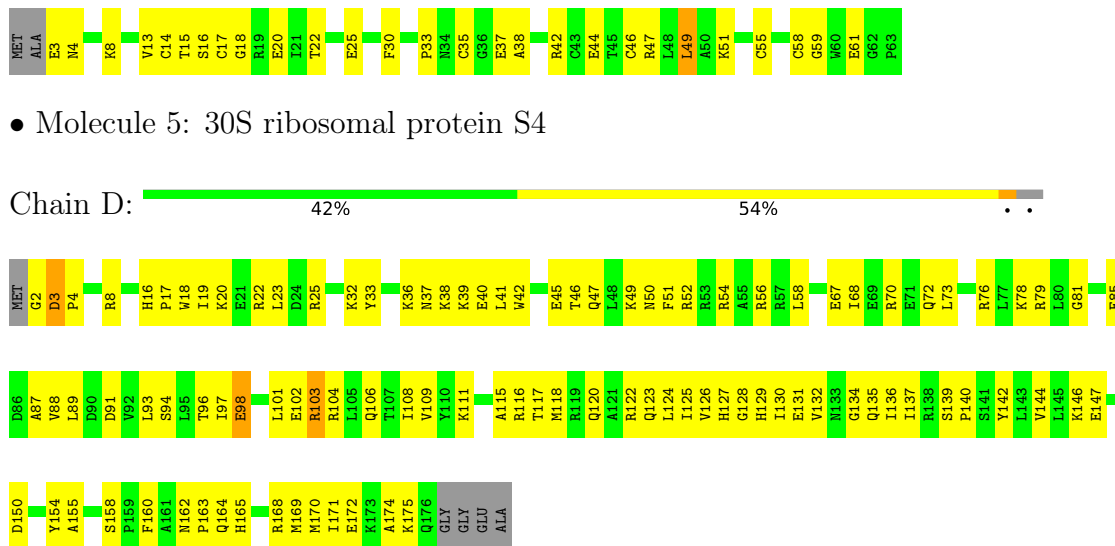
• Molecule 3: 30S ribosomal protein S2

Chain B: 56% 41%



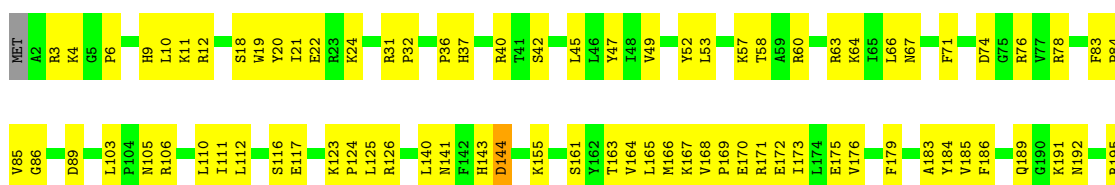
• Molecule 4: Zn-ribbon RNA-binding protein involved in translation

Chain C: 54% 41%



• Molecule 6: 30S ribosomal protein S4e

Chain E: 58% 42%





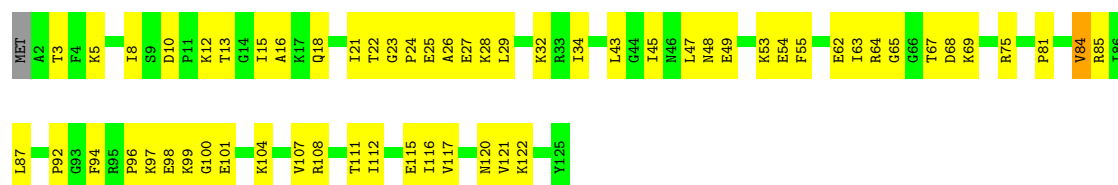
• Molecule 7: 30S ribosomal protein S5

Chain F: 53% 44%



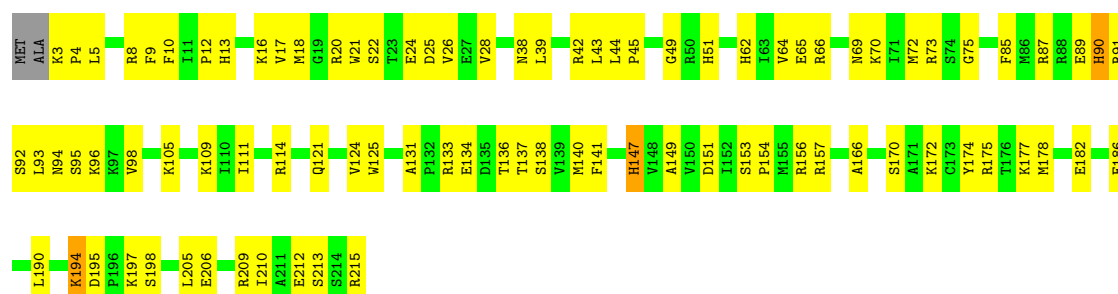
• Molecule 8: 30S ribosomal protein S6e

Chain G: 52% 46%



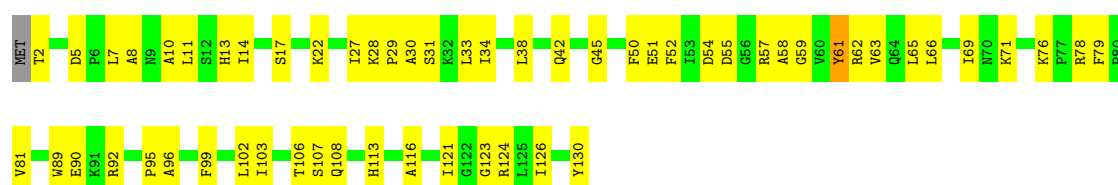
• Molecule 9: 30S ribosomal protein S7

Chain H: 58% 40%

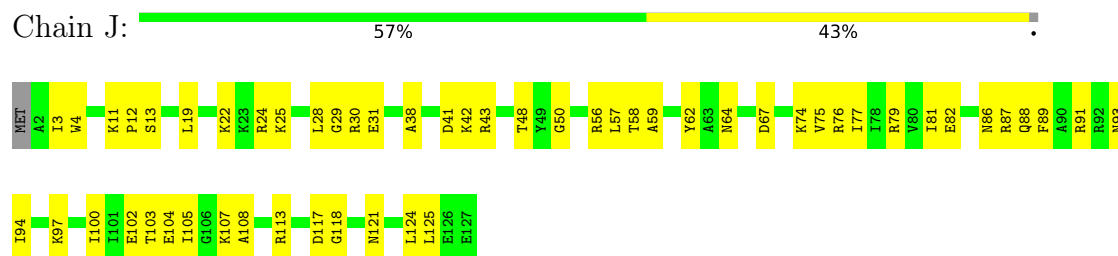


• Molecule 10: 30S ribosomal protein S8

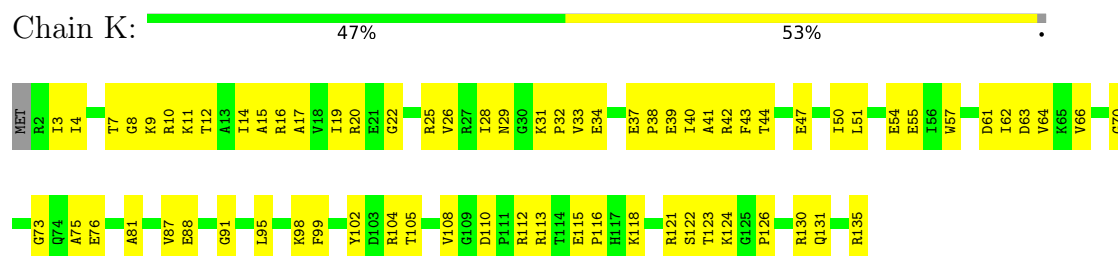
Chain I: 55% 43%



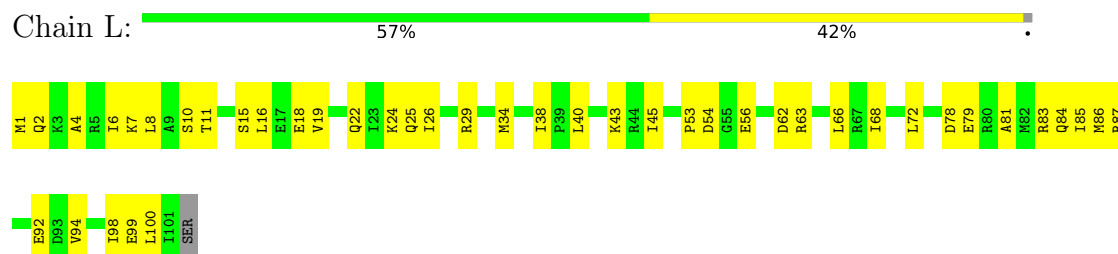
- Molecule 11: 30S ribosomal protein S8e



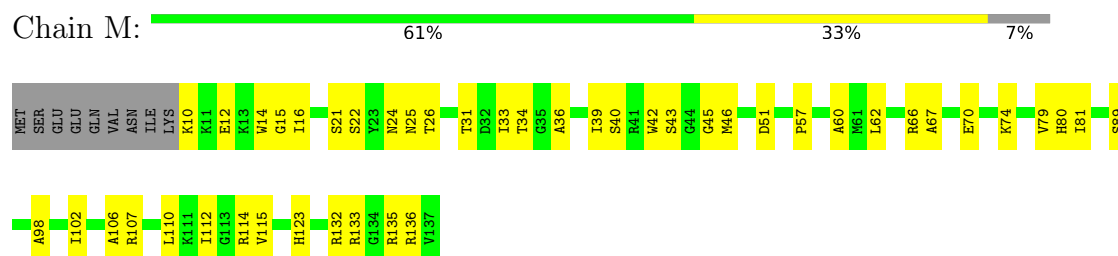
- Molecule 12: 30S ribosomal protein S9



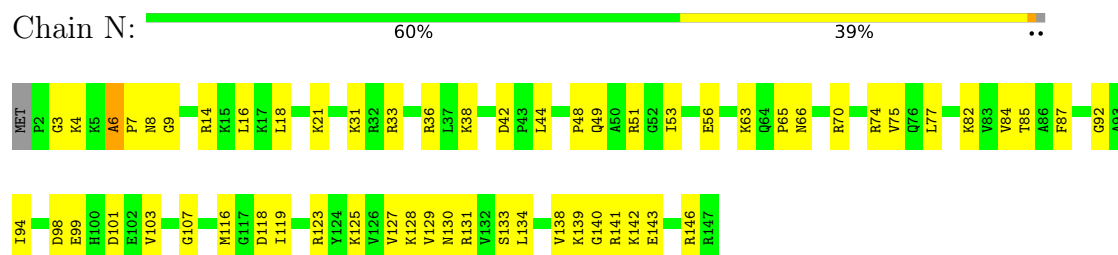
- Molecule 13: 30S ribosomal protein S10



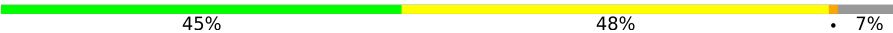
- Molecule 14: 30S ribosomal protein S11

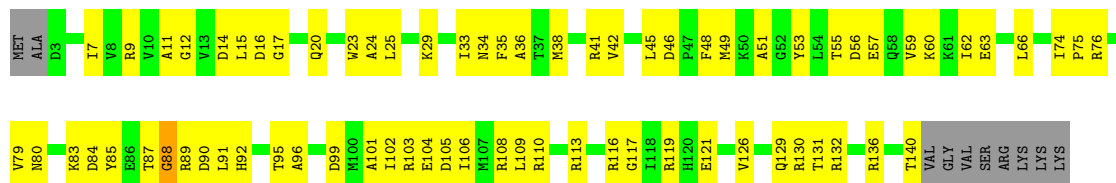


- Molecule 15: 30S ribosomal protein S12

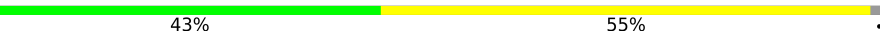


- Molecule 16: 30S ribosomal protein S13

Chain O:  45% 48% 7%



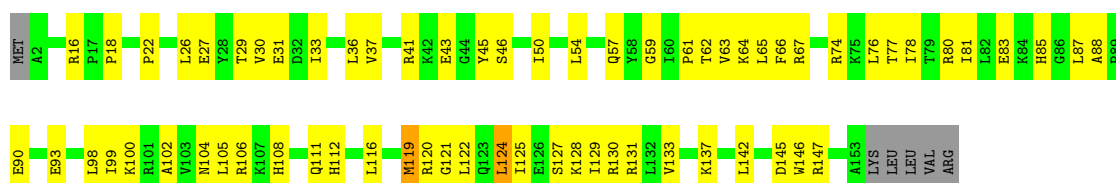
- Molecule 17: 30S ribosomal protein S14 type Z

Chain P:  43% 55%



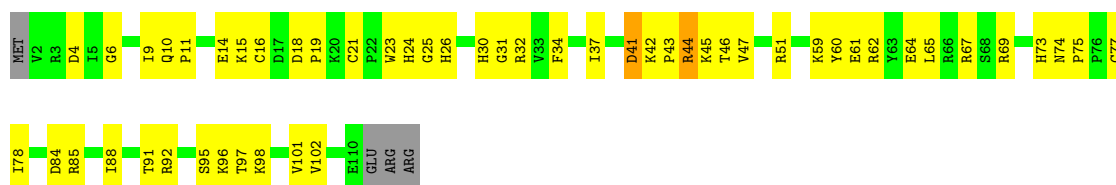
- Molecule 18: 30S ribosomal protein S15

Chain Q:  54% 41%



- Molecule 19: 30S ribosomal protein S17

Chain R:  50% 44%



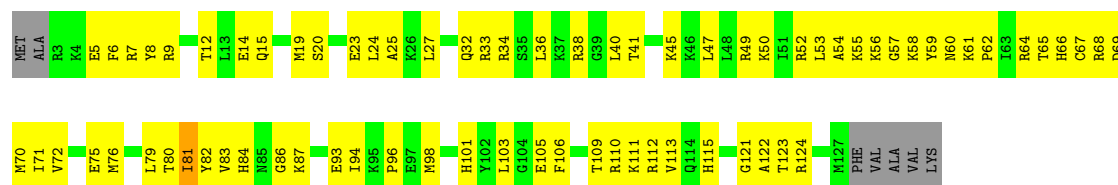
- Molecule 20: 30S ribosomal protein S17e

Chain S:  55% 43%



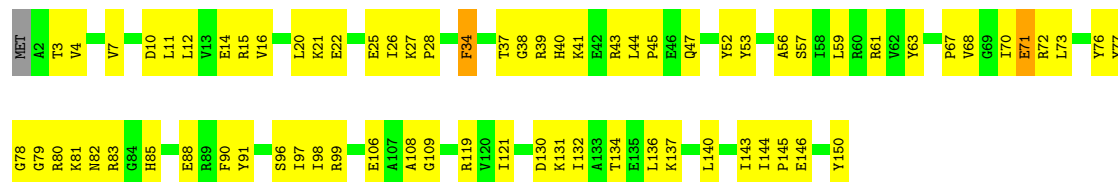
- Molecule 21: 30S ribosomal protein S19

Chain T:  39% 55% 5%



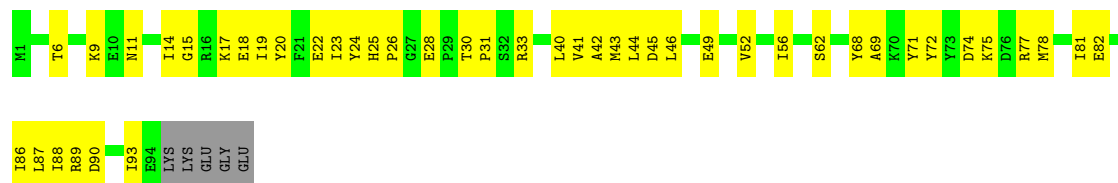
• Molecule 22: 30S ribosomal protein S19e

Chain U: 51% 47%



• Molecule 23: 30S ribosomal protein S24e

Chain V: 49% 45% 5%



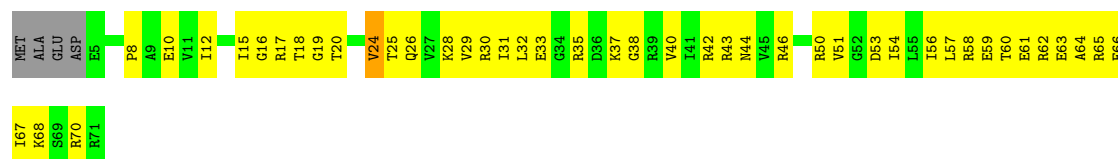
• Molecule 24: 30S ribosomal protein S27e

Chain W: 57% 40%



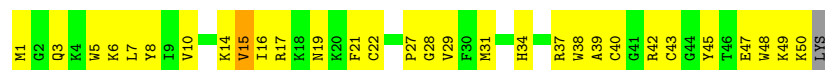
• Molecule 25: 30S ribosomal protein S28e

Chain X: 32% 61% 6%

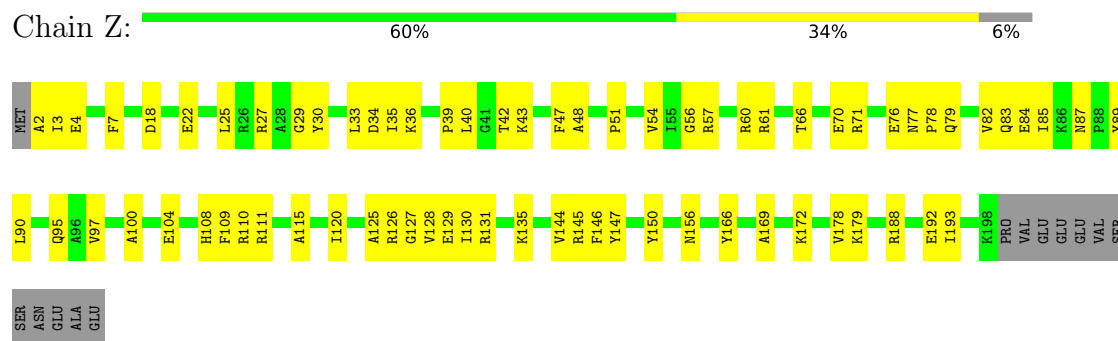


• Molecule 26: 30S ribosomal protein S27ae

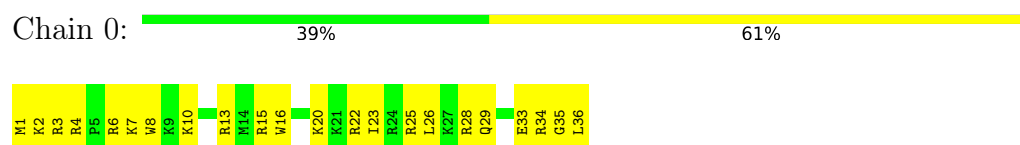
Chain Y: 39% 57%



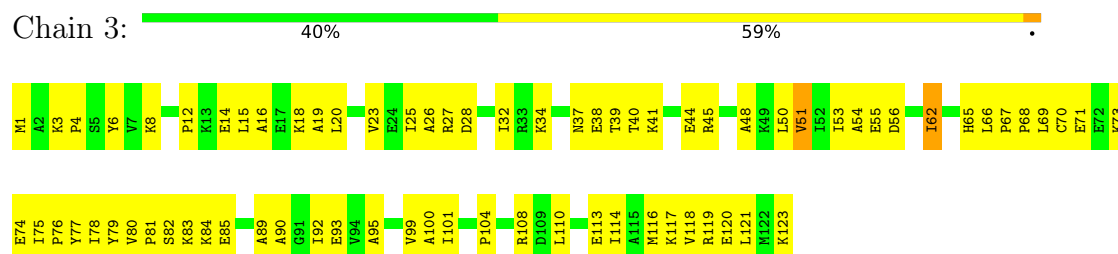
- Molecule 27: 30S ribosomal protein S3



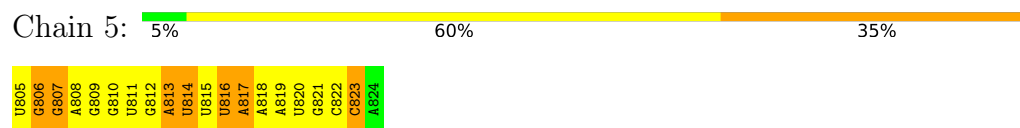
- Molecule 28: 50S ribosomal protein L41e



- Molecule 29: 50S ribosomal protein L7Ae



- Molecule 30: mRNA



- Molecule 31: initiator Met-tRNA fMet from E. coli (A1U72 variant)

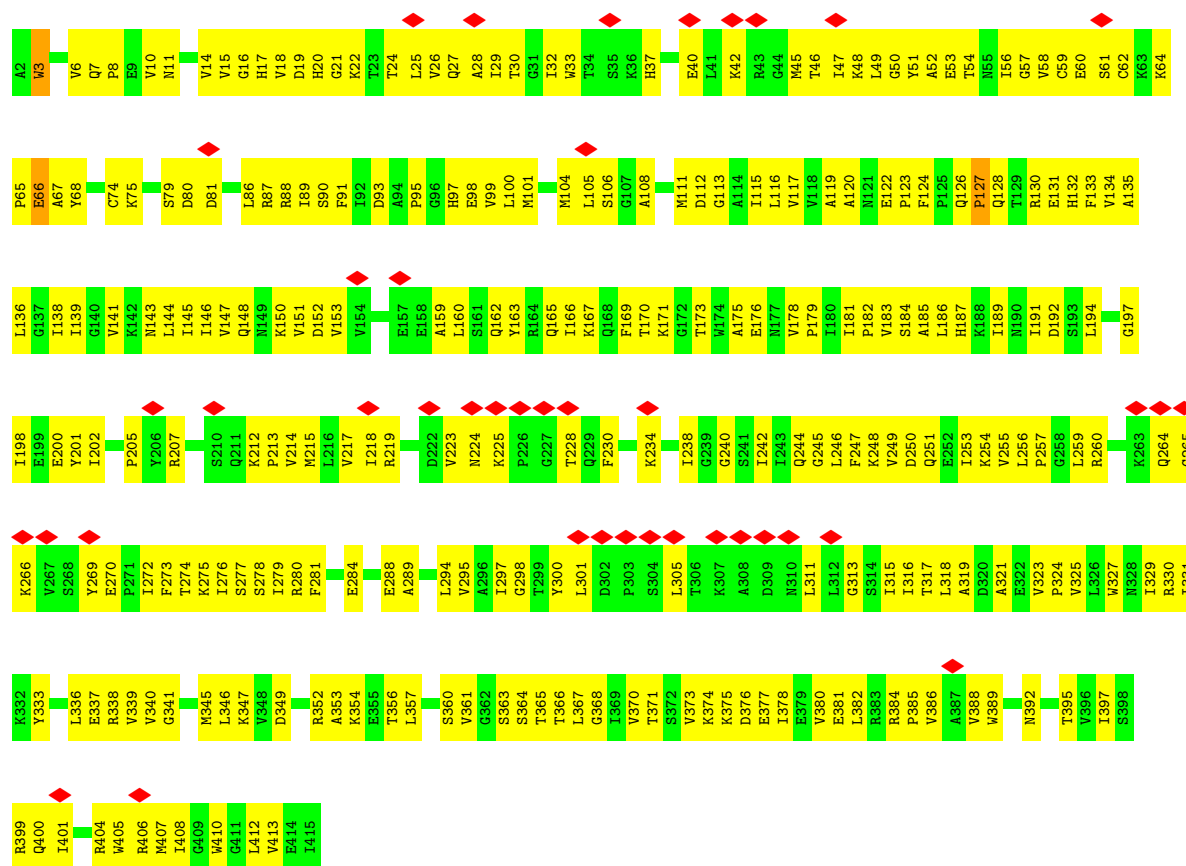


- Molecule 32: Translation initiation factor 1A

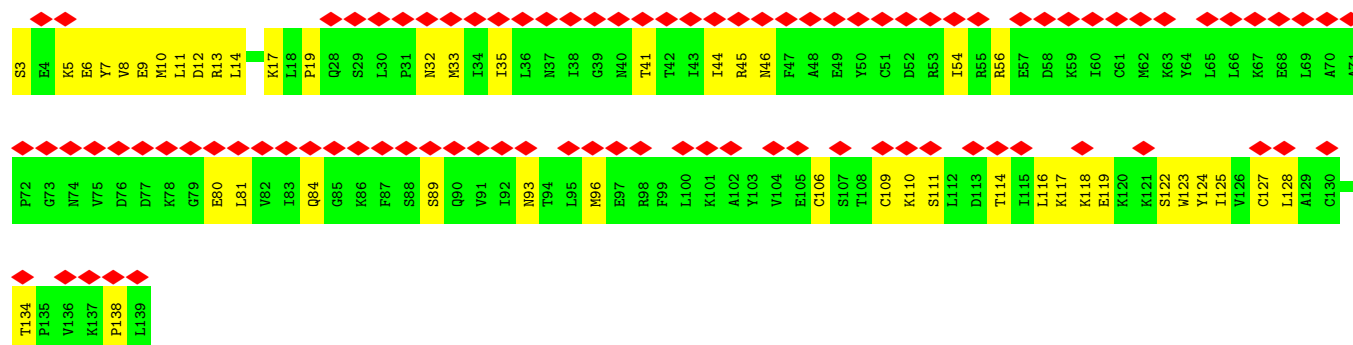




• Molecule 33: Translation initiation factor 2 subunit gamma

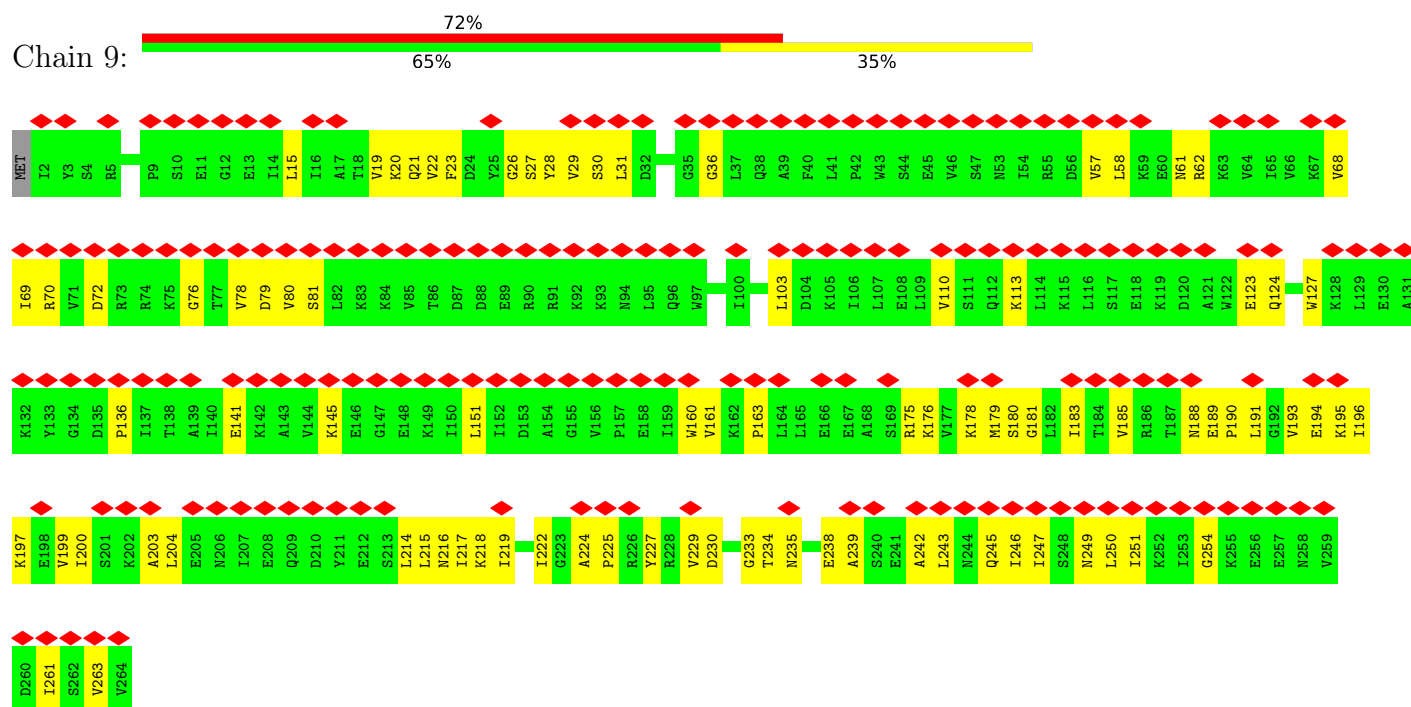


• Molecule 34: Translation initiation factor 2 subunit beta



● Molecule 35: Translation initiation factor 2 subunit alpha

Chain 9:



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	34000	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.044	Depositor
Minimum map value	-0.007	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.004	Depositor
Map size (Å)	379.32, 379.32, 379.32	wwPDB
Map dimensions	348, 348, 348	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.09, 1.09, 1.09	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: 5MU, MA6, LHH, OMC, 5MC, A2M, PSU, 5HM, MG, 6MZ, 4AC, H2U, GNP, UR3, B8H, 4SU, ZN

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	2	0.60	0/35019	0.59	0/54586
2	A	0.56	0/1559	0.72	0/2090
3	B	0.55	1/1602 (0.1%)	0.72	0/2165
4	C	0.51	0/496	0.64	0/673
5	D	0.60	1/1494 (0.1%)	0.72	0/2003
6	E	0.57	0/2032	0.74	2/2742 (0.1%)
7	F	0.64	0/1838	0.78	3/2478 (0.1%)
8	G	0.44	0/993	0.64	0/1329
9	H	0.52	1/1757 (0.1%)	0.71	0/2359
10	I	0.65	0/1055	0.85	0/1415
11	J	0.53	0/1005	0.76	0/1339
12	K	0.52	0/1081	0.73	0/1449
13	L	0.46	0/825	0.66	0/1107
14	M	0.53	0/982	0.72	0/1322
15	N	0.59	0/1165	0.78	2/1547 (0.1%)
16	O	0.49	0/1135	0.74	0/1526
17	P	0.50	0/465	0.77	1/613 (0.2%)
18	Q	0.53	0/1290	0.66	0/1734
19	R	0.61	1/923 (0.1%)	0.72	0/1247
20	S	0.46	0/565	0.60	0/747
21	T	0.49	0/1037	0.72	0/1385
22	U	0.49	0/1253	0.72	1/1689 (0.1%)
23	V	0.52	0/808	0.71	0/1086
24	W	0.47	0/488	0.73	0/659
25	X	0.46	0/538	0.68	0/719
26	Y	0.32	0/420	0.65	0/559
27	Z	0.49	0/1572	0.67	1/2110 (0.0%)
28	0	0.63	0/349	0.86	0/451
29	3	0.34	0/953	0.75	1/1284 (0.1%)
30	5	0.48	0/481	0.50	0/748
31	4	0.44	1/1699 (0.1%)	0.54	0/2648

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	6	0.41	0/793	0.73	0/1072
33	7	0.33	0/3272	0.66	0/4430
34	8	0.16	0/1045	0.39	0/1400
35	9	0.18	0/2050	0.42	1/2760 (0.0%)
All	All	0.54	5/74039 (0.0%)	0.64	12/107471 (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
7	F	0	1
18	Q	0	1
All	All	0	2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	H	194	LYS	C-N	-8.22	1.20	1.33
19	R	41	ASP	CA-CB	-5.61	1.36	1.53
3	B	30	LYS	CA-C	-5.24	1.45	1.52
5	D	98	GLU	CA-C	-5.17	1.45	1.52
31	4	8	4SU	O3'-P	5.04	1.61	1.56

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	N	143	GLU	CA-C-N	-7.82	107.21	122.70
15	N	143	GLU	C-N-CA	-7.82	107.21	122.70
17	P	46	VAL	N-CA-C	-7.05	106.43	113.20
27	Z	3	ILE	N-CA-C	-6.35	107.06	113.47
7	F	165	LEU	CA-C-N	-6.26	117.02	122.96
7	F	165	LEU	C-N-CA	-6.26	117.02	122.96
22	U	38	GLY	N-CA-C	5.94	119.31	111.70
6	E	49	VAL	CA-C-N	-5.64	113.39	122.24
6	E	49	VAL	C-N-CA	-5.64	113.39	122.24
35	9	222	ILE	N-CA-C	-5.09	108.54	113.53
29	3	62	ILE	N-CA-C	-5.04	107.55	112.29
7	F	170	VAL	N-CA-C	-5.01	106.56	111.77

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	F	5	TRP	Peptide
18	Q	106	ARG	Peptide

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	32291	0	16316	2019	0
2	A	1533	0	1627	100	0
3	B	1571	0	1630	70	0
4	C	482	0	461	25	0
5	D	1470	0	1542	99	0
6	E	1983	0	2060	82	0
7	F	1808	0	1879	92	0
8	G	977	0	1037	58	0
9	H	1720	0	1775	92	0
10	I	1034	0	1069	58	0
11	J	996	0	1076	52	0
12	K	1065	0	1121	75	0
13	L	817	0	871	34	0
14	M	964	0	994	43	0
15	N	1148	0	1248	46	0
16	O	1116	0	1152	76	0
17	P	455	0	475	30	0
18	Q	1262	0	1331	54	0
19	R	900	0	921	54	0
20	S	558	0	595	33	0
21	T	1018	0	1086	74	0
22	U	1223	0	1263	63	0
23	V	790	0	806	40	0
24	W	481	0	512	21	0
25	X	536	0	571	44	0
26	Y	408	0	413	35	0
27	Z	1550	0	1637	58	0
28	0	343	0	407	24	0
29	3	941	0	994	91	0
30	5	430	0	215	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	4	1622	0	830	134	0
32	6	777	0	806	54	0
33	7	3213	0	3331	347	0
34	8	1032	0	1073	41	0
35	9	2025	0	2133	80	0
36	2	31	0	0	0	0
36	4	1	0	0	0	0
36	5	1	0	0	0	0
36	7	1	0	0	0	0
37	C	2	0	0	0	0
37	F	1	0	0	0	0
37	P	1	0	0	0	0
37	R	1	0	0	0	0
37	W	1	0	0	0	0
38	7	8	0	8	2	0
39	7	32	0	13	4	0
40	2	40	0	0	18	0
40	K	1	0	0	0	0
40	Q	1	0	0	0	0
All	All	70661	0	55278	3945	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 32.

All (3945) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:140:A:N6	1:2:229:G:H1	1.36	1.23
33:7:213:PRO:HA	33:7:244:GLN:O	1.39	1.22
33:7:240:GLY:O	33:7:294:LEU:HA	1.57	1.04
31:4:74:C:H41	33:7:33:TRP:CD1	1.75	1.03
1:2:1300:C:OP1	22:U:39:ARG:NH2	1.96	0.97
1:2:465:G:O6	1:2:512:G:N2	1.99	0.95
31:4:74:C:H41	33:7:33:TRP:NE1	1.65	0.93
31:4:21:A:O2'	31:4:22:G:N7	2.01	0.92
1:2:337:C:N3	11:J:25:LYS:NZ	2.18	0.92
1:2:1262:A:H2'	1:2:1263:A:H8	1.36	0.91
1:2:17:4AC:O7	7:F:192:ARG:NH2	2.04	0.91
1:2:520:G:OP1	15:N:38:LYS:NZ	2.04	0.91
1:2:321:G:H2'	1:2:322:A:H8	1.37	0.90
1:2:1229:G:N2	1:2:1233:4AC:O2	2.04	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:46:G:H2'	1:2:47:G:H8	1.36	0.89
31:4:3:C:O2	31:4:71:C:N4	2.05	0.89
1:2:849:G:OP2	15:N:4:LYS:NZ	2.06	0.89
1:2:1134:G:OP1	20:S:5:ARG:NH2	2.06	0.88
1:2:1020:A:N3	27:Z:135:LYS:NZ	2.20	0.88
7:F:133:CYS:SG	7:F:139:HIS:CE1	2.60	0.88
1:2:17:4AC:H5	7:F:192:ARG:HH21	1.39	0.87
1:2:651:G:OP1	2:A:43:LYS:NZ	2.07	0.86
23:V:23:ILE:HD13	23:V:31:PRO:HG2	1.57	0.86
1:2:262:U:H2'	1:2:263:G:H8	1.38	0.86
1:2:1342:G:OP2	13:L:63:ARG:NH1	2.09	0.86
23:V:43:MET:HG2	23:V:44:LEU:HD12	1.56	0.86
33:7:325:VAL:HB	33:7:385:PRO:HB2	1.58	0.86
29:3:27:ARG:HH11	29:3:90:ALA:HA	1.41	0.85
1:2:1400:C:O2	1:2:1443:G:N2	2.09	0.85
1:2:300:G:N2	1:2:319:4AC:N3	2.25	0.85
33:7:98:GLU:HA	33:7:101:MET:HB2	1.58	0.85
1:2:333:G:N2	1:2:336:A:OP2	2.08	0.84
9:H:131:ALA:HB1	9:H:157:ARG:HB3	1.59	0.84
33:7:152:ASP:OD2	33:7:187:HIS:ND1	2.10	0.84
1:2:1271:U:H4'	1:2:1273:A:H2	1.43	0.84
1:2:1417:U:H2'	1:2:1418:C:C6	2.13	0.83
1:2:1453:G:N7	33:7:352:ARG:NH1	2.26	0.83
20:S:5:ARG:O	20:S:10:LYS:NZ	2.10	0.83
15:N:77:LEU:HD12	15:N:82:LYS:HB2	1.61	0.83
34:8:8:VAL:HA	34:8:11:LEU:HB3	1.61	0.83
33:7:59:CYS:H	33:7:67:ALA:HB1	1.44	0.83
9:H:26:VAL:HG12	9:H:121:GLN:HB2	1.58	0.82
26:Y:47:GLU:O	26:Y:50:LYS:NZ	2.12	0.82
1:2:1480:G:OP1	28:0:20:LYS:NZ	2.11	0.82
29:3:56:ASP:HB3	29:3:83:LYS:HE3	1.61	0.82
1:2:876:U:OP2	28:0:2:LYS:NZ	2.13	0.82
1:2:1425:G:H2'	1:2:1426:A:H8	1.44	0.82
4:C:17:CYS:SG	4:C:18:GLY:N	2.52	0.82
13:L:83:ARG:HG2	13:L:87:ARG:HH12	1.45	0.82
31:4:18:G:N1	31:4:55:PSU:O2'	2.11	0.82
1:2:1453:G:C5	33:7:352:ARG:HD2	2.14	0.82
1:2:1389:C:N3	1:2:1454:G:N1	2.27	0.81
33:7:27:GLN:HE21	33:7:33:TRP:HB3	1.45	0.81
1:2:702:C:H2'	1:2:703:4AC:H6	1.59	0.81
29:3:18:LYS:HB3	29:3:110:LEU:HD22	1.62	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:7:339:VAL:HB	33:7:345:MET:HA	1.62	0.81
1:2:784:G:O6	1:2:1498:C:N4	2.14	0.81
33:7:365:THR:H	33:7:384:ARG:HH11	1.28	0.81
1:2:1233:4AC:N3	1:2:1251:G:N1	2.29	0.81
33:7:48:LYS:NZ	33:7:49:LEU:O	2.14	0.81
33:7:277:SER:N	33:7:298:GLY:O	2.13	0.81
1:2:478:C:H2'	1:2:479:4AC:H6	1.61	0.81
1:2:998:C:H2'	1:2:999:G:H8	1.46	0.81
7:F:153:ARG:HB2	7:F:188:LEU:HD12	1.62	0.81
13:L:62:ASP:OD1	17:P:54:LYS:NZ	2.14	0.81
1:2:126:A:N6	1:2:194:A:N7	2.29	0.81
1:2:1389:C:N4	1:2:1454:G:O6	2.12	0.81
33:7:361:VAL:HB	33:7:364:SER:HB2	1.60	0.81
1:2:1204:C:O2'	21:T:124:ARG:NH1	2.13	0.81
1:2:641:G:OP1	2:A:119:ARG:NH1	2.14	0.80
18:Q:137:LYS:NZ	18:Q:146:TRP:O	2.14	0.80
1:2:1400:C:N3	1:2:1443:G:N1	2.25	0.80
1:2:1034:C:OP2	40:2:1701:HOH:O	1.98	0.80
22:U:27:LYS:NZ	22:U:28:PRO:O	2.14	0.80
1:2:1219:G:OP2	22:U:41:LYS:NZ	2.14	0.80
4:C:22:THR:N	4:C:25:GLU:OE2	2.13	0.80
2:A:52:THR:H	14:M:114:ARG:HH22	1.30	0.80
1:2:869:G:O2'	1:2:871:A:N6	2.13	0.80
25:X:16:GLY:O	25:X:26:GLN:N	2.14	0.80
1:2:423:U:OP2	1:2:424:C:N4	2.13	0.80
15:N:65:PRO:O	15:N:66:ASN:ND2	2.15	0.80
33:7:17:HIS:HE1	33:7:97:HIS:HD2	1.30	0.80
29:3:104:PRO:O	29:3:108:ARG:NH1	2.13	0.80
1:2:1290:G:N2	1:2:1293:A:OP2	2.15	0.79
1:2:49:G:N2	1:2:409:C:O2	2.15	0.79
1:2:1395:G:H1'	1:2:1449:G:H22	1.47	0.79
19:R:75:PRO:HD2	19:R:78:ILE:HD11	1.62	0.79
5:D:155:ALA:HB3	5:D:158:SER:HB2	1.65	0.79
1:2:861:G:H3'	28:0:1:MET:HE2	1.64	0.79
18:Q:26:LEU:HD11	18:Q:61:PRO:HD2	1.63	0.79
25:X:42:ARG:NH1	25:X:66:GLU:OE1	2.15	0.79
1:2:311:C:H2'	1:2:312:G:H8	1.48	0.79
1:2:1083:C:H2'	1:2:1084:C:H6	1.47	0.79
1:2:1262:A:H2'	1:2:1263:A:C8	2.17	0.79
1:2:1191:C:OP1	17:P:9:ARG:NH2	2.15	0.79
1:2:581:C:H2'	1:2:582:G:H8	1.47	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:627:G:H2'	1:2:628:G:C8	2.18	0.79
1:2:16:C:N4	1:2:32:G:O6	2.16	0.79
1:2:26:C:OP1	7:F:151:SER:OG	1.99	0.79
1:2:1137:G:O6	1:2:1147:4AC:N4	2.15	0.79
21:T:19:MET:HG2	21:T:20:SER:H	1.46	0.79
1:2:695:A:H2'	1:2:696:A:C8	2.18	0.79
10:I:5:ASP:OD2	10:I:8:ALA:N	2.16	0.79
33:7:74:CYS:HB3	33:7:79:SER:HB3	1.64	0.79
1:2:782:A:OP1	28:0:3:ARG:NH2	2.16	0.78
1:2:817:U:OP1	2:A:128:ARG:NH2	2.15	0.78
1:2:1460:G:H21	32:6:36:TRP:HE1	1.28	0.78
31:4:22:G:O2'	31:4:23:C:O4'	2.02	0.78
1:2:93:C:H2'	1:2:94:G:H8	1.47	0.78
1:2:372:A:OP2	15:N:51:ARG:NH1	2.16	0.78
1:2:381:C:H42	1:2:398:A:H62	1.30	0.78
1:2:547:G:N7	40:2:1711:HOH:O	2.16	0.78
1:2:1415:U:O2	1:2:1428:G:N2	2.15	0.78
16:O:9:ARG:NH1	16:O:12:GLY:O	2.15	0.78
1:2:46:G:H2'	1:2:47:G:C8	2.18	0.78
1:2:303:4AC:H2'	1:2:304:G:H8	1.48	0.78
1:2:1131:A:H62	1:2:1151:G:H22	1.29	0.78
22:U:14:GLU:OE1	22:U:53:TYR:OH	2.01	0.78
1:2:879:A:H2'	1:2:880:A:H8	1.48	0.78
1:2:1197:C:OP1	21:T:110:ARG:NH1	2.16	0.78
23:V:72:TYR:OH	23:V:82:GLU:OE2	2.01	0.78
1:2:187:G:O6	1:2:200:C:N4	2.17	0.78
1:2:321:G:H2'	1:2:322:A:C8	2.18	0.78
29:3:118:VAL:HA	29:3:121:LEU:HB2	1.66	0.78
20:S:32:LYS:O	20:S:47:ARG:NH1	2.16	0.78
31:4:29:G:H2'	31:4:30:G:H8	1.49	0.78
16:O:105:ASP:OD1	16:O:108:ARG:NH1	2.16	0.77
31:4:5:G:H2'	31:4:6:G:C8	2.19	0.77
1:2:359:C:H3'	1:2:360:G:H21	1.49	0.77
1:2:1311:G:OP2	9:H:85:PHE:N	2.15	0.77
1:2:1358:U:N3	1:2:1359:G:N7	2.32	0.77
29:3:3:LYS:HD3	29:3:4:PRO:HD2	1.65	0.77
34:8:5:LYS:O	34:8:9:GLU:HB2	1.84	0.77
1:2:1488:MA6:OP1	28:0:22:ARG:NH1	2.17	0.77
27:Z:144:VAL:HG12	27:Z:145:ARG:H	1.49	0.77
33:7:66:GLU:OE1	34:8:17:LYS:NZ	2.18	0.77
33:7:75:LYS:HG2	34:8:124:TYR:HB2	1.67	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:372:A:H2'	1:2:373:A2M:H8	1.65	0.77
1:2:1211:C:OP2	9:H:91:ARG:NH1	2.18	0.77
16:O:16:ASP:OD1	16:O:17:GLY:N	2.16	0.77
2:A:54:LYS:HA	2:A:58:GLY:HA3	1.67	0.76
33:7:51:TYR:CZ	33:7:294:LEU:HB3	2.21	0.76
35:9:235:ASN:ND2	35:9:238:GLU:OE2	2.17	0.76
26:Y:29:VAL:HG12	29:3:41:LYS:HD3	1.66	0.76
7:F:93:ASP:O	7:F:126:ARG:NH2	2.19	0.76
9:H:72:MET:HA	9:H:93:LEU:HD12	1.66	0.76
32:6:48:ARG:HG3	32:6:78:LYS:HG2	1.67	0.76
1:2:119:C:O3'	1:2:299:G:N2	2.18	0.76
33:7:74:CYS:O	33:7:79:SER:N	2.18	0.76
1:2:1349:A:O3'	9:H:70:LYS:NZ	2.18	0.76
35:9:180:SER:OG	35:9:230:ASP:OD1	2.04	0.76
19:R:95:SER:OG	19:R:96:LYS:N	2.19	0.76
1:2:906:U:H5''	1:2:907:A:H5''	1.67	0.75
1:2:948:G:OP1	40:2:1702:HOH:O	2.04	0.75
30:5:823:C:O2'	32:6:57:ARG:NH1	2.18	0.75
1:2:263:G:H4'	19:R:46:THR:HG21	1.68	0.75
10:I:31:SER:H	10:I:34:ILE:HD12	1.51	0.75
33:7:98:GLU:HB2	33:7:128:GLN:HE21	1.51	0.75
1:2:975:G:H4'	26:Y:1:MET:HE3	1.68	0.75
1:2:1399:C:N4	1:2:1444:G:O6	2.15	0.75
5:D:36:LYS:N	5:D:40:GLU:OE1	2.19	0.75
1:2:1136:C:N4	1:2:1148:G:O6	2.15	0.75
33:7:260:ARG:NH2	33:7:269:TYR:OH	2.19	0.75
9:H:43:LEU:N	12:K:102:TYR:OH	2.20	0.75
19:R:37:ILE:HG22	19:R:85:ARG:HG2	1.69	0.75
1:2:632:A:H62	1:2:691:G:H1	1.32	0.75
1:2:1206:C:O2'	12:K:130:ARG:NH2	2.19	0.75
8:G:75:ARG:HD2	8:G:92:PRO:HG2	1.69	0.75
1:2:203:A:H2'	1:2:204:G:H8	1.51	0.74
1:2:1415:U:H3	1:2:1428:G:H1	1.35	0.74
11:J:104:GLU:HG3	11:J:105:ILE:HG23	1.70	0.74
27:Z:2:ALA:N	27:Z:4:GLU:OE1	2.20	0.74
5:D:78:LYS:O	5:D:146:LYS:NZ	2.17	0.74
29:3:12:PRO:HD2	29:3:15:LEU:HD22	1.68	0.74
1:2:185:G:H2'	1:2:186:G:H8	1.52	0.74
1:2:1010:G:H2'	1:2:1011:A:H8	1.53	0.74
1:2:1425:G:H2'	1:2:1426:A:C8	2.21	0.74
33:7:182:PRO:HB2	34:8:14:LEU:HD22	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1378:5HM:H8	1:2:1379:G:H8	1.52	0.74
1:2:295:G:H2'	1:2:296:U:C6	2.23	0.74
1:2:428:C:H2'	1:2:429:A:H8	1.52	0.74
1:2:531:U:O2'	10:I:92:ARG:NH1	2.20	0.74
1:2:576:U:OP1	6:E:24:LYS:NZ	2.20	0.74
19:R:24:HIS:HE1	19:R:77:CYS:SG	2.03	0.74
33:7:248:LYS:HD3	33:7:288:GLU:HB2	1.68	0.74
1:2:140:A:N1	1:2:229:G:N2	2.34	0.74
1:2:1013:G:N2	1:2:1184:4AC:N3	2.35	0.74
8:G:85:ARG:NH1	8:G:104:LYS:O	2.21	0.74
20:S:14:ARG:O	20:S:18:ASN:ND2	2.19	0.74
33:7:106:SER:HA	33:7:363:SER:HA	1.69	0.74
16:O:57:GLU:HA	16:O:60:LYS:HD3	1.70	0.74
6:E:3:ARG:HE	6:E:4:LYS:HZ3	1.34	0.74
19:R:18:ASP:OD2	19:R:45:LYS:NZ	2.20	0.74
6:E:19:TRP:O	6:E:52:TYR:OH	2.04	0.73
8:G:32:LYS:HB2	8:G:112:ILE:HD12	1.71	0.73
1:2:992:U:OP1	17:P:3:LYS:NZ	2.18	0.73
1:2:1481:U:H2'	1:2:1482:A:H8	1.53	0.73
7:F:105:GLU:OE2	27:Z:110:ARG:NE	2.21	0.73
1:2:643:A:H2'	1:2:644:C:H6	1.54	0.73
1:2:1316:C:O2'	12:K:131:GLN:HG3	1.87	0.73
5:D:171:ILE:HG22	5:D:175:LYS:HZ1	1.54	0.73
27:Z:131:ARG:HH21	27:Z:145:ARG:HB2	1.53	0.73
6:E:144:ASP:N	6:E:144:ASP:OD1	2.21	0.73
1:2:253:U:O4'	1:2:865:G:N2	2.22	0.73
1:2:725:G:N7	40:2:1711:HOH:O	2.21	0.73
23:V:9:LYS:HB3	23:V:18:GLU:HB2	1.71	0.73
1:2:1010:G:H2'	1:2:1011:A:C8	2.23	0.73
3:B:149:TYR:OH	4:C:44:GLU:OE2	2.04	0.73
3:B:73:ARG:HH12	3:B:159:LYS:HE3	1.54	0.72
11:J:103:THR:HG23	11:J:105:ILE:H	1.54	0.72
27:Z:42:THR:OG1	27:Z:77:ASN:O	2.07	0.72
1:2:476:G:O6	1:2:506:C:N4	2.18	0.72
21:T:83:VAL:HG12	21:T:84:HIS:H	1.54	0.72
23:V:6:THR:OG1	23:V:22:GLU:OE1	2.06	0.72
33:7:134:VAL:HG11	33:7:340:VAL:HG21	1.71	0.72
1:2:1214:U:O2'	9:H:91:ARG:O	2.07	0.72
32:6:60:TRP:O	32:6:85:ARG:NH1	2.22	0.72
1:2:262:U:H2'	1:2:263:G:C8	2.24	0.72
1:2:1508:C:O2	30:5:807:G:N2	2.22	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:735:G:H2'	1:2:736:G:H8	1.54	0.72
1:2:1219:G:H2'	1:2:1220:G:H8	1.54	0.72
8:G:68:ASP:OD2	8:G:69:LYS:N	2.23	0.72
17:P:21:CYS:SG	17:P:22:ILE:N	2.62	0.72
27:Z:56:GLY:HA2	27:Z:61:ARG:HD3	1.71	0.72
1:2:930:A:C2	21:T:87:LYS:HB3	2.25	0.72
1:2:1458:G:H2'	1:2:1459:A:H8	1.55	0.72
12:K:17:ALA:HB2	12:K:81:ALA:HB1	1.69	0.72
27:Z:100:ALA:HB1	27:Z:169:ALA:HB2	1.69	0.72
29:3:50:LEU:HD13	29:3:104:PRO:HG3	1.70	0.72
1:2:972:G:O2'	1:2:1001:A:N1	2.23	0.72
1:2:1396:G:H1	1:2:1448:C:H1'	1.55	0.72
28:0:29:GLN:HB3	28:0:33:GLU:CD	2.15	0.72
33:7:184:SER:OG	39:7:502:GNP:O6	2.07	0.72
33:7:197:GLY:HA2	33:7:200:GLU:HG2	1.72	0.72
1:2:333:G:H21	1:2:335:G:H3'	1.54	0.72
28:0:1:MET:HE1	28:0:23:ILE:HG21	1.71	0.72
35:9:179:MET:HE2	35:9:239:ALA:HB3	1.72	0.72
1:2:353:A:OP2	1:2:354:C:N4	2.23	0.72
1:2:859:G:N2	1:2:881:C:N3	2.38	0.72
2:A:52:THR:OG1	2:A:53:LEU:N	2.23	0.72
16:O:11:ALA:N	16:O:63:GLU:OE2	2.23	0.72
23:V:6:THR:N	23:V:20:TYR:O	2.22	0.72
34:8:6:GLU:HA	34:8:9:GLU:HB3	1.72	0.72
1:2:1491:U:OP1	14:M:136:ARG:NH2	2.23	0.71
4:C:3:GLU:HB2	7:F:230:PRO:HD2	1.70	0.71
1:2:361:C:O2'	1:2:363:G:OP1	2.09	0.71
1:2:1400:C:N4	1:2:1443:G:O6	2.20	0.71
3:B:169:TRP:HD1	3:B:195:PHE:HE2	1.37	0.71
14:M:25:ASN:OD1	14:M:26:THR:N	2.20	0.71
1:2:267:G:H2'	1:2:268:G:C8	2.25	0.71
1:2:287:G:OP2	19:R:69:ARG:NH2	2.23	0.71
1:2:955:A:O2'	1:2:1015:G:OP2	2.07	0.71
33:7:144:LEU:HB3	33:7:178:VAL:HG11	1.72	0.71
1:2:834:G:OP1	7:F:153:ARG:NH2	2.21	0.71
1:2:1234:G:H21	1:2:1249:A:H62	1.36	0.71
33:7:191:ILE:HG23	33:7:194:LEU:HD23	1.71	0.71
1:2:1274:G:N2	40:2:1717:HOH:O	2.24	0.71
33:7:56:ILE:HG22	33:7:86:LEU:HD13	1.73	0.71
1:2:112:A:H2'	1:2:113:G:O4'	1.89	0.71
1:2:1273:A:N7	1:2:1275:U:N3	2.39	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:175:GLU:OE2	6:E:235:ARG:NH2	2.23	0.71
33:7:249:VAL:HA	33:7:276:ILE:HB	1.73	0.71
35:9:19:VAL:HA	35:9:29:VAL:HG12	1.71	0.71
1:2:1112:A:H2'	1:2:1113:G:H8	1.55	0.71
3:B:163:ALA:O	3:B:166:LEU:N	2.22	0.71
4:C:14:CYS:HB3	4:C:17:CYS:SG	2.30	0.71
15:N:101:ASP:OD1	15:N:146:ARG:NH1	2.24	0.71
1:2:1182:C:H2'	1:2:1183:C:C6	2.26	0.70
1:2:1260:U:H3	22:U:61:ARG:HH21	1.39	0.70
23:V:74:ASP:OD1	23:V:75:LYS:N	2.24	0.70
28:0:10:LYS:NZ	28:0:13:ARG:O	2.23	0.70
25:X:15:ILE:HD12	25:X:26:GLN:HG3	1.73	0.70
26:Y:31:MET:HA	26:Y:40:CYS:HA	1.71	0.70
1:2:1169:U:H2'	1:2:1171:G:C8	2.26	0.70
35:9:239:ALA:HA	35:9:242:ALA:HB3	1.72	0.70
1:2:222:A:C5	1:2:223:G:H1'	2.27	0.70
2:A:196:GLU:OE1	2:A:196:GLU:N	2.24	0.70
1:2:144:G:O6	1:2:173:C:N4	2.25	0.70
1:2:183:U:H2'	1:2:184:G:H8	1.57	0.70
1:2:973:A:C6	29:3:92:ILE:HG21	2.27	0.70
1:2:1480:G:H1	1:2:1493:C:H42	1.36	0.70
6:E:196:LYS:NZ	6:E:243:PRO:O	2.24	0.70
1:2:93:C:H2'	1:2:94:G:C8	2.26	0.70
1:2:451:A:H3'	1:2:452:G:H8	1.55	0.70
31:4:74:C:N4	33:7:33:TRP:CD1	2.57	0.70
31:4:76:A:H5''	33:7:223:VAL:HG22	1.74	0.70
33:7:49:LEU:HD21	33:7:104:MET:HA	1.74	0.70
1:2:825:U:O4	40:2:1703:HOH:O	2.07	0.70
1:2:926:G:H2'	1:2:927:U:C6	2.27	0.70
1:2:991:G:OP1	17:P:2:ALA:N	2.24	0.70
17:P:41:HIS:O	17:P:44:ARG:N	2.24	0.70
16:O:46:ASP:OD2	16:O:49:MET:N	2.25	0.70
1:2:642:U:OP2	2:A:190:LYS:NZ	2.24	0.69
8:G:87:LEU:HD12	8:G:104:LYS:HZ3	1.57	0.69
16:O:119:ARG:HB2	16:O:126:VAL:HG22	1.74	0.69
21:T:79:LEU:HG	21:T:80:THR:H	1.57	0.69
8:G:10:ASP:OD1	8:G:12:LYS:N	2.25	0.69
12:K:15:ALA:HA	12:K:66:VAL:HG12	1.73	0.69
13:L:43:LYS:HB3	13:L:68:ILE:HB	1.73	0.69
19:R:21:CYS:HB3	19:R:24:HIS:HB2	1.73	0.69
33:7:183:VAL:HG21	33:7:194:LEU:HD22	1.74	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:148:A:C2	1:2:149:A:H1'	2.28	0.69
3:B:70:VAL:O	3:B:118:THR:OG1	2.08	0.69
1:2:903:C:H2'	1:2:904:A:C8	2.27	0.69
1:2:1312:G:H2'	1:2:1313:A:C8	2.27	0.69
1:2:1321:G:H22	1:2:1347:G:H2'	1.56	0.69
1:2:1479:4AC:N3	1:2:1495:G:N2	2.39	0.69
1:2:1494:G:OP2	14:M:132:ARG:NH2	2.26	0.69
11:J:88:GLN:OE1	11:J:91:ARG:NH2	2.25	0.69
12:K:17:ALA:HA	12:K:64:VAL:HG12	1.74	0.69
21:T:32:GLN:N	21:T:32:GLN:OE1	2.25	0.69
14:M:107:ARG:O	25:X:35:ARG:NH2	2.25	0.69
31:4:47:U:H5''	31:4:48:C:H5'	1.74	0.69
31:4:74:C:H5	33:7:33:TRP:HE1	1.39	0.69
1:2:580:A:OP1	5:D:54:ARG:NH2	2.25	0.69
1:2:1334:A:OP2	17:P:32:ARG:NH2	2.26	0.69
1:2:1417:U:H2'	1:2:1418:C:H6	1.55	0.69
21:T:5:GLU:OE2	21:T:7:ARG:NE	2.25	0.69
1:2:627:G:H2'	1:2:628:G:H8	1.56	0.69
1:2:928:U:H1'	21:T:113:VAL:HG23	1.74	0.69
29:3:32:ILE:HD11	29:3:34:LYS:HE3	1.73	0.69
31:4:44:A:H3'	31:4:45:G:C8	2.28	0.69
1:2:1261:A:H2	1:2:1327:G:H1'	1.57	0.69
8:G:75:ARG:HB2	8:G:107:VAL:HG21	1.74	0.69
33:7:331:ILE:HG12	33:7:413:VAL:HG12	1.74	0.69
20:S:47:ARG:HA	20:S:50:ILE:HD12	1.75	0.69
1:2:205:G:O2'	11:J:64:ASN:ND2	2.26	0.69
1:2:1239:4AC:OP2	22:U:99:ARG:NE	2.24	0.69
1:2:1509:U:O2	30:5:806:G:N1	2.26	0.69
33:7:98:GLU:HG2	33:7:406:ARG:HH11	1.58	0.69
34:8:56:ARG:HH22	34:8:116:LEU:HB2	1.58	0.69
1:2:474:A:C4	5:D:18:TRP:NE1	2.61	0.68
9:H:133:ARG:HG3	25:X:58:ARG:HD2	1.75	0.68
16:O:63:GLU:HA	16:O:66:LEU:HD12	1.73	0.68
1:2:966:C:H2'	1:2:967:G:H8	1.59	0.68
2:A:52:THR:N	14:M:114:ARG:HH22	1.90	0.68
34:8:109:CYS:SG	34:8:111:SER:OG	2.50	0.68
18:Q:63:VAL:O	18:Q:65:LEU:N	2.25	0.68
31:4:18:G:OP2	31:4:60:U:O2'	2.07	0.68
35:9:31:LEU:O	35:9:36:GLY:HA2	1.94	0.68
1:2:466:G:N3	1:2:467:G:N2	2.42	0.68
1:2:731:4AC:C2	1:2:732:G:C8	2.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:202:ILE:HG12	6:E:213:VAL:HG12	1.73	0.68
1:2:344:C:H2'	1:2:345:C:H6	1.58	0.68
1:2:554:G:H2'	1:2:555:G:H8	1.57	0.68
1:2:1155:G:O2'	1:2:1156:G:O5'	2.10	0.68
5:D:171:ILE:O	5:D:175:LYS:NZ	2.24	0.68
10:I:27:ILE:HB	10:I:61:TYR:HB2	1.75	0.68
33:7:30:THR:HG21	33:7:52:ALA:HB1	1.75	0.68
1:2:413:G:O2'	1:2:463:A:N1	2.21	0.68
1:2:814:A:H1'	2:A:134:GLN:HE21	1.57	0.68
1:2:957:4AC:O7	1:2:957:4AC:H5	1.91	0.68
7:F:122:ILE:HD13	7:F:206:TYR:HD1	1.59	0.68
1:2:154:G:OP1	8:G:18:GLN:NE2	2.23	0.68
1:2:458:G:H3'	1:2:459:G:H8	1.59	0.68
1:2:759:A:O2'	1:2:761:A:N6	2.17	0.68
1:2:786:A:N6	1:2:1498:C:N3	2.42	0.68
31:4:43:A:H2'	31:4:44:A:H8	1.59	0.68
1:2:299:G:OP1	40:2:1704:HOH:O	2.11	0.68
35:9:183:ILE:HG13	35:9:227:TYR:HB2	1.75	0.68
1:2:163:G:H2'	1:2:164:G:H8	1.59	0.68
1:2:529:A:O2'	1:2:532:G:O2'	2.12	0.68
1:2:930:A:H2	21:T:87:LYS:HB3	1.58	0.68
1:2:1083:C:H2'	1:2:1084:C:C6	2.29	0.68
1:2:1240:G:OP2	22:U:99:ARG:NH2	2.27	0.68
6:E:42:SER:HA	6:E:85:VAL:O	1.93	0.68
19:R:15:LYS:HD2	19:R:24:HIS:HD2	1.59	0.68
1:2:926:G:H2'	1:2:927:U:H6	1.59	0.68
5:D:168:ARG:NH1	5:D:172:GLU:OE2	2.27	0.68
12:K:12:THR:H	12:K:113:ARG:HH22	1.41	0.68
33:7:150:LYS:HB3	33:7:153:VAL:HG12	1.75	0.68
1:2:89:G:H3'	1:2:90:G:H8	1.59	0.67
1:2:925:G:H21	21:T:122:ALA:HB1	1.56	0.67
5:D:172:GLU:HA	5:D:175:LYS:HE2	1.75	0.67
29:3:50:LEU:HB2	29:3:101:ILE:HG12	1.75	0.67
35:9:239:ALA:O	35:9:243:LEU:N	2.27	0.67
12:K:104:ARG:HE	12:K:108:VAL:HG21	1.58	0.67
1:2:1279:G:N3	1:2:1305:G:N2	2.41	0.67
17:P:29:PRO:HB2	17:P:40:ARG:HB3	1.76	0.67
1:2:1183:C:O2'	1:2:1188:A:N6	2.27	0.67
17:P:4:ALA:O	17:P:8:LYS:NZ	2.27	0.67
1:2:976:A:OP2	1:2:1000:G:N2	2.28	0.67
33:7:60:GLU:N	33:7:60:GLU:OE2	2.26	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:K:55:GLU:OE1	12:K:55:GLU:N	2.28	0.67
33:7:330:ARG:NH2	33:7:377:GLU:OE1	2.27	0.67
1:2:1261:A:C2	1:2:1327:G:H1'	2.30	0.67
1:2:1378:5HM:H8	1:2:1379:G:C8	2.29	0.67
3:B:142:ASP:OD1	3:B:143:THR:N	2.22	0.67
9:H:131:ALA:O	9:H:157:ARG:NH2	2.28	0.67
27:Z:4:GLU:H	27:Z:4:GLU:CD	2.03	0.67
30:5:807:G:H2'	30:5:808:A:C8	2.30	0.67
32:6:41:CYS:SG	32:6:42:GLU:N	2.67	0.67
1:2:37:C:H2'	1:2:38:A:H8	1.60	0.67
1:2:232:C:H2'	1:2:233:G:H8	1.59	0.67
1:2:278:C:H2'	1:2:279:A:H8	1.59	0.67
8:G:26:ALA:HA	8:G:29:LEU:HD21	1.76	0.67
32:6:74:VAL:O	32:6:79:ARG:NH1	2.28	0.67
1:2:643:A:H2'	1:2:644:C:C6	2.30	0.67
1:2:843:A:O2'	1:2:844:A:H3'	1.95	0.66
1:2:916:G:OP1	40:2:1706:HOH:O	2.12	0.66
1:2:1133:U:O4'	1:2:1156:G:N2	2.28	0.66
18:Q:120:ARG:HH11	18:Q:124:LEU:HD21	1.59	0.66
24:W:55:ILE:HG22	24:W:57:ARG:HH12	1.59	0.66
1:2:337:C:H4'	1:2:338:A:H5''	1.77	0.66
1:2:1147:4AC:O7	1:2:1147:4AC:H5	1.95	0.66
32:6:40:ARG:NH1	32:6:41:CYS:O	2.29	0.66
1:2:1116:A:O2'	1:2:1117:G:O5'	2.12	0.66
1:2:1266:C:H2'	1:2:1267:G:H8	1.59	0.66
16:O:83:LYS:HE2	21:T:9:ARG:HH12	1.61	0.66
22:U:137:LYS:NZ	22:U:150:TYR:O	2.26	0.66
1:2:50:G:N2	1:2:408:C:N3	2.43	0.66
1:2:848:4AC:O7	1:2:848:4AC:H5	1.95	0.66
1:2:972:G:N2	1:2:973:A:N1	2.43	0.66
1:2:1422:C:O2	1:2:1423:G:N1	2.28	0.66
2:A:118:LEU:HA	2:A:192:LEU:HD13	1.77	0.66
5:D:56:ARG:HD3	7:F:160:PRO:HG3	1.76	0.66
26:Y:48:TRP:O	26:Y:50:LYS:NZ	2.22	0.66
1:2:446:U:O2'	1:2:449:A:N7	2.23	0.66
1:2:718:4AC:O7	1:2:719:G:N1	2.27	0.66
1:2:848:4AC:O3'	10:I:76:LYS:HG2	1.96	0.66
1:2:851:4AC:H2'	1:2:852:G:H8	1.60	0.66
5:D:116:ARG:CZ	5:D:174:ALA:HB2	2.26	0.66
33:7:248:LYS:N	33:7:251:GLN:OE1	2.28	0.66
1:2:1391:G:N1	1:2:1451:G:N7	2.43	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:33:VAL:HG11	2:A:51:VAL:HG11	1.76	0.66
7:F:150:GLY:HA3	7:F:196:ASN:HD22	1.59	0.66
1:2:1193:4AC:O7	1:2:1193:4AC:H5	1.95	0.66
1:2:1209:U:OP1	40:2:1707:HOH:O	2.13	0.66
1:2:1458:G:H2'	1:2:1459:A:C8	2.30	0.66
5:D:104:ARG:NH2	5:D:140:PRO:O	2.29	0.66
12:K:135:ARG:NH1	31:4:35:A:OP2	2.29	0.66
31:4:10:G:H22	31:4:26:G:H1'	1.60	0.66
1:2:563:G:H21	10:I:124:ARG:HH21	1.43	0.66
1:2:860:A:O2'	28:0:4:ARG:NH1	2.26	0.66
1:2:1381:C:H2'	1:2:1382:A:C8	2.30	0.66
13:L:38:ILE:HB	13:L:72:LEU:HB3	1.76	0.66
21:T:6:PHE:CD2	21:T:96:PRO:HB3	2.31	0.66
33:7:146:ILE:HG21	33:7:166:ILE:HG21	1.78	0.66
1:2:443:G:O2'	23:V:30:THR:O	2.14	0.66
1:2:1294:C:N4	21:T:69:ASP:OD1	2.29	0.66
2:A:102:THR:HG21	2:A:129:ARG:HA	1.76	0.66
19:R:15:LYS:NZ	19:R:16:CYS:O	2.24	0.66
35:9:247:ILE:HG21	35:9:263:VAL:HB	1.76	0.66
1:2:313:G:N2	5:D:3:ASP:OD2	2.29	0.66
1:2:251:G:C2	1:2:294:G:C2	2.85	0.65
1:2:390:A:H2'	1:2:391:A:C8	2.31	0.65
1:2:903:C:H2'	1:2:904:A:H8	1.61	0.65
1:2:993:C:H2'	1:2:994:U:C6	2.30	0.65
1:2:1224:A:C5	1:2:1261:A:N7	2.64	0.65
1:2:1433:G:H2'	1:2:1434:U:C6	2.32	0.65
1:2:1452:A:C2	33:7:373:VAL:HB	2.31	0.65
29:3:40:THR:HG23	29:3:41:LYS:HG3	1.77	0.65
1:2:292:U:OP1	11:J:13:SER:OG	2.15	0.65
1:2:553:G:N2	1:2:722:G:N7	2.45	0.65
5:D:46:THR:HG22	5:D:50:ASN:HD21	1.61	0.65
20:S:61:LYS:HB2	20:S:66:ILE:HD12	1.77	0.65
29:3:73:LYS:HZ3	29:3:75:ILE:HB	1.60	0.65
33:7:269:TYR:CE1	33:7:385:PRO:HD2	2.31	0.65
1:2:638:G:H2'	1:2:639:G:O4'	1.96	0.65
13:L:8:LEU:HB3	13:L:16:LEU:HD11	1.78	0.65
1:2:703:4AC:OP1	2:A:139:ARG:NH1	2.29	0.65
1:2:1350:U:N3	1:2:1351:A:N1	2.44	0.65
10:I:51:GLU:OE2	10:I:62:ARG:NH1	2.29	0.65
33:7:108:ALA:HB1	33:7:139:ILE:HG13	1.78	0.65
33:7:260:ARG:HA	33:7:269:TYR:HA	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:7:333:TYR:CE1	33:7:378:ILE:HB	2.31	0.65
33:7:365:THR:H	33:7:384:ARG:NH1	1.94	0.65
1:2:203:A:H2'	1:2:204:G:C8	2.30	0.65
1:2:1232:C:H2'	1:2:1233:4AC:H6	1.79	0.65
2:A:12:ASP:OD2	2:A:13:LYS:N	2.30	0.65
2:A:52:THR:HG23	2:A:55:ASP:H	1.62	0.65
2:A:172:ALA:HB2	2:A:184:ALA:HB3	1.78	0.65
27:Z:4:GLU:OE2	27:Z:4:GLU:N	2.25	0.65
27:Z:4:GLU:O	27:Z:7:PHE:N	2.30	0.65
1:2:1328:C:H2'	1:2:1329:G:H8	1.61	0.65
11:J:57:LEU:HG	11:J:118:GLY:HA2	1.78	0.65
12:K:135:ARG:NH2	31:4:33:U:OP2	2.30	0.65
33:7:24:THR:HG21	33:7:186:LEU:HA	1.77	0.65
33:7:364:SER:HB3	33:7:384:ARG:HH12	1.61	0.65
35:9:69:ILE:HG22	35:9:70:ARG:HG3	1.79	0.65
1:2:525:U:O4	40:2:1705:HOH:O	2.11	0.65
1:2:1321:G:N2	1:2:1347:G:N3	2.45	0.65
5:D:46:THR:O	5:D:50:ASN:ND2	2.29	0.65
5:D:94:SER:HG	7:F:161:ARG:HH21	1.42	0.65
33:7:50:GLY:HA3	33:7:93:ASP:HB2	1.79	0.65
1:2:1198:U:H3	1:2:1296:C:H6	1.44	0.65
16:O:57:GLU:OE1	16:O:57:GLU:N	2.20	0.65
27:Z:82:VAL:HG12	27:Z:83:GLN:H	1.61	0.65
33:7:317:THR:HG22	33:7:318:LEU:H	1.61	0.65
1:2:1386:C:H2'	1:2:1387:A:C8	2.32	0.65
33:7:24:THR:HB	33:7:185:ALA:HB1	1.78	0.65
6:E:57:LYS:HG3	6:E:58:THR:HG23	1.79	0.64
7:F:128:CYS:SG	7:F:139:HIS:CE1	2.90	0.64
1:2:306:G:N2	1:2:309:A:OP2	2.30	0.64
1:2:344:C:H2'	1:2:345:C:C6	2.32	0.64
1:2:1468:A:C4	1:2:1469:6MZ:H8	2.33	0.64
8:G:68:ASP:OD1	8:G:108:ARG:NE	2.30	0.64
16:O:80:ASN:HB2	16:O:92:HIS:CG	2.32	0.64
28:O:7:LYS:O	28:O:13:ARG:NH1	2.28	0.64
32:6:77:ASP:H	32:6:79:ARG:HH12	1.44	0.64
1:2:1287:G:OP2	21:T:33:ARG:NH2	2.30	0.64
21:T:109:THR:HG23	21:T:110:ARG:HG3	1.79	0.64
29:3:116:MET:O	29:3:120:GLU:HG2	1.98	0.64
11:J:76:ARG:NH1	11:J:77:ILE:O	2.30	0.64
1:2:379:4AC:N4	1:2:400:G:O6	2.29	0.64
1:2:582:G:C2	1:2:583:G:C8	2.84	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:930:A:O2'	1:2:957:4AC:O2'	2.14	0.64
1:2:949:A:OP1	40:2:1709:HOH:O	2.14	0.64
13:L:6:ILE:HG22	13:L:98:ILE:HG12	1.79	0.64
19:R:34:PHE:HD1	19:R:51:ARG:HE	1.43	0.64
33:7:130:ARG:HH21	33:7:340:VAL:HA	1.63	0.64
1:2:224:G:O2'	1:2:225:C:O5'	2.15	0.64
1:2:543:G:OP1	40:2:1708:HOH:O	2.14	0.64
1:2:632:A:N7	1:2:691:G:N2	2.34	0.64
1:2:710:A:H2'	1:2:711:A:H8	1.61	0.64
1:2:1007:C:H2'	1:2:1008:G:C8	2.31	0.64
1:2:1309:C:O2'	9:H:175:ARG:NH1	2.31	0.64
11:J:108:ALA:HA	11:J:125:LEU:H	1.62	0.64
13:L:53:PRO:O	17:P:40:ARG:NH2	2.31	0.64
1:2:407:C:H2'	1:2:408:C:H6	1.62	0.64
1:2:915:U:OP1	40:2:1710:HOH:O	2.15	0.64
1:2:1086:C:H2'	1:2:1087:C:C6	2.33	0.64
1:2:1347:G:O2'	1:2:1348:A:O5'	2.13	0.64
19:R:41:ASP:OD1	19:R:41:ASP:N	2.24	0.64
21:T:32:GLN:HG3	21:T:71:ILE:HD13	1.79	0.64
33:7:65:PRO:O	33:7:67:ALA:N	2.30	0.64
1:2:128:C:O2'	1:2:271:A:N3	2.24	0.64
1:2:833:G:H2'	1:2:834:G:C8	2.33	0.64
1:2:1440:C:H2'	1:2:1441:U:C6	2.32	0.64
1:2:1475:U:O2'	1:2:1476:A:O5'	2.10	0.64
9:H:195:ASP:OD1	9:H:197:LYS:N	2.30	0.64
10:I:113:HIS:HA	10:I:116:ALA:HB3	1.80	0.64
1:2:57:U:O2	1:2:370:C:O2'	2.15	0.64
1:2:164:G:H2'	1:2:165:G:H8	1.62	0.64
1:2:1041:4AC:O7	1:2:1041:4AC:H5	1.97	0.64
16:O:55:THR:OG1	16:O:56:ASP:N	2.30	0.64
27:Z:57:ARG:O	27:Z:60:ARG:NE	2.30	0.64
35:9:196:ILE:O	35:9:200:ILE:HG12	1.98	0.64
1:2:368:C:H2'	1:2:369:G:C8	2.33	0.64
1:2:703:4AC:O7	1:2:703:4AC:H5	1.98	0.64
23:V:46:LEU:HB3	23:V:71:TYR:CE1	2.33	0.64
1:2:209:A:O2'	1:2:210:A:O5'	2.16	0.63
1:2:1236:C:OP2	22:U:71:GLU:HB2	1.97	0.63
9:H:141:PHE:CZ	25:X:65:ARG:HD3	2.32	0.63
33:7:132:HIS:O	33:7:136:LEU:HG	1.98	0.63
33:7:254:LYS:NZ	33:7:321:ALA:O	2.31	0.63
33:7:279:ILE:HG21	33:7:289:ALA:HB2	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:268:G:P	11:J:113:ARG:HE	2.21	0.63
1:2:521:C:H2'	1:2:522:C:C6	2.33	0.63
1:2:854:C:H2'	1:2:855:U:H6	1.62	0.63
29:3:20:LEU:HD21	29:3:81:PRO:HD2	1.79	0.63
1:2:323:G:H2'	1:2:324:A:C8	2.33	0.63
1:2:793:C:H4'	10:I:13:HIS:ND1	2.13	0.63
2:A:120:VAL:HG12	2:A:189:ILE:HG12	1.80	0.63
21:T:40:LEU:HB2	21:T:45:LYS:HE3	1.79	0.63
24:W:15:PHE:HB2	24:W:64:LEU:HG	1.80	0.63
1:2:37:C:H2'	1:2:38:A:C8	2.34	0.63
1:2:818:C:H2'	1:2:819:G:H8	1.63	0.63
17:P:39:CYS:HB2	17:P:42:CYS:SG	2.38	0.63
31:4:44:A:H3'	31:4:45:G:H8	1.63	0.63
11:J:38:ALA:HB3	11:J:59:ALA:HB1	1.81	0.63
29:3:69:LEU:O	29:3:73:LYS:NZ	2.31	0.63
2:A:185:GLU:OE1	2:A:185:GLU:N	2.32	0.63
7:F:56:GLU:N	7:F:56:GLU:OE2	2.31	0.63
19:R:14:GLU:HG3	19:R:15:LYS:H	1.62	0.63
26:Y:6:LYS:HG3	26:Y:7:LEU:HG	1.81	0.63
33:7:97:HIS:HB3	33:7:99:VAL:HG12	1.80	0.63
33:7:167:LYS:O	33:7:171:LYS:HG2	1.97	0.63
1:2:333:G:N2	1:2:335:G:H3'	2.13	0.63
1:2:354:C:O2	1:2:355:G:N2	2.31	0.63
1:2:1131:A:N6	1:2:1154:A:N7	2.46	0.63
1:2:1402:A:H2'	1:2:1403:G:H8	1.63	0.63
16:O:76:ARG:NH1	16:O:90:ASP:OD2	2.32	0.63
33:7:98:GLU:HB3	33:7:404:ARG:HG2	1.80	0.63
1:2:512:G:P	5:D:37:ASN:HB2	2.39	0.63
1:2:1182:C:H2'	1:2:1183:C:H6	1.63	0.63
2:A:48:VAL:O	14:M:34:THR:OG1	2.16	0.63
1:2:66:C:H2'	1:2:67:G:H8	1.62	0.63
1:2:1396:G:H22	1:2:1448:C:H1'	1.63	0.63
5:D:78:LYS:NZ	5:D:85:GLU:O	2.23	0.63
5:D:171:ILE:HG22	5:D:175:LYS:NZ	2.14	0.63
12:K:70:GLY:O	12:K:73:GLY:N	2.31	0.63
32:6:94:LEU:HG	32:6:99:LYS:HB2	1.79	0.63
33:7:26:VAL:HA	33:7:29:ILE:HG12	1.81	0.63
7:F:20:THR:HG22	7:F:21:LYS:H	1.64	0.62
30:5:823:C:H4'	32:6:57:ARG:HG3	1.80	0.62
33:7:163:TYR:OH	34:8:3:SER:O	2.14	0.62
3:B:44:ASP:OD2	3:B:47:LYS:NZ	2.33	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:4:74:C:N4	33:7:33:TRP:NE1	2.44	0.62
33:7:162:GLN:O	33:7:166:ILE:HG13	1.98	0.62
35:9:185:VAL:HG22	35:9:261:ILE:HG12	1.81	0.62
1:2:442:A:H2'	1:2:443:G:H8	1.62	0.62
6:E:164:VAL:HG12	6:E:176:VAL:HG22	1.81	0.62
14:M:40:SER:OG	14:M:70:GLU:OE1	2.13	0.62
18:Q:83:GLU:HG2	18:Q:88:ALA:HB2	1.80	0.62
31:4:10:G:N2	31:4:26:G:H1'	2.15	0.62
32:6:28:VAL:HG22	32:6:39:VAL:HG12	1.80	0.62
33:7:360:SER:HA	33:7:365:THR:HA	1.80	0.62
1:2:872:A:O2'	1:2:1482:A:OP1	2.18	0.62
1:2:1280:A:H3'	1:2:1281:U:H6	1.64	0.62
17:P:31:ILE:HG22	17:P:33:ILE:H	1.63	0.62
31:4:8:4SU:O2'	31:4:13:C:N4	2.32	0.62
32:6:68:ILE:HG12	32:6:84:TYR:O	2.00	0.62
33:7:130:ARG:NH2	33:7:340:VAL:HA	2.15	0.62
33:7:256:LEU:HD12	33:7:257:PRO:HA	1.81	0.62
1:2:582:G:C4	1:2:591:G:N2	2.67	0.62
1:2:1062:U:C2	1:2:1063:G:C8	2.86	0.62
1:2:1386:C:H2'	1:2:1387:A:H8	1.65	0.62
1:2:1450:U:H2'	1:2:1451:G:H5'	1.80	0.62
7:F:150:GLY:HA3	7:F:196:ASN:ND2	2.15	0.62
18:Q:27:GLU:OE1	18:Q:27:GLU:N	2.32	0.62
35:9:254:GLY:HA3	35:9:261:ILE:HD12	1.80	0.62
1:2:263:G:C2	1:2:264:G:C8	2.88	0.62
1:2:343:U:H4'	8:G:104:LYS:HE3	1.81	0.62
1:2:511:4AC:O7	1:2:511:4AC:H5	1.99	0.62
1:2:691:G:H2'	1:2:692:G:H8	1.64	0.62
1:2:1453:G:OP2	33:7:352:ARG:NH1	2.33	0.62
5:D:123:GLN:HE21	5:D:127:HIS:CE1	2.17	0.62
33:7:115:ILE:HG12	33:7:145:ILE:HB	1.80	0.62
1:2:185:G:H2'	1:2:186:G:C8	2.35	0.62
1:2:255:A:N1	1:2:287:G:O2'	2.32	0.62
1:2:269:G:O2'	1:2:270:U:O4'	2.18	0.62
1:2:458:G:H3'	1:2:459:G:C8	2.35	0.62
1:2:914:G:N2	12:K:131:GLN:HE22	1.98	0.62
1:2:991:G:H3'	1:2:992:U:H6	1.64	0.62
1:2:1133:U:O5'	20:S:5:ARG:NH2	2.28	0.62
1:2:1219:G:C4	1:2:1220:G:C8	2.88	0.62
7:F:20:THR:N	7:F:46:GLU:OE2	2.33	0.62
1:2:82:C:H2'	1:2:83:C:H6	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:485:C:OP1	32:6:54:LYS:NZ	2.30	0.62
1:2:914:G:H21	12:K:131:GLN:HE22	1.47	0.62
8:G:98:GLU:HB3	8:G:101:GLU:OE2	2.00	0.62
15:N:84:VAL:HG12	15:N:85:THR:H	1.64	0.62
29:3:101:ILE:HD11	29:3:104:PRO:HB3	1.80	0.62
32:6:55:LEU:C	32:6:57:ARG:H	2.07	0.62
33:7:183:VAL:HG11	33:7:194:LEU:HB2	1.80	0.62
1:2:55:A:C6	1:2:315:A:C5	2.88	0.62
1:2:467:G:H2'	1:2:468:C:O4'	2.00	0.62
1:2:519:G:H2'	1:2:520:G:H8	1.65	0.62
1:2:648:4AC:N3	1:2:677:G:N1	2.48	0.62
1:2:1133:U:OP2	20:S:3:LYS:NZ	2.24	0.62
1:2:1395:G:N3	1:2:1449:G:N1	2.48	0.62
1:2:1419:C:OP1	8:G:64:ARG:NH1	2.33	0.62
2:A:132:THR:O	2:A:135:GLU:N	2.29	0.62
5:D:58:LEU:O	5:D:70:ARG:NH2	2.29	0.62
33:7:144:LEU:HD23	33:7:178:VAL:HG21	1.81	0.62
5:D:139:SER:OG	5:D:142:TYR:HB2	2.00	0.62
21:T:12:THR:HG1	21:T:15:GLN:H	1.48	0.62
24:W:30:PHE:HD2	24:W:32:HIS:H	1.47	0.62
1:2:636:4AC:O7	1:2:636:4AC:H5	2.00	0.61
1:2:1131:A:H62	1:2:1151:G:N2	1.97	0.61
5:D:45:GLU:OE2	5:D:49:LYS:NZ	2.29	0.61
6:E:86:GLY:N	6:E:89:ASP:OD2	2.24	0.61
13:L:4:ALA:HA	13:L:100:LEU:HA	1.81	0.61
1:2:127:A:OP2	1:2:196:G:N2	2.30	0.61
1:2:981:C:N3	26:Y:37:ARG:NH2	2.46	0.61
1:2:1392:A:O2'	1:2:1393:G:H8	1.83	0.61
2:A:11:LYS:O	2:A:15:LYS:N	2.28	0.61
19:R:15:LYS:HD2	19:R:24:HIS:CD2	2.34	0.61
1:2:96:C:H2'	1:2:97:A:H8	1.65	0.61
1:2:718:4AC:C7	1:2:719:G:H1	2.12	0.61
1:2:996:G:O2'	1:2:997:C:O4'	2.18	0.61
1:2:1086:C:H2'	1:2:1087:C:H6	1.65	0.61
3:B:36:ARG:NH2	3:B:38:ASP:OD2	2.33	0.61
8:G:34:ILE:HG23	8:G:63:ILE:HB	1.83	0.61
16:O:99:ASP:OD1	16:O:99:ASP:N	2.28	0.61
29:3:74:GLU:HG2	29:3:75:ILE:H	1.66	0.61
29:3:85:GLU:N	29:3:85:GLU:OE1	2.32	0.61
33:7:105:LEU:HD21	33:7:135:ALA:HB1	1.82	0.61
1:2:394:4AC:N4	1:2:395:G:O6	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:854:C:H2'	1:2:855:U:C6	2.35	0.61
1:2:1392:A:O2'	1:2:1393:G:O5'	2.17	0.61
10:I:55:ASP:N	10:I:55:ASP:OD1	2.32	0.61
33:7:353:ALA:HB1	33:7:370:VAL:HG13	1.83	0.61
1:2:1217:G:O2'	22:U:43:ARG:HD2	2.00	0.61
2:A:47:ARG:HD3	14:M:34:THR:HG21	1.82	0.61
31:4:14:A:N6	31:4:15:G:N3	2.48	0.61
1:2:168:A:O2'	1:2:169:A:O4'	2.15	0.61
1:2:302:C:H1'	5:D:2:GLY:N	2.15	0.61
1:2:303:4AC:HM72	1:2:313:G:O6	1.99	0.61
1:2:1365:U:H2'	1:2:1366:G:N7	2.15	0.61
5:D:135:GLN:OE1	5:D:136:ILE:N	2.33	0.61
7:F:63:GLN:HA	7:F:89:VAL:HG12	1.82	0.61
15:N:6:ALA:HB3	15:N:7:PRO:HD3	1.81	0.61
23:V:88:ILE:HG13	23:V:93:ILE:HD11	1.80	0.61
32:6:49:CYS:SG	32:6:50:ARG:N	2.74	0.61
1:2:946:G:O2'	1:2:947:G:OP2	2.16	0.61
1:2:1085:C:H2'	1:2:1086:C:H6	1.66	0.61
1:2:1217:G:H4'	22:U:43:ARG:HE	1.66	0.61
18:Q:102:ALA:HB2	18:Q:125:ILE:HG21	1.82	0.61
24:W:45:THR:OG1	24:W:47:VAL:O	2.18	0.61
33:7:148:GLN:OE1	34:8:7:TYR:OH	2.13	0.61
1:2:164:G:H2'	1:2:165:G:C8	2.36	0.61
1:2:208:G:H2'	1:2:208:G:N3	2.15	0.61
1:2:620:U:C5	10:I:57:ARG:HB2	2.36	0.61
2:A:12:ASP:CG	35:9:22:VAL:HB	2.26	0.61
23:V:46:LEU:HB3	23:V:71:TYR:CD1	2.35	0.61
33:7:325:VAL:HB	33:7:385:PRO:CB	2.27	0.61
33:7:382:LEU:HD23	33:7:384:ARG:O	2.00	0.61
1:2:479:4AC:N4	1:2:504:G:O6	2.30	0.61
1:2:548:U:OP2	1:2:725:G:N1	2.32	0.61
1:2:790:G:C2	1:2:791:G:C8	2.88	0.61
1:2:1000:G:H2'	29:3:38:GLU:OE2	2.01	0.61
25:X:67:ILE:HD13	25:X:70:ARG:HA	1.82	0.61
1:2:714:G:N2	1:2:716:U:C4	2.69	0.61
1:2:1091:U:O2	1:2:1254:A:H2'	2.00	0.61
1:2:1138:G:H1	1:2:1146:C:H42	1.49	0.61
5:D:17:PRO:HG2	5:D:18:TRP:CE3	2.36	0.61
7:F:149:GLU:OE2	7:F:150:GLY:N	2.31	0.61
12:K:22:GLY:HA3	12:K:61:ASP:CG	2.26	0.61
13:L:92:GLU:OE2	13:L:92:GLU:N	2.29	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:O:33:ILE:O	16:O:36:ALA:N	2.31	0.61
17:P:10:LYS:HD3	17:P:11:PRO:HD2	1.83	0.61
21:T:84:HIS:CD2	21:T:86:GLY:H	2.19	0.61
25:X:67:ILE:HG12	25:X:68:LYS:H	1.66	0.61
29:3:71:GLU:OE1	29:3:71:GLU:N	2.33	0.61
1:2:148:A:C5	1:2:149:A:C8	2.89	0.60
1:2:247:G:H2'	1:2:248:G:C8	2.37	0.60
1:2:487:G:OP1	15:N:92:GLY:N	2.30	0.60
1:2:1279:G:H1	1:2:1305:G:HO2'	1.49	0.60
1:2:1457:G:H2'	1:2:1458:G:H8	1.66	0.60
2:A:73:ASP:OD1	2:A:74:VAL:N	2.34	0.60
11:J:79:ARG:NH1	11:J:102:GLU:OE2	2.33	0.60
12:K:47:GLU:OE2	12:K:102:TYR:OH	2.15	0.60
15:N:9:GLY:O	19:R:62:ARG:NE	2.33	0.60
28:0:8:TRP:HE1	28:0:16:TRP:CD1	2.18	0.60
31:4:9:G:O4'	31:4:46:A:H1'	2.00	0.60
31:4:76:A:H62	33:7:234:LYS:HE2	1.66	0.60
1:2:303:4AC:O7	1:2:303:4AC:H5	2.01	0.60
9:H:22:SER:OG	9:H:24:GLU:OE1	2.19	0.60
13:L:7:LYS:NZ	13:L:99:GLU:OE1	2.25	0.60
26:Y:47:GLU:OE1	26:Y:47:GLU:N	2.33	0.60
1:2:315:A:OP2	40:2:1712:HOH:O	2.16	0.60
1:2:1392:A:O2'	1:2:1393:G:O4'	2.19	0.60
10:I:28:LYS:HB3	10:I:29:PRO:HD3	1.84	0.60
25:X:18:THR:HG22	25:X:19:GLY:H	1.65	0.60
29:3:37:ASN:HD21	29:3:62:ILE:HG21	1.63	0.60
33:7:19:ASP:H	39:7:502:GNP:HNB3	1.49	0.60
1:2:627:G:C2	1:2:628:G:C5	2.89	0.60
1:2:666:C:C2	1:2:667:U:C5	2.90	0.60
1:2:1093:C:H42	1:2:1119:C:H41	1.48	0.60
1:2:1381:C:H2'	1:2:1382:A:H8	1.65	0.60
26:Y:39:ALA:HA	26:Y:45:TYR:O	2.00	0.60
30:5:811:U:C2	30:5:812:G:C8	2.88	0.60
33:7:101:MET:HE2	33:7:131:GLU:HG3	1.82	0.60
1:2:366:G:OP2	40:2:1713:HOH:O	2.16	0.60
1:2:476:G:N1	1:2:506:C:N3	2.37	0.60
1:2:582:G:N1	1:2:583:G:N7	2.50	0.60
1:2:911:G:P	9:H:156:ARG:HH22	2.24	0.60
6:E:216:GLU:HG2	6:E:217:ASP:O	2.01	0.60
14:M:133:ARG:HB3	14:M:136:ARG:HH11	1.66	0.60
31:4:50:U:O2	31:4:64:G:O6	2.19	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:6:95:LEU:O	32:6:98:GLY:N	2.33	0.60
33:7:219:ARG:HB2	38:7:501:MET:HE2	1.82	0.60
1:2:69:G:C6	1:2:103:G:N1	2.70	0.60
1:2:559:G:C6	1:2:614:G:C6	2.90	0.60
1:2:1339:C:H2'	1:2:1340:G:H8	1.67	0.60
2:A:23:TYR:HE1	2:A:32:GLU:HB2	1.67	0.60
29:3:70:CYS:HA	29:3:75:ILE:HG21	1.82	0.60
1:2:69:G:C4	1:2:103:G:N2	2.70	0.60
1:2:817:U:P	2:A:128:ARG:HH22	2.24	0.60
1:2:914:G:H2'	1:2:915:U:C6	2.37	0.60
12:K:3:ILE:HG22	12:K:20:ARG:HB3	1.82	0.60
12:K:7:THR:OG1	12:K:8:GLY:N	2.33	0.60
13:L:10:SER:OG	13:L:11:THR:N	2.35	0.60
23:V:86:ILE:HG23	23:V:87:LEU:HD12	1.82	0.60
28:0:34:ARG:HB3	33:7:371:THR:OG1	2.01	0.60
1:2:1353:G:O2'	1:2:1354:U:O4'	2.19	0.60
5:D:165:HIS:O	5:D:168:ARG:N	2.35	0.60
14:M:22:SER:HG	14:M:25:ASN:H	1.47	0.60
33:7:240:GLY:O	33:7:294:LEU:CA	2.42	0.60
34:8:125:ILE:HD12	34:8:134:THR:HG23	1.84	0.60
1:2:1221:G:OP1	22:U:57:SER:OG	2.16	0.60
1:2:1491:U:H2'	1:2:1492:A:H8	1.66	0.60
9:H:66:ARG:HA	9:H:69:ASN:HD21	1.66	0.60
15:N:139:LYS:HD2	15:N:141:ARG:HH11	1.67	0.60
18:Q:90:GLU:OE1	18:Q:90:GLU:N	2.33	0.60
33:7:329:ILE:HG21	33:7:386:VAL:HG11	1.83	0.60
1:2:886:A:C5	1:2:887:G:C8	2.89	0.60
1:2:1068:C:OP1	3:B:95:ARG:NH2	2.35	0.60
1:2:1391:G:H21	33:7:352:ARG:NE	2.00	0.60
6:E:166:MET:HE1	6:E:171:ARG:HG3	1.84	0.60
33:7:15:VAL:HB	33:7:132:HIS:ND1	2.17	0.60
33:7:68:TYR:HB2	33:7:192:ASP:OD1	2.02	0.60
1:2:126:A:C6	1:2:194:A:N7	2.69	0.59
1:2:1316:C:H1'	12:K:131:GLN:NE2	2.17	0.59
7:F:143:PHE:HB2	10:I:95:PRO:HB2	1.83	0.59
8:G:28:LYS:O	8:G:32:LYS:NZ	2.34	0.59
11:J:86:ASN:OD1	11:J:87:ARG:N	2.35	0.59
29:3:23:VAL:HB	29:3:89:ALA:HB1	1.84	0.59
31:4:34:C:C2	31:4:35:A:C8	2.90	0.59
33:7:58:VAL:HG23	33:7:86:LEU:HD11	1.83	0.59
33:7:163:TYR:HB2	34:8:7:TYR:CZ	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:55:A:C6	1:2:315:A:C6	2.90	0.59
1:2:433:C:H2'	1:2:434:U:C6	2.37	0.59
1:2:1114:G:C2	1:2:1115:G:C5	2.90	0.59
1:2:1148:G:H2'	1:2:1149:G:C8	2.37	0.59
1:2:1211:C:C2	1:2:1310:U:H5	2.20	0.59
1:2:1283:G:OP1	16:O:116:ARG:NH2	2.35	0.59
1:2:1321:G:N7	12:K:112:ARG:NE	2.50	0.59
33:7:327:TRP:NE1	33:7:382:LEU:O	2.29	0.59
1:2:347:G:N1	1:2:348:G:N7	2.50	0.59
1:2:474:A:C2	5:D:18:TRP:NE1	2.69	0.59
1:2:648:4AC:O7	1:2:648:4AC:H5	2.03	0.59
1:2:991:G:C5	1:2:992:U:C4	2.91	0.59
1:2:1452:A:C8	33:7:352:ARG:NE	2.66	0.59
6:E:40:ARG:HH22	6:E:189:GLN:CD	2.09	0.59
35:9:61:ASN:HB2	35:9:62:ARG:HH21	1.67	0.59
1:2:666:C:H2'	1:2:667:U:C6	2.37	0.59
1:2:1171:G:C2	1:2:1172:G:C8	2.90	0.59
1:2:1235:A:H62	1:2:1248:G:H21	1.49	0.59
1:2:1453:G:H21	33:7:354:LYS:HG3	1.68	0.59
1:2:352:U:H3'	1:2:354:C:N4	2.18	0.59
1:2:911:G:C2	1:2:912:G:N7	2.71	0.59
1:2:1476:A:C5	1:2:1499:G:C2	2.90	0.59
31:4:60:U:P	31:4:61:C:H41	2.25	0.59
33:7:51:TYR:CE1	33:7:90:SER:HB2	2.38	0.59
1:2:85:U:H1'	1:2:89:G:N2	2.18	0.59
1:2:637:G:N1	1:2:703:4AC:N3	2.40	0.59
1:2:825:U:H5	1:2:842:U:H5	1.49	0.59
1:2:873:G:H2'	1:2:874:G:H8	1.67	0.59
1:2:966:C:H2'	1:2:967:G:C8	2.37	0.59
5:D:130:ILE:HG22	5:D:131:GLU:H	1.68	0.59
18:Q:145:ASP:O	18:Q:147:ARG:NH1	2.35	0.59
1:2:116:A:C5	1:2:118:A:C5	2.89	0.59
1:2:337:C:OP2	11:J:25:LYS:N	2.36	0.59
1:2:1036:C:H2'	1:2:1037:G:H8	1.66	0.59
6:E:179:PHE:HE2	6:E:202:ILE:HD11	1.67	0.59
1:2:31:G:C2	1:2:32:G:C8	2.90	0.59
1:2:1140:G:N2	1:2:1143:A:OP2	2.32	0.59
1:2:1278:G:H21	1:2:1307:A:H62	1.48	0.59
1:2:1311:G:P	9:H:85:PHE:H	2.26	0.59
1:2:1331:G:N2	1:2:1340:G:C4	2.71	0.59
3:B:166:LEU:HG	3:B:170:ILE:HD11	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:U:56:ALA:O	22:U:59:LEU:N	2.36	0.59
35:9:204:LEU:HG	35:9:217:ILE:HG21	1.83	0.59
1:2:126:A:N7	1:2:194:A:N6	2.51	0.59
1:2:305:U:OP2	5:D:8:ARG:NH1	2.35	0.59
1:2:1148:G:H2'	1:2:1149:G:H8	1.67	0.59
1:2:1509:U:N3	30:5:805:U:O4	2.35	0.59
2:A:24:ALA:HB3	2:A:31:VAL:H	1.67	0.59
8:G:98:GLU:CD	8:G:99:LYS:H	2.10	0.59
23:V:33:ARG:HH22	23:V:89:ARG:HE	1.51	0.59
31:4:43:A:H2'	31:4:44:A:C8	2.38	0.59
33:7:323:VAL:HG12	33:7:389:TRP:HA	1.84	0.59
35:9:20:LYS:HD3	35:9:30:SER:OG	2.02	0.59
1:2:162:G:H2'	1:2:163:G:H8	1.67	0.59
1:2:163:G:H5'	8:G:65:GLY:HA3	1.85	0.59
1:2:183:U:O4'	11:J:121:ASN:ND2	2.35	0.59
1:2:437:U:N3	1:2:462:U:N3	2.50	0.59
1:2:1402:A:H2'	1:2:1403:G:C8	2.37	0.59
5:D:116:ARG:HH12	5:D:170:MET:HE3	1.68	0.59
10:I:90:GLU:OE2	10:I:113:HIS:NE2	2.36	0.59
13:L:24:LYS:HG3	13:L:34:MET:HE1	1.85	0.59
21:T:12:THR:OG1	21:T:15:GLN:N	2.23	0.59
25:X:8:PRO:HB2	25:X:32:LEU:HD21	1.83	0.59
1:2:337:C:H4'	1:2:338:A:C5'	2.33	0.58
1:2:1150:A:H3'	1:2:1151:G:H8	1.68	0.58
1:2:1452:A:H2	33:7:373:VAL:HB	1.65	0.58
33:7:145:ILE:HD11	33:7:202:ILE:HG13	1.84	0.58
1:2:638:G:C5	1:2:639:G:C8	2.91	0.58
1:2:775:G:H8	1:2:775:G:OP2	1.87	0.58
1:2:955:A:H8	1:2:1175:A:C6	2.21	0.58
1:2:1505:C:N3	30:5:810:G:N1	2.51	0.58
3:B:169:TRP:HD1	3:B:195:PHE:CE2	2.18	0.58
8:G:3:THR:OG1	8:G:21:ILE:O	2.16	0.58
35:9:31:LEU:O	35:9:36:GLY:CA	2.51	0.58
1:2:55:A:C5	1:2:315:A:C6	2.92	0.58
1:2:338:A:H2'	1:2:341:G:O6	2.04	0.58
1:2:390:A:H2'	1:2:391:A:H8	1.68	0.58
1:2:758:G:H2'	1:2:759:A:H8	1.68	0.58
1:2:833:G:H2'	1:2:834:G:H8	1.66	0.58
1:2:1239:4AC:N4	1:2:1244:G:O6	2.33	0.58
1:2:1279:G:O2'	1:2:1305:G:N2	2.34	0.58
1:2:1396:G:N1	1:2:1448:C:H1'	2.17	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1481:U:H2'	1:2:1482:A:C8	2.34	0.58
5:D:94:SER:OG	7:F:161:ARG:NH2	2.21	0.58
13:L:83:ARG:O	13:L:87:ARG:NH1	2.37	0.58
24:W:29:VAL:HG12	24:W:30:PHE:H	1.67	0.58
31:4:17:C:H5''	31:4:17(A):U:H3'	1.84	0.58
31:4:29:G:N3	31:4:30:G:C8	2.71	0.58
1:2:278:C:H2'	1:2:279:A:C8	2.38	0.58
1:2:1117:G:C5	1:2:1118:G:N1	2.71	0.58
1:2:1492:A:H5''	1:2:1493:C:OP2	2.03	0.58
2:A:122:ALA:HB2	2:A:186:ILE:HG23	1.85	0.58
19:R:11:PRO:HB3	19:R:23:TRP:CZ3	2.37	0.58
27:Z:36:LYS:HB3	27:Z:43:LYS:HE3	1.84	0.58
33:7:133:PHE:HD1	33:7:136:LEU:HD12	1.68	0.58
1:2:620:U:O2'	1:2:621:G:O5'	2.19	0.58
1:2:803:G:H2'	1:2:804:G:O4'	2.03	0.58
1:2:838:C:H2'	1:2:839:4AC:H5	1.84	0.58
1:2:1247:G:C4	1:2:1248:G:H1'	2.38	0.58
1:2:1323:A:H62	1:2:1347:G:N2	2.01	0.58
1:2:1388:C:H2'	1:2:1389:C:H6	1.67	0.58
21:T:93:GLU:N	21:T:93:GLU:OE2	2.37	0.58
1:2:1131:A:N6	1:2:1151:G:H22	2.00	0.58
1:2:1321:G:O6	12:K:10:ARG:NH2	2.33	0.58
16:O:105:ASP:HA	16:O:108:ARG:NH1	2.19	0.58
21:T:47:LEU:HD13	21:T:67:CYS:SG	2.43	0.58
30:5:812:G:C2	30:5:813:A:C4	2.90	0.58
31:4:16:C:H4'	31:4:60:U:H1'	1.84	0.58
32:6:42:GLU:HB2	32:6:104:PHE:CZ	2.39	0.58
33:7:28:ALA:HB1	33:7:191:ILE:HG13	1.86	0.58
33:7:179:PRO:HB3	33:7:201:TYR:CE2	2.39	0.58
1:2:163:G:H2'	1:2:164:G:C8	2.39	0.58
1:2:1239:4AC:O7	1:2:1239:4AC:H5	2.03	0.58
9:H:12:PRO:HG3	12:K:43:PHE:HE1	1.68	0.58
12:K:12:THR:N	12:K:113:ARG:HH12	2.01	0.58
15:N:63:LYS:HG2	15:N:118:ASP:O	2.04	0.58
33:7:357:LEU:HD22	33:7:399:ARG:HA	1.86	0.58
1:2:151:C:N3	1:2:165:G:N1	2.52	0.58
1:2:470:G:C2	1:2:471:G:N7	2.71	0.58
1:2:694:G:N2	1:2:698:G:C4	2.71	0.58
9:H:20:ARG:HB3	9:H:21:TRP:CE2	2.39	0.58
29:3:27:ARG:NH1	29:3:90:ALA:HA	2.16	0.58
1:2:190:C:H5'	6:E:155:LYS:HD2	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:488:C:H42	1:2:494:C:N4	2.01	0.58
1:2:1310:U:O2'	9:H:85:PHE:O	2.18	0.58
1:2:1359:G:C6	1:2:1360:C:C4	2.91	0.58
1:2:1398:G:O2'	1:2:1399:C:O5'	2.22	0.58
1:2:1453:G:H1'	33:7:353:ALA:O	2.04	0.58
2:A:14:TRP:CD1	2:A:15:LYS:HG2	2.39	0.58
27:Z:192:GLU:OE1	27:Z:192:GLU:N	2.37	0.58
35:9:235:ASN:HB2	35:9:238:GLU:HB3	1.86	0.58
1:2:14:U:H5	7:F:184:TRP:CD2	2.22	0.58
1:2:81:U:H2'	1:2:82:C:C6	2.39	0.58
1:2:407:C:H2'	1:2:408:C:C6	2.39	0.58
1:2:828:4AC:O7	1:2:828:4AC:H5	2.04	0.58
1:2:1038:U:O2'	3:B:103:ASN:OD1	2.21	0.58
1:2:1393:G:N3	33:7:375:LYS:HE3	2.19	0.58
12:K:115:GLU:CD	12:K:126:PRO:HG2	2.29	0.58
33:7:135:ALA:O	33:7:139:ILE:HG12	2.03	0.58
1:2:140:A:H61	1:2:229:G:H1	0.64	0.57
1:2:173:C:H2'	1:2:174:C:H6	1.68	0.57
1:2:311:C:H2'	1:2:312:G:C8	2.34	0.57
1:2:705:G:H2'	1:2:706:C:H6	1.69	0.57
1:2:1292:A:OP2	21:T:38:ARG:NH2	2.37	0.57
1:2:1446:U:H2'	1:2:1447:C:C6	2.39	0.57
3:B:64:PRO:HB3	3:B:179:ARG:HH12	1.69	0.57
11:J:89:PHE:O	11:J:93:ASN:N	2.37	0.57
20:S:53:TYR:O	20:S:57:LEU:HG	2.04	0.57
27:Z:111:ARG:O	27:Z:115:ALA:CB	2.52	0.57
31:4:76:A:HO2'	38:7:501:MET:N	2.02	0.57
33:7:357:LEU:HD21	33:7:399:ARG:HG3	1.86	0.57
33:7:361:VAL:O	33:7:364:SER:N	2.28	0.57
34:8:3:SER:HB2	34:8:6:GLU:HB3	1.86	0.57
1:2:314:G:O2'	5:D:3:ASP:OD1	2.22	0.57
1:2:581:C:H2'	1:2:582:G:C8	2.34	0.57
1:2:731:4AC:H2'	1:2:732:G:H8	1.69	0.57
1:2:1136:C:N3	1:2:1148:G:N1	2.51	0.57
1:2:1378:5HM:H6	1:2:1378:5HM:H11	1.86	0.57
12:K:104:ARG:NE	12:K:108:VAL:HG21	2.18	0.57
1:2:144:G:N2	1:2:145:G:C4	2.72	0.57
1:2:336:A:O2'	1:2:337:C:O5'	2.21	0.57
1:2:838:C:H2'	1:2:839:4AC:H6	1.86	0.57
1:2:1220:G:O2'	22:U:10:ASP:OD1	2.21	0.57
2:A:46:ASN:HA	2:A:70:GLN:HE21	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:17:PRO:HG2	5:D:18:TRP:CZ3	2.38	0.57
14:M:133:ARG:HG2	14:M:136:ARG:HD3	1.85	0.57
16:O:87:THR:O	16:O:89:ARG:N	2.37	0.57
19:R:73:HIS:HA	19:R:98:LYS:HZ2	1.69	0.57
35:9:175:ARG:NH2	35:9:234:THR:O	2.37	0.57
1:2:389:G:N2	1:2:393:C:N3	2.53	0.57
1:2:474:A:N3	5:D:18:TRP:NE1	2.41	0.57
1:2:554:G:H1	1:2:619:U:H3	1.50	0.57
1:2:724:U:O4	1:2:725:G:N1	2.38	0.57
1:2:732:G:N2	1:2:779:G:H1'	2.20	0.57
1:2:749:A:H5'	1:2:750:C:OP2	2.05	0.57
1:2:1020:A:H62	1:2:1174:C:H42	1.50	0.57
1:2:1078:C:O2'	27:Z:156:ASN:ND2	2.37	0.57
7:F:114:ILE:HG22	7:F:118:LYS:NZ	2.19	0.57
12:K:28:ILE:O	12:K:31:LYS:N	2.29	0.57
21:T:8:TYR:HD2	21:T:9:ARG:HG2	1.69	0.57
33:7:367:LEU:HD12	33:7:368:GLY:H	1.69	0.57
1:2:529:A:HO2'	1:2:532:G:HO2'	1.52	0.57
1:2:951:C:C2	1:2:952:C:C6	2.92	0.57
8:G:115:GLU:OE1	8:G:115:GLU:N	2.38	0.57
1:2:170:U:O2	1:2:211:A:N6	2.38	0.57
1:2:391:A:H4'	6:E:67:ASN:HD22	1.69	0.57
1:2:480:G:C6	1:2:504:G:C6	2.93	0.57
1:2:1452:A:H2'	33:7:352:ARG:HB2	1.87	0.57
1:2:1460:G:H2'	1:2:1461:A:N3	2.19	0.57
1:2:633:G:O6	1:2:707:U:O2	2.22	0.57
9:H:215:ARG:OXT	25:X:62:ARG:NH2	2.37	0.57
33:7:274:THR:OG1	33:7:275:LYS:N	2.38	0.57
35:9:194:GLU:OE2	35:9:197:LYS:NZ	2.36	0.57
35:9:204:LEU:HD21	35:9:246:ILE:HG23	1.86	0.57
1:2:155:G:H5''	8:G:5:LYS:NZ	2.20	0.57
1:2:372:A:C5	1:2:373:A2M:N7	2.72	0.57
1:2:424:C:O2	1:2:426:G:N2	2.38	0.57
1:2:484:G:H4'	1:2:485:C:H5''	1.87	0.57
8:G:68:ASP:HA	8:G:116:ILE:HD13	1.87	0.57
1:2:179:G:C2	1:2:180:G:C8	2.93	0.57
1:2:360:G:H4'	1:2:361:C:OP2	2.05	0.57
1:2:735:G:H2'	1:2:736:G:C8	2.38	0.57
1:2:934:G:C2	1:2:935:G:C8	2.93	0.57
1:2:1385:C:N4	1:2:1457:G:O6	2.37	0.57
1:2:1467:UR3:H5	30:5:820:U:H5'	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:43:LYS:O	13:L:68:ILE:N	2.28	0.57
22:U:67:PRO:HA	22:U:119:ARG:O	2.04	0.57
1:2:64:U:H2'	1:2:65:G:C8	2.39	0.57
5:D:129:HIS:ND1	5:D:158:SER:OG	2.32	0.57
31:4:74:C:H41	33:7:33:TRP:HE1	1.51	0.57
32:6:55:LEU:HD12	32:6:82:ILE:HG22	1.87	0.57
33:7:361:VAL:N	33:7:364:SER:O	2.38	0.57
1:2:193:G:H21	6:E:207:MET:HA	1.70	0.56
1:2:726:A:C8	1:2:727:G:C8	2.93	0.56
1:2:860:A:H2	1:2:861:G:N2	2.02	0.56
1:2:1342:G:P	13:L:63:ARG:HH12	2.27	0.56
2:A:12:ASP:O	2:A:16:LEU:N	2.38	0.56
7:F:50:ILE:HD11	7:F:118:LYS:HB3	1.86	0.56
9:H:17:VAL:HG12	9:H:18:MET:HG3	1.87	0.56
9:H:140:MET:HE2	25:X:20:THR:HA	1.86	0.56
11:J:75:VAL:HG11	11:J:105:ILE:HD13	1.87	0.56
20:S:32:LYS:HG3	20:S:47:ARG:HH12	1.70	0.56
27:Z:111:ARG:O	27:Z:115:ALA:HB2	2.05	0.56
33:7:26:VAL:O	33:7:30:THR:OG1	2.11	0.56
33:7:53:GLU:OE1	33:7:88:ARG:NH1	2.37	0.56
33:7:248:LYS:HB3	33:7:251:GLN:CD	2.30	0.56
1:2:426:G:H8	1:2:426:G:O5'	1.89	0.56
1:2:1195:G:C2	1:2:1196:G:C8	2.93	0.56
1:2:1328:C:H2'	1:2:1329:G:C8	2.38	0.56
7:F:50:ILE:HG13	7:F:51:ASP:N	2.20	0.56
7:F:114:ILE:HG22	7:F:118:LYS:HZ1	1.70	0.56
16:O:80:ASN:HB2	16:O:92:HIS:ND1	2.20	0.56
33:7:364:SER:HB3	33:7:384:ARG:NH1	2.20	0.56
1:2:17:4AC:O7	1:2:17:4AC:H5	2.04	0.56
1:2:651:G:C6	1:2:652:G:C2	2.94	0.56
1:2:891:U:H2'	1:2:892:U:H6	1.70	0.56
1:2:935:G:O2'	1:2:1173:U:OP1	2.18	0.56
1:2:1002:C:H2'	1:2:1003:G:C8	2.39	0.56
1:2:1411:C:O2'	11:J:31:GLU:OE1	2.22	0.56
1:2:1443:G:H2'	1:2:1444:G:C8	2.40	0.56
1:2:1493:C:N4	1:2:1494:G:O6	2.39	0.56
2:A:111:THR:HA	2:A:117:LYS:HA	1.86	0.56
7:F:144:THR:HG22	7:F:157:ILE:HA	1.86	0.56
9:H:215:ARG:NH1	25:X:59:GLU:OE1	2.37	0.56
27:Z:70:GLU:CD	27:Z:71:ARG:HG3	2.30	0.56
29:3:40:THR:HG23	29:3:41:LYS:H	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:7:256:LEU:HD23	33:7:315:ILE:HD11	1.88	0.56
1:2:189:A:O3'	6:E:155:LYS:NZ	2.38	0.56
1:2:190:C:H2'	1:2:191:U:C6	2.40	0.56
1:2:382:A:C2	1:2:383:A:C8	2.94	0.56
4:C:16:SER:OG	4:C:46:CYS:HB3	2.05	0.56
7:F:166:VAL:HG11	7:F:184:TRP:HD1	1.71	0.56
12:K:10:ARG:NH1	12:K:110:ASP:OD2	2.38	0.56
12:K:26:VAL:HA	12:K:62:ILE:O	2.05	0.56
23:V:18:GLU:OE1	23:V:18:GLU:N	2.34	0.56
33:7:318:LEU:HB2	33:7:321:ALA:HB2	1.87	0.56
1:2:79:C:H2'	1:2:80:G:H8	1.69	0.56
1:2:240:G:C2	1:2:241:G:C8	2.93	0.56
1:2:267:G:C2	1:2:268:G:C6	2.94	0.56
1:2:323:G:H2'	1:2:324:A:H8	1.69	0.56
1:2:338:A:C6	1:2:341:G:C2	2.93	0.56
6:E:20:TYR:HB2	6:E:52:TYR:OH	2.06	0.56
6:E:116:SER:OG	6:E:117:GLU:N	2.33	0.56
9:H:137:THR:OG1	9:H:138:SER:N	2.38	0.56
22:U:22:GLU:N	22:U:22:GLU:OE1	2.38	0.56
24:W:17:ARG:HD2	24:W:28:ILE:HG12	1.88	0.56
27:Z:39:PRO:O	27:Z:40:LEU:HG	2.05	0.56
33:7:269:TYR:CD1	33:7:385:PRO:HD2	2.40	0.56
1:2:79:C:H2'	1:2:80:G:C8	2.41	0.56
1:2:868:4AC:O7	1:2:868:4AC:H5	2.05	0.56
1:2:1290:G:O2'	1:2:1292:A:N7	2.30	0.56
1:2:1345:G:C4	1:2:1346:C:C5	2.93	0.56
1:2:1506:U:H2'	1:2:1507:C:C6	2.40	0.56
14:M:43:SER:HB2	14:M:46:MET:HG3	1.88	0.56
32:6:72:TRP:O	32:6:74:VAL:N	2.38	0.56
1:2:243:C:H2'	1:2:244:G:H8	1.70	0.56
1:2:536:C:H2'	1:2:537:U:C6	2.40	0.56
1:2:710:A:H2'	1:2:711:A:C8	2.39	0.56
1:2:1065:U:OP2	3:B:95:ARG:HD3	2.06	0.56
1:2:1319:U:N3	1:2:1351:A:H2	2.04	0.56
3:B:138:VAL:HG23	3:B:152:LEU:HD23	1.87	0.56
31:4:76:A:N6	33:7:278:SER:HB2	2.20	0.56
35:9:15:LEU:HD11	35:9:31:LEU:HD22	1.87	0.56
1:2:145:G:N2	1:2:146:A:N1	2.53	0.56
1:2:286:4AC:O7	1:2:286:4AC:H5	2.04	0.56
1:2:441:G:H2'	1:2:442:A:H8	1.71	0.56
1:2:442:A:H2'	1:2:443:G:C8	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:445:G:OP2	23:V:33:ARG:NH1	2.38	0.56
1:2:691:G:H2'	1:2:692:G:C8	2.41	0.56
1:2:695:A:H2'	1:2:696:A:H8	1.70	0.56
1:2:717:C:OP2	18:Q:16:ARG:NH2	2.39	0.56
1:2:1121:C:O2	12:K:16:ARG:NH1	2.38	0.56
1:2:1234:G:HO2'	1:2:1257:C:HO2'	1.54	0.56
1:2:1323:A:H62	1:2:1347:G:H21	1.54	0.56
8:G:62:GLU:OE1	8:G:62:GLU:N	2.39	0.56
9:H:44:LEU:HD12	9:H:45:PRO:HD2	1.88	0.56
12:K:34:GLU:OE1	22:U:150:TYR:OH	2.24	0.56
21:T:98:MET:HE2	21:T:106:PHE:CE1	2.41	0.56
22:U:21:LYS:HA	22:U:52:TYR:HE1	1.71	0.56
33:7:194:LEU:O	33:7:198:ILE:HG12	2.06	0.56
1:2:140:A:N6	1:2:229:G:N1	2.16	0.56
1:2:748:A:N6	1:2:769:A:N3	2.54	0.56
1:2:814:A:H1'	2:A:134:GLN:NE2	2.20	0.56
1:2:1068:C:C4	1:2:1069:G:N7	2.74	0.56
1:2:1449:G:H2'	1:2:1450:U:O4'	2.06	0.56
7:F:66:LEU:HD11	7:F:174:ILE:HD11	1.88	0.56
12:K:41:ALA:O	12:K:44:THR:N	2.29	0.56
19:R:59:LYS:HG2	19:R:60:TYR:CE2	2.41	0.56
25:X:33:GLU:HA	25:X:37:LYS:HG3	1.88	0.56
34:8:127:CYS:SG	34:8:128:LEU:N	2.78	0.56
1:2:516:G:C2	1:2:517:G:C8	2.94	0.56
1:2:1319:U:C2	1:2:1351:A:H2	2.24	0.56
12:K:10:ARG:HD3	12:K:76:GLU:HB3	1.86	0.56
25:X:12:ILE:HG12	25:X:29:VAL:HA	1.88	0.56
26:Y:10:VAL:HG23	26:Y:15:VAL:HG12	1.88	0.56
31:4:3:C:H2'	31:4:4:G:O4'	2.05	0.56
33:7:275:LYS:HB2	33:7:300:TYR:CE2	2.40	0.56
35:9:123:GLU:HA	35:9:127:TRP:HD1	1.71	0.56
1:2:185:G:C4	1:2:186:G:C8	2.94	0.55
1:2:437:U:O2	1:2:462:U:O2	2.23	0.55
1:2:1321:G:N2	1:2:1347:G:H2'	2.20	0.55
1:2:1356:C:H2'	1:2:1357:C:H6	1.71	0.55
9:H:98:VAL:HG22	12:K:40:ILE:HD11	1.87	0.55
33:7:14:VAL:HG12	33:7:115:ILE:HB	1.89	0.55
1:2:868:4AC:H2'	1:2:869:G:H8	1.71	0.55
1:2:1133:U:OP1	20:S:5:ARG:NE	2.29	0.55
1:2:1453:G:C4	33:7:352:ARG:HD2	2.41	0.55
2:A:108:PHE:CE1	2:A:143:GLN:HB2	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:217:ASP:N	6:E:217:ASP:OD1	2.38	0.55
9:H:28:VAL:HG12	9:H:124:VAL:HG13	1.88	0.55
11:J:88:GLN:HB2	11:J:91:ARG:NH2	2.20	0.55
31:4:10:G:H2'	31:4:11:A:H8	1.70	0.55
1:2:838:C:H2'	1:2:839:4AC:C5	2.37	0.55
1:2:845:G:C6	1:2:846:C:N4	2.75	0.55
1:2:1130:G:N7	20:S:44:LYS:NZ	2.55	0.55
1:2:1334:A:P	17:P:32:ARG:HH22	2.29	0.55
4:C:13:VAL:HG22	4:C:20:GLU:HB3	1.87	0.55
16:O:84:ASP:HB3	16:O:87:THR:O	2.05	0.55
28:0:34:ARG:CZ	33:7:381:GLU:HB2	2.35	0.55
29:3:4:PRO:HG3	29:3:55:GLU:HB3	1.87	0.55
33:7:6:VAL:HG11	33:7:87:ARG:HH21	1.71	0.55
33:7:50:GLY:N	33:7:93:ASP:O	2.25	0.55
33:7:130:ARG:HH12	33:7:338:ARG:HE	1.54	0.55
1:2:56:C:OP2	1:2:374:A:N6	2.30	0.55
1:2:923:G:O2'	1:2:942:C:O2'	2.25	0.55
1:2:1396:G:N2	1:2:1448:C:H1'	2.22	0.55
5:D:70:ARG:HD3	5:D:89:LEU:HD22	1.87	0.55
22:U:25:GLU:HG3	22:U:108:ALA:HA	1.89	0.55
1:2:523:A:H2'	1:2:524:C:O4'	2.05	0.55
1:2:541:G:C2	1:2:788:G:C8	2.93	0.55
1:2:832:G:H2'	1:2:833:G:H8	1.72	0.55
1:2:1263:A:O2'	9:H:96:LYS:HE3	2.07	0.55
1:2:1403:G:H2'	1:2:1404:G:O4'	2.07	0.55
5:D:163:PRO:HA	5:D:168:ARG:HD2	1.87	0.55
11:J:42:LYS:O	11:J:58:THR:OG1	2.23	0.55
13:L:10:SER:HB2	13:L:94:VAL:HG22	1.87	0.55
21:T:25:ALA:HB1	21:T:33:ARG:HG3	1.88	0.55
28:0:29:GLN:O	28:0:33:GLU:N	2.23	0.55
31:4:64:G:H2'	31:4:65:C:O4'	2.07	0.55
33:7:24:THR:HG23	33:7:27:GLN:OE1	2.06	0.55
1:2:178:A:C2	1:2:179:G:H1'	2.41	0.55
1:2:237:A:H2'	1:2:238:U:C6	2.42	0.55
1:2:607:A:C5	1:2:608:U:C4	2.95	0.55
1:2:1247:G:C2	1:2:1248:G:H1'	2.41	0.55
33:7:255:VAL:HG12	33:7:272:ILE:HB	1.89	0.55
33:7:259:LEU:O	33:7:270:GLU:N	2.39	0.55
1:2:1202:5MC:H3'	16:O:136:ARG:HH12	1.71	0.55
1:2:1388:C:H2'	1:2:1389:C:C6	2.42	0.55
1:2:1470:C:C4	1:2:1473:G:C6	2.94	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:168:VAL:HB	6:E:169:PRO:HD3	1.87	0.55
10:I:52:PHE:HE1	10:I:54:ASP:HB2	1.72	0.55
21:T:83:VAL:HG12	21:T:84:HIS:N	2.21	0.55
23:V:74:ASP:OD2	23:V:77:ARG:N	2.26	0.55
27:Z:83:GLN:HG3	27:Z:84:GLU:H	1.71	0.55
31:4:34:C:H2'	31:4:35:A:H8	1.71	0.55
31:4:76:A:H61	33:7:278:SER:HB2	1.71	0.55
1:2:237:A:H2'	1:2:238:U:H6	1.72	0.55
1:2:310:G:O3'	19:R:59:LYS:NZ	2.23	0.55
1:2:320:G:C2	1:2:321:G:C8	2.95	0.55
1:2:519:G:H2'	1:2:520:G:C8	2.42	0.55
1:2:727:G:C6	1:2:728:G:H1'	2.42	0.55
1:2:810:U:H3'	1:2:812:C:N4	2.22	0.55
7:F:130:SER:HB2	7:F:158:PRO:HB2	1.89	0.55
8:G:54:GLU:N	8:G:54:GLU:OE1	2.40	0.55
33:7:51:TYR:HE1	33:7:90:SER:HB2	1.70	0.55
34:8:12:ASP:OD1	34:8:13:ARG:N	2.39	0.55
1:2:82:C:H2'	1:2:83:C:C6	2.42	0.55
1:2:183:U:H2'	1:2:184:G:C8	2.38	0.55
1:2:927:U:H2'	1:2:928:U:C6	2.42	0.55
21:T:80:THR:OG1	21:T:93:GLU:HG3	2.07	0.55
25:X:63:GLU:N	25:X:63:GLU:OE2	2.39	0.55
29:3:39:THR:HG21	29:3:100:ALA:HB3	1.88	0.55
33:7:276:ILE:HG23	33:7:297:ILE:HG23	1.89	0.55
1:2:162:G:O2'	8:G:120:ASN:ND2	2.39	0.55
1:2:368:C:H2'	1:2:369:G:H8	1.72	0.55
1:2:563:G:N2	10:I:124:ARG:HH21	2.05	0.55
1:2:1429:U:H2'	1:2:1430:C:C6	2.42	0.55
1:2:1440:C:H2'	1:2:1441:U:C5	2.41	0.55
31:4:9:G:H21	31:4:45:G:H2'	1.71	0.55
32:6:38:ASP:OD1	32:6:48:ARG:HG2	2.06	0.55
1:2:236:G:C6	1:2:237:A:C5	2.95	0.54
1:2:512:G:OP2	5:D:38:LYS:N	2.32	0.54
1:2:572:G:C2	1:2:598:U:C4	2.95	0.54
1:2:722:G:OP2	18:Q:131:ARG:NH1	2.32	0.54
1:2:867:C:H5	1:2:868:4AC:C7	2.21	0.54
1:2:869:G:N2	1:2:871:A:OP1	2.40	0.54
1:2:879:A:H2'	1:2:880:A:C8	2.37	0.54
1:2:941:A:C5	1:2:942:C:N3	2.75	0.54
1:2:946:G:OP2	17:P:40:ARG:NE	2.33	0.54
1:2:1035:U:OP1	7:F:80:ARG:NH1	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:13:LEU:HG	3:B:18:HIS:HE1	1.71	0.54
6:E:179:PHE:CE2	6:E:202:ILE:HD11	2.42	0.54
1:2:858:G:H2'	1:2:859:G:C8	2.42	0.54
1:2:1310:U:H4'	1:2:1311:G:O5'	2.07	0.54
1:2:1380:U:H2'	1:2:1381:C:H6	1.71	0.54
9:H:10:PHE:H	12:K:42:ARG:HH12	1.53	0.54
16:O:7:ILE:HD13	16:O:16:ASP:HA	1.89	0.54
18:Q:120:ARG:NH1	18:Q:124:LEU:HD11	2.23	0.54
21:T:52:ARG:O	21:T:56:LYS:N	2.40	0.54
29:3:23:VAL:HG12	29:3:90:ALA:HB2	1.89	0.54
30:5:813:A:C6	30:5:814:U:C4	2.94	0.54
31:4:6:G:C2	31:4:7:G:H1'	2.42	0.54
32:6:77:ASP:H	32:6:79:ARG:NH1	2.06	0.54
33:7:17:HIS:HB3	33:7:20:HIS:CE1	2.43	0.54
33:7:213:PRO:HB3	33:7:246:LEU:H	1.71	0.54
33:7:248:LYS:O	33:7:251:GLN:HB2	2.07	0.54
1:2:22:G:H4'	7:F:79:ARG:HH21	1.71	0.54
1:2:471:G:C6	1:2:472:G:C6	2.96	0.54
1:2:484:G:N2	1:2:495:G:O6	2.38	0.54
1:2:695:A:C2	1:2:696:A:C5	2.95	0.54
1:2:1022:G:C6	1:2:1178:A:N1	2.76	0.54
1:2:1113:G:C2	1:2:1114:G:C5	2.94	0.54
5:D:162:ASN:O	5:D:164:GLN:N	2.34	0.54
7:F:35:HIS:ND1	7:F:36:GLU:HG3	2.22	0.54
9:H:38:ASN:OD1	9:H:39:LEU:N	2.40	0.54
1:2:418:G:H4'	5:D:170:MET:HE2	1.89	0.54
1:2:546:4AC:O7	1:2:546:4AC:H5	2.07	0.54
1:2:657:G:O5'	1:2:657:G:H8	1.91	0.54
1:2:738:C:C2	1:2:776:G:N2	2.75	0.54
1:2:1041:4AC:O2	1:2:1047:G:N2	2.40	0.54
7:F:179:GLY:O	7:F:181:GLN:HG3	2.07	0.54
14:M:98:ALA:O	14:M:102:ILE:HG22	2.07	0.54
32:6:23:GLN:HE22	32:6:68:ILE:HD12	1.72	0.54
33:7:135:ALA:O	33:7:138:ILE:HB	2.08	0.54
1:2:69:G:C6	1:2:70:U:C4	2.96	0.54
1:2:1266:C:H2'	1:2:1267:G:C8	2.41	0.54
1:2:1292:A:H5'	21:T:41:THR:HG21	1.88	0.54
1:2:1448:C:O2'	1:2:1449:G:O5'	2.22	0.54
2:A:27:PHE:HZ	2:A:83:PHE:HB2	1.73	0.54
3:B:54:VAL:HA	3:B:57:LYS:HG2	1.90	0.54
18:Q:104:ASN:OD1	18:Q:104:ASN:N	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:R:19:PRO:O	19:R:26:HIS:N	2.31	0.54
26:Y:8:TYR:HB3	26:Y:17:ARG:HG3	1.88	0.54
33:7:254:LYS:HB3	33:7:319:ALA:HA	1.89	0.54
34:8:33:MET:HA	34:8:46:ASN:HD21	1.72	0.54
35:9:245:GLN:OE1	35:9:249:ASN:ND2	2.40	0.54
1:2:123:G:C4'	19:R:32:ARG:HH21	2.20	0.54
1:2:1419:C:C2'	1:2:1420:U:H5'	2.38	0.54
1:2:1506:U:O2	30:5:809:G:C2	2.61	0.54
33:7:162:GLN:NE2	33:7:165:GLN:OE1	2.41	0.54
1:2:346:A:H2'	1:2:347:G:O4'	2.08	0.54
1:2:687:C:O2'	1:2:688:A:OP1	2.21	0.54
1:2:897:G:H22	30:5:818:A:H3'	1.73	0.54
1:2:955:A:H8	1:2:1175:A:N1	2.06	0.54
16:O:80:ASN:HB2	16:O:92:HIS:CE1	2.42	0.54
20:S:27:ASP:OD1	20:S:29:GLU:N	2.33	0.54
33:7:52:ALA:HB3	33:7:91:PHE:HB2	1.90	0.54
35:9:242:ALA:O	35:9:245:GLN:NE2	2.40	0.54
1:2:643:A:C6	1:2:644:C:C4	2.96	0.54
1:2:839:4AC:H5	1:2:839:4AC:O7	2.08	0.54
1:2:964:G:N1	1:2:1186:A:OP2	2.38	0.54
1:2:1212:A:N7	1:2:1275:U:N3	2.56	0.54
29:3:18:LYS:O	29:3:110:LEU:HB3	2.08	0.54
31:4:75:C:H2'	31:4:76:A:H5'	1.90	0.54
33:7:15:VAL:HB	33:7:132:HIS:CG	2.43	0.54
1:2:98:C:H2'	1:2:99:C:C6	2.43	0.54
1:2:1362:C:H2'	1:2:1363:C:H6	1.72	0.54
1:2:1419:C:H2'	1:2:1420:U:H5'	1.90	0.54
6:E:10:LEU:HD12	6:E:11:LYS:H	1.73	0.54
18:Q:105:LEU:HD23	18:Q:122:LEU:HD12	1.90	0.54
31:4:38:A:C5	31:4:39:C:C6	2.96	0.54
33:7:224:ASN:HB3	33:7:228:THR:HG21	1.89	0.54
33:7:376:ASP:CG	33:7:377:GLU:HG3	2.33	0.54
1:2:174:C:H2'	1:2:175:C:H6	1.73	0.54
1:2:244:G:C2	1:2:245:G:N7	2.75	0.54
1:2:554:G:H2'	1:2:555:G:C8	2.40	0.54
1:2:815:G:H2'	1:2:816:C:H6	1.73	0.54
1:2:861:G:N7	28:0:2:LYS:HG2	2.23	0.54
1:2:924:C:H4'	1:2:936:A:H61	1.72	0.54
1:2:1453:G:C6	33:7:352:ARG:HD2	2.42	0.54
1:2:1480:G:H2'	1:2:1481:U:C6	2.42	0.54
3:B:75:TYR:CZ	3:B:161:ARG:HD3	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:7:244:GLN:N	33:7:244:GLN:OE1	2.41	0.54
1:2:632:A:H5'	1:2:633:G:OP2	2.08	0.53
1:2:639:G:C6	1:2:640:G:N7	2.76	0.53
1:2:1048:C:O2	1:2:1048:C:H2'	2.08	0.53
1:2:1479:4AC:OP2	28:0:15:ARG:NE	2.39	0.53
1:2:1491:U:H5''	14:M:136:ARG:HH22	1.72	0.53
3:B:188:PHE:CE1	3:B:190:ILE:HD13	2.43	0.53
29:3:118:VAL:HA	29:3:121:LEU:HD12	1.89	0.53
32:6:67:VAL:HG11	32:6:82:ILE:HG12	1.88	0.53
1:2:193:G:H2'	1:2:194:A:O4'	2.08	0.53
1:2:436:U:C4	1:2:437:U:C6	2.96	0.53
1:2:1393:G:O2'	33:7:375:LYS:HD2	2.09	0.53
21:T:98:MET:HA	21:T:101:HIS:CD2	2.43	0.53
25:X:59:GLU:C	25:X:61:GLU:H	2.16	0.53
26:Y:21:PHE:HB3	26:Y:28:GLY:H	1.74	0.53
33:7:272:ILE:HD13	33:7:305:LEU:HD11	1.90	0.53
1:2:46:G:O6	1:2:412:A:N6	2.41	0.53
1:2:518:U:C2	1:2:519:G:C8	2.96	0.53
1:2:779:G:O6	40:2:1714:HOH:O	2.18	0.53
1:2:911:G:C2	1:2:912:G:C8	2.97	0.53
1:2:1184:4AC:O7	1:2:1184:4AC:H5	2.09	0.53
1:2:1333:C:OP1	17:P:19:ARG:NH2	2.41	0.53
1:2:1341:C:H3'	12:K:122:SER:HB3	1.90	0.53
1:2:1459:A:N6	1:2:1460:G:O6	2.41	0.53
3:B:171:LEU:O	3:B:175:ILE:N	2.41	0.53
8:G:48:ASN:HD21	8:G:55:PHE:HB2	1.72	0.53
31:4:50:U:H2'	31:4:51:C:C6	2.44	0.53
1:2:158:A:C5	1:2:159:A:C5	2.96	0.53
1:2:918:A:O2'	1:2:1307:A:N3	2.38	0.53
1:2:923:G:OP2	16:O:130:ARG:NH1	2.42	0.53
1:2:1064:G:H2'	1:2:1065:U:H6	1.73	0.53
1:2:1339:C:H2'	1:2:1340:G:C8	2.43	0.53
3:B:142:ASP:HB2	3:B:158:ASN:ND2	2.24	0.53
33:7:98:GLU:HG2	33:7:406:ARG:NH1	2.24	0.53
33:7:122:GLU:HG2	33:7:126:GLN:HG3	1.90	0.53
1:2:182:C:H4'	11:J:117:ASP:OD2	2.09	0.53
1:2:1014:A:H2	1:2:1175:A:N3	2.07	0.53
1:2:1020:A:N6	1:2:1180:G:C6	2.77	0.53
1:2:1406:G:O2'	1:2:1437:A:N6	2.41	0.53
8:G:94:PHE:CZ	8:G:96:PRO:HA	2.44	0.53
10:I:106:THR:HG23	10:I:108:GLN:H	1.72	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Q:98:LEU:HB3	18:Q:129:ILE:HD11	1.90	0.53
24:W:17:ARG:HG2	24:W:64:LEU:CD2	2.39	0.53
33:7:392:ASN:N	33:7:413:VAL:O	2.33	0.53
1:2:50:G:N2	1:2:408:C:C2	2.77	0.53
1:2:64:U:H2'	1:2:65:G:H8	1.73	0.53
1:2:246:C:H2'	1:2:247:G:C8	2.43	0.53
1:2:330:A:C6	1:2:342:G:C6	2.96	0.53
1:2:394:4AC:O7	1:2:394:4AC:H5	2.09	0.53
1:2:614:G:C2	1:2:615:G:C8	2.97	0.53
1:2:851:4AC:O2'	1:2:852:G:H5'	2.08	0.53
1:2:937:U:C2	1:2:941:A:N1	2.77	0.53
1:2:1389:C:O2	1:2:1454:G:N2	2.37	0.53
2:A:132:THR:HA	2:A:135:GLU:HB3	1.89	0.53
26:Y:5:TRP:HH2	29:3:65:HIS:ND1	2.06	0.53
29:3:73:LYS:NZ	29:3:75:ILE:HB	2.22	0.53
1:2:955:A:C8	1:2:1175:A:N1	2.76	0.53
1:2:1023:G:O5'	1:2:1023:G:H8	1.92	0.53
1:2:1234:G:H21	1:2:1249:A:N6	2.06	0.53
1:2:1417:U:C2	1:2:1418:C:C5	2.97	0.53
3:B:131:ILE:HG12	3:B:149:TYR:CD1	2.43	0.53
6:E:224:ASP:N	6:E:224:ASP:OD1	2.42	0.53
7:F:62:ASN:CG	7:F:91:ASN:HA	2.34	0.53
7:F:207:ASN:HA	7:F:210:LYS:HG3	1.91	0.53
23:V:17:LYS:HD2	23:V:71:TYR:CD2	2.44	0.53
25:X:26:GLN:HE21	25:X:67:ILE:HB	1.74	0.53
27:Z:70:GLU:HB3	27:Z:78:PRO:HG3	1.91	0.53
27:Z:109:PHE:CZ	27:Z:110:ARG:HG3	2.43	0.53
31:4:59:A:H2'	31:4:60:U:O4'	2.09	0.53
1:2:181:C:H2'	1:2:182:C:H6	1.73	0.53
1:2:304:G:O6	1:2:312:G:N1	2.42	0.53
1:2:869:G:HO2'	1:2:871:A:H62	1.53	0.53
1:2:1042:G:N1	1:2:1046:G:C6	2.77	0.53
1:2:1232:C:H2'	1:2:1233:4AC:C6	2.39	0.53
1:2:1392:A:O2'	1:2:1393:G:C8	2.61	0.53
2:A:98:ARG:O	2:A:101:THR:OG1	2.25	0.53
8:G:84:VAL:HG12	8:G:85:ARG:H	1.73	0.53
15:N:119:ILE:O	15:N:119:ILE:HG13	2.09	0.53
19:R:30:HIS:ND1	19:R:30:HIS:O	2.42	0.53
23:V:41:VAL:O	23:V:45:ASP:HA	2.09	0.53
23:V:52:VAL:HA	23:V:90:ASP:OD2	2.09	0.53
30:5:806:G:C2	30:5:807:G:H1'	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:4:12:G:O6	31:4:24:U:N3	2.42	0.53
31:4:53:G:C2	31:4:62:C:C2	2.97	0.53
33:7:79:SER:OG	33:7:81:ASP:OD1	2.19	0.53
1:2:1115:G:C5	1:2:1116:A:N6	2.76	0.53
1:2:1263:A:H2'	1:2:1264:C:H5'	1.89	0.53
15:N:70:ARG:HH21	15:N:118:ASP:CG	2.16	0.53
21:T:54:ALA:HA	21:T:58:LYS:O	2.09	0.53
23:V:56:ILE:O	23:V:56:ILE:HG13	2.08	0.53
26:Y:17:ARG:HH12	29:3:44:GLU:CD	2.17	0.53
35:9:22:VAL:HA	35:9:27:SER:OG	2.09	0.53
35:9:103:LEU:HD11	35:9:136:PRO:HB2	1.91	0.53
1:2:97:A:H2'	1:2:98:C:H6	1.74	0.53
1:2:1241:A:C6	1:2:1242:A:C6	2.97	0.53
1:2:1395:G:N2	1:2:1448:C:O2	2.41	0.53
30:5:808:A:C6	30:5:809:G:N7	2.77	0.53
1:2:529:A:C2	1:2:533:G:C5	2.97	0.52
1:2:697:G:N2	1:2:733:A:OP1	2.42	0.52
1:2:838:C:H2'	1:2:839:4AC:C6	2.39	0.52
1:2:1470:C:C5	1:2:1473:G:C5	2.98	0.52
5:D:123:GLN:HA	5:D:126:VAL:HG12	1.91	0.52
8:G:23:GLY:O	8:G:27:GLU:HG2	2.09	0.52
12:K:32:PRO:HB3	22:U:150:TYR:CE2	2.43	0.52
29:3:114:ILE:HA	29:3:117:LYS:HB2	1.90	0.52
31:4:60:U:OP1	31:4:61:C:N4	2.42	0.52
32:6:23:GLN:HE21	32:6:68:ILE:HB	1.75	0.52
32:6:27:VAL:O	32:6:40:ARG:HB3	2.09	0.52
1:2:541:G:N1	1:2:788:G:N7	2.58	0.52
1:2:815:G:H2'	1:2:816:C:C6	2.45	0.52
1:2:1449:G:H2'	1:2:1450:U:C4'	2.38	0.52
29:3:54:ALA:HA	29:3:80:VAL:HB	1.92	0.52
33:7:181:ILE:HD13	33:7:194:LEU:HA	1.90	0.52
34:8:5:LYS:O	34:8:9:GLU:CB	2.56	0.52
1:2:236:G:H2'	1:2:237:A:O4'	2.10	0.52
1:2:386:C:H2'	1:2:387:G:C8	2.45	0.52
1:2:387:G:C6	1:2:395:G:N1	2.77	0.52
1:2:561:A:O2'	1:2:562:A:OP2	2.26	0.52
1:2:772:C:H2'	1:2:772:C:O2	2.09	0.52
1:2:986:U:N3	1:2:988:A:OP2	2.42	0.52
1:2:996:G:O2'	1:2:997:C:O5'	2.26	0.52
1:2:1324:C:H2'	1:2:1325:C:H6	1.74	0.52
1:2:1435:C:O2'	1:2:1436:G:OP1	2.27	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1479:4AC:C2	1:2:1495:G:N2	2.72	0.52
3:B:25:THR:O	3:B:28:MET:N	2.42	0.52
4:C:3:GLU:CB	7:F:230:PRO:HD2	2.38	0.52
8:G:8:ILE:O	8:G:16:ALA:HB1	2.09	0.52
9:H:182:GLU:O	9:H:186:GLU:HG2	2.09	0.52
26:Y:38:TRP:HB2	26:Y:47:GLU:OE2	2.09	0.52
31:4:29:G:H2'	31:4:30:G:C8	2.37	0.52
33:7:353:ALA:CB	33:7:370:VAL:HG13	2.39	0.52
33:7:374:LYS:HE2	33:7:375:LYS:H	1.74	0.52
1:2:393:C:H3'	1:2:394:4AC:H6	1.92	0.52
1:2:417:C:H2'	1:2:418:G:H8	1.75	0.52
1:2:466:G:C2	1:2:467:G:N2	2.69	0.52
1:2:479:4AC:O7	1:2:479:4AC:H5	2.09	0.52
1:2:652:G:H22	1:2:673:C:N4	2.08	0.52
1:2:1029:G:O2'	1:2:1164:G:N2	2.43	0.52
1:2:1181:C:H2'	1:2:1182:C:C6	2.45	0.52
1:2:1476:A:C2	1:2:1477:G:C5	2.97	0.52
2:A:11:LYS:HD2	35:9:21:GLN:HB3	1.91	0.52
3:B:187:GLU:O	3:B:189:LYS:HG2	2.10	0.52
5:D:67:GLU:OE1	5:D:68:ILE:HG13	2.10	0.52
7:F:58:ASN:HA	7:F:63:GLN:NE2	2.24	0.52
9:H:89:GLU:O	9:H:90:HIS:ND1	2.42	0.52
13:L:100:LEU:HD23	13:L:100:LEU:H	1.73	0.52
14:M:89:SER:O	14:M:89:SER:OG	2.17	0.52
21:T:79:LEU:O	21:T:94:ILE:N	2.39	0.52
21:T:101:HIS:HB3	21:T:105:GLU:OE1	2.09	0.52
29:3:18:LYS:HB2	29:3:114:ILE:HD11	1.92	0.52
33:7:95:PRO:HD2	33:7:104:MET:HB3	1.91	0.52
1:2:162:G:H2'	1:2:163:G:C8	2.45	0.52
1:2:306:G:H4'	1:2:523:A:H4'	1.91	0.52
2:A:119:ARG:HB2	2:A:192:LEU:HD11	1.91	0.52
18:Q:46:SER:O	18:Q:50:ILE:HG13	2.09	0.52
32:6:19:PRO:HB3	32:6:23:GLN:HB2	1.91	0.52
33:7:17:HIS:CG	33:7:128:GLN:HB2	2.45	0.52
33:7:273:PHE:HB2	35:9:190:PRO:HG3	1.92	0.52
1:2:861:G:O2'	1:2:877:G:O6	2.26	0.52
1:2:945:C:C5	1:2:947:G:C5	2.96	0.52
1:2:1194:G:N3	1:2:1195:G:C8	2.78	0.52
1:2:1320:A:C4	1:2:1322:U:C4	2.98	0.52
31:4:30:G:C2	31:4:31:G:C8	2.97	0.52
33:7:11:ASN:HA	33:7:90:SER:OG	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:7:101:MET:O	33:7:104:MET:HG3	2.10	0.52
33:7:151:VAL:HG11	34:8:14:LEU:HD23	1.92	0.52
1:2:419:U:C2	1:2:420:G:C8	2.98	0.52
1:2:666:C:H2'	1:2:667:U:H6	1.74	0.52
1:2:738:C:N3	1:2:776:G:C2	2.78	0.52
1:2:755:U:H2'	1:2:756:U:O4'	2.10	0.52
1:2:792:G:H2'	1:2:793:C:H6	1.75	0.52
1:2:839:4AC:N3	1:2:840:G:C5	2.78	0.52
1:2:910:A:O3'	9:H:156:ARG:NH2	2.39	0.52
1:2:982:A:H2'	1:2:983:G:C8	2.43	0.52
1:2:1321:G:O2'	1:2:1322:U:OP2	2.28	0.52
3:B:101:MET:SD	3:B:112:PRO:HG2	2.50	0.52
5:D:125:ILE:O	5:D:128:GLY:N	2.26	0.52
6:E:12:ARG:HH21	6:E:22:GLU:HG3	1.75	0.52
10:I:50:PHE:CB	10:I:63:VAL:HG22	2.40	0.52
12:K:4:ILE:HG21	12:K:88:GLU:OE1	2.09	0.52
13:L:25:GLN:O	13:L:29:ARG:N	2.39	0.52
31:4:7:G:H2'	31:4:49:G:C8	2.45	0.52
35:9:194:GLU:HA	35:9:197:LYS:HD2	1.91	0.52
1:2:97:A:H2'	1:2:98:C:C6	2.45	0.52
1:2:274:G:H3'	1:2:276:C:H41	1.75	0.52
1:2:300:G:H1	1:2:319:4AC:H4	1.58	0.52
1:2:514:G:H2'	1:2:515:U:C6	2.44	0.52
1:2:796:G:H1	1:2:829:G:H21	1.58	0.52
1:2:1172:G:H2'	1:2:1173:U:C6	2.44	0.52
3:B:13:LEU:O	3:B:16:GLY:N	2.37	0.52
5:D:116:ARG:NH1	5:D:170:MET:HE3	2.25	0.52
6:E:66:LEU:HD21	6:E:71:PHE:CD2	2.45	0.52
8:G:97:LYS:HD2	8:G:97:LYS:O	2.10	0.52
16:O:132:ARG:HG2	16:O:132:ARG:O	2.09	0.52
17:P:23:ARG:HH11	17:P:42:CYS:HB3	1.75	0.52
35:9:183:ILE:O	35:9:227:TYR:N	2.39	0.52
1:2:231:C:H2'	1:2:232:C:H6	1.75	0.52
1:2:712:C:H2'	1:2:713:G:H8	1.75	0.52
1:2:793:C:H2'	1:2:794:U:C6	2.45	0.52
1:2:894:G:N2	1:2:1369:C:C2	2.78	0.52
1:2:1233:4AC:O2	1:2:1251:G:N2	2.43	0.52
1:2:1379:G:C2	1:2:1380:U:C5	2.97	0.52
1:2:1494:G:N7	14:M:132:ARG:NH1	2.55	0.52
3:B:169:TRP:CD1	3:B:195:PHE:HE2	2.23	0.52
8:G:5:LYS:N	8:G:117:VAL:O	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:63:ILE:HA	8:G:121:VAL:HG12	1.92	0.52
12:K:4:ILE:O	12:K:19:ILE:HG22	2.10	0.52
15:N:134:LEU:O	15:N:138:VAL:HG23	2.10	0.52
31:4:13:C:H2'	31:4:14:A:H5''	1.90	0.52
1:2:143:G:O6	1:2:174:C:N4	2.43	0.52
1:2:158:A:H2'	1:2:159:A:C8	2.45	0.52
1:2:379:4AC:O7	1:2:379:4AC:H5	2.10	0.52
1:2:424:C:O2'	1:2:425:U:OP2	2.26	0.52
1:2:517:G:C2	1:2:518:U:C4	2.97	0.52
1:2:529:A:H5''	1:2:530:U:OP1	2.10	0.52
1:2:533:G:C6	1:2:534:G:C5	2.98	0.52
1:2:543:G:N2	1:2:544:G:C4	2.77	0.52
1:2:628:G:C4	1:2:629:G:C8	2.97	0.52
1:2:714:G:OP1	24:W:12:ARG:NH2	2.42	0.52
1:2:723:G:H2'	1:2:724:U:O4'	2.10	0.52
1:2:1049:G:C5	1:2:1050:U:C4	2.99	0.52
1:2:1141:A:C2	1:2:1143:A:C6	2.98	0.52
1:2:1196:G:H2'	1:2:1197:C:C6	2.45	0.52
1:2:1224:A:C6	1:2:1261:A:C5	2.98	0.52
1:2:1241:A:H2'	1:2:1242:A:H8	1.75	0.52
1:2:1310:U:O2	9:H:174:TYR:OH	2.28	0.52
2:A:105:ASP:OD1	2:A:106:GLY:N	2.43	0.52
7:F:173:LYS:O	7:F:176:ARG:N	2.42	0.52
10:I:81:VAL:HG22	10:I:123:GLY:O	2.09	0.52
11:J:87:ARG:HE	11:J:88:GLN:HB3	1.75	0.52
12:K:26:VAL:HG23	12:K:62:ILE:HG22	1.91	0.52
20:S:41:VAL:HG11	20:S:47:ARG:HB3	1.92	0.52
33:7:200:GLU:HG3	33:7:201:TYR:N	2.25	0.52
34:8:114:THR:HG23	34:8:127:CYS:HA	1.92	0.52
1:2:643:A:C4	1:2:644:C:C5	2.99	0.51
1:2:722:G:H2'	1:2:723:G:C8	2.45	0.51
1:2:1194:G:C2	1:2:1195:G:C8	2.98	0.51
1:2:1241:A:C2	1:2:1242:A:C4	2.98	0.51
1:2:1396:G:N7	1:2:1397:G:H8	2.08	0.51
1:2:1474:G:H4'	1:2:1475:U:H5''	1.92	0.51
6:E:103:LEU:O	6:E:111:ILE:HG12	2.10	0.51
31:4:14:A:C6	31:4:15:G:H1'	2.45	0.51
31:4:26:G:C2	31:4:27:U:C5	2.98	0.51
31:4:55:PSU:O2'	31:4:57:A:N7	2.40	0.51
33:7:336:LEU:HD12	33:7:337:GLU:H	1.74	0.51
1:2:423:U:O2'	1:2:424:C:O5'	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:705:G:H2'	1:2:706:C:C6	2.44	0.51
1:2:1451:G:O2'	1:2:1452:A:H5''	2.10	0.51
10:I:106:THR:OG1	10:I:107:SER:N	2.44	0.51
20:S:26:ARG:NH2	20:S:59:ARG:HB2	2.25	0.51
33:7:89:ILE:HD12	33:7:91:PHE:CZ	2.45	0.51
33:7:280:ARG:HG3	33:7:284:GLU:O	2.10	0.51
1:2:106:C:C4	1:2:107:G:C5	2.97	0.51
1:2:549:A:H2'	1:2:550:G:O4'	2.10	0.51
1:2:641:G:H5''	1:2:642:U:OP2	2.11	0.51
1:2:802:G:C4	1:2:823:G:N2	2.77	0.51
1:2:1501:U:C2	1:2:1502:C:C5	2.98	0.51
9:H:13:HIS:CE1	12:K:54:GLU:HG3	2.44	0.51
9:H:25:ASP:OD1	9:H:25:ASP:N	2.43	0.51
9:H:147:HIS:CD2	9:H:147:HIS:H	2.21	0.51
19:R:84:ASP:N	19:R:84:ASP:OD1	2.42	0.51
33:7:313:GLY:HA3	33:7:363:SER:O	2.10	0.51
33:7:400:GLN:O	33:7:400:GLN:NE2	2.43	0.51
34:8:122:SER:HA	34:8:138:PRO:HD3	1.92	0.51
1:2:218:C:N4	1:2:219:G:C5	2.79	0.51
1:2:218:C:H2'	1:2:219:G:O4'	2.10	0.51
1:2:543:G:H2'	1:2:544:G:C8	2.45	0.51
1:2:626:4AC:O7	1:2:626:4AC:H5	2.08	0.51
1:2:643:A:C4	1:2:644:C:C6	2.99	0.51
1:2:643:A:C5	1:2:644:C:C5	2.98	0.51
1:2:795:A:H2'	1:2:796:G:H8	1.76	0.51
1:2:875:C:N3	1:2:876:U:C5	2.78	0.51
1:2:911:G:C2	1:2:912:G:C5	2.97	0.51
1:2:939:5MC:HM52	1:2:940:A:C2	2.45	0.51
1:2:1144:A:H8	1:2:1144:A:OP2	1.94	0.51
1:2:1338:U:P	22:U:83:ARG:HH22	2.32	0.51
16:O:15:LEU:HD13	16:O:24:ALA:HB3	1.92	0.51
18:Q:67:ARG:HD3	18:Q:74:ARG:O	2.10	0.51
25:X:18:THR:O	25:X:24:VAL:HG22	2.11	0.51
27:Z:48:ALA:O	27:Z:85:ILE:HG13	2.11	0.51
31:4:7:G:C2	31:4:67:C:C4	2.98	0.51
1:2:116:A:C4	1:2:118:A:C5	2.98	0.51
1:2:334:A:H4'	11:J:50:GLY:O	2.11	0.51
1:2:484:G:N2	1:2:495:G:C6	2.78	0.51
1:2:604:G:N3	1:2:605:G:C8	2.78	0.51
1:2:738:C:C2	1:2:776:G:C2	2.98	0.51
1:2:788:G:C2	1:2:789:C:C4	2.99	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:851:4AC:H5	1:2:851:4AC:O7	2.09	0.51
1:2:995:U:H2'	1:2:996:G:O4'	2.11	0.51
1:2:1131:A:C6	1:2:1154:A:N7	2.78	0.51
1:2:1293:A:C4	1:2:1297:G:C8	2.99	0.51
1:2:1446:U:H2'	1:2:1447:C:H6	1.76	0.51
1:2:1457:G:H2'	1:2:1458:G:C8	2.46	0.51
7:F:163:LEU:HD11	7:F:184:TRP:HE1	1.75	0.51
11:J:41:ASP:HA	11:J:59:ALA:HB3	1.93	0.51
16:O:20:GLN:HB2	16:O:23:TRP:HD1	1.75	0.51
16:O:113:ARG:HH12	16:O:121:GLU:CD	2.18	0.51
17:P:21:CYS:SG	17:P:24:CYS:N	2.78	0.51
33:7:215:MET:HE2	33:7:316:ILE:HD12	1.91	0.51
1:2:126:A:C2	1:2:195:A:N3	2.79	0.51
1:2:308:G:N1	1:2:309:A:C5	2.78	0.51
1:2:849:G:P	10:I:76:LYS:HG2	2.51	0.51
1:2:1260:U:H3	22:U:61:ARG:NH2	2.06	0.51
6:E:140:LEU:O	6:E:141:ASN:ND2	2.44	0.51
15:N:103:VAL:HG12	15:N:129:VAL:HG22	1.92	0.51
33:7:397:ILE:HG23	33:7:408:ILE:HG22	1.92	0.51
1:2:163:G:C2	1:2:164:G:C5	2.99	0.51
1:2:998:C:H2'	1:2:999:G:C8	2.35	0.51
1:2:1000:G:O5'	1:2:1000:G:H8	1.92	0.51
1:2:1279:G:C2	1:2:1305:G:N3	2.78	0.51
1:2:1393:G:OP1	33:7:374:LYS:HD3	2.11	0.51
1:2:1451:G:HO2'	1:2:1452:A:H8	1.59	0.51
12:K:25:ARG:HB2	22:U:150:TYR:CD1	2.46	0.51
22:U:37:THR:HG23	22:U:41:LYS:HE3	1.93	0.51
27:Z:166:TYR:HB2	27:Z:179:LYS:HG2	1.93	0.51
28:O:25:ARG:O	28:O:26:LEU:HD22	2.10	0.51
31:4:29:G:C2	31:4:30:G:C8	2.99	0.51
33:7:22:LYS:O	33:7:26:VAL:HG22	2.09	0.51
34:8:54:ILE:HG13	34:8:56:ARG:HB2	1.91	0.51
1:2:32:G:H2'	1:2:33:A:C8	2.45	0.51
1:2:78:G:H2'	1:2:79:C:C6	2.46	0.51
1:2:173:C:C2	1:2:174:C:C5	2.99	0.51
1:2:276:C:H2'	1:2:277:C:H6	1.76	0.51
1:2:299:G:O6	1:2:320:G:C5	2.63	0.51
1:2:733:A:C4	1:2:734:A:C8	2.99	0.51
1:2:1358:U:C2	1:2:1359:G:C8	2.99	0.51
2:A:88:LEU:HD13	2:A:187:ARG:O	2.11	0.51
3:B:167:ILE:H	3:B:167:ILE:HD12	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:F:135:CYS:C	7:F:136:ARG:HD3	2.36	0.51
9:H:18:MET:HE1	9:H:105:LYS:HB2	1.93	0.51
9:H:65:GLU:O	9:H:69:ASN:ND2	2.44	0.51
20:S:2:GLY:C	20:S:4:ILE:H	2.19	0.51
20:S:61:LYS:HA	20:S:66:ILE:HB	1.92	0.51
22:U:97:ILE:H	22:U:97:ILE:HD12	1.75	0.51
1:2:75:G:H2'	1:2:76:G:C8	2.46	0.51
1:2:83:C:H2'	1:2:84:C:C6	2.46	0.51
1:2:98:C:H2'	1:2:99:C:H6	1.75	0.51
1:2:373:A2M:HM'1	1:2:374:A:C4	2.45	0.51
1:2:647:C:H2'	1:2:648:4AC:H6	1.92	0.51
1:2:647:C:N4	1:2:678:G:C6	2.79	0.51
1:2:745:G:C5	1:2:746:C:C5	2.99	0.51
1:2:772:C:C2	1:2:773:C:C5	2.98	0.51
1:2:795:A:H2'	1:2:796:G:C8	2.45	0.51
1:2:952:C:O2'	1:2:953:U:OP1	2.23	0.51
1:2:1026:G:C6	1:2:1027:C:C4	2.99	0.51
1:2:1194:G:H2'	1:2:1195:G:H8	1.76	0.51
8:G:75:ARG:CD	8:G:92:PRO:HG2	2.40	0.51
11:J:41:ASP:N	11:J:41:ASP:OD1	2.36	0.51
29:3:73:LYS:HE2	29:3:75:ILE:HB	1.92	0.51
1:2:423:U:H2'	1:2:424:C:C2	2.46	0.51
1:2:742:G:H2'	1:2:743:G:O4'	2.11	0.51
1:2:806:G:C6	1:2:819:G:C6	2.99	0.51
1:2:883:U:O2'	1:2:884:A:H5'	2.11	0.51
1:2:1019:C:H4'	1:2:1020:A:H5''	1.93	0.51
1:2:1361:U:H2'	1:2:1362:C:C6	2.46	0.51
1:2:1452:A:H8	33:7:352:ARG:HH21	1.57	0.51
1:2:1470:C:C4	1:2:1473:G:C5	2.99	0.51
2:A:117:LYS:HG3	2:A:192:LEU:HD22	1.91	0.51
3:B:182:ILE:HG22	3:B:183:SER:H	1.76	0.51
5:D:56:ARG:HG2	7:F:132:GLU:HG2	1.92	0.51
7:F:122:ILE:HD13	7:F:206:TYR:CD1	2.44	0.51
9:H:49:GLY:HA2	9:H:51:HIS:CE1	2.46	0.51
15:N:84:VAL:HG12	15:N:85:THR:N	2.26	0.51
16:O:99:ASP:HB2	16:O:103:ARG:NH2	2.25	0.51
30:5:812:G:C4	30:5:813:A:C8	3.00	0.51
31:4:58:A:O2'	31:4:60:U:OP2	2.18	0.51
32:6:72:TRP:C	32:6:74:VAL:H	2.19	0.51
33:7:64:LYS:HG3	33:7:65:PRO:HB3	1.91	0.51
33:7:247:PHE:O	33:7:288:GLU:HG2	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:7:249:VAL:HG12	33:7:250:ASP:CG	2.35	0.51
1:2:65:G:H2'	1:2:66:C:C6	2.46	0.50
1:2:266:G:C6	1:2:267:G:N7	2.79	0.50
1:2:268:G:OP1	11:J:113:ARG:HG2	2.11	0.50
1:2:674:C:C2	1:2:675:C:C5	2.99	0.50
1:2:1114:G:N1	1:2:1115:G:C6	2.79	0.50
1:2:1132:C:C4	1:2:1134:G:C8	3.00	0.50
1:2:1324:C:OP1	12:K:124:LYS:NZ	2.34	0.50
1:2:1366:G:H8	1:2:1366:G:O5'	1.95	0.50
25:X:66:GLU:CD	25:X:67:ILE:H	2.18	0.50
26:Y:37:ARG:HA	26:Y:49:LYS:H	1.75	0.50
30:5:806:G:N3	30:5:807:G:H1'	2.25	0.50
32:6:20:GLU:O	32:6:23:GLN:HG3	2.11	0.50
35:9:151:LEU:HD12	35:9:161:VAL:HG13	1.93	0.50
1:2:582:G:C2	1:2:583:G:N7	2.79	0.50
1:2:582:G:N1	1:2:583:G:C5	2.80	0.50
1:2:991:G:C6	1:2:992:U:C4	3.00	0.50
1:2:1176:G:O2'	17:P:26:GLN:OE1	2.15	0.50
1:2:1190:C:O2'	1:2:1191:C:O5'	2.29	0.50
1:2:1346:C:C2	1:2:1347:G:C8	3.00	0.50
1:2:1396:G:H22	1:2:1448:C:C1'	2.24	0.50
3:B:166:LEU:O	3:B:169:TRP:N	2.43	0.50
5:D:73:LEU:O	5:D:76:ARG:N	2.43	0.50
31:4:4:G:C2	31:4:70:G:C6	2.99	0.50
31:4:7:G:C2	31:4:49:G:C5	2.99	0.50
33:7:49:LEU:HD11	33:7:104:MET:HA	1.93	0.50
1:2:580:A:N6	1:2:593:G:C6	2.80	0.50
1:2:685:G:N7	14:M:123:HIS:ND1	2.59	0.50
1:2:758:G:C8	1:2:759:A:C8	2.98	0.50
1:2:808:G:C6	1:2:809:C:C4	3.00	0.50
1:2:1022:G:C6	1:2:1023:G:C5	2.98	0.50
1:2:1152:G:N2	1:2:1154:A:OP2	2.45	0.50
1:2:1180:G:C6	1:2:1181:C:C4	2.99	0.50
1:2:1353:G:H4'	25:X:17:ARG:NE	2.26	0.50
1:2:1380:U:H2'	1:2:1381:C:O4'	2.11	0.50
5:D:106:GLN:NE2	5:D:122:ARG:HB2	2.26	0.50
26:Y:22:CYS:HB2	26:Y:29:VAL:HG23	1.93	0.50
1:2:29:C:O2'	1:2:884:A:N1	2.42	0.50
1:2:256:G:O6	1:2:287:G:N1	2.45	0.50
1:2:474:A:C6	1:2:475:A:N1	2.80	0.50
1:2:540:A:H5''	1:2:541:G:OP2	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:719:G:O6	18:Q:64:LYS:NZ	2.44	0.50
1:2:759:A:N3	1:2:761:A:C5	2.80	0.50
2:A:11:LYS:HG3	35:9:22:VAL:O	2.11	0.50
9:H:121:GLN:O	9:H:124:VAL:HB	2.11	0.50
10:I:71:LYS:HB3	10:I:130:TYR:CE2	2.46	0.50
15:N:31:LYS:O	15:N:33:ARG:N	2.45	0.50
29:3:76:PRO:HB3	29:3:119:ARG:HH21	1.77	0.50
33:7:27:GLN:NE2	33:7:33:TRP:HB3	2.20	0.50
33:7:175:ALA:O	33:7:178:VAL:HG22	2.11	0.50
35:9:214:LEU:HD12	35:9:233:GLY:HA3	1.92	0.50
1:2:55:A:N6	1:2:315:A:N6	2.60	0.50
1:2:418:G:H2'	1:2:419:U:H6	1.76	0.50
1:2:634:G:O6	1:2:707:U:N3	2.44	0.50
1:2:831:A:C6	1:2:832:G:C4	3.00	0.50
1:2:974:U:HO2'	26:Y:3:GLN:HE21	1.53	0.50
1:2:1053:A:C6	1:2:1054:C:C4	2.99	0.50
1:2:1207:G:C6	1:2:1208:C:N4	2.79	0.50
1:2:1208:C:H2'	1:2:1209:U:C6	2.46	0.50
1:2:1376:OMC:HM22	1:2:1377:C:H5'	1.94	0.50
16:O:129:GLN:OE1	16:O:129:GLN:N	2.44	0.50
35:9:110:VAL:HG13	35:9:163:PRO:HB2	1.94	0.50
35:9:218:LYS:HG3	35:9:230:ASP:OD2	2.11	0.50
1:2:116:A:C6	1:2:118:A:C2	2.99	0.50
1:2:893:G:C2	1:2:1370:A:C2	3.00	0.50
1:2:951:C:H42	17:P:15:GLY:HA3	1.76	0.50
1:2:1028:4AC:O7	1:2:1028:4AC:H5	2.10	0.50
1:2:1044:G:H2'	1:2:1045:A:C8	2.46	0.50
1:2:1101:U:H2'	1:2:1102:C:C6	2.47	0.50
1:2:1125:G:C2	1:2:1126:G:C5	2.99	0.50
1:2:1202:5MC:H3'	16:O:136:ARG:NH1	2.27	0.50
5:D:70:ARG:O	5:D:73:LEU:HB3	2.12	0.50
21:T:72:VAL:HG23	21:T:76:MET:SD	2.51	0.50
24:W:17:ARG:NH2	24:W:26:GLU:OE1	2.45	0.50
33:7:24:THR:HG21	33:7:186:LEU:HD12	1.93	0.50
1:2:531:U:H5''	1:2:532:G:H2'	1.94	0.50
1:2:825:U:H5	1:2:842:U:C5	2.29	0.50
1:2:973:A:H8	29:3:34:LYS:HB2	1.75	0.50
1:2:1345:G:H2'	1:2:1346:C:H6	1.76	0.50
2:A:99:ARG:HG2	2:A:100:ARG:HG3	1.93	0.50
5:D:32:LYS:HG3	5:D:33:TYR:CE2	2.47	0.50
8:G:22:THR:OG1	8:G:23:GLY:N	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:190:LEU:HB3	9:H:198:SER:HB3	1.93	0.50
20:S:27:ASP:OD1	20:S:28:PHE:N	2.44	0.50
27:Z:47:PHE:HD1	27:Z:84:GLU:O	1.95	0.50
1:2:219:G:C2	1:2:223:G:C6	3.00	0.50
1:2:465:G:O2'	1:2:466:G:H5'	2.12	0.50
1:2:578:C:H2'	1:2:579:C:C6	2.46	0.50
1:2:821:C:H5''	24:W:5:ARG:NH1	2.27	0.50
1:2:1039:A:N1	1:2:1067:A:C6	2.80	0.50
1:2:1241:A:C6	1:2:1242:A:C5	3.00	0.50
6:E:197:GLY:HA3	6:E:216:GLU:O	2.11	0.50
23:V:44:LEU:HB3	23:V:46:LEU:HD21	1.94	0.50
30:5:816:U:H2'	30:5:817:A:H8	1.77	0.50
33:7:339:VAL:O	33:7:345:MET:HG2	2.11	0.50
1:2:545:C:N4	1:2:546:4AC:HM72	2.26	0.50
1:2:1002:C:H2'	1:2:1003:G:H8	1.77	0.50
1:2:1242:A:H2'	1:2:1243:A:H8	1.77	0.50
1:2:1265:C:C2	1:2:1266:C:C5	3.00	0.50
1:2:1469:6MZ:N3	1:2:1469:6MZ:H2'	2.26	0.50
2:A:18:GLN:HB3	2:A:38:ALA:O	2.12	0.50
8:G:47:LEU:HB3	8:G:49:GLU:HG2	1.93	0.50
16:O:57:GLU:H	16:O:57:GLU:CD	2.09	0.50
29:3:14:GLU:HG3	29:3:15:LEU:HD12	1.94	0.50
29:3:74:GLU:HG2	29:3:75:ILE:N	2.26	0.50
32:6:72:TRP:CH2	32:6:81:ASP:HB2	2.47	0.50
33:7:40:GLU:OE1	33:7:47:ILE:HB	2.12	0.50
35:9:31:LEU:HD11	35:9:78:VAL:HG11	1.94	0.50
1:2:121:U:H2'	1:2:122:C:C6	2.47	0.49
1:2:606:G:C2	1:2:607:A:C5	3.00	0.49
1:2:655:G:N1	1:2:656:G:C5	2.80	0.49
1:2:1039:A:O4'	3:B:103:ASN:ND2	2.45	0.49
1:2:1465:C:C4	1:2:1466:G:N7	2.80	0.49
7:F:91:ASN:ND2	7:F:93:ASP:HB3	2.27	0.49
15:N:7:PRO:O	15:N:9:GLY:N	2.41	0.49
26:Y:40:CYS:O	26:Y:42:ARG:N	2.44	0.49
31:4:31:G:H2'	31:4:32:OMC:H6	1.76	0.49
32:6:78:LYS:H	32:6:79:ARG:CZ	2.25	0.49
33:7:10:VAL:O	33:7:90:SER:OG	2.30	0.49
33:7:20:HIS:HB3	33:7:117:VAL:HG23	1.93	0.49
1:2:239:G:O2'	6:E:6:PRO:HB3	2.11	0.49
1:2:319:4AC:O7	1:2:319:4AC:H5	2.11	0.49
1:2:347:G:C2	1:2:348:G:C8	3.00	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:369:G:C5	1:2:370:C:C4	3.00	0.49
1:2:865:G:N1	1:2:866:G:N2	2.60	0.49
1:2:866:G:N2	1:2:876:U:O2	2.26	0.49
1:2:1056:U:H2'	1:2:1058:A:OP2	2.12	0.49
1:2:1062:U:N3	1:2:1063:G:N7	2.60	0.49
1:2:1093:C:H42	1:2:1119:C:N4	2.09	0.49
1:2:1505:C:C2	30:5:810:G:C2	3.00	0.49
2:A:132:THR:C	2:A:135:GLU:H	2.18	0.49
6:E:185:VAL:HG21	6:E:230:ALA:HB1	1.94	0.49
8:G:67:THR:O	8:G:116:ILE:HG23	2.12	0.49
31:4:20:H2U:H3'	31:4:22:G:OP1	2.13	0.49
31:4:63:G:C2	31:4:64:G:C8	2.99	0.49
1:2:28:G:H1'	1:2:885:A:H61	1.77	0.49
1:2:116:A:C5	1:2:118:A:C6	3.00	0.49
1:2:464:A:C2	1:2:513:A:C5	3.00	0.49
1:2:466:G:C4	1:2:467:G:N1	2.81	0.49
1:2:466:G:O2'	1:2:467:G:H5'	2.12	0.49
1:2:863:A:C6	1:2:864:C:N4	2.81	0.49
1:2:904:A:O2'	1:2:906:U:OP1	2.20	0.49
1:2:1289:U:H2'	1:2:1290:G:C8	2.47	0.49
1:2:1485:G:H22	1:2:1487:MA6:H3'	1.77	0.49
6:E:10:LEU:HD12	6:E:11:LYS:N	2.26	0.49
17:P:16:LYS:NZ	17:P:28:GLY:O	2.40	0.49
18:Q:29:THR:OG1	18:Q:30:VAL:N	2.45	0.49
20:S:23:GLU:OE2	20:S:34:LYS:HD2	2.11	0.49
22:U:131:LYS:O	22:U:134:THR:OG1	2.24	0.49
35:9:181:GLY:O	35:9:229:VAL:N	2.45	0.49
1:2:89:G:C2	1:2:90:G:C4	3.00	0.49
1:2:174:C:H2'	1:2:175:C:C6	2.47	0.49
1:2:452:G:C6	1:2:453:C:C4	3.00	0.49
1:2:1013:G:N2	1:2:1184:4AC:C2	2.75	0.49
1:2:1085:C:H2'	1:2:1086:C:C6	2.46	0.49
2:A:116:TYR:CD2	2:A:155:PHE:CG	2.99	0.49
7:F:50:ILE:O	7:F:54:LEU:N	2.36	0.49
10:I:51:GLU:N	10:I:51:GLU:OE1	2.46	0.49
28:0:28:ARG:HG2	28:0:29:GLN:NE2	2.27	0.49
29:3:16:ALA:O	29:3:20:LEU:HB2	2.12	0.49
31:4:10:G:C2	31:4:11:A:C8	3.00	0.49
32:6:95:LEU:HD13	32:6:100:ILE:O	2.12	0.49
33:7:113:GLY:HA2	33:7:143:ASN:HB2	1.95	0.49
35:9:68:VAL:HA	35:9:80:VAL:HG12	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:32:G:H2'	1:2:33:A:H8	1.77	0.49
1:2:117:C:OP2	11:J:11:LYS:HE2	2.13	0.49
1:2:418:G:H2'	1:2:419:U:C6	2.47	0.49
1:2:636:4AC:N4	1:2:704:G:O6	2.46	0.49
1:2:990:G:N2	1:2:995:U:O4	2.40	0.49
1:2:1233:4AC:O7	1:2:1233:4AC:H5	2.11	0.49
1:2:1362:C:C2	1:2:1363:C:C5	3.01	0.49
1:2:1401:U:N3	1:2:1402:A:C5	2.80	0.49
2:A:11:LYS:HZ2	2:A:13:LYS:H	1.60	0.49
6:E:18:SER:C	6:E:19:TRP:HD1	2.20	0.49
9:H:38:ASN:HD22	9:H:62:HIS:N	2.09	0.49
11:J:88:GLN:HB2	11:J:91:ARG:HH21	1.77	0.49
25:X:67:ILE:HG12	25:X:68:LYS:N	2.26	0.49
27:Z:30:TYR:OH	27:Z:33:LEU:HD23	2.13	0.49
33:7:366:THR:HG21	33:7:382:LEU:HD21	1.93	0.49
34:8:9:GLU:OE1	34:8:10:MET:HG3	2.12	0.49
35:9:69:ILE:HD11	35:9:81:SER:HB2	1.93	0.49
1:2:215:A:H2'	1:2:216:G:C8	2.47	0.49
1:2:528:U:O4	1:2:855:U:O2'	2.22	0.49
1:2:591:G:C2	1:2:592:U:N3	2.81	0.49
1:2:917:G:H2'	1:2:917:G:N3	2.27	0.49
1:2:930:A:C5	1:2:931:A:C6	3.01	0.49
1:2:982:A:H2'	1:2:983:G:H8	1.76	0.49
1:2:1115:G:N1	1:2:1116:A:N1	2.61	0.49
1:2:1115:G:C2	1:2:1116:A:C2	3.00	0.49
1:2:1234:G:N2	1:2:1249:A:H62	2.08	0.49
1:2:1271:U:H4'	1:2:1273:A:C2	2.34	0.49
7:F:214:THR:HB	7:F:215:PRO:HD2	1.94	0.49
9:H:10:PHE:HE2	9:H:12:PRO:HB3	1.78	0.49
9:H:73:ARG:NH2	9:H:75:GLY:O	2.37	0.49
17:P:20:ARG:NH1	17:P:27:TYR:OH	2.44	0.49
33:7:46:THR:HB	33:7:95:PRO:HA	1.95	0.49
1:2:245:G:C5	1:2:246:C:C5	3.01	0.49
1:2:267:G:C2	1:2:268:G:C5	3.01	0.49
1:2:689:G:C6	1:2:691:G:C4	2.99	0.49
1:2:964:G:O2'	1:2:1009:A:N1	2.36	0.49
1:2:1112:A:C2	1:2:1113:G:C5	3.00	0.49
1:2:1476:A:C6	1:2:1499:G:C2	3.01	0.49
3:B:75:TYR:CE2	3:B:161:ARG:HD3	2.47	0.49
4:C:22:THR:O	4:C:25:GLU:HG2	2.13	0.49
4:C:55:CYS:HB3	4:C:58:CYS:HB2	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:L:56:GLU:OE1	13:L:56:GLU:N	2.46	0.49
18:Q:33:ILE:O	18:Q:37:VAL:HG23	2.11	0.49
29:3:66:LEU:HB2	29:3:67:PRO:HD3	1.93	0.49
31:4:75:C:H1'	33:7:225:LYS:HE3	1.94	0.49
33:7:50:GLY:C	33:7:93:ASP:H	2.21	0.49
34:8:35:ILE:HG12	34:8:44:ILE:HG12	1.94	0.49
1:2:206:C:O3'	11:J:43:ARG:NH1	2.38	0.49
1:2:313:G:C2	1:2:314:G:H1'	2.48	0.49
1:2:467:G:N7	1:2:468:C:C4	2.80	0.49
1:2:741:G:C4	1:2:742:G:C8	3.01	0.49
1:2:813:G:N1	1:2:815:G:C4	2.80	0.49
1:2:849:G:C6	1:2:850:C:N4	2.80	0.49
1:2:1013:G:H22	1:2:1184:4AC:C4	2.25	0.49
1:2:1192:C:H5''	1:2:1193:4AC:OP2	2.11	0.49
1:2:1437:A:C2	1:2:1438:G:H1'	2.48	0.49
4:C:4:ASN:ND2	4:C:4:ASN:O	2.45	0.49
4:C:16:SER:OG	4:C:17:CYS:N	2.45	0.49
14:M:106:ALA:HB2	14:M:112:ILE:HD11	1.95	0.49
18:Q:130:ARG:O	18:Q:133:VAL:HG12	2.12	0.49
27:Z:56:GLY:CA	27:Z:61:ARG:HB2	2.43	0.49
27:Z:109:PHE:CE1	27:Z:110:ARG:HG3	2.47	0.49
33:7:242:ILE:HG21	33:7:246:LEU:HA	1.94	0.49
34:8:33:MET:HE1	34:8:96:MET:HG2	1.94	0.49
34:8:114:THR:HG21	34:8:125:ILE:HG23	1.93	0.49
1:2:49:G:N2	1:2:409:C:C2	2.80	0.49
1:2:263:G:C2	1:2:282:A:C2	3.00	0.49
1:2:593:G:N1	1:2:594:G:C5	2.81	0.49
1:2:638:G:C6	1:2:639:G:C5	3.00	0.49
1:2:739:A:N6	1:2:775:G:O6	2.45	0.49
1:2:832:G:C2	1:2:833:G:C5	3.01	0.49
1:2:1395:G:O2'	1:2:1449:G:N2	2.46	0.49
1:2:1413:G:C6	1:2:1431:G:C6	3.01	0.49
1:2:1482:A:O2'	1:2:1483:G:H5'	2.13	0.49
2:A:116:TYR:N	2:A:116:TYR:CD1	2.81	0.49
7:F:53:LEU:O	7:F:54:LEU:HD23	2.12	0.49
13:L:83:ARG:HG2	13:L:87:ARG:NH1	2.21	0.49
16:O:45:LEU:HD23	16:O:45:LEU:H	1.78	0.49
18:Q:93:GLU:OE1	18:Q:93:GLU:N	2.46	0.49
19:R:44:ARG:O	19:R:46:THR:HG23	2.12	0.49
20:S:65:LYS:HE3	20:S:67:LEU:HD11	1.93	0.49
21:T:81:ILE:HD11	21:T:103:LEU:HD21	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:7:80:ASP:OD1	34:8:119:GLU:HA	2.13	0.49
35:9:224:ALA:HB3	35:9:225:PRO:HD3	1.95	0.49
1:2:156:G:N2	1:2:158:A:H5''	2.28	0.49
1:2:171:C:H2'	1:2:172:C:O4'	2.12	0.49
1:2:485:C:H2'	1:2:486:A:O4'	2.13	0.49
1:2:576:U:P	6:E:24:LYS:HZ1	2.34	0.49
1:2:588:A:H5'	1:2:589:C:OP2	2.13	0.49
1:2:789:C:H2'	1:2:790:G:H8	1.77	0.49
1:2:984:G:O6	1:2:993:C:N4	2.46	0.49
1:2:1127:G:C6	1:2:1128:G:N7	2.81	0.49
1:2:1324:C:H2'	1:2:1325:C:C6	2.48	0.49
1:2:1380:U:C2	1:2:1381:C:C6	3.00	0.49
2:A:27:PHE:CZ	2:A:83:PHE:HB2	2.48	0.49
2:A:100:ARG:HA	2:A:129:ARG:HE	1.78	0.49
12:K:25:ARG:HB2	22:U:150:TYR:HD1	1.78	0.49
33:7:273:PHE:HB2	35:9:190:PRO:CG	2.43	0.49
33:7:289:ALA:HB2	33:7:295:VAL:HG21	1.95	0.49
33:7:324:PRO:HD2	33:7:388:VAL:HG13	1.94	0.49
34:8:116:LEU:HG	34:8:123:TRP:CD1	2.48	0.49
1:2:179:G:C2	1:2:208:G:H1'	2.47	0.48
1:2:606:G:H2'	1:2:607:A:C8	2.48	0.48
1:2:610:C:O2'	10:I:78:ARG:NH1	2.46	0.48
1:2:688:A:OP2	2:A:129:ARG:NH2	2.46	0.48
1:2:993:C:C2	1:2:994:U:C5	3.01	0.48
1:2:1160:G:C2	1:2:1161:G:C8	3.01	0.48
1:2:1241:A:H2'	1:2:1242:A:C8	2.47	0.48
1:2:1279:G:N2	1:2:1305:G:N3	2.61	0.48
7:F:24:MET:O	7:F:27:LYS:N	2.46	0.48
16:O:117:GLY:O	16:O:121:GLU:HG3	2.12	0.48
25:X:15:ILE:HD11	25:X:28:LYS:N	2.28	0.48
27:Z:144:VAL:HG12	27:Z:145:ARG:N	2.22	0.48
30:5:819:A:C6	31:4:37:A:C2	3.01	0.48
32:6:16:VAL:HG11	32:6:93:TRP:CZ3	2.47	0.48
1:2:157:A:H2'	1:2:158:A:O4'	2.13	0.48
1:2:193:G:C6	1:2:194:A:N1	2.81	0.48
1:2:255:A:N7	1:2:288:A:C5	2.81	0.48
1:2:268:G:O2'	1:2:269:G:OP1	2.26	0.48
1:2:295:G:H2'	1:2:296:U:C5	2.48	0.48
1:2:529:A:C2	1:2:533:G:N7	2.81	0.48
1:2:570:G:H2'	1:2:571:C:O4'	2.13	0.48
1:2:643:A:C2	1:2:644:C:C2	3.01	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:980:C:C4	1:2:990:G:C5	3.01	0.48
1:2:1133:U:C4	1:2:1156:G:C4	3.00	0.48
1:2:1272:C:N4	9:H:177:LYS:HA	2.28	0.48
1:2:1476:A:N6	1:2:1499:G:C6	2.81	0.48
8:G:96:PRO:C	8:G:98:GLU:H	2.21	0.48
10:I:31:SER:OG	10:I:33:LEU:N	2.46	0.48
18:Q:90:GLU:H	18:Q:90:GLU:CD	2.19	0.48
25:X:67:ILE:HG23	25:X:70:ARG:H	1.78	0.48
32:6:16:VAL:HG21	32:6:93:TRP:HZ3	1.78	0.48
33:7:127:PRO:HB2	33:7:128:GLN:OE1	2.13	0.48
1:2:90:G:C4	1:2:91:G:C8	3.01	0.48
1:2:372:A:C4	1:2:373:A2M:N7	2.82	0.48
1:2:615:G:C2	1:2:616:G:C8	3.01	0.48
1:2:894:G:H2'	1:2:895:C:O4'	2.12	0.48
1:2:1112:A:N3	1:2:1113:G:C8	2.81	0.48
10:I:31:SER:OG	10:I:34:ILE:HG13	2.13	0.48
25:X:18:THR:HG22	25:X:19:GLY:N	2.27	0.48
27:Z:70:GLU:OE1	27:Z:71:ARG:HG3	2.13	0.48
27:Z:150:TYR:CD1	27:Z:150:TYR:N	2.79	0.48
1:2:412:A:C2	1:2:413:G:C8	3.01	0.48
1:2:435:U:OP2	1:2:435:U:H6	1.95	0.48
1:2:981:C:O2	26:Y:37:ARG:NE	2.47	0.48
1:2:1167:G:H2'	1:2:1168:G:O4'	2.13	0.48
1:2:1364:U:C2	1:2:1365:U:C5	3.02	0.48
1:2:1398:G:O2'	1:2:1399:C:H6	1.96	0.48
1:2:1401:U:C2	1:2:1402:A:C8	3.01	0.48
1:2:1407:A:N7	1:2:1437:A:C6	2.81	0.48
2:A:11:LYS:NZ	2:A:12:ASP:OD2	2.46	0.48
10:I:50:PHE:HB3	10:I:63:VAL:HG22	1.94	0.48
13:L:18:GLU:HG3	13:L:19:VAL:HG13	1.96	0.48
26:Y:27:PRO:O	29:3:45:ARG:NE	2.25	0.48
29:3:92:ILE:HG13	29:3:93:GLU:H	1.79	0.48
33:7:8:PRO:HD2	33:7:281:PHE:CE1	2.48	0.48
34:8:44:ILE:HD12	34:8:81:LEU:HD23	1.94	0.48
35:9:123:GLU:HA	35:9:127:TRP:CD1	2.48	0.48
1:2:22:G:C2	1:2:23:A:C4	3.01	0.48
1:2:465:G:H2'	1:2:466:G:C8	2.49	0.48
1:2:1421:U:O2'	1:2:1422:C:H5'	2.14	0.48
4:C:4:ASN:HB3	4:C:8:LYS:HZ3	1.79	0.48
7:F:142:PRO:HB2	7:F:143:PHE:HD2	1.78	0.48
8:G:3:THR:HB	8:G:22:THR:HB	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:G:87:LEU:HD12	8:G:104:LYS:NZ	2.28	0.48
11:J:56:ARG:HD3	11:J:56:ARG:HA	1.63	0.48
18:Q:74:ARG:HH11	18:Q:80:ARG:HD3	1.79	0.48
27:Z:104:GLU:HB3	27:Z:169:ALA:HB1	1.95	0.48
31:4:54:5MU:H72	31:4:55:PSU:C2	2.47	0.48
33:7:138:ILE:HG23	33:7:410:TRP:HB2	1.95	0.48
1:2:391:A:C2	1:2:392:A:C5	3.01	0.48
1:2:547:G:N2	1:2:728:G:C6	2.82	0.48
1:2:704:G:H2'	1:2:705:G:H8	1.79	0.48
1:2:753:G:C2	1:2:764:C:C2	3.02	0.48
1:2:793:C:H2'	1:2:794:U:H6	1.78	0.48
1:2:794:U:C4	1:2:841:U:C5	3.01	0.48
1:2:860:A:H2	1:2:861:G:H21	1.59	0.48
1:2:962:G:H5'	17:P:3:LYS:HG2	1.95	0.48
1:2:1147:4AC:H5'	1:2:1148:G:OP2	2.14	0.48
1:2:1484:G:C2	1:2:1485:G:C8	3.01	0.48
1:2:1502:C:C2	1:2:1503:A:C8	3.01	0.48
4:C:49:LEU:HD12	4:C:49:LEU:O	2.14	0.48
8:G:21:ILE:HD12	8:G:25:GLU:HB3	1.95	0.48
12:K:38:PRO:O	12:K:41:ALA:N	2.43	0.48
16:O:80:ASN:N	16:O:92:HIS:ND1	2.61	0.48
18:Q:108:HIS:C	18:Q:108:HIS:CD2	2.92	0.48
23:V:19:ILE:HB	23:V:69:ALA:O	2.14	0.48
31:4:8:4SU:H4'	31:4:21:A:H61	1.78	0.48
1:2:80:G:C6	1:2:94:G:C6	3.02	0.48
1:2:323:G:H8	1:2:323:G:O5'	1.96	0.48
1:2:425:U:O5'	1:2:425:U:H6	1.96	0.48
1:2:595:G:C2	1:2:596:G:H1'	2.48	0.48
1:2:687:C:N4	1:2:688:A:N1	2.62	0.48
1:2:813:G:C5	1:2:815:G:H1'	2.49	0.48
1:2:1118:G:N7	1:2:1119:C:C4	2.81	0.48
1:2:1405:U:C2	1:2:1406:G:C8	3.01	0.48
1:2:1476:A:H2'	1:2:1477:G:H8	1.79	0.48
2:A:45:LEU:HD11	2:A:72:TYR:C	2.38	0.48
3:B:128:LYS:O	3:B:131:ILE:N	2.47	0.48
9:H:10:PHE:H	12:K:42:ARG:NH1	2.11	0.48
15:N:98:ASP:OD1	15:N:99:GLU:N	2.46	0.48
16:O:101:ALA:HA	16:O:104:GLU:HG2	1.95	0.48
18:Q:85:HIS:C	18:Q:87:LEU:H	2.22	0.48
20:S:37:GLU:CD	20:S:37:GLU:H	2.22	0.48
21:T:49:ARG:O	21:T:53:LEU:HG	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:7:51:TYR:CE2	33:7:294:LEU:HB3	2.48	0.48
1:2:120:G:C2	1:2:247:G:C2	3.02	0.48
1:2:141:G:C6	1:2:176:A:C6	3.02	0.48
1:2:466:G:N2	1:2:467:G:H22	2.12	0.48
1:2:930:A:C2	21:T:87:LYS:HE2	2.49	0.48
1:2:1025:C:H2'	1:2:1026:G:H8	1.77	0.48
1:2:1061:G:N1	1:2:1062:U:C4	2.81	0.48
1:2:1444:G:C5	1:2:1445:C:C4	3.02	0.48
2:A:116:TYR:N	2:A:116:TYR:HD1	2.11	0.48
5:D:22:ARG:HG3	5:D:25:ARG:NH2	2.29	0.48
7:F:70:LEU:HD23	7:F:70:LEU:H	1.79	0.48
12:K:51:LEU:HD21	12:K:98:LYS:HB3	1.96	0.48
15:N:14:ARG:NH2	19:R:65:LEU:HB3	2.28	0.48
23:V:28:GLU:N	23:V:28:GLU:OE1	2.47	0.48
23:V:62:SER:O	23:V:62:SER:OG	2.27	0.48
33:7:58:VAL:HG23	33:7:86:LEU:CD1	2.43	0.48
33:7:289:ALA:CB	33:7:295:VAL:HG21	2.44	0.48
1:2:486:A:N6	1:2:487:G:C4	2.81	0.48
1:2:781:A:C8	1:2:783:A:C8	3.02	0.48
1:2:925:G:H2'	1:2:926:G:O4'	2.14	0.48
1:2:1219:G:O2'	1:2:1220:G:O4'	2.31	0.48
1:2:1239:4AC:O2	1:2:1245:G:N2	2.47	0.48
1:2:1437:A:C4	1:2:1438:G:C8	3.02	0.48
2:A:196:GLU:H	2:A:196:GLU:CD	2.16	0.48
3:B:78:LYS:HB3	3:B:79:PRO:HD3	1.95	0.48
7:F:122:ILE:HD11	7:F:202:PHE:CE1	2.48	0.48
29:3:75:ILE:HG12	29:3:77:TYR:HB3	1.94	0.48
33:7:127:PRO:O	33:7:341:GLY:HA2	2.14	0.48
33:7:130:ARG:HH22	33:7:338:ARG:HG3	1.78	0.48
1:2:316:G:N2	5:D:4:PRO:HD2	2.29	0.48
1:2:504:G:C6	1:2:505:G:C5	3.02	0.48
1:2:680:G:H3'	1:2:681:G:H8	1.77	0.48
1:2:886:A:H2'	1:2:886:A:N3	2.29	0.48
1:2:958:G:C2	1:2:959:G:C8	3.01	0.48
1:2:1197:C:H5''	1:2:1198:U:H5''	1.96	0.48
1:2:1331:G:OP2	1:2:1333:C:N4	2.47	0.48
1:2:1337:A:C6	1:2:1339:C:C2	3.02	0.48
3:B:118:THR:O	3:B:140:LEU:HB2	2.13	0.48
6:E:3:ARG:HH21	6:E:4:LYS:NZ	2.12	0.48
6:E:37:HIS:CD2	6:E:144:ASP:HB3	2.49	0.48
6:E:74:ASP:OD2	6:E:123:LYS:NZ	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:I:42:GLN:O	10:I:45:GLY:N	2.39	0.48
14:M:133:ARG:CG	14:M:136:ARG:HD3	2.44	0.48
15:N:48:PRO:O	15:N:49:GLN:HG3	2.14	0.48
15:N:87:PHE:O	15:N:125:LYS:HA	2.14	0.48
27:Z:25:LEU:O	27:Z:25:LEU:HD23	2.13	0.48
29:3:73:LYS:CE	29:3:75:ILE:HB	2.43	0.48
32:6:13:VAL:HG12	32:6:14:ILE:H	1.79	0.48
33:7:217:VAL:HG11	33:7:238:ILE:HG23	1.96	0.48
1:2:188:U:H1'	1:2:189:A:N7	2.29	0.47
1:2:263:G:C6	1:2:282:A:N1	2.82	0.47
1:2:481:G:C4	1:2:482:U:C5	3.02	0.47
1:2:759:A:N3	1:2:761:A:C6	2.82	0.47
1:2:871:A:C5	1:2:872:A:N1	2.81	0.47
1:2:1039:A:C2	1:2:1067:A:C2	3.02	0.47
3:B:13:LEU:HG	3:B:18:HIS:CE1	2.48	0.47
4:C:33:PRO:C	4:C:35:CYS:H	2.22	0.47
9:H:24:GLU:OE2	9:H:24:GLU:N	2.47	0.47
23:V:33:ARG:NH2	23:V:89:ARG:HG2	2.29	0.47
31:4:29:G:C4	31:4:30:G:C8	3.02	0.47
33:7:75:LYS:HZ1	34:8:119:GLU:CD	2.22	0.47
35:9:113:LYS:HD3	35:9:113:LYS:HA	1.65	0.47
1:2:273:C:N4	1:2:274:G:C6	2.82	0.47
1:2:402:G:N3	1:2:403:G:C8	2.82	0.47
1:2:412:A:O2'	1:2:413:G:H5'	2.14	0.47
1:2:451:A:N3	1:2:452:G:H1'	2.29	0.47
1:2:891:U:C2	1:2:892:U:C5	3.02	0.47
1:2:919:G:N2	1:2:1209:U:O2	2.47	0.47
1:2:986:U:H6	1:2:986:U:O5'	1.98	0.47
1:2:1453:G:C5	1:2:1454:G:C8	3.03	0.47
2:A:15:LYS:O	2:A:16:LEU:HD23	2.14	0.47
9:H:85:PHE:CD2	9:H:87:ARG:NH2	2.82	0.47
10:I:31:SER:N	10:I:34:ILE:HD12	2.26	0.47
16:O:109:LEU:HD13	16:O:116:ARG:HB3	1.96	0.47
19:R:64:GLU:HG2	19:R:65:LEU:N	2.29	0.47
24:W:16:LEU:O	24:W:28:ILE:HA	2.14	0.47
27:Z:130:ILE:HG23	27:Z:146:PHE:HD2	1.79	0.47
33:7:360:SER:O	33:7:395:THR:HA	2.14	0.47
1:2:236:G:C4	1:2:237:A:C8	3.02	0.47
1:2:321:G:C2	1:2:322:A:C5	3.03	0.47
1:2:465:G:C6	1:2:466:G:N1	2.82	0.47
1:2:513:A:H4'	1:2:514:G:O5'	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:655:G:C2	1:2:656:G:C4	3.02	0.47
1:2:1028:4AC:H5''	1:2:1029:G:OP2	2.13	0.47
1:2:1083:C:C2	1:2:1084:C:C5	3.02	0.47
1:2:1434:U:O5'	1:2:1434:U:H6	1.98	0.47
2:A:42:GLU:OE2	2:A:42:GLU:N	2.45	0.47
5:D:32:LYS:HG3	5:D:33:TYR:CD2	2.49	0.47
5:D:129:HIS:CG	5:D:158:SER:HG	2.29	0.47
11:J:11:LYS:HB3	11:J:12:PRO:HD2	1.96	0.47
14:M:39:ILE:O	14:M:74:LYS:NZ	2.48	0.47
16:O:95:THR:OG1	16:O:96:ALA:N	2.48	0.47
18:Q:41:ARG:C	18:Q:43:GLU:H	2.23	0.47
18:Q:100:LYS:HE3	18:Q:100:LYS:HB3	1.76	0.47
19:R:34:PHE:HE1	19:R:51:ARG:HH21	1.63	0.47
23:V:78:MET:HB3	23:V:78:MET:HE2	1.66	0.47
29:3:16:ALA:HA	29:3:20:LEU:HD13	1.97	0.47
29:3:77:TYR:HE1	29:3:123:LYS:HA	1.80	0.47
30:5:811:U:N3	30:5:812:G:N7	2.62	0.47
33:7:138:ILE:HG12	33:7:410:TRP:HB3	1.96	0.47
1:2:46:G:C6	1:2:412:A:C6	3.02	0.47
1:2:444:U:H2'	1:2:445:G:C8	2.48	0.47
1:2:539:A:N7	1:2:540:A:C6	2.82	0.47
1:2:886:A:C6	1:2:887:G:C8	3.02	0.47
1:2:1235:A:C6	1:2:1236:C:C2	3.01	0.47
1:2:1272:C:C4	9:H:177:LYS:HA	2.49	0.47
1:2:1302:C:C2	1:2:1303:G:C8	3.02	0.47
2:A:177:LYS:O	2:A:177:LYS:HD3	2.15	0.47
7:F:175:LEU:HD21	7:F:205:LEU:HD11	1.95	0.47
18:Q:16:ARG:HH21	18:Q:62:THR:HG21	1.78	0.47
25:X:25:THR:O	25:X:44:ASN:HA	2.14	0.47
33:7:14:VAL:CG2	33:7:93:ASP:HA	2.44	0.47
33:7:65:PRO:C	33:7:67:ALA:H	2.21	0.47
33:7:357:LEU:O	33:7:367:LEU:HD12	2.14	0.47
1:2:46:G:C2	1:2:47:G:C5	3.03	0.47
1:2:401:G:H2'	1:2:402:G:C8	2.48	0.47
1:2:831:A:C5	1:2:832:G:C8	3.02	0.47
1:2:1022:G:C5	1:2:1178:A:N1	2.83	0.47
1:2:1046:G:C2	1:2:1047:G:C8	3.03	0.47
1:2:1220:G:C2	1:2:1221:G:C8	3.02	0.47
1:2:1303:G:C2	1:2:1304:U:C6	3.02	0.47
1:2:1408:G:O6	1:2:1436:G:N2	2.47	0.47
1:2:1452:A:C5	33:7:352:ARG:HG3	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:23:LEU:HD23	5:D:23:LEU:HA	1.63	0.47
5:D:162:ASN:C	5:D:164:GLN:H	2.20	0.47
5:D:169:MET:HA	5:D:172:GLU:OE1	2.14	0.47
8:G:87:LEU:HA	8:G:104:LYS:HD3	1.96	0.47
9:H:206:GLU:O	9:H:210:ILE:HG12	2.15	0.47
10:I:57:ARG:O	10:I:59:GLY:N	2.47	0.47
13:L:19:VAL:HA	13:L:22:GLN:HB2	1.96	0.47
20:S:40:ASN:OD1	27:Z:193:ILE:HG23	2.14	0.47
31:4:21:A:C8	31:4:46:A:C2	3.02	0.47
32:6:39:VAL:HG23	32:6:47:ARG:HB2	1.96	0.47
1:2:604:G:C2	1:2:605:G:C5	3.03	0.47
1:2:863:A:C6	1:2:878:A:N7	2.83	0.47
1:2:970:A:C2	1:2:1005:G:C4	3.02	0.47
1:2:993:C:H2'	1:2:994:U:H6	1.75	0.47
1:2:1066:A:C8	3:B:125:GLN:NE2	2.83	0.47
1:2:1224:A:C5	1:2:1261:A:C5	3.02	0.47
1:2:1244:G:C6	1:2:1245:G:C5	3.03	0.47
1:2:1346:C:N4	1:2:1347:G:C6	2.83	0.47
1:2:1361:U:H2'	1:2:1362:C:H6	1.80	0.47
1:2:1378:5HM:O2	1:2:1468:A:C6	2.67	0.47
10:I:79:PHE:O	10:I:124:ARG:HA	2.14	0.47
18:Q:121:GLY:O	18:Q:125:ILE:HG13	2.14	0.47
22:U:21:LYS:HA	22:U:52:TYR:CE1	2.48	0.47
29:3:113:GLU:OE1	29:3:114:ILE:HG12	2.14	0.47
30:5:812:G:C6	30:5:813:A:C5	3.03	0.47
31:4:4:G:O2'	31:4:5:G:H5'	2.14	0.47
33:7:269:TYR:HE1	33:7:385:PRO:HD2	1.77	0.47
1:2:41:G:O6	1:2:516:G:C5	2.68	0.47
1:2:186:G:C2	1:2:187:G:N7	2.83	0.47
1:2:313:G:H21	5:D:3:ASP:CG	2.21	0.47
1:2:373:A2M:HM'1	1:2:374:A:N3	2.29	0.47
1:2:429:A:C6	1:2:430:C:C4	3.02	0.47
1:2:525:U:C2	1:2:527:U:C4	3.02	0.47
1:2:588:A:H8	1:2:589:C:C5	2.33	0.47
1:2:616:G:C2	1:2:617:C:C6	3.02	0.47
1:2:618:C:C4	1:2:619:U:O4	2.68	0.47
1:2:665:C:C2	1:2:666:C:C5	3.03	0.47
1:2:691:G:OP2	1:2:799:G:N2	2.47	0.47
1:2:917:G:N1	1:2:1311:G:C6	2.83	0.47
1:2:1082:G:H5'	12:K:113:ARG:HG3	1.97	0.47
1:2:1094:C:H4'	1:2:1095:A:H8	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1112:A:H2'	1:2:1113:G:C8	2.44	0.47
1:2:1141:A:C5	1:2:1143:A:C5	3.03	0.47
1:2:1148:G:C2	1:2:1149:G:C4	3.03	0.47
1:2:1180:G:C6	1:2:1181:C:N4	2.82	0.47
1:2:1252:U:H5''	1:2:1253:A:H5'	1.96	0.47
1:2:1404:G:H2'	1:2:1405:U:O4'	2.15	0.47
3:B:166:LEU:O	3:B:170:ILE:HG13	2.15	0.47
9:H:5:LEU:HA	9:H:8:ARG:HB3	1.97	0.47
10:I:95:PRO:HG2	10:I:99:PHE:HB3	1.97	0.47
12:K:95:LEU:HD12	12:K:95:LEU:HA	1.75	0.47
14:M:10:LYS:NZ	14:M:12:GLU:HB2	2.30	0.47
20:S:23:GLU:HB3	20:S:24:PHE:CE1	2.49	0.47
21:T:65:THR:OG1	21:T:66:HIS:N	2.47	0.47
27:Z:82:VAL:HG12	27:Z:83:GLN:N	2.29	0.47
29:3:23:VAL:HA	29:3:26:ALA:HB3	1.96	0.47
33:7:249:VAL:HG23	33:7:279:ILE:HG13	1.97	0.47
33:7:269:TYR:HE1	33:7:384:ARG:HB2	1.80	0.47
35:9:180:SER:HA	35:9:230:ASP:HA	1.95	0.47
1:2:145:G:H2'	1:2:146:A:C8	2.50	0.47
1:2:226:U:HO2'	1:2:227:C:H6	1.60	0.47
1:2:312:G:O2'	1:2:313:G:H5'	2.15	0.47
1:2:424:C:H4'	1:2:425:U:H5	1.80	0.47
1:2:494:C:H2'	1:2:495:G:H5'	1.96	0.47
1:2:519:G:N3	1:2:520:G:C8	2.82	0.47
1:2:590:4AC:O7	1:2:590:4AC:H5	2.15	0.47
1:2:637:G:C2	1:2:704:G:C5	3.03	0.47
1:2:793:C:H4'	10:I:13:HIS:CE1	2.49	0.47
1:2:891:U:H2'	1:2:892:U:C6	2.50	0.47
1:2:989:A:H2'	1:2:991:G:N7	2.30	0.47
1:2:1109:G:C2	1:2:1110:G:C8	3.03	0.47
1:2:1116:A:C6	1:2:1117:G:N2	2.83	0.47
1:2:1479:4AC:O7	1:2:1479:4AC:H5	2.14	0.47
4:C:55:CYS:SG	4:C:58:CYS:N	2.73	0.47
11:J:89:PHE:CG	11:J:94:ILE:HB	2.50	0.47
21:T:19:MET:HE1	21:T:27:LEU:HD12	1.97	0.47
23:V:11:ASN:O	23:V:15:GLY:N	2.46	0.47
33:7:15:VAL:HA	33:7:22:LYS:HZ3	1.79	0.47
35:9:215:LEU:HG	35:9:233:GLY:HA2	1.97	0.47
1:2:94:G:H2'	1:2:95:C:C6	2.50	0.47
1:2:205:G:C6	1:2:206:C:C4	3.03	0.47
1:2:645:C:H2'	1:2:646:C:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:685:G:C6	1:2:686:C:C4	3.02	0.47
1:2:769:A:C2	1:2:770:G:H1'	2.50	0.47
1:2:770:G:H2'	1:2:771:U:C6	2.49	0.47
1:2:897:G:N1	1:2:1474:G:N7	2.63	0.47
1:2:1304:U:O2'	16:O:29:LYS:NZ	2.47	0.47
1:2:1329:G:C6	1:2:1342:G:N1	2.82	0.47
4:C:14:CYS:CB	4:C:17:CYS:SG	2.98	0.47
12:K:51:LEU:HD23	12:K:99:PHE:CD1	2.50	0.47
13:L:83:ARG:CZ	13:L:83:ARG:HB2	2.44	0.47
16:O:38:MET:O	16:O:42:VAL:HG22	2.15	0.47
21:T:8:TYR:HE2	21:T:9:ARG:HE	1.63	0.47
22:U:68:VAL:O	22:U:119:ARG:N	2.44	0.47
23:V:81:ILE:HG13	23:V:82:GLU:N	2.30	0.47
31:4:36:U:H2'	31:4:37:A:C8	2.50	0.47
31:4:60:U:H5''	31:4:61:C:C5	2.50	0.47
33:7:248:LYS:O	33:7:276:ILE:HD12	2.15	0.47
1:2:27:U:H2'	1:2:28:G:C8	2.50	0.47
1:2:99:C:H2'	1:2:100:G:O4'	2.14	0.47
1:2:105:A:C2	1:2:336:A:N1	2.83	0.47
1:2:255:A:C2	1:2:291:A:C4	3.03	0.47
1:2:672:U:C5	1:2:673:C:C5	3.03	0.47
1:2:1261:A:H2'	1:2:1262:A:C8	2.49	0.47
1:2:1398:G:C2	1:2:1399:C:C2	3.03	0.47
1:2:1409:G:C6	1:2:1435:C:N3	2.83	0.47
3:B:4:GLU:O	3:B:4:GLU:HG3	2.15	0.47
5:D:124:LEU:HA	5:D:124:LEU:HD23	1.61	0.47
6:E:126:ARG:HB3	6:E:143:HIS:HB3	1.96	0.47
8:G:99:LYS:HD2	8:G:100:GLY:N	2.30	0.47
9:H:3:LYS:HB3	9:H:4:PRO:HD3	1.97	0.47
13:L:85:ILE:O	13:L:86:MET:HE2	2.15	0.47
19:R:4:ASP:OD1	19:R:6:GLY:N	2.41	0.47
22:U:106:GLU:O	22:U:109:GLY:N	2.48	0.47
25:X:18:THR:C	25:X:24:VAL:HG22	2.40	0.47
31:4:17:C:H4'	31:4:61:C:H5'	1.96	0.47
33:7:24:THR:HA	33:7:27:GLN:HB2	1.96	0.47
1:2:66:C:H2'	1:2:67:G:C8	2.48	0.46
1:2:203:A:C2	1:2:204:G:C5	3.03	0.46
1:2:223:G:H2'	1:2:224:G:C8	2.50	0.46
1:2:605:G:C2	1:2:606:G:C8	3.02	0.46
1:2:751:4AC:H5	1:2:751:4AC:O7	2.15	0.46
1:2:991:G:H3'	1:2:992:U:C6	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1098:C:H2'	1:2:1099:C:H6	1.80	0.46
1:2:1214:U:C2	9:H:93:LEU:HG	2.50	0.46
1:2:1224:A:C5	1:2:1261:A:C8	3.03	0.46
1:2:1349:A:C6	1:2:1350:U:C4	3.03	0.46
7:F:14:ASP:OD1	7:F:14:ASP:N	2.48	0.46
9:H:209:ARG:O	9:H:212:GLU:HG3	2.15	0.46
12:K:39:GLU:HG3	12:K:42:ARG:HH21	1.80	0.46
14:M:16:ILE:HD12	14:M:80:HIS:HB2	1.97	0.46
19:R:42:LYS:HD3	19:R:42:LYS:HA	1.65	0.46
21:T:20:SER:OG	21:T:24:LEU:N	2.48	0.46
30:5:807:G:H2'	30:5:808:A:H8	1.79	0.46
1:2:123:G:O4'	19:R:32:ARG:NH2	2.43	0.46
1:2:296:U:H5'	15:N:36:ARG:HH22	1.79	0.46
1:2:621:G:C4	1:2:720:A:C6	3.03	0.46
1:2:770:G:C4	1:2:771:U:C5	3.04	0.46
1:2:1022:G:C6	1:2:1178:A:C6	3.03	0.46
1:2:1162:G:H2'	1:2:1163:C:O4'	2.15	0.46
1:2:1168:G:H2'	1:2:1169:U:O4'	2.15	0.46
1:2:1242:A:OP2	22:U:96:SER:OG	2.32	0.46
1:2:1324:C:C2	1:2:1325:C:C5	3.03	0.46
1:2:1466:G:N1	1:2:1467:UR3:H3U1	2.30	0.46
4:C:42:ARG:NH2	4:C:47:ARG:HA	2.30	0.46
18:Q:30:VAL:HG23	18:Q:31:GLU:OE1	2.15	0.46
18:Q:127:SER:OG	18:Q:128:LYS:N	2.48	0.46
32:6:16:VAL:O	32:6:18:LEU:N	2.48	0.46
1:2:276:C:OP2	19:R:96:LYS:HD2	2.16	0.46
1:2:479:4AC:C2	1:2:505:G:N2	2.77	0.46
1:2:559:G:C5	1:2:560:U:C4	3.03	0.46
1:2:569:G:C6	1:2:570:G:C5	3.03	0.46
1:2:648:4AC:H2'	1:2:649:G:O4'	2.15	0.46
1:2:778:U:H5	1:2:779:G:C5	2.33	0.46
1:2:966:C:C2	1:2:967:G:C8	3.03	0.46
1:2:1115:G:C5	1:2:1116:A:C6	3.04	0.46
1:2:1147:4AC:H6	1:2:1147:4AC:H5''	1.96	0.46
1:2:1289:U:C4	1:2:1290:G:C5	3.04	0.46
1:2:1390:C:H5''	1:2:1391:G:OP2	2.16	0.46
1:2:1427:G:C4	1:2:1428:G:C8	3.04	0.46
1:2:1450:U:H2'	1:2:1451:G:C5'	2.45	0.46
1:2:1457:G:O2'	1:2:1458:G:H5'	2.15	0.46
2:A:145:ILE:HD11	2:A:171:ILE:HG22	1.97	0.46
3:B:167:ILE:O	3:B:171:LEU:HB2	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:87:ALA:HB1	5:D:91:ASP:HB2	1.98	0.46
6:E:167:LYS:HE3	6:E:170:GLU:HB3	1.97	0.46
22:U:40:HIS:CE1	22:U:78:GLY:HA2	2.50	0.46
23:V:17:LYS:HG3	23:V:71:TYR:HB3	1.97	0.46
33:7:144:LEU:HD21	33:7:146:ILE:HD11	1.98	0.46
33:7:146:ILE:HB	33:7:179:PRO:O	2.15	0.46
33:7:301:LEU:O	35:9:193:VAL:HG13	2.15	0.46
35:9:178:LYS:NZ	35:9:180:SER:HB2	2.30	0.46
1:2:89:G:C3'	1:2:90:G:H8	2.27	0.46
1:2:173:C:H2'	1:2:174:C:C6	2.50	0.46
1:2:185:G:C5	1:2:186:G:N7	2.84	0.46
1:2:196:G:N7	19:R:26:HIS:CG	2.84	0.46
1:2:401:G:C2	1:2:402:G:C4	3.03	0.46
1:2:733:A:H62	1:2:780:U:H3	1.64	0.46
1:2:733:A:C6	1:2:734:A:C5	3.04	0.46
1:2:772:C:N3	1:2:773:C:C5	2.83	0.46
1:2:833:G:C2	1:2:834:G:C5	3.03	0.46
1:2:894:G:N2	1:2:1369:C:O2	2.49	0.46
1:2:1006:C:O2'	1:2:1007:C:H5'	2.16	0.46
1:2:1224:A:N7	1:2:1261:A:C8	2.83	0.46
1:2:1252:U:OP1	1:2:1252:U:H3'	2.16	0.46
1:2:1386:C:N3	1:2:1457:G:N2	2.57	0.46
3:B:187:GLU:HA	3:B:189:LYS:HE3	1.96	0.46
7:F:132:GLU:O	7:F:134:ARG:N	2.49	0.46
19:R:18:ASP:N	19:R:18:ASP:OD1	2.46	0.46
27:Z:18:ASP:O	27:Z:22:GLU:HG3	2.15	0.46
32:6:55:LEU:C	32:6:57:ARG:N	2.73	0.46
1:2:26:C:C2	1:2:27:U:C5	3.04	0.46
1:2:168:A:C8	1:2:169:A:C6	3.04	0.46
1:2:262:U:OP1	19:R:96:LYS:HD3	2.16	0.46
1:2:369:G:C6	1:2:370:C:C4	3.03	0.46
1:2:392:A:H5''	6:E:64:LYS:HE2	1.98	0.46
1:2:709:G:N1	1:2:710:A:C5	2.83	0.46
1:2:973:A:C5	29:3:92:ILE:HG21	2.50	0.46
1:2:976:A:C5	1:2:1001:A:C4	3.04	0.46
4:C:59:GLY:O	4:C:61:GLU:HG3	2.16	0.46
6:E:112:LEU:HA	6:E:112:LEU:HD23	1.56	0.46
6:E:185:VAL:HG22	6:E:186:PHE:H	1.81	0.46
7:F:175:LEU:HD23	7:F:175:LEU:HA	1.45	0.46
9:H:121:GLN:HG3	9:H:125:TRP:CZ3	2.51	0.46
10:I:55:ASP:O	18:Q:18:PRO:HB3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:O:99:ASP:HB2	16:O:103:ARG:HH21	1.80	0.46
16:O:105:ASP:HA	16:O:108:ARG:HH12	1.80	0.46
19:R:11:PRO:HA	19:R:23:TRP:CH2	2.51	0.46
24:W:21:ILE:HG12	24:W:59:LYS:NZ	2.30	0.46
31:4:25:C:C2	31:4:26:G:C8	3.04	0.46
32:6:97:LYS:HB3	32:6:99:LYS:HD3	1.97	0.46
33:7:191:ILE:O	33:7:194:LEU:HB3	2.15	0.46
1:2:22:G:H2'	1:2:23:A:H8	1.81	0.46
1:2:41:G:H2'	1:2:42:C:C6	2.51	0.46
1:2:108:G:C2	1:2:109:C:C6	3.03	0.46
1:2:178:A:N3	1:2:209:A:N1	2.64	0.46
1:2:315:A:N6	1:2:316:G:O6	2.49	0.46
1:2:334:A:N6	1:2:335:G:C2	2.84	0.46
1:2:685:G:C5	1:2:686:C:C4	3.04	0.46
1:2:731:4AC:H2'	1:2:732:G:C8	2.50	0.46
1:2:781:A:H5''	1:2:783:A:N7	2.30	0.46
1:2:851:4AC:CM7	15:N:3:GLY:H	2.27	0.46
1:2:1306:A:C2	1:2:1307:A:C5	3.04	0.46
1:2:1404:G:C2	1:2:1440:C:N3	2.84	0.46
1:2:1431:G:H2'	1:2:1432:G:H8	1.80	0.46
3:B:68:LEU:HD21	3:B:110:PHE:CE2	2.51	0.46
13:L:1:MET:HG3	13:L:2:GLN:H	1.81	0.46
15:N:42:ASP:O	15:N:44:LEU:N	2.49	0.46
31:4:14:A:C8	31:4:22:G:C2	3.04	0.46
33:7:7:GLN:HB2	33:7:281:PHE:CE2	2.50	0.46
33:7:311:LEU:H	33:7:311:LEU:HD23	1.81	0.46
1:2:44:A:C6	1:2:406:A:C8	3.04	0.46
1:2:157:A:O4'	1:2:353:A:C8	2.69	0.46
1:2:193:G:N2	6:E:207:MET:HA	2.31	0.46
1:2:331:C:C2	1:2:332:U:C5	3.04	0.46
1:2:451:A:C2	1:2:452:G:H1'	2.51	0.46
1:2:465:G:C2	1:2:466:G:C2	3.03	0.46
1:2:641:G:C2	1:2:642:U:C4	3.04	0.46
1:2:651:G:N1	1:2:652:G:N2	2.63	0.46
1:2:1042:G:C2	1:2:1046:G:C2	3.04	0.46
1:2:1053:A:C5	1:2:1054:C:C4	3.03	0.46
1:2:1298:C:H4'	1:2:1336:C:H4'	1.98	0.46
1:2:1396:G:C2	1:2:1448:C:H1'	2.51	0.46
1:2:1398:G:OP2	1:2:1398:G:H8	1.99	0.46
7:F:107:GLY:O	7:F:110:ILE:N	2.48	0.46
25:X:53:ASP:O	25:X:54:ILE:HD13	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:7:3:TRP:HZ2	33:7:57:GLY:HA3	1.81	0.46
33:7:353:ALA:HB2	33:7:373:VAL:HG23	1.97	0.46
33:7:356:THR:HB	33:7:367:LEU:HD11	1.98	0.46
35:9:141:GLU:O	35:9:145:LYS:NZ	2.47	0.46
1:2:59:A:N6	1:2:112:A:C4	2.84	0.46
1:2:490:G:H5''	15:N:116:MET:HE2	1.98	0.46
1:2:559:G:C2	1:2:560:U:C2	3.04	0.46
1:2:600:G:C2	1:2:601:C:C5	3.03	0.46
1:2:799:G:C4	1:2:800:U:C6	3.03	0.46
1:2:911:G:N3	1:2:912:G:C8	2.84	0.46
1:2:1031:C:H6	1:2:1031:C:O5'	1.99	0.46
1:2:1140:G:N1	1:2:1143:A:OP2	2.46	0.46
1:2:1264:C:C2	1:2:1265:C:C5	3.04	0.46
1:2:1399:C:C2	1:2:1400:C:C6	3.04	0.46
1:2:1419:C:C4	1:2:1420:U:C4	3.04	0.46
1:2:1429:U:H2'	1:2:1430:C:H6	1.80	0.46
5:D:33:TYR:HA	5:D:118:MET:SD	2.56	0.46
9:H:212:GLU:HA	9:H:215:ARG:HG2	1.97	0.46
11:J:3:ILE:O	11:J:29:GLY:N	2.41	0.46
11:J:62:TYR:CG	11:J:74:LYS:HE3	2.51	0.46
12:K:87:VAL:O	12:K:91:GLY:HA2	2.16	0.46
20:S:27:ASP:OD2	20:S:29:GLU:HB3	2.16	0.46
22:U:47:GLN:OE1	22:U:47:GLN:N	2.32	0.46
22:U:90:PHE:CD1	22:U:91:TYR:N	2.84	0.46
29:3:1:MET:H1	29:3:53:ILE:HD12	1.80	0.46
29:3:48:ALA:HB1	29:3:51:VAL:HB	1.98	0.46
31:4:29:G:C2	31:4:30:G:C5	3.03	0.46
31:4:34:C:H2'	31:4:35:A:C8	2.51	0.46
32:6:20:GLU:H	32:6:23:GLN:CD	2.19	0.46
33:7:138:ILE:CD1	33:7:410:TRP:HB3	2.46	0.46
34:8:41:THR:HG22	34:8:84:GLN:HA	1.96	0.46
35:9:247:ILE:HG22	35:9:251:ILE:HD11	1.97	0.46
1:2:566:C:H2'	1:2:567:C:H6	1.81	0.46
1:2:745:G:C6	1:2:746:C:C4	3.04	0.46
1:2:831:A:C2	1:2:832:G:H1'	2.50	0.46
1:2:871:A:N7	1:2:872:A:C6	2.84	0.46
1:2:892:U:C2	1:2:893:G:C8	3.04	0.46
1:2:938:B8H:C2	1:2:939:5MC:HM51	2.44	0.46
1:2:1113:G:N1	1:2:1114:G:C5	2.84	0.46
1:2:1247:G:C5	1:2:1248:G:H1'	2.51	0.46
1:2:1368:A:N6	1:2:1470:C:H5'	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1386:C:C2	1:2:1387:A:C8	3.04	0.46
1:2:1388:C:C2	1:2:1389:C:C5	3.04	0.46
5:D:102:GLU:O	5:D:104:ARG:N	2.49	0.46
5:D:111:LYS:HD2	5:D:111:LYS:HA	1.76	0.46
6:E:172:GLU:OE2	6:E:173:ILE:N	2.49	0.46
6:E:191:LYS:HB3	6:E:191:LYS:HE2	1.70	0.46
9:H:92:SER:OG	9:H:94:ASN:ND2	2.48	0.46
18:Q:77:THR:OG1	18:Q:80:ARG:HB2	2.16	0.46
19:R:42:LYS:HB2	19:R:43:PRO:HD3	1.98	0.46
22:U:70:ILE:O	22:U:73:LEU:N	2.49	0.46
31:4:14:A:C6	31:4:22:G:O4'	2.69	0.46
31:4:51:C:H2'	31:4:52:G:O4'	2.16	0.46
33:7:333:TYR:HE1	33:7:378:ILE:HB	1.78	0.46
33:7:346:LEU:HD12	33:7:347:LYS:O	2.16	0.46
34:8:11:LEU:HA	34:8:14:LEU:HB2	1.98	0.46
34:8:89:SER:O	34:8:93:ASN:ND2	2.37	0.46
1:2:196:G:H2'	1:2:196:G:N3	2.31	0.46
1:2:252:A:C2	1:2:254:U:C4	3.04	0.46
1:2:582:G:H2'	1:2:582:G:N3	2.30	0.46
1:2:690:U:O4	30:5:808:A:O2'	2.23	0.46
1:2:702:C:C2	1:2:703:4AC:C5	2.98	0.46
1:2:711:A:H2'	1:2:712:C:O4'	2.16	0.46
1:2:782:A:N6	1:2:1478:C:H1'	2.31	0.46
1:2:1321:G:N2	1:2:1347:G:C4	2.84	0.46
1:2:1323:A:N6	1:2:1347:G:N2	2.64	0.46
1:2:1392:A:H5'	1:2:1452:A:H61	1.81	0.46
1:2:1395:G:C2	1:2:1449:G:C6	3.03	0.46
1:2:1407:A:H2'	1:2:1407:A:N3	2.30	0.46
1:2:1508:C:C2	30:5:807:G:N2	2.83	0.46
2:A:100:ARG:HG2	2:A:129:ARG:HH21	1.81	0.46
2:A:167:ILE:HB	2:A:186:ILE:HD11	1.97	0.46
3:B:135:ILE:HG13	3:B:136:PRO:O	2.16	0.46
9:H:134:GLU:HA	9:H:151:ASP:HA	1.97	0.46
9:H:194:LYS:HB2	9:H:194:LYS:HE3	1.78	0.46
21:T:84:HIS:CD2	21:T:84:HIS:C	2.94	0.46
30:5:816:U:C2	30:5:817:A:C8	3.04	0.46
33:7:144:LEU:O	33:7:145:ILE:HD13	2.16	0.46
33:7:214:VAL:HB	33:7:244:GLN:NE2	2.31	0.46
33:7:329:ILE:HD12	33:7:331:ILE:HD11	1.98	0.46
1:2:164:G:C2	1:2:165:G:C5	3.03	0.45
1:2:336:A:C2	1:2:338:A:C8	3.04	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:496:G:OP1	1:2:496:G:H2'	2.16	0.45
1:2:678:G:H2'	1:2:679:G:C8	2.51	0.45
1:2:999:G:H3'	1:2:1000:G:C8	2.51	0.45
1:2:1467:UR3:C5	30:5:820:U:H5'	2.46	0.45
5:D:76:ARG:O	5:D:79:ARG:N	2.49	0.45
5:D:106:GLN:O	5:D:109:VAL:HG12	2.16	0.45
6:E:47:TYR:HD1	6:E:47:TYR:HA	1.57	0.45
6:E:205:PHE:CE2	6:E:211:ASP:HA	2.51	0.45
7:F:50:ILE:HG13	7:F:51:ASP:H	1.80	0.45
8:G:81:PRO:HG3	8:G:111:THR:HB	1.98	0.45
21:T:34:ARG:O	21:T:36:LEU:N	2.49	0.45
21:T:53:LEU:O	21:T:57:GLY:N	2.48	0.45
29:3:34:LYS:NZ	29:3:92:ILE:HG22	2.30	0.45
29:3:114:ILE:O	29:3:118:VAL:HG22	2.16	0.45
31:4:26:G:C6	31:4:27:U:C4	3.04	0.45
33:7:11:ASN:H	33:7:112:ASP:HB2	1.81	0.45
1:2:132:C:O2'	1:2:133:C:OP1	2.30	0.45
1:2:149:A:H5'	1:2:150:C:OP2	2.16	0.45
1:2:205:G:C2	1:2:206:C:C2	3.05	0.45
1:2:359:C:C2	1:2:360:G:C2	3.04	0.45
1:2:402:G:C2	1:2:403:G:C8	3.04	0.45
1:2:705:G:C4	1:2:706:C:C5	3.04	0.45
1:2:709:G:C2	1:2:710:A:C5	3.04	0.45
1:2:734:A:N6	1:2:780:U:N3	2.64	0.45
1:2:738:C:H2'	1:2:739:A:O4'	2.15	0.45
1:2:862:U:C4	1:2:877:G:N2	2.85	0.45
1:2:999:G:H2'	1:2:999:G:N3	2.31	0.45
1:2:1192:C:N4	1:2:1193:4AC:HM72	2.30	0.45
1:2:1329:G:C4	1:2:1342:G:N2	2.84	0.45
1:2:1480:G:H2'	1:2:1481:U:H6	1.82	0.45
6:E:31:ARG:HG3	6:E:32:PRO:HD2	1.97	0.45
9:H:114:ARG:HH12	9:H:186:GLU:CD	2.24	0.45
9:H:172:LYS:NZ	9:H:186:GLU:HB2	2.31	0.45
25:X:62:ARG:HD2	25:X:62:ARG:HA	1.77	0.45
29:3:48:ALA:HB1	29:3:100:ALA:HB1	1.98	0.45
30:5:808:A:N1	30:5:809:G:C5	2.85	0.45
31:4:37:A:C2	31:4:38:A:C4	3.03	0.45
32:6:88:GLN:NE2	32:6:91:VAL:HG11	2.31	0.45
33:7:45:MET:O	33:7:47:ILE:HG13	2.17	0.45
33:7:53:GLU:OE2	33:7:281:PHE:HD1	2.00	0.45
33:7:234:LYS:NZ	33:7:277:SER:HB3	2.30	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:67:G:C6	1:2:363:G:C5	3.04	0.45
1:2:124:G:H2'	1:2:125:U:C6	2.51	0.45
1:2:124:G:H2'	1:2:125:U:H6	1.80	0.45
1:2:157:A:H2'	1:2:158:A:C8	2.52	0.45
1:2:383:A:C2	1:2:384:U:C4	3.05	0.45
1:2:671:A:C5	1:2:672:U:C5	3.04	0.45
1:2:759:A:H1'	1:2:761:A:N7	2.31	0.45
1:2:781:A:H8	1:2:783:A:C8	2.35	0.45
1:2:904:A:C6	1:2:907:A:C4	3.04	0.45
1:2:1126:G:C2	1:2:1127:G:C4	3.05	0.45
1:2:1142:U:O2'	1:2:1143:A:O5'	2.26	0.45
1:2:1157:G:H3'	1:2:1158:G:H5''	1.97	0.45
3:B:26:LYS:O	3:B:26:LYS:HD3	2.17	0.45
3:B:43:LEU:HD23	3:B:155:PRO:HB2	1.98	0.45
13:L:26:ILE:HG21	13:L:84:GLN:CB	2.46	0.45
16:O:46:ASP:CG	16:O:48:PHE:H	2.25	0.45
18:Q:22:PRO:HB3	18:Q:66:PHE:HE1	1.80	0.45
19:R:47:VAL:HG13	19:R:74:ASN:HB2	1.98	0.45
24:W:25:ASN:OD1	24:W:26:GLU:N	2.49	0.45
29:3:15:LEU:O	29:3:19:ALA:HB3	2.16	0.45
31:4:12:G:C6	31:4:24:U:C2	3.04	0.45
33:7:144:LEU:HD12	33:7:145:ILE:N	2.31	0.45
33:7:378:ILE:HG12	33:7:380:VAL:HG23	1.98	0.45
1:2:30:C:H5''	1:2:31:G:OP2	2.16	0.45
1:2:144:G:H2'	1:2:145:G:C8	2.52	0.45
1:2:464:A:O2'	1:2:465:G:N7	2.43	0.45
1:2:604:G:H2'	1:2:605:G:H8	1.82	0.45
1:2:793:C:C2	1:2:794:U:C5	3.03	0.45
1:2:1041:4AC:H3'	1:2:1041:4AC:H6	1.98	0.45
1:2:1173:U:H2'	1:2:1174:C:H5''	1.99	0.45
1:2:1236:C:P	22:U:72:ARG:HE	2.39	0.45
2:A:131:GLN:OE1	2:A:131:GLN:N	2.38	0.45
6:E:110:LEU:HD23	6:E:110:LEU:HA	1.76	0.45
6:E:183:ALA:O	6:E:198:ARG:HG3	2.16	0.45
7:F:53:LEU:HD23	7:F:53:LEU:HA	1.65	0.45
16:O:108:ARG:NH1	16:O:108:ARG:HB2	2.31	0.45
31:4:17:C:OP1	31:4:60:U:O2'	2.33	0.45
31:4:25:C:C4	31:4:26:G:C8	3.04	0.45
33:7:45:MET:HE2	33:7:97:HIS:ND1	2.32	0.45
33:7:374:LYS:HD2	33:7:374:LYS:HA	1.82	0.45
1:2:80:G:C6	1:2:81:U:C4	3.04	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:90:G:C6	1:2:91:G:C5	3.05	0.45
1:2:470:G:C8	1:2:501:A:C4	3.04	0.45
1:2:520:G:H5''	1:2:521:C:OP2	2.17	0.45
1:2:595:G:C4	1:2:596:G:C8	3.05	0.45
1:2:945:C:C4	1:2:947:G:C5	3.05	0.45
1:2:1053:A:H2'	1:2:1054:C:C6	2.52	0.45
1:2:1081:C:H2'	1:2:1082:G:C8	2.52	0.45
1:2:1086:C:C2	1:2:1127:G:N2	2.85	0.45
1:2:1166:C:C5	1:2:1167:G:C5	3.05	0.45
1:2:1398:G:O2'	1:2:1399:C:O4'	2.33	0.45
1:2:1420:U:O2'	1:2:1421:U:H2'	2.17	0.45
1:2:1424:G:N1	1:2:1425:G:C5	2.84	0.45
1:2:1484:G:C4	1:2:1485:G:C8	3.05	0.45
2:A:148:LYS:HD3	2:A:148:LYS:C	2.42	0.45
7:F:44:ILE:HG22	7:F:119:LEU:HD23	1.98	0.45
10:I:65:LEU:C	10:I:66:LEU:HD12	2.42	0.45
16:O:33:ILE:HG23	16:O:34:ASN:H	1.82	0.45
18:Q:116:LEU:O	18:Q:119:MET:N	2.50	0.45
19:R:101:VAL:HG22	19:R:102:VAL:O	2.16	0.45
26:Y:42:ARG:NH2	26:Y:43:CYS:SG	2.89	0.45
29:3:4:PRO:C	29:3:6:TYR:H	2.24	0.45
33:7:86:LEU:O	33:7:87:ARG:HB2	2.15	0.45
35:9:178:LYS:NZ	35:9:179:MET:O	2.34	0.45
1:2:63:A:C5	1:2:64:U:C5	3.05	0.45
1:2:142:G:N1	1:2:143:G:C5	2.85	0.45
1:2:218:C:C4	1:2:219:G:C8	3.04	0.45
1:2:314:G:H2'	1:2:314:G:N3	2.31	0.45
1:2:359:C:H2'	1:2:360:G:N3	2.32	0.45
1:2:470:G:C5	1:2:501:A:C2	3.04	0.45
1:2:582:G:O6	1:2:590:4AC:HM72	2.17	0.45
1:2:718:4AC:C7	1:2:719:G:N1	2.77	0.45
1:2:832:G:C2	1:2:833:G:C4	3.05	0.45
1:2:1451:G:O2'	33:7:352:ARG:NH2	2.49	0.45
1:2:1471:A:N6	1:2:1473:G:C2	2.85	0.45
1:2:1481:U:C2	1:2:1482:A:C8	3.05	0.45
2:A:44:VAL:HG22	2:A:47:ARG:CZ	2.46	0.45
2:A:171:ILE:C	2:A:173:LYS:H	2.24	0.45
6:E:3:ARG:HH21	6:E:4:LYS:HZ1	1.65	0.45
6:E:76:ARG:HB2	6:E:78:ARG:NH2	2.32	0.45
9:H:153:SER:OG	9:H:154:PRO:HD2	2.17	0.45
9:H:166:ALA:O	9:H:170:SER:OG	2.19	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:K:118:LYS:HA	12:K:118:LYS:HD3	1.75	0.45
14:M:12:GLU:HB3	14:M:14:TRP:HE1	1.82	0.45
15:N:4:LYS:NZ	15:N:8:ASN:HD22	2.14	0.45
23:V:11:ASN:OD1	23:V:14:ILE:N	2.46	0.45
24:W:29:VAL:HG12	24:W:30:PHE:N	2.31	0.45
25:X:29:VAL:O	25:X:40:VAL:HG13	2.16	0.45
27:Z:51:PRO:HA	27:Z:54:VAL:HG12	1.97	0.45
1:2:67:G:C4	1:2:340:G:N2	2.85	0.45
1:2:809:C:H3'	1:2:810:U:C6	2.51	0.45
1:2:951:C:C4	1:2:952:C:C5	3.05	0.45
1:2:1261:A:C6	1:2:1262:A:C6	3.05	0.45
5:D:131:GLU:OE2	5:D:134:GLY:HA2	2.17	0.45
13:L:78:ASP:O	13:L:81:ALA:N	2.43	0.45
14:M:33:ILE:HG23	14:M:34:THR:N	2.31	0.45
16:O:9:ARG:HA	16:O:14:ASP:HA	1.98	0.45
18:Q:26:LEU:HD21	18:Q:59:GLY:O	2.16	0.45
21:T:52:ARG:O	21:T:56:LYS:HG2	2.17	0.45
25:X:59:GLU:O	25:X:61:GLU:N	2.50	0.45
26:Y:27:PRO:HG2	29:3:45:ARG:HG2	1.98	0.45
28:0:4:ARG:HD2	28:0:7:LYS:HE2	1.98	0.45
29:3:25:ILE:HA	29:3:28:ASP:OD1	2.17	0.45
29:3:82:SER:OG	29:3:83:LYS:N	2.41	0.45
31:4:22:G:H2'	31:4:23:C:C6	2.52	0.45
33:7:300:TYR:HB3	35:9:191:LEU:HD23	1.99	0.45
33:7:329:ILE:HG21	33:7:386:VAL:CG1	2.46	0.45
1:2:22:G:N3	1:2:23:A:C8	2.85	0.45
1:2:44:A:C2	1:2:406:A:C5	3.04	0.45
1:2:174:C:C2	1:2:175:C:C5	3.04	0.45
1:2:304:G:C6	1:2:312:G:N1	2.85	0.45
1:2:656:G:OP1	14:M:25:ASN:ND2	2.50	0.45
1:2:694:G:N1	1:2:698:G:C6	2.84	0.45
1:2:1196:G:C2	1:2:1197:C:C4	3.04	0.45
1:2:1397:G:C2	1:2:1398:G:N7	2.85	0.45
1:2:1424:G:C2	1:2:1425:G:C4	3.04	0.45
7:F:58:ASN:OD1	7:F:58:ASN:N	2.45	0.45
7:F:120:ASN:O	7:F:122:ILE:HG23	2.17	0.45
10:I:17:SER:O	10:I:22:LYS:HB2	2.17	0.45
10:I:55:ASP:OD2	24:W:8:ILE:HG12	2.16	0.45
18:Q:45:TYR:HD1	18:Q:45:TYR:HA	1.58	0.45
22:U:73:LEU:HA	22:U:73:LEU:HD23	1.51	0.45
33:7:100:LEU:HA	33:7:100:LEU:HD12	1.61	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:7:213:PRO:HG3	33:7:245:GLY:HA3	1.98	0.45
33:7:347:LYS:HG3	33:7:349:ASP:OD1	2.16	0.45
34:8:106:CYS:HB2	34:8:110:LYS:HA	1.99	0.45
1:2:69:G:N3	1:2:103:G:N2	2.65	0.45
1:2:211:A:N1	1:2:229:G:O2'	2.47	0.45
1:2:225:C:O2'	1:2:226:U:H5'	2.17	0.45
1:2:273:C:C4	1:2:274:G:C5	3.04	0.45
1:2:702:C:H2'	1:2:703:4AC:C6	2.40	0.45
1:2:739:A:N1	1:2:775:G:C6	2.85	0.45
1:2:959:G:H2'	1:2:960:G:H8	1.82	0.45
1:2:1020:A:N1	1:2:1180:G:C4	2.85	0.45
1:2:1135:C:H2'	1:2:1136:C:C6	2.52	0.45
1:2:1238:C:N3	1:2:1246:G:C2	2.85	0.45
1:2:1294:C:C2	1:2:1295:U:C5	3.04	0.45
1:2:1313:A:O2'	31:4:40:C:O2'	2.35	0.45
1:2:1324:C:P	12:K:124:LYS:HZ1	2.37	0.45
1:2:1430:C:H2'	1:2:1431:G:H8	1.82	0.45
8:G:94:PHE:CE2	8:G:96:PRO:HA	2.51	0.45
18:Q:57:GLN:HG3	24:W:37:VAL:HG13	1.98	0.45
21:T:20:SER:OG	21:T:23:GLU:HB3	2.17	0.45
21:T:61:LYS:HG3	21:T:62:PRO:HD2	1.98	0.45
27:Z:126:ARG:HH12	27:Z:188:ARG:NH1	2.15	0.45
27:Z:179:LYS:HB2	27:Z:179:LYS:HE3	1.84	0.45
31:4:52:G:C6	31:4:63:G:C6	3.05	0.45
31:4:52:G:C2	31:4:53:G:C8	3.05	0.45
1:2:55:A:C5	1:2:315:A:C5	3.05	0.45
1:2:69:G:C2	1:2:70:U:C2	3.05	0.45
1:2:133:C:H2'	1:2:134:C:C6	2.51	0.45
1:2:186:G:H1	1:2:200:C:H42	1.64	0.45
1:2:470:G:C2	1:2:471:G:C5	3.05	0.45
1:2:631:G:OP1	2:A:132:THR:N	2.50	0.45
1:2:726:A:H8	1:2:727:G:C8	2.34	0.45
1:2:741:G:N1	1:2:773:C:C4	2.85	0.45
1:2:770:G:C2	1:2:771:U:C2	3.05	0.45
1:2:950:A:N1	1:2:1293:A:C4	2.85	0.45
1:2:1092:G:H5'	1:2:1254:A:O2'	2.17	0.45
1:2:1098:C:H2'	1:2:1099:C:C6	2.52	0.45
1:2:1147:4AC:H6	1:2:1147:4AC:C5'	2.47	0.45
1:2:1466:G:H21	1:2:1488:MA6:C2	2.30	0.45
2:A:17:LYS:HD3	2:A:39:ASP:OD1	2.17	0.45
2:A:121:MET:SD	2:A:188:LYS:HB3	2.57	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:46:THR:HG22	5:D:50:ASN:ND2	2.30	0.45
8:G:32:LYS:HA	8:G:32:LYS:HD3	1.72	0.45
19:R:9:ILE:HG13	19:R:10:GLN:H	1.82	0.45
19:R:60:TYR:O	19:R:62:ARG:HG3	2.17	0.45
25:X:12:ILE:HD13	25:X:30:ARG:HB3	1.99	0.45
26:Y:5:TRP:HB3	29:3:37:ASN:ND2	2.31	0.45
26:Y:17:ARG:NH1	29:3:44:GLU:OE2	2.50	0.45
27:Z:188:ARG:HH11	27:Z:188:ARG:H	1.65	0.45
29:3:40:THR:HG23	29:3:41:LYS:N	2.32	0.45
30:5:821:G:N1	31:4:35:A:C6	2.85	0.45
31:4:19:G:N2	31:4:57:A:H1'	2.32	0.45
33:7:26:VAL:HG21	33:7:93:ASP:OD1	2.16	0.45
35:9:219:ILE:HD12	35:9:229:VAL:HG23	1.98	0.45
1:2:187:G:C6	1:2:200:C:C4	3.05	0.44
1:2:200:C:H2'	1:2:201:C:C6	2.51	0.44
1:2:451:A:C4	1:2:452:G:C8	3.05	0.44
1:2:656:G:OP2	14:M:45:GLY:HA3	2.17	0.44
1:2:814:A:O3'	2:A:134:GLN:NE2	2.44	0.44
1:2:975:G:N1	29:3:38:GLU:OE1	2.40	0.44
1:2:1153:A:H2'	1:2:1154:A:O4'	2.17	0.44
1:2:1391:G:C6	1:2:1451:G:N7	2.85	0.44
1:2:1479:4AC:N3	1:2:1495:G:C2	2.84	0.44
2:A:124:VAL:HG12	2:A:125:ILE:N	2.33	0.44
5:D:78:LYS:HE2	5:D:78:LYS:HB3	1.74	0.44
5:D:154:TYR:HE1	5:D:160:PHE:HD2	1.64	0.44
7:F:143:PHE:HE1	7:F:211:VAL:HG21	1.81	0.44
10:I:102:LEU:HD12	10:I:102:LEU:HA	1.71	0.44
10:I:107:SER:O	10:I:107:SER:OG	2.29	0.44
14:M:10:LYS:CE	14:M:12:GLU:HB2	2.47	0.44
15:N:94:ILE:HD12	15:N:94:ILE:HA	1.85	0.44
26:Y:15:VAL:O	26:Y:16:ILE:HD13	2.17	0.44
32:6:26:GLY:O	32:6:66:LEU:HD12	2.16	0.44
35:9:19:VAL:HG12	35:9:29:VAL:HG12	1.99	0.44
35:9:20:LYS:HE2	35:9:28:TYR:HB3	1.99	0.44
1:2:22:G:N2	1:2:23:A:C4	2.85	0.44
1:2:54:G:C4	1:2:374:A:N7	2.86	0.44
1:2:115:A:C6	1:2:249:C:C4	3.06	0.44
1:2:317:C:H2'	1:2:318:C:C6	2.52	0.44
1:2:428:C:H2'	1:2:429:A:C8	2.42	0.44
1:2:652:G:C8	1:2:653:U:H5	2.34	0.44
1:2:685:G:C5	1:2:686:C:C5	3.06	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:724:U:N3	1:2:725:G:C4	2.85	0.44
1:2:768:U:C2	1:2:769:A:C8	3.05	0.44
1:2:771:U:H5''	1:2:772:C:OP2	2.17	0.44
1:2:804:G:H2'	1:2:805:C:C6	2.52	0.44
1:2:1273:A:C8	1:2:1275:U:N3	2.85	0.44
1:2:1403:G:C2	1:2:1441:U:N3	2.85	0.44
1:2:1451:G:O2'	1:2:1452:A:H8	1.99	0.44
1:2:1452:A:C8	33:7:352:ARG:NH2	2.84	0.44
1:2:1476:A:C2	1:2:1477:G:C4	3.05	0.44
3:B:21:THR:H	3:B:143:THR:HG21	1.83	0.44
3:B:21:THR:HG22	3:B:22:GLN:N	2.32	0.44
9:H:42:ARG:HH21	9:H:45:PRO:HA	1.81	0.44
18:Q:120:ARG:NH1	18:Q:124:LEU:HD21	2.31	0.44
20:S:2:GLY:O	20:S:4:ILE:N	2.49	0.44
21:T:53:LEU:HA	21:T:56:LYS:HB2	1.99	0.44
22:U:70:ILE:O	22:U:72:ARG:N	2.50	0.44
26:Y:38:TRP:C	26:Y:40:CYS:H	2.25	0.44
31:4:28:C:H42	31:4:42:G:H1	1.64	0.44
33:7:105:LEU:HD23	33:7:105:LEU:HA	1.84	0.44
33:7:138:ILE:HG22	33:7:139:ILE:HD13	1.98	0.44
1:2:206:C:H4'	11:J:43:ARG:HH22	1.82	0.44
1:2:259:A:H2	1:2:283:A:N6	2.14	0.44
1:2:295:G:H2'	1:2:296:U:H6	1.77	0.44
1:2:366:G:C6	1:2:367:G:N7	2.86	0.44
1:2:662:A:C6	1:2:663:A:C5	3.05	0.44
1:2:711:A:H4'	1:2:823:G:O2'	2.17	0.44
1:2:713:G:N1	1:2:714:G:C5	2.85	0.44
1:2:858:G:N2	1:2:882:U:O2	2.50	0.44
1:2:865:G:C2	1:2:866:G:N2	2.86	0.44
1:2:1046:G:C4	1:2:1047:G:C8	3.06	0.44
1:2:1064:G:C4	1:2:1065:U:C5	3.05	0.44
1:2:1237:C:H2'	1:2:1238:C:C6	2.53	0.44
1:2:1268:C:H2'	1:2:1269:C:H6	1.81	0.44
1:2:1289:U:C2	1:2:1290:G:C8	3.04	0.44
1:2:1365:U:H2'	1:2:1366:G:C8	2.52	0.44
4:C:37:GLU:HG2	4:C:38:ALA:N	2.32	0.44
10:I:11:LEU:HA	10:I:14:ILE:HG22	1.99	0.44
11:J:4:TRP:HB2	11:J:28:LEU:HD22	1.99	0.44
16:O:51:ALA:C	16:O:53:TYR:H	2.26	0.44
16:O:83:LYS:CE	21:T:9:ARG:HH12	2.29	0.44
21:T:123:THR:OG1	31:4:30:G:OP1	2.35	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:106:C:C5	1:2:107:G:N7	2.86	0.44
1:2:195:A:C5	1:2:197:G:C5	3.06	0.44
1:2:322:A:H2'	1:2:323:G:C8	2.52	0.44
1:2:334:A:H2'	1:2:335:G:O4'	2.18	0.44
1:2:470:G:C2	1:2:471:G:C8	3.06	0.44
1:2:662:A:C5	1:2:663:A:C5	3.05	0.44
1:2:1037:G:H2'	1:2:1038:U:C6	2.52	0.44
1:2:1046:G:N1	1:2:1047:G:C5	2.85	0.44
1:2:1085:C:C2	1:2:1128:G:C2	3.06	0.44
1:2:1272:C:C5	9:H:177:LYS:HD3	2.52	0.44
3:B:168:TYR:HD1	3:B:168:TYR:HA	1.68	0.44
6:E:40:ARG:NH2	6:E:189:GLN:OE1	2.23	0.44
6:E:184:TYR:CE2	6:E:238:PRO:HD3	2.52	0.44
15:N:134:LEU:HD12	15:N:134:LEU:HA	1.69	0.44
16:O:7:ILE:HD12	16:O:14:ASP:OD2	2.18	0.44
16:O:15:LEU:HD21	16:O:25:LEU:HD22	1.99	0.44
16:O:106:ILE:O	16:O:110:ARG:HG3	2.18	0.44
22:U:25:GLU:HB2	22:U:26:ILE:HD12	2.00	0.44
25:X:31:ILE:HG23	25:X:38:GLY:H	1.82	0.44
27:Z:76:GLU:C	27:Z:78:PRO:HD3	2.43	0.44
29:3:23:VAL:O	29:3:27:ARG:N	2.50	0.44
31:4:34:C:N3	31:4:35:A:N7	2.66	0.44
31:4:54:5MU:H72	31:4:55:PSU:O2	2.17	0.44
33:7:244:GLN:O	33:7:244:GLN:HG2	2.17	0.44
1:2:22:G:C2	1:2:23:A:C5	3.06	0.44
1:2:155:G:H2'	1:2:156:G:H8	1.81	0.44
1:2:211:A:N3	1:2:213:G:H1'	2.33	0.44
1:2:517:G:C2	1:2:518:U:C5	3.06	0.44
1:2:563:G:C2	1:2:611:U:C2	3.05	0.44
1:2:688:A:H4'	1:2:689:G:O4'	2.18	0.44
1:2:761:A:C6	1:2:762:C:C4	3.05	0.44
1:2:945:C:C4	1:2:947:G:C6	3.05	0.44
1:2:1289:U:H2'	1:2:1290:G:H8	1.81	0.44
4:C:42:ARG:NH1	4:C:47:ARG:HG3	2.32	0.44
11:J:4:TRP:HH2	11:J:19:LEU:HD11	1.82	0.44
15:N:128:LYS:HB3	15:N:128:LYS:HE2	1.60	0.44
16:O:79:VAL:HG12	16:O:91:LEU:O	2.16	0.44
16:O:113:ARG:NH1	16:O:121:GLU:OE2	2.51	0.44
21:T:50:LYS:HD2	21:T:59:TYR:CZ	2.52	0.44
29:3:113:GLU:OE2	29:3:117:LYS:NZ	2.38	0.44
30:5:823:C:HO2'	32:6:57:ARG:HH11	1.58	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:6:75:GLN:HB3	32:6:79:ARG:HH12	1.82	0.44
33:7:27:GLN:HA	33:7:32:ILE:O	2.18	0.44
33:7:230:PHE:HD2	35:9:219:ILE:O	2.00	0.44
33:7:251:GLN:O	33:7:275:LYS:HA	2.17	0.44
35:9:72:ASP:O	35:9:76:GLY:N	2.51	0.44
35:9:176:LYS:HZ3	35:9:178:LYS:HA	1.82	0.44
1:2:99:C:C2	1:2:100:G:C8	3.06	0.44
1:2:253:U:C6	1:2:865:G:N2	2.86	0.44
1:2:373:A2M:HM'3	1:2:373:A2M:H1'	1.53	0.44
1:2:391:A:H4'	6:E:67:ASN:ND2	2.31	0.44
1:2:695:A:C6	1:2:696:A:C6	3.06	0.44
1:2:739:A:C6	1:2:775:G:C6	3.05	0.44
1:2:1071:G:C6	1:2:1072:C:N4	2.85	0.44
1:2:1180:G:C4	1:2:1181:C:C5	3.06	0.44
1:2:1242:A:H2'	1:2:1243:A:C8	2.53	0.44
1:2:1351:A:N7	1:2:1352:C:N4	2.65	0.44
1:2:1373:C:C4	1:2:1375:G:C2	3.06	0.44
1:2:1386:C:N4	1:2:1457:G:H1	2.15	0.44
1:2:1452:A:H3'	33:7:352:ARG:CZ	2.47	0.44
2:A:59:ASP:OD1	2:A:59:ASP:N	2.47	0.44
3:B:148:SER:O	3:B:148:SER:OG	2.31	0.44
5:D:56:ARG:CG	7:F:132:GLU:HG2	2.47	0.44
9:H:16:LYS:HD2	9:H:22:SER:HB2	1.99	0.44
30:5:810:G:H2'	30:5:811:U:H6	1.83	0.44
31:4:10:G:N3	31:4:11:A:C8	2.85	0.44
31:4:73:A:C8	31:4:73:A:O5'	2.70	0.44
1:2:34:G:C6	1:2:523:A:C2	3.05	0.44
1:2:78:G:H2'	1:2:79:C:H6	1.83	0.44
1:2:180:G:C6	1:2:181:C:C4	3.06	0.44
1:2:197:G:C4	1:2:198:U:C5	3.06	0.44
1:2:205:G:C4	1:2:206:C:C5	3.05	0.44
1:2:246:C:O2'	1:2:247:G:H5'	2.18	0.44
1:2:651:G:C6	1:2:652:G:N1	2.86	0.44
1:2:665:C:N3	1:2:666:C:C5	2.86	0.44
1:2:799:G:C4	1:2:800:U:C5	3.06	0.44
1:2:856:G:C2	1:2:857:G:C8	3.05	0.44
1:2:976:A:C8	1:2:977:A:H1'	2.53	0.44
1:2:991:G:C4	1:2:992:U:C5	3.06	0.44
1:2:1015:G:N2	1:2:1016:G:C5	2.85	0.44
1:2:1022:G:C6	1:2:1023:G:C6	3.05	0.44
1:2:1453:G:N9	33:7:352:ARG:HB3	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:189:LYS:C	3:B:190:ILE:HD12	2.43	0.44
9:H:16:LYS:O	9:H:43:LEU:HA	2.18	0.44
11:J:104:GLU:CG	11:J:105:ILE:HG23	2.44	0.44
21:T:12:THR:HG21	21:T:14:GLU:OE1	2.18	0.44
26:Y:15:VAL:HG13	29:3:68:PRO:HB2	1.99	0.44
29:3:40:THR:O	29:3:44:GLU:HB2	2.18	0.44
31:4:25:C:C4	31:4:26:G:N7	2.85	0.44
31:4:31:G:C4	31:4:32:OMC:C5	3.05	0.44
33:7:21:GLY:H	39:7:502:GNP:PB	2.38	0.44
33:7:133:PHE:CE2	33:7:173:THR:HG21	2.53	0.44
33:7:259:LEU:N	33:7:272:ILE:HD11	2.33	0.44
33:7:264:GLN:O	33:7:266:LYS:N	2.50	0.44
1:2:508:G:C2	1:2:509:C:C4	3.05	0.44
1:2:663:A:H8	1:2:663:A:O5'	2.00	0.44
1:2:676:G:C6	1:2:677:G:C5	3.05	0.44
1:2:714:G:C2	1:2:716:U:C4	3.06	0.44
1:2:738:C:C4	1:2:776:G:N1	2.86	0.44
1:2:757:A:N1	1:2:758:G:N2	2.66	0.44
1:2:804:G:H2'	1:2:805:C:H6	1.83	0.44
1:2:925:G:C6	1:2:926:G:C5	3.06	0.44
1:2:926:G:H22	21:T:115:HIS:CE1	2.36	0.44
1:2:957:4AC:HM72	1:2:1195:G:O6	2.17	0.44
1:2:1026:G:C2	1:2:1027:C:C2	3.06	0.44
1:2:1154:A:OP1	12:K:104:ARG:NH2	2.49	0.44
1:2:1219:G:N3	1:2:1220:G:C8	2.86	0.44
1:2:1272:C:O5'	1:2:1272:C:H6	2.01	0.44
1:2:1316:C:O2'	1:2:1317:C:H5'	2.17	0.44
2:A:75:LYS:HE2	2:A:75:LYS:HB3	1.73	0.44
2:A:88:LEU:HD13	2:A:187:ARG:HA	2.00	0.44
4:C:35:CYS:HB3	4:C:37:GLU:CD	2.43	0.44
5:D:132:VAL:O	5:D:135:GLN:N	2.51	0.44
6:E:125:LEU:O	6:E:163:THR:HG23	2.18	0.44
7:F:25:LEU:HD23	7:F:25:LEU:HA	1.85	0.44
7:F:75:THR:C	7:F:77:SER:H	2.26	0.44
16:O:113:ARG:NH1	16:O:121:GLU:OE1	2.40	0.44
33:7:120:ALA:HB2	33:7:148:GLN:HG2	2.00	0.44
1:2:289:A:H2	19:R:67:ARG:HG3	1.83	0.44
1:2:437:U:C4	1:2:438:C:C5	3.06	0.44
1:2:509:C:H2'	1:2:510:C:H6	1.82	0.44
1:2:531:U:H4'	10:I:92:ARG:NH2	2.33	0.44
1:2:627:G:C2	1:2:628:G:C6	3.06	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:791:G:C2	1:2:792:G:N7	2.85	0.44
1:2:878:A:C6	1:2:879:A:C5	3.05	0.44
1:2:898:G:OP2	1:2:1472:A:C8	2.71	0.44
1:2:963:C:C4	1:2:1186:A:C2	3.06	0.44
1:2:1066:A:O4'	3:B:98:PRO:HG2	2.18	0.44
1:2:1071:G:N1	1:2:1072:C:C4	2.85	0.44
1:2:1083:C:C2	1:2:1153:A:N1	2.86	0.44
1:2:1098:C:C2	1:2:1116:A:H2	2.36	0.44
1:2:1106:C:C6	1:2:1107:U:C5	3.06	0.44
1:2:1182:C:C4	1:2:1183:C:C4	3.06	0.44
1:2:1331:G:C2	1:2:1340:G:C2	3.06	0.44
1:2:1341:C:O2'	1:2:1342:G:OP1	2.29	0.44
1:2:1425:G:C2	1:2:1426:A:C5	3.05	0.44
3:B:166:LEU:HD12	3:B:166:LEU:HA	1.75	0.44
3:B:179:ARG:O	3:B:181:GLU:N	2.50	0.44
5:D:150:ASP:N	5:D:150:ASP:OD1	2.37	0.44
10:I:106:THR:OG1	10:I:121:ILE:HD12	2.17	0.44
22:U:11:LEU:HB3	22:U:136:LEU:HD21	2.00	0.44
32:6:75:GLN:HB3	32:6:79:ARG:NH1	2.32	0.44
32:6:77:ASP:HB3	32:6:78:LYS:HD2	1.98	0.44
33:7:15:VAL:O	33:7:116:LEU:HA	2.18	0.44
33:7:171:LYS:HD3	33:7:176:GLU:HG2	2.00	0.44
1:2:73:A:O2'	1:2:74:G:OP2	2.34	0.43
1:2:91:G:H3'	1:2:92:A:H8	1.83	0.43
1:2:151:C:C2	1:2:165:G:C2	3.06	0.43
1:2:168:A:C4	1:2:169:A:C2	3.06	0.43
1:2:196:G:C6	19:R:26:HIS:HB3	2.53	0.43
1:2:238:U:H2'	1:2:239:G:O4'	2.18	0.43
1:2:284:G:C2	1:2:285:C:C6	3.06	0.43
1:2:447:A:C6	1:2:448:A:C5	3.06	0.43
1:2:578:C:H2'	1:2:579:C:H6	1.84	0.43
1:2:800:U:H2'	1:2:801:C:C5	2.53	0.43
1:2:837:G:H5''	1:2:838:C:H6	1.83	0.43
1:2:859:G:O6	1:2:860:A:N6	2.50	0.43
1:2:962:G:N1	1:2:1190:C:N3	2.66	0.43
1:2:997:C:N3	1:2:998:C:C4	2.85	0.43
1:2:1042:G:N2	1:2:1046:G:N3	2.65	0.43
1:2:1061:G:C4	1:2:1062:U:C5	3.06	0.43
1:2:1158:G:C2	1:2:1159:C:C5	3.05	0.43
1:2:1341:C:H3'	12:K:122:SER:CB	2.48	0.43
1:2:1483:G:C4	1:2:1484:G:C8	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:96:PHE:CE2	3:B:100:THR:HG21	2.53	0.43
3:B:169:TRP:CG	3:B:192:VAL:HG12	2.52	0.43
6:E:205:PHE:CD2	6:E:211:ASP:HA	2.53	0.43
10:I:57:ARG:C	10:I:59:GLY:H	2.24	0.43
10:I:76:LYS:O	10:I:78:ARG:N	2.51	0.43
16:O:34:ASN:HA	22:U:44:LEU:HD11	1.99	0.43
24:W:38:ARG:HB2	24:W:43:GLY:O	2.18	0.43
29:3:73:LYS:O	29:3:123:LYS:NZ	2.37	0.43
31:4:26:G:H2'	31:4:26:G:N3	2.33	0.43
33:7:8:PRO:HD2	33:7:281:PHE:CZ	2.52	0.43
33:7:47:ILE:HA	33:7:100:LEU:HD23	2.00	0.43
33:7:87:ARG:HA	33:7:87:ARG:HD3	1.67	0.43
33:7:122:GLU:HG3	33:7:123:PRO:HD2	1.99	0.43
33:7:160:LEU:HD11	34:8:8:VAL:CG2	2.48	0.43
33:7:256:LEU:HD11	33:7:325:VAL:HG11	1.99	0.43
35:9:178:LYS:HA	35:9:178:LYS:HD2	1.83	0.43
1:2:175:C:C2	1:2:176:A:C8	3.06	0.43
1:2:246:C:H2'	1:2:247:G:H8	1.83	0.43
1:2:391:A:H2'	1:2:392:A:C8	2.53	0.43
1:2:393:C:N4	1:2:394:4AC:C7	2.81	0.43
1:2:452:G:H5''	1:2:453:C:OP2	2.18	0.43
1:2:539:A:C5	1:2:540:A:N1	2.86	0.43
1:2:827:C:H2'	1:2:828:4AC:H6	1.99	0.43
1:2:1037:G:H2'	1:2:1038:U:H6	1.83	0.43
1:2:1113:G:N1	1:2:1114:G:C6	2.86	0.43
1:2:1300:C:H2'	1:2:1301:G:H8	1.83	0.43
1:2:1337:A:C4	1:2:1339:C:C5	3.06	0.43
1:2:1348:A:C2	1:2:1349:A:C8	3.06	0.43
2:A:123:MET:HE2	2:A:187:ARG:NH1	2.33	0.43
3:B:63:ASP:HB3	3:B:65:GLN:OE1	2.18	0.43
8:G:25:GLU:O	8:G:43:LEU:HD11	2.18	0.43
9:H:156:ARG:HH21	25:X:46:ARG:HH21	1.66	0.43
9:H:174:TYR:HE2	9:H:175:ARG:CZ	2.31	0.43
13:L:79:GLU:OE1	13:L:79:GLU:N	2.45	0.43
15:N:56:GLU:OE2	15:N:74:ARG:HG3	2.18	0.43
19:R:60:TYR:C	19:R:61:GLU:HG2	2.43	0.43
21:T:12:THR:OG1	21:T:14:GLU:N	2.51	0.43
24:W:20:CYS:SG	24:W:23:CYS:N	2.80	0.43
31:4:21:A:OP1	31:4:21:A:H3'	2.18	0.43
33:7:134:VAL:HG13	33:7:407:MET:HE1	1.99	0.43
1:2:53:4AC:O7	1:2:53:4AC:H5	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:94:G:C6	1:2:95:C:N4	2.87	0.43
1:2:607:A:H2'	1:2:608:U:C6	2.52	0.43
1:2:694:G:N1	1:2:698:G:C5	2.86	0.43
1:2:696:A:N3	1:2:697:G:C8	2.87	0.43
1:2:732:G:H5''	1:2:733:A:OP1	2.17	0.43
1:2:832:G:N3	1:2:833:G:C8	2.87	0.43
1:2:904:A:N6	1:2:907:A:C2	2.87	0.43
1:2:1115:G:C6	1:2:1116:A:N1	2.86	0.43
1:2:1387:A:C6	1:2:1457:G:N2	2.86	0.43
1:2:1439:C:H2'	1:2:1440:C:C6	2.53	0.43
1:2:1459:A:N1	1:2:1460:G:C6	2.85	0.43
1:2:1460:G:H5''	1:2:1461:A:OP1	2.18	0.43
2:A:113:LYS:HE2	2:A:152:GLU:O	2.18	0.43
6:E:124:PRO:C	6:E:125:LEU:HD12	2.43	0.43
7:F:149:GLU:HB3	7:F:200:ALA:HB2	2.01	0.43
9:H:178:MET:HE3	9:H:178:MET:HB2	1.84	0.43
18:Q:29:THR:O	18:Q:33:ILE:N	2.50	0.43
22:U:4:VAL:HG22	22:U:63:TYR:HE1	1.84	0.43
22:U:63:TYR:HD2	22:U:121:ILE:HD13	1.83	0.43
22:U:146:GLU:OE1	22:U:146:GLU:N	2.51	0.43
28:0:34:ARG:HD3	33:7:371:THR:OG1	2.18	0.43
31:4:36:U:H2'	31:4:37:A:H8	1.83	0.43
35:9:203:ALA:HB2	35:9:250:LEU:HD23	1.98	0.43
1:2:326:G:C2	1:2:327:G:C4	3.06	0.43
1:2:391:A:H2'	1:2:392:A:H8	1.83	0.43
1:2:440:G:C6	1:2:457:G:C6	3.06	0.43
1:2:633:G:N3	1:2:633:G:H2'	2.33	0.43
1:2:795:A:N7	1:2:830:U:C2	2.87	0.43
1:2:797:G:O6	1:2:828:4AC:HM72	2.18	0.43
1:2:798:U:O2'	1:2:1509:U:OP1	2.30	0.43
1:2:840:G:H5''	1:2:841:U:OP1	2.18	0.43
1:2:909:A:OP2	40:2:1715:HOH:O	2.20	0.43
1:2:983:G:C2	1:2:994:U:N3	2.86	0.43
1:2:1022:G:C6	1:2:1178:A:N6	2.85	0.43
1:2:1252:U:H5'	1:2:1253:A:C2	2.54	0.43
1:2:1433:G:C5	1:2:1434:U:C4	3.06	0.43
1:2:1508:C:H2'	1:2:1509:U:O4'	2.19	0.43
2:A:49:VAL:HG12	2:A:69:PHE:O	2.19	0.43
11:J:93:ASN:O	11:J:94:ILE:HD13	2.18	0.43
15:N:123:ARG:NH1	15:N:123:ARG:HB2	2.33	0.43
16:O:56:ASP:O	16:O:60:LYS:HG3	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S:32:LYS:HG3	20:S:47:ARG:NH1	2.33	0.43
22:U:34:PHE:N	22:U:34:PHE:CD1	2.81	0.43
22:U:76:TYR:CD2	22:U:77:TYR:HE2	2.36	0.43
26:Y:14:LYS:HA	26:Y:14:LYS:HD3	1.70	0.43
29:3:16:ALA:O	29:3:20:LEU:HD13	2.18	0.43
31:4:4:G:H1'	31:4:70:G:N2	2.32	0.43
1:2:20:U:O4	1:2:28:G:C2	2.71	0.43
1:2:143:G:N3	1:2:144:G:C8	2.86	0.43
1:2:181:C:C2	1:2:182:C:C5	3.07	0.43
1:2:366:G:C2	1:2:367:G:C8	3.07	0.43
1:2:367:G:H2'	1:2:368:C:H6	1.84	0.43
1:2:385:G:C2	1:2:398:A:N1	2.87	0.43
1:2:483:G:O2'	1:2:484:G:OP2	2.30	0.43
1:2:633:G:C6	1:2:708:G:C6	3.07	0.43
1:2:838:C:C2	1:2:839:4AC:O7	2.72	0.43
1:2:964:G:N7	1:2:1186:A:N6	2.66	0.43
1:2:978:G:N1	1:2:979:G:C5	2.87	0.43
1:2:1134:G:H2'	1:2:1135:C:H6	1.83	0.43
1:2:1274:G:C2	1:2:1309:C:C2	3.07	0.43
1:2:1289:U:H2'	1:2:1290:G:O4'	2.18	0.43
1:2:1322:U:H5	1:2:1347:G:N2	2.16	0.43
1:2:1340:G:C6	1:2:1341:C:C4	3.07	0.43
1:2:1351:A:C8	1:2:1352:C:C4	3.07	0.43
1:2:1412:C:H2'	1:2:1413:G:O4'	2.18	0.43
5:D:115:ALA:HB1	5:D:120:GLN:OE1	2.18	0.43
7:F:195:VAL:O	7:F:198:ALA:N	2.51	0.43
9:H:73:ARG:HE	9:H:75:GLY:CA	2.32	0.43
11:J:107:LYS:O	11:J:125:LEU:N	2.51	0.43
12:K:116:PRO:O	12:K:126:PRO:HG3	2.19	0.43
14:M:31:THR:HA	14:M:39:ILE:HG13	1.99	0.43
20:S:66:ILE:C	20:S:67:LEU:HD12	2.43	0.43
22:U:143:ILE:HG13	22:U:144:ILE:HD12	2.00	0.43
27:Z:87:ASN:O	27:Z:89:TYR:N	2.51	0.43
30:5:807:G:C2	30:5:808:A:C4	3.07	0.43
31:4:3:C:C2	31:4:71:C:N4	2.83	0.43
31:4:25:C:N3	31:4:26:G:C8	2.86	0.43
33:7:119:ALA:HB3	33:7:122:GLU:HB3	1.99	0.43
35:9:19:VAL:O	35:9:61:ASN:HA	2.19	0.43
1:2:41:G:H4'	15:N:133:SER:OG	2.19	0.43
1:2:148:A:C6	1:2:149:A:C4	3.06	0.43
1:2:222:A:N7	1:2:223:G:H1'	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:255:A:C5	1:2:288:A:C6	3.06	0.43
1:2:270:U:H5''	11:J:30:ARG:NH1	2.33	0.43
1:2:336:A:HO2'	1:2:337:C:P	2.42	0.43
1:2:383:A:H2'	1:2:384:U:C6	2.54	0.43
1:2:673:C:C2	1:2:674:C:C5	3.07	0.43
1:2:776:G:H5'	1:2:777:C:OP2	2.19	0.43
1:2:1099:C:C2	1:2:1115:G:N2	2.87	0.43
1:2:1224:A:C2	1:2:1261:A:C6	3.07	0.43
7:F:107:GLY:O	7:F:108:ILE:C	2.61	0.43
8:G:24:PRO:HA	8:G:27:GLU:HB2	2.00	0.43
9:H:93:LEU:HD12	9:H:93:LEU:O	2.19	0.43
16:O:41:ARG:NH2	22:U:45:PRO:O	2.51	0.43
29:3:83:LYS:HD3	29:3:95:ALA:CB	2.49	0.43
29:3:84:LYS:H	29:3:84:LYS:HD3	1.83	0.43
1:2:146:A:H8	1:2:146:A:OP2	2.01	0.43
1:2:179:G:N1	1:2:208:G:H1'	2.33	0.43
1:2:790:G:N3	1:2:790:G:H2'	2.33	0.43
1:2:862:U:C5	1:2:877:G:N2	2.87	0.43
1:2:1101:U:H2'	1:2:1102:C:H6	1.84	0.43
1:2:1196:G:H2'	1:2:1197:C:H6	1.84	0.43
1:2:1320:A:C4	1:2:1322:U:N3	2.87	0.43
1:2:1323:A:N6	1:2:1347:G:H21	2.16	0.43
1:2:1387:A:C6	1:2:1457:G:C2	3.07	0.43
1:2:1387:A:N1	1:2:1456:G:O6	2.51	0.43
1:2:1397:G:C2	1:2:1398:G:C8	3.06	0.43
2:A:117:LYS:C	2:A:118:LEU:HD12	2.44	0.43
3:B:21:THR:O	3:B:41:TYR:HB2	2.18	0.43
4:C:35:CYS:HB3	4:C:37:GLU:OE2	2.18	0.43
7:F:102:HIS:O	7:F:109:ALA:HA	2.18	0.43
9:H:136:THR:OG1	9:H:137:THR:N	2.50	0.43
9:H:186:GLU:O	9:H:190:LEU:HG	2.18	0.43
12:K:37:GLU:N	12:K:38:PRO:HD2	2.34	0.43
12:K:63:ASP:N	12:K:63:ASP:OD1	2.50	0.43
16:O:35:PHE:CE1	16:O:92:HIS:CE1	3.07	0.43
16:O:121:GLU:HG3	16:O:121:GLU:H	1.65	0.43
22:U:7:VAL:HG21	22:U:12:LEU:HD12	2.01	0.43
23:V:40:LEU:C	23:V:42:ALA:N	2.77	0.43
24:W:30:PHE:HE2	24:W:32:HIS:HB2	1.84	0.43
29:3:53:ILE:O	29:3:80:VAL:HG23	2.19	0.43
30:5:813:A:N3	30:5:813:A:H2'	2.34	0.43
31:4:74:C:N4	33:7:33:TRP:HE1	2.11	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:7:144:LEU:O	33:7:179:PRO:HD2	2.19	0.43
33:7:264:GLN:O	33:7:266:LYS:HG2	2.18	0.43
33:7:400:GLN:HB3	33:7:405:TRP:NE1	2.34	0.43
35:9:238:GLU:O	35:9:242:ALA:N	2.50	0.43
1:2:141:G:C5	1:2:142:G:C8	3.06	0.43
1:2:143:G:C2	1:2:144:G:C8	3.07	0.43
1:2:308:G:C2	1:2:309:A:C8	3.06	0.43
1:2:384:U:N3	1:2:385:G:C8	2.87	0.43
1:2:415:G:C6	1:2:416:C:C4	3.06	0.43
1:2:647:C:H2'	1:2:648:4AC:C6	2.47	0.43
1:2:660:G:OP1	14:M:135:ARG:NH1	2.50	0.43
1:2:662:A:OP2	14:M:51:ASP:HB2	2.19	0.43
1:2:695:A:N7	18:Q:120:ARG:NE	2.45	0.43
1:2:740:G:N1	1:2:774:U:O4	2.52	0.43
1:2:755:U:C2	1:2:756:U:C6	3.07	0.43
1:2:778:U:O4	1:2:779:G:C2	2.71	0.43
1:2:913:G:O2'	1:2:914:G:OP1	2.31	0.43
1:2:930:A:C5	1:2:931:A:N1	2.87	0.43
1:2:1037:G:C4	1:2:1038:U:C5	3.07	0.43
1:2:1046:G:C6	1:2:1047:G:N7	2.87	0.43
1:2:1134:G:C2	1:2:1135:C:C5	3.06	0.43
1:2:1141:A:C8	1:2:1143:A:C8	3.07	0.43
1:2:1207:G:C2	1:2:1208:C:C4	3.07	0.43
1:2:1211:C:C2	1:2:1310:U:C5	3.05	0.43
1:2:1220:G:N1	1:2:1221:G:C5	2.87	0.43
1:2:1241:A:C4	1:2:1242:A:C8	3.07	0.43
1:2:1274:G:N1	1:2:1309:C:C2	2.87	0.43
1:2:1285:G:C2	1:2:1301:G:C6	3.07	0.43
1:2:1485:G:N2	1:2:1487:MA6:H3'	2.34	0.43
2:A:64:HIS:CE1	2:A:92:TYR:CZ	3.07	0.43
2:A:194:GLU:OE1	2:A:195:PRO:HD3	2.19	0.43
3:B:136:PRO:HG3	4:C:30:PHE:HB3	2.00	0.43
4:C:49:LEU:CD1	4:C:51:LYS:HE2	2.49	0.43
5:D:162:ASN:HD22	5:D:164:GLN:HB2	1.84	0.43
6:E:66:LEU:HD21	6:E:71:PHE:HD2	1.84	0.43
12:K:47:GLU:HA	12:K:50:ILE:HG22	2.00	0.43
13:L:40:LEU:HD23	13:L:40:LEU:HA	1.63	0.43
23:V:81:ILE:HG13	23:V:82:GLU:HG2	2.00	0.43
29:3:27:ARG:HD3	29:3:90:ALA:HB1	2.00	0.43
31:4:51:C:C2	31:4:64:G:C6	3.07	0.43
33:7:352:ARG:HG2	33:7:353:ALA:H	1.82	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:8:45:ARG:HA	34:8:80:GLU:HG2	2.00	0.43
1:2:155:G:H2'	1:2:156:G:C8	2.54	0.43
1:2:204:G:C2	1:2:205:G:C4	3.07	0.43
1:2:575:A:C5	1:2:576:U:C6	3.07	0.43
1:2:580:A:C4	1:2:581:C:C5	3.07	0.43
1:2:788:G:N1	1:2:851:4AC:N3	2.67	0.43
1:2:863:A:C6	1:2:878:A:C8	3.07	0.43
1:2:1078:C:H1'	1:2:1162:G:N2	2.34	0.43
1:2:1327:G:C2	1:2:1344:G:C2	3.07	0.43
1:2:1446:U:O5'	1:2:1446:U:H6	2.01	0.43
3:B:157:ASN:O	3:B:159:LYS:N	2.52	0.43
6:E:192:ASN:HB3	6:E:195:ARG:HD3	2.01	0.43
7:F:93:ASP:OD1	7:F:227:ARG:HA	2.18	0.43
12:K:57:TRP:O	12:K:57:TRP:CD1	2.72	0.43
12:K:121:ARG:C	12:K:123:THR:H	2.27	0.43
17:P:26:GLN:NE2	17:P:39:CYS:SG	2.91	0.43
21:T:66:HIS:O	21:T:68:ARG:N	2.52	0.43
21:T:70:MET:SD	21:T:71:ILE:N	2.91	0.43
23:V:43:MET:HE3	23:V:43:MET:HB2	1.67	0.43
25:X:15:ILE:HG22	25:X:70:ARG:HG2	2.00	0.43
27:Z:18:ASP:OD1	27:Z:30:TYR:OH	2.22	0.43
29:3:8:LYS:HD2	29:3:79:TYR:OH	2.19	0.43
33:7:17:HIS:CG	33:7:18:VAL:N	2.86	0.43
33:7:124:PHE:HZ	33:7:169:PHE:HB2	1.84	0.43
33:7:144:LEU:O	33:7:178:VAL:HB	2.18	0.43
33:7:212:LYS:O	33:7:214:VAL:HG23	2.18	0.43
35:9:69:ILE:N	35:9:79:ASP:O	2.39	0.43
1:2:92:A:C6	1:2:93:C:C4	3.06	0.43
1:2:155:G:H5''	8:G:5:LYS:HZ2	1.82	0.43
1:2:263:G:N3	1:2:264:G:C8	2.87	0.43
1:2:323:G:OP1	11:J:22:LYS:HE2	2.19	0.43
1:2:388:G:O2'	1:2:389:G:H5'	2.18	0.43
1:2:695:A:C2	1:2:696:A:C4	3.06	0.43
1:2:722:G:N3	1:2:723:G:N7	2.67	0.43
1:2:778:U:H5	1:2:779:G:C4	2.37	0.43
1:2:808:G:C2	1:2:809:C:C2	3.06	0.43
1:2:898:G:O6	1:2:1365:U:N3	2.52	0.43
1:2:1061:G:C6	1:2:1062:U:C4	3.07	0.43
2:A:11:LYS:NZ	2:A:13:LYS:HG3	2.33	0.43
7:F:12:VAL:HA	7:F:15:GLU:HG2	2.00	0.43
8:G:13:THR:CG2	8:G:15:ILE:HG22	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:K:7:THR:HA	12:K:15:ALA:O	2.19	0.43
15:N:31:LYS:C	15:N:33:ARG:H	2.27	0.43
22:U:16:VAL:HG12	22:U:132:ILE:HG21	2.01	0.43
22:U:98:ILE:H	22:U:98:ILE:HG13	1.56	0.43
27:Z:147:TYR:N	27:Z:147:TYR:CD1	2.86	0.43
29:3:6:TYR:O	29:3:8:LYS:NZ	2.52	0.43
29:3:32:ILE:HG13	29:3:34:LYS:HG2	1.99	0.43
33:7:281:PHE:CZ	33:7:295:VAL:HB	2.54	0.43
34:8:6:GLU:HG3	34:8:9:GLU:OE1	2.18	0.43
35:9:124:GLN:OE1	35:9:160:TRP:NE1	2.52	0.43
1:2:531:U:C4	1:2:532:G:C5	3.07	0.42
1:2:668:A:H5'	1:2:670:A:H5'	2.02	0.42
1:2:790:G:C5	1:2:849:G:N2	2.87	0.42
1:2:1007:C:H2'	1:2:1008:G:H8	1.78	0.42
1:2:1016:G:H2'	1:2:1017:U:C6	2.54	0.42
1:2:1040:C:O2'	1:2:1041:4AC:H5'	2.19	0.42
1:2:1083:C:C2	1:2:1153:A:C2	3.07	0.42
1:2:1285:G:N1	1:2:1301:G:C6	2.87	0.42
1:2:1386:C:H42	1:2:1457:G:H1	1.65	0.42
1:2:1437:A:C5	1:2:1438:G:C8	3.07	0.42
2:A:168:ALA:HB1	2:A:184:ALA:O	2.19	0.42
5:D:96:THR:OG1	5:D:98:GLU:N	2.52	0.42
5:D:97:ILE:HG13	5:D:101:LEU:HD12	2.01	0.42
5:D:102:GLU:C	5:D:104:ARG:H	2.27	0.42
5:D:146:LYS:HE3	5:D:146:LYS:HB2	1.37	0.42
10:I:38:LEU:HD23	10:I:38:LEU:HA	1.75	0.42
15:N:18:LEU:HD23	15:N:18:LEU:HA	1.85	0.42
16:O:59:VAL:HA	16:O:62:ILE:HB	2.01	0.42
18:Q:76:LEU:HB3	18:Q:81:ILE:HD11	2.01	0.42
20:S:23:GLU:HB3	20:S:24:PHE:CZ	2.54	0.42
21:T:81:ILE:HG13	21:T:82:TYR:N	2.30	0.42
22:U:81:LYS:HG2	22:U:82:ASN:N	2.34	0.42
31:4:3:C:C2	31:4:4:G:C8	3.07	0.42
31:4:53:G:N2	31:4:54:5MU:H1'	2.34	0.42
32:6:74:VAL:O	32:6:79:ARG:HD2	2.18	0.42
32:6:102:GLN:OE1	32:6:102:GLN:N	2.52	0.42
1:2:105:A:N7	1:2:335:G:C5	2.87	0.42
1:2:267:G:N1	1:2:268:G:O6	2.52	0.42
1:2:484:G:N7	1:2:496:G:C5	2.87	0.42
1:2:524:C:C5	1:2:525:U:C6	3.06	0.42
1:2:631:G:OP1	2:A:131:GLN:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:950:A:C4	1:2:1293:A:C2	3.06	0.42
1:2:961:G:C2	1:2:1191:C:N3	2.87	0.42
1:2:1070:A:C2	1:2:1071:G:C5	3.07	0.42
1:2:1098:C:N3	1:2:1116:A:C2	2.87	0.42
1:2:1157:G:O2'	1:2:1158:G:OP1	2.25	0.42
1:2:1169:U:H2'	1:2:1171:G:H8	1.79	0.42
1:2:1312:G:C6	1:2:1313:A:C6	3.08	0.42
1:2:1413:G:N1	1:2:1414:A:C5	2.88	0.42
1:2:1424:G:C2	1:2:1425:G:C5	3.06	0.42
1:2:1486:G:O6	1:2:1487:MA6:H92	2.20	0.42
5:D:39:LYS:HA	5:D:42:TRP:CE3	2.53	0.42
6:E:105:ASN:CG	6:E:106:ARG:H	2.25	0.42
7:F:94:GLY:O	7:F:124:ILE:HG12	2.19	0.42
8:G:48:ASN:O	8:G:53:LYS:HD3	2.19	0.42
9:H:205:LEU:HD23	9:H:205:LEU:HA	1.91	0.42
12:K:44:THR:HB	12:K:75:ALA:HB1	2.00	0.42
21:T:103:LEU:HD12	21:T:103:LEU:HA	1.65	0.42
29:3:32:ILE:HD12	29:3:99:VAL:HG13	2.01	0.42
29:3:76:PRO:HG3	29:3:119:ARG:NH2	2.34	0.42
30:5:813:A:C5	30:5:814:U:C5	3.07	0.42
32:6:23:GLN:NE2	32:6:68:ILE:HD12	2.33	0.42
32:6:62:ARG:N	32:6:65:ASP:OD2	2.51	0.42
33:7:54:THR:HB	33:7:89:ILE:HD11	1.99	0.42
1:2:13:A:N3	7:F:166:VAL:HG23	2.34	0.42
1:2:67:G:C6	1:2:363:G:C6	3.07	0.42
1:2:89:G:H3'	1:2:90:G:C8	2.47	0.42
1:2:187:G:C5	1:2:188:U:C4	3.07	0.42
1:2:207:C:H6	1:2:207:C:O5'	2.02	0.42
1:2:209:A:O2'	1:2:210:A:O4'	2.35	0.42
1:2:539:A:C6	1:2:540:A:N1	2.87	0.42
1:2:576:U:O2	1:2:576:U:H2'	2.19	0.42
1:2:637:G:N2	1:2:704:G:C5	2.87	0.42
1:2:817:U:N3	1:2:818:C:C5	2.87	0.42
1:2:819:G:C6	1:2:820:C:C4	3.07	0.42
1:2:1095:A:H2'	1:2:1096:G:H8	1.82	0.42
1:2:1279:G:C4	1:2:1305:G:N2	2.87	0.42
1:2:1397:G:H2'	1:2:1397:G:N3	2.35	0.42
1:2:1444:G:N7	1:2:1445:C:N4	2.67	0.42
3:B:28:MET:O	3:B:32:ILE:HG12	2.20	0.42
5:D:47:GLN:O	5:D:51:PHE:CD2	2.72	0.42
6:E:237:LYS:HD3	6:E:237:LYS:HA	1.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:111:ILE:HD13	9:H:111:ILE:HA	1.84	0.42
15:N:21:LYS:HB3	15:N:21:LYS:HE2	1.84	0.42
16:O:83:LYS:HA	16:O:88:GLY:O	2.18	0.42
16:O:90:ASP:C	16:O:91:LEU:HD12	2.44	0.42
18:Q:111:GLN:C	18:Q:112:HIS:HD2	2.28	0.42
22:U:40:HIS:CD2	22:U:79:GLY:N	2.88	0.42
23:V:49:GLU:OE1	23:V:49:GLU:N	2.52	0.42
25:X:43:ARG:HA	25:X:64:ALA:HB3	2.01	0.42
25:X:66:GLU:OE2	25:X:67:ILE:HG22	2.19	0.42
26:Y:5:TRP:HH2	29:3:65:HIS:HD1	1.65	0.42
26:Y:22:CYS:HB2	26:Y:29:VAL:O	2.19	0.42
30:5:807:G:C5	30:5:808:A:C5	3.07	0.42
31:4:28:C:N4	31:4:43:A:C6	2.88	0.42
33:7:27:GLN:HE21	33:7:33:TRP:CB	2.25	0.42
33:7:64:LYS:HA	33:7:65:PRO:HA	1.87	0.42
33:7:106:SER:CA	33:7:363:SER:HA	2.45	0.42
33:7:256:LEU:HB3	33:7:315:ILE:HD11	2.01	0.42
1:2:110:U:H2'	1:2:111:C:C6	2.54	0.42
1:2:440:G:C6	1:2:441:G:N7	2.87	0.42
1:2:509:C:C2	1:2:510:C:C5	3.07	0.42
1:2:533:G:C5	1:2:534:G:C8	3.08	0.42
1:2:559:G:C6	1:2:560:U:C4	3.08	0.42
1:2:605:G:N3	1:2:606:G:C8	2.87	0.42
1:2:614:G:C6	1:2:615:G:N7	2.87	0.42
1:2:671:A:C6	1:2:672:U:C4	3.06	0.42
1:2:698:G:C2	1:2:699:C:C2	3.07	0.42
1:2:718:4AC:C7	1:2:719:G:H22	2.33	0.42
1:2:1084:C:C2	1:2:1129:G:C2	3.08	0.42
1:2:1120:A:H2'	1:2:1120:A:N3	2.35	0.42
1:2:1321:G:HO2'	1:2:1322:U:P	2.43	0.42
1:2:1453:G:C8	33:7:352:ARG:NH1	2.87	0.42
1:2:1503:A:C6	1:2:1504:C:C4	3.08	0.42
2:A:13:LYS:O	2:A:17:LYS:NZ	2.34	0.42
2:A:45:LEU:HD12	2:A:45:LEU:HA	1.76	0.42
9:H:141:PHE:CE2	25:X:65:ARG:HD3	2.54	0.42
13:L:15:SER:OG	13:L:18:GLU:OE2	2.31	0.42
14:M:110:LEU:H	14:M:110:LEU:HD12	1.84	0.42
17:P:28:GLY:O	17:P:30:ILE:N	2.52	0.42
18:Q:74:ARG:CZ	18:Q:74:ARG:HB2	2.49	0.42
25:X:50:ARG:HD3	25:X:51:VAL:H	1.84	0.42
27:Z:108:HIS:CE1	27:Z:109:PHE:HD1	2.36	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:7:223:VAL:O	33:7:225:LYS:HD2	2.18	0.42
35:9:20:LYS:N	35:9:28:TYR:O	2.42	0.42
35:9:23:PHE:HZ	35:9:28:TYR:CE1	2.38	0.42
35:9:216:ASN:OD1	35:9:217:ILE:N	2.52	0.42
1:2:13:A:C6	1:2:15:U:N3	2.87	0.42
1:2:76:G:O6	1:2:97:A:N1	2.53	0.42
1:2:141:G:C6	1:2:142:G:C5	3.07	0.42
1:2:632:A:H1'	1:2:700:G:O4'	2.20	0.42
1:2:649:G:C2	1:2:676:G:C6	3.08	0.42
1:2:813:G:C2	1:2:815:G:C8	3.07	0.42
1:2:950:A:C6	1:2:1293:A:C4	3.07	0.42
1:2:991:G:C2	1:2:992:U:C2	3.07	0.42
1:2:1068:C:N4	1:2:1069:G:N7	2.68	0.42
1:2:1373:C:C5	1:2:1375:G:C2	3.08	0.42
6:E:40:ARG:CZ	6:E:40:ARG:HB3	2.49	0.42
6:E:60:ARG:O	6:E:63:ARG:HB3	2.20	0.42
9:H:20:ARG:HG2	9:H:109:LYS:NZ	2.35	0.42
14:M:81:ILE:HB	14:M:115:VAL:HG23	2.01	0.42
19:R:73:HIS:HA	19:R:98:LYS:NZ	2.33	0.42
23:V:25:HIS:HB2	23:V:28:GLU:CD	2.44	0.42
24:W:20:CYS:SG	24:W:23:CYS:HB2	2.59	0.42
25:X:57:LEU:HD13	25:X:60:THR:H	1.83	0.42
31:4:22:G:C2	31:4:23:C:C4	3.07	0.42
32:6:94:LEU:HD12	32:6:94:LEU:HA	1.78	0.42
33:7:130:ARG:NH1	33:7:338:ARG:HE	2.16	0.42
33:7:247:PHE:CE2	33:7:316:ILE:HG22	2.55	0.42
33:7:340:VAL:HG23	33:7:341:GLY:N	2.34	0.42
1:2:46:G:C6	1:2:412:A:N6	2.88	0.42
1:2:74:G:C6	1:2:75:G:C5	3.07	0.42
1:2:244:G:N2	1:2:245:G:C5	2.87	0.42
1:2:503:C:H2'	1:2:504:G:O4'	2.19	0.42
1:2:650:G:N1	1:2:675:C:C4	2.87	0.42
1:2:754:A:C5	1:2:755:U:C5	3.07	0.42
1:2:788:G:O6	1:2:851:4AC:N4	2.51	0.42
1:2:964:G:H8	1:2:964:G:O5'	2.03	0.42
1:2:1032:A:N6	1:2:1074:A:H5'	2.34	0.42
1:2:1061:G:C2	1:2:1062:U:C4	3.06	0.42
1:2:1097:U:H2'	1:2:1098:C:H5'	2.00	0.42
1:2:1202:5MC:H4'	16:O:140:THR:HA	2.00	0.42
1:2:1299:C:H2'	1:2:1300:C:C6	2.55	0.42
1:2:1411:C:N3	1:2:1433:G:N1	2.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:15:LYS:HD3	2:A:15:LYS:HA	1.85	0.42
2:A:23:TYR:HD1	2:A:23:TYR:HA	1.63	0.42
6:E:229:TYR:HD1	6:E:229:TYR:HA	1.71	0.42
7:F:66:LEU:HD12	7:F:86:LEU:HD23	2.01	0.42
7:F:165:LEU:HG	7:F:181:GLN:O	2.20	0.42
10:I:130:TYR:O	10:I:130:TYR:CG	2.72	0.42
14:M:79:VAL:HG22	14:M:80:HIS:O	2.19	0.42
16:O:102:ILE:HG13	16:O:103:ARG:N	2.33	0.42
19:R:91:THR:OG1	19:R:92:ARG:N	2.41	0.42
23:V:20:TYR:CZ	23:V:68:TYR:CD1	3.07	0.42
27:Z:34:ASP:O	27:Z:35:ILE:HD13	2.19	0.42
31:4:9:G:N2	31:4:45:G:N3	2.68	0.42
31:4:58:A:O2'	31:4:59:A:O5'	2.38	0.42
33:7:98:GLU:C	33:7:404:ARG:HG3	2.44	0.42
33:7:175:ALA:HB1	33:7:178:VAL:CG2	2.49	0.42
33:7:249:VAL:CG2	33:7:279:ILE:HG13	2.49	0.42
34:8:116:LEU:HD11	34:8:123:TRP:HB3	2.01	0.42
35:9:23:PHE:HB2	35:9:26:GLY:O	2.19	0.42
35:9:189:GLU:OE1	35:9:191:LEU:HB2	2.19	0.42
1:2:116:A:C2	1:2:118:A:C4	3.07	0.42
1:2:193:G:H8	1:2:193:G:H3'	1.85	0.42
1:2:219:G:N2	1:2:222:A:C8	2.88	0.42
1:2:265:U:H2'	1:2:266:G:O4'	2.19	0.42
1:2:322:A:H5''	11:J:24:ARG:NH2	2.34	0.42
1:2:466:G:C5	1:2:467:G:N1	2.88	0.42
1:2:656:G:P	14:M:45:GLY:HA3	2.60	0.42
1:2:778:U:C5	1:2:779:G:C2	3.07	0.42
1:2:1115:G:O2'	1:2:1116:A:C8	2.60	0.42
1:2:1143:A:H2'	1:2:1144:A:C8	2.55	0.42
1:2:1145:G:O5'	20:S:4:ILE:HD13	2.20	0.42
1:2:1244:G:C2	1:2:1245:G:C4	3.07	0.42
1:2:1252:U:H5'	1:2:1253:A:N3	2.34	0.42
1:2:1310:U:C2	9:H:174:TYR:OH	2.73	0.42
1:2:1322:U:H5	1:2:1347:G:H21	1.68	0.42
1:2:1345:G:N3	1:2:1346:C:C6	2.88	0.42
1:2:1414:A:N1	1:2:1430:C:C4	2.88	0.42
1:2:1427:G:C2	1:2:1428:G:C8	3.07	0.42
1:2:1446:U:H2'	1:2:1447:C:C5	2.54	0.42
2:A:53:LEU:HA	2:A:53:LEU:HD12	1.79	0.42
3:B:97:LEU:O	3:B:97:LEU:HD12	2.20	0.42
5:D:147:GLU:HG3	5:D:147:GLU:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:H:62:HIS:HE1	9:H:64:VAL:HG23	1.85	0.42
12:K:9:LYS:HB2	12:K:9:LYS:HE3	1.79	0.42
18:Q:50:ILE:HG22	18:Q:54:LEU:HD13	2.02	0.42
19:R:37:ILE:CG2	19:R:85:ARG:HG2	2.45	0.42
23:V:11:ASN:O	23:V:15:GLY:CA	2.68	0.42
31:4:23:C:C4	31:4:24:U:C5	3.08	0.42
31:4:41:C:H2'	31:4:42:G:H8	1.83	0.42
33:7:143:ASN:HB3	33:7:202:ILE:HG12	2.01	0.42
35:9:185:VAL:HB	35:9:227:TYR:CE1	2.55	0.42
35:9:191:LEU:HD23	35:9:191:LEU:HA	1.78	0.42
1:2:78:G:C4	1:2:79:C:C5	3.08	0.42
1:2:139:G:H2'	1:2:140:A:O4'	2.20	0.42
1:2:268:G:OP1	11:J:97:LYS:HB2	2.19	0.42
1:2:372:A:C4	1:2:373:A2M:C8	3.03	0.42
1:2:559:G:N1	1:2:614:G:C5	2.88	0.42
1:2:859:G:C6	1:2:860:A:N6	2.88	0.42
1:2:937:U:OP1	40:2:1716:HOH:O	2.22	0.42
1:2:962:G:C2	1:2:1190:C:C2	3.07	0.42
1:2:1068:C:N4	1:2:1069:G:C5	2.88	0.42
1:2:1285:G:C6	1:2:1301:G:O6	2.73	0.42
2:A:93:ILE:HG13	2:A:94:ARG:N	2.35	0.42
6:E:225:THR:HG22	6:E:226:LEU:N	2.35	0.42
7:F:206:TYR:O	7:F:208:THR:N	2.53	0.42
9:H:136:THR:HA	9:H:149:ALA:HA	2.02	0.42
14:M:21:SER:OG	14:M:22:SER:N	2.53	0.42
16:O:83:LYS:HB3	21:T:9:ARG:HH12	1.85	0.42
22:U:15:ARG:NE	22:U:136:LEU:HD13	2.34	0.42
25:X:10:GLU:O	25:X:29:VAL:HB	2.20	0.42
33:7:48:LYS:HZ3	33:7:49:LEU:HB2	1.85	0.42
35:9:57:VAL:HG13	35:9:58:LEU:HD23	2.02	0.42
1:2:14:U:O2	1:2:307:A:C4	2.73	0.42
1:2:22:G:H2'	1:2:23:A:C8	2.55	0.42
1:2:55:A:C2	1:2:315:A:C8	3.07	0.42
1:2:173:C:N3	1:2:174:C:C5	2.88	0.42
1:2:223:G:H2'	1:2:224:G:O4'	2.19	0.42
1:2:255:A:O2'	1:2:288:A:N6	2.53	0.42
1:2:267:G:H5'	11:J:97:LYS:HD2	2.02	0.42
1:2:268:G:N1	1:2:277:C:C2	2.87	0.42
1:2:403:G:H2'	1:2:403:G:N3	2.35	0.42
1:2:477:G:N2	1:2:500:U:C6	2.88	0.42
1:2:658:G:H8	14:M:24:ASN:ND2	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:863:A:C5	1:2:864:C:N4	2.88	0.42
1:2:964:G:OP2	1:2:1186:A:N6	2.53	0.42
1:2:1244:G:C4	1:2:1245:G:C8	3.08	0.42
1:2:1392:A:C8	1:2:1451:G:N2	2.88	0.42
1:2:1416:C:H2'	1:2:1417:U:C6	2.55	0.42
7:F:141:VAL:HG13	7:F:142:PRO:HD2	2.00	0.42
14:M:62:LEU:O	14:M:66:ARG:HG3	2.20	0.42
16:O:113:ARG:NH1	16:O:121:GLU:CD	2.78	0.42
20:S:50:ILE:H	20:S:50:ILE:HG13	1.72	0.42
21:T:55:LYS:HE2	21:T:75:GLU:O	2.20	0.42
26:Y:45:TYR:CE1	26:Y:47:GLU:HB3	2.55	0.42
27:Z:87:ASN:C	27:Z:89:TYR:H	2.27	0.42
27:Z:95:GLN:HG3	27:Z:120:ILE:HD11	2.01	0.42
29:3:34:LYS:HZ3	29:3:92:ILE:HG22	1.84	0.42
30:5:807:G:C6	30:5:808:A:C6	3.08	0.42
33:7:49:LEU:HD22	33:7:95:PRO:HD3	2.01	0.42
33:7:274:THR:HA	35:9:190:PRO:HB3	2.02	0.42
33:7:356:THR:O	33:7:357:LEU:HD23	2.19	0.42
35:9:189:GLU:CD	35:9:191:LEU:H	2.28	0.42
1:2:28:G:H8	1:2:28:G:O5'	2.02	0.42
1:2:185:G:N3	1:2:186:G:C8	2.88	0.42
1:2:321:G:C4	1:2:322:A:N7	2.88	0.42
1:2:604:G:C2	1:2:605:G:C8	3.07	0.42
1:2:662:A:C6	1:2:663:A:C4	3.08	0.42
1:2:679:G:H2'	1:2:680:G:C8	2.55	0.42
1:2:738:C:O4'	1:2:870:C:N4	2.51	0.42
1:2:962:G:N2	1:2:1190:C:C2	2.88	0.42
1:2:989:A:C4	1:2:991:G:N7	2.88	0.42
1:2:1141:A:C4	1:2:1143:A:C5	3.08	0.42
7:F:62:ASN:OD1	7:F:91:ASN:HA	2.20	0.42
7:F:144:THR:HA	7:F:156:LEU:O	2.20	0.42
10:I:61:TYR:HD1	10:I:61:TYR:HA	1.75	0.42
18:Q:74:ARG:HD2	18:Q:80:ARG:NE	2.34	0.42
22:U:80:ARG:HD2	22:U:88:GLU:HG2	2.01	0.42
28:0:35:GLY:N	28:0:36:LEU:HD12	2.35	0.42
33:7:17:HIS:CE1	33:7:97:HIS:HD2	2.21	0.42
33:7:138:ILE:HD11	33:7:407:MET:SD	2.60	0.42
33:7:218:ILE:HG23	33:7:219:ARG:HG3	2.02	0.42
33:7:300:TYR:O	35:9:193:VAL:HG22	2.20	0.42
33:7:401:ILE:HD12	33:7:406:ARG:CD	2.50	0.42
35:9:235:ASN:OD1	35:9:239:ALA:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:148:A:N3	1:2:149:A:HI'	2.34	0.41
1:2:632:A:C2	1:2:699:C:C4	3.08	0.41
1:2:644:C:H2'	1:2:645:C:H6	1.85	0.41
1:2:722:G:N2	1:2:723:G:C5	2.88	0.41
1:2:819:G:C6	1:2:820:C:N4	2.88	0.41
1:2:1126:G:C4	1:2:1127:G:C8	3.08	0.41
1:2:1509:U:O2	30:5:806:G:C2	2.72	0.41
5:D:67:GLU:C	5:D:67:GLU:CD	2.87	0.41
5:D:137:ILE:HG22	5:D:139:SER:H	1.84	0.41
7:F:21:LYS:HB3	7:F:21:LYS:HE3	1.67	0.41
7:F:62:ASN:HB3	7:F:90:GLY:O	2.19	0.41
7:F:132:GLU:OE1	7:F:132:GLU:N	2.53	0.41
10:I:50:PHE:HB2	10:I:63:VAL:HG22	2.02	0.41
12:K:29:ASN:OD1	12:K:66:VAL:HG22	2.20	0.41
14:M:42:TRP:CD1	14:M:67:ALA:HA	2.55	0.41
15:N:84:VAL:CG1	15:N:85:THR:H	2.32	0.41
16:O:62:ILE:HD13	16:O:62:ILE:HA	1.82	0.41
16:O:74:ILE:HA	16:O:75:PRO:HD3	1.86	0.41
16:O:108:ARG:HB2	16:O:108:ARG:CZ	2.50	0.41
18:Q:98:LEU:O	18:Q:99:ILE:C	2.63	0.41
19:R:97:THR:O	19:R:97:THR:HG22	2.20	0.41
21:T:94:ILE:HA	21:T:98:MET:SD	2.60	0.41
26:Y:42:ARG:HG3	26:Y:43:CYS:N	2.35	0.41
31:4:14:A:N6	31:4:22:G:O4'	2.53	0.41
31:4:26:G:C2	31:4:27:U:C6	3.08	0.41
31:4:34:C:C2	31:4:35:A:N7	2.87	0.41
31:4:63:G:N2	31:4:64:G:C8	2.88	0.41
32:6:94:LEU:HD23	32:6:100:ILE:HG23	2.02	0.41
33:7:144:LEU:HD12	33:7:145:ILE:H	1.85	0.41
33:7:215:MET:HE1	33:7:238:ILE:O	2.20	0.41
33:7:340:VAL:HG23	33:7:341:GLY:H	1.85	0.41
34:8:3:SER:O	34:8:3:SER:OG	2.28	0.41
1:2:32:G:C4	1:2:33:A:N7	2.88	0.41
1:2:155:G:H5''	8:G:5:LYS:HZ1	1.85	0.41
1:2:181:C:H2'	1:2:182:C:C6	2.54	0.41
1:2:230:C:C2	1:2:231:C:C5	3.08	0.41
1:2:231:C:H2'	1:2:232:C:C6	2.53	0.41
1:2:344:C:C2	1:2:345:C:C5	3.08	0.41
1:2:574:A:C6	1:2:575:A:C4	3.07	0.41
1:2:574:A:H8	1:2:574:A:O5'	2.03	0.41
1:2:831:A:C4	1:2:832:G:C8	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:832:G:H2'	1:2:833:G:C8	2.51	0.41
1:2:863:A:C5	1:2:878:A:N7	2.88	0.41
1:2:911:G:OP1	9:H:156:ARG:NH2	2.53	0.41
1:2:1070:A:C2	1:2:1071:G:C8	3.08	0.41
1:2:1234:G:C2	1:2:1250:G:O6	2.73	0.41
1:2:1452:A:H3'	33:7:352:ARG:NH2	2.34	0.41
2:A:157:ASP:O	2:A:160:LEU:HB3	2.19	0.41
3:B:190:ILE:HG23	3:B:191:PRO:HD2	2.02	0.41
6:E:9:HIS:O	6:E:31:ARG:HD2	2.19	0.41
6:E:207:MET:HE2	19:R:31:GLY:O	2.20	0.41
8:G:48:ASN:ND2	8:G:55:PHE:HB2	2.35	0.41
10:I:7:LEU:O	10:I:10:ALA:N	2.51	0.41
11:J:67:ASP:OD1	11:J:124:LEU:HB2	2.20	0.41
14:M:57:PRO:O	14:M:60:ALA:HB3	2.19	0.41
17:P:28:GLY:O	17:P:30:ILE:HG13	2.20	0.41
17:P:41:HIS:O	17:P:42:CYS:C	2.63	0.41
18:Q:36:LEU:HD23	18:Q:36:LEU:HA	1.87	0.41
21:T:8:TYR:O	21:T:9:ARG:HD3	2.19	0.41
27:Z:78:PRO:O	27:Z:79:GLN:HG3	2.20	0.41
27:Z:128:VAL:HG22	27:Z:129:GLU:N	2.35	0.41
31:4:7:G:H2'	31:4:49:G:H8	1.84	0.41
31:4:14:A:H2'	31:4:14:A:N3	2.35	0.41
31:4:19:G:N2	31:4:57:A:O2'	2.52	0.41
31:4:48:C:N3	31:4:59:A:C4	2.87	0.41
33:7:111:MET:O	33:7:141:VAL:HG21	2.19	0.41
33:7:148:GLN:NE2	33:7:159:ALA:HA	2.35	0.41
35:9:195:LYS:O	35:9:199:VAL:HG13	2.19	0.41
1:2:112:A:C6	1:2:113:G:C4	3.08	0.41
1:2:268:G:N1	1:2:277:C:O2	2.54	0.41
1:2:333:G:O5'	1:2:333:G:H8	2.03	0.41
1:2:517:G:H2'	1:2:518:U:C6	2.56	0.41
1:2:791:G:C2	1:2:792:G:C5	3.09	0.41
1:2:808:G:H2'	1:2:809:C:C6	2.55	0.41
1:2:1042:G:C6	1:2:1046:G:C6	3.08	0.41
1:2:1172:G:O2'	13:L:54:ASP:OD2	2.38	0.41
1:2:1379:G:C2	1:2:1380:U:C4	3.08	0.41
3:B:17:VAL:HG22	3:B:163:ALA:HB1	2.01	0.41
5:D:81:GLY:HA3	5:D:103:ARG:NH2	2.35	0.41
16:O:113:ARG:HA	16:O:113:ARG:HD2	1.50	0.41
19:R:21:CYS:O	19:R:25:GLY:N	2.50	0.41
21:T:23:GLU:O	21:T:23:GLU:HG2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:Y:15:VAL:CG1	29:3:68:PRO:HB2	2.51	0.41
27:Z:90:LEU:HD21	27:Z:125:ALA:HB2	2.02	0.41
30:5:810:G:H2'	30:5:811:U:C6	2.55	0.41
31:4:11:A:C2	31:4:25:C:C2	3.08	0.41
33:7:24:THR:CG2	33:7:186:LEU:HA	2.49	0.41
33:7:25:LEU:HD23	33:7:25:LEU:HA	1.83	0.41
33:7:51:TYR:CG	33:7:294:LEU:HD13	2.55	0.41
1:2:55:A:C8	1:2:315:A:C2	3.08	0.41
1:2:91:G:N3	1:2:91:G:H2'	2.34	0.41
1:2:201:C:H2'	1:2:202:C:H6	1.85	0.41
1:2:252:A:C2	1:2:254:U:N3	2.88	0.41
1:2:276:C:OP1	19:R:96:LYS:HB2	2.20	0.41
1:2:386:C:H2'	1:2:387:G:H8	1.84	0.41
1:2:529:A:C2	1:2:533:G:C8	3.08	0.41
1:2:643:A:C5	1:2:644:C:C4	3.08	0.41
1:2:818:C:C2	1:2:819:G:C8	3.08	0.41
1:2:975:G:H2'	1:2:1000:G:N2	2.36	0.41
1:2:1015:G:O2'	1:2:1016:G:H5'	2.20	0.41
1:2:1203:G:N2	1:2:1204:C:C2	2.89	0.41
1:2:1271:U:O2'	1:2:1272:C:OP2	2.36	0.41
1:2:1401:U:H2'	1:2:1402:A:C8	2.55	0.41
1:2:1488:MA6:H3'	1:2:1488:MA6:H8	2.02	0.41
2:A:152:GLU:OE1	2:A:152:GLU:N	2.53	0.41
5:D:39:LYS:C	5:D:41:LEU:N	2.77	0.41
5:D:135:GLN:HG3	5:D:136:ILE:O	2.20	0.41
7:F:137:ARG:HA	7:F:138:PRO:HD3	1.79	0.41
10:I:69:ILE:HD13	10:I:69:ILE:HG21	1.86	0.41
15:N:107:GLY:O	15:N:125:LYS:HG2	2.20	0.41
17:P:23:ARG:NH1	17:P:42:CYS:HB3	2.35	0.41
21:T:79:LEU:HA	21:T:79:LEU:HD12	1.72	0.41
22:U:41:LYS:HA	22:U:41:LYS:HD3	1.84	0.41
22:U:144:ILE:HA	22:U:145:PRO:HD3	1.87	0.41
25:X:15:ILE:HD11	25:X:28:LYS:HB2	2.02	0.41
32:6:93:TRP:CD2	32:6:93:TRP:C	2.97	0.41
33:7:133:PHE:HA	33:7:136:LEU:HD12	2.03	0.41
33:7:260:ARG:HB2	33:7:269:TYR:CE2	2.56	0.41
1:2:65:G:C6	1:2:66:C:C4	3.09	0.41
1:2:130:U:O2	1:2:239:G:C2	2.74	0.41
1:2:149:A:H2'	1:2:149:A:N3	2.35	0.41
1:2:330:A:H2'	1:2:331:C:H6	1.85	0.41
1:2:436:U:O2	1:2:436:U:H2'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:465:G:C5	1:2:466:G:C6	3.07	0.41
1:2:467:G:C8	1:2:468:C:C2	3.09	0.41
1:2:599:C:H4'	1:2:600:G:O5'	2.20	0.41
1:2:679:G:H2'	1:2:680:G:O4'	2.19	0.41
1:2:790:G:C5	1:2:849:G:C2	3.08	0.41
1:2:896:G:C6	1:2:1366:G:N1	2.88	0.41
1:2:995:U:O2'	26:Y:34:HIS:ND1	2.49	0.41
1:2:1022:G:H8	1:2:1022:G:O5'	2.04	0.41
1:2:1116:A:C5	1:2:1117:G:C2	3.09	0.41
1:2:1201:A:C2	21:T:115:HIS:CD2	3.08	0.41
1:2:1239:4AC:H5''	1:2:1240:G:OP2	2.21	0.41
3:B:4:GLU:HB2	3:B:5:TYR:CD2	2.55	0.41
5:D:16:HIS:ND1	5:D:17:PRO:HD2	2.35	0.41
5:D:19:ILE:O	5:D:20:LYS:C	2.63	0.41
5:D:39:LYS:O	5:D:41:LEU:N	2.53	0.41
5:D:88:VAL:O	5:D:89:LEU:C	2.64	0.41
5:D:117:THR:OG1	5:D:118:MET:N	2.53	0.41
6:E:12:ARG:CZ	6:E:21:ILE:HD11	2.51	0.41
6:E:161:SER:O	6:E:161:SER:OG	2.38	0.41
7:F:91:ASN:HD21	7:F:93:ASP:HB3	1.85	0.41
12:K:22:GLY:HA3	12:K:61:ASP:OD2	2.20	0.41
15:N:127:VAL:HG23	15:N:128:LYS:N	2.35	0.41
18:Q:78:ILE:H	18:Q:78:ILE:HG13	1.61	0.41
18:Q:142:LEU:HD23	18:Q:142:LEU:HA	1.73	0.41
19:R:64:GLU:HG2	19:R:65:LEU:H	1.86	0.41
27:Z:57:ARG:HB3	27:Z:60:ARG:HD2	2.02	0.41
31:4:43:A:O2'	31:4:44:A:H5'	2.20	0.41
33:7:17:HIS:CG	33:7:18:VAL:H	2.38	0.41
33:7:105:LEU:HD22	33:7:139:ILE:HD11	2.02	0.41
33:7:138:ILE:HD13	33:7:410:TRP:HB3	2.01	0.41
33:7:147:VAL:HG11	33:7:183:VAL:HG22	2.02	0.41
1:2:139:G:C6	1:2:140:A:N7	2.89	0.41
1:2:485:C:C2	1:2:486:A:C8	3.08	0.41
1:2:621:G:N3	1:2:720:A:C2	2.89	0.41
1:2:652:G:OP1	2:A:13:LYS:HE2	2.20	0.41
1:2:671:A:C4	1:2:672:U:C6	3.09	0.41
1:2:731:4AC:O7	1:2:731:4AC:H5	2.18	0.41
1:2:886:A:C2	28:0:6:ARG:NH2	2.88	0.41
1:2:1037:G:C6	1:2:1038:U:C4	3.08	0.41
1:2:1218:C:H5'	22:U:43:ARG:HB2	2.03	0.41
1:2:1262:A:C2	1:2:1263:A:C5	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:1337:A:C5	1:2:1339:C:C4	3.09	0.41
1:2:1346:C:N4	1:2:1347:G:O6	2.54	0.41
1:2:1380:U:O4'	1:2:1487:MA6:H4'	2.21	0.41
1:2:1395:G:N2	1:2:1449:G:C6	2.89	0.41
5:D:19:ILE:HD13	5:D:19:ILE:HA	1.85	0.41
9:H:18:MET:HE2	9:H:18:MET:HB3	1.79	0.41
9:H:73:ARG:C	9:H:75:GLY:N	2.78	0.41
14:M:34:THR:HG23	14:M:36:ALA:H	1.86	0.41
15:N:31:LYS:HB2	15:N:31:LYS:HE3	1.62	0.41
18:Q:31:GLU:OE1	18:Q:31:GLU:N	2.54	0.41
27:Z:66:THR:O	27:Z:70:GLU:HG3	2.21	0.41
29:3:14:GLU:HG3	29:3:15:LEU:N	2.34	0.41
29:3:83:LYS:HD3	29:3:95:ALA:HB1	2.03	0.41
31:4:31:G:H2'	31:4:32:OMC:C6	2.55	0.41
33:7:62:CYS:SG	33:7:79:SER:HB2	2.60	0.41
33:7:205:PRO:HB2	33:7:207:ARG:HH11	1.86	0.41
33:7:276:ILE:CG2	33:7:297:ILE:HG23	2.49	0.41
34:8:106:CYS:SG	34:8:127:CYS:HB2	2.60	0.41
1:2:160:C:H2'	1:2:161:U:O4'	2.21	0.41
1:2:229:G:N3	1:2:229:G:H2'	2.34	0.41
1:2:367:G:N2	1:2:368:C:C2	2.89	0.41
1:2:417:C:H2'	1:2:418:G:C8	2.56	0.41
1:2:544:G:C2	1:2:545:C:C6	3.09	0.41
1:2:607:A:H1'	10:I:107:SER:OG	2.20	0.41
1:2:640:G:C2	1:2:701:C:C2	3.08	0.41
1:2:676:G:C4	1:2:677:G:C8	3.08	0.41
1:2:959:G:H2'	1:2:960:G:C8	2.55	0.41
1:2:1056:U:O2	1:2:1060:U:N3	2.54	0.41
1:2:1079:C:C2	1:2:1080:G:C8	3.09	0.41
1:2:1088:A:C6	1:2:1125:G:O6	2.73	0.41
1:2:1096:G:H4'	12:K:3:ILE:HD13	2.02	0.41
1:2:1125:G:H4'	1:2:1126:G:OP1	2.21	0.41
1:2:1131:A:C6	1:2:1154:A:C5	3.09	0.41
1:2:1166:C:N4	1:2:1167:G:C4	2.89	0.41
1:2:1181:C:C4	1:2:1182:C:N4	2.89	0.41
1:2:1200:C:H2'	16:O:131:THR:OG1	2.20	0.41
1:2:1304:U:C4	1:2:1305:G:C5	3.09	0.41
1:2:1316:C:H1'	12:K:131:GLN:HE21	1.84	0.41
1:2:1362:C:H2'	1:2:1363:C:C6	2.55	0.41
1:2:1401:U:H2'	1:2:1402:A:O4'	2.21	0.41
2:A:121:MET:O	2:A:187:ARG:NH2	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:129:HIS:CE1	5:D:158:SER:HG	2.28	0.41
6:E:53:LEU:HD23	6:E:53:LEU:HA	1.91	0.41
14:M:15:GLY:O	14:M:16:ILE:HD13	2.20	0.41
15:N:140:GLY:C	15:N:142:LYS:H	2.29	0.41
16:O:87:THR:C	16:O:89:ARG:H	2.27	0.41
23:V:24:TYR:CE1	23:V:26:PRO:HG3	2.55	0.41
25:X:32:LEU:O	25:X:37:LYS:HG3	2.21	0.41
28:O:8:TRP:NE1	28:O:16:TRP:CD1	2.88	0.41
34:8:117:LYS:HG2	34:8:118:LYS:N	2.36	0.41
35:9:180:SER:O	35:9:243:LEU:HD21	2.21	0.41
1:2:48:G:H2'	1:2:49:G:C8	2.56	0.41
1:2:103:G:O2'	1:2:104:G:O5'	2.30	0.41
1:2:196:G:C5	19:R:26:HIS:HB3	2.56	0.41
1:2:229:G:C2	1:2:230:C:C5	3.09	0.41
1:2:236:G:C5	1:2:237:A:N7	2.89	0.41
1:2:259:A:H2	1:2:283:A:C6	2.38	0.41
1:2:274:G:C4	1:2:276:C:C5	3.09	0.41
1:2:415:G:C4	1:2:460:A:C6	3.08	0.41
1:2:505:G:H2'	1:2:506:C:C6	2.55	0.41
1:2:554:G:N3	1:2:555:G:C8	2.88	0.41
1:2:655:G:C4	1:2:656:G:C8	3.08	0.41
1:2:803:G:C4	1:2:804:G:C8	3.09	0.41
1:2:917:G:C2	1:2:918:A:C8	3.09	0.41
1:2:1169:U:H5''	1:2:1170:A:OP2	2.21	0.41
1:2:1312:G:C2	1:2:1313:A:C4	3.09	0.41
1:2:1332:U:H3'	1:2:1333:C:C6	2.55	0.41
3:B:96:PHE:HE2	3:B:100:THR:HG21	1.85	0.41
7:F:84:ARG:NH1	7:F:195:VAL:HG21	2.36	0.41
7:F:148:LYS:HE2	7:F:148:LYS:HB3	1.73	0.41
7:F:162:GLY:N	7:F:182:ASP:OD2	2.29	0.41
11:J:25:LYS:HG2	11:J:25:LYS:O	2.21	0.41
12:K:12:THR:H	12:K:113:ARG:NH2	2.12	0.41
16:O:80:ASN:HB2	16:O:92:HIS:CD2	2.56	0.41
22:U:20:LEU:HA	22:U:20:LEU:HD23	1.82	0.41
31:4:52:G:N3	31:4:53:G:C8	2.89	0.41
32:6:94:LEU:HG	32:6:94:LEU:O	2.20	0.41
33:7:16:GLY:H	33:7:132:HIS:CD2	2.38	0.41
33:7:183:VAL:HB	33:7:191:ILE:HD13	2.01	0.41
33:7:253:ILE:O	33:7:273:PHE:HA	2.20	0.41
1:2:18:G:C6	1:2:31:G:C6	3.09	0.41
1:2:154:G:C4	1:2:162:G:C6	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:195:A:N7	1:2:197:G:C6	2.89	0.41
1:2:198:U:N3	1:2:199:C:C5	2.88	0.41
1:2:289:A:C2	19:R:67:ARG:HG3	2.56	0.41
1:2:294:G:C6	1:2:295:G:N7	2.88	0.41
1:2:322:A:C2	1:2:323:G:C5	3.09	0.41
1:2:351:C:N3	1:2:357:G:N1	2.68	0.41
1:2:572:G:C2	1:2:600:G:C6	3.09	0.41
1:2:580:A:C6	1:2:581:C:C4	3.09	0.41
1:2:612:G:C5	1:2:613:C:C5	3.09	0.41
1:2:754:A:N3	1:2:754:A:H2'	2.36	0.41
1:2:778:U:O4	1:2:779:G:N2	2.54	0.41
1:2:790:G:H21	10:I:2:THR:N	2.18	0.41
1:2:819:G:C4	1:2:820:C:C5	3.09	0.41
1:2:897:G:N2	30:5:818:A:C4	2.89	0.41
1:2:950:A:C6	1:2:1293:A:C5	3.09	0.41
1:2:1118:G:H2'	1:2:1119:C:O4'	2.21	0.41
1:2:1139:C:C4	1:2:1140:G:C5	3.08	0.41
1:2:1149:G:C4	1:2:1150:A:C8	3.09	0.41
1:2:1242:A:C4	1:2:1243:A:C8	3.09	0.41
1:2:1267:G:H2'	1:2:1268:C:H6	1.85	0.41
1:2:1324:C:O2	9:H:95:SER:OG	2.38	0.41
1:2:1402:A:N1	1:2:1441:U:C4	2.89	0.41
1:2:1437:A:C6	1:2:1438:G:C5	3.09	0.41
1:2:1441:U:H2'	1:2:1442:A:C8	2.56	0.41
2:A:60:PHE:N	2:A:60:PHE:CD1	2.88	0.41
3:B:21:THR:HG22	3:B:22:GLN:H	1.86	0.41
3:B:127:MET:O	3:B:131:ILE:HG13	2.21	0.41
5:D:108:ILE:HD13	5:D:108:ILE:HA	1.84	0.41
5:D:135:GLN:HE22	23:V:62:SER:HB2	1.85	0.41
5:D:142:TYR:HE2	5:D:144:VAL:HA	1.85	0.41
6:E:18:SER:C	6:E:19:TRP:CD1	2.98	0.41
6:E:45:LEU:HD12	6:E:45:LEU:HA	1.72	0.41
6:E:203:LYS:HG2	6:E:204:LYS:N	2.36	0.41
8:G:10:ASP:OD2	8:G:13:THR:HG22	2.21	0.41
8:G:12:LYS:HD3	8:G:12:LYS:HA	1.75	0.41
10:I:103:ILE:HG21	10:I:126:ILE:HD11	2.03	0.41
12:K:10:ARG:HG2	12:K:11:LYS:HG2	2.03	0.41
12:K:105:THR:HG22	12:K:105:THR:O	2.20	0.41
15:N:53:ILE:O	15:N:75:VAL:HA	2.21	0.41
16:O:85:TYR:O	16:O:85:TYR:CG	2.73	0.41
19:R:10:GLN:OE1	19:R:11:PRO:HD2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:X:60:THR:O	25:X:60:THR:HG22	2.21	0.41
27:Z:27:ARG:C	27:Z:29:GLY:H	2.29	0.41
29:3:75:ILE:HG23	29:3:75:ILE:O	2.21	0.41
30:5:819:A:N6	31:4:37:A:C2	2.88	0.41
30:5:823:C:H4'	32:6:57:ARG:CG	2.47	0.41
33:7:15:VAL:HG21	33:7:136:LEU:HD21	2.01	0.41
33:7:52:ALA:O	33:7:90:SER:HA	2.21	0.41
33:7:170:THR:HB	33:7:175:ALA:O	2.21	0.41
33:7:269:TYR:CE1	33:7:384:ARG:HB2	2.55	0.41
1:2:116:A:C4	1:2:118:A:C8	3.09	0.41
1:2:141:G:C6	1:2:142:G:N7	2.89	0.41
1:2:158:A:C6	1:2:159:A:C6	3.09	0.41
1:2:172:C:H2'	1:2:173:C:H6	1.86	0.41
1:2:293:C:H2'	1:2:294:G:H8	1.86	0.41
1:2:320:G:N1	1:2:321:G:C5	2.89	0.41
1:2:428:C:C2	1:2:429:A:C8	3.09	0.41
1:2:525:U:N3	1:2:527:U:C4	2.89	0.41
1:2:566:C:H2'	1:2:567:C:C6	2.56	0.41
1:2:686:C:H3'	1:2:687:C:C5	2.56	0.41
1:2:778:U:H5	1:2:779:G:C6	2.39	0.41
1:2:1053:A:C6	1:2:1063:G:N1	2.89	0.41
1:2:1117:G:C5	1:2:1118:G:C6	3.09	0.41
1:2:1166:C:C4	1:2:1167:G:C4	3.09	0.41
1:2:1300:C:H2'	1:2:1301:G:C8	2.56	0.41
1:2:1360:C:O2'	1:2:1361:U:H5'	2.20	0.41
1:2:1484:G:N3	1:2:1485:G:C8	2.89	0.41
6:E:166:MET:CE	6:E:171:ARG:HG3	2.51	0.41
9:H:9:PHE:HD1	12:K:34:GLU:O	2.04	0.41
10:I:76:LYS:HD2	10:I:76:LYS:HA	1.74	0.41
10:I:81:VAL:HG12	10:I:89:TRP:HE1	1.86	0.41
20:S:55:THR:O	20:S:59:ARG:HG2	2.21	0.41
22:U:57:SER:O	22:U:61:ARG:HG2	2.21	0.41
23:V:74:ASP:CG	23:V:75:LYS:N	2.78	0.41
31:4:71:C:O3'	33:7:42:LYS:HE3	2.21	0.41
33:7:61:SER:OG	33:7:79:SER:OG	2.37	0.41
33:7:357:LEU:CD2	33:7:399:ARG:HA	2.50	0.41
1:2:114:U:O2	1:2:114:U:H2'	2.20	0.40
1:2:162:G:C2	1:2:163:G:C5	3.09	0.40
1:2:185:G:N1	1:2:202:C:N3	2.69	0.40
1:2:229:G:C2	1:2:230:C:C6	3.09	0.40
1:2:255:A:C6	1:2:288:A:C2	3.09	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:311:C:N4	1:2:312:G:O6	2.54	0.40
1:2:367:G:N1	1:2:368:C:C4	2.90	0.40
1:2:575:A:N7	1:2:576:U:C5	2.89	0.40
1:2:576:U:N3	1:2:577:C:C5	2.89	0.40
1:2:642:U:C2	1:2:643:A:C8	3.10	0.40
1:2:686:C:C5	1:2:687:C:N4	2.89	0.40
1:2:782:A:C6	1:2:1498:C:H5	2.39	0.40
1:2:925:G:H21	21:T:122:ALA:CB	2.28	0.40
1:2:987:G:OP2	21:T:64:ARG:NH2	2.21	0.40
1:2:1166:C:N4	1:2:1167:G:C2	2.89	0.40
1:2:1358:U:C4	1:2:1359:G:N7	2.87	0.40
1:2:1375:G:C2	1:2:1376:OMC:O2	2.74	0.40
2:A:22:ILE:HB	2:A:33:VAL:O	2.21	0.40
3:B:163:ALA:C	3:B:165:ALA:N	2.78	0.40
9:H:73:ARG:C	9:H:75:GLY:H	2.28	0.40
11:J:100:ILE:HG12	11:J:125:LEU:HD13	2.03	0.40
18:Q:41:ARG:O	18:Q:43:GLU:N	2.54	0.40
33:7:255:VAL:HG23	33:7:316:ILE:HG12	2.03	0.40
33:7:357:LEU:HD23	33:7:357:LEU:HA	1.73	0.40
34:8:32:ASN:O	34:8:46:ASN:ND2	2.54	0.40
1:2:108:G:H21	1:2:363:G:H5'	1.86	0.40
1:2:124:G:N1	1:2:243:C:N3	2.69	0.40
1:2:200:C:O2'	1:2:201:C:H5'	2.21	0.40
1:2:220:U:C4	1:2:221:A:C4	3.08	0.40
1:2:326:G:C4	1:2:327:G:C8	3.08	0.40
1:2:410:C:O2'	1:2:587:A:N3	2.53	0.40
1:2:476:G:C2	1:2:478:C:C4	3.10	0.40
1:2:539:A:C5	1:2:540:A:C6	3.09	0.40
1:2:666:C:N3	1:2:667:U:C4	2.89	0.40
1:2:852:G:H2'	1:2:853:C:H6	1.86	0.40
1:2:946:G:N3	1:2:946:G:H2'	2.36	0.40
1:2:1003:G:H8	1:2:1003:G:OP2	2.04	0.40
1:2:1079:C:O2'	17:P:56:GLU:OE2	2.11	0.40
1:2:1122:U:O2'	12:K:14:ILE:HD13	2.21	0.40
1:2:1133:U:H3'	20:S:5:ARG:HH22	1.85	0.40
1:2:1137:G:N2	1:2:1148:G:H1'	2.36	0.40
1:2:1279:G:N2	1:2:1305:G:HO2'	2.19	0.40
2:A:17:LYS:HD3	2:A:17:LYS:HA	1.90	0.40
3:B:164:LEU:HD23	3:B:164:LEU:HA	1.93	0.40
5:D:52:ARG:NH2	5:D:93:LEU:HD22	2.36	0.40
5:D:56:ARG:HB3	7:F:132:GLU:HG2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:83:PHE:HA	6:E:84:PRO:HD3	1.88	0.40
6:E:123:LYS:O	6:E:165:LEU:HD13	2.21	0.40
6:E:217:ASP:OD1	6:E:221:GLU:HB2	2.20	0.40
7:F:13:LEU:O	7:F:13:LEU:HD23	2.22	0.40
7:F:131:TRP:CZ2	10:I:96:ALA:O	2.74	0.40
8:G:29:LEU:O	8:G:32:LYS:HG2	2.22	0.40
8:G:122:LYS:HE3	8:G:122:LYS:HB2	1.68	0.40
9:H:210:ILE:HA	9:H:213:SER:OG	2.21	0.40
12:K:108:VAL:O	12:K:108:VAL:HG12	2.21	0.40
15:N:130:ASN:O	15:N:131:ARG:HB2	2.20	0.40
16:O:99:ASP:O	16:O:102:ILE:HG12	2.21	0.40
21:T:60:ASN:OD1	21:T:60:ASN:N	2.37	0.40
21:T:121:GLY:O	21:T:123:THR:N	2.53	0.40
29:3:113:GLU:CD	29:3:117:LYS:HG3	2.46	0.40
33:7:313:GLY:HA2	33:7:363:SER:HB3	2.03	0.40
33:7:392:ASN:HB3	33:7:412:LEU:HB3	2.02	0.40
1:2:35:G:C6	1:2:36:C:C5	3.09	0.40
1:2:154:G:C6	1:2:155:G:C5	3.09	0.40
1:2:187:G:H2'	1:2:188:U:C6	2.56	0.40
1:2:200:C:H2'	1:2:201:C:H6	1.87	0.40
1:2:202:C:C2	1:2:203:A:C8	3.09	0.40
1:2:233:G:C2	1:2:234:A:C5	3.09	0.40
1:2:269:G:N7	11:J:113:ARG:NH2	2.69	0.40
1:2:331:C:C2	1:2:332:U:C6	3.09	0.40
1:2:547:G:O2'	1:2:548:U:H5'	2.21	0.40
1:2:733:A:C5	1:2:781:A:C6	3.10	0.40
1:2:773:C:C2	1:2:774:U:C5	3.09	0.40
1:2:896:G:C2	1:2:898:G:C8	3.09	0.40
1:2:950:A:C2	1:2:1293:A:N3	2.90	0.40
1:2:992:U:C2	1:2:993:C:C5	3.09	0.40
1:2:1062:U:H2'	1:2:1063:G:O4'	2.21	0.40
1:2:1130:G:C8	20:S:44:LYS:NZ	2.90	0.40
1:2:1214:U:O2	9:H:93:LEU:N	2.54	0.40
1:2:1241:A:N3	1:2:1242:A:C8	2.89	0.40
1:2:1268:C:C2	1:2:1269:C:C5	3.09	0.40
1:2:1273:A:H5''	1:2:1274:G:OP2	2.21	0.40
1:2:1294:C:N3	1:2:1295:U:C5	2.89	0.40
1:2:1298:C:H2'	1:2:1299:C:H6	1.85	0.40
7:F:205:LEU:O	7:F:208:THR:OG1	2.37	0.40
10:I:81:VAL:HG23	10:I:81:VAL:O	2.22	0.40
11:J:42:LYS:H	11:J:59:ALA:HB3	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:J:75:VAL:HB	11:J:104:GLU:OE2	2.21	0.40
13:L:45:ILE:HD11	13:L:66:LEU:HD23	2.04	0.40
21:T:111:LYS:HG2	21:T:112:ARG:O	2.20	0.40
22:U:140:LEU:HD12	22:U:140:LEU:HA	1.91	0.40
27:Z:127:GLY:HA3	27:Z:150:TYR:O	2.21	0.40
27:Z:172:LYS:HD2	27:Z:172:LYS:HA	1.81	0.40
28:O:20:LYS:HE3	28:O:20:LYS:HB2	1.57	0.40
29:3:78:ILE:C	29:3:79:TYR:HD1	2.29	0.40
33:7:259:LEU:HD21	35:9:188:ASN:HD21	1.85	0.40
1:2:121:U:H2'	1:2:122:C:O4'	2.21	0.40
1:2:628:G:C2	1:2:629:G:C4	3.09	0.40
1:2:638:G:C6	1:2:639:G:N7	2.89	0.40
1:2:689:G:N7	1:2:691:G:H1'	2.36	0.40
1:2:709:G:C2	1:2:710:A:C4	3.10	0.40
1:2:955:A:C8	1:2:1175:A:C6	3.07	0.40
1:2:989:A:C5	1:2:991:G:C5	3.10	0.40
1:2:1104:C:N3	1:2:1110:G:C6	2.89	0.40
1:2:1152:G:H21	1:2:1154:A:H5''	1.85	0.40
1:2:1249:A:N3	1:2:1249:A:H2'	2.36	0.40
1:2:1261:A:H2'	1:2:1262:A:H8	1.86	0.40
1:2:1300:C:P	22:U:39:ARG:HH22	2.39	0.40
1:2:1359:G:C5	1:2:1360:C:C5	3.08	0.40
2:A:113:LYS:HE2	2:A:152:GLU:C	2.46	0.40
2:A:118:LEU:HD21	2:A:191:VAL:HG12	2.03	0.40
3:B:72:VAL:HG23	3:B:94:GLY:O	2.21	0.40
5:D:68:ILE:O	5:D:72:GLN:N	2.48	0.40
6:E:86:GLY:O	6:E:89:ASP:HB2	2.22	0.40
9:H:154:PRO:O	9:H:157:ARG:HB2	2.21	0.40
10:I:30:ALA:HB3	10:I:58:ALA:O	2.21	0.40
11:J:81:ILE:HD12	11:J:82:GLU:OE2	2.21	0.40
15:N:77:LEU:HA	15:N:77:LEU:HD23	1.77	0.40
17:P:16:LYS:HE3	17:P:16:LYS:HB3	1.96	0.40
22:U:3:THR:HG22	22:U:130:ASP:OD2	2.22	0.40
31:4:50:U:H2'	31:4:51:C:C5	2.56	0.40
33:7:49:LEU:HB3	33:7:218:ILE:HD11	2.03	0.40
33:7:134:VAL:CG1	33:7:340:VAL:HG21	2.48	0.40
33:7:152:ASP:OD2	33:7:189:ILE:HD11	2.21	0.40
39:7:502:GNP:O1A	39:7:502:GNP:H2'	2.21	0.40
1:2:56:C:O2'	1:2:57:U:OP1	2.38	0.40
1:2:346:A:C4	1:2:347:G:C8	3.09	0.40
1:2:398:A:H3'	1:2:399:C:C6	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:520:G:C2	1:2:521:C:C5	3.10	0.40
1:2:618:C:H2'	1:2:619:U:C6	2.56	0.40
1:2:738:C:C4	1:2:739:A:N7	2.90	0.40
1:2:925:G:C5	1:2:926:G:C8	3.10	0.40
1:2:980:C:O5'	1:2:980:C:H6	2.04	0.40
1:2:1062:U:N3	1:2:1063:G:C5	2.89	0.40
1:2:1070:A:N1	1:2:1071:G:C5	2.90	0.40
1:2:1097:U:H2'	1:2:1097:U:O2	2.21	0.40
1:2:1107:U:C2	1:2:1109:G:C6	3.09	0.40
1:2:1128:G:C2	1:2:1129:G:C5	3.10	0.40
1:2:1150:A:C4	1:2:1151:G:C8	3.09	0.40
1:2:1211:C:H4'	1:2:1308:G:N2	2.36	0.40
1:2:1215:G:C2	1:2:1216:G:C5	3.09	0.40
1:2:1278:G:C6	1:2:1279:G:C6	3.09	0.40
1:2:1390:C:O5'	1:2:1390:C:H6	2.04	0.40
1:2:1411:C:C2	1:2:1433:G:C2	3.09	0.40
1:2:1480:G:C2	1:2:1481:U:C4	3.10	0.40
2:A:141:ILE:HA	2:A:144:GLU:OE1	2.22	0.40
6:E:167:LYS:HE3	6:E:170:GLU:CB	2.51	0.40
8:G:25:GLU:OE1	8:G:45:ILE:HG22	2.21	0.40
8:G:96:PRO:C	8:G:98:GLU:N	2.80	0.40
12:K:26:VAL:O	12:K:33:VAL:HG23	2.21	0.40
13:L:45:ILE:HG13	13:L:45:ILE:O	2.21	0.40
14:M:22:SER:OG	14:M:24:ASN:N	2.51	0.40
15:N:7:PRO:CG	15:N:16:LEU:HD13	2.52	0.40
16:O:83:LYS:HB3	21:T:9:ARG:NH1	2.37	0.40
18:Q:111:GLN:C	18:Q:112:HIS:CD2	2.99	0.40
21:T:55:LYS:NZ	21:T:79:LEU:HB2	2.36	0.40
24:W:6:ASN:CG	24:W:7:VAL:HG13	2.46	0.40
31:4:15:G:H1	31:4:21:A:H2	1.63	0.40
31:4:46:A:H8	31:4:46:A:OP2	2.04	0.40
31:4:63:G:C2	31:4:64:G:N7	2.89	0.40
33:7:37:HIS:CD2	33:7:48:LYS:HB2	2.57	0.40
33:7:88:ARG:HG3	33:7:88:ARG:HH21	1.87	0.40
33:7:327:TRP:HE1	33:7:382:LEU:C	2.25	0.40
33:7:330:ARG:HG3	33:7:330: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 PDB entries followed by that with respect to all EM entries.

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	A	186/199 (94%)	157 (84%)	29 (16%)	0	100	100
3	B	194/202 (96%)	162 (84%)	32 (16%)	0	100	100
4	C	59/63 (94%)	43 (73%)	16 (27%)	0	100	100
5	D	173/180 (96%)	140 (81%)	32 (18%)	1 (1%)	21	58
6	E	240/243 (99%)	179 (75%)	60 (25%)	1 (0%)	30	66
7	F	227/236 (96%)	172 (76%)	55 (24%)	0	100	100
8	G	122/125 (98%)	97 (80%)	25 (20%)	0	100	100
9	H	211/215 (98%)	171 (81%)	40 (19%)	0	100	100
10	I	127/130 (98%)	96 (76%)	31 (24%)	0	100	100
11	J	124/127 (98%)	91 (73%)	33 (27%)	0	100	100
12	K	132/135 (98%)	107 (81%)	25 (19%)	0	100	100
13	L	99/102 (97%)	86 (87%)	13 (13%)	0	100	100
14	M	126/137 (92%)	105 (83%)	21 (17%)	0	100	100
15	N	144/147 (98%)	104 (72%)	39 (27%)	1 (1%)	18	54
16	O	136/148 (92%)	107 (79%)	28 (21%)	1 (1%)	18	54
17	P	53/56 (95%)	40 (76%)	13 (24%)	0	100	100
18	Q	150/158 (95%)	127 (85%)	23 (15%)	0	100	100
19	R	107/113 (95%)	80 (75%)	27 (25%)	0	100	100
20	S	64/67 (96%)	54 (84%)	10 (16%)	0	100	100
21	T	123/132 (93%)	94 (76%)	29 (24%)	0	100	100
22	U	147/150 (98%)	125 (85%)	22 (15%)	0	100	100
23	V	92/99 (93%)	69 (75%)	23 (25%)	0	100	100
24	W	61/65 (94%)	45 (74%)	16 (26%)	0	100	100
25	X	65/71 (92%)	48 (74%)	17 (26%)	0	100	100
26	Y	48/51 (94%)	28 (58%)	20 (42%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	Z	195/210 (93%)	152 (78%)	43 (22%)	0	100	100
28	0	34/36 (94%)	22 (65%)	12 (35%)	0	100	100
29	3	121/123 (98%)	96 (79%)	25 (21%)	0	100	100
32	6	93/113 (82%)	78 (84%)	15 (16%)	0	100	100
33	7	412/414 (100%)	363 (88%)	46 (11%)	3 (1%)	18	54
34	8	125/129 (97%)	113 (90%)	12 (10%)	0	100	100
35	9	247/254 (97%)	234 (95%)	13 (5%)	0	100	100
All	All	4437/4630 (96%)	3585 (81%)	845 (19%)	7 (0%)	44	77

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	O	88	GLY
33	7	66	GLU
5	D	103	ARG
33	7	265	GLY
15	N	6	ALA
6	E	36	PRO
33	7	127	PRO

5.3.2 Protein sidechains ⓘ

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

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	A	161/167 (96%)	158 (98%)	3 (2%)	50	66
3	B	168/173 (97%)	167 (99%)	1 (1%)	78	80
4	C	54/55 (98%)	52 (96%)	2 (4%)	30	51
5	D	158/160 (99%)	157 (99%)	1 (1%)	78	80
6	E	213/214 (100%)	212 (100%)	1 (0%)	81	81
7	F	192/198 (97%)	190 (99%)	2 (1%)	68	75
8	G	107/108 (99%)	106 (99%)	1 (1%)	70	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	H	183/184 (100%)	181 (99%)	2 (1%)	65	73
10	I	106/107 (99%)	105 (99%)	1 (1%)	70	75
11	J	102/103 (99%)	101 (99%)	1 (1%)	68	75
12	K	110/111 (99%)	110 (100%)	0	100	100
13	L	90/91 (99%)	90 (100%)	0	100	100
14	M	95/104 (91%)	95 (100%)	0	100	100
15	N	120/121 (99%)	120 (100%)	0	100	100
16	O	115/123 (94%)	115 (100%)	0	100	100
17	P	45/46 (98%)	45 (100%)	0	100	100
18	Q	137/143 (96%)	135 (98%)	2 (2%)	57	70
19	R	98/102 (96%)	96 (98%)	2 (2%)	48	65
20	S	60/61 (98%)	60 (100%)	0	100	100
21	T	109/114 (96%)	108 (99%)	1 (1%)	70	75
22	U	126/127 (99%)	123 (98%)	3 (2%)	43	63
23	V	86/90 (96%)	86 (100%)	0	100	100
24	W	54/56 (96%)	54 (100%)	0	100	100
25	X	57/60 (95%)	55 (96%)	2 (4%)	32	53
26	Y	41/42 (98%)	39 (95%)	2 (5%)	22	45
27	Z	156/168 (93%)	154 (99%)	2 (1%)	61	71
28	0	34/34 (100%)	34 (100%)	0	100	100
29	3	99/99 (100%)	98 (99%)	1 (1%)	68	75
32	6	83/99 (84%)	83 (100%)	0	100	100
33	7	356/356 (100%)	355 (100%)	1 (0%)	86	84
34	8	117/118 (99%)	116 (99%)	1 (1%)	70	75
35	9	226/228 (99%)	226 (100%)	0	100	100
All	All	3858/3962 (97%)	3826 (99%)	32 (1%)	70	77

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	23	TYR
2	A	116	TYR
2	A	178	ILE

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Mol	Chain	Res	Type
3	B	12	TYR
4	C	15	THR
4	C	49	LEU
5	D	3	ASP
6	E	144	ASP
7	F	37	ILE
7	F	201	VAL
8	G	84	VAL
9	H	90	HIS
9	H	147	HIS
10	I	61	TYR
11	J	48	THR
18	Q	119	MET
18	Q	124	LEU
19	R	44	ARG
19	R	88	ILE
21	T	81	ILE
22	U	34	PHE
22	U	71	GLU
22	U	85	HIS
25	X	24	VAL
25	X	56	ILE
26	Y	15	VAL
26	Y	19	ASN
27	Z	97	VAL
27	Z	178	VAL
29	3	51	VAL
33	7	3	TRP
34	8	19	PRO

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (59) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	64	HIS
2	A	70	GLN
2	A	134	GLN
2	A	164	ASN
3	B	18	HIS
4	C	4	ASN
5	D	50	ASN
5	D	123	GLN
5	D	162	ASN

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Mol	Chain	Res	Type
6	E	9	HIS
6	E	147	ASN
7	F	91	ASN
7	F	181	GLN
7	F	196	ASN
7	F	207	ASN
8	G	48	ASN
8	G	118	GLN
8	G	120	ASN
9	H	13	HIS
9	H	46	HIS
9	H	51	HIS
9	H	69	ASN
9	H	94	ASN
9	H	147	HIS
9	H	164	ASN
9	H	193	ASN
10	I	9	ASN
10	I	16	ASN
11	J	64	ASN
11	J	83	ASN
12	K	131	GLN
13	L	2	GLN
14	M	18	HIS
15	N	8	ASN
15	N	66	ASN
17	P	34	HIS
18	Q	112	HIS
19	R	26	HIS
19	R	71	HIS
20	S	22	ASN
20	S	48	ASN
21	T	66	HIS
21	T	84	HIS
21	T	115	HIS
22	U	40	HIS
24	W	27	GLN
24	W	32	HIS
25	X	26	GLN
27	Z	50	ASN
27	Z	77	ASN
27	Z	95	GLN

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Mol	Chain	Res	Type
27	Z	123	ASN
27	Z	156	ASN
32	6	88	GLN
33	7	97	HIS
33	7	143	ASN
33	7	162	GLN
33	7	400	GLN
34	8	84	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1496/1497 (99%)	518 (34%)	19 (1%)
30	5	19/20 (95%)	9 (47%)	0
31	4	75/76 (98%)	33 (44%)	1 (1%)
All	All	1590/1593 (99%)	560 (35%)	20 (1%)

All (560) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	14	U
1	2	15	U
1	2	16	C
1	2	23	A
1	2	30	C
1	2	31	G
1	2	33	A
1	2	44	A
1	2	45	U
1	2	49	G
1	2	52	C
1	2	54	G
1	2	55	A
1	2	56	C
1	2	57	U
1	2	58	A
1	2	59	A
1	2	60	G
1	2	62	C
1	2	72	A
1	2	73	A

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Mol	Chain	Res	Type
1	2	74	G
1	2	82	C
1	2	86	U
1	2	87	C
1	2	88	U
1	2	91	G
1	2	92	A
1	2	95	C
1	2	99	C
1	2	110	U
1	2	111	C
1	2	117	C
1	2	118	A
1	2	119	C
1	2	126	A
1	2	127	A
1	2	128	C
1	2	132	C
1	2	133	C
1	2	143	G
1	2	146	A
1	2	149	A
1	2	150	C
1	2	153	C
1	2	154	G
1	2	156	G
1	2	157	A
1	2	164	G
1	2	168	A
1	2	169	A
1	2	178	A
1	2	179	G
1	2	187	G
1	2	188	U
1	2	189	A
1	2	196	G
1	2	201	C
1	2	203	A
1	2	204	G
1	2	209	A
1	2	210	A
1	2	211	A

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Mol	Chain	Res	Type
1	2	212	G
1	2	214	G
1	2	217	C
1	2	222	A
1	2	224	G
1	2	225	C
1	2	226	U
1	2	227	C
1	2	249	C
1	2	251	G
1	2	253	U
1	2	255	A
1	2	256	G
1	2	258	U
1	2	260	G
1	2	268	G
1	2	269	G
1	2	274	G
1	2	275	G
1	2	276	C
1	2	277	C
1	2	283	A
1	2	286	4AC
1	2	288	A
1	2	292	U
1	2	298	C
1	2	299	G
1	2	301	G
1	2	305	U
1	2	307	A
1	2	308	G
1	2	315	A
1	2	319	4AC
1	2	322	A
1	2	323	G
1	2	324	A
1	2	333	G
1	2	334	A
1	2	336	A
1	2	337	C
1	2	338	A
1	2	339	C

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Mol	Chain	Res	Type
1	2	341	G
1	2	344	C
1	2	354	C
1	2	358	G
1	2	361	C
1	2	362	A
1	2	363	G
1	2	367	G
1	2	371	G
1	2	373	A2M
1	2	374	A
1	2	375	C
1	2	376	C
1	2	379	4AC
1	2	381	C
1	2	382	A
1	2	390	A
1	2	391	A
1	2	393	C
1	2	394	4AC
1	2	397	G
1	2	402	G
1	2	406	A
1	2	407	C
1	2	408	C
1	2	409	C
1	2	415	G
1	2	421	C
1	2	422	C
1	2	423	U
1	2	424	C
1	2	425	U
1	2	426	G
1	2	430	C
1	2	431	G
1	2	435	U
1	2	436	U
1	2	437	U
1	2	440	G
1	2	443	G
1	2	446	U
1	2	447	A

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Mol	Chain	Res	Type
1	2	448	A
1	2	452	G
1	2	456	C
1	2	459	G
1	2	460	A
1	2	462	U
1	2	463	A
1	2	464	A
1	2	465	G
1	2	466	G
1	2	470	G
1	2	472	G
1	2	473	C
1	2	475	A
1	2	477	G
1	2	478	C
1	2	480	G
1	2	482	U
1	2	483	G
1	2	484	G
1	2	485	C
1	2	491	C
1	2	493	G
1	2	495	G
1	2	496	G
1	2	497	U
1	2	498	A
1	2	499	A
1	2	502	C
1	2	504	G
1	2	507	G
1	2	509	C
1	2	511	4AC
1	2	513	A
1	2	515	U
1	2	516	G
1	2	518	U
1	2	519	G
1	2	520	G
1	2	521	C
1	2	524	C
1	2	525	U

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Mol	Chain	Res	Type
1	2	526	A
1	2	527	U
1	2	529	A
1	2	530	U
1	2	531	U
1	2	532	G
1	2	533	G
1	2	536	C
1	2	537	U
1	2	538	A
1	2	539	A
1	2	541	G
1	2	542	C
1	2	546	4AC
1	2	547	G
1	2	552	C
1	2	554	G
1	2	561	A
1	2	571	C
1	2	575	A
1	2	580	A
1	2	585	U
1	2	586	C
1	2	587	A
1	2	588	A
1	2	589	C
1	2	595	G
1	2	596	G
1	2	598	U
1	2	600	G
1	2	620	U
1	2	621	G
1	2	622	G
1	2	624	A
1	2	630	A
1	2	632	A
1	2	633	G
1	2	642	U
1	2	646	C
1	2	648	4AC
1	2	649	G
1	2	654	A

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Mol	Chain	Res	Type
1	2	655	G
1	2	661	A
1	2	668	A
1	2	670	A
1	2	677	G
1	2	679	G
1	2	681	G
1	2	683	C
1	2	686	C
1	2	687	C
1	2	688	A
1	2	690	U
1	2	691	G
1	2	694	G
1	2	698	G
1	2	701	C
1	2	715	G
1	2	716	U
1	2	722	G
1	2	727	G
1	2	731	4AC
1	2	733	A
1	2	739	A
1	2	740	G
1	2	743	G
1	2	744	A
1	2	748	A
1	2	749	A
1	2	752	G
1	2	759	A
1	2	760	U
1	2	761	A
1	2	767	G
1	2	770	G
1	2	775	G
1	2	776	G
1	2	777	C
1	2	778	U
1	2	782	A
1	2	784	G
1	2	785	G
1	2	786	A

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Mol	Chain	Res	Type
1	2	787	U
1	2	788	G
1	2	789	C
1	2	795	A
1	2	796	G
1	2	809	C
1	2	812	C
1	2	813	G
1	2	819	G
1	2	823	G
1	2	824	G
1	2	829	G
1	2	835	A
1	2	836	A
1	2	837	G
1	2	838	C
1	2	841	U
1	2	843	A
1	2	844	A
1	2	848	4AC
1	2	853	C
1	2	856	G
1	2	868	4AC
1	2	870	C
1	2	873	G
1	2	875	C
1	2	885	A
1	2	886	A
1	2	892	U
1	2	897	G
1	2	905	C
1	2	906	U
1	2	914	G
1	2	915	U
1	2	926	G
1	2	928	U
1	2	932	U
1	2	936	A
1	2	938	B8H
1	2	939	5MC
1	2	940	A
1	2	941	A

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Mol	Chain	Res	Type
1	2	943	G
1	2	946	G
1	2	947	G
1	2	950	A
1	2	953	U
1	2	962	G
1	2	965	A
1	2	966	C
1	2	968	G
1	2	969	C
1	2	970	A
1	2	971	G
1	2	974	U
1	2	975	G
1	2	976	A
1	2	977	A
1	2	978	G
1	2	980	C
1	2	986	U
1	2	990	G
1	2	991	G
1	2	992	U
1	2	996	G
1	2	997	C
1	2	999	G
1	2	1000	G
1	2	1001	A
1	2	1002	C
1	2	1003	G
1	2	1004	C
1	2	1005	G
1	2	1011	A
1	2	1018	G
1	2	1019	C
1	2	1028	4AC
1	2	1029	G
1	2	1032	A
1	2	1040	C
1	2	1043	U
1	2	1047	G
1	2	1049	G
1	2	1051	C

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Mol	Chain	Res	Type
1	2	1055	U
1	2	1057	A
1	2	1058	A
1	2	1059	G
1	2	1060	U
1	2	1065	U
1	2	1066	A
1	2	1067	A
1	2	1068	C
1	2	1071	G
1	2	1078	C
1	2	1090	U
1	2	1098	C
1	2	1105	G
1	2	1106	C
1	2	1107	U
1	2	1108	C
1	2	1109	G
1	2	1114	G
1	2	1116	A
1	2	1117	G
1	2	1119	C
1	2	1123	C
1	2	1126	G
1	2	1131	A
1	2	1133	U
1	2	1134	G
1	2	1136	C
1	2	1141	A
1	2	1142	U
1	2	1143	A
1	2	1144	A
1	2	1147	4AC
1	2	1155	G
1	2	1156	G
1	2	1157	G
1	2	1158	G
1	2	1161	G
1	2	1163	C
1	2	1170	A
1	2	1171	G
1	2	1174	C

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Mol	Chain	Res	Type
1	2	1175	A
1	2	1184	4AC
1	2	1185	G
1	2	1186	A
1	2	1187	A
1	2	1189	C
1	2	1190	C
1	2	1192	C
1	2	1195	G
1	2	1197	C
1	2	1199	A
1	2	1200	C
1	2	1201	A
1	2	1203	G
1	2	1211	C
1	2	1212	A
1	2	1214	U
1	2	1215	G
1	2	1221	G
1	2	1229	G
1	2	1230	U
1	2	1232	C
1	2	1234	G
1	2	1236	C
1	2	1239	4AC
1	2	1244	G
1	2	1245	G
1	2	1248	G
1	2	1249	A
1	2	1254	A
1	2	1260	U
1	2	1264	C
1	2	1273	A
1	2	1274	G
1	2	1276	U
1	2	1277	C
1	2	1279	G
1	2	1284	C
1	2	1294	C
1	2	1303	G
1	2	1309	C
1	2	1310	U

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Mol	Chain	Res	Type
1	2	1311	G
1	2	1312	G
1	2	1313	A
1	2	1319	U
1	2	1322	U
1	2	1327	G
1	2	1333	C
1	2	1338	U
1	2	1340	G
1	2	1342	G
1	2	1344	G
1	2	1347	G
1	2	1348	A
1	2	1350	U
1	2	1354	U
1	2	1356	C
1	2	1361	U
1	2	1364	U
1	2	1366	G
1	2	1368	A
1	2	1369	C
1	2	1371	C
1	2	1372	A
1	2	1383	C
1	2	1385	C
1	2	1386	C
1	2	1388	C
1	2	1391	G
1	2	1393	G
1	2	1394	C
1	2	1395	G
1	2	1397	G
1	2	1398	G
1	2	1399	C
1	2	1401	U
1	2	1404	G
1	2	1412	C
1	2	1416	C
1	2	1419	C
1	2	1420	U
1	2	1424	G
1	2	1436	G

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Mol	Chain	Res	Type
1	2	1437	A
1	2	1440	C
1	2	1441	U
1	2	1444	G
1	2	1445	C
1	2	1449	G
1	2	1450	U
1	2	1451	G
1	2	1452	A
1	2	1453	G
1	2	1454	G
1	2	1456	G
1	2	1457	G
1	2	1459	A
1	2	1461	A
1	2	1462	A
1	2	1463	G
1	2	1466	G
1	2	1467	UR3
1	2	1471	A
1	2	1472	A
1	2	1473	G
1	2	1475	U
1	2	1476	A
1	2	1480	G
1	2	1486	G
1	2	1489	C
1	2	1492	A
1	2	1493	C
1	2	1494	G
1	2	1497	U
1	2	1498	C
1	2	1499	G
1	2	1505	C
1	2	1508	C
30	5	806	G
30	5	807	G
30	5	813	A
30	5	814	U
30	5	815	U
30	5	816	U
30	5	817	A

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Mol	Chain	Res	Type
30	5	822	C
30	5	823	C
31	4	3	C
31	4	6	G
31	4	7	G
31	4	9	G
31	4	12	G
31	4	13	C
31	4	14	A
31	4	15	G
31	4	16	C
31	4	17	C
31	4	18	G
31	4	20	H2U
31	4	21	A
31	4	22	G
31	4	23	C
31	4	25	C
31	4	26	G
31	4	31	G
31	4	46	A
31	4	49	G
31	4	52	G
31	4	55	PSU
31	4	58	A
31	4	59	A
31	4	60	U
31	4	66	C
31	4	69	C
31	4	71	C
31	4	72	U
31	4	73	A
31	4	74	C
31	4	75	C
31	4	76	A

All (20) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	87	C
1	2	132	C
1	2	168	A

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Mol	Chain	Res	Type
1	2	209	A
1	2	268	G
1	2	461	A
1	2	599	C
1	2	618	C
1	2	632	A
1	2	687	C
1	2	913	G
1	2	952	C
1	2	998	C
1	2	1106	C
1	2	1155	G
1	2	1341	C
1	2	1347	G
1	2	1435	C
1	2	1448	C
31	4	73	A

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	4AC	2	319	1	21,24,25	1.20	3 (14%)	29,34,37	1.48	4 (13%)
1	4AC	2	53	1	21,24,25	1.06	2 (9%)	29,34,37	1.48	5 (17%)
1	4AC	2	868	1	21,24,25	1.23	3 (14%)	29,34,37	1.37	4 (13%)
1	MA6	2	1488	1	23,26,27	1.43	4 (17%)	34,38,41	2.01	7 (20%)
1	LHH	2	250	1	22,25,26	2.45	8 (36%)	29,35,38	1.20	2 (6%)
1	4AC	2	479	1	21,24,25	1.13	3 (14%)	29,34,37	1.59	5 (17%)
1	4AC	2	1233	1	21,24,25	1.09	2 (9%)	29,34,37	1.53	4 (13%)
1	A2M	2	373	1	22,25,26	1.61	4 (18%)	31,36,39	2.80	12 (38%)
1	4AC	2	1239	1	21,24,25	1.15	2 (9%)	29,34,37	1.87	4 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	4AC	2	1479	1	21,24,25	1.10	3 (14%)	29,34,37	1.50	4 (13%)
1	4AC	2	394	1	21,24,25	1.02	2 (9%)	29,34,37	1.66	5 (17%)
1	4AC	2	851	1	21,24,25	1.24	3 (14%)	29,34,37	1.57	4 (13%)
1	4AC	2	303	1	21,24,25	1.16	3 (14%)	29,34,37	1.44	3 (10%)
1	4AC	2	1041	1	21,24,25	1.01	2 (9%)	29,34,37	1.98	4 (13%)
1	4AC	2	590	1,36	21,24,25	1.15	3 (14%)	29,34,37	1.47	4 (13%)
1	4AC	2	636	1	21,24,25	1.12	3 (14%)	29,34,37	1.60	4 (13%)
31	OMC	4	32	31	19,22,23	0.99	2 (10%)	26,31,34	1.13	2 (7%)
31	H2U	4	20	31	18,21,22	1.10	2 (11%)	21,30,33	2.24	1 (4%)
1	4AC	2	828	1	21,24,25	1.01	1 (4%)	29,34,37	1.64	4 (13%)
1	4AC	2	17	1	21,24,25	1.06	2 (9%)	29,34,37	1.77	5 (17%)
1	4AC	2	648	1	21,24,25	1.20	3 (14%)	29,34,37	1.85	7 (24%)
1	4AC	2	751	1	21,24,25	1.13	3 (14%)	29,34,37	1.26	4 (13%)
1	4AC	2	839	1	21,24,25	1.13	2 (9%)	29,34,37	1.80	6 (20%)
1	6MZ	2	1469	1,36	22,25,26	1.39	3 (13%)	30,36,39	2.26	8 (26%)
1	4AC	2	848	1	21,24,25	1.12	2 (9%)	29,34,37	1.75	4 (13%)
1	4AC	2	1193	1	21,24,25	1.13	2 (9%)	29,34,37	2.00	5 (17%)
1	5HM	2	1378	1	19,23,24	2.94	7 (36%)	25,33,36	0.64	0
1	UR3	2	1467	1	19,22,23	1.10	2 (10%)	26,32,35	1.50	5 (19%)
31	5MU	4	54	31	19,22,23	1.44	6 (31%)	28,32,35	2.05	8 (28%)
1	4AC	2	1147	1	21,24,25	1.12	3 (14%)	29,34,37	2.24	6 (20%)
1	4AC	2	703	1	21,24,25	1.07	2 (9%)	29,34,37	1.82	6 (20%)
1	4AC	2	731	1	21,24,25	1.16	3 (14%)	29,34,37	1.37	5 (17%)
31	4SU	4	8	31	18,21,22	1.79	5 (27%)	26,30,33	2.15	4 (15%)
1	OMC	2	1376	1	19,22,23	0.90	2 (10%)	26,31,34	0.76	0
1	4AC	2	626	1	21,24,25	1.05	3 (14%)	29,34,37	1.41	4 (13%)
1	4AC	2	1184	1	21,24,25	1.06	3 (14%)	29,34,37	1.39	4 (13%)
1	4AC	2	546	1	21,24,25	1.03	2 (9%)	29,34,37	1.44	3 (10%)
1	5MC	2	939	1	18,22,23	1.05	2 (11%)	26,32,35	1.25	3 (11%)
1	B8H	2	938	1	19,22,23	0.82	0	22,32,35	1.52	3 (13%)
1	4AC	2	1028	1	21,24,25	1.05	3 (14%)	29,34,37	1.62	4 (13%)
1	4AC	2	718	1	21,24,25	1.08	2 (9%)	29,34,37	1.18	3 (10%)
1	4AC	2	957	1	21,24,25	1.12	1 (4%)	29,34,37	2.29	7 (24%)
31	PSU	4	55	31	18,21,22	1.38	2 (11%)	22,30,33	1.85	3 (13%)
1	4AC	2	511	1	21,24,25	1.15	3 (14%)	29,34,37	1.87	6 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MA6	2	1487	1	23,26,27	1.49	4 (17%)	34,38,41	2.06	10 (29%)
1	4AC	2	379	1	21,24,25	1.08	3 (14%)	29,34,37	1.55	5 (17%)
1	5MC	2	1202	1	18,22,23	1.00	1 (5%)	26,32,35	1.21	1 (3%)
1	4AC	2	286	1	21,24,25	1.11	2 (9%)	29,34,37	1.64	7 (24%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	4AC	2	319	1	-	4/11/29/30	0/2/2/2
1	4AC	2	53	1	-	0/11/29/30	0/2/2/2
1	4AC	2	868	1	-	2/11/29/30	0/2/2/2
1	MA6	2	1488	1	-	0/11/29/30	0/3/3/3
1	LHH	2	250	1	-	1/13/31/32	0/2/2/2
1	4AC	2	479	1	-	3/11/29/30	0/2/2/2
1	4AC	2	1233	1	-	0/11/29/30	0/2/2/2
1	A2M	2	373	1	-	1/9/27/28	0/3/3/3
1	4AC	2	1239	1	-	2/11/29/30	0/2/2/2
1	4AC	2	1479	1	-	0/11/29/30	0/2/2/2
1	4AC	2	394	1	-	2/11/29/30	0/2/2/2
1	4AC	2	851	1	-	4/11/29/30	0/2/2/2
1	4AC	2	303	1	-	0/11/29/30	0/2/2/2
1	4AC	2	1041	1	-	0/11/29/30	0/2/2/2
1	4AC	2	590	1,36	-	2/11/29/30	0/2/2/2
1	4AC	2	636	1	-	0/11/29/30	0/2/2/2
31	OMC	4	32	31	-	2/9/27/28	0/2/2/2
31	H2U	4	20	31	-	4/7/38/39	0/2/2/2
1	4AC	2	828	1	-	0/11/29/30	0/2/2/2
1	4AC	2	17	1	-	0/11/29/30	0/2/2/2
1	4AC	2	648	1	-	2/11/29/30	0/2/2/2
1	4AC	2	751	1	-	0/11/29/30	0/2/2/2
1	4AC	2	839	1	-	1/11/29/30	0/2/2/2
1	6MZ	2	1469	1,36	-	2/9/27/28	0/3/3/3
1	4AC	2	848	1	-	2/11/29/30	0/2/2/2
1	4AC	2	1193	1	-	0/11/29/30	0/2/2/2
1	5HM	2	1378	1	-	2/9/27/28	0/2/2/2
1	UR3	2	1467	1	-	6/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
31	5MU	4	54	31	-	1/7/25/26	0/2/2/2
1	4AC	2	1147	1	-	2/11/29/30	0/2/2/2
1	4AC	2	703	1	-	0/11/29/30	0/2/2/2
1	4AC	2	731	1	-	3/11/29/30	0/2/2/2
31	4SU	4	8	31	-	5/7/25/26	0/2/2/2
1	OMC	2	1376	1	-	2/9/27/28	0/2/2/2
1	4AC	2	626	1	-	2/11/29/30	0/2/2/2
1	4AC	2	1184	1	-	2/11/29/30	0/2/2/2
1	4AC	2	546	1	-	2/11/29/30	0/2/2/2
1	5MC	2	939	1	-	0/7/25/26	0/2/2/2
1	B8H	2	938	1	-	3/7/25/26	0/2/2/2
1	4AC	2	1028	1	-	2/11/29/30	0/2/2/2
1	4AC	2	718	1	-	0/11/29/30	0/2/2/2
1	4AC	2	957	1	-	1/11/29/30	0/2/2/2
31	PSU	4	55	31	-	0/7/25/26	0/2/2/2
1	4AC	2	511	1	-	2/11/29/30	0/2/2/2
1	MA6	2	1487	1	-	1/11/29/30	0/3/3/3
1	4AC	2	379	1	-	2/11/29/30	0/2/2/2
1	5MC	2	1202	1	-	2/7/25/26	0/2/2/2
1	4AC	2	286	1	-	5/11/29/30	0/2/2/2

All (133) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2	1378	5HM	C4-N3	6.29	1.44	1.34
1	2	250	LHH	C4-N4	6.05	1.48	1.39
1	2	250	LHH	C7-N4	5.67	1.47	1.37
1	2	1378	5HM	C2-N3	5.46	1.47	1.36
1	2	1378	5HM	C4-N4	5.36	1.48	1.34
1	2	1378	5HM	C6-C5	4.88	1.48	1.34
31	4	8	4SU	C4-S4	-4.50	1.59	1.68
1	2	250	LHH	O2-C2	-4.33	1.15	1.23
1	2	1469	6MZ	C5-C4	4.13	1.46	1.39
1	2	1488	MA6	C5-C4	3.98	1.46	1.39
1	2	1378	5HM	C6-N1	3.83	1.44	1.38
1	2	1378	5HM	O2-C2	-3.63	1.17	1.23
1	2	373	A2M	C5-N7	-3.55	1.32	1.39
1	2	319	4AC	C4-N3	-3.50	1.26	1.32
31	4	55	PSU	C6-C5	3.50	1.39	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
31	4	8	4SU	C4-N3	-3.48	1.33	1.37
1	2	851	4AC	C4-N3	-3.41	1.26	1.32
1	2	1487	MA6	C5-C4	3.41	1.45	1.39
1	2	373	A2M	C5-C4	3.38	1.45	1.39
1	2	731	4AC	C4-N3	-3.37	1.27	1.32
1	2	1487	MA6	C5-N7	-3.30	1.32	1.39
1	2	250	LHH	C2-N1	-3.26	1.32	1.40
1	2	868	4AC	C4-N3	-3.23	1.27	1.32
1	2	303	4AC	C4-N3	-3.21	1.27	1.32
1	2	1488	MA6	C5-N7	-3.18	1.33	1.39
1	2	1233	4AC	C4-N3	-3.13	1.27	1.32
1	2	1487	MA6	C4-N9	-3.13	1.30	1.37
1	2	868	4AC	C4-N4	-3.12	1.35	1.39
1	2	839	4AC	C4-N3	-3.12	1.27	1.32
1	2	648	4AC	C4-N3	-3.11	1.27	1.32
1	2	1202	5MC	C6-N1	-3.09	1.32	1.38
1	2	373	A2M	C8-N9	-3.08	1.32	1.37
1	2	1378	5HM	C2-N1	3.03	1.46	1.40
1	2	590	4AC	C4-N3	-3.02	1.27	1.32
1	2	479	4AC	C4-N3	-2.99	1.27	1.32
1	2	636	4AC	C4-N3	-2.97	1.27	1.32
1	2	751	4AC	C4-N3	-2.91	1.27	1.32
1	2	250	LHH	C6-N1	-2.87	1.31	1.38
1	2	1479	4AC	C4-N3	-2.86	1.27	1.32
1	2	939	5MC	C6-C5	2.83	1.39	1.34
1	2	1193	4AC	C4-N3	-2.82	1.27	1.32
1	2	53	4AC	C5-C4	2.81	1.46	1.40
31	4	20	H2U	C4-N3	-2.80	1.32	1.37
1	2	379	4AC	C4-N3	-2.80	1.27	1.32
1	2	1028	4AC	C4-N3	-2.79	1.28	1.32
1	2	1487	MA6	C8-N9	-2.79	1.32	1.37
31	4	20	H2U	C2-N3	-2.77	1.33	1.38
1	2	1184	4AC	C4-N3	-2.76	1.28	1.32
1	2	511	4AC	C4-N3	-2.74	1.28	1.32
1	2	718	4AC	C5-C4	2.72	1.46	1.40
1	2	250	LHH	C2-N3	-2.71	1.30	1.36
31	4	54	5MU	C2-N1	2.70	1.42	1.38
1	2	828	4AC	C5-C4	2.69	1.46	1.40
1	2	590	4AC	C5-C4	2.68	1.46	1.40
1	2	626	4AC	C4-N3	-2.63	1.28	1.32
1	2	319	4AC	C4-N4	-2.62	1.35	1.39
1	2	939	5MC	C6-N1	-2.62	1.33	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2	1239	4AC	C4-N3	-2.61	1.28	1.32
1	2	751	4AC	C5-C4	2.59	1.46	1.40
1	2	479	4AC	C5-C4	2.59	1.46	1.40
1	2	1469	6MZ	C5-N7	-2.59	1.34	1.39
1	2	286	4AC	C5-C4	2.59	1.46	1.40
1	2	53	4AC	C4-N3	-2.56	1.28	1.32
1	2	373	A2M	C4-N9	-2.56	1.32	1.37
31	4	54	5MU	C4-N3	-2.55	1.34	1.38
1	2	648	4AC	C4-N4	-2.55	1.36	1.39
1	2	1467	UR3	C5-C4	-2.54	1.37	1.43
1	2	286	4AC	C4-N3	-2.53	1.28	1.32
1	2	546	4AC	C4-N3	-2.53	1.28	1.32
1	2	1147	4AC	C6-C5	-2.50	1.29	1.35
31	4	55	PSU	C4-N3	-2.49	1.34	1.38
1	2	703	4AC	C4-N3	-2.49	1.28	1.32
1	2	718	4AC	C4-N3	-2.48	1.28	1.32
1	2	957	4AC	C4-N3	-2.48	1.28	1.32
31	4	8	4SU	C2-N1	2.45	1.42	1.38
31	4	54	5MU	C6-C5	2.45	1.38	1.34
1	2	17	4AC	C4-N3	-2.44	1.28	1.32
1	2	394	4AC	C4-N3	-2.44	1.28	1.32
1	2	848	4AC	C4-N3	-2.40	1.28	1.32
31	4	32	OMC	C5-C4	-2.40	1.37	1.42
1	2	1184	4AC	C5-C4	2.38	1.45	1.40
1	2	731	4AC	C4-N4	-2.35	1.36	1.39
1	2	479	4AC	C4-N4	-2.33	1.36	1.39
1	2	839	4AC	C4-N4	-2.32	1.36	1.39
1	2	17	4AC	C4-N4	-2.31	1.36	1.39
31	4	32	OMC	C6-N1	-2.30	1.32	1.38
1	2	1239	4AC	C4-N4	-2.30	1.36	1.39
1	2	626	4AC	C4-N4	-2.27	1.36	1.39
31	4	8	4SU	C5-C4	-2.26	1.39	1.42
31	4	54	5MU	C6-N1	-2.26	1.34	1.38
1	2	379	4AC	C4-N4	-2.25	1.36	1.39
1	2	851	4AC	C5-C4	2.24	1.45	1.40
31	4	54	5MU	C2-N3	-2.23	1.34	1.38
1	2	1469	6MZ	C5-C6	2.22	1.47	1.41
31	4	54	5MU	C4-C5	2.21	1.48	1.44
1	2	1147	4AC	C4-N3	-2.21	1.29	1.32
1	2	848	4AC	C4-N4	-2.20	1.36	1.39
1	2	868	4AC	C5-C4	2.19	1.45	1.40
1	2	379	4AC	C5-C4	2.19	1.45	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2	648	4AC	C5-C4	2.19	1.45	1.40
1	2	1147	4AC	C4-N4	-2.19	1.36	1.39
1	2	303	4AC	C5-C4	2.19	1.45	1.40
1	2	1233	4AC	C5-C4	2.18	1.45	1.40
1	2	636	4AC	C5-C4	2.18	1.45	1.40
1	2	250	LHH	O7-C7	-2.17	1.18	1.23
1	2	1184	4AC	C4-N4	-2.16	1.36	1.39
1	2	1488	MA6	C4-N9	-2.16	1.32	1.37
1	2	511	4AC	C4-N4	-2.15	1.36	1.39
1	2	1479	4AC	C4-N4	-2.15	1.36	1.39
1	2	303	4AC	C4-N4	-2.14	1.36	1.39
1	2	1376	OMC	C5-C4	-2.14	1.38	1.42
1	2	636	4AC	C4-N4	-2.14	1.36	1.39
1	2	626	4AC	C5-C4	2.13	1.45	1.40
31	4	8	4SU	C6-C5	2.12	1.40	1.35
1	2	1028	4AC	C5-C4	2.12	1.45	1.40
1	2	751	4AC	C4-N4	-2.12	1.36	1.39
1	2	546	4AC	C5-C4	2.11	1.45	1.40
1	2	1028	4AC	C4-N4	-2.10	1.36	1.39
1	2	590	4AC	C4-N4	-2.10	1.36	1.39
1	2	1193	4AC	C4-N4	-2.09	1.36	1.39
1	2	511	4AC	C5-C4	2.09	1.45	1.40
1	2	250	LHH	C6-C5	2.08	1.39	1.35
1	2	1467	UR3	C6-N1	-2.08	1.33	1.38
1	2	1041	4AC	C5-C4	2.08	1.45	1.40
1	2	703	4AC	C5-C4	2.07	1.45	1.40
1	2	731	4AC	C5-C4	2.06	1.45	1.40
1	2	394	4AC	C5-C4	2.05	1.45	1.40
1	2	851	4AC	C4-N4	-2.05	1.36	1.39
1	2	319	4AC	C5-C4	2.04	1.45	1.40
1	2	1479	4AC	C5-C4	2.03	1.45	1.40
1	2	1376	OMC	C6-N1	-2.03	1.33	1.38
1	2	1488	MA6	C8-N9	-2.03	1.33	1.37
1	2	1041	4AC	C4-N3	-2.01	1.29	1.32

All (218) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	4	20	H2U	C4-N3-C2	-9.61	117.82	125.79
1	2	373	A2M	C2'-C1'-N9	-8.09	99.91	113.53
1	2	373	A2M	C5-C4-N3	-7.03	117.58	126.75
31	4	8	4SU	C4-N3-C2	-6.85	120.68	127.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	1469	6MZ	C5-C4-N3	-6.58	118.16	126.75
1	2	1488	MA6	C5-C4-N3	-6.50	118.28	126.75
1	2	1147	4AC	C5-C4-N4	-6.34	111.91	122.92
1	2	957	4AC	N4-C4-N3	6.19	124.24	113.85
1	2	1193	4AC	O7-C7-N4	5.84	131.27	121.82
1	2	373	A2M	N3-C4-N9	5.78	136.60	127.08
31	4	55	PSU	N1-C2-N3	5.76	121.65	115.13
1	2	1041	4AC	C5-C4-N4	-5.69	113.04	122.92
1	2	957	4AC	O7-C7-N4	5.64	130.95	121.82
1	2	1041	4AC	O7-C7-N4	5.64	130.95	121.82
1	2	1487	MA6	C5-C4-N3	-5.60	119.44	126.75
1	2	957	4AC	C5-C4-N4	-5.59	113.22	122.92
1	2	648	4AC	O7-C7-N4	5.56	130.82	121.82
1	2	1147	4AC	O7-C7-N4	5.55	130.80	121.82
1	2	1147	4AC	N4-C4-N3	5.53	123.13	113.85
1	2	1239	4AC	O7-C7-N4	5.41	130.58	121.82
1	2	938	B8H	C4-N3-C2	-5.41	120.35	127.35
1	2	839	4AC	O7-C7-N4	5.35	130.48	121.82
31	4	8	4SU	C5-C4-N3	5.29	119.59	114.69
1	2	848	4AC	O7-C7-N4	5.26	130.34	121.82
1	2	1041	4AC	N4-C4-N3	5.26	122.68	113.85
1	2	1193	4AC	C5-C4-N4	-5.17	113.94	122.92
1	2	17	4AC	O7-C7-N4	5.14	130.14	121.82
1	2	319	4AC	O7-C7-N4	5.04	129.98	121.82
1	2	1028	4AC	O7-C7-N4	5.01	129.93	121.82
1	2	511	4AC	O7-C7-N4	5.01	129.92	121.82
1	2	1193	4AC	N4-C4-N3	4.99	122.23	113.85
1	2	479	4AC	O7-C7-N4	4.93	129.79	121.82
1	2	1469	6MZ	N3-C4-N9	4.88	135.12	127.08
1	2	1467	UR3	C4-N3-C2	-4.88	119.97	124.56
1	2	1233	4AC	O7-C7-N4	4.84	129.66	121.82
1	2	636	4AC	O7-C7-N4	4.83	129.63	121.82
1	2	1202	5MC	C5-C6-N1	-4.79	118.41	123.34
31	4	54	5MU	C4-N3-C2	-4.79	121.15	127.35
1	2	511	4AC	C5-C4-N4	-4.79	114.61	122.92
1	2	53	4AC	O7-C7-N4	4.78	129.55	121.82
1	2	703	4AC	O7-C7-N4	4.77	129.54	121.82
31	4	54	5MU	C5-C4-N3	4.76	119.37	115.31
1	2	848	4AC	N4-C4-N3	4.75	121.82	113.85
1	2	1479	4AC	O7-C7-N4	4.73	129.47	121.82
1	2	394	4AC	N4-C4-N3	4.72	121.78	113.85
1	2	379	4AC	O7-C7-N4	4.72	129.46	121.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	848	4AC	C5-C4-N4	-4.71	114.74	122.92
1	2	703	4AC	C5-C4-N4	-4.65	114.85	122.92
31	4	8	4SU	N3-C2-N1	4.61	121.02	114.89
1	2	703	4AC	N4-C4-N3	4.60	121.58	113.85
1	2	731	4AC	O7-C7-N4	4.58	129.23	121.82
1	2	1239	4AC	C5-C4-N4	-4.53	115.05	122.92
1	2	626	4AC	O7-C7-N4	4.49	129.08	121.82
1	2	851	4AC	O7-C7-N4	4.48	129.07	121.82
1	2	17	4AC	C5-C4-N4	-4.47	115.15	122.92
1	2	286	4AC	O7-C7-N4	4.44	129.00	121.82
1	2	828	4AC	O7-C7-N4	4.43	128.98	121.82
1	2	1488	MA6	N3-C4-N9	4.42	134.37	127.08
1	2	394	4AC	O7-C7-N4	4.42	128.96	121.82
1	2	828	4AC	C5-C4-N4	-4.40	115.27	122.92
1	2	1469	6MZ	C2-N3-C4	4.40	122.14	111.75
1	2	511	4AC	N4-C4-N3	4.39	121.22	113.85
1	2	868	4AC	O7-C7-N4	4.38	128.91	121.82
31	4	54	5MU	N3-C2-N1	4.30	120.60	114.89
1	2	303	4AC	O7-C7-N4	4.30	128.77	121.82
1	2	1487	MA6	C2-N1-C6	4.29	121.90	111.75
1	2	1184	4AC	O7-C7-N4	4.24	128.68	121.82
1	2	1469	6MZ	C6-C5-N7	4.24	136.97	132.39
1	2	1487	MA6	N3-C4-N9	4.23	134.06	127.08
1	2	1239	4AC	N4-C4-N3	4.23	120.95	113.85
1	2	17	4AC	N4-C4-N3	4.21	120.92	113.85
1	2	648	4AC	C5-C4-N4	-4.19	115.64	122.92
1	2	1488	MA6	C2-N1-C6	4.15	121.55	111.75
1	2	839	4AC	N4-C4-N3	4.14	120.80	113.85
1	2	546	4AC	N4-C4-N3	4.05	120.66	113.85
1	2	590	4AC	O2-C2-N3	-4.03	115.77	122.33
1	2	751	4AC	O7-C7-N4	4.03	128.34	121.82
1	2	1479	4AC	CM7-C7-N4	-4.01	108.36	115.29
31	4	55	PSU	O2-C2-N1	-4.00	118.39	122.79
1	2	828	4AC	N4-C4-N3	3.99	120.55	113.85
1	2	546	4AC	O7-C7-N4	3.98	128.26	121.82
1	2	718	4AC	O7-C7-N4	3.96	128.23	121.82
1	2	636	4AC	C5-C4-N4	-3.94	116.08	122.92
31	4	54	5MU	O4-C4-C5	-3.82	120.47	124.90
1	2	957	4AC	C1'-N1-C2	3.78	126.85	118.42
1	2	839	4AC	C5-C4-N4	-3.78	116.36	122.92
1	2	53	4AC	CM7-C7-N4	-3.76	108.79	115.29
1	2	373	A2M	C2-N3-C4	3.71	120.52	111.75

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	636	4AC	N4-C4-N3	3.70	120.06	113.85
1	2	939	5MC	C5-C6-N1	-3.69	119.54	123.34
1	2	1028	4AC	C5-C4-N4	-3.69	116.51	122.92
1	2	1469	6MZ	N1-C2-N3	-3.68	122.85	128.60
1	2	590	4AC	O7-C7-N4	3.66	127.74	121.82
1	2	546	4AC	C5-C4-N4	-3.66	116.57	122.92
1	2	479	4AC	CM7-C7-N4	-3.65	108.98	115.29
1	2	1488	MA6	C2-N3-C4	3.63	120.32	111.75
1	2	373	A2M	C4-N9-C8	3.63	109.66	105.73
1	2	394	4AC	C5-C4-N4	-3.59	116.69	122.92
1	2	648	4AC	N4-C4-N3	3.56	119.83	113.85
1	2	379	4AC	C5-C4-N4	-3.54	116.76	122.92
1	2	1487	MA6	C4-C5-N7	-3.53	106.32	110.62
1	2	373	A2M	C4-C5-N7	-3.52	106.33	110.62
1	2	1028	4AC	N4-C4-N3	3.51	119.75	113.85
1	2	626	4AC	C5-C4-N4	-3.51	116.82	122.92
1	2	1233	4AC	C5-C4-N4	-3.50	116.83	122.92
1	2	286	4AC	C5-C4-N4	-3.50	116.84	122.92
1	2	303	4AC	N4-C4-N3	3.46	119.66	113.85
31	4	55	PSU	C4-N3-C2	-3.44	121.38	126.34
1	2	286	4AC	N4-C4-N3	3.42	119.59	113.85
1	2	303	4AC	C5-C4-N4	-3.41	117.00	122.92
1	2	1233	4AC	N4-C4-N3	3.41	119.57	113.85
1	2	868	4AC	CM7-C7-N4	-3.40	109.41	115.29
1	2	1479	4AC	N4-C4-N3	3.40	119.56	113.85
1	2	1488	MA6	C4-C5-N7	-3.39	106.49	110.62
1	2	1487	MA6	C2-N3-C4	3.36	119.68	111.75
1	2	1469	6MZ	C4-C5-N7	-3.35	106.54	110.62
1	2	373	A2M	C5-N7-C8	3.35	108.26	103.51
1	2	839	4AC	CM7-C7-N4	-3.34	109.52	115.29
1	2	1184	4AC	C5-C4-N4	-3.33	117.14	122.92
1	2	851	4AC	C5-C4-N4	-3.31	117.17	122.92
1	2	1028	4AC	CM7-C7-N4	-3.30	109.58	115.29
1	2	1479	4AC	C5-C4-N4	-3.23	117.30	122.92
31	4	32	OMC	O2-C2-N3	-3.22	117.10	122.33
31	4	54	5MU	C5-C6-N1	-3.17	120.07	123.34
1	2	379	4AC	CM7-C7-N4	-3.13	109.88	115.29
1	2	626	4AC	N4-C4-N3	3.10	119.06	113.85
1	2	1239	4AC	CM7-C7-N4	-3.09	109.94	115.29
1	2	1147	4AC	C1'-N1-C2	3.09	125.31	118.42
1	2	250	LHH	N4-C4-N3	3.05	118.97	113.85
1	2	479	4AC	C5-C4-N4	-3.05	117.63	122.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	1467	UR3	C3U-N3-C2	3.04	122.64	117.31
1	2	17	4AC	CM7-C7-N4	-3.04	110.03	115.29
31	4	8	4SU	C5-C4-S4	-3.01	120.58	124.47
1	2	648	4AC	CM7-C7-N4	-3.01	110.09	115.29
1	2	379	4AC	N4-C4-N3	3.00	118.89	113.85
1	2	1147	4AC	CM7-C7-N4	-2.99	110.11	115.29
1	2	851	4AC	O2-C2-N3	-2.95	117.53	122.33
1	2	319	4AC	CM7-C7-N4	-2.95	110.20	115.29
1	2	851	4AC	N4-C4-N3	2.94	118.79	113.85
1	2	319	4AC	C5-C4-N4	-2.93	117.83	122.92
1	2	319	4AC	N4-C4-N3	2.92	118.75	113.85
1	2	373	A2M	N9-C8-N7	-2.92	109.92	113.91
1	2	286	4AC	C1'-N1-C2	2.91	124.92	118.42
1	2	957	4AC	C1'-N1-C6	-2.91	114.49	120.84
1	2	731	4AC	CM7-C7-N4	-2.91	110.27	115.29
1	2	718	4AC	CM7-C7-N4	-2.90	110.28	115.29
1	2	1487	MA6	C4-N9-C8	2.89	108.86	105.73
1	2	1467	UR3	C1'-N1-C2	2.88	121.85	116.99
1	2	511	4AC	CM7-C7-N4	-2.84	110.37	115.29
1	2	626	4AC	CM7-C7-N4	-2.81	110.43	115.29
1	2	1233	4AC	CM7-C7-N4	-2.80	110.45	115.29
1	2	868	4AC	C5-C4-N4	-2.79	118.08	122.92
1	2	1041	4AC	CM7-C7-N4	-2.76	110.52	115.29
1	2	590	4AC	O2-C2-N1	2.75	124.56	118.89
1	2	1487	MA6	N1-C2-N3	-2.74	124.31	128.60
1	2	1487	MA6	C5-N7-C8	2.73	107.39	103.51
1	2	1488	MA6	N1-C2-N3	-2.72	124.35	128.60
1	2	839	4AC	C1'-N1-C2	2.69	124.42	118.42
1	2	479	4AC	O2-C2-N3	-2.68	117.98	122.33
1	2	1184	4AC	N4-C4-N3	2.67	118.34	113.85
1	2	53	4AC	C5-C4-N4	-2.65	118.31	122.92
1	2	648	4AC	O2-C2-N3	-2.64	118.04	122.33
1	2	1184	4AC	CM7-C7-N4	-2.62	110.75	115.29
1	2	394	4AC	C1'-N1-C2	2.62	124.26	118.42
1	2	751	4AC	CM7-C7-N4	-2.61	110.78	115.29
1	2	939	5MC	C5-C4-N3	-2.60	118.87	121.67
1	2	1193	4AC	CM7-C7-N4	-2.58	110.82	115.29
1	2	1469	6MZ	C5-N7-C8	2.55	107.12	103.51
1	2	479	4AC	N4-C4-N3	2.53	118.09	113.85
1	2	1487	MA6	N1-C6-N6	2.52	119.84	117.08
1	2	751	4AC	C5-C4-N4	-2.51	118.56	122.92
1	2	286	4AC	O2-C2-N3	-2.50	118.26	122.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
31	4	32	OMC	C1'-N1-C2	2.50	124.00	118.42
1	2	590	4AC	CM7-C7-N4	-2.49	110.98	115.29
1	2	848	4AC	CM7-C7-N4	-2.46	111.03	115.29
31	4	54	5MU	C5M-C5-C4	2.46	121.47	118.77
1	2	938	B8H	N3-C2-N1	2.46	117.80	115.14
1	2	731	4AC	N4-C4-N3	2.46	117.98	113.85
1	2	286	4AC	CM7-C7-N4	-2.44	111.08	115.29
1	2	250	LHH	C5-C6-N1	-2.42	117.76	121.81
1	2	1467	UR3	C6-N1-C2	-2.41	119.63	121.79
1	2	373	A2M	C5'-C4'-C3'	-2.39	106.21	115.18
1	2	53	4AC	N4-C4-N3	2.37	117.84	113.85
1	2	957	4AC	O7-C7-CM7	-2.34	117.71	122.06
1	2	373	A2M	N3-C2-N1	-2.33	124.96	128.60
31	4	54	5MU	C1'-N1-C2	2.32	121.76	117.57
1	2	703	4AC	C1'-N1-C2	2.31	123.58	118.42
1	2	731	4AC	C5-C4-N4	-2.30	118.92	122.92
1	2	1488	MA6	C5-N7-C8	2.30	106.78	103.51
1	2	511	4AC	C1'-N1-C2	2.29	123.53	118.42
1	2	957	4AC	CM7-C7-N4	-2.29	111.33	115.29
1	2	511	4AC	O2-C2-N3	-2.26	118.65	122.33
1	2	1193	4AC	O7-C7-CM7	-2.23	117.91	122.06
1	2	938	B8H	O4'-C1'-C2'	2.23	108.29	105.14
1	2	286	4AC	C1'-N1-C6	-2.22	116.01	120.84
1	2	373	A2M	C1'-N9-C8	-2.21	122.14	127.14
1	2	53	4AC	O2-C2-N3	-2.21	118.74	122.33
1	2	1487	MA6	N9-C8-N7	-2.19	110.92	113.91
1	2	703	4AC	C1'-N1-C6	-2.17	116.11	120.84
31	4	54	5MU	C1'-N1-C6	-2.17	117.51	121.12
1	2	636	4AC	CM7-C7-N4	-2.16	111.56	115.29
1	2	703	4AC	CM7-C7-N4	-2.15	111.58	115.29
1	2	868	4AC	N4-C4-N3	2.15	117.46	113.85
1	2	648	4AC	C1'-N1-C2	2.14	123.20	118.42
1	2	939	5MC	N4-C4-N3	2.13	122.36	118.48
1	2	828	4AC	CM7-C7-N4	-2.12	111.62	115.29
1	2	751	4AC	N4-C4-N3	2.11	117.39	113.85
1	2	648	4AC	C4-N3-C2	-2.11	117.25	120.12
1	2	373	A2M	C3'-C2'-C1'	2.09	106.81	102.89
1	2	731	4AC	O2-C2-N3	-2.08	118.95	122.33
1	2	394	4AC	O7-C7-CM7	-2.07	118.22	122.06
1	2	1469	6MZ	C2-N1-C6	2.06	122.17	115.25
1	2	839	4AC	O2-C2-N3	-2.04	119.01	122.33
1	2	1467	UR3	O3'-C3'-C2'	-2.04	105.22	111.82

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	718	4AC	C5-C4-N4	-2.04	119.38	122.92
1	2	1147	4AC	C1'-N1-C6	-2.01	116.45	120.84
1	2	17	4AC	O2-C2-N3	-2.00	119.07	122.33
1	2	379	4AC	O2-C2-N3	-2.00	119.07	122.33

There are no chirality outliers.

All (79) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	2	250	LHH	C1'-C2'-O2'-C1
1	2	286	4AC	C3'-C4'-C5'-O5'
1	2	373	A2M	C1'-C2'-O2'-CM'
1	2	379	4AC	C3'-C4'-C5'-O5'
1	2	511	4AC	O4'-C4'-C5'-O5'
1	2	511	4AC	C3'-C4'-C5'-O5'
1	2	546	4AC	C3'-C4'-C5'-O5'
1	2	648	4AC	O4'-C4'-C5'-O5'
1	2	848	4AC	O4'-C4'-C5'-O5'
1	2	868	4AC	C3'-C4'-C5'-O5'
1	2	1028	4AC	O4'-C4'-C5'-O5'
1	2	1147	4AC	C3'-C4'-C5'-O5'
1	2	1239	4AC	C3'-C4'-C5'-O5'
1	2	1467	UR3	C2'-C1'-N1-C6
31	4	8	4SU	C2'-C1'-N1-C2
31	4	8	4SU	C2'-C1'-N1-C6
31	4	20	H2U	O4'-C1'-N1-C6
1	2	379	4AC	O4'-C4'-C5'-O5'
1	2	546	4AC	O4'-C4'-C5'-O5'
1	2	648	4AC	C3'-C4'-C5'-O5'
1	2	731	4AC	O4'-C4'-C5'-O5'
1	2	731	4AC	C3'-C4'-C5'-O5'
1	2	848	4AC	C3'-C4'-C5'-O5'
1	2	868	4AC	O4'-C4'-C5'-O5'
1	2	1028	4AC	C3'-C4'-C5'-O5'
1	2	1202	5MC	C3'-C4'-C5'-O5'
1	2	1239	4AC	O4'-C4'-C5'-O5'
1	2	1467	UR3	O4'-C4'-C5'-O5'
31	4	8	4SU	O4'-C1'-N1-C2
1	2	479	4AC	O4'-C4'-C5'-O5'
1	2	1147	4AC	O4'-C4'-C5'-O5'
1	2	1202	5MC	O4'-C4'-C5'-O5'
1	2	1376	OMC	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
1	2	1376	OMC	O4'-C4'-C5'-O5'
1	2	1467	UR3	C3'-C4'-C5'-O5'
1	2	1467	UR3	C2'-C1'-N1-C2
1	2	286	4AC	O4'-C4'-C5'-O5'
31	4	8	4SU	O4'-C1'-N1-C6
1	2	1184	4AC	O4'-C4'-C5'-O5'
1	2	626	4AC	O4'-C4'-C5'-O5'
1	2	1184	4AC	C3'-C4'-C5'-O5'
1	2	1469	6MZ	C2'-C1'-N9-C4
1	2	938	B8H	O4'-C4'-C5'-O5'
1	2	851	4AC	C2'-C1'-N1-C6
1	2	1469	6MZ	C2'-C1'-N9-C8
1	2	319	4AC	O4'-C4'-C5'-O5'
1	2	938	B8H	C3'-C4'-C5'-O5'
1	2	1378	5HM	C4-C5-CM5-OM5
31	4	32	OMC	C2'-C1'-N1-C2
1	2	479	4AC	C3'-C4'-C5'-O5'
1	2	851	4AC	O4'-C1'-N1-C6
1	2	1467	UR3	O4'-C1'-N1-C6
1	2	394	4AC	C4'-C5'-O5'-P
31	4	32	OMC	C2'-C1'-N1-C6
31	4	20	H2U	C2'-C1'-N1-C2
31	4	20	H2U	C2'-C1'-N1-C6
1	2	1467	UR3	O4'-C1'-N1-C2
31	4	20	H2U	O4'-C1'-N1-C2
1	2	286	4AC	C2'-C1'-N1-C6
1	2	851	4AC	O4'-C1'-N1-C2
1	2	1487	MA6	C2'-C1'-N9-C8
1	2	286	4AC	C2'-C1'-N1-C2
1	2	590	4AC	C2'-C1'-N1-C6
1	2	626	4AC	C3'-C4'-C5'-O5'
1	2	319	4AC	O4'-C1'-N1-C6
1	2	590	4AC	C2'-C1'-N1-C2
1	2	938	B8H	O4'-C1'-C5-C6
1	2	394	4AC	C2'-C1'-N1-C2
1	2	479	4AC	C2'-C1'-N1-C2
1	2	839	4AC	C2'-C1'-N1-C2
1	2	851	4AC	C2'-C1'-N1-C2
31	4	8	4SU	C4'-C5'-O5'-P
1	2	319	4AC	C2'-C1'-N1-C6
1	2	957	4AC	C2'-C1'-N1-C2
31	4	54	5MU	C2'-C1'-N1-C2

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Mol	Chain	Res	Type	Atoms
1	2	319	4AC	C3'-C4'-C5'-O5'
1	2	1378	5HM	C6-C5-CM5-OM5
1	2	731	4AC	C2'-C1'-N1-C2
1	2	286	4AC	C4'-C5'-O5'-P

There are no ring outliers.

47 monomers are involved in 148 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	2	319	4AC	3	0
1	2	53	4AC	1	0
1	2	868	4AC	3	0
1	2	1488	MA6	3	0
1	2	479	4AC	4	0
1	2	1233	4AC	6	0
1	2	373	A2M	7	0
1	2	1239	4AC	5	0
1	2	1479	4AC	5	0
1	2	394	4AC	4	0
1	2	851	4AC	6	0
1	2	303	4AC	3	0
1	2	1041	4AC	4	0
1	2	590	4AC	2	0
1	2	636	4AC	2	0
31	4	32	OMC	3	0
31	4	20	H2U	1	0
1	2	828	4AC	3	0
1	2	17	4AC	3	0
1	2	648	4AC	5	0
1	2	751	4AC	1	0
1	2	839	4AC	7	0
1	2	1469	6MZ	2	0
1	2	848	4AC	2	0
1	2	1193	4AC	3	0
1	2	1378	5HM	4	0
1	2	1467	UR3	3	0
31	4	54	5MU	3	0
1	2	1147	4AC	5	0
1	2	703	4AC	6	0
1	2	731	4AC	4	0
31	4	8	4SU	2	0
1	2	1376	OMC	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	2	626	4AC	1	0
1	2	1184	4AC	4	0
1	2	546	4AC	2	0
1	2	939	5MC	2	0
1	2	938	B8H	1	0
1	2	1028	4AC	2	0
1	2	718	4AC	4	0
1	2	957	4AC	3	0
31	4	55	PSU	4	0
1	2	511	4AC	1	0
1	2	1487	MA6	4	0
1	2	379	4AC	2	0
1	2	1202	5MC	3	0
1	2	286	4AC	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 42 ligands modelled in this entry, 40 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
39	GNP	7	502	36	33,34,34	1.27	5 (15%)	46,54,54	0.76	2 (4%)
38	MET	7	501	-	6,7,8	0.50	0	2,7,9	0.39	0

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
39	GNP	7	502	36	-	7/18/38/38	0/3/3/3
38	MET	7	501	-	-	2/5/6/8	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
39	7	502	GNP	PB-O3A	4.26	1.64	1.59
39	7	502	GNP	PB-O1B	3.18	1.51	1.46
39	7	502	GNP	PG-N3B	2.80	1.70	1.63
39	7	502	GNP	PG-O1G	2.60	1.50	1.46
39	7	502	GNP	PB-O2B	-2.07	1.51	1.56

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
39	7	502	GNP	PB-O3A-PA	-2.95	122.22	132.62
39	7	502	GNP	O3G-PG-O1G	-2.32	107.63	113.45

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
39	7	502	GNP	PB-N3B-PG-O1G
39	7	502	GNP	PG-N3B-PB-O1B
39	7	502	GNP	C5'-O5'-PA-O3A
39	7	502	GNP	O4'-C4'-C5'-O5'
38	7	501	MET	CA-CB-CG-SD
38	7	501	MET	N-CA-CB-CG
39	7	502	GNP	C5'-O5'-PA-O1A
39	7	502	GNP	C3'-C4'-C5'-O5'
39	7	502	GNP	C4'-C5'-O5'-PA

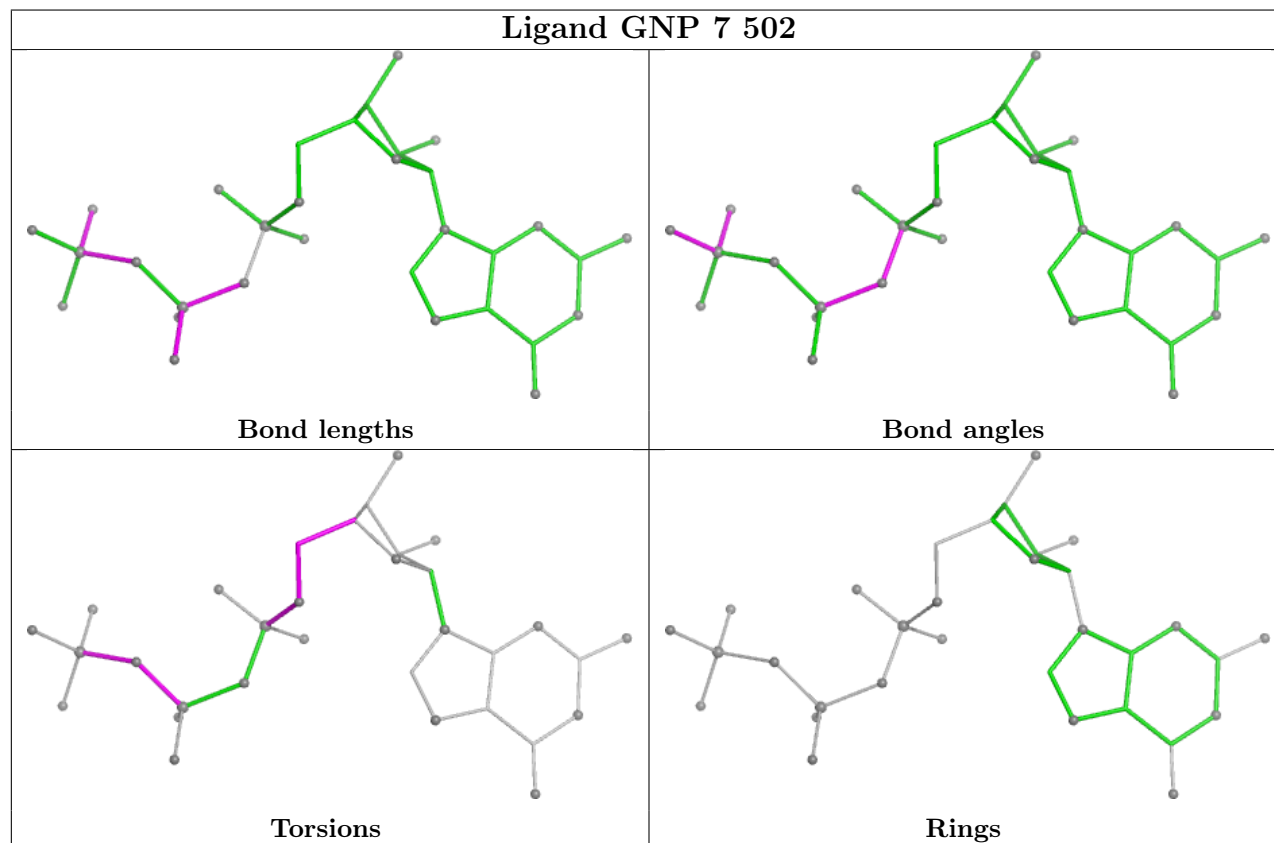
There are no ring outliers.

2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
39	7	502	GNP	4	0
38	7	501	MET	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
35	9	2
34	8	1

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Mol	Chain	Number of breaks
9	H	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	8	19:PRO	C	28:GLN	N	14.63
1	9	47:SER	C	53:ASN	N	11.57
1	9	169:SER	C	175:ARG	N	8.00
1	H	194:LYS	C	195:ASP	N	1.20

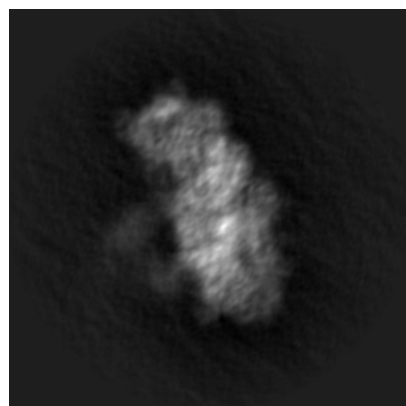
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10320. These allow visual inspection of the internal detail of the map and identification of artifacts.

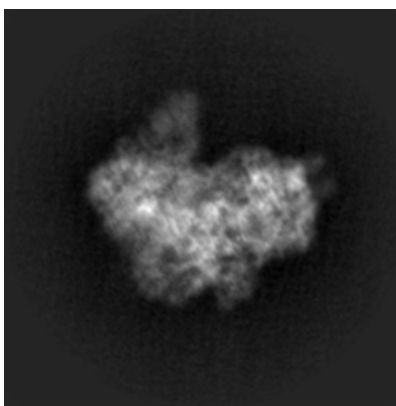
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

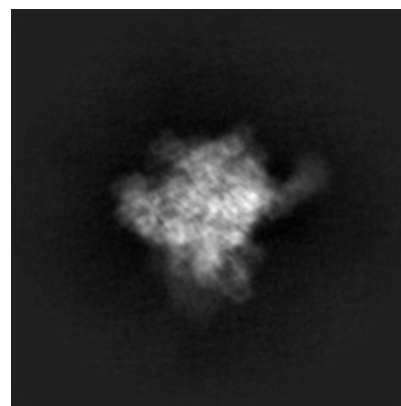
6.1.1 Primary map



X

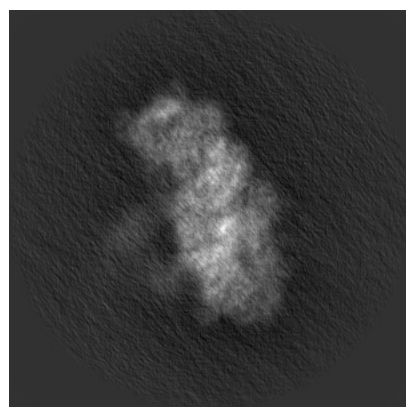


Y

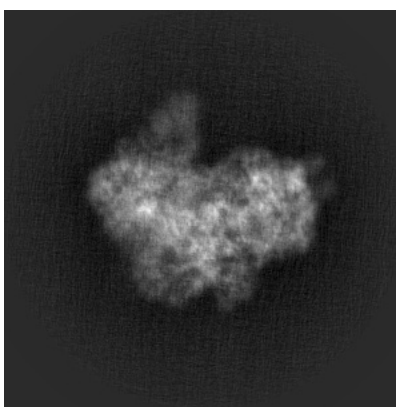


Z

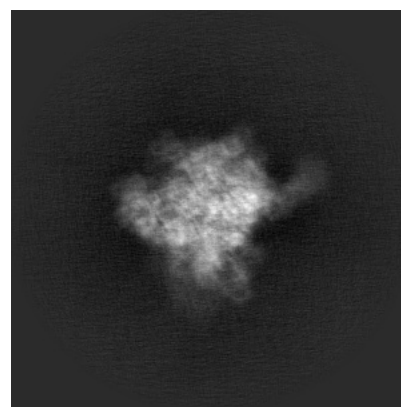
6.1.2 Raw map



X



Y

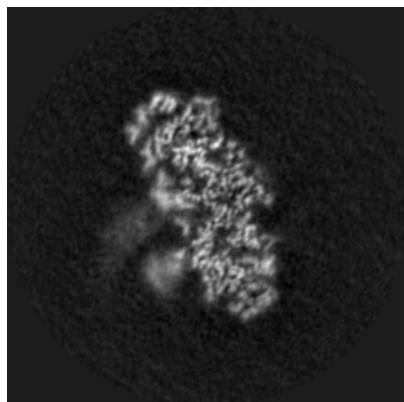


Z

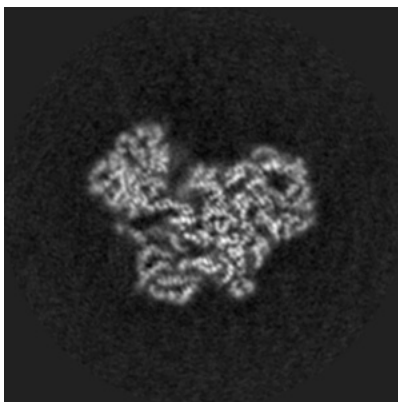
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

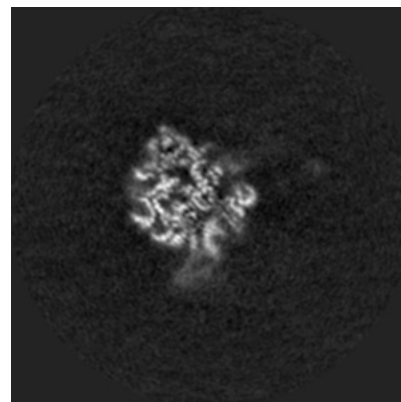
6.2.1 Primary map



X Index: 174

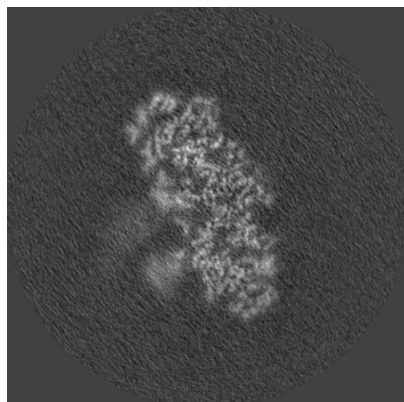


Y Index: 174

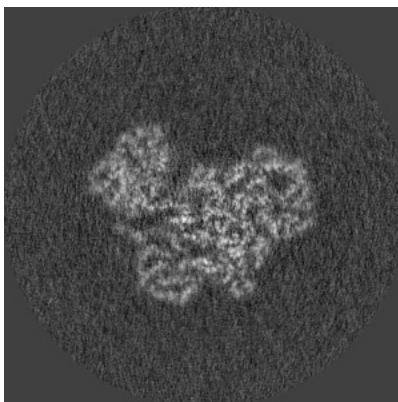


Z Index: 174

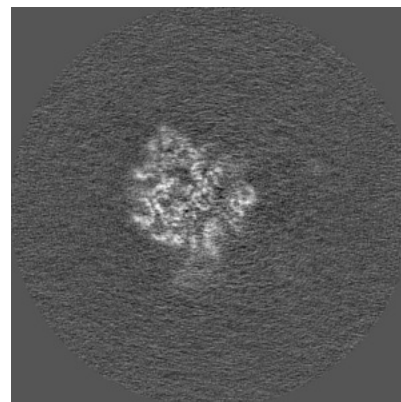
6.2.2 Raw map



X Index: 174



Y Index: 174

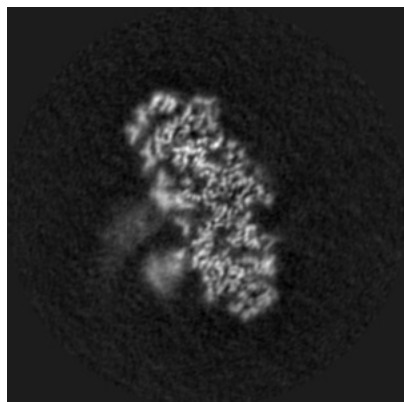


Z Index: 174

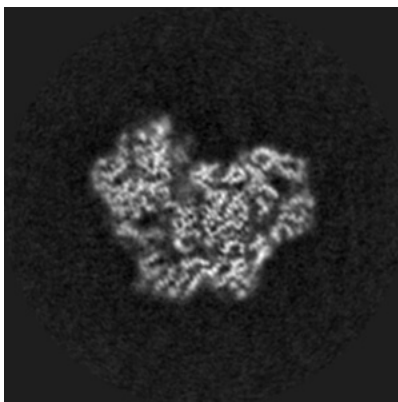
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

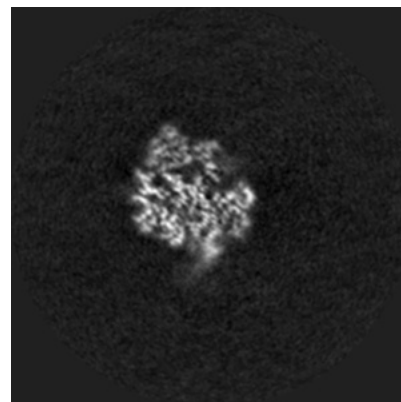
6.3.1 Primary map



X Index: 174

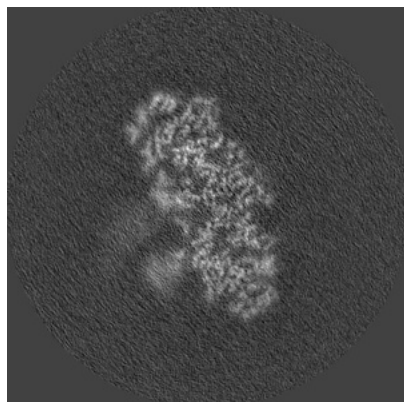


Y Index: 178

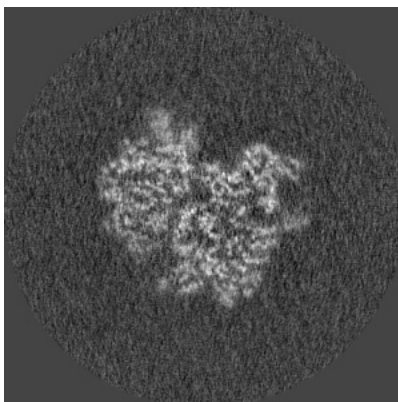


Z Index: 180

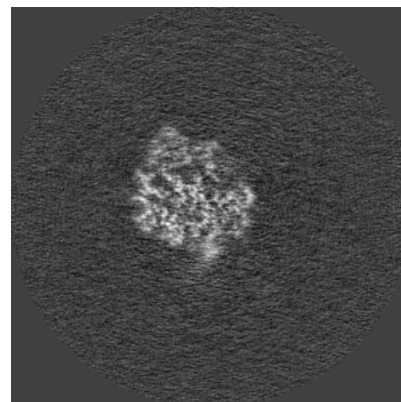
6.3.2 Raw map



X Index: 174



Y Index: 185

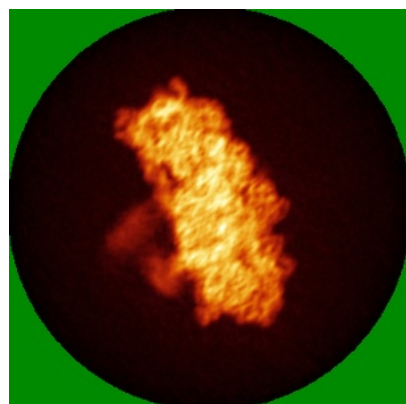


Z Index: 180

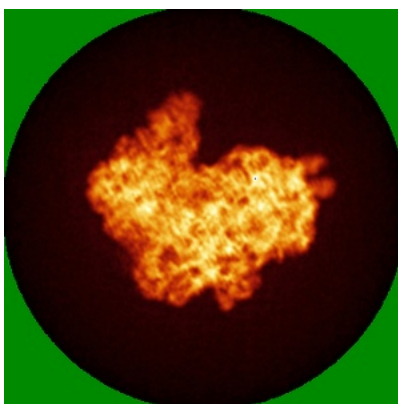
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

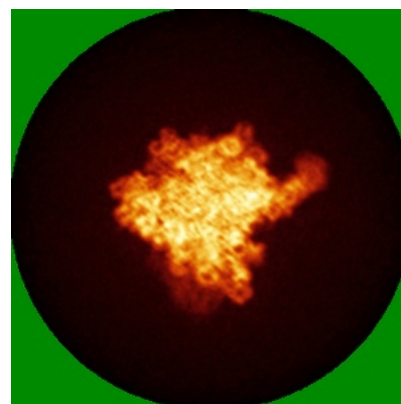
6.4.1 Primary map



X

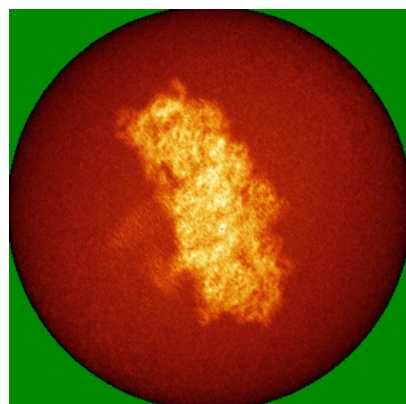


Y

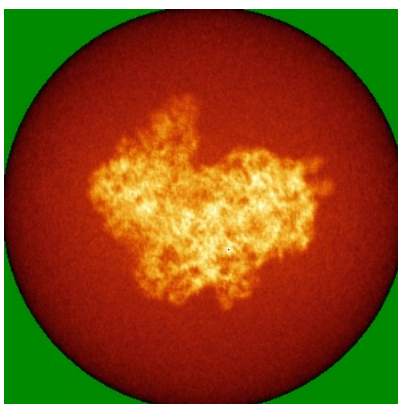


Z

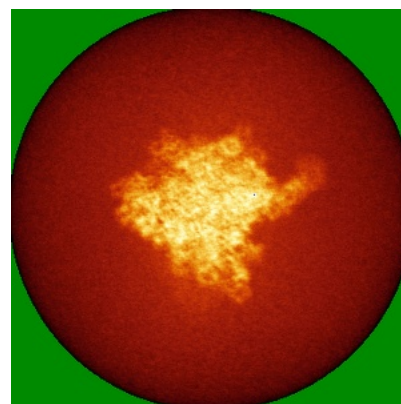
6.4.2 Raw map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



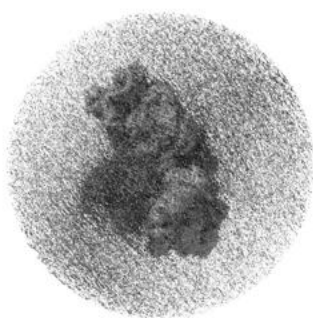
Y



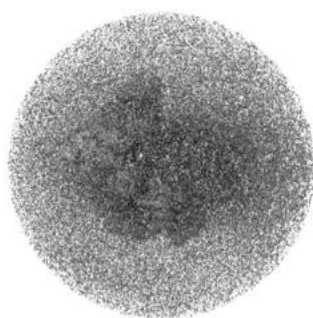
Z

The images above show the 3D surface view of the map at the recommended contour level 0.004. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

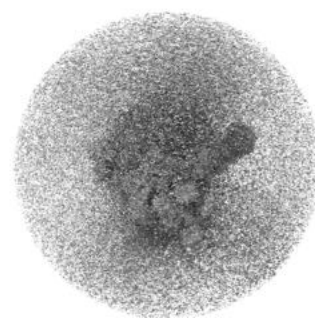
6.5.2 Raw map



X



Y



Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

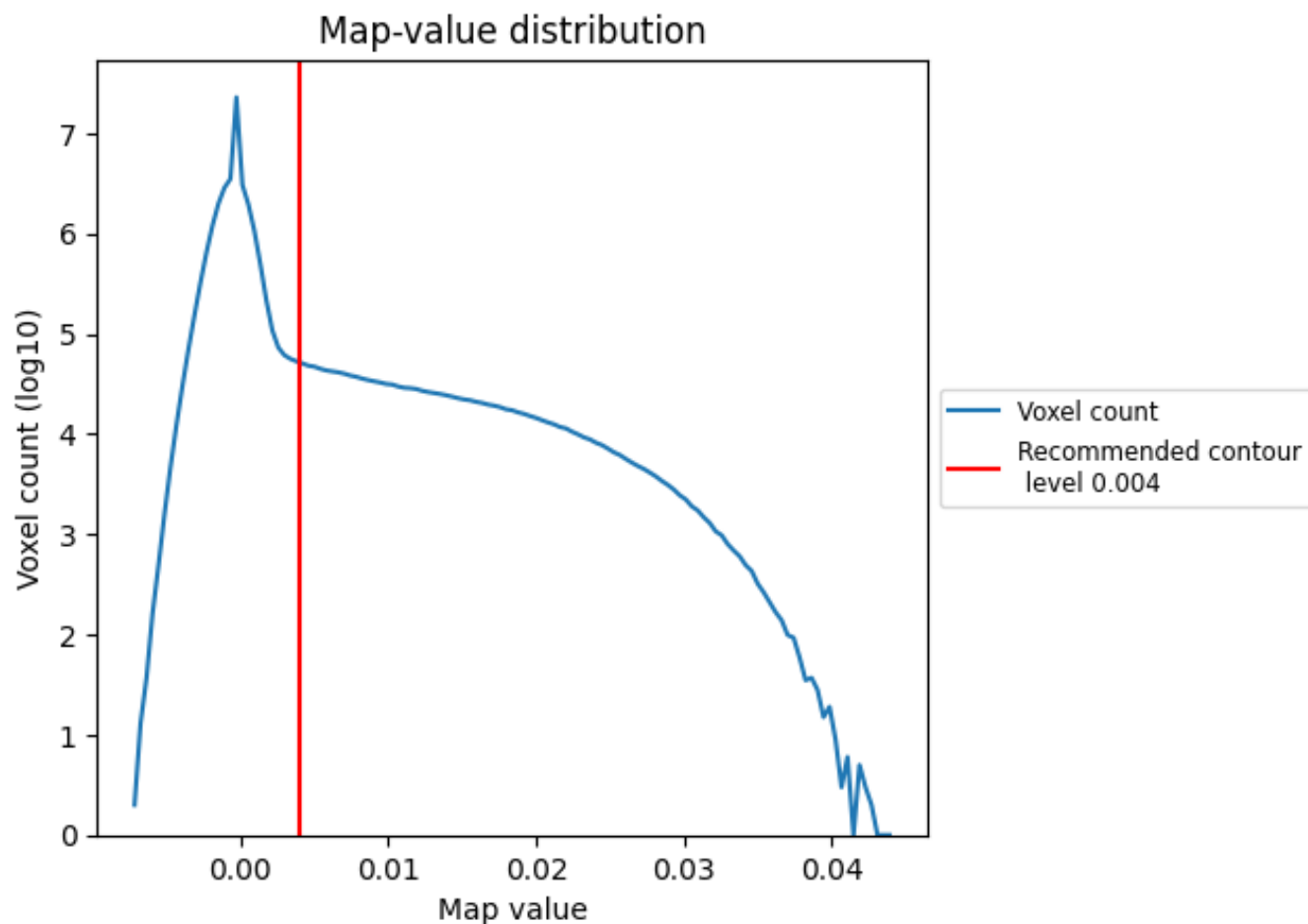
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

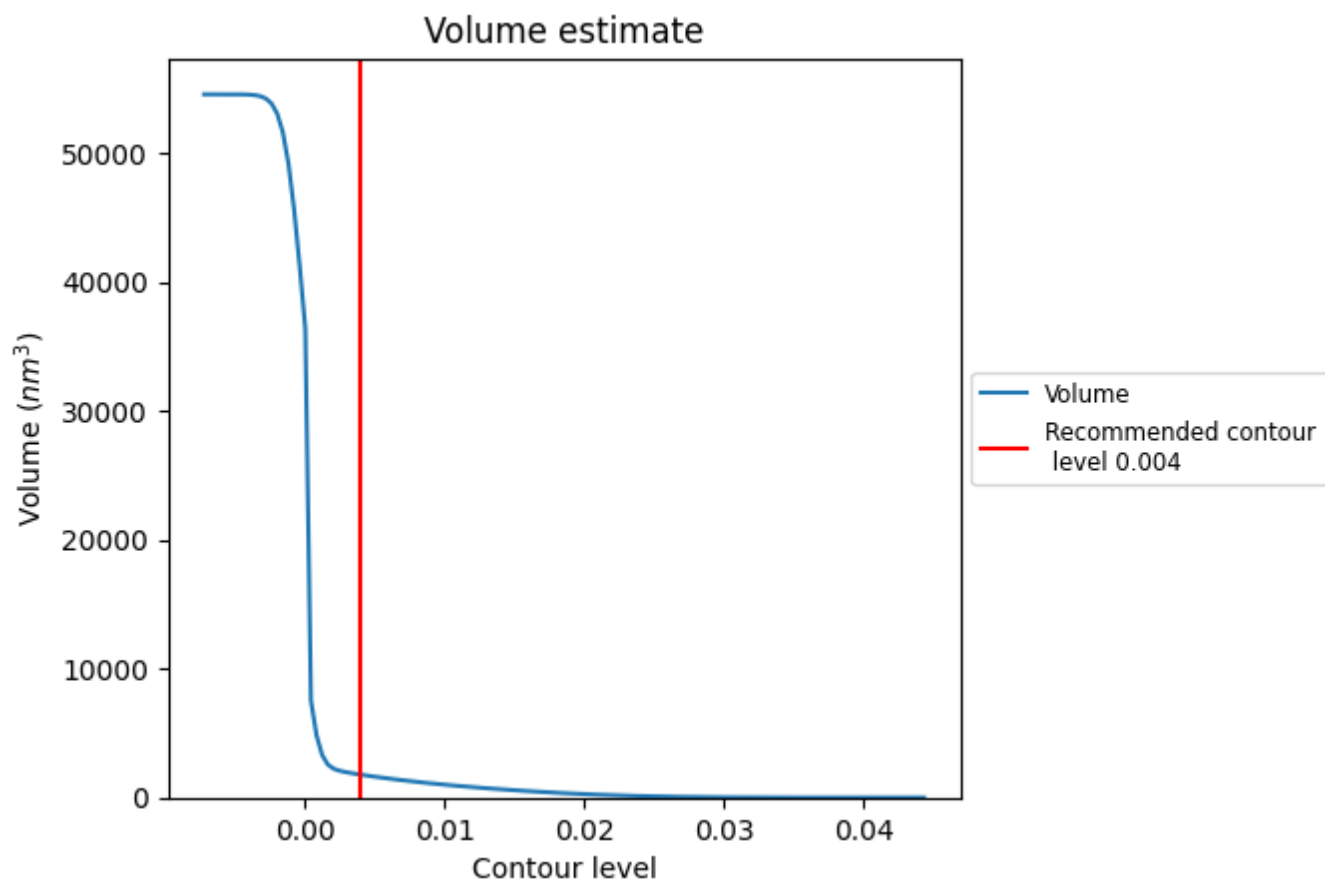
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

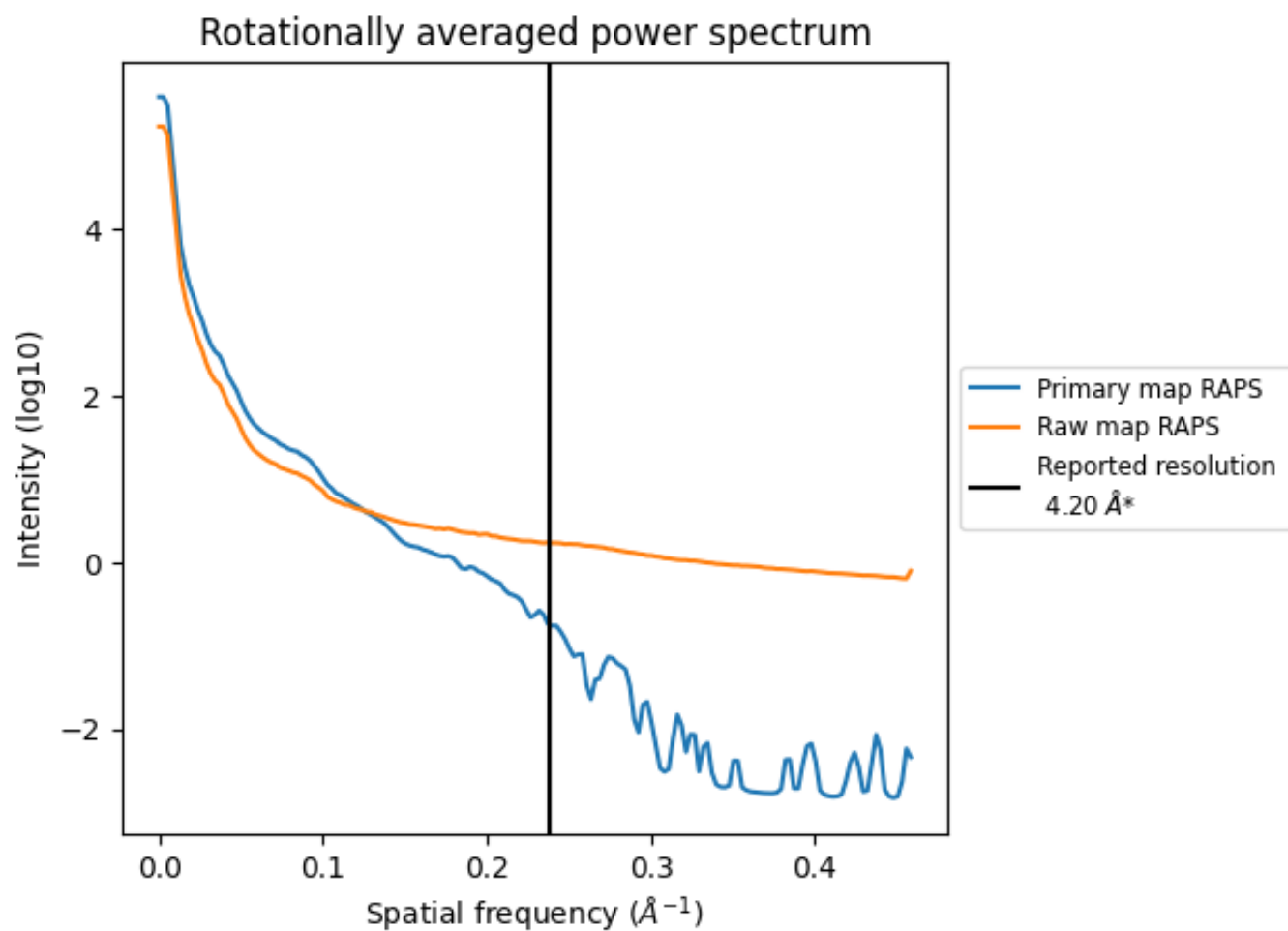
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1784 nm^3 ; this corresponds to an approximate mass of 1611 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

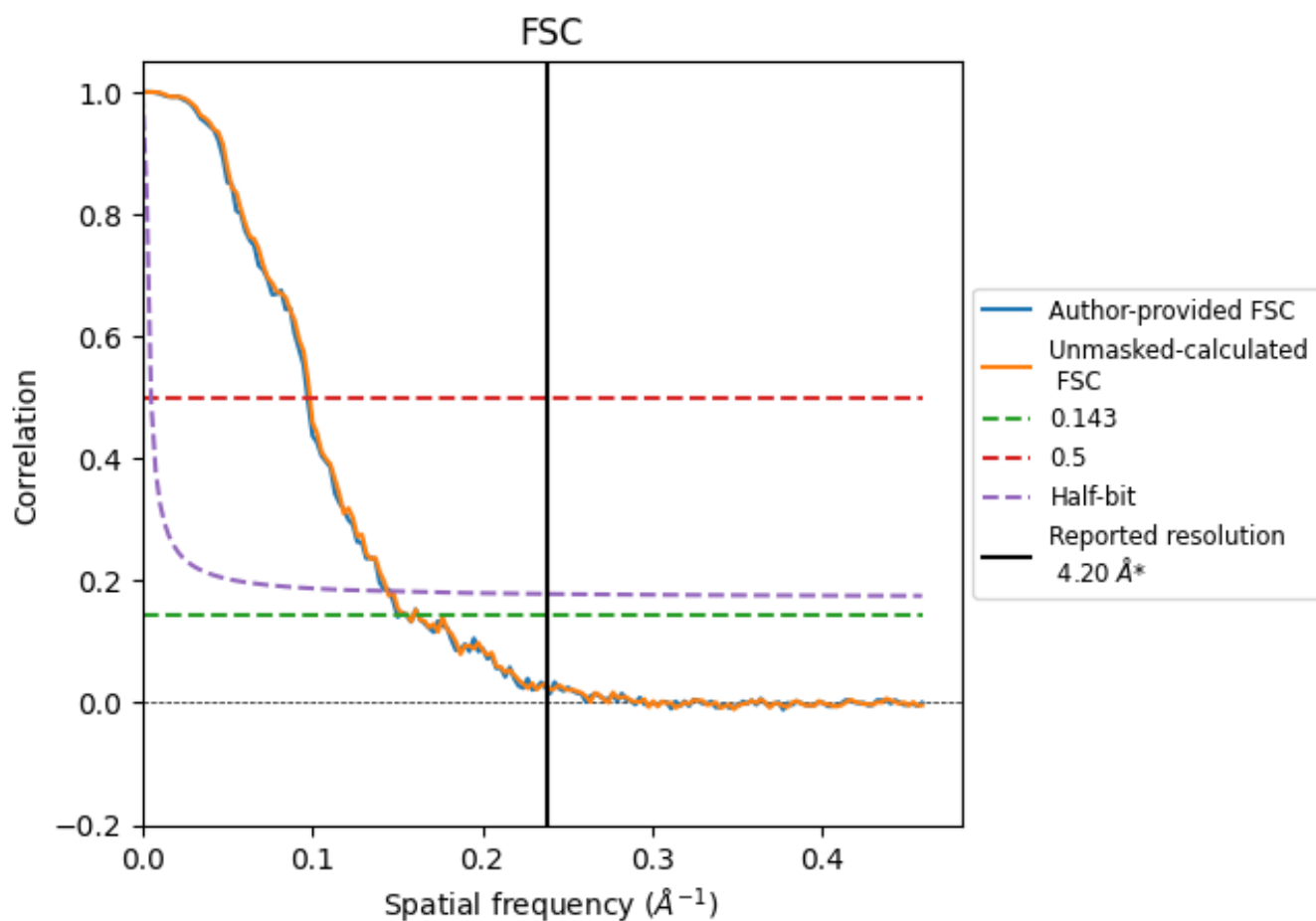


*Reported resolution corresponds to spatial frequency of 0.238 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.238 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.20	-	-
Author-provided FSC curve	6.67	10.29	6.87
Unmasked-calculated*	6.41	10.14	6.93

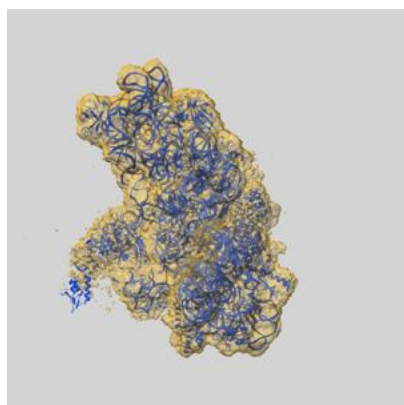
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 6.67 differs from the reported value 4.2 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.41 differs from the reported value 4.2 by more than 10 %

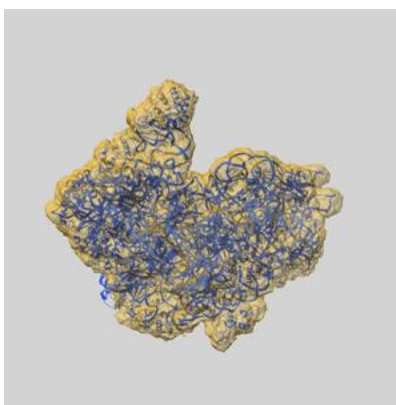
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10320 and PDB model 6SW9. Per-residue inclusion information can be found in section 3 on page 13.

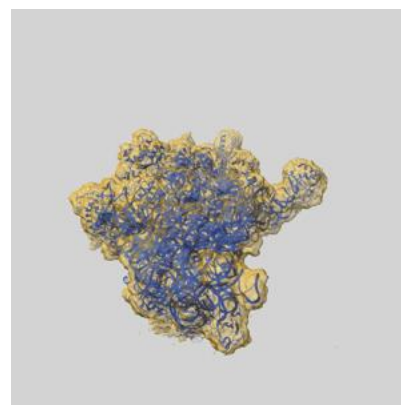
9.1 Map-model overlay [i](#)



X



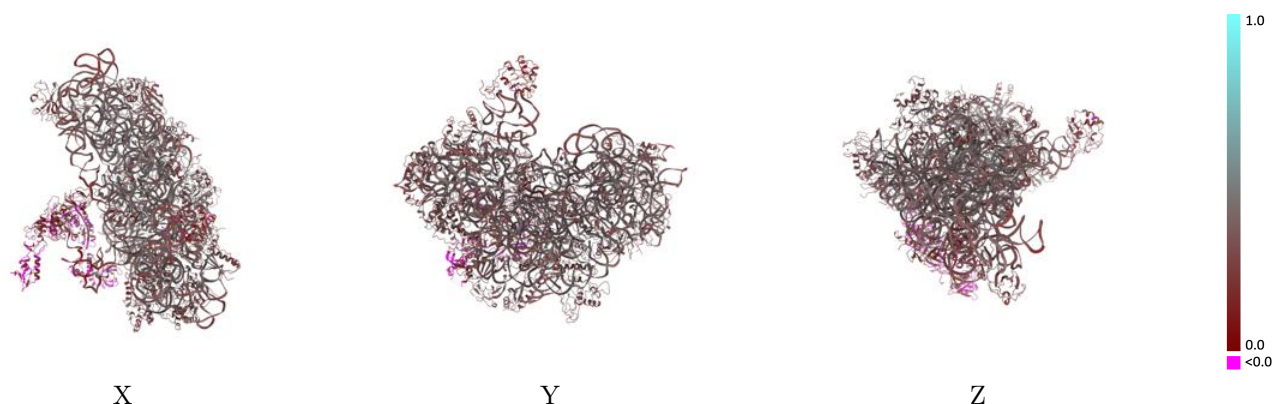
Y



Z

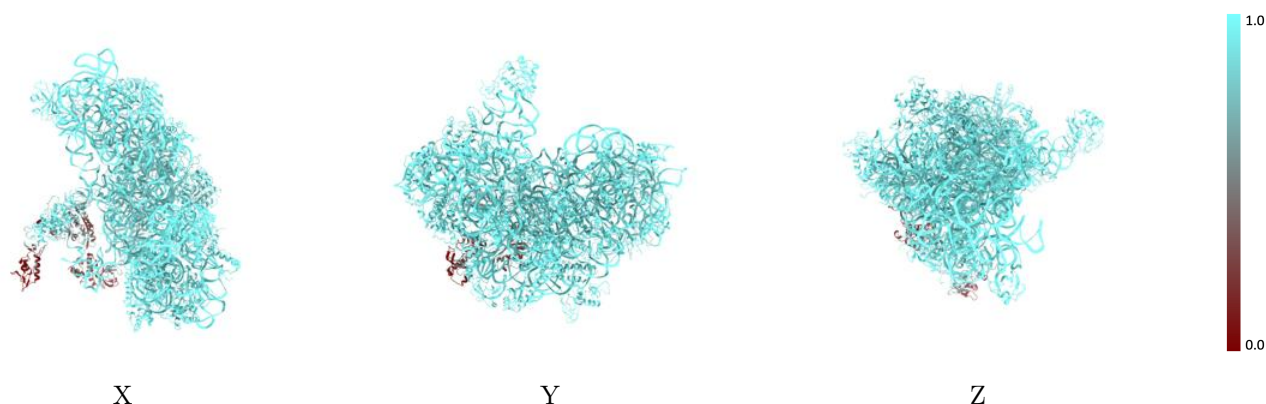
The images above show the 3D surface view of the map at the recommended contour level 0.004 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



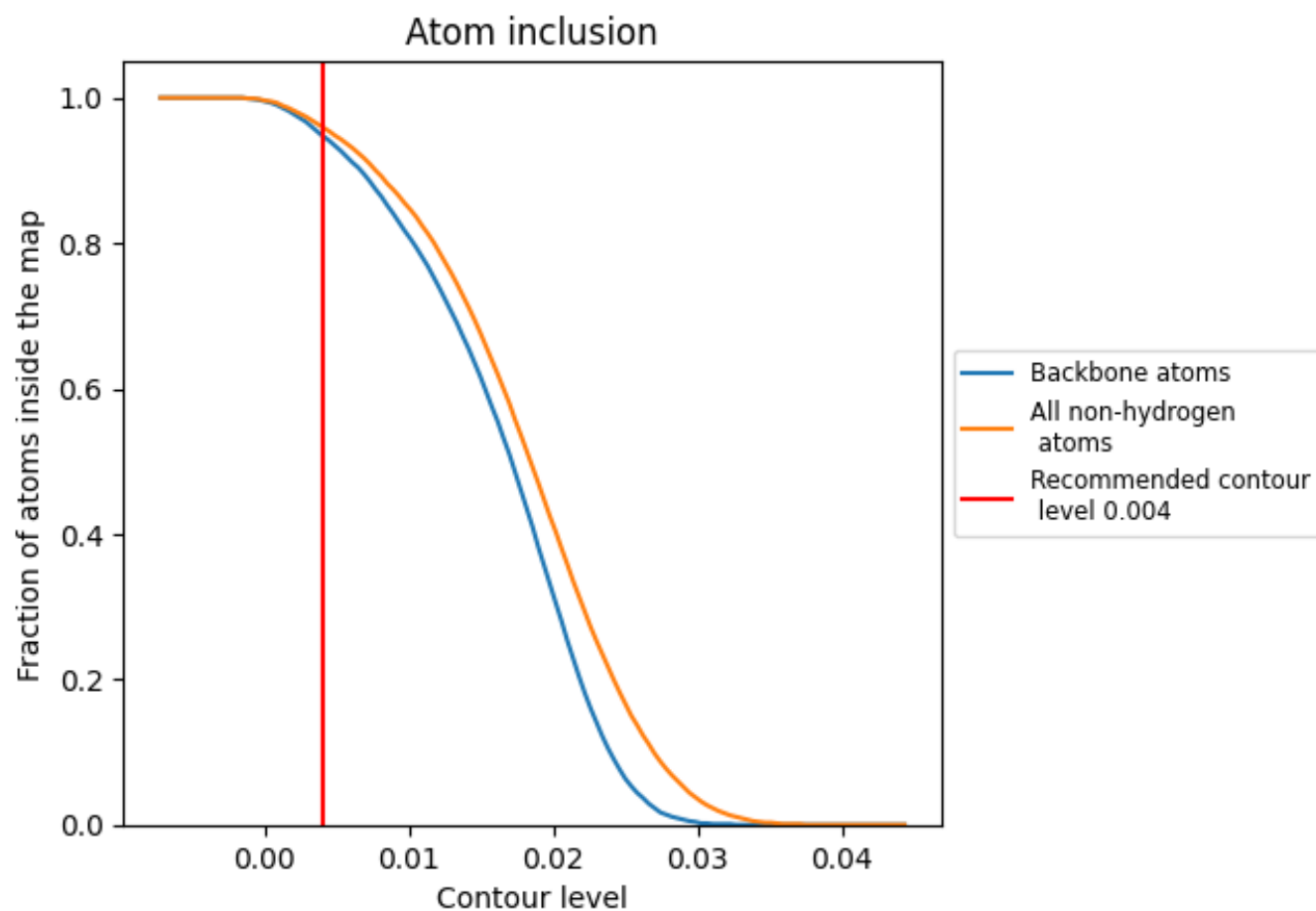
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.004).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 96% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.004) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9600	 0.3370
0	 0.9970	 0.3730
2	 1.0000	 0.3830
3	 1.0000	 0.2200
4	 0.9870	 0.2310
5	 0.9980	 0.3390
6	 1.0000	 0.2490
7	 0.8600	 0.1420
8	 0.2740	 0.0540
9	 0.2580	 0.0380
A	 0.9960	 0.3430
B	 0.9970	 0.3580
C	 0.9940	 0.3660
D	 1.0000	 0.3580
E	 0.9990	 0.3700
F	 0.9930	 0.3750
G	 0.9980	 0.3170
H	 0.9960	 0.3410
I	 0.9980	 0.3770
J	 0.9980	 0.3550
K	 0.9980	 0.3510
L	 0.9980	 0.3520
M	 1.0000	 0.3570
N	 0.9980	 0.3830
O	 0.9980	 0.3280
P	 1.0000	 0.3630
Q	 0.9980	 0.3450
R	 0.9990	 0.3900
S	 0.9850	 0.3060
T	 0.9930	 0.3340
U	 0.9980	 0.3410
V	 0.9990	 0.3440
W	 0.9960	 0.3620
X	 1.0000	 0.3480
Y	 0.9900	 0.2050
Z	 0.9950	 0.3530

