



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 08:03 PM GMT

PDB ID : 1I94
Title : CRYSTAL STRUCTURES OF THE SMALL RIBOSOMAL SUBUNIT WITH TETRACYCLINE, EDEINE AND IF3
Authors : Pioletti, M.; Schlutzen, F.; Harms, J.; Zarivach, R.; Gluehmann, M.; Avila, H.; Bartels, H.; Jacobi, C.; Hartsch, T.; Yonath, A.; Franceschi, F.
Deposited on : 2001-03-18
Resolution : 3.20 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

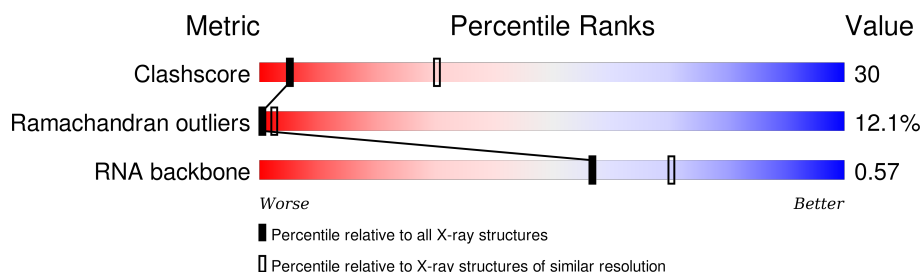
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	1024 (3.22-3.18)
Ramachandran outliers	100387	1004 (3.22-3.18)
RNA backbone	2183	1079 (3.70-2.70)

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

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	1514	
2	B	255	
3	C	238	
4	D	208	
5	E	161	
6	F	101	
7	G	155	

Continued on next page...

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Mol	Chain	Length	Quality of chain
8	H	138	 74%20%5% •
9	I	128	 69%28% • •
10	J	104	 57%32%6%6%
11	K	128	 48%42%5% •
12	L	131	 77%17%6%
13	M	125	 42%30% • 26%
14	N	60	 57%30%13%
15	O	88	 63%30%8%
16	P	88	 58%36%6%
17	Q	104	 67%25%8%
18	R	87	 51%33%10%6%
19	S	92	 61%24% • 13%
20	T	105	 44%41%10%6%
21	U	26	 50%27%15%8%

2 Entry composition [i](#)

There are 24 unique types of molecules in this entry. The entry contains 45618 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1514	Total	C	N	O	P	0	0	0
			32534	14482	6022	10517	1513			

- Molecule 2 is a protein called 30S RIBOSOMAL PROTEIN S2.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	249	Total	C	N	O	0	0	0
			1229	731	249	249			

- Molecule 3 is a protein called 30S RIBOSOMAL PROTEIN S3.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	206	Total	C	N	O	0	0	0
			1009	597	206	206			

- Molecule 4 is a protein called 30S RIBOSOMAL PROTEIN S4.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	D	208	Total	C	N	O	0	0	0
			1022	606	208	208			

- Molecule 5 is a protein called 30S RIBOSOMAL PROTEIN S5.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
5	E	156	Total	C	N	O	0	0	0
			763	451	156	156			

- Molecule 6 is a protein called 30S RIBOSOMAL PROTEIN S6.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
6	F	101	Total	C	N	O	0	0	0
			502	300	101	101			

- Molecule 7 is a protein called 30S RIBOSOMAL PROTEIN S7.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
7	G	155	Total	C	N	O	0	0	0
			767	457	155	155			

- Molecule 8 is a protein called 30S RIBOSOMAL PROTEIN S8.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
8	H	138	Total	C	N	O	0	0	0
			677	401	138	138			

- Molecule 9 is a protein called 30S RIBOSOMAL PROTEIN S9.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
9	I	127	Total	C	N	O	0	0	0
			621	367	127	127			

- Molecule 10 is a protein called 30S RIBOSOMAL PROTEIN S10.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
10	J	98	Total	C	N	O	0	0	0
			485	289	98	98			

- Molecule 11 is a protein called 30S RIBOSOMAL PROTEIN S11.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
11	K	123	Total	C	N	O	0	0	0
			602	356	123	123			

- Molecule 12 is a protein called 30S RIBOSOMAL PROTEIN S12.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
12	L	131	Total	C	N	O	0	0	0
			643	381	131	131			

- Molecule 13 is a protein called 30S RIBOSOMAL PROTEIN S13.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
13	M	93	Total	C	N	O	0	0	0
			458	272	93	93			

- Molecule 14 is a protein called 30S RIBOSOMAL PROTEIN S14.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
14	N	60	Total	C	N	O	0	0	0
			296	176	60	60			

- Molecule 15 is a protein called 30S RIBOSOMAL PROTEIN S15.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
15	O	88	Total	C	N	O	0	0	0
			434	258	88	88			

- Molecule 16 is a protein called 30S RIBOSOMAL PROTEIN S16.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
16	P	88	Total	C	N	O	0	0	0
			434	258	88	88			

- Molecule 17 is a protein called 30S RIBOSOMAL PROTEIN S17.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
17	Q	104	Total	C	N	O	0	0	0
			514	306	104	104			

- Molecule 18 is a protein called 30S RIBOSOMAL PROTEIN S18.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
18	R	82	Total	C	N	O	0	0	0
			405	241	82	82			

- Molecule 19 is a protein called 30S RIBOSOMAL PROTEIN S19.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
19	S	80	Total	C	N	O	0	0	0
			394	234	80	80			

- Molecule 20 is a protein called 30S RIBOSOMAL PROTEIN S20.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
20	T	99	Total	C	N	O	0	0	0
			489	291	99	99			

- Molecule 21 is a protein called 30S RIBOSOMAL PROTEIN THX.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
21	U	24	Total	C	N	O	0	0	0
			115	67	24	24			

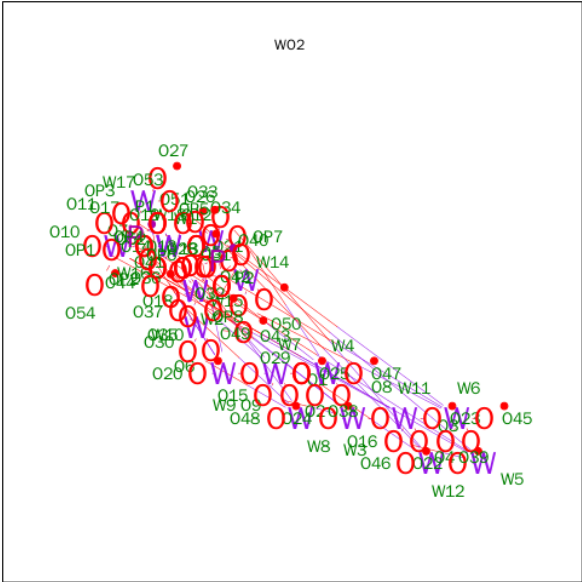
- Molecule 22 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
22	P	1	Total	Mg	0	0
			1	1		
22	G	1	Total	Mg	0	0
			1	1		
22	J	1	Total	Mg	0	0
			1	1		
22	Q	2	Total	Mg	0	0
			2	2		
22	D	2	Total	Mg	0	0
			2	2		
22	K	1	Total	Mg	0	0
			1	1		
22	E	1	Total	Mg	0	0
			1	1		
22	A	60	Total	Mg	0	0
			60	60		
22	T	3	Total	Mg	0	0
			3	3		
22	L	3	Total	Mg	0	0
			3	3		

- Molecule 23 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 24 is OCTADECATUNGSTENYL DIPHOSPHATE (three-letter code: WO2) (formula: O₆₂P₂W₁₈).



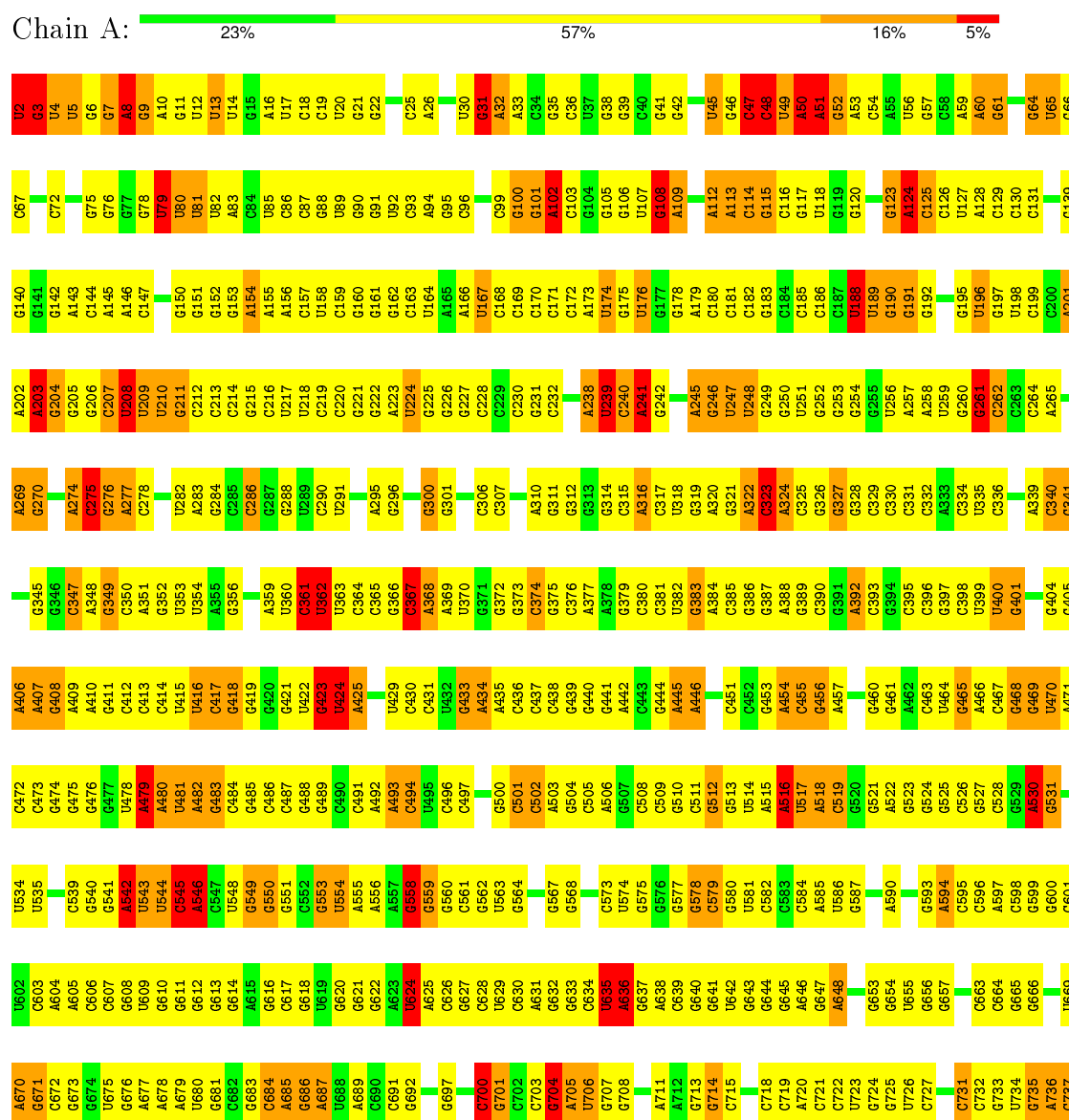
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
24	B	1	Total	O	P	W	0	0
			82	62	2	18		
24	B	1	Total	O	P	W	0	0
			82	62	2	18		
24	C	1	Total	O	P	W	0	0
			82	62	2	18		
24	B	1	Total	O	P	W	0	0
			82	62	2	18		
24	E	1	Total	O	P	W	0	0
			82	62	2	18		
24	G	1	Total	O	P	W	0	0
			82	62	2	18		
24	G	1	Total	O	P	W	0	0
			82	62	2	18		
24	R	1	Total	O	P	W	0	0
			82	62	2	18		
24	J	1	Total	O	P	W	0	0
			82	62	2	18		
24	H	1	Total	O	P	W	0	0
			82	62	2	18		
24	A	1	Total	O	P	W	0	0
			82	62	2	18		
24	D	1	Total	O	P	W	0	0
			82	62	2	18		
24	T	1	Total	O	P	W	0	0
			82	62	2	18		
24	K	1	Total	O	P	W	0	0
			82	62	2	18		

3 Residue-property plots

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

Note EDS was not executed.

• Molecule 1: 16S rRNA



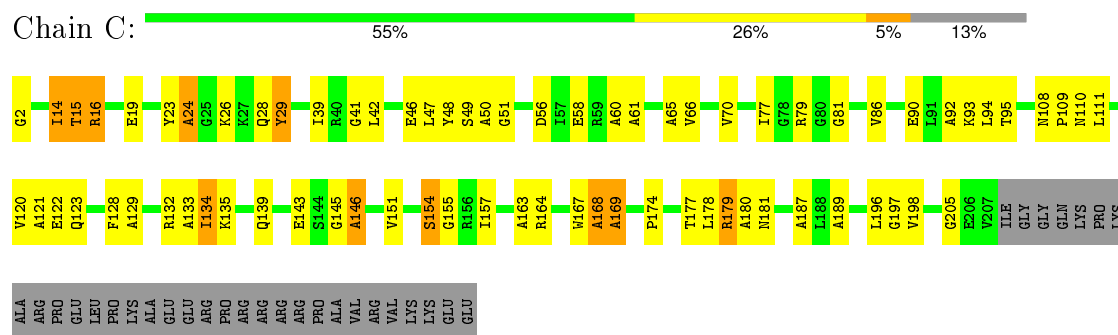
A1470	C1471	C1472	C1473	C1474	C1475	C1476	C1477	C1478	C1479	A1480	C1481	C1482	C1483	C1484	C1485	C1486	C1487	C1488	C1489	C1490	C1491	C1492	C1493	C1494	C1495	C1496	C1497	C1498	C1499	C1500	C1501	C1502	C1503	C1504	C1505	C1506	C1507	C1508	C1509	C1510	C1511	C1512	C1513	C1514	C1515																																																																																																																																																																																																																																																																																																																																											
U1407	C1408	C1409	C1410	C1411	C1412	C1413	C1414	C1415	C1416	C1417	C1418	C1419	C1420	C1421	C1422	C1423	C1424	C1425	C1426	C1427	C1428	C1429	C1430	C1431	C1432	C1433	C1434	C1435	C1436	C1437	C1438	C1439	C1440	C1441	C1442	C1443	C1444	C1445	C1446	C1447	C1448	C1449	C1450	C1451	C1452	C1453	C1454	C1455																																																																																																																																																																																																																																																																																																																																								
G1342	C1343	C1344	C1345	C1346	C1347	C1348	C1349	C1350	C1351	C1352	C1353	C1354	C1355	C1356	C1357	C1358	C1359	C1360	C1361	C1362	C1363	C1364	C1365	C1366	C1367	C1368	C1369	C1370	C1371	C1372	C1373	C1374	C1375	C1376	C1377	C1378	C1379	C1380	C1381	C1382	C1383	C1384	C1385	C1386	C1387	C1388	C1389	C1390	C1391	C1392	C1393	C1394	C1395	C1396	C1397	C1398	C1399	C1400	C1401	C1402	C1403	C1404	C1405	C1406	C1407	C1408	C1409	C1410	C1411	C1412	C1413	C1414	C1415	C1416	C1417	C1418	C1419	C1420	C1421	C1422	C1423	C1424	C1425	C1426	C1427	C1428	C1429	C1430	C1431	C1432	C1433	C1434	C1435	C1436	C1437	C1438	C1439	C1440	C1441	C1442	C1443	C1444	C1445	C1446	C1447	C1448	C1449	C1450	C1451	C1452	C1453	C1454	C1455																																																																																																																																																																																																																																																																							
G1276	C1277	C1278	C1279	C1280	C1281	C1282	C1283	C1284	C1285	C1286	C1287	C1288	C1289	C1290	C1291	C1292	C1293	C1294	C1295	C1296	C1297	C1298	C1299	C1300	C1301	C1302	C1303	C1304	C1305	C1306	C1307	C1308	C1309	C1310	C1311	C1312	C1313	C1314	C1315	C1316	C1317	C1318	C1319	C1320	C1321	C1322	C1323	C1324	C1325	C1326	C1327	C1328	C1329	C1330	C1331	C1332	C1333	C1334	C1335	C1336	C1337	C1338	C1339	C1340	C1341	C1342	C1343	C1344	C1345	C1346	C1347	C1348	C1349	C1350	C1351	C1352	C1353	C1354	C1355	C1356	C1357	C1358	C1359	C1360	C1361	C1362	C1363	C1364	C1365	C1366	C1367	C1368	C1369	C1370	C1371	C1372	C1373	C1374	C1375	C1376	C1377	C1378	C1379	C1380	C1381	C1382	C1383	C1384	C1385	C1386	C1387	C1388	C1389	C1390	C1391	C1392	C1393	C1394	C1395	C1396	C1397	C1398	C1399	C1400	C1401	C1402	C1403	C1404	C1405	C1406	C1407	C1408	C1409	C1410	C1411	C1412	C1413	C1414	C1415	C1416	C1417	C1418	C1419	C1420	C1421	C1422	C1423	C1424	C1425	C1426	C1427	C1428	C1429	C1430	C1431	C1432	C1433	C1434	C1435	C1436	C1437	C1438	C1439	C1440	C1441	C1442	C1443	C1444	C1445	C1446	C1447	C1448	C1449	C1450	C1451	C1452	C1453	C1454	C1455																																																																																																																																																																																																					
C1209	C1210	C1211	C1212	C1213	C1214	C1215	C1216	C1217	C1218	C1219	C1220	C1221	C1222	C1223	C1224	C1225	C1226	C1227	C1228	C1229	C1230	C1231	C1232	C1233	C1234	C1235	C1236	C1237	C1238	C1239	C1240	C1241	C1242	C1243	C1244	C1245	C1246	C1247	C1248	C1249	C1250	C1251	C1252	C1253	C1254	C1255	C1256	C1257	C1258	C1259	C1260	C1261	C1262	C1263	C1264	C1265	C1266	C1267	C1268	C1269	C1270	C1271	C1272	C1273	C1274	C1275	C1276	C1277	C1278	C1279	C1280	C1281	C1282	C1283	C1284	C1285	C1286	C1287	C1288	C1289	C1290	C1291	C1292	C1293	C1294	C1295	C1296	C1297	C1298	C1299	C1300	C1301	C1302	C1303	C1304	C1305	C1306	C1307	C1308	C1309	C1310	C1311	C1312	C1313	C1314	C1315	C1316	C1317	C1318	C1319	C1320	C1321	C1322	C1323	C1324	C1325	C1326	C1327	C1328	C1329	C1330	C1331	C1332	C1333	C1334	C1335	C1336	C1337	C1338	C1339	C1340	C1341	C1342	C1343	C1344	C1345	C1346	C1347	C1348	C1349	C1350	C1351	C1352	C1353	C1354	C1355	C1356	C1357	C1358	C1359	C1360	C1361	C1362	C1363	C1364	C1365	C1366	C1367	C1368	C1369	C1370	C1371	C1372	C1373	C1374	C1375	C1376	C1377	C1378	C1379	C1380	C1381	C1382	C1383	C1384	C1385	C1386	C1387	C1388	C1389	C1390	C1391	C1392	C1393	C1394	C1395	C1396	C1397	C1398	C1399	C1400	C1401	C1402	C1403	C1404	C1405	C1406	C1407	C1408	C1409	C1410	C1411	C1412	C1413	C1414	C1415	C1416	C1417	C1418	C1419	C1420	C1421	C1422	C1423	C1424	C1425	C1426	C1427	C1428	C1429	C1430	C1431	C1432	C1433	C1434	C1435	C1436	C1437	C1438	C1439	C1440	C1441	C1442	C1443	C1444	C1445	C1446	C1447	C1448	C1449	C1450	C1451	C1452	C1453	C1454	C1455																																																																																																																																		
C1143	C1144	C1145	C1146	C1147	C1148	C1149	C1150	C1151	C1152	C1153	C1154	C1155	C1156	C1157	C1158	C1159	C1160	C1161	C1162	C1163	C1164	C1165	C1166	C1167	C1168	C1169	C1170	C1171	C1172	C1173	C1174	C1175	C1176	C1177	C1178	C1179	C1180	C1181	C1182	C1183	C1184	C1185	C1186	C1187	C1188	C1189	C1190	C1191	C1192	C1193	C1194	C1195	C1196	C1197	C1198	C1199	C1200	C1201	C1202	C1203	C1204	C1205	C1206	C1207	C1208	C1209	C1210	C1211	C1212	C1213	C1214	C1215	C1216	C1217	C1218	C1219	C1220	C1221	C1222	C1223	C1224	C1225	C1226	C1227	C1228	C1229	C1230	C1231	C1232	C1233	C1234	C1235	C1236	C1237	C1238	C1239	C1240	C1241	C1242	C1243	C1244	C1245	C1246	C1247	C1248	C1249	C1250	C1251	C1252	C1253	C1254	C1255	C1256	C1257	C1258	C1259	C1260	C1261	C1262	C1263	C1264	C1265	C1266	C1267	C1268	C1269	C1270	C1271	C1272	C1273	C1274	C1275	C1276	C1277	C1278	C1279	C1280	C1281	C1282	C1283	C1284	C1285	C1286	C1287	C1288	C1289	C1290	C1291	C1292	C1293	C1294	C1295	C1296	C1297	C1298	C1299	C1300	C1301	C1302	C1303	C1304	C1305	C1306	C1307	C1308	C1309	C1310	C1311	C1312	C1313	C1314	C1315	C1316	C1317	C1318	C1319	C1320	C1321	C1322	C1323	C1324	C1325	C1326	C1327	C1328	C1329	C1330	C1331	C1332	C1333	C1334	C1335	C1336	C1337	C1338	C1339	C1340	C1341	C1342	C1343	C1344	C1345	C1346	C1347	C1348	C1349	C1350	C1351	C1352	C1353	C1354	C1355	C1356	C1357	C1358	C1359	C1360	C1361	C1362	C1363	C1364	C1365	C1366	C1367	C1368	C1369	C1370	C1371	C1372	C1373	C1374	C1375	C1376	C1377	C1378	C1379	C1380	C1381	C1382	C1383	C1384	C1385	C1386	C1387	C1388	C1389	C1390	C1391	C1392	C1393	C1394	C1395	C1396	C1397	C1398	C1399	C1400	C1401	C1402	C1403	C1404	C1405	C1406	C1407	C1408	C1409	C1410	C1411	C1412	C1413	C1414	C1415	C1416	C1417	C1418	C1419	C1420	C1421	C1422	C1423	C1424	C1425	C1426	C1427	C1428	C1429	C1430	C1431	C1432	C1433	C1434	C1435	C1436	C1437	C1438	C1439	C1440	C1441	C1442	C1443	C1444	C1445	C1446	C1447	C1448	C1449	C1450	C1451	C1452	C1453	C1454	C1455																																																																
U1077	C1080	G1081	C1082	C1083	C1084	C1085	C1086	C1087	C1088	C1089	C1090	C1091	C1092	C1093	C1094	C1095	C1096	C1097	C1098	C1099	C1100	C1101	C1102	C1103	C1104	C1105	C1106	C1107	C1108	C1109	C1110	C1111	C1112	C1113	C1114	C1115	C1116	C1117	C1118	C1119	C1120	C1121	C1122	C1123	C1124	C1125	C1126	C1127	C1128	C1129	C1130	C1131	C1132	C1133	C1134	C1135	C1136	C1137	C1138	C1139	C1140	C1141	C1142	C1143	C1144	C1145	C1146	C1147	C1148	C1149	C1150	C1151	C1152	C1153	C1154	C1155	C1156	C1157	C1158	C1159	C1160	C1161	C1162	C1163	C1164	C1165	C1166	C1167	C1168	C1169	C1170	C1171	C1172	C1173	C1174	C1175	C1176	C1177	C1178	C1179	C1180	C1181	C1182	C1183	C1184	C1185	C1186	C1187	C1188	C1189	C1190	C1191	C1192	C1193	C1194	C1195	C1196	C1197	C1198	C1199	C1200	C1201	C1202	C1203	C1204	C1205	C1206	C1207	C1208	C1209	C1210	C1211	C1212	C1213	C1214	C1215	C1216	C1217	C1218	C1219	C1220	C1221	C1222	C1223	C1224	C1225	C1226	C1227	C1228	C1229	C1230	C1231	C1232	C1233	C1234	C1235	C1236	C1237	C1238	C1239	C1240	C1241	C1242	C1243	C1244	C1245	C1246	C1247	C1248	C1249	C1250	C1251	C1252	C1253	C1254	C1255	C1256	C1257	C1258	C1259	C1260	C1261	C1262	C1263	C1264	C1265	C1266	C1267	C1268	C1269	C1270	C1271	C1272	C1273	C1274	C1275	C1276	C1277	C1278	C1279	C1280	C1281	C1282	C1283	C1284	C1285	C1286	C1287	C1288	C1289	C1290	C1291	C1292	C1293	C1294	C1295	C1296	C1297	C1298	C1299	C1300	C1301	C1302	C1303	C1304	C1305	C1306	C1307	C1308	C1309	C1310	C1311	C1312	C1313	C1314	C1315	C1316	C1317	C1318	C1319	C1320	C1321	C1322	C1323	C1324	C1325	C1326	C1327	C1328	C1329	C1330	C1331	C1332	C1333	C1334	C1335	C1336	C1337	C1338	C1339	C1340	C1341	C1342	C1343	C1344	C1345	C1346	C1347	C1348	C1349	C1350	C1351	C1352	C1353	C1354	C1355	C1356	C1357	C1358	C1359	C1360	C1361	C1362	C1363	C1364	C1365	C1366	C1367	C1368	C1369	C1370	C1371	C1372	C1373	C1374	C1375	C1376	C1377	C1378	C1379	C1380	C1381	C1382	C1383	C1384	C1385	C1386	C1387	C1388	C1389	C1390	C1391	C1392	C1393	C1394	C1395	C1396	C1397	C1398	C1399	C1400	C1401	C1402	C1403	C1404	C1405	C1406	C1407	C1408	C1409	C1410	C1411	C1412	C1413	C1414	C1415	C1416	C1417	C1418	C1419	C1420	C1421	C1422	C1423	C1424	C1425	C1426	C1427	C1428	C1429	C1430	C1431	C1432	C1433	C1434	C1435	C1436	C1437	C1438	C1439	C1440	C1441	C1442	C1443	C1444	C1445	C1446	C1447	C1448	C1449	C1450	C1451	C1452	C1453	C1454	C1455
A877	A878	A879	A880	A881	A882	A883	A884	A885	A886	A887	A888	A889	A890	A891	A892	A893	A894	A895	A896	A897	A898	A899	A900	A901	A902	A903	A904	A905	A906	A907	A908	A909	A910	A911	A912	A913	A914	A915	A916	A917	A918	A919	A920	A921	A922	A923	A924	A925	A926	A927	A928																																																																																																																																																																																																																																																																																																																																					

• Molecule 2: 30S RIBOSOMAL PROTEIN S2

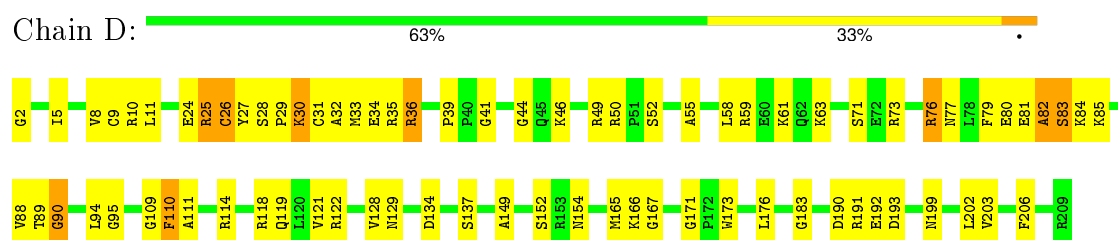
Chain B:  62% 29% 7%

P2	P3	P4	P5	P6	P7	P8	P9	P10	P11	P12	P13	P14	P15	P16	P17	P18	P19	P20	P21	P22	P23	P24	P25	P26	P27	P28	P29	P30	P31	P32	P33	P34	P35	P36	P37	P38	P39	P40	P41	P42	P43	P44	P45	P46	P47	P48	P49	P50	P51	P52	P53	P54	P55	P56	P57	P58	P59	P60	P61	P62	P63	P64	P65	P66	P67	P68	P69	P70	P71	P72	P73	P74	P75	P76	P77	P78	P79	P80	P81	P82	P83	P84	P85	P86	P87	P88	P89	P90	P91	P92	P93	P94	P95	P96	P97	P98	P99	P100																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
L102	L103	L104	L105	L106	L107	L108	L109	L110	L111	L112	L113	L114	L115	L116	L117	L118	L119	L120	L121	L122	L123	L124	L125	L126	L127	L128	L129	L130	L131	L132	L133	L134	L135	L136	L137	L138	L139	L140	L141	L142	L143	L144	L145	L146	L147	L148	L149	L150	L151	L152	L153	L154	L155	L156	L157	L158	L159	L160	L161	L162	L163	L164	L165	L166	L167	L168	L169	L170	L171	L172	L173	L174	L175	L176	L177	L178	L179	L180	L181	L182	L183	L184	L185	L186	L187	L188	L189	L190	L191	L192	L193	L194	L195	L196	L197	L198	L199	L200	L201	L202	L203	L204	L205	L206	L207	L208	L209	L210	L211	L212	L213	L214	L215	L216	L217	L218	L219	L220	L221	L222	L223	L224	L225	L226	L227	L228	L229	L230	L231	L232	L233	L234	L235	L236	L237	L238	L239	L240	L241	L242	L243	L244	L245	L246	L247	L248	L249	L250	L251	L252	L253	L254	L255	L256	L257	L258	L259	L260	L261	L262	L263	L264	L265	L266	L267	L268	L269	L270	L271	L272	L273	L274	L275	L276	L277	L278	L279	L280	L281	L282	L283	L284	L285	L286	L287	L288	L289	L290	L291	L292	L293	L294	L295	L296	L297	L298	L299	L300																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
R226	R227	R228	R229	R230	R231	R232	R233	R234	R235	R236	R237	R238	R239	R240	R241	R242	R243	R244	R245	R246	R247	R248	R249	R250	R251	R252	R253	R254	R255	R256	R257	R258	R259	R260	R261	R262	R263	R264	R265	R266	R267	R268	R269	R270	R271	R272	R273	R274	R275	R276	R277	R278	R279	R280	R281	R282	R283	R284	R285	R286	R287	R288	R289	R290	R291	R292	R293	R294	R295	R296	R297	R298	R299	R300																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																												
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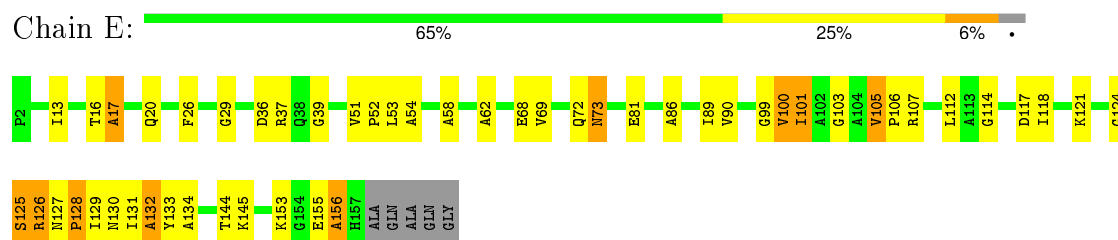
- Molecule 3: 30S RIBOSOMAL PROTEIN S3



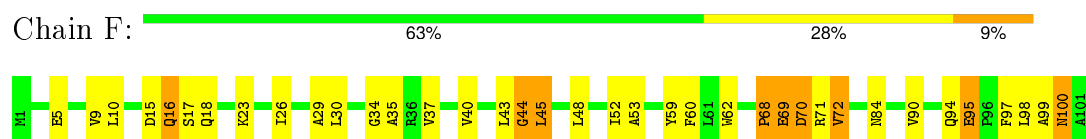
- Molecule 4: 30S RIBOSOMAL PROTEIN S4



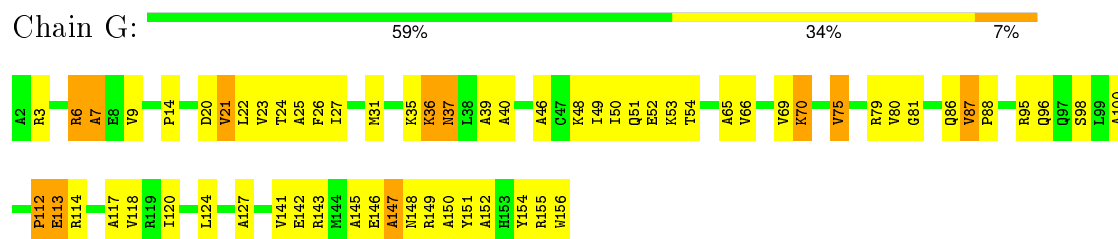
• Molecule 5: 30S RIBOSOMAL PROTEIN S5



- Molecule 6: 30S RIBOSOMAL PROTEIN S6

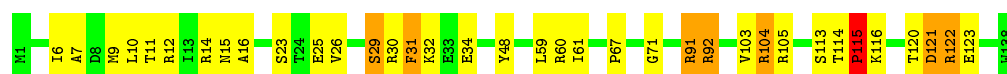


- Molecule 7: 30S RIBOSOMAL PROTEIN S7

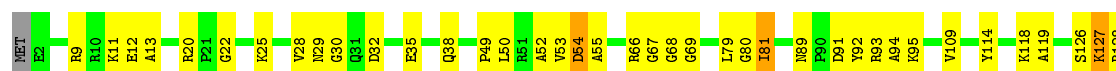


- Molecule 8: 30S RIBOSOMAL PROTEIN S8





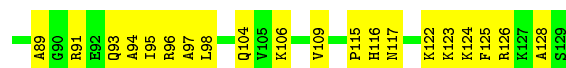
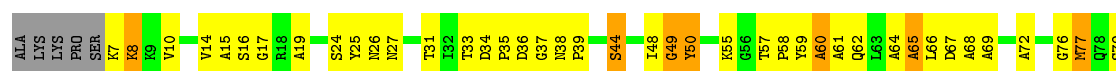
• Molecule 9: 30S RIBOSOMAL PROTEIN S9



• Molecule 10: 30S RIBOSOMAL PROTEIN S10



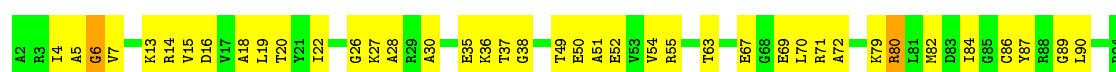
• Molecule 11: 30S RIBOSOMAL PROTEIN S11



• Molecule 12: 30S RIBOSOMAL PROTEIN S12



• Molecule 13: 30S RIBOSOMAL PROTEIN S13



• Molecule 14: 30S RIBOSOMAL PROTEIN S14



- Molecule 15: 30S RIBOSOMAL PROTEIN S15

Chain O: 



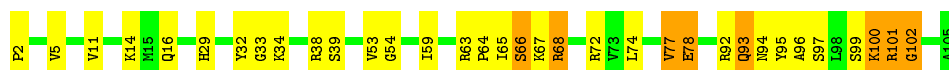
- Molecule 16: 30S RIBOSOMAL PROTEIN S16

Chain P: 



- Molecule 17: 30S RIBOSOMAL PROTEIN S17

Chain Q: 



- Molecule 18: 30S RIBOSOMAL PROTEIN S18

Chain R: 



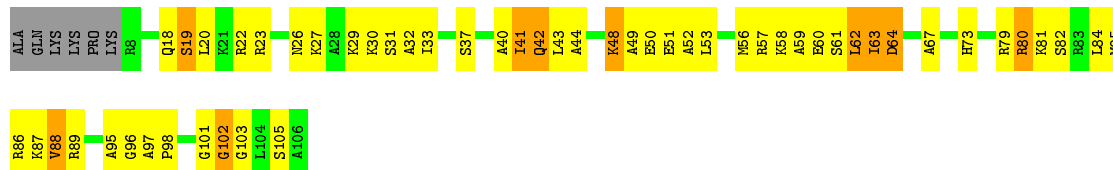
- Molecule 19: 30S RIBOSOMAL PROTEIN S19

Chain S: 



- Molecule 20: 30S RIBOSOMAL PROTEIN S20

Chain T: 



- Molecule 21: 30S RIBOSOMAL PROTEIN THX

Chain U: 



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	406.30 Å 406.30 Å 173.10 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	35.00 – 3.20	Depositor
% Data completeness (in resolution range)	(Not available) (35.00-3.20)	Depositor
R_{merge}	0.01	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 0.9	Depositor
R, R_{free}	0.203 , 0.245	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	45618	wwPDB-VP
Average B, all atoms (Å ²)	81.0	wwPDB-VP

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG, WO2

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.67	4/36417 (0.0%)	0.81	56/56838 (0.1%)
2	B	0.37	0/1228	0.70	1/1708 (0.1%)
3	C	0.41	0/1008	0.66	0/1397
4	D	0.45	0/1021	0.66	0/1417
5	E	0.65	0/762	1.02	0/1055
6	F	0.40	0/501	0.75	0/698
7	G	0.36	0/766	0.68	1/1066 (0.1%)
8	H	0.56	0/676	0.79	1/937 (0.1%)
9	I	0.37	0/620	0.71	0/858
10	J	0.35	0/484	0.68	0/673
11	K	0.44	0/601	0.76	0/832
12	L	0.49	0/642	0.86	0/890
13	M	0.30	0/457	0.69	0/634
14	N	0.40	0/295	0.79	0/409
15	O	0.55	0/433	0.85	0/601
16	P	0.56	0/433	0.85	0/601
17	Q	0.54	0/513	0.89	0/713
18	R	0.42	0/404	0.65	0/561
19	S	0.31	0/393	0.71	0/545
20	T	0.38	0/488	0.65	0/678
21	U	0.43	0/114	0.67	0/155
All	All	0.62	4/48256 (0.0%)	0.80	59/73266 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	67

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	738	G	C5-C6	-6.53	1.35	1.42
1	A	2	U	N1-C2	5.27	1.43	1.38
1	A	952	A	C5-C6	-5.19	1.36	1.41
1	A	1084	A	C5-C6	-5.14	1.36	1.41

All (59) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	47	C	N1-C1'-C2'	9.78	126.71	114.00
1	A	241	A	N9-C1'-C2'	9.41	126.23	114.00
1	A	13	U	N1-C1'-C2'	8.96	125.65	114.00
1	A	362	U	N1-C1'-C2'	8.83	125.48	114.00
1	A	558	G	N9-C1'-C2'	8.24	124.71	114.00
1	A	1481	G	N9-C1'-C2'	7.70	124.01	114.00
1	A	31	G	N9-C1'-C2'	7.67	123.96	114.00
1	A	636	A	N9-C1'-C2'	7.49	123.74	114.00
1	A	1031	U	N1-C1'-C2'	7.43	123.65	114.00
1	A	323	C	N1-C1'-C2'	7.16	123.30	114.00
1	A	1483	U	N1-C1'-C2'	7.11	123.24	114.00
1	A	1303	C	N1-C1'-C2'	6.87	122.93	114.00
1	A	1479	A	N9-C1'-C2'	6.83	122.88	114.00
1	A	624	U	N1-C1'-C2'	6.55	122.52	114.00
1	A	367	C	N1-C1'-C2'	6.41	122.33	114.00
1	A	542	A	N9-C1'-C2'	6.38	122.29	114.00
1	A	558	G	C2'-C3'-O3'	6.37	123.89	113.70
1	A	545	C	N1-C1'-C2'	6.26	122.14	114.00
1	A	1280	A	N9-C1'-C2'	6.21	122.08	114.00
1	A	102	A	N9-C1'-C2'	6.17	122.03	114.00
1	A	1505	U	C2'-C3'-O3'	6.11	123.47	113.70
1	A	937	U	N1-C1'-C2'	6.09	121.92	114.00
1	A	542	A	C2'-C3'-O3'	5.95	123.22	113.70
1	A	188	U	N1-C1'-C2'	5.94	121.72	114.00
1	A	945	A	N9-C1'-C2'	5.93	121.71	114.00
1	A	800	C	N1-C1'-C2'	5.92	121.70	114.00
1	A	798	A	N9-C1'-C2'	5.85	121.60	114.00
1	A	803	U	N1-C1'-C2'	5.84	121.59	114.00
1	A	700	C	C2'-C3'-O3'	5.84	123.04	113.70
1	A	100	G	N9-C1'-C2'	-5.83	105.58	112.00
1	A	361	C	N1-C1'-C2'	5.76	121.49	114.00
1	A	516	A	N9-C1'-C2'	5.64	121.34	114.00
1	A	203	A	N9-C1'-C2'	5.60	121.28	114.00
1	A	1035	G	O4'-C1'-N9	5.58	112.67	108.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	50	A	N9-C1'-C2'	5.55	121.21	114.00
1	A	261	G	O4'-C1'-N9	-5.54	103.77	108.20
1	A	239	U	N1-C1'-C2'	5.51	121.17	114.00
1	A	241	A	C4'-C3'-O3'	-5.50	97.85	109.40
1	A	1362	U	C2'-C3'-O3'	5.50	122.50	113.70
1	A	1279	C	N1-C1'-C2'	5.48	121.13	114.00
1	A	1475	U	N1-C1'-C2'	5.43	121.05	114.00
1	A	801	G	N9-C1'-C2'	5.39	121.01	114.00
7	G	150	ALA	N-CA-C	5.38	125.53	111.00
1	A	51	A	N9-C1'-C2'	5.35	120.95	114.00
8	H	115	PRO	N-CA-CB	5.34	109.71	103.30
1	A	1505	U	N1-C1'-C2'	5.33	120.92	114.00
1	A	1346	U	C2'-C3'-O3'	5.33	122.22	113.70
1	A	530	A	N9-C1'-C2'	5.31	120.90	114.00
1	A	1261	A	N9-C1'-C2'	5.29	120.88	114.00
1	A	300	G	N9-C1'-C2'	5.28	120.86	114.00
1	A	636	A	O4'-C1'-N9	5.20	112.36	108.20
1	A	635	U	N1-C1'-C2'	5.14	120.68	114.00
1	A	13	U	C4'-C3'-O3'	-5.13	98.63	109.40
1	A	286	C	N1-C1'-C2'	-5.11	106.38	112.00
1	A	959	U	N1-C1'-C2'	5.10	120.64	114.00
1	A	108	G	C2'-C3'-O3'	5.09	121.84	113.70
1	A	559	G	O4'-C1'-N9	5.06	112.25	108.20
2	B	2	PRO	N-CA-CB	5.02	109.32	103.30
1	A	479	A	N9-C1'-C2'	5.00	120.50	114.00

There are no chirality outliers.

All (67) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	101	G	Sidechain
1	A	1031	U	Sidechain
1	A	1049	A	Sidechain
1	A	1068	U	Sidechain
1	A	1106	G	Sidechain
1	A	1121	G	Sidechain
1	A	1130	U	Sidechain
1	A	1162	G	Sidechain
1	A	1163	G	Sidechain
1	A	1175	U	Sidechain
1	A	1205	G	Sidechain
1	A	124	A	Sidechain

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Mol	Chain	Res	Type	Group
1	A	1261	A	Sidechain
1	A	1278	C	Sidechain
1	A	1303	C	Sidechain
1	A	1326	U	Sidechain
1	A	1328	G	Sidechain
1	A	1332	U	Sidechain
1	A	1352	G	Sidechain
1	A	1362	U	Sidechain
1	A	1383	G	Sidechain
1	A	1432	C	Sidechain
1	A	1479	A	Sidechain
1	A	1483	U	Sidechain
1	A	1503	G	Sidechain
1	A	174	U	Sidechain
1	A	196	U	Sidechain
1	A	2	U	Sidechain
1	A	208	U	Sidechain
1	A	224	U	Sidechain
1	A	239	U	Sidechain
1	A	241	A	Sidechain
1	A	261	G	Sidechain
1	A	275	C	Sidechain
1	A	3	G	Sidechain
1	A	367	C	Sidechain
1	A	374	C	Sidechain
1	A	400	U	Sidechain
1	A	423	G	Sidechain
1	A	424	U	Sidechain
1	A	45	U	Sidechain
1	A	47	C	Sidechain
1	A	478	U	Sidechain
1	A	48	C	Sidechain
1	A	49	U	Sidechain
1	A	50	A	Sidechain
1	A	51	A	Sidechain
1	A	512	G	Sidechain
1	A	516	A	Sidechain
1	A	546	A	Sidechain
1	A	551	G	Sidechain
1	A	553	G	Sidechain
1	A	554	U	Sidechain
1	A	558	G	Sidechain

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Mol	Chain	Res	Type	Group
1	A	594	A	Sidechain
1	A	704	G	Sidechain
1	A	784	U	Sidechain
1	A	79	U	Sidechain
1	A	8	A	Sidechain
1	A	809	C	Sidechain
1	A	842	A	Sidechain
1	A	847	U	Sidechain
1	A	867	G	Sidechain
1	A	877	A	Sidechain
1	A	896	A	Sidechain
1	A	897	U	Sidechain
1	A	970	G	Sidechain

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	A	32534	0	16424	1447	1
2	B	1229	0	560	61	0
3	C	1009	0	502	47	0
4	D	1022	0	452	50	0
5	E	763	0	377	52	0
6	F	502	0	226	24	0
7	G	767	0	374	48	0
8	H	677	0	299	26	0
9	I	621	0	307	28	0
10	J	485	0	209	21	0
11	K	602	0	300	57	0
12	L	643	0	299	20	0
13	M	458	0	223	24	0
14	N	296	0	142	23	0
15	O	434	0	188	27	0
16	P	434	0	204	22	0
17	Q	514	0	219	22	0
18	R	405	0	179	28	0
19	S	394	0	171	12	0
20	T	489	0	253	32	2

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
21	U	115	0	51	15	0
22	A	60	0	0	0	0
22	D	2	0	0	0	0
22	E	1	0	0	0	0
22	G	1	0	0	0	0
22	J	1	0	0	0	0
22	K	1	0	0	0	0
22	L	3	0	0	0	0
22	P	1	0	0	0	0
22	Q	2	0	0	0	0
22	T	3	0	0	0	0
23	D	1	0	0	0	0
23	N	1	0	0	0	0
24	A	82	0	0	0	0
24	B	246	0	0	4	0
24	C	82	0	0	1	0
24	D	82	0	0	0	0
24	E	82	0	0	9	1
24	G	164	0	0	5	0
24	H	82	0	0	0	0
24	J	82	0	0	3	0
24	K	82	0	0	5	2
24	R	82	0	0	4	0
24	T	82	0	0	0	0
All	All	45618	0	21959	2034	3

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 30.

All (2034) 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)
18:R:45:SER:CB	24:R:1008:WO2:O52	1.72	1.38
7:G:148:ASN:CB	24:G:1006:WO2:O51	1.97	1.11
1:A:530:A:H4'	1:A:531:G:O5'	1.49	1.10
2:B:75:LYS:CB	24:B:1004:WO2:O26	2.01	1.09
1:A:424:U:O2'	1:A:425:A:H5''	1.53	1.06
1:A:238:A:H4'	1:A:239:U:C5'	1.89	1.03
1:A:849:A:O2'	1:A:850:A:H3'	1.57	1.02
5:E:153:LYS:O	24:E:1005:WO2:O49	1.76	1.02
1:A:1494:G:H5'	1:A:1494:G:H8	1.20	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1098:C:H2'	1:A:1099:G:H5''	1.43	0.97
1:A:100:G:H2'	1:A:101:G:H5'	1.45	0.97
11:K:8:LYS:N	24:K:1014:WO2:O44	1.97	0.97
1:A:923:A:H2'	1:A:924:G:H8	1.29	0.96
1:A:1139:A:H1'	1:A:1162:G:N2	1.80	0.96
11:K:44:SER:O	11:K:64:ALA:HB2	1.67	0.95
1:A:1286:G:H22	1:A:1312:G:H2'	1.30	0.95
1:A:1417:G:H2'	1:A:1418:U:C6	2.02	0.94
7:G:151:TYR:CB	24:G:1006:WO2:O48	2.16	0.93
11:K:8:LYS:CB	24:K:1014:WO2:O14	2.16	0.92
1:A:251:U:H2'	1:A:252:G:H8	1.35	0.92
16:P:2:VAL:O	16:P:64:ALA:HA	1.69	0.91
1:A:1388:U:H2'	1:A:1389:C:C6	2.05	0.91
1:A:1286:G:N2	1:A:1312:G:H2'	1.84	0.91
1:A:238:A:H4'	1:A:239:U:O5'	1.69	0.91
1:A:923:A:H2'	1:A:924:G:C8	2.05	0.91
1:A:3:G:N7	1:A:595:C:H1'	1.85	0.91
4:D:25:ARG:O	4:D:27:TYR:N	2.04	0.90
1:A:670:A:H4'	1:A:671:G:O5'	1.69	0.90
1:A:1176:C:H3'	1:A:1177:U:H5'	1.52	0.90
1:A:442:A:H62	1:A:470:U:H3	0.94	0.90
1:A:143:A:H2'	1:A:144:C:H6	1.35	0.89
1:A:501:C:H3'	1:A:513:G:H8	1.38	0.88
1:A:368:A:H1'	1:A:465:G:N3	1.88	0.88
5:E:153:LYS:C	24:E:1005:WO2:O49	2.12	0.87
1:A:1267:A:H3'	1:A:1268:A:H5''	1.57	0.87
1:A:899:G:H4'	5:E:20:GLN:HA	1.53	0.87
1:A:1141:U:H5'	1:A:1142:G:OP1	1.74	0.87
1:A:1494:G:H5'	1:A:1494:G:C8	2.09	0.86
1:A:251:U:H2'	1:A:252:G:C8	2.10	0.86
1:A:274:A:H5''	1:A:275:C:H3'	1.57	0.86
1:A:92:U:H2'	1:A:93:C:C6	2.10	0.86
1:A:1046:G:H4'	1:A:1047:U:C5'	2.06	0.86
1:A:100:G:C2'	1:A:101:G:H5'	2.06	0.86
1:A:800:C:H1'	1:A:802:A:H5'	1.57	0.85
1:A:1083:A:H4'	1:A:1084:A:O5'	1.75	0.85
1:A:433:G:H4'	1:A:434:A:OP1	1.74	0.85
1:A:648:A:H2'	1:A:708:G:N2	1.90	0.85
4:D:25:ARG:C	4:D:27:TYR:H	1.78	0.85
1:A:353:U:H2'	1:A:354:U:C6	2.12	0.85
2:B:75:LYS:N	24:B:1004:WO2:O26	2.09	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:190:G:H4'	1:A:191:G:OP2	1.78	0.84
11:K:27:ASN:HA	11:K:55:LYS:O	1.77	0.84
1:A:94:A:O2'	1:A:95:G:H5'	1.78	0.84
1:A:1419:C:H42	1:A:1441:G:H1	1.23	0.84
6:F:45:LEU:H	6:F:59:TYR:HA	1.41	0.84
1:A:1303:C:O2'	1:A:1304:G:H5'	1.78	0.83
16:P:37:GLY:HA3	16:P:50:LYS:O	1.77	0.83
5:E:125:SER:O	5:E:127:ASN:N	2.11	0.83
1:A:392:A:H5'	1:A:393:C:OP1	1.77	0.83
1:A:482:A:O2'	1:A:483:G:C8	2.31	0.83
1:A:1381:C:H4'	1:A:1382:C:O5'	1.77	0.83
1:A:1218:C:H3'	1:A:1219:A:H5'	1.60	0.82
1:A:175:G:O2'	1:A:176:U:H5'	1.79	0.82
15:O:2:PRO:O	15:O:3:ILE:O	1.98	0.82
1:A:400:U:H3'	1:A:401:G:H5'	1.61	0.81
1:A:143:A:H2'	1:A:144:C:C6	2.14	0.81
1:A:801:G:HO2'	1:A:803:U:H5	1.29	0.81
1:A:217:U:H2'	1:A:218:U:C6	2.14	0.81
1:A:726:U:H2'	1:A:727:C:C6	2.15	0.81
1:A:453:G:H3'	1:A:454:A:H5''	1.63	0.80
1:A:1046:G:O2'	1:A:1171:G:N2	2.13	0.80
1:A:1068:U:H3	1:A:1081:G:H22	1.30	0.80
1:A:1312:G:HO2'	1:A:1313:A:H8	1.28	0.80
1:A:500:G:C6	1:A:514:U:H1'	2.17	0.80
1:A:1046:G:H4'	1:A:1047:U:H5''	1.63	0.80
1:A:1465:G:H2'	1:A:1466:G:C8	2.17	0.79
1:A:105:G:H4'	1:A:384:A:H5''	1.63	0.79
7:G:152:ALA:HB1	11:K:89:ALA:HB1	1.65	0.79
1:A:1384:C:H2'	1:A:1385:C:C6	2.18	0.78
1:A:372:G:O2'	1:A:373:G:H5'	1.83	0.78
1:A:1328:G:N2	1:A:1355:G:H2'	1.98	0.78
5:E:90:VAL:O	5:E:121:LYS:N	2.14	0.78
1:A:1404:G:H2'	1:A:1405:G:C8	2.19	0.78
1:A:1267:A:C3'	1:A:1268:A:H5''	2.12	0.78
1:A:731:C:OP2	1:A:731:C:H6	1.66	0.77
1:A:995:G:H2'	1:A:996:C:C6	2.19	0.77
1:A:2:U:H4'	1:A:3:G:N2	1.98	0.77
1:A:1176:C:H3'	1:A:1177:U:C5'	2.14	0.77
1:A:721:C:H2'	1:A:722:C:H6	1.50	0.77
1:A:578:G:H2'	1:A:624:U:O4	1.85	0.77
5:E:51:VAL:O	5:E:54:ALA:HB3	1.83	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1115:G:H2'	1:A:1116:G:H8	1.50	0.77
1:A:264:C:H2'	1:A:265:A:H8	1.51	0.76
1:A:801:G:O2'	1:A:803:U:H5	1.67	0.76
1:A:777:A:H2'	1:A:778:C:H6	1.48	0.76
1:A:389:G:H2'	1:A:390:C:H6	1.50	0.76
1:A:775:A:O2'	1:A:776:U:H5'	1.86	0.76
5:E:90:VAL:CB	5:E:121:LYS:CB	2.63	0.76
2:B:82:ARG:O	2:B:85:ALA:HB3	1.86	0.76
4:D:32:ALA:C	4:D:34:GLU:H	1.88	0.76
1:A:647:G:H22	1:A:724:G:H1	1.34	0.76
1:A:1270:A:H2'	1:A:1271:G:H5'	1.67	0.76
1:A:353:U:H2'	1:A:354:U:H6	1.48	0.76
1:A:217:U:H2'	1:A:218:U:H6	1.51	0.75
1:A:60:A:H4'	1:A:61:G:O5'	1.86	0.75
1:A:1199:C:H2'	1:A:1200:U:C6	2.21	0.75
1:A:574:U:H2'	1:A:575:G:H8	1.52	0.75
1:A:1220:A:H1'	1:A:1222:G:C4	2.20	0.75
1:A:867:G:HO2'	1:A:883:G:H1	1.34	0.74
1:A:505:C:H2'	1:A:506:A:H5'	1.67	0.74
11:K:15:ALA:C	11:K:77:MET:HA	2.06	0.74
1:A:830:G:O2'	1:A:831:G:H5'	1.88	0.74
1:A:185:C:H2'	1:A:186:C:C6	2.22	0.74
1:A:445:A:H2	1:A:464:U:C4	2.05	0.74
1:A:1465:G:H2'	1:A:1466:G:H8	1.50	0.74
1:A:1098:C:C2'	1:A:1099:G:H5''	2.17	0.74
1:A:56:U:H2'	1:A:57:G:H8	1.53	0.74
1:A:549:G:H4'	1:A:550:G:OP1	1.87	0.74
21:U:2:GLY:O	21:U:4:GLY:N	2.20	0.74
1:A:1450:A:H2'	1:A:1451:G:C8	2.22	0.74
1:A:1506:G:H4'	1:A:1507:G:OP2	1.86	0.73
1:A:1450:A:H2'	1:A:1451:G:H8	1.53	0.73
1:A:892:A:H2'	1:A:893:G:H5'	1.68	0.73
1:A:562:G:H5'	1:A:711:A:H1'	1.69	0.73
1:A:904:G:H4'	1:A:1480:A:N7	2.01	0.73
1:A:700:C:O2'	1:A:701:G:OP2	2.05	0.73
1:A:275:C:H4'	1:A:276:G:OP2	1.86	0.73
1:A:1374:G:O2'	1:A:1479:A:H5''	1.88	0.73
7:G:52:GLU:O	7:G:54:THR:N	2.22	0.73
5:E:130:ASN:O	5:E:134:ALA:HB2	1.88	0.73
1:A:3:G:N3	1:A:3:G:H3'	2.03	0.73
7:G:147:ALA:O	24:G:1006:WO2:O51	2.06	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:I:12:GLU:O	9:I:67:GLY:O	2.06	0.73
1:A:429:U:H2'	1:A:430:C:C6	2.24	0.73
1:A:315:C:H2'	1:A:316:A:C8	2.23	0.73
1:A:1221:U:H4'	1:A:1222:G:OP2	1.88	0.73
11:K:15:ALA:O	11:K:77:MET:HA	1.89	0.73
17:Q:5:VAL:HA	17:Q:59:ILE:O	1.89	0.73
1:A:3:G:C8	1:A:595:C:H1'	2.23	0.72
1:A:1200:U:H2'	1:A:1201:G:H8	1.52	0.72
1:A:515:A:H2'	1:A:516:A:H5'	1.71	0.72
1:A:1200:U:H2'	1:A:1201:G:C8	2.25	0.72
17:Q:95:TYR:O	17:Q:97:SER:N	2.22	0.72
9:I:13:ALA:HA	9:I:67:GLY:O	1.89	0.72
1:A:543:U:H5''	1:A:544:U:O5'	1.90	0.72
1:A:400:U:H5''	1:A:401:G:O4'	1.90	0.72
1:A:994:A:H2'	1:A:995:G:O4'	1.88	0.72
1:A:777:A:H2'	1:A:778:C:C6	2.24	0.72
12:L:105:TYR:O	12:L:107:ALA:N	2.22	0.72
1:A:1244:C:H2'	1:A:1245:C:C6	2.24	0.71
1:A:264:C:H2'	1:A:265:A:C8	2.25	0.71
4:D:82:ALA:O	4:D:84:LYS:N	2.23	0.71
1:A:295:A:H1'	1:A:548:U:O2	1.90	0.71
2:B:105:PHE:O	2:B:107:THR:N	2.23	0.71
1:A:442:A:N6	1:A:470:U:H3	1.80	0.71
5:E:155:GLU:CB	24:E:1005:WO2:O48	2.39	0.71
1:A:1283:U:O2'	1:A:1284:C:OP1	2.09	0.71
1:A:869:A:O2'	1:A:1397:G:H4'	1.91	0.71
1:A:381:C:O2'	1:A:382:U:H5'	1.89	0.71
1:A:3:G:O6	1:A:594:A:N3	2.24	0.71
1:A:445:A:H2	1:A:464:U:C5	2.09	0.71
4:D:121:VAL:O	4:D:134:ASP:HA	1.90	0.70
1:A:1499:U:O2'	1:A:1500:G:H5'	1.91	0.70
1:A:1384:C:O2	1:A:1477:A:N1	2.23	0.70
13:M:79:LYS:O	13:M:82:MET:N	2.23	0.70
15:O:3:ILE:O	15:O:4:THR:CB	2.37	0.70
18:R:47:THR:C	18:R:49:LYS:H	1.91	0.70
1:A:1479:A:H2	1:A:1482:G:H22	1.40	0.70
1:A:484:C:H2'	1:A:485:G:H8	1.55	0.70
7:G:79:ARG:C	7:G:81:GLY:H	1.94	0.70
1:A:640:G:O2'	1:A:641:G:H5'	1.91	0.70
1:A:669:U:O4	1:A:686:G:N3	2.24	0.69
20:T:19:SER:O	20:T:22:ARG:N	2.24	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:92:U:H2'	1:A:93:C:H6	1.58	0.69
1:A:1190:C:O2'	1:A:1191:C:H5'	1.92	0.69
16:P:7:ALA:O	16:P:17:TYR:HA	1.91	0.69
1:A:952:A:O2'	1:A:953:G:OP2	2.10	0.69
12:L:9:GLN:O	12:L:12:ARG:O	2.10	0.69
1:A:981:G:C2	1:A:982:A:H1'	2.27	0.69
1:A:1040:G:H2'	1:A:1041:C:C6	2.28	0.69
1:A:454:A:O2'	1:A:455:C:H5''	1.93	0.69
1:A:721:C:H2'	1:A:722:C:C6	2.28	0.69
16:P:9:PHE:O	16:P:10:GLY:O	2.09	0.69
1:A:314:G:O2'	1:A:315:C:H5'	1.93	0.69
1:A:35:G:H21	12:L:118:SER:CB	2.06	0.69
14:N:23:ARG:HA	14:N:30:ALA:HB2	1.74	0.69
1:A:1042:C:O2'	1:A:1043:G:H5'	1.92	0.69
18:R:37:VAL:O	18:R:39:VAL:N	2.26	0.69
1:A:1312:G:O2'	1:A:1313:A:H8	1.76	0.69
1:A:238:A:H4'	1:A:239:U:H5'	1.73	0.68
1:A:2:U:H4'	1:A:3:G:H22	1.54	0.68
1:A:1013:G:H2'	1:A:1014:G:H8	1.58	0.68
1:A:1114:C:H2'	1:A:1115:G:C8	2.29	0.68
9:I:118:LYS:O	9:I:119:ALA:HB3	1.92	0.68
1:A:752:G:H4'	1:A:1490:A:H4'	1.75	0.68
16:P:27:LYS:O	16:P:29:ASP:N	2.25	0.68
6:F:9:VAL:HA	6:F:59:TYR:O	1.92	0.68
1:A:327:G:H2'	1:A:328:G:H8	1.58	0.68
1:A:1012:A:H2'	1:A:1013:G:H5'	1.75	0.68
1:A:486:C:O2'	1:A:487:C:H5'	1.94	0.68
18:R:45:SER:CB	24:R:1008:WO2:OP5	2.42	0.68
1:A:982:A:H5''	1:A:1003:U:C5	2.29	0.68
3:C:92:ALA:C	3:C:94:LEU:H	1.95	0.68
1:A:78:G:C3'	1:A:79:U:H5''	2.23	0.68
1:A:790:A:H2'	1:A:791:C:C6	2.29	0.68
1:A:1152:G:H2'	1:A:1153:C:H6	1.59	0.68
3:C:14:ILE:O	3:C:16:ARG:N	2.26	0.68
1:A:411:G:H1	1:A:422:U:H3	1.42	0.68
7:G:152:ALA:HB2	11:K:58:PRO:CB	2.24	0.68
1:A:209:U:H5''	1:A:210:U:OP1	1.94	0.68
1:A:387:G:H2'	1:A:388:A:H8	1.58	0.67
1:A:937:U:H2'	1:A:937:U:O2	1.94	0.67
1:A:1290:G:N2	1:A:1310:A:H1'	2.08	0.67
1:A:453:G:C6	1:A:455:C:H5'	2.29	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:505:C:C2'	1:A:506:A:H5'	2.24	0.67
1:A:635:U:O4	1:A:735:G:H2'	1.95	0.67
1:A:501:C:H4'	1:A:502:C:O5'	1.95	0.67
1:A:981:G:N2	1:A:982:A:H1'	2.09	0.67
1:A:736:A:H4'	1:A:737:C:H5''	1.77	0.67
1:A:56:U:H2'	1:A:57:G:C8	2.29	0.67
1:A:51:A:O2'	1:A:52:G:OP2	2.12	0.67
1:A:669:U:C4	1:A:670:A:N7	2.63	0.67
1:A:1152:G:H2'	1:A:1153:C:C6	2.30	0.67
1:A:1207:C:H4'	1:A:1208:A:OP1	1.94	0.67
1:A:460:G:O2'	1:A:461:G:H5'	1.95	0.67
14:N:23:ARG:HA	14:N:30:ALA:CB	2.25	0.67
13:M:26:GLY:O	13:M:28:ALA:N	2.27	0.67
2:B:100:GLY:O	2:B:102:LEU:N	2.28	0.66
1:A:64:G:H4'	1:A:65:U:H5''	1.75	0.66
1:A:1287:A:H62	1:A:1312:G:H1'	1.58	0.66
2:B:105:PHE:C	2:B:107:THR:H	1.97	0.66
21:U:3:LYS:O	21:U:11:GLY:HA2	1.95	0.66
4:D:25:ARG:C	4:D:27:TYR:N	2.49	0.66
1:A:1447:G:H2'	1:A:1448:G:H8	1.59	0.66
1:A:1282:U:H2'	1:A:1282:U:O2	1.93	0.66
1:A:484:C:H2'	1:A:485:G:C8	2.31	0.66
1:A:1231:A:H2'	1:A:1232:A:C8	2.30	0.66
1:A:952:A:H8	1:A:952:A:H5'	1.60	0.66
1:A:952:A:H4'	1:A:953:G:C5'	2.26	0.66
1:A:1211:C:O2'	1:A:1212:G:H5'	1.95	0.66
1:A:1370:C:O2'	1:A:1371:C:H5'	1.96	0.66
1:A:586:U:H2'	1:A:587:G:H8	1.60	0.66
1:A:603:C:H2'	1:A:604:A:O4'	1.95	0.66
10:J:18:ALA:CB	24:J:1009:WO2:O20	2.43	0.66
1:A:1487:U:H2'	1:A:1488:G:C8	2.31	0.66
1:A:803:U:H4'	1:A:804:G:OP2	1.94	0.66
1:A:701:G:H1'	11:K:116:HIS:HA	1.78	0.66
1:A:937:U:H3	1:A:1206:A:H62	1.42	0.66
1:A:64:G:H4'	1:A:65:U:C5'	2.26	0.66
1:A:75:G:O2'	1:A:76:G:H5'	1.96	0.66
11:K:8:LYS:HA	24:K:1014:WO2:O37	1.95	0.66
14:N:40:CYS:O	14:N:42:ILE:N	2.28	0.66
1:A:384:A:H2'	1:A:385:C:O4'	1.97	0.65
1:A:487:C:H1'	1:A:493:A:C4	2.31	0.65
1:A:212:C:H2'	1:A:213:C:C6	2.31	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:114:THR:C	8:H:116:LYS:H	1.98	0.65
1:A:1139:A:H5''	1:A:1140:C:OP1	1.96	0.65
1:A:123:G:H4'	1:A:124:A:O5'	1.95	0.65
1:A:1139:A:H1'	1:A:1162:G:H22	1.58	0.65
1:A:1477:A:O2'	1:A:1478:C:H5'	1.97	0.65
1:A:3:G:H4'	1:A:4:U:O5'	1.96	0.65
1:A:50:A:N6	1:A:356:G:H4'	2.11	0.65
1:A:952:A:H4'	1:A:953:G:H5'	1.78	0.65
18:R:47:THR:O	18:R:49:LYS:N	2.29	0.65
1:A:1266:A:H4'	1:A:1267:A:C8	2.32	0.65
1:A:1267:A:H3'	1:A:1268:A:C5'	2.27	0.65
1:A:1485:G:H2'	1:A:1486:C:C6	2.31	0.65
1:A:1404:G:H2'	1:A:1405:G:H8	1.61	0.65
1:A:496:C:H2'	1:A:497:C:C6	2.30	0.65
2:B:75:LYS:CA	24:B:1004:WO2:O26	2.43	0.65
12:L:119:LYS:O	12:L:120:TYR:CB	2.45	0.65
1:A:1125:G:H2'	1:A:1126:G:C8	2.32	0.65
1:A:114:C:H5'	1:A:115:G:OP1	1.97	0.65
12:L:26:ALA:O	12:L:27:LEU:O	2.14	0.65
1:A:441:G:O6	1:A:469:G:H2'	1.97	0.64
1:A:22:G:H4'	1:A:862:G:C8	2.32	0.64
1:A:1252:G:H2'	1:A:1253:G:C8	2.32	0.64
1:A:45:U:H2'	1:A:46:G:C8	2.32	0.64
1:A:867:G:O2'	1:A:868:U:P	2.56	0.64
1:A:902:G:C6	1:A:904:G:N7	2.66	0.64
1:A:319:G:N2	1:A:322:A:C8	2.65	0.64
1:A:203:A:H1'	1:A:204:G:O4'	1.97	0.64
10:J:50:ILE:HA	10:J:60:ARG:HA	1.78	0.64
6:F:44:GLY:HA2	6:F:60:PHE:H	1.61	0.64
1:A:3:G:O6	1:A:594:A:C4	2.51	0.64
17:Q:92:ARG:O	17:Q:94:ASN:N	2.31	0.64
1:A:1244:C:H2'	1:A:1245:C:H6	1.62	0.64
14:N:42:ILE:C	14:N:44:LEU:H	2.00	0.64
1:A:185:C:H2'	1:A:186:C:H6	1.61	0.64
1:A:389:G:H2'	1:A:390:C:C6	2.32	0.64
1:A:7:G:H4'	1:A:8:A:OP1	1.96	0.64
4:D:32:ALA:C	4:D:34:GLU:N	2.51	0.64
1:A:1056:G:H4'	2:B:103:THR:O	1.97	0.64
1:A:1182:A:H4'	1:A:1183:G:O5'	1.98	0.64
1:A:350:C:C4	1:A:351:A:N7	2.66	0.64
1:A:4:U:H2'	1:A:4:U:O2	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:269:A:O2'	1:A:270:G:H8	1.81	0.64
1:A:963:A:H2'	1:A:964:G:C8	2.32	0.64
1:A:740:U:H2'	1:A:741:G:O4'	1.98	0.64
1:A:1231:A:H5''	9:I:67:GLY:HA2	1.80	0.64
1:A:586:U:H2'	1:A:587:G:C8	2.33	0.64
10:J:90:LEU:O	24:J:1009:WO2:O49	2.16	0.64
1:A:340:C:H5'	1:A:341:G:C4	2.33	0.64
1:A:454:A:C2'	1:A:455:C:H5''	2.28	0.63
1:A:387:G:H2'	1:A:388:A:C8	2.33	0.63
1:A:1206:A:C2'	1:A:1207:C:H5'	2.28	0.63
2:B:43:ASP:O	2:B:45:GLN:N	2.32	0.63
7:G:154:TYR:O	7:G:156:TRP:N	2.31	0.63
14:N:11:LYS:O	14:N:12:ARG:C	2.35	0.63
1:A:1098:C:H2'	1:A:1099:G:C5'	2.26	0.63
1:A:261:G:H21	1:A:264:C:H5	1.46	0.63
1:A:376:C:H2'	1:A:377:A:O4'	1.97	0.63
1:A:1026:A:H2'	1:A:1027:C:H5'	1.81	0.63
1:A:108:G:H1'	1:A:109:A:N7	2.13	0.63
1:A:475:G:H2'	1:A:476:G:H8	1.62	0.63
1:A:1038:U:H5'	3:C:163:ALA:HB2	1.81	0.63
1:A:1206:A:H2'	1:A:1207:C:H5'	1.81	0.63
1:A:339:A:H5''	1:A:340:C:H5	1.63	0.63
1:A:156:A:H2'	1:A:157:C:H5'	1.79	0.63
1:A:1130:U:H2'	1:A:1131:C:O4'	1.98	0.63
1:A:1231:A:H4'	9:I:68:GLY:N	2.14	0.63
7:G:117:ALA:O	7:G:120:ILE:N	2.32	0.63
1:A:275:C:C2	17:Q:38:ARG:HA	2.33	0.63
1:A:1215:C:O2'	1:A:1216:U:H5'	1.98	0.63
1:A:123:G:H2'	1:A:189:U:OP1	1.99	0.63
1:A:1337:G:H2'	1:A:1338:A:C8	2.33	0.63
1:A:580:G:C8	1:A:581:U:C5	2.87	0.63
1:A:1163:G:O2'	1:A:1164:A:OP2	2.16	0.63
1:A:1477:A:C2'	1:A:1478:C:H5'	2.28	0.63
1:A:574:U:H2'	1:A:575:G:C8	2.34	0.63
1:A:979:G:H2'	1:A:980:G:C8	2.33	0.63
1:A:123:G:O2'	1:A:189:U:H5''	1.99	0.63
1:A:521:G:O2'	1:A:522:A:H5'	1.98	0.63
1:A:1087:A:H2'	1:A:1088:G:H8	1.64	0.62
1:A:971:A:H2'	1:A:971:A:N3	2.14	0.62
1:A:463:C:O2'	1:A:464:U:H5'	1.98	0.62
1:A:379:G:H2'	1:A:380:C:C6	2.34	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1351:C:H2'	1:A:1352:G:O4'	1.99	0.62
1:A:946:A:C2'	1:A:947:C:H5'	2.28	0.62
7:G:141:VAL:O	7:G:143:ARG:N	2.32	0.62
1:A:1422:C:H2'	1:A:1423:G:O4'	1.98	0.62
1:A:841:A:H2'	1:A:842:A:C8	2.35	0.62
1:A:684:C:O2'	1:A:685:A:OP2	2.17	0.62
1:A:316:A:H2	1:A:327:G:H22	1.46	0.62
1:A:969:U:H4'	1:A:970:G:O5'	2.00	0.62
1:A:867:G:O2'	1:A:868:U:OP2	2.16	0.62
1:A:1267:A:C2'	1:A:1268:A:H5''	2.29	0.62
1:A:801:G:H3'	1:A:802:A:C5'	2.30	0.62
1:A:316:A:O2'	1:A:317:C:H5'	1.99	0.62
1:A:639:C:C6	1:A:639:C:H3'	2.35	0.62
1:A:919:G:H2'	1:A:920:U:H6	1.63	0.62
17:Q:67:LYS:O	17:Q:68:ARG:CB	2.47	0.62
1:A:241:A:N6	1:A:276:G:H1'	2.15	0.62
1:A:329:C:H2'	1:A:330:C:C6	2.34	0.61
12:L:50:SER:O	12:L:51:ALA:HB2	2.00	0.61
1:A:1111:C:O5'	1:A:1112:A:H5'	2.00	0.61
1:A:931:G:O2'	1:A:932:U:H5'	2.00	0.61
1:A:322:A:H4'	1:A:323:C:OP1	2.00	0.61
8:H:48:TYR:HA	8:H:60:ARG:O	2.00	0.61
4:D:165:MET:O	4:D:167:GLY:N	2.33	0.61
1:A:992:A:H2'	1:A:993:A:C8	2.35	0.61
1:A:1038:U:C5'	3:C:163:ALA:HB2	2.29	0.61
1:A:8:A:N3	1:A:8:A:H2'	2.16	0.61
1:A:66:G:C2'	1:A:67:C:H5'	2.31	0.61
1:A:1039:G:H2'	1:A:1040:G:H5'	1.81	0.61
1:A:1393:C:H2'	1:A:1394:C:C6	2.35	0.61
12:L:105:TYR:C	12:L:107:ALA:H	2.03	0.61
1:A:1422:C:O2'	1:A:1423:G:H5'	2.01	0.61
10:J:78:ASN:O	10:J:80:LYS:N	2.33	0.61
1:A:239:U:O2	1:A:239:U:H2'	2.00	0.61
1:A:100:G:H2'	1:A:101:G:C5'	2.26	0.61
1:A:1300:A:H5'	1:A:1301:C:OP1	2.01	0.61
1:A:4:U:H5'	1:A:5:U:OP1	2.00	0.60
1:A:1049:A:HO2'	1:A:1050:G:H8	1.47	0.60
3:C:92:ALA:C	3:C:94:LEU:N	2.54	0.60
1:A:1237:A:O3'	1:A:1238:U:H4'	2.01	0.60
1:A:534:U:H2'	1:A:535:U:C6	2.36	0.60
1:A:672:C:H2'	1:A:673:G:O4'	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:669:U:H5	1:A:686:G:H21	1.49	0.60
1:A:261:G:H22	1:A:265:A:H62	1.49	0.60
1:A:203:A:C6	1:A:216:C:H4'	2.36	0.60
2:B:31:TYR:O	2:B:32:ILE:O	2.19	0.60
7:G:151:TYR:N	24:G:1006:WO2:O49	2.30	0.60
1:A:898:U:H2'	1:A:899:G:O4'	2.00	0.60
1:A:1485:G:H2'	1:A:1486:C:H6	1.65	0.60
1:A:1197:G:O2'	1:A:1198:C:H5'	2.01	0.60
1:A:937:U:O2'	1:A:1204:C:H5'	2.01	0.60
1:A:919:G:O2'	1:A:920:U:H5'	2.01	0.60
1:A:323:C:O2	1:A:323:C:H2'	2.01	0.60
12:L:120:TYR:O	12:L:121:GLY:C	2.40	0.60
1:A:1031:U:H1'	1:A:1182:A:N7	2.17	0.60
1:A:819:G:O2'	1:A:820:G:H5'	2.02	0.60
1:A:406:A:N6	1:A:408:G:N2	2.50	0.60
1:A:876:C:H2'	1:A:877:A:C8	2.37	0.60
1:A:849:A:HO2'	1:A:850:A:P	2.24	0.60
1:A:1286:G:H5'	21:U:4:GLY:HA3	1.83	0.60
1:A:990:U:H3	1:A:995:G:H1	1.47	0.60
1:A:578:G:H5''	1:A:579:C:OP1	2.01	0.60
1:A:1116:G:H1	1:A:1123:C:N4	1.99	0.60
7:G:52:GLU:C	7:G:54:THR:H	2.04	0.60
1:A:911:C:H4'	1:A:912:A:OP1	2.02	0.60
15:O:58:MET:O	15:O:62:GLN:N	2.22	0.60
1:A:146:A:N6	1:A:163:C:N3	2.50	0.60
1:A:648:A:N3	1:A:715:C:H2'	2.16	0.60
20:T:84:LEU:C	20:T:86:ARG:H	2.05	0.60
1:A:248:U:H2'	1:A:249:G:H8	1.67	0.60
1:A:327:G:O2'	1:A:328:G:H5'	2.01	0.59
4:D:80:GLU:O	4:D:81:GLU:C	2.39	0.59
4:D:32:ALA:O	4:D:34:GLU:N	2.35	0.59
18:R:10:LYS:C	18:R:12:ALA:H	2.05	0.59
1:A:1279:C:H2'	1:A:1279:C:O2	2.02	0.59
1:A:3:G:N7	1:A:595:C:C1'	2.64	0.59
3:C:92:ALA:O	3:C:94:LEU:N	2.35	0.59
7:G:75:VAL:HA	7:G:88:PRO:HA	1.83	0.59
1:A:1252:G:H2'	1:A:1253:G:H8	1.64	0.59
6:F:15:ASP:O	6:F:17:SER:N	2.35	0.59
1:A:1511:A:H5''	1:A:1512:C:C5	2.37	0.59
1:A:633:G:O2'	1:A:634:C:H5'	2.02	0.59
1:A:926:A:H2'	1:A:927:U:C6	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1246:G:C6	1:A:1247:G:C6	2.90	0.59
4:D:88:VAL:O	4:D:89:THR:C	2.41	0.59
1:A:1265:C:H3'	1:A:1266:A:H8	1.68	0.59
1:A:707:G:O2'	1:A:708:G:H5'	2.02	0.59
1:A:1013:G:H2'	1:A:1014:G:C8	2.35	0.59
1:A:139:G:O2'	1:A:140:G:H5'	2.02	0.59
1:A:988:G:H2'	1:A:989:G:H8	1.66	0.59
1:A:1408:C:O2'	1:A:1409:U:H5'	2.02	0.59
1:A:1232:A:O2'	1:A:1352:G:H5'	2.02	0.59
1:A:334:C:H2'	1:A:335:U:C6	2.37	0.59
2:B:144:ARG:O	2:B:147:LYS:N	2.35	0.59
1:A:1035:G:O6	1:A:1180:U:H2'	2.03	0.59
1:A:625:A:C8	8:H:115:PRO:HA	2.38	0.59
1:A:1135:C:O2'	1:A:1136:G:H5'	2.03	0.59
1:A:1274:G:H2'	1:A:1275:G:O4'	2.03	0.59
1:A:1119:C:H4'	1:A:1120:G:C2	2.38	0.59
1:A:1376:A:N7	1:A:1478:C:H4'	2.17	0.59
1:A:503:A:N1	1:A:519:C:H1'	2.18	0.59
19:S:15:LEU:O	19:S:19:VAL:N	2.31	0.59
8:H:25:GLU:HA	8:H:59:LEU:O	2.01	0.59
1:A:1122:C:H2'	1:A:1123:C:H6	1.68	0.59
2:B:20:GLU:O	2:B:22:LYS:N	2.29	0.59
1:A:584:C:O2'	1:A:585:A:H5'	2.02	0.58
11:K:94:ALA:O	11:K:97:ALA:HB3	2.02	0.58
1:A:2:U:H4'	1:A:3:G:C2	2.38	0.58
1:A:94:A:C4	1:A:95:G:C8	2.91	0.58
1:A:1328:G:O2'	1:A:1329:U:OP2	2.21	0.58
5:E:131:ILE:HA	5:E:134:ALA:HB3	1.85	0.58
1:A:1150:A:H2'	1:A:1151:A:C8	2.39	0.58
1:A:1111:C:H4'	1:A:1112:A:H5'	1.85	0.58
1:A:631:A:H2'	1:A:632:G:H8	1.66	0.58
1:A:1017:A:H2'	1:A:1018:G:H8	1.68	0.58
5:E:129:ILE:O	5:E:132:ALA:HB3	2.04	0.58
1:A:703:C:H2'	1:A:704:G:C8	2.37	0.58
10:J:62:HIS:CB	14:N:59:ALA:HB3	2.34	0.58
1:A:1286:G:N2	1:A:1312:G:C2'	2.62	0.58
5:E:39:GLY:O	5:E:69:VAL:N	2.26	0.58
1:A:195:G:H2'	1:A:196:U:C6	2.39	0.58
1:A:1287:A:N6	1:A:1312:G:H1'	2.19	0.58
1:A:1172:A:H2'	1:A:1173:C:C6	2.38	0.58
1:A:190:G:N2	1:A:258:A:H4'	2.19	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:789:C:O2'	1:A:790:A:H5'	2.03	0.58
8:H:114:THR:O	8:H:116:LYS:N	2.36	0.58
1:A:1109:G:N2	1:A:1128:A:H62	2.01	0.58
1:A:838:G:O2'	1:A:839:C:H5'	2.03	0.58
1:A:848:U:H5''	1:A:849:A:OP2	2.04	0.58
1:A:105:G:H5'	1:A:384:A:H4'	1.86	0.58
1:A:800:C:C1'	1:A:802:A:H5'	2.31	0.58
1:A:1231:A:H4'	9:I:68:GLY:H	1.67	0.58
1:A:952:A:H4'	1:A:953:G:O5'	2.04	0.58
1:A:503:A:H2'	1:A:504:G:O4'	2.04	0.58
5:E:124:GLY:O	5:E:125:SER:C	2.42	0.58
1:A:78:G:H3'	1:A:79:U:H5''	1.84	0.58
1:A:246:G:O2'	1:A:247:U:P	2.62	0.58
1:A:849:A:O2'	1:A:850:A:C3'	2.44	0.58
1:A:1049:A:O2'	1:A:1050:G:H8	1.85	0.58
1:A:891:A:O2'	1:A:892:A:H5'	2.04	0.58
1:A:534:U:H2'	1:A:535:U:H6	1.68	0.58
1:A:1118:U:H5''	1:A:1119:C:OP2	2.04	0.58
11:K:19:ALA:HA	11:K:31:THR:O	2.04	0.58
16:P:11:SER:O	16:P:12:LYS:C	2.41	0.58
1:A:1400:A:H2'	1:A:1401:G:H5'	1.85	0.58
1:A:1220:A:H1'	1:A:1222:G:N9	2.19	0.58
1:A:444:G:N7	1:A:465:G:O6	2.36	0.58
4:D:82:ALA:O	4:D:83:SER:C	2.41	0.58
13:M:84:ILE:C	13:M:86:CYS:H	2.07	0.58
1:A:798:A:H62	1:A:1486:C:H1'	1.68	0.58
16:P:6:LEU:HA	16:P:18:ARG:O	2.03	0.58
1:A:21:G:H2'	1:A:22:G:C8	2.39	0.57
1:A:173:A:O2'	1:A:174:U:H5'	2.04	0.57
1:A:1478:C:C6	1:A:1481:G:N7	2.72	0.57
1:A:604:A:H2'	1:A:605:A:O4'	2.04	0.57
1:A:997:C:O2'	1:A:998:U:H5'	2.03	0.57
11:K:115:PRO:C	11:K:117:ASN:H	2.08	0.57
15:O:30:ALA:O	15:O:33:THR:N	2.37	0.57
1:A:66:G:O2'	1:A:67:C:H5'	2.05	0.57
1:A:1231:A:H5''	9:I:67:GLY:CA	2.34	0.57
1:A:581:U:C2	1:A:582:C:C5	2.91	0.57
1:A:352:G:O2'	1:A:353:U:H5'	2.04	0.57
1:A:381:C:C2'	1:A:382:U:H5'	2.34	0.57
15:O:80:ALA:O	15:O:84:LYS:N	2.37	0.57
1:A:439:G:O2'	1:A:440:G:H5'	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:20:THR:C	13:M:22:ILE:H	2.08	0.57
1:A:19:C:O2'	1:A:20:U:H5'	2.04	0.57
1:A:899:G:H2'	1:A:900:A:C8	2.40	0.57
17:Q:95:TYR:C	17:Q:97:SER:N	2.58	0.57
12:L:117:ARG:O	12:L:118:SER:C	2.43	0.57
1:A:340:C:H5'	1:A:341:G:C5	2.39	0.57
1:A:1064:G:O2'	1:A:1065:U:H5'	2.03	0.57
9:I:28:VAL:O	9:I:30:GLY:N	2.38	0.57
9:I:9:ARG:HA	9:I:13:ALA:O	2.04	0.57
11:K:33:THR:HA	11:K:39:PRO:HA	1.86	0.57
1:A:761:G:H2'	1:A:762:C:O4'	2.05	0.57
1:A:1311:U:C2'	1:A:1312:G:H5'	2.34	0.57
18:R:37:VAL:O	18:R:40:LEU:N	2.38	0.57
8:H:6:ILE:O	8:H:9:MET:N	2.37	0.57
1:A:453:G:H3'	1:A:454:A:C5'	2.34	0.57
1:A:1110:C:O2'	1:A:1112:A:C8	2.51	0.57
1:A:1063:G:H2'	1:A:1064:G:H8	1.70	0.57
1:A:1445:A:H2'	1:A:1446:G:O4'	2.05	0.57
16:P:78:GLY:C	16:P:80:PHE:H	2.07	0.57
1:A:832:G:H8	1:A:848:U:O4	1.87	0.57
1:A:1474:G:C2'	1:A:1475:U:H5'	2.35	0.57
1:A:442:A:N7	1:A:470:U:O4	2.38	0.57
1:A:433:G:C4'	1:A:434:A:OP1	2.49	0.57
4:D:82:ALA:O	4:D:85:LYS:N	2.37	0.57
1:A:790:A:H2'	1:A:791:C:H6	1.69	0.57
1:A:203:A:H4'	1:A:204:G:O5'	2.04	0.57
1:A:1417:G:H2'	1:A:1418:U:H6	1.63	0.57
1:A:613:G:O2'	1:A:614:G:H5'	2.04	0.57
1:A:1046:G:N2	1:A:1171:G:O2'	2.38	0.57
1:A:1464:G:O2'	1:A:1465:G:H5'	2.05	0.57
1:A:731:C:O2'	1:A:732:C:H6	1.88	0.57
17:Q:95:TYR:C	17:Q:97:SER:H	2.08	0.57
1:A:933:U:H2'	1:A:934:U:C6	2.40	0.57
1:A:475:G:H2'	1:A:476:G:C8	2.40	0.57
1:A:819:G:H2'	1:A:820:G:O5'	2.05	0.57
13:M:18:ALA:O	13:M:20:THR:N	2.38	0.57
19:S:42:PRO:O	19:S:44:MET:N	2.38	0.57
20:T:64:ASP:HA	20:T:67:ALA:HB3	1.86	0.57
1:A:890:A:H4'	1:A:891:A:O5'	2.05	0.56
1:A:892:A:C2'	1:A:893:G:H5'	2.33	0.56
1:A:205:G:O2'	1:A:206:G:H5'	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:54:VAL:O	13:M:55:ARG:C	2.43	0.56
2:B:178:ARG:O	8:H:71:GLY:HA2	2.05	0.56
7:G:79:ARG:C	7:G:81:GLY:N	2.59	0.56
7:G:143:ARG:C	7:G:145:ALA:H	2.07	0.56
12:L:50:SER:O	12:L:51:ALA:CB	2.53	0.56
1:A:221:G:O2'	1:A:222:G:H5'	2.05	0.56
1:A:945:A:H4'	1:A:946:A:OP2	2.05	0.56
1:A:1003:U:H2'	1:A:1004:G:C8	2.40	0.56
1:A:245:A:H1'	1:A:247:U:C4	2.40	0.56
1:A:988:G:H2'	1:A:989:G:C8	2.39	0.56
1:A:631:A:O2'	1:A:632:G:H5'	2.04	0.56
5:E:16:THR:O	5:E:17:ALA:O	2.23	0.56
1:A:1497:G:O2'	1:A:1498:G:H5'	2.04	0.56
1:A:1026:A:C2'	1:A:1027:C:H5'	2.35	0.56
2:B:236:TYR:O	2:B:237:ALA:HB3	2.04	0.56
15:O:8:LYS:O	15:O:9:GLN:C	2.43	0.56
1:A:1497:G:H2'	1:A:1498:G:H8	1.70	0.56
1:A:369:A:N1	1:A:386:G:O4'	2.39	0.56
1:A:156:A:C2'	1:A:157:C:H5'	2.36	0.56
1:A:32:A:OP2	1:A:393:C:O2'	2.22	0.56
1:A:373:G:C6	1:A:374:C:N4	2.74	0.56
1:A:1206:A:N3	1:A:1206:A:H2'	2.19	0.56
14:N:9:LYS:C	14:N:11:LYS:H	2.09	0.56
4:D:8:VAL:O	4:D:11:LEU:N	2.27	0.56
1:A:958:U:H2'	1:A:959:U:C5	2.41	0.56
1:A:359:A:H2'	1:A:360:U:C2	2.40	0.56
3:C:39:ILE:O	3:C:42:LEU:N	2.39	0.56
1:A:2:U:O3'	1:A:3:G:C2	2.59	0.56
1:A:399:U:H2'	1:A:400:U:C6	2.41	0.56
1:A:1395:A:O2'	1:A:1396:U:H5'	2.06	0.56
1:A:1407:U:H2'	1:A:1408:C:H6	1.70	0.56
11:K:122:LYS:O	11:K:123:LYS:C	2.44	0.56
3:C:205:GLY:C	24:C:1003:WO2:O48	2.44	0.56
1:A:766:C:O2'	1:A:767:C:H5'	2.05	0.56
1:A:866:A:H4'	1:A:867:G:OP1	2.06	0.56
1:A:1279:C:O2'	1:A:1280:A:OP2	2.20	0.56
1:A:483:G:O2'	1:A:484:C:H5'	2.06	0.56
16:P:36:ILE:O	16:P:51:VAL:HA	2.06	0.56
2:B:193:ASP:C	2:B:195:ASP:H	2.08	0.56
7:G:95:ARG:O	7:G:96:GLN:C	2.43	0.56
1:A:1310:A:O2'	1:A:1311:U:H5'	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1502:G:O2'	1:A:1503:G:H5'	2.06	0.56
1:A:946:A:H2'	1:A:947:C:H5'	1.88	0.56
1:A:795:C:O2'	1:A:796:U:P	2.64	0.56
1:A:435:A:H3'	1:A:436:C:C6	2.40	0.56
1:A:1220:A:N1	1:A:1279:C:H5	2.03	0.55
21:U:12:LYS:O	21:U:15:ARG:N	2.39	0.55
1:A:157:C:H2'	1:A:158:U:C6	2.41	0.55
10:J:63:PHE:HA	14:N:59:ALA:H	1.71	0.55
1:A:763:A:O2'	1:A:764:A:H5''	2.06	0.55
1:A:966:C:O2'	1:A:967:C:H5'	2.06	0.55
1:A:1043:G:O2'	1:A:1044:U:H5'	2.06	0.55
1:A:511:C:O2'	1:A:518:A:H2'	2.05	0.55
1:A:802:A:H5''	1:A:803:U:OP2	2.05	0.55
1:A:731:C:OP2	1:A:731:C:C6	2.55	0.55
1:A:505:C:H2'	1:A:506:A:C5'	2.36	0.55
1:A:496:C:H2'	1:A:497:C:H6	1.70	0.55
1:A:1295:C:H2'	1:A:1296:U:C6	2.40	0.55
1:A:1331:A:H8	1:A:1331:A:O5'	1.89	0.55
1:A:942:A:O2'	1:A:943:G:OP2	2.23	0.55
1:A:1323:C:O2'	1:A:1324:G:H5'	2.07	0.55
13:M:16:ASP:O	13:M:30:ALA:HB1	2.06	0.55
1:A:445:A:N7	1:A:465:G:N1	2.55	0.55
2:B:100:GLY:O	2:B:101:MET:C	2.44	0.55
16:P:52:ASP:O	16:P:53:VAL:C	2.45	0.55
1:A:310:A:H5''	1:A:312:G:OP2	2.05	0.55
1:A:238:A:C2	1:A:241:A:C8	2.95	0.55
1:A:257:A:C6	1:A:258:A:C6	2.94	0.55
1:A:56:U:O2'	1:A:57:G:H5'	2.06	0.55
1:A:982:A:H5''	1:A:1003:U:C4	2.41	0.55
3:C:132:ARG:O	3:C:133:ALA:C	2.45	0.55
1:A:713:G:N7	1:A:714:G:H1'	2.20	0.55
1:A:714:G:H5'	1:A:749:A:H4'	1.88	0.55
1:A:923:A:C2	1:A:1217:A:C2	2.95	0.55
7:G:141:VAL:C	7:G:143:ARG:H	2.09	0.55
9:I:89:ASN:C	9:I:91:ASP:H	2.10	0.55
9:I:93:ARG:O	9:I:95:LYS:N	2.40	0.55
1:A:1289:U:H2'	1:A:1290:G:C8	2.42	0.55
11:K:44:SER:O	11:K:64:ALA:CB	2.47	0.55
2:B:236:TYR:O	2:B:237:ALA:CB	2.55	0.55
1:A:11:G:H2'	1:A:12:U:O4'	2.07	0.55
1:A:665:G:O2'	1:A:666:G:H5'	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1311:U:H2'	1:A:1312:G:H5'	1.87	0.55
1:A:1228:U:O2'	1:A:1229:A:H5'	2.06	0.55
1:A:1454:C:H2'	1:A:1455:C:C6	2.42	0.55
1:A:1102:G:H2'	1:A:1103:U:H6	1.71	0.55
11:K:7:LYS:O	11:K:8:LYS:CB	2.55	0.55
1:A:385:C:H2'	1:A:386:G:C8	2.42	0.55
1:A:893:G:H2'	1:A:894:G:H8	1.72	0.55
4:D:79:PHE:O	4:D:82:ALA:HB3	2.07	0.55
1:A:951:A:H5'	1:A:952:A:OP1	2.07	0.55
1:A:1323:C:H2'	1:A:1324:G:H8	1.72	0.55
1:A:849:A:O2'	1:A:850:A:O5'	2.15	0.55
1:A:445:A:C2	1:A:464:U:C4	2.92	0.55
1:A:723:U:OP2	15:O:2:PRO:HA	2.07	0.55
7:G:79:ARG:O	7:G:81:GLY:N	2.40	0.55
1:A:64:G:H4'	1:A:65:U:O5'	2.07	0.55
1:A:870:C:H2'	1:A:871:G:H8	1.72	0.54
15:O:51:HIS:O	15:O:54:ARG:N	2.27	0.54
11:K:24:SER:O	11:K:26:ASN:N	2.40	0.54
1:A:1494:G:C5'	1:A:1494:G:H8	2.08	0.54
1:A:1140:C:H2'	1:A:1140:C:O2	2.06	0.54
1:A:1151:A:H2'	1:A:1152:G:O4'	2.06	0.54
1:A:820:G:H2'	1:A:821:G:O4'	2.07	0.54
1:A:160:G:O2'	1:A:161:G:H5'	2.07	0.54
16:P:23:ASP:C	16:P:25:ARG:N	2.58	0.54
7:G:146:GLU:O	7:G:147:ALA:HB2	2.08	0.54
16:P:2:VAL:HA	16:P:22:THR:O	2.07	0.54
1:A:1475:U:O2'	1:A:1476:A:P	2.65	0.54
1:A:1266:A:HO2'	1:A:1267:A:P	2.31	0.54
1:A:979:G:H2'	1:A:980:G:H8	1.72	0.54
9:I:89:ASN:C	9:I:91:ASP:N	2.61	0.54
11:K:57:THR:O	11:K:60:ALA:HB3	2.08	0.54
1:A:181:C:O2'	1:A:182:C:H5'	2.07	0.54
20:T:29:LYS:O	20:T:32:ALA:HB3	2.08	0.54
1:A:1264:G:O2'	1:A:1265:C:H5'	2.08	0.54
1:A:1350:G:O2'	1:A:1351:C:H5'	2.07	0.54
1:A:1447:G:H2'	1:A:1448:G:C8	2.41	0.54
1:A:1510:C:H4'	1:A:1512:C:H41	1.72	0.54
7:G:65:ALA:HB1	7:G:127:ALA:HB3	1.90	0.54
1:A:922:G:C2	1:A:923:A:C8	2.96	0.54
1:A:1374:G:O2'	1:A:1479:A:C5'	2.53	0.54
1:A:1463:G:H2'	1:A:1464:G:C8	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:788:C:H2'	1:A:789:C:C6	2.43	0.54
1:A:639:C:C6	1:A:639:C:C3'	2.90	0.54
1:A:718:C:O2'	1:A:719:C:H5'	2.07	0.54
1:A:47:C:C6	1:A:360:U:H2'	2.43	0.54
1:A:434:A:N6	1:A:480:A:H1'	2.23	0.54
1:A:51:A:H4'	1:A:52:G:C5'	2.38	0.54
1:A:954:A:N3	1:A:954:A:H3'	2.23	0.54
2:B:44:LEU:C	2:B:46:LYS:H	2.10	0.54
1:A:1142:G:O2'	1:A:1143:C:H5'	2.08	0.54
1:A:143:A:O2'	1:A:144:C:H5'	2.07	0.54
1:A:686:G:H5''	1:A:687:A:H5'	1.90	0.54
2:B:104:ASN:O	2:B:105:PHE:C	2.46	0.54
1:A:937:U:H3	1:A:1206:A:N6	2.04	0.54
1:A:112:A:H4'	1:A:113:A:O5'	2.08	0.54
1:A:112:A:O2'	1:A:113:A:OP2	2.25	0.54
1:A:350:C:C2	1:A:351:A:C8	2.96	0.54
1:A:581:U:H2'	1:A:582:C:C6	2.43	0.54
2:B:170:GLU:O	2:B:173:ALA:HB3	2.08	0.54
1:A:1388:U:O5'	1:A:1388:U:H6	1.90	0.53
1:A:669:U:H3	1:A:670:A:H62	1.55	0.53
1:A:1396:U:H2'	1:A:1397:G:H8	1.73	0.53
5:E:130:ASN:O	5:E:134:ALA:CB	2.56	0.53
1:A:51:A:H4'	1:A:52:G:O5'	2.07	0.53
3:C:60:ALA:O	3:C:61:ALA:HB3	2.07	0.53
2:B:3:VAL:O	2:B:5:ILE:N	2.41	0.53
1:A:105:G:C4'	1:A:384:A:H5''	2.37	0.53
1:A:798:A:H5''	1:A:800:C:N4	2.23	0.53
1:A:1419:C:H2'	1:A:1420:G:C8	2.44	0.53
7:G:52:GLU:C	7:G:54:THR:N	2.60	0.53
1:A:544:U:O2'	1:A:545:C:OP1	2.24	0.53
1:A:945:A:H5''	1:A:946:A:OP2	2.08	0.53
8:H:114:THR:C	8:H:116:LYS:N	2.62	0.53
1:A:437:C:O2'	1:A:438:C:H5'	2.08	0.53
3:C:109:PRO:C	3:C:111:LEU:H	2.11	0.53
1:A:1051:C:H2'	1:A:1052:U:O5'	2.09	0.53
3:C:139:GLN:O	3:C:143:GLU:N	2.36	0.53
1:A:858:G:H2'	1:A:859:C:O4'	2.09	0.53
1:A:1235:C:H2'	1:A:1236:G:C8	2.44	0.53
11:K:59:TYR:C	11:K:61:ALA:N	2.61	0.53
1:A:1202:G:OP1	1:A:1302:C:N3	2.41	0.53
15:O:6:GLU:O	15:O:7:GLU:C	2.46	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:190:ASP:O	4:D:193:ASP:N	2.41	0.53
4:D:109:GLY:O	4:D:111:ALA:N	2.40	0.53
3:C:145:GLY:O	3:C:146:ALA:O	2.27	0.53
1:A:424:U:H1'	1:A:425:A:C8	2.44	0.53
1:A:1122:C:H2'	1:A:1123:C:C6	2.44	0.53
1:A:933:U:O2'	1:A:934:U:H5'	2.09	0.53
9:I:28:VAL:C	9:I:30:GLY:H	2.12	0.53
1:A:795:C:O2'	1:A:796:U:H6	1.91	0.53
1:A:1402:C:O2'	1:A:1403:G:H5'	2.08	0.53
1:A:66:G:N2	1:A:166:A:C2	2.76	0.53
14:N:42:ILE:O	14:N:44:LEU:N	2.41	0.53
1:A:1511:A:H5''	1:A:1512:C:H5	1.74	0.53
7:G:124:LEU:O	7:G:127:ALA:HB3	2.09	0.53
1:A:1309:C:O2'	1:A:1310:A:H5'	2.07	0.53
1:A:902:G:H1'	1:A:1479:A:C4	2.44	0.53
1:A:106:G:C1'	1:A:349:G:H5''	2.39	0.53
4:D:76:ARG:O	4:D:79:PHE:N	2.42	0.53
1:A:1246:G:C2	1:A:1252:G:C2	2.96	0.53
1:A:625:A:C6	1:A:626:C:C4	2.97	0.53
16:P:45:THR:O	16:P:47:ASP:N	2.41	0.53
24:B:1001:WO2:O49	24:B:1004:WO2:OP5	2.27	0.53
1:A:832:G:C6	1:A:833:C:C4	2.97	0.53
11:K:8:LYS:CB	24:K:1014:WO2:O5	2.56	0.53
1:A:209:U:H4'	1:A:210:U:H5''	1.91	0.53
1:A:114:C:H41	1:A:230:C:H3'	1.74	0.53
2:B:144:ARG:O	2:B:145:LEU:C	2.47	0.53
11:K:62:GLN:O	11:K:65:ALA:N	2.42	0.53
3:C:168:ALA:O	3:C:169:ALA:HB2	2.09	0.53
5:E:155:GLU:O	5:E:156:ALA:HB3	2.08	0.53
1:A:501:C:O2'	1:A:502:C:OP2	2.27	0.53
1:A:364:C:H2'	1:A:365:C:H6	1.74	0.53
1:A:171:C:O2'	1:A:172:C:H5'	2.09	0.53
1:A:26:A:N6	1:A:541:G:H1'	2.24	0.53
1:A:742:A:H2'	1:A:743:G:H5'	1.91	0.53
1:A:1318:G:H5''	1:A:1319:G:OP1	2.09	0.53
1:A:485:G:OP1	12:L:116:SER:O	2.26	0.53
5:E:131:ILE:O	5:E:134:ALA:HB3	2.09	0.53
12:L:105:TYR:C	12:L:107:ALA:N	2.60	0.53
1:A:952:A:HO2'	1:A:953:G:P	2.32	0.53
4:D:94:LEU:O	4:D:95:GLY:C	2.47	0.53
13:M:69:GLU:O	13:M:72:ALA:HB3	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1375:U:O4'	1:A:1479:A:H5'	2.09	0.52
1:A:684:C:H5''	1:A:686:G:O4'	2.09	0.52
1:A:1056:G:C6	1:A:1084:A:N6	2.77	0.52
1:A:983:A:H2'	1:A:984:C:O4'	2.09	0.52
1:A:842:A:H2'	1:A:843:C:C6	2.44	0.52
5:E:13:ILE:HA	5:E:29:GLY:O	2.09	0.52
2:B:242:ALA:O	2:B:243:GLU:CB	2.56	0.52
1:A:1370:C:H2'	1:A:1371:C:H6	1.73	0.52
10:J:6:ILE:O	10:J:71:LEU:O	2.27	0.52
20:T:41:ILE:O	20:T:43:LEU:N	2.42	0.52
1:A:1231:A:H2'	1:A:1232:A:H8	1.73	0.52
1:A:1038:U:O2'	1:A:1039:G:H5'	2.09	0.52
1:A:958:U:C2	1:A:959:U:C5	2.97	0.52
2:B:44:LEU:C	2:B:46:LYS:N	2.63	0.52
3:C:79:ARG:C	3:C:81:GLY:H	2.13	0.52
3:C:48:TYR:C	3:C:50:ALA:H	2.12	0.52
1:A:1222:G:H2'	1:A:1223:C:C6	2.44	0.52
1:A:1139:A:H4'	1:A:1140:C:O5'	2.10	0.52
1:A:66:G:H2'	1:A:67:C:H5'	1.90	0.52
1:A:1328:G:C2'	1:A:1329:U:OP2	2.57	0.52
1:A:509:C:OP1	1:A:890:A:H3'	2.09	0.52
20:T:41:ILE:O	20:T:42:GLN:C	2.47	0.52
11:K:34:ASP:O	11:K:36:ASP:N	2.42	0.52
1:A:1291:G:O2'	1:A:1292:G:H5'	2.09	0.52
3:C:28:GLN:O	3:C:29:TYR:C	2.47	0.52
1:A:1217:A:O2'	1:A:1285:G:H4'	2.10	0.52
1:A:1084:A:H2'	1:A:1085:C:C6	2.45	0.52
1:A:581:U:H2'	1:A:582:C:H6	1.73	0.52
13:M:18:ALA:C	13:M:20:THR:N	2.62	0.52
1:A:274:A:N3	1:A:276:G:N2	2.57	0.52
1:A:1163:G:H4'	1:A:1164:A:O5'	2.08	0.52
1:A:79:U:H3	1:A:83:A:H62	1.56	0.52
1:A:926:A:C5	1:A:927:U:C4	2.98	0.52
2:B:20:GLU:C	2:B:22:LYS:H	2.11	0.52
1:A:713:G:C5	1:A:714:G:H1'	2.44	0.52
1:A:413:C:O2'	1:A:414:C:H5'	2.09	0.52
2:B:63:MET:C	2:B:65:GLY:H	2.13	0.52
1:A:691:C:H2'	1:A:692:G:H8	1.74	0.52
1:A:147:C:H42	1:A:163:C:N4	2.08	0.52
1:A:1012:A:C2'	1:A:1013:G:H5'	2.40	0.52
1:A:908:C:H2'	1:A:909:C:H6	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:36:LYS:O	7:G:37:ASN:C	2.47	0.52
1:A:178:G:H2'	1:A:179:A:H8	1.74	0.52
1:A:823:C:H4'	1:A:825:C:N3	2.24	0.52
1:A:1327:A:N1	1:A:1356:A:H5''	2.25	0.52
1:A:982:A:H2'	1:A:983:A:H5'	1.91	0.52
1:A:269:A:H4'	1:A:270:G:O5'	2.08	0.52
1:A:340:C:O2'	1:A:341:G:OP2	2.20	0.52
2:B:134:GLU:HA	2:B:137:ARG:CB	2.40	0.52
1:A:675:U:O2'	1:A:677:A:N7	2.40	0.52
1:A:1082:C:O5'	1:A:1082:C:H6	1.93	0.52
1:A:380:C:N4	1:A:381:C:N4	2.58	0.52
1:A:154:A:O5'	1:A:154:A:H8	1.92	0.52
1:A:1102:G:O2'	1:A:1103:U:H5'	2.10	0.52
1:A:320:A:N6	1:A:321:G:N1	2.58	0.52
5:E:112:LEU:C	5:E:114:GLY:N	2.63	0.52
1:A:473:C:O5'	1:A:473:C:H6	1.92	0.52
1:A:397:G:C6	1:A:398:C:C5	2.98	0.52
1:A:934:U:H1'	1:A:937:U:C5	2.45	0.52
1:A:50:A:O2'	1:A:52:G:C8	2.62	0.52
3:C:180:ALA:O	3:C:181:ASN:CB	2.58	0.52
11:K:15:ALA:CA	11:K:77:MET:HA	2.41	0.51
1:A:317:C:O2'	1:A:318:U:H5'	2.10	0.51
1:A:1346:U:O2'	1:A:1347:G:OP1	2.23	0.51
1:A:911:C:C4'	1:A:912:A:OP1	2.58	0.51
1:A:245:A:H4'	1:A:246:G:O5'	2.08	0.51
1:A:1248:C:O2	1:A:1308:C:H4'	2.09	0.51
1:A:1258:C:H2'	1:A:1259:U:H5'	1.91	0.51
11:K:48:ILE:O	11:K:49:GLY:C	2.48	0.51
11:K:79:SER:HA	11:K:104:GLN:O	2.10	0.51
1:A:1100:C:O4'	1:A:1160:A:H1'	2.09	0.51
3:C:23:TYR:O	3:C:24:ALA:HB2	2.09	0.51
1:A:1195:C:H5''	1:A:1196:G:OP2	2.09	0.51
1:A:937:U:O2'	1:A:938:U:OP2	2.28	0.51
7:G:21:VAL:O	7:G:23:VAL:N	2.43	0.51
1:A:1034:U:O4	1:A:1181:C:H2'	2.10	0.51
1:A:190:G:H22	1:A:258:A:H4'	1.76	0.51
1:A:549:G:C4'	1:A:550:G:OP1	2.57	0.51
1:A:886:A:H2'	1:A:887:C:O4'	2.10	0.51
1:A:610:G:O2'	1:A:611:G:H5'	2.10	0.51
1:A:1021:C:H2'	1:A:1022:U:C6	2.46	0.51
1:A:125:C:OP1	1:A:258:A:H4'	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:892:A:H2'	1:A:893:G:C5'	2.40	0.51
1:A:796:U:OP1	1:A:881:C:H5'	2.10	0.51
3:C:48:TYR:O	3:C:50:ALA:N	2.44	0.51
1:A:656:G:H2'	1:A:657:G:C8	2.45	0.51
1:A:1479:A:H2	1:A:1482:G:N2	2.06	0.51
20:T:30:LYS:O	20:T:31:SER:C	2.49	0.51
1:A:423:G:O2'	1:A:424:U:P	2.69	0.51
1:A:798:A:N1	1:A:1506:G:H2'	2.24	0.51
1:A:597:A:H2'	1:A:598:C:C6	2.45	0.51
1:A:597:A:C2	1:A:610:G:C2	2.98	0.51
19:S:16:LEU:C	19:S:18:LYS:H	2.14	0.51
1:A:87:C:H2'	1:A:88:G:H8	1.76	0.51
1:A:82:U:H2'	1:A:83:A:C8	2.45	0.51
1:A:642:U:O2'	1:A:643:G:H5'	2.11	0.51
13:M:49:THR:O	13:M:52:GLU:N	2.44	0.51
1:A:85:U:H2'	1:A:86:C:C6	2.46	0.51
1:A:1289:U:H2'	1:A:1290:G:H8	1.76	0.51
1:A:1267:A:H2'	1:A:1268:A:H5''	1.91	0.51
14:N:28:GLY:O	14:N:30:ALA:N	2.44	0.51
1:A:919:G:H2'	1:A:920:U:C6	2.46	0.51
7:G:31:MET:HA	7:G:39:ALA:HB2	1.92	0.51
15:O:16:ALA:C	15:O:18:PHE:H	2.14	0.51
9:I:118:LYS:O	9:I:119:ALA:CB	2.58	0.51
1:A:231:G:H2'	1:A:232:C:O4'	2.11	0.51
15:O:27:VAL:O	15:O:28:GLN:C	2.49	0.51
1:A:795:C:O2'	1:A:796:U:C6	2.63	0.51
7:G:35:LYS:O	7:G:36:LYS:C	2.48	0.51
1:A:120:G:O3'	17:Q:2:PRO:N	2.43	0.51
7:G:24:THR:O	7:G:27:ILE:N	2.43	0.51
1:A:561:C:H42	1:A:746:G:H1	1.57	0.51
10:J:18:ALA:O	10:J:19:SER:C	2.49	0.51
1:A:116:C:H5''	1:A:306:C:O2'	2.11	0.51
1:A:1407:U:C2	1:A:1408:C:C5	2.99	0.51
1:A:1296:U:C4	1:A:1297:G:C6	2.99	0.51
1:A:526:C:O2'	1:A:527:G:H5'	2.11	0.51
6:F:5:GLU:O	6:F:90:VAL:HA	2.11	0.51
1:A:198:U:H1'	20:T:103:GLY:HA2	1.93	0.51
1:A:322:A:O3'	1:A:323:C:C4'	2.59	0.50
17:Q:92:ARG:O	17:Q:93:GLN:C	2.50	0.50
1:A:635:U:O2'	1:A:636:A:H5''	2.10	0.50
1:A:270:G:H5'	17:Q:14:LYS:CB	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:11:LYS:O	14:N:13:THR:N	2.44	0.50
1:A:329:C:O5'	1:A:329:C:H6	1.94	0.50
6:F:97:PHE:O	6:F:98:LEU:C	2.50	0.50
1:A:1140:C:C2'	1:A:1140:C:O2	2.59	0.50
1:A:488:G:C6	1:A:518:A:C2	2.98	0.50
1:A:500:G:O6	1:A:514:U:H1'	2.11	0.50
1:A:500:G:N2	1:A:516:A:OP2	2.44	0.50
1:A:385:C:H2'	1:A:386:G:H8	1.76	0.50
1:A:648:A:H2'	1:A:708:G:H21	1.73	0.50
5:E:127:ASN:O	5:E:129:ILE:N	2.45	0.50
1:A:731:C:HO2'	1:A:732:C:H6	1.59	0.50
1:A:521:G:OP1	12:L:114:LYS:N	2.44	0.50
1:A:911:C:H5'	1:A:912:A:OP1	2.12	0.50
1:A:436:C:H6	1:A:436:C:O5'	1.95	0.50
1:A:87:C:H2'	1:A:88:G:C8	2.46	0.50
18:R:7:LYS:N	18:R:11:GLU:N	2.59	0.50
1:A:1250:A:H5'	21:U:18:TYR:O	2.11	0.50
17:Q:63:ARG:O	17:Q:64:PRO:C	2.47	0.50
17:Q:65:ILE:O	17:Q:66:SER:CB	2.60	0.50
1:A:1384:C:H2'	1:A:1385:C:O4'	2.12	0.50
1:A:1474:G:H2'	1:A:1475:U:H5'	1.93	0.50
1:A:670:A:HO2'	1:A:671:G:P	2.33	0.50
1:A:145:A:C2	1:A:146:A:H1'	2.46	0.50
1:A:1080:C:O2'	1:A:1081:G:H5'	2.11	0.50
1:A:981:G:N2	1:A:1020:C:N3	2.59	0.50
4:D:176:LEU:HA	4:D:183:GLY:HA2	1.94	0.50
18:R:17:SER:O	18:R:19:LYS:N	2.45	0.50
7:G:48:LYS:O	7:G:50:ILE:N	2.45	0.50
11:K:95:ILE:O	11:K:98:LEU:N	2.41	0.50
1:A:1039:G:C2'	1:A:1040:G:H5'	2.41	0.50
1:A:1039:G:H2'	1:A:1040:G:C5'	2.41	0.50
1:A:627:G:C5	1:A:628:C:C5	2.99	0.50
1:A:468:G:H4'	1:A:469:G:O5'	2.11	0.50
1:A:1012:A:H2'	1:A:1013:G:C5'	2.41	0.50
20:T:84:LEU:O	20:T:86:ARG:N	2.44	0.50
1:A:1063:G:H2'	1:A:1064:G:C8	2.47	0.50
1:A:359:A:C2	1:A:360:U:O4	2.64	0.50
1:A:795:C:H1'	1:A:796:U:C5	2.46	0.50
1:A:1070:G:H21	1:A:1149:A:H61	1.60	0.50
5:E:100:VAL:O	5:E:118:ILE:O	2.29	0.50
1:A:669:U:N3	1:A:670:A:N7	2.60	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:59:TYR:O	11:K:61:ALA:N	2.45	0.50
11:K:58:PRO:O	11:K:61:ALA:HB3	2.12	0.50
1:A:862:G:H1'	1:A:891:A:N1	2.26	0.50
1:A:982:A:H2'	1:A:983:A:C5'	2.42	0.50
1:A:212:C:H2'	1:A:213:C:H6	1.75	0.50
1:A:1205:G:H4'	1:A:1206:A:OP1	2.11	0.50
1:A:1206:A:C3'	1:A:1207:C:H5'	2.42	0.50
1:A:1108:U:O5'	1:A:1108:U:H6	1.94	0.50
5:E:105:VAL:O	5:E:106:PRO:C	2.48	0.50
11:K:68:ALA:O	11:K:72:ALA:CB	2.60	0.50
1:A:539:C:O2'	1:A:540:G:H5'	2.12	0.50
20:T:61:SER:O	20:T:62:LEU:C	2.50	0.50
1:A:4:U:C2'	1:A:4:U:O2	2.59	0.50
1:A:54:C:H42	1:A:352:G:H1	1.59	0.50
1:A:800:C:H4'	1:A:801:G:O5'	2.11	0.50
1:A:261:G:O2'	1:A:262:C:P	2.70	0.50
1:A:775:A:H2'	1:A:777:A:N7	2.25	0.50
1:A:1018:G:N2	1:A:1019:C:H1'	2.27	0.50
1:A:47:C:HO2'	1:A:48:C:P	2.33	0.50
9:I:89:ASN:O	9:I:91:ASP:N	2.45	0.50
20:T:32:ALA:O	20:T:33:ILE:C	2.50	0.50
20:T:30:LYS:O	20:T:33:ILE:N	2.45	0.50
1:A:1514:U:H4'	1:A:1515:C:OP1	2.12	0.50
1:A:817:C:H2'	1:A:818:U:C6	2.47	0.50
1:A:423:G:H4'	1:A:424:U:O5'	2.12	0.50
1:A:720:A:C2	1:A:721:C:C2	3.00	0.50
14:N:42:ILE:C	14:N:44:LEU:N	2.65	0.50
1:A:215:G:O2'	1:A:216:C:H5'	2.12	0.50
1:A:625:A:C2	8:H:113:SER:O	2.65	0.50
11:K:68:ALA:O	11:K:72:ALA:HB2	2.11	0.50
1:A:621:G:O2'	1:A:622:G:H5'	2.11	0.50
1:A:1442:C:H2'	1:A:1443:C:O4'	2.11	0.50
3:C:121:ALA:HB2	3:C:187:ALA:HB1	1.94	0.50
1:A:1281:G:O2'	1:A:1282:U:H6	1.94	0.50
1:A:1287:A:C2	1:A:1313:A:H1'	2.47	0.50
1:A:516:A:O2'	1:A:517:U:OP1	2.27	0.50
1:A:578:G:C5	1:A:624:U:C5	3.00	0.50
5:E:131:ILE:CA	5:E:134:ALA:HB3	2.42	0.50
1:A:952:A:C4'	1:A:953:G:H5'	2.42	0.50
1:A:980:G:H2'	1:A:981:G:O4'	2.12	0.50
14:N:22:THR:O	14:N:23:ARG:O	2.30	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:748:G:H1	1:A:795:C:H2'	1.76	0.50
1:A:599:G:H2'	1:A:600:G:C8	2.47	0.50
11:K:59:TYR:C	11:K:61:ALA:H	2.15	0.49
1:A:373:G:N2	1:A:381:C:C2	2.80	0.49
2:B:81:VAL:O	2:B:85:ALA:HB2	2.11	0.49
1:A:546:A:H1'	1:A:549:G:O2'	2.12	0.49
1:A:928:G:HO2'	1:A:947:C:HO2'	1.60	0.49
1:A:963:A:H2'	1:A:964:G:H8	1.76	0.49
1:A:1402:C:H2'	1:A:1403:G:H8	1.77	0.49
7:G:37:ASN:O	7:G:40:ALA:HB3	2.12	0.49
17:Q:32:TYR:O	17:Q:34:LYS:N	2.45	0.49
19:S:46:GLY:O	19:S:47:HIS:O	2.30	0.49
1:A:1139:A:H1'	1:A:1162:G:C2	2.45	0.49
1:A:1162:G:O2'	1:A:1163:G:C8	2.65	0.49
1:A:801:G:H2'	1:A:802:A:H5''	1.94	0.49
1:A:993:A:H2'	1:A:994:A:C8	2.47	0.49
1:A:563:U:H2'	1:A:564:G:O4'	2.12	0.49
1:A:1109:G:H21	1:A:1128:A:H62	1.59	0.49
1:A:438:C:H2'	1:A:439:G:C8	2.47	0.49
1:A:414:C:O2'	1:A:415:U:H5'	2.11	0.49
1:A:1000:G:H2'	1:A:1001:G:H8	1.77	0.49
1:A:996:C:H6	1:A:996:C:O5'	1.95	0.49
1:A:1231:A:C5'	9:I:68:GLY:H	2.25	0.49
1:A:949:C:O2'	1:A:950:G:H5'	2.12	0.49
10:J:18:ALA:HB2	24:J:1009:WO2:O20	2.11	0.49
1:A:269:A:HO2'	1:A:270:G:H8	1.50	0.49
16:P:78:GLY:C	16:P:80:PHE:N	2.65	0.49
1:A:599:G:H2'	1:A:600:G:H8	1.76	0.49
1:A:198:U:O2'	1:A:199:C:H5'	2.12	0.49
17:Q:29:HIS:CB	17:Q:32:TYR:H	2.26	0.49
19:S:40:ILE:O	19:S:67:VAL:O	2.30	0.49
2:B:51:LEU:O	2:B:52:GLU:C	2.50	0.49
1:A:515:A:H2'	1:A:516:A:C5'	2.39	0.49
1:A:516:A:H2'	1:A:518:A:OP2	2.12	0.49
1:A:516:A:HO2'	1:A:517:U:P	2.35	0.49
1:A:368:A:O2'	1:A:369:A:H5'	2.11	0.49
1:A:890:A:H1'	1:A:891:A:O4'	2.12	0.49
1:A:327:G:H2'	1:A:328:G:C8	2.43	0.49
1:A:1026:A:H2'	1:A:1027:C:C5'	2.42	0.49
1:A:1508:A:C5	1:A:1509:U:C4	3.01	0.49
2:B:141:GLU:O	2:B:143:GLU:N	2.45	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:222:ILE:O	2:B:225:ALA:HB2	2.12	0.49
1:A:1155:G:O2'	1:A:1156:G:H5'	2.11	0.49
4:D:149:ALA:HB3	4:D:152:SER:CB	2.42	0.49
2:B:77:ALA:O	2:B:79:ASP:N	2.45	0.49
1:A:92:U:C2	1:A:93:C:C5	3.00	0.49
1:A:397:G:O2'	1:A:398:C:H5'	2.12	0.49
5:E:86:ALA:HB3	5:E:125:SER:CB	2.42	0.49
1:A:1488:G:H2'	1:A:1489:U:O4'	2.13	0.49
1:A:320:A:H2'	1:A:321:G:O4'	2.12	0.49
2:B:69:LEU:HA	2:B:91:PRO:O	2.13	0.49
13:M:5:ALA:O	13:M:6:GLY:C	2.51	0.49
12:L:127:GLU:C	12:L:129:ALA:H	2.15	0.49
1:A:904:G:O2'	1:A:905:G:H5'	2.13	0.49
1:A:163:C:H2'	1:A:164:U:C6	2.48	0.49
1:A:500:G:C2'	1:A:501:C:OP2	2.60	0.49
1:A:106:G:H1'	1:A:349:G:C5'	2.42	0.49
1:A:479:A:H1'	1:A:480:A:C8	2.47	0.49
1:A:941:A:N6	1:A:942:A:N6	2.60	0.49
1:A:1130:U:C5	1:A:1131:C:C4	3.00	0.49
1:A:764:A:C2	1:A:1491:C:H4'	2.47	0.49
1:A:1323:C:H2'	1:A:1324:G:C8	2.47	0.49
19:S:12:ASP:C	19:S:14:HIS:H	2.16	0.49
7:G:6:ARG:O	7:G:7:ALA:O	2.31	0.49
1:A:100:G:N7	1:A:101:G:N2	2.60	0.49
1:A:1506:G:C4'	1:A:1507:G:OP2	2.56	0.49
1:A:1395:A:C4	1:A:1465:G:N2	2.80	0.49
1:A:952:A:O5'	1:A:953:G:H5'	2.12	0.49
1:A:921:G:H2'	1:A:1319:G:O6	2.13	0.49
13:M:71:ARG:O	13:M:72:ALA:C	2.50	0.49
1:A:907:C:C2'	1:A:908:C:H5'	2.42	0.49
2:B:94:ASN:O	2:B:95:GLN:O	2.31	0.49
9:I:32:ASP:O	9:I:35:GLU:N	2.43	0.49
1:A:278:C:O5'	1:A:278:C:H6	1.96	0.49
1:A:1385:C:H2'	1:A:1386:C:C6	2.46	0.49
1:A:369:A:C2	1:A:370:U:C2	3.00	0.49
1:A:993:A:H1'	1:A:1199:C:O2'	2.13	0.49
1:A:208:U:O2'	1:A:209:U:P	2.71	0.49
1:A:1424:G:N3	1:A:1424:G:H3'	2.28	0.49
1:A:1201:G:H2'	1:A:1202:G:H8	1.78	0.49
2:B:105:PHE:C	2:B:107:THR:N	2.62	0.49
1:A:1189:C:H6	1:A:1189:C:O5'	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:945:A:C4'	1:A:946:A:OP2	2.60	0.49
1:A:1038:U:H5'	3:C:163:ALA:CB	2.42	0.49
13:M:18:ALA:C	13:M:20:THR:H	2.16	0.49
1:A:748:G:N1	1:A:795:C:H2'	2.27	0.49
7:G:36:LYS:O	7:G:39:ALA:N	2.46	0.49
5:E:112:LEU:C	5:E:114:GLY:H	2.15	0.49
2:B:216:SER:O	2:B:219:VAL:N	2.46	0.49
1:A:1146:G:C2	1:A:1147:C:C4	3.01	0.49
4:D:171:GLY:C	4:D:173:TRP:H	2.15	0.49
1:A:1476:A:O2'	1:A:1497:G:H5''	2.12	0.49
1:A:1236:G:O2'	1:A:1239:G:H1'	2.13	0.49
1:A:1468:G:N2	1:A:1469:A:H62	2.11	0.49
1:A:430:C:H2'	1:A:431:C:H6	1.78	0.49
1:A:981:G:N3	1:A:982:A:H1'	2.28	0.49
1:A:1208:A:C2	1:A:1209:C:H1'	2.48	0.49
1:A:937:U:O2	1:A:937:U:C2'	2.61	0.49
1:A:714:G:OP1	1:A:749:A:H1'	2.12	0.49
1:A:817:C:H2'	1:A:818:U:H6	1.78	0.49
1:A:770:A:H2'	1:A:771:U:H6	1.76	0.49
10:J:81:THR:C	10:J:83:GLU:H	2.15	0.49
1:A:916:G:C6	1:A:917:C:N4	2.81	0.49
1:A:282:U:O2'	1:A:283:A:H5'	2.13	0.49
1:A:501:C:H3'	1:A:513:G:C8	2.31	0.48
1:A:395:C:H2'	1:A:396:C:C6	2.48	0.48
1:A:794:C:H4'	1:A:878:A:H61	1.77	0.48
1:A:1229:A:H2'	1:A:1230:C:C6	2.48	0.48
1:A:1261:A:H2'	1:A:1262:U:H5'	1.95	0.48
2:B:75:LYS:C	2:B:77:ALA:H	2.16	0.48
1:A:544:U:H4'	1:A:545:C:OP2	2.12	0.48
1:A:946:A:O2'	1:A:947:C:H5'	2.13	0.48
1:A:1510:C:H4'	1:A:1512:C:N4	2.28	0.48
8:H:120:THR:O	8:H:122:ARG:N	2.46	0.48
1:A:1419:C:H2'	1:A:1420:G:H8	1.77	0.48
1:A:947:C:H4'	1:A:949:C:C5	2.48	0.48
1:A:631:A:H2'	1:A:632:G:C8	2.46	0.48
8:H:120:THR:O	8:H:121:ASP:C	2.51	0.48
11:K:109:VAL:HA	18:R:85:LEU:O	2.14	0.48
1:A:758:G:H2'	1:A:759:G:O4'	2.14	0.48
21:U:13:ILE:O	21:U:16:GLY:N	2.42	0.48
1:A:1503:G:O2'	1:A:1504:C:H5'	2.13	0.48
1:A:577:G:C2'	1:A:578:G:H5'	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1410:A:N1	1:A:1450:A:C6	2.81	0.48
1:A:17:U:H2'	1:A:18:C:C6	2.49	0.48
1:A:315:C:H2'	1:A:316:A:H8	1.72	0.48
1:A:946:A:H2'	1:A:947:C:C5'	2.42	0.48
1:A:1108:U:H2'	1:A:1109:G:H8	1.78	0.48
1:A:842:A:O2'	1:A:843:C:H5'	2.13	0.48
15:O:28:GLN:O	15:O:29:VAL:C	2.51	0.48
1:A:180:C:O2'	20:T:82:SER:HA	2.12	0.48
2:B:88:ALA:O	2:B:90:MET:N	2.47	0.48
17:Q:100:LYS:O	17:Q:102:GLY:N	2.47	0.48
6:F:68:PRO:O	6:F:69:GLU:C	2.52	0.48
1:A:1495:A:H2'	1:A:1496:A:C8	2.48	0.48
1:A:727:C:H4'	1:A:829:G:O2'	2.13	0.48
1:A:788:C:H2'	1:A:789:C:H6	1.77	0.48
1:A:1205:G:N2	1:A:1344:C:N3	2.62	0.48
1:A:205:G:C2'	1:A:206:G:H5'	2.44	0.48
19:S:16:LEU:C	19:S:18:LYS:N	2.67	0.48
1:A:745:C:H2'	1:A:746:G:C8	2.48	0.48
4:D:52:SER:O	4:D:55:ALA:N	2.46	0.48
6:F:71:ARG:O	6:F:72:VAL:C	2.52	0.48
1:A:508:C:H6	1:A:508:C:O5'	1.96	0.48
1:A:1056:G:C6	1:A:1084:A:C6	3.01	0.48
2:B:100:GLY:C	2:B:102:LEU:N	2.67	0.48
1:A:159:C:H2'	1:A:160:G:C8	2.47	0.48
1:A:1167:G:H2'	1:A:1168:G:O5'	2.13	0.48
1:A:276:G:O2'	1:A:277:A:OP2	2.30	0.48
1:A:1219:A:C6	1:A:1220:A:N7	2.81	0.48
11:K:64:ALA:C	11:K:66:LEU:H	2.16	0.48
1:A:1347:G:C6	1:A:1348:C:N3	2.82	0.48
6:F:44:GLY:HA2	6:F:60:PHE:N	2.27	0.48
1:A:1422:C:C2'	1:A:1423:G:H5'	2.43	0.48
1:A:1135:C:H2'	1:A:1136:G:O4'	2.13	0.48
1:A:675:U:H1'	1:A:678:A:N7	2.28	0.48
13:M:49:THR:O	13:M:50:GLU:C	2.51	0.48
3:C:128:PHE:O	3:C:129:ALA:C	2.51	0.48
2:B:201:ILE:O	2:B:203:GLY:N	2.43	0.48
20:T:79:ARG:O	20:T:80:ARG:C	2.51	0.48
1:A:801:G:H3'	1:A:802:A:H5'	1.96	0.48
20:T:18:GLN:O	20:T:19:SER:C	2.51	0.48
2:B:141:GLU:O	2:B:142:LEU:C	2.51	0.48
1:A:1120:G:H3'	1:A:1120:G:N3	2.29	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1295:C:H2'	1:A:1296:U:H6	1.78	0.48
1:A:907:C:H2'	1:A:908:C:H5'	1.96	0.48
1:A:1021:C:H2'	1:A:1022:U:H6	1.79	0.48
18:R:67:ALA:O	18:R:69:THR:N	2.47	0.48
1:A:80:U:H2'	1:A:81:U:OP1	2.14	0.48
1:A:1286:G:O2'	1:A:1287:A:H8	1.97	0.48
1:A:1286:G:H5'	21:U:4:GLY:C	2.34	0.48
1:A:1140:C:C2	1:A:1142:G:C8	3.02	0.48
5:E:125:SER:C	5:E:127:ASN:N	2.67	0.48
1:A:45:U:H2'	1:A:46:G:H8	1.77	0.48
1:A:330:C:O2'	1:A:331:C:H5'	2.12	0.48
15:O:27:VAL:O	15:O:30:ALA:HB3	2.14	0.48
20:T:88:VAL:O	20:T:89:ARG:C	2.50	0.48
1:A:416:U:O2'	1:A:417:C:P	2.71	0.48
4:D:199:ASN:O	4:D:202:LEU:N	2.38	0.48
8:H:31:PHE:O	8:H:34:GLU:N	2.45	0.48
5:E:144:THR:O	5:E:145:LYS:CB	2.62	0.48
19:S:70:LYS:O	19:S:72:GLY:N	2.47	0.48
1:A:201:A:H2'	1:A:202:A:C8	2.48	0.48
1:A:469:G:C2'	1:A:470:U:OP2	2.62	0.48
1:A:801:G:C3'	1:A:802:A:C5'	2.91	0.48
1:A:1467:C:O2'	1:A:1468:G:H5'	2.14	0.48
1:A:1328:G:O2'	1:A:1329:U:P	2.72	0.48
7:G:51:GLN:O	7:G:54:THR:O	2.32	0.48
1:A:950:G:H3'	1:A:951:A:H5''	1.96	0.48
1:A:167:U:H1'	1:A:203:A:C6	2.48	0.48
7:G:141:VAL:C	7:G:143:ARG:N	2.68	0.48
6:F:99:ALA:O	6:F:100:ASN:CB	2.61	0.48
1:A:1432:C:H5''	1:A:1433:G:OP1	2.14	0.48
9:I:50:LEU:CB	9:I:55:ALA:HB3	2.44	0.48
18:R:47:THR:C	18:R:49:LYS:N	2.59	0.47
5:E:81:GLU:HA	5:E:90:VAL:HA	1.95	0.47
1:A:543:U:C5'	1:A:544:U:O5'	2.61	0.47
1:A:1336:G:O2'	1:A:1337:G:H5'	2.14	0.47
15:O:7:GLU:O	15:O:10:LYS:N	2.47	0.47
5:E:105:VAL:O	5:E:107:ARG:N	2.46	0.47
3:C:122:GLU:O	3:C:123:GLN:C	2.52	0.47
1:A:617:C:O2'	1:A:618:G:H5'	2.14	0.47
1:A:347:C:H4'	1:A:349:G:OP1	2.14	0.47
1:A:444:G:OP1	1:A:445:A:O3'	2.33	0.47
1:A:379:G:H2'	1:A:380:C:H6	1.76	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1232:A:H1'	1:A:1351:C:O2'	2.13	0.47
15:O:7:GLU:O	15:O:10:LYS:CB	2.62	0.47
11:K:57:THR:O	11:K:60:ALA:N	2.47	0.47
7:G:36:LYS:O	7:G:40:ALA:N	2.44	0.47
12:L:29:GLY:O	12:L:30:ALA:O	2.32	0.47
8:H:29:SER:O	8:H:30:ARG:C	2.53	0.47
1:A:368:A:C1'	1:A:465:G:H1'	2.44	0.47
1:A:937:U:O2'	1:A:938:U:P	2.72	0.47
1:A:123:G:O2'	1:A:124:A:OP2	2.32	0.47
1:A:1508:A:H2'	1:A:1509:U:C6	2.49	0.47
1:A:1511:A:H3'	1:A:1512:C:C6	2.49	0.47
20:T:56:MET:O	20:T:60:GLU:N	2.43	0.47
1:A:831:G:H3'	1:A:848:U:H3	1.79	0.47
5:E:155:GLU:N	24:E:1005:WO2:O43	2.48	0.47
1:A:1171:G:HO2'	1:A:1172:A:P	2.38	0.47
1:A:1084:A:H2'	1:A:1085:C:H6	1.79	0.47
1:A:396:C:O2'	1:A:604:A:N3	2.45	0.47
1:A:609:U:H2'	1:A:610:G:C8	2.49	0.47
11:K:95:ILE:O	11:K:96:ARG:C	2.53	0.47
5:E:52:PRO:O	5:E:53:LEU:C	2.53	0.47
1:A:1076:G:H5''	1:A:1077:U:H5	1.79	0.47
1:A:1221:U:C4'	1:A:1222:G:OP2	2.60	0.47
1:A:1286:G:H5''	21:U:5:ASP:N	2.29	0.47
1:A:144:C:C2	1:A:145:A:C8	3.02	0.47
1:A:805:C:O2'	1:A:806:G:H5'	2.14	0.47
1:A:1420:G:C6	1:A:1421:C:N4	2.82	0.47
1:A:639:C:H3'	1:A:639:C:H6	1.75	0.47
7:G:143:ARG:C	7:G:145:ALA:N	2.66	0.47
20:T:84:LEU:C	20:T:86:ARG:N	2.68	0.47
3:C:151:VAL:O	3:C:167:TRP:O	2.32	0.47
1:A:1286:G:H5'	21:U:4:GLY:CA	2.45	0.47
1:A:648:A:H2'	1:A:708:G:H22	1.77	0.47
1:A:775:A:C5	1:A:777:A:N6	2.82	0.47
1:A:1452:G:H2'	1:A:1453:G:H8	1.80	0.47
1:A:167:U:H5'	1:A:203:A:O4'	2.15	0.47
1:A:1237:A:H5''	1:A:1238:U:OP1	2.14	0.47
6:F:26:ILE:O	6:F:29:ALA:HB3	2.14	0.47
7:G:69:VAL:O	7:G:70:LYS:C	2.53	0.47
1:A:1494:G:C8	1:A:1494:G:C5'	2.92	0.47
1:A:2:U:H4'	1:A:3:G:N1	2.30	0.47
4:D:31:CYS:O	4:D:32:ALA:HB3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:471:A:H2'	1:A:472:C:O4'	2.15	0.47
1:A:1468:G:N2	1:A:1469:A:N6	2.63	0.47
1:A:653:G:C6	1:A:720:A:N6	2.82	0.47
1:A:577:G:H2'	1:A:578:G:H5'	1.95	0.47
1:A:16:A:N1	1:A:896:A:H2	2.13	0.47
5:E:131:ILE:HA	5:E:134:ALA:CB	2.44	0.47
1:A:952:A:C8	1:A:952:A:H5'	2.45	0.47
3:C:154:SER:CB	3:C:197:GLY:H	2.28	0.47
1:A:1206:A:C2'	1:A:1207:C:C5'	2.91	0.47
1:A:1335:C:O2'	1:A:1336:G:H5'	2.15	0.47
8:H:26:VAL:O	8:H:59:LEU:N	2.46	0.47
11:K:17:GLY:HA3	11:K:33:THR:O	2.14	0.47
1:A:150:G:C2	1:A:160:G:C2	3.02	0.47
15:O:16:ALA:O	15:O:18:PHE:N	2.47	0.47
8:H:31:PHE:O	8:H:32:LYS:C	2.51	0.47
1:A:567:G:H2'	1:A:568:G:H8	1.80	0.47
1:A:469:G:H2'	1:A:470:U:OP2	2.15	0.47
1:A:105:G:H21	1:A:349:G:H5'	1.79	0.47
1:A:368:A:C2	1:A:369:A:C8	3.02	0.47
1:A:798:A:H4'	1:A:800:C:C4	2.50	0.47
1:A:397:G:H4'	1:A:603:C:O2	2.15	0.47
1:A:388:A:O2'	1:A:389:G:H5'	2.15	0.47
1:A:1393:C:H2'	1:A:1394:C:H6	1.78	0.47
1:A:413:C:H2'	1:A:414:C:C6	2.50	0.47
1:A:418:G:H3'	1:A:418:G:N3	2.29	0.47
1:A:873:C:O2'	1:A:874:C:H5'	2.14	0.47
5:E:153:LYS:CA	24:E:1005:WO2:O49	2.63	0.47
1:A:1387:G:O2'	1:A:1388:U:H5'	2.15	0.47
1:A:990:U:H2'	1:A:991:G:H5'	1.97	0.47
1:A:361:C:O2'	1:A:362:U:P	2.73	0.47
1:A:364:C:H2'	1:A:365:C:C6	2.50	0.47
1:A:429:U:H2'	1:A:430:C:H6	1.74	0.47
1:A:214:C:C4	1:A:215:G:N7	2.82	0.47
1:A:1423:G:H4'	1:A:1424:G:C5	2.50	0.47
11:K:24:SER:C	11:K:26:ASN:H	2.17	0.47
1:A:169:C:O2'	1:A:170:C:H5'	2.15	0.47
13:M:36:LYS:O	13:M:38:GLY:N	2.47	0.47
1:A:1398:G:H2'	1:A:1399:G:O4'	2.15	0.47
1:A:445:A:N7	1:A:465:G:C2	2.83	0.47
1:A:1239:G:H2'	1:A:1240:C:C6	2.50	0.47
1:A:1485:G:H2'	1:A:1486:C:O4'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:400:U:O4	4:D:2:GLY:HA3	2.15	0.47
1:A:751:A:H2'	1:A:752:G:O4'	2.15	0.47
1:A:942:A:C2	1:A:946:A:C2	3.03	0.46
1:A:1206:A:C2	1:A:1207:C:C4	3.04	0.46
1:A:932:U:H2'	1:A:933:U:H5'	1.97	0.46
1:A:1108:U:H2'	1:A:1109:G:O4'	2.15	0.46
1:A:156:A:H2'	1:A:157:C:C5'	2.44	0.46
7:G:124:LEU:O	7:G:127:ALA:N	2.46	0.46
1:A:691:C:O2'	1:A:692:G:H5'	2.14	0.46
7:G:26:PHE:O	7:G:27:ILE:C	2.52	0.46
11:K:69:ALA:O	11:K:72:ALA:N	2.48	0.46
1:A:130:C:H2'	1:A:131:C:H6	1.79	0.46
5:E:155:GLU:O	5:E:156:ALA:CB	2.62	0.46
21:U:2:GLY:O	21:U:3:LYS:C	2.54	0.46
5:E:90:VAL:N	5:E:121:LYS:O	2.48	0.46
6:F:15:ASP:O	6:F:18:GLN:N	2.48	0.46
1:A:764:A:C2	1:A:1491:C:C4'	2.99	0.46
15:O:51:HIS:O	15:O:52:SER:C	2.53	0.46
11:K:57:THR:O	11:K:60:ALA:CB	2.64	0.46
1:A:171:C:H2'	1:A:172:C:H6	1.78	0.46
3:C:46:GLU:O	3:C:48:TYR:N	2.44	0.46
3:C:48:TYR:C	3:C:50:ALA:N	2.68	0.46
11:K:49:GLY:O	11:K:50:TYR:C	2.53	0.46
1:A:253:G:H2'	1:A:254:G:H8	1.81	0.46
1:A:1219:A:C2	1:A:1222:G:N3	2.83	0.46
1:A:670:A:O2'	1:A:671:G:OP2	2.31	0.46
1:A:1176:C:C3'	1:A:1177:U:C5'	2.91	0.46
16:P:9:PHE:C	16:P:10:GLY:O	2.54	0.46
12:L:109:GLY:HA3	12:L:121:GLY:O	2.15	0.46
1:A:8:A:H4'	1:A:9:G:OP1	2.15	0.46
6:F:15:ASP:O	6:F:16:GLN:C	2.54	0.46
16:P:23:ASP:O	16:P:24:ALA:C	2.54	0.46
1:A:1341:A:C2	1:A:1342:G:H1'	2.51	0.46
1:A:1051:C:C2'	1:A:1052:U:O5'	2.63	0.46
1:A:609:U:H2'	1:A:610:G:H8	1.80	0.46
1:A:525:G:N2	1:A:526:C:C2	2.83	0.46
4:D:61:LYS:C	4:D:63:LYS:N	2.68	0.46
1:A:1357:A:H2'	1:A:1358:U:O4'	2.15	0.46
9:I:20:ARG:O	9:I:22:GLY:N	2.42	0.46
14:N:54:PRO:C	14:N:56:VAL:H	2.18	0.46
1:A:720:A:H2'	1:A:721:C:C6	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:365:C:C2	1:A:366:G:C8	3.04	0.46
1:A:153:G:H2'	1:A:155:A:OP2	2.14	0.46
1:A:927:U:H6	1:A:927:U:O5'	1.98	0.46
13:M:87:TYR:C	13:M:89:GLY:N	2.66	0.46
1:A:764:A:H2'	1:A:765:A:H5'	1.97	0.46
1:A:734:U:H1'	15:O:23:GLY:O	2.15	0.46
1:A:1496:A:H2'	1:A:1497:G:H5'	1.97	0.46
1:A:669:U:C4	1:A:686:G:N3	2.84	0.46
1:A:163:C:O2'	1:A:164:U:H5'	2.16	0.46
1:A:720:A:O2'	1:A:721:C:H5'	2.15	0.46
1:A:1115:G:H2'	1:A:1116:G:C8	2.41	0.46
17:Q:59:ILE:HA	17:Q:72:ARG:O	2.15	0.46
1:A:65:U:C1'	1:A:206:G:H4'	2.45	0.46
5:E:17:ALA:H	5:E:26:PHE:HA	1.78	0.46
2:B:65:GLY:O	2:B:66:GLY:O	2.34	0.46
5:E:155:GLU:O	24:E:1005:WO2:O9	2.33	0.46
1:A:594:A:H2	1:A:613:G:H22	1.62	0.46
1:A:562:G:C6	1:A:563:U:C4	3.04	0.46
1:A:1191:C:H4'	1:A:1195:C:H41	1.80	0.46
14:N:12:ARG:O	14:N:13:THR:C	2.53	0.46
1:A:820:G:C2	1:A:821:G:H1'	2.51	0.46
16:P:11:SER:O	16:P:12:LYS:O	2.34	0.46
1:A:1166:G:O2'	1:A:1167:G:H5'	2.16	0.46
11:K:91:ARG:O	11:K:93:GLN:N	2.40	0.46
1:A:1480:A:O2'	1:A:1481:G:OP1	2.32	0.46
1:A:798:A:H2'	1:A:1503:G:H21	1.80	0.46
1:A:553:G:O4'	1:A:803:U:C2	2.68	0.46
1:A:862:G:O2'	1:A:863:G:H5'	2.16	0.46
1:A:157:C:O2'	1:A:158:U:H5'	2.16	0.46
16:P:71:ARG:O	16:P:72:ARG:C	2.54	0.46
4:D:24:GLU:O	4:D:26:CYS:N	2.49	0.46
1:A:1267:A:C3'	1:A:1268:A:C5'	2.90	0.46
1:A:1328:G:H21	1:A:1355:G:H2'	1.80	0.46
1:A:1150:A:N1	1:A:1151:A:C2	2.83	0.46
13:M:20:THR:C	13:M:22:ILE:N	2.69	0.46
1:A:1455:C:H6	1:A:1455:C:O5'	1.99	0.46
13:M:51:ALA:O	13:M:52:GLU:C	2.54	0.46
1:A:901:C:O5'	1:A:901:C:H6	1.98	0.46
9:I:49:PRO:O	9:I:52:ALA:HB3	2.15	0.46
1:A:512:G:H5'	1:A:516:A:C2	2.50	0.46
1:A:106:G:H1'	1:A:349:G:H5''	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:463:C:H2'	1:A:464:U:O4'	2.16	0.46
1:A:1047:U:H4'	1:A:1048:C:O5'	2.16	0.46
1:A:1056:G:N1	1:A:1084:A:C6	2.84	0.46
1:A:724:G:H2'	1:A:725:G:O4'	2.16	0.46
1:A:731:C:O2'	1:A:732:C:C6	2.67	0.46
1:A:209:U:C5'	1:A:210:U:OP1	2.64	0.46
1:A:116:C:OP1	1:A:307:C:H5'	2.16	0.46
1:A:925:C:O2'	1:A:926:A:H5'	2.16	0.46
1:A:607:C:H2'	1:A:608:G:H8	1.81	0.46
1:A:1434:G:H2'	1:A:1435:G:H8	1.81	0.46
21:U:10:ARG:O	21:U:11:GLY:C	2.54	0.46
1:A:1046:G:C4'	1:A:1047:U:C5'	2.87	0.46
6:F:43:LEU:O	6:F:44:GLY:O	2.34	0.46
19:S:42:PRO:C	19:S:44:MET:N	2.70	0.46
1:A:958:U:H2'	1:A:959:U:C6	2.51	0.46
1:A:181:C:H2'	1:A:182:C:O4'	2.16	0.46
1:A:954:A:O2'	1:A:956:C:OP2	2.16	0.46
20:T:58:LYS:O	20:T:59:ALA:C	2.55	0.46
1:A:811:A:H2'	1:A:812:G:O4'	2.16	0.46
10:J:39:PRO:O	10:J:40:LEU:CB	2.64	0.46
1:A:276:G:O2'	1:A:277:A:P	2.74	0.45
1:A:1285:G:N1	1:A:1313:A:OP2	2.47	0.45
1:A:990:U:C2'	1:A:991:G:H5'	2.46	0.45
1:A:969:U:O2'	1:A:970:G:OP2	2.34	0.45
1:A:704:G:H4'	1:A:705:A:O4'	2.17	0.45
1:A:222:G:O2'	1:A:223:A:H5'	2.16	0.45
1:A:1073:U:O2	1:A:1075:A:C8	2.69	0.45
1:A:118:U:O3'	1:A:616:G:N2	2.49	0.45
1:A:689:A:H8	1:A:689:A:O5'	1.99	0.45
4:D:35:ARG:O	4:D:36:ARG:CB	2.63	0.45
1:A:1290:G:H22	1:A:1310:A:H1'	1.81	0.45
1:A:1374:G:H2'	1:A:1375:U:O4'	2.17	0.45
1:A:1479:A:C6	1:A:1481:G:C2	3.04	0.45
11:K:76:GLY:O	11:K:77:MET:C	2.55	0.45
1:A:295:A:H2'	1:A:296:G:H5'	1.98	0.45
1:A:170:C:H2'	1:A:171:C:C6	2.50	0.45
7:G:20:ASP:O	7:G:21:VAL:C	2.54	0.45
19:S:5:LEU:O	19:S:6:LYS:CB	2.64	0.45
1:A:1477:A:H2'	1:A:1478:C:H5'	1.96	0.45
1:A:1043:G:N2	1:A:1178:G:H1'	2.30	0.45
1:A:445:A:O2'	1:A:446:A:OP2	2.34	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:899:G:H2'	1:A:900:A:H8	1.80	0.45
20:T:19:SER:O	20:T:20:LEU:C	2.55	0.45
1:A:1189:C:O2'	1:A:1190:C:H5'	2.17	0.45
1:A:1204:C:C5'	1:A:1205:G:H5''	2.46	0.45
1:A:1215:C:H5'	1:A:1347:G:OP1	2.16	0.45
1:A:8:A:O3'	1:A:9:G:O4'	2.33	0.45
5:E:36:ASP:O	5:E:37:ARG:CB	2.65	0.45
15:O:78:TYR:O	15:O:79:ARG:C	2.55	0.45
10:J:9:ARG:HA	10:J:68:HIS:O	2.16	0.45
1:A:523:G:H2'	1:A:524:G:O4'	2.16	0.45
7:G:112:PRO:O	7:G:113:GLU:C	2.55	0.45
1:A:412:C:H42	1:A:421:G:H1	1.63	0.45
1:A:1327:A:O2'	1:A:1328:G:P	2.74	0.45
1:A:1201:G:C4	1:A:1202:G:C8	3.04	0.45
18:R:37:VAL:O	18:R:38:GLU:C	2.54	0.45
1:A:1345:A:N3	1:A:1345:A:H2'	2.31	0.45
1:A:178:G:H2'	1:A:179:A:C8	2.50	0.45
1:A:568:G:N3	1:A:856:C:H4'	2.31	0.45
1:A:973:A:H2'	1:A:974:U:C6	2.51	0.45
8:H:91:ARG:O	8:H:92:ARG:C	2.54	0.45
3:C:86:VAL:O	3:C:90:GLU:N	2.41	0.45
1:A:849:A:HO2'	1:A:850:A:C5'	2.25	0.45
1:A:1268:A:H2'	1:A:1269:A:C8	2.52	0.45
1:A:740:U:OP1	1:A:805:C:O2'	2.31	0.45
1:A:191:G:C6	1:A:192:G:N7	2.85	0.45
1:A:895:A:H2'	1:A:896:A:O4'	2.16	0.45
1:A:678:A:H2'	1:A:679:A:C8	2.50	0.45
1:A:679:A:N1	1:A:780:C:O2'	2.46	0.45
1:A:599:G:N2	1:A:608:G:C4	2.85	0.45
1:A:88:G:H2'	1:A:89:U:O4'	2.17	0.45
1:A:1146:G:C2	1:A:1154:G:C6	3.05	0.45
1:A:1139:A:C6	1:A:1161:A:C5	3.05	0.45
1:A:38:G:H22	1:A:392:A:H5''	1.80	0.45
5:E:89:ILE:HA	5:E:121:LYS:O	2.16	0.45
1:A:988:G:N2	1:A:998:U:H1'	2.32	0.45
1:A:642:U:C2'	1:A:643:G:H5'	2.46	0.45
6:F:68:PRO:O	6:F:70:ASP:N	2.50	0.45
4:D:202:LEU:O	4:D:203:VAL:C	2.53	0.45
1:A:424:U:O2'	1:A:425:A:C5'	2.44	0.45
1:A:1162:G:C2	1:A:1163:G:N2	2.85	0.45
1:A:32:A:H2'	1:A:33:A:C8	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:317:C:C2'	1:A:318:U:H5'	2.46	0.45
1:A:1344:C:H5'	1:A:1345:A:O5'	2.17	0.45
1:A:203:A:O2'	1:A:204:G:C8	2.68	0.45
3:C:39:ILE:C	3:C:41:GLY:N	2.68	0.45
1:A:1296:U:H2'	1:A:1297:G:O4'	2.17	0.45
1:A:770:A:H2'	1:A:771:U:C6	2.52	0.45
1:A:663:C:H2'	1:A:664:C:H6	1.82	0.45
10:J:16:LEU:O	10:J:17:ASP:C	2.55	0.45
1:A:595:C:O2	1:A:612:G:N2	2.50	0.45
1:A:106:G:H2'	1:A:107:U:O4'	2.17	0.45
1:A:369:A:C2	1:A:386:G:O4'	2.70	0.45
1:A:375:G:N1	1:A:379:G:C6	2.85	0.45
1:A:544:U:O2'	1:A:545:C:P	2.75	0.45
1:A:953:G:OP1	14:N:31:ARG:O	2.34	0.45
11:K:62:GLN:HA	11:K:97:ALA:HB2	1.99	0.45
1:A:1102:G:H2'	1:A:1103:U:C6	2.50	0.45
20:T:56:MET:O	20:T:59:ALA:HB3	2.17	0.45
6:F:48:LEU:HA	18:R:77:GLY:O	2.16	0.45
1:A:3:G:O6	1:A:594:A:C2	2.70	0.45
1:A:801:G:O2'	1:A:803:U:C5	2.48	0.45
1:A:396:C:H1'	1:A:605:A:H1'	1.98	0.45
1:A:38:G:H22	1:A:392:A:C5'	2.29	0.45
1:A:323:C:C2'	1:A:324:A:OP2	2.64	0.45
1:A:1210:A:H2'	1:A:1211:C:C6	2.52	0.45
13:M:70:LEU:O	13:M:71:ARG:C	2.55	0.45
18:R:67:ALA:C	18:R:69:THR:N	2.69	0.45
9:I:79:LEU:O	9:I:80:GLY:C	2.56	0.45
10:J:27:ALA:C	10:J:29:ARG:H	2.20	0.45
1:A:225:G:H2'	1:A:226:G:O4'	2.17	0.45
1:A:1046:G:C4'	1:A:1047:U:H5'	2.47	0.45
1:A:397:G:C2	1:A:398:C:C6	3.05	0.45
1:A:16:A:N1	1:A:896:A:C2	2.85	0.45
1:A:542:A:H4'	1:A:543:U:O5'	2.17	0.45
1:A:295:A:H2'	1:A:296:G:O4'	2.16	0.45
1:A:1206:A:H4'	1:A:1207:C:OP1	2.16	0.45
1:A:637:G:H2'	1:A:638:A:O4'	2.16	0.45
1:A:115:G:H2'	1:A:116:C:H6	1.82	0.45
1:A:214:C:H2'	1:A:215:G:O4'	2.17	0.45
1:A:8:A:N3	1:A:8:A:C2'	2.80	0.45
1:A:1053:C:C2	1:A:1087:A:C2	3.05	0.45
20:T:86:ARG:O	20:T:87:LYS:C	2.55	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:K:115:PRO:C	11:K:117:ASN:N	2.71	0.45
1:A:823:C:H5''	1:A:824:U:OP1	2.15	0.45
1:A:227:G:C4	1:A:228:C:C6	3.05	0.45
1:A:126:C:O2'	1:A:127:U:H5'	2.17	0.45
1:A:680:U:H2'	1:A:681:G:H5'	1.99	0.45
2:B:4:GLU:C	2:B:6:THR:H	2.21	0.45
9:I:53:VAL:O	9:I:54:ASP:CB	2.65	0.45
1:A:1309:C:H2'	1:A:1310:A:H8	1.82	0.44
4:D:30:LYS:C	4:D:32:ALA:H	2.21	0.44
1:A:516:A:O2'	1:A:517:U:P	2.75	0.44
1:A:1127:C:O2'	1:A:1128:A:O5'	2.32	0.44
4:D:89:THR:O	4:D:90:GLY:O	2.34	0.44
1:A:625:A:N3	8:H:113:SER:O	2.50	0.44
2:B:163:PHE:HA	2:B:185:ILE:O	2.17	0.44
14:N:55:GLY:O	14:N:57:ARG:N	2.49	0.44
1:A:463:C:C2'	1:A:464:U:H5'	2.46	0.44
5:E:127:ASN:O	5:E:128:PRO:C	2.53	0.44
1:A:117:G:H4'	1:A:286:C:O2'	2.17	0.44
1:A:8:A:O2'	5:E:103:GLY:HA2	2.17	0.44
1:A:1182:A:O2'	1:A:1183:G:OP2	2.31	0.44
1:A:152:G:H2'	1:A:153:G:H5'	1.99	0.44
1:A:339:A:H5''	1:A:340:C:C5	2.47	0.44
1:A:1100:C:O2'	1:A:1101:C:H5'	2.17	0.44
7:G:114:ARG:CB	24:G:1007:WO2:O49	2.65	0.44
1:A:1099:G:H5'	1:A:1099:G:H8	1.83	0.44
1:A:442:A:OP2	1:A:469:G:N2	2.50	0.44
1:A:163:C:H2'	1:A:164:U:H6	1.82	0.44
1:A:369:A:H2'	1:A:370:U:C6	2.52	0.44
1:A:54:C:C5	1:A:347:C:C5	3.05	0.44
1:A:1205:G:O2'	1:A:1206:A:P	2.76	0.44
1:A:585:A:C6	1:A:586:U:N3	2.86	0.44
1:A:1341:A:H2'	1:A:1342:G:O4'	2.17	0.44
1:A:689:A:C8	1:A:689:A:H3'	2.53	0.44
9:I:80:GLY:O	9:I:81:ILE:C	2.55	0.44
6:F:52:ILE:O	6:F:53:ALA:HB3	2.17	0.44
4:D:25:ARG:O	4:D:28:SER:N	2.50	0.44
1:A:1390:A:C6	1:A:1391:C:N4	2.84	0.44
1:A:1206:A:H2'	1:A:1207:C:C5'	2.46	0.44
2:B:44:LEU:O	2:B:46:LYS:N	2.49	0.44
1:A:825:C:H6	1:A:825:C:O5'	2.00	0.44
1:A:745:C:H2'	1:A:746:G:H8	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:187:ALA:O	3:C:198:VAL:N	2.49	0.44
16:P:71:ARG:O	16:P:74:LEU:N	2.50	0.44
3:C:19:GLU:O	3:C:56:ASP:HA	2.17	0.44
11:K:8:LYS:N	24:K:1014:WO2:O5	2.51	0.44
1:A:1219:A:N7	1:A:1284:C:H1'	2.32	0.44
1:A:1222:G:H2'	1:A:1223:C:H6	1.80	0.44
1:A:144:C:O2	1:A:145:A:C8	2.70	0.44
1:A:501:C:H1'	1:A:512:G:C6	2.53	0.44
1:A:105:G:N2	1:A:349:G:H5'	2.33	0.44
2:B:104:ASN:O	2:B:107:THR:N	2.51	0.44
5:E:100:VAL:O	5:E:101:ILE:CB	2.66	0.44
4:D:152:SER:C	4:D:154:ASN:H	2.21	0.44
1:A:1428:C:H2'	1:A:1429:C:C6	2.52	0.44
1:A:404:G:H2'	1:A:405:G:O4'	2.17	0.44
1:A:605:A:C8	1:A:606:C:C5	3.05	0.44
1:A:1396:U:H2'	1:A:1397:G:C8	2.52	0.44
1:A:16:A:O2'	1:A:17:U:H5'	2.18	0.44
7:G:51:GLN:C	7:G:54:THR:O	2.56	0.44
1:A:1111:C:O2'	1:A:1112:A:OP2	2.24	0.44
1:A:1509:U:H3	1:A:1511:A:H62	1.66	0.44
1:A:335:U:C2	1:A:345:G:N2	2.86	0.44
19:S:42:PRO:C	19:S:44:MET:H	2.21	0.44
9:I:92:TYR:O	9:I:93:ARG:C	2.54	0.44
1:A:226:G:C2	1:A:227:G:C8	3.06	0.44
4:D:128:VAL:O	4:D:129:ASN:CB	2.65	0.44
2:B:175:ARG:O	2:B:176:GLU:C	2.55	0.44
12:L:122:THR:O	12:L:123:LYS:C	2.56	0.44
1:A:683:G:O4'	1:A:687:A:H1'	2.17	0.44
1:A:937:U:N3	1:A:1206:A:N7	2.65	0.44
3:C:39:ILE:O	3:C:41:GLY:N	2.51	0.44
20:T:41:ILE:O	20:T:44:ALA:N	2.51	0.44
5:E:37:ARG:HA	5:E:114:GLY:CA	2.46	0.44
1:A:655:U:O2'	1:A:656:G:H5'	2.18	0.44
7:G:6:ARG:O	7:G:7:ALA:C	2.56	0.44
18:R:20:ALA:O	18:R:21:LYS:C	2.56	0.44
4:D:114:ARG:O	4:D:118:ARG:N	2.46	0.44
20:T:37:SER:O	20:T:40:ALA:HB3	2.17	0.44
6:F:94:GLN:O	6:F:95:GLU:O	2.35	0.44
18:R:45:SER:HA	24:R:1008:WO2:O21	2.17	0.44
1:A:1220:A:C6	1:A:1279:C:C5	3.05	0.44
21:U:5:ASP:O	21:U:11:GLY:HA3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1085:C:H2'	1:A:1086:G:O4'	2.18	0.44
9:I:11:LYS:O	9:I:12:GLU:CB	2.65	0.44
1:A:1109:G:N2	1:A:1126:G:N2	2.65	0.44
1:A:230:C:O2'	1:A:231:G:H5'	2.17	0.44
13:M:86:CYS:O	13:M:89:GLY:N	2.47	0.44
1:A:1106:G:OP1	10:J:35:SER:C	2.56	0.44
1:A:275:C:C4'	1:A:276:G:OP2	2.62	0.44
1:A:1284:C:N4	1:A:1285:G:C5	2.86	0.44
1:A:1386:C:O5'	1:A:1386:C:H6	1.99	0.44
1:A:373:G:O6	1:A:374:C:N4	2.51	0.44
1:A:50:A:N6	1:A:356:G:C4'	2.79	0.44
1:A:415:U:H1'	1:A:419:G:N2	2.33	0.44
2:B:222:ILE:O	2:B:225:ALA:N	2.43	0.44
1:A:733:G:N3	15:O:23:GLY:HA3	2.32	0.44
14:N:16:PHE:O	14:N:17:LYS:C	2.56	0.44
2:B:166:ASP:C	2:B:168:THR:H	2.21	0.44
1:A:1367:G:O2'	1:A:1368:G:H5'	2.18	0.44
1:A:421:G:H2'	1:A:422:U:C6	2.53	0.43
1:A:384:A:C6	1:A:385:C:H1'	2.53	0.43
1:A:899:G:C2	1:A:1378:A:C2	3.06	0.43
1:A:543:U:C4'	1:A:544:U:O5'	2.65	0.43
20:T:20:LEU:O	20:T:23:ARG:N	2.51	0.43
1:A:269:A:O2'	1:A:270:G:C8	2.59	0.43
1:A:954:A:H2'	1:A:955:A:H5''	2.00	0.43
1:A:597:A:C6	1:A:598:C:C4	3.06	0.43
18:R:21:LYS:O	18:R:22:VAL:C	2.56	0.43
1:A:1412:C:O2'	1:A:1413:C:H5'	2.18	0.43
1:A:888:U:H2'	1:A:889:C:C6	2.53	0.43
8:H:11:THR:O	8:H:14:ARG:N	2.51	0.43
3:C:177:THR:O	3:C:179:ARG:N	2.43	0.43
1:A:554:U:O5'	1:A:554:U:H6	2.01	0.43
1:A:1234:G:C6	1:A:1235:C:C4	3.06	0.43
1:A:1391:C:H6	1:A:1391:C:O5'	2.01	0.43
1:A:373:G:C6	1:A:374:C:C4	3.06	0.43
1:A:929:U:H5'	1:A:949:C:N4	2.34	0.43
1:A:1348:C:H2'	1:A:1349:C:H6	1.83	0.43
1:A:1275:G:O2'	1:A:1276:G:H5'	2.18	0.43
1:A:1076:G:HO2'	1:A:1077:U:P	2.40	0.43
1:A:227:G:H2'	1:A:228:C:H6	1.83	0.43
1:A:128:A:C8	1:A:129:C:C5	3.06	0.43
1:A:1029:G:O2'	1:A:1030:G:H5'	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:39:PRO:O	4:D:44:GLY:HA3	2.19	0.43
1:A:410:A:H2'	1:A:411:G:O4'	2.19	0.43
1:A:142:G:H2'	1:A:143:A:H8	1.83	0.43
1:A:259:U:C4	1:A:260:G:C5	3.06	0.43
1:A:95:G:H2'	1:A:96:C:C6	2.53	0.43
15:O:2:PRO:C	15:O:3:ILE:O	2.56	0.43
1:A:991:G:C2	1:A:995:G:O6	2.72	0.43
1:A:653:G:C6	1:A:654:G:C5	3.07	0.43
13:M:79:LYS:O	13:M:80:ARG:C	2.56	0.43
1:A:911:C:N4	1:A:1326:U:C2	2.86	0.43
4:D:89:THR:O	4:D:90:GLY:C	2.57	0.43
1:A:320:A:N7	1:A:321:G:C5	2.87	0.43
1:A:80:U:C2'	1:A:81:U:OP1	2.65	0.43
1:A:1254:G:H2'	1:A:1255:G:O4'	2.19	0.43
5:E:72:GLN:O	5:E:73:ASN:CB	2.66	0.43
1:A:1142:G:C2'	1:A:1143:C:H5''	2.48	0.43
1:A:2:U:H5''	1:A:594:A:C2	2.53	0.43
1:A:479:A:C2	1:A:480:A:C6	3.06	0.43
1:A:1329:U:H2'	1:A:1330:A:H8	1.83	0.43
1:A:775:A:H2'	1:A:777:A:C8	2.53	0.43
1:A:981:G:N2	1:A:1020:C:C2	2.86	0.43
4:D:8:VAL:O	4:D:10:ARG:N	2.51	0.43
1:A:764:A:H2	1:A:1491:C:C4'	2.31	0.43
2:B:42:ILE:O	2:B:44:LEU:N	2.51	0.43
1:A:170:C:O2'	1:A:171:C:H5'	2.18	0.43
13:M:13:LYS:O	13:M:14:ARG:C	2.55	0.43
3:C:189:ALA:N	3:C:196:LEU:O	2.51	0.43
1:A:421:G:H4'	4:D:41:GLY:O	2.18	0.43
1:A:1481:G:O2'	1:A:1482:G:C5	2.71	0.43
1:A:1266:A:O2'	1:A:1267:A:P	2.76	0.43
1:A:1049:A:H1'	1:A:1050:G:O4'	2.18	0.43
5:E:124:GLY:O	5:E:126:ARG:N	2.52	0.43
1:A:1204:C:O5'	1:A:1205:G:H5''	2.17	0.43
10:J:50:ILE:CA	10:J:60:ARG:HA	2.46	0.43
1:A:963:A:C6	1:A:964:G:C6	3.07	0.43
1:A:173:A:H2'	1:A:174:U:O4'	2.18	0.43
1:A:438:C:H2'	1:A:439:G:H8	1.82	0.43
1:A:864:G:N2	1:A:887:C:O2	2.51	0.43
17:Q:100:LYS:O	17:Q:101:ARG:C	2.56	0.43
1:A:42:G:O5'	1:A:42:G:H8	2.01	0.43
1:A:1133:A:OP1	10:J:41:PRO:HA	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:241:A:H62	1:A:276:G:H1'	1.83	0.43
1:A:867:G:C2'	1:A:868:U:OP2	2.67	0.43
1:A:239:U:C6	1:A:871:G:C2	3.06	0.43
1:A:1142:G:H2'	1:A:1143:C:C5'	2.49	0.43
1:A:468:G:O2'	1:A:469:G:OP2	2.36	0.43
1:A:352:G:C2'	1:A:353:U:H5'	2.49	0.43
1:A:723:U:O2'	1:A:724:G:H5'	2.19	0.43
1:A:35:G:H2'	1:A:36:C:C6	2.53	0.43
1:A:793:C:H1'	1:A:876:C:H41	1.83	0.43
1:A:171:C:H2'	1:A:172:C:C6	2.53	0.43
1:A:975:G:O2'	1:A:976:C:H5'	2.19	0.43
1:A:1305:A:H2'	1:A:1306:C:O4'	2.19	0.43
1:A:72:C:H42	1:A:90:G:H1	1.67	0.43
1:A:601:C:N4	1:A:606:C:H42	2.17	0.43
2:B:141:GLU:O	2:B:144:ARG:N	2.52	0.43
1:A:596:C:O2	1:A:611:G:C2	2.72	0.43
10:J:79:ARG:C	10:J:81:THR:N	2.71	0.43
1:A:240:C:O2'	1:A:241:A:H5'	2.19	0.43
1:A:1141:U:O2	1:A:1163:G:C6	2.71	0.43
1:A:670:A:C4'	1:A:671:G:O5'	2.54	0.43
1:A:480:A:O2'	1:A:481:U:OP1	2.27	0.43
1:A:970:G:HO2'	1:A:971:A:P	2.40	0.43
1:A:335:U:O2'	1:A:336:C:H5'	2.18	0.43
11:K:62:GLN:HA	11:K:65:ALA:HB3	1.99	0.43
1:A:748:G:N2	1:A:795:C:O2'	2.51	0.43
2:B:63:MET:C	2:B:65:GLY:N	2.71	0.43
1:A:596:C:H2'	1:A:597:A:C8	2.54	0.43
1:A:539:C:C2'	1:A:540:G:H5'	2.49	0.43
1:A:882:U:H2'	1:A:883:G:H5'	2.00	0.43
21:U:12:LYS:O	21:U:16:GLY:N	2.51	0.43
1:A:543:U:H4'	1:A:544:U:C5'	2.49	0.43
1:A:1040:G:C5	1:A:1041:C:C4	3.06	0.43
11:K:115:PRO:O	11:K:117:ASN:N	2.41	0.43
15:O:30:ALA:O	15:O:31:LEU:C	2.57	0.43
1:A:620:G:O2'	1:A:621:G:H5'	2.18	0.43
1:A:1220:A:H2'	1:A:1220:A:N3	2.34	0.43
1:A:190:G:O6	1:A:259:U:H5''	2.19	0.43
1:A:94:A:H2'	1:A:95:G:H8	1.83	0.43
1:A:362:U:C6	1:A:389:G:N2	2.87	0.43
1:A:890:A:O2'	1:A:891:A:P	2.77	0.43
18:R:36:ASN:O	18:R:37:VAL:C	2.56	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:123:G:O2'	1:A:189:U:C6	2.72	0.43
1:A:956:C:H41	1:A:1341:A:H62	1.67	0.43
2:B:62:ALA:O	2:B:65:GLY:N	2.49	0.43
1:A:779:C:C4	1:A:780:C:C5	3.07	0.43
18:R:23:LYS:O	18:R:24:ALA:HB3	2.19	0.43
16:P:3:LYS:CB	16:P:65:GLN:O	2.67	0.43
8:H:12:ARG:O	8:H:16:ALA:HB2	2.18	0.43
1:A:798:A:N6	1:A:1486:C:H1'	2.33	0.42
1:A:1190:C:C2'	1:A:1191:C:H5'	2.48	0.42
1:A:1204:C:H5''	1:A:1205:G:H5''	2.00	0.42
1:A:970:G:O2'	1:A:971:A:OP1	2.28	0.42
1:A:182:C:N3	1:A:183:G:N7	2.67	0.42
11:K:67:ASP:O	11:K:68:ALA:C	2.56	0.42
7:G:66:VAL:O	7:G:69:VAL:N	2.45	0.42
1:A:663:C:O5'	1:A:663:C:H6	2.01	0.42
4:D:119:GLN:O	4:D:122:ARG:N	2.52	0.42
1:A:368:A:H1'	1:A:465:G:H1'	1.99	0.42
5:E:132:ALA:O	5:E:133:TYR:C	2.56	0.42
1:A:653:G:O2'	1:A:654:G:H5'	2.19	0.42
1:A:322:A:N3	1:A:324:A:H1'	2.34	0.42
1:A:1194:A:C5	1:A:1196:G:C8	3.06	0.42
3:C:92:ALA:HA	3:C:95:THR:O	2.19	0.42
1:A:1136:G:O2'	1:A:1137:G:H5'	2.19	0.42
1:A:25:C:H2'	1:A:26:A:C8	2.54	0.42
4:D:71:SER:C	4:D:73:ARG:N	2.67	0.42
18:R:55:ARG:O	18:R:57:GLY:N	2.53	0.42
18:R:46:GLU:N	24:R:1008:WO2:O21	2.52	0.42
1:A:1387:G:C2	1:A:1474:G:C2	3.07	0.42
1:A:259:U:H6	1:A:259:U:O5'	2.03	0.42
1:A:94:A:N3	1:A:95:G:C8	2.87	0.42
1:A:929:U:H5'	1:A:949:C:H41	1.84	0.42
1:A:980:G:H2'	1:A:981:G:C8	2.53	0.42
1:A:451:C:C2	1:A:460:G:C2	3.07	0.42
1:A:439:G:N1	1:A:474:G:C6	2.87	0.42
1:A:642:U:H2'	1:A:643:G:O4'	2.19	0.42
15:O:73:GLU:O	15:O:74:ASP:CB	2.66	0.42
1:A:968:U:O4	1:A:1193:U:H1'	2.18	0.42
1:A:1281:G:O2'	1:A:1282:U:C6	2.72	0.42
1:A:613:G:O5'	1:A:613:G:H8	2.02	0.42
1:A:504:G:O5'	12:L:73:GLU:HA	2.18	0.42
1:A:91:G:H2'	1:A:92:U:O4'	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:94:ASN:O	17:Q:95:TYR:C	2.58	0.42
1:A:970:G:O2'	1:A:971:A:P	2.78	0.42
8:H:9:MET:O	8:H:10:LEU:C	2.58	0.42
1:A:1144:C:C2	1:A:1156:G:C2	3.07	0.42
1:A:1431:A:H2'	1:A:1432:C:OP1	2.19	0.42
1:A:1305:A:O2'	1:A:1306:C:H5'	2.19	0.42
6:F:40:VAL:HA	6:F:62:TRP:O	2.19	0.42
20:T:50:GLU:O	20:T:53:LEU:N	2.51	0.42
6:F:10:LEU:HA	6:F:84:ASN:O	2.19	0.42
1:A:240:C:H2'	1:A:241:A:H5'	2.01	0.42
1:A:445:A:O2'	1:A:446:A:P	2.77	0.42
1:A:1505:U:O2'	1:A:1507:G:H5'	2.19	0.42
1:A:653:G:C6	1:A:654:G:C6	3.07	0.42
10:J:50:ILE:HA	10:J:60:ARG:CA	2.46	0.42
1:A:1031:U:H1'	1:A:1182:A:C5	2.55	0.42
2:B:193:ASP:O	2:B:195:ASP:N	2.51	0.42
1:A:628:C:O2'	1:A:629:U:H5'	2.19	0.42
1:A:1168:G:C6	1:A:1169:A:C5	3.07	0.42
18:R:67:ALA:C	18:R:69:THR:H	2.23	0.42
6:F:23:LYS:O	6:F:26:ILE:N	2.52	0.42
18:R:16:PRO:O	18:R:18:ARG:N	2.52	0.42
5:E:99:GLY:O	5:E:117:ASP:HA	2.19	0.42
1:A:219:C:H2'	1:A:220:C:C6	2.55	0.42
1:A:256:U:O2	1:A:258:A:C8	2.73	0.42
11:K:76:GLY:O	11:K:77:MET:O	2.37	0.42
1:A:364:C:OP2	1:A:383:G:N2	2.43	0.42
1:A:493:A:H5''	1:A:494:C:OP1	2.20	0.42
1:A:1345:A:H1'	1:A:1347:G:N7	2.35	0.42
1:A:223:A:H2'	1:A:224:U:H6	1.84	0.42
1:A:795:C:HO2'	1:A:796:U:H5	1.64	0.42
1:A:10:A:H2'	1:A:11:G:H8	1.85	0.42
3:C:120:VAL:O	3:C:121:ALA:C	2.56	0.42
13:M:5:ALA:O	13:M:7:VAL:N	2.52	0.42
3:C:51:GLY:O	3:C:70:VAL:HA	2.20	0.42
1:A:1436:C:O2'	1:A:1437:A:H5'	2.19	0.42
1:A:288:G:H5'	1:A:593:G:C2	2.54	0.42
1:A:697:G:N3	1:A:760:A:H1'	2.35	0.42
1:A:423:G:HO2'	1:A:424:U:P	2.42	0.42
1:A:274:A:H4'	1:A:275:C:O5'	2.19	0.42
1:A:1050:G:N2	1:A:1172:A:N3	2.65	0.42
1:A:95:G:H2'	1:A:96:C:H6	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:316:A:C2	1:A:317:C:C4	3.08	0.42
1:A:295:A:H2'	1:A:296:G:C5'	2.50	0.42
1:A:1192:U:O2'	1:A:1194:A:C2	2.66	0.42
1:A:78:G:H2'	1:A:79:U:H5''	2.02	0.42
1:A:1336:G:C2	1:A:1337:G:C4	3.08	0.42
1:A:418:G:N2	1:A:419:G:C8	2.87	0.42
1:A:419:G:H8	1:A:419:G:O5'	2.03	0.42
1:A:691:C:H2'	1:A:692:G:C8	2.53	0.42
4:D:171:GLY:C	4:D:173:TRP:N	2.73	0.42
1:A:1399:G:O2'	1:A:1460:A:N6	2.47	0.42
1:A:1458:U:H2'	1:A:1459:G:O4'	2.19	0.42
5:E:156:ALA:O	24:E:1005:WO2:O20	2.37	0.42
1:A:1268:A:N6	1:A:1269:A:N6	2.67	0.42
1:A:862:G:N3	1:A:891:A:C2	2.87	0.42
1:A:1053:C:O2'	1:A:1054:G:H5'	2.20	0.42
1:A:1415:A:C8	1:A:1445:A:C6	3.08	0.42
1:A:958:U:H2'	1:A:959:U:H5	1.83	0.42
4:D:190:ASP:O	4:D:192:GLU:N	2.53	0.42
1:A:620:G:H2'	1:A:621:G:H8	1.83	0.42
12:L:127:GLU:O	12:L:128:ALA:HB3	2.19	0.42
1:A:126:C:C2'	1:A:127:U:H5'	2.50	0.42
1:A:1428:C:H2'	1:A:1429:C:H6	1.85	0.42
4:D:26:CYS:HA	4:D:31:CYS:CB	2.50	0.42
1:A:1506:G:H5''	1:A:1507:G:OP2	2.20	0.42
1:A:57:G:N2	1:A:383:G:O6	2.53	0.42
1:A:1451:G:H2'	1:A:1452:G:C8	2.55	0.42
1:A:984:C:H6	1:A:984:C:O5'	2.02	0.42
1:A:1206:A:N3	1:A:1206:A:C2'	2.82	0.42
1:A:1348:C:H2'	1:A:1349:C:C6	2.55	0.42
1:A:1348:C:O2'	1:A:1349:C:H5'	2.20	0.42
1:A:159:C:H2'	1:A:160:G:H8	1.82	0.42
2:B:42:ILE:C	2:B:44:LEU:H	2.23	0.42
1:A:1291:G:H2'	1:A:1292:G:C8	2.55	0.42
1:A:527:G:C5	1:A:528:C:C5	3.07	0.42
4:D:203:VAL:O	4:D:206:PHE:N	2.47	0.42
1:A:974:U:O5'	1:A:974:U:H6	2.03	0.42
1:A:1427:G:C2	1:A:1428:C:C5	3.07	0.42
1:A:41:G:O2'	1:A:42:G:H5'	2.19	0.42
1:A:1362:U:O2'	1:A:1363:U:OP2	2.31	0.42
1:A:409:A:OP2	1:A:423:G:N2	2.38	0.42
1:A:1309:C:C4	1:A:1310:A:N7	2.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1374:G:H2'	1:A:1375:U:H6	1.85	0.42
1:A:66:G:H2'	1:A:67:C:C5'	2.49	0.42
1:A:1382:C:H5''	1:A:1383:G:OP2	2.19	0.42
1:A:992:A:C8	1:A:993:A:N7	2.88	0.42
1:A:535:U:H5''	12:L:87:GLY:O	2.19	0.42
1:A:819:G:C2'	1:A:820:G:O5'	2.67	0.42
11:K:62:GLN:HA	11:K:97:ALA:CB	2.50	0.42
2:B:193:ASP:C	2:B:195:ASP:N	2.74	0.42
1:A:749:A:N6	1:A:750:A:C2	2.88	0.42
1:A:1103:U:O2'	1:A:1104:U:H5'	2.20	0.42
1:A:180:C:O3'	20:T:82:SER:CB	2.68	0.42
7:G:24:THR:O	7:G:25:ALA:C	2.58	0.42
1:A:1514:U:H2'	1:A:1515:C:C6	2.55	0.42
6:F:100:ASN:CB	18:R:28:GLU:H	2.32	0.42
20:T:56:MET:O	20:T:57:ARG:C	2.58	0.42
3:C:58:GLU:H	3:C:65:ALA:HB3	1.85	0.42
1:A:424:U:H4'	1:A:425:A:O5'	2.20	0.41
1:A:3:G:O2'	1:A:4:U:H5''	2.20	0.41
4:D:28:SER:O	4:D:30:LYS:N	2.53	0.41
1:A:1036:C:O2	1:A:1177:U:C4	2.73	0.41
1:A:1043:G:C2	1:A:1178:G:N3	2.88	0.41
1:A:401:G:C4	1:A:479:A:C5	3.08	0.41
1:A:482:A:O2'	1:A:483:G:O5'	2.33	0.41
1:A:17:U:H4'	1:A:1062:A:O4'	2.20	0.41
1:A:1352:G:O2'	1:A:1353:G:H5'	2.20	0.41
1:A:78:G:C2'	1:A:79:U:H5''	2.50	0.41
1:A:672:C:H2'	1:A:673:G:C8	2.55	0.41
1:A:911:C:C5	1:A:1326:U:C6	3.07	0.41
1:A:246:G:HO2'	1:A:247:U:P	2.43	0.41
1:A:247:U:H2'	1:A:248:U:C5	2.55	0.41
5:E:39:GLY:O	5:E:68:GLU:HA	2.20	0.41
16:P:78:GLY:O	16:P:80:PHE:N	2.53	0.41
1:A:1491:C:H2'	1:A:1492:C:C6	2.55	0.41
1:A:955:A:C6	1:A:1299:A:C5	3.08	0.41
11:K:34:ASP:C	11:K:36:ASP:H	2.22	0.41
1:A:608:G:C6	1:A:609:U:C4	3.08	0.41
1:A:416:U:H4'	1:A:417:C:OP2	2.20	0.41
3:C:108:ASN:C	3:C:110:ASN:N	2.73	0.41
14:N:14:PRO:O	14:N:15:LYS:CB	2.67	0.41
1:A:851:G:C2'	1:A:852:C:H5'	2.50	0.41
1:A:409:A:O2'	1:A:410:A:H5'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1312:G:O2'	1:A:1313:A:C8	2.61	0.41
1:A:1497:G:O2'	1:A:1498:G:C5'	2.68	0.41
1:A:445:A:C2	1:A:464:U:C5	2.99	0.41
1:A:804:G:O2'	1:A:805:C:H5'	2.20	0.41
1:A:374:C:H2'	1:A:375:G:C8	2.54	0.41
1:A:945:A:C5'	1:A:946:A:OP2	2.68	0.41
1:A:963:A:H2'	1:A:964:G:O4'	2.20	0.41
1:A:764:A:C5	1:A:785:A:C2	3.08	0.41
11:K:49:GLY:O	11:K:50:TYR:O	2.38	0.41
8:H:15:ASN:O	8:H:16:ALA:C	2.59	0.41
15:O:87:ILE:O	15:O:88:ARG:O	2.39	0.41
1:A:250:G:H5'	17:Q:16:GLN:O	2.20	0.41
2:B:184:VAL:O	2:B:198:ASP:CB	2.68	0.41
1:A:239:U:O4	1:A:883:G:H1'	2.20	0.41
1:A:1236:G:C2	1:A:1264:G:C2	3.08	0.41
1:A:398:C:H2'	1:A:399:U:H6	1.85	0.41
1:A:1466:G:C2	1:A:1467:C:C2	3.08	0.41
1:A:673:G:H8	1:A:673:G:O5'	2.03	0.41
1:A:246:G:N2	1:A:248:U:O4	2.54	0.41
13:M:87:TYR:O	13:M:90:LEU:N	2.40	0.41
1:A:1077:U:H5'	1:A:1091:C:O2	2.20	0.41
1:A:972:C:N3	1:A:1028:A:O2'	2.43	0.41
19:S:34:TRP:O	19:S:36:ARG:N	2.46	0.41
5:E:58:ALA:O	5:E:62:ALA:HB2	2.20	0.41
1:A:1478:C:C2	1:A:1481:G:O6	2.73	0.41
1:A:502:C:C2'	1:A:503:A:O5'	2.69	0.41
1:A:1240:C:O2'	1:A:1265:C:H1'	2.20	0.41
1:A:1504:C:O2'	1:A:1505:U:H5'	2.20	0.41
1:A:1202:G:N2	1:A:1203:G:H1'	2.36	0.41
8:H:6:ILE:O	8:H:7:ALA:C	2.59	0.41
1:A:1291:G:H2'	1:A:1292:G:H8	1.86	0.41
8:H:122:ARG:O	8:H:123:GLU:C	2.58	0.41
1:A:1436:C:C2	1:A:1437:A:C8	3.09	0.41
1:A:456:G:H2'	1:A:457:A:O4'	2.21	0.41
1:A:1015:G:H2'	1:A:1016:G:O4'	2.20	0.41
1:A:772:U:O5'	1:A:772:U:H6	2.03	0.41
1:A:207:C:OP2	1:A:207:C:H6	2.03	0.41
1:A:175:G:C2'	1:A:176:U:OP2	2.69	0.41
1:A:454:A:H2'	1:A:455:C:H5''	2.01	0.41
1:A:1199:C:H2'	1:A:1200:U:C5	2.54	0.41
1:A:961:C:N3	1:A:1203:G:C2	2.89	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:211:G:H2'	1:A:212:C:C6	2.55	0.41
1:A:639:C:H6	1:A:639:C:O5'	2.04	0.41
1:A:1109:G:H21	1:A:1128:A:N6	2.18	0.41
1:A:154:A:C6	1:A:155:A:C2	3.09	0.41
1:A:1274:G:O2'	1:A:1275:G:H5'	2.21	0.41
1:A:561:C:N4	1:A:746:G:H1	2.17	0.41
1:A:1514:U:H2'	1:A:1515:C:C5	2.56	0.41
11:K:37:GLY:O	11:K:38:ASN:C	2.59	0.41
3:C:155:GLY:HA2	3:C:164:ARG:O	2.20	0.41
18:R:45:SER:C	18:R:47:THR:N	2.73	0.41
1:A:1279:C:C2'	1:A:1279:C:O2	2.68	0.41
1:A:162:G:C2	1:A:163:C:C4	3.09	0.41
1:A:369:A:C2	1:A:370:U:N3	2.89	0.41
1:A:53:A:N6	1:A:54:C:C4	2.89	0.41
1:A:190:G:H22	1:A:258:A:C4'	2.33	0.41
11:K:15:ALA:H	11:K:77:MET:H	1.69	0.41
1:A:752:G:N2	1:A:794:C:H1'	2.36	0.41
1:A:112:A:H5''	1:A:113:A:H5'	2.02	0.41
10:J:59:SER:O	10:J:60:ARG:O	2.39	0.41
1:A:705:A:O2'	1:A:706:U:C6	2.72	0.41
1:A:1400:A:C2'	1:A:1401:G:H5'	2.48	0.41
3:C:109:PRO:C	3:C:111:LEU:N	2.74	0.41
1:A:1249:A:C2	1:A:1250:A:C6	3.08	0.41
3:C:134:ILE:O	3:C:135:LYS:C	2.58	0.41
8:H:104:ARG:O	8:H:105:ARG:C	2.58	0.41
8:H:23:SER:HA	8:H:61:ILE:O	2.21	0.41
1:A:423:G:O2'	1:A:424:U:OP2	2.36	0.41
1:A:1290:G:N1	1:A:1310:A:C4	2.88	0.41
1:A:1287:A:N6	1:A:1312:G:O2'	2.53	0.41
1:A:1139:A:N6	1:A:1161:A:N7	2.69	0.41
1:A:441:G:H3'	1:A:469:G:N2	2.36	0.41
1:A:500:G:C5	1:A:514:U:H1'	2.54	0.41
5:E:130:ASN:O	5:E:134:ALA:N	2.53	0.41
1:A:323:C:O2	1:A:323:C:C2'	2.66	0.41
1:A:210:U:O2'	1:A:211:G:P	2.79	0.41
1:A:65:U:H1'	1:A:206:G:H4'	2.03	0.41
1:A:1112:A:OP2	1:A:1113:G:P	2.79	0.41
1:A:785:A:H2'	1:A:786:G:H5'	2.03	0.41
2:B:4:GLU:C	2:B:6:THR:N	2.73	0.41
1:A:1437:A:H2'	1:A:1438:G:O4'	2.21	0.41
1:A:240:C:C2'	1:A:241:A:H5'	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:275:C:O2	17:Q:39:SER:N	2.54	0.41
1:A:1036:C:OP2	1:A:1178:G:OP2	2.38	0.41
1:A:502:C:H2'	1:A:503:A:O5'	2.21	0.41
1:A:261:G:O2'	1:A:262:C:O5'	2.38	0.41
1:A:123:G:H4'	1:A:124:A:C5'	2.51	0.41
7:G:46:ALA:HB2	7:G:117:ALA:HA	2.01	0.41
1:A:630:C:H2'	1:A:631:A:H8	1.86	0.41
7:G:95:ARG:O	7:G:98:SER:N	2.54	0.41
20:T:61:SER:O	20:T:63:ILE:N	2.53	0.41
4:D:49:ARG:O	4:D:50:ARG:C	2.59	0.41
5:E:153:LYS:N	24:E:1005:WO2:O49	2.54	0.41
1:A:1281:G:HO2'	1:A:1282:U:P	2.44	0.41
1:A:143:A:C4	1:A:144:C:C5	3.09	0.41
1:A:488:G:H2'	1:A:489:G:H8	1.86	0.41
1:A:726:U:H6	1:A:726:U:O5'	2.04	0.41
1:A:99:C:O2	1:A:374:C:H4'	2.21	0.41
1:A:961:C:N4	1:A:1202:G:H1	2.19	0.41
1:A:1351:C:C2'	1:A:1352:G:O4'	2.67	0.41
1:A:486:C:H2'	1:A:487:C:H6	1.85	0.41
1:A:736:A:H4'	1:A:737:C:C5'	2.47	0.41
1:A:1210:A:O2'	1:A:1211:C:H5'	2.21	0.41
1:A:1108:U:H2'	1:A:1109:G:C8	2.55	0.41
1:A:113:A:C5	1:A:115:G:C6	3.09	0.41
16:P:53:VAL:O	16:P:54:GLU:C	2.60	0.41
4:D:109:GLY:O	4:D:110:PHE:C	2.57	0.41
1:A:1402:C:H2'	1:A:1403:G:C8	2.55	0.41
1:A:102:A:H2'	1:A:321:G:N2	2.36	0.41
1:A:1258:C:C2'	1:A:1259:U:H5'	2.50	0.41
1:A:643:G:H2'	1:A:644:G:O4'	2.21	0.41
1:A:197:G:C6	1:A:198:U:C4	3.09	0.41
18:R:15:ARG:O	18:R:17:SER:N	2.54	0.41
1:A:627:G:C6	1:A:628:C:C5	3.09	0.41
1:A:758:G:O2'	1:A:759:G:H5'	2.21	0.41
20:T:50:GLU:O	20:T:52:ALA:N	2.54	0.41
1:A:59:A:H3'	1:A:326:G:H22	1.85	0.41
1:A:1471:G:O2'	1:A:1472:U:H5'	2.20	0.41
1:A:834:C:O2	1:A:834:C:H2'	2.20	0.41
1:A:1314:A:C2	1:A:1315:G:H1'	2.56	0.41
1:A:1472:U:H2'	1:A:1473:C:C6	2.56	0.41
10:J:20:ALA:O	10:J:21:GLN:C	2.58	0.41
4:D:58:LEU:O	4:D:59:ARG:C	2.59	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:26:ASN:O	20:T:27:LYS:C	2.60	0.41
1:A:1220:A:N1	1:A:1279:C:C5	2.88	0.41
1:A:1281:G:O2'	1:A:1282:U:O5'	2.36	0.41
21:U:12:LYS:O	21:U:13:ILE:C	2.58	0.41
1:A:1036:C:O2'	1:A:1037:A:H5''	2.21	0.41
1:A:1042:C:HO2'	1:A:1043:G:H5'	1.84	0.41
1:A:142:G:O2'	1:A:143:A:H5'	2.20	0.41
1:A:601:C:N4	1:A:606:C:N4	2.68	0.41
1:A:1466:G:H2'	1:A:1467:C:O4'	2.21	0.41
1:A:374:C:C5	1:A:375:G:N7	2.89	0.41
1:A:543:U:H5''	1:A:544:U:C5'	2.51	0.41
1:A:123:G:N2	1:A:188:U:O2'	2.54	0.41
14:N:9:LYS:C	14:N:11:LYS:N	2.74	0.41
1:A:795:C:O2'	1:A:796:U:OP2	2.39	0.41
1:A:965:G:O2'	1:A:966:C:H5'	2.20	0.41
1:A:11:G:C5	1:A:12:U:C5	3.09	0.41
1:A:1368:G:O2'	1:A:1369:G:H5'	2.21	0.41
2:B:246:GLU:O	2:B:247:THR:O	2.39	0.41
1:A:738:G:C6	1:A:739:C:N4	2.88	0.41
1:A:831:G:N1	1:A:832:G:C5	2.89	0.40
24:E:1005:WO2:O44	8:H:67:PRO:CB	2.69	0.40
1:A:1282:U:C2'	1:A:1282:U:O2	2.64	0.40
1:A:801:G:C2'	1:A:802:A:H5''	2.51	0.40
1:A:726:U:H2'	1:A:727:C:H6	1.80	0.40
1:A:154:A:C6	1:A:341:G:C6	3.09	0.40
1:A:1179:G:H2'	1:A:1180:U:C6	2.56	0.40
15:O:16:ALA:C	15:O:18:PHE:N	2.74	0.40
14:N:17:LYS:C	14:N:19:ARG:H	2.23	0.40
1:A:797:A:N7	1:A:799:A:C4	2.89	0.40
1:A:290:C:O2'	1:A:291:U:H5'	2.22	0.40
1:A:923:A:C4	1:A:924:G:N7	2.89	0.40
21:U:10:ARG:O	21:U:12:LYS:N	2.54	0.40
1:A:1480:A:H4'	1:A:1481:G:OP2	2.22	0.40
1:A:594:A:N7	1:A:595:C:C5	2.90	0.40
1:A:1177:U:OP1	1:A:1178:G:H5'	2.21	0.40
1:A:374:C:H2'	1:A:375:G:H8	1.87	0.40
1:A:373:G:C2	1:A:381:C:C2	3.09	0.40
1:A:928:G:O2'	1:A:929:U:H5'	2.20	0.40
1:A:932:U:H2'	1:A:933:U:C5'	2.51	0.40
14:N:40:CYS:O	14:N:43:CYS:N	2.54	0.40
2:B:20:GLU:C	2:B:22:LYS:N	2.73	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:439:G:C2'	1:A:440:G:H5'	2.51	0.40
11:K:123:LYS:O	11:K:125:PHE:N	2.53	0.40
1:A:1077:U:C5'	1:A:1091:C:O2	2.69	0.40
9:I:127:LYS:O	9:I:128:ARG:C	2.59	0.40
1:A:1282:U:O4	1:A:1284:C:H1'	2.22	0.40
1:A:1384:C:O2	1:A:1477:A:C2	2.73	0.40
1:A:1049:A:O2'	1:A:1050:G:P	2.79	0.40
1:A:1353:G:O3'	9:I:69:GLY:HA3	2.22	0.40
1:A:543:U:H4'	1:A:544:U:O5'	2.21	0.40
1:A:329:C:H2'	1:A:330:C:H6	1.81	0.40
1:A:1237:A:O3'	1:A:1238:U:C4'	2.69	0.40
1:A:173:A:C2'	1:A:174:U:H5'	2.51	0.40
15:O:7:GLU:O	15:O:8:LYS:C	2.59	0.40
1:A:955:A:N1	1:A:1299:A:C5	2.89	0.40
1:A:1076:G:O2'	1:A:1077:U:OP2	2.33	0.40
14:N:54:PRO:O	14:N:56:VAL:N	2.54	0.40
6:F:30:LEU:C	6:F:35:ALA:HB3	2.42	0.40
18:R:53:ARG:O	18:R:54:ARG:C	2.59	0.40
7:G:86:GLN:O	7:G:87:VAL:O	2.40	0.40
20:T:101:GLY:O	20:T:102:GLY:O	2.38	0.40
1:A:1497:G:H2'	1:A:1498:G:C8	2.53	0.40
1:A:1042:C:C4	3:C:2:GLY:HA3	2.55	0.40
1:A:400:U:C3'	1:A:401:G:H5'	2.42	0.40
1:A:1390:A:H2'	1:A:1391:C:C6	2.56	0.40
1:A:1469:A:H3'	1:A:1470:A:C8	2.56	0.40
1:A:573:C:O2'	1:A:574:U:H5'	2.22	0.40
17:Q:92:ARG:C	17:Q:94:ASN:N	2.75	0.40
1:A:1039:G:H5''	3:C:154:SER:CB	2.52	0.40
1:A:638:A:C2	1:A:639:C:C2	3.09	0.40
1:A:969:U:O2'	1:A:970:G:P	2.80	0.40
1:A:331:C:H2'	1:A:332:C:H6	1.85	0.40
6:F:15:ASP:C	6:F:17:SER:N	2.73	0.40
15:O:29:VAL:O	15:O:30:ALA:C	2.59	0.40
9:I:28:VAL:C	9:I:30:GLY:N	2.74	0.40
1:A:150:G:O2'	1:A:151:G:H5'	2.21	0.40
1:A:179:A:C6	1:A:180:C:C4	3.09	0.40
17:Q:77:VAL:O	17:Q:78:GLU:CB	2.69	0.40
1:A:466:A:H2'	1:A:467:C:O4'	2.22	0.40
1:A:1284:C:C5	1:A:1285:G:N7	2.90	0.40
1:A:1139:A:C5	1:A:1161:A:C6	3.09	0.40
1:A:1042:C:C5	3:C:2:GLY:HA3	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:143:A:N3	1:A:144:C:C6	2.90	0.40
1:A:399:U:H2'	1:A:400:U:H6	1.86	0.40
1:A:990:U:H2'	1:A:991:G:C5'	2.52	0.40
1:A:261:G:N2	1:A:264:C:C5	2.88	0.40
1:A:1410:A:H2'	1:A:1411:C:C6	2.57	0.40
3:C:15:THR:O	3:C:16:ARG:CB	2.69	0.40
1:A:1370:C:HO2'	1:A:1371:C:H5'	1.87	0.40
1:A:248:U:H2'	1:A:249:G:C8	2.52	0.40
1:A:997:C:C2'	1:A:998:U:H5'	2.52	0.40
1:A:31:G:N1	1:A:48:C:H5''	2.37	0.40
1:A:526:C:C2'	1:A:527:G:H5'	2.52	0.40
1:A:1097:C:C2	1:A:1167:G:N2	2.90	0.40
11:K:14:VAL:O	11:K:16:SER:N	2.49	0.40
1:A:645:G:H2'	1:A:646:A:C8	2.56	0.40
1:A:1243:C:H6	1:A:1243:C:O5'	2.04	0.40
2:B:110:GLN:O	2:B:113:HIS:N	2.51	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:T:50:GLU:N	24:K:1014:WO2:O25[3_555]	1.97	0.23
1:A:407:A:OP1	24:E:1005:WO2:O54[7_557]	2.07	0.13
20:T:48:LYS:CB	24:K:1014:WO2:O48[3_555]	2.07	0.13

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	B	247/255 (97%)	151 (61%)	60 (24%)	36 (15%)	0 1
3	C	204/238 (86%)	134 (66%)	50 (24%)	20 (10%)	1 4

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	D	206/208 (99%)	143 (69%)	45 (22%)	18 (9%)	1	5
5	E	154/161 (96%)	115 (75%)	29 (19%)	10 (6%)	1	13
6	F	99/101 (98%)	75 (76%)	13 (13%)	11 (11%)	0	3
7	G	153/155 (99%)	85 (56%)	45 (29%)	23 (15%)	0	1
8	H	136/138 (99%)	106 (78%)	21 (15%)	9 (7%)	1	12
9	I	125/128 (98%)	89 (71%)	25 (20%)	11 (9%)	1	5
10	J	96/104 (92%)	61 (64%)	17 (18%)	18 (19%)	0	0
11	K	121/128 (94%)	87 (72%)	20 (16%)	14 (12%)	0	3
12	L	129/131 (98%)	76 (59%)	40 (31%)	13 (10%)	1	4
13	M	91/125 (73%)	52 (57%)	29 (32%)	10 (11%)	0	3
14	N	58/60 (97%)	34 (59%)	13 (22%)	11 (19%)	0	0
15	O	86/88 (98%)	58 (67%)	18 (21%)	10 (12%)	0	3
16	P	86/88 (98%)	57 (66%)	19 (22%)	10 (12%)	0	3
17	Q	102/104 (98%)	74 (72%)	13 (13%)	15 (15%)	0	1
18	R	80/87 (92%)	46 (58%)	19 (24%)	15 (19%)	0	0
19	S	78/92 (85%)	55 (70%)	15 (19%)	8 (10%)	1	4
20	T	97/105 (92%)	47 (48%)	30 (31%)	20 (21%)	0	0
21	U	22/26 (85%)	11 (50%)	7 (32%)	4 (18%)	0	0
All	All	2370/2522 (94%)	1556 (66%)	528 (22%)	286 (12%)	0	2

All (286) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	4	GLU
2	B	13	ALA
2	B	32	ILE
2	B	44	LEU
2	B	89	GLY
2	B	95	GLN
2	B	106	LYS
2	B	229	VAL
2	B	243	GLU
2	B	247	THR
3	C	15	THR
3	C	16	ARG
3	C	24	ALA

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Mol	Chain	Res	Type
3	C	146	ALA
3	C	154	SER
4	D	26	CYS
4	D	36	ARG
4	D	82	ALA
4	D	83	SER
4	D	166	LYS
5	E	17	ALA
6	F	44	GLY
6	F	69	GLU
6	F	100	ASN
7	G	7	ALA
7	G	21	VAL
7	G	36	LYS
7	G	147	ALA
7	G	155	ARG
8	H	91	ARG
8	H	103	VAL
8	H	122	ARG
9	I	25	LYS
9	I	29	ASN
9	I	38	GLN
9	I	94	ALA
10	J	34	VAL
10	J	39	PRO
10	J	55	LYS
10	J	79	ARG
11	K	8	LYS
11	K	10	VAL
11	K	50	TYR
11	K	77	MET
12	L	27	LEU
12	L	30	ALA
12	L	51	ALA
12	L	106	ASP
12	L	121	GLY
13	M	27	LYS
13	M	80	ARG
14	N	12	ARG
14	N	23	ARG
14	N	29	ARG
14	N	41	ARG

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Mol	Chain	Res	Type
15	O	3	ILE
15	O	74	ASP
15	O	88	ARG
16	P	12	LYS
17	Q	66	SER
17	Q	78	GLU
17	Q	96	ALA
17	Q	99	SER
18	R	22	VAL
18	R	30	ASP
18	R	37	VAL
18	R	38	GLU
19	S	6	LYS
19	S	47	HIS
19	S	71	LEU
20	T	42	GLN
20	T	49	ALA
20	T	63	ILE
20	T	73	HIS
21	U	3	LYS
2	B	21	ARG
2	B	66	GLY
2	B	78	GLN
2	B	101	MET
2	B	141	GLU
2	B	237	ALA
3	C	47	LEU
3	C	77	ILE
3	C	134	ILE
4	D	9	CYS
4	D	25	ARG
4	D	33	MET
4	D	46	LYS
4	D	90	GLY
4	D	110	PHE
4	D	191	ARG
5	E	125	SER
5	E	126	ARG
5	E	156	ALA
6	F	16	GLN
6	F	34	GLY
6	F	45	LEU

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Mol	Chain	Res	Type
6	F	70	ASP
6	F	72	VAL
7	G	22	LEU
7	G	53	LYS
7	G	75	VAL
7	G	113	GLU
7	G	142	GLU
8	H	121	ASP
9	I	66	ARG
9	I	114	TYR
9	I	127	LYS
10	J	54	PHE
10	J	60	ARG
10	J	72	VAL
10	J	83	GLU
10	J	90	LEU
11	K	25	TYR
11	K	44	SER
11	K	49	GLY
11	K	124	LYS
12	L	14	GLY
12	L	45	PRO
12	L	116	SER
12	L	127	GLU
13	M	6	GLY
13	M	19	LEU
13	M	37	THR
13	M	63	THR
13	M	67	GLU
14	N	26	ARG
14	N	31	ARG
14	N	43	CYS
15	O	4	THR
15	O	5	LYS
15	O	17	ARG
15	O	30	ALA
16	P	10	GLY
16	P	28	ARG
16	P	53	VAL
17	Q	33	GLY
17	Q	53	VAL
17	Q	54	GLY

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Mol	Chain	Res	Type
17	Q	68	ARG
17	Q	74	LEU
17	Q	93	GLN
18	R	17	SER
18	R	18	ARG
18	R	36	ASN
18	R	56	THR
18	R	60	GLY
19	S	43	GLU
20	T	51	GLU
20	T	85	MET
20	T	102	GLY
2	B	8	LYS
2	B	43	ASP
2	B	53	ARG
2	B	77	ALA
2	B	142	LEU
2	B	188	ALA
2	B	202	PRO
2	B	226	ARG
2	B	230	VAL
3	C	29	TYR
3	C	49	SER
3	C	93	LYS
3	C	178	LEU
4	D	30	LYS
4	D	77	ASN
5	E	73	ASN
7	G	3	ARG
7	G	37	ASN
7	G	49	ILE
7	G	80	VAL
7	G	100	ALA
8	H	115	PRO
10	J	24	VAL
10	J	40	LEU
11	K	60	ALA
11	K	126	ARG
11	K	128	ALA
12	L	117	ARG
14	N	55	GLY
16	P	54	GLU

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Mol	Chain	Res	Type
17	Q	100	LYS
17	Q	101	ARG
18	R	19	LYS
18	R	21	LYS
18	R	68	LYS
19	S	35	SER
19	S	69	HIS
20	T	41	ILE
20	T	48	LYS
20	T	80	ARG
2	B	5	ILE
2	B	62	ALA
2	B	76	GLN
3	C	66	VAL
3	C	179	ARG
4	D	5	ILE
4	D	29	PRO
4	D	137	SER
5	E	101	ILE
7	G	6	ARG
7	G	87	VAL
7	G	149	ARG
8	H	29	SER
8	H	104	ARG
10	J	28	ARG
10	J	30	SER
11	K	35	PRO
11	K	65	ALA
11	K	106	LYS
12	L	120	TYR
13	M	35	GLU
16	P	29	ASP
16	P	46	PRO
16	P	83	GLU
17	Q	11	VAL
18	R	41	LYS
19	S	30	LEU
20	T	19	SER
20	T	62	LEU
20	T	64	ASP
20	T	95	ALA
20	T	105	SER

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Mol	Chain	Res	Type
21	U	13	ILE
2	B	25	ASN
2	B	45	GLN
2	B	55	PHE
2	B	104	ASN
3	C	26	LYS
3	C	168	ALA
3	C	169	ALA
4	D	76	ARG
5	E	100	VAL
5	E	105	VAL
5	E	128	PRO
5	E	132	ALA
6	F	95	GLU
8	H	92	ARG
9	I	54	ASP
9	I	109	VAL
10	J	51	ARG
10	J	58	ASP
10	J	88	LEU
12	L	134	LYS
13	M	4	ILE
14	N	14	PRO
15	O	19	PRO
16	P	19	ILE
17	Q	102	GLY
18	R	16	PRO
19	S	66	MET
20	T	81	LYS
21	U	5	ASP
21	U	11	GLY
2	B	194	PRO
2	B	233	SER
3	C	14	ILE
3	C	174	PRO
7	G	70	LYS
8	H	31	PHE
9	I	126	SER
15	O	29	VAL
17	Q	77	VAL
20	T	88	VAL
2	B	166	ASP

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Mol	Chain	Res	Type
6	F	37	VAL
6	F	68	PRO
7	G	9	VAL
7	G	112	PRO
13	M	15	VAL
15	O	23	GLY
18	R	48	GLY
20	T	97	ALA
2	B	231	GLU
7	G	118	VAL
10	J	36	GLY
12	L	25	PRO
20	T	96	GLY
3	C	157	ILE
9	I	81	ILE
16	P	79	VAL
20	T	98	PRO
7	G	14	PRO
10	J	82	ILE
14	N	13	THR
14	N	56	VAL

5.3.2 Protein sidechains ⓘ

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1513/1514 (99%)	280 (18%)	140 (9%)

All (280) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	4	U
1	A	5	U
1	A	6	G
1	A	8	A
1	A	9	G
1	A	13	U
1	A	14	U

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Mol	Chain	Res	Type
1	A	31	G
1	A	32	A
1	A	39	G
1	A	47	C
1	A	48	C
1	A	49	U
1	A	50	A
1	A	51	A
1	A	52	G
1	A	61	G
1	A	65	U
1	A	79	U
1	A	80	U
1	A	81	U
1	A	102	A
1	A	103	C
1	A	109	A
1	A	113	A
1	A	114	C
1	A	115	G
1	A	124	A
1	A	125	C
1	A	154	A
1	A	168	C
1	A	176	U
1	A	188	U
1	A	189	U
1	A	190	G
1	A	191	G
1	A	201	A
1	A	203	A
1	A	204	G
1	A	207	C
1	A	209	U
1	A	210	U
1	A	211	G
1	A	238	A
1	A	239	U
1	A	240	C
1	A	242	G
1	A	246	G
1	A	247	U

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Mol	Chain	Res	Type
1	A	248	U
1	A	261	G
1	A	262	C
1	A	270	G
1	A	275	C
1	A	276	G
1	A	277	A
1	A	284	G
1	A	300	G
1	A	301	G
1	A	311	G
1	A	316	A
1	A	323	C
1	A	324	A
1	A	325	C
1	A	327	G
1	A	341	G
1	A	347	C
1	A	348	A
1	A	349	G
1	A	362	U
1	A	363	U
1	A	367	C
1	A	368	A
1	A	383	G
1	A	392	A
1	A	401	G
1	A	406	A
1	A	407	A
1	A	408	G
1	A	416	U
1	A	417	C
1	A	418	G
1	A	423	G
1	A	424	U
1	A	425	A
1	A	434	A
1	A	446	A
1	A	454	A
1	A	455	C
1	A	456	G
1	A	465	G

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Mol	Chain	Res	Type
1	A	468	G
1	A	469	G
1	A	470	U
1	A	480	A
1	A	481	U
1	A	483	G
1	A	491	C
1	A	492	A
1	A	493	A
1	A	494	C
1	A	501	C
1	A	502	C
1	A	510	G
1	A	516	A
1	A	517	U
1	A	519	C
1	A	531	G
1	A	542	A
1	A	543	U
1	A	544	U
1	A	545	C
1	A	546	A
1	A	549	G
1	A	550	G
1	A	555	A
1	A	556	A
1	A	558	G
1	A	559	G
1	A	560	G
1	A	579	C
1	A	590	A
1	A	635	U
1	A	636	A
1	A	648	A
1	A	670	A
1	A	671	G
1	A	676	G
1	A	684	C
1	A	685	A
1	A	686	G
1	A	687	A
1	A	701	G

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Mol	Chain	Res	Type
1	A	704	G
1	A	705	A
1	A	706	U
1	A	714	G
1	A	731	C
1	A	736	A
1	A	737	C
1	A	738	G
1	A	760	A
1	A	764	A
1	A	776	U
1	A	796	U
1	A	798	A
1	A	800	C
1	A	801	G
1	A	802	A
1	A	803	U
1	A	804	G
1	A	811	A
1	A	822	U
1	A	823	C
1	A	824	U
1	A	825	C
1	A	835	G
1	A	847	U
1	A	848	U
1	A	849	A
1	A	850	A
1	A	851	G
1	A	862	G
1	A	866	A
1	A	867	G
1	A	868	U
1	A	879	G
1	A	891	A
1	A	903	G
1	A	911	C
1	A	912	A
1	A	922	G
1	A	937	U
1	A	938	U
1	A	943	G

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Mol	Chain	Res	Type
1	A	945	A
1	A	946	A
1	A	948	G
1	A	949	C
1	A	951	A
1	A	952	A
1	A	953	G
1	A	954	A
1	A	959	U
1	A	960	A
1	A	969	U
1	A	970	G
1	A	971	A
1	A	982	A
1	A	983	A
1	A	1002	G
1	A	1004	G
1	A	1005	C
1	A	1032	G
1	A	1036	C
1	A	1046	G
1	A	1047	U
1	A	1048	C
1	A	1050	G
1	A	1067	U
1	A	1068	U
1	A	1083	A
1	A	1084	A
1	A	1099	G
1	A	1107	U
1	A	1108	U
1	A	1111	C
1	A	1112	A
1	A	1113	G
1	A	1118	U
1	A	1119	C
1	A	1120	G
1	A	1121	G
1	A	1127	C
1	A	1128	A
1	A	1140	C
1	A	1141	U

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Mol	Chain	Res	Type
1	A	1142	G
1	A	1164	A
1	A	1165	G
1	A	1177	U
1	A	1178	G
1	A	1181	C
1	A	1182	A
1	A	1183	G
1	A	1193	U
1	A	1205	G
1	A	1206	A
1	A	1207	C
1	A	1208	A
1	A	1220	A
1	A	1221	U
1	A	1222	G
1	A	1238	U
1	A	1261	A
1	A	1262	U
1	A	1263	C
1	A	1266	A
1	A	1267	A
1	A	1280	A
1	A	1281	G
1	A	1284	C
1	A	1286	G
1	A	1301	C
1	A	1303	C
1	A	1304	G
1	A	1319	G
1	A	1327	A
1	A	1328	G
1	A	1329	U
1	A	1345	A
1	A	1346	U
1	A	1347	G
1	A	1363	U
1	A	1376	A
1	A	1377	C
1	A	1379	C
1	A	1380	A
1	A	1382	C

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Mol	Chain	Res	Type
1	A	1383	G
1	A	1426	A
1	A	1432	C
1	A	1433	G
1	A	1469	A
1	A	1476	A
1	A	1479	A
1	A	1480	A
1	A	1481	G
1	A	1483	U
1	A	1484	A
1	A	1494	G
1	A	1495	A
1	A	1506	G
1	A	1507	G
1	A	1510	C
1	A	1511	A
1	A	1512	C
1	A	1513	C
1	A	1514	U
1	A	1515	C

All (140) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	3	G
1	A	7	G
1	A	8	A
1	A	13	U
1	A	30	U
1	A	31	G
1	A	47	C
1	A	48	C
1	A	50	A
1	A	51	A
1	A	60	A
1	A	64	G
1	A	102	A
1	A	108	G
1	A	112	A
1	A	114	C
1	A	123	G

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Mol	Chain	Res	Type
1	A	167	U
1	A	189	U
1	A	190	G
1	A	203	A
1	A	208	U
1	A	210	U
1	A	238	A
1	A	241	A
1	A	245	A
1	A	246	G
1	A	261	G
1	A	269	A
1	A	274	A
1	A	275	C
1	A	276	G
1	A	322	A
1	A	323	C
1	A	324	A
1	A	340	C
1	A	361	C
1	A	362	U
1	A	416	U
1	A	423	G
1	A	424	U
1	A	433	G
1	A	445	A
1	A	454	A
1	A	468	G
1	A	469	G
1	A	479	A
1	A	480	A
1	A	482	A
1	A	491	C
1	A	492	A
1	A	494	C
1	A	501	C
1	A	516	A
1	A	518	A
1	A	530	A
1	A	542	A
1	A	543	U
1	A	544	U

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Mol	Chain	Res	Type
1	A	545	C
1	A	549	G
1	A	558	G
1	A	578	G
1	A	624	U
1	A	635	U
1	A	636	A
1	A	670	A
1	A	684	C
1	A	686	G
1	A	700	C
1	A	704	G
1	A	735	G
1	A	736	A
1	A	795	C
1	A	798	A
1	A	800	C
1	A	801	G
1	A	802	A
1	A	803	U
1	A	848	U
1	A	849	A
1	A	850	A
1	A	861	U
1	A	866	A
1	A	867	G
1	A	890	A
1	A	911	C
1	A	937	U
1	A	942	A
1	A	945	A
1	A	951	A
1	A	952	A
1	A	959	U
1	A	969	U
1	A	970	G
1	A	1031	U
1	A	1046	G
1	A	1047	U
1	A	1049	A
1	A	1067	U
1	A	1083	A

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Mol	Chain	Res	Type
1	A	1111	C
1	A	1117	U
1	A	1127	C
1	A	1139	A
1	A	1162	G
1	A	1163	G
1	A	1171	G
1	A	1182	A
1	A	1195	C
1	A	1205	G
1	A	1206	A
1	A	1207	C
1	A	1220	A
1	A	1221	U
1	A	1266	A
1	A	1279	C
1	A	1283	U
1	A	1300	A
1	A	1303	C
1	A	1326	U
1	A	1327	A
1	A	1328	G
1	A	1345	A
1	A	1346	U
1	A	1362	U
1	A	1376	A
1	A	1378	A
1	A	1381	C
1	A	1382	C
1	A	1425	G
1	A	1432	C
1	A	1475	U
1	A	1479	A
1	A	1480	A
1	A	1483	U
1	A	1494	G
1	A	1505	U
1	A	1506	G
1	A	1514	U

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 91 ligands modelled in this entry, 77 are monoatomic - leaving 14 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$
24	WO2	A	1576	-	54,116,116	54.94	10 (18%)	6,348,348	12.84	2 (33%)
24	WO2	B	1001	-	54,116,116	54.94	10 (18%)	6,348,348	12.83	2 (33%)
24	WO2	B	1002	-	54,116,116	54.93	11 (20%)	6,348,348	12.82	2 (33%)
24	WO2	B	1004	-	54,116,116	54.92	10 (18%)	6,348,348	12.82	2 (33%)
24	WO2	C	1003	-	54,116,116	54.93	10 (18%)	6,348,348	12.83	2 (33%)
24	WO2	D	1012	-	54,116,116	54.93	11 (20%)	6,348,348	12.82	2 (33%)
24	WO2	E	1005	-	54,116,116	54.92	11 (20%)	6,348,348	12.82	2 (33%)
24	WO2	G	1006	-	54,116,116	54.93	10 (18%)	6,348,348	12.83	2 (33%)
24	WO2	G	1007	-	54,116,116	54.94	11 (20%)	6,348,348	12.83	2 (33%)
24	WO2	H	1010	-	54,116,116	54.94	10 (18%)	6,348,348	12.83	2 (33%)
24	WO2	J	1009	-	54,116,116	54.93	10 (18%)	6,348,348	12.83	2 (33%)
24	WO2	K	1014	-	54,116,116	54.94	10 (18%)	6,348,348	12.83	2 (33%)
24	WO2	R	1008	-	54,116,116	54.94	10 (18%)	6,348,348	12.84	2 (33%)
24	WO2	T	1013	-	54,116,116	54.93	10 (18%)	6,348,348	12.82	2 (33%)

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
24	WO2	A	1576	-	-	0/0/624/624	0/0/35/35
24	WO2	B	1001	-	-	0/0/624/624	0/0/35/35
24	WO2	B	1002	-	-	0/0/624/624	0/0/35/35
24	WO2	B	1004	-	-	0/0/624/624	0/0/35/35
24	WO2	C	1003	-	-	0/0/624/624	0/0/35/35
24	WO2	D	1012	-	-	0/0/624/624	0/0/35/35
24	WO2	E	1005	-	-	0/0/624/624	0/0/35/35
24	WO2	G	1006	-	-	0/0/624/624	0/0/35/35
24	WO2	G	1007	-	-	0/0/624/624	0/0/35/35
24	WO2	H	1010	-	-	0/0/624/624	0/0/35/35
24	WO2	J	1009	-	-	0/0/624/624	0/0/35/35
24	WO2	K	1014	-	-	0/0/624/624	0/0/35/35
24	WO2	R	1008	-	-	0/0/624/624	0/0/35/35
24	WO2	T	1013	-	-	0/0/624/624	0/0/35/35

All (144) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	B	1002	WO2	W11-O10	-3.20	1.78	1.90
24	A	1576	WO2	W11-O10	-3.20	1.78	1.90
24	K	1014	WO2	W11-O10	-3.19	1.78	1.90
24	B	1001	WO2	W11-O10	-3.19	1.78	1.90
24	T	1013	WO2	W11-O10	-3.18	1.78	1.90
24	H	1010	WO2	W11-O10	-3.18	1.78	1.90
24	B	1004	WO2	W11-O10	-3.18	1.78	1.90
24	G	1007	WO2	W11-O10	-3.17	1.78	1.90
24	R	1008	WO2	W11-O10	-3.17	1.78	1.90
24	C	1003	WO2	W11-O10	-3.17	1.78	1.90
24	G	1006	WO2	W11-O10	-3.17	1.78	1.90
24	J	1009	WO2	W11-O10	-3.17	1.78	1.90
24	D	1012	WO2	W11-O10	-3.16	1.78	1.90
24	E	1005	WO2	W11-O10	-3.15	1.79	1.90
24	B	1002	WO2	W9-O9	-2.30	1.82	1.90
24	D	1012	WO2	W9-O9	-2.29	1.82	1.90
24	A	1576	WO2	W9-O9	-2.29	1.82	1.90
24	H	1010	WO2	W9-O9	-2.28	1.82	1.90
24	G	1007	WO2	W9-O9	-2.28	1.82	1.90
24	T	1013	WO2	W9-O9	-2.27	1.82	1.90
24	R	1008	WO2	W9-O9	-2.26	1.82	1.90
24	C	1003	WO2	W9-O9	-2.26	1.82	1.90
24	B	1004	WO2	W9-O9	-2.26	1.82	1.90
24	B	1001	WO2	W9-O9	-2.26	1.82	1.90
24	G	1006	WO2	W9-O9	-2.25	1.82	1.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	E	1005	WO2	W9-O9	-2.25	1.82	1.90
24	J	1009	WO2	W9-O9	-2.24	1.82	1.90
24	K	1014	WO2	W9-O9	-2.24	1.82	1.90
24	J	1009	WO2	W11-O16	-2.23	1.83	1.94
24	E	1005	WO2	W11-O16	-2.21	1.83	1.94
24	G	1007	WO2	W11-O16	-2.21	1.83	1.94
24	B	1002	WO2	W11-O16	-2.21	1.83	1.94
24	D	1012	WO2	W11-O16	-2.20	1.83	1.94
24	C	1003	WO2	W11-O16	-2.20	1.83	1.94
24	G	1006	WO2	W11-O16	-2.20	1.83	1.94
24	R	1008	WO2	W11-O16	-2.20	1.83	1.94
24	A	1576	WO2	W11-O16	-2.20	1.83	1.94
24	B	1001	WO2	W11-O16	-2.20	1.83	1.94
24	B	1004	WO2	W11-O16	-2.20	1.83	1.94
24	T	1013	WO2	W11-O16	-2.19	1.83	1.94
24	H	1010	WO2	W11-O16	-2.17	1.83	1.94
24	K	1014	WO2	W11-O16	-2.17	1.83	1.94
24	B	1002	WO2	W5-O16	2.01	2.05	1.94
24	G	1007	WO2	W5-O16	2.01	2.05	1.94
24	D	1012	WO2	W5-O16	2.01	2.05	1.94
24	E	1005	WO2	W5-O16	2.01	2.05	1.94
24	E	1005	WO2	P2-OP7	2.35	1.57	1.53
24	R	1008	WO2	P2-OP7	2.38	1.57	1.53
24	B	1001	WO2	P2-OP7	2.38	1.57	1.53
24	B	1004	WO2	P2-OP7	2.39	1.57	1.53
24	K	1014	WO2	P2-OP7	2.40	1.57	1.53
24	D	1012	WO2	P2-OP7	2.41	1.57	1.53
24	C	1003	WO2	P2-OP7	2.41	1.57	1.53
24	G	1007	WO2	P2-OP7	2.42	1.57	1.53
24	J	1009	WO2	P2-OP7	2.42	1.57	1.53
24	B	1002	WO2	P2-OP7	2.43	1.57	1.53
24	A	1576	WO2	P2-OP7	2.43	1.57	1.53
24	H	1010	WO2	P2-OP7	2.44	1.57	1.53
24	T	1013	WO2	P2-OP7	2.45	1.57	1.53
24	D	1012	WO2	P1-OP3	2.47	1.58	1.53
24	G	1006	WO2	P1-OP3	2.48	1.58	1.53
24	G	1006	WO2	P2-OP7	2.49	1.58	1.53
24	C	1003	WO2	P1-OP3	2.49	1.58	1.53
24	B	1001	WO2	P1-OP3	2.50	1.58	1.53
24	B	1002	WO2	P1-OP3	2.51	1.58	1.53
24	E	1005	WO2	P1-OP3	2.52	1.58	1.53
24	K	1014	WO2	P1-OP3	2.52	1.58	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	B	1004	WO2	P1-OP3	2.52	1.58	1.53
24	G	1007	WO2	P1-OP3	2.53	1.58	1.53
24	R	1008	WO2	P1-OP3	2.54	1.58	1.53
24	T	1013	WO2	P1-OP3	2.54	1.58	1.53
24	A	1576	WO2	P1-OP3	2.55	1.58	1.53
24	H	1010	WO2	P1-OP3	2.55	1.58	1.53
24	J	1009	WO2	P1-OP3	2.57	1.58	1.53
24	D	1012	WO2	W3-O8	2.63	1.99	1.90
24	B	1002	WO2	W3-O8	2.64	1.99	1.90
24	B	1001	WO2	W3-O8	2.64	1.99	1.90
24	J	1009	WO2	W3-O8	2.65	1.99	1.90
24	G	1006	WO2	W3-O8	2.65	1.99	1.90
24	A	1576	WO2	W3-O8	2.65	1.99	1.90
24	C	1003	WO2	P1-OP1	2.65	1.58	1.53
24	B	1004	WO2	W3-O8	2.66	1.99	1.90
24	G	1007	WO2	W3-O8	2.66	1.99	1.90
24	E	1005	WO2	P1-OP1	2.66	1.58	1.53
24	T	1013	WO2	W3-O8	2.66	1.99	1.90
24	K	1014	WO2	W3-O8	2.66	1.99	1.90
24	E	1005	WO2	W3-O8	2.67	2.00	1.90
24	H	1010	WO2	W3-O8	2.68	2.00	1.90
24	R	1008	WO2	W3-O8	2.68	2.00	1.90
24	B	1004	WO2	P1-OP1	2.68	1.58	1.53
24	H	1010	WO2	P1-OP1	2.69	1.58	1.53
24	C	1003	WO2	W3-O8	2.69	2.00	1.90
24	T	1013	WO2	P1-OP1	2.69	1.58	1.53
24	K	1014	WO2	P1-OP1	2.70	1.58	1.53
24	B	1002	WO2	P1-OP1	2.70	1.58	1.53
24	J	1009	WO2	P1-OP1	2.71	1.58	1.53
24	R	1008	WO2	P1-OP1	2.73	1.58	1.53
24	A	1576	WO2	P1-OP1	2.74	1.58	1.53
24	D	1012	WO2	P1-OP1	2.76	1.58	1.53
24	G	1007	WO2	P1-OP1	2.76	1.58	1.53
24	B	1001	WO2	P1-OP1	2.78	1.58	1.53
24	G	1006	WO2	P1-OP1	2.82	1.58	1.53
24	G	1007	WO2	W3-O11	3.77	2.03	1.90
24	J	1009	WO2	W3-O11	3.77	2.03	1.90
24	K	1014	WO2	W3-O11	3.77	2.03	1.90
24	E	1005	WO2	W3-O11	3.77	2.03	1.90
24	D	1012	WO2	W3-O11	3.77	2.03	1.90
24	B	1002	WO2	W3-O11	3.77	2.03	1.90
24	B	1001	WO2	W3-O11	3.78	2.04	1.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	H	1010	WO2	W3-O11	3.78	2.04	1.90
24	A	1576	WO2	W3-O11	3.79	2.04	1.90
24	R	1008	WO2	W3-O11	3.79	2.04	1.90
24	T	1013	WO2	W3-O11	3.80	2.04	1.90
24	C	1003	WO2	W3-O11	3.80	2.04	1.90
24	G	1006	WO2	W3-O11	3.81	2.04	1.90
24	B	1004	WO2	W3-O11	3.82	2.04	1.90
24	B	1002	WO2	W9-O12	3.89	2.04	1.90
24	K	1014	WO2	W9-O12	3.89	2.04	1.90
24	T	1013	WO2	W9-O12	3.90	2.04	1.90
24	B	1001	WO2	W9-O12	3.90	2.04	1.90
24	G	1007	WO2	W9-O12	3.90	2.04	1.90
24	A	1576	WO2	W9-O12	3.91	2.04	1.90
24	C	1003	WO2	W9-O12	3.91	2.04	1.90
24	J	1009	WO2	W9-O12	3.92	2.04	1.90
24	R	1008	WO2	W9-O12	3.92	2.04	1.90
24	B	1004	WO2	W9-O12	3.92	2.04	1.90
24	E	1005	WO2	W9-O12	3.92	2.04	1.90
24	H	1010	WO2	W9-O12	3.93	2.04	1.90
24	D	1012	WO2	W9-O12	3.93	2.04	1.90
24	G	1006	WO2	W9-O12	3.94	2.04	1.90
24	E	1005	WO2	P2-OP5	403.40	8.55	1.53
24	B	1004	WO2	P2-OP5	403.46	8.56	1.53
24	D	1012	WO2	P2-OP5	403.49	8.56	1.53
24	T	1013	WO2	P2-OP5	403.49	8.56	1.53
24	B	1002	WO2	P2-OP5	403.50	8.56	1.53
24	G	1006	WO2	P2-OP5	403.50	8.56	1.53
24	C	1003	WO2	P2-OP5	403.52	8.56	1.53
24	J	1009	WO2	P2-OP5	403.52	8.56	1.53
24	K	1014	WO2	P2-OP5	403.54	8.56	1.53
24	G	1007	WO2	P2-OP5	403.55	8.56	1.53
24	R	1008	WO2	P2-OP5	403.55	8.56	1.53
24	H	1010	WO2	P2-OP5	403.56	8.56	1.53
24	B	1001	WO2	P2-OP5	403.57	8.56	1.53
24	A	1576	WO2	P2-OP5	403.58	8.56	1.53

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	G	1007	WO2	OP6-P2-OP5	-29.13	61.91	111.62
24	A	1576	WO2	OP6-P2-OP5	-29.13	61.92	111.62
24	R	1008	WO2	OP6-P2-OP5	-29.12	61.93	111.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	K	1014	WO2	OP6-P2-OP5	-29.12	61.94	111.62
24	B	1001	WO2	OP6-P2-OP5	-29.12	61.94	111.62
24	H	1010	WO2	OP6-P2-OP5	-29.11	61.94	111.62
24	J	1009	WO2	OP6-P2-OP5	-29.11	61.94	111.62
24	C	1003	WO2	OP6-P2-OP5	-29.11	61.95	111.62
24	G	1006	WO2	OP6-P2-OP5	-29.10	61.96	111.62
24	T	1013	WO2	OP6-P2-OP5	-29.10	61.96	111.62
24	E	1005	WO2	OP6-P2-OP5	-29.10	61.97	111.62
24	B	1004	WO2	OP6-P2-OP5	-29.09	61.98	111.62
24	D	1012	WO2	OP6-P2-OP5	-29.09	61.98	111.62
24	B	1002	WO2	OP6-P2-OP5	-29.09	61.98	111.62
24	H	1010	WO2	OP7-P2-OP5	-11.71	91.63	111.62
24	R	1008	WO2	OP7-P2-OP5	-11.71	91.64	111.62
24	K	1014	WO2	OP7-P2-OP5	-11.71	91.64	111.62
24	B	1001	WO2	OP7-P2-OP5	-11.71	91.64	111.62
24	D	1012	WO2	OP7-P2-OP5	-11.70	91.65	111.62
24	G	1006	WO2	OP7-P2-OP5	-11.69	91.67	111.62
24	A	1576	WO2	OP7-P2-OP5	-11.69	91.67	111.62
24	C	1003	WO2	OP7-P2-OP5	-11.68	91.69	111.62
24	J	1009	WO2	OP7-P2-OP5	-11.67	91.70	111.62
24	B	1002	WO2	OP7-P2-OP5	-11.67	91.70	111.62
24	T	1013	WO2	OP7-P2-OP5	-11.67	91.70	111.62
24	G	1007	WO2	OP7-P2-OP5	-11.67	91.71	111.62
24	B	1004	WO2	OP7-P2-OP5	-11.66	91.72	111.62
24	E	1005	WO2	OP7-P2-OP5	-11.65	91.73	111.62

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

9 monomers are involved in 34 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
24	B	1001	WO2	1	0
24	B	1004	WO2	4	0
24	C	1003	WO2	1	0
24	E	1005	WO2	9	1
24	G	1006	WO2	4	0
24	G	1007	WO2	1	0
24	J	1009	WO2	3	0
24	K	1014	WO2	5	2
24	R	1008	WO2	4	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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

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

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

6.3 Carbohydrates [i](#)

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

6.4 Ligands [i](#)

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

6.5 Other polymers [i](#)

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