



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2020 – 07:39 PM BST

PDB ID : 1XMO
Title : Crystal Structure of mnm5U34t6A37-tRNA^{Lys}UUU Complexed with AAG-mRNA in the Decoding Center
Authors : Murphy, F.V.; Ramakrishnan, V.; Malkiewicz, A.; Agris, P.F.
Deposited on : 2004-10-04
Resolution : 3.25 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

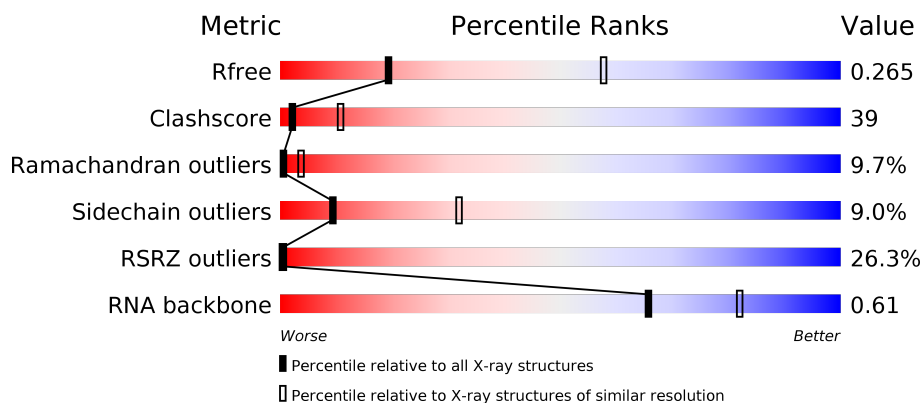
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.25 Å.

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



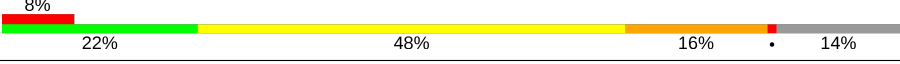
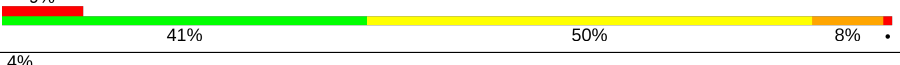
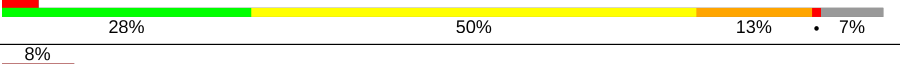
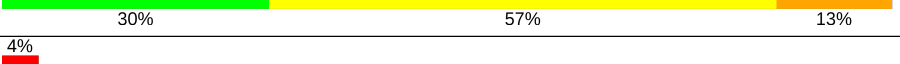
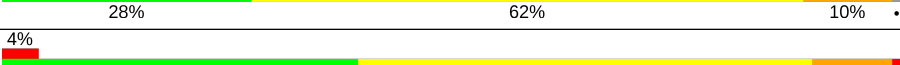
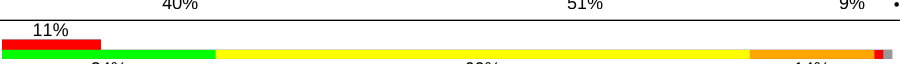
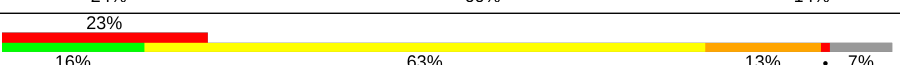
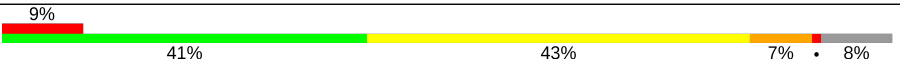
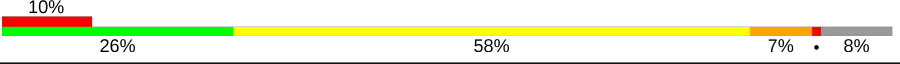
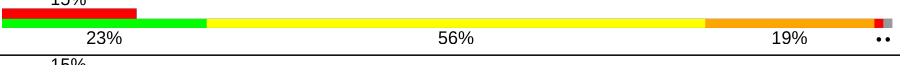
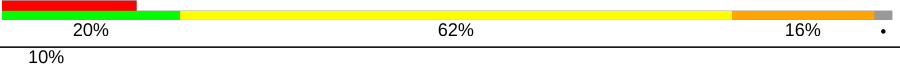
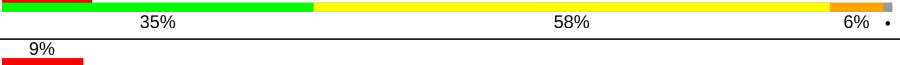

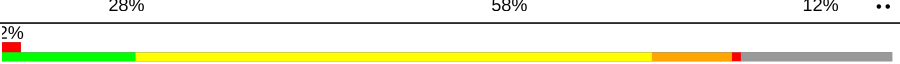
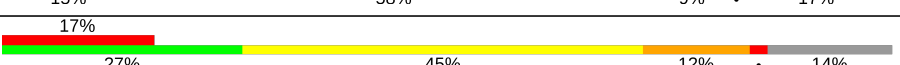
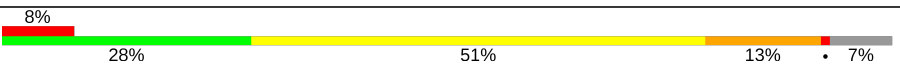
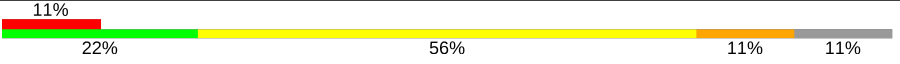
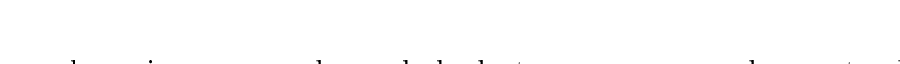
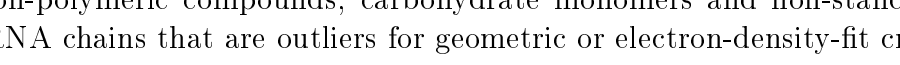
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1191 (3.30-3.22)
Clashscore	141614	1251 (3.30-3.22)
Ramachandran outliers	138981	1229 (3.30-3.22)
Sidechain outliers	138945	1228 (3.30-3.22)
RSRZ outliers	127900	1154 (3.30-3.22)
RNA backbone	3102	1072 (3.62-2.90)

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

Mol	Chain	Length	Quality of chain
1	A	1522	<div> <div>52%</div> <div>28% 55% 14% ..</div> </div>
2	W	3	<div> <div>100%</div> <div>33% 67%</div> </div>
3	X	11	<div> <div>27%</div> <div>36% 45% 18%</div> </div>
4	B	256	<div> <div>7%</div> <div>15% 65% 9% • 9%</div> </div>

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Mol	Chain	Length	Quality of chain
5	C	239	
6	D	209	
7	E	162	
8	F	101	
9	G	156	
10	H	138	
11	I	128	
12	J	105	
13	K	129	
14	L	135	
15	M	126	
16	N	61	
17	O	89	
18	P	88	
19	Q	105	
20	R	88	
21	S	93	
22	T	106	
23	V	27	

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
25	MG	A	1562	-	-	-	X
25	MG	A	1566	-	-	-	X
25	MG	A	1575	-	-	-	X
25	MG	A	1595	-	-	-	X
25	MG	A	1596	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
25	MG	A	1607	-	-	-	X
25	MG	A	1622	-	-	-	X
25	MG	A	1634	-	-	-	X
25	MG	A	210	-	-	-	X
25	MG	A	493	-	-	-	X
3	T6A	X	37	X	-	-	-

2 Entry composition [i](#)

There are 26 unique types of molecules in this entry. The entry contains 52063 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1507	Total	C	N	O	P	0	0	0
			32380	14414	5990	10470	1506			

- Molecule 2 is a RNA chain called A-Site Messenger RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	W	3	Total	C	N	O	P	0	0	0
			64	30	15	17	2			

- Molecule 3 is a RNA chain called Anticodon Transfer RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	X	11	Total	C	N	O	P	0	0	0
			239	110	38	81	10			

- Molecule 4 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	B	234	Total	C	N	O	S	0	0	0
			1900	1213	341	341	5			

- Molecule 5 is a protein called 30S ribosomal protein S3.

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

- Molecule 6 is a protein called 30S ribosomal protein S4.

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

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

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

- Molecule 8 is a protein called 30S ribosomal protein S6.

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

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

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

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

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

- Molecule 11 is a protein called 30S ribosomal protein S9.

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

- Molecule 12 is a protein called 30S ribosomal protein S10.

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

- Molecule 13 is a protein called 30S ribosomal protein S11.

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

- Molecule 14 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
14	L	124	Total	C	N	O	S	0	0	0
			970	611	195	163	1			

- Molecule 15 is a protein called 30S ribosomal protein S13.

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

- Molecule 16 is a protein called 30S ribosomal protein S14.

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

- Molecule 17 is a protein called 30S ribosomal protein S15.

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

- Molecule 18 is a protein called 30S ribosomal protein S16.

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

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

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

- Molecule 20 is a protein called 30S ribosomal protein S18.

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
21	S	80	Total	C	N	O	S	0	0	0
			647	414	119	112	2			

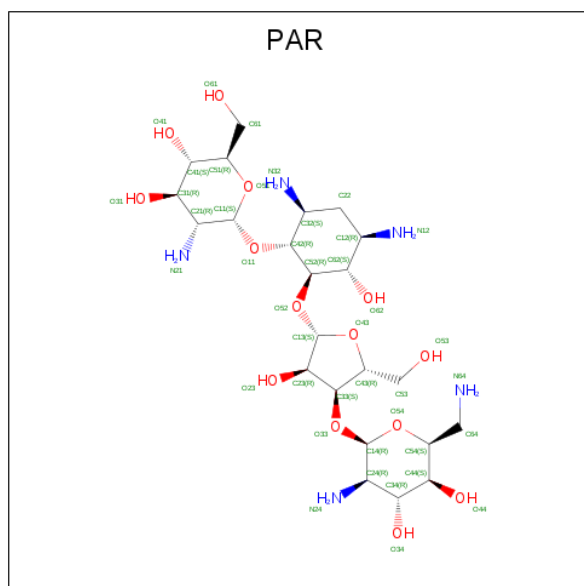
- Molecule 22 is a protein called 30S ribosomal protein S20.

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

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

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
23	V	24	Total	C	N	O	0	0	0
			208	128	50	30			

- Molecule 24 is PAROMOMYCIN (three-letter code: PAR) (formula: $C_{23}H_{45}N_5O_{14}$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
24	A	1	Total	C	N	O	0	0
			42	23	5	14		

- Molecule 25 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
25	X	2	Total	Mg	0	0
			2	2		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
25	J	1	Total 1	Mg 1	0	0
25	A	104	Total 104	Mg 104	0	0

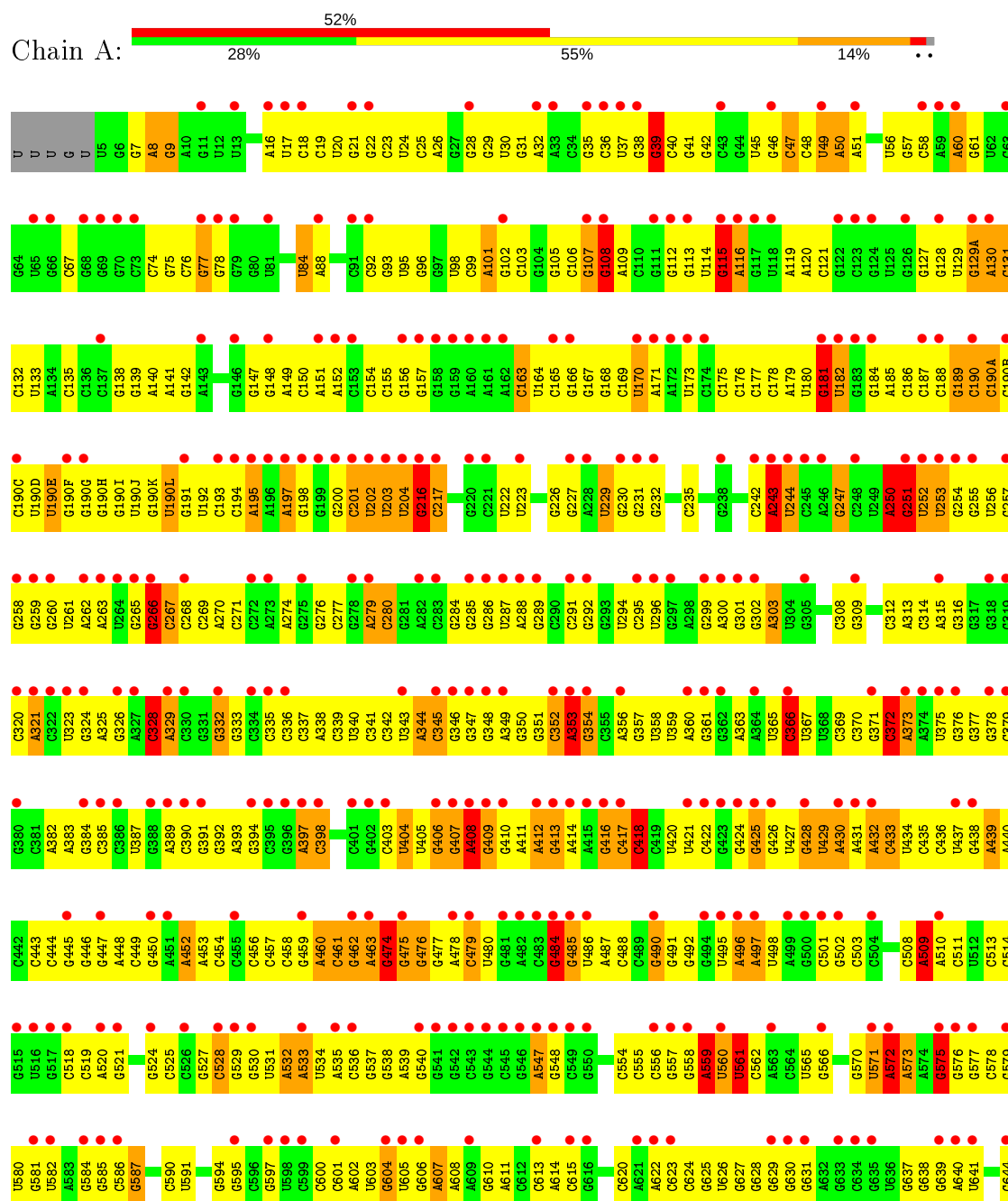
- Molecule 26 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

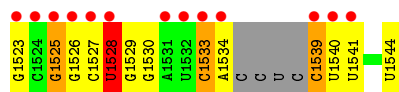
3 Residue-property plots

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

• Molecule 1: 16S ribosomal RNA



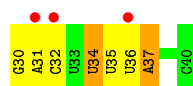
G1461	G1392	A1382	G1270	C1208	C1145	U1085	C1029	A968	C904	G836	G769	A706	G645
G1462	U1393	A1383	G1271	C1209	A1146	U1086	G1030	A969	U905	G837	G770	C707	U646
G1463	A1394	C1385	G1272	C1210	C1187	G1087	C	C970	G906	G838	G775	C708	C647
G1464	C1395	U1211	G1273	U1211	U1148	G1088	G	G971	A907	U839	G776	C709	A648
G1465	A1396	C1212	G1274	U1212	C1149	G1089	A	C972	A908	U840	A777	G710	G649
G1466	C1397	U1213	A1275	U1213	U1150	U1090	G1031	G973	A909	U841	A778	G711	G650
G1467	G1398	C1214	G1276	C1214	A1151	U1091	G1032	A974	C910	C848	C779	A712	C651
G1468	A1399	A1152	U1277	G1215	C1153	A1092	G1033	A975	U911	C849	A780	G713	U652
G1469	C1399	C1153	U1278	G1216	C1154	U093	G1034	G976	C912	U850	A781	G714	A653
G1470	C1400	G1154	A1279	C1217	G1155	U094	G1035	A977	A913	G851	A782	A715	G654
G1471	C1401	U1155	A1280	C1218	U1156	U095	A1035	A978	A914	G852	A783	A716	A655
G1472	C1402	A1156	U1281	U1219	G1157	C1096	G1036	C979	A915	G853	C717	G717	C656
G1473	C1403	C1157	U1282	G1220	A1158	C1097	G1037	C980	A916	G854	C718	G718	G657
G1474	A1404	C1158	G1283	G1221	C1159	C1098	C1038	U981	G917	G855	G785	C719	G658
G1475	G1405	U1159	A1284	G1222	G1160	U099	C1039	U982	A918	C856	G786	C720	U659
G1476	U1406	C1161	A1285	G1223	C1162	C1100	U1040	U983	A919	C857	A787	G721	G660
G1477	C1407	C1162	A1286	G1224	C1163	A1101	G1041	C984	U920	G858	U788	G722	G661
G1478	G1412	G1163	A1287	C1225	C1164	A1102	A1042	C985	U921	A859	U789	A723	U662
G1479	A1413	C1165	A1288	G1226	U1164	C1103	C1043	A986	G922	A860	A790	G724	A663
G1480	U1414	U1165	A1289	A1227	G1166	G1104	A1044	G987	A923	G861	G791	G725	G664
G1481	C1352	C1166	G1290	C1228	C1167	U105	C1045	G988	C924	C862	A792	G726	A665
G1482	G1353	A1167	A1291	A1229	G1168	G1106	A1046	C989	G925	U863	U793	G727	G666
G1483	C1354	A1168	U1292	C1230	C1169	C1107	G1047	C990	A864	U864	A794	A728	G667
G1484	G1355	A1169	G1293	G1231	A1169	G1108	G1048	U991	G927	A865	C795	G729	G668
G1485	C1356	G1171	C1294	U1232	C1171	C1109	U1049	U992	G928	C866	C796	A730	U669
G1486	A1357	G1174	G1295	G1233	G1174	A1110	G1050	G993	G929	G867	C797	G731	G670
G1487	C1358	U1175	C1296	C1234	C1175	A1111	C1051	A994	C934	C868	G798	C732	G671
G1488	G1359	A1176	C1297	U1235	C1176	C1112	C1052	A995	A935	C869	G799	C735	U672
G1489	C1360	G1177	A1298	C1236	C1177	C1113	G1053	A996	A936	U870	G800	C736	G673
G1490	A1361	C1178	C1299	C1237	C1178	C1114	C1054	U1000	A937	A872	U801	A737	G674
G1491	C1362	G1179	A1300	A1238	C1179	C1115	A1055	A1001	A938	A873	A802	C738	A675
G1492	C1363	U1179	U1301	C1239	C1180	C1116	U1056	G	G939	G874	G803	C739	U677
G1493	A1364	G1180	U1302	U1240	C1181	G1117	G1057	U1002	C940	C875	U804	C740	U678
G1494	C1365	G1181	C1303	G1241	C1182	C1118	C1058	G1003	G941	C876	C806	G741	C679
G1495	G1366	A1182	G1304	C1242	C1183	C1119	C1059	A1004	G942	C877	A807	G742	C680
G1496	C1367	G1183	C1305	C1243	C1184	G1120	G1060	A1005	U943	G878	G811	U743	C681
G1497	A1368	G1184	A1306	C1244	C1185	U1121	C1061	C1006	G944	C879	C812	C744	G682
G1498	C1369	G1186	U1307	G1248	G1186	U1122	U1062	C1007	G945	C880	U813	C745	G683
G1499	A1433	C1369	A1248	C1249	C1187	A1123	C1063	C1008	A946	G881	U814	A746	A684
G1500	C1433	G1370	G1311	G1250	C1188	U1124	C1064	C1009	G947	C882	A815	C747	G685
G1501	A1434	G1371	G1312	A1251	C1189	U1125	U1065	G1010	C948	C883	A816	C748	U686
G1502	G1435	U1372	U1313	C1252	C1190	U1126	C1066	G1011	A949	U884	A817	G750	A687
G1503	U1436	C1373	C1314	A1252	C1191	G1127	A1067	U1012	U950	G885	C817	C751	G688
G1504	C1437	G1374	U1315	G1253	C1192	C1128	G1068	G1013	G951	G886	G818	U751	C689
G1505	G1438	A1375	G1316	C1254	C1193	C129	C1069	A1014	U952	G887	A819	G752	G690
G1506	C1439	C1376	A1317	U1255	U1194	A1130	U1070	A1015	G953	G888	U820	A753	G691
G1507	G1440	C1377	C1318	A1256	C1195	C1131	C1071	A1016	A889	G889	G821	G754	U692
G1508	A1441	G1378	A1319	G1257	U1196	C1132	G1072	G1017	U955	G890	G825	G755	G693
G1509	C1442	C1379	G1320	G1258	G1197	G1133	U1073	C1018	A958	G891	C826	C756	A694
G1510	A1443	U1380	C1321	C1259	G1198	U1134	G1074	C1019	A959	G895	U827	U757	A695
G1511	C1444	C1381	C1322	C1260	U1199	U1135	C1075	U1020	U960	C896	A828	G758	A696
G1512	G1445	C1382	G1323	A1261	C1200	U1136	G1076	G1021	U961	C897	A759	G760	U697
G1513	A1451	C1383	A1324	C1262	A1201	G1138	U1077	G1022	C962	C898	G829	G761	G698
G1514	C1452	G1384	C1325	C1263	G1202	G1139	U1078	G1023	G899	G899	U831	G762	C701
G1515	G1453	U1385	G1326	C1264	C1203	C1140	G1079	G1024	A900	C832	U833	G763	A702
G1516	A1454	C1386	C1327	G1265	A1204	C1141	A1080	U1025	A901	C833	C834	A764	G703
G1517	C1455	C1387	C1328	G1266	U1205	G1142	G1081	G1026	A965	U834	A767	A768	U705
G1518	G1456	C1388	A1329	C1267	U1206	G1143	G1082	G1027	G903	U835			
G1519	U1457	U1389	U1330	A1268	G1207	G1144	G1084	C1028					
G1520	A1458	C1390	G1331	A1269									
G1521	C1459	U1391											
G1522	A1460												



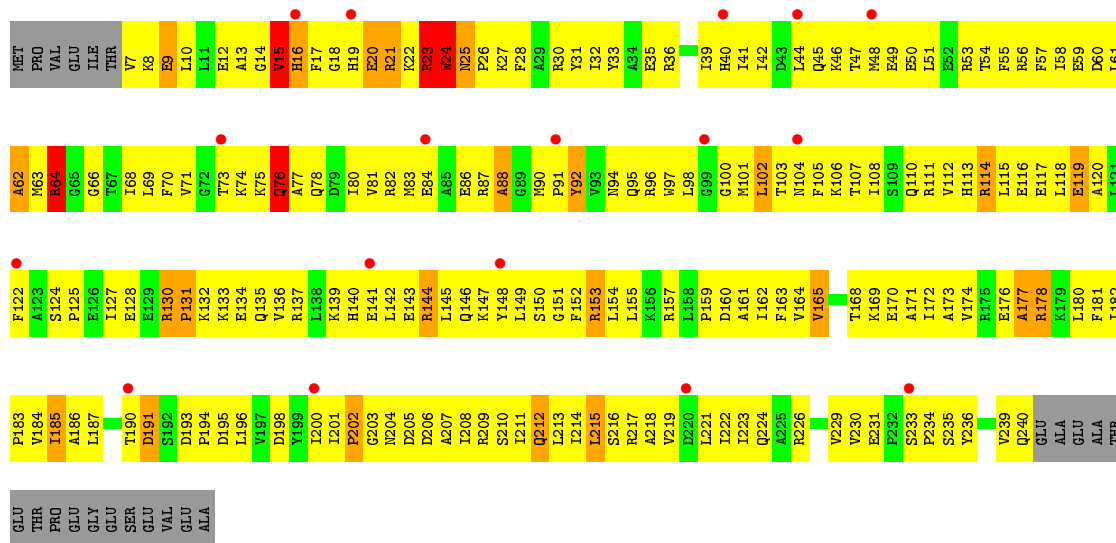
• Molecule 2: A-Site Messenger RNA



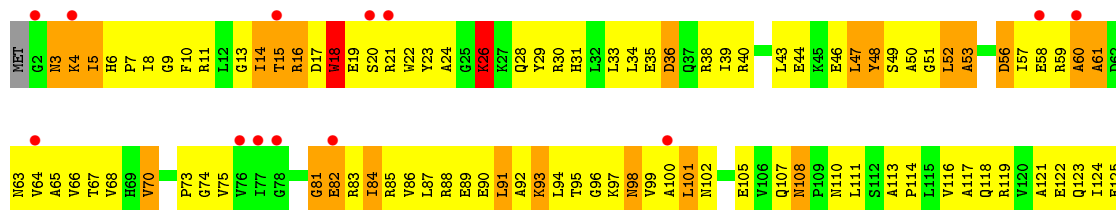
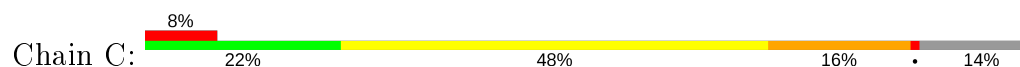
• Molecule 3: Anticodon Transfer RNA

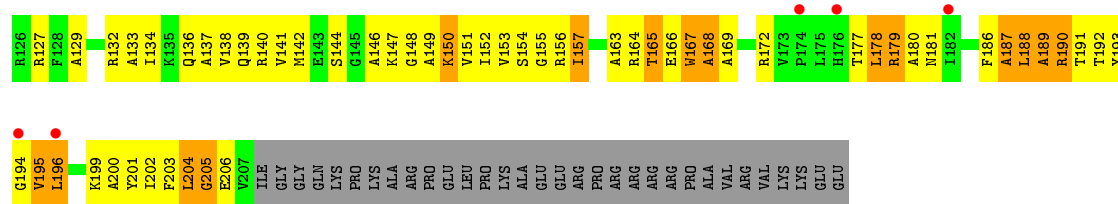


• Molecule 4: 30S ribosomal protein S2

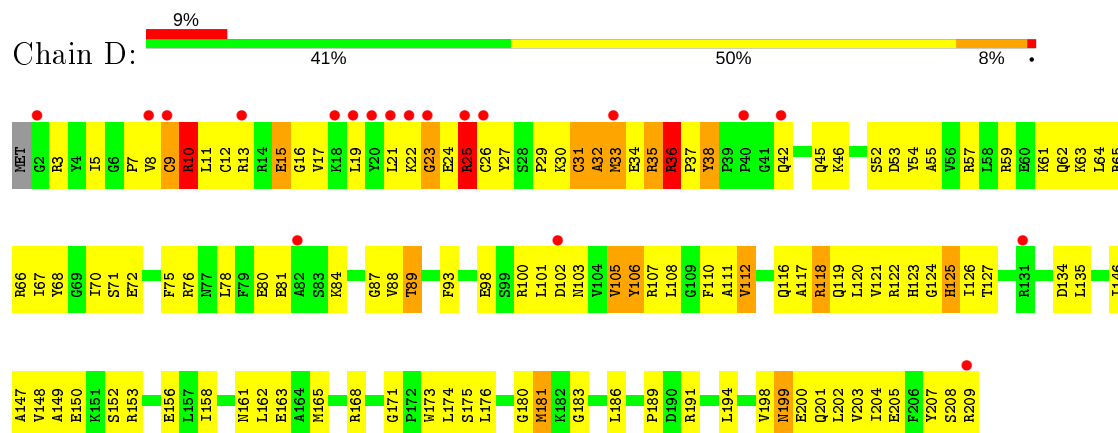


• Molecule 5: 30S ribosomal protein S3

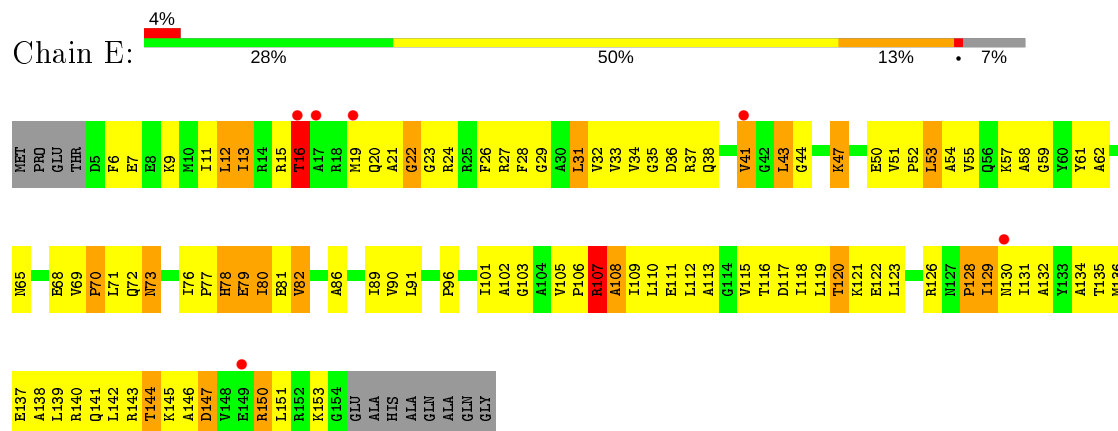




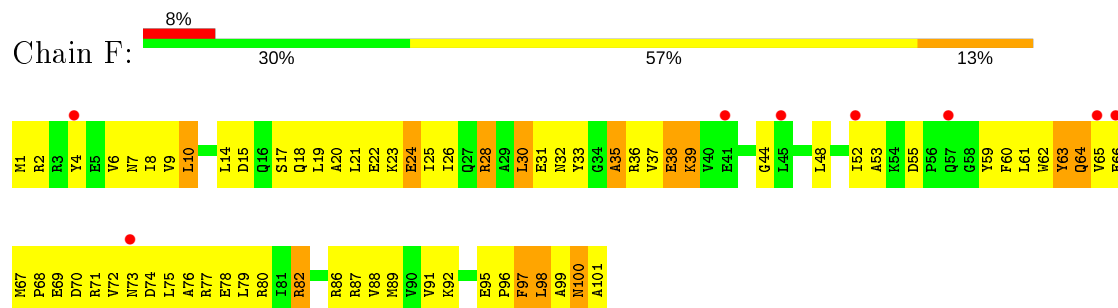
• Molecule 6: 30S ribosomal protein S4



• Molecule 7: 30S ribosomal protein S5

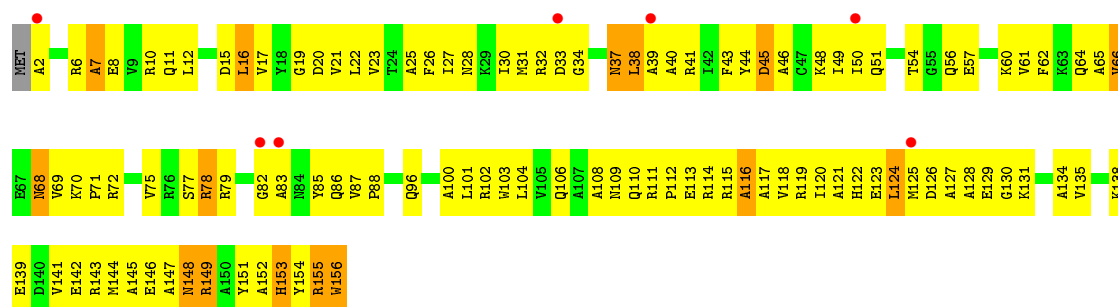


• Molecule 8: 30S ribosomal protein S6

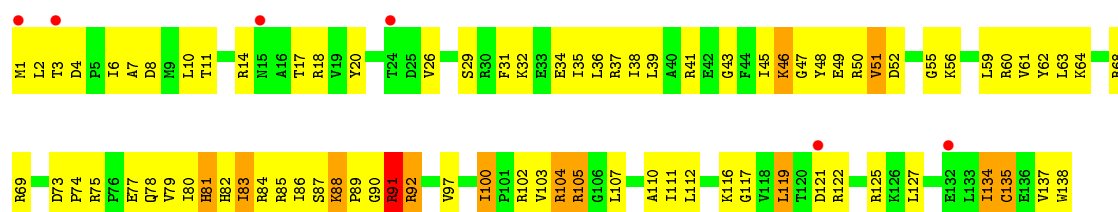


• Molecule 9: 30S ribosomal protein S7

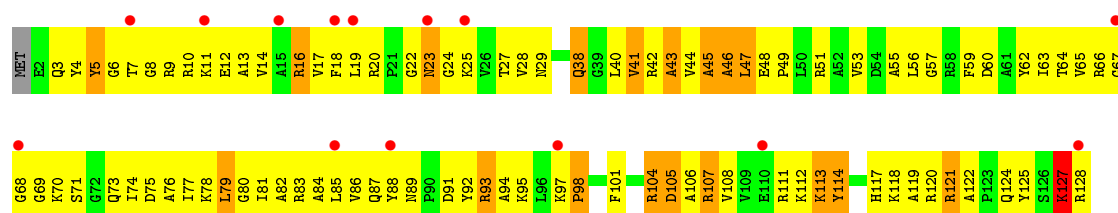




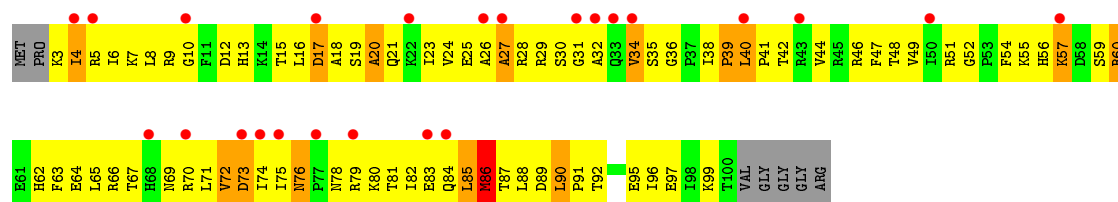
- Molecule 10: 30S ribosomal protein S8



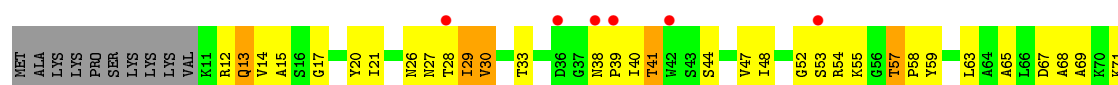
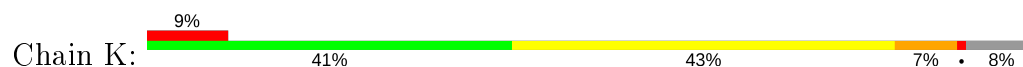
- Molecule 11: 30S ribosomal protein S9

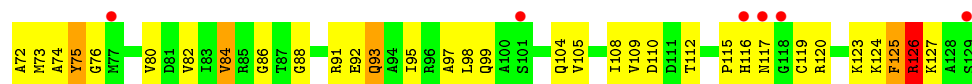


- Molecule 12: 30S ribosomal protein S10

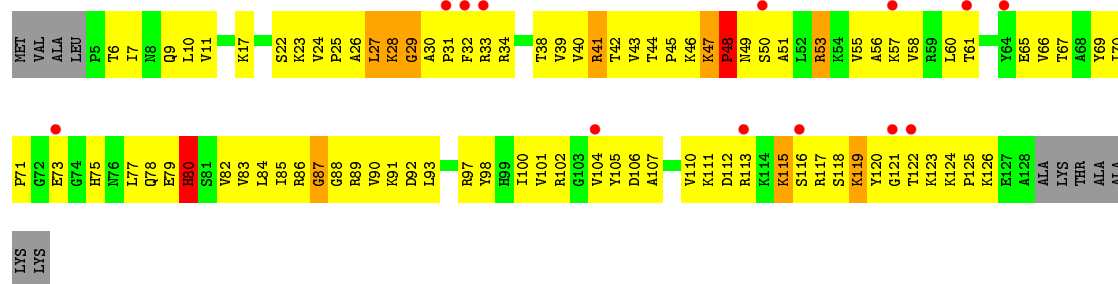


- Molecule 13: 30S ribosomal protein S11

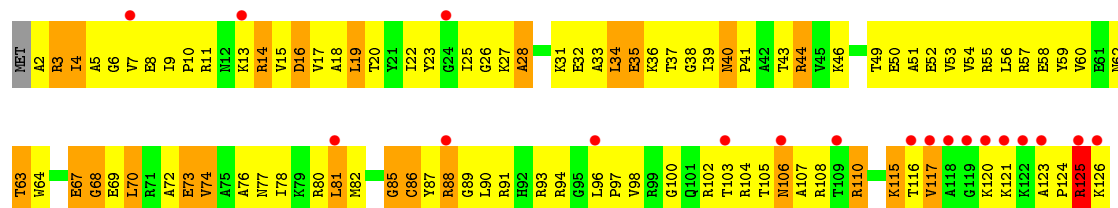




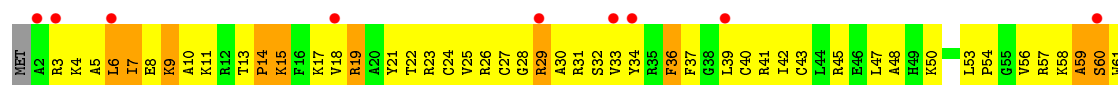
• Molecule 14: 30S ribosomal protein S12



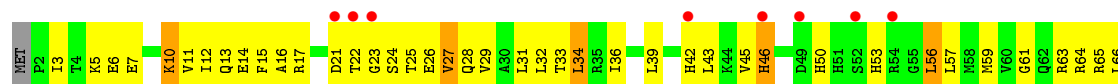
• Molecule 15: 30S ribosomal protein S13



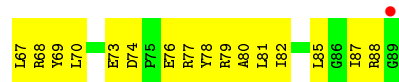
• Molecule 16: 30S ribosomal protein S14

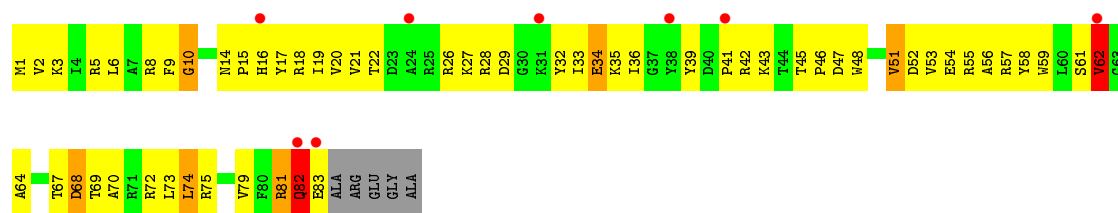


• Molecule 17: 30S ribosomal protein S15

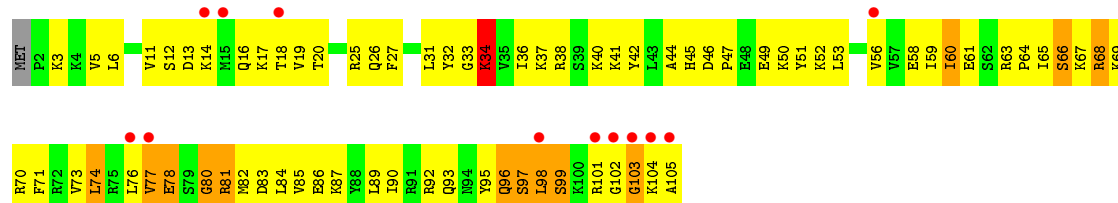


• Molecule 18: 30S ribosomal protein S16

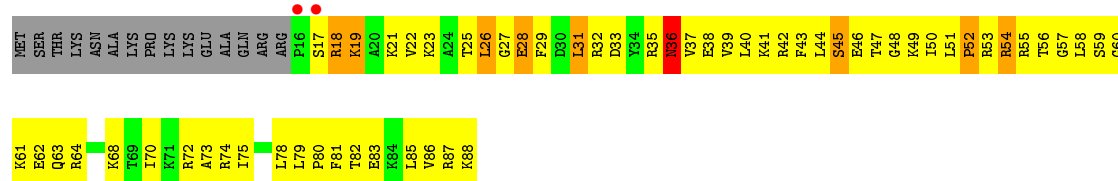
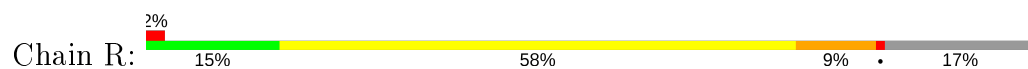




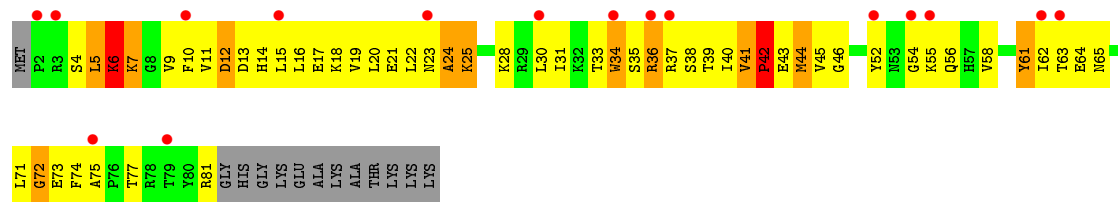
- Molecule 19: 30S ribosomal protein S17



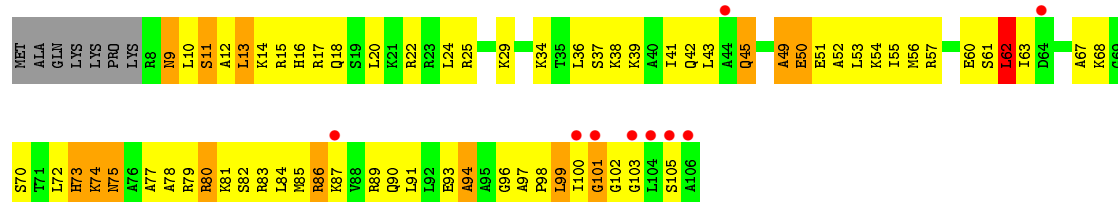
- Molecule 20: 30S ribosomal protein S18



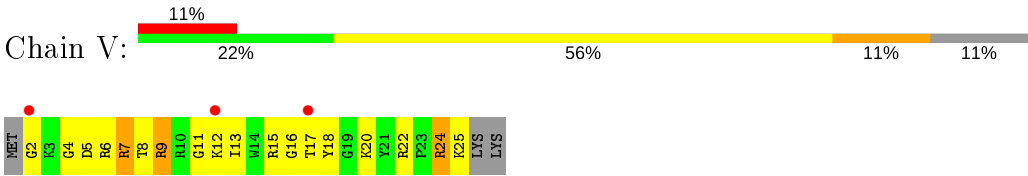
- Molecule 21: 30S ribosomal protein S19



- Molecule 22: 30S ribosomal protein S20



● Molecule 23: 30S ribosomal protein Thx



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	400.81Å 400.81Å 176.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	99.00 – 3.25 200.41 – 3.23	Depositor EDS
% Data completeness (in resolution range)	5.0 (99.00-3.25) 88.5 (200.41-3.23)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.14	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.05 (at 3.26Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.231 , 0.284 0.215 , 0.265	Depositor DCC
R_{free} test set	10562 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	85.2	Xtriage
Anisotropy	0.267	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 146.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	52063	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.22% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG, T6A, PAR, MNU

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	0.57	2/36244 (0.0%)	0.74	36/56567 (0.1%)
2	W	0.55	0/72	0.95	1/111 (0.9%)
3	X	0.41	0/203	0.78	0/311
4	B	0.34	0/1935	0.65	0/2609
5	C	0.36	0/1636	0.63	0/2205
6	D	0.39	0/1733	0.65	0/2318
7	E	0.44	0/1162	0.74	0/1564
8	F	0.32	0/856	0.59	0/1154
9	G	0.35	0/1276	0.61	0/1709
10	H	0.44	0/1136	0.75	0/1527
11	I	0.35	0/1029	0.63	0/1378
12	J	0.35	0/805	0.69	0/1082
13	K	0.41	0/900	0.68	0/1213
14	L	0.45	0/986	0.77	0/1320
15	M	0.35	0/1008	0.67	0/1347
16	N	0.43	0/501	0.74	0/664
17	O	0.36	0/745	0.63	0/992
18	P	0.47	0/716	0.74	0/963
19	Q	0.47	0/870	0.77	0/1159
20	R	0.35	0/603	0.65	0/799
21	S	0.32	0/661	0.63	0/890
22	T	0.41	0/764	0.77	0/1006
23	V	0.42	0/212	0.72	0/277
All	All	0.52	2/56053 (0.0%)	0.73	37/83165 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	4	60
3	X	1	0
All	All	5	60

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1361	G	C3'-O3'	5.22	1.49	1.42
1	A	1361	G	O3'-P	5.14	1.67	1.61

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	575	G	C2'-C3'-O3'	9.66	130.74	109.50
1	A	115	G	C2'-C3'-O3'	9.52	130.44	109.50
1	A	559	A	C2'-C3'-O3'	9.37	130.12	109.50
1	A	243	A	C2'-C3'-O3'	9.32	130.01	109.50
1	A	1528	U	C2'-C3'-O3'	8.97	129.23	109.50
1	A	181	G	C2'-C3'-O3'	8.89	129.06	109.50
1	A	1498	U	C2'-C3'-O3'	8.36	127.90	109.50
1	A	1503	A	C2'-C3'-O3'	7.72	126.48	109.50
1	A	792	A	C2'-C3'-O3'	7.46	125.91	109.50
1	A	366	C	C2'-C3'-O3'	7.18	125.30	109.50
1	A	509	A	C2'-C3'-O3'	7.12	125.17	109.50
1	A	1505	G	C2'-C3'-O3'	7.11	125.14	109.50
1	A	965	A	C2'-C3'-O3'	6.87	124.70	113.70
1	A	812	C	C2'-C3'-O3'	6.74	124.48	113.70
1	A	1346	A	C2'-C3'-O3'	6.65	124.34	113.70
1	A	484	G	C2'-C3'-O3'	6.62	124.29	113.70
1	A	1299	A	N9-C1'-C2'	6.45	122.38	114.00
1	A	372	C	C2'-C3'-O3'	6.40	123.94	113.70
1	A	266	G	C2'-C3'-O3'	6.19	123.60	113.70
1	A	353	A	C5'-C4'-O4'	-6.19	101.67	109.10
1	A	108	G	O4'-C1'-N9	6.16	113.13	108.20
1	A	1502	A	N9-C1'-C2'	5.96	121.75	114.00
1	A	687	A	C2'-C3'-O3'	5.91	123.16	113.70
1	A	418	C	N1-C1'-C2'	5.87	121.63	114.00
1	A	60	A	C2'-C3'-O3'	5.80	122.98	113.70
1	A	960	U	C2'-C3'-O3'	5.70	122.81	113.70
1	A	108	G	O4'-C4'-C3'	-5.66	98.34	104.00
1	A	760	G	N9-C1'-C2'	-5.65	105.79	112.00
1	A	1281	U	N1-C1'-C2'	5.62	121.30	114.00
1	A	328	C	C2'-C3'-O3'	5.44	122.41	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	W	1	A	O5'-C5'-C4'	5.36	121.88	111.70
1	A	1528	U	C4'-C3'-O3'	5.33	123.65	113.00
1	A	575	G	O4'-C1'-N9	-5.31	103.95	108.20
1	A	1454	G	N9-C1'-C2'	-5.29	106.18	112.00
1	A	243	A	C4'-C3'-O3'	5.07	123.13	113.00
1	A	1504	G	OP2-P-O3'	5.04	116.30	105.20
1	A	572	A	N9-C1'-C2'	5.03	120.54	114.00

All (5) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	181	G	C3'
1	A	243	A	C3'
1	A	559	A	C3'
1	A	1528	U	C3'
3	X	37	T6A	C14

All (60) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1048	G	Sidechain
1	A	1054	C	Sidechain
1	A	107	G	Sidechain
1	A	1073	U	Sidechain
1	A	1077	G	Sidechain
1	A	108	G	Sidechain
1	A	1235	U	Sidechain
1	A	1281	U	Sidechain
1	A	1299	A	Sidechain
1	A	1345	U	Sidechain
1	A	1361	G	Sidechain
1	A	1396	A	Sidechain
1	A	1402	C	Sidechain
1	A	1414	U	Sidechain
1	A	1502	A	Sidechain
1	A	1510	U	Sidechain
1	A	1519	A	Sidechain
1	A	1522	U	Sidechain
1	A	1525	G	Sidechain
1	A	170	U	Sidechain
1	A	197	A	Sidechain
1	A	216	G	Sidechain

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Mol	Chain	Res	Type	Group
1	A	226	G	Sidechain
1	A	229	U	Sidechain
1	A	250	A	Sidechain
1	A	251	G	Sidechain
1	A	253	U	Sidechain
1	A	274	A	Sidechain
1	A	303	A	Sidechain
1	A	387	U	Sidechain
1	A	39	G	Sidechain
1	A	404	U	Sidechain
1	A	408	A	Sidechain
1	A	474	G	Sidechain
1	A	490	G	Sidechain
1	A	528	C	Sidechain
1	A	529	G	Sidechain
1	A	561	U	Sidechain
1	A	571	U	Sidechain
1	A	572	A	Sidechain
1	A	573	A	Sidechain
1	A	575	G	Sidechain
1	A	587	G	Sidechain
1	A	604	G	Sidechain
1	A	657	G	Sidechain
1	A	664	G	Sidechain
1	A	682	G	Sidechain
1	A	727	G	Sidechain
1	A	741	G	Sidechain
1	A	77	G	Sidechain
1	A	785	G	Sidechain
1	A	84	U	Sidechain
1	A	860	A	Sidechain
1	A	870	U	Sidechain
1	A	879	C	Sidechain
1	A	898	G	Sidechain
1	A	901	A	Sidechain
1	A	911	U	Sidechain
1	A	912	C	Sidechain
1	A	960	U	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	32380	0	16346	1337	0
2	W	64	0	35	4	0
3	X	239	0	127	7	0
4	B	1900	0	1951	305	0
5	C	1612	0	1677	245	0
6	D	1703	0	1764	150	0
7	E	1146	0	1207	140	0
8	F	843	0	857	102	0
9	G	1257	0	1296	131	0
10	H	1116	0	1177	112	0
11	I	1011	0	1043	153	0
12	J	792	0	835	127	0
13	K	885	0	904	71	0
14	L	970	0	1057	130	0
15	M	997	0	1072	155	0
16	N	492	0	530	67	0
17	O	734	0	771	78	0
18	P	700	0	720	81	0
19	Q	857	0	930	125	0
20	R	597	0	668	100	0
21	S	647	0	673	83	0
22	T	762	0	856	87	0
23	V	208	0	221	19	0
24	A	42	0	45	2	0
25	A	104	0	0	0	0
25	J	1	0	0	0	0
25	X	2	0	0	0	0
26	D	1	0	0	0	0
26	N	1	0	0	1	0
All	All	52063	0	36762	3496	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 39.

All (3496) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1489:G:H2'	1:A:1490:C:H5''	1.26	1.10
6:D:36:ARG:H	6:D:37:PRO:HD3	1.13	1.08
5:C:179:ARG:HG2	5:C:180:ALA:H	0.98	1.06
5:C:26:LYS:HD3	5:C:26:LYS:H	1.14	1.06
4:B:132:LYS:HA	4:B:135:GLN:HB3	1.36	1.05
1:A:1116:C:H2'	1:A:1117:G:H5''	1.36	1.05
1:A:928:G:H4'	1:A:1533:C:H5'	1.39	1.04
1:A:1489:G:C2'	1:A:1490:C:H5''	1.87	1.03
1:A:201:C:C4'	1:A:216:G:H21	1.71	1.03
1:A:929:G:OP1	1:A:1533:C:H2'	1.58	1.03
1:A:243:A:H4'	1:A:244:U:H5'	1.39	1.02
1:A:630:G:H2'	1:A:631:G:H5'	1.37	1.02
5:C:196:LEU:H	5:C:196:LEU:HD23	1.21	1.01
22:T:54:LYS:HG2	22:T:57:ARG:HH22	1.25	1.01
12:J:46:ARG:HD3	12:J:64:GLU:HB3	1.43	1.01
1:A:1057:G:H5''	5:C:154:SER:HB2	1.39	1.00
4:B:80:ILE:HD11	4:B:208:ILE:HG23	1.42	1.00
1:A:839:U:H5'	1:A:840:C:C5	1.97	1.00
5:C:179:ARG:HG2	5:C:180:ALA:N	1.77	0.99
1:A:190(L):U:H5'	1:A:190(L):U:H6	1.29	0.98
5:C:14:ILE:HG22	5:C:15:THR:H	1.27	0.98
14:L:60:LEU:HD11	14:L:85:ILE:HD12	1.45	0.97
1:A:266:G:H5''	1:A:268:C:H41	1.30	0.96
16:N:27:CYS:HG	26:N:307:ZN:ZN	0.78	0.96
14:L:47:LYS:HB3	14:L:48:PRO:HD3	1.47	0.96
6:D:36:ARG:HG3	6:D:38:TYR:HE2	1.30	0.96
14:L:60:LEU:HD21	14:L:66:VAL:HG22	1.48	0.96
11:I:106:ALA:O	11:I:108:VAL:HG23	1.66	0.95
21:S:17:GLU:HA	21:S:20:LEU:HG	1.49	0.95
7:E:80:ILE:HD11	7:E:91:LEU:HB2	1.47	0.95
1:A:972:C:H4'	12:J:57:LYS:HD3	1.47	0.95
21:S:20:LEU:HA	21:S:23:ASN:HD22	1.30	0.94
1:A:838:G:H2'	1:A:839:U:H5''	1.50	0.94
7:E:107:ARG:HH11	7:E:107:ARG:HB2	1.32	0.94
8:F:7:ASN:HB2	8:F:89:MET:HB3	1.48	0.94
5:C:129:ALA:HB3	5:C:132:ARG:HE	1.32	0.94
4:B:101:MET:HE3	4:B:108:ILE:HD13	1.46	0.94
12:J:90:LEU:H	12:J:91:PRO:HD2	1.32	0.93
1:A:939:G:H5''	9:G:102:ARG:HH22	1.32	0.93
21:S:55:LYS:HG2	21:S:56:GLN:HE21	1.34	0.93
4:B:48:MET:HA	4:B:51:LEU:HD12	1.50	0.92
1:A:582:U:H1'	19:Q:105:ALA:HA	1.50	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:114:TYR:H	11:I:114:TYR:HD1	1.12	0.92
5:C:179:ARG:CG	5:C:180:ALA:H	1.81	0.92
15:M:5:ALA:HB3	15:M:8:GLU:HG3	1.52	0.91
1:A:1095:U:H2'	1:A:1096:C:C6	2.04	0.91
4:B:18:GLY:HA2	4:B:41:ILE:HA	1.52	0.91
12:J:34:VAL:HG22	12:J:74:ILE:HG22	1.54	0.90
12:J:90:LEU:H	12:J:91:PRO:CD	1.84	0.90
14:L:126:LYS:H	14:L:126:LYS:HD2	1.33	0.90
1:A:760:G:H22	19:Q:105:ALA:N	1.68	0.90
17:O:87:ILE:HG22	17:O:88:ARG:HE	1.36	0.90
1:A:1356:G:H2'	1:A:1357:A:C8	2.06	0.90
15:M:81:LEU:HD23	15:M:81:LEU:H	1.37	0.89
1:A:1443:G:H5''	1:A:1446:A:H5'	1.53	0.89
10:H:90:GLY:O	10:H:91:ARG:HB2	1.72	0.89
4:B:92:TYR:CE1	4:B:151:GLY:HA3	2.07	0.89
6:D:36:ARG:HG3	6:D:38:TYR:CE2	2.07	0.89
5:C:179:ARG:HD3	5:C:206:GLU:HB3	1.55	0.89
4:B:178:ARG:HH11	4:B:178:ARG:HG3	1.37	0.89
1:A:1116:C:C2'	1:A:1117:G:H5''	2.03	0.88
17:O:26:GLU:HA	17:O:81:LEU:HD11	1.51	0.88
11:I:9:ARG:HG2	11:I:14:VAL:HG22	1.56	0.88
5:C:108:ASN:ND2	5:C:111:LEU:HG	1.87	0.88
7:E:78:HIS:HD2	10:H:107:LEU:HD12	1.39	0.88
5:C:123:GLN:HE22	5:C:140:ARG:HH22	1.14	0.88
16:N:24:CYS:HB3	16:N:28:GLY:H	1.38	0.88
11:I:43:ALA:HA	11:I:74:ILE:HD13	1.54	0.88
1:A:1034:G:H21	1:A:1035:A:H62	1.22	0.87
14:L:41:ARG:HG2	14:L:42:THR:H	1.40	0.87
1:A:200:G:N2	1:A:216:G:H2'	1.90	0.87
1:A:839:U:H5'	1:A:840:C:H5	1.36	0.87
1:A:953:G:H1'	15:M:125:ARG:HA	1.54	0.87
8:F:101:ALA:HA	20:R:28:GLU:HG3	1.56	0.87
1:A:1016:A:H2'	1:A:1017:G:O4'	1.75	0.87
9:G:22:LEU:O	9:G:25:ALA:HB3	1.74	0.86
1:A:409:G:OP2	1:A:431:A:H5'	1.76	0.86
6:D:36:ARG:N	6:D:37:PRO:HD3	1.89	0.86
7:E:51:VAL:HB	7:E:52:PRO:HD3	1.57	0.86
11:I:10:ARG:HG2	11:I:75:ASP:HB2	1.58	0.86
6:D:81:GLU:HA	6:D:84:LYS:HD2	1.57	0.85
1:A:1135:U:H4'	1:A:1136:U:H5	1.40	0.85
1:A:1124:G:H5'	12:J:35:SER:O	1.76	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1316:G:H5''	16:N:17:LYS:HD2	1.58	0.85
1:A:382:A:H2'	1:A:383:A:C8	2.12	0.85
14:L:47:LYS:HB3	14:L:48:PRO:CD	2.05	0.85
1:A:459:G:N1	1:A:461:C:H5''	1.90	0.85
23:V:6:ARG:HD3	23:V:15:ARG:NH1	1.91	0.85
1:A:382:A:H2'	1:A:383:A:H8	1.42	0.85
1:A:371:G:O2'	1:A:372:C:H5'	1.76	0.85
1:A:1435:G:H2'	1:A:1436:U:C6	2.13	0.84
17:O:16:ALA:HB1	17:O:21:ASP:HB3	1.59	0.84
21:S:30:LEU:O	21:S:31:ILE:HD13	1.76	0.84
1:A:406:G:H1	1:A:436:C:H42	1.23	0.84
1:A:630:G:C2'	1:A:631:G:H5'	2.06	0.84
1:A:1201:A:H4'	1:A:1202:G:O5'	1.78	0.84
18:P:21:VAL:HG12	18:P:33:ILE:HD12	1.60	0.84
1:A:328:C:H2'	1:A:328:C:O2	1.75	0.84
5:C:18:TRP:HE3	5:C:18:TRP:H	1.22	0.84
10:H:20:TYR:CE2	10:H:75:ARG:HD2	2.13	0.84
12:J:48:THR:HA	12:J:62:HIS:HD2	1.42	0.83
4:B:200:ILE:HG22	4:B:201:ILE:H	1.41	0.83
8:F:100:ASN:HB2	20:R:23:LYS:HE3	1.60	0.83
1:A:939:G:H5''	9:G:102:ARG:NH2	1.92	0.83
5:C:156:ARG:H	5:C:163:ALA:HA	1.43	0.83
1:A:664:G:H22	1:A:741:G:H1	1.27	0.83
1:A:975:A:O5'	1:A:976:G:H5'	1.78	0.83
1:A:203:U:H4'	1:A:204:U:O3'	1.78	0.82
1:A:235:C:H5'	19:Q:70:ARG:HG2	1.60	0.82
11:I:114:TYR:CD2	12:J:60:ARG:HB2	2.14	0.82
5:C:52:LEU:HD23	5:C:52:LEU:H	1.44	0.82
1:A:476:G:H2'	1:A:479:C:N4	1.94	0.82
14:L:77:LEU:HD21	14:L:107:ALA:HA	1.60	0.82
11:I:93:ARG:NH1	11:I:93:ARG:HB3	1.94	0.82
1:A:474:G:N3	1:A:474:G:H3'	1.95	0.82
1:A:1057:G:H5''	5:C:154:SER:CB	2.08	0.82
1:A:476:G:H2'	1:A:479:C:H42	1.45	0.81
9:G:16:LEU:H	9:G:16:LEU:HD22	1.45	0.81
18:P:28:ARG:HH11	18:P:28:ARG:HG2	1.45	0.81
9:G:70:LYS:HB3	9:G:96:GLN:HG2	1.61	0.81
22:T:57:ARG:NH1	22:T:102:GLY:HA3	1.94	0.81
18:P:81:ARG:NE	18:P:81:ARG:HA	1.95	0.81
22:T:67:ALA:HA	22:T:73:HIS:H	1.46	0.81
8:F:67:MET:HE2	8:F:72:VAL:HG22	1.62	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:38:ILE:HB	12:J:71:LEU:HB2	1.63	0.81
8:F:26:ILE:O	8:F:30:LEU:HB2	1.79	0.81
1:A:579:G:H5'	1:A:728:A:H1'	1.60	0.81
22:T:54:LYS:HG2	22:T:57:ARG:NH2	1.94	0.81
7:E:11:ILE:HG22	7:E:12:LEU:HD12	1.63	0.80
5:C:150:LYS:HE2	5:C:152:ILE:HD11	1.63	0.80
8:F:28:ARG:HA	8:F:28:ARG:CZ	2.11	0.80
12:J:25:GLU:HB3	12:J:29:ARG:HE	1.45	0.80
18:P:81:ARG:HE	18:P:81:ARG:HA	1.46	0.80
4:B:19:HIS:HB2	4:B:204:ASN:ND2	1.97	0.80
5:C:3:ASN:HD22	5:C:3:ASN:N	1.79	0.80
4:B:77:ALA:HB1	4:B:80:ILE:HD12	1.62	0.80
10:H:116:LYS:NZ	10:H:127:LEU:HB3	1.96	0.80
9:G:120:ILE:H	9:G:120:ILE:HD12	1.47	0.80
11:I:65:VAL:HG21	11:I:73:GLN:HB3	1.63	0.80
12:J:4:ILE:HD12	12:J:74:ILE:HG13	1.63	0.80
1:A:1148:U:H2'	1:A:1149:C:O4'	1.82	0.80
1:A:1349:A:H2'	1:A:1350:A:H8	1.47	0.79
5:C:93:LYS:HE2	5:C:93:LYS:HA	1.63	0.79
9:G:15:ASP:HB3	9:G:19:GLY:N	1.97	0.79
5:C:190:ARG:HD2	5:C:190:ARG:H	1.48	0.79
20:R:47:THR:HA	20:R:83:GLU:HB2	1.64	0.79
4:B:218:ALA:O	4:B:222:ILE:HG13	1.82	0.79
4:B:84:GLU:HB3	4:B:219:VAL:HG21	1.64	0.79
19:Q:98:LEU:HA	19:Q:102:GLY:HA2	1.64	0.79
1:A:1527:C:O2'	1:A:1528:U:H5'	1.81	0.79
4:B:91:PRO:HG3	4:B:154:LEU:HB2	1.64	0.79
1:A:1137:C:H4'	1:A:1138:G:C2	2.18	0.79
13:K:14:VAL:HG21	13:K:40:ILE:HD11	1.64	0.79
10:H:83:ILE:O	10:H:83:ILE:HG23	1.83	0.78
1:A:1054:C:N4	3:X:34:MNU:H1'	1.98	0.78
1:A:406:G:H21	6:D:119:GLN:HE22	1.30	0.78
4:B:15:VAL:HG11	4:B:209:ARG:HG2	1.63	0.78
5:C:134:ILE:HD11	5:C:153:VAL:HG23	1.65	0.78
19:Q:12:SER:HB3	19:Q:20:THR:HB	1.65	0.78
12:J:84:GLN:O	12:J:88:LEU:HD12	1.83	0.78
6:D:111:ALA:HB2	6:D:120:LEU:HD12	1.65	0.78
9:G:38:LEU:HA	9:G:41:ARG:HG3	1.65	0.78
1:A:1106:G:H5''	5:C:172:ARG:HG2	1.65	0.78
7:E:122:GLU:O	7:E:123:LEU:HD23	1.84	0.78
1:A:376:G:H2'	1:A:377:G:H8	1.48	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:92:TYR:HE1	4:B:151:GLY:HA3	1.47	0.78
6:D:8:VAL:HG11	6:D:21:LEU:HB3	1.66	0.78
1:A:1250:A:H5''	11:I:68:GLY:H	1.48	0.78
1:A:1101:A:H4'	1:A:1102:A:O5'	1.85	0.77
1:A:1250:A:H4'	11:I:68:GLY:H	1.47	0.77
10:H:97:VAL:HA	10:H:100:ILE:HD11	1.65	0.77
18:P:22:THR:HA	18:P:33:ILE:HG13	1.67	0.77
12:J:30:SER:OG	12:J:81:THR:HA	1.83	0.77
15:M:4:ILE:HG22	15:M:5:ALA:N	1.99	0.77
1:A:1229:A:H2'	1:A:1230:C:H6	1.48	0.77
4:B:115:LEU:HD21	4:B:153:ARG:HH22	1.49	0.77
1:A:1490:C:H5'	1:A:1490:C:H6	1.47	0.77
4:B:142:LEU:O	4:B:146:GLN:HG2	1.85	0.77
5:C:86:VAL:O	5:C:89:GLU:HB3	1.85	0.77
14:L:25:PRO:C	14:L:27:LEU:H	1.87	0.77
5:C:56:ASP:O	5:C:57:ILE:HG13	1.84	0.77
15:M:36:LYS:HD2	15:M:59:TYR:CZ	2.19	0.77
1:A:760:G:H22	19:Q:105:ALA:H	1.28	0.77
1:A:1154:G:H2'	1:A:1155:G:H8	1.50	0.77
8:F:60:PHE:O	8:F:61:LEU:HD23	1.84	0.77
11:I:8:GLY:HA2	11:I:79:LEU:HD13	1.67	0.77
1:A:760:G:H1	19:Q:105:ALA:HB2	1.48	0.77
1:A:1140:C:H2'	1:A:1141:C:H6	1.50	0.77
1:A:1262:C:H42	1:A:1273:G:H1	1.32	0.77
11:I:16:ARG:HD3	11:I:64:THR:HB	1.67	0.77
11:I:114:TYR:CE2	12:J:60:ARG:HB2	2.19	0.77
1:A:190(L):U:H5'	1:A:190(L):U:C6	2.18	0.77
14:L:124:LYS:HD2	14:L:125:PRO:HD2	1.67	0.77
1:A:838:G:C2'	1:A:839:U:H5''	2.13	0.77
16:N:9:LYS:HD3	16:N:10:ALA:N	1.99	0.77
1:A:1140:C:H2'	1:A:1141:C:C6	2.20	0.76
9:G:23:VAL:O	9:G:27:ILE:HG13	1.85	0.76
11:I:11:LYS:O	11:I:12:GLU:HB3	1.83	0.76
14:L:6:THR:OG1	14:L:9:GLN:HG3	1.84	0.76
14:L:126:LYS:N	14:L:126:LYS:HD2	1.99	0.76
14:L:55:VAL:HG12	14:L:56:ALA:N	1.99	0.76
21:S:17:GLU:HA	21:S:20:LEU:CG	2.13	0.76
1:A:706:A:O2'	13:K:29:ILE:HD11	1.85	0.76
5:C:64:VAL:HG23	5:C:99:VAL:HG11	1.67	0.76
15:M:34:LEU:HD13	15:M:41:PRO:HA	1.66	0.76
15:M:62:ASN:O	15:M:63:THR:HB	1.85	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:Q:27:PHE:CZ	19:Q:36:ILE:HD11	2.20	0.76
1:A:1391:U:H2'	1:A:1392:G:C8	2.21	0.76
7:E:76:ILE:HG22	7:E:78:HIS:H	1.50	0.76
1:A:1313:U:OP2	21:S:6:LYS:HA	1.85	0.76
4:B:132:LYS:HB3	4:B:136:VAL:HG23	1.67	0.76
5:C:26:LYS:N	5:C:26:LYS:HD3	1.98	0.76
1:A:1141:C:O2'	1:A:1142:G:H5'	1.86	0.76
1:A:1502:A:H2	1:A:1505:G:H1	1.32	0.76
1:A:781:A:H2'	1:A:782:A:H5'	1.68	0.76
1:A:1366:C:H2'	1:A:1367:C:H6	1.50	0.76
1:A:243:A:C4'	1:A:244:U:H5'	2.14	0.76
14:L:47:LYS:CB	14:L:48:PRO:HD3	2.15	0.76
1:A:954:G:H4'	15:M:120:LYS:HB2	1.67	0.76
15:M:78:ILE:HA	15:M:81:LEU:HD21	1.65	0.76
1:A:409:G:OP1	1:A:429:U:H1'	1.86	0.76
5:C:191:THR:HG21	5:C:193:TYR:CZ	2.20	0.76
6:D:38:TYR:CD1	6:D:45:GLN:HG3	2.21	0.75
16:N:14:PRO:O	16:N:15:LYS:HB2	1.84	0.75
1:A:1161:C:H2'	1:A:1162:C:C6	2.20	0.75
4:B:20:GLU:O	4:B:39:ILE:HG23	1.85	0.75
5:C:141:VAL:HG11	5:C:202:ILE:HG12	1.67	0.75
7:E:80:ILE:CD1	7:E:91:LEU:HB2	2.17	0.75
9:G:54:THR:HG22	9:G:56:GLN:H	1.49	0.75
15:M:81:LEU:HD12	15:M:88:ARG:HG2	1.67	0.75
12:J:48:THR:HA	12:J:62:HIS:CD2	2.21	0.75
17:O:65:ARG:NH1	17:O:65:ARG:HB2	2.00	0.75
19:Q:97:SER:HB2	19:Q:102:GLY:O	1.87	0.75
5:C:116:VAL:HG21	5:C:202:ILE:HD11	1.69	0.75
7:E:7:GLU:HB3	7:E:112:LEU:HD11	1.68	0.75
13:K:91:ARG:C	13:K:93:GLN:H	1.87	0.75
1:A:459:G:H21	1:A:462:G:N2	1.84	0.75
5:C:196:LEU:N	5:C:196:LEU:HD23	2.01	0.75
23:V:6:ARG:HD3	23:V:15:ARG:HH12	1.50	0.75
1:A:201:C:H4'	1:A:216:G:H21	1.48	0.74
14:L:34:ARG:O	14:L:61:THR:HG23	1.87	0.74
17:O:77:ARG:O	17:O:80:ALA:HB3	1.87	0.74
1:A:1360:A:H2'	1:A:1361:G:C8	2.22	0.74
1:A:1196:U:H5''	1:A:1197:G:H5'	1.69	0.74
1:A:409:G:H5'	1:A:430:A:C5	2.23	0.74
7:E:43:LEU:HD11	7:E:132:ALA:HB1	1.68	0.74
1:A:203:U:O3'	1:A:204:U:H4'	1.87	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:406:G:H1	1:A:436:C:N4	1.85	0.74
1:A:877:C:O2	10:H:3:THR:HG21	1.88	0.74
6:D:38:TYR:HE1	6:D:45:GLN:HE21	1.31	0.74
1:A:1010:G:H2'	1:A:1011:G:H8	1.52	0.74
1:A:755:G:OP2	17:O:65:ARG:HD2	1.87	0.74
6:D:24:GLU:O	6:D:25:ARG:HB2	1.86	0.74
6:D:36:ARG:H	6:D:37:PRO:CD	1.96	0.74
1:A:1250:A:C5'	11:I:68:GLY:H	2.01	0.74
19:Q:45:HIS:NE2	19:Q:47:PRO:HG3	2.02	0.74
1:A:458:C:H42	1:A:463:A:H3'	1.52	0.74
4:B:101:MET:N	4:B:108:ILE:HD12	2.03	0.74
14:L:43:VAL:HG12	14:L:44:THR:N	2.02	0.74
14:L:46:LYS:HE2	14:L:47:LYS:HB2	1.68	0.74
4:B:124:SER:HB2	4:B:125:PRO:HD2	1.67	0.74
11:I:44:VAL:HG12	11:I:51:ARG:HH12	1.52	0.74
14:L:75:HIS:HD2	14:L:77:LEU:H	1.33	0.74
5:C:110:ASN:HD22	5:C:140:ARG:HB3	1.53	0.74
14:L:53:ARG:HG2	14:L:69:TYR:HE1	1.53	0.74
1:A:1490:C:O2'	1:A:1491:G:H5'	1.88	0.74
4:B:57:PHE:CE2	4:B:61:LEU:HD11	2.22	0.74
8:F:48:LEU:HD13	8:F:52:ILE:HD12	1.69	0.74
14:L:27:LEU:O	14:L:29:GLY:N	2.20	0.74
17:O:36:ILE:HA	17:O:59:MET:HE1	1.70	0.74
10:H:121:ASP:HB2	10:H:125:ARG:HH21	1.52	0.73
15:M:49:THR:HG22	15:M:51:ALA:H	1.52	0.73
1:A:250:A:H4'	1:A:251:G:O5'	1.88	0.73
4:B:82:ARG:HA	4:B:92:TYR:CE2	2.23	0.73
18:P:34:GLU:OE2	18:P:55:ARG:HD3	1.88	0.73
20:R:19:LYS:H	20:R:19:LYS:HD2	1.54	0.73
1:A:1125:U:H3	12:J:5:ARG:HH21	1.34	0.73
1:A:1118:C:H1'	1:A:1179:A:C4	2.24	0.73
6:D:38:TYR:HD1	6:D:45:GLN:HG3	1.53	0.73
1:A:267:C:H2'	1:A:268:C:H6	1.53	0.73
6:D:26:CYS:HA	6:D:31:CYS:HB2	1.71	0.73
1:A:953:G:H1'	15:M:125:ARG:CA	2.19	0.73
5:C:10:PHE:CZ	5:C:178:LEU:HD13	2.23	0.73
1:A:1443:G:H5''	1:A:1446:A:C5'	2.19	0.73
1:A:149:A:H2'	1:A:150:C:C6	2.23	0.73
1:A:701:C:H5'	1:A:703:G:O4'	1.88	0.73
1:A:730:G:N2	1:A:765:G:H5''	2.04	0.73
14:L:110:VAL:O	14:L:122:THR:HG22	1.87	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:S:15:LEU:HD12	21:S:16:LEU:N	2.03	0.73
1:A:190:C:H4'	1:A:190(A):C:OP1	1.88	0.73
4:B:27:LYS:HE2	4:B:195:ASP:HB2	1.70	0.73
4:B:66:GLY:HA2	4:B:160:ASP:OD2	1.89	0.73
4:B:182:ILE:HD12	4:B:182:ILE:H	1.54	0.72
5:C:134:ILE:HD11	5:C:153:VAL:CG2	2.19	0.72
6:D:118:ARG:HH21	6:D:118:ARG:HG3	1.54	0.72
1:A:1064:G:H4'	1:A:1065:U:C5'	2.19	0.72
1:A:1135:U:H4'	1:A:1136:U:C5	2.22	0.72
1:A:954:G:H21	1:A:1227:A:H62	1.35	0.72
4:B:18:GLY:N	4:B:41:ILE:HG23	2.05	0.72
5:C:150:LYS:HG3	5:C:169:ALA:HB2	1.69	0.72
15:M:13:LYS:HG2	15:M:44:ARG:HH21	1.54	0.72
15:M:3:ARG:HA	15:M:9:ILE:HG13	1.70	0.72
1:A:1281:U:H5'	1:A:1282:C:C5	2.25	0.72
11:I:4:TYR:CE2	11:I:88:TYR:HA	2.24	0.72
14:L:86:ARG:HG3	14:L:86:ARG:HH11	1.54	0.72
20:R:53:ARG:NH1	20:R:60:GLY:N	2.37	0.72
1:A:1489:G:H2'	1:A:1490:C:C5'	2.14	0.72
10:H:116:LYS:HZ2	10:H:127:LEU:HB3	1.54	0.72
1:A:977:A:H2'	1:A:978:A:H5''	1.70	0.72
5:C:47:LEU:HD23	5:C:68:VAL:HG11	1.71	0.72
13:K:110:ASP:HB2	20:R:88:LYS:NZ	2.03	0.72
1:A:1437:C:H2'	1:A:1438:G:H8	1.55	0.72
6:D:3:ARG:HD2	6:D:118:ARG:CZ	2.18	0.72
15:M:23:TYR:HB2	15:M:67:GLU:OE2	1.90	0.72
21:S:14:HIS:O	21:S:18:LYS:HB2	1.89	0.72
12:J:54:PHE:O	12:J:55:LYS:HG2	1.90	0.72
14:L:75:HIS:CD2	14:L:77:LEU:H	2.07	0.72
1:A:335:C:H2'	1:A:336:C:H6	1.55	0.71
4:B:73:THR:HG21	4:B:96:ARG:HH11	1.54	0.71
15:M:69:GLU:O	15:M:72:ALA:HB3	1.90	0.71
9:G:49:ILE:N	9:G:49:ILE:HD12	2.05	0.71
5:C:129:ALA:HB3	5:C:132:ARG:NE	2.02	0.71
1:A:760:G:N2	19:Q:104:LYS:H	1.87	0.71
7:E:81:GLU:HG2	7:E:90:VAL:HG22	1.72	0.71
1:A:129(A):G:O2'	1:A:190(E):U:H2'	1.90	0.71
1:A:1142:G:H2'	1:A:1143:G:O4'	1.89	0.71
1:A:1226:C:H4'	1:A:1227:A:OP1	1.89	0.71
1:A:193:C:H2'	1:A:194:C:C6	2.25	0.71
1:A:460:A:H62	1:A:463:A:N6	1.88	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:51:LEU:HD22	4:B:55:PHE:HE1	1.53	0.71
1:A:1145:C:HO2'	1:A:1146:A:H8	1.38	0.71
1:A:269:C:H2'	1:A:270:A:C8	2.25	0.71
1:A:408:A:OP1	1:A:408:A:H3'	1.90	0.71
10:H:60:ARG:HG3	10:H:60:ARG:HH11	1.55	0.71
1:A:101:A:O2'	1:A:102:G:H5'	1.90	0.71
5:C:20:SER:HB3	5:C:22:TRP:NE1	2.05	0.71
7:E:105:VAL:HB	7:E:106:PRO:HD3	1.71	0.71
18:P:55:ARG:O	18:P:58:TYR:HB3	1.91	0.71
9:G:113:GLU:HG2	9:G:119:ARG:HG2	1.73	0.71
15:M:81:LEU:CD2	15:M:81:LEU:H	2.04	0.71
1:A:333:G:H4'	22:T:16:HIS:CD2	2.26	0.70
4:B:47:THR:O	4:B:51:LEU:HG	1.90	0.70
10:H:51:VAL:HG12	10:H:52:ASP:H	1.56	0.70
1:A:1057:G:O2'	1:A:1058:G:H5'	1.91	0.70
1:A:1106:G:OP1	5:C:172:ARG:HD3	1.91	0.70
1:A:1152:A:H5'	12:J:70:ARG:NH2	2.07	0.70
1:A:1401:G:N2	1:A:1402:C:H1'	2.05	0.70
1:A:424:G:H3'	1:A:424:G:N3	2.06	0.70
5:C:3:ASN:HD22	5:C:3:ASN:H	1.39	0.70
1:A:1298:C:C4	9:G:114:ARG:HD2	2.26	0.70
13:K:33:THR:HG22	13:K:39:PRO:HA	1.72	0.70
5:C:15:THR:O	5:C:16:ARG:HB2	1.91	0.70
1:A:1435:G:H2'	1:A:1436:U:H6	1.55	0.70
16:N:59:ALA:O	16:N:60:SER:HB3	1.90	0.70
1:A:1005:A:H1'	1:A:1026:G:N2	2.06	0.70
1:A:1114:C:H2'	1:A:1115:C:H6	1.55	0.70
1:A:370:C:O2'	1:A:371:G:H5'	1.92	0.70
4:B:71:VAL:O	4:B:165:VAL:HG23	1.92	0.70
6:D:153:ARG:HH22	6:D:180:GLY:HA2	1.56	0.70
4:B:68:ILE:H	4:B:90:MET:HE1	1.57	0.70
6:D:61:LYS:HD2	6:D:207:TYR:OH	1.91	0.70
1:A:163:C:O2'	1:A:164:U:H5'	1.91	0.70
1:A:186:C:H2'	1:A:187:C:H6	1.57	0.70
8:F:31:GLU:HA	8:F:35:ALA:HB2	1.73	0.70
23:V:5:ASP:O	23:V:11:GLY:HA3	1.92	0.70
1:A:186:C:H2'	1:A:187:C:C6	2.27	0.69
1:A:666:G:H5'	1:A:726:C:H1'	1.73	0.69
6:D:191:ARG:HD2	6:D:191:ARG:O	1.92	0.69
21:S:6:LYS:HD3	21:S:6:LYS:H	1.55	0.69
1:A:1352:C:H2'	1:A:1353:G:C8	2.27	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1397:C:H4'	1:A:1398:A:OP2	1.92	0.69
1:A:1510:U:H2'	1:A:1511:G:C8	2.27	0.69
5:C:190:ARG:HH11	5:C:190:ARG:HG2	1.57	0.69
11:I:44:VAL:HG12	11:I:51:ARG:NH1	2.06	0.69
8:F:100:ASN:HD22	20:R:23:LYS:HG2	1.57	0.69
1:A:190(L):U:H6	1:A:190(L):U:C5'	2.05	0.69
1:A:975:A:H8	1:A:975:A:H5'	1.55	0.69
5:C:180:ALA:HB1	5:C:203:PHE:CE1	2.27	0.69
17:O:87:ILE:HG22	17:O:88:ARG:NE	2.08	0.69
22:T:11:SER:HA	22:T:13:LEU:CD1	2.22	0.69
1:A:1368:G:O2'	1:A:1369:C:H5'	1.92	0.69
1:A:243:A:H4'	1:A:244:U:C5'	2.18	0.69
1:A:946:A:H2'	1:A:947:G:C8	2.27	0.69
8:F:44:GLY:HA2	8:F:59:TYR:CZ	2.28	0.69
9:G:147:ALA:C	9:G:148:ASN:HD22	1.95	0.69
9:G:22:LEU:HD21	9:G:66:VAL:HG21	1.75	0.69
7:E:78:HIS:CD2	10:H:107:LEU:HD12	2.25	0.69
1:A:1152:A:H2'	1:A:1153:C:C6	2.27	0.69
20:R:86:VAL:HG12	20:R:87:ARG:H	1.57	0.69
22:T:75:ASN:OD1	22:T:75:ASN:N	2.25	0.69
1:A:269:C:H2'	1:A:270:A:H8	1.56	0.69
4:B:146:GLN:O	4:B:150:SER:HB3	1.93	0.69
8:F:30:LEU:HD22	8:F:35:ALA:CB	2.22	0.69
14:L:55:VAL:HG11	14:L:67:THR:HG23	1.73	0.69
16:N:22:THR:OG1	16:N:33:VAL:HG21	1.92	0.69
19:Q:45:HIS:O	19:Q:47:PRO:HD3	1.92	0.69
1:A:1053:G:C3'	1:A:1054:C:H5'	2.23	0.69
4:B:219:VAL:C	4:B:221:LEU:H	1.94	0.69
1:A:409:G:N2	1:A:433:C:OP1	2.26	0.69
4:B:178:ARG:HH21	4:B:196:LEU:C	1.95	0.69
9:G:148:ASN:N	9:G:148:ASN:HD22	1.90	0.69
10:H:38:ILE:N	10:H:38:ILE:HD12	2.06	0.69
5:C:180:ALA:HB1	5:C:203:PHE:HE1	1.57	0.69
5:C:64:VAL:HG12	5:C:66:VAL:HG23	1.75	0.69
8:F:9:VAL:HB	8:F:87:ARG:HB2	1.74	0.69
10:H:38:ILE:H	10:H:38:ILE:HD12	1.58	0.69
11:I:114:TYR:HD1	11:I:114:TYR:N	1.89	0.69
15:M:26:GLY:O	15:M:28:ALA:N	2.26	0.69
1:A:1281:U:H5'	1:A:1282:C:H5	1.58	0.69
1:A:1127:G:H21	1:A:1146:A:H62	1.39	0.69
1:A:114:U:O2'	1:A:115:G:H5'	1.93	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:26:LYS:CD	5:C:26:LYS:H	1.89	0.69
5:C:52:LEU:HD23	5:C:52:LEU:N	2.07	0.69
17:O:76:GLU:HA	17:O:79:ARG:HH21	1.57	0.69
1:A:338:A:H2'	1:A:339:C:C6	2.28	0.68
18:P:75:ARG:HH11	18:P:75:ARG:HG3	1.57	0.68
4:B:130:ARG:HD3	4:B:131:PRO:HD2	1.75	0.68
11:I:48:GLU:N	11:I:49:PRO:HD2	2.08	0.68
12:J:6:ILE:HA	12:J:97:GLU:O	1.93	0.68
1:A:975:A:C8	1:A:975:A:H5'	2.28	0.68
5:C:38:ARG:HH11	5:C:38:ARG:HG3	1.58	0.68
18:P:20:VAL:HG21	18:P:32:TYR:CG	2.28	0.68
5:C:150:LYS:HB3	5:C:201:TYR:HB2	1.75	0.68
7:E:15:ARG:O	7:E:16:THR:HB	1.93	0.68
8:F:10:LEU:CD1	8:F:59:TYR:HB3	2.23	0.68
15:M:34:LEU:HD22	15:M:39:ILE:HB	1.74	0.68
1:A:1161:C:H2'	1:A:1162:C:H6	1.59	0.68
4:B:87:ARG:HH11	4:B:234:PRO:HD2	1.57	0.68
9:G:15:ASP:HB3	9:G:19:GLY:H	1.59	0.68
11:I:11:LYS:O	11:I:11:LYS:HG2	1.93	0.68
11:I:104:ARG:HD3	11:I:104:ARG:O	1.93	0.68
11:I:93:ARG:CB	11:I:93:ARG:HH11	2.07	0.68
12:J:89:ASP:HB2	12:J:91:PRO:HD2	1.74	0.68
13:K:110:ASP:HB2	20:R:88:LYS:HZ2	1.57	0.68
17:O:87:ILE:HG22	17:O:88:ARG:H	1.57	0.68
18:P:74:LEU:O	18:P:79:VAL:HG23	1.92	0.68
19:Q:20:THR:HG21	19:Q:41:LYS:HD2	1.75	0.68
4:B:159:PRO:HB2	4:B:161:ALA:O	1.93	0.68
5:C:193:TYR:CD1	5:C:194:GLY:N	2.61	0.68
4:B:124:SER:O	4:B:127:ILE:HG12	1.94	0.68
6:D:153:ARG:NH1	6:D:181:MET:HB2	2.09	0.68
1:A:1367:C:H4'	12:J:48:THR:HG21	1.76	0.68
1:A:1065:U:H4'	1:A:1066:C:O5'	1.93	0.68
4:B:30:ARG:HG3	4:B:31:TYR:CD2	2.29	0.68
5:C:58:GLU:O	5:C:59:ARG:HG3	1.94	0.68
10:H:119:LEU:HD23	10:H:119:LEU:N	2.09	0.68
12:J:35:SER:HB2	12:J:72:VAL:O	1.93	0.68
19:Q:67:LYS:HA	19:Q:70:ARG:HH12	1.59	0.68
1:A:1015:A:H2'	1:A:1016:A:C8	2.29	0.67
1:A:1401:G:C2	1:A:1402:C:H1'	2.30	0.67
4:B:12:GLU:C	4:B:14:GLY:H	1.97	0.67
5:C:14:ILE:HG22	5:C:15:THR:N	2.04	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1152:A:H5''	12:J:13:HIS:CD2	2.29	0.67
12:J:71:LEU:O	12:J:72:VAL:HB	1.94	0.67
13:K:67:ASP:OD2	13:K:71:LYS:HE3	1.95	0.67
19:Q:18:THR:HG23	19:Q:69:LYS:HE3	1.75	0.67
1:A:1343:G:H2'	1:A:1344:C:C6	2.29	0.67
11:I:6:GLY:N	11:I:84:ALA:HB2	2.08	0.67
6:D:3:ARG:NE	6:D:3:ARG:HA	2.10	0.67
10:H:46:LYS:HG3	10:H:64:LYS:HG2	1.75	0.67
20:R:46:GLU:CD	20:R:46:GLU:H	1.97	0.67
21:S:20:LEU:HA	21:S:23:ASN:ND2	2.08	0.67
1:A:919:A:O2'	1:A:920:U:H5'	1.95	0.67
11:I:42:ARG:HG2	11:I:42:ARG:HH11	1.59	0.67
1:A:1249:C:H2'	1:A:1250:A:H5'	1.77	0.67
1:A:1347:G:O2'	1:A:1348:U:P	2.52	0.67
7:E:80:ILE:H	7:E:80:ILE:HD12	1.59	0.67
17:O:39:LEU:HD22	17:O:56:LEU:HB2	1.77	0.67
20:R:52:PRO:HD2	20:R:55:ARG:HG3	1.76	0.67
8:F:10:LEU:HD12	8:F:59:TYR:HB3	1.77	0.67
15:M:8:GLU:OE1	15:M:22:ILE:HA	1.94	0.67
1:A:1229:A:H2'	1:A:1230:C:C6	2.29	0.67
4:B:71:VAL:HG23	4:B:164:VAL:HA	1.76	0.67
9:G:145:ALA:C	9:G:147:ALA:H	1.97	0.67
1:A:1250:A:C4'	11:I:68:GLY:H	2.08	0.67
1:A:291:C:O2'	1:A:292:G:H5'	1.95	0.67
4:B:14:GLY:O	4:B:15:VAL:HG13	1.95	0.67
14:L:27:LEU:C	14:L:29:GLY:H	1.97	0.67
15:M:13:LYS:HA	15:M:44:ARG:HE	1.59	0.67
8:F:101:ALA:CA	20:R:28:GLU:HG3	2.24	0.67
1:A:969:A:H61	15:M:126:LYS:HE3	1.60	0.66
22:T:11:SER:HA	22:T:13:LEU:HD11	1.76	0.66
5:C:117:ALA:HB2	5:C:200:ALA:HB2	1.77	0.66
6:D:33:MET:O	6:D:37:PRO:HG3	1.95	0.66
11:I:127:LYS:O	11:I:128:ARG:HB2	1.95	0.66
1:A:1329:A:O2'	1:A:1330:U:H5'	1.94	0.66
4:B:19:HIS:ND1	4:B:204:ASN:HB3	2.10	0.66
1:A:1145:C:O2'	1:A:1146:A:H8	1.78	0.66
4:B:63:MET:HG3	4:B:63:MET:O	1.95	0.66
5:C:136:GLN:O	5:C:139:GLN:HB2	1.96	0.66
1:A:1189:C:OP1	12:J:51:ARG:NH2	2.28	0.66
1:A:452:A:O2'	1:A:453:A:H8	1.79	0.66
1:A:736:C:OP1	20:R:68:LYS:HD2	1.95	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:G:26:PHE:CE2	9:G:30:ILE:HD11	2.30	0.66
21:S:42:PRO:O	21:S:45:VAL:HG23	1.95	0.66
1:A:760:G:N2	19:Q:104:LYS:N	2.43	0.66
1:A:860:A:H2'	1:A:861:G:O4'	1.94	0.66
4:B:101:MET:HE2	4:B:108:ILE:HG21	1.77	0.66
1:A:1152:A:H5'	12:J:70:ARG:HH22	1.60	0.66
1:A:190(I):G:O2'	1:A:190(J):U:H5'	1.96	0.66
1:A:26:A:N6	1:A:558:G:H1'	2.11	0.66
1:A:328:C:C2'	1:A:328:C:O2	2.44	0.66
1:A:731:G:OP1	1:A:766:A:H1'	1.95	0.66
14:L:33:ARG:HD2	14:L:61:THR:OG1	1.96	0.66
15:M:3:ARG:HA	15:M:8:GLU:O	1.96	0.66
1:A:722:A:H4'	1:A:723:U:C4	2.31	0.66
4:B:207:ALA:H	4:B:211:ILE:HD11	1.59	0.66
5:C:10:PHE:O	5:C:178:LEU:HD11	1.95	0.66
15:M:36:LYS:HD2	15:M:59:TYR:OH	1.96	0.66
20:R:55:ARG:HB3	20:R:55:ARG:NH1	2.11	0.66
1:A:1038:C:H2'	1:A:1039:C:C6	2.31	0.66
13:K:91:ARG:C	13:K:93:GLN:N	2.50	0.66
1:A:1236:A:H2'	1:A:1237:C:C6	2.31	0.66
18:P:54:GLU:OE2	18:P:55:ARG:HG2	1.95	0.66
1:A:1228:C:OP1	15:M:115:LYS:HE3	1.96	0.65
15:M:56:LEU:C	15:M:56:LEU:HD23	2.17	0.65
18:P:28:ARG:HG2	18:P:29:ASP:OD2	1.96	0.65
21:S:39:THR:HG22	21:S:40:ILE:N	2.11	0.65
22:T:97:ALA:O	22:T:99:LEU:N	2.29	0.65
1:A:190(H):G:O2'	1:A:190(I):G:H5'	1.97	0.65
1:A:939:G:H2'	1:A:940:C:H6	1.61	0.65
4:B:132:LYS:HA	4:B:135:GLN:CB	2.21	0.65
1:A:1412:C:H2'	1:A:1413:A:C8	2.32	0.65
1:A:235:C:H1'	19:Q:61:GLU:OE1	1.96	0.65
4:B:17:PHE:HD1	4:B:18:GLY:N	1.95	0.65
1:A:1191:A:OP1	5:C:4:LYS:HE3	1.96	0.65
6:D:3:ARG:HD2	6:D:118:ARG:NH2	2.12	0.65
14:L:27:LEU:C	14:L:29:GLY:N	2.50	0.65
4:B:115:LEU:HD23	4:B:116:GLU:N	2.10	0.65
7:E:7:GLU:O	7:E:34:VAL:HA	1.97	0.65
9:G:141:VAL:O	9:G:144:MET:HB2	1.96	0.65
1:A:897:C:H5''	19:Q:101:ARG:HH22	1.60	0.65
20:R:43:PHE:HA	20:R:51:LEU:HD12	1.79	0.65
1:A:1000:U:H2'	1:A:1001:A:H8	1.61	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:130:A:OP2	1:A:190(E):U:H2'	1.97	0.65
1:A:501:C:H2'	1:A:502:G:H8	1.61	0.65
20:R:19:LYS:HD2	20:R:19:LYS:N	2.11	0.65
1:A:1250:A:H4'	11:I:68:GLY:N	2.11	0.65
13:K:33:THR:HG22	13:K:39:PRO:CA	2.27	0.65
23:V:6:ARG:O	23:V:12:LYS:HE3	1.97	0.65
1:A:1262:C:H2'	1:A:1263:C:H6	1.61	0.65
1:A:669:U:H2'	1:A:670:G:H8	1.61	0.65
4:B:143:GLU:O	4:B:147:LYS:HG3	1.97	0.65
8:F:100:ASN:O	20:R:28:GLU:HA	1.97	0.65
9:G:49:ILE:H	9:G:49:ILE:HD12	1.60	0.65
12:J:49:VAL:HG13	16:N:41:ARG:HB2	1.79	0.65
1:A:1032:G:H2'	1:A:1033:G:O4'	1.96	0.65
1:A:1190:G:OP1	5:C:4:LYS:HA	1.97	0.65
6:D:29:PRO:HA	6:D:34:GLU:OE1	1.96	0.65
7:E:137:GLU:O	7:E:141:GLN:HG3	1.96	0.65
17:O:21:ASP:OD2	17:O:24:SER:HB3	1.96	0.65
1:A:1226:C:H5''	15:M:103:THR:OG1	1.96	0.65
1:A:163:C:C2'	1:A:164:U:H5'	2.26	0.65
1:A:404:U:O2'	1:A:405:U:H5'	1.96	0.65
4:B:212:GLN:NE2	4:B:216:SER:HB3	2.11	0.65
9:G:85:TYR:O	9:G:87:VAL:HG23	1.96	0.65
4:B:222:ILE:HG22	4:B:226:ARG:NH2	2.11	0.65
5:C:14:ILE:O	5:C:16:ARG:N	2.31	0.65
8:F:19:LEU:HD21	8:F:23:LYS:HD2	1.79	0.65
8:F:69:GLU:O	8:F:72:VAL:HG23	1.97	0.65
17:O:39:LEU:HD23	17:O:39:LEU:C	2.16	0.65
1:A:1339:A:H2'	1:A:1340:A:O4'	1.98	0.64
1:A:791:G:H2'	1:A:792:A:H5'	1.78	0.64
1:A:9:G:H5'	7:E:122:GLU:OE2	1.97	0.64
5:C:186:PHE:CG	5:C:187:ALA:N	2.65	0.64
10:H:112:LEU:HD23	10:H:119:LEU:O	1.97	0.64
12:J:34:VAL:HG12	12:J:35:SER:N	2.12	0.64
15:M:8:GLU:C	15:M:9:ILE:HD12	2.17	0.64
16:N:9:LYS:C	16:N:9:LYS:HD3	2.17	0.64
1:A:1149:C:H2'	1:A:1150:U:H6	1.61	0.64
1:A:337:C:H2'	1:A:338:A:H8	1.61	0.64
12:J:90:LEU:N	12:J:91:PRO:HD2	2.10	0.64
17:O:74:ASP:OD1	17:O:76:GLU:HB3	1.97	0.64
21:S:42:PRO:O	21:S:44:MET:N	2.29	0.64
1:A:99:C:H2'	1:A:101:A:C8	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1475:G:H2'	1:A:1476:G:H8	1.61	0.64
7:E:33:VAL:HG11	7:E:109:ILE:HA	1.79	0.64
12:J:25:GLU:C	12:J:27:ALA:H	2.00	0.64
1:A:149:A:H2'	1:A:150:C:H6	1.61	0.64
5:C:64:VAL:CG2	5:C:99:VAL:HG11	2.27	0.64
11:I:9:ARG:HA	11:I:13:ALA:O	1.96	0.64
12:J:76:ASN:HD22	12:J:78:ASN:HD21	1.45	0.64
17:O:65:ARG:HH11	17:O:65:ARG:HB2	1.59	0.64
1:A:1056:U:H5'	5:C:163:ALA:HB2	1.78	0.64
1:A:1441:G:H4'	1:A:1442:G:C2	2.33	0.64
1:A:76:C:O2'	1:A:77:G:H5'	1.96	0.64
5:C:19:GLU:HB3	5:C:40:ARG:HH21	1.63	0.64
6:D:8:VAL:O	6:D:10:ARG:N	2.31	0.64
1:A:1343:G:H2'	1:A:1344:C:H6	1.61	0.64
1:A:1369:C:H2'	1:A:1370:G:C8	2.33	0.64
4:B:132:LYS:HG2	4:B:135:GLN:OE1	1.98	0.64
4:B:116:GLU:HG2	4:B:153:ARG:HH12	1.63	0.64
5:C:20:SER:HB3	5:C:22:TRP:HE1	1.61	0.64
8:F:44:GLY:HA2	8:F:59:TYR:CE1	2.32	0.64
13:K:33:THR:HA	13:K:39:PRO:HA	1.78	0.64
18:P:28:ARG:NH1	18:P:28:ARG:HG2	2.11	0.64
1:A:254:G:OP1	19:Q:67:LYS:O	2.16	0.64
1:A:371:G:C2'	1:A:372:C:H5'	2.28	0.64
5:C:52:LEU:CD2	5:C:52:LEU:H	2.10	0.64
7:E:34:VAL:HG12	7:E:62:ALA:HB1	1.79	0.64
9:G:22:LEU:HD11	9:G:101:LEU:HD21	1.80	0.64
20:R:25:THR:O	20:R:26:LEU:HB2	1.98	0.64
20:R:39:VAL:O	20:R:42:ARG:HB2	1.98	0.64
21:S:16:LEU:O	21:S:19:VAL:HG12	1.97	0.64
7:E:107:ARG:CB	7:E:107:ARG:HH11	2.09	0.64
7:E:150:ARG:HH11	7:E:150:ARG:HG3	1.63	0.64
14:L:86:ARG:HG3	14:L:86:ARG:NH1	2.13	0.64
1:A:1330:U:H2'	1:A:1331:G:H5'	1.80	0.64
1:A:792:A:H4'	1:A:793:U:H5''	1.78	0.64
11:I:81:ILE:O	11:I:85:LEU:HB2	1.98	0.64
1:A:972:C:C4'	12:J:57:LYS:HD3	2.25	0.64
12:J:75:ILE:HG22	12:J:76:ASN:H	1.63	0.64
13:K:84:VAL:HG23	13:K:109:VAL:O	1.97	0.64
14:L:110:VAL:HG12	14:L:111:LYS:N	2.12	0.64
1:A:22:G:H2'	1:A:23:C:C6	2.33	0.64
1:A:337:C:H2'	1:A:338:A:C8	2.33	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:463:A:H2	18:P:82:GLN:HG3	1.63	0.64
1:A:794:A:H2'	1:A:795:C:C6	2.32	0.64
4:B:182:ILE:HD12	4:B:182:ILE:N	2.13	0.64
4:B:187:LEU:HD13	4:B:214:ILE:HG21	1.80	0.64
9:G:31:MET:SD	9:G:34:GLY:HA2	2.38	0.64
12:J:6:ILE:HG13	12:J:71:LEU:O	1.97	0.64
15:M:81:LEU:HD23	15:M:81:LEU:N	2.10	0.64
15:M:88:ARG:HG3	15:M:98:VAL:HG11	1.79	0.64
1:A:1196:U:H5''	1:A:1197:G:C5'	2.28	0.63
1:A:1208:C:H2'	1:A:1209:C:H6	1.61	0.63
1:A:287:U:O2'	1:A:288:A:H5'	1.97	0.63
1:A:761:G:H5'	19:Q:103:GLY:N	2.13	0.63
11:I:118:LYS:O	11:I:119:ALA:HB3	1.98	0.63
20:R:36:ASN:O	20:R:39:VAL:HG12	1.97	0.63
22:T:79:ARG:HD2	22:T:83:ARG:HH12	1.62	0.63
4:B:239:VAL:HG12	4:B:240:GLN:NE2	2.12	0.63
6:D:25:ARG:HE	6:D:30:LYS:HB2	1.62	0.63
7:E:80:ILE:N	7:E:80:ILE:HD12	2.13	0.63
9:G:41:ARG:O	9:G:45:ASP:HB2	1.97	0.63
11:I:22:GLY:HA3	11:I:60:ASP:HB2	1.79	0.63
19:Q:82:MET:HA	19:Q:85:VAL:HG23	1.77	0.63
21:S:22:LEU:HD22	21:S:28:LYS:HB2	1.79	0.63
1:A:1236:A:H4'	1:A:1304:G:H4'	1.80	0.63
4:B:92:TYR:CD1	4:B:151:GLY:HA3	2.33	0.63
20:R:47:THR:HG22	20:R:48:GLY:H	1.63	0.63
21:S:22:LEU:HD23	21:S:25:LYS:NZ	2.13	0.63
21:S:52:TYR:HA	21:S:56:GLN:O	1.98	0.63
1:A:338:A:H2	1:A:351:G:H22	1.46	0.63
1:A:959:A:H3'	1:A:960:U:H5''	1.80	0.63
4:B:60:ASP:O	4:B:64:ARG:HB2	1.97	0.63
5:C:64:VAL:HB	5:C:99:VAL:HG21	1.80	0.63
12:J:25:GLU:HA	12:J:28:ARG:HB3	1.81	0.63
19:Q:95:TYR:O	19:Q:97:SER:N	2.31	0.63
21:S:39:THR:HG22	21:S:40:ILE:H	1.64	0.63
1:A:530:G:O6	2:W:3:G:H1'	1.98	0.63
1:A:627:G:O2'	1:A:628:G:H5'	1.98	0.63
4:B:101:MET:CE	4:B:108:ILE:HD13	2.26	0.63
5:C:133:ALA:O	5:C:136:GLN:HB3	1.98	0.63
6:D:76:ARG:HH11	6:D:76:ARG:HG2	1.64	0.63
7:E:129:ILE:H	7:E:129:ILE:HD12	1.64	0.63
14:L:55:VAL:CG1	14:L:67:THR:HG23	2.28	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:P:17:TYR:HE1	18:P:41:PRO:CG	2.11	0.63
1:A:1305:G:C5'	23:V:4:GLY:HA3	2.28	0.63
1:A:1497:G:O2'	1:A:1498:U:H5'	1.98	0.63
1:A:407:G:H3'	1:A:431:A:OP1	1.99	0.63
1:A:524:G:H2'	1:A:525:C:C6	2.34	0.63
11:I:107:ARG:HH11	11:I:107:ARG:HB3	1.63	0.63
12:J:17:ASP:O	12:J:21:GLN:HB2	1.98	0.63
14:L:110:VAL:CG2	14:L:120:TYR:HB3	2.28	0.63
1:A:1064:G:H4'	1:A:1065:U:H5'	1.79	0.63
1:A:353:A:H5'	1:A:353:A:H8	1.64	0.63
21:S:20:LEU:HD12	21:S:21:GLU:N	2.14	0.63
1:A:132:C:O2'	1:A:133:U:H5'	1.98	0.63
1:A:1475:G:H2'	1:A:1476:G:C8	2.33	0.63
7:E:35:GLY:N	7:E:112:LEU:HD12	2.14	0.63
8:F:80:ARG:HH11	8:F:80:ARG:HG2	1.63	0.63
19:Q:60:ILE:HD13	19:Q:61:GLU:H	1.64	0.63
4:B:87:ARG:HH21	4:B:219:VAL:HB	1.62	0.62
5:C:6:HIS:NE2	5:C:8:ILE:HB	2.14	0.62
8:F:6:VAL:O	8:F:62:TRP:HA	1.98	0.62
19:Q:69:LYS:O	19:Q:70:ARG:HD2	1.98	0.62
1:A:1319:A:OP1	21:S:5:LEU:HD11	1.99	0.62
21:S:7:LYS:O	21:S:7:LYS:HG2	1.99	0.62
1:A:1279:A:H5''	1:A:1280:A:OP1	2.00	0.62
1:A:459:G:N2	1:A:462:G:N2	2.46	0.62
1:A:575:G:OP1	1:A:575:G:H4'	1.97	0.62
5:C:124:ILE:HD11	5:C:153:VAL:HG21	1.81	0.62
15:M:115:LYS:HE3	15:M:115:LYS:H	1.63	0.62
15:M:40:ASN:HD22	15:M:41:PRO:CD	2.13	0.62
15:M:60:VAL:O	15:M:63:THR:HG22	1.98	0.62
18:P:17:TYR:HE1	18:P:41:PRO:HG2	1.64	0.62
20:R:44:LEU:HD21	20:R:70:ILE:HD13	1.81	0.62
1:A:333:G:H4'	22:T:16:HIS:NE2	2.13	0.62
1:A:1086:U:H3	1:A:1099:G:H22	1.46	0.62
1:A:267:C:H2'	1:A:268:C:C6	2.33	0.62
1:A:445:G:H2'	1:A:446:G:H8	1.63	0.62
1:A:501:C:H2'	1:A:502:G:C8	2.33	0.62
4:B:15:VAL:CG1	4:B:209:ARG:HG2	2.29	0.62
14:L:40:VAL:O	14:L:40:VAL:HG12	1.98	0.62
1:A:376:G:OP2	18:P:67:THR:HG21	2.00	0.62
20:R:45:SER:C	20:R:47:THR:H	2.02	0.62
1:A:1525:G:O2'	1:A:1526:G:H5'	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:216:G:H5'	1:A:217:C:O5'	1.99	0.62
1:A:760:G:N1	19:Q:105:ALA:HB2	2.14	0.62
5:C:108:ASN:HD22	5:C:111:LEU:HG	1.61	0.62
5:C:14:ILE:CG2	5:C:15:THR:H	2.01	0.62
5:C:59:ARG:HG2	5:C:63:ASN:O	1.99	0.62
1:A:190(L):U:O2'	1:A:191:G:H5'	1.98	0.62
7:E:41:VAL:HG13	7:E:113:ALA:HA	1.81	0.62
1:A:1125:U:H3	12:J:5:ARG:NH2	1.96	0.62
1:A:791:G:H2'	1:A:792:A:C5'	2.30	0.62
4:B:25:ASN:HD22	4:B:25:ASN:C	2.03	0.62
11:I:97:LYS:HB3	11:I:98:PRO:HD3	1.82	0.62
14:L:43:VAL:HG12	14:L:44:THR:H	1.65	0.62
1:A:1137:C:H4'	1:A:1138:G:N2	2.14	0.62
1:A:1262:C:H2'	1:A:1263:C:C6	2.34	0.62
1:A:737:A:H2'	1:A:738:C:C6	2.35	0.62
7:E:101:ILE:HD12	7:E:119:LEU:HD21	1.82	0.62
9:G:75:VAL:HG22	9:G:86:GLN:HB3	1.81	0.62
10:H:51:VAL:HG21	10:H:60:ARG:HG2	1.81	0.62
11:I:5:TYR:C	11:I:5:TYR:CD1	2.73	0.62
16:N:9:LYS:HG3	16:N:21:TYR:O	2.00	0.62
1:A:760:G:H1	19:Q:105:ALA:CB	2.12	0.62
1:A:1514:C:H2'	1:A:1515:C:H6	1.64	0.62
6:D:146:ILE:N	6:D:146:ILE:HD12	2.13	0.62
8:F:31:GLU:HA	8:F:35:ALA:CB	2.30	0.62
1:A:1205:U:C1'	5:C:195:VAL:HG21	2.30	0.62
1:A:1251:A:H2'	1:A:1252:A:C8	2.34	0.62
13:K:82:VAL:HG23	13:K:105:VAL:HG13	1.82	0.62
18:P:28:ARG:NH1	18:P:29:ASP:OD2	2.33	0.62
4:B:81:VAL:HG12	4:B:92:TYR:HD2	1.65	0.61
5:C:10:PHE:CE2	5:C:178:LEU:HD13	2.35	0.61
16:N:4:LYS:HA	16:N:7:ILE:CD1	2.30	0.61
19:Q:81:ARG:HE	19:Q:84:LEU:HD11	1.65	0.61
1:A:1355:G:O2'	1:A:1356:G:H5'	2.01	0.61
1:A:193:C:H2'	1:A:194:C:H6	1.65	0.61
1:A:475:G:H2'	1:A:476:G:H5''	1.81	0.61
1:A:677:U:H3	1:A:713:G:H22	1.45	0.61
4:B:178:ARG:NH1	4:B:178:ARG:HG3	2.10	0.61
4:B:35:GLU:HA	4:B:39:ILE:O	1.98	0.61
5:C:64:VAL:HB	5:C:99:VAL:CB	2.30	0.61
6:D:119:GLN:HG2	6:D:123:HIS:CD2	2.35	0.61
1:A:1149:C:H2'	1:A:1150:U:C6	2.35	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1195:C:H3'	1:A:1196:U:H5'	1.82	0.61
5:C:154:SER:O	5:C:165:THR:HA	2.01	0.61
8:F:100:ASN:HD22	20:R:23:LYS:CG	2.12	0.61
10:H:36:LEU:HA	10:H:39:LEU:HD23	1.83	0.61
11:I:12:GLU:HG3	11:I:12:GLU:O	2.00	0.61
14:L:55:VAL:CG1	14:L:56:ALA:N	2.63	0.61
1:A:1027:C:H1'	1:A:1036:G:H22	1.66	0.61
1:A:1337:G:H5''	1:A:1338:G:OP1	2.01	0.61
1:A:67:C:O2'	1:A:171:A:H1'	1.99	0.61
1:A:620:C:N1	6:D:135:LEU:HD13	2.15	0.61
9:G:145:ALA:O	9:G:147:ALA:N	2.34	0.61
9:G:75:VAL:O	9:G:75:VAL:HG13	2.00	0.61
14:L:38:THR:HG22	14:L:39:VAL:HG23	1.82	0.61
19:Q:14:LYS:HD2	19:Q:14:LYS:H	1.64	0.61
22:T:54:LYS:HE3	22:T:100:ILE:HD12	1.82	0.61
1:A:1351:U:O2'	1:A:1352:C:H5'	2.01	0.61
1:A:299:G:H2'	1:A:300:A:C8	2.36	0.61
7:E:53:LEU:O	7:E:57:LYS:HB2	2.00	0.61
14:L:82:VAL:O	14:L:106:ASP:HB2	2.00	0.61
1:A:952:U:H1'	15:M:126:LYS:O	2.00	0.61
17:O:53:HIS:HE1	17:O:57:LEU:HD22	1.66	0.61
20:R:37:VAL:HG12	20:R:41:LYS:HE2	1.81	0.61
1:A:1352:C:H2'	1:A:1353:G:H8	1.63	0.61
1:A:760:G:H21	19:Q:104:LYS:H	1.48	0.61
1:A:761:G:H5'	19:Q:102:GLY:HA3	1.81	0.61
4:B:71:VAL:CG2	4:B:164:VAL:HA	2.30	0.61
5:C:155:GLY:HA2	5:C:164:ARG:H	1.65	0.61
13:K:69:ALA:O	13:K:73:MET:HG2	2.00	0.61
20:R:39:VAL:HG13	20:R:40:LEU:N	2.16	0.61
1:A:156:G:O2'	1:A:157:G:H5'	2.00	0.61
5:C:196:LEU:H	5:C:196:LEU:CD2	2.01	0.61
11:I:120:ARG:O	11:I:122:ALA:N	2.34	0.61
11:I:17:VAL:HG21	11:I:80:GLY:HA3	1.82	0.61
1:A:761:G:H4'	19:Q:103:GLY:O	2.00	0.61
14:L:89:ARG:HA	14:L:97:ARG:HA	1.83	0.61
17:O:17:ARG:HH11	17:O:17:ARG:HG3	1.65	0.61
22:T:43:LEU:HD13	22:T:51:GLU:HG3	1.83	0.61
1:A:1034:G:N2	1:A:1035:A:H62	1.96	0.61
1:A:135:C:O2	18:P:1:MET:HB2	2.01	0.61
1:A:975:A:H4'	1:A:976:G:H5'	1.83	0.61
8:F:82:ARG:HE	8:F:82:ARG:HA	1.65	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:Q:19:VAL:HG23	19:Q:44:ALA:HB3	1.83	0.61
1:A:1386:G:O2'	1:A:1387:G:H5'	2.01	0.60
1:A:393:A:O2'	1:A:394:G:H5'	2.00	0.60
1:A:839:U:O2	1:A:839:U:H2'	2.01	0.60
4:B:18:GLY:H	4:B:41:ILE:HG23	1.63	0.60
6:D:12:CYS:SG	6:D:19:LEU:HB2	2.41	0.60
6:D:25:ARG:HE	6:D:30:LYS:CB	2.14	0.60
1:A:921:U:O2	7:E:19:MET:HB2	2.01	0.60
13:K:14:VAL:HG21	13:K:40:ILE:CD1	2.31	0.60
15:M:54:VAL:O	15:M:58:GLU:HG2	2.01	0.60
1:A:463:A:C2	18:P:82:GLN:HG3	2.36	0.60
19:Q:95:TYR:HA	19:Q:98:LEU:HD11	1.82	0.60
1:A:1366:C:H2'	1:A:1367:C:C6	2.33	0.60
5:C:149:ALA:O	5:C:150:LYS:HB2	2.01	0.60
6:D:205:GLU:HA	6:D:208:SER:HB2	1.83	0.60
16:N:4:LYS:HA	16:N:7:ILE:HD12	1.83	0.60
1:A:1260:C:O5'	1:A:1284:C:H4'	2.01	0.60
4:B:103:THR:HG23	4:B:176:GLU:OE1	2.01	0.60
4:B:178:ARG:NH2	4:B:196:LEU:O	2.34	0.60
7:E:6:PHE:HB3	7:E:34:VAL:HG22	1.82	0.60
16:N:3:ARG:NH1	16:N:6:LEU:HD11	2.15	0.60
1:A:1238:A:N7	1:A:1303:C:H1'	2.16	0.60
1:A:1347:G:O2'	1:A:1348:U:OP2	2.18	0.60
1:A:254:G:O2'	1:A:255:G:H5'	2.01	0.60
1:A:835:U:OP1	20:R:64:ARG:NH2	2.33	0.60
1:A:939:G:H2'	1:A:940:C:C6	2.36	0.60
4:B:12:GLU:O	4:B:14:GLY:N	2.34	0.60
11:I:43:ALA:CA	11:I:74:ILE:HD13	2.27	0.60
16:N:37:PHE:CE2	16:N:53:LEU:HD13	2.35	0.60
1:A:1182:G:O2'	1:A:1183:A:OP2	2.19	0.60
7:E:12:LEU:C	7:E:12:LEU:HD22	2.21	0.60
1:A:112:G:N2	1:A:354:G:H5'	2.17	0.60
1:A:1262:C:N4	1:A:1273:G:H1	1.99	0.60
1:A:538:G:OP2	14:L:115:LYS:HG3	2.01	0.60
10:H:14:ARG:O	10:H:18:ARG:HD3	2.02	0.60
18:P:45:THR:HB	18:P:46:PRO:HD2	1.83	0.60
19:Q:59:ILE:CG2	19:Q:71:PHE:HB3	2.32	0.60
21:S:63:THR:HG22	21:S:64:GLU:N	2.15	0.60
22:T:39:LYS:CD	22:T:55:ILE:HD13	2.32	0.60
1:A:865:A:H2'	1:A:866:C:C6	2.37	0.60
4:B:221:LEU:O	4:B:221:LEU:HD13	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:47:LEU:CD2	5:C:68:VAL:HG11	2.32	0.60
15:M:91:ARG:HB2	15:M:98:VAL:HG13	1.83	0.60
15:M:94:ARG:NH1	21:S:81:ARG:HH11	1.97	0.60
19:Q:78:GLU:HG3	19:Q:78:GLU:O	2.00	0.60
20:R:52:PRO:O	20:R:56:THR:HG23	2.00	0.60
1:A:761:G:H5'	19:Q:102:GLY:C	2.22	0.60
1:A:960:U:O2	1:A:960:U:H2'	2.02	0.60
11:I:114:TYR:CE2	12:J:59:SER:O	2.55	0.60
12:J:42:THR:HG23	12:J:67:THR:O	2.02	0.60
18:P:6:LEU:HD11	18:P:73:LEU:HD12	1.82	0.60
1:A:1321:C:H42	21:S:37:ARG:NH1	1.98	0.60
1:A:138:G:O2'	1:A:139:G:H5'	2.02	0.60
1:A:344:A:H5''	1:A:345:C:H5	1.67	0.60
18:P:74:LEU:HB3	18:P:79:VAL:HG21	1.82	0.60
15:M:94:ARG:HH12	21:S:81:ARG:HD3	1.67	0.60
22:T:67:ALA:HA	22:T:73:HIS:N	2.17	0.60
3:X:34:MNU:H2'	3:X:35:U:C6	2.36	0.60
3:X:36:U:H2'	3:X:37:T6A:H8	1.66	0.60
1:A:1208:C:H2'	1:A:1209:C:C6	2.36	0.60
1:A:1234:C:O2'	1:A:1235:U:H5'	2.02	0.60
1:A:1342:C:O2'	1:A:1343:G:H5'	2.02	0.60
1:A:853:G:O2'	1:A:854:G:H5'	2.02	0.60
4:B:60:ASP:OD1	4:B:64:ARG:HD2	2.02	0.60
4:B:84:GLU:OE1	4:B:216:SER:HA	2.01	0.60
5:C:97:LYS:O	5:C:98:ASN:HB3	2.02	0.60
18:P:18:ARG:NH1	18:P:32:TYR:OH	2.35	0.60
22:T:72:LEU:O	22:T:73:HIS:O	2.19	0.60
1:A:129:U:H5'	1:A:129(A):G:OP1	2.02	0.59
4:B:12:GLU:HG2	4:B:44:LEU:HD22	1.82	0.59
9:G:49:ILE:CD1	9:G:49:ILE:H	2.14	0.59
14:L:48:PRO:C	14:L:49:ASN:HD22	2.05	0.59
1:A:953:G:C1'	15:M:125:ARG:HA	2.28	0.59
17:O:88:ARG:HE	17:O:88:ARG:N	2.00	0.59
15:M:94:ARG:HH12	21:S:81:ARG:HH11	1.49	0.59
1:A:1072:G:H2'	1:A:1073:U:C6	2.37	0.59
4:B:131:PRO:HB2	4:B:133:LYS:HG3	1.84	0.59
5:C:148:GLY:HA3	5:C:172:ARG:O	2.02	0.59
10:H:116:LYS:HD3	10:H:127:LEU:HD12	1.84	0.59
1:A:1250:A:H5''	11:I:68:GLY:N	2.16	0.59
1:A:112:G:H21	1:A:354:G:H5'	1.67	0.59
1:A:1428:A:H2'	1:A:1429:C:C6	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:556:C:O2'	1:A:557:G:H5'	2.01	0.59
1:A:622:A:C8	1:A:623:C:C6	2.91	0.59
1:A:750:G:N3	17:O:23:GLY:HA3	2.17	0.59
4:B:27:LYS:CE	4:B:195:ASP:HB2	2.33	0.59
5:C:147:LYS:HE2	5:C:205:GLY:HA2	1.84	0.59
1:A:716:A:N3	13:K:117:ASN:O	2.36	0.59
14:L:71:PRO:O	14:L:102:ARG:HD2	2.02	0.59
18:P:81:ARG:HE	18:P:81:ARG:CA	2.14	0.59
1:A:1321:C:O2'	21:S:77:THR:HG21	2.03	0.59
1:A:418:C:H6	1:A:425:G:H1	1.47	0.59
5:C:147:LYS:HE3	5:C:203:PHE:CE2	2.37	0.59
9:G:103:TRP:HD1	9:G:106:GLN:NE2	2.00	0.59
15:M:4:ILE:HG22	15:M:5:ALA:H	1.68	0.59
1:A:974:A:OP1	16:N:31:ARG:HD3	2.01	0.59
20:R:33:ASP:OD2	20:R:36:ASN:HB2	2.02	0.59
5:C:58:GLU:HB3	12:J:92:THR:HG21	1.84	0.59
14:L:58:VAL:O	14:L:65:GLU:HA	2.02	0.59
1:A:1292:U:H2'	1:A:1293:G:C8	2.38	0.59
1:A:1363:A:H1'	1:A:1365:G:N7	2.17	0.59
1:A:1391:U:H2'	1:A:1392:G:H8	1.65	0.59
1:A:425:G:H2'	1:A:426:G:O4'	2.03	0.59
4:B:97:TRP:CE2	4:B:101:MET:HG3	2.37	0.59
4:B:200:ILE:O	4:B:201:ILE:HG13	2.03	0.59
4:B:30:ARG:HD2	4:B:31:TYR:CE2	2.37	0.59
6:D:76:ARG:HG2	6:D:76:ARG:NH1	2.18	0.59
8:F:10:LEU:HD12	8:F:10:LEU:H	1.66	0.59
8:F:30:LEU:HD22	8:F:35:ALA:HB1	1.85	0.59
11:I:93:ARG:C	11:I:95:LYS:H	2.04	0.59
1:A:1490:C:C5'	1:A:1490:C:H6	2.14	0.59
4:B:47:THR:HA	4:B:202:PRO:HG2	1.84	0.59
5:C:189:ALA:HB3	5:C:196:LEU:O	2.03	0.59
5:C:23:TYR:CD2	5:C:24:ALA:N	2.71	0.59
6:D:36:ARG:N	6:D:37:PRO:CD	2.60	0.59
12:J:24:VAL:O	12:J:28:ARG:HD3	2.02	0.59
1:A:1051:C:O2'	1:A:1052:U:H5'	2.02	0.59
1:A:1053:G:C4'	1:A:1054:C:H5'	2.33	0.59
1:A:28:G:O2'	1:A:296:U:OP1	2.20	0.59
7:E:15:ARG:O	7:E:16:THR:CB	2.51	0.59
8:F:98:LEU:HD22	8:F:101:ALA:HB2	1.84	0.59
19:Q:78:GLU:CD	19:Q:81:ARG:HD2	2.23	0.59
21:S:12:ASP:HB3	21:S:14:HIS:CE1	2.38	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:T:53:LEU:O	22:T:56:MET:HB3	2.03	0.59
22:T:56:MET:HG2	22:T:84:LEU:CD1	2.32	0.59
1:A:1054:C:H42	3:X:34:MNU:H1'	1.66	0.59
1:A:1519:A:H3'	1:A:1520:G:C5'	2.32	0.59
1:A:625:G:H4'	18:P:16:HIS:CD2	2.38	0.59
1:A:840:C:H4'	1:A:841:U:OP1	2.02	0.59
1:A:908:A:H2'	1:A:909:A:C8	2.38	0.59
1:A:918:A:H2'	1:A:919:A:C8	2.38	0.59
4:B:127:ILE:HG13	4:B:128:GLU:OE1	2.03	0.59
6:D:70:ILE:HG22	6:D:71:SER:N	2.17	0.59
10:H:127:LEU:HD23	10:H:127:LEU:N	2.18	0.59
13:K:86:GLY:H	13:K:112:THR:HG23	1.66	0.59
15:M:14:ARG:NH1	15:M:14:ARG:HB3	2.18	0.59
8:F:97:PHE:HB2	20:R:32:ARG:NH2	2.18	0.59
1:A:1499:A:O2'	1:A:1500:A:H5'	2.03	0.59
5:C:73:PRO:C	5:C:75:VAL:H	2.06	0.59
5:C:88:ARG:HE	5:C:101:LEU:HB3	1.67	0.59
8:F:22:GLU:OE1	8:F:82:ARG:HD3	2.02	0.59
11:I:93:ARG:CB	11:I:93:ARG:NH1	2.63	0.59
12:J:5:ARG:HB2	12:J:99:LYS:O	2.03	0.59
14:L:28:LYS:C	14:L:30:ALA:H	2.06	0.59
14:L:39:VAL:HA	14:L:79:GLU:CD	2.23	0.59
1:A:1281:U:H4'	1:A:1282:C:OP2	2.02	0.58
1:A:1289:A:H2'	1:A:1290:G:H5'	1.85	0.58
1:A:203:U:H5'	1:A:216:G:OP1	2.03	0.58
7:E:126:ARG:CG	7:E:126:ARG:HH11	2.15	0.58
9:G:21:VAL:HG23	9:G:22:LEU:N	2.18	0.58
13:K:84:VAL:HG11	13:K:91:ARG:HD3	1.85	0.58
19:Q:31:LEU:HG	19:Q:32:TYR:CE2	2.37	0.58
1:A:151:A:H2'	1:A:152:A:O4'	2.03	0.58
1:A:201:C:H4'	1:A:216:G:N2	2.17	0.58
1:A:738:C:H5''	8:F:69:GLU:HB3	1.85	0.58
4:B:22:LYS:HG3	4:B:35:GLU:OE1	2.02	0.58
9:G:79:ARG:HH11	9:G:83:ALA:N	2.01	0.58
10:H:35:ILE:HG22	10:H:39:LEU:HD21	1.85	0.58
10:H:87:SER:C	10:H:88:LYS:HG2	2.23	0.58
11:I:113:LYS:N	11:I:113:LYS:HD2	2.17	0.58
13:K:54:ARG:O	13:K:57:THR:HG23	2.03	0.58
1:A:969:A:N6	15:M:126:LYS:HE3	2.17	0.58
1:A:948:C:O2'	1:A:949:A:H5'	2.03	0.58
5:C:191:THR:HG22	5:C:192:THR:N	2.18	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:93:LYS:HD3	5:C:94:LEU:HD12	1.85	0.58
13:K:54:ARG:O	13:K:57:THR:CG2	2.51	0.58
14:L:117:ARG:NH2	14:L:124:LYS:HD3	2.19	0.58
19:Q:97:SER:HB2	19:Q:103:GLY:C	2.23	0.58
1:A:188:C:H5'	1:A:189:G:OP2	2.03	0.58
1:A:669:U:H2'	1:A:670:G:C8	2.38	0.58
4:B:139:LYS:HD3	4:B:139:LYS:O	2.03	0.58
4:B:230:VAL:HG12	4:B:231:GLU:N	2.18	0.58
8:F:36:ARG:HH11	8:F:36:ARG:HG2	1.68	0.58
12:J:12:ASP:HB3	12:J:15:THR:CG2	2.33	0.58
17:O:87:ILE:HG22	17:O:88:ARG:N	2.19	0.58
1:A:1505:G:H2'	1:A:1541:U:OP2	2.04	0.58
1:A:412:A:H2'	1:A:413:G:H5'	1.85	0.58
5:C:107:GLN:O	5:C:108:ASN:HB3	2.04	0.58
5:C:5:ILE:HD12	5:C:5:ILE:O	2.03	0.58
11:I:10:ARG:HG2	11:I:75:ASP:CB	2.31	0.58
19:Q:81:ARG:HE	19:Q:84:LEU:CD1	2.16	0.58
1:A:154:C:H2'	1:A:155:C:H6	1.69	0.58
1:A:266:G:H5''	1:A:268:C:N4	2.11	0.58
1:A:954:G:H2'	1:A:955:U:H6	1.68	0.58
12:J:47:PHE:HB2	12:J:63:PHE:HB2	1.86	0.58
18:P:19:ILE:HG22	18:P:36:ILE:HG13	1.86	0.58
1:A:1184:G:H2'	1:A:1185:G:H8	1.69	0.58
1:A:1218:C:H2'	1:A:1219:U:C6	2.38	0.58
1:A:1513:A:H2'	1:A:1514:C:C6	2.38	0.58
1:A:262:A:C6	1:A:263:A:C6	2.91	0.58
4:B:139:LYS:HE3	4:B:143:GLU:OE2	2.03	0.58
4:B:17:PHE:CD1	4:B:18:GLY:N	2.71	0.58
4:B:88:ALA:CB	4:B:90:MET:HG2	2.33	0.58
5:C:123:GLN:NE2	5:C:140:ARG:HH22	1.94	0.58
1:A:877:C:H1'	10:H:3:THR:CG2	2.33	0.58
10:H:82:HIS:O	10:H:83:ILE:HB	2.01	0.58
12:J:89:ASP:OD2	12:J:91:PRO:HD2	2.04	0.58
14:L:83:VAL:HG22	14:L:100:ILE:HG23	1.86	0.58
16:N:8:GLU:O	16:N:11:LYS:HB2	2.03	0.58
17:O:33:THR:HG23	17:O:63:ARG:NH1	2.19	0.58
18:P:67:THR:HG22	18:P:69:THR:H	1.69	0.58
1:A:357:G:O2'	1:A:358:U:H5'	2.04	0.58
1:A:614:A:H2'	1:A:615:C:C6	2.39	0.58
4:B:44:LEU:HA	4:B:47:THR:OG1	2.04	0.58
4:B:82:ARG:HA	4:B:92:TYR:HE2	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:191:THR:HG21	5:C:193:TYR:CE2	2.39	0.58
6:D:34:GLU:O	6:D:35:ARG:HB2	2.03	0.58
1:A:1318:A:H4'	21:S:10:PHE:CE2	2.39	0.58
1:A:1054:C:O2'	1:A:1055:A:H5''	2.03	0.58
1:A:459:G:H1	1:A:461:C:H5''	1.67	0.58
1:A:690:G:H2'	1:A:691:G:O4'	2.04	0.58
1:A:945:G:C2	1:A:946:A:C8	2.91	0.58
4:B:144:ARG:HG3	4:B:145:LEU:N	2.19	0.58
6:D:32:ALA:O	6:D:33:MET:C	2.41	0.58
8:F:99:ALA:CB	20:R:31:LEU:HD12	2.34	0.58
10:H:59:LEU:O	10:H:61:VAL:HG23	2.03	0.58
10:H:20:TYR:HE2	10:H:75:ARG:HD2	1.65	0.58
20:R:47:THR:HB	20:R:49:LYS:HG2	1.86	0.58
1:A:1095:U:H2'	1:A:1096:C:H6	1.67	0.58
1:A:1127:G:N2	1:A:1146:A:H62	2.01	0.58
1:A:141:A:O2'	1:A:142:G:H5'	2.04	0.58
1:A:21:G:H2'	1:A:22:G:C8	2.38	0.58
1:A:335:C:O2'	1:A:336:C:H5'	2.03	0.58
1:A:353:A:H5'	1:A:353:A:C8	2.38	0.58
1:A:547:A:H4'	1:A:548:G:O5'	2.03	0.58
1:A:590:C:O2'	1:A:591:U:H5'	2.04	0.58
1:A:895:G:H2'	1:A:896:C:C6	2.38	0.58
4:B:101:MET:HE3	4:B:108:ILE:CD1	2.28	0.58
5:C:193:TYR:HD1	5:C:194:GLY:N	2.02	0.58
10:H:103:VAL:HG21	10:H:110:ALA:HB2	1.84	0.58
15:M:50:GLU:O	15:M:54:VAL:HG23	2.04	0.58
15:M:56:LEU:O	15:M:56:LEU:HD23	2.03	0.58
1:A:1193:G:O2'	1:A:1194:U:H5'	2.04	0.57
1:A:420:U:O5'	1:A:424:G:H8	1.86	0.57
1:A:49:U:O2'	1:A:50:A:H2'	2.04	0.57
6:D:24:GLU:HA	6:D:24:GLU:OE1	2.03	0.57
8:F:95:GLU:H	8:F:95:GLU:CD	2.07	0.57
8:F:98:LEU:HD23	8:F:99:ALA:H	1.69	0.57
10:H:6:ILE:HG13	10:H:31:PHE:CE2	2.39	0.57
22:T:11:SER:C	22:T:13:LEU:HD12	2.24	0.57
1:A:1153:C:H2'	1:A:1154:G:H8	1.68	0.57
1:A:1437:C:H2'	1:A:1438:G:C8	2.39	0.57
1:A:184:G:H2'	1:A:185:A:H8	1.67	0.57
1:A:255:G:H1'	19:Q:16:GLN:NE2	2.19	0.57
1:A:314:C:O2'	1:A:315:A:H5'	2.04	0.57
9:G:149:ARG:HA	9:G:149:ARG:HE	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:7:THR:HG22	11:I:8:GLY:N	2.19	0.57
1:A:1174:G:O2'	1:A:1175:G:H5'	2.04	0.57
1:A:1349:A:C4	1:A:1350:A:C8	2.92	0.57
1:A:1358:U:H3'	1:A:1359:C:H6	1.69	0.57
4:B:87:ARG:NH1	4:B:233:SER:HA	2.18	0.57
5:C:73:PRO:O	5:C:75:VAL:N	2.30	0.57
11:I:93:ARG:O	11:I:95:LYS:N	2.33	0.57
1:A:444:C:O2'	1:A:445:G:H5'	2.04	0.57
1:A:983:A:H5'	1:A:984:C:OP2	2.04	0.57
14:L:119:LYS:HD2	14:L:119:LYS:H	1.68	0.57
1:A:195:A:H4'	22:T:68:LYS:HE2	1.86	0.57
1:A:1216:G:H5''	16:N:5:ALA:HB2	1.87	0.57
1:A:1370:G:O2'	1:A:1371:G:H5'	2.04	0.57
1:A:1521:G:H2'	1:A:1522:U:C6	2.40	0.57
1:A:252:U:H2'	1:A:253:U:C6	2.39	0.57
1:A:308:C:H2'	1:A:309:G:H8	1.70	0.57
1:A:459:G:H3'	1:A:460:A:H5''	1.86	0.57
7:E:72:GLN:O	7:E:73:ASN:HB3	2.05	0.57
8:F:60:PHE:C	8:F:61:LEU:HD23	2.25	0.57
12:J:87:THR:O	12:J:88:LEU:HG	2.04	0.57
13:K:105:VAL:O	13:K:105:VAL:HG12	2.05	0.57
17:O:26:GLU:OE1	17:O:77:ARG:HD2	2.04	0.57
19:Q:60:ILE:HD13	19:Q:61:GLU:N	2.19	0.57
22:T:43:LEU:HD12	22:T:52:ALA:HA	1.86	0.57
1:A:1342:C:O2'	11:I:124:GLN:HB2	2.05	0.57
1:A:1372:U:OP1	11:I:71:SER:HB3	2.04	0.57
1:A:407:G:O2'	1:A:408:A:OP1	2.21	0.57
1:A:713:G:H2'	1:A:714:G:C8	2.40	0.57
4:B:97:TRP:CZ2	4:B:102:LEU:HD13	2.40	0.57
4:B:115:LEU:CD2	4:B:153:ARG:HH22	2.17	0.57
4:B:180:LEU:O	4:B:181:PHE:HB2	2.04	0.57
5:C:191:THR:HG22	5:C:193:TYR:H	1.69	0.57
5:C:83:ARG:O	5:C:86:VAL:N	2.37	0.57
6:D:25:ARG:C	6:D:27:TYR:H	2.07	0.57
7:E:77:PRO:O	7:E:78:HIS:HB3	2.05	0.57
13:K:21:ILE:HG12	13:K:30:VAL:HG13	1.87	0.57
14:L:24:VAL:HG12	14:L:24:VAL:O	2.03	0.57
20:R:53:ARG:HH12	20:R:60:GLY:N	2.02	0.57
1:A:1243:C:H2'	1:A:1244:C:C6	2.39	0.57
13:K:29:ILE:C	13:K:29:ILE:HD12	2.25	0.57
1:A:1329:A:C2'	1:A:1330:U:H5'	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:190(A):C:H42	1:A:190(H):G:H1	1.53	0.57
1:A:895:G:H2'	1:A:896:C:H6	1.69	0.57
5:C:110:ASN:ND2	5:C:140:ARG:HB3	2.20	0.57
6:D:38:TYR:HE1	6:D:45:GLN:NE2	2.03	0.57
7:E:79:GLU:HA	7:E:91:LEU:O	2.05	0.57
9:G:11:GLN:C	9:G:12:LEU:HD12	2.25	0.57
13:K:95:ILE:HG21	13:K:108:ILE:HD13	1.86	0.57
15:M:74:VAL:O	15:M:77:ASN:HB3	2.04	0.57
19:Q:97:SER:OG	19:Q:103:GLY:HA2	2.05	0.57
19:Q:50:LYS:HG2	19:Q:50:LYS:O	2.04	0.57
4:B:184:VAL:O	4:B:198:ASP:HB2	2.04	0.57
4:B:163:PHE:CD1	4:B:185:ILE:HB	2.40	0.57
4:B:88:ALA:HB3	4:B:90:MET:HG2	1.87	0.57
9:G:28:ASN:O	9:G:31:MET:HB3	2.05	0.57
14:L:55:VAL:HG12	14:L:56:ALA:H	1.66	0.57
15:M:14:ARG:HH11	15:M:14:ARG:CB	2.18	0.57
19:Q:12:SER:HB3	19:Q:20:THR:CB	2.34	0.57
1:A:409:G:H3'	1:A:431:A:N7	2.18	0.57
4:B:101:MET:CA	4:B:108:ILE:HD12	2.34	0.57
9:G:108:ALA:O	9:G:119:ARG:HD2	2.05	0.57
15:M:15:VAL:HG23	15:M:43:THR:O	2.05	0.57
16:N:27:CYS:SG	16:N:43:CYS:SG	3.02	0.57
1:A:1286:A:C2	23:V:18:TYR:OH	2.58	0.57
1:A:1161:C:H2'	1:A:1162:C:C5	2.40	0.56
4:B:97:TRP:HZ2	4:B:102:LEU:HD13	1.70	0.56
9:G:64:GLN:O	9:G:68:ASN:HB2	2.05	0.56
11:I:49:PRO:HG2	11:I:81:ILE:HG22	1.87	0.56
1:A:1375:A:O2'	1:A:1376:U:H5'	2.05	0.56
1:A:409:G:H2'	1:A:409:G:N3	2.19	0.56
10:H:11:THR:HA	10:H:14:ARG:NH1	2.19	0.56
1:A:1038:C:H2'	1:A:1039:C:H6	1.70	0.56
1:A:1064:G:H4'	1:A:1065:U:H5''	1.86	0.56
1:A:1241:G:H2'	1:A:1242:C:C6	2.40	0.56
1:A:1347:G:C2'	1:A:1348:U:OP2	2.54	0.56
1:A:41:G:H2'	1:A:42:G:H8	1.69	0.56
1:A:409:G:H1	1:A:433:C:C5'	2.19	0.56
1:A:624:C:H2'	1:A:625:G:H8	1.69	0.56
5:C:114:PRO:O	5:C:118:GLN:HB2	2.05	0.56
7:E:76:ILE:HG23	7:E:77:PRO:HD2	1.88	0.56
10:H:45:ILE:C	10:H:47:GLY:H	2.09	0.56
13:K:124:LYS:HE2	13:K:125:PHE:CZ	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1392:G:O2'	1:A:1393:U:H5'	2.05	0.56
1:A:231:G:O2'	1:A:232:G:H5'	2.05	0.56
1:A:338:A:H2'	1:A:339:C:H6	1.68	0.56
4:B:134:GLU:C	4:B:136:VAL:H	2.07	0.56
12:J:9:ARG:HG3	12:J:9:ARG:O	2.05	0.56
14:L:43:VAL:CG1	14:L:44:THR:N	2.68	0.56
18:P:17:TYR:CE1	18:P:41:PRO:HG2	2.40	0.56
6:D:162:LEU:O	6:D:165:MET:HB2	2.05	0.56
10:H:49:GLU:HG2	10:H:62:TYR:HE2	1.71	0.56
11:I:85:LEU:O	11:I:92:TYR:HD1	1.89	0.56
20:R:55:ARG:HB3	20:R:55:ARG:HH11	1.69	0.56
1:A:408:A:H5''	1:A:429:U:O2'	2.05	0.56
5:C:18:TRP:N	5:C:18:TRP:CE3	2.71	0.56
9:G:65:ALA:O	9:G:69:VAL:HG23	2.06	0.56
10:H:38:ILE:CD1	10:H:38:ILE:H	2.18	0.56
10:H:41:ARG:C	10:H:43:GLY:H	2.08	0.56
15:M:73:GLU:O	15:M:77:ASN:N	2.34	0.56
1:A:1329:A:P	15:M:28:ALA:HB3	2.45	0.56
1:A:1402:C:O2	1:A:1500:A:N1	2.39	0.56
1:A:16:A:C2'	1:A:17:U:H5'	2.35	0.56
1:A:129(A):G:N3	1:A:190(E):U:H5'	2.21	0.56
4:B:115:LEU:HD21	4:B:153:ARG:NH2	2.18	0.56
4:B:137:ARG:HB3	4:B:137:ARG:NH1	2.21	0.56
4:B:51:LEU:HD22	4:B:55:PHE:CE1	2.38	0.56
5:C:48:TYR:HA	5:C:52:LEU:HD22	1.87	0.56
6:D:10:ARG:C	6:D:12:CYS:N	2.59	0.56
1:A:923:A:OP1	7:E:21:ALA:HB2	2.06	0.56
14:L:71:PRO:HG2	14:L:102:ARG:HG3	1.88	0.56
19:Q:59:ILE:HG23	19:Q:71:PHE:HB3	1.87	0.56
1:A:1039:C:O2'	1:A:1040:U:H5'	2.05	0.56
1:A:750:G:H21	17:O:23:GLY:HA3	1.71	0.56
1:A:926:G:H5'	1:A:927:G:O5'	2.05	0.56
5:C:28:GLN:HA	5:C:31:HIS:HD2	1.71	0.56
7:E:13:ILE:HA	7:E:29:GLY:O	2.06	0.56
11:I:97:LYS:N	11:I:98:PRO:CD	2.68	0.56
12:J:7:LYS:O	12:J:97:GLU:HB2	2.04	0.56
14:L:82:VAL:HG12	14:L:106:ASP:OD1	2.05	0.56
14:L:89:ARG:NE	14:L:97:ARG:HG2	2.21	0.56
1:A:1118:C:H6	1:A:1118:C:O5'	1.89	0.56
1:A:147:G:O2'	1:A:148:G:H5'	2.06	0.56
1:A:200:G:H21	1:A:216:G:H2'	1.68	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:475:G:C2	1:A:476:G:C8	2.94	0.56
10:H:73:ASP:OD2	10:H:75:ARG:HB2	2.06	0.56
11:I:114:TYR:HE2	12:J:59:SER:O	1.89	0.56
1:A:107:G:C2'	1:A:108:G:H5'	2.36	0.56
1:A:190(L):U:C2'	1:A:191:G:H5'	2.36	0.56
1:A:266:G:H5'	1:A:266:G:C8	2.40	0.56
4:B:10:LEU:HA	4:B:48:MET:SD	2.45	0.56
7:E:28:PHE:CD2	7:E:51:VAL:HG22	2.41	0.56
7:E:57:LYS:HG2	7:E:61:TYR:CE2	2.41	0.56
12:J:39:PRO:O	12:J:69:ASN:O	2.23	0.56
12:J:38:ILE:CB	12:J:71:LEU:HB2	2.34	0.56
1:A:39:G:O2'	1:A:40:C:H5'	2.06	0.56
5:C:138:VAL:HG22	5:C:151:VAL:HG23	1.88	0.56
5:C:30:ARG:CZ	5:C:30:ARG:HB3	2.36	0.56
11:I:63:ILE:CD1	11:I:81:ILE:HD11	2.36	0.56
19:Q:27:PHE:CD1	19:Q:27:PHE:C	2.79	0.56
22:T:70:SER:HA	22:T:73:HIS:CD2	2.41	0.56
1:A:1128:C:H5'	11:I:16:ARG:NH2	2.20	0.55
1:A:1202:G:O2'	1:A:1203:C:H5'	2.06	0.55
1:A:41:G:H2'	1:A:42:G:C8	2.40	0.55
1:A:900:A:H2'	1:A:901:A:C8	2.40	0.55
7:E:51:VAL:O	7:E:54:ALA:HB3	2.05	0.55
7:E:68:GLU:O	7:E:70:PRO:HD3	2.06	0.55
10:H:84:ARG:O	10:H:135:CYS:HB2	2.06	0.55
11:I:17:VAL:HG11	11:I:81:ILE:HA	1.87	0.55
20:R:73:ALA:CB	20:R:79:LEU:HD12	2.37	0.55
1:A:149:A:O2'	1:A:150:C:H5'	2.06	0.55
1:A:449:C:H2'	1:A:450:G:O4'	2.06	0.55
4:B:97:TRP:CD2	4:B:101:MET:HG3	2.40	0.55
4:B:15:VAL:HG21	4:B:209:ARG:CG	2.37	0.55
4:B:31:TYR:HE1	4:B:200:ILE:HD13	1.70	0.55
4:B:87:ARG:NH2	4:B:219:VAL:HB	2.22	0.55
7:E:107:ARG:O	7:E:108:ALA:C	2.42	0.55
8:F:14:LEU:HA	8:F:18:GLN:HE21	1.72	0.55
11:I:10:ARG:O	11:I:11:LYS:C	2.45	0.55
12:J:12:ASP:OD2	12:J:13:HIS:N	2.39	0.55
18:P:51:VAL:HG11	18:P:74:LEU:HD22	1.88	0.55
22:T:100:ILE:O	22:T:100:ILE:HG22	2.06	0.55
1:A:1153:C:H2'	1:A:1154:G:C8	2.42	0.55
1:A:580:U:H2'	1:A:581:G:O4'	2.07	0.55
4:B:239:VAL:HG12	4:B:240:GLN:HE22	1.70	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:3:ASN:N	5:C:3:ASN:ND2	2.50	0.55
5:C:82:GLU:O	5:C:85:ARG:HB3	2.06	0.55
1:A:333:G:H4'	22:T:16:HIS:HE2	1.71	0.55
1:A:1010:G:H2'	1:A:1011:G:C8	2.38	0.55
1:A:1381:U:O2'	1:A:1382:C:H5'	2.06	0.55
1:A:781:A:H2'	1:A:782:A:C5'	2.35	0.55
1:A:865:A:O2'	1:A:866:C:H5'	2.06	0.55
1:A:920:U:H2'	1:A:921:U:C6	2.41	0.55
4:B:106:LYS:O	4:B:110:GLN:HG3	2.07	0.55
4:B:15:VAL:HG21	4:B:209:ARG:HG3	1.87	0.55
4:B:178:ARG:HH11	4:B:178:ARG:CG	2.13	0.55
5:C:156:ARG:O	5:C:157:ILE:C	2.44	0.55
10:H:55:GLY:C	10:H:56:LYS:HD2	2.27	0.55
1:A:974:A:OP2	16:N:41:ARG:NH1	2.37	0.55
17:O:78:TYR:CZ	17:O:82:ILE:HD11	2.42	0.55
1:A:1128:C:H6	1:A:1128:C:O5'	1.89	0.55
1:A:1514:C:H2'	1:A:1515:C:C6	2.42	0.55
1:A:302:G:H5''	14:L:17:LYS:NZ	2.22	0.55
1:A:437:U:C2'	1:A:438:G:H5'	2.36	0.55
1:A:984:C:H2'	1:A:985:C:C6	2.42	0.55
4:B:23:ARG:NH1	4:B:24:TRP:HA	2.21	0.55
4:B:51:LEU:O	4:B:55:PHE:HD1	1.89	0.55
5:C:134:ILE:O	5:C:138:VAL:HG23	2.07	0.55
6:D:62:GLN:NE2	6:D:65:ARG:HH12	2.05	0.55
8:F:98:LEU:HD23	8:F:99:ALA:N	2.21	0.55
16:N:14:PRO:O	16:N:15:LYS:CB	2.54	0.55
1:A:256:U:H2'	1:A:257:G:C8	2.42	0.55
1:A:475:G:H2'	1:A:476:G:C5'	2.37	0.55
1:A:447:G:H2'	1:A:485:G:N2	2.22	0.55
5:C:153:VAL:HG12	5:C:154:SER:N	2.21	0.55
10:H:60:ARG:HH11	10:H:60:ARG:CG	2.20	0.55
12:J:63:PHE:CE1	16:N:45:ARG:HG3	2.42	0.55
17:O:24:SER:OG	17:O:27:VAL:HG23	2.06	0.55
18:P:53:VAL:CG2	18:P:54:GLU:N	2.70	0.55
1:A:463:A:C2	18:P:82:GLN:HB2	2.42	0.55
22:T:13:LEU:H	22:T:13:LEU:HD12	1.71	0.55
1:A:103:C:P	22:T:17:ARG:HH11	2.29	0.55
22:T:57:ARG:HB2	22:T:57:ARG:HH11	1.72	0.55
22:T:89:ARG:O	22:T:93:GLU:HG2	2.06	0.55
1:A:84:U:H2'	1:A:88:A:C8	2.41	0.55
4:B:16:HIS:HB3	4:B:44:LEU:HD21	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:70:ILE:HD11	6:D:100:ARG:HD2	1.88	0.55
7:E:135:THR:HG22	7:E:136:MET:N	2.21	0.55
8:F:72:VAL:C	8:F:74:ASP:H	2.08	0.55
10:H:18:ARG:NH2	10:H:81:HIS:O	2.37	0.55
11:I:45:ALA:O	11:I:48:GLU:N	2.39	0.55
11:I:53:VAL:HG21	11:I:85:LEU:HD21	1.89	0.55
22:T:50:GLU:HG3	22:T:100:ILE:HD12	1.88	0.55
1:A:1249:C:C2'	1:A:1250:A:H5'	2.36	0.55
1:A:190(E):U:O2'	19:Q:63:ARG:NH2	2.39	0.55
1:A:404:U:H2'	1:A:405:U:H6	1.71	0.55
1:A:826:C:H2'	1:A:827:U:C6	2.42	0.55
1:A:838:G:C3'	1:A:839:U:H5''	2.37	0.55
1:A:974:A:H8	1:A:974:A:OP1	1.90	0.55
4:B:10:LEU:C	4:B:12:GLU:H	2.11	0.55
7:E:126:ARG:HG2	7:E:126:ARG:HH11	1.71	0.55
10:H:39:LEU:H	10:H:39:LEU:HD22	1.72	0.55
12:J:9:ARG:HB3	12:J:9:ARG:NH1	2.22	0.55
1:A:1064:G:C4'	1:A:1065:U:H5'	2.37	0.55
1:A:1330:U:C2'	1:A:1331:G:H5'	2.37	0.55
1:A:942:G:C2	1:A:943:U:C6	2.95	0.55
4:B:131:PRO:C	4:B:133:LYS:H	2.10	0.55
4:B:88:ALA:HB1	4:B:226:ARG:HH22	1.72	0.55
5:C:64:VAL:HB	5:C:99:VAL:CG2	2.37	0.55
11:I:4:TYR:O	11:I:18:PHE:HA	2.07	0.55
14:L:126:LYS:H	14:L:126:LYS:CD	2.14	0.55
19:Q:40:LYS:HD3	19:Q:42:TYR:CZ	2.41	0.55
1:A:1318:A:H4'	21:S:10:PHE:CZ	2.42	0.55
1:A:1413:A:O2'	1:A:1414:U:H5'	2.07	0.55
1:A:554:C:H2'	1:A:555:C:C6	2.42	0.55
1:A:977:A:C2'	1:A:978:A:H5''	2.36	0.55
4:B:210:SER:C	4:B:212:GLN:H	2.11	0.55
4:B:213:LEU:O	4:B:217:ARG:HG2	2.07	0.55
5:C:147:LYS:HE2	5:C:205:GLY:H	1.71	0.55
7:E:59:GLY:O	7:E:62:ALA:HB3	2.07	0.55
9:G:71:PRO:HD3	9:G:103:TRP:CZ3	2.42	0.55
1:A:1123:A:H2	12:J:39:PRO:HG3	1.71	0.55
15:M:49:THR:C	15:M:51:ALA:H	2.10	0.55
1:A:761:G:H5'	19:Q:102:GLY:CA	2.37	0.55
22:T:100:ILE:O	22:T:102:GLY:N	2.39	0.55
1:A:1106:G:H5''	5:C:172:ARG:CG	2.36	0.54
1:A:1451:A:H8	1:A:1451:A:O5'	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:260:G:H2'	1:A:261:U:C6	2.42	0.54
1:A:397:A:H5'	1:A:398:C:OP1	2.07	0.54
1:A:639:G:O2'	1:A:640:A:H5'	2.06	0.54
1:A:1205:U:H1'	5:C:195:VAL:HG21	1.90	0.54
10:H:74:PRO:O	10:H:75:ARG:C	2.46	0.54
18:P:81:ARG:C	18:P:83:GLU:H	2.08	0.54
1:A:582:U:C1'	19:Q:105:ALA:HA	2.30	0.54
20:R:53:ARG:NH1	20:R:59:SER:C	2.61	0.54
21:S:9:VAL:HG12	21:S:10:PHE:N	2.22	0.54
1:A:1005:A:H1'	1:A:1026:G:C2	2.42	0.54
1:A:1025:U:H5'	1:A:1026:G:OP1	2.07	0.54
1:A:528:C:H5'	1:A:535:A:C6	2.42	0.54
1:A:744:C:H2'	1:A:745:C:C6	2.42	0.54
1:A:989:C:O2'	1:A:990:C:H5'	2.07	0.54
4:B:69:LEU:HD23	4:B:69:LEU:C	2.28	0.54
6:D:70:ILE:CG2	6:D:71:SER:N	2.71	0.54
8:F:38:GLU:O	8:F:39:LYS:HB3	2.07	0.54
8:F:72:VAL:C	8:F:74:ASP:N	2.57	0.54
9:G:125:MET:O	9:G:128:ALA:HB3	2.07	0.54
10:H:97:VAL:O	10:H:100:ILE:HG13	2.07	0.54
17:O:87:ILE:CG2	17:O:88:ARG:HH21	2.20	0.54
19:Q:11:VAL:C	19:Q:53:LEU:HD11	2.28	0.54
20:R:38:GLU:OE1	20:R:38:GLU:N	2.40	0.54
20:R:43:PHE:C	20:R:51:LEU:HD12	2.28	0.54
1:A:1305:G:O2'	1:A:1331:G:N2	2.40	0.54
1:A:445:G:O2'	1:A:446:G:H5'	2.07	0.54
1:A:456:C:H2'	1:A:457:C:C6	2.42	0.54
1:A:478:A:H2'	1:A:479:C:H5''	1.88	0.54
4:B:114:ARG:HD2	4:B:141:GLU:OE2	2.07	0.54
7:E:96:PRO:HA	7:E:117:ASP:OD2	2.07	0.54
10:H:134:ILE:O	10:H:135:CYS:HB3	2.07	0.54
20:R:53:ARG:C	20:R:55:ARG:N	2.60	0.54
21:S:30:LEU:C	21:S:31:ILE:HD13	2.28	0.54
1:A:1120:G:H2'	1:A:1121:U:C6	2.42	0.54
1:A:1230:C:O2'	1:A:1231:G:H5'	2.07	0.54
1:A:1300:G:HO2'	1:A:1301:U:H6	1.55	0.54
1:A:1406:U:O2'	1:A:1407:C:H5'	2.07	0.54
4:B:115:LEU:HD12	4:B:145:LEU:HB3	1.88	0.54
4:B:36:ARG:HB2	4:B:41:ILE:HD11	1.89	0.54
4:B:78:GLN:HG2	4:B:94:ASN:CG	2.28	0.54
5:C:51:GLY:O	5:C:70:VAL:HA	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:126:ILE:HG22	6:D:127:THR:N	2.23	0.54
9:G:152:ALA:O	9:G:154:TYR:N	2.40	0.54
9:G:69:VAL:HA	9:G:138:LYS:HG3	1.88	0.54
13:K:91:ARG:O	13:K:93:GLN:N	2.40	0.54
19:Q:5:VAL:O	19:Q:6:LEU:HD23	2.08	0.54
22:T:16:HIS:CE1	22:T:20:LEU:HD11	2.42	0.54
1:A:390:C:H2'	1:A:391:G:H8	1.72	0.54
5:C:93:LYS:HE2	5:C:93:LYS:CA	2.36	0.54
9:G:110:GLN:OE1	9:G:110:GLN:HA	2.06	0.54
14:L:55:VAL:CG1	14:L:56:ALA:H	2.18	0.54
15:M:88:ARG:HH11	15:M:88:ARG:CB	2.19	0.54
3:X:30:G:H2'	3:X:30:G:N3	2.23	0.54
1:A:1305:G:N2	1:A:1331:G:H1'	2.22	0.54
1:A:1480:G:H2'	1:A:1481:U:C6	2.42	0.54
1:A:17:U:H2'	1:A:18:C:C6	2.42	0.54
1:A:744:C:H2'	1:A:745:C:H6	1.72	0.54
1:A:811:C:H4'	1:A:900:A:N6	2.22	0.54
4:B:162:ILE:O	4:B:185:ILE:HG13	2.07	0.54
4:B:201:ILE:O	4:B:203:GLY:N	2.41	0.54
5:C:119:ARG:O	5:C:122:GLU:HB2	2.07	0.54
11:I:49:PRO:CG	11:I:81:ILE:HG22	2.38	0.54
15:M:17:VAL:O	15:M:20:THR:HB	2.08	0.54
19:Q:63:ARG:HG2	19:Q:64:PRO:HD2	1.89	0.54
1:A:1168:A:H2'	1:A:1169:A:C8	2.43	0.54
1:A:1323:G:H2'	1:A:1324:A:C8	2.42	0.54
1:A:409:G:N3	1:A:409:G:C2'	2.71	0.54
1:A:673:G:H2'	1:A:674:G:C8	2.43	0.54
5:C:190:ARG:HD2	5:C:190:ARG:N	2.21	0.54
18:P:42:ARG:O	18:P:43:LYS:C	2.45	0.54
1:A:1221:G:O2'	1:A:1222:G:H5'	2.08	0.54
1:A:1256:A:H5'	1:A:1258:G:H1'	1.89	0.54
1:A:1300:G:O2'	1:A:1301:U:H6	1.91	0.54
8:F:2:ARG:CZ	8:F:69:GLU:HG2	2.37	0.54
9:G:44:TYR:C	9:G:46:ALA:N	2.60	0.54
11:I:25:LYS:HB2	11:I:60:ASP:OD1	2.08	0.54
14:L:45:PRO:HD3	14:L:51:ALA:O	2.08	0.54
15:M:81:LEU:O	15:M:86:CYS:HB3	2.08	0.54
16:N:9:LYS:C	16:N:11:LYS:H	2.10	0.54
22:T:82:SER:O	22:T:86:ARG:HB2	2.07	0.54
1:A:1033:G:H2'	1:A:1034:G:H8	1.73	0.54
1:A:1104:G:H2'	1:A:1105:A:H8	1.73	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:474:G:N3	1:A:474:G:C3'	2.70	0.54
1:A:594:G:H2'	1:A:595:G:H5'	1.89	0.54
1:A:723:U:O2	1:A:723:U:H2'	2.08	0.54
4:B:101:MET:HA	4:B:108:ILE:HD12	1.90	0.54
6:D:15:GLU:HG2	6:D:63:LYS:HG3	1.90	0.54
15:M:2:ALA:O	15:M:4:ILE:HG13	2.08	0.54
1:A:1312:G:O2'	1:A:1313:U:H5'	2.08	0.54
1:A:976:G:C8	1:A:1358:U:O2	2.60	0.54
1:A:113:G:H1'	1:A:354:G:H5'	1.89	0.54
1:A:539:A:H2'	1:A:540:G:C8	2.43	0.54
6:D:24:GLU:O	6:D:25:ARG:CB	2.55	0.54
6:D:62:GLN:HE22	6:D:65:ARG:HH12	1.56	0.54
7:E:147:ASP:N	7:E:147:ASP:OD1	2.32	0.54
10:H:34:GLU:O	10:H:37:ARG:HB2	2.07	0.54
11:I:63:ILE:HD11	11:I:81:ILE:HD11	1.90	0.54
15:M:121:LYS:N	15:M:121:LYS:HD2	2.23	0.54
19:Q:98:LEU:O	19:Q:99:SER:HB3	2.08	0.54
22:T:100:ILE:O	22:T:101:GLY:C	2.46	0.54
1:A:192:U:H4'	22:T:102:GLY:O	2.07	0.54
1:A:1126:U:H2'	1:A:1127:G:O4'	2.08	0.53
1:A:390:C:H2'	1:A:391:G:C8	2.43	0.53
1:A:951:G:O2'	1:A:952:U:H5'	2.08	0.53
4:B:130:ARG:CD	4:B:131:PRO:HD2	2.37	0.53
4:B:219:VAL:C	4:B:221:LEU:N	2.61	0.53
5:C:20:SER:O	16:N:54:PRO:HB3	2.08	0.53
7:E:128:PRO:HG2	7:E:129:ILE:H	1.74	0.53
7:E:91:LEU:HB3	7:E:118:ILE:HD11	1.90	0.53
15:M:5:ALA:HB3	15:M:8:GLU:CG	2.32	0.53
20:R:59:SER:OG	20:R:62:GLU:HG3	2.07	0.53
1:A:167:G:O2'	1:A:168:G:H5'	2.07	0.53
1:A:201:C:O4'	1:A:216:G:N2	2.41	0.53
1:A:645:C:O2'	1:A:646:U:H5'	2.07	0.53
1:A:750:G:H1'	17:O:22:THR:OG1	2.08	0.53
6:D:153:ARG:HD2	6:D:181:MET:HE3	1.90	0.53
7:E:144:THR:HG22	7:E:147:ASP:OD1	2.08	0.53
8:F:14:LEU:HA	8:F:18:GLN:NE2	2.24	0.53
8:F:28:ARG:HA	8:F:28:ARG:NE	2.24	0.53
8:F:8:ILE:HD11	8:F:79:LEU:HD13	1.89	0.53
9:G:145:ALA:C	9:G:147:ALA:N	2.61	0.53
12:J:9:ARG:HD2	12:J:95:GLU:OE1	2.08	0.53
22:T:43:LEU:CD1	22:T:52:ALA:HA	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:403:C:O2'	1:A:404:U:H5'	2.08	0.53
1:A:448:A:C4	1:A:487:A:C2	2.96	0.53
1:A:487:A:H2'	1:A:488:C:O4'	2.08	0.53
4:B:177:ALA:O	4:B:180:LEU:N	2.41	0.53
6:D:108:LEU:HB3	6:D:110:PHE:CE1	2.44	0.53
6:D:153:ARG:HH12	6:D:180:GLY:C	2.11	0.53
10:H:4:ASP:OD2	10:H:85:ARG:NH1	2.41	0.53
12:J:28:ARG:O	12:J:28:ARG:HG2	2.08	0.53
16:N:26:ARG:CZ	16:N:47:LEU:HD21	2.38	0.53
19:Q:96:GLN:O	19:Q:97:SER:HB3	2.08	0.53
20:R:79:LEU:HD22	20:R:80:PRO:HD2	1.90	0.53
20:R:88:LYS:HG2	20:R:88:LYS:OXT	2.07	0.53
1:A:959:A:C2	1:A:1222:G:O4'	2.61	0.53
1:A:1487:G:O2'	1:A:1488:G:H5'	2.07	0.53
1:A:929:G:P	1:A:1533:C:H2'	2.49	0.53
1:A:340:U:H2'	1:A:341:C:C6	2.43	0.53
4:B:178:ARG:CG	4:B:178:ARG:NH1	2.70	0.53
5:C:30:ARG:CB	5:C:30:ARG:NH1	2.71	0.53
9:G:120:ILE:H	9:G:120:ILE:CD1	2.21	0.53
11:I:17:VAL:CG2	11:I:80:GLY:HA3	2.38	0.53
15:M:3:ARG:CA	15:M:9:ILE:HG13	2.38	0.53
18:P:53:VAL:O	18:P:55:ARG:N	2.42	0.53
21:S:46:GLY:HA2	21:S:61:TYR:HE2	1.73	0.53
1:A:975:A:O2'	1:A:976:G:OP2	2.23	0.53
4:B:91:PRO:HB3	4:B:151:GLY:O	2.09	0.53
6:D:150:GLU:HA	6:D:153:ARG:HG2	1.90	0.53
15:M:20:THR:HG23	15:M:26:GLY:HA2	1.89	0.53
19:Q:59:ILE:HG22	19:Q:71:PHE:CD1	2.43	0.53
1:A:1251:A:H1'	1:A:1369:C:HO2'	1.73	0.53
1:A:707:C:O2'	1:A:708:C:H5'	2.09	0.53
1:A:975:A:H4'	1:A:976:G:C5'	2.38	0.53
4:B:12:GLU:C	4:B:14:GLY:N	2.60	0.53
4:B:111:ARG:HB3	4:B:149:LEU:HD11	1.90	0.53
5:C:40:ARG:HB3	5:C:44:GLU:CD	2.29	0.53
9:G:151:TYR:HE1	13:K:54:ARG:CZ	2.22	0.53
9:G:49:ILE:N	9:G:49:ILE:CD1	2.71	0.53
10:H:83:ILE:CG2	10:H:83:ILE:O	2.55	0.53
12:J:16:LEU:O	12:J:18:ALA:N	2.41	0.53
13:K:41:THR:HG21	13:K:71:LYS:HB3	1.90	0.53
17:O:26:GLU:O	17:O:27:VAL:C	2.47	0.53
18:P:6:LEU:HD23	18:P:17:TYR:CG	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:P:22:THR:HA	18:P:33:ILE:CG1	2.37	0.53
1:A:1497:G:C2'	1:A:1498:U:H5'	2.39	0.53
1:A:202:U:H5'	1:A:216:G:O2'	2.08	0.53
4:B:163:PHE:HD1	4:B:185:ILE:HB	1.73	0.53
5:C:81:GLY:O	5:C:84:ILE:HG22	2.08	0.53
9:G:88:PRO:HB2	9:G:149:ARG:HH21	1.73	0.53
13:K:30:VAL:HG21	13:K:65:ALA:HA	1.91	0.53
18:P:69:THR:O	18:P:72:ARG:HB3	2.09	0.53
20:R:35:ARG:O	20:R:37:VAL:HG23	2.08	0.53
8:F:91:VAL:HG11	20:R:72:ARG:NH1	2.24	0.53
1:A:1054:C:OP1	1:A:1197:G:OP1	2.26	0.53
1:A:201:C:O2	1:A:203:U:H1'	2.09	0.53
1:A:92:C:O2'	1:A:93:G:H5'	2.08	0.53
4:B:132:LYS:HB3	4:B:136:VAL:CG2	2.39	0.53
4:B:144:ARG:HA	4:B:147:LYS:HD2	1.91	0.53
4:B:45:GLN:O	4:B:49:GLU:HG3	2.09	0.53
12:J:31:GLY:CA	12:J:76:ASN:HD21	2.22	0.53
15:M:59:TYR:CG	15:M:59:TYR:O	2.61	0.53
1:A:254:G:OP1	19:Q:68:ARG:HB3	2.09	0.53
1:A:942:G:H2'	1:A:943:U:H6	1.73	0.53
10:H:103:VAL:CG2	10:H:110:ALA:HB2	2.39	0.53
7:E:143:ARG:HH12	10:H:77:GLU:CD	2.12	0.53
18:P:17:TYR:CE1	18:P:41:PRO:CG	2.92	0.53
18:P:75:ARG:NH1	18:P:75:ARG:HG3	2.21	0.53
19:Q:82:MET:O	19:Q:83:ASP:C	2.47	0.53
1:A:1195:C:H3'	1:A:1196:U:C5'	2.39	0.53
1:A:154:C:H2'	1:A:155:C:C6	2.44	0.53
1:A:941:G:O2'	1:A:942:G:H5'	2.08	0.53
4:B:23:ARG:HH12	4:B:191:ASP:HA	1.74	0.53
5:C:181:ASN:O	5:C:204:LEU:HD12	2.09	0.53
6:D:199:ASN:ND2	6:D:201:GLN:HB2	2.24	0.53
9:G:120:ILE:N	9:G:120:ILE:HD12	2.18	0.53
11:I:48:GLU:N	11:I:49:PRO:CD	2.71	0.53
12:J:85:LEU:O	12:J:87:THR:N	2.42	0.53
14:L:85:ILE:HG23	14:L:98:TYR:HB3	1.91	0.53
15:M:53:VAL:O	15:M:57:ARG:HB2	2.09	0.53
19:Q:76:LEU:C	19:Q:76:LEU:HD23	2.30	0.53
21:S:71:LEU:O	21:S:73:GLU:N	2.42	0.53
1:A:1010:G:N2	1:A:1020:U:H1'	2.23	0.52
1:A:1423:G:O2'	1:A:1424:C:H5'	2.10	0.52
4:B:144:ARG:HG3	4:B:145:LEU:H	1.72	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:35:GLU:OE1	5:C:97:LYS:HE3	2.08	0.52
5:C:43:LEU:HD22	5:C:68:VAL:HG21	1.91	0.52
8:F:4:TYR:CE2	8:F:72:VAL:HG21	2.44	0.52
9:G:23:VAL:HG13	9:G:43:PHE:CE2	2.43	0.52
9:G:61:VAL:O	9:G:64:GLN:HB3	2.08	0.52
11:I:49:PRO:HB3	11:I:82:ALA:HB2	1.91	0.52
12:J:63:PHE:HE1	16:N:45:ARG:HG3	1.74	0.52
14:L:28:LYS:C	14:L:30:ALA:N	2.63	0.52
1:A:761:G:C5'	19:Q:102:GLY:HA3	2.38	0.52
1:A:1035:A:O2'	1:A:1036:G:H5'	2.10	0.52
1:A:650:G:O2'	1:A:651:C:H5'	2.09	0.52
1:A:750:G:N2	17:O:23:GLY:HA3	2.23	0.52
4:B:112:VAL:C	4:B:114:ARG:H	2.13	0.52
4:B:69:LEU:HD12	4:B:155:LEU:HD11	1.92	0.52
6:D:11:LEU:HD22	6:D:66:ARG:NE	2.24	0.52
9:G:44:TYR:C	9:G:46:ALA:H	2.12	0.52
17:O:12:ILE:C	17:O:14:GLU:H	2.12	0.52
1:A:1010:G:H22	1:A:1020:U:H1'	1.73	0.52
1:A:22:G:H2'	1:A:23:C:H6	1.75	0.52
8:F:99:ALA:HB2	20:R:31:LEU:HD12	1.91	0.52
9:G:111:ARG:HE	9:G:123:GLU:HA	1.75	0.52
11:I:69:GLY:O	11:I:73:GLN:HG3	2.09	0.52
15:M:6:GLY:O	15:M:7:VAL:HG22	2.09	0.52
17:O:82:ILE:HD13	17:O:88:ARG:CG	2.39	0.52
19:Q:66:SER:O	19:Q:70:ARG:NH1	2.43	0.52
19:Q:86:GLU:O	19:Q:87:LYS:C	2.47	0.52
1:A:1060:C:O2'	1:A:1061:G:H5'	2.10	0.52
1:A:458:C:H2'	1:A:459:G:H8	1.73	0.52
4:B:222:ILE:HG22	4:B:226:ARG:HH21	1.75	0.52
7:E:129:ILE:N	7:E:129:ILE:HD12	2.24	0.52
12:J:38:ILE:O	12:J:70:ARG:HA	2.09	0.52
13:K:74:ALA:C	13:K:76:GLY:H	2.12	0.52
15:M:49:THR:C	15:M:51:ALA:N	2.61	0.52
20:R:53:ARG:HG2	20:R:63:GLN:HG2	1.91	0.52
1:A:1513:A:C2	1:A:1523:G:C6	2.97	0.52
1:A:16:A:O2'	1:A:17:U:H5'	2.10	0.52
1:A:625:G:H2'	1:A:626:U:C6	2.44	0.52
1:A:975:A:C5'	1:A:976:G:H5'	2.39	0.52
4:B:71:VAL:HG21	4:B:164:VAL:HG22	1.91	0.52
6:D:118:ARG:NH2	6:D:118:ARG:HG3	2.23	0.52
6:D:61:LYS:NZ	6:D:72:GLU:OE2	2.43	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:23:ILE:HG22	12:J:72:VAL:HG11	1.90	0.52
15:M:15:VAL:HG12	15:M:19:LEU:HD12	1.90	0.52
15:M:37:THR:CG2	15:M:55:ARG:HD2	2.39	0.52
17:O:21:ASP:CG	17:O:24:SER:HB3	2.29	0.52
1:A:1068:G:N7	1:A:1094:G:H2'	2.25	0.52
1:A:1427:U:O2'	1:A:1428:A:H5'	2.10	0.52
1:A:312:C:H2'	1:A:313:A:C8	2.44	0.52
1:A:407:G:C3'	1:A:431:A:OP1	2.58	0.52
1:A:620:C:C2	6:D:135:LEU:HD13	2.45	0.52
1:A:74:C:O2'	1:A:75:G:H5'	2.10	0.52
9:G:75:VAL:HG23	9:G:87:VAL:C	2.30	0.52
21:S:15:LEU:HD12	21:S:15:LEU:C	2.29	0.52
21:S:22:LEU:CD2	21:S:28:LYS:HB2	2.40	0.52
1:A:407:G:O2'	1:A:408:A:P	2.67	0.52
1:A:509:A:H5'	6:D:54:TYR:HD2	1.75	0.52
4:B:54:THR:O	4:B:58:ILE:HG13	2.10	0.52
7:E:103:GLY:O	7:E:106:PRO:HD2	2.09	0.52
7:E:43:LEU:H	7:E:65:ASN:ND2	2.08	0.52
9:G:15:ASP:CB	9:G:20:ASP:H	2.23	0.52
10:H:6:ILE:HD12	10:H:35:ILE:HD12	1.91	0.52
12:J:71:LEU:O	12:J:72:VAL:CB	2.58	0.52
14:L:47:LYS:CB	14:L:48:PRO:CD	2.79	0.52
14:L:92:ASP:C	14:L:93:LEU:HD23	2.30	0.52
14:L:88:GLY:H	14:L:98:TYR:HA	1.75	0.52
15:M:91:ARG:NH2	15:M:103:THR:HG21	2.25	0.52
18:P:15:PRO:O	18:P:16:HIS:ND1	2.42	0.52
18:P:46:PRO:HG2	18:P:47:ASP:H	1.74	0.52
18:P:53:VAL:C	18:P:55:ARG:N	2.62	0.52
1:A:1510:U:H2'	1:A:1511:G:H8	1.71	0.52
1:A:460:A:N7	1:A:462:G:N2	2.44	0.52
1:A:738:C:H2'	1:A:739:C:H6	1.75	0.52
6:D:65:ARG:HB2	6:D:75:PHE:CD1	2.45	0.52
9:G:138:LYS:C	9:G:138:LYS:HD3	2.30	0.52
10:H:91:ARG:HG3	14:L:7:ILE:HG13	1.91	0.52
12:J:4:ILE:CD1	12:J:74:ILE:HG13	2.37	0.52
20:R:48:GLY:H	20:R:82:THR:HA	1.74	0.52
1:A:1193:G:C2'	1:A:1194:U:H5'	2.39	0.52
1:A:201:C:C4'	1:A:216:G:N2	2.56	0.52
1:A:222:U:H2'	1:A:223:U:C6	2.45	0.52
1:A:513:C:H2'	1:A:514:C:C6	2.44	0.52
1:A:792:A:H4'	1:A:793:U:C5'	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:144:ARG:HD2	4:B:145:LEU:HD23	1.92	0.52
14:L:33:ARG:O	14:L:84:LEU:HD12	2.09	0.52
1:A:981:U:H5'	16:N:21:TYR:CE1	2.45	0.52
16:N:9:LYS:NZ	16:N:22:THR:HA	2.25	0.52
19:Q:104:LYS:O	19:Q:105:ALA:HB3	2.10	0.52
1:A:359:U:O2'	1:A:360:A:H5'	2.10	0.52
1:A:975:A:C4'	1:A:976:G:H5'	2.39	0.52
4:B:187:LEU:HD12	4:B:201:ILE:HG22	1.92	0.52
5:C:39:ILE:HG22	5:C:40:ARG:N	2.25	0.52
7:E:102:ALA:HB2	7:E:120:THR:HB	1.91	0.52
8:F:14:LEU:HD13	8:F:19:LEU:HA	1.91	0.52
10:H:137:VAL:HG12	10:H:138:TRP:N	2.23	0.52
12:J:7:LYS:HB2	12:J:97:GLU:CB	2.39	0.52
14:L:119:LYS:N	14:L:119:LYS:HD2	2.24	0.52
15:M:34:LEU:CD2	15:M:39:ILE:HB	2.38	0.52
1:A:1062:U:H2'	1:A:1063:C:C6	2.45	0.51
1:A:586:C:O2'	1:A:587:G:H5'	2.09	0.51
1:A:865:A:H2'	1:A:866:C:H6	1.76	0.51
1:A:943:U:H2'	1:A:944:G:H5'	1.90	0.51
1:A:986:A:H2'	1:A:987:G:C8	2.45	0.51
6:D:70:ILE:HD11	6:D:100:ARG:CD	2.40	0.51
11:I:9:ARG:CG	11:I:14:VAL:HG22	2.34	0.51
1:A:1123:A:H4'	12:J:36:GLY:HA3	1.92	0.51
15:M:40:ASN:HD22	15:M:41:PRO:HD2	1.74	0.51
20:R:19:LYS:H	20:R:19:LYS:CD	2.22	0.51
22:T:13:LEU:N	22:T:13:LEU:HD12	2.25	0.51
1:A:1372:U:O2'	1:A:1373:G:H5'	2.09	0.51
1:A:200:G:H2'	1:A:216:G:N2	2.25	0.51
1:A:984:C:H2'	1:A:985:C:H6	1.74	0.51
4:B:200:ILE:HG22	4:B:201:ILE:N	2.18	0.51
4:B:92:TYR:HE1	4:B:151:GLY:CA	2.20	0.51
4:B:92:TYR:CD1	4:B:92:TYR:N	2.78	0.51
5:C:157:ILE:CD1	5:C:166:GLU:HB2	2.40	0.51
5:C:180:ALA:O	5:C:181:ASN:HB3	2.10	0.51
5:C:186:PHE:O	5:C:187:ALA:HB2	2.09	0.51
7:E:11:ILE:HB	7:E:31:LEU:HB3	1.91	0.51
8:F:23:LYS:HA	8:F:26:ILE:HB	1.92	0.51
11:I:111:ARG:HG2	11:I:112:LYS:N	2.23	0.51
1:A:1150:U:O2	12:J:39:PRO:HG3	2.10	0.51
12:J:47:PHE:CZ	16:N:37:PHE:HE1	2.28	0.51
17:O:53:HIS:CE1	17:O:57:LEU:HD22	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:R:47:THR:HG22	20:R:48:GLY:N	2.25	0.51
1:A:1130:A:OP2	1:A:1131:G:H5''	2.11	0.51
1:A:1288:A:H1'	1:A:1352:C:O2'	2.10	0.51
1:A:1412:C:H2'	1:A:1413:A:H8	1.73	0.51
1:A:1507:A:C2	1:A:1508:G:C4	2.98	0.51
1:A:686:U:O4	1:A:703:G:H1'	2.10	0.51
1:A:909:A:H2'	1:A:910:C:O4'	2.10	0.51
4:B:7:VAL:C	4:B:8:LYS:HD2	2.30	0.51
5:C:28:GLN:HA	5:C:31:HIS:CD2	2.46	0.51
6:D:202:LEU:O	6:D:203:VAL:C	2.49	0.51
1:A:653:A:P	10:H:56:LYS:HZ1	2.34	0.51
11:I:46:ALA:O	11:I:49:PRO:HD2	2.10	0.51
11:I:4:TYR:HD1	11:I:19:LEU:O	1.93	0.51
11:I:84:ALA:C	11:I:86:VAL:H	2.13	0.51
12:J:34:VAL:HG12	12:J:35:SER:H	1.73	0.51
12:J:89:ASP:CB	12:J:91:PRO:HD2	2.41	0.51
13:K:58:PRO:HB2	13:K:93:GLN:HG3	1.93	0.51
17:O:67:LEU:O	17:O:70:LEU:N	2.44	0.51
1:A:267:C:P	19:Q:67:LYS:HB2	2.51	0.51
1:A:1513:A:C2	1:A:1523:G:C5	2.99	0.51
1:A:1515:C:O2'	1:A:1516:G:H5'	2.11	0.51
1:A:45:U:H2'	1:A:46:G:C8	2.46	0.51
1:A:640:A:O2'	1:A:641:U:H5'	2.09	0.51
1:A:818:G:O2'	1:A:819:A:H5'	2.11	0.51
7:E:129:ILE:H	7:E:129:ILE:CD1	2.23	0.51
7:E:11:ILE:CG2	7:E:12:LEU:HD12	2.38	0.51
8:F:80:ARG:NH1	8:F:88:VAL:HB	2.26	0.51
9:G:115:ARG:O	9:G:116:ALA:C	2.48	0.51
10:H:86:ILE:HG12	10:H:135:CYS:HA	1.92	0.51
14:L:119:LYS:CD	14:L:119:LYS:H	2.23	0.51
1:A:950:U:OP2	15:M:102:ARG:HD2	2.11	0.51
15:M:10:PRO:O	15:M:11:ARG:HB2	2.10	0.51
18:P:26:ARG:HG3	18:P:27:LYS:N	2.25	0.51
19:Q:56:VAL:CG2	19:Q:81:ARG:HD3	2.41	0.51
21:S:45:VAL:HG12	21:S:46:GLY:N	2.24	0.51
1:A:1003:G:N1	1:A:1004:A:H1'	2.26	0.51
1:A:1021:G:O2'	1:A:1022:G:H5'	2.10	0.51
1:A:1209:C:O2'	1:A:1210:C:H5'	2.11	0.51
1:A:1392:G:O2'	1:A:1502:A:H5''	2.10	0.51
1:A:193:C:O3'	22:T:61:SER:HB2	2.11	0.51
1:A:411:A:C2	1:A:417:C:O2	2.63	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:584:G:H2'	1:A:585:G:C8	2.45	0.51
5:C:6:HIS:CD2	5:C:8:ILE:H	2.29	0.51
10:H:104:ARG:CZ	10:H:138:TRP:CZ3	2.93	0.51
11:I:12:GLU:O	11:I:12:GLU:CG	2.58	0.51
11:I:13:ALA:HA	11:I:67:GLY:O	2.10	0.51
12:J:60:ARG:HH11	12:J:60:ARG:HG2	1.76	0.51
21:S:17:GLU:O	21:S:21:GLU:HG3	2.10	0.51
22:T:34:LYS:O	22:T:37:SER:HB2	2.11	0.51
22:T:39:LYS:HD3	22:T:55:ILE:HD13	1.91	0.51
1:A:1064:G:N2	1:A:1190:G:H2'	2.25	0.51
1:A:384:G:H2'	1:A:385:C:C6	2.45	0.51
4:B:100:GLY:C	4:B:108:ILE:HD12	2.31	0.51
4:B:17:PHE:HD1	4:B:18:GLY:H	1.56	0.51
5:C:38:ARG:HG3	5:C:38:ARG:NH1	2.24	0.51
9:G:135:VAL:O	9:G:139:GLU:HG3	2.11	0.51
9:G:15:ASP:HB3	9:G:20:ASP:H	1.76	0.51
19:Q:68:ARG:HH11	19:Q:68:ARG:HG2	1.74	0.51
1:A:109:A:H2'	1:A:326:G:N2	2.26	0.51
1:A:376:G:H2'	1:A:377:G:C8	2.36	0.51
1:A:965:A:C6	1:A:969:A:C2	2.99	0.51
4:B:212:GLN:O	4:B:213:LEU:C	2.48	0.51
5:C:26:LYS:CD	5:C:26:LYS:N	2.67	0.51
7:E:107:ARG:NH1	7:E:107:ARG:HB2	2.14	0.51
8:F:33:TYR:HA	8:F:71:ARG:CZ	2.40	0.51
9:G:38:LEU:C	9:G:38:LEU:HD12	2.31	0.51
1:A:1425:U:H2'	1:A:1426:C:C6	2.44	0.51
1:A:173:U:H5	1:A:198:G:HO2'	1.54	0.51
1:A:332:G:O2'	1:A:333:G:H5'	2.11	0.51
1:A:35:G:H2'	1:A:36:C:C6	2.46	0.51
1:A:825:G:O2'	1:A:826:C:H5'	2.11	0.51
1:A:1298:C:H2'	9:G:114:ARG:NH1	2.26	0.51
14:L:83:VAL:HG21	14:L:100:ILE:HD13	1.92	0.51
15:M:91:ARG:HB3	15:M:98:VAL:HG22	1.91	0.51
16:N:25:VAL:HG12	16:N:39:LEU:HD23	1.92	0.51
1:A:1006:C:H2'	1:A:1007:C:H6	1.75	0.51
1:A:1358:U:H2'	1:A:1359:C:O4'	2.10	0.51
1:A:1519:A:H3'	1:A:1520:G:H5'	1.91	0.51
1:A:538:G:O2'	1:A:539:A:H5'	2.11	0.51
4:B:118:LEU:O	4:B:120:ALA:N	2.44	0.51
4:B:16:HIS:CE1	4:B:214:ILE:HG12	2.46	0.51
8:F:67:MET:CE	8:F:72:VAL:HG22	2.38	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:I:107:ARG:HB3	11:I:107:ARG:NH1	2.26	0.51
11:I:53:VAL:CG2	11:I:85:LEU:HD21	2.40	0.51
12:J:7:LYS:HB2	12:J:97:GLU:HB2	1.93	0.51
14:L:110:VAL:HG21	14:L:120:TYR:HB3	1.93	0.51
14:L:26:ALA:O	14:L:27:LEU:O	2.29	0.51
14:L:43:VAL:CG1	14:L:44:THR:H	2.21	0.51
15:M:49:THR:HB	15:M:52:GLU:HG3	1.93	0.51
18:P:21:VAL:HG21	18:P:59:TRP:CD1	2.46	0.51
21:S:58:VAL:HG21	21:S:75:ALA:HA	1.91	0.51
1:A:1315:U:H2'	1:A:1316:G:C8	2.46	0.51
1:A:1325:C:H4'	23:V:17:THR:HG21	1.93	0.51
1:A:139:G:O2'	1:A:140:A:H5'	2.11	0.51
4:B:96:ARG:HH12	4:B:169:LYS:NZ	2.08	0.51
1:A:427:U:OP1	6:D:13:ARG:NH2	2.43	0.51
9:G:152:ALA:C	9:G:154:TYR:H	2.14	0.51
14:L:113:ARG:HB2	14:L:122:THR:HG21	1.93	0.51
20:R:39:VAL:CG1	20:R:40:LEU:N	2.74	0.51
20:R:45:SER:C	20:R:47:THR:N	2.64	0.51
1:A:1003:G:C6	1:A:1004:A:H1'	2.46	0.50
1:A:1367:C:C2	1:A:1368:G:C8	2.99	0.50
1:A:19:C:O2'	1:A:20:U:H5'	2.11	0.50
4:B:115:LEU:CD2	4:B:116:GLU:N	2.74	0.50
4:B:182:ILE:CD1	4:B:182:ILE:H	2.21	0.50
10:H:36:LEU:CD1	10:H:59:LEU:HD13	2.41	0.50
10:H:97:VAL:HA	10:H:100:ILE:CD1	2.40	0.50
12:J:96:ILE:HG22	12:J:97:GLU:N	2.25	0.50
17:O:7:GLU:O	17:O:11:VAL:HG23	2.11	0.50
19:Q:63:ARG:HG2	19:Q:64:PRO:CD	2.42	0.50
1:A:247:G:OP2	19:Q:99:SER:HB2	2.11	0.50
1:A:1182:G:H4'	1:A:1183:A:O5'	2.11	0.50
1:A:959:A:H2'	1:A:960:U:O4'	2.11	0.50
4:B:15:VAL:HG11	4:B:209:ARG:CG	2.39	0.50
11:I:5:TYR:C	11:I:84:ALA:HB2	2.31	0.50
14:L:6:THR:HG1	14:L:9:GLN:HG3	1.76	0.50
1:A:960:U:H1'	1:A:1223:C:H5'	1.93	0.50
1:A:1226:C:O2'	1:A:1227:A:H5'	2.11	0.50
1:A:1290:G:H2'	1:A:1291:G:H8	1.76	0.50
1:A:1426:C:H2'	1:A:1427:U:H6	1.76	0.50
1:A:939:G:H5''	9:G:102:ARG:CZ	2.42	0.50
4:B:80:ILE:CD1	4:B:208:ILE:HG23	2.29	0.50
5:C:191:THR:HG21	5:C:193:TYR:CE1	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:32:ALA:HB2	12:J:76:ASN:OD1	2.11	0.50
14:L:86:ARG:HB3	14:L:101:VAL:HG23	1.94	0.50
14:L:87:GLY:HA2	14:L:98:TYR:HA	1.94	0.50
16:N:36:PHE:O	16:N:36:PHE:CD1	2.65	0.50
17:O:82:ILE:HD13	17:O:88:ARG:HG3	1.93	0.50
1:A:1399:C:C2	1:A:1502:A:N6	2.80	0.50
1:A:203:U:H4'	1:A:216:G:P	2.52	0.50
1:A:409:G:N2	1:A:431:A:O2'	2.44	0.50
1:A:456:C:O2'	1:A:457:C:H5'	2.12	0.50
1:A:26:A:H61	1:A:558:G:H1'	1.77	0.50
1:A:730:G:H21	1:A:765:G:H5''	1.74	0.50
1:A:952:U:O2'	1:A:953:G:H5'	2.12	0.50
1:A:1101:A:C8	4:B:172:ILE:HD13	2.46	0.50
4:B:77:ALA:HB3	4:B:211:ILE:HD13	1.94	0.50
5:C:20:SER:HB3	5:C:22:TRP:CD1	2.47	0.50
7:E:144:THR:CG2	7:E:146:ALA:H	2.25	0.50
9:G:25:ALA:O	9:G:28:ASN:HB2	2.11	0.50
14:L:53:ARG:CG	14:L:69:TYR:HE1	2.23	0.50
14:L:60:LEU:CD1	14:L:85:ILE:HD12	2.29	0.50
15:M:94:ARG:HH12	21:S:81:ARG:CD	2.25	0.50
1:A:242:C:H2'	1:A:243:A:H5'	1.93	0.50
1:A:646:U:H2'	1:A:647:C:C6	2.46	0.50
1:A:707:C:H2'	1:A:708:C:H6	1.76	0.50
4:B:137:ARG:C	4:B:139:LYS:H	2.14	0.50
4:B:122:PHE:CZ	4:B:139:LYS:HG2	2.47	0.50
4:B:28:PHE:CD2	4:B:190:THR:HA	2.47	0.50
4:B:51:LEU:CD2	4:B:55:PHE:HE1	2.22	0.50
4:B:92:TYR:N	4:B:92:TYR:HD1	2.09	0.50
1:A:1056:U:C5'	5:C:163:ALA:HB2	2.42	0.50
1:A:1073:U:OP1	7:E:57:LYS:HE2	2.11	0.50
10:H:116:LYS:HZ3	10:H:127:LEU:HB3	1.71	0.50
14:L:55:VAL:HG11	14:L:67:THR:CG2	2.41	0.50
20:R:46:GLU:N	20:R:46:GLU:CD	2.64	0.50
1:A:1314:C:H3'	21:S:6:LYS:HZ2	1.77	0.50
1:A:1085:U:H3'	1:A:1086:U:C5	2.46	0.50
1:A:1086:U:H3	1:A:1099:G:N2	2.09	0.50
1:A:1220:G:N3	21:S:54:GLY:HA2	2.27	0.50
1:A:28:G:O2'	1:A:29:G:H5'	2.12	0.50
4:B:101:MET:CE	4:B:108:ILE:HG21	2.41	0.50
4:B:178:ARG:HH21	4:B:196:LEU:HA	1.76	0.50
6:D:121:VAL:O	6:D:134:ASP:HA	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:E:16:THR:HG21	7:E:27:ARG:HB2	1.92	0.50
7:E:80:ILE:O	7:E:80:ILE:HD12	2.12	0.50
9:G:75:VAL:CG2	9:G:86:GLN:HB3	2.40	0.50
15:M:105:THR:O	15:M:106:ASN:C	2.48	0.50
17:O:10:LYS:HD2	17:O:10:LYS:C	2.32	0.50
19:Q:63:ARG:HG2	19:Q:64:PRO:N	2.27	0.50
19:Q:92:ARG:O	19:Q:95:TYR:HB2	2.12	0.50
1:A:1000:U:H2'	1:A:1001:A:C8	2.45	0.50
1:A:1031:G:N3	1:A:1031:G:H2'	2.26	0.50
1:A:129(A):G:O2'	1:A:130:A:OP2	2.29	0.50
1:A:1413:A:H2	1:A:1487:G:H22	1.59	0.50
1:A:802:A:H2'	1:A:803:G:H5'	1.92	0.50
1:A:938:A:N6	1:A:939:G:C6	2.80	0.50
4:B:183:PRO:HA	4:B:198:ASP:OD2	2.10	0.50
4:B:82:ARG:HG2	4:B:86:GLU:OE1	2.12	0.50
5:C:165:THR:O	5:C:165:THR:HG22	2.11	0.50
8:F:19:LEU:HD23	8:F:20:ALA:N	2.26	0.50
10:H:38:ILE:N	10:H:38:ILE:CD1	2.74	0.50
10:H:51:VAL:HG21	10:H:60:ARG:CG	2.40	0.50
12:J:25:GLU:O	12:J:27:ALA:N	2.41	0.50
12:J:80:LYS:HA	12:J:83:GLU:HB2	1.93	0.50
14:L:41:ARG:HG2	14:L:42:THR:N	2.20	0.50
17:O:61:GLY:O	17:O:64:ARG:HG2	2.11	0.50
1:A:1293:G:O2'	1:A:1294:G:H5'	2.12	0.50
1:A:168:G:O2'	1:A:169:C:H5'	2.12	0.50
1:A:359:U:H2'	1:A:360:A:H8	1.77	0.50
1:A:408:A:OP1	1:A:431:A:OP2	2.29	0.50
1:A:456:C:H2'	1:A:457:C:H6	1.76	0.50
4:B:178:ARG:HH21	4:B:196:LEU:CA	2.25	0.50
4:B:19:HIS:CD2	4:B:204:ASN:HA	2.47	0.50
4:B:19:HIS:HB2	4:B:204:ASN:HD22	1.74	0.50
5:C:139:GLN:HA	5:C:139:GLN:NE2	2.27	0.50
5:C:64:VAL:HB	5:C:99:VAL:HB	1.93	0.50
9:G:21:VAL:HG23	9:G:22:LEU:H	1.77	0.50
10:H:48:TYR:CD1	10:H:48:TYR:C	2.82	0.50
15:M:15:VAL:O	15:M:18:ALA:HB3	2.11	0.50
15:M:34:LEU:HD13	15:M:41:PRO:CA	2.38	0.50
16:N:27:CYS:HB3	16:N:43:CYS:SG	2.52	0.50
5:C:29:TYR:OH	16:N:54:PRO:HG2	2.12	0.50
17:O:5:LYS:HB2	17:O:6:GLU:OE2	2.11	0.50
19:Q:17:LYS:HA	19:Q:46:ASP:O	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1428:A:H2'	1:A:1429:C:H6	1.77	0.50
1:A:102:G:N3	1:A:151:A:H2	2.10	0.50
1:A:594:G:C2'	1:A:595:G:H5'	2.42	0.50
1:A:831:U:H2'	1:A:832:C:H6	1.77	0.50
4:B:115:LEU:HD23	4:B:115:LEU:C	2.33	0.50
6:D:150:GLU:HA	6:D:153:ARG:CG	2.42	0.50
6:D:65:ARG:HB2	6:D:75:PHE:CE1	2.47	0.50
10:H:102:ARG:O	10:H:102:ARG:HG3	2.12	0.50
1:A:694:A:H5'	13:K:53:SER:HB3	1.94	0.50
14:L:89:ARG:HG2	14:L:97:ARG:HG2	1.93	0.50
15:M:5:ALA:O	15:M:6:GLY:C	2.50	0.50
15:M:85:GLY:O	15:M:86:CYS:O	2.29	0.50
18:P:46:PRO:HG2	18:P:47:ASP:N	2.27	0.50
18:P:67:THR:HG22	18:P:68:ASP:N	2.27	0.50
20:R:43:PHE:CA	20:R:51:LEU:HD12	2.42	0.50
1:A:107:G:H2'	1:A:108:G:H5'	1.94	0.49
1:A:193:C:H4'	22:T:60:GLU:HG2	1.94	0.49
1:A:792:A:C4	1:A:794:A:C6	3.00	0.49
4:B:59:GLU:O	4:B:62:ALA:HB3	2.12	0.49
4:B:88:ALA:C	4:B:90:MET:H	2.16	0.49
6:D:35:ARG:O	6:D:36:ARG:CB	2.60	0.49
10:H:41:ARG:C	10:H:43:GLY:N	2.66	0.49
12:J:34:VAL:HG11	12:J:72:VAL:HG13	1.93	0.49
15:M:63:THR:HG23	15:M:64:TRP:CG	2.47	0.49
18:P:53:VAL:O	18:P:54:GLU:C	2.51	0.49
20:R:18:ARG:H	20:R:19:LYS:HD2	1.77	0.49
1:A:1366:C:C2	1:A:1367:C:C5	3.00	0.49
1:A:190(F):G:H4'	1:A:190(G):G:OP2	2.11	0.49
1:A:392:G:H2'	1:A:393:A:H8	1.77	0.49
5:C:23:TYR:CG	5:C:24:ALA:N	2.80	0.49
5:C:83:ARG:HH11	5:C:83:ARG:HG3	1.77	0.49
5:C:87:LEU:O	5:C:91:LEU:HB2	2.12	0.49
6:D:64:LEU:HD12	6:D:75:PHE:CZ	2.46	0.49
7:E:128:PRO:O	7:E:130:ASN:N	2.45	0.49
15:M:7:VAL:HG23	15:M:7:VAL:O	2.12	0.49
17:O:3:ILE:HD13	17:O:34:LEU:HD13	1.94	0.49
18:P:74:LEU:HD13	18:P:79:VAL:HG21	1.94	0.49
20:R:22:VAL:O	20:R:22:VAL:HG12	2.11	0.49
20:R:21:LYS:CG	20:R:57:GLY:HA3	2.42	0.49
1:A:192:U:H1'	22:T:103:GLY:HA3	1.94	0.49
22:T:60:GLU:O	22:T:63:ILE:HB	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:T:36:LEU:HD12	22:T:62:LEU:HD12	1.93	0.49
1:A:1105:A:H2'	1:A:1106:G:H8	1.78	0.49
1:A:1256:A:C5'	1:A:1258:G:H1'	2.43	0.49
1:A:1238:A:H5'	1:A:1336:C:H41	1.77	0.49
1:A:613:C:O2'	1:A:614:A:H5'	2.13	0.49
1:A:780:A:O2'	1:A:781:A:H5''	2.11	0.49
1:A:882:C:O2'	1:A:883:C:H5'	2.12	0.49
1:A:943:U:C2'	1:A:944:G:H5'	2.42	0.49
7:E:51:VAL:HB	7:E:52:PRO:CD	2.37	0.49
4:B:178:ARG:HH22	10:H:68:ARG:HH22	1.60	0.49
11:I:83:ARG:O	11:I:86:VAL:HB	2.12	0.49
8:F:97:PHE:HB2	20:R:32:ARG:HH21	1.77	0.49
21:S:7:LYS:H	21:S:7:LYS:HD3	1.78	0.49
1:A:1114:C:H2'	1:A:1115:C:C6	2.42	0.49
1:A:1300:G:O2'	1:A:1301:U:P	2.69	0.49
1:A:131:C:H2'	1:A:132:C:C6	2.48	0.49
1:A:1415:G:H2'	1:A:1416:G:H8	1.78	0.49
1:A:560:U:H5'	1:A:566:G:N2	2.27	0.49
4:B:137:ARG:HB3	4:B:137:ARG:HH11	1.78	0.49
4:B:77:ALA:HB2	4:B:211:ILE:HD12	1.94	0.49
7:E:150:ARG:NH1	7:E:150:ARG:HG3	2.26	0.49
8:F:18:GLN:O	8:F:21:LEU:HB3	2.12	0.49
1:A:737:A:H1'	8:F:73:ASN:HD21	1.77	0.49
8:F:80:ARG:NH1	8:F:80:ARG:HG2	2.27	0.49
12:J:79:ARG:O	12:J:83:GLU:HB2	2.12	0.49
13:K:27:ASN:HB2	13:K:55:LYS:HB3	1.93	0.49
14:L:24:VAL:HG13	14:L:98:TYR:HE2	1.76	0.49
17:O:78:TYR:C	17:O:80:ALA:N	2.66	0.49
19:Q:6:LEU:O	19:Q:59:ILE:N	2.45	0.49
20:R:29:PHE:CE1	20:R:31:LEU:HG	2.47	0.49
1:A:115:G:H1'	1:A:116:A:N7	2.27	0.49
1:A:1184:G:H2'	1:A:1185:G:C8	2.48	0.49
1:A:1349:A:P	11:I:118:LYS:NZ	2.85	0.49
1:A:16:A:H2'	1:A:17:U:H5'	1.94	0.49
1:A:1112:C:N3	5:C:178:LEU:N	2.61	0.49
6:D:120:LEU:HD23	6:D:125:HIS:HD2	1.77	0.49
9:G:129:GLU:OE1	9:G:131:LYS:HE2	2.12	0.49
10:H:35:ILE:HG23	10:H:111:ILE:HG21	1.93	0.49
15:M:108:ARG:N	15:M:108:ARG:HD2	2.27	0.49
15:M:13:LYS:HA	15:M:44:ARG:NE	2.27	0.49
15:M:37:THR:HG23	15:M:55:ARG:HG2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:R:21:LYS:HG2	20:R:57:GLY:HA3	1.94	0.49
22:T:93:GLU:O	22:T:94:ALA:HB2	2.12	0.49
23:V:9:ARG:NH1	23:V:22:ARG:HG3	2.27	0.49
1:A:1097:C:H2'	1:A:1098:C:C6	2.47	0.49
1:A:127:G:O2'	1:A:128:G:H5'	2.13	0.49
1:A:1491:G:C5	24:A:1545:PAR:H21	2.48	0.49
1:A:294:U:H2'	1:A:295:C:C6	2.47	0.49
1:A:409:G:H1	1:A:433:C:H5'	1.77	0.49
1:A:675:A:H1'	13:K:116:HIS:CD2	2.48	0.49
1:A:757:U:O2'	1:A:879:C:H1'	2.13	0.49
6:D:200:GLU:O	6:D:201:GLN:C	2.51	0.49
7:E:20:GLN:O	7:E:21:ALA:C	2.51	0.49
9:G:37:ASN:O	9:G:40:ALA:HB3	2.13	0.49
11:I:4:TYR:CZ	11:I:88:TYR:HD1	2.30	0.49
14:L:50:SER:O	14:L:51:ALA:HB2	2.13	0.49
15:M:33:ALA:C	15:M:35:GLU:H	2.16	0.49
15:M:91:ARG:CB	15:M:98:VAL:HG22	2.43	0.49
20:R:57:GLY:O	20:R:58:LEU:HD23	2.13	0.49
1:A:1014:A:C2	1:A:1219:U:H1'	2.46	0.49
1:A:1486:G:H2'	1:A:1487:G:O4'	2.13	0.49
1:A:754:C:H3'	1:A:754:C:O2	2.12	0.49
4:B:14:GLY:C	4:B:15:VAL:HG22	2.32	0.49
5:C:179:ARG:CG	5:C:180:ALA:N	2.52	0.49
10:H:17:THR:HB	10:H:78:GLN:OE1	2.13	0.49
12:J:12:ASP:HB3	12:J:15:THR:HG22	1.94	0.49
14:L:110:VAL:CG1	14:L:111:LYS:N	2.75	0.49
16:N:37:PHE:CE2	16:N:56:VAL:HG21	2.47	0.49
17:O:39:LEU:CD2	17:O:56:LEU:HB2	2.42	0.49
1:A:1101:A:C4'	1:A:1102:A:O5'	2.58	0.49
1:A:1109:C:H2'	1:A:1110:A:O4'	2.12	0.49
1:A:1140:C:C6	1:A:1141:C:H5	2.30	0.49
1:A:1285:A:H1'	1:A:1286:A:OP2	2.13	0.49
1:A:349:A:H2'	1:A:350:G:O5'	2.12	0.49
1:A:488:C:H6	1:A:488:C:O5'	1.96	0.49
1:A:840:C:C4'	1:A:841:U:OP1	2.61	0.49
5:C:30:ARG:HH11	5:C:30:ARG:HB2	1.77	0.49
6:D:30:LYS:O	6:D:32:ALA:N	2.41	0.49
7:E:43:LEU:N	7:E:136:MET:HE2	2.28	0.49
7:E:77:PRO:O	7:E:78:HIS:CB	2.61	0.49
14:L:86:ARG:O	14:L:87:GLY:O	2.31	0.49
16:N:21:TYR:HD2	16:N:22:THR:O	1.96	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:750:G:C2	17:O:23:GLY:HA3	2.48	0.49
19:Q:3:LYS:HB3	19:Q:60:ILE:CD1	2.43	0.49
21:S:33:THR:HG22	21:S:35:SER:H	1.78	0.49
22:T:39:LYS:HD3	22:T:55:ILE:HG21	1.94	0.49
1:A:1424:C:H2'	1:A:1425:U:C6	2.48	0.49
1:A:625:G:H2'	1:A:626:U:H6	1.77	0.49
1:A:877:C:O2'	1:A:878:G:H5'	2.12	0.49
4:B:204:ASN:O	4:B:206:ASP:N	2.45	0.49
4:B:77:ALA:CB	4:B:211:ILE:HD13	2.43	0.49
5:C:204:LEU:N	5:C:204:LEU:HD12	2.28	0.49
5:C:36:ASP:N	5:C:36:ASP:OD2	2.44	0.49
5:C:58:GLU:O	5:C:64:VAL:HA	2.11	0.49
5:C:64:VAL:O	5:C:99:VAL:HB	2.13	0.49
6:D:105:VAL:HG12	6:D:106:TYR:N	2.28	0.49
7:E:144:THR:HG22	7:E:146:ALA:N	2.28	0.49
12:J:25:GLU:HB3	12:J:29:ARG:NE	2.23	0.49
12:J:39:PRO:O	12:J:40:LEU:HB2	2.12	0.49
14:L:39:VAL:H	14:L:57:LYS:HB2	1.78	0.49
1:A:974:A:P	16:N:41:ARG:HH12	2.36	0.49
17:O:14:GLU:HG3	17:O:15:PHE:CD1	2.47	0.49
19:Q:45:HIS:CD2	19:Q:47:PRO:HG3	2.48	0.49
1:A:1157:A:H4'	1:A:1158:C:O5'	2.13	0.49
1:A:1291:G:H4'	11:I:38:GLN:O	2.13	0.49
1:A:176:C:OP1	22:T:29:LYS:HE2	2.12	0.49
1:A:448:A:O2'	1:A:449:C:H5'	2.12	0.49
1:A:460:A:N6	1:A:463:A:N6	2.61	0.49
1:A:98:U:O2'	1:A:99:C:H5'	2.12	0.49
6:D:64:LEU:O	6:D:64:LEU:HD13	2.13	0.49
7:E:102:ALA:HB1	7:E:120:THR:HG21	1.93	0.49
7:E:16:THR:CG2	7:E:27:ARG:HB2	2.42	0.49
1:A:1250:A:H4'	11:I:68:GLY:CA	2.42	0.49
12:J:4:ILE:HB	12:J:74:ILE:HG13	1.95	0.49
1:A:953:G:N7	15:M:104:ARG:NH2	2.58	0.49
15:M:13:LYS:HD3	15:M:14:ARG:N	2.28	0.49
17:O:50:HIS:O	17:O:53:HIS:HB3	2.13	0.49
8:F:60:PHE:CE2	20:R:78:LEU:HD21	2.48	0.49
1:A:1003:G:H2'	1:A:1003:G:N3	2.28	0.48
1:A:1042:G:O2'	1:A:1043:C:H5'	2.13	0.48
1:A:1054:C:C2'	1:A:1055:A:H5''	2.42	0.48
1:A:1056:U:H5'	5:C:163:ALA:CB	2.42	0.48
1:A:1091:U:O2	1:A:1093:A:C8	2.66	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1347:G:H2'	1:A:1373:G:H1	1.78	0.48
1:A:363:A:OP1	14:L:33:ARG:HD3	2.12	0.48
1:A:600:C:H2'	1:A:601:C:H6	1.77	0.48
1:A:781:A:OP1	1:A:1523:G:H5'	2.12	0.48
1:A:831:U:O2'	1:A:832:C:H5'	2.13	0.48
6:D:165:MET:O	6:D:168:ARG:HB2	2.13	0.48
6:D:108:LEU:HD21	6:D:174:LEU:HD22	1.95	0.48
12:J:25:GLU:O	12:J:29:ARG:HG3	2.13	0.48
12:J:69:ASN:O	12:J:70:ARG:HD3	2.13	0.48
15:M:3:ARG:HH22	15:M:7:VAL:HG12	1.78	0.48
17:O:76:GLU:HA	17:O:79:ARG:HE	1.77	0.48
22:T:73:HIS:O	22:T:74:LYS:HB2	2.12	0.48
22:T:75:ASN:O	22:T:78:ALA:HB3	2.13	0.48
1:A:1003:G:H1	1:A:1004:A:HO2'	1.60	0.48
1:A:1031:G:H4'	1:A:1032:G:C8	2.48	0.48
1:A:1356:G:H2'	1:A:1357:A:H8	1.73	0.48
1:A:1423:G:H2'	1:A:1424:C:H6	1.78	0.48
1:A:1521:G:H2'	1:A:1522:U:H6	1.78	0.48
1:A:190(K):G:C2'	1:A:190(L):U:H5''	2.44	0.48
1:A:491:G:O2'	1:A:492:G:H5'	2.13	0.48
1:A:718:G:H5'	1:A:719:C:OP2	2.13	0.48
1:A:760:G:H1	19:Q:105:ALA:CA	2.26	0.48
1:A:848:C:H2'	1:A:849:C:H6	1.77	0.48
1:A:934:C:C4	1:A:1345:U:C5	3.02	0.48
5:C:139:GLN:CA	5:C:139:GLN:HE21	2.26	0.48
5:C:157:ILE:HD11	5:C:166:GLU:HB2	1.95	0.48
6:D:38:TYR:N	6:D:38:TYR:CD2	2.80	0.48
9:G:48:LYS:O	9:G:51:GLN:HB2	2.12	0.48
16:N:23:ARG:NH1	16:N:30:ALA:HB2	2.28	0.48
1:A:1294:G:O2'	1:A:1295:G:H5'	2.13	0.48
1:A:1237:C:H4'	1:A:1334:G:N2	2.28	0.48
1:A:409:G:H2'	1:A:431:A:C8	2.49	0.48
1:A:519:C:H2'	1:A:520:A:O4'	2.14	0.48
1:A:600:C:H2'	1:A:601:C:C6	2.48	0.48
1:A:954:G:C4	1:A:955:U:C6	3.02	0.48
4:B:77:ALA:HB2	4:B:211:ILE:CD1	2.43	0.48
7:E:24:ARG:HB3	7:E:24:ARG:NH1	2.28	0.48
7:E:36:ASP:O	7:E:37:ARG:HB2	2.13	0.48
9:G:115:ARG:HB2	9:G:118:VAL:CG2	2.43	0.48
11:I:114:TYR:CD1	11:I:114:TYR:N	2.62	0.48
17:O:66:LEU:O	17:O:69:TYR:HB3	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:P:6:LEU:HD23	18:P:17:TYR:CD1	2.48	0.48
20:R:36:ASN:ND2	20:R:38:GLU:CD	2.67	0.48
1:A:1053:G:C4	1:A:1199:U:C5	3.01	0.48
1:A:1489:G:C3'	1:A:1490:C:H5''	2.42	0.48
1:A:942:G:N3	1:A:943:U:C6	2.81	0.48
1:A:991:U:O2	1:A:993:G:H8	1.97	0.48
4:B:20:GLU:O	4:B:39:ILE:CG2	2.58	0.48
5:C:127:ARG:HG2	5:C:127:ARG:O	2.12	0.48
5:C:153:VAL:CG1	5:C:154:SER:N	2.76	0.48
5:C:60:ALA:O	5:C:61:ALA:HB2	2.12	0.48
10:H:112:LEU:HG	10:H:112:LEU:O	2.13	0.48
10:H:60:ARG:NH1	10:H:60:ARG:CG	2.75	0.48
10:H:63:LEU:N	10:H:63:LEU:HD22	2.28	0.48
10:H:81:HIS:N	10:H:81:HIS:ND1	2.60	0.48
11:I:117:HIS:C	11:I:118:LYS:HG3	2.33	0.48
11:I:3:GLN:HB2	11:I:20:ARG:HG2	1.95	0.48
13:K:52:GLY:H	13:K:55:LYS:HE2	1.77	0.48
14:L:47:LYS:CG	14:L:48:PRO:HD3	2.43	0.48
1:A:1320:C:N4	21:S:37:ARG:HD3	2.29	0.48
22:T:41:ILE:O	22:T:45:GLN:HB2	2.13	0.48
1:A:1104:G:P	4:B:111:ARG:HD2	2.54	0.48
1:A:1049:U:H1'	1:A:1201:A:N7	2.28	0.48
1:A:445:G:H2'	1:A:446:G:C8	2.47	0.48
5:C:28:GLN:O	5:C:31:HIS:N	2.46	0.48
6:D:22:LYS:O	6:D:23:GLY:C	2.51	0.48
8:F:38:GLU:HB2	8:F:64:GLN:HG2	1.96	0.48
8:F:63:TYR:CD1	8:F:63:TYR:N	2.82	0.48
15:M:56:LEU:C	15:M:56:LEU:CD2	2.82	0.48
1:A:1226:C:H5'	15:M:96:LEU:HD13	1.96	0.48
16:N:26:ARG:NH2	16:N:47:LEU:HD21	2.28	0.48
3:X:31:A:H2'	3:X:32:C:C6	2.48	0.48
1:A:1292:U:H2'	1:A:1293:G:H8	1.79	0.48
1:A:285:G:O2'	1:A:286:G:H5'	2.14	0.48
1:A:475:G:N2	1:A:476:G:C8	2.82	0.48
4:B:122:PHE:HA	4:B:127:ILE:CG2	2.44	0.48
4:B:184:VAL:N	4:B:198:ASP:OD2	2.34	0.48
5:C:40:ARG:HB3	5:C:44:GLU:HG3	1.96	0.48
20:R:87:ARG:O	20:R:88:LYS:HB3	2.13	0.48
21:S:17:GLU:HA	21:S:20:LEU:CD2	2.43	0.48
1:A:1029:C:H1'	1:A:1033:G:N2	2.29	0.48
1:A:1064:G:H22	1:A:1190:G:H2'	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1207:G:H2'	1:A:1208:C:H6	1.79	0.48
1:A:1221:G:C2'	1:A:1222:G:H5'	2.44	0.48
1:A:175:C:H2'	1:A:176:C:H6	1.78	0.48
1:A:129(A):G:O2'	1:A:190(E):U:H5''	2.14	0.48
1:A:408:A:H4'	1:A:409:G:OP1	2.14	0.48
1:A:486:U:O2'	1:A:487:A:H5'	2.14	0.48
1:A:604:G:O2'	1:A:605:U:H5'	2.13	0.48
7:E:144:THR:HG22	7:E:146:ALA:H	1.78	0.48
11:I:114:TYR:HD2	12:J:60:ARG:HB2	1.72	0.48
15:M:40:ASN:HD22	15:M:41:PRO:N	2.11	0.48
15:M:91:ARG:HH22	15:M:103:THR:HG21	1.79	0.48
1:A:1320:C:H41	21:S:37:ARG:HD3	1.78	0.48
21:S:71:LEU:C	21:S:73:GLU:H	2.17	0.48
1:A:1117:G:O3'	11:I:104:ARG:HD2	2.14	0.48
1:A:56:U:H2'	1:A:57:G:C8	2.49	0.48
1:A:797:C:H2'	1:A:798:G:H8	1.79	0.48
4:B:9:GLU:OE2	4:B:213:LEU:HD11	2.13	0.48
9:G:51:GLN:OE1	9:G:51:GLN:HA	2.14	0.48
10:H:36:LEU:HD12	10:H:59:LEU:HD13	1.94	0.48
11:I:125:TYR:HE1	11:I:128:ARG:HB3	1.79	0.48
12:J:48:THR:HG23	12:J:62:HIS:NE2	2.29	0.48
14:L:56:ALA:HB2	14:L:70:ILE:HD11	1.95	0.48
1:A:958:A:C8	21:S:55:LYS:HD2	2.48	0.48
1:A:1380:U:O2'	1:A:1381:U:OP2	2.28	0.48
1:A:112:G:H4'	1:A:389:A:H5''	1.96	0.48
1:A:458:C:H42	1:A:463:A:C3'	2.23	0.48
1:A:731:G:O2'	1:A:732:C:H5'	2.14	0.48
1:A:861:G:O2'	1:A:862:C:H5'	2.14	0.48
1:A:95:U:O2'	1:A:96:G:H5'	2.14	0.48
1:A:994:A:H2'	1:A:994:A:N3	2.29	0.48
4:B:54:THR:O	4:B:57:PHE:HB3	2.14	0.48
5:C:139:GLN:O	5:C:142:MET:N	2.46	0.48
14:L:32:PHE:HB3	14:L:84:LEU:HD11	1.95	0.48
15:M:4:ILE:CG2	15:M:5:ALA:N	2.70	0.48
15:M:88:ARG:HG3	15:M:98:VAL:CG1	2.42	0.48
19:Q:80:GLY:O	19:Q:81:ARG:HB3	2.14	0.48
1:A:1375:A:C2'	1:A:1376:U:H5'	2.44	0.48
1:A:1461:G:O2'	1:A:1462:G:H5'	2.14	0.48
1:A:176:C:O2'	1:A:177:C:H5'	2.13	0.48
1:A:353:A:H8	1:A:353:A:C5'	2.27	0.48
1:A:408:A:H4'	1:A:429:U:H1'	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:559:A:H4'	1:A:560:U:O3'	2.13	0.48
1:A:991:U:C4	1:A:1212:U:H1'	2.49	0.48
4:B:107:THR:O	4:B:110:GLN:N	2.41	0.48
4:B:46:LYS:HA	4:B:49:GLU:HB2	1.96	0.48
6:D:38:TYR:HD2	6:D:38:TYR:N	2.12	0.48
11:I:42:ARG:O	11:I:43:ALA:C	2.52	0.48
11:I:28:VAL:HA	11:I:63:ILE:O	2.14	0.48
11:I:95:LYS:C	11:I:98:PRO:HD2	2.34	0.48
12:J:9:ARG:CB	12:J:9:ARG:HH11	2.27	0.48
16:N:41:ARG:HG3	16:N:42:ILE:N	2.28	0.48
17:O:33:THR:HG23	17:O:63:ARG:HH12	1.78	0.48
18:P:19:ILE:HG22	18:P:36:ILE:CG1	2.44	0.48
1:A:1248:A:H2'	1:A:1249:C:C6	2.49	0.47
1:A:163:C:H2'	1:A:164:U:O4'	2.14	0.47
1:A:312:C:H2'	1:A:313:A:H8	1.78	0.47
14:L:104:VAL:O	14:L:105:TYR:HB2	2.14	0.47
14:L:120:TYR:O	14:L:122:THR:HG23	2.14	0.47
15:M:13:LYS:O	15:M:14:ARG:C	2.52	0.47
15:M:31:LYS:O	15:M:35:GLU:HB2	2.13	0.47
15:M:37:THR:HG22	15:M:55:ARG:HD2	1.96	0.47
16:N:3:ARG:O	16:N:7:ILE:HG13	2.13	0.47
16:N:47:LEU:O	16:N:48:ALA:C	2.52	0.47
1:A:760:G:N2	19:Q:105:ALA:N	2.50	0.47
21:S:63:THR:HG22	21:S:65:ASN:H	1.78	0.47
1:A:1007:C:H2'	1:A:1008:C:C6	2.49	0.47
1:A:1060:C:C2	1:A:1198:G:C2	3.02	0.47
1:A:1330:U:OP1	15:M:23:TYR:O	2.33	0.47
1:A:1443:G:C5'	1:A:1446:A:H5'	2.36	0.47
1:A:19:C:H5''	7:E:86:ALA:CB	2.44	0.47
1:A:335:C:H2'	1:A:336:C:C6	2.41	0.47
1:A:459:G:H3'	1:A:460:A:C5'	2.44	0.47
1:A:687:A:H4'	1:A:688:G:O5'	2.14	0.47
5:C:178:LEU:O	5:C:179:ARG:HB2	2.14	0.47
8:F:96:PRO:O	8:F:98:LEU:N	2.46	0.47
11:I:55:ALA:O	11:I:57:GLY:N	2.47	0.47
12:J:25:GLU:CB	12:J:29:ARG:HH21	2.26	0.47
5:C:58:GLU:HB3	12:J:92:THR:CG2	2.44	0.47
14:L:7:ILE:O	14:L:11:VAL:HG23	2.14	0.47
14:L:25:PRO:C	14:L:27:LEU:N	2.59	0.47
19:Q:90:ILE:O	19:Q:93:GLN:HB3	2.14	0.47
1:A:1060:C:C2	1:A:1198:G:N2	2.82	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1113:C:O2'	1:A:1114:C:H5'	2.15	0.47
1:A:1196:U:H4'	1:A:1197:G:OP2	2.14	0.47
1:A:1227:A:H3'	1:A:1227:A:H8	1.79	0.47
1:A:448:A:H2'	1:A:449:C:C6	2.49	0.47
1:A:474:G:OP1	1:A:475:G:C8	2.67	0.47
1:A:828:A:H2'	1:A:829:G:O4'	2.13	0.47
1:A:977:A:O2'	1:A:979:C:OP2	2.32	0.47
4:B:216:SER:O	4:B:219:VAL:HG23	2.14	0.47
5:C:87:LEU:C	5:C:89:GLU:H	2.16	0.47
7:E:144:THR:CB	7:E:147:ASP:OD1	2.62	0.47
10:H:104:ARG:NH2	10:H:138:TRP:CZ3	2.82	0.47
11:I:5:TYR:HB2	11:I:18:PHE:CD2	2.48	0.47
13:K:33:THR:HB	13:K:38:ASN:O	2.13	0.47
17:O:88:ARG:HE	17:O:88:ARG:H	1.63	0.47
20:R:37:VAL:HG12	20:R:41:LYS:CE	2.43	0.47
21:S:38:SER:OG	21:S:71:LEU:HD13	2.14	0.47
21:S:4:SER:O	21:S:5:LEU:CB	2.63	0.47
22:T:10:LEU:O	22:T:12:ALA:N	2.47	0.47
1:A:201:C:O5'	1:A:216:G:N2	2.47	0.47
1:A:321:A:H62	1:A:328:C:H1'	1.79	0.47
1:A:356:A:O2'	1:A:357:G:H5'	2.14	0.47
1:A:408:A:C4'	1:A:429:U:O2'	2.62	0.47
1:A:458:C:N4	1:A:463:A:H3'	2.25	0.47
6:D:3:ARG:HE	6:D:3:ARG:HA	1.79	0.47
7:E:128:PRO:O	7:E:129:ILE:C	2.52	0.47
8:F:67:MET:CE	8:F:72:VAL:HA	2.45	0.47
8:F:67:MET:HE1	8:F:72:VAL:HG13	1.95	0.47
9:G:62:PHE:HA	9:G:124:LEU:CD2	2.45	0.47
12:J:10:GLY:H	12:J:16:LEU:HD11	1.79	0.47
12:J:3:LYS:C	12:J:4:ILE:HG13	2.35	0.47
14:L:71:PRO:HB2	14:L:120:TYR:HE2	1.78	0.47
14:L:9:GLN:O	14:L:10:LEU:C	2.53	0.47
16:N:28:GLY:O	16:N:30:ALA:N	2.47	0.47
21:S:40:ILE:HD13	21:S:62:ILE:HG13	1.95	0.47
1:A:1090:U:H2'	1:A:1091:U:C6	2.49	0.47
1:A:1195:C:H2'	1:A:1197:G:H5'	1.95	0.47
1:A:279:A:OP2	19:Q:95:TYR:OH	2.26	0.47
5:C:65:ALA:HB1	5:C:67:THR:OG1	2.13	0.47
6:D:45:GLN:O	6:D:46:LYS:C	2.51	0.47
10:H:6:ILE:HD12	10:H:35:ILE:CD1	2.45	0.47
12:J:34:VAL:HG22	12:J:74:ILE:CG2	2.35	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:28:LYS:O	14:L:30:ALA:N	2.47	0.47
23:V:6:ARG:CD	23:V:15:ARG:HH12	2.25	0.47
1:A:1287:A:H2'	1:A:1288:A:C8	2.50	0.47
1:A:1350:A:C2	1:A:1351:U:C2	3.02	0.47
1:A:1474:G:O2'	1:A:1475:G:H5'	2.15	0.47
1:A:191:G:N2	22:T:85:MET:HE1	2.30	0.47
1:A:408:A:H5''	6:D:22:LYS:NZ	2.30	0.47
1:A:839:U:C2'	1:A:839:U:O2	2.63	0.47
1:A:865:A:C6	1:A:866:C:C4	3.02	0.47
1:A:883:C:O2'	1:A:884:U:H5'	2.15	0.47
1:A:1104:G:OP1	4:B:111:ARG:HD2	2.13	0.47
5:C:5:ILE:HD13	5:C:10:PHE:HB2	1.96	0.47
5:C:66:VAL:HG12	5:C:66:VAL:O	2.14	0.47
6:D:31:CYS:O	6:D:33:MET:N	2.48	0.47
11:I:45:ALA:O	11:I:46:ALA:C	2.53	0.47
12:J:8:LEU:HD12	12:J:20:ALA:HB1	1.96	0.47
11:I:114:TYR:HD2	12:J:60:ARG:HD2	1.80	0.47
13:K:27:ASN:OD1	13:K:28:THR:N	2.48	0.47
16:N:32:SER:HB2	16:N:41:ARG:HB3	1.96	0.47
18:P:22:THR:HA	18:P:33:ILE:CD1	2.45	0.47
1:A:1197:G:H3'	1:A:1197:G:OP1	2.14	0.47
1:A:1228:C:H4'	15:M:116:THR:HA	1.95	0.47
1:A:1251:A:H1'	1:A:1369:C:O2'	2.13	0.47
1:A:1441:G:H4'	1:A:1442:G:N1	2.29	0.47
1:A:1405:G:P	24:A:1545:PAR:O34	2.73	0.47
1:A:370:C:C2'	1:A:371:G:H5'	2.45	0.47
1:A:397:A:N3	1:A:397:A:H3'	2.29	0.47
1:A:743:U:H2'	1:A:744:C:C6	2.50	0.47
1:A:864:A:H2'	1:A:865:A:C8	2.49	0.47
5:C:147:LYS:HE2	5:C:205:GLY:CA	2.45	0.47
5:C:33:LEU:HD21	16:N:53:LEU:HD21	1.97	0.47
9:G:112:PRO:HD2	9:G:113:GLU:OE2	2.13	0.47
10:H:121:ASP:HB2	10:H:125:ARG:NH2	2.25	0.47
17:O:46:HIS:N	17:O:46:HIS:ND1	2.63	0.47
22:T:57:ARG:HB2	22:T:57:ARG:NH1	2.29	0.47
1:A:1300:G:C2'	1:A:1301:U:OP2	2.62	0.47
1:A:1358:U:H3'	1:A:1359:C:C6	2.49	0.47
1:A:409:G:P	1:A:429:U:O2	2.72	0.47
1:A:708:C:O2'	1:A:709:G:H5'	2.15	0.47
1:A:865:A:C5	1:A:866:C:C4	3.02	0.47
1:A:897:C:H5''	19:Q:101:ARG:NH2	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:15:GLU:CG	6:D:63:LYS:HG3	2.45	0.47
7:E:121:LYS:HE3	7:E:123:LEU:CD2	2.44	0.47
9:G:117:ALA:HA	9:G:120:ILE:HD13	1.97	0.47
9:G:87:VAL:HG13	9:G:88:PRO:HD2	1.96	0.47
11:I:113:LYS:N	11:I:113:LYS:CD	2.78	0.47
11:I:127:LYS:HE3	11:I:127:LYS:CA	2.45	0.47
11:I:63:ILE:HD13	11:I:77:ILE:HG23	1.97	0.47
12:J:44:VAL:HG21	12:J:66:ARG:HH21	1.79	0.47
14:L:40:VAL:HG21	14:L:77:LEU:O	2.13	0.47
15:M:19:LEU:O	15:M:22:ILE:HG13	2.15	0.47
17:O:31:LEU:O	17:O:34:LEU:HB3	2.15	0.47
18:P:53:VAL:HG22	18:P:54:GLU:N	2.29	0.47
22:T:22:ARG:O	22:T:25:ARG:N	2.48	0.47
22:T:53:LEU:O	22:T:56:MET:N	2.48	0.47
1:A:1345:U:C2	1:A:1377:A:C2	3.03	0.47
1:A:1495:U:H2'	1:A:1496:C:H6	1.78	0.47
1:A:603:U:H2'	1:A:604:G:H8	1.80	0.47
4:B:16:HIS:NE2	4:B:214:ILE:CG1	2.78	0.47
4:B:71:VAL:CG2	4:B:164:VAL:HG22	2.45	0.47
7:E:21:ALA:O	7:E:23:GLY:N	2.47	0.47
7:E:57:LYS:HG2	7:E:61:TYR:HE2	1.79	0.47
8:F:76:ALA:O	8:F:80:ARG:HG3	2.15	0.47
10:H:1:MET:HG2	10:H:2:LEU:N	2.30	0.47
11:I:45:ALA:O	11:I:48:GLU:HB2	2.15	0.47
1:A:1296:C:H5''	15:M:14:ARG:HD2	1.97	0.47
15:M:62:ASN:O	15:M:63:THR:CB	2.61	0.47
20:R:53:ARG:HH11	20:R:59:SER:C	2.19	0.47
20:R:47:THR:HG23	20:R:83:GLU:H	1.79	0.47
21:S:4:SER:O	21:S:5:LEU:HG	2.15	0.47
1:A:1018:C:H6	1:A:1018:C:O5'	1.98	0.47
1:A:1154:G:H2'	1:A:1155:G:C8	2.40	0.47
1:A:325:A:H2'	1:A:326:G:O4'	2.14	0.47
1:A:428:G:OP2	6:D:7:PRO:HG3	2.14	0.47
1:A:848:C:H2'	1:A:849:C:C6	2.50	0.47
1:A:968:A:OP2	11:I:128:ARG:NH2	2.48	0.47
4:B:207:ALA:O	4:B:211:ILE:HG13	2.14	0.47
5:C:172:ARG:NH1	5:C:203:PHE:CE2	2.82	0.47
5:C:92:ALA:HA	5:C:95:THR:OG1	2.15	0.47
9:G:57:GLU:O	9:G:60:LYS:HB3	2.15	0.47
10:H:82:HIS:O	10:H:83:ILE:CB	2.63	0.47
11:I:8:GLY:CA	11:I:79:LEU:HB3	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:25:GLU:HB2	12:J:29:ARG:HH21	1.79	0.47
18:P:20:VAL:HG23	18:P:35:LYS:HA	1.96	0.47
19:Q:27:PHE:CE1	19:Q:36:ILE:HD11	2.50	0.47
1:A:1126:U:OP2	1:A:1281:U:O2	2.33	0.47
1:A:1480:G:H2'	1:A:1481:U:H6	1.79	0.47
1:A:459:G:C6	1:A:461:C:H5''	2.49	0.47
1:A:908:A:H2'	1:A:909:A:H8	1.79	0.47
5:C:137:ALA:O	5:C:141:VAL:HG23	2.14	0.47
5:C:172:ARG:HB3	5:C:172:ARG:HH11	1.80	0.47
5:C:196:LEU:N	5:C:196:LEU:CD2	2.71	0.47
1:A:1190:G:H3'	5:C:3:ASN:OD1	2.14	0.47
6:D:98:GLU:HG2	6:D:189:PRO:HG3	1.97	0.47
7:E:57:LYS:HB2	7:E:57:LYS:HE3	1.67	0.47
8:F:75:LEU:O	8:F:78:GLU:HB3	2.15	0.47
9:G:152:ALA:C	9:G:154:TYR:N	2.67	0.47
9:G:78:ARG:HB2	9:G:156:TRP:CH2	2.50	0.47
10:H:4:ASP:OD2	10:H:89:PRO:HD3	2.14	0.47
11:I:78:LYS:HE3	11:I:101:PHE:CD2	2.49	0.47
15:M:19:LEU:HD21	15:M:56:LEU:HD21	1.97	0.47
1:A:227:G:O2'	18:P:62:VAL:HG11	2.15	0.47
19:Q:52:LYS:N	19:Q:52:LYS:HD2	2.30	0.47
20:R:87:ARG:HH11	20:R:87:ARG:HG3	1.80	0.47
1:A:1290:G:H2'	1:A:1291:G:C8	2.50	0.46
1:A:836:G:C6	1:A:851:G:C6	3.03	0.46
4:B:120:ALA:C	4:B:122:PHE:H	2.18	0.46
7:E:24:ARG:CB	7:E:24:ARG:HH11	2.28	0.46
9:G:38:LEU:C	9:G:40:ALA:N	2.68	0.46
11:I:92:TYR:O	11:I:93:ARG:C	2.53	0.46
13:K:68:ALA:O	13:K:72:ALA:HB2	2.15	0.46
14:L:39:VAL:HA	14:L:79:GLU:OE1	2.15	0.46
15:M:78:ILE:O	15:M:81:LEU:HD23	2.15	0.46
17:O:87:ILE:HG22	17:O:88:ARG:HH21	1.80	0.46
20:R:53:ARG:O	20:R:57:GLY:N	2.42	0.46
21:S:13:ASP:OD2	21:S:14:HIS:N	2.46	0.46
21:S:15:LEU:HD23	21:S:33:THR:HG21	1.97	0.46
21:S:63:THR:CG2	21:S:64:GLU:N	2.78	0.46
15:M:94:ARG:NH1	21:S:81:ARG:HD3	2.30	0.46
22:T:56:MET:HG2	22:T:84:LEU:HD11	1.97	0.46
1:A:1329:A:N7	23:V:7:ARG:NH2	2.63	0.46
1:A:1349:A:H2'	1:A:1350:A:C8	2.37	0.46
1:A:448:A:OP2	1:A:485:G:N2	2.37	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:657:G:O2'	1:A:658:G:H5'	2.15	0.46
1:A:697:U:H2'	1:A:698:G:H5'	1.97	0.46
1:A:806:C:O2'	1:A:807:A:H5'	2.16	0.46
4:B:25:ASN:ND2	4:B:25:ASN:C	2.68	0.46
6:D:98:GLU:OE2	6:D:107:ARG:NE	2.47	0.46
9:G:43:PHE:O	9:G:46:ALA:HB3	2.15	0.46
14:L:28:LYS:HG2	14:L:28:LYS:O	2.15	0.46
14:L:78:GLN:O	14:L:80:HIS:N	2.45	0.46
19:Q:33:GLY:O	19:Q:34:LYS:C	2.53	0.46
20:R:53:ARG:CG	20:R:63:GLN:HG2	2.44	0.46
1:A:1055:A:C2	1:A:1056:U:H1'	2.50	0.46
1:A:216:G:H5'	1:A:217:C:P	2.55	0.46
1:A:539:A:H2'	1:A:540:G:H8	1.79	0.46
1:A:556:C:C2'	1:A:557:G:H5'	2.46	0.46
1:A:570:G:N2	1:A:571:U:C2	2.83	0.46
1:A:791:G:C2'	1:A:792:A:C5'	2.92	0.46
1:A:858:G:O2'	1:A:859:A:H5'	2.16	0.46
4:B:144:ARG:HA	4:B:147:LYS:CE	2.45	0.46
4:B:68:ILE:HG22	4:B:69:LEU:N	2.30	0.46
9:G:44:TYR:O	9:G:46:ALA:N	2.48	0.46
10:H:104:ARG:CZ	10:H:138:TRP:CH2	2.98	0.46
18:P:17:TYR:HE1	18:P:41:PRO:HG3	1.80	0.46
19:Q:81:ARG:HG3	19:Q:81:ARG:O	2.16	0.46
20:R:42:ARG:HH11	20:R:42:ARG:HG3	1.80	0.46
22:T:72:LEU:O	22:T:73:HIS:C	2.52	0.46
1:A:1097:C:O2'	1:A:1168:A:H1'	2.15	0.46
1:A:1283:G:O2'	1:A:1284:C:H5'	2.15	0.46
1:A:217:C:P	1:A:461:C:H41	2.38	0.46
1:A:390:C:O3'	18:P:28:ARG:NH2	2.48	0.46
11:I:112:LYS:C	11:I:112:LYS:HD3	2.35	0.46
13:K:40:ILE:HG22	13:K:41:THR:OG1	2.15	0.46
15:M:39:ILE:HD12	15:M:56:LEU:HD12	1.98	0.46
15:M:53:VAL:HG12	15:M:57:ARG:HH21	1.80	0.46
18:P:75:ARG:NH1	18:P:82:GLN:HE22	2.13	0.46
19:Q:25:ARG:HG2	19:Q:25:ARG:O	2.16	0.46
21:S:11:VAL:HG22	21:S:39:THR:H	1.81	0.46
1:A:1036:G:O2'	1:A:1037:C:H5'	2.16	0.46
1:A:1043:C:O2'	1:A:1044:A:H5'	2.15	0.46
1:A:1057:G:C2'	1:A:1058:G:H5'	2.45	0.46
1:A:1072:G:H2'	1:A:1073:U:H6	1.81	0.46
1:A:1224:G:H1	1:A:1362:C:H42	1.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1438:G:H2'	1:A:1439:C:C6	2.51	0.46
1:A:284:G:H2'	1:A:285:G:H8	1.80	0.46
1:A:706:A:H1'	13:K:29:ILE:CD1	2.45	0.46
1:A:84:U:H2'	1:A:88:A:H8	1.78	0.46
1:A:967:C:O3'	11:I:128:ARG:CZ	2.64	0.46
6:D:207:TYR:C	6:D:209:ARG:H	2.18	0.46
7:E:43:LEU:HD23	7:E:44:GLY:H	1.81	0.46
9:G:16:LEU:H	9:G:16:LEU:CD2	2.22	0.46
11:I:104:ARG:O	11:I:105:ASP:C	2.54	0.46
13:K:17:GLY:O	13:K:80:VAL:HA	2.16	0.46
15:M:63:THR:HG23	15:M:64:TRP:CD2	2.50	0.46
17:O:17:ARG:NH1	17:O:17:ARG:HG3	2.29	0.46
17:O:78:TYR:C	17:O:80:ALA:H	2.19	0.46
1:A:333:G:C4'	22:T:16:HIS:CD2	2.98	0.46
22:T:87:LYS:O	22:T:91:LEU:HG	2.16	0.46
1:A:1104:G:H2'	1:A:1105:A:C8	2.50	0.46
1:A:1120:G:H2'	1:A:1121:U:H6	1.81	0.46
1:A:1522:U:H2'	1:A:1523:G:H8	1.79	0.46
1:A:424:G:N3	1:A:424:G:C3'	2.77	0.46
1:A:625:G:O2'	1:A:626:U:H5'	2.15	0.46
1:A:647:C:H2'	1:A:648:A:C8	2.51	0.46
1:A:814:A:N7	1:A:816:A:C4	2.83	0.46
1:A:855:G:H2'	1:A:856:C:C6	2.51	0.46
4:B:78:GLN:HG2	4:B:94:ASN:ND2	2.30	0.46
5:C:28:GLN:O	5:C:29:TYR:C	2.53	0.46
8:F:21:LEU:O	8:F:24:GLU:HB3	2.15	0.46
9:G:103:TRP:O	9:G:104:LEU:C	2.54	0.46
9:G:135:VAL:O	9:G:138:LYS:HB3	2.16	0.46
9:G:15:ASP:OD2	9:G:16:LEU:N	2.48	0.46
10:H:35:ILE:HG23	10:H:111:ILE:HD13	1.97	0.46
10:H:64:LYS:O	10:H:79:VAL:HG23	2.16	0.46
19:Q:44:ALA:HB1	19:Q:73:VAL:HG22	1.98	0.46
22:T:45:GLN:HA	22:T:91:LEU:HD13	1.98	0.46
1:A:1060:C:H4'	12:J:52:GLY:N	2.31	0.46
1:A:1108:G:H4'	1:A:1191:A:O4'	2.15	0.46
1:A:1190:G:C2'	1:A:1191:A:OP2	2.63	0.46
1:A:1306:A:H2'	1:A:1307:U:O4'	2.16	0.46
1:A:1328:C:O2'	1:A:1329:A:H5'	2.14	0.46
1:A:57:G:H2'	1:A:58:C:C6	2.51	0.46
1:A:731:G:H5'	1:A:766:A:H4'	1.97	0.46
1:A:836:G:OP1	20:R:61:LYS:NZ	2.44	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:143:GLU:O	4:B:147:LYS:HE3	2.16	0.46
4:B:33:TYR:HB3	4:B:41:ILE:O	2.15	0.46
6:D:127:THR:CG2	6:D:147:ALA:HB3	2.46	0.46
7:E:43:LEU:HD23	7:E:44:GLY:N	2.31	0.46
10:H:46:LYS:HG3	10:H:64:LYS:CG	2.43	0.46
12:J:28:ARG:HH11	12:J:28:ARG:HG2	1.79	0.46
13:K:120:ARG:NH2	13:K:126:ARG:NH1	2.63	0.46
14:L:124:LYS:O	14:L:125:PRO:C	2.53	0.46
1:A:302:G:H5''	14:L:17:LYS:HZ1	1.78	0.46
20:R:28:GLU:OE1	20:R:28:GLU:N	2.48	0.46
1:A:1117:G:H21	1:A:1180:A:H1'	1.80	0.46
1:A:337:C:N4	1:A:338:A:H62	2.13	0.46
1:A:840:C:O5'	1:A:840:C:H6	1.98	0.46
5:C:178:LEU:O	5:C:179:ARG:CB	2.63	0.46
6:D:87:GLY:O	6:D:89:THR:N	2.49	0.46
7:E:15:ARG:HG3	7:E:15:ARG:NH1	2.31	0.46
10:H:31:PHE:O	10:H:35:ILE:HG13	2.16	0.46
11:I:117:HIS:O	11:I:118:LYS:HG3	2.16	0.46
12:J:16:LEU:O	12:J:17:ASP:C	2.52	0.46
14:L:7:ILE:HG22	14:L:11:VAL:HG23	1.98	0.46
18:P:8:ARG:C	18:P:9:PHE:HD2	2.19	0.46
22:T:100:ILE:O	22:T:100:ILE:CG2	2.63	0.46
22:T:101:GLY:O	22:T:102:GLY:C	2.53	0.46
23:V:24:ARG:O	23:V:25:LYS:CB	2.64	0.46
1:A:1357:A:C8	1:A:1358:U:H5	2.34	0.46
1:A:407:G:H2'	1:A:431:A:OP1	2.15	0.46
1:A:501:C:O2'	1:A:502:G:H5'	2.16	0.46
1:A:740:U:H4'	17:O:42:HIS:CD2	2.51	0.46
1:A:954:G:H2'	1:A:955:U:O4'	2.15	0.46
6:D:162:LEU:HD12	6:D:181:MET:SD	2.56	0.46
7:E:34:VAL:O	7:E:34:VAL:HG13	2.15	0.46
8:F:101:ALA:CB	20:R:28:GLU:HG3	2.45	0.46
9:G:46:ALA:HA	9:G:49:ILE:HD13	1.98	0.46
10:H:31:PHE:O	10:H:34:GLU:HB2	2.16	0.46
17:O:78:TYR:O	17:O:80:ALA:N	2.49	0.46
18:P:43:LYS:HG2	18:P:48:TRP:CE2	2.51	0.46
19:Q:67:LYS:O	19:Q:68:ARG:HB3	2.15	0.46
20:R:79:LEU:CD2	20:R:80:PRO:HD2	2.45	0.46
21:S:14:HIS:O	21:S:18:LYS:HE3	2.16	0.46
22:T:90:GLN:O	22:T:93:GLU:HB2	2.15	0.46
1:A:1439:C:OP1	22:T:38:LYS:NZ	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:346:G:C2'	1:A:347:G:H5'	2.46	0.46
1:A:903:G:H2'	1:A:904:C:C6	2.51	0.46
4:B:105:PHE:O	4:B:106:LYS:C	2.54	0.46
4:B:30:ARG:HG3	4:B:31:TYR:N	2.31	0.46
4:B:91:PRO:HG2	4:B:155:LEU:HG	1.97	0.46
5:C:139:GLN:HA	5:C:139:GLN:HE21	1.81	0.46
5:C:139:GLN:O	5:C:140:ARG:C	2.54	0.46
8:F:76:ALA:C	8:F:78:GLU:N	2.69	0.46
11:I:1117:G:H4'	11:I:104:ARG:NH1	2.31	0.46
11:I:113:LYS:H	11:I:119:ALA:HA	1.80	0.46
1:A:1401:G:C2	1:A:1402:C:C1'	2.98	0.45
1:A:748:C:OP2	1:A:748:C:H6	1.99	0.45
4:B:137:ARG:HA	4:B:140:HIS:HD2	1.80	0.45
6:D:19:LEU:HD22	6:D:67:ILE:HG12	1.97	0.45
9:G:108:ALA:C	9:G:110:GLN:H	2.18	0.45
9:G:111:ARG:HE	9:G:123:GLU:CA	2.29	0.45
9:G:148:ASN:N	9:G:148:ASN:ND2	2.62	0.45
11:I:5:TYR:HA	11:I:17:VAL:O	2.16	0.45
11:I:43:ALA:HA	11:I:74:ILE:CD1	2.36	0.45
18:P:74:LEU:HB3	18:P:79:VAL:CG2	2.46	0.45
1:A:1423:G:H2'	1:A:1424:C:C6	2.51	0.45
1:A:1431:C:C2'	1:A:1432:G:H5'	2.46	0.45
1:A:1504:G:O2'	1:A:1505:G:OP2	2.31	0.45
1:A:352:C:N3	1:A:356:A:N6	2.64	0.45
1:A:392:G:H2'	1:A:393:A:C8	2.51	0.45
1:A:730:G:N3	1:A:765:G:H4'	2.32	0.45
4:B:102:LEU:HD12	4:B:102:LEU:N	2.32	0.45
4:B:108:ILE:HG22	4:B:152:PHE:CE2	2.52	0.45
6:D:78:LEU:HB3	6:D:93:PHE:HE2	1.81	0.45
7:E:135:THR:O	7:E:138:ALA:HB3	2.17	0.45
8:F:62:TRP:C	8:F:63:TYR:CD1	2.90	0.45
12:J:25:GLU:C	12:J:27:ALA:N	2.69	0.45
13:K:74:ALA:O	13:K:76:GLY:N	2.49	0.45
14:L:39:VAL:HA	14:L:79:GLU:HG2	1.98	0.45
18:P:10:GLY:HA3	18:P:14:ASN:O	2.15	0.45
19:Q:61:GLU:HA	19:Q:71:PHE:CD1	2.50	0.45
20:R:55:ARG:CB	20:R:55:ARG:HH11	2.30	0.45
1:A:1305:G:OP1	23:V:2:GLY:N	2.50	0.45
1:A:1288:A:C6	1:A:1289:A:C5	3.04	0.45
1:A:934:C:H5	1:A:1344:C:H2'	1.82	0.45
1:A:1490:C:H5'	1:A:1490:C:C6	2.39	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:252:U:H2'	1:A:253:U:C5	2.52	0.45
1:A:718:G:O5'	13:K:117:ASN:ND2	2.49	0.45
1:A:720:C:H2'	1:A:721:G:C8	2.51	0.45
1:A:723:U:H5''	1:A:724:G:OP2	2.17	0.45
4:B:210:SER:C	4:B:212:GLN:N	2.68	0.45
4:B:27:LYS:HZ3	4:B:195:ASP:HB2	1.80	0.45
6:D:126:ILE:CG2	6:D:127:THR:N	2.79	0.45
7:E:107:ARG:O	7:E:110:LEU:N	2.49	0.45
10:H:10:LEU:HD23	10:H:83:ILE:HD11	1.99	0.45
1:A:1249:C:O2'	11:I:73:GLN:NE2	2.50	0.45
12:J:32:ALA:H	12:J:76:ASN:HD21	1.65	0.45
12:J:9:ARG:CB	12:J:9:ARG:NH1	2.79	0.45
15:M:108:ARG:NE	15:M:108:ARG:HA	2.31	0.45
1:A:163:C:H2'	1:A:164:U:C5'	2.46	0.45
1:A:748:C:O2'	1:A:749:C:C6	2.65	0.45
1:A:8:A:C6	6:D:209:ARG:HA	2.52	0.45
4:B:97:TRP:CZ2	4:B:101:MET:HB2	2.51	0.45
4:B:84:GLU:HB3	4:B:219:VAL:CG2	2.40	0.45
5:C:195:VAL:O	5:C:195:VAL:HG12	2.17	0.45
6:D:163:GLU:C	6:D:165:MET:H	2.20	0.45
7:E:143:ARG:HD3	7:E:143:ARG:HA	1.60	0.45
1:A:939:G:C5'	9:G:102:ARG:HH22	2.18	0.45
10:H:105:ARG:HG3	10:H:105:ARG:HH11	1.81	0.45
13:K:123:LYS:O	13:K:124:LYS:C	2.55	0.45
15:M:125:ARG:C	15:M:125:ARG:HD2	2.36	0.45
15:M:14:ARG:HH11	15:M:14:ARG:HB3	1.79	0.45
17:O:67:LEU:O	17:O:68:ARG:C	2.54	0.45
1:A:1495:U:H2'	1:A:1496:C:C6	2.52	0.45
1:A:38:G:N1	1:A:397:A:OP1	2.34	0.45
1:A:740:U:O2'	1:A:741:G:H5'	2.17	0.45
1:A:742:G:H2'	1:A:743:U:O4'	2.16	0.45
1:A:938:A:C6	1:A:939:G:C5	3.05	0.45
7:E:144:THR:O	7:E:145:LYS:C	2.55	0.45
7:E:151:LEU:HD11	10:H:77:GLU:OE2	2.16	0.45
7:E:35:GLY:H	7:E:112:LEU:HD12	1.81	0.45
9:G:122:HIS:HA	9:G:125:MET:HE3	1.97	0.45
9:G:6:ARG:O	9:G:7:ALA:C	2.55	0.45
10:H:11:THR:O	10:H:14:ARG:N	2.50	0.45
10:H:35:ILE:CG2	10:H:111:ILE:HD13	2.47	0.45
10:H:35:ILE:O	10:H:39:LEU:HD22	2.17	0.45
11:I:24:GLY:HA3	11:I:57:GLY:HA2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:K:109:VAL:HA	20:R:85:LEU:O	2.16	0.45
14:L:11:VAL:HG21	19:Q:34:LYS:HG2	1.99	0.45
14:L:53:ARG:CD	14:L:93:LEU:HD21	2.47	0.45
14:L:24:VAL:HG13	14:L:98:TYR:CE2	2.50	0.45
15:M:116:THR:HG22	15:M:117:VAL:N	2.32	0.45
15:M:14:ARG:NH1	15:M:14:ARG:CB	2.79	0.45
15:M:59:TYR:O	15:M:59:TYR:CD1	2.69	0.45
1:A:277:C:OP1	19:Q:41:LYS:HE3	2.17	0.45
19:Q:65:ILE:O	19:Q:66:SER:HB3	2.15	0.45
19:Q:67:LYS:CA	19:Q:70:ARG:HH12	2.29	0.45
21:S:63:THR:HG21	21:S:65:ASN:HD22	1.81	0.45
1:A:1227:A:OP2	15:M:96:LEU:HD21	2.17	0.45
1:A:1275:A:O2'	1:A:1276:G:H5'	2.16	0.45
1:A:1314:C:OP2	21:S:6:LYS:HD2	2.17	0.45
1:A:1347:G:C2'	1:A:1373:G:H1	2.28	0.45
1:A:1519:A:C3'	1:A:1520:G:H5'	2.47	0.45
1:A:344:A:H5''	1:A:345:C:C5	2.50	0.45
1:A:432:A:O3'	1:A:433:C:H6	1.99	0.45
1:A:437:U:O2'	1:A:438:G:H5'	2.17	0.45
1:A:502:G:H2'	1:A:503:C:C6	2.52	0.45
1:A:560:U:H4'	1:A:561:U:H5''	1.99	0.45
1:A:660:G:C2	1:A:746:A:C2	3.05	0.45
1:A:662:G:O2'	1:A:663:A:H5'	2.17	0.45
1:A:954:G:C5	1:A:955:U:C5	3.05	0.45
1:A:961:U:H2'	1:A:962:C:O4'	2.16	0.45
7:E:119:LEU:HD23	7:E:119:LEU:HA	1.59	0.45
7:E:15:ARG:O	7:E:27:ARG:O	2.35	0.45
9:G:77:SER:O	9:G:156:TRP:HH2	2.00	0.45
10:H:137:VAL:CG1	10:H:138:TRP:N	2.79	0.45
10:H:46:LYS:N	10:H:64:LYS:HG3	2.31	0.45
11:I:27:THR:HG22	11:I:28:VAL:N	2.32	0.45
12:J:86:MET:N	12:J:86:MET:SD	2.89	0.45
14:L:22:SER:OG	14:L:23:LYS:N	2.49	0.45
16:N:18:VAL:HG23	16:N:19:ARG:H	1.82	0.45
17:O:11:VAL:O	17:O:14:GLU:HB3	2.17	0.45
17:O:45:VAL:HB	17:O:46:HIS:ND1	2.32	0.45
17:O:76:GLU:CA	17:O:79:ARG:HH21	2.25	0.45
19:Q:20:THR:CG2	19:Q:41:LYS:HD2	2.46	0.45
19:Q:58:GLU:HB2	19:Q:74:LEU:HB3	1.98	0.45
1:A:1347:G:N2	1:A:1373:G:H2'	2.31	0.45
1:A:1402:C:H2'	1:A:1403:C:O4'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1451:A:O2'	1:A:1452:C:OP1	2.31	0.45
1:A:1403:C:H1'	1:A:1500:A:N1	2.32	0.45
1:A:826:C:H2'	1:A:827:U:H6	1.81	0.45
5:C:199:LYS:HB3	5:C:201:TYR:HE1	1.82	0.45
5:C:34:LEU:HD23	5:C:34:LEU:O	2.15	0.45
7:E:144:THR:HG23	7:E:145:LYS:N	2.32	0.45
7:E:55:VAL:O	7:E:58:ALA:HB3	2.16	0.45
8:F:71:ARG:HA	8:F:74:ASP:OD2	2.17	0.45
10:H:10:LEU:CD2	10:H:83:ILE:HD11	2.47	0.45
12:J:24:VAL:HG12	12:J:24:VAL:O	2.16	0.45
15:M:20:THR:C	15:M:22:ILE:H	2.19	0.45
17:O:59:MET:HB2	17:O:59:MET:HE3	1.77	0.45
21:S:17:GLU:CA	21:S:20:LEU:HG	2.35	0.45
22:T:39:LYS:CE	22:T:55:ILE:HD13	2.47	0.45
1:A:1167:A:C6	1:A:1168:A:C6	3.04	0.45
1:A:1380:U:O2'	1:A:1381:U:P	2.75	0.45
1:A:337:C:N4	1:A:338:A:N6	2.64	0.45
1:A:439:A:C4	1:A:497:A:C2	3.04	0.45
1:A:833:U:H2'	1:A:834:C:H6	1.82	0.45
1:A:969:A:C2'	1:A:970:C:H5'	2.47	0.45
1:A:987:G:O2'	1:A:988:G:H5'	2.17	0.45
4:B:207:ALA:H	4:B:211:ILE:CD1	2.28	0.45
5:C:35:GLU:CD	5:C:59:ARG:HH22	2.20	0.45
9:G:116:ALA:HA	9:G:119:ARG:CZ	2.46	0.45
9:G:117:ALA:O	9:G:118:VAL:C	2.55	0.45
9:G:15:ASP:O	9:G:19:GLY:HA2	2.17	0.45
14:L:41:ARG:CG	14:L:42:THR:H	2.18	0.45
21:S:15:LEU:HD21	21:S:38:SER:OG	2.16	0.45
1:A:1069:C:H2'	1:A:1070:U:O5'	2.16	0.45
1:A:1085:U:H3'	1:A:1086:U:H5	1.82	0.45
1:A:1137:C:H4'	1:A:1138:G:N1	2.31	0.45
1:A:1370:G:C2	1:A:1371:G:C8	3.05	0.45
1:A:1477:C:O2'	1:A:1478:C:H5'	2.17	0.45
1:A:665:A:H2'	1:A:732:C:O2	2.17	0.45
4:B:144:ARG:HA	4:B:147:LYS:CD	2.46	0.45
5:C:88:ARG:HG2	5:C:101:LEU:HB2	1.99	0.45
6:D:112:VAL:CG2	6:D:161:ASN:HD21	2.29	0.45
6:D:3:ARG:HH12	6:D:70:ILE:HA	1.82	0.45
7:E:28:PHE:O	7:E:47:LYS:HA	2.17	0.45
8:F:30:LEU:HD22	8:F:35:ALA:HB2	1.99	0.45
8:F:1:MET:HB3	8:F:66:GLU:HG2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:G:38:LEU:C	9:G:40:ALA:H	2.20	0.45
1:A:1280:A:O4'	12:J:41:PRO:HG3	2.17	0.45
12:J:79:ARG:HG2	12:J:79:ARG:HH11	1.82	0.45
19:Q:97:SER:OG	19:Q:98:LEU:N	2.50	0.45
21:S:41:VAL:HB	21:S:42:PRO:HD2	1.99	0.45
1:A:1202:G:O4'	16:N:29:ARG:HD3	2.17	0.45
1:A:1321:C:H42	21:S:37:ARG:HH12	1.65	0.45
1:A:1426:C:H2'	1:A:1427:U:C6	2.52	0.45
1:A:1525:G:P	13:K:120:ARG:HH22	2.39	0.45
1:A:280:C:O2	19:Q:38:ARG:HG3	2.16	0.45
1:A:624:C:H2'	1:A:625:G:C8	2.50	0.45
1:A:690:G:C6	1:A:691:G:C6	3.06	0.45
1:A:781:A:C5	1:A:802:A:C2	3.05	0.45
4:B:134:GLU:C	4:B:136:VAL:N	2.71	0.45
4:B:187:LEU:HD12	4:B:201:ILE:CG2	2.47	0.45
4:B:27:LYS:O	4:B:194:PRO:HG3	2.17	0.45
5:C:147:LYS:HE2	5:C:205:GLY:N	2.31	0.45
6:D:199:ASN:HD21	6:D:201:GLN:HB2	1.81	0.45
8:F:36:ARG:NH1	8:F:36:ARG:HG2	2.31	0.45
9:G:115:ARG:HB2	9:G:118:VAL:HG21	1.99	0.45
12:J:39:PRO:HA	12:J:70:ARG:HH11	1.82	0.45
15:M:13:LYS:HG2	15:M:44:ARG:NH2	2.29	0.45
15:M:88:ARG:HH11	15:M:88:ARG:HB2	1.82	0.45
17:O:10:LYS:HD2	17:O:10:LYS:O	2.17	0.45
18:P:1:MET:CE	18:P:3:LYS:HD2	2.47	0.45
19:Q:63:ARG:O	19:Q:64:PRO:C	2.56	0.45
20:R:57:GLY:C	20:R:58:LEU:HD23	2.37	0.45
1:A:1311:G:N2	1:A:1327:C:C2	2.85	0.44
1:A:20:U:O2'	1:A:21:G:H5'	2.17	0.44
1:A:352:C:H4'	1:A:354:G:OP1	2.17	0.44
1:A:372:C:O2'	1:A:373:A:OP2	2.31	0.44
1:A:37:U:O2'	1:A:38:G:H5'	2.17	0.44
1:A:532:A:C2'	1:A:533:A:OP1	2.65	0.44
1:A:737:A:H2'	1:A:738:C:H6	1.81	0.44
1:A:778:G:C5	1:A:779:C:C5	3.05	0.44
4:B:21:ARG:HB2	4:B:22:LYS:H	1.51	0.44
5:C:6:HIS:CD2	5:C:8:ILE:HB	2.52	0.44
7:E:121:LYS:HE3	7:E:123:LEU:HD23	2.00	0.44
8:F:10:LEU:HD12	8:F:59:TYR:O	2.17	0.44
10:H:119:LEU:CD2	10:H:119:LEU:N	2.80	0.44
10:H:134:ILE:HG22	10:H:135:CYS:N	2.31	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:707:C:H4'	13:K:20:TYR:CG	2.52	0.44
9:G:151:TYR:HE1	13:K:54:ARG:NH2	2.16	0.44
15:M:96:LEU:HB3	15:M:97:PRO:HD2	1.99	0.44
17:O:6:GLU:O	17:O:7:GLU:C	2.55	0.44
18:P:43:LYS:HG3	18:P:48:TRP:CD2	2.51	0.44
19:Q:58:GLU:OE1	19:Q:74:LEU:HD13	2.17	0.44
1:A:1328:C:P	23:V:20:LYS:HZ1	2.40	0.44
1:A:1227:A:H3'	1:A:1227:A:C8	2.52	0.44
1:A:1237:C:C4'	1:A:1334:G:N2	2.80	0.44
1:A:1344:C:O2'	1:A:1345:U:H5'	2.17	0.44
1:A:1349:A:P	11:I:118:LYS:HZ3	2.41	0.44
1:A:286:G:H2'	1:A:287:U:O4'	2.17	0.44
1:A:407:G:C2'	1:A:408:A:OP1	2.66	0.44
4:B:100:GLY:O	4:B:101:MET:C	2.54	0.44
4:B:200:ILE:CG2	4:B:201:ILE:H	2.20	0.44
4:B:63:MET:O	4:B:64:ARG:HB2	2.17	0.44
5:C:17:ASP:HB2	5:C:21:ARG:HH21	1.82	0.44
6:D:163:GLU:C	6:D:165:MET:N	2.70	0.44
7:E:35:GLY:CA	7:E:112:LEU:HD12	2.47	0.44
7:E:6:PHE:HB3	7:E:34:VAL:CG2	2.47	0.44
8:F:25:ILE:HD12	8:F:82:ARG:HD2	1.98	0.44
9:G:116:ALA:O	9:G:117:ALA:C	2.55	0.44
10:H:7:ALA:O	10:H:8:ASP:C	2.55	0.44
13:K:69:ALA:O	13:K:72:ALA:HB3	2.17	0.44
14:L:23:LYS:O	14:L:24:VAL:HG23	2.17	0.44
20:R:79:LEU:HD23	20:R:79:LEU:HA	1.84	0.44
22:T:72:LEU:C	22:T:73:HIS:O	2.56	0.44
1:A:1070:U:O2'	1:A:1071:C:H5'	2.17	0.44
1:A:201:C:C5'	1:A:216:G:H21	2.28	0.44
1:A:676:A:H1'	13:K:115:PRO:HB3	1.98	0.44
1:A:738:C:H2'	1:A:739:C:C6	2.52	0.44
1:A:969:A:O2'	1:A:970:C:H5'	2.17	0.44
4:B:23:ARG:O	4:B:24:TRP:O	2.34	0.44
5:C:178:LEU:HD12	5:C:178:LEU:HA	1.70	0.44
6:D:105:VAL:HG12	6:D:117:ALA:HB1	2.00	0.44
9:G:116:ALA:HA	9:G:119:ARG:NH2	2.32	0.44
9:G:138:LYS:HE2	9:G:142:GLU:OE1	2.17	0.44
15:M:53:VAL:O	15:M:53:VAL:HG12	2.16	0.44
20:R:86:VAL:O	20:R:87:ARG:HB2	2.17	0.44
1:A:1320:C:C2	21:S:72:GLY:HA3	2.53	0.44
22:T:16:HIS:O	22:T:17:ARG:C	2.56	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1060:C:O4'	12:J:52:GLY:HA2	2.17	0.44
1:A:1190:G:O2'	1:A:1191:A:P	2.75	0.44
1:A:1399:C:C2	1:A:1401:G:C5	3.05	0.44
1:A:316:G:OP2	1:A:351:G:O2'	2.35	0.44
1:A:369:C:O2'	1:A:370:C:H5'	2.17	0.44
1:A:622:A:C8	1:A:623:C:C5	3.06	0.44
1:A:644:G:O2'	1:A:645:C:H5'	2.18	0.44
5:C:111:LEU:HD21	5:C:144:SER:O	2.17	0.44
8:F:25:ILE:HD12	8:F:82:ARG:HH11	1.82	0.44
12:J:34:VAL:CG1	12:J:35:SER:N	2.79	0.44
13:K:58:PRO:O	13:K:59:TYR:C	2.55	0.44
17:O:16:ALA:HA	17:O:21:ASP:OD1	2.17	0.44
17:O:76:GLU:OE1	17:O:79:ARG:NH2	2.50	0.44
1:A:324:G:OP1	22:T:22:ARG:NH1	2.51	0.44
1:A:1060:C:H5''	12:J:51:ARG:HB3	1.99	0.44
1:A:1539:C:C2	1:A:1540:U:H5	2.34	0.44
1:A:190(K):G:C3'	1:A:190(L):U:H5''	2.48	0.44
1:A:349:A:C2'	1:A:350:G:O5'	2.66	0.44
1:A:413:G:H1'	1:A:416:G:N2	2.33	0.44
4:B:10:LEU:C	4:B:12:GLU:N	2.71	0.44
4:B:48:MET:O	4:B:51:LEU:HB2	2.18	0.44
4:B:80:ILE:HD11	4:B:208:ILE:CG2	2.31	0.44
5:C:134:ILE:CG2	5:C:168:ALA:HB3	2.48	0.44
5:C:87:LEU:C	5:C:89:GLU:N	2.70	0.44
5:C:91:LEU:O	5:C:95:THR:HG23	2.18	0.44
7:E:139:LEU:O	7:E:141:GLN:N	2.51	0.44
8:F:67:MET:HB2	8:F:68:PRO:CD	2.47	0.44
9:G:16:LEU:HD22	9:G:16:LEU:N	2.23	0.44
9:G:70:LYS:HG2	9:G:100:ALA:HB2	2.00	0.44
1:A:303:A:P	14:L:17:LYS:HZ1	2.41	0.44
17:O:28:GLN:O	17:O:29:VAL:C	2.55	0.44
17:O:70:LEU:HG	17:O:78:TYR:HB2	1.98	0.44
20:R:53:ARG:C	20:R:55:ARG:H	2.20	0.44
20:R:52:PRO:HB2	20:R:54:ARG:HG3	1.99	0.44
21:S:71:LEU:C	21:S:73:GLU:N	2.71	0.44
21:S:6:LYS:HB2	21:S:7:LYS:HD3	1.99	0.44
1:A:1054:C:O2'	1:A:1055:A:C5'	2.65	0.44
1:A:1121:U:O2'	1:A:1122:U:H5'	2.17	0.44
1:A:1399:C:H4'	1:A:1400:C:O5'	2.17	0.44
1:A:1406:U:C2'	1:A:1407:C:H5'	2.47	0.44
1:A:1431:C:H2'	1:A:1432:G:H5'	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:409:G:H5'	1:A:430:A:C6	2.52	0.44
1:A:50:A:N6	1:A:361:G:H4'	2.32	0.44
4:B:104:ASN:OD1	4:B:107:THR:HB	2.17	0.44
4:B:27:LYS:NZ	4:B:195:ASP:HB2	2.32	0.44
5:C:191:THR:CG2	5:C:192:THR:N	2.81	0.44
6:D:106:TYR:C	6:D:106:TYR:CD2	2.90	0.44
8:F:25:ILE:HD12	8:F:82:ARG:NH1	2.32	0.44
14:L:38:THR:HB	14:L:57:LYS:HB3	1.98	0.44
15:M:80:ARG:C	15:M:82:MET:N	2.71	0.44
20:R:53:ARG:O	20:R:55:ARG:N	2.50	0.44
21:S:28:LYS:HB3	21:S:31:ILE:HD11	1.99	0.44
1:A:1160:G:C6	1:A:1181:G:O6	2.71	0.44
1:A:1197:G:OP1	1:A:1198:G:OP2	2.36	0.44
1:A:1368:G:OP2	11:I:112:LYS:HD3	2.18	0.44
1:A:24:U:O2'	1:A:25:C:H5'	2.18	0.44
4:B:115:LEU:O	4:B:118:LEU:N	2.49	0.44
7:E:15:ARG:HD3	7:E:26:PHE:CD2	2.52	0.44
7:E:71:LEU:O	7:E:72:GLN:HG2	2.17	0.44
7:E:72:GLN:O	7:E:73:ASN:CB	2.65	0.44
8:F:19:LEU:C	8:F:21:LEU:N	2.71	0.44
1:A:707:C:O2	13:K:39:PRO:HD3	2.18	0.44
15:M:123:ALA:O	15:M:124:PRO:C	2.56	0.44
19:Q:51:TYR:CE1	19:Q:73:VAL:HG11	2.52	0.44
1:A:1053:G:H4'	1:A:1054:C:H5'	1.98	0.44
1:A:1160:G:C6	1:A:1161:C:C4	3.06	0.44
1:A:1160:G:O2'	1:A:1161:C:H5'	2.18	0.44
1:A:1190:G:C3'	5:C:3:ASN:OD1	2.66	0.44
1:A:1305:G:OP2	1:A:1305:G:C8	2.71	0.44
1:A:378:G:O2'	1:A:379:C:H5'	2.18	0.44
1:A:554:C:H2'	1:A:555:C:H6	1.82	0.44
1:A:584:G:H2'	1:A:585:G:H8	1.82	0.44
1:A:572:A:H5''	1:A:917:G:H4'	2.00	0.44
1:A:992:U:O2'	1:A:993:G:P	2.76	0.44
4:B:9:GLU:O	4:B:12:GLU:N	2.51	0.44
4:B:193:ASP:OD1	4:B:196:LEU:HB2	2.17	0.44
5:C:180:ALA:O	5:C:205:GLY:O	2.36	0.44
7:E:126:ARG:CG	7:E:126:ARG:NH1	2.75	0.44
1:A:1081:G:OP1	7:E:16:THR:HG23	2.18	0.44
7:E:32:VAL:HG12	7:E:33:VAL:N	2.33	0.44
11:I:78:LYS:HE3	11:I:101:PHE:HD2	1.83	0.44
11:I:80:GLY:O	11:I:83:ARG:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:33:LEU:HD11	16:N:53:LEU:HD23	1.99	0.44
16:N:59:ALA:O	16:N:60:SER:CB	2.62	0.44
19:Q:85:VAL:O	19:Q:89:LEU:HG	2.18	0.44
20:R:51:LEU:HA	20:R:52:PRO:HD3	1.82	0.44
22:T:63:ILE:HD13	22:T:80:ARG:HB2	1.98	0.44
1:A:1270:C:H6	1:A:1270:C:O5'	2.01	0.44
1:A:1345:U:C4	1:A:1377:A:C2	3.05	0.44
1:A:391:G:C6	1:A:392:G:C5	3.05	0.44
1:A:460:A:H62	1:A:463:A:H62	1.64	0.44
1:A:407:G:N2	1:A:496:A:O2'	2.50	0.44
1:A:817:C:H4'	1:A:818:G:OP1	2.18	0.44
5:C:43:LEU:HD22	5:C:47:LEU:HD22	1.99	0.44
8:F:37:VAL:HA	8:F:65:VAL:HG12	1.98	0.44
14:L:65:GLU:N	14:L:65:GLU:CD	2.71	0.44
5:C:29:TYR:CZ	16:N:54:PRO:HG2	2.53	0.44
1:A:1006:C:O2'	1:A:1007:C:H5'	2.18	0.43
1:A:1192:C:C5	1:A:1193:G:C8	3.06	0.43
1:A:1370:G:C2	1:A:1371:G:N7	2.85	0.43
1:A:1345:U:C2	1:A:1377:A:N1	2.86	0.43
1:A:279:A:H5''	1:A:280:C:H3'	2.00	0.43
1:A:303:A:P	14:L:17:LYS:NZ	2.91	0.43
1:A:452:A:O2'	1:A:453:A:C8	2.65	0.43
4:B:143:GLU:C	4:B:147:LYS:HE3	2.38	0.43
4:B:36:ARG:HD2	4:B:41:ILE:CD1	2.48	0.43
5:C:177:THR:O	5:C:179:ARG:N	2.50	0.43
6:D:16:GLY:C	6:D:33:MET:HE1	2.38	0.43
12:J:23:ILE:CG2	12:J:72:VAL:HG11	2.47	0.43
20:R:27:GLY:O	20:R:29:PHE:HD2	2.01	0.43
20:R:74:ARG:O	20:R:75:ILE:C	2.56	0.43
22:T:74:LYS:HB3	22:T:75:ASN:H	1.53	0.43
1:A:1060:C:O2	1:A:1198:G:C2	2.72	0.43
1:A:1072:G:H2'	1:A:1073:U:O4'	2.18	0.43
1:A:1168:A:C6	1:A:1169:A:C6	3.06	0.43
1:A:1364:U:O2'	1:A:1365:G:H5'	2.18	0.43
1:A:418:C:C5	1:A:426:G:N1	2.86	0.43
1:A:586:C:C2'	1:A:587:G:H5'	2.48	0.43
1:A:975:A:H4'	1:A:976:G:O5'	2.18	0.43
4:B:24:TRP:HB3	4:B:40:HIS:CE1	2.53	0.43
4:B:83:MET:HE2	4:B:235:SER:HB3	2.00	0.43
4:B:82:ARG:NH1	4:B:92:TYR:OH	2.51	0.43
5:C:190:ARG:NH1	5:C:190:ARG:HG2	2.28	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:51:GLY:C	5:C:70:VAL:HG12	2.38	0.43
6:D:3:ARG:CA	6:D:3:ARG:NE	2.80	0.43
8:F:30:LEU:HD21	8:F:65:VAL:HG11	1.99	0.43
9:G:139:GLU:O	9:G:143:ARG:HG3	2.17	0.43
19:Q:51:TYR:HE2	19:Q:76:LEU:HB2	1.83	0.43
19:Q:82:MET:O	19:Q:85:VAL:N	2.51	0.43
20:R:35:ARG:O	20:R:37:VAL:N	2.47	0.43
1:A:1354:C:O2'	1:A:1355:G:H5'	2.18	0.43
1:A:1521:G:O2'	1:A:1522:U:H5'	2.17	0.43
1:A:328:C:H4'	1:A:329:A:H5'	2.01	0.43
1:A:113:G:H1'	1:A:354:G:C5'	2.48	0.43
1:A:447:G:H2'	1:A:485:G:H22	1.83	0.43
1:A:597:G:C4	1:A:644:G:C2	3.07	0.43
1:A:783:C:O2'	1:A:784:C:H5'	2.17	0.43
6:D:8:VAL:HG11	6:D:21:LEU:CB	2.43	0.43
8:F:75:LEU:HD13	8:F:75:LEU:C	2.38	0.43
9:G:12:LEU:HD12	9:G:12:LEU:N	2.33	0.43
10:H:83:ILE:HG13	10:H:137:VAL:HG22	2.00	0.43
10:H:29:SER:OG	10:H:32:LYS:HG3	2.17	0.43
10:H:87:SER:OG	10:H:92:ARG:HA	2.18	0.43
1:A:1302:U:C5	15:M:17:VAL:HG21	2.52	0.43
1:A:178:C:O2'	1:A:179:A:H5'	2.18	0.43
1:A:252:U:H2'	1:A:253:U:H6	1.81	0.43
1:A:443:C:H2'	1:A:444:C:H6	1.82	0.43
1:A:490:G:H2'	1:A:491:G:H8	1.84	0.43
1:A:19:C:O2	1:A:572:A:H2	2.00	0.43
1:A:602:A:O2'	1:A:603:U:H5'	2.18	0.43
5:C:155:GLY:C	5:C:157:ILE:N	2.70	0.43
1:A:1112:C:O2	5:C:179:ARG:HB3	2.17	0.43
5:C:57:ILE:HG23	5:C:64:VAL:HG13	2.01	0.43
6:D:112:VAL:HG23	6:D:116:GLN:OE1	2.18	0.43
6:D:59:ARG:HA	6:D:59:ARG:NE	2.33	0.43
7:E:78:HIS:HB2	7:E:79:GLU:OE1	2.19	0.43
8:F:33:TYR:HA	8:F:71:ARG:NH2	2.33	0.43
9:G:46:ALA:C	9:G:48:LYS:N	2.72	0.43
10:H:48:TYR:HB2	10:H:60:ARG:O	2.18	0.43
5:C:34:LEU:CD1	16:N:25:VAL:HG21	2.48	0.43
16:N:57:ARG:CG	16:N:58:LYS:N	2.80	0.43
17:O:25:THR:O	17:O:25:THR:HG22	2.19	0.43
20:R:74:ARG:HB3	20:R:81:PHE:CE1	2.54	0.43
22:T:14:LYS:O	22:T:18:GLN:HG3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1061:G:C6	1:A:1062:U:N3	2.86	0.43
1:A:1108:G:H5'	1:A:1191:A:H4'	2.00	0.43
1:A:1450:U:H2'	1:A:1452:C:C5	2.54	0.43
1:A:190(K):G:H2'	1:A:190(L):U:H5''	2.00	0.43
1:A:339:C:H2'	1:A:340:U:H6	1.83	0.43
1:A:348:G:N3	1:A:348:G:H2'	2.32	0.43
1:A:607:A:O2'	1:A:608:A:H5'	2.18	0.43
1:A:831:U:H2'	1:A:832:C:C6	2.54	0.43
4:B:130:ARG:HB3	4:B:134:GLU:OE1	2.19	0.43
4:B:24:TRP:N	4:B:24:TRP:CD1	2.85	0.43
4:B:57:PHE:CZ	4:B:61:LEU:HD21	2.53	0.43
5:C:50:ALA:CB	5:C:70:VAL:HG11	2.48	0.43
6:D:124:GLY:O	6:D:126:ILE:N	2.52	0.43
6:D:70:ILE:HG22	6:D:71:SER:O	2.18	0.43
7:E:144:THR:HB	7:E:147:ASP:OD1	2.19	0.43
10:H:69:ARG:NE	10:H:75:ARG:O	2.48	0.43
15:M:105:THR:HG22	15:M:106:ASN:H	1.83	0.43
17:O:3:ILE:CD1	17:O:34:LEU:HD22	2.48	0.43
2:W:2:A:H5'	2:W:2:A:H8	1.84	0.43
1:A:1179:A:O2'	1:A:1180:A:H5'	2.19	0.43
1:A:1157:A:H1'	1:A:1181:G:N2	2.34	0.43
1:A:1250:A:C5'	11:I:68:GLY:N	2.77	0.43
1:A:131:C:H2'	1:A:132:C:H6	1.83	0.43
1:A:437:U:H2'	1:A:438:G:H5'	1.99	0.43
1:A:603:U:H2'	1:A:604:G:C8	2.54	0.43
1:A:578:C:O2'	1:A:728:A:N3	2.43	0.43
1:A:802:A:C2'	1:A:803:G:H5'	2.48	0.43
1:A:803:G:H2'	1:A:804:U:O4'	2.18	0.43
1:A:978:A:C5	1:A:1319:A:C2	3.06	0.43
5:C:47:LEU:N	5:C:47:LEU:HD12	2.34	0.43
5:C:5:ILE:O	5:C:5:ILE:CD1	2.66	0.43
6:D:64:LEU:HD12	6:D:75:PHE:HZ	1.84	0.43
7:E:69:VAL:HG21	7:E:113:ALA:HB1	1.99	0.43
8:F:62:TRP:C	8:F:63:TYR:HD1	2.22	0.43
11:I:87:GLN:C	11:I:89:ASN:N	2.72	0.43
12:J:65:LEU:C	12:J:65:LEU:HD23	2.39	0.43
14:L:53:ARG:HG2	14:L:69:TYR:CE1	2.43	0.43
14:L:92:ASP:O	14:L:93:LEU:HD23	2.18	0.43
18:P:9:PHE:CE1	18:P:18:ARG:CZ	3.01	0.43
1:A:375:U:O2'	18:P:28:ARG:HD2	2.19	0.43
19:Q:19:VAL:CG2	19:Q:44:ALA:HB3	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:S:33:THR:HG22	21:S:34:TRP:N	2.32	0.43
1:A:1320:C:O2	21:S:72:GLY:HA3	2.19	0.43
1:A:141:A:H1'	1:A:182:U:O2	2.18	0.43
1:A:1431:C:H2'	1:A:1432:G:C5'	2.49	0.43
1:A:359:U:H2'	1:A:360:A:C8	2.54	0.43
1:A:416:G:N3	1:A:416:G:H3'	2.33	0.43
4:B:97:TRP:HH2	4:B:176:GLU:CD	2.22	0.43
4:B:46:LYS:O	4:B:50:GLU:HB2	2.19	0.43
5:C:121:ALA:O	5:C:125:GLU:HG3	2.19	0.43
5:C:179:ARG:O	5:C:180:ALA:HB3	2.19	0.43
5:C:186:PHE:CE2	5:C:188:LEU:HD22	2.53	0.43
5:C:89:GLU:O	5:C:93:LYS:HB2	2.19	0.43
7:E:115:VAL:HG12	7:E:116:THR:N	2.33	0.43
11:I:38:GLN:OE1	11:I:38:GLN:HA	2.18	0.43
11:I:93:ARG:C	11:I:95:LYS:N	2.71	0.43
14:L:117:ARG:O	14:L:119:LYS:O	2.37	0.43
15:M:33:ALA:O	15:M:35:GLU:N	2.52	0.43
15:M:94:ARG:HH12	21:S:81:ARG:NH1	2.12	0.43
17:O:53:HIS:O	17:O:56:LEU:N	2.51	0.43
18:P:56:ALA:O	18:P:57:ARG:C	2.57	0.43
18:P:69:THR:O	18:P:70:ALA:C	2.57	0.43
19:Q:74:LEU:HD23	19:Q:74:LEU:O	2.18	0.43
21:S:22:LEU:C	21:S:24:ALA:H	2.20	0.43
1:A:1320:C:N3	21:S:36:ARG:HG3	2.34	0.43
21:S:45:VAL:HG12	21:S:46:GLY:H	1.84	0.43
1:A:1346:A:C8	1:A:1348:U:C2	3.07	0.43
1:A:1372:U:H2'	1:A:1373:G:C5'	2.49	0.43
1:A:1520:G:C2	1:A:1521:G:C5	3.07	0.43
1:A:243:A:C5'	1:A:244:U:H5'	2.48	0.43
1:A:279:A:H4'	1:A:280:C:OP2	2.17	0.43
1:A:294:U:H2'	1:A:295:C:H6	1.83	0.43
1:A:560:U:O2'	1:A:561:U:OP2	2.24	0.43
1:A:601:C:O2'	1:A:602:A:H5'	2.18	0.43
1:A:692:U:OP1	13:K:124:LYS:HE3	2.19	0.43
1:A:718:G:C5'	1:A:719:C:OP2	2.66	0.43
1:A:77:G:O2'	1:A:78:G:H5'	2.18	0.43
4:B:20:GLU:HB2	4:B:190:THR:HB	2.01	0.43
5:C:151:VAL:O	5:C:152:ILE:HG13	2.19	0.43
5:C:73:PRO:C	5:C:75:VAL:N	2.68	0.43
6:D:116:GLN:O	6:D:119:GLN:N	2.51	0.43
6:D:67:ILE:HG22	6:D:68:TYR:N	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:80:GLU:HA	6:D:80:GLU:OE2	2.18	0.43
9:G:15:ASP:HB3	9:G:19:GLY:CA	2.49	0.43
9:G:26:PHE:HB2	9:G:62:PHE:HZ	1.83	0.43
9:G:32:ARG:O	9:G:33:ASP:HB2	2.18	0.43
12:J:96:ILE:CG2	12:J:97:GLU:N	2.82	0.43
14:L:119:LYS:O	14:L:120:TYR:HB2	2.19	0.43
15:M:31:LYS:C	15:M:33:ALA:N	2.71	0.43
1:A:1116:C:H2'	1:A:1117:G:C5'	2.27	0.43
1:A:1263:C:O2'	1:A:1264:C:H5'	2.18	0.43
1:A:652:U:C5	1:A:752:G:C4	3.07	0.43
1:A:757:U:H2'	1:A:758:G:O4'	2.18	0.43
1:A:791:G:C2'	1:A:792:A:H5'	2.47	0.43
1:A:920:U:H2'	1:A:921:U:H6	1.80	0.43
4:B:58:ILE:O	4:B:61:LEU:HB2	2.19	0.43
4:B:7:VAL:O	4:B:7:VAL:HG23	2.18	0.43
4:B:9:GLU:HB2	4:B:217:ARG:HH12	1.83	0.43
5:C:52:LEU:CD2	5:C:118:GLN:HE22	2.32	0.43
5:C:91:LEU:HD21	5:C:99:VAL:HG23	2.00	0.43
6:D:112:VAL:HG22	6:D:161:ASN:ND2	2.34	0.43
7:E:53:LEU:HD22	7:E:57:LYS:HZ1	1.84	0.43
8:F:32:ASN:HD22	8:F:32:ASN:N	2.16	0.43
8:F:44:GLY:CA	8:F:59:TYR:CE1	3.01	0.43
9:G:15:ASP:OD2	9:G:44:TYR:OH	2.28	0.43
13:K:33:THR:HB	13:K:38:ASN:C	2.39	0.43
15:M:20:THR:C	15:M:22:ILE:N	2.72	0.43
17:O:57:LEU:HA	17:O:57:LEU:HD12	1.51	0.43
17:O:73:GLU:HA	17:O:73:GLU:OE1	2.19	0.43
20:R:26:LEU:HD11	20:R:39:VAL:HG23	2.01	0.43
22:T:61:SER:O	22:T:62:LEU:C	2.56	0.43
22:T:68:LYS:HA	22:T:68:LYS:HD2	1.83	0.43
1:A:1371:G:C2	1:A:1372:U:C6	3.06	0.43
1:A:1424:C:H2'	1:A:1425:U:O4'	2.19	0.43
1:A:169:C:O2'	1:A:170:U:H5'	2.19	0.43
1:A:300:A:H2'	1:A:301:G:O4'	2.19	0.43
1:A:41:G:O2'	1:A:42:G:H5'	2.18	0.43
1:A:647:C:H2'	1:A:648:A:H8	1.83	0.43
1:A:653:A:P	10:H:56:LYS:NZ	2.91	0.43
1:A:709:G:C6	1:A:710:G:C5	3.06	0.43
1:A:916:G:O2'	1:A:917:G:H5'	2.18	0.43
4:B:124:SER:HB2	4:B:125:PRO:CD	2.44	0.43
4:B:91:PRO:HA	4:B:154:LEU:HD12	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:187:LEU:CD1	4:B:214:ILE:HG21	2.45	0.43
5:C:30:ARG:NH1	5:C:30:ARG:HB3	2.33	0.43
5:C:40:ARG:HB3	5:C:44:GLU:OE1	2.18	0.43
7:E:31:LEU:HD22	7:E:43:LEU:HD21	2.01	0.43
8:F:19:LEU:HD23	8:F:19:LEU:C	2.39	0.43
8:F:48:LEU:HD21	8:F:60:PHE:CE1	2.54	0.43
9:G:101:LEU:O	9:G:102:ARG:C	2.57	0.43
11:I:93:ARG:CZ	11:I:93:ARG:HB3	2.47	0.43
14:L:69:TYR:HB2	14:L:90:VAL:HG21	2.01	0.43
15:M:33:ALA:C	15:M:35:GLU:N	2.73	0.43
19:Q:3:LYS:HD3	19:Q:61:GLU:O	2.18	0.43
1:A:1203:C:H2'	1:A:1204:A:H8	1.84	0.42
1:A:1478:C:H2'	1:A:1479:C:C6	2.54	0.42
1:A:1516:G:H2'	1:A:1518:A:OP2	2.19	0.42
1:A:342:C:O2'	1:A:343:U:H5'	2.19	0.42
1:A:502:G:P	14:L:118:SER:HG	2.42	0.42
4:B:118:LEU:O	4:B:119:GLU:C	2.56	0.42
4:B:73:THR:HB	4:B:170:GLU:OE2	2.19	0.42
5:C:90:GLU:HA	5:C:93:LYS:HB2	2.00	0.42
6:D:162:LEU:HD23	6:D:165:MET:HG3	2.00	0.42
7:E:21:ALA:O	7:E:22:GLY:C	2.56	0.42
9:G:118:VAL:O	9:G:121:ALA:HB3	2.19	0.42
11:I:127:LYS:HE3	11:I:127:LYS:HA	2.01	0.42
11:I:65:VAL:O	11:I:66:ARG:HB2	2.19	0.42
15:M:23:TYR:CB	15:M:67:GLU:HA	2.49	0.42
18:P:74:LEU:CB	18:P:79:VAL:HG21	2.49	0.42
19:Q:40:LYS:HE2	19:Q:42:TYR:CE2	2.54	0.42
8:F:100:ASN:ND2	20:R:23:LYS:HG2	2.31	0.42
21:S:22:LEU:HA	21:S:25:LYS:NZ	2.33	0.42
22:T:53:LEU:CD1	22:T:101:GLY:HA2	2.49	0.42
1:A:1201:A:HO2'	1:A:1202:G:P	2.42	0.42
1:A:929:G:H5''	1:A:1533:C:C5	2.55	0.42
1:A:180:U:H2'	1:A:181:G:H5'	2.01	0.42
1:A:190(H):G:C2'	1:A:190(I):G:H5'	2.49	0.42
1:A:344:A:H4'	1:A:345:C:OP2	2.19	0.42
1:A:478:A:H3'	1:A:479:C:C5'	2.49	0.42
1:A:610:G:O2'	1:A:611:A:H5'	2.19	0.42
1:A:954:G:H2'	1:A:955:U:C6	2.52	0.42
6:D:110:PHE:CD2	6:D:148:VAL:HG22	2.54	0.42
11:I:106:ALA:O	11:I:107:ARG:C	2.56	0.42
11:I:93:ARG:HB2	11:I:93:ARG:HH11	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:K:74:ALA:C	13:K:76:GLY:N	2.72	0.42
15:M:34:LEU:CD1	15:M:41:PRO:HA	2.43	0.42
17:O:39:LEU:HD23	17:O:39:LEU:O	2.19	0.42
1:A:1286:A:H2	23:V:18:TYR:HH	1.61	0.42
1:A:107:G:N7	22:T:15:ARG:NH2	2.59	0.42
1:A:1123:A:H2'	1:A:1124:G:O4'	2.19	0.42
1:A:1357:A:C5	1:A:1358:U:C5	3.07	0.42
1:A:695:A:H2'	1:A:696:A:C8	2.54	0.42
1:A:946:A:C6	1:A:947:G:C6	3.08	0.42
4:B:148:TYR:CD2	4:B:148:TYR:N	2.84	0.42
4:B:42:ILE:HG21	4:B:202:PRO:O	2.20	0.42
5:C:70:VAL:O	5:C:105:GLU:HA	2.18	0.42
5:C:11:ARG:O	5:C:14:ILE:O	2.38	0.42
6:D:149:ALA:HB3	6:D:152:SER:HB2	2.00	0.42
6:D:33:MET:HA	6:D:37:PRO:HA	2.00	0.42
9:G:153:HIS:ND1	9:G:153:HIS:N	2.66	0.42
10:H:91:ARG:NH1	19:Q:33:GLY:HA3	2.35	0.42
11:I:42:ARG:NH1	11:I:42:ARG:HG2	2.30	0.42
12:J:28:ARG:NH1	12:J:28:ARG:HG2	2.33	0.42
13:K:69:ALA:O	13:K:72:ALA:N	2.52	0.42
15:M:2:ALA:HB3	15:M:53:VAL:HG11	2.01	0.42
15:M:90:LEU:HD22	15:M:93:ARG:HD2	2.01	0.42
19:Q:26:GLN:O	19:Q:27:PHE:HB3	2.19	0.42
20:R:86:VAL:HG12	20:R:87:ARG:N	2.30	0.42
21:S:39:THR:CG2	21:S:40:ILE:N	2.80	0.42
1:A:1319:A:OP2	21:S:5:LEU:HD21	2.20	0.42
1:A:363:A:C2	14:L:31:PRO:HG2	2.54	0.42
1:A:46:G:H2'	1:A:366:C:C5	2.54	0.42
1:A:848:C:O2'	1:A:849:C:H5'	2.19	0.42
1:A:866:C:H2'	1:A:867:G:O4'	2.20	0.42
4:B:164:VAL:O	4:B:186:ALA:HA	2.20	0.42
1:A:1206:G:H1'	5:C:193:TYR:O	2.18	0.42
5:C:30:ARG:HB2	5:C:30:ARG:NH1	2.33	0.42
7:E:110:LEU:HD13	7:E:118:ILE:HG21	2.01	0.42
8:F:55:ASP:CB	8:F:86:ARG:HH12	2.31	0.42
8:F:37:VAL:HG22	8:F:65:VAL:CG1	2.50	0.42
11:I:10:ARG:O	11:I:13:ALA:N	2.53	0.42
13:K:13:GLN:HA	13:K:75:TYR:O	2.19	0.42
13:K:95:ILE:O	13:K:99:GLN:HG3	2.19	0.42
14:L:39:VAL:HA	14:L:79:GLU:CG	2.49	0.42
1:A:521:G:OP1	14:L:73:GLU:O	2.36	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:M:87:TYR:C	15:M:89:GLY:N	2.71	0.42
18:P:33:ILE:O	18:P:34:GLU:HB2	2.19	0.42
19:Q:31:LEU:HG	19:Q:32:TYR:CD2	2.54	0.42
20:R:29:PHE:CZ	20:R:31:LEU:HG	2.55	0.42
1:A:1453:G:H2'	1:A:1454:G:O4'	2.20	0.42
1:A:1455:G:O2'	1:A:1459:C:H5'	2.19	0.42
1:A:741:G:O2'	1:A:742:G:H5'	2.19	0.42
1:A:791:G:H2'	1:A:792:A:H5''	2.00	0.42
1:A:958:A:N3	1:A:985:C:O2'	2.45	0.42
1:A:966:G:H2'	1:A:967:C:O4'	2.19	0.42
4:B:212:GLN:HE22	4:B:216:SER:HB3	1.81	0.42
4:B:230:VAL:CG1	4:B:231:GLU:N	2.81	0.42
4:B:24:TRP:CZ3	4:B:26:PRO:HA	2.55	0.42
4:B:16:HIS:CB	4:B:44:LEU:HD21	2.48	0.42
5:C:30:ARG:CB	5:C:30:ARG:CZ	2.98	0.42
6:D:36:ARG:HA	6:D:38:TYR:CE2	2.55	0.42
9:G:149:ARG:HG2	13:K:59:TYR:CE1	2.55	0.42
1:A:587:G:OP1	10:H:89:PRO:HB3	2.19	0.42
12:J:38:ILE:HD12	12:J:71:LEU:CB	2.50	0.42
14:L:120:TYR:O	14:L:122:THR:N	2.52	0.42
14:L:53:ARG:HD2	14:L:93:LEU:HD21	2.00	0.42
21:S:45:VAL:HA	21:S:62:ILE:HG22	2.02	0.42
1:A:1205:U:O2'	5:C:195:VAL:CG2	2.68	0.42
1:A:1237:C:C4'	1:A:1334:G:H21	2.33	0.42
1:A:1416:G:C2	1:A:1485:U:O2	2.73	0.42
1:A:1415:G:C4	1:A:1416:G:C8	3.06	0.42
1:A:1470:G:O2'	1:A:1471:G:H5'	2.18	0.42
1:A:1511:G:H2'	1:A:1512:U:O4'	2.19	0.42
1:A:397:A:H5'	1:A:398:C:P	2.60	0.42
1:A:412:A:H2'	1:A:413:G:C5'	2.50	0.42
1:A:420:U:H5'	1:A:424:G:H1'	2.01	0.42
1:A:439:A:H2'	1:A:440:A:O4'	2.20	0.42
1:A:624:C:O2'	1:A:625:G:H5'	2.19	0.42
1:A:990:C:H5''	1:A:1018:C:H5'	2.02	0.42
4:B:170:GLU:O	4:B:173:ALA:HB3	2.19	0.42
4:B:16:HIS:NE2	4:B:214:ILE:HG12	2.35	0.42
11:I:23:ASN:ND2	11:I:23:ASN:O	2.52	0.42
13:K:110:ASP:HB2	20:R:88:LYS:HZ1	1.82	0.42
13:K:126:ARG:HB3	13:K:127:LYS:H	1.48	0.42
13:K:14:VAL:O	13:K:15:ALA:HB3	2.19	0.42
15:M:9:ILE:N	15:M:9:ILE:HD12	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:N:47:LEU:O	16:N:50:LYS:N	2.52	0.42
18:P:6:LEU:HD21	18:P:73:LEU:HD11	2.02	0.42
19:Q:76:LEU:C	19:Q:76:LEU:CD2	2.87	0.42
20:R:26:LEU:HD21	20:R:39:VAL:CG2	2.50	0.42
22:T:49:ALA:O	22:T:52:ALA:HB3	2.20	0.42
1:A:1305:G:H5'	23:V:4:GLY:HA3	1.99	0.42
1:A:105:G:H2'	1:A:106:C:C6	2.54	0.42
1:A:114:U:H2'	1:A:115:G:C8	2.55	0.42
1:A:1250:A:H2'	1:A:1251:A:C8	2.54	0.42
1:A:1303:C:N4	1:A:1304:G:C6	2.87	0.42
1:A:1346:A:C5	9:G:10:ARG:NH2	2.88	0.42
1:A:1505:G:H3'	1:A:1505:G:C8	2.54	0.42
1:A:300:A:H1'	1:A:565:U:O2	2.20	0.42
1:A:320:C:H2'	1:A:321:A:C8	2.54	0.42
1:A:602:A:C2	1:A:637:G:C2	3.07	0.42
1:A:929:G:H5''	1:A:1533:C:C6	2.54	0.42
4:B:77:ALA:HB3	4:B:211:ILE:HG21	2.02	0.42
5:C:14:ILE:CG2	5:C:15:THR:N	2.72	0.42
5:C:92:ALA:O	5:C:93:LYS:C	2.58	0.42
6:D:207:TYR:C	6:D:209:ARG:N	2.73	0.42
7:E:15:ARG:HH11	7:E:15:ARG:HG3	1.84	0.42
8:F:31:GLU:CA	8:F:35:ALA:HB2	2.47	0.42
9:G:116:ALA:O	9:G:119:ARG:HB2	2.19	0.42
11:I:40:LEU:O	11:I:41:VAL:C	2.57	0.42
11:I:84:ALA:C	11:I:86:VAL:N	2.73	0.42
12:J:90:LEU:N	12:J:91:PRO:CD	2.61	0.42
15:M:110:ARG:HH11	15:M:110:ARG:CG	2.32	0.42
15:M:72:ALA:O	15:M:76:ALA:HB3	2.20	0.42
5:C:34:LEU:HD12	16:N:25:VAL:HG21	2.02	0.42
16:N:3:ARG:O	16:N:4:LYS:C	2.57	0.42
1:A:1305:G:H5''	23:V:4:GLY:HA3	1.99	0.42
23:V:6:ARG:O	23:V:8:THR:N	2.45	0.42
1:A:1053:G:O6	1:A:1199:U:H2'	2.19	0.42
1:A:1333:A:H2'	1:A:1334:G:O4'	2.20	0.42
1:A:1396:A:H4'	1:A:1397:C:H5''	2.02	0.42
1:A:258:G:O2'	1:A:259:G:H5'	2.19	0.42
1:A:47:C:H5''	1:A:365:U:C6	2.55	0.42
1:A:458:C:C2'	1:A:459:G:H8	2.33	0.42
1:A:475:G:C2'	1:A:476:G:H5''	2.47	0.42
1:A:605:U:O2'	1:A:606:G:H5'	2.19	0.42
1:A:737:A:H1'	8:F:73:ASN:ND2	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:928:G:H4'	1:A:1533:C:C5'	2.29	0.42
4:B:44:LEU:O	4:B:47:THR:N	2.53	0.42
4:B:87:ARG:O	4:B:88:ALA:HB2	2.20	0.42
5:C:132:ARG:O	5:C:136:GLN:N	2.47	0.42
1:A:1377:A:O2'	9:G:2:ALA:HB3	2.20	0.42
10:H:117:GLY:O	10:H:119:LEU:CD2	2.68	0.42
11:I:42:ARG:O	11:I:44:VAL:N	2.52	0.42
11:I:44:VAL:O	11:I:51:ARG:NH1	2.52	0.42
12:J:55:LYS:HG3	12:J:56:HIS:N	2.35	0.42
17:O:43:LEU:HD11	17:O:53:HIS:HA	2.01	0.42
19:Q:69:LYS:C	19:Q:70:ARG:HD2	2.40	0.42
20:R:17:SER:H	20:R:19:LYS:NZ	2.18	0.42
22:T:54:LYS:CE	22:T:100:ILE:HD12	2.48	0.42
1:A:1256:A:H2	1:A:1277:C:C4	2.38	0.42
1:A:532:A:H2'	1:A:533:A:OP1	2.20	0.42
1:A:602:A:H2'	1:A:603:U:O4'	2.20	0.42
1:A:904:C:O2'	1:A:905:U:H5'	2.20	0.42
1:A:927:G:H2'	1:A:928:G:H8	1.85	0.42
4:B:103:THR:HA	4:B:180:LEU:HD11	2.01	0.42
6:D:101:LEU:HD12	6:D:101:LEU:O	2.19	0.42
6:D:180:GLY:O	6:D:181:MET:C	2.58	0.42
6:D:61:LYS:NZ	6:D:62:GLN:NE2	2.67	0.42
7:E:70:PRO:O	7:E:77:PRO:HD3	2.20	0.42
8:F:68:PRO:O	8:F:69:GLU:C	2.58	0.42
13:K:97:ALA:O	13:K:98:LEU:C	2.57	0.42
15:M:59:TYR:O	15:M:63:THR:HG21	2.20	0.42
18:P:21:VAL:HG21	18:P:59:TRP:CG	2.55	0.42
19:Q:40:LYS:HD3	19:Q:42:TYR:OH	2.19	0.42
19:Q:81:ARG:HB2	19:Q:81:ARG:CZ	2.50	0.42
22:T:39:LYS:HE3	22:T:55:ILE:HD13	2.02	0.42
22:T:96:GLY:O	22:T:97:ALA:HB3	2.18	0.42
23:V:17:THR:O	23:V:22:ARG:HD3	2.20	0.42
3:X:36:U:H2'	3:X:37:T6A:C8	2.52	0.42
1:A:1037:C:H2'	1:A:1038:C:C6	2.55	0.42
1:A:1054:C:H2'	1:A:1055:A:H5''	2.01	0.42
1:A:1520:G:H2'	1:A:1521:G:C8	2.55	0.42
1:A:409:G:OP2	1:A:431:A:C5'	2.57	0.42
1:A:440:A:C6	1:A:495:U:C2	3.08	0.42
1:A:462:G:O2'	18:P:82:GLN:NE2	2.53	0.42
1:A:604:G:H2'	1:A:605:U:H6	1.84	0.42
1:A:665:A:H2'	1:A:725:G:N2	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:833:U:H2'	1:A:834:C:C6	2.54	0.42
1:A:851:G:O2'	1:A:852:G:H5'	2.19	0.42
4:B:32:ILE:HD13	4:B:40:HIS:CD2	2.55	0.42
5:C:46:GLU:C	5:C:48:TYR:H	2.23	0.42
6:D:110:PHE:N	6:D:110:PHE:CD1	2.87	0.42
1:A:559:A:P	7:E:126:ARG:NH2	2.93	0.42
7:E:76:ILE:HG23	7:E:142:LEU:HD13	2.01	0.42
7:E:50:GLU:OE1	7:E:53:LEU:HD12	2.20	0.42
10:H:82:HIS:CG	10:H:83:ILE:H	2.38	0.42
11:I:118:LYS:HZ2	11:I:118:LYS:HB2	1.85	0.42
11:I:78:LYS:HD2	11:I:78:LYS:O	2.20	0.42
16:N:29:ARG:HB3	16:N:40:CYS:CB	2.49	0.42
17:O:21:ASP:OD1	17:O:24:SER:HB3	2.20	0.42
19:Q:102:GLY:O	19:Q:103:GLY:O	2.38	0.42
20:R:44:LEU:HD23	20:R:50:ILE:HA	2.01	0.42
1:A:735:C:H1'	20:R:75:ILE:HD11	2.02	0.42
20:R:47:THR:CG2	20:R:83:GLU:H	2.33	0.42
1:A:1284:C:H3'	1:A:1285:A:C8	2.55	0.41
1:A:1349:A:C6	1:A:1374:A:C8	3.08	0.41
1:A:768:A:H4'	1:A:1523:G:N2	2.35	0.41
1:A:358:U:H2'	1:A:359:U:C6	2.55	0.41
1:A:454:C:H4'	18:P:68:ASP:OD2	2.20	0.41
1:A:836:G:H2'	1:A:837:G:H8	1.85	0.41
1:A:923:A:O4'	1:A:1398:A:C2	2.72	0.41
1:A:965:A:N1	1:A:969:A:C2	2.88	0.41
1:A:992:U:O2'	1:A:993:G:OP2	2.32	0.41
4:B:78:GLN:HG2	4:B:94:ASN:OD1	2.20	0.41
6:D:102:ASP:CG	6:D:103:ASN:N	2.74	0.41
7:E:82:VAL:HG11	7:E:134:ALA:O	2.20	0.41
8:F:52:ILE:O	8:F:53:ALA:HB3	2.20	0.41
8:F:74:ASP:O	8:F:77:ARG:N	2.53	0.41
1:A:1539:C:O2	9:G:82:GLY:HA3	2.20	0.41
10:H:11:THR:CB	10:H:14:ARG:HH12	2.32	0.41
13:K:48:ILE:CD1	13:K:63:LEU:HB2	2.50	0.41
1:A:625:G:OP1	18:P:9:PHE:O	2.38	0.41
1:A:484:G:H5'	1:A:486:U:O4'	2.20	0.41
1:A:536:C:H2'	1:A:537:G:C8	2.56	0.41
1:A:673:G:N2	1:A:674:G:C2	2.87	0.41
1:A:754:C:C3'	1:A:754:C:O2	2.67	0.41
1:A:782:A:H2'	1:A:783:C:O4'	2.20	0.41
1:A:575:G:C5	1:A:881:G:C2	3.07	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:915:A:H2'	1:A:916:G:H5'	2.02	0.41
4:B:169:LYS:HD3	4:B:170:GLU:OE2	2.20	0.41
4:B:201:ILE:HG21	4:B:214:ILE:HG21	2.02	0.41
4:B:53:ARG:O	4:B:56:ARG:HB3	2.21	0.41
6:D:194:LEU:HD22	6:D:194:LEU:N	2.35	0.41
8:F:15:ASP:OD1	8:F:17:SER:HB2	2.20	0.41
11:I:28:VAL:O	11:I:29:ASN:HB2	2.20	0.41
14:L:119:LYS:N	14:L:119:LYS:CD	2.83	0.41
14:L:86:ARG:O	14:L:86:ARG:HG3	2.19	0.41
15:M:16:ASP:OD1	15:M:16:ASP:N	2.47	0.41
15:M:67:GLU:O	15:M:68:GLY:C	2.58	0.41
16:N:17:LYS:HG3	16:N:18:VAL:N	2.34	0.41
16:N:5:ALA:C	16:N:7:ILE:H	2.23	0.41
16:N:60:SER:O	16:N:61:TRP:HB3	2.20	0.41
17:O:32:LEU:O	17:O:33:THR:C	2.59	0.41
1:A:1050:G:O2'	1:A:1051:C:H5'	2.21	0.41
1:A:1255:G:O2'	1:A:1258:G:N3	2.51	0.41
1:A:376:G:N3	1:A:389:A:C2	2.88	0.41
1:A:662:G:H2'	1:A:663:A:C8	2.56	0.41
1:A:778:G:O2'	1:A:779:C:H5'	2.20	0.41
4:B:137:ARG:HA	4:B:140:HIS:CD2	2.55	0.41
4:B:75:LYS:O	4:B:76:GLN:C	2.59	0.41
6:D:10:ARG:O	6:D:13:ARG:N	2.53	0.41
6:D:110:PHE:N	6:D:110:PHE:HD1	2.18	0.41
6:D:146:ILE:N	6:D:146:ILE:CD1	2.82	0.41
7:E:131:ILE:HD13	7:E:131:ILE:HA	1.82	0.41
7:E:20:GLN:C	7:E:21:ALA:O	2.58	0.41
8:F:63:TYR:HD1	8:F:63:TYR:N	2.18	0.41
9:G:23:VAL:HG12	9:G:27:ILE:HD11	2.02	0.41
10:H:45:ILE:C	10:H:47:GLY:N	2.73	0.41
11:I:118:LYS:O	11:I:119:ALA:CB	2.64	0.41
12:J:32:ALA:C	12:J:34:VAL:H	2.23	0.41
15:M:59:TYR:O	15:M:63:THR:CG2	2.69	0.41
16:N:11:LYS:C	16:N:13:THR:N	2.74	0.41
22:T:77:ALA:O	22:T:78:ALA:C	2.58	0.41
1:A:1112:C:O2	5:C:178:LEU:O	2.39	0.41
1:A:129:U:O2'	1:A:130:A:H2'	2.20	0.41
1:A:276:G:O2'	1:A:277:C:H5'	2.21	0.41
1:A:851:G:H2'	1:A:852:G:H8	1.85	0.41
1:A:924:C:H5'	1:A:1399:C:OP2	2.20	0.41
1:A:974:A:C8	1:A:974:A:OP1	2.73	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:215:LEU:O	4:B:218:ALA:HB3	2.20	0.41
6:D:176:LEU:HA	6:D:183:GLY:HA2	2.01	0.41
7:E:131:ILE:O	7:E:134:ALA:HB3	2.20	0.41
11:I:42:ARG:O	11:I:45:ALA:N	2.42	0.41
14:L:83:VAL:CG2	14:L:100:ILE:HG23	2.50	0.41
1:A:1085:U:C2	1:A:1094:G:O6	2.73	0.41
1:A:163:C:H2'	1:A:164:U:H5'	1.98	0.41
1:A:323:U:H2'	1:A:324:G:O4'	2.20	0.41
1:A:346:G:O2'	1:A:347:G:H5'	2.18	0.41
1:A:692:U:H1'	1:A:695:A:N7	2.36	0.41
1:A:22:G:H4'	1:A:885:G:C8	2.55	0.41
4:B:118:LEU:HD13	4:B:142:LEU:HB2	2.02	0.41
4:B:26:PRO:C	4:B:28:PHE:H	2.23	0.41
4:B:55:PHE:O	4:B:56:ARG:C	2.57	0.41
4:B:70:PHE:CD1	4:B:70:PHE:N	2.89	0.41
4:B:8:LYS:O	4:B:9:GLU:C	2.58	0.41
5:C:113:ALA:O	5:C:114:PRO:C	2.58	0.41
5:C:172:ARG:HB3	5:C:172:ARG:NH1	2.35	0.41
5:C:33:LEU:CD2	16:N:53:LEU:HD21	2.51	0.41
5:C:83:ARG:NH1	5:C:83:ARG:HG3	2.35	0.41
9:G:50:ILE:O	9:G:54:THR:HB	2.21	0.41
10:H:134:ILE:HD12	10:H:134:ILE:HA	1.81	0.41
10:H:20:TYR:CE1	10:H:78:GLN:NE2	2.88	0.41
11:I:47:LEU:C	11:I:49:PRO:HD2	2.41	0.41
16:N:53:LEU:HB3	16:N:56:VAL:HB	2.02	0.41
19:Q:95:TYR:O	19:Q:98:LEU:HD12	2.20	0.41
1:A:103:C:P	22:T:17:ARG:NH1	2.92	0.41
1:A:1151:A:H5''	12:J:42:THR:OG1	2.21	0.41
1:A:1227:A:C8	1:A:1227:A:C3'	3.04	0.41
1:A:1234:C:C2'	1:A:1235:U:H5'	2.51	0.41
1:A:128:G:C6	1:A:129:U:C4	3.09	0.41
1:A:1302:U:H5	15:M:17:VAL:HG21	1.85	0.41
1:A:1451:A:O3'	1:A:1452:C:H6	2.04	0.41
1:A:458:C:H2'	1:A:459:G:O4'	2.20	0.41
5:C:51:GLY:O	5:C:53:ALA:N	2.44	0.41
6:D:105:VAL:HG12	6:D:117:ALA:CB	2.51	0.41
6:D:125:HIS:HA	6:D:149:ALA:HB3	2.03	0.41
6:D:54:TYR:O	6:D:55:ALA:C	2.58	0.41
10:H:35:ILE:O	10:H:36:LEU:C	2.58	0.41
11:I:48:GLU:OE2	11:I:51:ARG:HD2	2.20	0.41
12:J:78:ASN:O	12:J:82:ILE:HD12	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:778:G:H1'	13:K:119:CYS:HB3	2.03	0.41
13:K:67:ASP:CG	13:K:71:LYS:HE3	2.41	0.41
15:M:31:LYS:O	15:M:35:GLU:OE1	2.39	0.41
15:M:70:LEU:HD23	15:M:70:LEU:O	2.20	0.41
23:V:13:ILE:O	23:V:16:GLY:N	2.39	0.41
1:A:533:A:C6	1:A:536:C:N3	2.88	0.41
1:A:664:G:N2	1:A:741:G:H1	2.07	0.41
1:A:748:C:O2'	1:A:749:C:H6	2.03	0.41
4:B:18:GLY:CA	4:B:41:ILE:HG23	2.49	0.41
5:C:15:THR:HB	5:C:181:ASN:HB2	2.02	0.41
5:C:6:HIS:HD2	5:C:7:PRO:HD2	1.85	0.41
6:D:202:LEU:O	6:D:205:GLU:N	2.53	0.41
7:E:24:ARG:CB	7:E:24:ARG:NH1	2.84	0.41
7:E:54:ALA:O	7:E:58:ALA:N	2.44	0.41
9:G:75:VAL:O	9:G:75:VAL:CG1	2.68	0.41
11:I:107:ARG:CB	11:I:107:ARG:NH1	2.84	0.41
11:I:17:VAL:HG11	11:I:81:ILE:CA	2.50	0.41
15:M:73:GLU:O	15:M:74:VAL:C	2.59	0.41
1:A:376:G:H5''	18:P:5:ARG:HD2	2.01	0.41
19:Q:34:LYS:HG3	19:Q:34:LYS:O	2.21	0.41
19:Q:60:ILE:CD1	19:Q:61:GLU:N	2.84	0.41
1:A:1096:C:H2'	1:A:1097:C:C6	2.55	0.41
1:A:1220:G:O2'	1:A:1221:G:H5'	2.20	0.41
1:A:1431:C:O2'	1:A:1432:G:H5'	2.21	0.41
1:A:628:G:H2'	1:A:629:G:C8	2.55	0.41
1:A:674:G:H2'	1:A:675:A:H8	1.86	0.41
1:A:994:A:N7	1:A:1216:G:H4'	2.36	0.41
4:B:102:LEU:CD1	4:B:102:LEU:N	2.84	0.41
4:B:144:ARG:CG	4:B:145:LEU:N	2.83	0.41
5:C:64:VAL:CB	5:C:99:VAL:HG11	2.50	0.41
6:D:173:TRP:O	6:D:186:LEU:HB2	2.20	0.41
7:E:77:PRO:HD2	7:E:142:LEU:HD13	2.03	0.41
7:E:50:GLU:O	7:E:51:VAL:C	2.59	0.41
7:E:9:LYS:NZ	7:E:111:GLU:OE1	2.53	0.41
9:G:38:LEU:O	9:G:40:ALA:N	2.54	0.41
11:I:46:ALA:C	11:I:48:GLU:H	2.23	0.41
15:M:80:ARG:C	15:M:82:MET:H	2.23	0.41
1:A:1048:G:OP1	16:N:3:ARG:HA	2.21	0.41
1:A:760:G:N3	19:Q:103:GLY:HA3	2.36	0.41
19:Q:13:ASP:OD2	19:Q:13:ASP:O	2.39	0.41
21:S:74:PHE:N	21:S:74:PHE:CD1	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1035:A:C2'	1:A:1036:G:H5'	2.51	0.41
1:A:1207:G:O2'	1:A:1208:C:H5'	2.20	0.41
1:A:1240:U:P	9:G:116:ALA:HB2	2.61	0.41
1:A:165:C:C2	1:A:166:G:C8	3.08	0.41
1:A:353:A:C8	1:A:353:A:C5'	3.03	0.41
1:A:802:A:H2'	1:A:803:G:C5'	2.50	0.41
4:B:27:LYS:NZ	4:B:193:ASP:OD2	2.53	0.41
4:B:87:ARG:HH11	4:B:233:SER:HA	1.85	0.41
4:B:30:ARG:C	4:B:32:ILE:H	2.23	0.41
5:C:133:ALA:O	5:C:137:ALA:N	2.41	0.41
5:C:39:ILE:HD12	5:C:57:ILE:CD1	2.51	0.41
5:C:8:ILE:HG22	5:C:9:GLY:N	2.36	0.41
6:D:11:LEU:HD22	6:D:66:ARG:CZ	2.50	0.41
6:D:153:ARG:CD	6:D:181:MET:HE3	2.50	0.41
11:I:8:GLY:HA3	11:I:79:LEU:HB3	2.02	0.41
12:J:16:LEU:O	12:J:19:SER:N	2.54	0.41
14:L:46:LYS:HG3	14:L:47:LYS:N	2.36	0.41
15:M:58:GLU:OE2	15:M:58:GLU:HA	2.21	0.41
12:J:47:PHE:CD2	16:N:34:TYR:HE2	2.39	0.41
5:C:13:GLY:HA2	16:N:57:ARG:CZ	2.51	0.41
18:P:58:TYR:O	18:P:61:SER:N	2.54	0.41
1:A:1048:G:H1'	1:A:1215:G:H5'	2.02	0.41
1:A:1231:G:H2'	1:A:1232:U:C6	2.56	0.41
1:A:1321:C:C5	1:A:1322:C:C2	3.09	0.41
1:A:1424:C:H2'	1:A:1425:U:H6	1.84	0.41
1:A:253:U:H2'	1:A:254:G:H8	1.86	0.41
1:A:443:C:H2'	1:A:444:C:C6	2.56	0.41
1:A:792:A:H1'	1:A:794:A:N7	2.36	0.41
4:B:128:GLU:HA	4:B:135:GLN:NE2	2.35	0.41
6:D:63:LYS:HD2	6:D:198:VAL:HG22	2.02	0.41
6:D:61:LYS:HZ1	6:D:62:GLN:NE2	2.19	0.41
9:G:31:MET:HA	9:G:39:ALA:HB2	2.03	0.41
11:I:44:VAL:O	11:I:51:ARG:NH2	2.54	0.41
13:K:26:ASN:O	13:K:27:ASN:CB	2.68	0.41
14:L:111:LYS:O	14:L:112:ASP:HB2	2.21	0.41
16:N:29:ARG:HH11	16:N:29:ARG:HG2	1.85	0.41
18:P:51:VAL:O	18:P:52:ASP:C	2.58	0.41
19:Q:51:TYR:C	19:Q:52:LYS:HD2	2.41	0.41
1:A:1096:C:H2'	1:A:1097:C:H6	1.85	0.41
1:A:1223:C:H3'	1:A:1224:G:H5''	2.03	0.41
1:A:1229:A:C2	1:A:1230:C:C4	3.09	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1320:C:H2'	1:A:1321:C:O4'	2.20	0.41
1:A:1360:A:C2'	1:A:1361:G:C8	3.00	0.41
1:A:1469:G:O2'	1:A:1470:G:H5'	2.21	0.41
1:A:791:G:N2	1:A:1497:G:O3'	2.54	0.41
4:B:134:GLU:HG2	4:B:137:ARG:HH21	1.86	0.41
6:D:148:VAL:HG11	6:D:158:ILE:HD13	2.03	0.41
6:D:52:SER:O	6:D:54:TYR:N	2.54	0.41
7:E:107:ARG:HG2	7:E:111:GLU:OE1	2.20	0.41
9:G:124:LEU:O	9:G:127:ALA:HB3	2.20	0.41
9:G:32:ARG:HE	9:G:32:ARG:HB3	1.75	0.41
9:G:66:VAL:HG12	9:G:70:LYS:HE3	2.02	0.41
11:I:70:LYS:O	11:I:74:ILE:HG13	2.21	0.41
14:L:70:ILE:HG12	14:L:100:ILE:HD12	2.02	0.41
15:M:67:GLU:HB3	15:M:68:GLY:H	1.46	0.41
18:P:20:VAL:HG21	18:P:32:TYR:CD2	2.55	0.41
19:Q:37:LYS:O	19:Q:38:ARG:HB2	2.21	0.41
19:Q:76:LEU:HD23	19:Q:77:VAL:N	2.36	0.41
20:R:53:ARG:O	20:R:54:ARG:C	2.58	0.41
22:T:61:SER:O	22:T:63:ILE:N	2.54	0.41
1:A:1544:U:O3'	2:W:1:A:C5'	2.68	0.41
2:W:1:A:H2'	2:W:2:A:H5'	2.03	0.41
1:A:1017:G:H2'	1:A:1018:C:C6	2.56	0.40
1:A:1129:C:OP1	11:I:62:TYR:OH	2.37	0.40
1:A:1152:A:H5''	12:J:13:HIS:CG	2.55	0.40
1:A:1221:G:OP1	21:S:36:ARG:HD3	2.21	0.40
1:A:937:A:C2	1:A:1379:G:C6	3.09	0.40
1:A:265:G:H2'	1:A:267:C:H5	1.86	0.40
1:A:109:A:C6	1:A:326:G:C6	3.09	0.40
1:A:961:U:O2'	1:A:962:C:H5'	2.21	0.40
4:B:107:THR:O	4:B:108:ILE:C	2.59	0.40
4:B:68:ILE:HB	4:B:90:MET:HE3	2.03	0.40
4:B:97:TRP:CE3	4:B:98:LEU:O	2.74	0.40
5:C:164:ARG:HH11	5:C:164:ARG:HB3	1.86	0.40
7:E:12:LEU:N	7:E:12:LEU:HD13	2.35	0.40
8:F:91:VAL:HG12	8:F:92:LYS:N	2.36	0.40
10:H:80:ILE:O	10:H:80:ILE:HG22	2.20	0.40
11:I:46:ALA:O	11:I:78:LYS:HG2	2.21	0.40
11:I:59:PHE:HZ	11:I:88:TYR:CZ	2.39	0.40
15:M:22:ILE:CD1	15:M:25:ILE:HD12	2.51	0.40
19:Q:104:LYS:HD3	19:Q:104:LYS:C	2.42	0.40
22:T:22:ARG:C	22:T:24:LEU:N	2.73	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:T:80:ARG:O	22:T:81:LYS:C	2.60	0.40
22:T:91:LEU:HD23	22:T:91:LEU:N	2.36	0.40
1:A:1140:C:H2'	1:A:1141:C:C5	2.53	0.40
1:A:1064:G:N2	1:A:1190:G:C2'	2.84	0.40
1:A:1229:A:C4	1:A:1230:C:C5	3.09	0.40
1:A:1240:U:OP2	9:G:116:ALA:HB2	2.21	0.40
1:A:1241:G:H2'	1:A:1242:C:H6	1.86	0.40
1:A:651:C:O2'	1:A:652:U:H5'	2.22	0.40
1:A:741:G:H5'	17:O:39:LEU:HD12	2.03	0.40
1:A:788:U:O2'	1:A:789:U:H5'	2.21	0.40
4:B:137:ARG:C	4:B:139:LYS:N	2.73	0.40
4:B:139:LYS:HD3	4:B:139:LYS:C	2.41	0.40
4:B:16:HIS:O	4:B:17:PHE:C	2.59	0.40
4:B:69:LEU:HD22	4:B:71:VAL:HG13	2.02	0.40
4:B:81:VAL:C	4:B:83:MET:N	2.74	0.40
5:C:167:TRP:HB3	5:C:168:ALA:H	1.44	0.40
5:C:180:ALA:HA	5:C:206:GLU:HA	2.03	0.40
5:C:40:ARG:HG3	5:C:40:ARG:HH11	1.87	0.40
6:D:61:LYS:HD2	6:D:207:TYR:CZ	2.56	0.40
6:D:61:LYS:O	6:D:62:GLN:C	2.59	0.40
1:A:559:A:OP2	7:E:126:ARG:NH2	2.54	0.40
9:G:21:VAL:CG2	9:G:22:LEU:N	2.85	0.40
12:J:80:LYS:HA	12:J:83:GLU:CB	2.51	0.40
13:K:29:ILE:HD12	13:K:30:VAL:N	2.36	0.40
13:K:54:ARG:O	13:K:57:THR:HG22	2.20	0.40
14:L:69:TYR:CD2	14:L:70:ILE:N	2.89	0.40
15:M:25:ILE:HG22	15:M:26:GLY:N	2.37	0.40
15:M:31:LYS:O	15:M:32:GLU:C	2.57	0.40
15:M:44:ARG:HB3	15:M:46:LYS:HG2	2.04	0.40
16:N:8:GLU:O	16:N:9:LYS:C	2.59	0.40
18:P:39:TYR:CE2	18:P:41:PRO:HG3	2.56	0.40
1:A:1014:A:H2	1:A:1219:U:H1'	1.87	0.40
1:A:270:A:H2'	1:A:271:C:C6	2.57	0.40
1:A:339:C:H2'	1:A:340:U:C6	2.57	0.40
1:A:604:G:C5	1:A:605:U:C5	3.09	0.40
1:A:637:G:O2'	1:A:638:G:H5'	2.20	0.40
1:A:671:G:H2'	1:A:672:U:O4'	2.22	0.40
1:A:682:G:O2'	1:A:683:G:H5'	2.21	0.40
1:A:960:U:O2	1:A:960:U:H5'	2.21	0.40
4:B:76:GLN:NE2	4:B:207:ALA:N	2.70	0.40
5:C:58:GLU:HB2	5:C:65:ALA:HB2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:100:ARG:HB3	6:D:102:ASP:OD1	2.21	0.40
6:D:116:GLN:O	6:D:117:ALA:C	2.59	0.40
6:D:33:MET:O	6:D:35:ARG:N	2.54	0.40
7:E:143:ARG:NH1	10:H:77:GLU:OE2	2.52	0.40
12:J:16:LEU:C	12:J:18:ALA:N	2.74	0.40
12:J:64:GLU:HG2	16:N:59:ALA:HA	2.02	0.40
14:L:71:PRO:HB2	14:L:120:TYR:CE2	2.55	0.40
15:M:19:LEU:O	15:M:22:ILE:CG1	2.69	0.40
18:P:55:ARG:O	18:P:56:ALA:C	2.58	0.40
19:Q:97:SER:CB	19:Q:103:GLY:C	2.89	0.40
21:S:4:SER:O	21:S:5:LEU:CG	2.69	0.40
1:A:1184:G:OP1	1:A:1184:G:H3'	2.22	0.40
1:A:1192:C:H2'	1:A:1193:G:O4'	2.21	0.40
1:A:1348:U:H2'	1:A:1349:A:H8	1.86	0.40
1:A:1345:U:C4	1:A:1377:A:N3	2.90	0.40
1:A:1427:U:H2'	1:A:1428:A:C8	2.57	0.40
1:A:190(L):U:H3	22:T:105:SER:CB	2.33	0.40
1:A:229:U:H2'	1:A:230:G:H8	1.87	0.40
1:A:46:G:O2'	1:A:365:U:H1'	2.21	0.40
1:A:664:G:OP1	20:R:64:ARG:HD2	2.21	0.40
1:A:925:G:C6	1:A:927:G:N7	2.89	0.40
1:A:953:G:O2'	15:M:125:ARG:HA	2.21	0.40
4:B:131:PRO:C	4:B:133:LYS:N	2.74	0.40
4:B:168:THR:O	4:B:171:ALA:HB2	2.22	0.40
4:B:194:PRO:C	4:B:196:LEU:H	2.24	0.40
4:B:223:ILE:O	4:B:226:ARG:HB2	2.22	0.40
6:D:204:ILE:HG22	6:D:208:SER:OG	2.22	0.40
7:E:32:VAL:O	7:E:43:LEU:HD23	2.21	0.40
8:F:37:VAL:O	8:F:39:LYS:N	2.54	0.40
11:I:76:ALA:O	11:I:79:LEU:N	2.54	0.40
13:K:86:GLY:N	13:K:112:THR:HG23	2.34	0.40
15:M:69:GLU:HG2	15:M:69:GLU:O	2.21	0.40
17:O:76:GLU:HA	17:O:79:ARG:NH2	2.31	0.40
20:R:73:ALA:HB3	20:R:79:LEU:HD12	2.04	0.40
22:T:10:LEU:CD1	22:T:12:ALA:H	2.35	0.40
22:T:36:LEU:HD12	22:T:62:LEU:CD1	2.51	0.40
1:A:1347:G:C6	11:I:107:ARG:NH2	2.75	0.40
1:A:718:G:C8	13:K:116:HIS:HB3	2.57	0.40
1:A:862:C:H2'	1:A:863:U:C6	2.57	0.40
4:B:45:GLN:HB3	4:B:49:GLU:OE2	2.21	0.40
4:B:55:PHE:HA	4:B:58:ILE:HG13	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:C:40:ARG:HB3	5:C:44:GLU:CG	2.51	0.40
6:D:102:ASP:CG	6:D:103:ASN:H	2.25	0.40
6:D:108:LEU:O	6:D:165:MET:HE2	2.22	0.40
6:D:112:VAL:HG22	6:D:161:ASN:HD21	1.86	0.40
7:E:12:LEU:CD1	7:E:12:LEU:N	2.85	0.40
7:E:144:THR:HG22	7:E:146:ALA:HB3	2.04	0.40
7:E:90:VAL:O	7:E:91:LEU:HD23	2.22	0.40
8:F:36:ARG:O	8:F:65:VAL:HA	2.22	0.40
11:I:8:GLY:HA2	11:I:79:LEU:HB3	2.04	0.40
16:N:9:LYS:C	16:N:11:LYS:N	2.74	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	B	232/256 (91%)	129 (56%)	80 (34%)	23 (10%)	0	3
5	C	204/239 (85%)	123 (60%)	48 (24%)	33 (16%)	0	1
6	D	206/209 (99%)	151 (73%)	38 (18%)	17 (8%)	1	5
7	E	148/162 (91%)	120 (81%)	18 (12%)	10 (7%)	1	8
8	F	99/101 (98%)	68 (69%)	24 (24%)	7 (7%)	1	7
9	G	153/156 (98%)	99 (65%)	41 (27%)	13 (8%)	1	5
10	H	136/138 (99%)	106 (78%)	25 (18%)	5 (4%)	3	19
11	I	125/128 (98%)	85 (68%)	27 (22%)	13 (10%)	0	3
12	J	96/105 (91%)	57 (59%)	23 (24%)	16 (17%)	0	1
13	K	117/129 (91%)	85 (73%)	26 (22%)	6 (5%)	2	13
14	L	122/135 (90%)	85 (70%)	24 (20%)	13 (11%)	0	3
15	M	123/126 (98%)	75 (61%)	30 (24%)	18 (15%)	0	1

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
16	N	58/61 (95%)	34 (59%)	16 (28%)	8 (14%)	0	1
17	O	86/89 (97%)	54 (63%)	28 (33%)	4 (5%)	2	14
18	P	81/88 (92%)	59 (73%)	16 (20%)	6 (7%)	1	7
19	Q	102/105 (97%)	75 (74%)	17 (17%)	10 (10%)	0	3
20	R	71/88 (81%)	50 (70%)	16 (22%)	5 (7%)	1	7
21	S	78/93 (84%)	56 (72%)	14 (18%)	8 (10%)	0	3
22	T	97/106 (92%)	56 (58%)	30 (31%)	11 (11%)	0	2
23	V	22/27 (82%)	18 (82%)	2 (9%)	2 (9%)	1	4
All	All	2356/2541 (93%)	1585 (67%)	543 (23%)	228 (10%)	0	4

All (228) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	B	13	ALA
4	B	15	VAL
4	B	16	HIS
4	B	21	ARG
4	B	24	TRP
4	B	64	ARG
4	B	205	ASP
5	C	15	THR
5	C	16	ARG
5	C	52	LEU
5	C	53	ALA
5	C	61	ALA
5	C	100	ALA
5	C	179	ARG
5	C	189	ALA
6	D	9	CYS
6	D	32	ALA
6	D	36	ARG
6	D	88	VAL
7	E	78	HIS
8	F	35	ALA
8	F	64	GLN
9	G	116	ALA
9	G	155	ARG
10	H	83	ILE
10	H	91	ARG

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Mol	Chain	Res	Type
11	I	41	VAL
11	I	46	ALA
11	I	121	ARG
12	J	34	VAL
12	J	60	ARG
12	J	86	MET
12	J	90	LEU
14	L	27	LEU
14	L	28	LYS
14	L	41	ARG
14	L	47	LYS
14	L	48	PRO
14	L	80	HIS
14	L	87	GLY
14	L	115	LYS
14	L	121	GLY
14	L	123	LYS
15	M	3	ARG
15	M	27	LYS
15	M	67	GLU
15	M	74	VAL
15	M	86	CYS
16	N	29	ARG
16	N	59	ALA
19	Q	81	ARG
19	Q	97	SER
19	Q	103	GLY
20	R	19	LYS
21	S	5	LEU
21	S	6	LYS
21	S	43	GLU
22	T	11	SER
22	T	49	ALA
22	T	73	HIS
22	T	94	ALA
22	T	98	PRO
22	T	99	LEU
4	B	23	ARG
4	B	62	ALA
4	B	76	GLN
4	B	119	GLU
5	C	18	TRP

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Mol	Chain	Res	Type
5	C	26	LYS
5	C	60	ALA
5	C	91	LEU
5	C	96	GLY
5	C	102	ASN
5	C	150	LYS
5	C	187	ALA
5	C	188	LEU
6	D	10	ARG
6	D	23	GLY
6	D	25	ARG
6	D	89	THR
6	D	125	HIS
6	D	181	MET
7	E	153	LYS
9	G	68	ASN
9	G	153	HIS
11	I	43	ALA
11	I	56	LEU
11	I	94	ALA
12	J	4	ILE
12	J	26	ALA
12	J	27	ALA
12	J	72	VAL
12	J	85	LEU
13	K	75	TYR
13	K	88	GLY
13	K	126	ARG
15	M	63	THR
15	M	68	GLY
15	M	117	VAL
16	N	15	LYS
18	P	62	VAL
19	Q	49	GLU
19	Q	77	VAL
19	Q	80	GLY
19	Q	96	GLN
19	Q	99	SER
20	R	36	ASN
21	S	25	LYS
21	S	44	MET
22	T	101	GLY

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Mol	Chain	Res	Type
23	V	7	ARG
23	V	9	ARG
4	B	20	GLU
5	C	4	LYS
5	C	81	GLY
5	C	195	VAL
6	D	5	ILE
6	D	175	SER
7	E	16	THR
7	E	22	GLY
7	E	107	ARG
7	E	108	ALA
7	E	140	ARG
8	F	97	PHE
9	G	7	ALA
9	G	66	VAL
9	G	78	ARG
9	G	146	GLU
10	H	122	ARG
11	I	105	ASP
12	J	17	ASP
12	J	57	LYS
12	J	73	ASP
13	K	12	ARG
14	L	91	LYS
15	M	14	ARG
15	M	38	GLY
16	N	36	PHE
16	N	60	SER
17	O	13	GLN
18	P	64	ALA
18	P	82	GLN
19	Q	66	SER
20	R	26	LEU
21	S	72	GLY
22	T	86	ARG
4	B	74	LYS
4	B	131	PRO
4	B	202	PRO
5	C	47	LEU
5	C	146	ALA
5	C	157	ILE

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Mol	Chain	Res	Type
6	D	31	CYS
6	D	33	MET
8	F	38	GLU
8	F	70	ASP
9	G	37	ASN
9	G	109	ASN
9	G	134	ALA
10	H	46	LYS
11	I	45	ALA
11	I	47	LEU
11	I	107	ARG
11	I	127	LYS
12	J	20	ALA
12	J	40	LEU
15	M	34	LEU
15	M	100	GLY
15	M	125	ARG
16	N	6	LEU
17	O	46	HIS
19	Q	34	LYS
20	R	45	SER
21	S	42	PRO
22	T	9	ASN
4	B	88	ALA
4	B	95	GLN
4	B	113	HIS
4	B	130	ARG
4	B	177	ALA
4	B	229	VAL
5	C	49	SER
5	C	98	ASN
5	C	108	ASN
5	C	168	ALA
6	D	53	ASP
7	E	128	PRO
8	F	100	ASN
10	H	135	CYS
14	L	116	SER
15	M	4	ILE
15	M	28	ALA
15	M	73	GLU
15	M	107	ALA

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Mol	Chain	Res	Type
16	N	19	ARG
17	O	85	LEU
18	P	34	GLU
20	R	52	PRO
21	S	24	ALA
22	T	50	GLU
22	T	62	LEU
5	C	82	GLU
5	C	178	LEU
5	C	205	GLY
6	D	35	ARG
6	D	171	GLY
7	E	129	ILE
8	F	39	LYS
9	G	17	VAL
9	G	130	GLY
11	I	93	ARG
13	K	92	GLU
15	M	85	GLY
4	B	165	VAL
4	B	174	VAL
12	J	76	ASN
18	P	10	GLY
12	J	39	PRO
5	C	14	ILE
11	I	98	PRO
13	K	47	VAL
17	O	27	VAL
18	P	51	VAL
5	C	74	GLY
5	C	84	ILE
7	E	70	PRO
14	L	29	GLY
16	N	14	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	B	202/220 (92%)	181 (90%)	21 (10%)	7	25
5	C	160/188 (85%)	145 (91%)	15 (9%)	8	30
6	D	180/181 (99%)	164 (91%)	16 (9%)	9	32
7	E	115/123 (94%)	96 (84%)	19 (16%)	2	10
8	F	90/90 (100%)	83 (92%)	7 (8%)	12	38
9	G	126/127 (99%)	115 (91%)	11 (9%)	10	34
10	H	119/119 (100%)	107 (90%)	12 (10%)	7	27
11	I	98/99 (99%)	87 (89%)	11 (11%)	6	23
12	J	87/92 (95%)	85 (98%)	2 (2%)	50	73
13	K	90/99 (91%)	79 (88%)	11 (12%)	5	20
14	L	104/111 (94%)	100 (96%)	4 (4%)	33	62
15	M	100/101 (99%)	88 (88%)	12 (12%)	5	20
16	N	49/50 (98%)	47 (96%)	2 (4%)	30	60
17	O	79/80 (99%)	76 (96%)	3 (4%)	33	62
18	P	72/74 (97%)	66 (92%)	6 (8%)	11	36
19	Q	96/97 (99%)	90 (94%)	6 (6%)	18	47
20	R	64/77 (83%)	59 (92%)	5 (8%)	12	38
21	S	71/80 (89%)	63 (89%)	8 (11%)	6	22
22	T	75/82 (92%)	67 (89%)	8 (11%)	6	25
23	V	19/22 (86%)	18 (95%)	1 (5%)	22	53
All	All	1996/2112 (94%)	1816 (91%)	180 (9%)	9	32

All (180) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	B	9	GLU
4	B	15	VAL
4	B	23	ARG
4	B	24	TRP
4	B	25	ASN
4	B	64	ARG
4	B	76	GLN
4	B	92	TYR
4	B	102	LEU
4	B	114	ARG
4	B	117	GLU

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Mol	Chain	Res	Type
4	B	144	ARG
4	B	153	ARG
4	B	157	ARG
4	B	178	ARG
4	B	185	ILE
4	B	191	ASP
4	B	212	GLN
4	B	215	LEU
4	B	224	GLN
4	B	236	TYR
5	C	3	ASN
5	C	5	ILE
5	C	18	TRP
5	C	26	LYS
5	C	36	ASP
5	C	48	TYR
5	C	56	ASP
5	C	70	VAL
5	C	93	LYS
5	C	101	LEU
5	C	165	THR
5	C	167	TRP
5	C	190	ARG
5	C	196	LEU
5	C	204	LEU
6	D	9	CYS
6	D	10	ARG
6	D	15	GLU
6	D	17	VAL
6	D	25	ARG
6	D	36	ARG
6	D	38	TYR
6	D	42	GLN
6	D	57	ARG
6	D	105	VAL
6	D	106	TYR
6	D	112	VAL
6	D	118	ARG
6	D	122	ARG
6	D	156	GLU
6	D	199	ASN
7	E	12	LEU

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Mol	Chain	Res	Type
7	E	13	ILE
7	E	16	THR
7	E	31	LEU
7	E	38	GLN
7	E	41	VAL
7	E	43	LEU
7	E	47	LYS
7	E	53	LEU
7	E	73	ASN
7	E	79	GLU
7	E	80	ILE
7	E	82	VAL
7	E	89	ILE
7	E	107	ARG
7	E	120	THR
7	E	144	THR
7	E	147	ASP
7	E	150	ARG
8	F	10	LEU
8	F	24	GLU
8	F	28	ARG
8	F	30	LEU
8	F	63	TYR
8	F	82	ARG
8	F	98	LEU
9	G	8	GLU
9	G	16	LEU
9	G	38	LEU
9	G	45	ASP
9	G	72	ARG
9	G	124	LEU
9	G	126	ASP
9	G	148	ASN
9	G	149	ARG
9	G	155	ARG
9	G	156	TRP
10	H	26	VAL
10	H	50	ARG
10	H	51	VAL
10	H	81	HIS
10	H	88	LYS
10	H	91	ARG

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Mol	Chain	Res	Type
10	H	92	ARG
10	H	100	ILE
10	H	104	ARG
10	H	105	ARG
10	H	119	LEU
10	H	134	ILE
11	I	5	TYR
11	I	16	ARG
11	I	23	ASN
11	I	38	GLN
11	I	79	LEU
11	I	91	ASP
11	I	104	ARG
11	I	113	LYS
11	I	114	TYR
11	I	121	ARG
11	I	127	LYS
12	J	73	ASP
12	J	86	MET
13	K	13	GLN
13	K	29	ILE
13	K	30	VAL
13	K	41	THR
13	K	44	SER
13	K	57	THR
13	K	84	VAL
13	K	93	GLN
13	K	104	GLN
13	K	125	PHE
13	K	126	ARG
14	L	48	PRO
14	L	53	ARG
14	L	80	HIS
14	L	119	LYS
15	M	16	ASP
15	M	19	LEU
15	M	35	GLU
15	M	40	ASN
15	M	44	ARG
15	M	70	LEU
15	M	81	LEU
15	M	88	ARG

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Mol	Chain	Res	Type
15	M	106	ASN
15	M	110	ARG
15	M	115	LYS
15	M	125	ARG
16	N	7	ILE
16	N	9	LYS
17	O	10	LYS
17	O	34	LEU
17	O	56	LEU
18	P	2	VAL
18	P	62	VAL
18	P	68	ASP
18	P	74	LEU
18	P	81	ARG
18	P	82	GLN
19	Q	34	LYS
19	Q	60	ILE
19	Q	68	ARG
19	Q	74	LEU
19	Q	78	GLU
19	Q	98	LEU
20	R	18	ARG
20	R	28	GLU
20	R	31	LEU
20	R	36	ASN
20	R	54	ARG
21	S	6	LYS
21	S	7	LYS
21	S	12	ASP
21	S	34	TRP
21	S	36	ARG
21	S	41	VAL
21	S	42	PRO
21	S	61	TYR
22	T	9	ASN
22	T	13	LEU
22	T	42	GLN
22	T	45	GLN
22	T	62	LEU
22	T	74	LYS
22	T	75	ASN
22	T	80	ARG

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Mol	Chain	Res	Type
23	V	24	ARG

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

Mol	Chain	Res	Type
4	B	25	ASN
4	B	40	HIS
4	B	140	HIS
4	B	212	GLN
4	B	240	GLN
5	C	6	HIS
5	C	31	HIS
5	C	69	HIS
5	C	108	ASN
5	C	110	ASN
5	C	118	GLN
5	C	123	GLN
5	C	139	GLN
6	D	42	GLN
6	D	45	GLN
6	D	62	GLN
6	D	119	GLN
6	D	123	HIS
6	D	161	ASN
6	D	199	ASN
7	E	65	ASN
7	E	73	ASN
7	E	78	HIS
8	F	7	ASN
8	F	18	GLN
8	F	27	GLN
8	F	32	ASN
8	F	57	GLN
8	F	64	GLN
8	F	100	ASN
9	G	37	ASN
9	G	106	GLN
9	G	148	ASN
11	I	23	ASN
11	I	73	GLN
12	J	13	HIS
12	J	56	HIS

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Mol	Chain	Res	Type
12	J	78	ASN
12	J	84	GLN
13	K	22	HIS
13	K	116	HIS
13	K	117	ASN
14	L	49	ASN
14	L	75	HIS
15	M	12	ASN
15	M	40	ASN
15	M	62	ASN
17	O	13	GLN
17	O	37	ASN
17	O	53	HIS
17	O	71	GLN
18	P	82	GLN
20	R	36	ASN
21	S	14	HIS
21	S	23	ASN
21	S	47	HIS
21	S	56	GLN
21	S	65	ASN
21	S	69	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1506/1522 (98%)	240 (15%)	62 (4%)
2	W	2/3 (66%)	1 (50%)	0
3	X	9/11 (81%)	0	0
All	All	1517/1536 (98%)	241 (15%)	62 (4%)

All (241) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	8	A
1	A	9	G
1	A	31	G
1	A	32	A
1	A	39	G
1	A	47	C
1	A	48	C

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Mol	Chain	Res	Type
1	A	49	U
1	A	50	A
1	A	51	A
1	A	60	A
1	A	61	G
1	A	101	A
1	A	116	A
1	A	120	A
1	A	121	C
1	A	129(A)	G
1	A	130	A
1	A	131	C
1	A	163	C
1	A	182	U
1	A	189	G
1	A	190	C
1	A	190(A)	C
1	A	190(B)	C
1	A	190(C)	C
1	A	190(D)	U
1	A	190(E)	U
1	A	190(L)	U
1	A	195	A
1	A	197	A
1	A	201	C
1	A	202	U
1	A	203	U
1	A	204	U
1	A	216	G
1	A	217	C
1	A	244	U
1	A	247	G
1	A	251	G
1	A	252	U
1	A	266	G
1	A	267	C
1	A	280	C
1	A	289	G
1	A	321	A
1	A	328	C
1	A	329	A
1	A	332	G

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Mol	Chain	Res	Type
1	A	345	C
1	A	352	C
1	A	353	A
1	A	354	G
1	A	367	U
1	A	373	A
1	A	397	A
1	A	398	C
1	A	406	G
1	A	407	G
1	A	408	A
1	A	409	G
1	A	410	G
1	A	412	A
1	A	413	G
1	A	414	A
1	A	416	G
1	A	417	C
1	A	418	C
1	A	421	U
1	A	422	C
1	A	425	G
1	A	429	U
1	A	430	A
1	A	432	A
1	A	433	C
1	A	434	U
1	A	435	C
1	A	439	A
1	A	452	A
1	A	460	A
1	A	461	C
1	A	462	G
1	A	463	A
1	A	474	G
1	A	475	G
1	A	476	G
1	A	477	G
1	A	479	C
1	A	480	U
1	A	484	G
1	A	485	G

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Mol	Chain	Res	Type
1	A	497	A
1	A	498	U
1	A	508	C
1	A	510	A
1	A	511	C
1	A	518	C
1	A	527	G
1	A	531	U
1	A	532	A
1	A	533	A
1	A	534	U
1	A	547	A
1	A	559	A
1	A	560	U
1	A	561	U
1	A	562	C
1	A	572	A
1	A	573	A
1	A	575	G
1	A	576	G
1	A	577	G
1	A	607	A
1	A	653	A
1	A	665	A
1	A	687	A
1	A	688	G
1	A	702	A
1	A	703	G
1	A	718	G
1	A	723	U
1	A	731	G
1	A	748	C
1	A	749	C
1	A	755	G
1	A	777	A
1	A	781	A
1	A	782	A
1	A	792	A
1	A	793	U
1	A	812	C
1	A	813	U
1	A	815	A

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Mol	Chain	Res	Type
1	A	817	C
1	A	828	A
1	A	839	U
1	A	840	C
1	A	841	U
1	A	848	C
1	A	859	A
1	A	902	G
1	A	914	A
1	A	926	G
1	A	927	G
1	A	934	C
1	A	935	A
1	A	945	G
1	A	960	U
1	A	961	U
1	A	966	G
1	A	968	A
1	A	969	A
1	A	974	A
1	A	975	A
1	A	976	G
1	A	977	A
1	A	992	U
1	A	993	G
1	A	994	A
1	A	1005	A
1	A	1024	G
1	A	1026	G
1	A	1031	G
1	A	1050	G
1	A	1054	C
1	A	1055	A
1	A	1065	U
1	A	1066	C
1	A	1068	G
1	A	1094	G
1	A	1095	U
1	A	1101	A
1	A	1102	A
1	A	1117	G
1	A	1124	G

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Mol	Chain	Res	Type
1	A	1125	U
1	A	1126	U
1	A	1129	C
1	A	1130	A
1	A	1132	C
1	A	1136	U
1	A	1138	G
1	A	1139	G
1	A	1145	C
1	A	1152	A
1	A	1159	U
1	A	1183	A
1	A	1184	G
1	A	1191	A
1	A	1196	U
1	A	1197	G
1	A	1201	A
1	A	1202	G
1	A	1212	U
1	A	1214	C
1	A	1225	A
1	A	1226	C
1	A	1227	A
1	A	1256	A
1	A	1257	U
1	A	1280	A
1	A	1281	U
1	A	1282	C
1	A	1286	A
1	A	1287	A
1	A	1290	G
1	A	1300	G
1	A	1301	U
1	A	1302	U
1	A	1320	C
1	A	1338	G
1	A	1346	A
1	A	1347	G
1	A	1348	U
1	A	1361	G
1	A	1362	C
1	A	1363	A

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Mol	Chain	Res	Type
1	A	1370	G
1	A	1381	U
1	A	1398	A
1	A	1442	G
1	A	1443	G
1	A	1446	A
1	A	1452	C
1	A	1490	C
1	A	1492	A
1	A	1498	U
1	A	1499	A
1	A	1502	A
1	A	1504	G
1	A	1505	G
1	A	1506	U
1	A	1517	G
1	A	1519	A
1	A	1520	G
1	A	1529	G
1	A	1530	G
1	A	1533	C
1	A	1534	A
1	A	1539	C
2	W	2	A

All (62) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	7	G
1	A	30	U
1	A	60	A
1	A	115	G
1	A	119	A
1	A	129(A)	G
1	A	181	G
1	A	243	A
1	A	250	A
1	A	251	G
1	A	266	G
1	A	279	A
1	A	328	C
1	A	344	A

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Mol	Chain	Res	Type
1	A	353	A
1	A	366	C
1	A	372	C
1	A	407	G
1	A	428	G
1	A	429	U
1	A	484	G
1	A	496	A
1	A	509	A
1	A	533	A
1	A	559	A
1	A	560	U
1	A	575	G
1	A	687	A
1	A	701	C
1	A	748	C
1	A	792	A
1	A	812	C
1	A	840	C
1	A	960	U
1	A	965	A
1	A	975	A
1	A	992	U
1	A	993	G
1	A	1049	U
1	A	1065	U
1	A	1067	A
1	A	1101	A
1	A	1182	G
1	A	1183	A
1	A	1190	G
1	A	1196	U
1	A	1201	A
1	A	1224	G
1	A	1226	C
1	A	1281	U
1	A	1285	A
1	A	1300	G
1	A	1346	A
1	A	1347	G
1	A	1380	U
1	A	1397	C

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Mol	Chain	Res	Type
1	A	1451	A
1	A	1498	U
1	A	1503	A
1	A	1504	G
1	A	1505	G
1	A	1528	U

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	T6A	X	37	3	24,34,35	1.34	3 (12%)	24,49,52	3.90	7 (29%)
3	MNU	X	34	3,2	17,24,25	1.01	1 (5%)	19,34,37	3.73	3 (15%)

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
3	T6A	X	37	3	1/1/9/11	4/15/41/42	0/3/3/3
3	MNU	X	34	3,2	-	3/7/28/29	0/2/2/2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	X	34	MNU	C4-N3	3.05	1.38	1.33
3	X	37	T6A	O14-C14	-3.02	1.34	1.43
3	X	37	T6A	C12-N11	-2.92	1.40	1.46
3	X	37	T6A	C15-C14	-2.78	1.43	1.51

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	X	34	MNU	C4-N3-C2	14.13	127.07	115.14
3	X	37	T6A	O14-C14-C15	11.99	145.26	109.74
3	X	37	T6A	C12-N11-C10	9.28	132.66	122.75
3	X	34	MNU	C5-C4-N3	-7.35	114.48	125.25
3	X	37	T6A	O14-C14-C12	-6.97	95.20	109.14
3	X	37	T6A	N6-C10-N11	6.46	122.78	113.76
3	X	37	T6A	O10-C10-N6	-4.37	116.23	123.62
3	X	37	T6A	C15-C14-C12	3.57	119.52	112.30
3	X	34	MNU	C6-C5-C4	2.55	119.66	115.73
3	X	37	T6A	C2-N1-C6	2.51	118.74	116.59

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	X	37	T6A	C14

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	X	37	T6A	C13-C12-C14-O14
3	X	34	MNU	C2'-C1'-N1-C6
3	X	37	T6A	N11-C12-C14-O14
3	X	37	T6A	C13-C12-N11-C10
3	X	34	MNU	C4-C5-C7-N8
3	X	37	T6A	C3'-C4'-C5'-O5'
3	X	34	MNU	C6-C5-C7-N8

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	X	37	T6A	2	0
3	X	34	MNU	3	0

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 110 ligands modelled in this entry, 109 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
24	PAR	A	1545	-	45,45,45	1.75	11 (24%)	64,67,67	1.21	5 (7%)

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	PAR	A	1545	-	-	4/18/94/94	0/4/4/4

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	A	1545	PAR	C64-C54	4.62	1.58	1.52
24	A	1545	PAR	O54-C14	4.06	1.52	1.41
24	A	1545	PAR	C31-C21	3.66	1.58	1.53
24	A	1545	PAR	O51-C11	2.97	1.49	1.41
24	A	1545	PAR	O33-C14	2.86	1.49	1.41
24	A	1545	PAR	O33-C33	2.75	1.51	1.43
24	A	1545	PAR	C44-C34	2.74	1.59	1.52
24	A	1545	PAR	O51-C51	2.46	1.50	1.44
24	A	1545	PAR	O54-C54	2.33	1.50	1.44
24	A	1545	PAR	C34-C24	2.30	1.56	1.53
24	A	1545	PAR	C11-C21	2.09	1.56	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	A	1545	PAR	O52-C13-C23	4.21	116.68	107.96
24	A	1545	PAR	O54-C54-C64	3.48	112.49	106.01

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
24	A	1545	PAR	O52-C13-O43	-3.27	107.89	111.43
24	A	1545	PAR	C14-O54-C54	3.13	119.83	113.69
24	A	1545	PAR	O33-C14-C24	2.97	113.33	108.22

There are no chirality outliers.

All (4) torsion outliers are listed below:

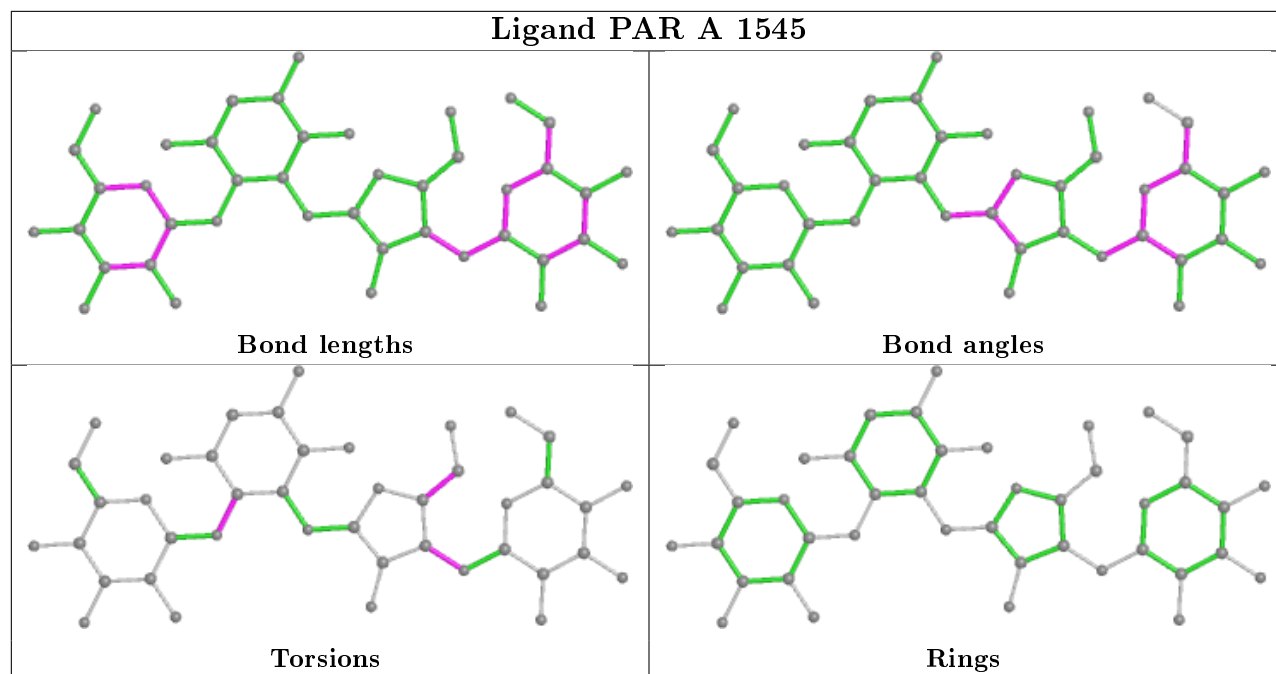
Mol	Chain	Res	Type	Atoms
24	A	1545	PAR	O43-C43-C53-O53
24	A	1545	PAR	C52-C42-O11-C11
24	A	1545	PAR	C23-C33-O33-C14
24	A	1545	PAR	C33-C43-C53-O53

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
24	A	1545	PAR	2	0

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	1507/1522 (99%)	2.20	794 (52%) 0 0	30, 65, 160, 200	0
2	W	3/3 (100%)	2.48	3 (100%) 0 0	56, 56, 63, 72	0
3	X	9/11 (81%)	1.94	3 (33%) 0 0	64, 101, 157, 157	0
4	B	234/256 (91%)	0.64	17 (7%) 15 14	37, 100, 173, 200	0
5	C	206/239 (86%)	0.70	18 (8%) 10 10	44, 93, 169, 200	0
6	D	208/209 (99%)	0.71	19 (9%) 9 10	33, 71, 149, 200	0
7	E	150/162 (92%)	0.71	6 (4%) 38 35	27, 63, 122, 200	0
8	F	101/101 (100%)	0.69	8 (7%) 12 12	48, 103, 154, 174	0
9	G	155/156 (99%)	0.63	7 (4%) 33 31	41, 81, 152, 200	0
10	H	138/138 (100%)	0.73	6 (4%) 35 33	20, 54, 113, 174	0
11	I	127/128 (99%)	0.81	14 (11%) 5 5	35, 90, 149, 178	0
12	J	98/105 (93%)	1.22	24 (24%) 0 0	44, 117, 186, 200	0
13	K	119/129 (92%)	0.82	12 (10%) 7 7	30, 67, 138, 187	0
14	L	124/135 (91%)	0.95	13 (10%) 6 6	31, 64, 139, 175	0
15	M	125/126 (99%)	1.23	19 (15%) 2 2	44, 85, 169, 200	0
16	N	60/61 (98%)	1.02	9 (15%) 2 2	42, 82, 139, 179	0
17	O	88/89 (98%)	0.85	9 (10%) 6 7	23, 76, 142, 192	0
18	P	83/88 (94%)	0.95	8 (9%) 8 8	27, 52, 96, 173	0
19	Q	104/105 (99%)	1.29	12 (11%) 4 4	22, 61, 146, 200	0
20	R	73/88 (82%)	0.74	2 (2%) 54 51	40, 79, 175, 188	0
21	S	80/93 (86%)	1.00	16 (20%) 1 1	62, 111, 162, 193	0
22	T	99/106 (93%)	0.84	9 (9%) 9 10	32, 58, 136, 168	0
23	V	24/27 (88%)	1.04	3 (12%) 3 3	41, 69, 118, 136	0
All	All	3915/4077 (96%)	1.37	1031 (26%) 0 0	20, 73, 159, 200	0

All (1031) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
19	Q	103	GLY	13.3
19	Q	104	LYS	12.9
15	M	120	LYS	11.3
1	A	202	U	11.2
19	Q	105	ALA	10.6
1	A	216	G	9.9
15	M	126	LYS	9.0
19	Q	102	GLY	9.0
1	A	407	G	8.5
12	J	31	GLY	8.5
1	A	1031	G	8.4
15	M	122	LYS	8.3
15	M	119	GLY	8.0
1	A	421	U	7.8
1	A	1034	G	7.8
18	P	83	GLU	7.6
1	A	1023	G	7.4
1	A	1026	G	7.2
1	A	1030	C	7.0
1	A	1129	C	6.9
1	A	423	G	6.9
1	A	1534	A	6.7
1	A	416	G	6.7
1	A	1027	C	6.7
17	O	22	THR	6.4
1	A	414	A	6.3
1	A	1533	C	6.2
15	M	118	ALA	6.1
12	J	10	GLY	6.0
1	A	1283	G	6.0
19	Q	101	ARG	6.0
21	S	54	GLY	5.9
1	A	203	U	5.8
6	D	2	GLY	5.7
15	M	7	VAL	5.7
1	A	413	G	5.7
20	R	16	PRO	5.7
15	M	123	ALA	5.6
1	A	1539	C	5.5
1	A	1540	U	5.5
20	R	17	SER	5.5
1	A	1127	G	5.4

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Mol	Chain	Res	Type	RSRZ
1	A	1024	G	5.3
1	A	1134	G	5.2
22	T	106	ALA	5.2
1	A	1038	C	5.1
1	A	1137	C	5.1
1	A	1019	C	5.1
1	A	1131	G	5.0
5	C	2	GLY	5.0
12	J	4	ILE	5.0
1	A	1033	G	5.0
1	A	412	A	5.0
1	A	1003	G	4.9
1	A	1269	A	4.8
1	A	1259	C	4.8
1	A	993	G	4.7
1	A	1011	G	4.7
1	A	424	G	4.7
1	A	1268	A	4.6
1	A	159	G	4.6
17	O	21	ASP	4.6
6	D	23	GLY	4.5
1	A	1006	C	4.5
15	M	125	ARG	4.5
1	A	1169	A	4.4
1	A	1258	G	4.4
1	A	1053	G	4.3
17	O	23	GLY	4.3
1	A	1144	G	4.3
1	A	959	A	4.3
1	A	1124	G	4.3
1	A	204	U	4.2
1	A	581	G	4.2
1	A	1017	G	4.2
1	A	1020	U	4.2
1	A	1016	A	4.2
11	I	68	GLY	4.2
1	A	848	C	4.1
1	A	1222	G	4.1
1	A	1002	G	4.1
1	A	666	G	4.1
1	A	1420	C	4.1
1	A	1035	A	4.1

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Mol	Chain	Res	Type	RSRZ
1	A	1334	G	4.0
1	A	1050	G	4.0
11	I	7	THR	4.0
15	M	116	THR	4.0
1	A	1287	A	4.0
1	A	1231	G	4.0
1	A	130	A	4.0
1	A	1221	G	3.9
6	D	33	MET	3.9
1	A	432	A	3.9
1	A	162	A	3.9
4	B	233	SER	3.9
17	O	89	GLY	3.9
1	A	1014	A	3.9
1	A	989	C	3.8
1	A	1126	U	3.8
1	A	1468	A	3.8
1	A	1361	G	3.8
1	A	849	C	3.8
1	A	1479	C	3.8
1	A	1300	G	3.8
1	A	160	A	3.8
1	A	380	G	3.8
1	A	510	A	3.8
22	T	105	SER	3.8
1	A	1277	C	3.8
1	A	1419	G	3.8
4	B	16	HIS	3.8
1	A	758	G	3.8
12	J	26	ALA	3.8
14	L	73	GLU	3.8
1	A	417	C	3.8
4	B	19	HIS	3.7
1	A	1048	G	3.7
1	A	1316	G	3.7
16	N	29	ARG	3.7
1	A	425	G	3.7
1	A	869	G	3.7
1	A	1467	G	3.7
1	A	478	A	3.7
1	A	1000	U	3.7
1	A	346	G	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	409	G	3.7
1	A	1356	G	3.7
1	A	752	G	3.7
1	A	1068	G	3.7
1	A	984	C	3.7
1	A	78	G	3.6
1	A	951	G	3.6
1	A	1022	G	3.6
21	S	63	THR	3.6
1	A	958	A	3.6
1	A	1140	C	3.6
1	A	1135	U	3.6
1	A	447	G	3.6
1	A	199	G	3.6
1	A	1417	G	3.6
15	M	106	ASN	3.6
4	B	190	THR	3.6
1	A	1255	G	3.6
7	E	17	ALA	3.6
1	A	415	A	3.6
1	A	1018	C	3.6
17	O	52	SER	3.6
1	A	517	G	3.6
1	A	1220	G	3.6
13	K	77	MET	3.6
1	A	1238	A	3.6
1	A	888	G	3.6
1	A	971	G	3.6
1	A	1274	G	3.6
1	A	1284	C	3.5
1	A	1001	A	3.5
1	A	714	G	3.5
1	A	1266	G	3.5
1	A	297	G	3.5
1	A	1084	G	3.5
8	F	41	GLU	3.5
1	A	800	G	3.5
1	A	51	A	3.5
16	N	6	LEU	3.5
1	A	426	G	3.5
1	A	494	G	3.5
1	A	529	G	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	343	U	3.5
1	A	1036	G	3.5
21	S	3	ARG	3.5
1	A	548	G	3.5
1	A	1304	G	3.5
1	A	1344	C	3.4
1	A	496	A	3.4
1	A	630	G	3.4
6	D	9	CYS	3.4
14	L	61	THR	3.4
1	A	497	A	3.4
9	G	83	ALA	3.4
1	A	725	G	3.4
1	A	1133	G	3.4
1	A	1421	G	3.4
5	C	21	ARG	3.4
1	A	483	C	3.4
1	A	1168	A	3.4
1	A	500	G	3.4
9	G	82	GLY	3.4
1	A	373	A	3.3
1	A	1237	C	3.3
1	A	1088	G	3.3
7	E	41	VAL	3.3
1	A	217	C	3.3
1	A	1303	C	3.3
1	A	108	G	3.3
1	A	112	G	3.3
1	A	1525	G	3.3
11	I	128	ARG	3.3
1	A	158	G	3.3
21	S	37	ARG	3.3
1	A	889	A	3.3
1	A	1518	A	3.3
6	D	42	GLN	3.3
1	A	1213	A	3.3
1	A	171	A	3.3
1	A	374	A	3.3
1	A	741	G	3.3
1	A	841	U	3.3
1	A	1519	A	3.3
1	A	745	C	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	1054	C	3.3
15	M	13	LYS	3.3
1	A	1526	G	3.3
21	S	62	ILE	3.3
5	C	64	VAL	3.3
1	A	864	A	3.2
1	A	22	G	3.2
1	A	1138	G	3.2
1	A	1335	C	3.2
1	A	484	G	3.2
1	A	837	G	3.2
1	A	1323	G	3.2
21	S	2	PRO	3.2
1	A	410	G	3.2
1	A	1202	G	3.2
1	A	1392	G	3.2
12	J	27	ALA	3.2
1	A	1040	U	3.2
1	A	482	A	3.2
1	A	816	A	3.2
1	A	1046	A	3.2
1	A	36	C	3.2
1	A	542	G	3.2
1	A	1010	G	3.2
1	A	315	A	3.2
1	A	687	A	3.2
1	A	291	C	3.2
1	A	1541	U	3.2
8	F	73	ASN	3.2
1	A	385	C	3.2
1	A	1097	C	3.2
1	A	459	G	3.2
1	A	730	G	3.2
1	A	898	G	3.2
1	A	556	C	3.2
12	J	33	GLN	3.2
15	M	121	LYS	3.2
1	A	278	G	3.2
1	A	947	G	3.2
7	E	16	THR	3.2
1	A	1326	C	3.2
1	A	991	U	3.2

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Mol	Chain	Res	Type	RSRZ
11	I	19	LEU	3.2
15	M	88	ARG	3.1
12	J	83	GLU	3.1
1	A	577	G	3.1
1	A	1094	G	3.1
5	C	76	VAL	3.1
1	A	198	G	3.1
1	A	1405	G	3.1
1	A	1441	G	3.1
1	A	1504	G	3.1
16	N	60	SER	3.1
4	B	99	GLY	3.1
1	A	1200	C	3.1
1	A	254	G	3.1
13	K	42	TRP	3.1
1	A	172	A	3.1
1	A	379	C	3.1
1	A	408	A	3.1
1	A	463	A	3.1
1	A	1228	C	3.1
1	A	157	G	3.1
22	T	100	ILE	3.1
1	A	1223	C	3.1
1	A	1430	C	3.1
10	H	24	THR	3.1
1	A	1043	C	3.1
23	V	2	GLY	3.1
1	A	361	G	3.1
1	A	1511	G	3.1
16	N	3	ARG	3.1
8	F	65	VAL	3.1
1	A	1177	G	3.1
1	A	1371	G	3.1
1	A	995	C	3.1
1	A	1248	A	3.1
1	A	1260	C	3.1
1	A	1282	C	3.0
9	G	33	ASP	3.0
6	D	26	CYS	3.0
1	A	70	G	3.0
1	A	1461	G	3.0
1	A	345	C	3.0

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Mol	Chain	Res	Type	RSRZ
16	N	33	VAL	3.0
1	A	354	G	3.0
1	A	878	G	3.0
11	I	23	ASN	3.0
1	A	1005	A	3.0
1	A	1318	A	3.0
1	A	1339	A	3.0
1	A	201	C	3.0
1	A	266	G	3.0
1	A	1109	C	3.0
6	D	18	LYS	3.0
1	A	336	C	3.0
1	A	1032	G	3.0
1	A	586	C	3.0
1	A	1251	A	3.0
1	A	481	G	3.0
1	A	1175	G	3.0
1	A	1370	G	3.0
11	I	67	GLY	3.0
1	A	245	C	3.0
1	A	726	C	3.0
5	C	77	ILE	3.0
1	A	320	C	3.0
1	A	634	C	3.0
1	A	1296	C	3.0
1	A	38	G	2.9
1	A	1224	G	2.9
1	A	16	A	2.9
1	A	1093	A	2.9
23	V	17	THR	2.9
1	A	173	U	2.9
1	A	925	G	2.9
1	A	960	U	2.9
13	K	117	ASN	2.9
8	F	4	TYR	2.9
1	A	697	U	2.9
14	L	113	ARG	2.9
1	A	102	G	2.9
1	A	259	G	2.9
1	A	347	G	2.9
1	A	1482	G	2.9
6	D	20	TYR	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	262	A	2.9
1	A	263	A	2.9
1	A	1176	A	2.9
1	A	1374	A	2.9
1	A	495	U	2.9
1	A	428	G	2.9
1	A	621	A	2.9
1	A	1434	A	2.9
1	A	1315	U	2.9
1	A	566	G	2.9
1	A	595	G	2.9
22	T	64	ASP	2.9
1	A	1080	A	2.9
4	B	220	ASP	2.9
1	A	181	G	2.9
1	A	251	G	2.9
1	A	789	U	2.9
1	A	901	A	2.9
12	J	32	ALA	2.9
1	A	398	C	2.9
1	A	362	G	2.9
1	A	1276	G	2.9
3	X	36	U	2.9
1	A	273	A	2.9
6	D	21	LEU	2.9
1	A	117	G	2.9
1	A	258	G	2.9
1	A	654	G	2.9
1	A	928	G	2.9
1	A	1363	A	2.9
11	I	85	LEU	2.9
18	P	41	PRO	2.9
1	A	479	C	2.8
1	A	122	G	2.8
1	A	384	G	2.8
1	A	575	G	2.8
1	A	622	A	2.8
1	A	371	G	2.8
1	A	438	G	2.8
1	A	691	G	2.8
1	A	1435	G	2.8
2	W	3	G	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	123	C	2.8
1	A	353	A	2.8
1	A	1503	A	2.8
1	A	437	U	2.8
1	A	780	A	2.8
1	A	1288	A	2.8
1	A	326	G	2.8
1	A	948	C	2.8
1	A	195	A	2.8
8	F	66	GLU	2.8
1	A	1348	U	2.8
21	S	52	TYR	2.8
1	A	285	G	2.8
1	A	524	G	2.8
1	A	701	C	2.8
19	Q	15	MET	2.8
1	A	1433	A	2.8
1	A	182	U	2.8
14	L	50	SER	2.8
1	A	299	G	2.8
14	L	57	LYS	2.8
1	A	264	U	2.8
1	A	288	A	2.8
1	A	1004	A	2.8
10	H	1	MET	2.8
1	A	124	G	2.8
1	A	585	G	2.8
1	A	1338	G	2.8
1	A	1355	G	2.8
1	A	572	A	2.8
1	A	996	A	2.8
1	A	1015	A	2.8
15	M	109	THR	2.8
15	M	117	VAL	2.8
1	A	183	G	2.7
1	A	450	G	2.7
1	A	1171	G	2.7
1	A	814	A	2.7
1	A	900	A	2.7
4	B	122	PHE	2.7
14	L	32	PHE	2.7
4	B	91	PRO	2.7

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Mol	Chain	Res	Type	RSRZ
12	J	73	ASP	2.7
1	A	422	C	2.7
1	A	375	U	2.7
1	A	196	A	2.7
1	A	872	A	2.7
4	B	40	HIS	2.7
6	D	22	LYS	2.7
1	A	165	C	2.7
1	A	536	C	2.7
1	A	323	U	2.7
1	A	760	G	2.7
1	A	861	G	2.7
1	A	1312	G	2.7
5	C	176	HIS	2.7
1	A	356	A	2.7
1	A	964	A	2.7
1	A	994	A	2.7
1	A	113	G	2.7
1	A	349	A	2.7
1	A	364	A	2.7
1	A	1191	A	2.7
1	A	66	G	2.7
1	A	1291	G	2.7
1	A	1401	G	2.7
1	A	37	U	2.7
1	A	190(B)	C	2.7
1	A	1219	U	2.7
1	A	431	A	2.7
1	A	502	G	2.7
1	A	662	G	2.7
1	A	1182	G	2.7
1	A	781	A	2.7
1	A	68	G	2.7
1	A	348	G	2.7
1	A	378	G	2.7
1	A	1029	C	2.7
1	A	1181	G	2.7
9	G	2	ALA	2.7
1	A	1234	C	2.7
1	A	644	G	2.7
6	D	25	ARG	2.6
1	A	327	A	2.6

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Mol	Chain	Res	Type	RSRZ
5	C	58	GLU	2.6
1	A	153	C	2.6
1	A	268	C	2.6
1	A	1007	C	2.6
1	A	629	G	2.6
1	A	798	G	2.6
1	A	1013	G	2.6
1	A	1061	G	2.6
1	A	152	A	2.6
1	A	924	C	2.6
1	A	1322	C	2.6
1	A	1527	C	2.6
1	A	683	G	2.6
1	A	874	G	2.6
1	A	1042	G	2.6
1	A	1108	G	2.6
7	E	130	ASN	2.6
10	H	121	ASP	2.6
1	A	1025	U	2.6
8	F	52	ILE	2.6
14	L	31	PRO	2.6
1	A	563	A	2.6
1	A	975	A	2.6
1	A	1130	A	2.6
1	A	879	C	2.6
1	A	220	G	2.6
1	A	305	G	2.6
1	A	685	G	2.6
1	A	692	U	2.6
1	A	731	G	2.6
1	A	1215	G	2.6
1	A	161	A	2.6
1	A	282	A	2.6
1	A	401	C	2.6
5	C	100	ALA	2.6
1	A	11	G	2.6
1	A	292	G	2.6
1	A	584	G	2.6
1	A	1523	G	2.6
1	A	59	A	2.6
22	T	104	LEU	2.6
1	A	934	C	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	253	U	2.6
6	D	19	LEU	2.6
1	A	28	G	2.6
1	A	319	G	2.6
14	L	122	THR	2.6
1	A	1069	C	2.6
1	A	1466	C	2.6
1	A	81	U	2.6
1	A	1528	U	2.6
1	A	462	G	2.6
1	A	1347	G	2.6
1	A	1497	G	2.6
1	A	1360	A	2.6
1	A	1492	A	2.6
1	A	1500	A	2.6
14	L	64	TYR	2.6
22	T	101	GLY	2.6
22	T	103	GLY	2.6
1	A	246	A	2.6
1	A	302	G	2.6
1	A	640	A	2.6
1	A	670	G	2.6
1	A	939	G	2.6
1	A	1475	G	2.6
1	A	1516	G	2.6
1	A	1520	G	2.6
1	A	330	C	2.6
1	A	352	C	2.6
1	A	652	U	2.6
1	A	797	C	2.6
1	A	982	U	2.6
1	A	300	A	2.5
1	A	547	A	2.5
1	A	715	A	2.5
1	A	914	A	2.5
1	A	137	C	2.5
1	A	1395	C	2.5
12	J	40	LEU	2.5
19	Q	98	LEU	2.5
21	S	23	ASN	2.5
6	D	209	ARG	2.5
1	A	244	U	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	767	A	2.5
1	A	69	G	2.5
1	A	275	G	2.5
1	A	445	G	2.5
10	H	3	THR	2.5
1	A	518	C	2.5
1	A	865	A	2.5
1	A	1208	C	2.5
1	A	1484	C	2.5
1	A	521	G	2.5
1	A	690	G	2.5
1	A	821	G	2.5
12	J	22	LYS	2.5
1	A	49	U	2.5
1	A	174	C	2.5
1	A	272	C	2.5
1	A	777	A	2.5
1	A	1357	A	2.5
19	Q	77	VAL	2.5
1	A	126	G	2.5
1	A	546	G	2.5
1	A	742	G	2.5
1	A	829	G	2.5
1	A	867	G	2.5
1	A	986	A	2.5
1	A	1275	A	2.5
1	A	1524	C	2.5
3	X	32	C	2.5
1	A	46	G	2.5
1	A	557	G	2.5
1	A	604	G	2.5
1	A	711	G	2.5
1	A	853	G	2.5
1	A	945	G	2.5
12	J	84	GLN	2.5
15	M	96	LEU	2.5
1	A	73	C	2.5
1	A	915	A	2.5
1	A	1460	A	2.5
1	A	170	U	2.5
1	A	1121	U	2.5
1	A	301	G	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	635	G	2.5
1	A	917	G	2.5
1	A	1271	G	2.5
1	A	1454	G	2.5
1	A	533	A	2.5
11	I	97	LYS	2.5
13	K	38	ASN	2.5
1	A	227	G	2.5
1	A	1295	G	2.5
1	A	880	C	2.5
1	A	985	C	2.5
1	A	1239	A	2.5
1	A	1398	A	2.5
1	A	1515	C	2.5
4	B	141	GLU	2.5
12	J	79	ARG	2.5
1	A	223	U	2.5
1	A	318	G	2.5
1	A	515	G	2.5
1	A	631	G	2.5
1	A	1079	G	2.5
1	A	1166	G	2.5
1	A	88	A	2.4
1	A	151	A	2.4
1	A	696	A	2.4
1	A	402	G	2.4
1	A	597	G	2.4
1	A	606	G	2.4
1	A	750	G	2.4
1	A	886	G	2.4
1	A	902	G	2.4
1	A	1198	G	2.4
11	I	15	ALA	2.4
21	S	75	ALA	2.4
1	A	118	U	2.4
1	A	228	A	2.4
1	A	675	A	2.4
1	A	1502	A	2.4
15	M	103	THR	2.4
5	C	60	ALA	2.4
1	A	252	U	2.4
1	A	713	G	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	776	G	2.4
1	A	990	C	2.4
1	A	1365	G	2.4
12	J	74	ILE	2.4
7	E	19	MET	2.4
1	A	194	C	2.4
1	A	1056	U	2.4
1	A	190(F)	G	2.4
1	A	430	A	2.4
1	A	887	G	2.4
1	A	1139	G	2.4
1	A	1180	A	2.4
18	P	38	TYR	2.4
1	A	193	C	2.4
1	A	732	C	2.4
1	A	1226	C	2.4
1	A	988	G	2.4
1	A	1154	G	2.4
11	I	110	GLU	2.4
15	M	81	LEU	2.4
6	D	82	ALA	2.4
1	A	187	C	2.4
1	A	188	C	2.4
1	A	756	C	2.4
1	A	1147	C	2.4
1	A	1362	C	2.4
1	A	232	G	2.4
1	A	576	G	2.4
1	A	668	G	2.4
1	A	775	G	2.4
1	A	836	G	2.4
1	A	1089	G	2.4
1	A	386	C	2.4
13	K	39	PRO	2.4
16	N	2	ALA	2.4
1	A	77	G	2.4
1	A	490	G	2.4
1	A	954	G	2.4
1	A	287	U	2.4
1	A	1083	U	2.4
1	A	43	C	2.4
4	B	84	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
5	C	82	GLU	2.4
1	A	782	A	2.4
5	C	182	ILE	2.4
1	A	146	G	2.4
1	A	190(G)	G	2.4
1	A	657	G	2.4
1	A	825	G	2.4
1	A	1178	G	2.4
1	A	366	C	2.4
1	A	866	C	2.4
1	A	1332	A	2.3
6	D	102	ASP	2.3
1	A	952	U	2.3
1	A	1532	U	2.3
14	L	116	SER	2.3
1	A	388	G	2.3
1	A	650	G	2.3
1	A	852	G	2.3
1	A	906	G	2.3
1	A	927	G	2.3
1	A	1021	G	2.3
1	A	1190	G	2.3
1	A	1447	G	2.3
1	A	242	C	2.3
12	J	34	VAL	2.3
13	K	28	THR	2.3
14	L	33	ARG	2.3
19	Q	18	THR	2.3
21	S	79	THR	2.3
2	W	2	A	2.3
1	A	813	U	2.3
1	A	1313	U	2.3
13	K	116	HIS	2.3
16	N	18	VAL	2.3
19	Q	56	VAL	2.3
1	A	184	G	2.3
1	A	309	G	2.3
1	A	667	G	2.3
1	A	623	C	2.3
1	A	1267	C	2.3
1	A	1328	C	2.3
1	A	1501	C	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	1285	A	2.3
1	A	868	C	2.3
5	C	4	LYS	2.3
13	K	53	SER	2.3
1	A	757	U	2.3
1	A	1301	U	2.3
1	A	1349	A	2.3
10	H	132	GLU	2.3
1	A	1218	C	2.3
1	A	688	G	2.3
1	A	876	G	2.3
1	A	881	G	2.3
1	A	1337	G	2.3
1	A	197	A	2.3
1	A	389	A	2.3
1	A	535	A	2.3
1	A	1102	A	2.3
21	S	34	TRP	2.3
9	G	50	ILE	2.3
17	O	49	ASP	2.3
18	P	62	VAL	2.3
12	J	5	ARG	2.3
1	A	248	C	2.3
1	A	395	C	2.3
1	A	645	C	2.3
1	A	681	C	2.3
1	A	738	C	2.3
1	A	826	C	2.3
1	A	834	C	2.3
1	A	1075	C	2.3
1	A	1195	C	2.3
1	A	115	G	2.3
1	A	156	G	2.3
1	A	296	U	2.3
1	A	605	U	2.3
1	A	682	G	2.3
1	A	1143	G	2.3
1	A	1364	U	2.3
1	A	1522	U	2.3
12	J	75	ILE	2.3
1	A	116	A	2.3
1	A	1375	A	2.3

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Mol	Chain	Res	Type	RSRZ
2	W	1	A	2.3
4	B	148	TYR	2.3
1	A	812	C	2.3
1	A	979	C	2.3
5	C	196	LEU	2.3
1	A	678	U	2.3
4	B	73	THR	2.3
1	A	129(A)	G	2.3
1	A	655	A	2.3
1	A	673	G	2.3
1	A	1256	A	2.3
11	I	11	LYS	2.3
21	S	55	LYS	2.3
21	S	15	LEU	2.3
1	A	91	C	2.3
1	A	891	U	2.3
1	A	698	G	2.3
1	A	1184	G	2.3
1	A	1286	A	2.3
1	A	1329	A	2.3
1	A	1333	A	2.3
1	A	1499	A	2.3
1	A	779	C	2.3
1	A	970	C	2.3
1	A	332	G	2.2
1	A	639	G	2.2
1	A	664	G	2.2
1	A	922	G	2.2
4	B	44	LEU	2.2
4	B	104	ASN	2.2
1	A	17	U	2.2
1	A	190	C	2.2
1	A	549	C	2.2
1	A	720	C	2.2
13	K	129	SER	2.2
17	O	46	HIS	2.2
1	A	838	G	2.2
1	A	944	G	2.2
1	A	1331	G	2.2
1	A	190(C)	C	2.2
1	A	295	C	2.2
1	A	403	C	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	599	C	2.2
1	A	321	A	2.2
1	A	965	A	2.2
1	A	486	U	2.2
1	A	616	G	2.2
1	A	769	G	2.2
1	A	1174	G	2.2
1	A	875	C	2.2
1	A	1098	C	2.2
1	A	1325	C	2.2
19	Q	14	LYS	2.2
1	A	21	G	2.2
1	A	35	G	2.2
1	A	148	G	2.2
1	A	200	G	2.2
1	A	799	G	2.2
1	A	916	G	2.2
1	A	1047	G	2.2
1	A	1106	G	2.2
1	A	526	C	2.2
1	A	1165	C	2.2
1	A	1354	C	2.2
5	C	194	GLY	2.2
12	J	17	ASP	2.2
1	A	279	A	2.2
1	A	1123	A	2.2
1	A	58	C	2.2
1	A	283	C	2.2
1	A	528	C	2.2
1	A	550	G	2.2
1	A	633	G	2.2
1	A	976	G	2.2
1	A	1197	G	2.2
1	A	1210	C	2.2
1	A	1264	C	2.2
1	A	1440	C	2.2
1	A	1469	G	2.2
22	T	44	ALA	2.2
1	A	1055	A	2.2
12	J	77	PRO	2.2
13	K	36	ASP	2.2
18	P	24	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	910	C	2.2
1	A	1321	C	2.2
1	A	396	G	2.2
1	A	530	G	2.2
1	A	541	G	2.2
1	A	885	G	2.2
12	J	68	HIS	2.2
1	A	788	U	2.2
1	A	1049	U	2.2
1	A	663	A	2.2
1	A	695	A	2.2
1	A	504	C	2.2
1	A	543	C	2.2
1	A	897	C	2.2
5	C	15	THR	2.2
12	J	50	ILE	2.2
1	A	107	G	2.2
1	A	286	G	2.2
1	A	289	G	2.2
1	A	755	G	2.2
1	A	1406	U	2.2
6	D	131	ARG	2.2
1	A	33	A	2.2
1	A	1067	A	2.2
1	A	1483	A	2.2
3	X	31	A	2.2
6	D	8	VAL	2.2
1	A	571	U	2.2
1	A	1376	U	2.2
1	A	1489	G	2.2
1	A	946	A	2.2
1	A	1157	A	2.2
12	J	43	ARG	2.2
17	O	42	HIS	2.2
17	O	54	ARG	2.2
1	A	221	C	2.1
1	A	390	C	2.1
1	A	613	C	2.1
1	A	1327	C	2.1
9	G	39	ALA	2.1
1	A	920	U	2.1
4	B	200	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	111	G	2.1
1	A	1373	G	2.1
5	C	78	GLY	2.1
1	A	143	A	2.1
1	A	919	A	2.1
1	A	501	C	2.1
1	A	1060	C	2.1
1	A	1389	C	2.1
5	C	20	SER	2.1
13	K	101	SER	2.1
1	A	560	U	2.1
1	A	961	U	2.1
5	C	174	PRO	2.1
1	A	397	A	2.1
1	A	485	G	2.1
1	A	499	A	2.1
1	A	737	A	2.1
1	A	903	G	2.1
22	T	87	LYS	2.1
1	A	598	U	2.1
1	A	1037	C	2.1
18	P	16	HIS	2.1
1	A	166	G	2.1
1	A	265	G	2.1
1	A	329	A	2.1
1	A	451	A	2.1
1	A	727	G	2.1
1	A	766	A	2.1
1	A	895	G	2.1
1	A	978	A	2.1
1	A	1201	A	2.1
1	A	1324	A	2.1
1	A	1346	A	2.1
1	A	1494	G	2.1
1	A	65	U	2.1
1	A	545	C	2.1
1	A	656	C	2.1
1	A	1209	C	2.1
1	A	1490	C	2.1
8	F	57	GLN	2.1
16	N	39	LEU	2.1
1	A	243	A	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	790	A	2.1
1	A	1250	A	2.1
1	A	255	G	2.1
1	A	376	G	2.1
1	A	391	G	2.1
1	A	406	G	2.1
1	A	540	G	2.1
1	A	544	G	2.1
1	A	786	G	2.1
1	A	1294	G	2.1
1	A	1521	G	2.1
1	A	322	C	2.1
10	H	15	ASN	2.1
1	A	520	A	2.1
1	A	704	A	2.1
1	A	938	A	2.1
1	A	1340	A	2.1
1	A	1531	A	2.1
1	A	335	C	2.1
21	S	36	ARG	2.1
8	F	45	LEU	2.1
15	M	24	GLY	2.1
1	A	60	A	2.1
1	A	660	G	2.1
1	A	674	G	2.1
1	A	1186	G	2.1
1	A	1253	G	2.1
1	A	1366	C	2.1
1	A	641	U	2.1
1	A	1306	A	2.1
18	P	31	LYS	2.1
1	A	615	C	2.1
1	A	770	C	2.1
1	A	579	G	2.1
1	A	1471	G	2.1
9	G	125	MET	2.1
1	A	1012	U	2.1
16	N	34	TYR	2.1
1	A	32	A	2.1
19	Q	76	LEU	2.1
1	A	18	C	2.1
1	A	601	C	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	840	C	2.1
1	A	1514	C	2.1
6	D	13	ARG	2.0
11	I	25	LYS	2.0
12	J	57	LYS	2.0
23	V	12	LYS	2.0
1	A	231	G	2.0
1	A	260	G	2.0
1	A	1164	G	2.0
1	A	13	U	2.0
1	A	705	U	2.0
14	L	104	VAL	2.0
1	A	1044	A	2.0
4	B	48	MET	2.0
18	P	82	GLN	2.0
1	A	63	C	2.0
1	A	92	C	2.0
1	A	1243	C	2.0
1	A	1383	C	2.0
1	A	1465	C	2.0
1	A	191	G	2.0
1	A	230	G	2.0
1	A	238	G	2.0
1	A	324	G	2.0
1	A	394	G	2.0
1	A	475	G	2.0
1	A	1505	G	2.0
11	I	18	PHE	2.0
7	E	149	GLU	2.0
1	A	819	A	2.0
1	A	1214	C	2.0
1	A	1297	C	2.0
12	J	70	ARG	2.0
14	L	121	GLY	2.0
1	A	516	U	2.0
1	A	582	U	2.0
1	A	858	G	2.0
1	A	1265	G	2.0
11	I	88	TYR	2.0
21	S	30	LEU	2.0
1	A	729	A	2.0
1	A	1280	A	2.0

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Mol	Chain	Res	Type	RSRZ
13	K	118	GLY	2.0
1	A	455	C	2.0
1	A	679	C	2.0
1	A	856	C	2.0
6	D	40	PRO	2.0
21	S	10	PHE	2.0
1	A	1062	U	2.0
1	A	79	G	2.0
1	A	128	G	2.0
1	A	257	G	2.0
1	A	558	G	2.0
1	A	803	G	2.0
1	A	1064	G	2.0
1	A	1074	G	2.0
1	A	360	A	2.0
1	A	609	A	2.0
1	A	665	A	2.0
1	A	334	C	2.0
1	A	904	C	2.0
1	A	1008	C	2.0
1	A	1066	C	2.0
1	A	1388	C	2.0
1	A	1402	C	2.0

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	T6A	X	37	32/33	0.89	0.34	76,80,80,80	0
3	MNU	X	34	23/24	0.90	0.37	56,96,115,115	0

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
25	MG	A	210	1/1	0.41	0.53	23,23,23,23	1
25	MG	A	1575	1/1	0.43	1.13	23,23,23,23	1
25	MG	A	1607	1/1	0.45	0.69	23,23,23,23	1
25	MG	A	1621	1/1	0.48	0.33	23,23,23,23	1
25	MG	A	493	1/1	0.57	1.21	23,23,23,23	1
25	MG	A	1596	1/1	0.58	1.50	23,23,23,23	1
25	MG	A	87	1/1	0.58	0.33	23,23,23,23	1
25	MG	A	1622	1/1	0.62	0.51	23,23,23,23	1
25	MG	A	1611	1/1	0.64	0.31	23,23,23,23	1
25	MG	A	211	1/1	0.67	0.34	23,23,23,23	0
25	MG	A	1627	1/1	0.67	0.28	23,23,23,23	1
25	MG	A	1595	1/1	0.69	1.31	23,23,23,23	1
25	MG	A	1619	1/1	0.74	0.23	23,23,23,23	1
25	MG	A	1620	1/1	0.74	0.29	23,23,23,23	1
25	MG	A	1616	1/1	0.74	0.30	23,23,23,23	1
25	MG	A	1566	1/1	0.76	0.53	23,23,23,23	1
25	MG	A	1632	1/1	0.76	0.26	23,23,23,23	1
25	MG	A	1634	1/1	0.76	0.43	23,23,23,23	1
25	MG	A	71	1/1	0.78	0.34	23,23,23,23	1
25	MG	A	441	1/1	0.78	0.22	23,23,23,23	1
25	MG	A	1562	1/1	0.79	0.77	23,23,23,23	1
25	MG	A	1615	1/1	0.79	0.27	23,23,23,23	1
25	MG	A	1633	1/1	0.79	0.34	23,23,23,23	1
25	MG	A	1580	1/1	0.80	0.31	23,23,23,23	1
25	MG	A	1561	1/1	0.80	0.28	23,23,23,23	1
25	MG	A	470	1/1	0.80	0.42	23,23,23,23	1
25	MG	A	1585	1/1	0.82	0.39	23,23,23,23	1
25	MG	A	1558	1/1	0.83	0.18	23,23,23,23	0
25	MG	A	1592	1/1	0.84	0.23	23,23,23,23	0
25	MG	A	1559	1/1	0.84	0.33	23,23,23,23	0
25	MG	A	1605	1/1	0.85	0.44	23,23,23,23	1
25	MG	A	1604	1/1	0.85	0.36	23,23,23,23	1
25	MG	A	1613	1/1	0.85	0.40	23,23,23,23	1
25	MG	A	1564	1/1	0.85	0.28	23,23,23,23	0
25	MG	A	1628	1/1	0.85	0.30	23,23,23,23	1
25	MG	A	1550	1/1	0.86	0.30	23,23,23,23	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
25	MG	A	1597	1/1	0.86	0.30	23,23,23,23	1
25	MG	A	471	1/1	0.86	0.29	23,23,23,23	1
25	MG	A	1548	1/1	0.88	0.32	23,23,23,23	1
25	MG	A	1612	1/1	0.88	0.28	23,23,23,23	1
25	MG	A	1560	1/1	0.88	0.26	23,23,23,23	0
25	MG	A	467	1/1	0.89	0.92	23,23,23,23	1
25	MG	A	466	1/1	0.89	0.42	23,23,23,23	1
25	MG	A	1554	1/1	0.90	0.31	23,23,23,23	1
25	MG	A	1549	1/1	0.90	0.41	23,23,23,23	1
25	MG	A	1569	1/1	0.90	0.23	23,23,23,23	1
25	MG	A	1581	1/1	0.90	0.46	23,23,23,23	1
25	MG	A	469	1/1	0.91	0.24	23,23,23,23	1
25	MG	A	1610	1/1	0.91	0.53	23,23,23,23	1
25	MG	A	1582	1/1	0.91	0.11	23,23,23,23	0
25	MG	A	1635	1/1	0.91	0.42	23,23,23,23	1
25	MG	A	1630	1/1	0.91	0.26	23,23,23,23	1
25	MG	A	1631	1/1	0.91	0.14	23,23,23,23	1
25	MG	A	1593	1/1	0.91	0.33	23,23,23,23	1
25	MG	A	1556	1/1	0.91	0.24	23,23,23,23	0
25	MG	A	1609	1/1	0.92	0.27	23,23,23,23	0
24	PAR	A	1545	42/42	0.92	0.39	25,25,25,25	0
25	MG	A	1571	1/1	0.92	0.15	23,23,23,23	0
25	MG	A	1606	1/1	0.92	0.50	23,23,23,23	1
25	MG	A	473	1/1	0.92	0.36	23,23,23,23	1
25	MG	A	1629	1/1	0.92	0.23	23,23,23,23	0
25	MG	A	1573	1/1	0.92	0.23	23,23,23,23	0
25	MG	A	1608	1/1	0.92	0.29	23,23,23,23	1
25	MG	A	1600	1/1	0.92	0.38	23,23,23,23	1
25	MG	A	1578	1/1	0.93	0.21	23,23,23,23	0
25	MG	A	1624	1/1	0.93	0.20	23,23,23,23	1
25	MG	A	1565	1/1	0.93	0.27	23,23,23,23	0
25	MG	A	1598	1/1	0.93	0.40	23,23,23,23	0
25	MG	A	1602	1/1	0.93	0.19	23,23,23,23	0
25	MG	A	214	1/1	0.93	0.37	23,23,23,23	1
25	MG	A	1599	1/1	0.93	0.26	23,23,23,23	1
25	MG	A	1603	1/1	0.94	0.30	23,23,23,23	1
25	MG	A	1568	1/1	0.94	0.16	23,23,23,23	0
25	MG	A	1589	1/1	0.94	0.33	23,23,23,23	0
25	MG	A	1577	1/1	0.94	0.15	23,23,23,23	0
25	MG	A	1563	1/1	0.94	0.47	23,23,23,23	1
25	MG	A	1601	1/1	0.94	0.67	23,23,23,23	1
25	MG	A	1583	1/1	0.94	0.16	23,23,23,23	0

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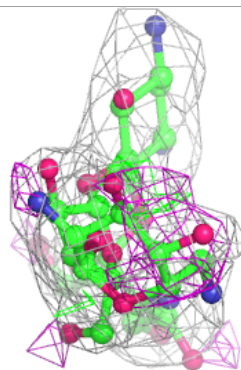
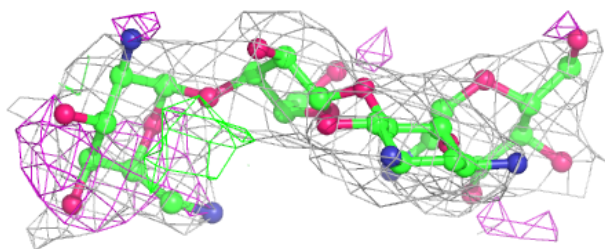
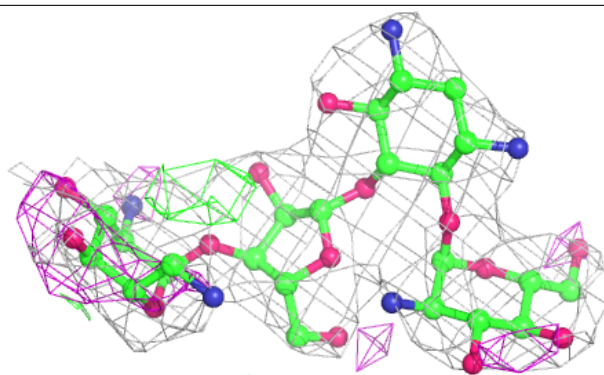
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
25	MG	A	1552	1/1	0.94	0.21	23,23,23,23	0
25	MG	X	502	1/1	0.94	0.31	23,23,23,23	1
25	MG	A	1570	1/1	0.95	0.20	23,23,23,23	0
25	MG	A	1547	1/1	0.95	0.34	23,23,23,23	0
25	MG	A	86	1/1	0.95	0.30	23,23,23,23	1
25	MG	A	1625	1/1	0.95	0.27	23,23,23,23	1
25	MG	A	1553	1/1	0.95	0.35	23,23,23,23	0
25	MG	A	1579	1/1	0.96	0.29	23,23,23,23	1
25	MG	A	1546	1/1	0.96	0.28	23,23,23,23	0
25	MG	X	500	1/1	0.96	0.23	23,23,23,23	1
25	MG	A	1587	1/1	0.96	0.13	23,23,23,23	0
25	MG	A	1551	1/1	0.96	0.24	23,23,23,23	0
25	MG	A	1567	1/1	0.96	0.32	23,23,23,23	0
25	MG	A	1590	1/1	0.96	0.25	23,23,23,23	0
25	MG	A	1617	1/1	0.96	0.18	23,23,23,23	1
25	MG	A	1586	1/1	0.96	0.18	23,23,23,23	1
25	MG	A	1591	1/1	0.96	0.29	23,23,23,23	1
25	MG	A	1618	1/1	0.97	0.23	23,23,23,23	0
25	MG	A	1594	1/1	0.97	0.23	23,23,23,23	1
25	MG	A	1588	1/1	0.97	0.28	23,23,23,23	0
25	MG	A	1574	1/1	0.97	0.22	23,23,23,23	0
25	MG	A	1623	1/1	0.97	0.40	23,23,23,23	1
25	MG	J	449	1/1	0.97	0.33	23,23,23,23	1
25	MG	A	1626	1/1	0.97	0.19	23,23,23,23	1
25	MG	A	1557	1/1	0.97	0.22	23,23,23,23	0
25	MG	A	1555	1/1	0.97	0.27	23,23,23,23	0
25	MG	A	1576	1/1	0.98	0.26	23,23,23,23	0
25	MG	A	1614	1/1	0.98	0.21	23,23,23,23	1
25	MG	A	1572	1/1	0.98	0.16	23,23,23,23	0
26	ZN	D	306	1/1	0.99	0.33	23,23,23,23	1
25	MG	A	1584	1/1	0.99	0.15	23,23,23,23	0
26	ZN	N	307	1/1	1.00	0.24	23,23,23,23	1

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around PAR A 1545:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.