



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 12:49 PM UTC

PDB ID : 6PPK / pdb_00006ppk
EMDB ID : EMD-20441
Title : RbgA+45SRbgA complex
Authors : Ortega, J.
Deposited on : 2019-07-07
Resolution : 4.40 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

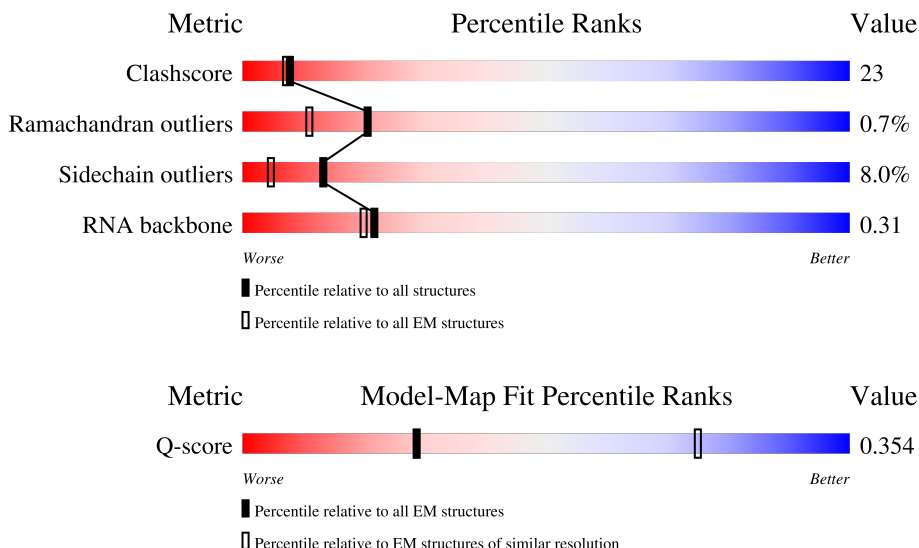
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

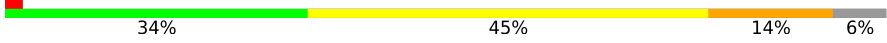
The reported resolution of this entry is 4.40 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	3132 (3.91 - 4.90)

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

Mol	Chain	Length	Quality of chain
1	A	2927	
2	B	119	
3	C	277	

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Mol	Chain	Length	Quality of chain
4	D	209	
5	E	207	
6	F	179	
7	G	179	
8	J	145	
9	K	122	
10	L	146	
11	N	120	
12	O	120	
13	P	115	
14	Q	118	
15	R	102	
16	S	113	
17	T	95	
18	U	103	
19	V	94	
20	Z	59	
21	b	59	
22	Y	66	
23	d	44	
24	W	282	

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	GNP	W	301	-	-	X	-

2 Entry composition

There are 25 unique types of molecules in this entry. The entry contains 80451 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2658	Total	C	N	O	P	0	0
			57112	25477	10569	18408	2658		

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	112	Total	C	N	O	P	0	0
			2395	1068	435	780	112		

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	260	Total	C	N	O	S	0	0
			2010	1253	392	359	6		

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	206	Total	C	N	O	S	0	0
			1569	985	289	290	5		

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	197	Total	C	N	O	S	0	0
			1511	951	280	278	2		

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	139	Total	C	N	O	S	0	0
			1090	694	190	199	7		

- Molecule 7 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	109	Total	C	N	O	S	0	0
			829	518	153	157	1		

- Molecule 8 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	J	141	Total	C	N	O	S	0	0
			1119	708	205	201	5		

- Molecule 9 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	K	122	Total	C	N	O	S	0	0
			920	571	173	172	4		

- Molecule 10 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	122	Total	C	N	O	S	0	0
			904	561	171	171	1		

- Molecule 11 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	N	118	Total	C	N	O	S	0	0
			947	580	185	178	4		

- Molecule 12 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	O	100	Total	C	N	O	0	0
			775	483	154	138		

- Molecule 13 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	P	114	Total	C	N	O	0	0
			936	595	184	157		

- Molecule 14 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Q	117	Total	C	N	O	S	0	0
			940	591	189	156	4		

- Molecule 15 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	R	100	Total	C	N	O	S	0	0
			781	498	138	145			

- Molecule 16 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	S	109	Total	C	N	O	S	0	0
			842	525	164	150	3		

- Molecule 17 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	T	90	Total	C	N	O	S	0	0
			724	452	133	136	3		

- Molecule 18 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	U	91	Total	C	N	O	S	0	0
			691	438	129	121	3		

- Molecule 19 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	V	78	Total	C	N	O	S	0	0
			604	375	118	111			

- Molecule 20 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Z	58	Total	C	N	O	S	0	0
			455	281	89	84	1		

- Molecule 21 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	b	53	Total	C	N	O	S	0	0
			418	258	84	69	7		

- Molecule 22 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Y	65	Total	C	N	O	S	0	0
			530	328	102	98	2		

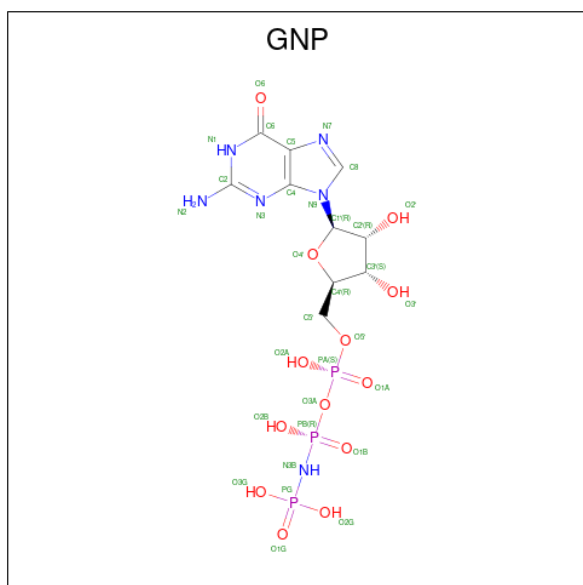
- Molecule 23 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	d	43	Total	C	N	O	S	0	0
			359	217	88	53	1		

- Molecule 24 is a protein called Ribosome biogenesis GTPase A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	252	Total	C	N	O	S	0	0
			1958	1250	343	359	6		

- Molecule 25 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (CCD ID: GNP) (formula: $C_{10}H_{17}N_6O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).

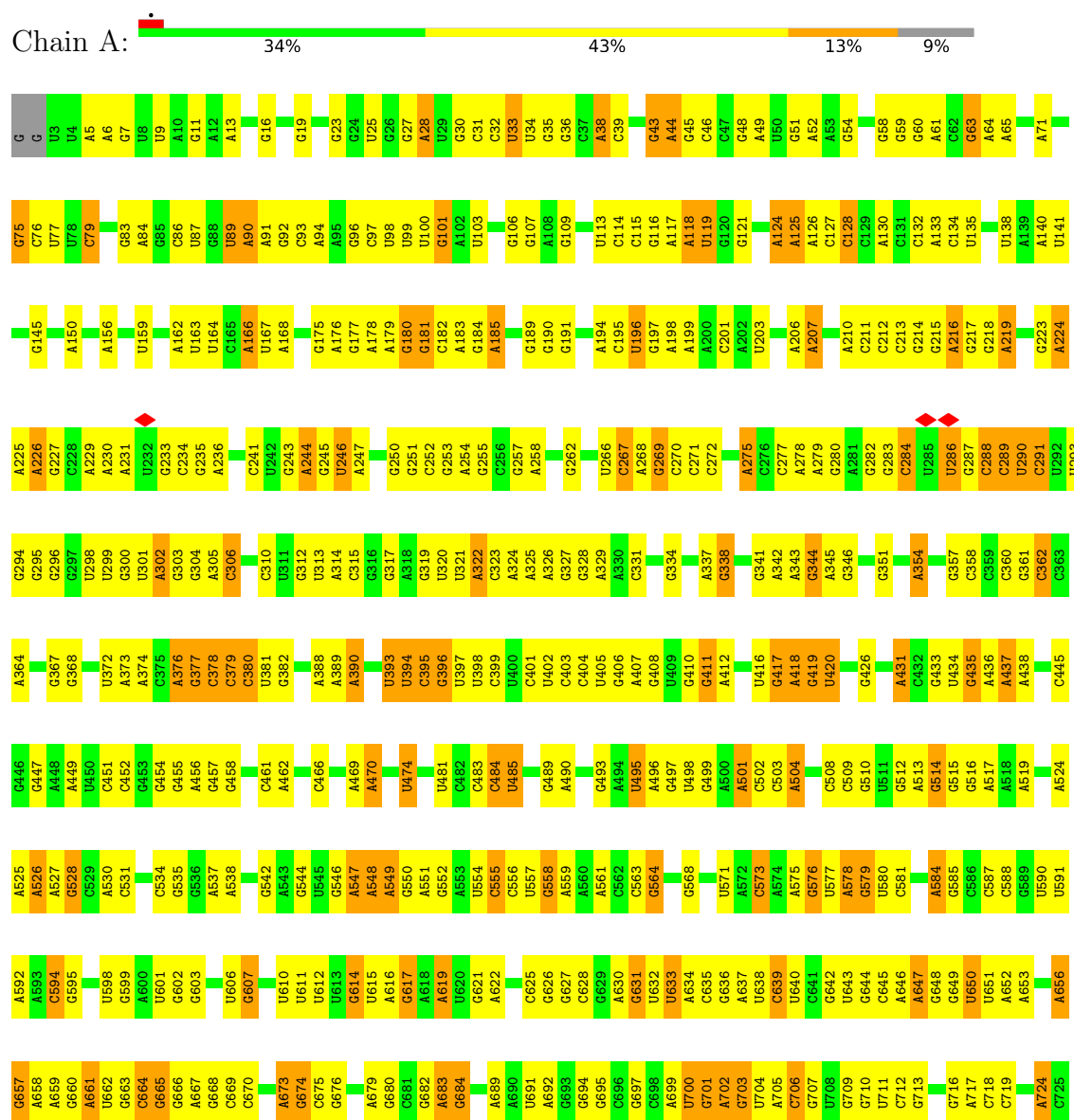


Mol	Chain	Residues	Atoms					AltConf
25	W	1	Total	C	N	O	P	0
			32	10	6	13	3	

3 Residue-property plots

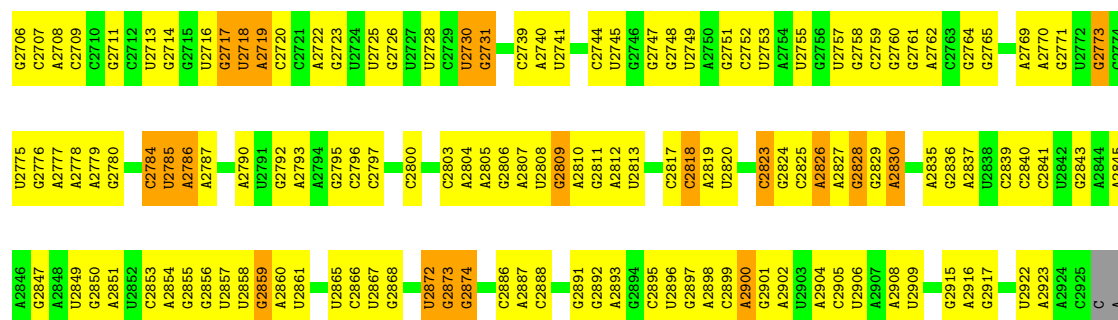
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: 23S rRNA

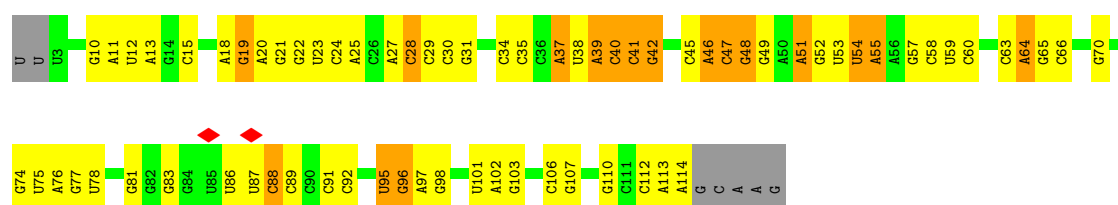


C1657	G1590	U1522	C1450	U1380	G1311	A1233	G1155	A1092	A1008	G	C872	U793	C726
G1658	G1591	U1523	C1455	A1381	G1312	G1236	G1156	G1093	A1011	G	U873	U794	A727
A1659	A1592	A1524	A1456	G1382	A1313	G1236	G1157	A1094	U1011	U	U874	G795	G728
C1660	A1593	G1525	A1456	U1383	A1313	G1236	G1158	G1095	U1011	U	U875	A796	G729
A1661	G1594	G1526	U1457	C1384	A1314	U1240	G1159	A1096	C1016	A	A876	A797	U730
C1662	U1595	C1527	U1458	G1385	A1315	U1241	G1160	A1097	U1017	C	G877	A798	G731
A1663	U1596	U1528	G1386	G1386	A1316	U1242	G1161	A1098	G1018	C	G877	A799	A732
G1664	C1597	G1529	G1387	G1387	G1317	U1243	G1168	C1099	A1019	G946	U881	G800	U733
G1665	U1598	U1530	A1460	A1388	G1322	A1244	G1169	G1102	A947	A948	A882	G801	C734
U1666	G1462	C1389	G1463	C1390	A1323	G1245	A1172	A1103	U949	U950	U886	G802	U735
A1667	A1464	U1391	A1464	U1391	G1324	G1247	A1173	U1104	U950	U950	U887	C803	A736
G1668	U1602	G1395	A1465	C1395	A1325	U1248	A1174	U1107	C951	U954	U888	G804	C737
A1672	U1603	G1396	U1327	C1396	A1326	U1249	A1175	G1108	U954	U954	U889	G805	C738
G1673	C1604	G1397	U1327	G1397	A1327	U1250	U1176	U1109	U955	U955	U890	G806	C739
G1674	C1605	A1540	A1332	C1398	A1328	U1251	U1177	G	C956	C956	G891	G807	U741
A1675	A1606	A1541	G1333	A1398	A1329	G1252	U1178	C	A956	A956	U892	A811	U742
C1683	C1607	A1542	U1333	A1399	A1330	U1257	U1179	U	A957	A957	U893	U816	U743
U1684	U1608	U1543	C1334	A1404	C1335	C1257	C1180	U	A958	A958	U894	C744	C745
A1685	C1613	C1544	A1335	A1405	A1336	U1258	C1181	A	C959	C959	A894	A746	A747
A1686	A1614	G1545	A1336	A1406	A1337	G1259	G1182	G	G963	G963	A895	G817	G747
G1687	A1615	G1476	C1337	G1410	G1338	G1264	G1183	A	A964	A964	A896	G818	U748
G1688	G1616	A1477	G1338	U1411	A1339	G1267	G1184	A	G967	G967	A897	G822	G749
U1689	A1617	G1478	A1340	U1412	A1340	U1268	G1185	G	A970	A970	U898	G823	U750
C1690	A1618	G1479	G1341	G1413	U1342	A1269	G1188	A1116	A971	A971	G903	G824	G751
A1691	A1619	A1481	U1342	G1414	C1343	U1272	A1189	G1117	U972	U972	G906	U826	A758
U1692	A1620	G1482	C1344	G1415	C1344	G1272	A1190	C	A973	A973	U907	G827	G759
C1693	G1621	G1482	U1345	U1416	U1345	G1275	U1193	C	A974	A974	A829	A829	U761
A1695	U1626	U1489	A1346	G1420	A1346	U1276	U1194	A	U1045	U1045	A908	A830	A762
G1696	A1627	A1490	U1347	A1421	G1348	G1277	A1199	A	A1054	A1054	U909	U831	A763
A1697	G1628	G1493	G1348	A1422	G1348	U1278	A1201	U1127	A1055	A1055	U910	G832	C764
U1704	C1629	G1494	C1349	A1423	G1349	G1279	A1202	U1128	A1056	A1056	G912	C833	A765
G1705	A1631	C1495	U1350	A1424	U1351	G1280	G1203	U1129	G1057	G1057	C914	C834	C766
G1706	G1632	G1496	U1352	C1425	U1352	G1281	U1204	U1130	U1058	U1058	A917	A835	U767
U1707	G1633	U1497	C1353	A1426	C1353	G1285	U1205	U1131	A1061	A1061	U918	A836	G768
U1708	U1634	U1498	U1354	G1427	C1354	A1286	G1206	U1132	A1062	A1062	U919	U837	A769
G1711	G1635	A1499	G1356	U1430	U1356	G1287	G1207	U1133	G1063	G1063	G920	C843	G773
G1712	U1500	U1501	G1359	G1431	U1355	U1288	G1208	A1134	U989	U989	G921	G852	G775
A1713	U1501	G1502	A1360	A1432	U1356	U1289	G1209	U	C990	C990	A922	C853	C777
A1714	G1503	G1503	A1361	A1433	A1361	A1293	U1213	G	A991	A991	U924	G854	C779
C1717	A1504	A1504	G1362	A1434	G1362	U1294	U1214	C	U1069	U1069	G925	G855	G780
G1718	U1505	U1505	G1363	U1435	U1295	U1295	U1215	G	G926	G926	U857	U857	A781
G1719	C1506	C1577	C1364	U1436	G1296	U1297	U	U	G927	G927	U858	U858	C783
G1720	U1507	U1507	C1364	C1437	U1297	U1297	C	A	G928	G928	C859	U860	C784
A1721	C1508	C1508	G1367	U1438	U1298	U1298	G1220	A	U993	U993	G929	G861	C785
G1726	U1579	U1579	U1368	U1439	G1299	G1299	G1221	A	C997	C997	C	U862	A786
A1727	G1512	G1512	C1369	G1440	U1300	U1300	G1222	A	G998	G998	C	A866	C787
U1733	U1513	U1513	C1370	U1441	U1301	U1301	U1221	A	A999	A999	U	U867	G788
A1734	A1516	A1516	C1371	A1442	A1302	A1302	G1223	A	G1000	G1000	C	A866	C789
A1735	A1517	A1517	C1372	C1443	U1303	U1303	G1223	A	U1001	U1001	C	U867	C790
G1736	A1518	A1518	G1376	C1444	G1304	G1304	G1227	A	A1003	A1003	C	A866	C791
A1738	A1519	A1519	G1377	C1445	A1305	A1305	G1228	A	U1004	U1004	C	U867	G792
C1739	U1520	U1520	G1378	U1446	U1306	U1306	G1231	A	A1005	A1005	C	U867	G792
	A1521	A1521	U1379	U1448	U1307	U1307	G1232	A	A1006	A1006	C	U867	G792
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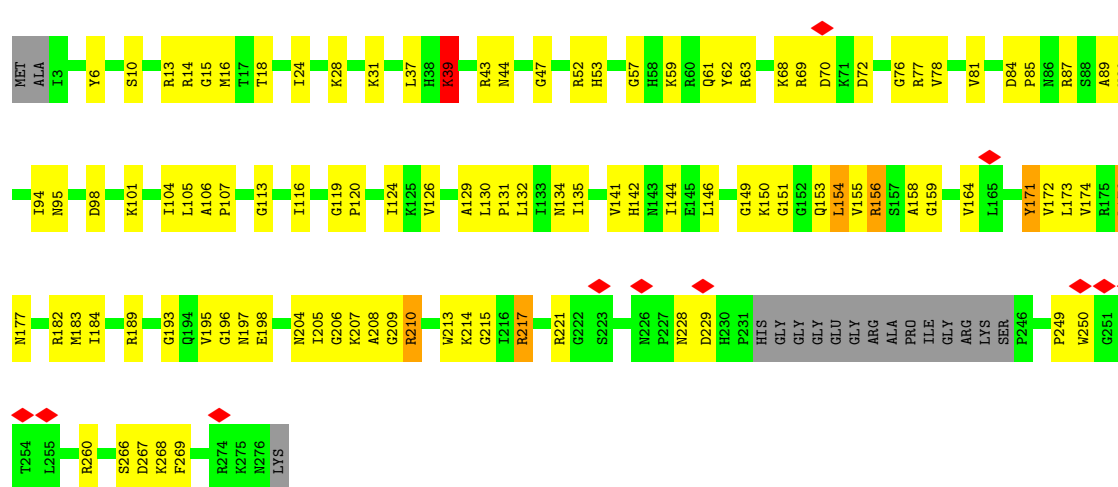




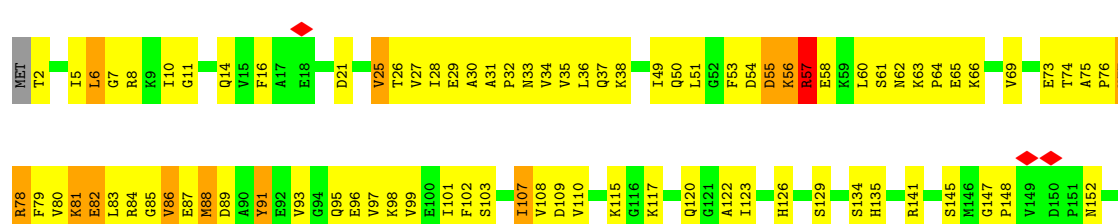
• Molecule 2: 5S rRNA



• Molecule 3: 50S ribosomal protein L2



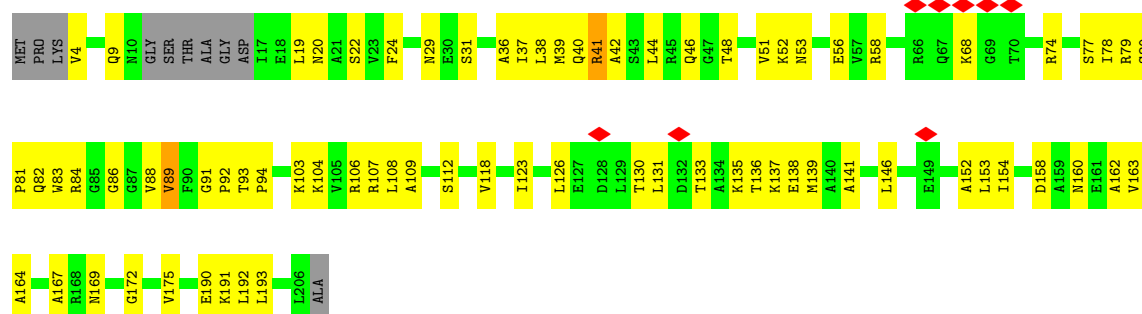
• Molecule 4: 50S ribosomal protein L3





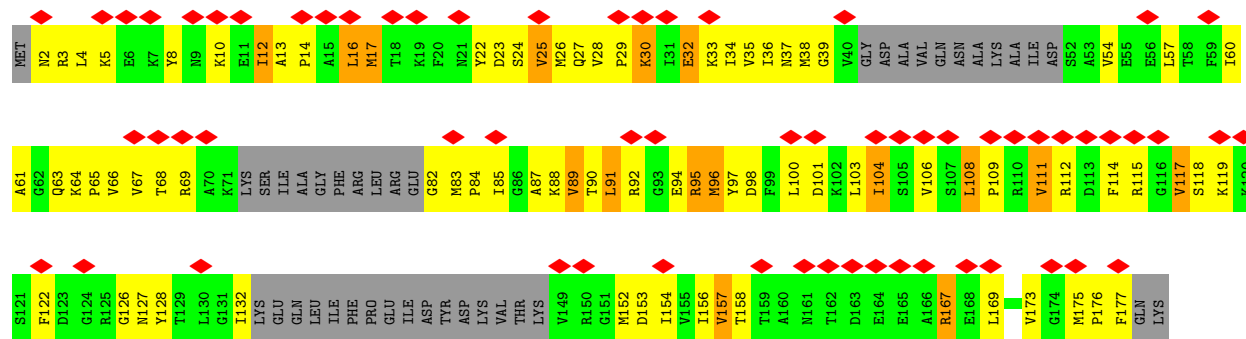
• Molecule 5: 50S ribosomal protein L4

Chain E: 58% 36% 5%



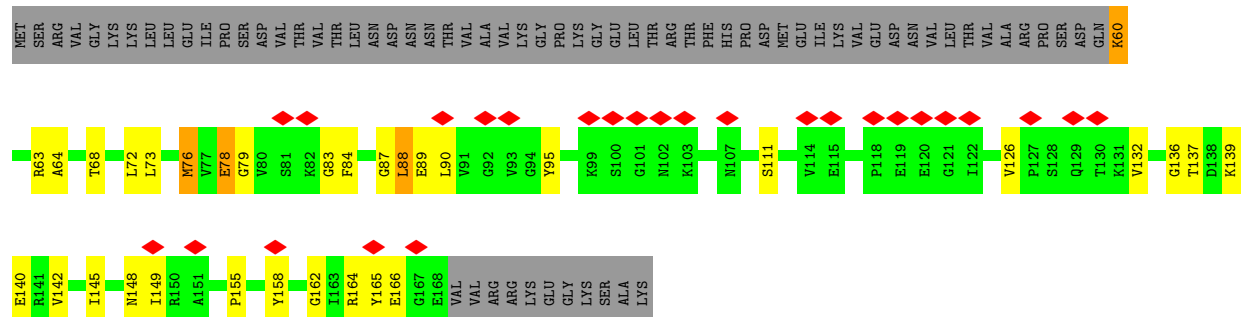
• Molecule 6: 50S ribosomal protein L5

Chain F: 35% 30% 39% 9% 22%



• Molecule 7: 50S ribosomal protein L6

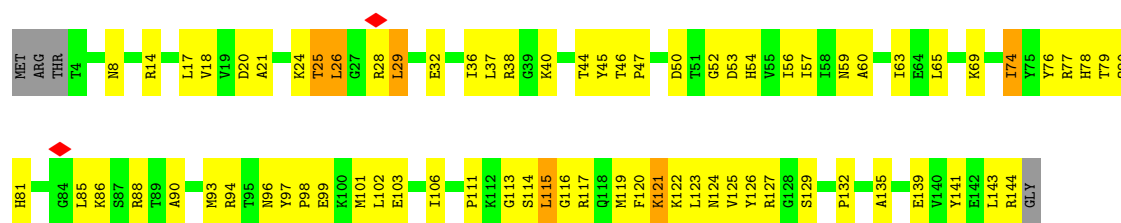
Chain G: 15% 42% 16% 39%



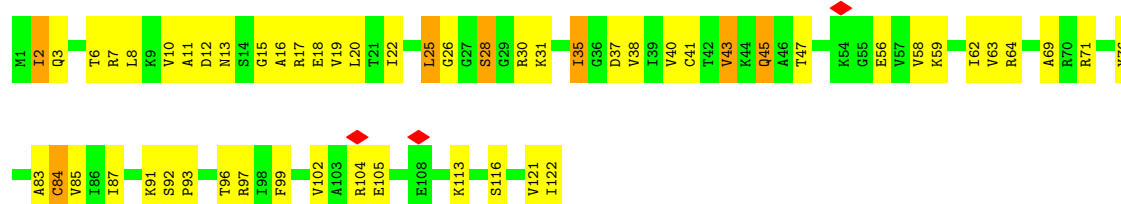
• Molecule 8: 50S ribosomal protein L13

Chain J: 46% 47% 5%

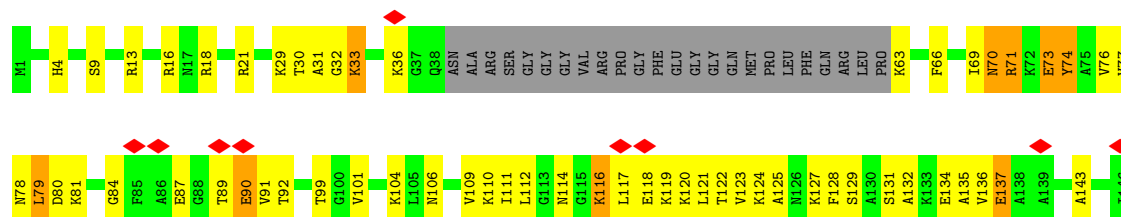
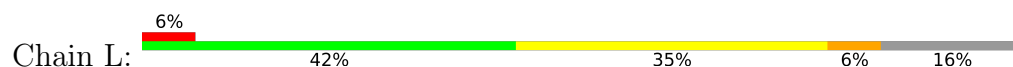




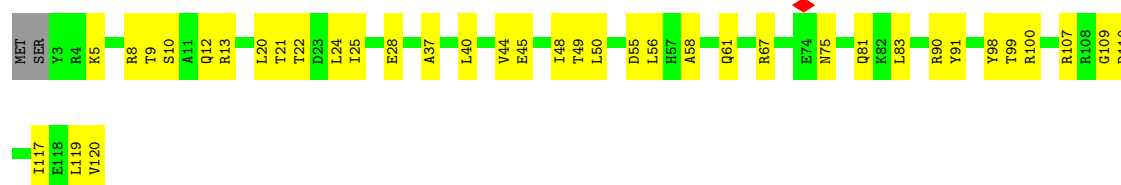
• Molecule 9: 50S ribosomal protein L14



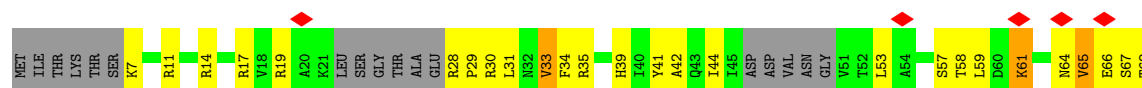
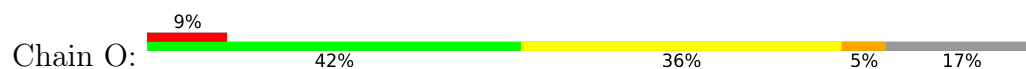
• Molecule 10: 50S ribosomal protein L15



• Molecule 11: 50S ribosomal protein L17



• Molecule 12: 50S ribosomal protein L18



Chain T:  71% 21% 5%

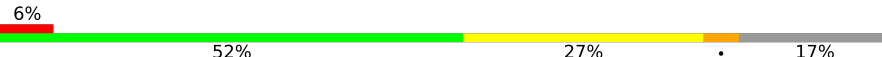


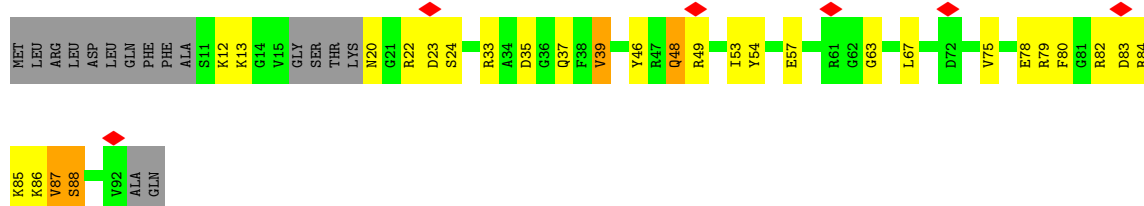
- Molecule 18: 50S ribosomal protein L24

Chain U:  50% 26% 11% 12%



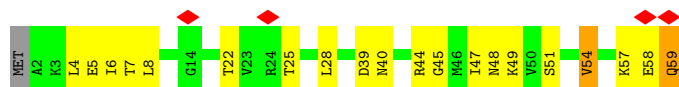
- Molecule 19: 50S ribosomal protein L27

Chain V:  6% 52% 27% 17%

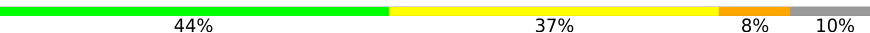


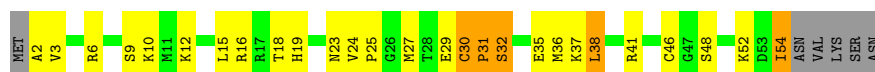
- Molecule 20: 50S ribosomal protein L30

Chain Z:  7% 64% 31% 2%



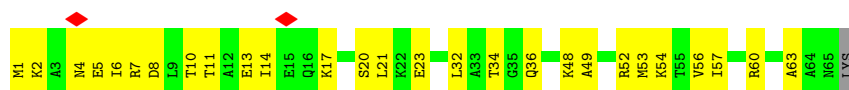
- Molecule 21: 50S ribosomal protein L32

Chain b:  44% 37% 8% 10%



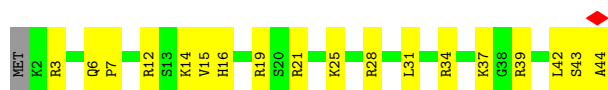
- Molecule 22: 50S ribosomal protein L29

Chain Y:  58% 41% 1%

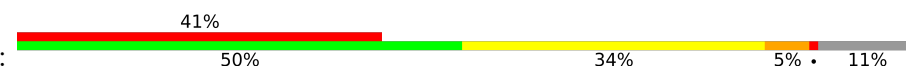


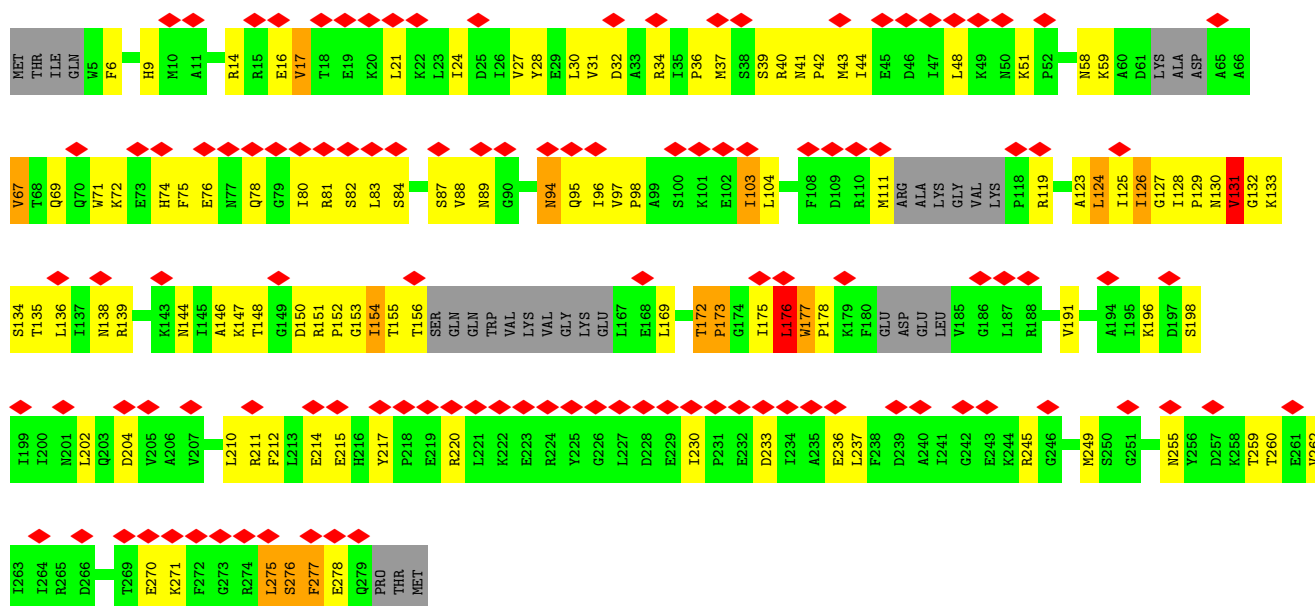
• Molecule 23: 50S ribosomal protein L34

Chain d:  57% 41%



• Molecule 24: Ribosome biogenesis GTPase A

Chain W:  41% 50% 34% 5% 11%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	81392	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	43	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.102	Depositor
Minimum map value	-0.047	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.017	Depositor
Map size (Å)	348.0, 348.0, 348.0	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.45, 1.45, 1.45	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.48	0/63968	0.51	4/99771 (0.0%)
2	B	0.30	0/2678	0.46	0/4174
3	C	0.39	0/2044	0.63	1/2741 (0.0%)
4	D	0.37	0/1591	0.69	3/2132 (0.1%)
5	E	0.41	0/1528	0.67	0/2061
6	F	0.25	0/1102	0.68	0/1476
7	G	0.24	0/841	0.59	2/1130 (0.2%)
8	J	0.35	0/1142	0.66	0/1537
9	K	0.35	0/927	1.08	10/1245 (0.8%)
10	L	0.33	0/910	0.58	0/1210
11	N	0.45	0/954	0.67	1/1276 (0.1%)
12	O	0.26	0/781	0.58	0/1042
13	P	0.34	0/949	0.72	2/1269 (0.2%)
14	Q	0.48	0/952	0.70	1/1266 (0.1%)
15	R	0.39	0/792	0.59	0/1063
16	S	0.44	0/851	0.68	0/1146
17	T	0.41	0/730	0.65	2/974 (0.2%)
18	U	0.31	0/698	0.84	4/929 (0.4%)
19	V	0.34	0/611	0.93	3/810 (0.4%)
20	Z	0.35	0/457	0.55	0/613
21	b	0.39	0/425	0.75	2/563 (0.4%)
22	Y	0.36	0/531	0.61	0/707
23	d	0.61	1/362 (0.3%)	0.63	0/473
24	W	0.27	0/1987	0.63	1/2680 (0.0%)
All	All	0.45	1/87811 (0.0%)	0.55	36/132288 (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
5	E	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
23	d	6	GLN	C-N	-5.70	1.28	1.33

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	K	2	ILE	CB-CA-C	18.89	137.56	111.49
19	V	82	ARG	CB-CA-C	13.83	134.21	111.26
19	V	82	ARG	N-CA-C	-12.52	95.34	112.12
9	K	2	ILE	N-CA-C	-12.42	92.19	109.45
18	U	84	LYS	N-CA-C	11.09	127.69	112.93
13	P	29	LEU	CB-CA-C	10.05	130.20	110.30
9	K	43	VAL	CB-CA-C	-9.83	98.21	110.99
18	U	84	LYS	CB-CA-C	-9.58	95.04	110.08
3	C	176	LEU	CB-CA-C	-9.22	94.50	110.45
9	K	97	ARG	CB-CA-C	-8.81	95.63	110.43
9	K	43	VAL	N-CA-C	8.48	120.76	107.28
19	V	88	SER	CB-CA-C	-7.54	97.38	110.95
4	D	103	SER	CB-CA-C	-7.46	95.94	113.02
18	U	5	LYS	N-CA-C	7.46	120.69	108.08
21	b	31	PRO	CB-CA-C	-7.40	99.87	111.04
9	K	56	GLU	CB-CA-C	7.39	122.84	109.62
4	D	57	ARG	CB-CA-C	-7.20	96.00	111.11
9	K	37	ASP	CB-CA-C	7.15	124.33	109.68
7	G	88	LEU	CB-CA-C	6.91	122.36	109.71
9	K	45	GLN	CB-CA-C	-6.84	98.17	109.80
4	D	103	SER	N-CA-C	-6.73	99.97	108.45
7	G	88	LEU	N-CA-C	-6.49	98.32	108.90
9	K	37	ASP	N-CA-C	-6.22	102.32	110.53
11	N	75	ASN	N-CA-C	-5.68	107.34	114.56
17	T	91	GLU	CA-C-N	5.67	131.90	121.70
17	T	91	GLU	C-N-CA	5.67	131.90	121.70
9	K	56	GLU	N-CA-C	-5.65	102.66	110.35
13	P	29	LEU	N-CA-C	-5.60	100.90	109.41
1	A	1107	U	P-O3'-C3'	5.52	128.47	120.20
18	U	97	SER	CB-CA-C	-5.41	110.31	116.54
24	W	176	LEU	CB-CA-C	-5.36	110.38	116.54
14	Q	103	LEU	CB-CA-C	-5.35	110.38	116.54
1	A	2785	U	P-O3'-C3'	5.32	128.18	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1245	G	P-O3'-C3'	5.20	127.99	120.20
21	b	32	SER	CB-CA-C	-5.12	101.62	114.11
1	A	2785	U	C2'-C3'-O3'	5.04	117.07	109.50

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	E	41	ARG	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	57112	0	28735	1159	0
2	B	2395	0	1212	65	0
3	C	2010	0	2100	139	0
4	D	1569	0	1635	189	0
5	E	1511	0	1598	62	0
6	F	1090	0	1136	203	0
7	G	829	0	851	52	0
8	J	1119	0	1159	96	0
9	K	920	0	977	77	0
10	L	904	0	957	82	0
11	N	947	0	978	34	0
12	O	775	0	807	79	0
13	P	936	0	1008	92	0
14	Q	940	0	1005	78	0
15	R	781	0	821	68	0
16	S	842	0	899	82	0
17	T	724	0	768	17	0
18	U	691	0	755	88	0
19	V	604	0	614	57	0
20	Z	455	0	491	20	0
21	b	418	0	439	45	0
22	Y	530	0	568	34	0
23	d	359	0	398	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
24	W	1958	0	1979	205	0
25	W	32	0	13	10	0
All	All	80451	0	51903	2608	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 23.

All (2608) 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)
10:L:117:LEU:CD2	10:L:136:VAL:HA	1.29	1.58
6:F:122:PHE:CE2	6:F:167:ARG:NH2	1.69	1.57
8:J:26:LEU:HA	8:J:29:LEU:CD1	1.40	1.50
13:P:33:VAL:HG21	13:P:77:PHE:CZ	1.48	1.47
24:W:81:ARG:NH1	24:W:103:ILE:CG1	1.79	1.45
13:P:94:LYS:HD2	13:P:118:ARG:NH2	1.18	1.42
7:G:87:GLY:CA	7:G:166:GLU:HG3	1.49	1.39
18:U:84:LYS:O	18:U:84:LYS:CE	1.69	1.39
24:W:58:ASN:ND2	24:W:132:GLY:CA	1.88	1.37
6:F:68:THR:CG2	6:F:88:LYS:HG3	1.54	1.36
6:F:122:PHE:HE2	6:F:167:ARG:NH2	0.85	1.34
2:B:55:A:C5'	6:F:23:ASP:CB	2.06	1.34
12:O:95:PHE:CE2	12:O:106:VAL:CG1	2.11	1.34
1:A:2280:G:O6	19:V:12:LYS:HB3	1.19	1.34
2:B:55:A:H5''	6:F:23:ASP:CB	1.55	1.33
1:A:1397:G:N2	1:A:1411:U:C5	1.95	1.33
1:A:1527:C:O2	1:A:1558:G:N2	1.60	1.33
2:B:55:A:C5'	6:F:23:ASP:HB3	1.59	1.32
1:A:2126:G:N2	1:A:2221:C:O2	1.60	1.32
24:W:58:ASN:ND2	24:W:132:GLY:HA3	0.99	1.31
1:A:2687:C:O2	1:A:2692:G:N2	1.65	1.30
10:L:137:GLU:OE1	10:L:143:ALA:HB2	1.13	1.30
8:J:76:TYR:CD1	8:J:85:LEU:HD11	1.67	1.29
13:P:33:VAL:CG2	13:P:77:PHE:CZ	2.14	1.29
12:O:95:PHE:HE2	12:O:106:VAL:CG1	1.41	1.29
4:D:83:LEU:CD2	4:D:203:LYS:HD2	1.60	1.28
10:L:79:LEU:CD2	10:L:117:LEU:HB2	1.64	1.27
12:O:35:ARG:HH12	12:O:105:ARG:NE	1.31	1.27
7:G:87:GLY:HA3	7:G:166:GLU:CG	1.65	1.27
8:J:126:TYR:CE2	8:J:132:PRO:HD2	1.69	1.26
6:F:8:TYR:CE1	6:F:30:LYS:NZ	2.03	1.26

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:10:ILE:HD11	4:D:29:GLU:OE1	1.28	1.26
1:A:2280:G:O6	19:V:12:LYS:CB	1.85	1.25
24:W:31:VAL:HG13	24:W:39:SER:OG	1.33	1.25
1:A:495:U:O2	5:E:84:ARG:HD2	1.29	1.25
1:A:2777:A:O2'	7:G:64:ALA:CA	1.83	1.25
13:P:94:LYS:CD	13:P:118:ARG:NH2	1.98	1.25
16:S:36:LEU:HD11	16:S:47:ILE:CG2	1.67	1.24
14:Q:95:LEU:HD12	15:R:11:GLN:CB	1.68	1.23
14:Q:95:LEU:HD11	15:R:11:GLN:O	1.37	1.23
6:F:122:PHE:HE2	6:F:167:ARG:CZ	1.52	1.22
24:W:154:ILE:HD11	24:W:172:THR:CG2	1.70	1.21
10:L:117:LEU:CD2	10:L:136:VAL:CA	2.19	1.20
24:W:37:MET:HE3	24:W:71:TRP:CZ3	1.75	1.20
24:W:67:VAL:HG21	24:W:276:SER:CB	1.69	1.20
6:F:108:LEU:CD1	6:F:176:PRO:HG3	1.72	1.18
1:A:2777:A:O2'	7:G:64:ALA:HA	1.37	1.18
3:C:94:ILE:HD11	3:C:104:ILE:CD1	1.74	1.17
24:W:67:VAL:HG21	24:W:276:SER:OG	1.40	1.17
20:Z:6:ILE:HG22	20:Z:28:LEU:HD11	1.26	1.17
10:L:117:LEU:HD23	10:L:136:VAL:HA	1.17	1.17
4:D:16:PHE:CZ	13:P:80:HIS:O	1.98	1.16
12:O:35:ARG:NH1	12:O:105:ARG:HG3	1.58	1.16
8:J:26:LEU:CA	8:J:29:LEU:HD11	1.76	1.16
9:K:76:TYR:HB2	13:P:76:THR:HB	1.27	1.16
10:L:117:LEU:HD21	10:L:136:VAL:HA	1.17	1.16
14:Q:92:ARG:HB2	15:R:11:GLN:CG	1.74	1.16
22:Y:21:LEU:CD1	22:Y:53:MET:HE1	1.76	1.16
7:G:78:GLU:HB3	7:G:84:PHE:HZ	1.08	1.16
1:A:673:A:C8	10:L:76:VAL:HG11	1.81	1.15
2:B:41:C:H5''	6:F:63:GLN:OE1	1.43	1.14
1:A:1659:A:N6	16:S:91:GLY:HA2	1.62	1.14
1:A:2280:G:C5	19:V:12:LYS:HE3	1.83	1.14
2:B:55:A:C5'	6:F:23:ASP:HB2	1.78	1.14
4:D:27:VAL:HG21	13:P:8:ILE:HD11	1.30	1.14
12:O:95:PHE:CE2	12:O:106:VAL:HG12	1.75	1.13
9:K:62:ILE:HA	9:K:84:CYS:SG	1.88	1.13
14:Q:92:ARG:CB	15:R:11:GLN:HG3	1.77	1.13
18:U:84:LYS:HE3	18:U:84:LYS:C	1.73	1.13
24:W:154:ILE:CD1	24:W:172:THR:HG21	1.78	1.12
6:F:3:ARG:NH2	6:F:101:ASP:OD2	1.82	1.12
18:U:45:SER:HG	18:U:55:GLY:N	1.46	1.12

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:30:ALA:HB1	4:D:53:PHE:CZ	1.84	1.12
16:S:86:ARG:NH2	16:S:96:ILE:HD11	1.64	1.12
18:U:41:VAL:HG12	18:U:43:LYS:HG3	1.32	1.12
1:A:738:C:C5'	3:C:217:ARG:HH22	1.62	1.12
24:W:67:VAL:CG2	24:W:276:SER:OG	1.98	1.12
24:W:81:ARG:NH1	24:W:103:ILE:HG12	1.64	1.12
24:W:127:GLY:O	24:W:175:ILE:HB	1.48	1.11
1:A:2282:G:H1	19:V:13:LYS:HG3	1.00	1.11
4:D:7:GLY:HA3	4:D:30:ALA:HB2	1.32	1.11
1:A:787:C:H1'	1:A:2010:A:N7	1.66	1.11
1:A:2342:C:H5''	6:F:88:LYS:HD3	1.33	1.10
16:S:38:LEU:HD13	21:b:38:LEU:HB3	1.21	1.10
1:A:702:A:H4'	1:A:703:G:H5'	1.16	1.10
2:B:53:U:O2'	6:F:26:MET:HG2	1.49	1.10
1:A:699:A:H5''	1:A:700:U:OP2	1.50	1.10
1:A:1527:C:O2	1:A:1558:G:C2	2.05	1.10
18:U:80:ARG:O	18:U:94:ALA:CB	1.98	1.10
1:A:2282:G:O6	19:V:13:LYS:HA	1.52	1.09
5:E:51:VAL:HG21	5:E:91:GLY:HA3	1.34	1.09
10:L:79:LEU:HD21	10:L:117:LEU:CB	1.81	1.09
1:A:920:G:C6	1:A:946:G:O6	2.05	1.09
4:D:10:ILE:HB	4:D:27:VAL:HG11	1.25	1.09
6:F:63:GLN:HG2	6:F:91:LEU:HB3	1.16	1.09
4:D:55:ASP:HA	4:D:77:LYS:HA	1.19	1.09
14:Q:95:LEU:HD11	15:R:11:GLN:C	1.76	1.09
6:F:68:THR:HG22	6:F:88:LYS:HE2	1.09	1.09
24:W:81:ARG:HH12	24:W:103:ILE:HG13	0.94	1.09
22:Y:21:LEU:HD12	22:Y:53:MET:HE1	1.17	1.09
3:C:94:ILE:HD11	3:C:104:ILE:HD11	1.33	1.08
24:W:126:ILE:CG2	24:W:175:ILE:HD11	1.82	1.08
1:A:738:C:H5'	3:C:217:ARG:NH2	1.66	1.08
2:B:53:U:H1'	6:F:26:MET:SD	1.91	1.08
24:W:81:ARG:HH11	24:W:103:ILE:CD1	1.66	1.08
1:A:2777:A:O2'	7:G:64:ALA:C	1.98	1.07
16:S:36:LEU:HD11	16:S:47:ILE:HG21	1.29	1.07
1:A:1288:G:H21	5:E:88:VAL:HG21	0.98	1.07
2:B:41:C:C5'	6:F:63:GLN:OE1	2.02	1.07
2:B:55:A:H5'	6:F:23:ASP:CB	1.84	1.06
4:D:50:GLN:HG2	4:D:82:GLU:OE1	1.52	1.06
14:Q:95:LEU:HD12	15:R:11:GLN:HB3	1.27	1.06
14:Q:108:GLN:OE1	15:R:45:ASN:ND2	1.88	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2342:C:C5'	6:F:88:LYS:HD3	1.85	1.06
4:D:10:ILE:CD1	4:D:29:GLU:OE1	2.02	1.06
16:S:38:LEU:CD1	21:b:38:LEU:HB3	1.85	1.06
18:U:82:GLY:N	18:U:93:VAL:O	1.89	1.06
7:G:78:GLU:HB3	7:G:84:PHE:CZ	1.91	1.05
9:K:22:ILE:HD12	9:K:40:VAL:HG12	1.33	1.05
13:P:33:VAL:CG2	13:P:77:PHE:CE2	2.38	1.05
21:b:38:LEU:HD11	21:b:41:ARG:HB2	1.33	1.05
8:J:24:LYS:O	8:J:29:LEU:HD21	1.55	1.05
4:D:11:GLY:H	4:D:27:VAL:HB	1.16	1.05
4:D:83:LEU:HD22	4:D:203:LYS:HD2	1.13	1.05
1:A:2667:G:OP2	4:D:84:ARG:NH1	1.90	1.05
11:N:28:GLU:HG3	11:N:119:LEU:HD12	1.38	1.05
24:W:81:ARG:NH1	24:W:103:ILE:HG13	1.50	1.05
15:R:48:VAL:HG22	15:R:53:VAL:HG23	1.06	1.04
6:F:63:GLN:HG2	6:F:91:LEU:CB	1.86	1.04
6:F:126:GLY:O	6:F:158:THR:OG1	1.74	1.04
9:K:25:LEU:CB	9:K:38:VAL:HG13	1.88	1.04
16:S:36:LEU:CD1	16:S:47:ILE:HG22	1.88	1.04
1:A:2342:C:O2'	6:F:37:ASN:ND2	1.91	1.04
8:J:76:TYR:HD1	8:J:85:LEU:HD11	0.90	1.04
19:V:39:VAL:CG2	19:V:75:VAL:HG23	1.88	1.04
12:O:95:PHE:CZ	12:O:106:VAL:HG13	1.93	1.03
1:A:1527:C:C2	1:A:1558:G:N2	2.26	1.03
19:V:53:ILE:HG13	19:V:67:LEU:HD11	1.36	1.03
24:W:37:MET:HE3	24:W:71:TRP:HZ3	1.08	1.03
1:A:673:A:H8	10:L:76:VAL:HG11	1.23	1.02
6:F:4:LEU:CD2	6:F:97:TYR:O	2.07	1.02
1:A:2703:G:H4'	9:K:30:ARG:HD3	1.37	1.02
2:B:53:U:O2'	6:F:26:MET:CG	2.07	1.02
22:Y:21:LEU:CD1	22:Y:53:MET:CE	2.37	1.02
1:A:2592:U:H4'	9:K:28:SER:OG	1.58	1.02
6:F:63:GLN:CB	6:F:90:THR:O	2.06	1.02
6:F:69:ARG:HA	6:F:84:PRO:HA	1.38	1.02
6:F:108:LEU:HD12	6:F:176:PRO:HG3	1.42	1.02
1:A:1288:G:N2	5:E:88:VAL:HG21	1.74	1.02
6:F:68:THR:HG22	6:F:88:LYS:CE	1.89	1.02
18:U:84:LYS:H	18:U:93:VAL:CG1	1.72	1.02
12:O:95:PHE:CE2	12:O:106:VAL:HG13	1.91	1.01
1:A:342:A:O5'	18:U:95:LYS:NZ	1.93	1.01
1:A:1397:G:C2	1:A:1411:U:H5	1.78	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:10:ILE:HB	4:D:27:VAL:CG1	1.91	1.01
4:D:30:ALA:CA	4:D:53:PHE:HZ	1.73	1.01
16:S:36:LEU:CD1	16:S:47:ILE:CG2	2.39	1.01
22:Y:21:LEU:HD12	22:Y:53:MET:CE	1.89	1.01
1:A:2282:G:N1	19:V:13:LYS:HG3	1.73	1.01
1:A:2777:A:O2'	7:G:64:ALA:O	1.77	1.01
1:A:342:A:C5'	18:U:95:LYS:NZ	2.24	1.00
1:A:2342:C:H5''	6:F:88:LYS:CD	1.90	1.00
1:A:2280:G:C6	19:V:12:LYS:HE3	1.94	1.00
1:A:1861:C:O2	1:A:2002:G:N2	1.94	1.00
6:F:8:TYR:HE1	6:F:30:LYS:NZ	1.48	1.00
19:V:39:VAL:HG21	19:V:75:VAL:CG2	1.91	1.00
1:A:669:C:H2'	1:A:670:C:C6	1.97	1.00
6:F:68:THR:CG2	6:F:88:LYS:CG	2.38	1.00
20:Z:8:LEU:HD23	20:Z:54:VAL:HG13	1.42	0.99
2:B:53:U:O2'	6:F:26:MET:SD	2.20	0.99
1:A:2282:G:H1	19:V:13:LYS:CG	1.74	0.99
8:J:26:LEU:CA	8:J:29:LEU:CD1	2.37	0.99
8:J:76:TYR:HD1	8:J:85:LEU:CD1	1.75	0.99
6:F:68:THR:HG23	6:F:88:LYS:HG3	1.43	0.99
1:A:2823:C:O2	1:A:2828:G:N2	1.93	0.99
8:J:126:TYR:CE2	8:J:132:PRO:CD	2.45	0.99
6:F:68:THR:HG21	6:F:88:LYS:HG3	1.41	0.99
10:L:117:LEU:HD23	10:L:136:VAL:CA	1.87	0.99
1:A:683:A:H8	10:L:114:ASN:OD1	1.45	0.98
24:W:127:GLY:H	24:W:175:ILE:CG1	1.76	0.98
4:D:30:ALA:CB	4:D:53:PHE:CZ	2.46	0.98
6:F:4:LEU:HD23	6:F:97:TYR:O	1.63	0.98
13:P:33:VAL:HG21	13:P:77:PHE:CE2	1.98	0.98
19:V:39:VAL:HG21	19:V:75:VAL:HG23	1.01	0.98
1:A:1858:A:N7	1:A:1859:C:C4	2.32	0.98
19:V:80:PHE:CZ	19:V:86:LYS:HD2	1.99	0.98
24:W:31:VAL:CG1	24:W:39:SER:OG	2.12	0.98
6:F:4:LEU:HD23	6:F:97:TYR:HA	1.46	0.98
18:U:82:GLY:CA	18:U:93:VAL:O	2.11	0.98
2:B:55:A:H5''	6:F:23:ASP:HB3	1.02	0.97
10:L:137:GLU:OE1	10:L:143:ALA:CB	2.10	0.97
24:W:67:VAL:HG21	24:W:276:SER:HB2	1.46	0.97
15:R:7:THR:HG21	15:R:35:PHE:CD1	2.00	0.97
24:W:81:ARG:HH11	24:W:103:ILE:CG1	1.58	0.97
1:A:342:A:H5''	18:U:95:LYS:NZ	1.80	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2552:G:O6	1:A:2569:C:N4	1.97	0.97
2:B:28:C:O2	2:B:52:G:N2	1.96	0.97
8:J:26:LEU:HB2	8:J:63:ILE:CG2	1.93	0.97
8:J:26:LEU:HD12	8:J:102:LEU:HD13	1.46	0.97
24:W:125:ILE:HD13	24:W:136:LEU:HD23	1.44	0.97
1:A:2557:U:H3	1:A:2564:G:H22	1.11	0.96
15:R:22:ILE:HD11	15:R:95:VAL:HB	1.45	0.96
24:W:31:VAL:HG13	24:W:39:SER:HG	1.14	0.96
4:D:30:ALA:HA	4:D:53:PHE:HZ	1.27	0.96
1:A:2280:G:N7	19:V:12:LYS:CE	2.29	0.96
12:O:95:PHE:CZ	12:O:106:VAL:CG1	2.48	0.96
1:A:683:A:OP2	10:L:112:LEU:HD22	1.66	0.96
4:D:49:ILE:HD13	4:D:91:TYR:CG	2.01	0.96
14:Q:95:LEU:HD12	15:R:11:GLN:HB2	1.47	0.95
6:F:4:LEU:HD23	6:F:97:TYR:CA	1.96	0.95
24:W:81:ARG:HH11	24:W:103:ILE:HD11	1.31	0.95
1:A:1553:A:N3	1:A:1555:A:N6	2.14	0.95
15:R:48:VAL:HG22	15:R:53:VAL:CG2	1.96	0.95
8:J:32:GLU:HG2	8:J:143:LEU:HG	1.49	0.95
2:B:41:C:H1'	6:F:92:ARG:HB2	1.48	0.95
6:F:34:ILE:CD1	6:F:96:MET:SD	2.54	0.95
24:W:126:ILE:HG21	24:W:175:ILE:HD11	1.48	0.94
1:A:1397:G:N2	1:A:1411:U:H5	1.44	0.94
4:D:35:VAL:HG21	4:D:91:TYR:HD1	1.31	0.94
24:W:126:ILE:HB	24:W:175:ILE:CG1	1.96	0.94
6:F:63:GLN:HG3	6:F:91:LEU:HA	1.48	0.94
10:L:125:ALA:HB3	10:L:128:PHE:CE1	2.01	0.94
1:A:77:U:H4'	22:Y:2:LYS:HG3	1.49	0.94
1:A:925:A:H62	1:A:947:A:C1'	1.79	0.94
21:b:38:LEU:CD1	21:b:41:ARG:HB2	1.96	0.94
6:F:132:ILE:HD13	6:F:154:ILE:HG13	1.50	0.94
8:J:26:LEU:HB2	8:J:63:ILE:HG21	1.46	0.94
1:A:125:A:N6	23:d:42:LEU:HD12	1.83	0.94
1:A:920:G:O6	1:A:946:G:O6	1.86	0.94
1:A:925:A:H62	1:A:947:A:H1'	1.32	0.94
15:R:31:GLU:HG2	15:R:32:THR:H	1.29	0.94
16:S:86:ARG:HH21	16:S:96:ILE:CD1	1.79	0.94
19:V:67:LEU:HD13	19:V:87:VAL:HG11	1.49	0.94
24:W:81:ARG:NH1	24:W:103:ILE:CD1	2.27	0.93
7:G:87:GLY:CA	7:G:166:GLU:CG	2.33	0.93
10:L:117:LEU:HD23	10:L:135:ALA:O	1.68	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:7:GLY:HA2	4:D:53:PHE:CE2	2.04	0.93
8:J:126:TYR:HE2	8:J:132:PRO:HD2	1.13	0.93
1:A:2361:C:OP1	19:V:84:ARG:NH1	2.02	0.93
1:A:2823:C:N3	1:A:2828:G:N1	2.17	0.93
4:D:29:GLU:HB3	4:D:185:LEU:CD2	1.98	0.93
3:C:173:LEU:CD2	3:C:183:MET:HG2	1.99	0.92
24:W:58:ASN:HD21	24:W:132:GLY:CA	1.59	0.92
4:D:32:PRO:HG3	4:D:98:LYS:HG2	1.51	0.92
13:P:94:LYS:CD	13:P:118:ARG:HH21	1.71	0.92
18:U:41:VAL:CG1	18:U:43:LYS:HG3	1.99	0.92
16:S:86:ARG:NH2	16:S:96:ILE:CD1	2.33	0.92
19:V:80:PHE:CE2	19:V:86:LYS:HG3	2.05	0.92
1:A:1397:G:N2	1:A:1411:U:C6	2.37	0.92
6:F:34:ILE:HD12	6:F:96:MET:SD	2.09	0.92
6:F:68:THR:HG21	6:F:88:LYS:CG	1.99	0.92
21:b:38:LEU:HD11	21:b:41:ARG:CB	2.00	0.92
24:W:74:HIS:O	24:W:78:GLN:HG3	1.69	0.92
1:A:495:U:O2	5:E:84:ARG:CD	2.16	0.91
6:F:63:GLN:CG	6:F:91:LEU:HA	2.00	0.91
15:R:24:LYS:HD2	15:R:91:PRO:HG3	1.50	0.91
9:K:58:VAL:HG12	9:K:59:LYS:N	1.83	0.91
1:A:2777:A:O4'	7:G:68:THR:CG2	2.19	0.91
9:K:58:VAL:HG12	9:K:59:LYS:H	1.35	0.91
12:O:35:ARG:NH1	12:O:105:ARG:NE	2.17	0.91
1:A:2230:C:O2	1:A:2251:G:N2	2.03	0.91
12:O:35:ARG:NH1	12:O:105:ARG:CG	2.33	0.91
1:A:2039:G:OP2	16:S:41:ARG:NH1	2.04	0.91
4:D:83:LEU:CD2	4:D:203:LYS:CD	2.48	0.91
12:O:35:ARG:HH11	12:O:105:ARG:HG3	1.23	0.91
24:W:126:ILE:CB	24:W:175:ILE:HD11	2.01	0.91
1:A:1659:A:H62	16:S:91:GLY:HA2	1.31	0.90
5:E:51:VAL:CG2	5:E:91:GLY:HA3	2.02	0.90
1:A:1529:G:N1	1:A:1552:C:N3	2.19	0.90
6:F:108:LEU:HD11	6:F:176:PRO:HG3	1.50	0.90
4:D:27:VAL:HG21	13:P:8:ILE:CD1	2.02	0.90
7:G:87:GLY:C	7:G:166:GLU:HG2	1.97	0.90
1:A:2093:C:H42	1:A:2475:G:H1	1.20	0.90
24:W:172:THR:N	24:W:173:PRO:CD	2.34	0.90
4:D:83:LEU:HD22	4:D:203:LYS:CD	2.02	0.89
14:Q:95:LEU:CD1	15:R:11:GLN:CB	2.49	0.89
16:S:12:ILE:HD13	16:S:43:ALA:HB2	1.55	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:U:84:LYS:O	18:U:84:LYS:HE3	0.72	0.89
1:A:2777:A:O4'	7:G:68:THR:HG22	1.71	0.89
1:A:683:A:C8	10:L:114:ASN:OD1	2.25	0.89
9:K:76:TYR:HB2	13:P:76:THR:CB	2.03	0.89
12:O:53:LEU:O	12:O:88:LYS:NZ	2.05	0.89
16:S:38:LEU:HD11	21:b:38:LEU:N	1.88	0.89
10:L:117:LEU:HD23	10:L:135:ALA:C	1.98	0.89
11:N:37:ALA:HB1	11:N:117:ILE:HD11	1.52	0.89
1:A:738:C:H5'	3:C:217:ARG:HH22	1.25	0.88
6:F:122:PHE:CE2	6:F:167:ARG:CZ	2.39	0.88
13:P:33:VAL:HG22	13:P:77:PHE:CZ	2.07	0.88
24:W:58:ASN:CG	24:W:131:VAL:O	2.16	0.88
8:J:26:LEU:HA	8:J:29:LEU:HD11	0.89	0.88
8:J:57:ILE:HD12	8:J:125:VAL:HG22	1.52	0.88
1:A:1830:G:OP2	3:C:153:GLN:NE2	2.06	0.88
1:A:2592:U:C4'	9:K:28:SER:OG	2.22	0.88
14:Q:92:ARG:HB2	15:R:11:GLN:HG3	0.91	0.88
10:L:117:LEU:HD22	10:L:136:VAL:HG12	1.56	0.87
14:Q:108:GLN:OE1	15:R:45:ASN:CG	2.16	0.87
15:R:48:VAL:HG12	15:R:50:ASN:O	1.75	0.87
15:R:48:VAL:CG2	15:R:53:VAL:HG23	1.99	0.87
4:D:55:ASP:HA	4:D:77:LYS:CA	2.02	0.87
6:F:4:LEU:HD23	6:F:97:TYR:C	1.99	0.87
9:K:25:LEU:HB3	9:K:38:VAL:HG13	1.53	0.87
13:P:33:VAL:HG21	13:P:77:PHE:HZ	0.90	0.87
16:S:86:ARG:HH21	16:S:96:ILE:HD11	1.32	0.87
1:A:787:C:H1'	1:A:2010:A:C8	2.09	0.87
1:A:673:A:C8	10:L:76:VAL:CG1	2.57	0.87
4:D:30:ALA:CA	4:D:53:PHE:CZ	2.57	0.87
13:P:12:THR:HG22	13:P:58:ILE:HD11	1.56	0.87
1:A:1353:C:H42	1:A:1377:G:H1	1.23	0.87
1:A:1858:A:N7	1:A:1859:C:N4	2.23	0.87
1:A:2809:G:OP2	8:J:121:LYS:HE2	1.75	0.87
6:F:4:LEU:HG	6:F:97:TYR:HD1	1.37	0.87
4:D:49:ILE:CD1	4:D:91:TYR:CG	2.58	0.86
7:G:87:GLY:C	7:G:166:GLU:CG	2.48	0.86
8:J:24:LYS:O	8:J:29:LEU:CD2	2.23	0.86
24:W:154:ILE:HD11	24:W:172:THR:HG21	0.89	0.86
8:J:25:THR:O	8:J:29:LEU:HG	1.75	0.86
6:F:5:LYS:NZ	6:F:94:GLU:OE2	2.07	0.86
12:O:35:ARG:HH12	12:O:105:ARG:HE	1.20	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:702:A:H4'	1:A:703:G:C5'	2.04	0.85
5:E:81:PRO:HB3	5:E:89:VAL:HG22	1.56	0.85
10:L:79:LEU:HD21	10:L:117:LEU:HB2	0.89	0.85
18:U:80:ARG:O	18:U:94:ALA:HB2	1.76	0.85
1:A:2284:G:H1	1:A:2304:C:H42	1.20	0.85
4:D:49:ILE:HD13	4:D:91:TYR:CD1	2.11	0.85
8:J:44:THR:HG22	14:Q:100:VAL:HG12	1.59	0.85
12:O:69:GLY:O	12:O:105:ARG:NH1	2.09	0.85
1:A:1659:A:N6	16:S:91:GLY:CA	2.39	0.85
1:A:2342:C:H4'	6:F:37:ASN:OD1	1.77	0.85
1:A:2777:A:C1'	7:G:68:THR:CG2	2.55	0.85
2:B:55:A:H8	6:F:24:SER:OG	1.59	0.85
24:W:127:GLY:H	24:W:175:ILE:HG13	1.39	0.85
18:U:80:ARG:O	18:U:94:ALA:HB1	1.75	0.85
24:W:172:THR:H	24:W:173:PRO:CD	1.89	0.85
8:J:26:LEU:HA	8:J:29:LEU:HD12	1.59	0.85
1:A:2280:G:C6	19:V:12:LYS:HB3	2.11	0.85
1:A:377:G:O2'	1:A:378:C:H6	1.60	0.84
1:A:84:A:OP2	18:U:4:LYS:HD3	1.76	0.84
1:A:2126:G:C2	1:A:2221:C:O2	2.29	0.84
4:D:54:ASP:O	4:D:78:ARG:HG3	1.76	0.84
1:A:342:A:C5'	18:U:95:LYS:HZ2	1.84	0.84
1:A:740:A:OP1	3:C:39:LYS:HE3	1.77	0.84
24:W:191:VAL:HG11	24:W:277:PHE:HZ	1.42	0.84
1:A:2684:G:HO2'	1:A:2693:G:H1	1.25	0.84
6:F:69:ARG:HA	6:F:84:PRO:CA	2.05	0.84
1:A:2280:G:C5	19:V:12:LYS:CE	2.60	0.84
24:W:71:TRP:HE1	24:W:278:GLU:C	1.85	0.84
6:F:69:ARG:HE	6:F:82:GLY:HA2	1.43	0.84
12:O:101:LEU:HD23	12:O:101:LEU:H	1.41	0.84
4:D:31:ALA:N	4:D:53:PHE:CE1	2.45	0.84
24:W:58:ASN:HD21	24:W:132:GLY:HA3	1.10	0.84
4:D:11:GLY:H	4:D:27:VAL:CB	1.91	0.83
4:D:49:ILE:O	4:D:82:GLU:HA	1.77	0.83
24:W:125:ILE:HD13	24:W:136:LEU:CD2	2.08	0.83
1:A:738:C:H5''	3:C:217:ARG:HH22	1.39	0.83
1:A:920:G:O6	1:A:946:G:C6	2.31	0.83
1:A:2687:C:O2	1:A:2692:G:C2	2.31	0.83
1:A:1858:A:C5	1:A:1859:C:C4	2.66	0.83
2:B:55:A:N6	6:F:26:MET:CE	2.40	0.83
3:C:94:ILE:HD11	3:C:104:ILE:HD13	1.60	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:341:G:OP1	18:U:82:GLY:O	1.97	0.83
1:A:787:C:C1'	1:A:2010:A:N7	2.41	0.83
1:A:699:A:C5'	1:A:700:U:OP2	2.26	0.83
24:W:126:ILE:HB	24:W:175:ILE:CD1	2.09	0.83
1:A:342:A:C5'	18:U:95:LYS:HZ1	1.91	0.83
4:D:107:ILE:HG22	4:D:205:ALA:CB	2.08	0.83
1:A:580:U:H2'	1:A:581:C:H6	1.43	0.83
2:B:35:C:O2'	12:O:103:HIS:NE2	2.11	0.82
12:O:28:ARG:HA	12:O:92:ASP:O	1.78	0.82
12:O:107:LYS:O	12:O:111:ASP:CG	2.22	0.82
12:O:75:THR:HG21	12:O:108:ALA:CB	2.09	0.82
1:A:343:A:OP2	18:U:95:LYS:NZ	2.12	0.82
1:A:1390:C:H2'	1:A:1391:U:C6	2.13	0.82
1:A:920:G:C5	1:A:946:G:O6	2.31	0.82
18:U:82:GLY:HA3	18:U:93:VAL:O	1.77	0.82
1:A:2777:A:C1'	7:G:68:THR:HG23	2.10	0.82
1:A:2340:A:C8	6:F:85:ILE:HD13	2.14	0.82
14:Q:95:LEU:CD1	15:R:11:GLN:O	2.26	0.82
1:A:1847:U:C6	3:C:153:GLN:O	2.33	0.81
19:V:80:PHE:CZ	19:V:86:LYS:CD	2.63	0.81
3:C:173:LEU:HD21	3:C:183:MET:HG2	1.59	0.81
6:F:122:PHE:CE2	6:F:167:ARG:NE	2.47	0.81
11:N:37:ALA:CB	11:N:117:ILE:HD11	2.11	0.81
1:A:647:A:N6	1:A:702:A:C8	2.49	0.81
3:C:94:ILE:CD1	3:C:104:ILE:CD1	2.59	0.81
13:P:64:VAL:HB	13:P:75:ARG:HB3	1.61	0.81
4:D:30:ALA:HA	4:D:53:PHE:CZ	2.15	0.81
24:W:37:MET:CE	24:W:71:TRP:CZ3	2.61	0.81
9:K:2:ILE:HD13	9:K:8:LEU:HD21	1.63	0.81
15:R:14:VAL:CG1	15:R:97:ILE:HG13	2.11	0.81
6:F:68:THR:CG2	6:F:88:LYS:HE2	2.03	0.81
9:K:25:LEU:HB2	9:K:38:VAL:O	1.80	0.81
24:W:58:ASN:OD1	24:W:131:VAL:O	1.99	0.81
24:W:126:ILE:HB	24:W:175:ILE:HD11	1.60	0.81
1:A:2359:G:N2	1:A:2414:C:O2	2.12	0.81
8:J:59:ASN:OD1	8:J:129:SER:HB3	1.80	0.81
10:L:137:GLU:CD	10:L:143:ALA:HB2	2.07	0.80
1:A:2536:C:N4	1:A:2611:G:C6	2.49	0.80
2:B:55:A:H5'	6:F:23:ASP:C	2.07	0.80
6:F:63:GLN:HB3	6:F:90:THR:O	1.81	0.80
1:A:380:C:H5'	18:U:2:HIS:CE1	2.16	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:34:VAL:HG11	4:D:74:THR:HG21	1.64	0.80
1:A:77:U:H4'	22:Y:2:LYS:CG	2.12	0.80
4:D:35:VAL:CG2	4:D:91:TYR:HD1	1.95	0.80
6:F:104:ILE:HA	6:F:108:LEU:HB2	1.61	0.80
24:W:43:MET:HB2	24:W:178:PRO:HG3	1.64	0.80
24:W:126:ILE:HB	24:W:175:ILE:HG13	1.64	0.80
1:A:2681:U:H3	1:A:2697:G:H1	1.30	0.80
10:L:79:LEU:CD2	10:L:117:LEU:CB	2.49	0.80
13:P:94:LYS:CD	13:P:118:ARG:HH22	1.91	0.79
1:A:1527:C:H1'	1:A:1558:G:N2	1.96	0.79
1:A:2703:G:C4'	9:K:30:ARG:HD3	2.12	0.79
4:D:55:ASP:HB3	4:D:77:LYS:HG2	1.63	0.79
6:F:8:TYR:CD1	6:F:30:LYS:NZ	2.49	0.79
6:F:61:ALA:HB1	6:F:91:LEU:CD2	2.11	0.79
6:F:104:ILE:HG23	6:F:108:LEU:HD12	1.62	0.79
1:A:317:G:H1	1:A:403:C:H42	1.31	0.79
1:A:2093:C:N4	1:A:2475:G:H1	1.80	0.79
9:K:25:LEU:HB2	9:K:38:VAL:HG13	1.62	0.79
9:K:58:VAL:CG1	9:K:59:LYS:H	1.95	0.79
1:A:783:C:H42	1:A:807:G:H1	1.31	0.79
1:A:1858:A:C8	1:A:1859:C:C5	2.69	0.79
1:A:1517:A:H61	1:A:1567:U:H3	1.30	0.79
1:A:2280:G:O6	19:V:12:LYS:HB2	1.80	0.79
6:F:118:SER:OG	6:F:177:PHE:CD1	2.35	0.79
1:A:377:G:O2'	1:A:378:C:C6	2.33	0.79
1:A:580:U:H2'	1:A:581:C:C6	2.17	0.79
24:W:153:GLY:HA3	25:W:301:GNP:O2G	1.82	0.79
1:A:1554:U:H5''	1:A:1555:A:C8	2.17	0.79
4:D:32:PRO:CG	4:D:98:LYS:HG2	2.12	0.79
24:W:127:GLY:H	24:W:175:ILE:HG12	1.48	0.79
1:A:2777:A:H1'	7:G:68:THR:CG2	2.13	0.78
6:F:4:LEU:HG	6:F:97:TYR:CD1	2.16	0.78
21:b:27:MET:HB3	21:b:36:MET:SD	2.24	0.78
1:A:1554:U:H5'	1:A:1555:A:N7	1.99	0.78
1:A:2557:U:H3	1:A:2564:G:N2	1.82	0.78
6:F:29:PRO:O	6:F:169:LEU:HD22	1.84	0.78
1:A:2280:G:N7	19:V:12:LYS:HE2	1.97	0.78
3:C:205:ILE:HG23	3:C:210:ARG:HB3	1.64	0.78
12:O:75:THR:HG21	12:O:108:ALA:HB3	1.65	0.78
6:F:8:TYR:HA	6:F:12:ILE:HB	1.66	0.78
4:D:35:VAL:CG2	4:D:91:TYR:CD1	2.67	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:Q:95:LEU:CD1	15:R:11:GLN:HB2	2.12	0.78
1:A:1362:G:H1	1:A:1370:C:H42	1.28	0.77
2:B:53:U:C1'	6:F:26:MET:SD	2.70	0.77
4:D:50:GLN:CG	4:D:82:GLU:OE1	2.30	0.77
6:F:69:ARG:NE	6:F:82:GLY:HA2	1.97	0.77
1:A:1551:C:H2'	1:A:1552:C:C6	2.20	0.77
24:W:156:THR:HG22	24:W:172:THR:HB	1.67	0.77
3:C:171:TYR:HE1	3:C:183:MET:SD	2.07	0.77
6:F:69:ARG:CA	6:F:84:PRO:HB3	2.14	0.77
18:U:84:LYS:H	18:U:93:VAL:HG11	1.47	0.77
18:U:84:LYS:H	18:U:93:VAL:HG12	1.50	0.77
1:A:2641:C:HO2'	21:b:2:ALA:N	1.82	0.77
1:A:2342:C:H1'	6:F:37:ASN:ND2	1.99	0.77
4:D:33:ASN:HB2	4:D:97:VAL:HG23	1.67	0.77
9:K:10:VAL:HG21	9:K:16:ALA:C	2.10	0.77
24:W:220:ARG:CZ	24:W:275:LEU:HD23	2.15	0.77
24:W:172:THR:H	24:W:173:PRO:HD3	1.48	0.77
6:F:4:LEU:HD22	6:F:97:TYR:O	1.83	0.76
1:A:77:U:O3'	22:Y:2:LYS:HG3	1.85	0.76
1:A:1526:G:N2	1:A:1558:G:N2	2.33	0.76
8:J:26:LEU:HA	8:J:29:LEU:CG	2.14	0.76
1:A:2280:G:N7	19:V:12:LYS:HE3	1.95	0.76
1:A:2777:A:H1'	7:G:68:THR:HG23	1.68	0.76
6:F:63:GLN:CG	6:F:90:THR:O	2.34	0.76
6:F:63:GLN:CG	6:F:91:LEU:HB3	2.09	0.76
14:Q:95:LEU:CD1	15:R:11:GLN:C	2.57	0.76
4:D:50:GLN:HG2	4:D:82:GLU:CD	2.10	0.76
1:A:925:A:N6	1:A:947:A:C1'	2.48	0.76
1:A:2900:A:HO2'	13:P:5:GLN:N	1.83	0.76
3:C:94:ILE:CD1	3:C:104:ILE:HD13	2.15	0.76
4:D:29:GLU:CB	4:D:185:LEU:CD2	2.62	0.76
1:A:77:U:C4'	22:Y:2:LYS:HG3	2.15	0.76
3:C:171:TYR:CZ	3:C:269:PHE:CE1	2.74	0.76
24:W:81:ARG:NH1	24:W:103:ILE:HD11	1.94	0.76
1:A:402:U:H2'	1:A:403:C:C6	2.21	0.75
1:A:1847:U:OP2	3:C:156:ARG:HD2	1.86	0.75
4:D:31:ALA:N	4:D:53:PHE:CZ	2.53	0.75
12:O:78:GLY:O	12:O:109:LEU:CD1	2.34	0.75
1:A:2129:G:N1	1:A:2218:U:O2	2.19	0.75
9:K:17:ARG:HB2	9:K:45:GLN:O	1.86	0.75
15:R:14:VAL:HG11	15:R:97:ILE:HG13	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:122:PHE:CZ	6:F:167:ARG:HB2	2.21	0.75
16:S:21:MET:HA	16:S:24:ILE:HD12	1.67	0.75
18:U:11:VAL:HG12	18:U:12:ILE:N	2.02	0.75
1:A:495:U:H1'	5:E:84:ARG:HG3	1.69	0.75
4:D:16:PHE:CE1	13:P:80:HIS:O	2.39	0.75
4:D:2:THR:O	4:D:86:VAL:HG13	1.86	0.75
4:D:108:VAL:O	4:D:205:ALA:HB2	1.86	0.75
24:W:151:ARG:N	24:W:152:PRO:HD2	2.02	0.75
4:D:6:LEU:H	4:D:33:ASN:HD21	1.35	0.75
15:R:5:ILE:HG22	15:R:7:THR:HG23	1.67	0.75
6:F:108:LEU:HD11	6:F:176:PRO:CG	2.17	0.74
15:R:7:THR:HG21	15:R:35:PHE:CG	2.21	0.74
16:S:29:VAL:HG12	16:S:55:ILE:HD11	1.69	0.74
4:D:11:GLY:N	4:D:27:VAL:HB	1.99	0.74
4:D:38:LYS:NZ	4:D:88:MET:HG2	2.02	0.74
8:J:36:ILE:CD1	8:J:141:TYR:HE2	2.00	0.74
16:S:38:LEU:CD1	21:b:38:LEU:CB	2.64	0.74
1:A:673:A:N7	10:L:112:LEU:HD12	2.02	0.74
1:A:2049:A:N7	21:b:6:ARG:NH1	2.33	0.74
12:O:35:ARG:HH12	12:O:105:ARG:CD	2.01	0.74
16:S:100:THR:HG22	16:S:101:SER:N	2.02	0.74
4:D:32:PRO:CB	4:D:98:LYS:HG2	2.16	0.74
16:S:39:THR:OG1	16:S:44:SER:OG	2.05	0.74
20:Z:6:ILE:CG2	20:Z:28:LEU:HD11	2.14	0.74
24:W:58:ASN:HD22	24:W:132:GLY:CA	1.77	0.74
2:B:55:A:N6	6:F:26:MET:HE2	2.02	0.74
24:W:58:ASN:ND2	24:W:131:VAL:O	2.19	0.74
1:A:2132:A:H61	1:A:2215:U:H3	1.34	0.74
6:F:17:MET:SD	6:F:22:TYR:CD2	2.80	0.74
6:F:122:PHE:CD2	6:F:167:ARG:NH2	2.50	0.74
9:K:58:VAL:CG1	9:K:59:LYS:N	2.50	0.74
24:W:127:GLY:N	24:W:175:ILE:HG13	2.02	0.74
1:A:683:A:N7	10:L:114:ASN:ND2	2.35	0.74
6:F:111:VAL:HB	6:F:114:PHE:HB3	1.69	0.74
19:V:67:LEU:CD1	19:V:87:VAL:HG11	2.18	0.74
24:W:154:ILE:CD1	24:W:172:THR:CG2	2.48	0.74
4:D:55:ASP:CB	4:D:77:LYS:HG2	2.18	0.74
24:W:220:ARG:HD2	24:W:275:LEU:HD21	1.69	0.74
24:W:172:THR:N	24:W:173:PRO:HD2	2.00	0.73
9:K:69:ALA:HB1	9:K:105:GLU:OE2	1.88	0.73
6:F:63:GLN:HG2	6:F:91:LEU:CA	2.18	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:738:C:C5'	3:C:217:ARG:NH2	2.34	0.73
24:W:150:ASP:HB3	24:W:152:PRO:HD2	1.70	0.73
4:D:32:PRO:HB3	4:D:98:LYS:CG	2.19	0.73
24:W:129:PRO:CG	24:W:176:LEU:HD23	2.19	0.73
4:D:49:ILE:CD1	4:D:91:TYR:CD2	2.70	0.73
4:D:55:ASP:CA	4:D:77:LYS:HA	2.10	0.73
13:P:33:VAL:HG22	13:P:77:PHE:CE2	2.19	0.73
1:A:925:A:N6	1:A:947:A:N9	2.36	0.73
16:S:29:VAL:CG1	16:S:55:ILE:HD11	2.18	0.73
18:U:84:LYS:N	18:U:93:VAL:CG1	2.51	0.73
1:A:643:U:H3	1:A:705:A:H61	1.32	0.73
1:A:2670:A:H5''	8:J:79:THR:HG21	1.71	0.73
8:J:36:ILE:HD11	8:J:141:TYR:HE2	1.54	0.73
21:b:27:MET:HE3	21:b:36:MET:HE3	1.71	0.73
6:F:95:ARG:HG3	6:F:95:ARG:O	1.87	0.72
15:R:19:THR:HG22	15:R:96:THR:HB	1.71	0.72
15:R:31:GLU:HG2	15:R:32:THR:N	2.01	0.72
24:W:58:ASN:HD22	24:W:132:GLY:HA3	0.93	0.72
8:J:36:ILE:HD13	8:J:141:TYR:CE2	2.24	0.72
8:J:50:ASP:HB2	8:J:115:LEU:HD13	1.70	0.72
9:K:64:ARG:HB2	9:K:83:ALA:H	1.54	0.72
2:B:55:A:C4'	6:F:23:ASP:HB2	2.19	0.72
13:P:50:VAL:HG13	13:P:63:THR:O	1.89	0.72
1:A:702:A:H2'	1:A:702:A:OP2	1.90	0.72
1:A:1793:G:H2'	1:A:1794:C:C6	2.24	0.72
1:A:2220:A:H2'	1:A:2221:C:C6	2.24	0.72
2:B:41:C:H5'	6:F:63:GLN:OE1	1.87	0.72
9:K:87:ILE:HD11	9:K:91:LYS:C	2.15	0.72
24:W:37:MET:SD	24:W:71:TRP:CH2	2.83	0.72
9:K:62:ILE:CA	9:K:84:CYS:SG	2.74	0.72
19:V:80:PHE:CE1	19:V:86:LYS:HD2	2.25	0.72
1:A:1573:C:O2	1:A:1594:G:N2	2.16	0.72
4:D:35:VAL:HG21	4:D:91:TYR:CD1	2.20	0.72
6:F:10:LYS:HG3	6:F:10:LYS:O	1.89	0.72
1:A:2342:C:C2'	6:F:37:ASN:HD21	2.01	0.72
3:C:171:TYR:CE1	3:C:183:MET:SD	2.83	0.72
6:F:61:ALA:HB1	6:F:91:LEU:HD23	1.71	0.72
6:F:63:GLN:HB2	6:F:90:THR:O	1.89	0.72
10:L:74:TYR:CZ	10:L:127:LYS:HG3	2.25	0.71
6:F:63:GLN:CG	6:F:91:LEU:CA	2.69	0.71
14:Q:90:VAL:O	14:Q:90:VAL:HG12	1.90	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:W:210:LEU:HD13	24:W:237:LEU:HD22	1.70	0.71
6:F:132:ILE:HD11	6:F:154:ILE:HB	1.71	0.71
8:J:99:GLU:OE2	8:J:127:ARG:HB2	1.89	0.71
22:Y:2:LYS:C	22:Y:2:LYS:HD3	2.16	0.71
24:W:129:PRO:CD	24:W:176:LEU:HD23	2.20	0.71
1:A:1529:G:N2	1:A:1552:C:O2	2.19	0.71
4:D:7:GLY:HA3	4:D:30:ALA:CB	2.16	0.71
14:Q:17:VAL:HG21	14:Q:32:TYR:HE1	1.55	0.71
24:W:151:ARG:N	24:W:152:PRO:CD	2.53	0.71
1:A:1858:A:C8	1:A:1859:C:C4	2.78	0.71
1:A:925:A:N6	1:A:947:A:H1'	2.05	0.71
24:W:150:ASP:CB	24:W:152:PRO:HD2	2.21	0.71
24:W:191:VAL:HG11	24:W:277:PHE:CZ	2.24	0.71
4:D:5:ILE:CG2	4:D:33:ASN:ND2	2.54	0.71
15:R:31:GLU:CG	15:R:32:THR:H	2.03	0.71
4:D:30:ALA:HB1	4:D:53:PHE:CE1	2.25	0.70
10:L:117:LEU:HD23	10:L:136:VAL:N	2.05	0.70
3:C:210:ARG:HA	3:C:213:TRP:HD1	1.55	0.70
7:G:60:LYS:NZ	7:G:60:LYS:HB3	2.05	0.70
10:L:91:VAL:HB	10:L:122:THR:O	1.91	0.70
24:W:153:GLY:N	25:W:301:GNP:O1G	2.24	0.70
2:B:41:C:H5''	6:F:63:GLN:CD	2.17	0.70
1:A:795:G:H5''	16:S:89:ALA:HB2	1.73	0.70
4:D:7:GLY:HA2	4:D:53:PHE:CD2	2.26	0.70
16:S:38:LEU:HD13	21:b:38:LEU:CB	2.11	0.70
1:A:2039:G:P	16:S:41:ARG:NH1	2.63	0.70
1:A:343:A:OP2	18:U:95:LYS:HD3	1.90	0.70
1:A:559:A:N3	14:Q:11:ARG:NH2	2.39	0.70
14:Q:95:LEU:CD1	15:R:11:GLN:HB3	2.16	0.70
3:C:205:ILE:CG2	3:C:210:ARG:HB3	2.20	0.70
24:W:129:PRO:HG3	24:W:176:LEU:HG	1.74	0.70
22:Y:21:LEU:CD1	22:Y:53:MET:HE2	2.21	0.70
1:A:2039:G:H5''	16:S:42:ALA:HB2	1.74	0.70
2:B:55:A:C8	6:F:24:SER:OG	2.39	0.70
14:Q:58:ARG:HE	14:Q:93:LYS:HE3	1.56	0.69
4:D:5:ILE:HG23	4:D:33:ASN:ND2	2.07	0.69
10:L:74:TYR:CD1	10:L:110:LYS:HB2	2.27	0.69
24:W:31:VAL:CG1	24:W:36:PRO:O	2.40	0.69
1:A:1564:C:C2	1:A:1565:U:C5	2.79	0.69
7:G:87:GLY:HA3	7:G:166:GLU:HG3	0.74	0.69
10:L:79:LEU:HD22	10:L:117:LEU:N	2.06	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:P:94:LYS:HB2	13:P:118:ARG:CZ	2.23	0.69
24:W:37:MET:CE	24:W:71:TRP:CH2	2.76	0.69
1:A:2298:A:C6	1:A:2299:G:C6	2.80	0.69
18:U:41:VAL:HG12	18:U:43:LYS:CG	2.18	0.69
6:F:38:MET:HE3	6:F:57:LEU:HD22	1.73	0.69
1:A:2667:G:P	4:D:84:ARG:HH22	2.15	0.69
1:A:2536:C:N4	1:A:2611:G:N1	2.41	0.69
10:L:74:TYR:OH	10:L:127:LYS:HG3	1.92	0.69
1:A:2290:C:C5	19:V:24:SER:HB2	2.28	0.69
4:D:29:GLU:HG3	4:D:29:GLU:O	1.91	0.69
4:D:29:GLU:CB	4:D:185:LEU:HD23	2.23	0.69
9:K:63:VAL:CG2	9:K:85:VAL:HG23	2.22	0.69
13:P:30:ARG:NE	13:P:47:GLU:OE1	2.26	0.69
8:J:36:ILE:CD1	8:J:141:TYR:CE2	2.76	0.68
24:W:31:VAL:HG11	24:W:36:PRO:O	1.92	0.68
1:A:1847:U:C5	3:C:153:GLN:O	2.46	0.68
24:W:220:ARG:CZ	24:W:275:LEU:CD2	2.71	0.68
1:A:2786:A:N1	7:G:68:THR:HG21	2.08	0.68
6:F:13:ALA:HB3	6:F:14:PRO:HD3	1.74	0.68
13:P:94:LYS:CE	13:P:118:ARG:HH22	2.06	0.68
1:A:787:C:C2	1:A:2010:A:N7	2.62	0.68
6:F:69:ARG:HB2	6:F:84:PRO:HB3	1.76	0.68
1:A:925:A:H3'	1:A:925:A:N3	2.09	0.68
1:A:2823:C:N4	1:A:2828:G:O6	2.27	0.68
1:A:380:C:H5'	18:U:2:HIS:NE2	2.08	0.68
4:D:7:GLY:CA	4:D:53:PHE:CE2	2.78	0.68
4:D:28:ILE:HD12	4:D:188:ILE:CD1	2.24	0.68
23:d:15:VAL:O	23:d:15:VAL:HG12	1.94	0.68
1:A:2859:G:OP1	4:D:57:ARG:NH1	2.27	0.67
4:D:31:ALA:N	4:D:53:PHE:HE1	1.90	0.67
9:K:62:ILE:HA	9:K:84:CYS:HG	1.58	0.67
9:K:63:VAL:HG12	9:K:64:ARG:HG3	1.76	0.67
19:V:53:ILE:CG1	19:V:67:LEU:HD11	2.21	0.67
4:D:29:GLU:HB3	4:D:185:LEU:HD22	1.76	0.67
16:S:38:LEU:HD11	21:b:38:LEU:H	1.56	0.67
24:W:153:GLY:HA3	25:W:301:GNP:PG	2.35	0.67
1:A:343:A:OP2	18:U:95:LYS:CE	2.42	0.67
1:A:925:A:N3	1:A:925:A:H5'	2.09	0.67
14:Q:44:ASN:HD22	15:R:76:TYR:H	1.42	0.67
1:A:2777:A:O4'	7:G:68:THR:HG23	1.94	0.67
6:F:60:ILE:HD13	6:F:152:MET:SD	2.34	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:S:100:THR:HG22	16:S:101:SER:H	1.60	0.67
1:A:343:A:OP2	18:U:95:LYS:CD	2.43	0.67
1:A:631:G:H22	10:L:33:LYS:HE2	1.59	0.67
1:A:2298:A:H2'	1:A:2299:G:C8	2.30	0.67
4:D:54:ASP:HB3	4:D:78:ARG:HD2	1.76	0.67
1:A:607:G:H1	1:A:622:A:H61	1.40	0.67
1:A:635:C:C2	1:A:636:G:N7	2.63	0.67
1:A:1242:U:H2'	1:A:1243:A:H8	1.59	0.67
1:A:1711:G:H4'	9:K:6:THR:HG23	1.77	0.67
6:F:33:LYS:HA	6:F:96:MET:HE1	1.76	0.67
1:A:224:A:H1'	1:A:236:A:H1'	1.76	0.66
1:A:998:G:H1	1:A:1011:C:H42	1.43	0.66
16:S:89:ALA:C	16:S:91:GLY:H	2.04	0.66
1:A:77:U:C3'	22:Y:2:LYS:HG3	2.25	0.66
4:D:2:THR:OG1	4:D:85:GLY:O	2.11	0.66
24:W:37:MET:HE3	24:W:71:TRP:CH2	2.30	0.66
1:A:738:C:OP1	3:C:217:ARG:NH1	2.28	0.66
1:A:897:G:H1	1:A:975:C:H42	1.42	0.66
13:P:97:ARG:HG3	13:P:99:LYS:H	1.60	0.66
24:W:135:THR:HA	24:W:138:ASN:HD21	1.60	0.66
6:F:64:LYS:HD2	6:F:65:PRO:HD2	1.77	0.66
24:W:97:VAL:N	24:W:98:PRO:HD2	2.11	0.66
1:A:1811:C:N3	1:A:2615:C:N4	2.44	0.66
1:A:2548:U:C5	1:A:2570:A:C6	2.84	0.66
8:J:113:GLY:O	8:J:117:ARG:NH1	2.28	0.66
12:O:78:GLY:HA3	12:O:109:LEU:HD13	1.77	0.66
18:U:79:THR:HG21	18:U:96:LYS:HG2	1.78	0.66
24:W:39:SER:O	24:W:128:ILE:HG12	1.95	0.66
1:A:1793:G:H2'	1:A:1794:C:H6	1.59	0.66
12:O:28:ARG:CG	12:O:92:ASP:O	2.44	0.66
17:T:3:ASP:N	17:T:3:ASP:OD1	2.27	0.66
22:Y:21:LEU:HD11	22:Y:53:MET:HE1	1.74	0.66
24:W:220:ARG:CD	24:W:275:LEU:HD21	2.25	0.66
1:A:342:A:P	18:U:95:LYS:CE	2.83	0.66
1:A:647:A:C6	1:A:702:A:C8	2.84	0.66
5:E:93:THR:OG1	5:E:94:PRO:HD2	1.95	0.66
8:J:25:THR:C	8:J:29:LEU:HD21	2.21	0.66
1:A:758:A:H61	1:A:767:U:H3	1.43	0.66
1:A:2000:A:H2'	1:A:2000:A:N3	2.10	0.66
9:K:87:ILE:HG13	9:K:93:PRO:HA	1.79	0.66
9:K:104:ARG:NH2	13:P:37:GLU:HA	2.10	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1759:U:O2	1:A:1759:U:H2'	1.96	0.65
12:O:95:PHE:HZ	12:O:106:VAL:HG13	1.60	0.65
18:U:92:ARG:NH1	18:U:101:LEU:O	2.26	0.65
6:F:16:LEU:O	6:F:16:LEU:HG	1.94	0.65
6:F:118:SER:OG	6:F:177:PHE:HD1	1.78	0.65
21:b:38:LEU:CD1	21:b:41:ARG:HD2	2.26	0.65
1:A:2704:A:H61	1:A:2761:G:H1	1.44	0.65
4:D:83:LEU:O	4:D:86:VAL:HG23	1.97	0.65
24:W:31:VAL:CG1	24:W:39:SER:HG	1.97	0.65
24:W:125:ILE:HG21	24:W:136:LEU:HD23	1.79	0.65
3:C:16:MET:HB3	3:C:206:GLY:HA3	1.79	0.65
8:J:44:THR:HG22	14:Q:100:VAL:CG1	2.27	0.65
1:A:1178:U:H5''	8:J:85:LEU:HD21	1.77	0.65
12:O:39:HIS:HB2	12:O:58:THR:OG1	1.97	0.65
16:S:70:VAL:HG12	16:S:71:ILE:N	2.11	0.65
1:A:1395:C:H42	1:A:1414:G:H1	1.42	0.65
9:K:17:ARG:N	9:K:45:GLN:O	2.29	0.65
1:A:2342:C:H5'	6:F:88:LYS:HD3	1.79	0.64
3:C:159:GLY:HA2	3:C:198:GLU:HG2	1.79	0.64
4:D:108:VAL:C	4:D:205:ALA:HB2	2.22	0.64
1:A:1554:U:C5'	1:A:1555:A:C8	2.80	0.64
3:C:53:HIS:HB2	3:C:217:ARG:O	1.97	0.64
1:A:1554:U:C5'	1:A:1555:A:N7	2.59	0.64
3:C:57:GLY:HA3	3:C:214:LYS:O	1.96	0.64
24:W:125:ILE:CG2	24:W:136:LEU:HD23	2.27	0.64
1:A:785:C:H42	1:A:805:G:H1	1.45	0.64
1:A:1757:G:N7	1:A:1759:U:C5	2.66	0.64
1:A:2364:A:OP1	12:O:17:ARG:NE	2.30	0.64
5:E:190:GLU:O	5:E:191:LYS:HG3	1.97	0.64
1:A:1267:G:OP2	14:Q:13:ARG:HG3	1.97	0.64
6:F:4:LEU:CD2	6:F:100:LEU:HB2	2.28	0.64
7:G:72:LEU:CD2	7:G:140:GLU:OE2	2.46	0.64
13:P:94:LYS:CG	13:P:118:ARG:NH2	2.61	0.64
16:S:38:LEU:O	21:b:25:PRO:HG3	1.96	0.64
1:A:2777:A:HO2'	7:G:64:ALA:C	1.87	0.64
3:C:142:HIS:HA	3:C:155:VAL:HG11	1.78	0.64
12:O:95:PHE:HE2	12:O:106:VAL:HG12	1.19	0.64
1:A:635:C:N3	1:A:636:G:N7	2.46	0.64
3:C:131:PRO:HA	3:C:189:ARG:HA	1.80	0.64
1:A:2111:A:N6	1:A:2266:G:O2'	2.30	0.64
6:F:29:PRO:O	6:F:169:LEU:CD2	2.44	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1348:G:H4'	23:d:7:PRO:HB2	1.79	0.64
1:A:1573:C:N3	1:A:1594:G:N1	2.37	0.64
1:A:2559:U:H6	1:A:2559:U:O5'	1.80	0.64
2:B:29:C:H1'	2:B:51:A:H61	1.62	0.64
6:F:38:MET:HE3	6:F:57:LEU:CD2	2.27	0.63
24:W:97:VAL:N	24:W:98:PRO:CD	2.60	0.63
18:U:45:SER:OG	18:U:55:GLY:N	2.26	0.63
1:A:2282:G:C6	19:V:13:LYS:HA	2.33	0.63
9:K:25:LEU:HD12	9:K:38:VAL:HG11	1.81	0.63
10:L:77:VAL:O	10:L:112:LEU:N	2.28	0.63
24:W:34:ARG:O	24:W:277:PHE:HB2	1.98	0.63
1:A:920:G:H8	1:A:920:G:O5'	1.81	0.63
12:O:95:PHE:HE2	12:O:106:VAL:HG11	1.51	0.63
1:A:495:U:C2	5:E:84:ARG:HD2	2.27	0.63
1:A:2667:G:P	4:D:84:ARG:HH12	2.18	0.63
18:U:41:VAL:CG1	18:U:43:LYS:CG	2.75	0.63
1:A:504:A:N7	1:A:519:A:N6	2.46	0.63
1:A:949:U:OP1	1:A:949:U:H4'	1.99	0.63
1:A:2002:G:H8	1:A:2002:G:O5'	1.82	0.63
3:C:87:ARG:HG3	3:C:89:ALA:H	1.62	0.63
6:F:13:ALA:HB3	6:F:14:PRO:CD	2.29	0.63
6:F:69:ARG:N	6:F:84:PRO:HB3	2.14	0.63
21:b:46:CYS:SG	21:b:48:SER:OG	2.45	0.63
1:A:1820:A:N6	1:A:1857:G:O2'	2.31	0.63
4:D:32:PRO:HB3	4:D:98:LYS:HG3	1.81	0.63
1:A:1861:C:O5'	1:A:1861:C:H6	1.81	0.63
1:A:2359:G:N1	1:A:2414:C:N3	2.35	0.63
12:O:71:THR:OG1	12:O:72:SER:N	2.30	0.63
1:A:776:G:OP2	3:C:13:ARG:NH2	2.32	0.63
1:A:2778:A:O4'	7:G:64:ALA:HB2	1.99	0.63
7:G:83:GLY:HA2	7:G:137:THR:HA	1.81	0.63
1:A:1847:U:O2'	3:C:154:LEU:HA	1.98	0.62
1:A:1656:C:H42	1:A:1666:U:H3	1.46	0.62
4:D:79:PHE:CG	4:D:199:LEU:HD22	2.33	0.62
24:W:134:SER:N	25:W:301:GNP:O1A	2.30	0.62
1:A:398:U:H2'	1:A:399:C:H6	1.64	0.62
1:A:927:G:H8	1:A:927:G:O5'	1.82	0.62
13:P:33:VAL:CG2	13:P:77:PHE:HZ	1.74	0.62
15:R:25:LEU:HD11	15:R:93:THR:HG21	1.80	0.62
1:A:1659:A:H62	16:S:91:GLY:CA	2.04	0.62
1:A:2218:U:O2	1:A:2218:U:H2'	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:78:GLU:CB	7:G:84:PHE:HZ	1.98	0.62
15:R:22:ILE:HD11	15:R:95:VAL:CB	2.25	0.62
19:V:54:TYR:CE1	19:V:84:ARG:HD3	2.35	0.62
1:A:2291:U:O2'	1:A:2292:C:H5'	1.99	0.62
8:J:24:LYS:C	8:J:29:LEU:HD21	2.24	0.62
8:J:77:ARG:NH1	8:J:86:LYS:HD3	2.15	0.62
3:C:195:VAL:HG12	3:C:196:GLY:N	2.15	0.62
4:D:25:VAL:HG11	4:D:187:LEU:HB3	1.82	0.62
1:A:732:A:H8	1:A:735:U:H3	1.48	0.62
12:O:29:PRO:HB2	12:O:44:ILE:HG23	1.81	0.62
14:Q:92:ARG:CG	15:R:11:GLN:HG3	2.30	0.62
18:U:11:VAL:CG1	18:U:12:ILE:N	2.63	0.62
1:A:886:U:H2'	1:A:887:C:C6	2.34	0.62
1:A:1631:A:H4'	1:A:1632:G:H4'	1.82	0.62
1:A:2674:G:N2	1:A:2796:C:OP2	2.33	0.62
1:A:2853:C:H2'	1:A:2854:A:H8	1.65	0.62
1:A:634:A:C5	1:A:635:C:C5	2.88	0.62
1:A:1527:C:H1'	1:A:1558:G:H21	1.63	0.62
1:A:1846:G:OP2	3:C:156:ARG:NH1	2.33	0.62
2:B:53:U:C2'	6:F:26:MET:SD	2.87	0.62
16:S:21:MET:SD	16:S:24:ILE:HD12	2.39	0.62
1:A:2289:C:O5'	1:A:2289:C:H6	1.83	0.61
1:A:2809:G:OP2	8:J:121:LYS:CE	2.47	0.61
1:A:1513:U:H3	1:A:1572:G:H1	1.48	0.61
7:G:89:GLU:N	7:G:164:ARG:O	2.17	0.61
10:L:117:LEU:HD21	10:L:136:VAL:CA	2.08	0.61
1:A:531:C:OP2	18:U:47:PRO:HG3	1.99	0.61
1:A:2342:C:C1'	6:F:37:ASN:ND2	2.62	0.61
3:C:142:HIS:ND1	3:C:193:GLY:O	2.33	0.61
6:F:132:ILE:CD1	6:F:154:ILE:HG13	2.29	0.61
24:W:135:THR:O	24:W:135:THR:HG22	2.00	0.61
1:A:116:G:OP1	23:d:19:ARG:NH2	2.34	0.61
1:A:1529:G:O6	1:A:1552:C:N4	2.27	0.61
1:A:2537:G:H8	1:A:2537:G:O5'	1.83	0.61
1:A:2560:A:H1'	1:A:2688:G:H5'	1.81	0.61
2:B:39:A:H2'	6:F:66:VAL:HG21	1.83	0.61
4:D:16:PHE:HZ	13:P:80:HIS:O	1.73	0.61
4:D:38:LYS:HZ3	4:D:88:MET:HG2	1.64	0.61
22:Y:8:ASP:HB2	22:Y:13:GLU:HB2	1.83	0.61
1:A:683:A:C8	10:L:114:ASN:CG	2.78	0.61
3:C:68:LYS:HD3	3:C:149:GLY:O	2.01	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:178:LYS:HB3	4:D:187:LEU:HD12	1.81	0.61
15:R:65:GLN:HG2	15:R:93:THR:HG23	1.82	0.61
16:S:38:LEU:HD11	21:b:38:LEU:CA	2.31	0.61
24:W:126:ILE:CG2	24:W:175:ILE:CD1	2.70	0.61
6:F:37:ASN:HB2	6:F:153:ASP:HB2	1.81	0.61
24:W:39:SER:O	24:W:128:ILE:CG1	2.49	0.61
3:C:132:LEU:HB3	3:C:172:VAL:HG21	1.81	0.61
4:D:107:ILE:HB	4:D:205:ALA:HB3	1.83	0.61
24:W:129:PRO:HG3	24:W:176:LEU:CG	2.31	0.61
1:A:2298:A:C5	1:A:2299:G:C5	2.89	0.61
1:A:2777:A:O2'	7:G:64:ALA:CB	2.49	0.61
3:C:94:ILE:CG1	3:C:104:ILE:HD13	2.31	0.61
9:K:10:VAL:HG21	9:K:16:ALA:O	2.01	0.61
9:K:63:VAL:HG21	9:K:85:VAL:HG23	1.82	0.61
18:U:80:ARG:O	18:U:94:ALA:CA	2.48	0.61
24:W:36:PRO:HB3	24:W:75:PHE:HE2	1.66	0.61
1:A:357:G:H2'	1:A:358:C:H6	1.66	0.60
1:A:530:A:H5''	18:U:47:PRO:HD3	1.82	0.60
10:L:71:ARG:HG2	10:L:73:GLU:OE1	2.01	0.60
22:Y:21:LEU:HD11	22:Y:53:MET:CE	2.31	0.60
1:A:77:U:H5'	22:Y:2:LYS:HB2	1.81	0.60
1:A:418:A:N6	1:A:449:A:OP2	2.35	0.60
1:A:2291:U:H2'	1:A:2292:C:C6	2.36	0.60
1:A:2324:C:OP1	12:O:14:ARG:NH1	2.34	0.60
6:F:4:LEU:HB3	6:F:97:TYR:HB3	1.83	0.60
6:F:68:THR:CG2	6:F:88:LYS:CD	2.79	0.60
12:O:29:PRO:CB	12:O:44:ILE:HG23	2.30	0.60
1:A:319:G:H1	1:A:401:C:H42	1.49	0.60
4:D:16:PHE:H	13:P:15:GLN:HE22	1.49	0.60
6:F:68:THR:HG22	6:F:88:LYS:HG3	1.75	0.60
10:L:117:LEU:HD22	10:L:136:VAL:CG1	2.28	0.60
13:P:30:ARG:HG2	13:P:47:GLU:HB2	1.83	0.60
1:A:607:G:H21	14:Q:37:GLN:HE22	1.47	0.60
1:A:790:A:C2	1:A:802:G:C2	2.89	0.60
1:A:1859:C:H2'	1:A:1860:G:H8	1.66	0.60
7:G:126:VAL:HG13	7:G:132:VAL:HG22	1.84	0.60
12:O:28:ARG:HG2	12:O:92:ASP:O	2.01	0.60
15:R:5:ILE:CG2	15:R:7:THR:HG23	2.31	0.60
1:A:1497:G:H1	1:A:1505:U:H3	1.50	0.60
1:A:1706:G:N2	1:A:2717:G:OP1	2.35	0.60
1:A:2132:A:N1	1:A:2215:U:O2	2.34	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:O:31:LEU:N	12:O:94:VAL:O	2.33	0.60
24:W:58:ASN:ND2	24:W:132:GLY:C	2.58	0.60
1:A:306:C:O2	1:A:411:G:N2	2.33	0.60
1:A:751:G:O2'	1:A:774:A:N6	2.34	0.60
1:A:998:G:H21	1:A:2296:A:H2	1.50	0.60
6:F:69:ARG:CB	6:F:84:PRO:HB3	2.30	0.60
12:O:28:ARG:N	12:O:29:PRO:HD3	2.16	0.60
24:W:32:ASP:HB2	24:W:131:VAL:HG21	1.82	0.60
1:A:644:G:OP1	5:E:29:ASN:ND2	2.34	0.60
1:A:743:U:H2'	1:A:744:C:H6	1.67	0.60
1:A:2342:C:H5''	6:F:88:LYS:HD2	1.81	0.60
1:A:2773:G:OP2	1:A:2784:C:N4	2.34	0.60
5:E:9:GLN:NE2	5:E:130:THR:O	2.33	0.60
5:E:81:PRO:HB3	5:E:89:VAL:CG2	2.28	0.60
8:J:25:THR:HG22	8:J:28:ARG:HB2	1.83	0.60
24:W:202:LEU:HB2	24:W:260:THR:HG21	1.84	0.60
1:A:417:G:OP2	1:A:470:A:N6	2.35	0.60
1:A:911:G:H1	1:A:959:C:H42	1.48	0.60
1:A:2343:A:H4'	6:F:35:VAL:HG21	1.84	0.60
14:Q:100:VAL:HG12	14:Q:100:VAL:O	2.01	0.60
1:A:528:G:H1	1:A:555:C:H42	1.49	0.60
1:A:1354:C:H42	1:A:1376:G:H1	1.48	0.60
1:A:1460:G:O2'	1:A:1631:A:N6	2.35	0.60
1:A:2132:A:N6	1:A:2215:U:H3	1.99	0.60
3:C:130:LEU:HD12	3:C:134:ASN:HB2	1.83	0.60
4:D:8:ARG:HH21	4:D:78:ARG:NH1	1.99	0.60
8:J:37:LEU:HD22	8:J:119:MET:HE3	1.83	0.60
16:S:31:GLU:OE1	21:b:36:MET:HE2	2.02	0.60
3:C:171:TYR:HH	3:C:269:PHE:HE1	1.48	0.60
5:E:164:ALA:HA	5:E:175:VAL:HG11	1.83	0.59
19:V:53:ILE:HG13	19:V:67:LEU:CD1	2.21	0.59
1:A:578:A:OP2	14:Q:38:GLN:NE2	2.35	0.59
1:A:1337:C:H42	1:A:1687:G:H1	1.49	0.59
1:A:2566:U:H2'	1:A:2567:C:C6	2.37	0.59
6:F:69:ARG:HA	6:F:84:PRO:CB	2.32	0.59
6:F:69:ARG:CA	6:F:84:PRO:CB	2.80	0.59
6:F:132:ILE:HD13	6:F:154:ILE:CG1	2.28	0.59
6:F:132:ILE:HB	6:F:152:MET:O	2.02	0.59
8:J:24:LYS:C	8:J:29:LEU:CD2	2.74	0.59
18:U:81:VAL:C	18:U:94:ALA:HA	2.27	0.59
24:W:156:THR:HG22	24:W:172:THR:CB	2.31	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:634:A:C4	1:A:635:C:C6	2.91	0.59
1:A:673:A:O2'	1:A:674:G:O4'	2.20	0.59
1:A:1055:A:OP1	8:J:40:LYS:NZ	2.35	0.59
9:K:63:VAL:HG13	9:K:102:VAL:HG13	1.84	0.59
9:K:64:ARG:NH2	9:K:99:PHE:O	2.36	0.59
20:Z:6:ILE:HG22	20:Z:28:LEU:CD1	2.18	0.59
1:A:1213:G:H1	1:A:1223:C:H42	1.48	0.59
4:D:110:VAL:HG11	4:D:192:VAL:HG13	1.84	0.59
5:E:24:PHE:HB3	5:E:118:VAL:HG21	1.84	0.59
1:A:515:G:OP2	23:d:37:LYS:NZ	2.35	0.59
1:A:601:U:O3'	8:J:114:SER:OG	2.15	0.59
1:A:787:C:O2	1:A:2010:A:N7	2.36	0.59
1:A:1599:U:H3'	1:A:1600:G:H21	1.66	0.59
1:A:1858:A:C5	1:A:1859:C:N3	2.70	0.59
1:A:2010:A:H2'	1:A:2010:A:N3	2.17	0.59
1:A:2291:U:O2'	1:A:2292:C:O4'	2.19	0.59
2:B:83:G:H1	2:B:89:C:H42	1.49	0.59
10:L:125:ALA:HB3	10:L:128:PHE:HE1	1.59	0.59
15:R:90:GLN:NE2	15:R:91:PRO:O	2.35	0.59
1:A:30:G:OP2	14:Q:5:LYS:NZ	2.34	0.59
1:A:84:A:N6	1:A:101:G:O2'	2.36	0.59
1:A:217:G:H21	1:A:219:A:H1'	1.67	0.59
1:A:1252:G:H21	1:A:1277:A:H62	1.51	0.59
1:A:2291:U:H2'	1:A:2292:C:H6	1.67	0.59
1:A:2655:C:H2'	1:A:2656:G:H8	1.66	0.59
6:F:8:TYR:HH	6:F:97:TYR:HE2	1.50	0.59
6:F:122:PHE:CZ	6:F:167:ARG:NE	2.70	0.59
12:O:69:GLY:O	12:O:105:ARG:CZ	2.51	0.59
16:S:100:THR:CG2	16:S:101:SER:H	2.16	0.59
19:V:80:PHE:CZ	19:V:86:LYS:CG	2.86	0.59
21:b:9:SER:HG	21:b:12:LYS:H	1.48	0.59
1:A:54:G:N2	1:A:115:C:O2	2.35	0.59
4:D:117:LYS:O	4:D:120:GLN:NE2	2.36	0.59
1:A:124:A:OP1	23:d:14:LYS:NZ	2.36	0.59
1:A:342:A:O5'	18:U:95:LYS:CE	2.51	0.59
1:A:364:A:N3	5:E:169:ASN:ND2	2.50	0.59
1:A:701:G:H8	1:A:701:G:O5'	1.85	0.59
1:A:1578:G:N2	1:A:1587:U:OP2	2.36	0.59
1:A:1828:G:OP1	3:C:260:ARG:NH1	2.35	0.59
4:D:83:LEU:HB3	4:D:86:VAL:CG2	2.33	0.59
4:D:83:LEU:HD21	4:D:203:LYS:HD2	1.76	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:S:38:LEU:CD1	21:b:38:LEU:CA	2.81	0.59
16:S:44:SER:N	16:S:45:PRO:HD2	2.18	0.59
1:A:647:A:C5	1:A:702:A:C5	2.91	0.59
1:A:740:A:OP1	3:C:39:LYS:CE	2.49	0.59
1:A:2128:U:H2'	1:A:2129:G:H8	1.68	0.59
1:A:513:A:OP1	23:d:34:ARG:NH2	2.36	0.59
1:A:917:A:H8	1:A:917:A:O5'	1.86	0.59
4:D:49:ILE:HD11	4:D:91:TYR:CG	2.38	0.59
4:D:79:PHE:HB3	4:D:199:LEU:HD22	1.85	0.59
1:A:530:A:H4'	18:U:45:SER:O	2.03	0.58
1:A:866:A:OP2	1:A:1228:G:N2	2.35	0.58
1:A:1801:G:N2	1:A:2008:C:O2	2.34	0.58
1:A:2112:G:N2	1:A:2265:U:O2	2.34	0.58
2:B:40:C:H4'	6:F:64:LYS:HB3	1.85	0.58
3:C:146:LEU:HD12	3:C:153:GLN:OE1	2.01	0.58
6:F:68:THR:CG2	6:F:88:LYS:CE	2.74	0.58
1:A:1526:G:N1	1:A:1558:G:N1	2.49	0.58
3:C:94:ILE:HG13	3:C:104:ILE:HG21	1.85	0.58
6:F:38:MET:HG2	6:F:87:ALA:O	2.03	0.58
6:F:169:LEU:O	6:F:173:VAL:HG23	2.02	0.58
10:L:79:LEU:CD2	10:L:117:LEU:CA	2.81	0.58
13:P:62:PHE:CD2	13:P:79:VAL:HG22	2.38	0.58
24:W:44:ILE:HG12	24:W:126:ILE:HD12	1.84	0.58
1:A:1397:G:O6	1:A:1410:G:C8	2.56	0.58
1:A:2169:G:N1	1:A:2181:C:O2	2.36	0.58
6:F:108:LEU:N	6:F:109:PRO:HD2	2.18	0.58
1:A:2873:G:O2'	1:A:2893:A:N6	2.36	0.58
8:J:25:THR:O	8:J:29:LEU:CG	2.49	0.58
24:W:130:ASN:N	25:W:301:GNP:O1B	2.36	0.58
1:A:2038:G:C5'	16:S:40:PRO:HB2	2.34	0.58
7:G:73:LEU:HA	7:G:76:MET:HE2	1.86	0.58
24:W:42:PRO:HD2	24:W:177:TRP:NE1	2.18	0.58
1:A:830:A:H2'	1:A:831:U:H4'	1.86	0.58
1:A:1563:G:C5	1:A:1564:C:C5	2.91	0.58
1:A:1738:U:O2	3:C:14:ARG:NH2	2.37	0.58
1:A:2426:G:H1	1:A:2448:U:H3	1.50	0.58
12:O:69:GLY:O	12:O:105:ARG:NH2	2.36	0.58
1:A:1338:G:H21	1:A:1686:A:H62	1.51	0.58
1:A:1711:G:N2	1:A:2023:C:N3	2.52	0.58
24:W:94:ASN:OD1	24:W:94:ASN:N	2.28	0.58
1:A:1231:G:H5''	10:L:32:GLY:HA2	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2186:G:N2	1:A:2187:A:N7	2.52	0.58
1:A:2669:G:H1	1:A:2803:C:H42	1.51	0.58
4:D:34:VAL:O	4:D:34:VAL:HG13	2.03	0.58
6:F:127:ASN:OD1	6:F:157:VAL:HG13	2.04	0.58
1:A:125:A:H62	23:d:42:LEU:HD12	1.65	0.58
1:A:1246:G:O6	1:A:1281:C:N4	2.36	0.58
1:A:1521:G:H22	1:A:1563:G:H1	1.52	0.58
1:A:1801:G:O6	1:A:2005:C:N4	2.37	0.58
1:A:2164:A:H62	1:A:2185:G:H21	1.51	0.58
1:A:2420:G:H22	1:A:2456:C:H1'	1.69	0.58
1:A:2592:U:H4'	9:K:28:SER:CB	2.33	0.58
4:D:5:ILE:HA	4:D:33:ASN:ND2	2.18	0.58
4:D:28:ILE:HD12	4:D:188:ILE:HD11	1.85	0.58
6:F:63:GLN:HG3	6:F:90:THR:O	2.03	0.58
6:F:108:LEU:CD1	6:F:176:PRO:CG	2.64	0.58
1:A:1390:C:H2'	1:A:1391:U:H6	1.65	0.58
1:A:2549:C:H42	1:A:2574:G:H1	1.52	0.58
1:A:2847:G:H5''	4:D:163:ARG:HE	1.68	0.58
8:J:111:PRO:O	8:J:116:GLY:HA3	2.03	0.58
11:N:24:LEU:HD23	11:N:44:VAL:HG11	1.85	0.58
11:N:45:GLU:OE2	11:N:98:TYR:N	2.37	0.58
12:O:30:ARG:HB2	12:O:96:ASP:OD2	2.03	0.58
24:W:59:LYS:N	25:W:301:GNP:O6	2.36	0.58
1:A:1245:G:O4'	10:L:4:HIS:NE2	2.36	0.57
1:A:1264:G:O2'	15:R:86:GLN:NE2	2.37	0.57
1:A:1322:G:N2	1:A:1325:A:OP2	2.37	0.57
1:A:1387:G:O6	1:A:1643:C:N4	2.37	0.57
1:A:2298:A:H2'	1:A:2299:G:H8	1.66	0.57
3:C:107:PRO:HA	3:C:195:VAL:HA	1.85	0.57
4:D:109:ASP:N	4:D:203:LYS:O	2.32	0.57
13:P:32:HIS:HB2	13:P:85:ALA:HB3	1.86	0.57
1:A:1651:G:O2'	1:A:1653:A:N6	2.37	0.57
1:A:2719:A:OP1	11:N:13:ARG:NH1	2.37	0.57
10:L:116:LYS:HG3	10:L:116:LYS:O	2.02	0.57
19:V:80:PHE:CE2	19:V:86:LYS:CG	2.85	0.57
1:A:1102:G:N2	1:A:1150:C:N3	2.52	0.57
2:B:41:C:Cl'	6:F:92:ARG:HB2	2.30	0.57
6:F:8:TYR:HE1	6:F:30:LYS:HZ1	0.71	0.57
9:K:71:ARG:HH12	9:K:104:ARG:HH11	1.52	0.57
15:R:24:LYS:HD2	15:R:91:PRO:CG	2.30	0.57
15:R:62:VAL:HA	15:R:95:VAL:HG22	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:S:36:LEU:HD12	16:S:47:ILE:HG22	1.82	0.57
16:S:78:GLU:OE1	16:S:99:ARG:NH1	2.37	0.57
18:U:4:LYS:H	18:U:92:ARG:HH21	1.51	0.57
1:A:635:C:N4	1:A:636:G:O6	2.38	0.57
6:F:24:SER:O	6:F:26:MET:N	2.33	0.57
6:F:34:ILE:HD11	6:F:96:MET:SD	2.44	0.57
1:A:517:A:OP1	5:E:79:ARG:NH2	2.37	0.57
1:A:684:G:C6	1:A:697:G:N1	2.73	0.57
1:A:1177:G:C5	8:J:78:HIS:CE1	2.92	0.57
1:A:1379:U:H2'	17:T:57:MET:HE3	1.87	0.57
3:C:210:ARG:CA	3:C:213:TRP:HD1	2.15	0.57
1:A:740:A:OP1	3:C:39:LYS:HG2	2.05	0.57
1:A:2294:U:O5'	1:A:2294:U:H6	1.87	0.57
1:A:2752:C:C4	1:A:2753:U:C5	2.93	0.57
1:A:65:A:N1	1:A:90:A:N6	2.52	0.57
1:A:1525:G:HO2'	1:A:1608:A:HO2'	1.51	0.57
1:A:1563:G:H2'	1:A:1564:C:H6	1.69	0.57
1:A:2026:A:H2'	1:A:2027:A:H8	1.70	0.57
1:A:2322:C:OP1	12:O:97:ARG:NH1	2.37	0.57
1:A:2559:U:OP1	1:A:2564:G:N2	2.38	0.57
9:K:87:ILE:HA	9:K:93:PRO:HA	1.87	0.57
15:R:48:VAL:CG1	15:R:50:ASN:O	2.51	0.57
24:W:148:THR:HG22	24:W:150:ASP:H	1.69	0.57
1:A:455:G:H1	1:A:466:C:H42	1.52	0.57
1:A:1069:U:H3'	1:A:1070:G:H8	1.69	0.57
1:A:2298:A:C6	1:A:2299:G:C5	2.92	0.57
18:U:85:VAL:HG21	18:U:91:VAL:H	1.69	0.57
21:b:38:LEU:HD11	21:b:41:ARG:HD2	1.87	0.57
1:A:1314:A:N7	1:A:1335:A:O2'	2.36	0.57
1:A:2281:G:H8	1:A:2281:G:O5'	1.88	0.57
2:B:30:C:H42	2:B:48:G:H1	1.53	0.57
4:D:33:ASN:N	4:D:97:VAL:O	2.37	0.57
14:Q:4:VAL:HG12	14:Q:5:LYS:N	2.19	0.57
1:A:1526:G:C2	1:A:1558:G:N2	2.73	0.57
11:N:55:ASP:HB3	11:N:58:ALA:H	1.69	0.57
1:A:166:A:H2'	1:A:167:U:C6	2.39	0.56
3:C:70:ASP:OD1	3:C:70:ASP:N	2.37	0.56
6:F:108:LEU:N	6:F:109:PRO:CD	2.67	0.56
12:O:78:GLY:O	12:O:109:LEU:HD12	2.04	0.56
13:P:28:THR:HA	13:P:48:GLY:O	2.05	0.56
15:R:58:VAL:HG13	15:R:100:ILE:HD13	1.85	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:S:12:ILE:HD13	16:S:43:ALA:CB	2.33	0.56
16:S:100:THR:CG2	16:S:101:SER:N	2.66	0.56
24:W:111:MET:SD	24:W:119:ARG:CB	2.93	0.56
1:A:138:U:N3	1:A:141:U:OP2	2.38	0.56
1:A:636:G:N2	1:A:712:C:O2	2.34	0.56
1:A:2325:U:O2	1:A:2366:G:N2	2.38	0.56
16:S:6:VAL:HG22	16:S:104:THR:HG22	1.87	0.56
21:b:38:LEU:CD1	21:b:41:ARG:CB	2.72	0.56
24:W:129:PRO:HD2	24:W:176:LEU:HD23	1.85	0.56
1:A:38:A:OP1	5:E:52:LYS:NZ	2.38	0.56
1:A:286:U:H3'	1:A:287:G:H8	1.70	0.56
1:A:342:A:H5''	18:U:95:LYS:HZ1	1.57	0.56
1:A:398:U:H2'	1:A:399:C:C6	2.40	0.56
1:A:2380:G:O2'	1:A:2395:A:N6	2.39	0.56
3:C:6:TYR:HD2	3:C:13:ARG:HD2	1.71	0.56
3:C:171:TYR:CE2	3:C:269:PHE:CE1	2.93	0.56
4:D:49:ILE:O	4:D:82:GLU:CA	2.53	0.56
6:F:69:ARG:CD	6:F:82:GLY:HA2	2.34	0.56
8:J:17:LEU:HD22	8:J:141:TYR:HB2	1.86	0.56
12:O:34:PHE:HB3	12:O:41:TYR:HB2	1.87	0.56
15:R:19:THR:HA	15:R:96:THR:HA	1.86	0.56
23:d:12:ARG:NH1	23:d:44:ALA:O	2.38	0.56
1:A:1342:G:HO2'	1:A:1687:G:HO2'	1.53	0.56
7:G:155:PRO:HA	7:G:162:GLY:HA3	1.86	0.56
11:N:119:LEU:C	11:N:120:VAL:HG23	2.30	0.56
13:P:34:LYS:O	13:P:83:LYS:NZ	2.37	0.56
16:S:13:ALA:HB3	16:S:16:LYS:HG3	1.86	0.56
19:V:80:PHE:CZ	19:V:86:LYS:HG3	2.40	0.56
1:A:2560:A:N6	1:A:2690:G:O6	2.38	0.56
2:B:101:U:H2'	2:B:102:A:H8	1.70	0.56
12:O:59:LEU:HG	12:O:59:LEU:O	2.04	0.56
21:b:38:LEU:CD1	21:b:41:ARG:CG	2.84	0.56
1:A:1657:C:N4	1:A:1664:G:O6	2.32	0.56
1:A:2703:G:H4'	9:K:30:ARG:CD	2.23	0.56
1:A:2722:A:H2'	1:A:2723:G:H8	1.69	0.56
1:A:2841:C:OP1	21:b:41:ARG:NH2	2.39	0.56
11:N:107:ARG:NE	11:N:110:ASP:OD2	2.30	0.56
14:Q:79:LEU:HD21	14:Q:106:PHE:HZ	1.70	0.56
21:b:38:LEU:HD11	21:b:41:ARG:CG	2.35	0.56
1:A:2277:C:O5'	1:A:2277:C:H6	1.88	0.56
6:F:63:GLN:HG2	6:F:91:LEU:HA	1.78	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:J:77:ARG:CZ	8:J:86:LYS:HD3	2.35	0.56
9:K:17:ARG:CB	9:K:45:GLN:O	2.52	0.56
9:K:87:ILE:HG13	9:K:92:SER:O	2.05	0.56
1:A:1243:A:O2'	5:E:41:ARG:NH1	2.38	0.56
1:A:1313:A:N6	1:A:1691:A:N7	2.53	0.56
10:L:117:LEU:HD22	10:L:136:VAL:CA	2.31	0.56
12:O:95:PHE:CE2	12:O:102:TYR:HE1	2.23	0.56
1:A:226:A:H8	1:A:454:G:H21	1.52	0.56
1:A:673:A:H61	1:A:682:G:H2'	1.71	0.56
1:A:776:G:OP2	3:C:207:LYS:NZ	2.39	0.56
1:A:861:C:H2'	1:A:862:U:H6	1.70	0.56
1:A:2066:A:H2'	1:A:2067:G:H8	1.69	0.56
4:D:107:ILE:CG2	4:D:205:ALA:CB	2.82	0.56
4:D:122:ALA:HB2	4:D:161:PRO:HD3	1.87	0.56
12:O:58:THR:O	12:O:68:THR:HB	2.06	0.56
15:R:24:LYS:HB2	15:R:91:PRO:HG2	1.88	0.56
19:V:53:ILE:HG22	19:V:85:LYS:HB2	1.87	0.56
1:A:344:G:OP2	18:U:80:ARG:NH2	2.39	0.56
1:A:1002:G:O2'	1:A:1005:A:N6	2.35	0.56
1:A:1614:A:P	3:C:210:ARG:HH22	2.29	0.56
1:A:2253:G:OP1	3:C:268:LYS:NZ	2.39	0.56
1:A:2340:A:H8	6:F:85:ILE:HD13	1.68	0.56
18:U:85:VAL:O	18:U:85:VAL:HG12	2.06	0.56
1:A:77:U:O3'	22:Y:2:LYS:CG	2.54	0.55
1:A:2548:U:C4	1:A:2570:A:C6	2.94	0.55
5:E:79:ARG:HG3	5:E:86:GLY:HA2	1.87	0.55
7:G:90:LEU:HD12	7:G:132:VAL:HG21	1.88	0.55
12:O:69:GLY:C	12:O:105:ARG:HH12	2.13	0.55
1:A:893:A:O2'	1:A:978:A:N6	2.40	0.55
1:A:1673:G:H1	1:A:1683:C:H42	1.54	0.55
6:F:34:ILE:HG13	6:F:96:MET:SD	2.45	0.55
6:F:38:MET:HE1	6:F:57:LEU:HD13	1.88	0.55
9:K:13:ASN:ND2	9:K:96:THR:OG1	2.33	0.55
9:K:104:ARG:HG2	9:K:104:ARG:O	2.06	0.55
11:N:90:ARG:NH1	11:N:91:TYR:OH	2.39	0.55
24:W:81:ARG:HH11	24:W:103:ILE:HG12	1.40	0.55
1:A:2074:C:O2	21:b:19:HIS:NE2	2.39	0.55
1:A:2906:U:O2'	11:N:99:THR:O	2.24	0.55
5:E:80:SER:HB3	5:E:83:TRP:CD1	2.41	0.55
5:E:152:ALA:N	5:E:172:GLY:O	2.38	0.55
9:K:13:ASN:HD22	9:K:96:THR:HG1	1.54	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:656:A:H61	1:A:662:U:H3	1.52	0.55
1:A:719:C:C2	1:A:856:G:C2	2.94	0.55
1:A:2130:G:H22	1:A:2217:U:H3	1.53	0.55
1:A:2895:C:C5'	11:N:61:GLN:HE22	2.20	0.55
2:B:34:C:N4	2:B:47:C:O2'	2.39	0.55
3:C:68:LYS:O	3:C:69:ARG:C	2.50	0.55
1:A:1200:G:OP2	14:Q:58:ARG:NH2	2.36	0.55
1:A:1578:G:O2'	1:A:1587:U:O4	2.20	0.55
6:F:69:ARG:N	6:F:84:PRO:CB	2.70	0.55
6:F:132:ILE:CD1	6:F:154:ILE:HB	2.35	0.55
13:P:66:LYS:NZ	13:P:67:ILE:O	2.40	0.55
24:W:58:ASN:HD21	24:W:132:GLY:N	2.04	0.55
1:A:546:G:N1	1:A:549:A:OP2	2.39	0.55
1:A:1707:U:C4	1:A:1708:U:C5	2.95	0.55
1:A:2301:U:O2	1:A:2301:U:H2'	2.07	0.55
1:A:2474:G:OP1	5:E:74:ARG:NH2	2.40	0.55
4:D:145:SER:O	4:D:158:LYS:NZ	2.40	0.55
12:O:35:ARG:NH1	12:O:105:ARG:CD	2.67	0.55
15:R:7:THR:HG22	15:R:37:ASP:OD2	2.06	0.55
1:A:223:G:H22	1:A:474:U:H2'	1.71	0.55
1:A:659:A:N1	5:E:46:GLN:NE2	2.54	0.55
1:A:1519:C:H42	1:A:1565:U:H3	1.53	0.55
1:A:2029:G:H2'	1:A:2030:A:H8	1.72	0.55
1:A:2684:G:O2'	1:A:2693:G:N1	2.35	0.55
1:A:2696:C:N3	7:G:111:SER:OG	2.39	0.55
3:C:78:VAL:HB	3:C:113:GLY:H	1.71	0.55
13:P:94:LYS:HD2	13:P:118:ARG:HH21	0.75	0.55
16:S:22:ASP:OD1	16:S:25:ARG:NH2	2.38	0.55
1:A:63:G:H2'	1:A:64:A:H8	1.71	0.55
1:A:557:U:H4'	1:A:1275:G:H4'	1.89	0.55
1:A:1757:G:C8	1:A:1759:U:C6	2.94	0.55
1:A:2171:G:N2	1:A:2179:U:O2	2.40	0.55
1:A:2231:C:H42	1:A:2250:G:H1	1.55	0.55
1:A:2342:C:C1'	6:F:37:ASN:HD21	2.20	0.55
1:A:2718:U:OP2	1:A:2748:G:N2	2.38	0.55
2:B:55:A:H5'	6:F:23:ASP:CA	2.37	0.55
4:D:11:GLY:O	4:D:27:VAL:HG23	2.05	0.55
16:S:89:ALA:C	16:S:91:GLY:N	2.65	0.55
1:A:564:G:O3'	16:S:18:ARG:NH1	2.40	0.55
1:A:765:A:H5''	1:A:766:C:H5	1.72	0.55
1:A:1044:C:OP2	14:Q:93:LYS:NZ	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2357:A:C6	1:A:2358:A:C6	2.95	0.55
2:B:42:G:N3	2:B:45:C:N4	2.42	0.55
9:K:35:ILE:HG21	9:K:105:GLU:OE1	2.07	0.55
14:Q:114:LYS:O	14:Q:118:ASN:ND2	2.39	0.55
1:A:2537:G:C6	1:A:2611:G:N1	2.75	0.55
4:D:181:ALA:O	4:D:184:ASN:ND2	2.40	0.55
16:S:18:ARG:NH2	16:S:76:VAL:O	2.35	0.55
22:Y:6:ILE:O	22:Y:6:ILE:HG13	2.07	0.55
1:A:376:A:C2	1:A:379:C:C5	2.95	0.54
3:C:15:GLY:O	3:C:204:ASN:ND2	2.40	0.54
4:D:93:VAL:O	4:D:93:VAL:HG13	2.08	0.54
9:K:7:ARG:HD3	9:K:18:GLU:OE1	2.07	0.54
12:O:39:HIS:CE1	12:O:59:LEU:HD13	2.42	0.54
1:A:1314:A:OP2	11:N:12:GLN:NE2	2.41	0.54
1:A:1546:G:N2	3:C:98:ASP:O	2.40	0.54
1:A:2291:U:O2'	1:A:2292:C:C5'	2.55	0.54
4:D:96:GLU:OE1	4:D:96:GLU:N	2.40	0.54
6:F:104:ILE:HD11	6:F:175:MET:SD	2.47	0.54
1:A:377:G:HO2'	1:A:378:C:H6	0.76	0.54
3:C:132:LEU:HD23	3:C:135:ILE:HD12	1.89	0.54
9:K:104:ARG:HH21	13:P:37:GLU:HA	1.72	0.54
13:P:27:ASP:OD1	13:P:27:ASP:N	2.40	0.54
13:P:67:ILE:HA	13:P:72:GLY:HA2	1.89	0.54
16:S:38:LEU:HD11	21:b:38:LEU:HB3	1.83	0.54
1:A:1585:A:N6	1:A:1587:U:O2	2.40	0.54
4:D:134:SER:OG	4:D:135:HIS:N	2.36	0.54
5:E:20:ASN:OD1	5:E:22:SER:OG	2.26	0.54
6:F:34:ILE:CG1	6:F:96:MET:SD	2.95	0.54
8:J:36:ILE:O	8:J:36:ILE:HG22	2.06	0.54
15:R:21:TYR:CZ	15:R:94:LYS:HD2	2.43	0.54
1:A:75:G:O3'	22:Y:48:LYS:NZ	2.40	0.54
1:A:304:G:H2'	1:A:305:A:H8	1.73	0.54
1:A:2049:A:OP1	14:Q:27:SER:OG	2.26	0.54
3:C:77:ARG:HB3	3:C:95:ASN:HB3	1.89	0.54
3:C:94:ILE:HG13	3:C:104:ILE:HD13	1.89	0.54
12:O:97:ARG:HG2	12:O:100:TYR:O	2.07	0.54
22:Y:10:THR:OG1	22:Y:11:THR:N	2.40	0.54
1:A:568:G:O2'	1:A:587:C:O2'	2.26	0.54
1:A:1059:A:O2'	14:Q:78:ARG:NH2	2.41	0.54
2:B:35:C:H42	2:B:46:A:H2	1.55	0.54
3:C:173:LEU:HD23	3:C:183:MET:HA	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:27:VAL:O	4:D:27:VAL:HG12	2.06	0.54
5:E:38:LEU:HD22	10:L:13:ARG:HH22	1.72	0.54
9:K:25:LEU:HB3	9:K:38:VAL:CG1	2.33	0.54
21:b:54:ILE:O	21:b:54:ILE:HG22	2.06	0.54
22:Y:49:ALA:HA	22:Y:52:ARG:HG2	1.89	0.54
24:W:58:ASN:HB2	25:W:301:GNP:O6	2.07	0.54
24:W:75:PHE:O	24:W:78:GLN:HB2	2.07	0.54
24:W:128:ILE:HG23	24:W:129:PRO:HD2	1.90	0.54
24:W:204:ASP:OD1	24:W:204:ASP:N	2.39	0.54
1:A:644:G:N2	1:A:650:U:OP1	2.38	0.54
1:A:2598:G:H2'	1:A:2599:G:H8	1.72	0.54
6:F:38:MET:CE	6:F:57:LEU:HD22	2.38	0.54
24:W:41:ASN:CG	24:W:175:ILE:HG22	2.32	0.54
1:A:250:G:OP1	1:A:435:G:N2	2.40	0.54
1:A:1133:G:H22	1:A:1148:C:H42	1.56	0.54
1:A:1713:A:H61	1:A:1721:A:H61	1.56	0.54
1:A:1858:A:C6	1:A:1859:C:N3	2.76	0.54
1:A:2308:G:N7	19:V:22:ARG:NH2	2.55	0.54
9:K:7:ARG:HH21	9:K:20:LEU:HD11	1.71	0.54
1:A:1334:C:OP1	11:N:67:ARG:NH2	2.40	0.54
2:B:77:G:H1	2:B:95:U:H3	1.56	0.54
6:F:38:MET:CE	6:F:57:LEU:HD13	2.37	0.54
7:G:79:GLY:O	7:G:83:GLY:N	2.41	0.54
1:A:967:G:N2	1:A:2298:A:OP2	2.40	0.54
1:A:1563:G:C4	1:A:1564:C:C6	2.95	0.54
4:D:5:ILE:HA	4:D:33:ASN:HD22	1.73	0.54
9:K:63:VAL:HG23	9:K:85:VAL:HG23	1.90	0.54
24:W:217:TYR:HB3	24:W:220:ARG:HG3	1.89	0.54
1:A:510:G:N2	1:A:513:A:OP2	2.38	0.53
1:A:527:A:H4'	18:U:43:LYS:HG2	1.89	0.53
1:A:726:C:H2'	1:A:727:A:C8	2.43	0.53
1:A:2344:U:O2	1:A:2344:U:H2'	2.07	0.53
1:A:2895:C:H5''	11:N:61:GLN:HE22	1.72	0.53
13:P:50:VAL:CG1	13:P:63:THR:O	2.57	0.53
1:A:118:A:H4'	1:A:119:U:H5'	1.89	0.53
1:A:767:U:H2'	1:A:768:G:H8	1.73	0.53
1:A:2015:G:O2'	24:W:198:SER:O	2.22	0.53
1:A:2872:U:OP1	13:P:99:LYS:NZ	2.40	0.53
4:D:51:LEU:O	4:D:80:VAL:HA	2.08	0.53
5:E:4:VAL:HG11	5:E:123:ILE:HD11	1.90	0.53
8:J:26:LEU:HB2	8:J:63:ILE:HG22	1.86	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:L:90:GLU:O	10:L:92:THR:HG23	2.08	0.53
1:A:719:C:C2	1:A:856:G:N2	2.76	0.53
1:A:724:A:O2'	1:A:2099:G:O2'	2.25	0.53
1:A:1474:C:OP2	3:C:28:LYS:NZ	2.41	0.53
5:E:158:ASP:N	5:E:158:ASP:OD1	2.40	0.53
8:J:65:LEU:HD13	8:J:69:LYS:HB2	1.89	0.53
13:P:89:VAL:HG12	13:P:90:VAL:N	2.24	0.53
13:P:94:LYS:CE	13:P:118:ARG:NH2	2.64	0.53
24:W:134:SER:CB	25:W:301:GNP:O1A	2.56	0.53
1:A:342:A:P	18:U:95:LYS:NZ	2.80	0.53
1:A:1862:C:H3'	1:A:1862:C:H6	1.74	0.53
4:D:21:ASP:OD1	4:D:21:ASP:N	2.38	0.53
15:R:25:LEU:HD12	15:R:25:LEU:O	2.08	0.53
24:W:67:VAL:CB	24:W:276:SER:OG	2.57	0.53
1:A:211:C:C2	1:A:212:C:C5	2.96	0.53
1:A:362:C:H42	1:A:377:G:H1	1.57	0.53
1:A:950:U:C4	1:A:951:C:C2	2.96	0.53
1:A:1572:G:O2'	1:A:1573:C:H6	1.91	0.53
1:A:2281:G:N7	19:V:12:LYS:NZ	2.56	0.53
1:A:2922:U:O2'	8:J:135:ALA:O	2.25	0.53
11:N:25:ILE:HD13	11:N:83:LEU:HD21	1.90	0.53
15:R:6:LYS:O	15:R:6:LYS:HD2	2.07	0.53
18:U:11:VAL:CG1	18:U:12:ILE:H	2.20	0.53
1:A:1587:U:H2'	1:A:1588:A:H8	1.73	0.53
1:A:1616:G:H4'	3:C:59:LYS:HD2	1.90	0.53
1:A:2713:U:OP2	13:P:54:ARG:NH1	2.41	0.53
2:B:75:U:O2	2:B:75:U:H2'	2.09	0.53
3:C:171:TYR:HB2	3:C:184:ILE:O	2.09	0.53
7:G:78:GLU:OE1	7:G:78:GLU:HA	2.06	0.53
12:O:31:LEU:HB3	12:O:95:PHE:HA	1.91	0.53
18:U:84:LYS:CE	18:U:84:LYS:C	2.54	0.53
1:A:683:A:OP1	10:L:131:SER:OG	2.25	0.53
1:A:1104:U:N3	1:A:1127:U:O2	2.42	0.53
1:A:1446:C:H2'	1:A:1447:C:C6	2.44	0.53
1:A:1613:C:H5''	3:C:18:THR:HG21	1.89	0.53
1:A:610:U:O4	15:R:79:LYS:NZ	2.41	0.53
1:A:662:U:H2'	1:A:663:G:H8	1.74	0.53
1:A:2561:G:H1'	1:A:2692:G:H21	1.74	0.53
1:A:2709:C:O2'	4:D:191:ASN:ND2	2.42	0.53
3:C:89:ALA:HA	3:C:158:ALA:HB2	1.90	0.53
4:D:102:PHE:HE2	4:D:108:VAL:HG12	1.73	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:J:25:THR:C	8:J:29:LEU:CD2	2.81	0.53
13:P:89:VAL:HG11	13:P:92:TYR:CE1	2.44	0.53
1:A:266:U:H2'	1:A:267:C:H4'	1.90	0.53
1:A:275:A:N7	1:A:296:G:N2	2.56	0.53
1:A:1296:G:N2	5:E:82:GLN:O	2.41	0.53
1:A:1546:G:O3'	3:C:101:LYS:NZ	2.42	0.53
16:S:89:ALA:O	16:S:91:GLY:N	2.41	0.53
24:W:177:TRP:HD1	24:W:178:PRO:HD2	1.73	0.53
8:J:46:THR:OG1	14:Q:64:ARG:NH2	2.42	0.53
10:L:92:THR:HA	10:L:124:LYS:HB2	1.90	0.53
12:O:95:PHE:CZ	12:O:106:VAL:HG12	2.24	0.53
20:Z:57:LYS:HG3	20:Z:57:LYS:O	2.08	0.53
24:W:28:TYR:HB2	24:W:125:ILE:HG12	1.91	0.53
24:W:41:ASN:OD1	24:W:44:ILE:N	2.38	0.53
1:A:435:G:O2'	1:A:437:A:OP2	2.24	0.52
1:A:1103:A:O2'	1:A:1132:A:N6	2.42	0.52
1:A:1572:G:O2'	1:A:1573:C:O4'	2.27	0.52
6:F:2:ASN:N	6:F:98:ASP:OD1	2.43	0.52
6:F:132:ILE:CD1	6:F:154:ILE:CG1	2.86	0.52
11:N:99:THR:OG1	11:N:100:ARG:N	2.41	0.52
14:Q:44:ASN:ND2	15:R:76:TYR:O	2.41	0.52
18:U:79:THR:CG2	18:U:96:LYS:HG2	2.37	0.52
1:A:1835:C:O2	3:C:44:ASN:ND2	2.41	0.52
1:A:2298:A:C4	1:A:2299:G:N7	2.77	0.52
1:A:2353:U:C2	1:A:2414:C:C5	2.97	0.52
4:D:83:LEU:HD21	4:D:203:LYS:CG	2.39	0.52
13:P:35:VAL:HG21	13:P:44:GLN:HE21	1.74	0.52
24:W:30:LEU:HD11	24:W:133:LYS:HA	1.89	0.52
1:A:342:A:P	18:U:95:LYS:HE3	2.48	0.52
1:A:925:A:C6	1:A:947:A:C4	2.97	0.52
1:A:1029:A:N6	1:A:1030:G:O6	2.43	0.52
1:A:1043:G:H1	1:A:1204:C:H42	1.57	0.52
1:A:1178:U:O4'	8:J:76:TYR:CZ	2.62	0.52
1:A:2281:G:O6	19:V:12:LYS:HD2	2.08	0.52
1:A:2886:C:H2'	1:A:2887:A:H8	1.73	0.52
3:C:120:PRO:O	3:C:134:ASN:ND2	2.42	0.52
4:D:29:GLU:HB2	4:D:185:LEU:HD23	1.91	0.52
4:D:83:LEU:HD21	4:D:203:LYS:CD	2.36	0.52
7:G:89:GLU:HB3	7:G:164:ARG:HB2	1.91	0.52
24:W:71:TRP:NE1	24:W:278:GLU:O	2.39	0.52
1:A:512:G:H21	1:A:731:G:H1'	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1614:A:OP1	3:C:210:ARG:NH2	2.40	0.52
1:A:1615:A:H5'	3:C:85:PRO:HB3	1.91	0.52
1:A:2066:A:H2'	1:A:2067:G:C8	2.44	0.52
1:A:2849:U:H3'	1:A:2850:G:H21	1.75	0.52
1:A:580:U:C2	1:A:581:C:C5	2.98	0.52
1:A:2093:C:O2	1:A:2093:C:H2'	2.09	0.52
1:A:2607:G:N7	4:D:145:SER:OG	2.41	0.52
1:A:2828:G:H2'	1:A:2829:G:H8	1.74	0.52
2:B:41:C:C5'	6:F:63:GLN:CD	2.78	0.52
4:D:108:VAL:N	4:D:205:ALA:HB2	2.25	0.52
6:F:36:ILE:HB	6:F:89:VAL:O	2.10	0.52
6:F:38:MET:SD	6:F:57:LEU:HD22	2.50	0.52
10:L:70:ASN:OD1	10:L:70:ASN:N	2.43	0.52
14:Q:99:ALA:HB1	14:Q:105:ALA:HB3	1.92	0.52
1:A:19:G:N1	1:A:568:G:C6	2.77	0.52
1:A:1425:C:H2'	1:A:1426:A:H8	1.75	0.52
1:A:1762:G:H2'	1:A:1763:G:H8	1.74	0.52
1:A:2086:G:H1'	21:b:3:VAL:HG21	1.92	0.52
1:A:2112:G:H1	1:A:2265:U:H3	1.58	0.52
1:A:2163:A:N7	1:A:2185:G:N1	2.46	0.52
1:A:2558:G:P	1:A:2558:G:H21	2.33	0.52
1:A:2717:G:N1	1:A:2749:U:OP2	2.41	0.52
12:O:75:THR:HG21	12:O:108:ALA:HB1	1.89	0.52
1:A:789:C:H2'	1:A:790:A:C8	2.44	0.52
1:A:1231:G:OP1	10:L:30:THR:OG1	2.26	0.52
1:A:2030:A:OP1	11:N:5:LYS:NZ	2.37	0.52
1:A:2224:U:H2'	1:A:2225:C:H6	1.74	0.52
4:D:55:ASP:HB3	4:D:77:LYS:NZ	2.25	0.52
13:P:45:ILE:O	13:P:45:ILE:HG23	2.10	0.52
13:P:46:PHE:CZ	13:P:66:LYS:HD3	2.44	0.52
14:Q:42:SER:OG	14:Q:43:GLY:N	2.42	0.52
16:S:70:VAL:CG1	16:S:71:ILE:N	2.72	0.52
18:U:79:THR:HG21	18:U:96:LYS:HB2	1.90	0.52
19:V:35:ASP:N	19:V:35:ASP:OD1	2.40	0.52
24:W:87:SER:OG	25:W:301:GNP:C6	2.58	0.52
24:W:210:LEU:HD13	24:W:237:LEU:CD2	2.40	0.52
1:A:342:A:P	18:U:95:LYS:HZ1	2.33	0.52
1:A:602:G:H2'	1:A:603:G:H8	1.74	0.52
1:A:1526:G:N2	1:A:1558:G:C2	2.78	0.52
1:A:1616:G:OP2	3:C:63:ARG:NH1	2.43	0.52
1:A:2670:A:H5''	8:J:79:THR:CG2	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2675:C:C5	1:A:2676:U:C5	2.98	0.52
2:B:37:A:O2'	2:B:45:C:O2	2.28	0.52
24:W:21:LEU:O	24:W:51:LYS:NZ	2.42	0.52
1:A:269:G:O2'	1:A:322:A:N6	2.43	0.52
1:A:2688:G:N2	1:A:2691:A:OP2	2.42	0.52
4:D:109:ASP:HB2	4:D:205:ALA:HA	1.92	0.52
12:O:78:GLY:O	12:O:109:LEU:HD11	2.10	0.52
18:U:84:LYS:N	18:U:93:VAL:HG11	2.19	0.52
24:W:74:HIS:NE2	24:W:78:GLN:OE1	2.43	0.52
1:A:77:U:OP1	22:Y:52:ARG:NH1	2.43	0.52
1:A:611:U:OP2	10:L:29:LYS:NZ	2.37	0.52
1:A:732:A:O5'	1:A:835:A:N6	2.43	0.52
1:A:1257:C:O2	1:A:1272:G:N2	2.35	0.52
1:A:2084:C:O2	1:A:2601:A:N6	2.43	0.52
6:F:33:LYS:O	6:F:157:VAL:HG23	2.10	0.52
18:U:45:SER:OG	18:U:55:GLY:O	2.28	0.52
23:d:15:VAL:O	23:d:15:VAL:CG1	2.57	0.52
24:W:75:PHE:HA	24:W:78:GLN:HG3	1.92	0.52
1:A:376:A:C2	1:A:379:C:C6	2.98	0.51
1:A:1364:C:N3	16:S:86:ARG:NH1	2.57	0.51
1:A:1382:G:O6	1:A:1442:A:N6	2.43	0.51
1:A:1708:U:O4	1:A:2027:A:N6	2.43	0.51
1:A:2298:A:N6	1:A:2299:G:C6	2.78	0.51
1:A:2342:C:O2'	6:F:37:ASN:CG	2.53	0.51
14:Q:66:ASN:OD1	14:Q:70:ARG:NH1	2.44	0.51
18:U:11:VAL:HG12	18:U:12:ILE:H	1.73	0.51
1:A:861:C:H2'	1:A:862:U:C6	2.45	0.51
1:A:2326:C:H42	1:A:2350:G:H1	1.58	0.51
4:D:63:LYS:HA	4:D:66:LYS:HB2	1.93	0.51
4:D:123:ILE:HD11	4:D:141:ARG:HA	1.91	0.51
21:b:18:THR:OG1	21:b:19:HIS:N	2.42	0.51
1:A:5:A:H61	1:A:2922:U:H3	1.58	0.51
1:A:2298:A:C4	1:A:2299:G:C8	2.99	0.51
1:A:2357:A:H61	1:A:2416:U:H3	1.58	0.51
4:D:32:PRO:HG3	4:D:98:LYS:CG	2.32	0.51
4:D:55:ASP:CA	4:D:77:LYS:HB3	2.39	0.51
6:F:96:MET:O	6:F:96:MET:HG3	2.11	0.51
7:G:60:LYS:NZ	7:G:60:LYS:CB	2.73	0.51
1:A:198:A:N6	1:A:201:C:OP2	2.43	0.51
1:A:594:C:OP1	15:R:92:TYR:OH	2.27	0.51
4:D:49:ILE:HD11	4:D:91:TYR:CD2	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:U:80:ARG:O	18:U:94:ALA:HA	2.10	0.51
1:A:559:A:O2'	1:A:1257:C:OP1	2.28	0.51
1:A:948:A:C5'	1:A:948:A:N3	2.73	0.51
1:A:970:A:O3'	19:V:37:GLN:NE2	2.44	0.51
1:A:1469:G:HO2'	1:A:1545:C:HO2'	1.51	0.51
1:A:1695:A:OP1	11:N:8:ARG:NH2	2.44	0.51
3:C:72:ASP:OD1	3:C:72:ASP:N	2.41	0.51
3:C:172:VAL:HG12	3:C:174:VAL:HG23	1.93	0.51
10:L:76:VAL:O	10:L:76:VAL:HG12	2.09	0.51
24:W:24:ILE:HG21	24:W:124:LEU:HB2	1.93	0.51
24:W:37:MET:SD	24:W:71:TRP:HH2	2.32	0.51
1:A:380:C:H2'	1:A:381:U:H6	1.76	0.51
1:A:719:C:N3	1:A:856:G:N1	2.57	0.51
1:A:1554:U:H3'	1:A:1555:A:C5'	2.39	0.51
1:A:2280:G:O6	19:V:12:LYS:HE3	2.09	0.51
7:G:72:LEU:HD22	7:G:140:GLU:OE2	2.09	0.51
10:L:74:TYR:CE1	10:L:127:LYS:HG3	2.44	0.51
19:V:53:ILE:CD1	19:V:67:LEU:CD1	2.89	0.51
24:W:39:SER:CA	24:W:128:ILE:HG13	2.41	0.51
4:D:79:PHE:CG	4:D:199:LEU:CD2	2.94	0.51
1:A:1099:C:H42	1:A:1152:G:H1	1.58	0.51
1:A:1306:G:OP2	16:S:15:ARG:NH2	2.44	0.51
1:A:1437:C:O3'	17:T:25:LYS:NZ	2.44	0.51
1:A:1554:U:H3'	1:A:1555:A:H5'	1.93	0.51
1:A:2082:G:O2'	4:D:152:ASN:ND2	2.39	0.51
1:A:2094:C:H2'	1:A:2095:C:H6	1.76	0.51
1:A:2824:G:C2	1:A:2826:A:H5''	2.46	0.51
10:L:91:VAL:CB	10:L:122:THR:O	2.59	0.51
16:S:53:SER:O	16:S:57:ASN:N	2.41	0.51
1:A:925:A:N3	1:A:925:A:C5'	2.74	0.51
1:A:947:A:H3'	1:A:948:A:C2	2.45	0.51
1:A:1129:U:N3	1:A:1132:A:OP2	2.42	0.51
1:A:1231:G:H2'	1:A:1232:G:H8	1.74	0.51
1:A:2230:C:H2'	1:A:2231:C:C6	2.46	0.51
1:A:2334:U:O4	6:F:39:GLY:HA3	2.10	0.51
4:D:156:LYS:O	8:J:81:HIS:ND1	2.34	0.51
5:E:139:MET:N	5:E:139:MET:SD	2.84	0.51
10:L:77:VAL:O	10:L:111:ILE:HA	2.11	0.51
16:S:29:VAL:HG12	16:S:29:VAL:O	2.10	0.51
1:A:1500:U:OP2	11:N:81:GLN:NE2	2.44	0.51
4:D:62:ASN:O	4:D:65:GLU:N	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:52:A:OP2	1:A:116:G:N1	2.44	0.50
1:A:1038:C:OP1	15:R:84:LYS:NZ	2.43	0.50
1:A:2003:C:OP1	24:W:144:ASN:ND2	2.39	0.50
3:C:171:TYR:CE2	3:C:269:PHE:CZ	2.99	0.50
1:A:573:C:N4	1:A:2072:C:OP2	2.44	0.50
1:A:615:U:O2'	1:A:617:G:OP2	2.27	0.50
1:A:948:A:N3	1:A:948:A:H5''	2.26	0.50
1:A:2153:G:N2	1:A:2203:C:N3	2.58	0.50
1:A:2688:G:O2'	1:A:2690:G:N7	2.38	0.50
5:E:103:LYS:HG3	5:E:106:ARG:HH21	1.77	0.50
6:F:69:ARG:HE	6:F:82:GLY:CA	2.20	0.50
24:W:67:VAL:HG23	24:W:276:SER:OG	2.07	0.50
1:A:357:G:C5	1:A:358:C:C5	3.00	0.50
1:A:455:G:H2'	1:A:456:A:H8	1.76	0.50
1:A:745:C:H5''	1:A:746:A:H5'	1.93	0.50
1:A:1304:G:OP1	21:b:16:ARG:NH2	2.42	0.50
1:A:2065:C:H2'	1:A:2066:A:H8	1.76	0.50
1:A:2777:A:C2'	7:G:64:ALA:HA	2.36	0.50
1:A:2847:G:O3'	4:D:163:ARG:NH2	2.44	0.50
1:A:2922:U:H2'	1:A:2923:A:C8	2.47	0.50
2:B:55:A:H1'	6:F:27:GLN:NE2	1.86	0.50
4:D:107:ILE:CB	4:D:205:ALA:HB3	2.41	0.50
8:J:25:THR:O	8:J:29:LEU:CD2	2.59	0.50
14:Q:92:ARG:HH12	14:Q:93:LYS:HE2	1.76	0.50
16:S:9:THR:OG1	16:S:102:HIS:NE2	2.44	0.50
24:W:191:VAL:CG1	24:W:277:PHE:HZ	2.19	0.50
1:A:638:U:H2'	1:A:639:C:C6	2.46	0.50
1:A:869:U:O4	1:A:882:A:N6	2.42	0.50
1:A:1370:C:O2'	1:A:1371:G:N2	2.41	0.50
1:A:1444:C:H2'	1:A:1445:A:H8	1.76	0.50
1:A:2218:U:O2	1:A:2218:U:C2'	2.60	0.50
1:A:2810:A:H5''	1:A:2811:G:H5'	1.93	0.50
8:J:47:PRO:O	8:J:115:LEU:HD11	2.11	0.50
13:P:56:GLY:N	13:P:60:GLU:OE2	2.44	0.50
13:P:63:THR:HA	13:P:75:ARG:O	2.11	0.50
16:S:53:SER:O	16:S:57:ASN:HB2	2.11	0.50
1:A:16:G:H4'	21:b:15:LEU:HG	1.94	0.50
1:A:19:G:C6	1:A:568:G:C6	3.00	0.50
1:A:1381:A:O2'	1:A:1383:U:OP2	2.29	0.50
1:A:1397:G:C2	1:A:1411:U:C5	2.66	0.50
1:A:1481:G:H1	1:A:1605:C:H42	1.60	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2038:G:H5''	16:S:40:PRO:HB2	1.92	0.50
3:C:61:GLN:O	3:C:63:ARG:NH2	2.40	0.50
3:C:195:VAL:CG1	3:C:196:GLY:N	2.74	0.50
4:D:69:VAL:O	4:D:73:GLU:N	2.44	0.50
8:J:44:THR:CG2	14:Q:100:VAL:HG12	2.36	0.50
9:K:93:PRO:HD2	9:K:113:LYS:HD3	1.92	0.50
1:A:657:G:H21	1:A:661:A:H62	1.59	0.50
1:A:2152:A:H62	1:A:2200:A:H4'	1.76	0.50
1:A:2818:C:HO2'	1:A:2917:G:H21	1.57	0.50
3:C:72:ASP:HB2	3:C:119:GLY:HA2	1.94	0.50
3:C:77:ARG:NH1	3:C:113:GLY:O	2.45	0.50
6:F:8:TYR:CD1	6:F:8:TYR:C	2.89	0.50
7:G:145:ILE:HA	7:G:148:ASN:HB2	1.94	0.50
24:W:31:VAL:HG13	24:W:39:SER:CB	2.37	0.50
1:A:504:A:H62	1:A:519:A:H62	1.60	0.50
1:A:563:C:OP2	21:b:10:LYS:NZ	2.40	0.50
1:A:635:C:C2	1:A:636:G:C8	2.99	0.50
1:A:997:C:OP1	2:B:88:C:N4	2.45	0.50
1:A:1040:C:HO2'	15:R:10:LYS:HZ2	1.58	0.50
1:A:1421:A:O3'	1:A:1621:G:N2	2.43	0.50
1:A:2541:C:OP1	4:D:129:SER:N	2.44	0.50
1:A:2610:G:N2	1:A:2639:C:OP2	2.45	0.50
1:A:2829:G:H2'	1:A:2830:A:O4'	2.11	0.50
6:F:33:LYS:CA	6:F:96:MET:HE1	2.39	0.50
10:L:73:GLU:HG2	10:L:73:GLU:O	2.11	0.50
12:O:102:TYR:OH	12:O:110:ALA:CB	2.60	0.50
16:S:8:ARG:HD3	16:S:102:HIS:CE1	2.47	0.50
16:S:20:VAL:O	16:S:20:VAL:HG12	2.12	0.50
16:S:81:THR:OG1	16:S:82:LEU:N	2.44	0.50
17:T:62:LYS:H	17:T:73:THR:HG22	1.75	0.50
1:A:380:C:H2'	1:A:381:U:C6	2.46	0.50
1:A:735:U:H2'	1:A:736:A:H8	1.77	0.50
1:A:1616:G:O3'	3:C:59:LYS:NZ	2.40	0.50
1:A:1745:A:H3'	1:A:1746:A:H8	1.76	0.50
1:A:2542:A:H3'	1:A:2543:U:H6	1.76	0.50
3:C:105:LEU:HD11	3:C:156:ARG:HG2	1.94	0.50
8:J:88:ARG:HH22	8:J:96:ASN:HD22	1.58	0.50
18:U:3:VAL:HG21	18:U:70:PRO:HD3	1.92	0.50
1:A:634:A:N7	1:A:635:C:C5	2.80	0.50
1:A:703:G:C2	1:A:704:U:C2	3.00	0.50
1:A:1023:G:H2'	1:A:1024:G:H8	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1419:G:H21	1:A:1617:A:H61	1.60	0.50
4:D:38:LYS:HZ1	4:D:88:MET:HG2	1.73	0.50
15:R:39:LEU:HB2	15:R:48:VAL:HG21	1.94	0.50
24:W:41:ASN:ND2	24:W:176:LEU:O	2.43	0.50
24:W:211:ARG:HA	24:W:214:GLU:HB2	1.94	0.50
1:A:342:A:H5''	18:U:95:LYS:HZ2	1.57	0.49
1:A:2039:G:OP1	16:S:41:ARG:HA	2.12	0.49
6:F:60:ILE:CD1	6:F:152:MET:SD	2.99	0.49
14:Q:79:LEU:HD21	14:Q:106:PHE:CZ	2.47	0.49
24:W:156:THR:CG2	24:W:172:THR:OG1	2.59	0.49
1:A:106:G:H4'	1:A:337:A:H5''	1.95	0.49
1:A:531:C:P	18:U:47:PRO:HG3	2.51	0.49
1:A:796:A:N7	1:A:1663:A:N6	2.60	0.49
1:A:1332:U:H2'	1:A:1333:C:H6	1.77	0.49
1:A:1493:C:H2'	1:A:1494:G:C8	2.47	0.49
1:A:1782:G:OP1	13:P:96:ARG:NH2	2.41	0.49
1:A:2292:C:O2'	1:A:2293:C:H5'	2.12	0.49
2:B:55:A:H62	6:F:26:MET:CE	2.17	0.49
6:F:68:THR:HG21	6:F:88:LYS:CD	2.40	0.49
12:O:35:ARG:NH1	12:O:105:ARG:HE	1.97	0.49
20:Z:39:ASP:OD1	20:Z:44:ARG:NH2	2.45	0.49
24:W:76:GLU:HA	24:W:80:ILE:O	2.12	0.49
24:W:123:ALA:HB3	24:W:169:LEU:HD21	1.94	0.49
24:W:220:ARG:NE	24:W:275:LEU:CD2	2.75	0.49
1:A:361:G:H1	1:A:378:C:H42	1.60	0.49
1:A:1246:G:H1'	1:A:1247:G:H5'	1.93	0.49
1:A:1301:U:H2'	1:A:1302:A:H8	1.76	0.49
1:A:1496:G:H1	1:A:1507:U:H3	1.60	0.49
1:A:1528:U:H4'	1:A:1529:G:H5'	1.94	0.49
1:A:1858:A:C8	1:A:1859:C:N4	2.80	0.49
1:A:1858:A:C6	1:A:1859:C:C2	3.00	0.49
1:A:2082:G:H2'	1:A:2083:A:H8	1.76	0.49
1:A:2573:G:N2	1:A:2675:C:O2'	2.37	0.49
1:A:2777:A:C2'	7:G:64:ALA:HB1	2.41	0.49
6:F:67:VAL:HA	6:F:87:ALA:HA	1.93	0.49
8:J:14:ARG:HH12	8:J:122:LYS:HE3	1.75	0.49
9:K:12:ASP:OD1	9:K:12:ASP:N	2.40	0.49
20:Z:7:THR:O	20:Z:54:VAL:HG12	2.12	0.49
24:W:40:ARG:O	24:W:128:ILE:HD11	2.11	0.49
24:W:191:VAL:CG1	24:W:277:PHE:CZ	2.95	0.49
1:A:19:G:N2	1:A:568:G:C4	2.80	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:621:G:H2'	1:A:622:A:C8	2.47	0.49
1:A:673:A:N7	10:L:76:VAL:HG13	2.27	0.49
1:A:727:A:H2'	1:A:728:G:H8	1.76	0.49
1:A:2326:C:O2	1:A:2327:A:H1'	2.11	0.49
1:A:2711:G:O2'	4:D:14:GLN:NE2	2.45	0.49
1:A:925:A:N3	1:A:925:A:C3'	2.73	0.49
1:A:1478:G:H2'	1:A:1479:G:C8	2.48	0.49
5:E:58:ARG:O	5:E:79:ARG:NH1	2.45	0.49
1:A:284:C:O2'	1:A:287:G:O6	2.31	0.49
1:A:796:A:H61	1:A:800:G:H21	1.60	0.49
1:A:1672:A:H2'	1:A:1673:G:H8	1.78	0.49
3:C:172:VAL:HG12	3:C:173:LEU:N	2.27	0.49
4:D:107:ILE:CG2	4:D:205:ALA:HB3	2.43	0.49
8:J:26:LEU:HD12	8:J:102:LEU:CD1	2.30	0.49
14:Q:94:MET:O	14:Q:97:ASP:OD1	2.30	0.49
16:S:38:LEU:HD11	21:b:38:LEU:CB	2.41	0.49
24:W:249:MET:HB3	24:W:255:ASN:HB2	1.94	0.49
1:A:2309:G:N7	19:V:22:ARG:NH2	2.61	0.49
1:A:2839:C:H3'	1:A:2840:C:H6	1.77	0.49
6:F:17:MET:CE	6:F:25:VAL:O	2.61	0.49
8:J:57:ILE:HD12	8:J:125:VAL:CG2	2.34	0.49
9:K:11:ALA:O	9:K:99:PHE:N	2.35	0.49
20:Z:22:THR:HG21	20:Z:49:LYS:HD3	1.93	0.49
24:W:31:VAL:CG1	24:W:36:PRO:HA	2.43	0.49
1:A:1557:G:H8	1:A:1557:G:O5'	1.95	0.49
1:A:2290:C:O4'	1:A:2417:A:H1'	2.13	0.49
1:A:2536:C:O5'	1:A:2536:C:H6	1.95	0.49
2:B:64:A:H2	2:B:66:C:H41	1.59	0.49
9:K:43:VAL:O	9:K:43:VAL:HG12	2.09	0.49
16:S:14:PRO:HG3	16:S:78:GLU:HB3	1.93	0.49
1:A:634:A:C8	1:A:635:C:C5	3.01	0.49
1:A:1518:G:H1	1:A:1566:G:H1	1.61	0.49
1:A:2024:U:O2	9:K:3:GLN:NE2	2.45	0.49
4:D:49:ILE:O	4:D:82:GLU:HB3	2.12	0.49
12:O:28:ARG:N	12:O:29:PRO:CD	2.74	0.49
21:b:38:LEU:HD11	21:b:41:ARG:CD	2.42	0.49
24:W:31:VAL:HG12	24:W:36:PRO:HA	1.94	0.49
1:A:337:A:O2'	1:A:338:G:O4'	2.31	0.49
1:A:761:U:N3	1:A:764:C:OP2	2.35	0.49
1:A:1557:G:H2'	1:A:1558:G:C8	2.48	0.49
3:C:126:VAL:HG23	3:C:193:GLY:HA3	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:Q:44:ASN:ND2	15:R:76:TYR:H	2.09	0.49
14:Q:86:SER:HB3	14:Q:116:GLN:HE21	1.78	0.49
1:A:527:A:O2'	18:U:43:LYS:HG2	2.13	0.48
1:A:869:U:H5	1:A:990:C:H1'	1.78	0.48
1:A:1471:G:N7	3:C:31:LYS:NZ	2.61	0.48
1:A:1616:G:H5''	3:C:61:GLN:HB2	1.95	0.48
1:A:2000:A:OP2	1:A:2000:A:H4'	2.13	0.48
1:A:2111:A:H3'	1:A:2112:G:H8	1.77	0.48
4:D:5:ILE:HG22	4:D:33:ASN:ND2	2.27	0.48
8:J:25:THR:HG23	8:J:28:ARG:H	1.76	0.48
8:J:26:LEU:CA	8:J:29:LEU:CG	2.87	0.48
15:R:86:GLN:NE2	15:R:87:GLY:O	2.41	0.48
18:U:79:THR:HB	18:U:94:ALA:HB1	1.95	0.48
22:Y:4:ASN:HA	22:Y:7:ARG:HH21	1.77	0.48
1:A:65:A:H5'	17:T:71:GLY:HA3	1.95	0.48
1:A:739:C:H2'	1:A:740:A:H8	1.77	0.48
1:A:2684:G:N2	1:A:2685:U:O4	2.37	0.48
7:G:60:LYS:HB3	7:G:60:LYS:HZ1	1.74	0.48
13:P:35:VAL:HB	13:P:42:ARG:HG3	1.95	0.48
14:Q:85:LEU:HB2	14:Q:116:GLN:HG3	1.95	0.48
24:W:129:PRO:HG3	24:W:176:LEU:CD2	2.43	0.48
1:A:279:A:H2'	1:A:280:G:H8	1.77	0.48
1:A:1554:U:C5'	1:A:1555:A:C5	2.96	0.48
1:A:2420:G:N1	1:A:2453:C:O2'	2.46	0.48
1:A:2850:G:H3'	1:A:2851:A:H8	1.79	0.48
10:L:125:ALA:HB3	10:L:128:PHE:CZ	2.45	0.48
24:W:81:ARG:HH12	24:W:103:ILE:CG1	1.66	0.48
1:A:357:G:C4	1:A:358:C:C5	3.01	0.48
1:A:1673:G:H2'	1:A:1674:G:C8	2.48	0.48
1:A:2233:C:H4'	3:C:150:LYS:HE2	1.95	0.48
1:A:2800:C:O2'	4:D:172:GLN:NE2	2.37	0.48
2:B:74:G:H2'	2:B:75:U:H6	1.78	0.48
8:J:26:LEU:CB	8:J:63:ILE:CG2	2.81	0.48
14:Q:110:ALA:O	14:Q:113:ALA:N	2.46	0.48
18:U:72:ASP:N	18:U:77:GLU:O	2.41	0.48
24:W:58:ASN:HD21	24:W:131:VAL:C	2.20	0.48
1:A:614:G:OP1	1:A:1018:G:O2'	2.25	0.48
1:A:910:A:O2'	2:B:98:G:N3	2.46	0.48
1:A:2342:C:C5'	6:F:88:LYS:CD	2.64	0.48
1:A:2605:G:O2'	1:A:2608:C:OP2	2.30	0.48
3:C:171:TYR:OH	3:C:269:PHE:HE1	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:27:VAL:CG2	13:P:8:ILE:HD11	2.21	0.48
24:W:58:ASN:ND2	24:W:131:VAL:C	2.71	0.48
1:A:743:U:H2'	1:A:744:C:C6	2.46	0.48
1:A:1482:G:O2'	1:A:1523:U:O2	2.30	0.48
1:A:2103:U:H3	1:A:2464:A:H61	1.61	0.48
1:A:2285:G:H2'	1:A:2286:U:C6	2.48	0.48
1:A:2291:U:O2	1:A:2307:A:H2	1.96	0.48
1:A:2344:U:O2	1:A:2344:U:C2'	2.60	0.48
1:A:2353:U:O2	1:A:2414:C:C5	2.67	0.48
1:A:2664:U:O2'	4:D:82:GLU:OE2	2.25	0.48
8:J:18:VAL:N	8:J:139:GLU:O	2.46	0.48
12:O:65:VAL:HB	12:O:68:THR:H	1.79	0.48
13:P:27:ASP:O	13:P:49:VAL:CG1	2.62	0.48
22:Y:2:LYS:HD3	22:Y:2:LYS:O	2.13	0.48
1:A:288:C:OP2	1:A:289:C:N4	2.46	0.48
1:A:833:C:H2'	1:A:834:C:H6	1.79	0.48
1:A:1178:U:H5''	8:J:85:LEU:CD2	2.44	0.48
1:A:1417:A:O2'	1:A:1419:G:OP2	2.29	0.48
1:A:1580:A:OP2	1:A:1581:A:N6	2.47	0.48
2:B:22:G:H22	2:B:57:G:H1	1.61	0.48
10:L:81:LYS:HB3	10:L:101:VAL:CG1	2.44	0.48
13:P:58:ILE:O	13:P:80:HIS:CD2	2.67	0.48
13:P:60:GLU:O	13:P:79:VAL:HG23	2.14	0.48
19:V:46:TYR:HB3	19:V:67:LEU:HD12	1.95	0.48
1:A:833:C:C2	1:A:834:C:C5	3.02	0.48
1:A:948:A:OP2	1:A:948:A:H2	1.97	0.48
1:A:2607:G:OP1	1:A:2643:A:N6	2.46	0.48
3:C:94:ILE:HG13	3:C:104:ILE:CG2	2.44	0.48
4:D:35:VAL:CG2	4:D:91:TYR:CE1	2.96	0.48
14:Q:79:LEU:O	14:Q:83:LEU:N	2.47	0.48
24:W:72:LYS:HG3	24:W:82:SER:OG	2.13	0.48
1:A:334:G:C2	1:A:394:U:C2	3.01	0.48
1:A:617:G:O2'	1:A:619:A:OP1	2.32	0.48
1:A:775:G:H5''	3:C:13:ARG:HH22	1.78	0.48
1:A:1519:C:O2	1:A:1566:G:N2	2.47	0.48
1:A:1598:C:OP1	1:A:1764:U:O2'	2.27	0.48
1:A:1847:U:HO2'	3:C:154:LEU:HA	1.76	0.48
1:A:2062:A:O2'	1:A:2064:G:OP2	2.32	0.48
1:A:2290:C:H5	19:V:24:SER:HB2	1.78	0.48
1:A:2293:C:N4	19:V:23:ASP:OD2	2.47	0.48
1:A:2369:A:H2'	1:A:2370:G:H8	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2552:G:H2'	1:A:2553:G:H8	1.79	0.48
5:E:153:LEU:HB3	5:E:192:LEU:HB2	1.96	0.48
13:P:78:PRO:O	13:P:84:ILE:HD12	2.14	0.48
14:Q:108:GLN:CD	15:R:45:ASN:CG	2.81	0.48
24:W:129:PRO:HD3	24:W:176:LEU:HA	1.96	0.48
1:A:206:A:N1	1:A:207:A:N6	2.62	0.48
1:A:302:A:H2'	1:A:303:G:C8	2.49	0.48
1:A:527:A:H4'	18:U:43:LYS:CD	2.44	0.48
1:A:673:A:N7	10:L:76:VAL:CG1	2.77	0.48
1:A:950:U:C4	1:A:951:C:N3	2.82	0.48
1:A:1160:G:H2'	1:A:1161:A:H8	1.79	0.48
1:A:2076:C:H2'	1:A:2077:G:C8	2.48	0.48
1:A:2313:C:O2'	1:A:2317:A:N6	2.46	0.48
2:B:27:A:N6	2:B:52:G:O6	2.46	0.48
11:N:21:THR:HG22	11:N:44:VAL:HG22	1.96	0.48
16:S:3:ALA:N	16:S:107:VAL:O	2.45	0.48
1:A:241:C:H42	1:A:262:G:H1	1.60	0.47
1:A:1433:U:H4'	1:A:1648:A:H4'	1.96	0.47
1:A:1673:G:H2'	1:A:1674:G:H8	1.79	0.47
2:B:102:A:H3'	2:B:103:G:H8	1.79	0.47
4:D:55:ASP:HB3	4:D:77:LYS:HZ3	1.79	0.47
8:J:90:ALA:O	8:J:94:ARG:N	2.46	0.47
9:K:113:LYS:O	9:K:116:SER:OG	2.26	0.47
12:O:70:ASP:OD1	12:O:70:ASP:N	2.30	0.47
14:Q:86:SER:OG	14:Q:112:ALA:O	2.31	0.47
1:A:167:U:H2'	1:A:168:A:H8	1.79	0.47
1:A:909:G:H22	1:A:963:G:H1'	1.79	0.47
1:A:2267:G:H1'	1:A:2269:C:H5	1.79	0.47
1:A:2320:U:OP1	1:A:2409:U:O2'	2.32	0.47
1:A:2853:C:H2'	1:A:2854:A:C8	2.47	0.47
9:K:87:ILE:HD11	9:K:92:SER:N	2.29	0.47
10:L:79:LEU:HD22	10:L:117:LEU:CA	2.44	0.47
13:P:90:VAL:HG12	13:P:91:ARG:HG3	1.96	0.47
1:A:351:G:N1	1:A:354:A:OP2	2.47	0.47
1:A:1827:U:O2	1:A:1831:A:H2	1.96	0.47
1:A:2469:C:H2'	1:A:2470:C:H4'	1.96	0.47
3:C:84:ASP:OD2	3:C:87:ARG:N	2.33	0.47
4:D:51:LEU:N	4:D:81:LYS:O	2.36	0.47
12:O:11:ARG:NH1	12:O:33:VAL:O	2.37	0.47
14:Q:90:VAL:O	14:Q:90:VAL:CG1	2.62	0.47
1:A:1054:A:OP2	8:J:38:ARG:NH1	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1446:C:O2	1:A:1640:G:N2	2.41	0.47
4:D:37:GLN:H	4:D:50:GLN:HB2	1.79	0.47
4:D:55:ASP:N	4:D:77:LYS:HB3	2.29	0.47
11:N:119:LEU:O	11:N:120:VAL:HG23	2.15	0.47
13:P:58:ILE:HA	13:P:80:HIS:HD2	1.78	0.47
1:A:746:A:H62	1:A:780:G:H21	1.62	0.47
1:A:776:G:C8	3:C:207:LYS:HE2	2.50	0.47
1:A:2364:A:OP1	12:O:17:ARG:HG3	2.14	0.47
1:A:2839:C:C6	1:A:2840:C:C5	3.02	0.47
2:B:40:C:C4'	6:F:64:LYS:HB3	2.44	0.47
3:C:72:ASP:OD2	3:C:189:ARG:NH2	2.44	0.47
10:L:74:TYR:CZ	10:L:127:LYS:CG	2.96	0.47
13:P:26:GLY:HA3	13:P:95:VAL:HG21	1.96	0.47
21:b:27:MET:CE	21:b:36:MET:HE3	2.43	0.47
24:W:42:PRO:CD	24:W:177:TRP:HE1	2.28	0.47
1:A:125:A:N6	23:d:42:LEU:CD1	2.67	0.47
1:A:744:C:H42	1:A:812:G:H1	1.63	0.47
1:A:2001:G:H8	1:A:2001:G:O5'	1.97	0.47
1:A:2015:G:H4'	24:W:198:SER:HB3	1.97	0.47
1:A:2113:C:H42	1:A:2264:G:H1	1.62	0.47
1:A:2275:G:C2	1:A:2455:A:C4	3.02	0.47
1:A:2357:A:N6	1:A:2416:U:H3	2.12	0.47
1:A:2537:G:N1	1:A:2611:G:C6	2.82	0.47
3:C:37:LEU:HB2	3:C:62:TYR:HB2	1.96	0.47
14:Q:45:TYR:HD1	14:Q:48:ARG:HH21	1.62	0.47
15:R:14:VAL:HG13	15:R:97:ILE:HG13	1.91	0.47
1:A:213:C:H2'	1:A:214:G:H8	1.79	0.47
1:A:379:C:C2	1:A:380:C:C5	3.02	0.47
1:A:1307:U:H2'	1:A:1308:A:H8	1.79	0.47
1:A:1446:C:H2'	1:A:1447:C:H6	1.80	0.47
1:A:1472:G:H5''	1:A:1473:A:H2'	1.96	0.47
1:A:1850:A:H2'	1:A:1851:G:H8	1.79	0.47
1:A:2261:C:H2'	1:A:2262:A:H8	1.80	0.47
4:D:32:PRO:CB	4:D:98:LYS:CG	2.83	0.47
4:D:55:ASP:HB2	4:D:77:LYS:HG2	1.94	0.47
5:E:4:VAL:HG22	5:E:19:LEU:HD11	1.97	0.47
8:J:88:ARG:NH1	8:J:97:TYR:OH	2.48	0.47
10:L:90:GLU:N	10:L:122:THR:OG1	2.47	0.47
12:O:78:GLY:CA	12:O:109:LEU:HD13	2.44	0.47
13:P:16:LEU:HG	13:P:80:HIS:CE1	2.49	0.47
24:W:58:ASN:OD1	24:W:58:ASN:N	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:W:83:LEU:HD22	24:W:95:GLN:HG3	1.96	0.47
24:W:211:ARG:O	24:W:215:GLU:N	2.43	0.47
1:A:632:U:C2	1:A:633:U:C5	3.03	0.47
1:A:912:C:O2	1:A:913:A:N6	2.47	0.47
1:A:2026:A:H2'	1:A:2027:A:C8	2.49	0.47
2:B:74:G:C4	2:B:75:U:C5	3.03	0.47
3:C:210:ARG:HA	3:C:213:TRP:CD1	2.42	0.47
10:L:91:VAL:N	10:L:122:THR:O	2.45	0.47
12:O:61:LYS:HD3	12:O:61:LYS:HA	1.36	0.47
20:Z:45:GLY:HA2	20:Z:48:ASN:HB2	1.97	0.47
1:A:302:A:H2'	1:A:303:G:H8	1.80	0.47
1:A:1384:C:H2'	1:A:1385:G:C8	2.50	0.47
1:A:1476:C:H2'	1:A:1477:A:C8	2.50	0.47
1:A:2874:G:O2'	1:A:2891:G:N2	2.48	0.47
1:A:2900:A:O2'	13:P:5:GLN:N	2.45	0.47
6:F:57:LEU:HD23	6:F:65:PRO:HB3	1.96	0.47
14:Q:60:LEU:O	14:Q:63:THR:OG1	2.28	0.47
15:R:96:THR:O	15:R:96:THR:HG23	2.15	0.47
22:Y:34:THR:OG1	22:Y:36:GLN:NE2	2.48	0.47
1:A:196:U:H2'	1:A:197:G:H8	1.80	0.47
1:A:635:C:O2	1:A:636:G:C8	2.68	0.47
1:A:1068:G:N2	1:A:1069:U:O4	2.48	0.47
1:A:1674:G:H2'	1:A:1675:A:C8	2.50	0.47
1:A:2703:G:C5'	9:K:30:ARG:HD3	2.44	0.47
9:K:22:ILE:CD1	9:K:40:VAL:HG12	2.24	0.47
13:P:28:THR:HG22	13:P:49:VAL:HG22	1.97	0.47
13:P:94:LYS:HB2	13:P:118:ARG:NE	2.29	0.47
22:Y:20:SER:HA	22:Y:23:GLU:HB2	1.96	0.47
1:A:293:U:H2'	1:A:294:G:H8	1.80	0.46
1:A:455:G:H2'	1:A:456:A:C8	2.50	0.46
1:A:1527:C:C1'	1:A:1558:G:N2	2.72	0.46
1:A:1819:C:H2'	1:A:1820:A:C4	2.50	0.46
1:A:2342:C:C4'	6:F:37:ASN:OD1	2.58	0.46
1:A:2384:C:OP1	19:V:33:ARG:NH2	2.47	0.46
5:E:163:VAL:HG12	5:E:175:VAL:HG12	1.97	0.46
6:F:28:VAL:HG13	6:F:28:VAL:O	2.14	0.46
8:J:60:ALA:HB2	8:J:126:TYR:O	2.14	0.46
8:J:106:ILE:HG21	8:J:123:LEU:HD13	1.96	0.46
16:S:10:VAL:HG12	16:S:11:ARG:N	2.30	0.46
16:S:70:VAL:CG1	16:S:71:ILE:H	2.28	0.46
19:V:48:GLN:NE2	19:V:53:ILE:H	2.13	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:679:A:O2'	1:A:2433:C:OP1	2.29	0.46
1:A:787:C:O2	1:A:2010:A:C8	2.68	0.46
1:A:1765:G:N2	1:A:1768:A:OP2	2.40	0.46
9:K:122:ILE:HD13	13:P:46:PHE:HE1	1.80	0.46
22:Y:6:ILE:HG22	22:Y:56:VAL:CG1	2.45	0.46
1:A:290:U:H1'	1:A:291:C:H5'	1.97	0.46
1:A:625:C:H2'	1:A:626:G:C8	2.50	0.46
1:A:984:G:H2'	1:A:985:G:H8	1.80	0.46
1:A:1581:A:O2'	1:A:1584:U:N3	2.49	0.46
1:A:1828:G:O2'	3:C:182:ARG:NH1	2.48	0.46
1:A:1849:U:OP1	3:C:177:ASN:ND2	2.48	0.46
1:A:2827:A:C5	1:A:2828:G:H1'	2.51	0.46
1:A:2828:G:H2'	1:A:2829:G:C8	2.51	0.46
1:A:2922:U:H2'	1:A:2923:A:H8	1.80	0.46
5:E:160:ASN:HB2	5:E:163:VAL:HG23	1.97	0.46
1:A:114:C:H2'	1:A:115:C:H6	1.79	0.46
1:A:461:C:H2'	1:A:462:A:C8	2.50	0.46
1:A:920:G:N7	1:A:946:G:O6	2.48	0.46
1:A:1595:U:H2'	1:A:1596:U:H6	1.81	0.46
1:A:1656:C:O2'	1:A:1657:C:O4'	2.34	0.46
1:A:2394:G:OP1	19:V:63:GLY:N	2.43	0.46
1:A:2423:C:N4	1:A:2450:G:O6	2.48	0.46
4:D:58:GLU:HA	4:D:61:SER:HB3	1.98	0.46
6:F:5:LYS:HZ3	6:F:94:GLU:CD	2.17	0.46
9:K:25:LEU:HD12	9:K:38:VAL:CG1	2.44	0.46
10:L:79:LEU:HD22	10:L:117:LEU:HB2	1.80	0.46
24:W:32:ASP:CB	24:W:131:VAL:HG21	2.45	0.46
1:A:121:G:O6	1:A:128:C:N4	2.46	0.46
1:A:664:C:O2'	1:A:665:G:O4'	2.34	0.46
1:A:919:U:H6	1:A:919:U:H5''	1.81	0.46
1:A:1818:A:OP2	3:C:221:ARG:NE	2.48	0.46
1:A:2704:A:H5'	9:K:30:ARG:HB3	1.97	0.46
10:L:21:ARG:HD3	10:L:21:ARG:HA	1.78	0.46
1:A:2471:C:H2'	1:A:2472:C:H6	1.81	0.46
6:F:4:LEU:CG	6:F:97:TYR:HD1	2.18	0.46
1:A:185:A:H61	1:A:218:G:H1	1.63	0.46
1:A:1355:U:H2'	1:A:1356:G:C8	2.51	0.46
4:D:35:VAL:HG22	4:D:91:TYR:CD1	2.48	0.46
9:K:11:ALA:HB2	9:K:83:ALA:HB1	1.98	0.46
9:K:87:ILE:HG13	9:K:92:SER:C	2.41	0.46
11:N:9:THR:O	11:N:13:ARG:N	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:P:94:LYS:HB2	13:P:118:ARG:NH2	2.30	0.46
14:Q:15:LYS:HD3	14:Q:15:LYS:HA	1.54	0.46
14:Q:69:ALA:O	14:Q:73:GLY:N	2.48	0.46
15:R:19:THR:HG22	15:R:96:THR:CB	2.45	0.46
17:T:52:ASP:HB2	17:T:84:THR:HG22	1.97	0.46
18:U:84:LYS:C	18:U:84:LYS:CD	2.85	0.46
19:V:57:GLU:O	19:V:88:SER:OG	2.30	0.46
1:A:211:C:H2'	1:A:212:C:H6	1.81	0.46
1:A:684:G:C6	1:A:697:G:C2	3.04	0.46
1:A:709:G:H2'	1:A:710:G:H8	1.80	0.46
1:A:776:G:O6	3:C:208:ALA:N	2.42	0.46
1:A:1058:U:OP2	14:Q:70:ARG:NH2	2.49	0.46
1:A:1577:C:H3'	1:A:1578:G:H8	1.80	0.46
1:A:2286:U:O5'	1:A:2286:U:H6	1.99	0.46
1:A:2562:U:H4'	1:A:2693:G:H4'	1.98	0.46
4:D:83:LEU:HB3	4:D:86:VAL:HG22	1.96	0.46
24:W:41:ASN:CG	24:W:175:ILE:CG2	2.88	0.46
24:W:129:PRO:CG	24:W:176:LEU:CD2	2.91	0.46
1:A:1537:G:H2'	1:A:1538:G:C8	2.50	0.46
1:A:1828:G:N2	3:C:154:LEU:HB3	2.30	0.46
1:A:2628:G:H2'	1:A:2629:A:H8	1.80	0.46
4:D:25:VAL:CG1	4:D:187:LEU:HB3	2.44	0.46
4:D:79:PHE:CB	4:D:199:LEU:HD22	2.46	0.46
8:J:53:ASP:OD1	8:J:53:ASP:N	2.47	0.46
10:L:81:LYS:HB3	10:L:101:VAL:HG13	1.98	0.46
15:R:64:LYS:O	15:R:94:LYS:N	2.49	0.46
24:W:74:HIS:O	24:W:78:GLN:CG	2.53	0.46
1:A:925:A:C5	1:A:947:A:N3	2.84	0.46
1:A:1043:G:OP1	14:Q:92:ARG:NH1	2.49	0.46
1:A:2895:C:H2'	1:A:2896:U:C6	2.51	0.46
8:J:32:GLU:CG	8:J:143:LEU:HG	2.33	0.46
8:J:78:HIS:HD2	8:J:85:LEU:HB2	1.81	0.46
14:Q:38:GLN:O	14:Q:42:SER:N	2.49	0.46
16:S:44:SER:N	16:S:45:PRO:CD	2.79	0.46
17:T:58:ASN:OD1	17:T:58:ASN:N	2.46	0.46
24:W:32:ASP:HB2	24:W:131:VAL:CG2	2.46	0.46
1:A:694:G:H2'	1:A:695:G:H8	1.81	0.45
1:A:956:A:H3'	1:A:959:C:H41	1.81	0.45
1:A:1151:U:N3	1:A:1152:G:N7	2.63	0.45
8:J:37:LEU:HD11	8:J:123:LEU:HD12	1.98	0.45
13:P:64:VAL:O	13:P:75:ARG:N	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:S:29:VAL:HG11	16:S:55:ILE:HD11	1.96	0.45
16:S:64:MET:HB3	16:S:69:LEU:HD21	1.97	0.45
20:Z:8:LEU:HG	20:Z:28:LEU:HD13	1.97	0.45
22:Y:34:THR:HG23	22:Y:36:GLN:H	1.81	0.45
23:d:3:ARG:HD3	23:d:3:ARG:HA	1.65	0.45
1:A:277:C:H2'	1:A:278:A:H8	1.80	0.45
1:A:638:U:H2'	1:A:639:C:H6	1.81	0.45
1:A:663:G:OP1	5:E:107:ARG:NH2	2.42	0.45
1:A:706:C:N4	1:A:707:G:O6	2.49	0.45
1:A:927:G:H2'	1:A:928:G:H8	1.82	0.45
1:A:950:U:H2'	1:A:951:C:O4'	2.15	0.45
1:A:1384:C:H2'	1:A:1385:G:H8	1.80	0.45
1:A:1458:U:O2	1:A:1460:G:N1	2.50	0.45
1:A:1618:A:OP1	3:C:61:GLN:NE2	2.49	0.45
1:A:2094:C:H2'	1:A:2095:C:C6	2.51	0.45
1:A:2469:C:C4	1:A:2470:C:H1'	2.51	0.45
4:D:28:ILE:HD12	4:D:188:ILE:HD12	1.98	0.45
5:E:137:LYS:O	5:E:141:ALA:N	2.46	0.45
14:Q:4:VAL:CG1	14:Q:5:LYS:N	2.79	0.45
14:Q:61:TRP:CD1	14:Q:97:ASP:OD1	2.69	0.45
15:R:40:PHE:H	15:R:48:VAL:HG23	1.81	0.45
24:W:39:SER:HA	24:W:128:ILE:HG13	1.97	0.45
24:W:59:LYS:HA	25:W:301:GNP:HN1	1.82	0.45
1:A:484:C:N3	1:A:485:U:C4	2.84	0.45
1:A:534:C:H2'	1:A:535:G:H8	1.80	0.45
1:A:726:C:H2'	1:A:727:A:H8	1.82	0.45
1:A:2353:U:O2	1:A:2414:C:C6	2.69	0.45
3:C:76:GLY:N	3:C:116:ILE:O	2.44	0.45
4:D:83:LEU:CB	4:D:86:VAL:CG2	2.95	0.45
13:P:78:PRO:HG2	13:P:81:THR:HG21	1.97	0.45
16:S:86:ARG:NH2	16:S:96:ILE:HD13	2.27	0.45
1:A:395:C:H2'	1:A:396:G:C8	2.51	0.45
1:A:416:U:H5''	1:A:417:G:H5''	1.99	0.45
1:A:547:A:H2'	1:A:548:A:H8	1.81	0.45
1:A:999:A:H2'	1:A:1000:G:H8	1.81	0.45
1:A:1066:A:O2'	1:A:1067:A:O5'	2.32	0.45
1:A:1478:G:H2'	1:A:1479:G:H8	1.82	0.45
1:A:1619:A:H2'	1:A:1620:A:C8	2.52	0.45
2:B:27:A:H2	2:B:54:U:H3	1.64	0.45
3:C:207:LYS:HG3	3:C:209:GLY:H	1.82	0.45
4:D:201:THR:HG22	4:D:203:LYS:HG3	1.96	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:J:29:LEU:HD11	8:J:63:ILE:CG2	2.46	0.45
8:J:37:LEU:O	8:J:52:GLY:HA3	2.16	0.45
8:J:98:PRO:HD2	8:J:127:ARG:HE	1.82	0.45
16:S:52:LYS:HD3	16:S:52:LYS:HA	1.45	0.45
17:T:31:ASP:OD1	17:T:32:VAL:N	2.49	0.45
24:W:129:PRO:CD	24:W:176:LEU:HA	2.47	0.45
1:A:1573:C:N4	1:A:1594:G:O6	2.42	0.45
1:A:1644:C:H2'	1:A:1645:C:H6	1.82	0.45
1:A:1847:U:O5'	3:C:156:ARG:HB3	2.16	0.45
24:W:34:ARG:NH1	24:W:270:GLU:OE1	2.46	0.45
24:W:40:ARG:HH22	24:W:78:GLN:HE22	1.64	0.45
1:A:79:C:O2'	1:A:390:A:N3	2.43	0.45
1:A:626:G:H2'	1:A:627:G:C8	2.51	0.45
1:A:669:C:C2'	1:A:670:C:C6	2.86	0.45
1:A:1160:G:H2'	1:A:1161:A:C8	2.51	0.45
1:A:1527:C:C2	1:A:1558:G:N1	2.84	0.45
1:A:2021:G:N2	1:A:2025:C:O2'	2.50	0.45
1:A:2717:G:N2	1:A:2751:G:O6	2.50	0.45
1:A:2770:A:H62	1:A:2792:G:H21	1.65	0.45
3:C:260:ARG:NH2	3:C:266:SER:OG	2.42	0.45
10:L:66:PHE:CD1	10:L:66:PHE:N	2.85	0.45
19:V:79:ARG:HA	19:V:85:LYS:HA	1.99	0.45
21:b:12:LYS:HA	21:b:15:LEU:HB2	1.99	0.45
22:Y:32:LEU:HD12	22:Y:32:LEU:HA	1.85	0.45
1:A:719:C:N3	1:A:856:G:C2	2.85	0.45
1:A:1207:C:O2'	15:R:23:GLU:OE1	2.31	0.45
1:A:1232:G:H2'	1:A:1233:A:H8	1.81	0.45
1:A:1734:A:H2'	1:A:1735:A:C8	2.51	0.45
1:A:2291:U:OP1	1:A:2416:U:O2'	2.34	0.45
1:A:2302:A:H2'	1:A:2303:A:C8	2.52	0.45
4:D:62:ASN:HB3	4:D:64:PRO:HG2	1.97	0.45
4:D:147:GLY:HA3	4:D:148:PRO:HD3	1.83	0.45
4:D:203:LYS:HE2	4:D:203:LYS:HB3	1.63	0.45
6:F:128:TYR:CD2	6:F:156:ILE:HD12	2.51	0.45
7:G:84:PHE:N	7:G:136:GLY:O	2.47	0.45
9:K:122:ILE:HD13	13:P:46:PHE:CE1	2.51	0.45
1:A:140:A:H1'	1:A:1448:U:H5'	1.99	0.45
1:A:530:A:O2'	18:U:55:GLY:HA2	2.17	0.45
1:A:787:C:N1	1:A:2010:A:N7	2.64	0.45
1:A:1026:A:N6	1:A:1027:A:N1	2.64	0.45
1:A:1359:G:N2	1:A:1370:C:H41	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2312:C:OP2	1:A:2418:G:O2'	2.34	0.45
1:A:2730:U:H5'	1:A:2731:G:H5''	1.97	0.45
1:A:2739:C:H2'	1:A:2740:A:C8	2.52	0.45
2:B:27:A:H3'	2:B:28:C:C6	2.51	0.45
3:C:146:LEU:HD21	3:C:154:LEU:HD21	1.99	0.45
4:D:11:GLY:C	4:D:27:VAL:HG23	2.42	0.45
6:F:8:TYR:O	6:F:8:TYR:HD1	1.99	0.45
11:N:20:LEU:O	11:N:24:LEU:N	2.50	0.45
12:O:101:LEU:H	12:O:101:LEU:CD2	2.18	0.45
13:P:89:VAL:CG1	13:P:90:VAL:N	2.80	0.45
21:b:30:CYS:SG	21:b:31:PRO:HD2	2.57	0.45
1:A:106:G:H2'	1:A:107:G:H8	1.81	0.45
1:A:784:C:N4	1:A:806:G:O6	2.50	0.45
1:A:1512:G:H1'	1:A:1593:A:H2	1.81	0.45
1:A:2744:C:H2'	1:A:2745:U:C6	2.52	0.45
4:D:55:ASP:HA	4:D:77:LYS:CB	2.45	0.45
4:D:55:ASP:OD2	4:D:75:ALA:CB	2.64	0.45
10:L:31:ALA:O	10:L:33:LYS:NZ	2.44	0.45
10:L:79:LEU:HD22	10:L:116:LYS:C	2.41	0.45
21:b:46:CYS:HG	21:b:48:SER:HG	1.27	0.45
22:Y:54:LYS:HD3	22:Y:57:ILE:HD12	1.99	0.45
1:A:243:G:OP2	1:A:244:A:O2'	2.31	0.45
1:A:1267:G:N7	14:Q:16:LYS:NZ	2.63	0.45
1:A:1326:A:H5'	11:N:107:ARG:HD2	1.99	0.45
1:A:1523:U:H5''	1:A:1524:A:C8	2.52	0.45
2:B:55:A:H4'	6:F:23:ASP:HB2	1.96	0.45
3:C:77:ARG:N	3:C:95:ASN:O	2.49	0.45
5:E:38:LEU:O	5:E:42:ALA:N	2.50	0.45
5:E:190:GLU:O	5:E:191:LYS:CG	2.64	0.45
14:Q:89:GLU:HG3	14:Q:91:ASN:HB2	1.97	0.45
20:Z:5:GLU:O	20:Z:57:LYS:HB3	2.17	0.45
24:W:212:PHE:CZ	24:W:276:SER:O	2.70	0.45
1:A:833:C:H2'	1:A:834:C:C6	2.52	0.44
1:A:1060:U:H2'	1:A:1061:A:C8	2.53	0.44
1:A:1385:G:H1	1:A:1645:C:H42	1.65	0.44
1:A:2356:A:O2'	1:A:2357:A:C8	2.70	0.44
1:A:2703:G:H5''	9:K:30:ARG:HD3	1.99	0.44
2:B:112:C:H2'	2:B:113:A:C8	2.52	0.44
1:A:918:U:H6	1:A:918:U:H5''	1.82	0.44
1:A:2349:A:O2'	1:A:2362:A:N6	2.51	0.44
3:C:205:ILE:O	3:C:210:ARG:HG2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:109:ALA:O	5:E:112:SER:OG	2.25	0.44
5:E:131:LEU:HB2	5:E:162:ALA:HB1	1.99	0.44
12:O:41:TYR:CD1	12:O:57:SER:OG	2.71	0.44
12:O:102:TYR:OH	12:O:110:ALA:HB3	2.17	0.44
18:U:84:LYS:O	18:U:85:VAL:C	2.60	0.44
21:b:38:LEU:HD13	21:b:41:ARG:HD2	1.99	0.44
1:A:675:C:N4	1:A:676:G:O6	2.51	0.44
1:A:888:A:H2'	1:A:889:A:H8	1.82	0.44
1:A:1042:A:H5'	14:Q:92:ARG:HH21	1.82	0.44
1:A:1476:C:H2'	1:A:1477:A:H8	1.82	0.44
1:A:1508:C:H2'	1:A:1509:C:H6	1.82	0.44
1:A:1614:A:H4'	3:C:214:LYS:HG2	1.99	0.44
1:A:2094:C:O5'	1:A:2094:C:H6	2.00	0.44
1:A:2292:C:C2'	1:A:2293:C:H5'	2.48	0.44
1:A:2539:C:O2	1:A:2607:G:N2	2.43	0.44
1:A:2748:G:H5'	13:P:99:LYS:HZ1	1.82	0.44
10:L:33:LYS:HD3	10:L:33:LYS:HA	1.59	0.44
12:O:103:HIS:CD2	12:O:103:HIS:O	2.70	0.44
14:Q:33:LYS:HE2	14:Q:33:LYS:HB3	1.74	0.44
18:U:84:LYS:CB	18:U:93:VAL:HG11	2.48	0.44
20:Z:5:GLU:OE2	20:Z:59:GLN:NE2	2.50	0.44
24:W:16:GLU:OE1	24:W:16:GLU:HA	2.17	0.44
1:A:304:G:H2'	1:A:305:A:C8	2.51	0.44
1:A:704:U:H2'	1:A:705:A:C8	2.52	0.44
1:A:950:U:O5'	1:A:950:U:H6	2.01	0.44
1:A:1572:G:O2'	1:A:1573:C:C6	2.71	0.44
1:A:1859:C:H2'	1:A:1860:G:C8	2.48	0.44
3:C:69:ARG:HE	3:C:129:ALA:HB2	1.82	0.44
9:K:26:GLY:HA3	9:K:30:ARG:HH21	1.82	0.44
10:L:91:VAL:HB	10:L:123:VAL:HA	1.99	0.44
21:b:38:LEU:CD1	21:b:41:ARG:CD	2.94	0.44
1:A:776:G:OP1	3:C:10:SER:OG	2.30	0.44
1:A:2099:G:H2'	1:A:2100:A:H8	1.83	0.44
1:A:2163:A:H2'	1:A:2164:A:H8	1.82	0.44
12:O:29:PRO:HB3	12:O:44:ILE:HG23	1.97	0.44
24:W:39:SER:C	24:W:128:ILE:HG13	2.43	0.44
1:A:426:G:O2'	1:A:2261:C:OP1	2.31	0.44
1:A:897:G:H1'	20:Z:25:THR:HG21	2.00	0.44
1:A:1564:C:O2	1:A:1564:C:H2'	2.16	0.44
1:A:1847:U:O4	3:C:153:GLN:HG2	2.18	0.44
1:A:2374:G:H5'	1:A:2376:C:H5'	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2703:G:O3'	9:K:30:ARG:HB3	2.17	0.44
1:A:2747:G:O2'	1:A:2872:U:OP1	2.29	0.44
1:A:2865:U:H5'	11:N:49:THR:HG21	1.99	0.44
4:D:126:HIS:CG	4:D:159:LEU:HB3	2.52	0.44
14:Q:50:ARG:HH21	15:R:73:VAL:HG22	1.83	0.44
1:A:431:A:N6	1:A:458:G:O6	2.51	0.44
1:A:738:C:O2'	3:C:43:ARG:NE	2.51	0.44
1:A:1214:U:O4	1:A:1221:A:N6	2.51	0.44
1:A:1587:U:H2'	1:A:1588:A:C8	2.53	0.44
1:A:2835:A:H62	1:A:2915:G:H21	1.66	0.44
6:F:69:ARG:HD3	6:F:82:GLY:HA2	1.99	0.44
11:N:9:THR:OG1	11:N:10:SER:N	2.46	0.44
11:N:22:THR:HG21	11:N:67:ARG:HB2	1.99	0.44
12:O:95:PHE:CD2	12:O:102:TYR:HE1	2.35	0.44
16:S:9:THR:HG23	16:S:100:THR:HG21	2.00	0.44
18:U:9:VAL:HG22	18:U:70:PRO:HA	2.00	0.44
20:Z:4:LEU:HD13	20:Z:58:GLU:CD	2.43	0.44
1:A:627:G:H2'	1:A:628:C:C6	2.52	0.44
1:A:684:G:C4	1:A:697:G:N2	2.86	0.44
1:A:760:G:O2'	1:A:766:C:N3	2.47	0.44
1:A:1314:A:O2'	1:A:1315:G:O4'	2.29	0.44
1:A:1735:A:H4'	24:W:245:ARG:HH12	1.82	0.44
1:A:2280:G:OP2	1:A:2280:G:H8	2.00	0.44
1:A:2539:C:H41	1:A:2604:C:N4	2.15	0.44
1:A:2581:U:OP1	24:W:196:LYS:NZ	2.51	0.44
1:A:2705:C:H2'	1:A:2706:G:H8	1.82	0.44
6:F:65:PRO:HB3	6:F:89:VAL:HG22	1.99	0.44
18:U:83:TYR:N	18:U:93:VAL:HG13	2.33	0.44
19:V:48:GLN:O	19:V:49:ARG:NH1	2.51	0.44
24:W:176:LEU:HD13	24:W:177:TRP:H	1.83	0.44
1:A:372:U:H4'	18:U:64:HIS:HD2	1.81	0.44
1:A:526:A:H1'	1:A:527:A:H5''	2.00	0.44
1:A:578:A:H4'	1:A:579:G:C8	2.53	0.44
1:A:745:C:HO2'	1:A:781:A:H61	1.64	0.44
1:A:925:A:N6	1:A:947:A:C4	2.86	0.44
1:A:1656:C:N4	1:A:1665:G:O6	2.51	0.44
1:A:2548:U:C4	1:A:2570:A:C5	3.05	0.44
4:D:29:GLU:HB2	4:D:185:LEU:CD2	2.44	0.44
4:D:54:ASP:O	4:D:78:ARG:CG	2.55	0.44
4:D:55:ASP:CB	4:D:77:LYS:CG	2.93	0.44
6:F:54:VAL:O	6:F:54:VAL:HG12	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:J:74:ILE:H	8:J:74:ILE:HG13	1.48	0.44
10:L:117:LEU:HD11	10:L:119:LYS:O	2.17	0.44
12:O:94:VAL:HG12	12:O:95:PHE:N	2.31	0.44
21:b:15:LEU:HD23	21:b:15:LEU:HA	1.81	0.44
1:A:244:A:H5'	1:A:246:U:H1'	1.99	0.43
1:A:1232:G:H2'	1:A:1233:A:C8	2.53	0.43
1:A:1508:C:H2'	1:A:1509:C:C6	2.53	0.43
1:A:1806:U:H2'	1:A:1807:U:H6	1.83	0.43
1:A:2024:U:O2	9:K:3:GLN:CD	2.61	0.43
1:A:2154:G:O6	1:A:2192:U:O2'	2.33	0.43
11:N:20:LEU:HD13	11:N:40:LEU:HD22	1.98	0.43
13:P:32:HIS:HD2	13:P:86:LYS:HB3	1.83	0.43
18:U:79:THR:HG21	18:U:96:LYS:CG	2.46	0.43
24:W:9:HIS:CD2	24:W:9:HIS:O	2.70	0.43
24:W:96:ILE:O	24:W:96:ILE:HG13	2.17	0.43
24:W:150:ASP:C	24:W:152:PRO:HD2	2.43	0.43
24:W:220:ARG:NE	24:W:275:LEU:HD21	2.33	0.43
1:A:393:U:C2	1:A:394:U:C5	3.06	0.43
1:A:1177:G:O2'	1:A:1179:A:N7	2.49	0.43
1:A:2376:C:H42	1:A:2399:G:H1	1.66	0.43
2:B:18:A:C4	2:B:19:G:H1'	2.53	0.43
4:D:99:VAL:C	4:D:101:ILE:H	2.26	0.43
12:O:35:ARG:HH12	12:O:105:ARG:CG	2.13	0.43
15:R:12:ILE:HG21	15:R:20:VAL:HG11	1.98	0.43
17:T:50:LYS:HE2	17:T:50:LYS:HB3	1.76	0.43
22:Y:60:ARG:HA	22:Y:63:ALA:HB3	1.99	0.43
24:W:88:VAL:C	24:W:139:ARG:HH12	2.26	0.43
1:A:827:G:N2	1:A:832:G:N7	2.65	0.43
1:A:2542:A:H3'	1:A:2543:U:C6	2.53	0.43
13:P:32:HIS:HB3	13:P:43:ILE:HD11	1.99	0.43
18:U:23:ILE:HA	18:U:35:VAL:HG22	2.00	0.43
24:W:58:ASN:HD21	24:W:132:GLY:C	2.18	0.43
1:A:888:A:H2'	1:A:889:A:C8	2.54	0.43
1:A:1717:C:H2'	1:A:1718:G:H8	1.82	0.43
1:A:2106:A:N3	1:A:2463:A:O2'	2.43	0.43
1:A:2298:A:C5	1:A:2299:G:N7	2.86	0.43
1:A:2307:A:OP2	19:V:20:ASN:ND2	2.51	0.43
1:A:2708:A:H4'	4:D:193:PRO:HB3	2.00	0.43
1:A:2823:C:C2	1:A:2828:G:N2	2.75	0.43
8:J:40:LYS:HA	8:J:40:LYS:HD3	1.72	0.43
12:O:42:ALA:CB	12:O:109:LEU:HD21	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:U:4:LYS:H	18:U:92:ARG:NH2	2.15	0.43
1:A:89:U:H3'	1:A:90:A:H2'	2.00	0.43
1:A:419:G:H22	1:A:447:G:H2'	1.83	0.43
1:A:514:G:OP2	23:d:34:ARG:NE	2.38	0.43
1:A:635:C:N3	1:A:636:G:C5	2.87	0.43
1:A:828:A:O2'	1:A:1817:C:O2'	2.33	0.43
1:A:892:U:H1'	1:A:894:A:H2	1.83	0.43
1:A:1646:G:OP2	17:T:58:ASN:ND2	2.34	0.43
1:A:2049:A:N1	1:A:2064:G:N2	2.67	0.43
1:A:2320:U:O2'	1:A:2403:C:O2	2.34	0.43
1:A:2757:U:H2'	1:A:2758:G:C8	2.53	0.43
3:C:68:LYS:HG2	3:C:151:GLY:N	2.34	0.43
5:E:37:ILE:HD13	5:E:37:ILE:HA	1.85	0.43
15:R:39:LEU:CB	15:R:48:VAL:HG21	2.48	0.43
18:U:2:HIS:ND1	18:U:2:HIS:N	2.66	0.43
18:U:7:ASP:OD1	18:U:7:ASP:N	2.50	0.43
23:d:43:SER:O	23:d:43:SER:OG	2.36	0.43
1:A:875:U:H2'	1:A:876:A:C8	2.54	0.43
1:A:929:G:H8	1:A:929:G:OP2	2.02	0.43
1:A:1178:U:O4'	8:J:76:TYR:CE2	2.71	0.43
1:A:1774:A:H3'	1:A:1775:G:H8	1.84	0.43
1:A:2126:G:N1	1:A:2221:C:C2	2.79	0.43
6:F:128:TYR:CD2	6:F:156:ILE:CD1	3.02	0.43
13:P:76:THR:O	13:P:76:THR:HG22	2.18	0.43
1:A:357:G:C4	1:A:358:C:C6	3.07	0.43
1:A:638:U:C2	1:A:639:C:C5	3.07	0.43
1:A:1081:U:H2'	1:A:1082:G:H8	1.84	0.43
1:A:1289:U:H2'	10:L:18:ARG:HH22	1.83	0.43
1:A:1412:A:H3'	1:A:1413:G:H8	1.83	0.43
1:A:2311:G:O2'	1:A:2419:U:O4	2.31	0.43
1:A:2318:G:H2'	1:A:2319:G:H8	1.84	0.43
1:A:2595:A:H4'	1:A:2596:G:H5''	2.00	0.43
1:A:2759:C:H2'	1:A:2760:G:C8	2.54	0.43
2:B:24:C:H3'	2:B:25:A:H8	1.83	0.43
3:C:141:VAL:HG13	3:C:144:ILE:HD11	2.00	0.43
4:D:30:ALA:C	4:D:53:PHE:HZ	2.24	0.43
4:D:83:LEU:CD2	4:D:203:LYS:CG	2.95	0.43
5:E:46:GLN:HG2	5:E:48:THR:HG23	1.99	0.43
8:J:8:ASN:OD1	8:J:8:ASN:N	2.46	0.43
17:T:91:GLU:HG3	17:T:92:ILE:HG12	2.00	0.43
19:V:49:ARG:HA	19:V:49:ARG:HD3	1.77	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:W:9:HIS:O	24:W:9:HIS:HD2	2.01	0.43
24:W:27:VAL:HG11	24:W:48:LEU:HD13	2.01	0.43
24:W:32:ASP:HA	24:W:131:VAL:CG2	2.48	0.43
1:A:342:A:OP1	18:U:95:LYS:CE	2.66	0.43
1:A:1575:A:N6	1:A:1591:G:O2'	2.52	0.43
1:A:1630:G:O2'	1:A:1631:A:O5'	2.28	0.43
2:B:21:G:H1	2:B:58:C:H42	1.67	0.43
2:B:40:C:H5''	6:F:64:LYS:HB3	2.00	0.43
3:C:44:ASN:HB3	3:C:47:GLY:H	1.82	0.43
3:C:90:ASN:HD21	3:C:197:ASN:HB2	1.83	0.43
3:C:176:LEU:O	3:C:177:ASN:C	2.56	0.43
4:D:31:ALA:O	4:D:53:PHE:HE1	2.00	0.43
5:E:104:LYS:O	5:E:108:LEU:N	2.52	0.43
5:E:137:LYS:HA	5:E:137:LYS:HD2	1.88	0.43
1:A:189:G:H2'	1:A:190:G:H8	1.83	0.43
1:A:2376:C:N4	1:A:2399:G:H1	2.16	0.43
4:D:10:ILE:HB	4:D:27:VAL:HG12	1.92	0.43
5:E:31:SER:OG	10:L:9:SER:OG	2.32	0.43
6:F:167:ARG:HB2	6:F:167:ARG:HE	1.55	0.43
8:J:26:LEU:CA	8:J:29:LEU:HG	2.49	0.43
11:N:55:ASP:OD1	11:N:56:LEU:N	2.52	0.43
24:W:156:THR:HG21	24:W:172:THR:OG1	2.18	0.43
1:A:86:C:HO2'	1:A:103:U:HO2'	1.65	0.43
1:A:796:A:H2'	1:A:797:A:H8	1.83	0.43
1:A:1626:U:H2'	1:A:1627:A:H8	1.84	0.43
1:A:2038:G:H2'	1:A:2039:G:H8	1.83	0.43
10:L:132:ALA:O	10:L:136:VAL:HG13	2.19	0.43
13:P:78:PRO:HG2	13:P:81:THR:CG2	2.49	0.43
16:S:86:ARG:HH21	16:S:96:ILE:HD13	1.76	0.43
20:Z:7:THR:O	20:Z:54:VAL:CG1	2.66	0.43
21:b:23:ASN:ND2	21:b:24:VAL:O	2.50	0.43
1:A:28:A:HO2'	1:A:626:G:HO2'	1.57	0.42
1:A:342:A:OP1	18:U:95:LYS:HE2	2.19	0.42
1:A:749:G:C2	1:A:778:C:C2	3.07	0.42
1:A:1042:A:H5'	14:Q:92:ARG:NH2	2.33	0.42
1:A:1518:G:H1	1:A:1566:G:H22	1.67	0.42
3:C:164:VAL:HG13	3:C:174:VAL:HG22	2.00	0.42
4:D:62:ASN:O	4:D:66:LYS:N	2.48	0.42
5:E:39:MET:HE3	5:E:39:MET:HB3	1.91	0.42
5:E:154:ILE:HG12	5:E:193:LEU:HD12	2.00	0.42
6:F:68:THR:HG22	6:F:88:LYS:CD	2.38	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:U:41:VAL:HG11	18:U:43:LYS:CG	2.49	0.42
20:Z:8:LEU:HD21	20:Z:28:LEU:CD1	2.49	0.42
20:Z:47:ILE:H	20:Z:47:ILE:HG13	1.70	0.42
24:W:40:ARG:NH2	24:W:75:PHE:CE1	2.87	0.42
1:A:77:U:C5'	22:Y:2:LYS:HB2	2.47	0.42
1:A:210:A:C8	1:A:211:C:C5	3.07	0.42
1:A:682:G:O6	10:L:110:LYS:NZ	2.50	0.42
1:A:1129:U:H3	1:A:1131:A:H3'	1.84	0.42
1:A:1288:G:N2	5:E:88:VAL:CG2	2.64	0.42
1:A:1388:A:H5'	1:A:1389:C:H5''	2.00	0.42
1:A:1858:A:N9	1:A:1859:C:C5	2.87	0.42
1:A:2120:U:H5''	1:A:2121:U:H2'	2.02	0.42
1:A:2148:A:H61	1:A:2200:A:H1'	1.84	0.42
1:A:2537:G:N1	1:A:2611:G:N1	2.67	0.42
1:A:2725:U:H2'	1:A:2726:G:C8	2.53	0.42
1:A:2901:G:H2'	1:A:2902:A:H8	1.82	0.42
2:B:55:A:C1'	6:F:27:GLN:NE2	2.63	0.42
3:C:164:VAL:HA	3:C:174:VAL:HG13	2.01	0.42
1:A:5:A:H2'	1:A:6:A:C8	2.54	0.42
1:A:1183:G:H2'	1:A:1184:G:C8	2.54	0.42
1:A:1733:U:N3	1:A:1745:A:OP1	2.53	0.42
1:A:2472:C:H2'	1:A:2473:G:C8	2.54	0.42
1:A:2566:U:H2'	1:A:2567:C:H6	1.82	0.42
1:A:2752:C:OP2	4:D:115:LYS:NZ	2.41	0.42
5:E:136:THR:HG22	5:E:167:ALA:H	1.84	0.42
10:L:129:SER:HB3	10:L:132:ALA:HB3	2.01	0.42
13:P:12:THR:HG22	13:P:58:ILE:CD1	2.38	0.42
13:P:30:ARG:HG2	13:P:47:GLU:CB	2.48	0.42
19:V:78:GLU:HB2	19:V:86:LYS:HD3	2.02	0.42
24:W:89:ASN:C	24:W:139:ARG:HH22	2.27	0.42
24:W:220:ARG:CZ	24:W:275:LEU:HD21	2.49	0.42
1:A:816:U:H2'	1:A:817:G:C8	2.54	0.42
1:A:1069:U:H3'	1:A:1070:G:C8	2.52	0.42
1:A:1315:G:H2'	1:A:1316:A:H8	1.85	0.42
1:A:1757:G:N7	1:A:1759:U:C6	2.87	0.42
1:A:2282:G:O6	19:V:13:LYS:CA	2.45	0.42
1:A:2321:U:OP1	1:A:2408:G:N2	2.45	0.42
1:A:2687:C:N3	1:A:2692:G:N1	2.60	0.42
3:C:90:ASN:HB2	3:C:106:ALA:HB3	2.01	0.42
4:D:31:ALA:HB1	4:D:32:PRO:HD2	2.01	0.42
4:D:55:ASP:CA	4:D:77:LYS:CB	2.96	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:13:ALA:N	6:F:14:PRO:HD2	2.34	0.42
6:F:17:MET:HE1	6:F:25:VAL:O	2.19	0.42
6:F:33:LYS:C	6:F:96:MET:HE1	2.44	0.42
9:K:15:GLY:O	9:K:47:THR:N	2.42	0.42
24:W:14:ARG:HA	24:W:17:VAL:HG12	2.02	0.42
24:W:277:PHE:HD1	24:W:277:PHE:HA	1.74	0.42
1:A:419:G:N2	1:A:420:U:O4	2.52	0.42
1:A:1117:G:H4'	1:A:1135:G:H2'	2.01	0.42
1:A:1759:U:H3	1:A:1774:A:H62	1.67	0.42
1:A:1850:A:H2'	1:A:1851:G:C8	2.55	0.42
1:A:1862:C:C3'	1:A:1862:C:C6	3.02	0.42
1:A:2072:C:H2'	1:A:2073:C:H6	1.85	0.42
1:A:2253:G:H4'	1:A:2255:C:C2	2.54	0.42
1:A:2299:G:H2'	1:A:2300:G:C8	2.55	0.42
6:F:128:TYR:HD2	6:F:156:ILE:HD12	1.84	0.42
10:L:16:ARG:HG2	10:L:18:ARG:HD2	2.02	0.42
13:P:27:ASP:O	13:P:49:VAL:HG12	2.19	0.42
13:P:28:THR:HA	13:P:49:VAL:HA	2.01	0.42
14:Q:80:MET:HA	14:Q:83:LEU:HB3	2.00	0.42
1:A:194:A:H2'	1:A:195:C:C6	2.55	0.42
1:A:1058:U:P	8:J:144:ARG:HH22	2.42	0.42
1:A:1489:U:N3	1:A:1597:C:O2	2.52	0.42
1:A:1564:C:N3	1:A:1565:U:C5	2.87	0.42
1:A:2392:U:H2'	1:A:2393:C:H6	1.82	0.42
1:A:2548:U:C5	1:A:2570:A:N6	2.88	0.42
1:A:2888:C:OP1	13:P:94:LYS:NZ	2.53	0.42
4:D:26:THR:HG21	4:D:192:VAL:HB	2.01	0.42
5:E:133:THR:H	5:E:138:GLU:CD	2.28	0.42
11:N:119:LEU:O	11:N:120:VAL:CG2	2.67	0.42
14:Q:86:SER:HB3	14:Q:116:GLN:HG2	2.02	0.42
20:Z:40:ASN:O	20:Z:44:ARG:N	2.51	0.42
24:W:127:GLY:O	24:W:175:ILE:CB	2.42	0.42
1:A:510:G:N1	1:A:514:G:O6	2.53	0.42
1:A:516:G:O6	23:d:39:ARG:NH2	2.53	0.42
1:A:776:G:C5	3:C:207:LYS:HB2	2.55	0.42
1:A:802:G:H2'	1:A:803:C:C6	2.55	0.42
1:A:929:G:OP2	1:A:929:G:C8	2.72	0.42
1:A:1529:G:H3'	1:A:1530:G:C8	2.55	0.42
1:A:2247:C:H2'	1:A:2248:G:H8	1.85	0.42
1:A:2709:C:H5'	4:D:193:PRO:HA	2.01	0.42
1:A:2873:G:H5''	13:P:97:ARG:HA	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:107:ILE:HG22	4:D:205:ALA:HB1	1.98	0.42
5:E:77:SER:OG	5:E:78:ILE:N	2.52	0.42
6:F:115:ARG:HE	6:F:115:ARG:HB2	1.74	0.42
6:F:132:ILE:CD1	6:F:154:ILE:CB	2.98	0.42
8:J:26:LEU:CD1	8:J:102:LEU:HD13	2.33	0.42
8:J:29:LEU:HD11	8:J:63:ILE:HG23	2.02	0.42
10:L:74:TYR:HH	10:L:127:LYS:HG3	1.85	0.42
12:O:35:ARG:HD3	12:O:100:TYR:CZ	2.55	0.42
17:T:14:THR:HG1	17:T:17:SER:H	1.61	0.42
17:T:53:LYS:HB3	17:T:82:LYS:HB3	2.01	0.42
24:W:220:ARG:NE	24:W:275:LEU:HD23	2.35	0.42
1:A:27:G:H21	1:A:558:G:H2'	1.85	0.42
1:A:987:A:H3'	1:A:988:G:H8	1.85	0.42
1:A:1553:A:H1'	1:A:1555:A:N1	2.35	0.42
1:A:1735:A:H5'	24:W:245:ARG:HH22	1.85	0.42
1:A:2295:A:C6	1:A:2301:U:C2	3.08	0.42
4:D:56:LYS:HB2	4:D:57:ARG:H	1.66	0.42
5:E:139:MET:HG3	5:E:167:ALA:HB2	2.01	0.42
8:J:20:ASP:OD1	8:J:21:ALA:N	2.53	0.42
24:W:42:PRO:HD2	24:W:177:TRP:HE1	1.82	0.42
1:A:132:C:H2'	1:A:133:A:H8	1.84	0.42
1:A:738:C:H42	1:A:818:G:H1	1.68	0.42
1:A:751:G:H2'	1:A:773:G:H22	1.85	0.42
1:A:790:A:O2'	1:A:1704:U:OP1	2.30	0.42
1:A:1046:A:OP2	1:A:1200:G:N1	2.37	0.42
1:A:1425:C:H2'	1:A:1426:A:C8	2.54	0.42
1:A:1614:A:P	3:C:210:ARG:NH2	2.92	0.42
1:A:2282:G:H2'	1:A:2283:C:H5'	2.01	0.42
1:A:2635:C:N4	1:A:2636:G:O6	2.52	0.42
2:B:64:A:OP2	2:B:106:C:N4	2.51	0.42
3:C:210:ARG:HA	3:C:210:ARG:HD2	1.63	0.42
4:D:30:ALA:C	4:D:53:PHE:CZ	2.97	0.42
6:F:8:TYR:CD1	6:F:8:TYR:O	2.73	0.42
7:G:139:LYS:HA	7:G:142:VAL:HG12	2.02	0.42
9:K:40:VAL:HG22	9:K:59:LYS:HG2	2.01	0.42
11:N:50:LEU:HD23	11:N:50:LEU:HA	1.88	0.42
12:O:39:HIS:HD2	12:O:41:TYR:HE1	1.68	0.42
13:P:30:ARG:HA	13:P:47:GLU:HA	2.00	0.42
14:Q:110:ALA:O	14:Q:113:ALA:HB3	2.20	0.42
15:R:40:PHE:H	15:R:48:VAL:CG2	2.33	0.42
19:V:48:GLN:HE22	19:V:53:ILE:H	1.68	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:Y:17:LYS:HD3	22:Y:17:LYS:HA	1.87	0.42
24:W:30:LEU:CD1	24:W:133:LYS:HA	2.49	0.42
24:W:129:PRO:HD3	24:W:176:LEU:CA	2.50	0.42
1:A:134:C:H2'	1:A:135:U:C6	2.55	0.42
1:A:247:A:H62	1:A:257:G:H21	1.67	0.42
1:A:407:A:H2'	1:A:408:G:H8	1.85	0.42
1:A:456:A:H2'	1:A:457:G:C8	2.55	0.42
1:A:575:A:O2'	1:A:576:G:N2	2.53	0.42
1:A:639:C:C2	1:A:640:U:C5	3.07	0.42
1:A:827:G:H21	1:A:830:A:H62	1.67	0.42
1:A:1060:U:H2'	1:A:1061:A:H8	1.85	0.42
1:A:1240:U:H2'	1:A:1241:C:C6	2.55	0.42
1:A:1564:C:C2	1:A:1565:U:H5	2.36	0.42
1:A:2151:U:H2'	1:A:2152:A:C8	2.55	0.42
1:A:2539:C:H41	1:A:2604:C:H42	1.68	0.42
1:A:2664:U:C4	1:A:2665:U:C5	3.08	0.42
1:A:2671:G:H2'	1:A:2672:G:H8	1.85	0.42
2:B:112:C:H2'	2:B:113:A:H8	1.85	0.42
3:C:94:ILE:CG1	3:C:104:ILE:CD1	2.98	0.42
9:K:35:ILE:HD13	9:K:35:ILE:HA	1.90	0.42
12:O:107:LYS:O	12:O:111:ASP:OD2	2.38	0.42
13:P:62:PHE:CE2	13:P:79:VAL:HG22	2.55	0.42
13:P:78:PRO:HG2	13:P:81:THR:HB	2.02	0.42
14:Q:27:SER:HB3	14:Q:31:LEU:HD13	2.01	0.42
17:T:54:VAL:HG22	17:T:81:VAL:HG13	2.02	0.42
23:d:25:LYS:HD2	23:d:28:ARG:HD2	2.01	0.42
24:W:233:ASP:HB3	24:W:236:GLU:HB3	2.02	0.42
1:A:43:G:H3'	1:A:44:A:C8	2.55	0.41
1:A:303:G:H2'	1:A:304:G:C8	2.54	0.41
1:A:1108:G:H1'	1:A:1134:A:C6	2.54	0.41
1:A:1808:U:H5''	1:A:1809:A:H5'	2.01	0.41
1:A:2128:U:H2'	1:A:2129:G:C8	2.52	0.41
8:J:103:GLU:HG2	8:J:120:PHE:HE1	1.85	0.41
13:P:31:VAL:HG22	13:P:87:ILE:HG12	2.01	0.41
14:Q:74:LEU:HD23	14:Q:74:LEU:HA	1.92	0.41
21:b:27:MET:HE3	21:b:36:MET:CE	2.45	0.41
22:Y:10:THR:O	22:Y:14:ILE:N	2.48	0.41
1:A:190:G:C2	1:A:213:C:O2	2.73	0.41
1:A:1554:U:H5'	1:A:1555:A:C5	2.55	0.41
1:A:1846:G:OP1	3:C:87:ARG:NH2	2.50	0.41
1:A:2298:A:C2'	1:A:2299:G:H8	2.32	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2434:G:H2'	1:A:2440:A:H61	1.85	0.41
1:A:2557:U:H2'	1:A:2558:G:H2'	2.02	0.41
1:A:2769:A:N6	1:A:2770:A:N1	2.68	0.41
2:B:76:A:H62	2:B:96:G:H21	1.67	0.41
5:E:51:VAL:CG1	5:E:92:PRO:HD2	2.49	0.41
5:E:135:LYS:HD2	5:E:135:LYS:HA	1.90	0.41
9:K:69:ALA:HB1	9:K:105:GLU:CD	2.44	0.41
10:L:79:LEU:HD22	10:L:117:LEU:CB	2.43	0.41
13:P:31:VAL:O	13:P:46:PHE:N	2.52	0.41
14:Q:54:LYS:HB2	14:Q:54:LYS:HE3	1.83	0.41
16:S:83:LYS:O	16:S:84:ARG:NH1	2.44	0.41
1:A:5:A:H2'	1:A:6:A:H8	1.86	0.41
1:A:213:C:H2'	1:A:214:G:C8	2.55	0.41
1:A:992:G:H2'	1:A:993:A:H8	1.85	0.41
1:A:1858:A:H2'	1:A:1859:C:C6	2.56	0.41
1:A:2667:G:P	4:D:84:ARG:NH2	2.87	0.41
3:C:52:ARG:HH12	3:C:249:PRO:HG3	1.85	0.41
23:d:21:ARG:HD2	23:d:31:LEU:HD21	2.01	0.41
24:W:39:SER:O	24:W:128:ILE:HG13	2.21	0.41
24:W:44:ILE:HD12	24:W:44:ILE:HA	1.95	0.41
1:A:89:U:OP2	1:A:90:A:O2'	2.30	0.41
1:A:241:C:O2'	1:A:652:A:O2'	2.32	0.41
1:A:527:A:H4'	18:U:43:LYS:CG	2.50	0.41
1:A:528:G:O2'	1:A:552:G:N2	2.53	0.41
1:A:626:G:H2'	1:A:627:G:H8	1.85	0.41
1:A:1072:A:H61	1:A:1173:A:H3'	1.84	0.41
1:A:1177:G:N7	8:J:78:HIS:CE1	2.89	0.41
1:A:2072:C:OP1	1:A:2806:G:O2'	2.38	0.41
1:A:2559:U:O2	7:G:158:TYR:OH	2.38	0.41
3:C:16:MET:HE2	3:C:16:MET:HB2	1.88	0.41
5:E:53:ASN:HB3	5:E:56:GLU:HG2	2.03	0.41
6:F:38:MET:HB2	6:F:87:ALA:H	1.86	0.41
9:K:87:ILE:HG13	9:K:93:PRO:CA	2.50	0.41
14:Q:87:GLY:HA2	15:R:49:GLY:HA2	2.01	0.41
24:W:31:VAL:HG12	24:W:32:ASP:N	2.34	0.41
1:A:33:U:H2'	1:A:493:G:N2	2.35	0.41
1:A:705:A:C5	1:A:706:C:C6	3.08	0.41
1:A:925:A:N7	1:A:947:A:H1'	2.36	0.41
1:A:1178:U:H2'	1:A:1179:A:C8	2.55	0.41
1:A:1205:U:H2'	1:A:1206:G:H8	1.86	0.41
1:A:1324:G:N2	1:A:1367:G:O3'	2.46	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1711:G:N2	1:A:2023:C:C2	2.89	0.41
1:A:2132:A:C2	1:A:2215:U:O2	2.74	0.41
3:C:57:GLY:CA	3:C:214:LYS:O	2.65	0.41
5:E:36:ALA:O	5:E:40:GLN:N	2.45	0.41
7:G:60:LYS:HB3	7:G:60:LYS:HE3	1.71	0.41
7:G:88:LEU:HD13	7:G:149:ILE:HG21	2.02	0.41
16:S:86:ARG:HH22	16:S:96:ILE:HD11	1.70	0.41
18:U:10:MET:HE3	18:U:10:MET:HB3	1.74	0.41
24:W:41:ASN:HB3	24:W:44:ILE:HG22	2.03	0.41
1:A:1711:G:H4'	9:K:6:THR:CG2	2.47	0.41
1:A:2836:G:H2'	1:A:2837:A:C8	2.55	0.41
1:A:2886:C:H2'	1:A:2887:A:C8	2.53	0.41
3:C:228:ASN:OD1	3:C:229:ASP:N	2.54	0.41
8:J:56:ILE:HG22	8:J:124:ASN:HD22	1.85	0.41
10:L:104:LYS:HE3	10:L:106:ASN:ND2	2.35	0.41
24:W:214:GLU:HG2	24:W:230:ILE:HG21	2.03	0.41
1:A:180:G:H2'	1:A:181:G:C8	2.56	0.41
1:A:653:A:H62	1:A:665:G:N2	2.18	0.41
1:A:727:A:H2'	1:A:728:G:C8	2.54	0.41
1:A:1094:A:OP2	1:A:1156:G:N2	2.54	0.41
1:A:2082:G:H2'	1:A:2083:A:C8	2.53	0.41
1:A:2292:C:H2'	1:A:2293:C:C6	2.56	0.41
1:A:2295:A:C4	1:A:2301:U:N3	2.88	0.41
1:A:2648:U:H5'	4:D:156:LYS:HG3	2.03	0.41
6:F:17:MET:HE2	6:F:25:VAL:O	2.20	0.41
8:J:29:LEU:HG	8:J:29:LEU:H	1.53	0.41
10:L:74:TYR:OH	10:L:127:LYS:CG	2.65	0.41
13:P:32:HIS:CE1	13:P:45:ILE:HG13	2.56	0.41
14:Q:43:GLY:HA2	14:Q:46:ALA:HB3	2.02	0.41
16:S:83:LYS:HE2	16:S:83:LYS:HB3	1.93	0.41
18:U:79:THR:HB	18:U:94:ALA:CB	2.50	0.41
20:Z:5:GLU:HB2	20:Z:57:LYS:HG2	2.03	0.41
24:W:32:ASP:CB	24:W:131:VAL:CG2	2.98	0.41
24:W:32:ASP:HA	24:W:131:VAL:HG22	2.02	0.41
1:A:286:U:H3'	1:A:287:G:C8	2.52	0.41
1:A:861:C:C2	1:A:862:U:C5	3.09	0.41
1:A:1298:C:H2'	1:A:1299:G:C8	2.56	0.41
1:A:1735:A:O3'	24:W:271:LYS:NZ	2.54	0.41
1:A:2234:C:H2'	1:A:2235:G:C8	2.55	0.41
1:A:2280:G:H8	1:A:2280:G:P	2.44	0.41
1:A:2302:A:O2'	1:A:2303:A:H5'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:O:28:ARG:HG3	12:O:92:ASP:O	2.19	0.41
17:T:91:GLU:HG3	17:T:92:ILE:H	1.86	0.41
21:b:27:MET:HE3	21:b:27:MET:HB2	1.95	0.41
23:d:15:VAL:O	23:d:16:HIS:ND1	2.53	0.41
24:W:36:PRO:O	24:W:39:SER:OG	2.33	0.41
1:A:96:G:H2'	1:A:97:C:C6	2.56	0.41
1:A:216:A:H2'	1:A:217:G:C8	2.56	0.41
1:A:303:G:H2'	1:A:304:G:H8	1.85	0.41
1:A:497:G:H1	1:A:501:A:P	2.44	0.41
1:A:584:A:H3'	1:A:585:G:H8	1.86	0.41
1:A:794:U:H4'	16:S:89:ALA:HB3	2.03	0.41
1:A:908:A:H2'	1:A:909:G:O4'	2.20	0.41
1:A:1241:C:H42	1:A:1285:G:H1	1.67	0.41
1:A:1439:U:H2'	1:A:1440:G:C8	2.56	0.41
1:A:1497:G:H2'	1:A:1504:A:H61	1.86	0.41
1:A:1843:G:H3'	1:A:1844:A:H2'	2.02	0.41
1:A:2247:C:H2'	1:A:2248:G:C8	2.56	0.41
1:A:2281:G:O5'	1:A:2281:G:C8	2.71	0.41
1:A:2342:C:HO2'	6:F:37:ASN:CG	2.27	0.41
1:A:2473:G:OP2	5:E:68:LYS:NZ	2.36	0.41
1:A:2620:C:N4	1:A:2621:G:O6	2.53	0.41
1:A:2777:A:C2'	7:G:64:ALA:CB	2.99	0.41
2:B:70:G:H21	2:B:102:A:H62	1.67	0.41
4:D:16:PHE:O	13:P:15:GLN:NE2	2.54	0.41
4:D:36:LEU:HD23	4:D:36:LEU:HA	1.88	0.41
4:D:50:GLN:HG2	4:D:82:GLU:OE2	2.19	0.41
4:D:56:LYS:HD2	4:D:60:LEU:HB2	2.02	0.41
4:D:86:VAL:HG11	4:D:91:TYR:CE2	2.55	0.41
5:E:44:LEU:HD23	5:E:44:LEU:HA	1.83	0.41
6:F:13:ALA:CB	6:F:14:PRO:CD	2.95	0.41
6:F:67:VAL:CG2	6:F:84:PRO:CG	2.99	0.41
6:F:117:VAL:HB	6:F:118:SER:H	1.58	0.41
7:G:76:MET:HE2	7:G:76:MET:HB2	1.92	0.41
7:G:87:GLY:O	7:G:166:GLU:HG2	2.17	0.41
8:J:93:MET:HE3	8:J:101:MET:HB2	2.02	0.41
9:K:87:ILE:CG1	9:K:92:SER:O	2.69	0.41
12:O:75:THR:OG1	12:O:108:ALA:HB1	2.21	0.41
14:Q:69:ALA:O	14:Q:74:LEU:N	2.54	0.41
16:S:77:ASP:OD1	16:S:77:ASP:N	2.53	0.41
17:T:5:ARG:HH11	17:T:5:ARG:HG3	1.86	0.41
17:T:57:MET:HB3	17:T:57:MET:HE2	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:W:36:PRO:HB3	24:W:75:PHE:CE2	2.52	0.41
24:W:128:ILE:CG2	24:W:129:PRO:HD2	2.51	0.41
1:A:1314:A:N3	1:A:1315:G:H1'	2.36	0.41
1:A:1644:C:C2	1:A:1645:C:C5	3.08	0.41
1:A:1672:A:H2'	1:A:1673:G:C8	2.55	0.41
1:A:1834:C:O3'	3:C:250:TRP:NE1	2.54	0.41
1:A:2536:C:C4	1:A:2611:G:N1	2.89	0.41
3:C:53:HIS:CB	3:C:217:ARG:O	2.66	0.41
3:C:68:LYS:O	3:C:69:ARG:O	2.38	0.41
7:G:90:LEU:HD22	7:G:95:TYR:HB3	2.02	0.41
8:J:45:TYR:O	14:Q:64:ARG:NE	2.38	0.41
24:W:75:PHE:HA	24:W:75:PHE:HD1	1.79	0.41
1:A:89:U:H3'	1:A:90:A:H8	1.85	0.40
1:A:217:G:N3	1:A:219:A:O2'	2.53	0.40
1:A:789:C:H42	1:A:802:G:H1	1.69	0.40
1:A:1326:A:N6	11:N:109:GLY:O	2.44	0.40
1:A:1572:G:O2'	1:A:1573:C:O5'	2.36	0.40
1:A:1694:G:H2'	1:A:1695:A:H8	1.86	0.40
1:A:2293:C:H2'	1:A:2294:U:C6	2.56	0.40
1:A:2707:C:H2'	1:A:2708:A:H8	1.86	0.40
4:D:55:ASP:CA	4:D:77:LYS:CA	2.87	0.40
4:D:75:ALA:HA	4:D:76:PRO:HD3	1.93	0.40
5:E:126:LEU:HD23	5:E:126:LEU:HA	1.87	0.40
8:J:14:ARG:HD3	8:J:14:ARG:HA	1.85	0.40
11:N:119:LEU:C	11:N:120:VAL:CG2	2.94	0.40
14:Q:5:LYS:HD2	14:Q:5:LYS:HA	1.91	0.40
16:S:70:VAL:HG12	16:S:71:ILE:H	1.81	0.40
20:Z:51:SER:O	20:Z:54:VAL:O	2.39	0.40
1:A:217:G:H2'	1:A:218:G:C8	2.56	0.40
1:A:527:A:C4'	18:U:43:LYS:HE2	2.51	0.40
1:A:1073:A:N6	1:A:1172:A:O4'	2.54	0.40
1:A:1359:G:H22	1:A:1370:C:H5	1.69	0.40
1:A:2103:U:O2'	1:A:2626:G:N3	2.55	0.40
1:A:2536:C:O5'	1:A:2536:C:C6	2.74	0.40
1:A:2705:C:H2'	1:A:2706:G:C8	2.56	0.40
4:D:2:THR:OG1	4:D:86:VAL:HA	2.21	0.40
6:F:30:LYS:HE3	6:F:30:LYS:HB3	1.26	0.40
12:O:95:PHE:CD1	12:O:110:ALA:HB2	2.56	0.40
13:P:77:PHE:HD1	13:P:77:PHE:HA	1.74	0.40
13:P:99:LYS:HD2	13:P:101:TYR:HE1	1.84	0.40
22:Y:21:LEU:HD13	22:Y:53:MET:HE2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:683:A:C8	10:L:114:ASN:ND2	2.86	0.40
1:A:684:G:C6	1:A:697:G:C6	3.10	0.40
1:A:783:C:O2	1:A:783:C:H2'	2.22	0.40
1:A:999:A:H2'	1:A:1000:G:C8	2.57	0.40
1:A:1176:U:N3	1:A:2055:U:OP2	2.54	0.40
1:A:1649:C:O2'	1:A:1655:A:N6	2.54	0.40
1:A:1862:C:H3'	1:A:1862:C:C6	2.56	0.40
1:A:2275:G:N2	1:A:2455:A:H1'	2.36	0.40
1:A:2777:A:H2'	7:G:64:ALA:HB1	2.02	0.40
1:A:2901:G:H2'	1:A:2902:A:C8	2.57	0.40
2:B:55:A:O2'	6:F:27:GLN:NE2	2.53	0.40
3:C:24:ILE:HG13	3:C:81:VAL:HG12	2.03	0.40
3:C:154:LEU:H	3:C:154:LEU:HG	1.55	0.40
6:F:118:SER:HB2	6:F:128:TYR:HE1	1.87	0.40
12:O:31:LEU:HD12	12:O:31:LEU:HA	1.99	0.40
13:P:10:ASP:N	13:P:10:ASP:OD1	2.53	0.40
24:W:6:PHE:CD2	24:W:176:LEU:HD11	2.56	0.40
1:A:211:C:N3	1:A:212:C:C5	2.89	0.40
1:A:509:C:H2'	1:A:510:G:H8	1.86	0.40
1:A:1314:A:H8	1:A:1314:A:H5''	1.86	0.40
1:A:1537:G:H2'	1:A:1538:G:H8	1.86	0.40
1:A:1601:A:N6	1:A:1603:U:O2	2.54	0.40
1:A:2008:C:H2'	1:A:2009:G:C8	2.56	0.40
3:C:37:LEU:HD12	3:C:37:LEU:HA	1.96	0.40
3:C:124:ILE:HG22	3:C:124:ILE:O	2.21	0.40
9:K:19:VAL:HG13	9:K:41:CYS:HB2	2.03	0.40
18:U:96:LYS:HA	18:U:96:LYS:HD3	1.60	0.40
19:V:53:ILE:CD1	19:V:67:LEU:HD12	2.50	0.40
24:W:259:THR:HA	24:W:262:VAL:HG22	2.02	0.40
1:A:293:U:H2'	1:A:294:G:C8	2.56	0.40
1:A:380:C:H4'	18:U:2:HIS:CE1	2.57	0.40
1:A:1507:U:H2'	1:A:1508:C:H6	1.87	0.40
12:O:35:ARG:HH12	12:O:105:ARG:CZ	2.19	0.40
16:S:20:VAL:O	16:S:20:VAL:CG1	2.69	0.40
24:W:146:ALA:O	24:W:147:LYS:HG3	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	256/277 (92%)	230 (90%)	24 (9%)	2 (1%)	16	52
4	D	204/209 (98%)	176 (86%)	27 (13%)	1 (0%)	24	62
5	E	193/207 (93%)	167 (86%)	26 (14%)	0	100	100
6	F	131/179 (73%)	114 (87%)	14 (11%)	3 (2%)	5	28
7	G	107/179 (60%)	93 (87%)	14 (13%)	0	100	100
8	J	139/145 (96%)	122 (88%)	17 (12%)	0	100	100
9	K	120/122 (98%)	100 (83%)	20 (17%)	0	100	100
10	L	118/146 (81%)	101 (86%)	16 (14%)	1 (1%)	16	52
11	N	116/120 (97%)	108 (93%)	8 (7%)	0	100	100
12	O	92/120 (77%)	84 (91%)	8 (9%)	0	100	100
13	P	112/115 (97%)	98 (88%)	13 (12%)	1 (1%)	14	49
14	Q	115/118 (98%)	105 (91%)	10 (9%)	0	100	100
15	R	98/102 (96%)	82 (84%)	15 (15%)	1 (1%)	12	47
16	S	107/113 (95%)	97 (91%)	9 (8%)	1 (1%)	14	49
17	T	88/95 (93%)	77 (88%)	11 (12%)	0	100	100
18	U	85/103 (82%)	62 (73%)	19 (22%)	4 (5%)	2	16
19	V	74/94 (79%)	67 (90%)	7 (10%)	0	100	100
20	Z	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
21	b	51/59 (86%)	42 (82%)	9 (18%)	0	100	100
22	Y	63/66 (96%)	55 (87%)	8 (13%)	0	100	100
23	d	41/44 (93%)	38 (93%)	3 (7%)	0	100	100
24	W	242/282 (86%)	213 (88%)	26 (11%)	3 (1%)	10	42
All	All	2608/2954 (88%)	2283 (88%)	308 (12%)	17 (1%)	20	55

All (17) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	R	24	LYS
16	S	90	MET
18	U	82	GLY
24	W	172	THR
3	C	215	GLY
4	D	206	VAL
6	F	117	VAL
18	U	47	PRO
24	W	173	PRO
3	C	39	LYS
6	F	32	GLU
24	W	131	VAL
13	P	108	GLY
18	U	6	GLY
18	U	91	VAL
6	F	25	VAL
10	L	84	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	215/225 (96%)	208 (97%)	7 (3%)	33	55
4	D	167/170 (98%)	149 (89%)	18 (11%)	6	22
5	E	164/170 (96%)	162 (99%)	2 (1%)	63	73
6	F	120/154 (78%)	101 (84%)	19 (16%)	2	13
7	G	88/151 (58%)	83 (94%)	5 (6%)	18	41
8	J	120/123 (98%)	112 (93%)	8 (7%)	15	37
9	K	101/101 (100%)	95 (94%)	6 (6%)	18	40
10	L	93/110 (84%)	71 (76%)	22 (24%)	1	5
11	N	98/100 (98%)	97 (99%)	1 (1%)	68	76
12	O	77/93 (83%)	66 (86%)	11 (14%)	3	15
13	P	99/100 (99%)	93 (94%)	6 (6%)	17	39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	Q	96/97 (99%)	89 (93%)	7 (7%)	13	34
15	R	83/84 (99%)	79 (95%)	4 (5%)	23	45
16	S	90/93 (97%)	79 (88%)	11 (12%)	5	19
17	T	81/85 (95%)	77 (95%)	4 (5%)	22	44
18	U	78/87 (90%)	63 (81%)	15 (19%)	1	9
19	V	61/74 (82%)	57 (93%)	4 (7%)	15	37
20	Z	52/53 (98%)	50 (96%)	2 (4%)	29	50
21	b	47/53 (89%)	39 (83%)	8 (17%)	2	11
22	Y	56/57 (98%)	54 (96%)	2 (4%)	31	52
23	d	38/39 (97%)	38 (100%)	0	100	100
24	W	205/244 (84%)	188 (92%)	17 (8%)	10	30
All	All	2229/2463 (90%)	2050 (92%)	179 (8%)	13	31

All (179) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	39	LYS
3	C	154	LEU
3	C	156	ARG
3	C	171	TYR
3	C	210	ARG
3	C	217	ARG
3	C	267	ASP
4	D	6	LEU
4	D	25	VAL
4	D	55	ASP
4	D	56	LYS
4	D	57	ARG
4	D	77	LYS
4	D	78	ARG
4	D	81	LYS
4	D	82	GLU
4	D	86	VAL
4	D	87	GLU
4	D	88	MET
4	D	89	ASP
4	D	91	TYR
4	D	95	GLN

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Mol	Chain	Res	Type
4	D	107	ILE
4	D	159	LEU
4	D	207	LYS
5	E	89	VAL
5	E	146	LEU
6	F	12	ILE
6	F	16	LEU
6	F	17	MET
6	F	30	LYS
6	F	32	GLU
6	F	83	MET
6	F	89	VAL
6	F	91	LEU
6	F	95	ARG
6	F	96	MET
6	F	103	LEU
6	F	104	ILE
6	F	106	VAL
6	F	108	LEU
6	F	111	VAL
6	F	112	ARG
6	F	119	LYS
6	F	157	VAL
6	F	167	ARG
7	G	60	LYS
7	G	63	ARG
7	G	76	MET
7	G	78	GLU
7	G	165	TYR
8	J	25	THR
8	J	26	LEU
8	J	29	LEU
8	J	54	HIS
8	J	74	ILE
8	J	80	GLN
8	J	115	LEU
8	J	121	LYS
9	K	25	LEU
9	K	28	SER
9	K	31	LYS
9	K	35	ILE
9	K	84	CYS

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Mol	Chain	Res	Type
9	K	121	VAL
10	L	33	LYS
10	L	36	LYS
10	L	63	LYS
10	L	69	ILE
10	L	70	ASN
10	L	71	ARG
10	L	73	GLU
10	L	74	TYR
10	L	78	ASN
10	L	79	LEU
10	L	80	ASP
10	L	87	GLU
10	L	89	THR
10	L	90	GLU
10	L	99	THR
10	L	109	VAL
10	L	116	LYS
10	L	118	GLU
10	L	120	LYS
10	L	121	LEU
10	L	134	GLU
10	L	137	GLU
11	N	48	ILE
12	O	7	LYS
12	O	19	ARG
12	O	33	VAL
12	O	61	LYS
12	O	64	ASN
12	O	65	VAL
12	O	66	GLU
12	O	67	SER
12	O	70	ASP
12	O	102	TYR
12	O	107	LYS
13	P	45	ILE
13	P	49	VAL
13	P	50	VAL
13	P	77	PHE
13	P	81	THR
13	P	113	ILE
14	Q	13	ARG

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Mol	Chain	Res	Type
14	Q	15	LYS
14	Q	17	VAL
14	Q	97	ASP
14	Q	98	LEU
14	Q	101	ASN
14	Q	107	ASN
15	R	6	LYS
15	R	10	LYS
15	R	22	ILE
15	R	25	LEU
16	S	38	LEU
16	S	39	THR
16	S	41	ARG
16	S	44	SER
16	S	46	ILE
16	S	49	LYS
16	S	50	VAL
16	S	51	LEU
16	S	52	LYS
16	S	53	SER
16	S	55	ILE
17	T	3	ASP
17	T	5	ARG
17	T	6	ASP
17	T	8	LEU
18	U	4	LYS
18	U	5	LYS
18	U	9	VAL
18	U	10	MET
18	U	46	LYS
18	U	81	VAL
18	U	84	LYS
18	U	89	LYS
18	U	90	LYS
18	U	91	VAL
18	U	92	ARG
18	U	95	LYS
18	U	96	LYS
18	U	97	SER
18	U	100	VAL
19	V	39	VAL
19	V	48	GLN

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Mol	Chain	Res	Type
19	V	83	ASP
19	V	87	VAL
20	Z	54	VAL
20	Z	59	GLN
21	b	29	GLU
21	b	30	CYS
21	b	32	SER
21	b	35	GLU
21	b	37	LYS
21	b	38	LEU
21	b	52	LYS
21	b	54	ILE
22	Y	1	MET
22	Y	5	GLU
24	W	17	VAL
24	W	67	VAL
24	W	69	GLN
24	W	84	SER
24	W	94	ASN
24	W	103	ILE
24	W	104	LEU
24	W	124	LEU
24	W	126	ILE
24	W	131	VAL
24	W	154	ILE
24	W	155	THR
24	W	176	LEU
24	W	177	TRP
24	W	275	LEU
24	W	276	SER
24	W	277	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (46) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	90	ASN
3	C	134	ASN
3	C	197	ASN
4	D	14	GLN
4	D	33	ASN
4	D	120	GLN
4	D	135	HIS

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Mol	Chain	Res	Type
4	D	152	ASN
5	E	40	GLN
5	E	179	ASN
6	F	37	ASN
7	G	129	GLN
8	J	41	HIS
8	J	78	HIS
8	J	124	ASN
9	K	3	GLN
9	K	4	GLN
10	L	17	ASN
10	L	78	ASN
10	L	106	ASN
11	N	57	HIS
11	N	61	GLN
11	N	81	GLN
13	P	44	GLN
13	P	80	HIS
14	Q	37	GLN
14	Q	44	ASN
14	Q	107	ASN
14	Q	116	GLN
14	Q	118	ASN
15	R	86	GLN
16	S	60	HIS
19	V	20	ASN
20	Z	19	GLN
20	Z	52	HIS
20	Z	59	GLN
22	Y	16	GLN
22	Y	31	GLN
22	Y	36	GLN
23	d	6	GLN
23	d	9	ASN
23	d	26	ASN
24	W	9	HIS
24	W	70	GLN
24	W	138	ASN
24	W	144	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2643/2927 (90%)	957 (36%)	55 (2%)
2	B	111/119 (93%)	38 (34%)	3 (2%)
All	All	2754/3046 (90%)	995 (36%)	58 (2%)

All (995) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	7	G
1	A	9	U
1	A	11	G
1	A	13	A
1	A	23	G
1	A	25	U
1	A	28	A
1	A	31	C
1	A	32	C
1	A	33	U
1	A	34	U
1	A	35	G
1	A	36	G
1	A	38	A
1	A	39	C
1	A	43	G
1	A	44	A
1	A	45	G
1	A	46	C
1	A	48	G
1	A	49	A
1	A	51	G
1	A	59	G
1	A	60	G
1	A	61	A
1	A	63	G
1	A	71	A
1	A	75	G
1	A	76	C
1	A	79	C
1	A	83	G
1	A	87	U
1	A	89	U
1	A	90	A
1	A	91	A
1	A	92	G

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Mol	Chain	Res	Type
1	A	93	C
1	A	94	A
1	A	98	U
1	A	100	U
1	A	101	G
1	A	109	G
1	A	113	U
1	A	117	A
1	A	118	A
1	A	119	U
1	A	124	A
1	A	125	A
1	A	126	A
1	A	127	C
1	A	128	C
1	A	130	A
1	A	145	G
1	A	150	A
1	A	156	A
1	A	159	U
1	A	162	A
1	A	163	U
1	A	164	U
1	A	166	A
1	A	175	G
1	A	176	A
1	A	177	G
1	A	178	A
1	A	179	A
1	A	180	G
1	A	181	G
1	A	182	C
1	A	184	G
1	A	185	A
1	A	191	G
1	A	196	U
1	A	199	A
1	A	203	U
1	A	207	A
1	A	215	G
1	A	216	A
1	A	219	A

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Mol	Chain	Res	Type
1	A	224	A
1	A	225	A
1	A	226	A
1	A	227	G
1	A	230	A
1	A	231	A
1	A	233	G
1	A	234	C
1	A	235	G
1	A	244	A
1	A	245	G
1	A	246	U
1	A	251	G
1	A	252	C
1	A	253	G
1	A	254	A
1	A	255	G
1	A	258	A
1	A	267	C
1	A	268	A
1	A	269	G
1	A	270	C
1	A	271	C
1	A	272	C
1	A	275	A
1	A	282	G
1	A	283	G
1	A	284	C
1	A	286	U
1	A	289	C
1	A	290	U
1	A	291	C
1	A	295	G
1	A	298	U
1	A	299	U
1	A	300	G
1	A	301	U
1	A	302	A
1	A	306	C
1	A	310	C
1	A	312	G
1	A	313	U

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Mol	Chain	Res	Type
1	A	314	A
1	A	315	C
1	A	320	U
1	A	321	U
1	A	322	A
1	A	323	C
1	A	324	A
1	A	325	A
1	A	326	A
1	A	327	G
1	A	328	G
1	A	329	A
1	A	331	C
1	A	338	G
1	A	344	G
1	A	345	A
1	A	346	G
1	A	354	A
1	A	360	C
1	A	362	C
1	A	367	G
1	A	368	G
1	A	373	A
1	A	374	A
1	A	376	A
1	A	378	C
1	A	379	C
1	A	380	C
1	A	382	G
1	A	388	A
1	A	389	A
1	A	390	A
1	A	393	U
1	A	394	U
1	A	395	C
1	A	396	G
1	A	397	U
1	A	404	C
1	A	405	U
1	A	406	G
1	A	410	G
1	A	411	G

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Mol	Chain	Res	Type
1	A	412	A
1	A	417	G
1	A	418	A
1	A	419	G
1	A	420	U
1	A	431	A
1	A	433	G
1	A	434	U
1	A	435	G
1	A	436	A
1	A	437	A
1	A	438	A
1	A	445	C
1	A	451	C
1	A	452	C
1	A	469	A
1	A	470	A
1	A	474	U
1	A	481	U
1	A	483	C
1	A	484	C
1	A	485	U
1	A	489	G
1	A	490	A
1	A	495	U
1	A	496	A
1	A	498	U
1	A	499	G
1	A	501	A
1	A	502	C
1	A	503	C
1	A	504	A
1	A	508	C
1	A	514	G
1	A	524	A
1	A	525	A
1	A	526	A
1	A	528	G
1	A	537	A
1	A	538	A
1	A	542	G
1	A	544	G

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Mol	Chain	Res	Type
1	A	547	A
1	A	548	A
1	A	549	A
1	A	550	G
1	A	551	A
1	A	554	U
1	A	555	C
1	A	556	C
1	A	558	G
1	A	561	A
1	A	564	G
1	A	571	U
1	A	573	C
1	A	576	G
1	A	577	U
1	A	578	A
1	A	579	G
1	A	584	A
1	A	588	C
1	A	590	U
1	A	591	U
1	A	592	A
1	A	594	C
1	A	595	G
1	A	598	U
1	A	599	G
1	A	606	U
1	A	607	G
1	A	612	U
1	A	614	G
1	A	616	A
1	A	617	G
1	A	619	A
1	A	630	A
1	A	631	G
1	A	633	U
1	A	637	A
1	A	639	C
1	A	642	G
1	A	645	C
1	A	646	A
1	A	648	G

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Mol	Chain	Res	Type
1	A	649	G
1	A	650	U
1	A	651	U
1	A	656	A
1	A	657	G
1	A	658	A
1	A	660	G
1	A	661	A
1	A	664	C
1	A	665	G
1	A	666	G
1	A	667	A
1	A	668	G
1	A	673	A
1	A	674	G
1	A	680	G
1	A	683	A
1	A	684	G
1	A	689	A
1	A	691	U
1	A	692	A
1	A	700	U
1	A	701	G
1	A	702	A
1	A	703	G
1	A	706	C
1	A	711	U
1	A	713	G
1	A	716	G
1	A	717	A
1	A	718	C
1	A	724	A
1	A	729	G
1	A	731	G
1	A	732	A
1	A	733	U
1	A	734	C
1	A	742	G
1	A	747	G
1	A	758	A
1	A	764	C
1	A	765	A

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Mol	Chain	Res	Type
1	A	766	C
1	A	769	A
1	A	773	G
1	A	774	A
1	A	775	G
1	A	776	G
1	A	777	C
1	A	782	A
1	A	783	C
1	A	784	C
1	A	785	C
1	A	787	C
1	A	788	G
1	A	792	G
1	A	793	U
1	A	794	U
1	A	795	G
1	A	796	A
1	A	799	A
1	A	811	A
1	A	812	G
1	A	817	G
1	A	822	G
1	A	823	G
1	A	825	G
1	A	829	A
1	A	830	A
1	A	831	U
1	A	832	G
1	A	835	A
1	A	836	A
1	A	838	C
1	A	843	C
1	A	847	A
1	A	852	G
1	A	853	C
1	A	856	G
1	A	858	U
1	A	859	C
1	A	866	A
1	A	872	C
1	A	874	U

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Mol	Chain	Res	Type
1	A	877	G
1	A	878	G
1	A	881	U
1	A	882	A
1	A	886	U
1	A	890	G
1	A	892	U
1	A	895	G
1	A	896	A
1	A	898	U
1	A	899	C
1	A	903	G
1	A	906	G
1	A	907	U
1	A	908	A
1	A	909	G
1	A	910	A
1	A	912	C
1	A	914	C
1	A	918	U
1	A	919	U
1	A	921	G
1	A	924	U
1	A	925	A
1	A	927	G
1	A	949	U
1	A	951	C
1	A	954	U
1	A	956	A
1	A	957	A
1	A	959	C
1	A	964	A
1	A	970	A
1	A	972	U
1	A	974	A
1	A	975	C
1	A	976	U
1	A	978	A
1	A	981	C
1	A	987	A
1	A	988	G
1	A	990	C

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Mol	Chain	Res	Type
1	A	991	A
1	A	992	G
1	A	1004	U
1	A	1005	A
1	A	1007	G
1	A	1008	A
1	A	1016	U
1	A	1019	A
1	A	1020	A
1	A	1028	C
1	A	1029	A
1	A	1030	G
1	A	1031	C
1	A	1034	A
1	A	1035	G
1	A	1037	C
1	A	1042	A
1	A	1043	G
1	A	1054	A
1	A	1055	A
1	A	1056	A
1	A	1058	U
1	A	1059	A
1	A	1063	G
1	A	1067	A
1	A	1068	G
1	A	1069	U
1	A	1070	G
1	A	1071	G
1	A	1072	A
1	A	1073	A
1	A	1074	A
1	A	1079	U
1	A	1092	A
1	A	1093	G
1	A	1096	A
1	A	1098	C
1	A	1102	G
1	A	1104	U
1	A	1107	U
1	A	1108	G
1	A	1117	G

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Mol	Chain	Res	Type
1	A	1128	U
1	A	1129	U
1	A	1130	A
1	A	1131	A
1	A	1134	A
1	A	1135	G
1	A	1148	C
1	A	1151	U
1	A	1153	G
1	A	1154	U
1	A	1158	G
1	A	1159	U
1	A	1168	G
1	A	1173	A
1	A	1174	A
1	A	1175	A
1	A	1176	U
1	A	1177	G
1	A	1178	U
1	A	1179	A
1	A	1180	C
1	A	1181	C
1	A	1182	G
1	A	1185	G
1	A	1188	A
1	A	1189	A
1	A	1190	A
1	A	1193	U
1	A	1194	A
1	A	1201	A
1	A	1202	A
1	A	1208	G
1	A	1209	G
1	A	1215	U
1	A	1222	A
1	A	1223	C
1	A	1227	G
1	A	1236	G
1	A	1246	G
1	A	1247	G
1	A	1248	C
1	A	1250	G

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Mol	Chain	Res	Type
1	A	1251	U
1	A	1252	G
1	A	1258	A
1	A	1259	G
1	A	1267	G
1	A	1269	A
1	A	1278	G
1	A	1279	C
1	A	1286	A
1	A	1288	G
1	A	1289	U
1	A	1293	A
1	A	1295	U
1	A	1296	G
1	A	1299	G
1	A	1305	A
1	A	1306	G
1	A	1311	G
1	A	1312	A
1	A	1313	A
1	A	1314	A
1	A	1315	G
1	A	1317	G
1	A	1326	A
1	A	1327	U
1	A	1335	A
1	A	1339	A
1	A	1340	A
1	A	1341	U
1	A	1342	G
1	A	1344	C
1	A	1345	U
1	A	1346	A
1	A	1350	U
1	A	1352	U
1	A	1353	C
1	A	1360	A
1	A	1363	G
1	A	1364	C
1	A	1367	G
1	A	1368	U
1	A	1369	C

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Mol	Chain	Res	Type
1	A	1372	C
1	A	1376	G
1	A	1380	U
1	A	1384	C
1	A	1388	A
1	A	1398	A
1	A	1404	A
1	A	1406	A
1	A	1417	A
1	A	1418	U
1	A	1423	A
1	A	1424	A
1	A	1427	G
1	A	1430	U
1	A	1431	G
1	A	1434	A
1	A	1435	U
1	A	1436	U
1	A	1439	U
1	A	1441	U
1	A	1442	A
1	A	1448	U
1	A	1449	C
1	A	1450	C
1	A	1455	C
1	A	1456	A
1	A	1459	U
1	A	1460	G
1	A	1462	G
1	A	1464	A
1	A	1466	U
1	A	1472	G
1	A	1473	A
1	A	1474	C
1	A	1490	A
1	A	1495	C
1	A	1497	G
1	A	1498	U
1	A	1499	A
1	A	1500	U
1	A	1501	U
1	A	1502	G

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Mol	Chain	Res	Type
1	A	1503	G
1	A	1505	U
1	A	1506	A
1	A	1507	U
1	A	1512	G
1	A	1513	U
1	A	1516	A
1	A	1519	C
1	A	1520	A
1	A	1521	G
1	A	1528	U
1	A	1529	G
1	A	1530	G
1	A	1535	U
1	A	1536	A
1	A	1539	C
1	A	1540	A
1	A	1541	A
1	A	1543	U
1	A	1544	C
1	A	1545	C
1	A	1553	A
1	A	1554	U
1	A	1555	A
1	A	1556	A
1	A	1561	G
1	A	1562	A
1	A	1565	U
1	A	1570	U
1	A	1573	C
1	A	1576	G
1	A	1578	G
1	A	1582	U
1	A	1584	U
1	A	1585	A
1	A	1586	G
1	A	1587	U
1	A	1589	G
1	A	1592	A
1	A	1596	U
1	A	1601	A
1	A	1606	A

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Mol	Chain	Res	Type
1	A	1607	C
1	A	1608	A
1	A	1615	A
1	A	1617	A
1	A	1626	U
1	A	1629	C
1	A	1631	A
1	A	1632	G
1	A	1634	U
1	A	1636	A
1	A	1638	A
1	A	1643	C
1	A	1644	C
1	A	1651	G
1	A	1652	C
1	A	1653	A
1	A	1654	A
1	A	1655	A
1	A	1656	C
1	A	1657	C
1	A	1658	G
1	A	1660	C
1	A	1661	A
1	A	1667	A
1	A	1668	G
1	A	1674	G
1	A	1685	A
1	A	1688	G
1	A	1690	G
1	A	1692	U
1	A	1693	C
1	A	1696	G
1	A	1697	A
1	A	1707	U
1	A	1708	U
1	A	1712	G
1	A	1713	A
1	A	1714	A
1	A	1719	G
1	A	1726	G
1	A	1727	A
1	A	1739	C

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Mol	Chain	Res	Type
1	A	1745	A
1	A	1752	G
1	A	1756	U
1	A	1758	U
1	A	1759	U
1	A	1762	G
1	A	1763	G
1	A	1771	C
1	A	1774	A
1	A	1776	A
1	A	1777	G
1	A	1778	A
1	A	1779	G
1	A	1780	C
1	A	1782	G
1	A	1785	G
1	A	1787	G
1	A	1788	A
1	A	1790	U
1	A	1791	A
1	A	1792	G
1	A	1793	G
1	A	1796	C
1	A	1797	A
1	A	1802	A
1	A	1803	C
1	A	1805	G
1	A	1808	U
1	A	1810	G
1	A	1811	C
1	A	1813	A
1	A	1815	A
1	A	1816	A
1	A	1818	A
1	A	1829	C
1	A	1830	G
1	A	1831	A
1	A	1832	A
1	A	1834	C
1	A	1837	U
1	A	1838	A
1	A	1839	A

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Mol	Chain	Res	Type
1	A	1844	A
1	A	1849	U
1	A	2001	G
1	A	2006	A
1	A	2009	G
1	A	2010	A
1	A	2011	U
1	A	2014	G
1	A	2015	G
1	A	2021	G
1	A	2022	U
1	A	2024	U
1	A	2026	A
1	A	2031	G
1	A	2032	A
1	A	2052	A
1	A	2059	A
1	A	2060	A
1	A	2062	A
1	A	2064	G
1	A	2065	C
1	A	2068	G
1	A	2072	C
1	A	2081	G
1	A	2084	C
1	A	2085	G
1	A	2086	G
1	A	2092	C
1	A	2093	C
1	A	2096	G
1	A	2097	U
1	A	2098	G
1	A	2105	U
1	A	2109	G
1	A	2111	A
1	A	2116	G
1	A	2121	U
1	A	2122	G
1	A	2124	A
1	A	2128	U
1	A	2131	U
1	A	2132	A

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Mol	Chain	Res	Type
1	A	2135	G
1	A	2136	C
1	A	2146	A
1	A	2147	U
1	A	2148	A
1	A	2149	G
1	A	2151	U
1	A	2155	A
1	A	2156	G
1	A	2157	C
1	A	2158	C
1	A	2159	U
1	A	2161	G
1	A	2162	G
1	A	2163	A
1	A	2165	A
1	A	2166	C
1	A	2168	G
1	A	2169	G
1	A	2178	C
1	A	2183	G
1	A	2187	A
1	A	2188	G
1	A	2190	C
1	A	2199	G
1	A	2200	A
1	A	2201	U
1	A	2202	A
1	A	2203	C
1	A	2217	U
1	A	2221	C
1	A	2222	C
1	A	2223	U
1	A	2227	A
1	A	2232	G
1	A	2233	C
1	A	2235	G
1	A	2240	U
1	A	2241	A
1	A	2242	U
1	A	2243	C
1	A	2244	G

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Mol	Chain	Res	Type
1	A	2246	G
1	A	2253	G
1	A	2254	A
1	A	2255	C
1	A	2260	U
1	A	2264	G
1	A	2267	G
1	A	2268	G
1	A	2274	U
1	A	2276	A
1	A	2283	C
1	A	2288	G
1	A	2291	U
1	A	2297	A
1	A	2301	U
1	A	2303	A
1	A	2304	C
1	A	2308	G
1	A	2311	G
1	A	2312	C
1	A	2315	A
1	A	2325	U
1	A	2328	G
1	A	2334	U
1	A	2335	U
1	A	2336	G
1	A	2337	G
1	A	2339	A
1	A	2340	A
1	A	2341	U
1	A	2342	C
1	A	2343	A
1	A	2344	U
1	A	2345	U
1	A	2346	C
1	A	2347	G
1	A	2348	C
1	A	2349	A
1	A	2351	A
1	A	2352	G
1	A	2356	A
1	A	2357	A

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Mol	Chain	Res	Type
1	A	2363	C
1	A	2364	A
1	A	2365	A
1	A	2373	U
1	A	2374	G
1	A	2375	A
1	A	2376	C
1	A	2377	U
1	A	2379	C
1	A	2387	A
1	A	2400	G
1	A	2401	G
1	A	2411	G
1	A	2412	G
1	A	2414	C
1	A	2420	G
1	A	2421	A
1	A	2430	U
1	A	2431	U
1	A	2435	C
1	A	2448	U
1	A	2452	U
1	A	2453	C
1	A	2454	A
1	A	2455	A
1	A	2456	C
1	A	2457	G
1	A	2458	G
1	A	2459	A
1	A	2460	U
1	A	2464	A
1	A	2468	A
1	A	2470	C
1	A	2541	C
1	A	2542	A
1	A	2543	U
1	A	2546	C
1	A	2547	A
1	A	2548	U
1	A	2549	C
1	A	2554	G
1	A	2556	C

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Mol	Chain	Res	Type
1	A	2557	U
1	A	2558	G
1	A	2559	U
1	A	2560	A
1	A	2561	G
1	A	2569	C
1	A	2572	G
1	A	2573	G
1	A	2575	U
1	A	2576	U
1	A	2579	G
1	A	2580	C
1	A	2581	U
1	A	2582	G
1	A	2583	U
1	A	2585	C
1	A	2593	A
1	A	2594	A
1	A	2595	A
1	A	2596	G
1	A	2597	C
1	A	2602	C
1	A	2603	G
1	A	2607	G
1	A	2610	G
1	A	2611	G
1	A	2616	A
1	A	2618	A
1	A	2619	A
1	A	2620	C
1	A	2621	G
1	A	2628	G
1	A	2631	A
1	A	2638	U
1	A	2639	C
1	A	2640	C
1	A	2642	U
1	A	2643	A
1	A	2644	U
1	A	2648	U
1	A	2650	G
1	A	2652	G

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Mol	Chain	Res	Type
1	A	2658	A
1	A	2659	G
1	A	2661	A
1	A	2663	A
1	A	2665	U
1	A	2668	A
1	A	2674	G
1	A	2675	C
1	A	2676	U
1	A	2677	G
1	A	2680	C
1	A	2686	A
1	A	2687	C
1	A	2703	G
1	A	2714	G
1	A	2717	G
1	A	2718	U
1	A	2719	A
1	A	2720	C
1	A	2728	U
1	A	2730	U
1	A	2731	G
1	A	2741	U
1	A	2755	U
1	A	2762	A
1	A	2764	G
1	A	2765	G
1	A	2771	G
1	A	2773	G
1	A	2775	U
1	A	2776	G
1	A	2779	A
1	A	2780	G
1	A	2784	C
1	A	2785	U
1	A	2786	A
1	A	2787	A
1	A	2790	A
1	A	2793	A
1	A	2795	G
1	A	2797	C
1	A	2804	A

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Mol	Chain	Res	Type
1	A	2805	A
1	A	2807	A
1	A	2808	U
1	A	2809	G
1	A	2813	U
1	A	2817	C
1	A	2818	C
1	A	2819	A
1	A	2820	U
1	A	2823	C
1	A	2825	C
1	A	2826	A
1	A	2828	G
1	A	2830	A
1	A	2843	G
1	A	2845	A
1	A	2855	G
1	A	2856	G
1	A	2857	U
1	A	2858	U
1	A	2859	G
1	A	2860	A
1	A	2861	U
1	A	2866	C
1	A	2867	U
1	A	2868	G
1	A	2872	U
1	A	2873	G
1	A	2874	G
1	A	2892	G
1	A	2897	G
1	A	2898	A
1	A	2899	C
1	A	2900	A
1	A	2904	A
1	A	2905	C
1	A	2908	A
1	A	2909	U
1	A	2916	A
2	B	10	G
2	B	11	A
2	B	12	U

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Mol	Chain	Res	Type
2	B	13	A
2	B	15	C
2	B	19	G
2	B	20	A
2	B	23	U
2	B	28	C
2	B	31	G
2	B	37	A
2	B	38	U
2	B	39	A
2	B	40	C
2	B	41	C
2	B	42	G
2	B	46	A
2	B	48	G
2	B	49	G
2	B	51	A
2	B	55	A
2	B	60	C
2	B	63	C
2	B	64	A
2	B	65	G
2	B	78	U
2	B	81	G
2	B	86	U
2	B	87	U
2	B	88	C
2	B	91	C
2	B	92	C
2	B	95	U
2	B	96	G
2	B	97	A
2	B	107	G
2	B	110	G
2	B	114	A

All (58) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	43	G
1	A	58	G
1	A	90	A

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Mol	Chain	Res	Type
1	A	99	U
1	A	124	A
1	A	163	U
1	A	175	G
1	A	183	A
1	A	229	A
1	A	252	C
1	A	271	C
1	A	288	C
1	A	377	G
1	A	405	U
1	A	417	G
1	A	419	G
1	A	549	A
1	A	647	A
1	A	649	G
1	A	664	C
1	A	666	G
1	A	683	A
1	A	717	A
1	A	733	U
1	A	837	U
1	A	1066	A
1	A	1103	A
1	A	1107	U
1	A	1245	G
1	A	1250	G
1	A	1314	A
1	A	1325	A
1	A	1339	A
1	A	1351	U
1	A	1362	G
1	A	1438	C
1	A	1455	C
1	A	1527	C
1	A	1535	U
1	A	1595	U
1	A	1630	G
1	A	1652	C
1	A	1656	C
1	A	1755	C
1	A	1779	G

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Mol	Chain	Res	Type
1	A	1784	A
1	A	2267	G
1	A	2334	U
1	A	2351	A
1	A	2454	A
1	A	2716	U
1	A	2784	C
1	A	2785	U
1	A	2812	A
1	A	2858	U
2	B	47	C
2	B	54	U
2	B	59	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	$\# Z > 2$
25	GNP	W	301	-	34,34,34	1.69	5 (14%)	47,54,54	1.81	7 (14%)

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
25	GNP	W	301	-	-	3/18/38/38	0/3/3/3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
25	W	301	GNP	PG-N3B	4.63	1.75	1.63
25	W	301	GNP	PB-N3B	4.60	1.75	1.63
25	W	301	GNP	C5-C4	3.18	1.47	1.38
25	W	301	GNP	C6-N1	-2.36	1.34	1.38
25	W	301	GNP	C5-N7	-2.02	1.35	1.39

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	W	301	GNP	C5-C4-N3	-6.14	118.62	128.39
25	W	301	GNP	C2-N3-C4	5.06	121.02	112.30
25	W	301	GNP	N9-C4-N3	4.54	135.04	125.95
25	W	301	GNP	C6-C5-N7	3.24	136.19	130.29
25	W	301	GNP	C4-C5-N7	-2.57	106.60	110.67
25	W	301	GNP	C3'-C2'-C1'	2.48	106.16	101.46
25	W	301	GNP	O6-C6-C5	-2.08	121.04	126.53

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
25	W	301	GNP	PG-N3B-PB-O1B
25	W	301	GNP	PA-O3A-PB-O2B
25	W	301	GNP	PA-O3A-PB-O1B

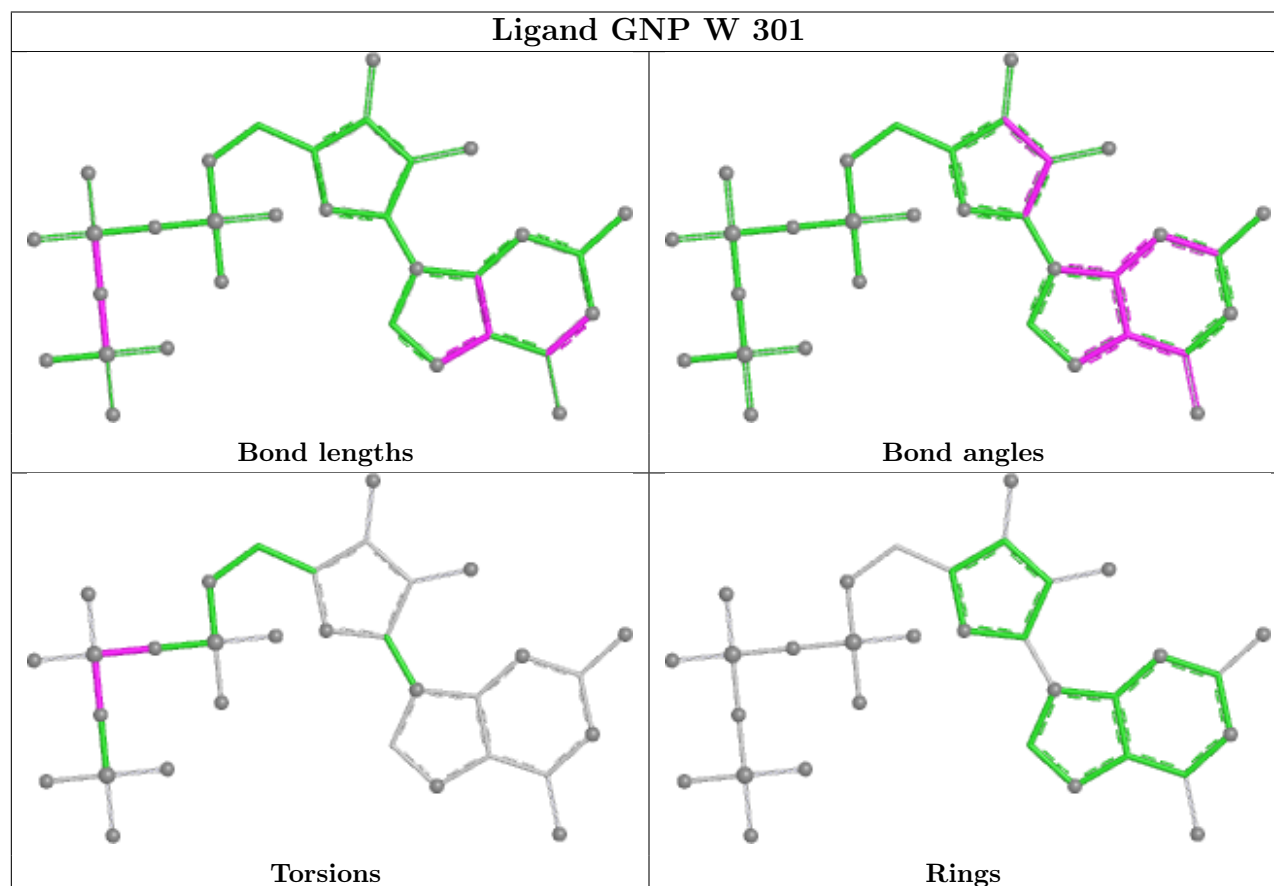
There are no ring outliers.

1 monomer is involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
25	W	301	GNP	10	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.

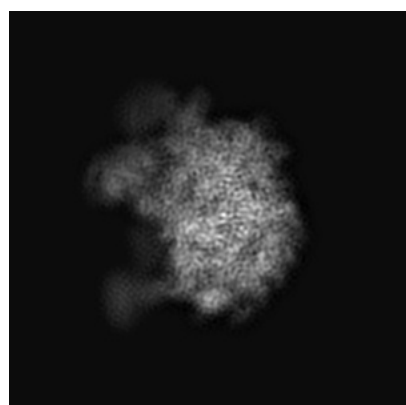
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20441. These allow visual inspection of the internal detail of the map and identification of artifacts.

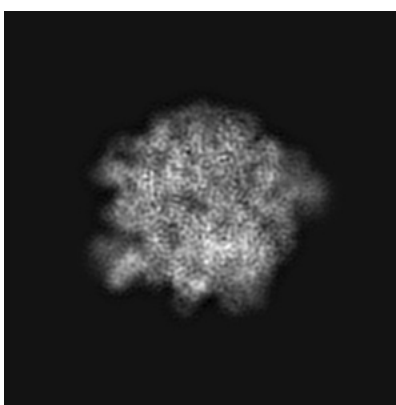
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

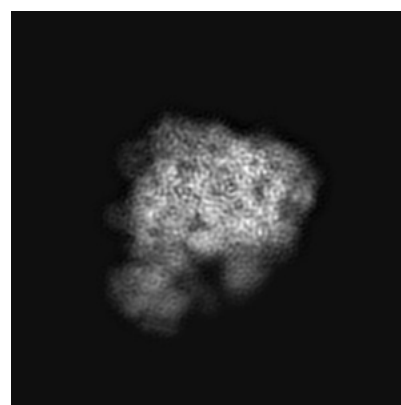
6.1.1 Primary map



X



Y

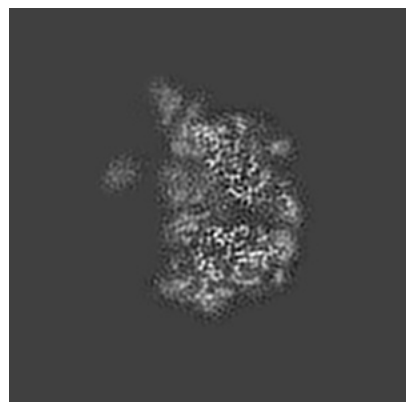


Z

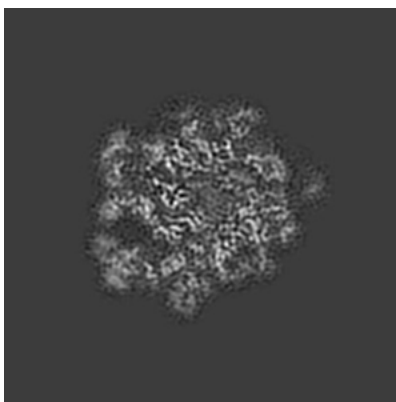
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

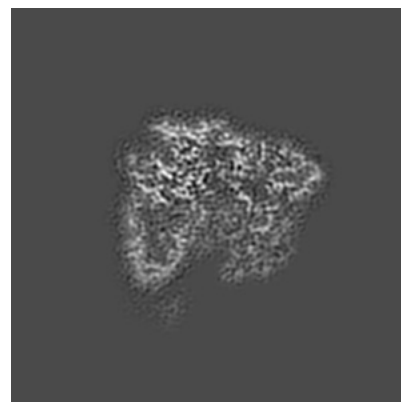
6.2.1 Primary map



X Index: 120



Y Index: 120

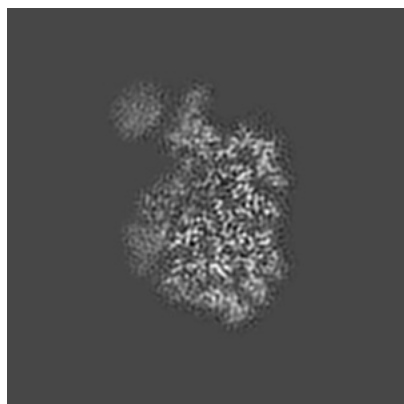


Z Index: 120

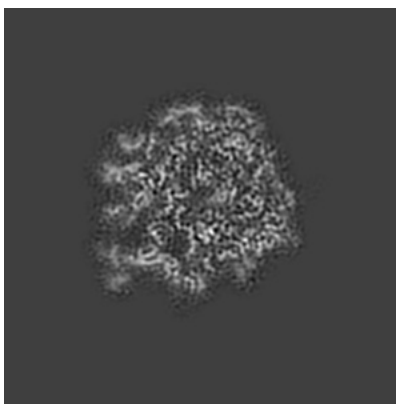
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

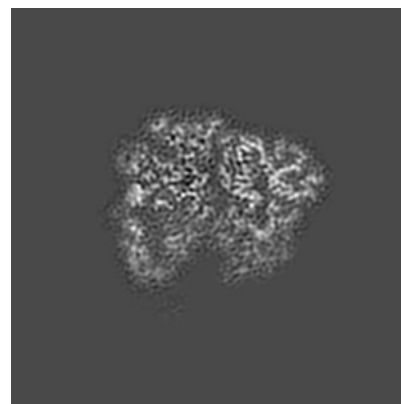
6.3.1 Primary map



X Index: 140



Y Index: 127

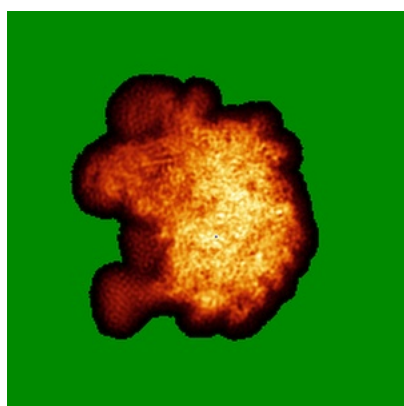


Z Index: 117

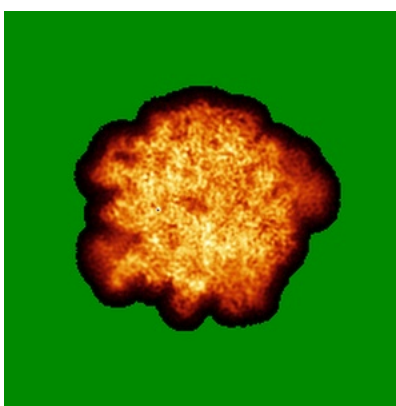
The images above show the largest variance slices of the map in three orthogonal directions.

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

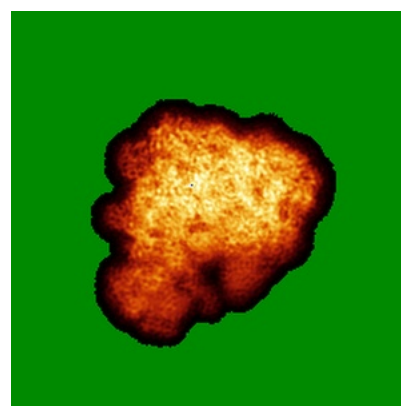
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views

This section was not generated.

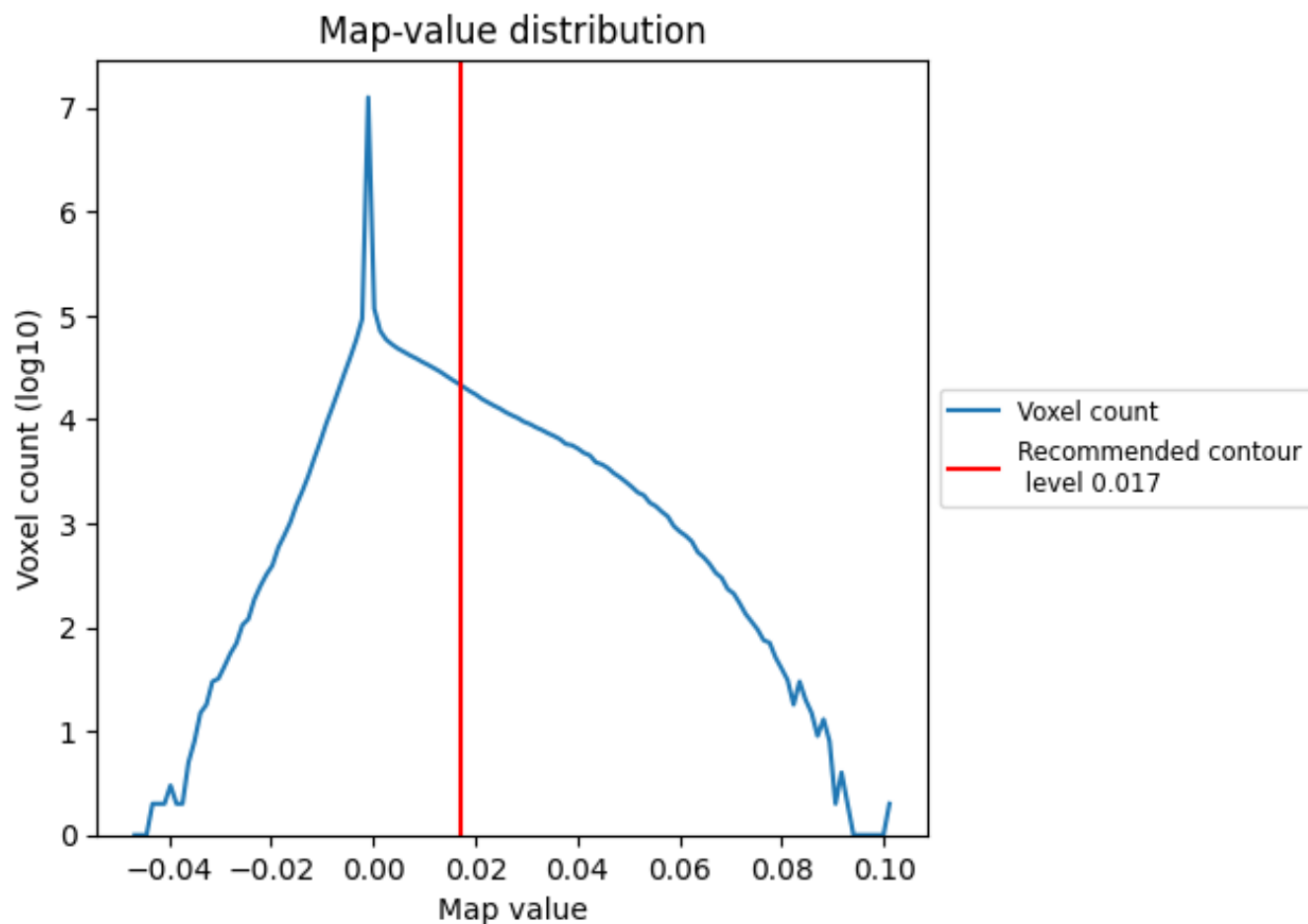
6.6 Mask visualisation

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

7 Map analysis [i](#)

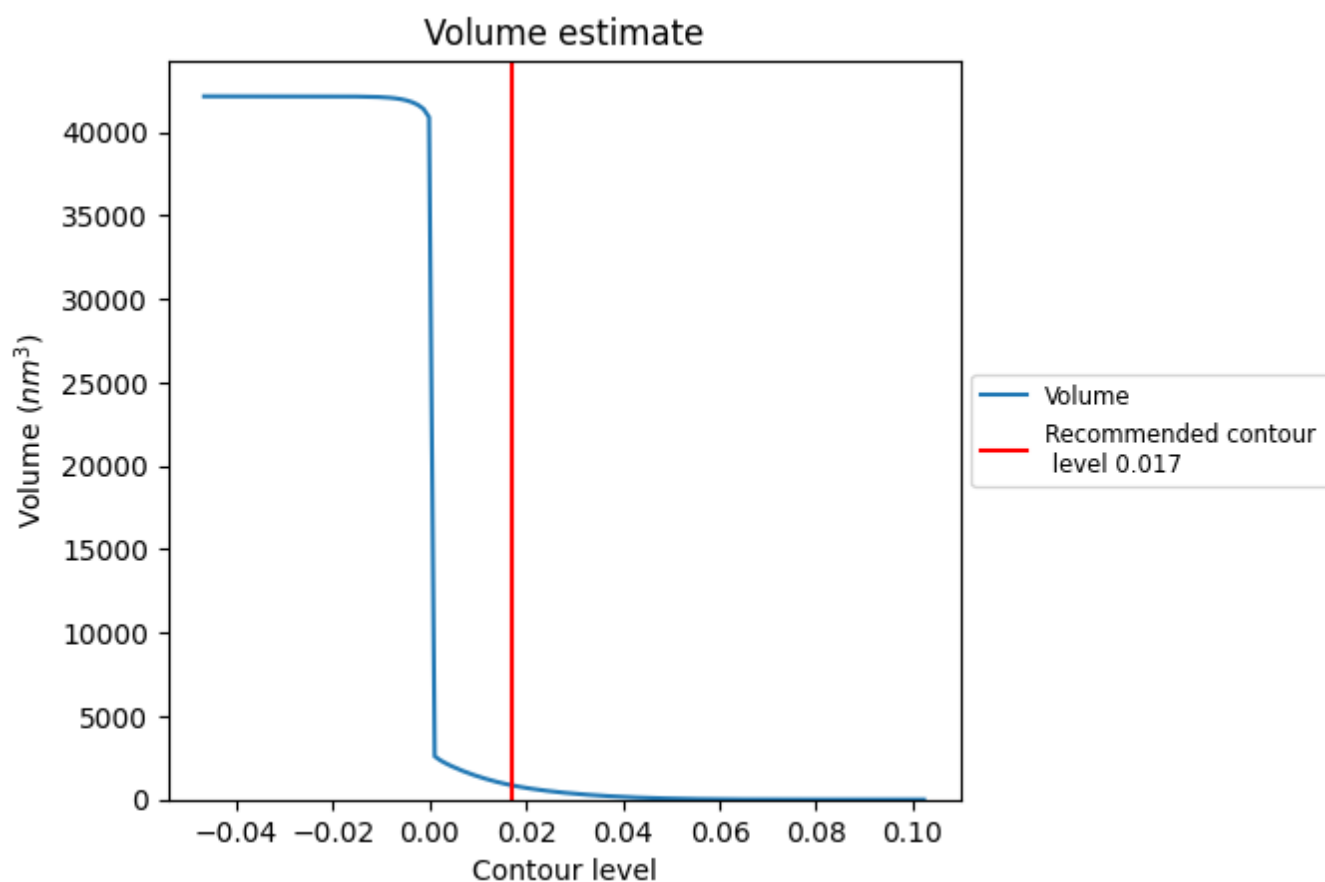
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

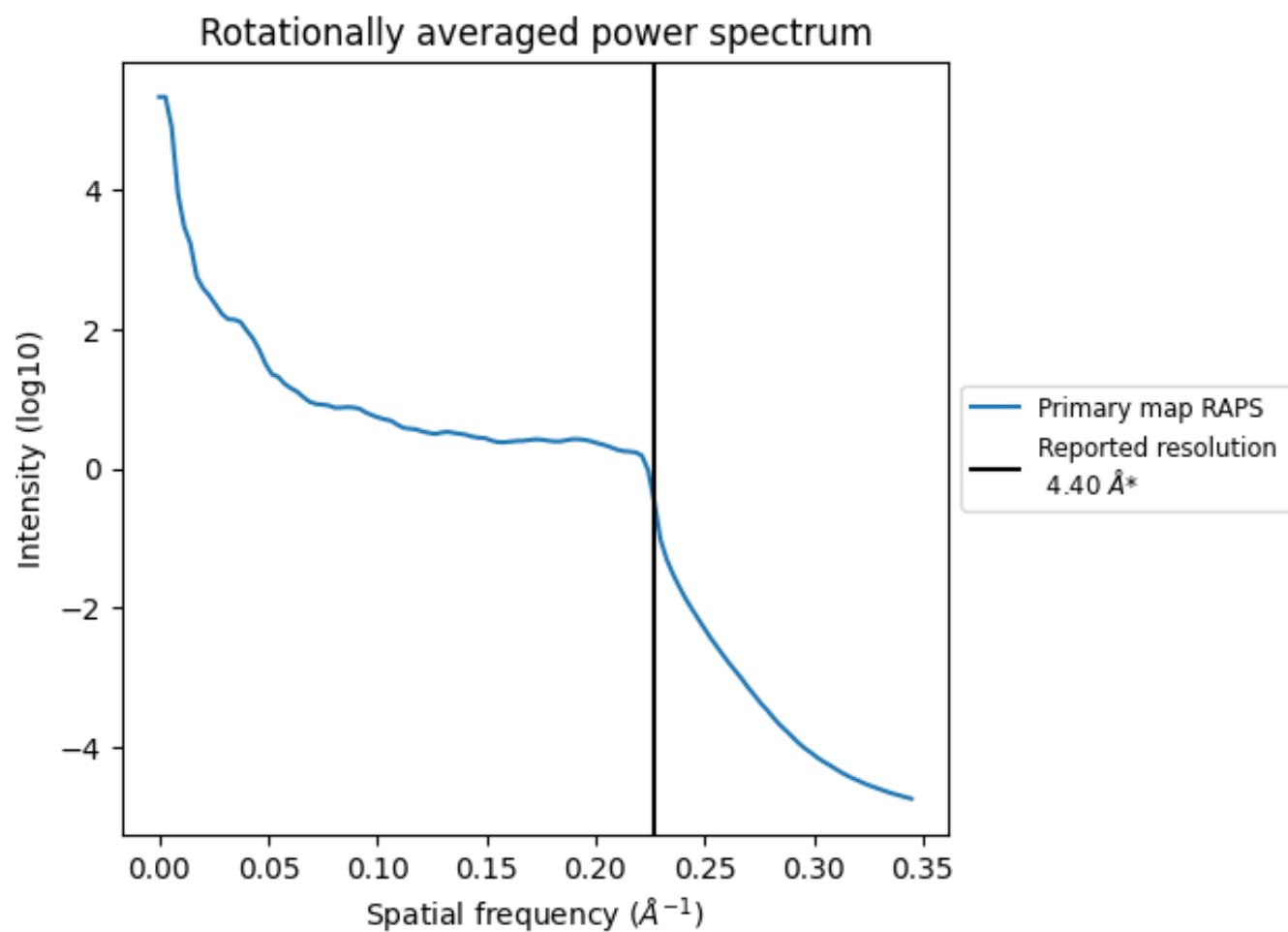
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 855 nm^3 ; this corresponds to an approximate mass of 772 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

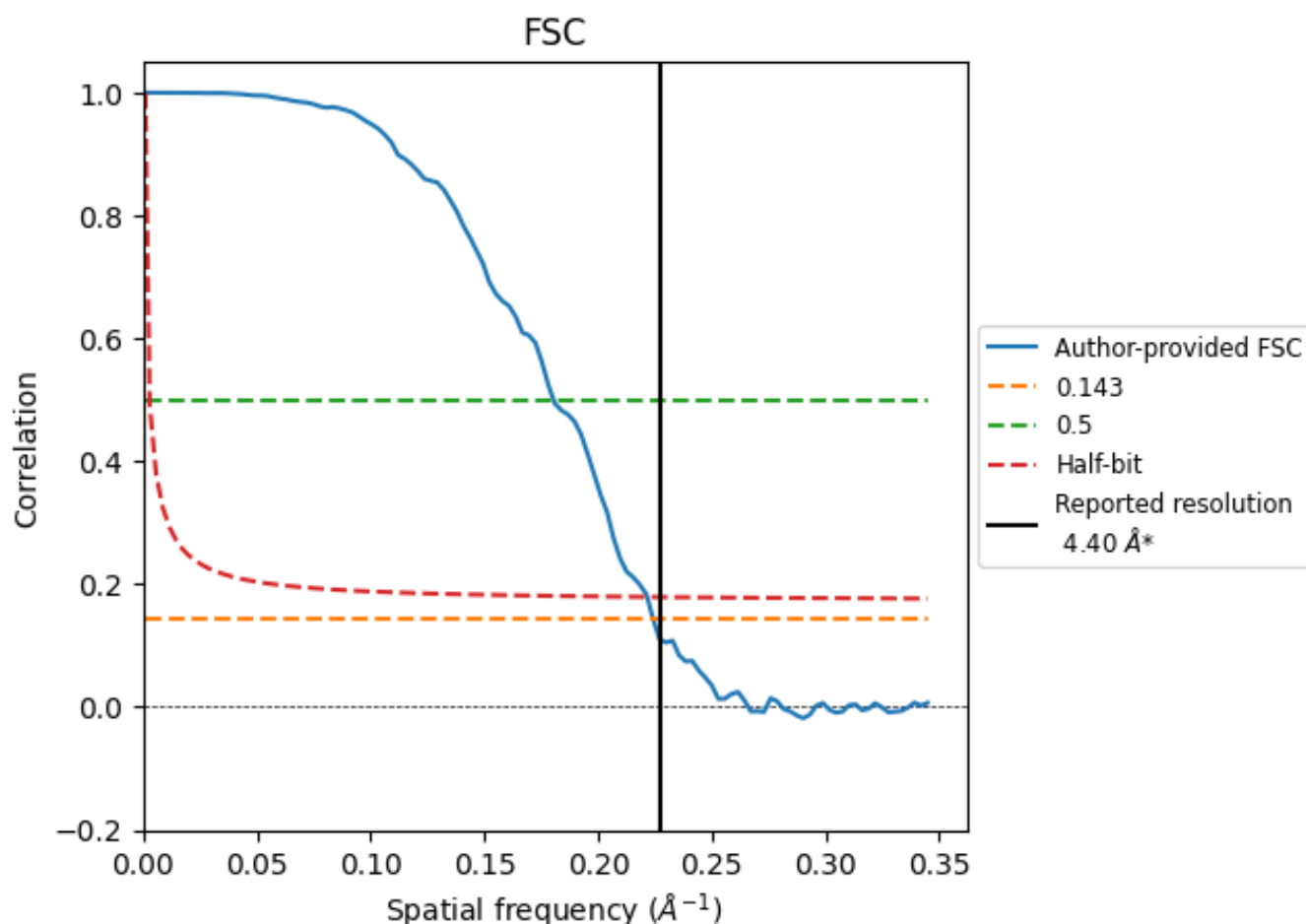


*Reported resolution corresponds to spatial frequency of 0.227 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.227 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.40	-	-
Author-provided FSC curve	4.46	5.54	4.51
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

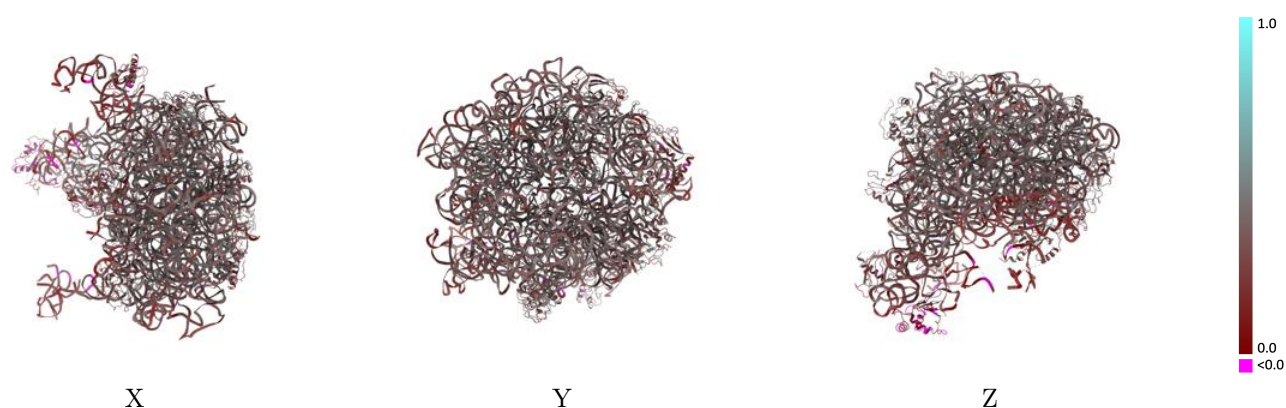
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-20441 and PDB model 6PPK. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)

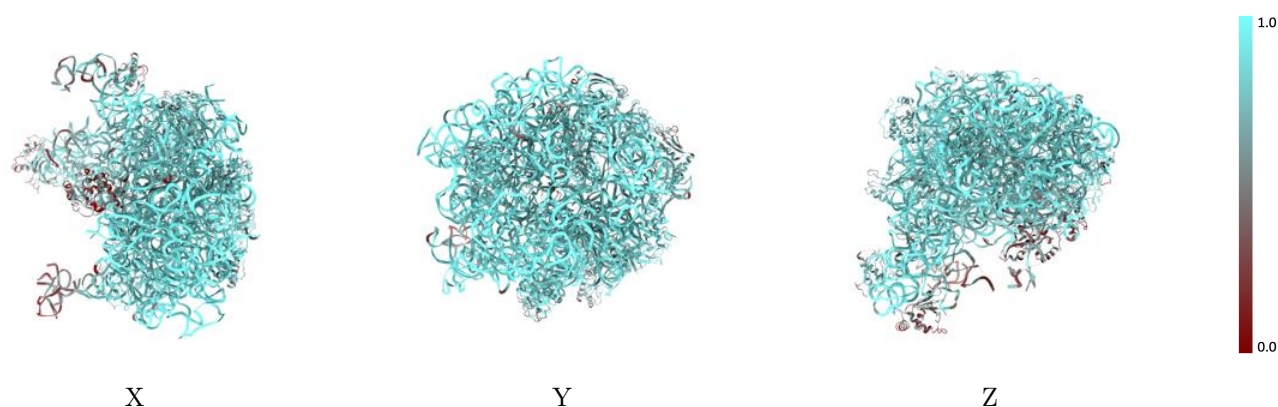
This section was not generated.

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



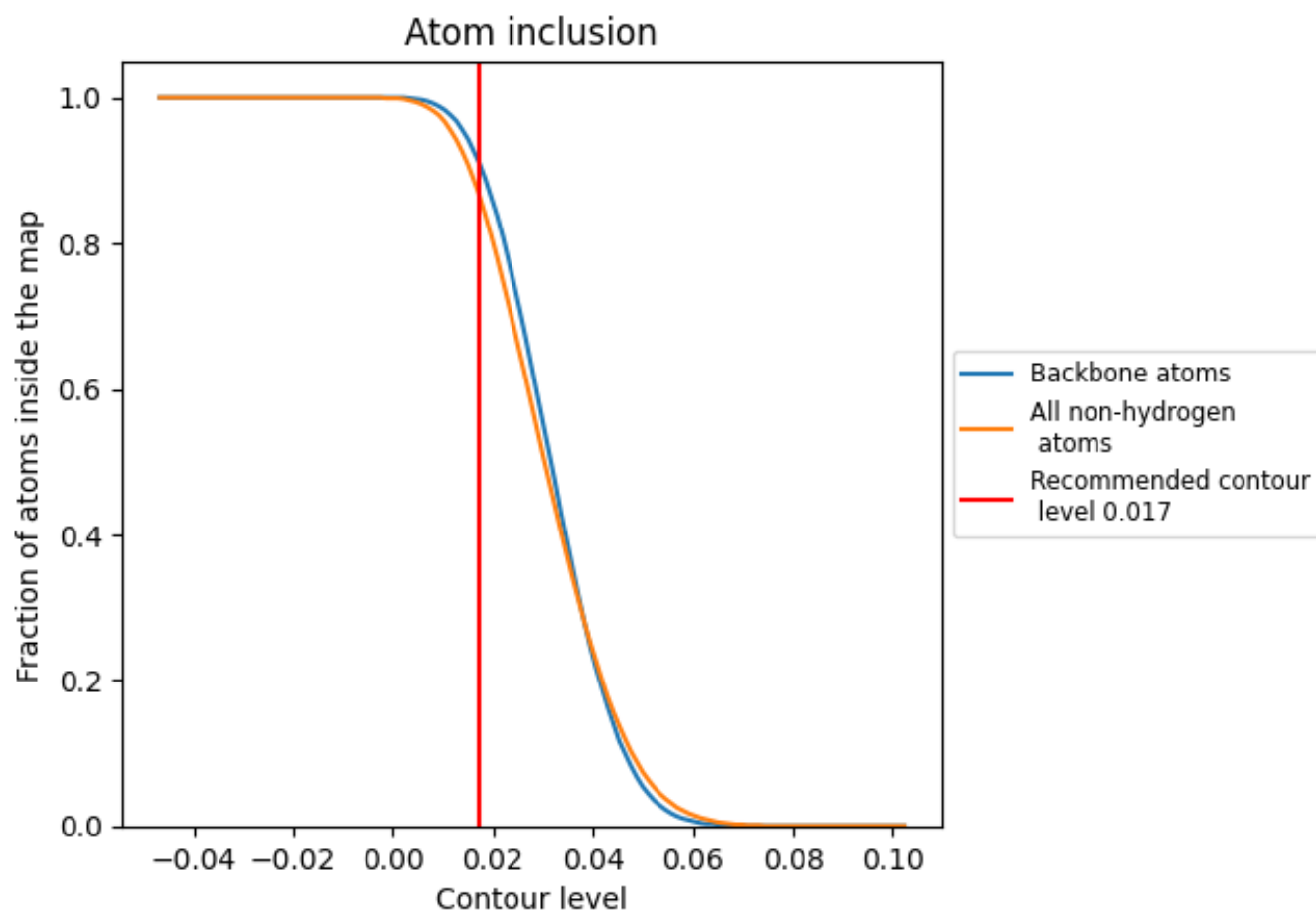
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.017).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 87% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.017) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8710	 0.3540
A	 0.9210	 0.3570
B	 0.8960	 0.3060
C	 0.7980	 0.3770
D	 0.7780	 0.3900
E	 0.7890	 0.3850
F	 0.4270	 0.1090
G	 0.5910	 0.2660
J	 0.7920	 0.3700
K	 0.8030	 0.3930
L	 0.7510	 0.3500
N	 0.8210	 0.3890
O	 0.6910	 0.2740
P	 0.7440	 0.3450
Q	 0.8490	 0.3740
R	 0.8300	 0.4010
S	 0.8060	 0.3960
T	 0.8390	 0.4080
U	 0.7820	 0.3500
V	 0.6980	 0.3630
W	 0.4270	 0.3160
Y	 0.8000	 0.3440
Z	 0.7330	 0.3500
b	 0.8200	 0.3980
d	 0.8750	 0.4290

