



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 03:24 PM UTC

PDB ID : 9BS0 / pdb_00009bs0
EMDB ID : EMD-44849
Title : YphC-treated 45SYphC particle. Class 5
Authors : Arpin, D.; Ortega, J.
Deposited on : 2024-05-12
Resolution : 3.30 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

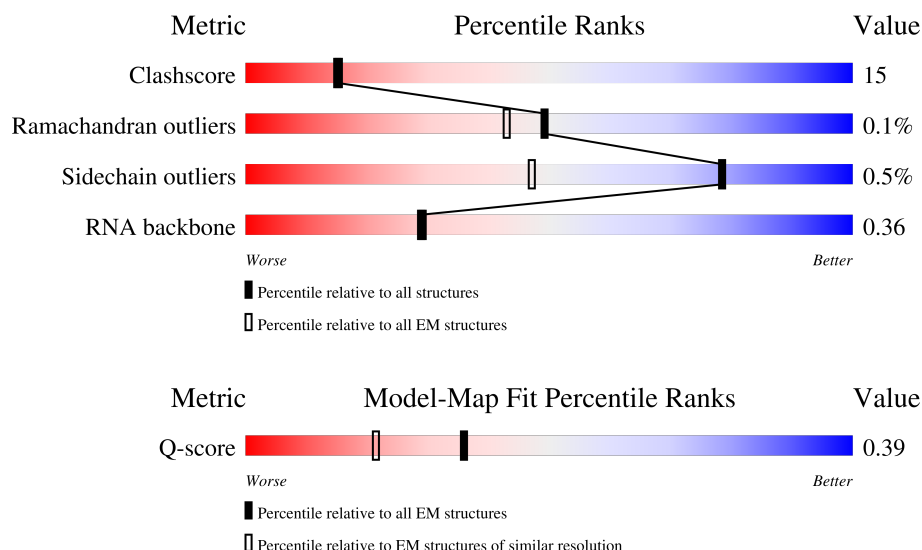
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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	15087 (2.80 - 3.80)

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	<div> <div>5%</div> <div>32%</div> <div>40%</div> <div>20%</div> <div>9%</div> </div>
2	B	119	<div> <div>23%</div> <div>36%</div> <div>34%</div> <div>7%</div> </div>
3	C	277	<div> <div>6%</div> <div>92%</div> </div>

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Mol	Chain	Length	Quality of chain
4	D	209	
5	E	207	
6	F	179	
7	G	145	
8	H	122	
9	I	146	
10	J	120	
11	K	115	
12	L	118	
13	M	102	
14	N	113	
15	O	95	
16	P	103	
17	Q	94	
18	R	66	
19	S	59	
20	T	59	
21	U	44	
22	V	120	
23	W	436	
24	Z	49	
25	Y	232	

2 Entry composition [i](#)

There are 26 unique types of molecules in this entry. The entry contains 81446 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	2678	Total	C	N	O	P	0	0
			57517	25661	10633	18545	2678		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	267	C	U	conflict	GB 1775206404
A	640	U	C	conflict	GB 1775206404
A	1558	C	G	conflict	GB 1775206404

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	111	Total	C	N	O	P	0	0
			2375	1059	433	772	111		

- Molecule 3 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	266	Total	C	N	O	S	0	0
			1977	1231	381	361	4		

- Molecule 4 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	184	Total	C	N	O	S	0	0
			1351	852	238	257	4		

- Molecule 5 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	205	Total	C	N	O	S	0	0
			1499	938	275	285	1		

- Molecule 6 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	65	Total	C	N	O	S	0	0
			468	288	87	91	2		

- Molecule 7 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	144	Total	C	N	O	S	0	0
			1121	709	206	202	4		

- Molecule 8 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	121	Total	C	N	O	S	0	0
			880	546	164	167	3		

- Molecule 9 is a protein called Large ribosomal subunit protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	117	Total	C	N	O	S	0	0
			854	532	161	160	1		

- Molecule 10 is a protein called Large ribosomal subunit protein bL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	119	Total	C	N	O	S	0	0
			933	572	185	172	4		

- Molecule 11 is a protein called Large ribosomal subunit protein bL19.

Mol	Chain	Residues	Atoms				AltConf	Trace
11	K	112	Total	C	N	O	0	0
			869	553	168	148		

- Molecule 12 is a protein called Large ribosomal subunit protein bL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	117	Total	C	N	O	S	0	0
			904	566	182	153	3		

- Molecule 13 is a protein called Large ribosomal subunit protein bL21.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	M	101	Total	C	N	O	0	0
			770	491	134	145		

- Molecule 14 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	N	109	Total	C	N	O	S	0
			824	514	158	150	2	0

- Molecule 15 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	O	91	Total	C	N	O	S	0
			725	452	133	137	3	0

- Molecule 16 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	P	93	Total	C	N	O	S	0
			686	433	127	124	2	0

- Molecule 17 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	Q	62	Total	C	N	O	0	0
			398	244	77	77		

- Molecule 18 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	R	65	Total	C	N	O	S	0
			500	305	97	96	2	0

- Molecule 19 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	S	58	Total	C	N	O	S	0
			447	275	87	84	1	0

- Molecule 20 is a protein called Large ribosomal subunit protein bL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	52	Total	C	N	O	S	0	0
			402	246	81	68	7		

- Molecule 21 is a protein called Large ribosomal subunit protein bL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	44	Total	C	N	O	S	0	0
			363	219	88	54	2		

- Molecule 22 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	106	Total	C	N	O	S	0	0
			739	455	142	142			

- Molecule 23 is a protein called GTPase Der.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	W	411	Total	C	N	O	S	0	0
			3064	1942	526	590	6		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
W	70	THR	ALA	conflict	UNP P50743
W	98	SER	ALA	conflict	UNP P50743
W	159	CYS	VAL	conflict	UNP P50743
W	217	ALA	SER	conflict	UNP P50743
W	262	GLY	ALA	conflict	UNP P50743
W	269	ASN	GLU	conflict	UNP P50743
W	292	ILE	VAL	conflict	UNP P50743
W	311	GLN	GLU	conflict	UNP P50743
W	315	GLU	ASP	conflict	UNP P50743
W	325	VAL	ILE	conflict	UNP P50743

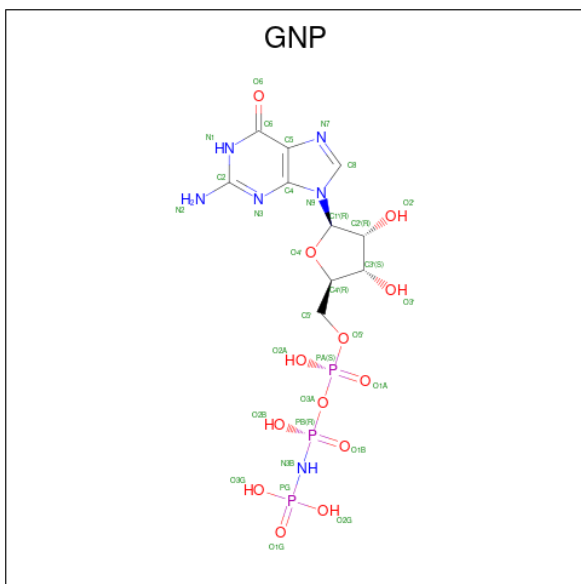
- Molecule 24 is a protein called Large ribosomal subunit protein bL33A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Z	47	Total	C	N	O	S	0	0
			373	227	71	72	3		

- Molecule 25 is a protein called Large ribosomal subunit protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	178	Total	C	N	O	S	0	0
			1343	857	227	255	4		

- Molecule 26 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (CCD ID: GNP) (formula: $\text{C}_{10}\text{H}_{17}\text{N}_6\text{O}_{13}\text{P}_3$).

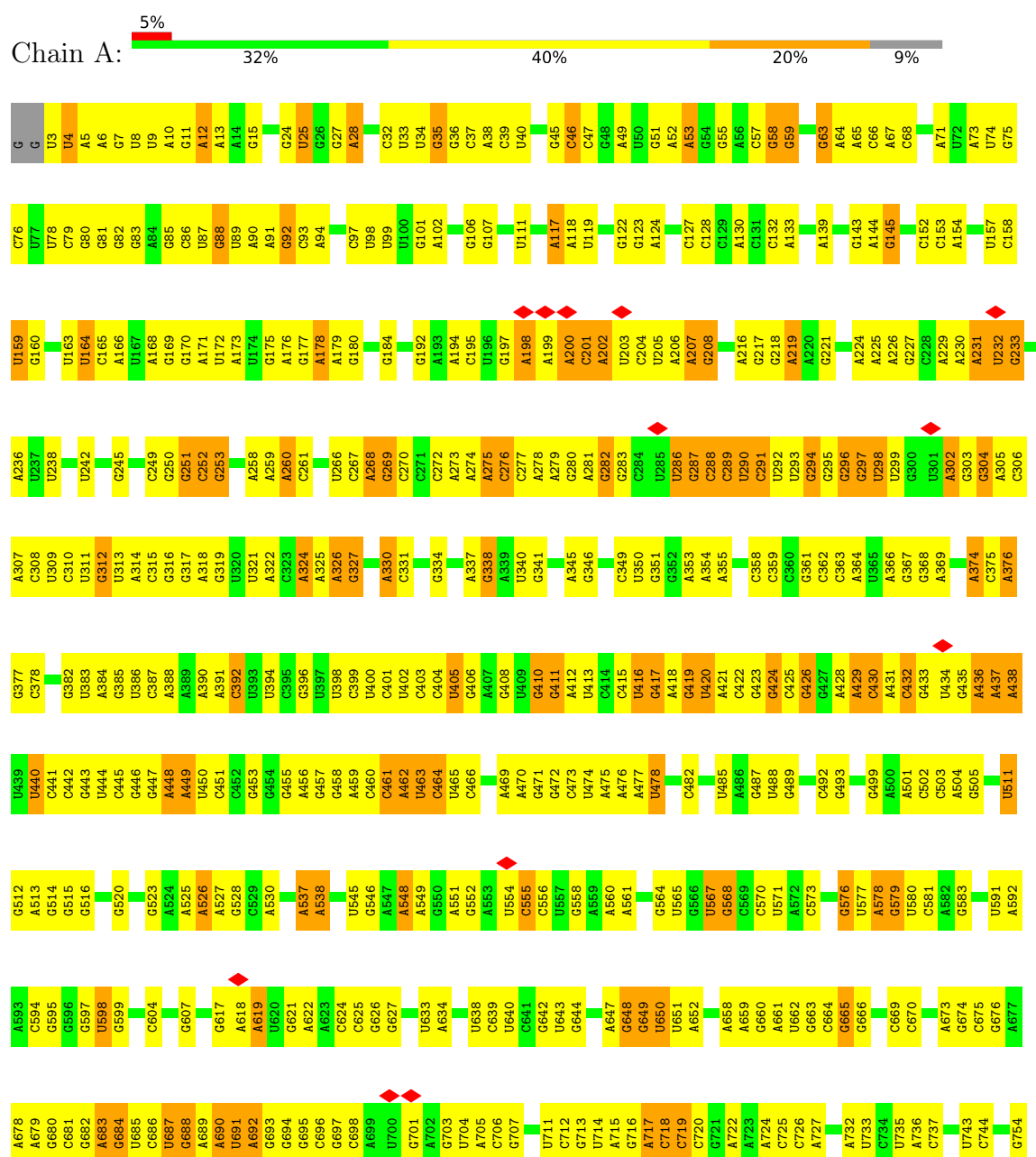


Mol	Chain	Residues	Atoms					AltConf
26	W	1	Total 32	C 10	N 6	O 13	P 3	0
26	W	1	Total 32	C 10	N 6	O 13	P 3	0

3 Residue-property plots

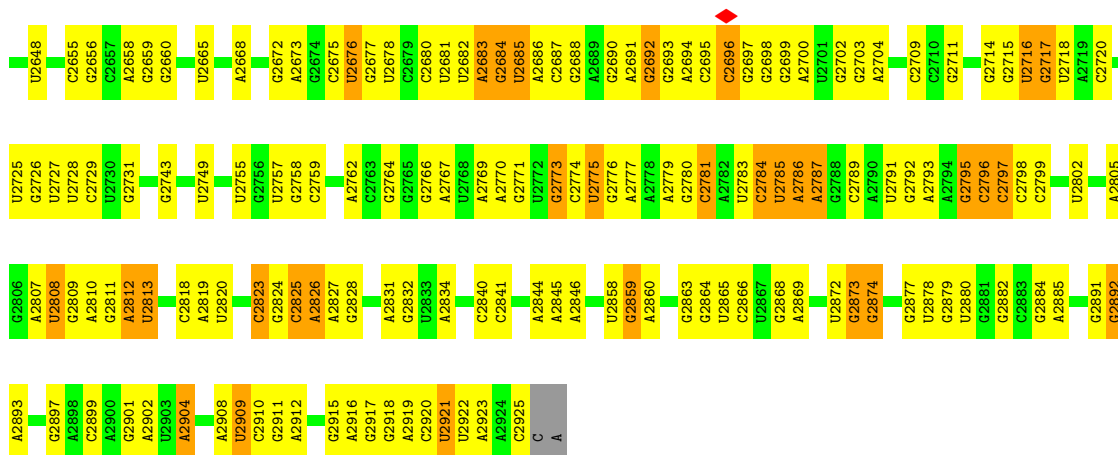
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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

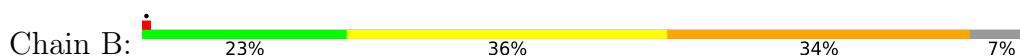


G1715	C1623	G1561	A1490	G1414	G1232	A1161	G	C1028	U960	C899	G823	U755
U1716	U1624	A1562	A1491	C1415	A1325	C1162	G	A1029	C961	U900	G824	U756
G1719	C1625	A1563	C1492	G1416	A1326	U1163	A	U1030	C962	G901	G825	C757
	U1626	C1564	C1493	A1417	U1327	A1244	U	C1031	G963	U902	U826	A758
A1722	C1629	U1565	G1494	G1418	C1328	U1165	G		A964	G903	G827	G759
A1723	G1630	G1566	G1495	G1419	G1329	G1246	U	C1037	U965	A904	A828	G760
A1724	A1631	U1567	G1496	G1420	C1330	C1247	U	A1042	U966	G905	U761	U761
U1725	G1632	A1568	G1497	A1424	C1331	C1168	G		G967	G906	A829	A762
G1726	G1633	C1569	A1498	C1425	U1332	C1169	G	A1046	C968	U907	A830	A763
A1727	U1634	U1570	U1500	A1426	C1333	G1170	C	A1047	C969	A908	U831	C764
C1728	G1635	G1571	U1501	G1427	U1251	G1171	U	A1048	A970	G909	A835	A765
		U1572	G1502	U1428	G1252	A1172	U	C1053	A971	A910	C766	C766
C1731	G1651	U1573	G1503	U1429	G1259	A1173	A	A1054	U972	G911	U837	U767
G1732	C1652	A1580	U1504	U1430	A1339	A1174	G	A1055	C973	C912	C838	G768
U1733	U1570	U1581	U1505	G1431	U1340	A1175	A	A1056	A974	A913	G839	A770
A1734	G1571	A1582	A1506	A1432	G1342	U1176	C	G1057		G914	A841	U771
A1735	A1654	U1583	U1507	U1433	G1343	U1177	C	U1058	A978	G915	G842	G772
G1736	C1655	G1584	C1508	A1434	C1344	U1178	A	A1059	U979	G916	C843	G773
	C1656	A1585	U1509	U1435	U1345	U1179	G	U1060	C980	A917	C844	G774
A1743	C1657	G1586	G1510	U1436	U1346	C1179	C	A1061	C981	U918	U844	A775
G1744		U1587	G1511	A1347	A1347	C1180	C	G1062	U982	G920	G776	G776
A1745	G1578	A1588	G1512	U1438	G1347	C1181	A	G1063	U983	C921	C777	C777
U1746	A1579	U1589	U1513	U1439	U1348	G1182	C	U1064	C984	A922	C778	C778
G1747	U1580	C1514	U1514	U1440	U1355	G1185	C	U1065	G985	C	G852	G779
	A1581	C1515	C1515	U1441	U1356	C1186	A	A1066	G986	U	C853	G780
G1750	U1582	A1516	C1516	A1442	G1358	U1187	U	A1067	A987	A	U854	
U1751	A1583	A1517	G1359	G1443	G1359	U1188	U	G1068	G988	G	G855	C783
G1752	U1584	G1518	A1360	A1444	A1360	U1189	U	U1069	U989	G	G856	C784
	A1585	C1519	G1362	A1445	A1361	G1192	A	G1070	C990	G	U857	C785
U1756	G1670	A1520	G1363	C1449	G1362	U1193	A	A1071	A991	C	U858	A786
G1757	U1671	U1521	C1364	U1455	G1364	A1194	A	A1072	C992	C	C859	C787
U1758	A1523	U1522	U1373	C1456	U1373	A1197	G	A1073	U995	C	G865	G788
U1759	A1524	G1523	U1374	U1457	U1374	A1198	G	A1074	C	C	A866	C789
	G1525	G1524	G1375	U1458	G1375	G1200	U	G1076	A999	U	G867	A790
G1764	U1593	G1526	U1376	U1459	G1376	A1201	C	A1077	G1000	A	U869	C791
G1765	U1594	C1527	U1379	G1460	G1379	G1209	G	U1078	U1001	C	A870	U793
C1766	U1595	U1528	U1380	A1461	G1379	A1210	U	U1079	G1002	C	G871	U794
A1767	C1597	G1530	U1384	C1462	U1384	C1211	A	G1080	A1003	G	C872	G795
U1768	U1598	A1533	G1385	U1463	G1385	C1212	A	U1081	U1004	G	U873	
G1769	U1599	U1534	G1386	A1464	U1386	U1212	U	G1082	A1005	U	U874	A799
C1770	G1600	U1535	G1387	A1465	G1387	U1213	A	U1083	U1006	U	U875	G800
		A1534	C1388	G1471	U1388	U1214	G	A1084	G1007	A	A876	U801
G1773	U1603	U1535	G1389	G1472	C1389	U1215	U	U1085	U1008	C	G877	G802
A1774	C1604	A1536	U1391	A1473	U1391	G1216	C	U1086	A1009	A	U878	C803
G1775	G1605	G1537	A1392	C1474	U1392	C1217	U	U1087	C1010	C	G879	G804
A1776	A1606	U1538	G1393	G1475	G1393	U1218	A	G1088	C1011	U	C880	G805
G1777	C1607	C1539	U1394	U1476	U1394	C1219	C	U1089	G1012	A948	G806	G807
A1778	U1608	A1540	A1392	A1477	A1392	G1220	U	U1090	U1013	U949	U808	A808
G1779	G1609	U1541	G1400	G1478	A1400	U1221	C	U1091	A1014	U950	U809	U809
C1780	U1610	A1542	A1401	A1479	G1401	C1222	G	G1092	G1015	A951	G810	G810
		C1545	U1480	U1480	A1404	U1223	U	U1093	U1016	G952	A888	A888
G1782	A1614	G1546	G1481	G1481	A1404	G1224	U	C1094	C1017	U953	G811	A811
C1783	G1615	U1547	A1482	U1482	G1318	G1225	C	G1095	A1020	C954	G812	G812
A1784	G1616	U1548	A1483	U1483	G1319	U1226	U	U1096	A1025	A955	G813	G813
G1785	A1617	U1549	A1484	U1484	U1320	G1227	A	A1097	A957	A896	G818	G818
	G1711	U1550	A1485	U1485	U1321	G1228	C	C1098	A1026	G897	G822	G822
A1789	G1712	C1551			G1322	U1229	A		U1027	U998		
U1790						G1231						

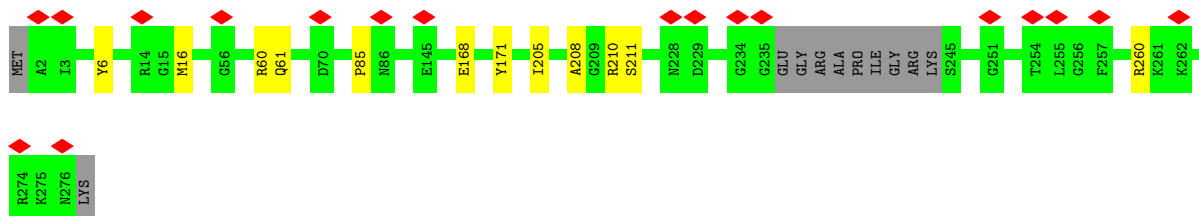
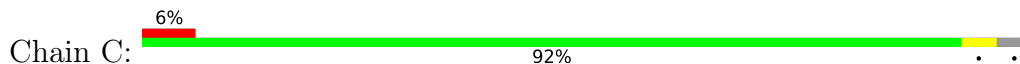




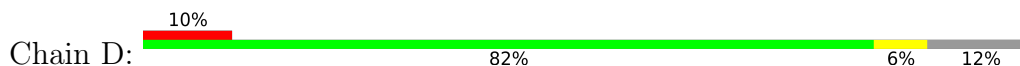
• Molecule 2: 5S rRNA



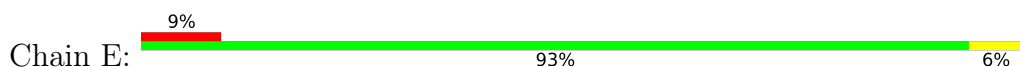
• Molecule 3: Large ribosomal subunit protein uL2

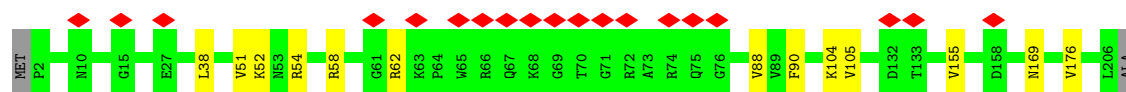


• Molecule 4: Large ribosomal subunit protein uL3

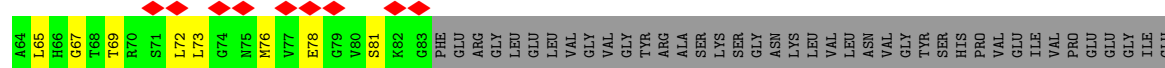
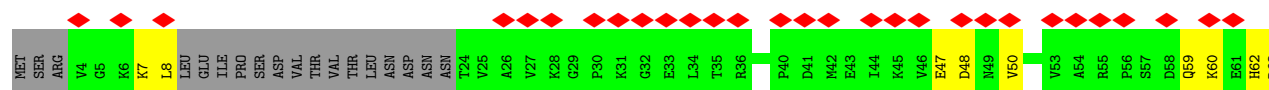


• Molecule 5: Large ribosomal subunit protein uL4

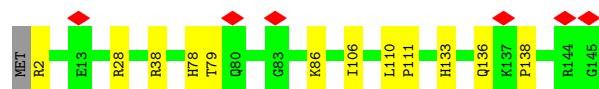
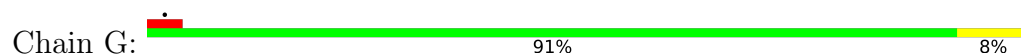




- Molecule 6: Large ribosomal subunit protein uL6



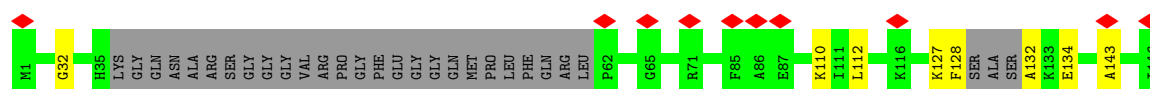
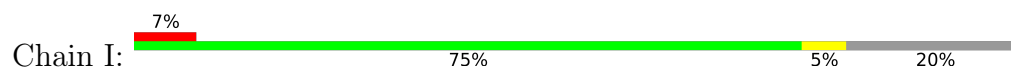
- Molecule 7: Large ribosomal subunit protein uL13



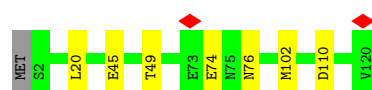
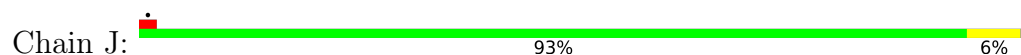
- Molecule 8: Large ribosomal subunit protein uL14



- Molecule 9: Large ribosomal subunit protein uL15

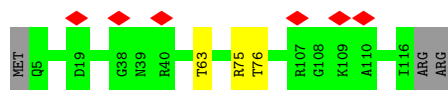


- Molecule 10: Large ribosomal subunit protein bL17

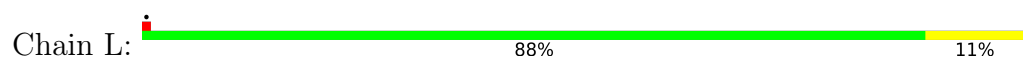


- Molecule 11: Large ribosomal subunit protein bL19

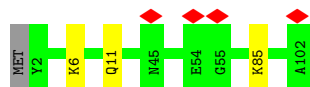




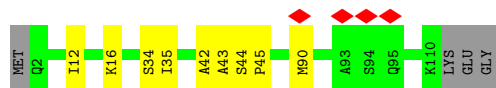
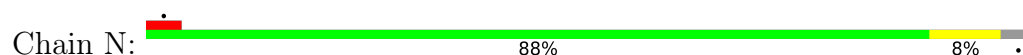
- Molecule 12: Large ribosomal subunit protein bL20



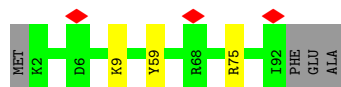
- Molecule 13: Large ribosomal subunit protein bL21



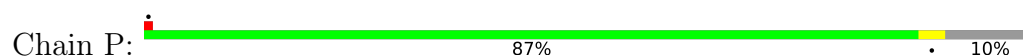
- Molecule 14: Large ribosomal subunit protein uL22



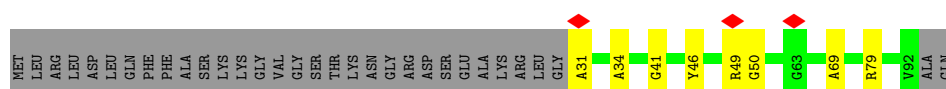
- Molecule 15: Large ribosomal subunit protein uL23



- Molecule 16: Large ribosomal subunit protein uL24



- Molecule 17: Large ribosomal subunit protein bL27



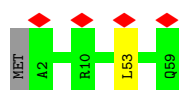
- Molecule 18: Large ribosomal subunit protein uL29

Chain R:  89% 9%



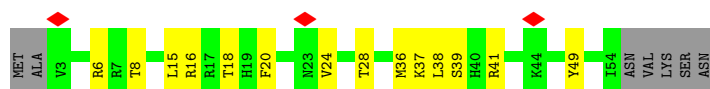
- Molecule 19: Large ribosomal subunit protein uL30

Chain S:  7% 97%

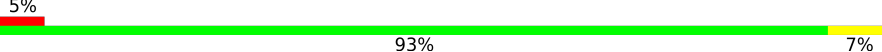


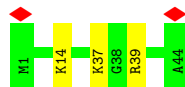
- Molecule 20: Large ribosomal subunit protein bL32

Chain T:  5% 64% 24% 12%




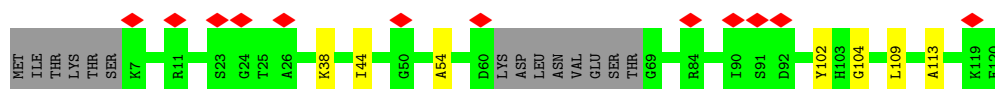
- Molecule 21: Large ribosomal subunit protein bL34

Chain U:  5% 93% 7%




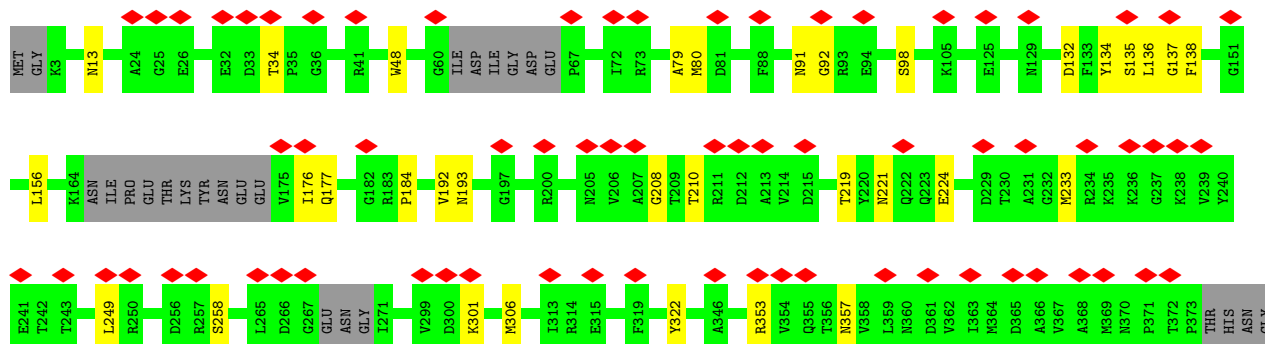
- Molecule 22: Large ribosomal subunit protein uL18

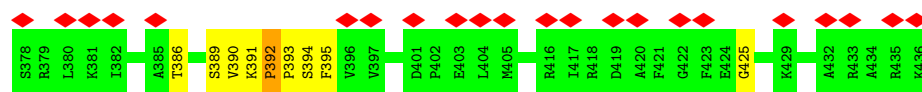
Chain V:  10% 82% 6% 12%



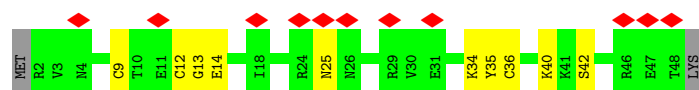
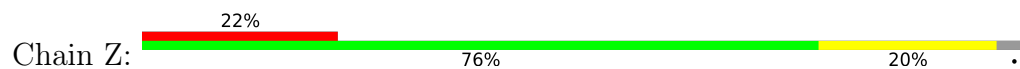
- Molecule 23: GTPase Der

Chain W:  21% 85% 9% 6%

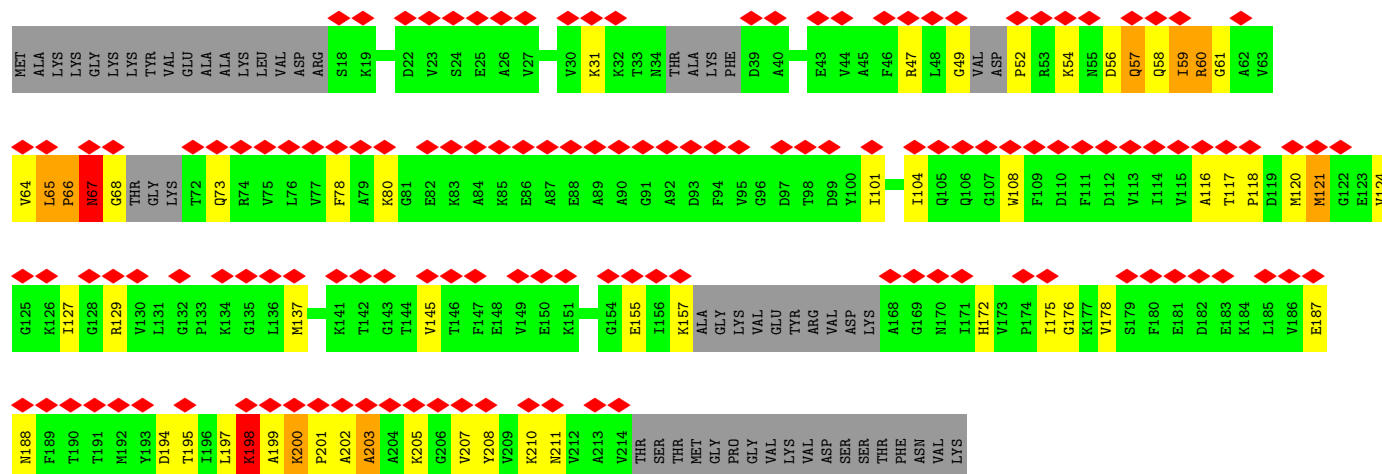




- Molecule 24: Large ribosomal subunit protein bL33A



- Molecule 25: Large ribosomal subunit protein uL1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	18086	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2750	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.941	Depositor
Minimum map value	-0.280	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.061	Depositor
Recommended contour level	0.255	Depositor
Map size (Å)	362.52002, 362.52002, 362.52002	wwPDB
Map dimensions	424, 424, 424	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.855, 0.855, 0.855	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	0.25	0/64420	0.35	0/100477
2	B	0.18	0/2655	0.32	0/4136
3	C	0.29	0/2011	0.63	0/2710
4	D	0.31	0/1365	0.68	0/1834
5	E	0.35	0/1516	0.60	0/2057
6	F	0.17	0/472	0.46	0/634
7	G	0.34	0/1144	0.64	0/1543
8	H	0.38	0/887	0.76	0/1200
9	I	0.30	0/860	0.67	0/1146
10	J	0.35	0/940	0.76	0/1260
11	K	0.38	0/882	0.69	0/1189
12	L	0.46	0/916	0.68	0/1224
13	M	0.28	0/781	0.62	0/1051
14	N	0.33	0/833	0.68	0/1125
15	O	0.39	0/731	0.75	0/977
16	P	0.32	0/694	0.70	0/928
17	Q	0.46	0/404	1.02	0/549
18	R	0.35	0/501	0.74	0/674
19	S	0.35	0/449	0.85	0/605
20	T	0.30	0/409	0.69	0/544
21	U	0.30	0/366	0.70	0/479
22	V	0.23	0/745	0.67	0/1006
23	W	0.32	0/3115	0.71	0/4237
24	Z	0.35	0/378	0.73	0/508
25	Y	0.39	0/1361	0.89	6/1833 (0.3%)
All	All	0.27	0/88835	0.45	6/133926 (0.0%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	Y	54	LYS	N-CA-CB	-8.77	98.45	110.56
25	Y	198	LYS	N-CA-C	-8.64	100.87	111.33
25	Y	54	LYS	N-CA-C	8.47	122.42	112.93
25	Y	61	GLY	N-CA-C	8.06	123.77	110.55
25	Y	176	GLY	N-CA-C	5.79	117.97	110.45
25	Y	203	ALA	N-CA-C	-5.71	104.04	111.74

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	57517	0	28951	1608	0
2	B	2375	0	1203	79	0
3	C	1977	0	1995	7	0
4	D	1351	0	1384	13	0
5	E	1499	0	1523	10	0
6	F	468	0	460	12	0
7	G	1121	0	1145	11	0
8	H	880	0	895	7	0
9	I	854	0	886	13	0
10	J	933	0	956	7	0
11	K	869	0	883	3	0
12	L	904	0	921	20	0
13	M	770	0	791	2	0
14	N	824	0	861	8	0
15	O	725	0	759	4	0
16	P	686	0	724	2	0
17	Q	398	0	311	12	0
18	R	500	0	491	5	0
19	S	447	0	469	1	0
20	T	402	0	403	12	0
21	U	363	0	399	3	0
22	V	739	0	700	5	0
23	W	3064	0	2926	74	0
24	Z	373	0	355	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
25	Y	1343	0	1366	123	0
26	W	64	0	26	2	0
All	All	81446	0	51783	1909	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 15.

All (1909) 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)
23:W:132:ASP:HA	25:Y:137:MET:CE	1.33	1.55
23:W:132:ASP:CA	25:Y:137:MET:HE1	1.44	1.42
23:W:389:SER:OG	23:W:394:SER:HB2	1.21	1.36
23:W:134:TYR:O	25:Y:129:ARG:CD	1.83	1.26
1:A:2351:A:H2	1:A:2361:C:N4	1.31	1.26
23:W:137:GLY:CA	25:Y:129:ARG:HD2	1.63	1.26
25:Y:116:ALA:HB1	25:Y:121:MET:CE	1.73	1.19
23:W:132:ASP:CA	25:Y:137:MET:CE	2.05	1.18
25:Y:59:ILE:CD1	25:Y:201:PRO:HG2	1.79	1.12
23:W:137:GLY:HA2	25:Y:129:ARG:CD	1.77	1.12
23:W:137:GLY:H	25:Y:129:ARG:NE	1.46	1.11
25:Y:59:ILE:HD12	25:Y:201:PRO:HG2	1.34	1.09
25:Y:116:ALA:HB1	25:Y:121:MET:HE1	1.10	1.05
23:W:134:TYR:C	25:Y:129:ARG:HE	1.64	1.05
23:W:132:ASP:HA	25:Y:137:MET:HE3	1.40	1.03
23:W:137:GLY:HA2	25:Y:129:ARG:HD2	1.03	1.02
23:W:137:GLY:CA	25:Y:129:ARG:CD	2.37	1.00
2:B:45:C:H1'	2:B:46:A:H2'	1.38	1.00
1:A:2351:A:C2	1:A:2361:C:N4	2.23	0.99
23:W:134:TYR:O	25:Y:129:ARG:CG	2.09	0.99
25:Y:59:ILE:CD1	25:Y:201:PRO:CG	2.40	0.99
25:Y:59:ILE:HD12	25:Y:201:PRO:CG	1.93	0.97
25:Y:116:ALA:CB	25:Y:121:MET:SD	2.52	0.97
23:W:132:ASP:C	25:Y:137:MET:HE1	1.89	0.97
23:W:137:GLY:H	25:Y:129:ARG:CD	1.78	0.97
1:A:2207:C:P	25:Y:211:ASN:HD22	1.88	0.96
1:A:1886:G:N2	1:A:1914:A:H62	1.62	0.96
1:A:1831:A:HO2'	1:A:1832:A:H8	0.99	0.96
23:W:138:PHE:N	25:Y:129:ARG:NH2	2.12	0.96
23:W:389:SER:OG	23:W:394:SER:CB	2.14	0.95
1:A:2777:A:N6	1:A:2783:U:H3	1.64	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:W:134:TYR:O	25:Y:129:ARG:NE	1.97	0.95
25:Y:121:MET:HE2	25:Y:121:MET:HA	1.48	0.95
23:W:134:TYR:C	25:Y:129:ARG:NE	2.25	0.94
23:W:134:TYR:O	25:Y:129:ARG:HG2	1.67	0.94
1:A:1886:G:H21	1:A:1914:A:H62	1.06	0.94
1:A:1883:A:H62	1:A:1917:G:N2	1.67	0.93
2:B:29:C:O2	2:B:51:A:N6	2.01	0.92
23:W:134:TYR:O	25:Y:129:ARG:HD3	1.67	0.92
1:A:2128:U:H3	1:A:2219:G:H1	0.95	0.92
1:A:1572:G:HO2'	1:A:1573:C:H6	1.18	0.92
23:W:137:GLY:N	25:Y:129:ARG:CD	2.33	0.92
25:Y:116:ALA:CB	25:Y:121:MET:HE1	1.98	0.92
1:A:159:U:H3	1:A:169:G:H1	0.96	0.90
1:A:1886:G:H21	1:A:1914:A:N6	1.70	0.90
23:W:132:ASP:HA	25:Y:137:MET:HE1	1.02	0.90
25:Y:117:THR:O	25:Y:121:MET:SD	2.29	0.90
23:W:389:SER:HG	23:W:394:SER:HB2	1.28	0.89
25:Y:116:ALA:HB3	25:Y:121:MET:SD	2.12	0.88
25:Y:101:ILE:CD1	25:Y:124:VAL:HG23	2.03	0.88
23:W:98:SER:H	25:Y:52:PRO:HD3	1.38	0.88
25:Y:67:ASN:HD21	25:Y:187:GLU:HB2	1.39	0.88
1:A:2330:A:H62	1:A:2343:A:H2	1.22	0.87
25:Y:101:ILE:HD13	25:Y:124:VAL:HG23	1.55	0.87
1:A:1081:U:H3	1:A:1166:G:H1	1.16	0.87
1:A:2293:C:O2	1:A:2305:G:N2	2.08	0.87
1:A:2293:C:C2	1:A:2305:G:C2	2.63	0.87
25:Y:116:ALA:HB1	25:Y:121:MET:SD	2.13	0.86
25:Y:117:THR:O	25:Y:121:MET:HG2	1.75	0.86
1:A:2129:G:H1	1:A:2218:U:H3	0.91	0.85
1:A:918:U:O2	1:A:953:G:N2	2.10	0.84
1:A:1220:G:H2'	1:A:1221:A:H8	1.38	0.84
1:A:2443:G:C6	1:A:2444:G:O6	2.31	0.84
1:A:1246:G:H1'	1:A:1247:G:H5'	1.60	0.84
1:A:2130:G:H1	1:A:2217:U:H3	1.26	0.84
1:A:2298:A:H2'	1:A:2299:G:C6	2.13	0.84
1:A:2359:G:H1'	17:Q:50:GLY:HA3	1.61	0.83
1:A:2681:U:H3	1:A:2697:G:H1	1.23	0.83
23:W:137:GLY:N	25:Y:129:ARG:NE	2.26	0.83
25:Y:117:THR:O	25:Y:121:MET:CG	2.27	0.83
1:A:2293:C:C2	1:A:2305:G:N2	2.47	0.82
1:A:688:G:N2	1:A:693:G:O6	2.13	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:Y:124:VAL:O	25:Y:127:ILE:HG22	1.78	0.82
1:A:2388:C:H2'	1:A:2389:A:H8	1.44	0.82
2:B:36:C:H2'	2:B:37:A:H4'	1.62	0.82
1:A:2395:A:H3'	1:A:2396:G:H8	1.42	0.81
1:A:1883:A:N6	1:A:1917:G:H21	1.79	0.81
1:A:1521:G:H22	1:A:1563:G:H1	1.24	0.81
23:W:132:ASP:CA	25:Y:137:MET:HE3	1.97	0.81
1:A:2321:U:O3'	1:A:2403:C:N4	2.14	0.81
1:A:1883:A:H62	1:A:1917:G:H21	1.26	0.80
1:A:2777:A:H62	1:A:2783:U:H3	0.84	0.80
1:A:2206:C:O3'	25:Y:211:ASN:ND2	2.14	0.80
1:A:1093:G:O2'	1:A:1157:A:N6	2.14	0.80
1:A:1087:U:O2	1:A:1160:G:O6	1.99	0.79
1:A:1871:G:O6	1:A:1927:U:C4	2.35	0.79
1:A:1444:C:H2'	1:A:1445:A:H8	1.45	0.79
1:A:1245:G:O6	1:A:1281:C:N4	2.16	0.79
1:A:1074:A:N6	1:A:1172:A:OP1	2.15	0.79
1:A:2332:G:H22	1:A:2343:A:H1'	1.48	0.79
25:Y:67:ASN:HB2	25:Y:188:ASN:HD21	1.47	0.79
1:A:1867:C:H4'	1:A:1868:G:H5'	1.64	0.79
1:A:2104:U:O2'	1:A:2626:G:N3	2.15	0.79
9:I:128:PHE:C	9:I:132:ALA:HB1	2.08	0.78
1:A:1757:G:O6	1:A:1775:G:N1	2.14	0.78
1:A:2414:C:O2'	17:Q:49:ARG:NH1	2.15	0.78
1:A:2162:G:H22	1:A:2183:G:H3'	1.49	0.78
1:A:2717:G:N1	1:A:2749:U:OP2	2.13	0.78
2:B:77:G:H1	2:B:95:U:H3	1.31	0.78
1:A:1518:G:N2	1:A:1567:U:O2	2.17	0.78
1:A:2295:A:N1	1:A:2301:U:O2'	2.17	0.78
1:A:2400:G:N7	1:A:2402:A:N6	2.31	0.77
1:A:2425:G:N3	1:A:2426:G:N1	2.32	0.77
1:A:2353:U:H5'	1:A:2354:G:H5''	1.66	0.77
1:A:63:G:H2'	1:A:64:A:H8	1.50	0.77
1:A:2882:G:N2	1:A:2885:A:OP2	2.18	0.77
25:Y:116:ALA:CB	25:Y:121:MET:CE	2.57	0.77
1:A:2137:U:O2	1:A:2210:G:N2	2.16	0.76
23:W:322:TYR:HB2	23:W:425:GLY:H	1.50	0.76
1:A:1220:G:H2'	1:A:1221:A:C8	2.19	0.76
23:W:132:ASP:N	25:Y:137:MET:CE	2.34	0.76
1:A:2467:U:H5''	1:A:2468:A:H5'	1.68	0.76
1:A:2771:G:H1	1:A:2791:U:H3	1.34	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2395:A:H3'	1:A:2396:G:C8	2.20	0.76
1:A:249:C:N4	1:A:250:G:O6	2.19	0.75
1:A:1870:U:O2'	1:A:1871:G:OP1	2.04	0.75
1:A:2389:A:H3'	1:A:2390:A:H8	1.51	0.75
1:A:1513:U:H3	1:A:1572:G:H1	1.34	0.75
1:A:955:C:H2'	1:A:956:A:C8	2.21	0.75
1:A:200:A:O2'	1:A:2459:A:N7	2.18	0.74
23:W:132:ASP:N	25:Y:137:MET:HE3	1.97	0.74
1:A:2161:G:OP2	1:A:2182:G:O2'	2.06	0.74
1:A:896:A:H2'	1:A:897:G:H8	1.52	0.74
1:A:2156:G:OP1	1:A:2202:A:N6	2.20	0.74
1:A:2349:A:H2'	1:A:2361:C:H5	1.51	0.74
1:A:2349:A:H2'	1:A:2361:C:C5	2.23	0.74
1:A:854:U:OP2	1:A:877:G:N2	2.21	0.73
9:I:128:PHE:C	9:I:132:ALA:CB	2.61	0.73
1:A:2086:G:H2'	1:A:2087:A:H8	1.52	0.73
1:A:2207:C:OP2	25:Y:211:ASN:ND2	2.20	0.73
1:A:2371:C:H1'	1:A:2372:U:H5'	1.70	0.73
1:A:1085:G:N1	1:A:1163:U:C2	2.56	0.73
1:A:2292:C:OP2	1:A:2307:A:N6	2.22	0.73
1:A:2099:G:H2'	1:A:2100:A:H8	1.55	0.72
1:A:2151:U:O4'	25:Y:172:HIS:NE2	2.23	0.72
1:A:2355:U:O2	1:A:2356:A:N6	2.21	0.72
1:A:2777:A:N7	1:A:2783:U:O4	2.22	0.72
1:A:28:A:N6	1:A:558:G:O2'	2.22	0.72
1:A:1517:A:H61	1:A:1567:U:H3	1.37	0.72
1:A:350:U:H3	1:A:354:A:H62	1.38	0.72
1:A:1085:G:C2	1:A:1163:U:C2	2.78	0.72
2:B:34:C:H41	2:B:45:C:H5	1.38	0.72
1:A:726:C:H2'	1:A:727:A:H8	1.54	0.72
1:A:2366:G:N2	1:A:2367:G:C2	2.58	0.72
1:A:2368:G:H3'	1:A:2369:A:H8	1.54	0.72
25:Y:121:MET:HE2	25:Y:121:MET:CA	2.20	0.72
1:A:2349:A:O2'	1:A:2365:A:N6	2.23	0.71
2:B:43:A:H5''	2:B:44:A:H8	1.54	0.71
1:A:1888:A:N6	1:A:1912:G:O2'	2.23	0.71
1:A:2291:U:H5''	1:A:2415:U:H3	1.54	0.71
1:A:2557:U:O2	1:A:2564:G:O6	2.09	0.71
1:A:268:A:N6	1:A:475:A:N7	2.39	0.71
1:A:1000:G:H1	1:A:1009:U:H3	1.39	0.71
1:A:505:G:O2'	1:A:516:G:O6	2.07	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1874:G:O6	1:A:1925:A:N1	2.24	0.71
1:A:2206:C:H3'	1:A:2207:C:H5''	1.73	0.71
24:Z:9:CYS:SG	24:Z:12:CYS:N	2.64	0.71
1:A:2426:G:N2	1:A:2427:U:O4	2.24	0.71
1:A:1568:G:N2	1:A:1569:A:O2'	2.24	0.71
1:A:2116:G:O6	1:A:2262:A:N6	2.25	0.70
1:A:327:G:N2	1:A:400:U:O2	2.24	0.70
1:A:376:A:O2'	1:A:378:C:OP2	2.08	0.70
1:A:1880:U:H3	1:A:1920:G:H1	1.39	0.70
1:A:2129:G:O6	1:A:2218:U:O4	2.09	0.70
1:A:1874:G:N1	1:A:1925:A:C2	2.59	0.70
1:A:918:U:N3	1:A:953:G:N1	2.38	0.70
1:A:1878:G:H2'	1:A:1879:G:C8	2.26	0.70
1:A:2591:U:H3	1:A:2595:A:H62	1.40	0.70
25:Y:201:PRO:HG2	25:Y:208:TYR:HE1	1.57	0.70
1:A:411:G:O2'	1:A:413:U:O4	2.09	0.70
1:A:2495:C:O2	1:A:2515:G:N1	2.20	0.70
1:A:2351:A:H2	1:A:2361:C:H41	0.74	0.70
1:A:314:A:O2'	1:A:316:G:N7	2.25	0.70
25:Y:200:LYS:HE3	25:Y:201:PRO:HD2	1.73	0.70
1:A:1085:G:C6	1:A:1163:U:N3	2.60	0.69
1:A:1914:A:O2'	1:A:1915:U:O5'	2.08	0.69
1:A:2181:C:N4	1:A:2182:G:O6	2.25	0.69
1:A:2401:G:N3	1:A:2402:A:N6	2.37	0.69
23:W:138:PHE:O	25:Y:129:ARG:NH2	2.25	0.69
1:A:1512:G:O2'	1:A:1594:G:O2'	2.09	0.69
1:A:2681:U:O4	1:A:2697:G:O6	2.10	0.69
1:A:2162:G:O6	1:A:2184:U:H2'	1.91	0.69
1:A:2133:C:H2'	1:A:2134:A:H8	1.58	0.69
1:A:2868:G:H2'	1:A:2869:A:H8	1.56	0.69
1:A:732:A:H8	1:A:735:U:H3	1.41	0.69
1:A:1046:A:OP2	1:A:1200:G:N1	2.20	0.69
1:A:1310:C:H5''	1:A:1311:G:H5'	1.73	0.69
1:A:2310:C:OP1	1:A:2312:C:O2'	2.10	0.69
1:A:2512:C:H3'	1:A:2513:G:H21	1.58	0.69
1:A:2133:C:H2'	1:A:2134:A:C8	2.28	0.69
1:A:2360:G:H1'	1:A:2364:A:N6	2.08	0.69
1:A:1474:C:N4	1:A:1618:A:OP2	2.26	0.69
1:A:785:C:O2'	1:A:786:A:OP1	2.10	0.68
1:A:2128:U:O4	1:A:2219:G:O6	2.10	0.68
12:L:58:ARG:NH1	12:L:93:LYS:NZ	2.41	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:251:G:H21	1:A:252:C:H5'	1.58	0.68
1:A:1166:G:H2'	1:A:1167:C:C6	2.28	0.68
1:A:2514:G:OP2	1:A:2514:G:N2	2.20	0.68
1:A:293:U:H2'	1:A:294:G:H8	1.57	0.68
1:A:2108:U:H2'	1:A:2109:G:H8	1.59	0.68
25:Y:67:ASN:HB2	25:Y:188:ASN:ND2	2.08	0.68
1:A:159:U:H3'	1:A:160:G:H8	1.57	0.68
1:A:896:A:H2'	1:A:897:G:C8	2.29	0.68
1:A:93:C:H2'	1:A:94:A:H8	1.58	0.68
1:A:2385:C:N4	1:A:2386:U:O2	2.27	0.68
17:Q:31:ALA:HA	17:Q:46:TYR:CB	2.24	0.68
1:A:692:A:N3	1:A:2378:G:N2	2.42	0.68
1:A:2489:U:O2'	1:A:2524:G:N2	2.26	0.68
1:A:1516:A:H62	1:A:1568:G:H8	1.42	0.68
1:A:160:G:O2'	1:A:168:A:N6	2.28	0.67
1:A:2124:A:N1	1:A:2224:U:O2'	2.26	0.67
25:Y:199:ALA:O	25:Y:201:PRO:HD3	1.95	0.67
1:A:754:G:H1	1:A:771:U:H3	1.39	0.67
1:A:1585:A:N6	1:A:1587:U:O2	2.26	0.67
1:A:1245:G:H1'	1:A:1246:G:H5'	1.76	0.67
1:A:1587:U:H2'	1:A:1588:A:H8	1.59	0.67
1:A:1214:U:H2'	1:A:1215:U:C6	2.28	0.67
1:A:1444:C:H2'	1:A:1445:A:C8	2.28	0.67
1:A:2143:A:O2'	1:A:2197:G:O6	2.12	0.67
1:A:2197:G:N1	1:A:2200:A:N1	2.43	0.67
23:W:138:PHE:H	25:Y:129:ARG:NH2	1.93	0.67
1:A:1090:U:O2'	1:A:1157:A:N1	2.28	0.67
1:A:1866:C:O2'	1:A:1868:G:N7	2.24	0.67
1:A:2810:A:H5''	1:A:2811:G:H5'	1.76	0.67
1:A:2413:G:OP1	1:A:2413:G:N2	2.28	0.67
1:A:1218:U:H2'	1:A:1220:G:H1'	1.78	0.66
1:A:2676:U:H3	1:A:2702:G:H1	1.40	0.66
1:A:2684:G:H1	1:A:2693:G:H3'	1.60	0.66
1:A:442:C:H2'	1:A:443:G:H8	1.60	0.66
1:A:2313:C:OP2	1:A:2418:G:N1	2.28	0.66
1:A:1831:A:O2'	1:A:1832:A:H8	1.75	0.66
2:B:53:U:O2'	2:B:55:A:N7	2.27	0.66
1:A:2145:G:H22	1:A:2164:A:H4'	1.59	0.66
25:Y:59:ILE:HG21	25:Y:208:TYR:OH	1.95	0.66
1:A:1871:G:O6	1:A:1927:U:O4	2.14	0.66
1:A:2293:C:N3	1:A:2305:G:N1	2.44	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2198:G:H21	1:A:2199:G:H1	1.43	0.66
1:A:2293:C:O2	1:A:2305:G:C2	2.48	0.66
1:A:2684:G:N2	1:A:2693:G:H2'	2.11	0.66
1:A:676:G:N2	1:A:679:A:OP2	2.29	0.66
1:A:286:U:H3'	1:A:287:G:H8	1.61	0.65
1:A:644:G:N2	1:A:650:U:OP1	2.29	0.65
1:A:917:A:C5	1:A:918:U:H1'	2.31	0.65
1:A:1094:A:O5'	1:A:1097:A:N6	2.29	0.65
1:A:2318:G:O2'	1:A:2375:A:N6	2.28	0.65
1:A:2491:U:H3	1:A:2518:G:H1	1.43	0.65
1:A:2655:C:H2'	1:A:2656:G:H8	1.59	0.65
1:A:2159:U:OP1	1:A:2189:G:N2	2.29	0.65
12:L:58:ARG:NH1	12:L:93:LYS:HZ1	1.95	0.65
1:A:688:G:N2	1:A:691:U:OP2	2.30	0.65
1:A:1085:G:O6	1:A:1164:C:N4	2.29	0.65
1:A:287:G:OP2	1:A:288:C:N4	2.28	0.65
1:A:403:C:H2'	1:A:404:C:C6	2.31	0.65
1:A:1709:A:H61	1:A:2025:C:H42	1.44	0.65
1:A:2544:C:H2'	1:A:2545:G:H8	1.62	0.65
1:A:1523:U:H5''	1:A:1524:A:H8	1.62	0.65
1:A:2163:A:N1	1:A:2188:G:O2'	2.30	0.65
1:A:197:G:H2'	1:A:198:A:C4	2.33	0.65
1:A:2404:G:OP1	1:A:2405:A:N6	2.29	0.65
1:A:546:G:N1	1:A:549:A:OP2	2.28	0.64
1:A:1521:G:N2	1:A:1563:G:H1	1.95	0.64
1:A:2779:A:O2'	1:A:2781:C:N4	2.23	0.64
23:W:132:ASP:HA	25:Y:137:MET:HE2	1.66	0.64
1:A:881:U:H1'	1:A:2387:A:C2	2.32	0.64
25:Y:59:ILE:HD11	25:Y:201:PRO:HG2	1.79	0.64
1:A:765:A:H5''	1:A:766:C:H5	1.61	0.64
1:A:1875:G:N2	1:A:1924:C:O2	2.29	0.64
1:A:1478:G:H2'	1:A:1479:G:C8	2.33	0.64
1:A:2302:A:OP2	1:A:2303:A:N6	2.30	0.64
1:A:2361:C:H4'	1:A:2362:A:OP1	1.96	0.64
1:A:2444:G:H3'	1:A:2445:C:C5	2.33	0.64
25:Y:59:ILE:CD1	25:Y:201:PRO:HG3	2.24	0.64
25:Y:66:PRO:C	25:Y:68:GLY:H	2.05	0.64
1:A:200:A:H4'	1:A:2459:A:H62	1.61	0.64
1:A:908:A:H2'	1:A:909:G:O4'	1.98	0.64
1:A:1263:G:N2	1:A:1266:A:OP2	2.30	0.64
1:A:1087:U:O2	1:A:1160:G:C6	2.51	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1883:A:H4'	23:W:221:ASN:HA	1.80	0.64
1:A:2175:C:H5''	1:A:2176:A:C8	2.33	0.64
1:A:1476:C:H2'	1:A:1477:A:H8	1.62	0.64
1:A:2400:G:H4'	1:A:2401:G:OP1	1.96	0.64
1:A:2771:G:N2	1:A:2791:U:O2	2.27	0.64
1:A:683:A:H4'	1:A:684:G:O5'	1.97	0.64
1:A:2552:G:H2'	1:A:2553:G:H8	1.63	0.64
1:A:2317:A:O5'	1:A:2318:G:N2	2.31	0.64
2:B:11:A:O2'	2:B:13:A:OP2	2.12	0.64
25:Y:195:THR:HA	25:Y:198:LYS:HE2	1.80	0.64
1:A:1070:G:H3'	1:A:1071:G:H5''	1.80	0.63
1:A:1485:A:H61	1:A:1600:G:H8	1.46	0.63
1:A:2103:U:H2'	1:A:2104:U:C2	2.33	0.63
1:A:2352:G:O6	1:A:2358:A:N6	2.30	0.63
1:A:2404:G:N2	1:A:2408:G:O6	2.31	0.63
1:A:2561:G:H21	1:A:2693:G:H5'	1.62	0.63
17:Q:41:GLY:HA2	17:Q:69:ALA:O	1.98	0.63
1:A:2207:C:P	25:Y:211:ASN:ND2	2.67	0.63
1:A:2406:A:N7	22:V:102:TYR:OH	2.31	0.63
25:Y:80:LYS:NZ	25:Y:120:MET:HB2	2.14	0.63
1:A:59:G:O2'	1:A:74:U:OP2	2.14	0.63
1:A:1046:A:H2'	1:A:1047:A:C8	2.33	0.63
1:A:1523:U:H5''	1:A:1524:A:C8	2.34	0.63
1:A:250:G:OP2	1:A:252:C:N4	2.32	0.63
1:A:757:C:H2'	1:A:758:A:H8	1.64	0.63
1:A:2111:A:N6	1:A:2266:G:O3'	2.32	0.63
1:A:2138:U:H3	1:A:2209:U:H3	1.47	0.63
1:A:353:A:N7	1:A:374:A:N6	2.46	0.63
1:A:873:U:O2	1:A:879:G:N1	2.32	0.63
1:A:2444:G:H3'	1:A:2445:C:C4	2.34	0.63
1:A:2844:A:O2'	1:A:2846:A:N7	2.26	0.63
2:B:22:G:O6	2:B:54:U:O2'	2.15	0.63
25:Y:101:ILE:HD11	25:Y:124:VAL:HG23	1.81	0.63
1:A:669:C:H2'	1:A:670:C:C6	2.34	0.62
1:A:1094:A:OP2	1:A:1156:G:N2	2.32	0.62
1:A:1511:C:H2'	1:A:1512:G:C8	2.33	0.62
1:A:1493:C:O2'	1:A:1592:A:N3	2.32	0.62
1:A:626:G:H2'	1:A:627:G:H8	1.64	0.62
1:A:1549:U:H2'	1:A:1550:C:C6	2.35	0.62
25:Y:194:ASP:HA	25:Y:197:LEU:HG	1.80	0.62
1:A:765:A:H3'	1:A:766:C:H6	1.63	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:47:GLU:N	6:F:50:VAL:O	2.33	0.62
1:A:1551:C:H2'	1:A:1552:C:C6	2.34	0.62
1:A:221:G:H22	1:A:238:U:H4'	1.65	0.62
25:Y:59:ILE:HD12	25:Y:201:PRO:HG3	1.81	0.62
1:A:2901:G:H2'	1:A:2902:A:H8	1.65	0.62
2:B:45:C:H4'	2:B:46:A:C5	2.35	0.62
1:A:1880:U:O2	1:A:1920:G:N2	2.33	0.61
1:A:83:G:N2	1:A:102:A:OP2	2.24	0.61
1:A:2129:G:N2	1:A:2218:U:O2	2.28	0.61
1:A:2163:A:N7	1:A:2185:G:N1	2.47	0.61
25:Y:78:PHE:HB3	25:Y:120:MET:HE3	1.81	0.61
25:Y:201:PRO:HD2	25:Y:208:TYR:CE1	2.35	0.61
1:A:652:A:OP2	1:A:665:G:N1	2.24	0.61
1:A:2490:C:H1'	1:A:2523:G:H22	1.64	0.61
1:A:2207:C:OP1	25:Y:47:ARG:HD2	2.01	0.61
1:A:2401:G:H2'	1:A:2402:A:C6	2.35	0.61
2:B:77:G:O6	2:B:95:U:O4	2.17	0.61
10:J:102:MET:SD	20:T:49:TYR:HD2	2.24	0.61
23:W:219:THR:HA	23:W:224:GLU:HA	1.83	0.61
1:A:960:U:H1'	1:A:961:C:H5	1.65	0.61
1:A:1519:C:H42	1:A:1566:G:H1	1.48	0.61
14:N:44:SER:HB3	14:N:45:PRO:HD3	1.83	0.61
23:W:137:GLY:H	25:Y:129:ARG:CZ	2.12	0.61
23:W:176:ILE:HG22	23:W:177:GLN:N	2.16	0.61
1:A:1231:G:OP1	9:I:32:GLY:HA2	2.01	0.61
1:A:2322:C:H42	1:A:2369:A:H61	1.48	0.61
1:A:2688:G:H1'	1:A:2691:A:N6	2.14	0.61
1:A:2841:C:O2	1:A:2908:A:O2'	2.17	0.61
23:W:134:TYR:CB	25:Y:129:ARG:HG2	2.31	0.61
1:A:1015:G:H2'	1:A:1016:U:C6	2.36	0.61
1:A:1218:U:H3	1:A:1221:A:H1'	1.65	0.61
1:A:1875:G:N1	1:A:1924:C:N3	2.48	0.61
1:A:2090:G:N2	1:A:2091:A:O2'	2.34	0.61
2:B:49:G:H2'	2:B:50:A:C8	2.36	0.61
1:A:692:A:H3'	1:A:693:G:H8	1.66	0.60
1:A:1085:G:O6	1:A:1163:U:C4	2.54	0.60
1:A:2160:U:H1'	1:A:2183:G:H5'	1.81	0.60
1:A:164:U:H2'	1:A:165:C:H6	1.65	0.60
1:A:2219:G:H2'	1:A:2220:A:H8	1.66	0.60
1:A:2412:G:O2'	1:A:2413:G:OP1	2.17	0.60
14:N:12:ILE:HD11	14:N:43:ALA:HB2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1573:C:H2'	1:A:1574:G:C8	2.37	0.60
1:A:2060:A:O3'	1:A:2061:G:N2	2.26	0.60
1:A:2434:G:H21	1:A:2441:A:H62	1.48	0.60
1:A:1085:G:N1	1:A:1163:U:N3	2.50	0.60
1:A:2357:A:H3'	1:A:2358:A:H5''	1.83	0.60
1:A:1029:A:N6	1:A:1030:G:O6	2.34	0.60
1:A:2301:U:H5''	1:A:2302:A:O4'	2.01	0.60
1:A:2218:U:H2'	1:A:2219:G:H8	1.66	0.60
1:A:2315:A:N6	1:A:2353:U:O3'	2.34	0.60
12:L:58:ARG:HH12	12:L:93:LYS:NZ	1.99	0.60
1:A:687:U:H2'	1:A:688:G:C4	2.36	0.60
1:A:875:U:H4'	1:A:878:G:C4	2.36	0.60
1:A:1497:G:N2	1:A:1505:U:H3	2.00	0.60
1:A:2164:A:OP1	1:A:2166:C:N4	2.34	0.60
1:A:2233:C:H2'	1:A:2234:C:H6	1.67	0.60
1:A:2440:A:H2'	1:A:2441:A:C8	2.36	0.60
1:A:2494:C:H2'	1:A:2495:C:C2	2.36	0.60
1:A:2685:U:N3	1:A:2694:A:C8	2.69	0.60
1:A:1347:A:H62	1:A:1651:G:H8	1.48	0.60
1:A:2766:G:H2'	1:A:2767:A:C8	2.36	0.60
1:A:1322:G:N2	1:A:1325:A:OP2	2.35	0.60
1:A:2160:U:O4'	1:A:2186:G:N2	2.34	0.60
1:A:164:U:H2'	1:A:165:C:C6	2.37	0.59
1:A:1085:G:C6	1:A:1163:U:C4	2.90	0.59
1:A:89:U:H5''	1:A:90:A:H2'	1.84	0.59
1:A:1080:G:O2'	1:A:1081:U:OP1	2.20	0.59
1:A:1362:G:O2'	1:A:1363:G:OP1	2.17	0.59
1:A:2291:U:H5''	1:A:2415:U:N3	2.17	0.59
1:A:2825:C:H3'	1:A:2826:A:H8	1.67	0.59
1:A:351:G:N2	1:A:354:A:OP2	2.35	0.59
1:A:704:U:H2'	1:A:705:A:C8	2.37	0.59
1:A:1529:G:H2'	1:A:1530:G:C8	2.37	0.59
1:A:1925:A:H2'	1:A:1926:G:C8	2.38	0.59
1:A:2070:U:H2'	1:A:2071:A:C8	2.37	0.59
1:A:2198:G:N2	1:A:2199:G:H1	2.01	0.59
1:A:2108:U:O2'	1:A:2109:G:OP1	2.21	0.59
1:A:2859:G:H21	1:A:2908:A:H62	1.48	0.59
2:B:45:C:O2'	2:B:46:A:H5''	2.01	0.59
23:W:391:LYS:CB	23:W:392:PRO:HD3	2.32	0.59
1:A:2361:C:N4	1:A:2365:A:H61	2.00	0.59
2:B:43:A:H5''	2:B:44:A:C8	2.37	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1431:G:H2'	1:A:1432:A:C8	2.37	0.59
1:A:2293:C:O2'	1:A:2294:U:O5'	2.20	0.59
23:W:137:GLY:N	25:Y:129:ARG:CZ	2.65	0.59
1:A:1509:C:H2'	1:A:1510:G:C8	2.38	0.59
1:A:1507:U:H2'	1:A:1508:C:C6	2.38	0.59
1:A:2144:G:O2'	1:A:2194:G:N2	2.35	0.59
1:A:2298:A:H2'	1:A:2299:G:C5	2.38	0.59
1:A:45:G:H5'	1:A:46:C:H5'	1.85	0.59
1:A:293:U:H2'	1:A:294:G:C8	2.37	0.59
1:A:337:A:O2'	1:A:338:G:O4'	2.20	0.59
1:A:1572:G:O2'	1:A:1573:C:H6	1.84	0.59
1:A:1876:A:H62	1:A:1922:C:H42	1.51	0.59
1:A:2123:A:H2'	1:A:2124:A:C8	2.38	0.59
1:A:2488:A:N1	1:A:2526:A:N6	2.50	0.59
22:V:109:LEU:O	22:V:113:ALA:N	2.36	0.59
1:A:2137:U:H3	1:A:2210:G:H1	1.48	0.58
1:A:2294:U:H1'	1:A:2295:A:H2'	1.85	0.58
1:A:2330:A:H3'	1:A:2331:U:C6	2.38	0.58
6:F:59:GLN:HB2	6:F:62:HIS:ND1	2.18	0.58
1:A:802:G:H2'	1:A:803:C:C6	2.38	0.58
1:A:918:U:O2	1:A:953:G:C2	2.57	0.58
1:A:1085:G:C2	1:A:1163:U:O2	2.56	0.58
1:A:2366:G:O2'	1:A:2367:G:OP1	2.20	0.58
1:A:2420:G:H4'	1:A:2421:A:C4	2.38	0.58
1:A:1529:G:H2'	1:A:1530:G:H8	1.67	0.58
1:A:231:A:H2'	1:A:233:G:H5''	1.85	0.58
1:A:957:A:C4	1:A:2294:U:H4'	2.39	0.58
1:A:1882:A:O2'	1:A:1917:G:N2	2.36	0.58
1:A:2162:G:N2	1:A:2183:G:O5'	2.37	0.58
1:A:2414:C:HO2'	17:Q:49:ARG:NH1	2.01	0.58
1:A:296:G:H2'	1:A:297:G:C8	2.39	0.58
1:A:852:G:O2'	1:A:853:C:OP1	2.21	0.58
1:A:1161:A:H2'	1:A:1162:C:C6	2.38	0.58
1:A:2103:U:H2'	1:A:2104:U:N1	2.18	0.58
1:A:2148:A:N6	1:A:2178:C:O2'	2.30	0.58
1:A:2317:A:C5	1:A:2319:G:N1	2.72	0.58
1:A:1008:A:H2'	1:A:1009:U:C6	2.38	0.58
1:A:2709:C:H1'	4:D:191:ASN:ND2	2.19	0.58
1:A:2865:U:H5''	10:J:49:THR:HG21	1.85	0.58
1:A:232:U:H4'	1:A:233:G:OP1	2.04	0.58
1:A:918:U:C2	1:A:953:G:N1	2.72	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1580:A:OP2	1:A:1581:A:N6	2.37	0.58
1:A:1162:C:O2'	1:A:1163:U:O4'	2.20	0.57
1:A:2367:G:N3	1:A:2368:G:N2	2.52	0.57
1:A:2728:U:H2'	1:A:2729:C:H6	1.69	0.57
1:A:576:G:O2'	1:A:578:A:N7	2.37	0.57
1:A:633:U:H2'	1:A:634:A:H8	1.69	0.57
1:A:685:U:H2'	1:A:686:C:C6	2.40	0.57
25:Y:80:LYS:HZ2	25:Y:120:MET:HB2	1.69	0.57
1:A:871:G:O2'	1:A:872:C:O5'	2.21	0.57
1:A:1201:A:H5''	12:L:55:ARG:HD3	1.85	0.57
1:A:1883:A:N6	1:A:1917:G:N2	2.41	0.57
1:A:2130:G:N2	1:A:2217:U:O2	2.30	0.57
23:W:389:SER:HG	23:W:394:SER:CB	2.10	0.57
1:A:432:C:O2'	1:A:435:G:N2	2.38	0.57
1:A:897:G:H2'	1:A:898:U:C6	2.39	0.57
1:A:1586:G:H2'	1:A:1587:U:C6	2.39	0.57
1:A:2859:G:N2	1:A:2908:A:H62	2.01	0.57
1:A:111:U:OP1	18:R:58:ARG:NH2	2.36	0.57
1:A:954:U:H2'	1:A:955:C:C6	2.39	0.57
1:A:1461:A:H2'	1:A:1462:G:O4'	2.05	0.57
1:A:1886:G:N2	1:A:1914:A:N6	2.37	0.57
1:A:200:A:O2'	1:A:201:C:O5'	2.23	0.57
1:A:2373:U:OP1	24:Z:34:LYS:NZ	2.36	0.57
1:A:2524:G:O2'	1:A:2525:C:O4'	2.23	0.57
1:A:2688:G:N2	1:A:2691:A:OP2	2.35	0.57
1:A:2716:U:H2'	1:A:2717:G:O4'	2.05	0.57
1:A:2728:U:H2'	1:A:2729:C:C6	2.40	0.57
1:A:2773:G:H5''	1:A:2784:C:H41	1.68	0.57
4:D:54:ASP:O	4:D:77:LYS:HA	2.05	0.57
6:F:78:GLU:O	6:F:81:SER:OG	2.14	0.57
25:Y:201:PRO:CD	25:Y:208:TYR:CE1	2.88	0.57
1:A:921:G:H1	1:A:950:U:H2'	1.69	0.57
1:A:1013:U:H2'	1:A:1014:A:H8	1.69	0.57
1:A:2204:U:C2	1:A:2205:A:H1'	2.40	0.57
1:A:2317:A:H3'	1:A:2318:G:N3	2.20	0.57
1:A:2443:G:H2'	1:A:2444:G:C8	2.39	0.57
25:Y:49:GLY:HA2	25:Y:210:LYS:HE3	1.87	0.57
1:A:5:A:H2'	1:A:6:A:H8	1.70	0.57
1:A:1079:U:H1'	1:A:1080:G:H5'	1.86	0.57
1:A:1913:A:H3'	1:A:1914:A:H8	1.70	0.57
1:A:2493:C:H2'	1:A:2494:C:C6	2.39	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2676:U:O4	1:A:2702:G:O6	2.23	0.57
8:H:11:ALA:HB1	8:H:99:PHE:HB2	1.86	0.57
1:A:2494:C:N4	1:A:2517:A:H61	2.02	0.57
1:A:999:A:H61	1:A:1010:C:H42	1.53	0.56
1:A:1304:G:OP1	20:T:16:ARG:NH2	2.38	0.56
1:A:1379:U:OP2	15:O:59:TYR:OH	2.20	0.56
1:A:287:G:H3'	1:A:288:C:C6	2.40	0.56
1:A:1509:C:H2'	1:A:1510:G:H8	1.70	0.56
1:A:1515:C:H2'	1:A:1516:A:C8	2.39	0.56
1:A:2251:G:H2'	1:A:2252:A:C8	2.40	0.56
1:A:2769:A:OP2	1:A:2792:G:N1	2.33	0.56
1:A:268:A:N6	1:A:474:U:O2'	2.38	0.56
1:A:463:U:O2'	1:A:464:C:OP1	2.23	0.56
1:A:662:U:H2'	1:A:663:G:H8	1.68	0.56
1:A:719:C:OP1	5:E:90:PHE:CZ	2.59	0.56
1:A:725:C:H2'	1:A:726:C:C6	2.41	0.56
1:A:795:G:C6	14:N:90:MET:HE1	2.41	0.56
1:A:1072:A:OP2	1:A:1180:C:O2'	2.23	0.56
1:A:1077:G:H2'	1:A:1078:A:H8	1.70	0.56
1:A:1476:C:H2'	1:A:1477:A:C8	2.40	0.56
1:A:1478:G:H2'	1:A:1479:G:H8	1.69	0.56
1:A:1497:G:H22	1:A:1505:U:H3	1.53	0.56
1:A:2066:A:H2'	1:A:2067:G:H8	1.68	0.56
1:A:2370:G:H2'	1:A:2371:C:C2	2.40	0.56
2:B:43:A:H2'	2:B:43:A:N3	2.20	0.56
12:L:58:ARG:HH12	12:L:93:LYS:HZ1	1.53	0.56
23:W:322:TYR:HB2	23:W:425:GLY:N	2.20	0.56
25:Y:59:ILE:HD13	25:Y:201:PRO:CG	2.34	0.56
1:A:92:G:H2'	1:A:93:C:C6	2.40	0.56
1:A:275:A:HO2'	1:A:305:A:HO2'	1.52	0.56
1:A:537:A:O2'	1:A:538:A:OP1	2.23	0.56
1:A:1515:C:H2'	1:A:1516:A:H8	1.69	0.56
1:A:1623:C:H2'	1:A:1624:U:C6	2.41	0.56
1:A:2427:U:O4	1:A:2449:C:N4	2.39	0.56
1:A:2709:C:H1'	4:D:191:ASN:HD22	1.70	0.56
1:A:769:A:H2'	1:A:770:A:H8	1.71	0.56
25:Y:197:LEU:O	25:Y:198:LYS:C	2.47	0.56
1:A:625:C:OP2	12:L:33:LYS:NZ	2.34	0.56
1:A:765:A:H3'	1:A:766:C:C6	2.40	0.56
1:A:981:C:H2'	1:A:982:U:H6	1.71	0.56
1:A:1065:U:H3	1:A:1188:A:H62	1.54	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1093:G:N1	1:A:1157:A:OP2	2.38	0.56
1:A:1706:G:N2	1:A:2717:G:OP1	2.39	0.56
1:A:1881:U:H5''	1:A:1917:G:C6	2.41	0.56
1:A:2233:C:H2'	1:A:2234:C:C6	2.40	0.56
1:A:913:A:N6	1:A:961:C:N3	2.54	0.56
1:A:1428:G:H2'	1:A:1429:U:C6	2.40	0.56
1:A:2325:U:O2'	1:A:2326:C:O5'	2.23	0.56
1:A:2566:U:H2'	1:A:2567:C:C6	2.41	0.56
1:A:2684:G:N2	1:A:2685:U:O4	2.39	0.56
1:A:1097:A:H2'	1:A:1098:C:C2	2.39	0.56
1:A:1656:C:HO2'	1:A:1657:C:H6	1.53	0.56
1:A:2184:U:O2'	1:A:2185:G:O4'	2.24	0.56
1:A:2376:C:H5	1:A:2410:C:C2	2.24	0.56
1:A:2429:G:N2	1:A:2446:C:O2'	2.39	0.56
1:A:24:G:H2'	1:A:25:U:C6	2.41	0.56
1:A:159:U:O4	1:A:169:G:O6	2.24	0.56
1:A:1884:G:O2'	1:A:1885:A:OP1	2.21	0.56
1:A:2377:U:H3'	1:A:2378:G:H5''	1.87	0.56
1:A:2491:U:H3	1:A:2518:G:H22	1.53	0.56
1:A:2516:G:H2'	1:A:2517:A:O4'	2.06	0.56
1:A:2686:A:H61	1:A:2693:G:H1'	1.71	0.56
2:B:47:C:OP2	2:B:47:C:H4'	2.02	0.56
1:A:57:C:O3'	15:O:75:ARG:NH2	2.38	0.56
1:A:2099:G:H2'	1:A:2100:A:C8	2.40	0.56
2:B:3:U:OP1	2:B:59:U:O2'	2.21	0.56
2:B:19:G:O2'	2:B:20:A:OP1	2.22	0.56
1:A:2114:C:N4	1:A:2115:U:O4	2.39	0.55
1:A:2834:A:OP2	1:A:2915:G:N1	2.24	0.55
1:A:286:U:H3'	1:A:287:G:C8	2.41	0.55
1:A:455:G:H2'	1:A:456:A:C8	2.42	0.55
1:A:530:A:H5''	16:P:46:LYS:HD3	1.88	0.55
1:A:1008:A:H2'	1:A:1009:U:H6	1.70	0.55
1:A:2111:A:H2'	1:A:2112:G:O4'	2.06	0.55
1:A:2219:G:H2'	1:A:2220:A:C8	2.40	0.55
1:A:2369:A:H2'	1:A:2370:G:N2	2.20	0.55
1:A:2380:G:H21	1:A:2395:A:H8	1.54	0.55
1:A:2773:G:OP2	1:A:2784:C:N4	2.39	0.55
2:B:95:U:H3'	2:B:96:G:H8	1.71	0.55
1:A:24:G:H2'	1:A:25:U:H6	1.72	0.55
1:A:391:A:H2'	1:A:392:C:C6	2.42	0.55
1:A:430:C:H41	1:A:432:C:H2'	1.70	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2293:C:N3	1:A:2305:G:C2	2.75	0.55
1:A:2802:U:OP1	4:D:168:GLN:NE2	2.38	0.55
1:A:302:A:H2'	1:A:303:G:C8	2.40	0.55
1:A:2120:U:OP2	1:A:2121:U:O2'	2.12	0.55
25:Y:175:ILE:HB	25:Y:188:ASN:HB3	1.89	0.55
1:A:1774:A:H3'	1:A:1775:G:H8	1.71	0.55
1:A:2318:G:H1'	1:A:2319:G:O5'	2.06	0.55
1:A:2351:A:H2'	1:A:2352:G:C8	2.41	0.55
1:A:2374:G:H4'	1:A:2375:A:H3'	1.89	0.55
1:A:2699:G:H2'	1:A:2700:A:H8	1.72	0.55
1:A:5:A:H2'	1:A:6:A:C8	2.41	0.55
1:A:1016:U:H2'	1:A:1017:C:C6	2.42	0.55
1:A:1870:U:HO2'	1:A:1871:G:P	2.27	0.55
1:A:2101:G:H2'	1:A:2102:C:C6	2.42	0.55
1:A:2434:G:N2	1:A:2441:A:H62	2.05	0.55
1:A:1081:U:O2	1:A:1166:G:N2	2.32	0.55
1:A:1094:A:H61	1:A:1158:G:H1'	1.71	0.55
1:A:1882:A:O2'	1:A:1883:A:N7	2.30	0.55
2:B:3:U:HO2'	2:B:4:G:H8	1.54	0.55
7:G:78:HIS:ND1	7:G:79:THR:O	2.40	0.55
1:A:259:A:H2'	1:A:260:A:C8	2.42	0.55
1:A:1924:C:H2'	1:A:1925:A:C8	2.42	0.55
1:A:2293:C:C2	1:A:2305:G:N1	2.75	0.55
1:A:274:A:N6	1:A:298:U:C2	2.75	0.55
1:A:1480:A:N6	1:A:1606:A:H61	2.05	0.55
1:A:2197:G:H2'	1:A:2198:G:H5''	1.89	0.55
1:A:2401:G:H21	1:A:2409:U:H3	1.53	0.55
5:E:52:LYS:O	5:E:88:VAL:HG22	2.07	0.55
1:A:2683:A:N1	1:A:2694:A:H5''	2.22	0.54
2:B:43:A:H3'	2:B:44:A:C8	2.42	0.54
25:Y:121:MET:CE	25:Y:121:MET:CA	2.86	0.54
1:A:296:G:O2'	1:A:297:G:O5'	2.24	0.54
1:A:455:G:H2'	1:A:456:A:H8	1.72	0.54
1:A:1061:A:H2'	1:A:1062:C:C6	2.42	0.54
1:A:2411:G:H1'	1:A:2412:G:H4'	1.89	0.54
1:A:704:U:H2'	1:A:705:A:H8	1.73	0.54
1:A:1303:U:H2'	1:A:1304:G:C8	2.43	0.54
1:A:1881:U:H2'	1:A:1917:G:C4	2.42	0.54
1:A:2322:C:P	1:A:2403:C:H41	2.30	0.54
1:A:1279:C:H2'	1:A:1280:G:C8	2.42	0.54
1:A:1339:A:H4'	1:A:1340:A:O5'	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1390:C:H2'	1:A:1391:U:C6	2.42	0.54
1:A:1918:A:H2'	1:A:1919:A:O4'	2.08	0.54
1:A:776:G:C2	1:A:1804:U:H1'	2.43	0.54
1:A:89:U:H3'	1:A:90:A:H8	1.73	0.54
1:A:2107:C:H2'	1:A:2108:U:C6	2.42	0.54
1:A:2164:A:H3'	1:A:2165:A:H8	1.71	0.54
1:A:2272:U:H2'	1:A:2463:A:N1	2.23	0.54
25:Y:67:ASN:HD21	25:Y:187:GLU:CB	2.17	0.54
1:A:219:A:H62	1:A:478:U:H5	1.56	0.54
1:A:1175:A:H1'	1:A:2545:G:H1'	1.88	0.54
1:A:1482:G:H21	1:A:1562:A:H8	1.55	0.54
1:A:2026:A:O5'	4:D:130:ARG:NE	2.37	0.54
7:G:78:HIS:CE1	7:G:79:THR:O	2.61	0.54
1:A:619:A:OP2	1:A:2084:C:N4	2.41	0.54
1:A:1927:U:H5'	1:A:1928:A:OP2	2.07	0.54
1:A:2083:A:O5'	1:A:2084:C:H5'	2.08	0.54
1:A:2688:G:N2	1:A:2690:G:H3'	2.22	0.54
6:F:65:LEU:O	6:F:69:THR:HG23	2.08	0.54
25:Y:73:GLN:O	25:Y:157:LYS:NZ	2.39	0.54
1:A:1063:G:H2'	1:A:1064:U:C6	2.43	0.54
1:A:1914:A:O2'	1:A:1915:U:H6	1.91	0.54
1:A:2368:G:H3'	1:A:2369:A:C8	2.38	0.54
1:A:2695:C:H2'	1:A:2696:C:O4'	2.08	0.54
1:A:684:G:H2'	1:A:685:U:C6	2.43	0.54
1:A:726:C:H2'	1:A:727:A:C8	2.39	0.54
1:A:768:G:H2'	1:A:769:A:C8	2.43	0.54
1:A:960:U:O2	1:A:961:C:N4	2.41	0.54
1:A:1455:C:O2'	1:A:1456:A:OP1	2.23	0.54
1:A:1549:U:H2'	1:A:1550:C:H6	1.72	0.54
1:A:1874:G:C6	1:A:1925:A:N1	2.76	0.54
1:A:2388:C:H2'	1:A:2389:A:C8	2.33	0.54
1:A:686:C:N4	1:A:695:G:O6	2.40	0.53
1:A:2066:A:H2'	1:A:2067:G:C8	2.43	0.53
1:A:2173:G:H2'	1:A:2175:C:H5'	1.89	0.53
15:O:9:LYS:O	18:R:29:ARG:HD3	2.09	0.53
1:A:2143:A:H3'	1:A:2144:G:H8	1.74	0.53
1:A:2401:G:H2'	1:A:2402:A:N6	2.22	0.53
23:W:176:ILE:CG2	23:W:177:GLN:N	2.71	0.53
1:A:679:A:O2'	1:A:2433:C:OP1	2.19	0.53
1:A:687:U:H2'	1:A:688:G:N9	2.23	0.53
1:A:844:U:OP1	5:E:62:ARG:NH1	2.40	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:898:U:H2'	1:A:899:C:C6	2.44	0.53
1:A:1871:G:C6	1:A:1927:U:N3	2.76	0.53
1:A:2156:G:H4'	1:A:2202:A:N1	2.24	0.53
1:A:2161:G:H4'	1:A:2162:G:H21	1.74	0.53
1:A:2333:G:O6	1:A:2342:C:O2'	2.23	0.53
1:A:2387:A:H2'	1:A:2388:C:C6	2.43	0.53
1:A:2878:U:H2'	1:A:2879:G:H8	1.72	0.53
23:W:138:PHE:C	25:Y:129:ARG:NH2	2.67	0.53
1:A:80:G:H21	1:A:337:A:H8	1.55	0.53
1:A:402:U:H2'	1:A:403:C:C6	2.44	0.53
1:A:2123:A:H2'	1:A:2124:A:H8	1.73	0.53
1:A:2218:U:H2'	1:A:2219:G:C8	2.43	0.53
1:A:2686:A:H2'	1:A:2687:C:O4'	2.08	0.53
1:A:2878:U:H2'	1:A:2879:G:C8	2.43	0.53
1:A:288:C:H2'	1:A:289:C:C6	2.44	0.53
1:A:1172:A:H4'	1:A:1173:A:H5''	1.90	0.53
1:A:1838:A:H2'	1:A:1839:A:C8	2.43	0.53
1:A:2385:C:H2'	1:A:2386:U:H4'	1.91	0.53
9:I:128:PHE:HE2	9:I:143:ALA:HB1	1.72	0.53
23:W:138:PHE:C	25:Y:129:ARG:HH22	2.16	0.53
1:A:2320:U:HO2'	1:A:2321:U:H6	1.55	0.53
1:A:2901:G:H2'	1:A:2902:A:C8	2.44	0.53
1:A:287:G:H3'	1:A:288:C:C5	2.43	0.53
1:A:761:U:H4'	1:A:764:C:H41	1.74	0.53
1:A:768:G:H2'	1:A:769:A:H8	1.72	0.53
1:A:1599:U:H3'	1:A:1600:G:H21	1.73	0.53
1:A:2207:C:H2'	1:A:2208:C:C6	2.44	0.53
1:A:403:C:H2'	1:A:404:C:H6	1.72	0.53
1:A:919:U:H2'	1:A:920:G:C8	2.44	0.53
1:A:951:C:H2'	1:A:952:A:H8	1.74	0.53
1:A:953:G:H2'	1:A:954:U:C6	2.43	0.53
1:A:1026:A:C2	1:A:1182:G:H4'	2.44	0.53
1:A:1200:G:P	12:L:58:ARG:HE	2.31	0.53
1:A:1571:G:O2'	1:A:1572:G:H5'	2.08	0.53
1:A:1587:U:H2'	1:A:1588:A:C8	2.43	0.53
1:A:2162:G:O2'	1:A:2163:A:H5'	2.09	0.53
1:A:410:G:H3'	1:A:411:G:H8	1.72	0.53
1:A:442:C:H2'	1:A:443:G:C8	2.43	0.53
1:A:633:U:H2'	1:A:634:A:C8	2.44	0.53
1:A:1088:G:H2'	1:A:1089:C:H6	1.73	0.53
1:A:1925:A:H2'	1:A:1926:G:H8	1.74	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:887:C:H2'	1:A:888:A:H8	1.74	0.52
1:A:1292:G:N2	12:L:33:LYS:HB3	2.24	0.52
1:A:1438:C:H2'	1:A:1439:U:C6	2.44	0.52
1:A:2454:A:H4'	1:A:2455:A:H3'	1.90	0.52
2:B:34:C:H2'	2:B:47:C:C5	2.44	0.52
1:A:694:G:H4'	1:A:2380:G:H5'	1.91	0.52
1:A:2494:C:H2'	1:A:2495:C:N3	2.24	0.52
23:W:136:LEU:HB2	25:Y:129:ARG:NH1	2.25	0.52
25:Y:117:THR:N	25:Y:121:MET:SD	2.82	0.52
1:A:65:A:H2'	1:A:66:C:H6	1.73	0.52
1:A:902:G:O6	1:A:903:G:N1	2.43	0.52
1:A:1674:G:H2'	1:A:1675:A:C8	2.44	0.52
1:A:2451:C:O2	23:W:249:LEU:HD23	2.09	0.52
2:B:84:G:N1	2:B:86:U:O2	2.42	0.52
20:T:39:SER:C	20:T:41:ARG:H	2.18	0.52
1:A:419:G:H4'	1:A:420:U:O5'	2.10	0.52
1:A:1493:C:H2'	1:A:1494:G:C8	2.45	0.52
1:A:1782:G:N2	1:A:1785:G:N3	2.57	0.52
2:B:10:G:N2	17:Q:79:ARG:NH1	2.57	0.52
7:G:136:GLN:O	7:G:138:PRO:HD3	2.09	0.52
18:R:42:ARG:O	18:R:46:VAL:HG23	2.10	0.52
1:A:288:C:H2'	1:A:289:C:C5	2.45	0.52
1:A:349:C:H2'	1:A:350:U:C6	2.45	0.52
1:A:1483:A:H2'	1:A:1484:U:C6	2.45	0.52
1:A:2318:G:H2'	1:A:2373:U:H5	1.73	0.52
1:A:911:G:O2'	1:A:912:C:H5'	2.09	0.52
1:A:2727:U:H2'	1:A:2728:U:C6	2.44	0.52
1:A:2785:U:O2'	1:A:2786:A:OP2	2.26	0.52
1:A:2825:C:H3'	1:A:2826:A:C8	2.45	0.52
2:B:20:A:H2'	2:B:21:G:C8	2.45	0.52
1:A:917:A:H3'	1:A:918:U:H4'	1.92	0.52
1:A:2378:G:OP1	1:A:2378:G:H4'	2.10	0.52
1:A:2826:A:H2'	1:A:2827:A:C8	2.45	0.52
1:A:2911:G:C2	1:A:2912:A:C4	2.97	0.52
1:A:78:U:H2'	1:A:79:C:C6	2.45	0.52
1:A:678:A:H2'	1:A:679:A:C8	2.44	0.52
1:A:1279:C:H2'	1:A:1280:G:H8	1.74	0.52
1:A:1458:U:O2	1:A:1460:G:N1	2.43	0.52
1:A:1756:U:H2'	1:A:1757:G:N2	2.24	0.52
1:A:2873:G:H22	1:A:2892:G:H1'	1.73	0.52
1:A:449:A:H2'	1:A:450:U:C6	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:580:U:H2'	1:A:581:C:C6	2.45	0.52
1:A:995:U:OP1	1:A:1007:G:N2	2.37	0.52
1:A:604:C:O2'	12:L:48:ARG:NH1	2.42	0.52
1:A:703:G:H2'	1:A:704:U:H6	1.75	0.52
2:B:39:A:H4'	2:B:40:C:OP1	2.09	0.52
13:M:6:LYS:HA	13:M:11:GLN:HA	1.91	0.52
15:O:9:LYS:O	18:R:29:ARG:CD	2.58	0.52
25:Y:104:ILE:HA	25:Y:108:TRP:HB2	1.90	0.52
1:A:1304:G:H8	1:A:1304:G:O5'	1.94	0.51
1:A:1767:A:H3'	1:A:1768:A:C8	2.45	0.51
1:A:2217:U:H2'	1:A:2218:U:C6	2.45	0.51
1:A:2390:A:H2'	1:A:2391:G:C8	2.45	0.51
1:A:2774:C:H2'	1:A:2775:U:C6	2.44	0.51
1:A:824:G:H2'	1:A:825:G:H8	1.75	0.51
1:A:1562:A:H3'	1:A:1563:G:H8	1.75	0.51
1:A:1861:C:H2'	1:A:1862:C:C2	2.45	0.51
1:A:2685:U:C2	1:A:2686:A:C8	2.98	0.51
1:A:2715:G:H2'	1:A:2716:U:C6	2.45	0.51
2:B:31:G:C2	2:B:32:U:H1'	2.45	0.51
1:A:777:C:OP1	1:A:1804:U:O2'	2.28	0.51
1:A:1831:A:O2'	1:A:1832:A:O5'	2.28	0.51
1:A:2879:G:H2'	1:A:2880:U:C6	2.46	0.51
1:A:417:G:OP2	1:A:470:A:N6	2.42	0.51
1:A:626:G:H2'	1:A:627:G:C8	2.43	0.51
1:A:872:C:H5'	1:A:2457:G:N1	2.25	0.51
1:A:1270:C:H2'	1:A:1271:U:C6	2.45	0.51
1:A:1387:G:H2'	1:A:1388:A:H5''	1.92	0.51
1:A:1517:A:N6	1:A:1567:U:H3	2.06	0.51
1:A:2759:C:O3'	4:D:173:ASN:CB	2.58	0.51
2:B:107:G:H2'	2:B:108:C:C6	2.45	0.51
1:A:179:A:H5''	1:A:180:G:OP2	2.09	0.51
1:A:756:U:H2'	1:A:757:C:C6	2.45	0.51
1:A:1521:G:H22	1:A:1563:G:H22	1.57	0.51
1:A:2796:C:O2'	1:A:2797:C:OP1	2.27	0.51
1:A:907:U:O2	1:A:964:A:N7	2.44	0.51
1:A:952:A:H2'	1:A:953:G:C8	2.46	0.51
1:A:1483:A:H2'	1:A:1484:U:H6	1.76	0.51
1:A:2161:G:H2'	1:A:2182:G:H21	1.75	0.51
12:L:58:ARG:CZ	12:L:93:LYS:HZ1	2.23	0.51
1:A:170:G:H2'	1:A:171:A:H8	1.75	0.51
1:A:805:G:H21	1:A:2010:A:N6	2.07	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1029:A:N7	1:A:1030:G:C6	2.79	0.51
1:A:1533:A:H2'	1:A:1534:A:C8	2.46	0.51
1:A:1819:C:H2'	1:A:1820:A:C8	2.46	0.51
1:A:324:A:H2'	1:A:325:A:C8	2.46	0.51
1:A:583:G:P	7:G:2:ARG:HH21	2.34	0.51
1:A:1087:U:H1'	1:A:1161:A:H2	1.76	0.51
1:A:1392:A:OP2	1:A:1416:G:N1	2.35	0.51
1:A:1828:G:OP1	3:C:260:ARG:NH1	2.33	0.51
1:A:2909:U:H2'	1:A:2910:C:O4'	2.10	0.51
7:G:106:ILE:HG22	7:G:110:LEU:HD23	1.93	0.51
25:Y:66:PRO:O	25:Y:68:GLY:N	2.44	0.51
1:A:290:U:O2'	1:A:291:C:O5'	2.27	0.51
1:A:567:U:H2'	1:A:568:G:N7	2.26	0.51
1:A:715:A:H2'	1:A:717:A:H62	1.76	0.51
1:A:1080:G:H2'	1:A:1081:U:C6	2.46	0.51
1:A:1513:U:H2'	1:A:1514:C:C6	2.46	0.51
1:A:2688:G:N2	1:A:2690:G:H5''	2.26	0.51
2:B:107:G:H2'	2:B:108:C:H6	1.76	0.51
3:C:6:TYR:CE2	3:C:16:MET:HE3	2.46	0.51
25:Y:120:MET:O	25:Y:120:MET:HG2	2.10	0.51
25:Y:124:VAL:O	25:Y:127:ILE:CG2	2.54	0.51
1:A:999:A:N6	1:A:1010:C:H42	2.09	0.51
1:A:1093:G:C6	1:A:1156:G:H2'	2.46	0.51
1:A:1153:G:H2'	1:A:1154:U:O4'	2.11	0.51
1:A:1243:A:H2'	1:A:1244:A:N3	2.26	0.51
1:A:1520:A:H3'	1:A:1521:G:H8	1.76	0.51
1:A:2129:G:N1	1:A:2218:U:N3	2.32	0.51
1:A:2361:C:H41	1:A:2365:A:H61	1.58	0.51
1:A:2757:U:H2'	1:A:2758:G:H8	1.76	0.51
2:B:40:C:H1'	2:B:44:A:H61	1.75	0.51
1:A:1326:A:O2'	1:A:1327:U:O5'	2.30	0.50
1:A:1438:C:O2'	1:A:1439:U:OP1	2.28	0.50
1:A:2305:G:P	1:A:2305:G:H8	2.35	0.50
1:A:2428:G:OP1	26:W:502:GNP:N2	2.44	0.50
1:A:2552:G:H2'	1:A:2553:G:C8	2.45	0.50
1:A:2555:G:H1	1:A:2566:U:H3	1.59	0.50
1:A:545:U:H2'	1:A:546:G:O4'	2.11	0.50
1:A:703:G:H2'	1:A:704:U:C6	2.46	0.50
1:A:980:C:HO2'	1:A:981:C:H6	1.57	0.50
14:N:12:ILE:CD1	14:N:43:ALA:HB2	2.42	0.50
1:A:1201:A:H5''	12:L:55:ARG:CD	2.41	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1390:C:O2'	1:A:1619:A:O2'	2.26	0.50
9:I:128:PHE:C	9:I:132:ALA:HB3	2.36	0.50
23:W:184:PRO:HD3	23:W:233:MET:C	2.36	0.50
1:A:706:C:H2'	1:A:707:G:H8	1.76	0.50
1:A:2161:G:H5''	1:A:2182:G:H1'	1.92	0.50
1:A:2378:G:N7	1:A:2398:A:N6	2.59	0.50
1:A:2440:A:H2'	1:A:2441:A:H8	1.77	0.50
1:A:2873:G:O2'	1:A:2893:A:N6	2.44	0.50
1:A:67:A:H1'	1:A:88:G:N2	2.26	0.50
1:A:492:C:H2'	1:A:493:G:C8	2.46	0.50
1:A:692:A:H3'	1:A:693:G:C8	2.45	0.50
1:A:720:C:OP1	5:E:54:ARG:NH1	2.44	0.50
1:A:830:A:H2'	1:A:831:U:H4'	1.93	0.50
1:A:871:G:N2	1:A:2387:A:N1	2.55	0.50
1:A:872:C:H5'	1:A:2457:G:C6	2.46	0.50
1:A:2102:C:C2	1:A:2103:U:N3	2.79	0.50
1:A:2425:G:H22	1:A:2450:G:H8	1.58	0.50
1:A:2545:G:H2'	1:A:2546:C:O4'	2.12	0.50
12:L:58:ARG:CZ	12:L:93:LYS:HE3	2.42	0.50
23:W:137:GLY:C	25:Y:129:ARG:HD2	2.35	0.50
25:Y:65:LEU:HD13	25:Y:66:PRO:HD2	1.94	0.50
25:Y:66:PRO:C	25:Y:68:GLY:N	2.70	0.50
25:Y:67:ASN:H	25:Y:67:ASN:ND2	2.08	0.50
1:A:475:A:H2'	1:A:476:A:C8	2.46	0.50
1:A:621:G:H2'	1:A:622:A:C8	2.47	0.50
1:A:1097:A:H5''	1:A:1098:C:C6	2.46	0.50
1:A:1428:G:H2'	1:A:1429:U:H6	1.76	0.50
1:A:2330:A:H3'	1:A:2331:U:H6	1.76	0.50
1:A:2398:A:O2'	1:A:2399:G:H8	1.94	0.50
1:A:194:A:H2'	1:A:195:C:H6	1.77	0.50
1:A:1077:G:H2'	1:A:1078:A:C8	2.47	0.50
1:A:1082:G:C5	1:A:1166:G:C6	2.99	0.50
1:A:1358:G:H2'	1:A:1359:G:C8	2.46	0.50
1:A:1521:G:N2	1:A:1563:G:H22	2.10	0.50
1:A:1752:G:C5	1:A:1785:G:C6	3.00	0.50
1:A:1774:A:H3'	1:A:1775:G:C8	2.47	0.50
1:A:1886:G:C2	1:A:1914:A:N6	2.79	0.50
1:A:2823:C:H3'	1:A:2824:G:H8	1.77	0.50
6:F:73:LEU:O	6:F:76:MET:HG2	2.11	0.50
8:H:96:THR:O	8:H:117:LEU:HD21	2.12	0.50
1:A:81:G:H2'	1:A:82:G:O4'	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:970:A:H5''	17:Q:34:ALA:HB3	1.92	0.50
1:A:1027:A:HO2'	1:A:2065:C:HO2'	1.47	0.50
1:A:1097:A:H2'	1:A:1098:C:N3	2.27	0.50
1:A:1769:G:H2'	1:A:1770:C:H6	1.77	0.50
1:A:2398:A:O2'	1:A:2399:G:O5'	2.30	0.50
1:A:2684:G:C2	1:A:2693:G:H2'	2.47	0.50
4:D:2:THR:HB	4:D:203:LYS:HZ1	1.77	0.50
1:A:982:U:H2'	1:A:983:U:C6	2.46	0.50
1:A:1053:C:H5''	1:A:1054:A:H2'	1.94	0.50
1:A:2107:C:H2'	1:A:2108:U:C5	2.47	0.50
1:A:2272:U:N3	1:A:2273:U:O4	2.45	0.50
1:A:2403:C:C4	1:A:2404:G:C8	3.00	0.50
1:A:2672:G:H2'	1:A:2673:A:C8	2.47	0.50
23:W:13:ASN:HD21	23:W:34:THR:HG22	1.77	0.50
1:A:93:C:H2'	1:A:94:A:C8	2.42	0.49
1:A:269:G:H2'	1:A:270:C:O4'	2.12	0.49
1:A:983:U:H2'	1:A:984:G:C8	2.47	0.49
1:A:1525:G:H2'	1:A:1526:G:C8	2.46	0.49
1:A:2162:G:N2	1:A:2183:G:H3'	2.24	0.49
1:A:2429:G:H2'	1:A:2430:U:O4'	2.12	0.49
1:A:2455:A:C8	1:A:2459:A:H5'	2.46	0.49
1:A:2690:G:H2'	1:A:2691:A:O4'	2.12	0.49
1:A:2786:A:H3'	1:A:2787:A:H5''	1.92	0.49
12:L:47:PHE:HA	12:L:50:ARG:NH1	2.27	0.49
14:N:35:ILE:HD11	20:T:24:VAL:HG23	1.94	0.49
23:W:134:TYR:C	25:Y:129:ARG:HG2	2.35	0.49
1:A:398:U:H2'	1:A:399:C:H6	1.75	0.49
1:A:922:A:H2'	1:A:949:U:H3	1.77	0.49
1:A:973:G:H2'	1:A:974:A:O4'	2.12	0.49
1:A:1087:U:C2'	1:A:1160:G:H1	2.25	0.49
1:A:2205:A:H2'	1:A:2206:C:H6	1.77	0.49
1:A:591:U:OP1	1:A:1259:G:O2'	2.28	0.49
1:A:642:G:H2'	1:A:643:U:C6	2.47	0.49
1:A:973:G:C6	1:A:974:A:C5	3.01	0.49
1:A:1320:G:H2'	1:A:1321:U:C6	2.47	0.49
1:A:1619:A:H2'	1:A:1620:A:H8	1.77	0.49
1:A:1828:G:N2	1:A:1848:A:OP2	2.36	0.49
1:A:2194:G:H3'	1:A:2195:G:C8	2.47	0.49
23:W:392:PRO:O	23:W:393:PRO:C	2.54	0.49
1:A:159:U:O2	1:A:169:G:N2	2.35	0.49
1:A:760:G:N2	1:A:766:C:H42	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1458:U:H1'	1:A:1460:G:C4	2.48	0.49
1:A:1545:C:C2	1:A:1546:G:C8	3.01	0.49
1:A:2144:G:O2'	1:A:2195:G:N2	2.46	0.49
1:A:2367:G:H1'	1:A:2368:G:H21	1.77	0.49
1:A:725:C:H2'	1:A:726:C:H6	1.76	0.49
1:A:957:A:N3	1:A:2294:U:H4'	2.27	0.49
1:A:1564:C:H2'	1:A:1565:U:C6	2.47	0.49
1:A:1634:U:H2'	1:A:1635:G:H8	1.78	0.49
1:A:1685:A:H2'	1:A:1686:A:H8	1.78	0.49
1:A:1854:G:H2'	1:A:1855:C:H6	1.76	0.49
1:A:2368:G:C8	1:A:2369:A:C8	3.00	0.49
1:A:2422:U:H5	1:A:2424:C:C5	2.30	0.49
1:A:2703:G:H2'	1:A:2704:A:C8	2.48	0.49
20:T:28:THR:O	20:T:37:LYS:N	2.44	0.49
1:A:217:G:H2'	1:A:218:G:C8	2.48	0.49
1:A:231:A:O2'	1:A:232:U:OP1	2.27	0.49
1:A:278:A:H2'	1:A:279:A:C8	2.48	0.49
1:A:283:G:N2	1:A:289:C:N3	2.60	0.49
1:A:560:A:H2'	1:A:561:A:H8	1.76	0.49
1:A:1619:A:H2'	1:A:1620:A:C8	2.48	0.49
1:A:2151:U:C4'	25:Y:172:HIS:CD2	2.95	0.49
1:A:2497:A:N6	1:A:2514:G:N7	2.55	0.49
1:A:2520:U:OP2	23:W:357:ASN:N	2.38	0.49
1:A:280:G:O6	1:A:291:C:N4	2.46	0.49
1:A:410:G:H3'	1:A:411:G:C8	2.47	0.49
1:A:1271:U:H2'	1:A:1272:G:H8	1.76	0.49
1:A:1750:G:H2'	1:A:1751:U:C6	2.47	0.49
1:A:2010:A:H2'	1:A:2010:A:N3	2.27	0.49
1:A:2171:G:C4	1:A:2172:C:H1'	2.48	0.49
1:A:2298:A:O2'	1:A:2299:G:O5'	2.30	0.49
1:A:2665:U:HO2'	4:D:46:TYR:HH	1.58	0.49
1:A:2793:A:H2'	1:A:2795:G:H21	1.78	0.49
25:Y:121:MET:SD	25:Y:145:VAL:HG13	2.52	0.49
1:A:460:C:N4	1:A:2439:G:H1	2.10	0.49
1:A:680:G:H2'	1:A:681:C:C6	2.48	0.49
1:A:1270:C:H2'	1:A:1271:U:H6	1.77	0.49
1:A:1292:G:H21	12:L:33:LYS:HD3	1.78	0.49
1:A:1354:C:H2'	1:A:1355:U:C6	2.48	0.49
1:A:2295:A:H1'	1:A:2296:A:C8	2.48	0.49
24:Z:35:TYR:HA	24:Z:42:SER:HA	1.94	0.49
1:A:1009:U:HO2'	1:A:1010:C:P	2.36	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2154:G:H2'	1:A:2155:A:N3	2.28	0.49
1:A:2320:U:O2'	1:A:2321:U:H6	1.96	0.49
1:A:2399:G:O2'	1:A:2400:G:O5'	2.28	0.49
1:A:2797:C:OP2	7:G:86:LYS:NZ	2.46	0.49
1:A:2864:G:H4'	10:J:45:GLU:HG2	1.94	0.49
10:J:74:GLU:C	10:J:76:ASN:N	2.70	0.49
20:T:38:LEU:HB2	20:T:41:ARG:HB2	1.95	0.49
1:A:27:G:O2'	1:A:558:G:N2	2.45	0.49
1:A:757:C:H2'	1:A:758:A:C8	2.45	0.49
1:A:865:G:N1	1:A:1229:U:OP2	2.37	0.49
1:A:951:C:H2'	1:A:952:A:C8	2.48	0.49
1:A:2464:A:H2'	1:A:2465:G:C8	2.48	0.49
1:A:2467:U:H2'	1:A:2470:C:C6	2.47	0.49
1:A:604:C:H1'	12:L:48:ARG:HH12	1.78	0.48
1:A:639:C:H2'	1:A:640:U:H6	1.78	0.48
1:A:955:C:H2'	1:A:956:A:H8	1.74	0.48
1:A:1272:G:H2'	1:A:1273:G:H8	1.78	0.48
1:A:1533:A:H2'	1:A:1534:A:H8	1.77	0.48
1:A:3:U:H2'	1:A:4:U:C6	2.47	0.48
1:A:398:U:H2'	1:A:399:C:C6	2.47	0.48
1:A:560:A:H2'	1:A:561:A:C8	2.49	0.48
1:A:687:U:O2'	1:A:688:G:OP1	2.30	0.48
1:A:912:C:H5''	1:A:913:A:C5	2.48	0.48
1:A:988:G:H2'	1:A:989:U:H6	1.76	0.48
1:A:1428:G:H5'	1:A:1573:C:OP1	2.14	0.48
1:A:1548:U:H2'	1:A:1549:U:H6	1.77	0.48
1:A:1877:A:O2'	1:A:1878:G:OP1	2.31	0.48
1:A:2159:U:H1'	1:A:2187:A:N6	2.28	0.48
1:A:525:A:O2'	1:A:526:A:O5'	2.29	0.48
1:A:1088:G:H2'	1:A:1089:C:C6	2.48	0.48
1:A:1384:C:H2'	1:A:1385:G:H8	1.78	0.48
1:A:2304:C:O2'	1:A:2305:G:O5'	2.30	0.48
1:A:2318:G:H4'	1:A:2319:G:OP1	2.13	0.48
2:B:38:U:O4	2:B:45:C:H5'	2.13	0.48
1:A:351:G:H22	1:A:354:A:P	2.36	0.48
1:A:684:G:C6	1:A:697:G:N1	2.82	0.48
1:A:760:G:H2'	1:A:761:U:C6	2.47	0.48
1:A:1519:C:N3	1:A:1566:G:C2	2.82	0.48
1:A:2392:U:H2'	1:A:2393:C:C6	2.49	0.48
1:A:2466:C:H2'	1:A:2467:U:C6	2.49	0.48
1:A:124:A:OP1	21:U:14:LYS:NZ	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:417:G:O2'	1:A:471:G:OP1	2.30	0.48
1:A:718:C:HO2'	1:A:719:C:H6	1.55	0.48
1:A:801:U:H2'	1:A:802:G:H8	1.78	0.48
1:A:2415:U:H3'	1:A:2416:U:H5''	1.96	0.48
1:A:2443:G:O6	1:A:2444:G:O6	2.30	0.48
2:B:40:C:O2'	2:B:44:A:N1	2.43	0.48
1:A:1219:C:H3'	1:A:1220:G:O4'	2.14	0.48
1:A:1223:C:H2'	1:A:1224:A:H8	1.79	0.48
1:A:1915:U:C2	1:A:1916:U:C5	3.01	0.48
1:A:2623:C:H2'	1:A:2624:G:O4'	2.13	0.48
1:A:58:G:O2'	1:A:59:G:OP1	2.29	0.48
1:A:1321:U:H2'	1:A:1322:G:O4'	2.14	0.48
1:A:1390:C:H2'	1:A:1391:U:H6	1.79	0.48
1:A:1525:G:H2'	1:A:1526:G:H8	1.78	0.48
1:A:2108:U:H2'	1:A:2109:G:C8	2.43	0.48
1:A:2129:G:H2'	1:A:2130:G:C8	2.48	0.48
1:A:2142:C:H3'	1:A:2197:G:OP1	2.13	0.48
1:A:2879:G:H2'	1:A:2880:U:H6	1.79	0.48
2:B:38:U:O2'	2:B:41:C:H4'	2.13	0.48
1:A:687:U:O2'	1:A:688:G:O4'	2.31	0.48
1:A:1656:C:O2'	1:A:1657:C:H5'	2.14	0.48
1:A:1889:G:O6	1:A:1912:G:H1'	2.14	0.48
1:A:2151:U:H4'	25:Y:172:HIS:CD2	2.49	0.48
1:A:2328:G:C2	1:A:2329:A:H1'	2.48	0.48
1:A:2404:G:O2'	1:A:2407:A:N1	2.47	0.48
1:A:2519:G:C8	23:W:357:ASN:HB2	2.49	0.48
1:A:2681:U:H2'	1:A:2682:U:O4'	2.13	0.48
2:B:35:C:H3'	2:B:36:C:C6	2.49	0.48
8:H:71:ARG:HE	11:K:75:ARG:NH1	2.12	0.48
1:A:457:G:H5''	1:A:458:G:H5''	1.96	0.48
1:A:462:A:N3	1:A:462:A:H2'	2.29	0.48
1:A:1767:A:H3'	1:A:1768:A:H8	1.79	0.48
1:A:1868:G:H2'	1:A:1869:G:O4'	2.14	0.48
1:A:1879:G:H2'	1:A:1880:U:C6	2.48	0.48
1:A:1914:A:HO2'	1:A:1915:U:H6	1.58	0.48
1:A:2330:A:N3	1:A:2330:A:H2'	2.29	0.48
1:A:583:G:OP2	7:G:2:ARG:NH2	2.46	0.48
1:A:683:A:OP2	9:I:112:LEU:HB3	2.13	0.48
1:A:962:C:H2'	1:A:963:G:O4'	2.14	0.48
1:A:1212:U:C2	1:A:1213:G:C8	3.01	0.48
1:A:1609:C:H2'	1:A:1610:U:C6	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2187:A:H4'	1:A:2188:G:O5'	2.13	0.48
1:A:2295:A:O2'	1:A:2296:A:H5''	2.12	0.48
1:A:2414:C:H2'	1:A:2415:U:H5''	1.95	0.48
1:A:2565:G:H2'	1:A:2566:U:C6	2.49	0.48
1:A:2593:A:C2	1:A:2676:U:H4'	2.49	0.48
2:B:31:G:N1	2:B:32:U:H1'	2.29	0.48
23:W:138:PHE:CA	25:Y:129:ARG:NH2	2.77	0.48
1:A:52:A:H2'	1:A:53:A:C8	2.49	0.47
1:A:1727:A:H2'	1:A:1728:C:C6	2.49	0.47
1:A:1731:C:H2'	1:A:1732:G:C8	2.49	0.47
1:A:1813:A:H4'	1:A:1814:A:O5'	2.15	0.47
1:A:1871:G:O2'	23:W:306:MET:HE1	2.14	0.47
1:A:2316:A:OP2	24:Z:25:ASN:ND2	2.47	0.47
1:A:2557:U:O2	1:A:2564:G:C6	2.67	0.47
1:A:2677:G:H2'	1:A:2678:U:H6	1.79	0.47
1:A:292:U:H2'	1:A:293:U:C6	2.49	0.47
1:A:597:G:H2'	1:A:598:U:C6	2.48	0.47
1:A:2048:U:H5	20:T:6:ARG:NH1	2.12	0.47
1:A:2132:A:O2'	1:A:2133:C:H5'	2.14	0.47
1:A:2178:C:H2'	1:A:2179:U:C6	2.49	0.47
1:A:2204:U:N3	1:A:2205:A:H1'	2.28	0.47
1:A:2266:G:C8	1:A:2268:G:O6	2.67	0.47
1:A:2316:A:N3	1:A:2318:G:H5''	2.29	0.47
1:A:2349:A:H4'	1:A:2350:G:OP1	2.14	0.47
1:A:2369:A:H2'	1:A:2370:G:H21	1.77	0.47
1:A:2561:G:N2	1:A:2692:G:O2'	2.47	0.47
14:N:34:SER:OG	20:T:36:MET:HG3	2.14	0.47
1:A:144:A:H2'	1:A:145:G:H8	1.80	0.47
1:A:273:A:C4	1:A:274:A:C8	3.02	0.47
1:A:304:G:C4	1:A:305:A:C8	3.03	0.47
1:A:638:U:H2'	1:A:639:C:C6	2.49	0.47
1:A:1505:U:O2'	1:A:1507:U:H5''	2.15	0.47
1:A:2321:U:H1'	1:A:2403:C:C4	2.49	0.47
3:C:60:ARG:HD3	3:C:85:PRO:HB2	1.95	0.47
1:A:35:G:H1'	1:A:501:A:C4	2.50	0.47
1:A:1187:U:H4'	1:A:1188:A:O4'	2.14	0.47
1:A:2135:G:H2'	1:A:2136:C:C6	2.50	0.47
1:A:2192:U:C2	1:A:2193:C:H1'	2.49	0.47
1:A:2376:C:O2'	1:A:2377:U:H5''	2.14	0.47
2:B:34:C:H42	2:B:47:C:H5''	1.79	0.47
2:B:64:A:H61	2:B:105:A:H3'	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:280:G:N1	1:A:291:C:N3	2.62	0.47
1:A:306:C:C2	1:A:307:A:C8	3.02	0.47
1:A:1214:U:H2'	1:A:1215:U:H6	1.75	0.47
1:A:1887:G:H2'	1:A:1912:G:N2	2.29	0.47
1:A:2355:U:H2'	1:A:2356:A:C8	2.49	0.47
1:A:2494:C:H2'	1:A:2495:C:C4	2.50	0.47
5:E:51:VAL:HG11	5:E:88:VAL:HG11	1.96	0.47
9:I:127:LYS:O	9:I:128:PHE:HB3	2.14	0.47
1:A:201:C:H4'	1:A:202:A:OP1	2.14	0.47
1:A:295:G:C6	1:A:296:G:C6	3.02	0.47
1:A:1071:G:H8	1:A:1071:G:OP1	1.98	0.47
1:A:1854:G:H2'	1:A:1855:C:C6	2.49	0.47
1:A:1884:G:H2'	1:A:1885:A:C8	2.49	0.47
1:A:2220:A:H2'	1:A:2221:C:C6	2.49	0.47
1:A:2291:U:H2'	1:A:2415:U:O4	2.15	0.47
1:A:2294:U:C2	1:A:2295:A:H2'	2.50	0.47
1:A:2373:U:H4'	1:A:2375:A:H2'	1.96	0.47
1:A:2433:C:N4	1:A:2443:G:O6	2.47	0.47
1:A:2443:G:H2'	1:A:2444:G:H8	1.77	0.47
1:A:2812:A:H2'	1:A:2813:U:C6	2.49	0.47
1:A:2874:G:O2'	1:A:2891:G:N2	2.47	0.47
4:D:6:LEU:HA	4:D:201:THR:HA	1.95	0.47
12:L:58:ARG:NH2	12:L:93:LYS:HZ1	2.12	0.47
1:A:153:C:H2'	1:A:154:A:H8	1.79	0.47
1:A:159:U:H3'	1:A:160:G:C8	2.45	0.47
1:A:340:U:H2'	1:A:341:G:O4'	2.15	0.47
1:A:350:U:O4	1:A:354:A:N7	2.48	0.47
1:A:1089:C:H2'	1:A:1090:U:O4'	2.14	0.47
1:A:1841:G:H2'	1:A:1842:C:C6	2.50	0.47
1:A:2119:A:N6	1:A:2259:G:O6	2.46	0.47
1:A:2519:G:H2'	1:A:2520:U:C6	2.50	0.47
1:A:2699:G:H2'	1:A:2700:A:C8	2.50	0.47
1:A:2759:C:H4'	4:D:173:ASN:CB	2.45	0.47
1:A:2831:A:H2'	1:A:2832:G:H8	1.78	0.47
1:A:2872:U:H2'	1:A:2873:G:O4'	2.14	0.47
2:B:3:U:O2'	2:B:4:G:H8	1.98	0.47
2:B:28:C:N4	2:B:53:U:H3	2.13	0.47
2:B:37:A:H1'	2:B:42:G:C2	2.49	0.47
2:B:64:A:N6	2:B:105:A:H3'	2.29	0.47
25:Y:104:ILE:HG12	25:Y:108:TRP:CD1	2.50	0.47
25:Y:118:PRO:HG3	25:Y:145:VAL:HG12	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:279:A:H2'	1:A:280:G:C8	2.50	0.47
1:A:766:C:H2'	1:A:767:U:C6	2.50	0.47
1:A:866:A:OP2	1:A:1228:G:N2	2.46	0.47
1:A:874:U:H4'	1:A:875:U:C2	2.49	0.47
1:A:903:G:HO2'	1:A:904:A:H8	1.61	0.47
1:A:906:G:O2'	1:A:963:G:O6	2.31	0.47
1:A:1317:G:H2'	1:A:1318:G:H8	1.80	0.47
1:A:2062:A:O2'	1:A:2064:G:OP2	2.30	0.47
1:A:2214:G:H2'	1:A:2215:U:C6	2.50	0.47
1:A:2302:A:H2'	1:A:2302:A:N3	2.29	0.47
2:B:37:A:H1'	2:B:42:G:N2	2.30	0.47
2:B:37:A:H8	2:B:42:G:C6	2.33	0.47
1:A:66:C:C2	1:A:67:A:C8	3.03	0.47
1:A:289:C:O2'	1:A:290:U:H6	1.98	0.47
1:A:1541:A:H2'	1:A:1542:A:C8	2.50	0.47
1:A:2132:A:H2'	1:A:2133:C:C6	2.50	0.47
1:A:2877:G:H2'	1:A:2878:U:C6	2.49	0.47
2:B:32:U:H2'	2:B:45:C:N4	2.30	0.47
25:Y:59:ILE:HD13	25:Y:201:PRO:HG3	1.94	0.47
1:A:318:A:H2'	1:A:319:G:C8	2.50	0.47
1:A:713:G:H2'	1:A:714:U:C6	2.50	0.47
1:A:1231:G:H5''	9:I:32:GLY:O	2.15	0.47
1:A:1458:U:H1'	1:A:1460:G:C5	2.50	0.47
1:A:2161:G:H2'	1:A:2182:G:N3	2.29	0.47
22:V:44:ILE:N	22:V:54:ALA:O	2.48	0.47
24:Z:12:CYS:CB	24:Z:36:CYS:SG	3.03	0.47
1:A:405:U:C4	1:A:406:G:N7	2.83	0.46
1:A:915:U:H2'	1:A:916:G:O4'	2.15	0.46
1:A:1245:G:H1'	1:A:1246:G:C5'	2.43	0.46
1:A:1555:A:C4	1:A:1556:A:C8	3.03	0.46
1:A:2161:G:H4'	1:A:2162:G:N2	2.30	0.46
1:A:2357:A:N6	1:A:2359:G:O6	2.48	0.46
1:A:2443:G:C4	1:A:2444:G:N7	2.82	0.46
1:A:7:G:H2'	1:A:8:U:H6	1.79	0.46
1:A:278:A:C6	1:A:294:G:C6	3.03	0.46
1:A:325:A:H2'	1:A:326:A:O4'	2.16	0.46
1:A:488:U:H2'	1:A:489:G:C8	2.50	0.46
1:A:648:G:O2'	1:A:649:G:H5''	2.15	0.46
1:A:764:C:C2	1:A:765:A:H1'	2.50	0.46
1:A:957:A:O4'	1:A:2294:U:H5'	2.16	0.46
1:A:1065:U:H3	1:A:1188:A:N6	2.12	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1524:A:H2'	1:A:1525:G:H8	1.79	0.46
1:A:1869:G:H2'	1:A:1870:U:C6	2.50	0.46
1:A:2172:C:H2'	1:A:2173:G:O4'	2.14	0.46
1:A:2260:U:H2'	1:A:2261:C:C6	2.49	0.46
1:A:2451:C:O2'	1:A:2452:U:OP1	2.29	0.46
1:A:2566:U:H2'	1:A:2567:C:H6	1.79	0.46
1:A:2757:U:H2'	1:A:2758:G:C8	2.50	0.46
1:A:2777:A:H4'	6:F:67:GLY:HA3	1.97	0.46
2:B:48:G:OP2	2:B:48:G:H2'	2.15	0.46
1:A:312:G:N2	1:A:405:U:O4'	2.49	0.46
1:A:786:A:H1'	1:A:787:C:H5	1.79	0.46
1:A:1087:U:H1'	1:A:1161:A:C2	2.51	0.46
1:A:1088:G:C5	1:A:1160:G:C6	3.03	0.46
1:A:1872:C:H5''	23:W:301:LYS:NZ	2.30	0.46
1:A:1875:G:C4	1:A:1876:A:C6	3.04	0.46
1:A:1919:A:H3'	1:A:1920:G:H8	1.80	0.46
1:A:2352:G:O3'	1:A:2353:U:H4'	2.09	0.46
2:B:5:G:H2'	2:B:6:U:O4'	2.15	0.46
2:B:25:A:H2'	2:B:26:C:O4'	2.16	0.46
23:W:135:SER:N	25:Y:129:ARG:HE	2.09	0.46
1:A:274:A:H3'	1:A:275:A:H8	1.81	0.46
1:A:957:A:N3	1:A:2293:C:O2'	2.34	0.46
1:A:1817:C:C2	1:A:1818:A:C8	3.03	0.46
1:A:1881:U:H4'	1:A:1882:A:OP2	2.12	0.46
1:A:2796:C:HO2'	1:A:2797:C:P	2.36	0.46
1:A:2884:G:H2'	1:A:2885:A:C8	2.50	0.46
24:Z:9:CYS:HB3	24:Z:14:GLU:H	1.80	0.46
1:A:948:A:H2'	1:A:949:U:O4'	2.16	0.46
1:A:969:C:H2'	17:Q:34:ALA:HB2	1.98	0.46
1:A:1346:A:H2'	1:A:1347:A:C8	2.51	0.46
1:A:1556:A:H2'	1:A:1557:G:O4'	2.16	0.46
1:A:2180:U:H1'	1:A:2181:C:H5	1.80	0.46
23:W:137:GLY:HA2	25:Y:129:ARG:HD3	1.85	0.46
25:Y:198:LYS:HE2	25:Y:198:LYS:HB2	1.76	0.46
1:A:64:A:H61	1:A:90:A:H61	1.64	0.46
1:A:1870:U:H3'	1:A:1871:G:H8	1.80	0.46
1:A:1881:U:H3'	1:A:1882:A:H8	1.81	0.46
1:A:1913:A:H2'	1:A:1914:A:O4'	2.15	0.46
1:A:2076:C:H2'	1:A:2077:G:H8	1.81	0.46
2:B:95:U:H3'	2:B:96:G:C8	2.50	0.46
25:Y:31:LYS:NZ	25:Y:178:VAL:O	2.38	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:312:G:H2'	1:A:313:U:C6	2.51	0.46
1:A:695:G:H2'	1:A:696:C:C6	2.51	0.46
1:A:1061:A:O2'	1:A:1062:C:H5'	2.15	0.46
1:A:1572:G:O2'	1:A:1573:C:O5'	2.32	0.46
1:A:2190:C:H2'	1:A:2191:A:O4'	2.16	0.46
1:A:2264:G:O2'	1:A:2265:U:OP1	2.29	0.46
2:B:26:C:OP2	22:V:38:LYS:CB	2.63	0.46
2:B:37:A:H1'	2:B:42:G:N1	2.31	0.46
25:Y:117:THR:C	25:Y:121:MET:SD	2.98	0.46
1:A:429:A:H2'	1:A:430:C:O4'	2.15	0.46
1:A:1080:G:C6	1:A:1168:G:C5	3.04	0.46
1:A:1524:A:H2'	1:A:1525:G:C8	2.51	0.46
1:A:1595:U:H2'	1:A:1596:U:H6	1.80	0.46
1:A:1869:G:H2'	1:A:1870:U:H6	1.81	0.46
1:A:1871:G:H2'	1:A:1872:C:C6	2.51	0.46
1:A:2162:G:OP1	1:A:2167:C:H1'	2.16	0.46
1:A:2560:A:N6	1:A:2561:G:O6	2.49	0.46
3:C:208:ALA:O	3:C:211:SER:OG	2.28	0.46
9:I:128:PHE:CE2	9:I:143:ALA:HB1	2.50	0.46
1:A:779:C:H2'	1:A:780:G:O4'	2.15	0.46
1:A:1529:G:O2'	1:A:1530:G:O4'	2.33	0.46
1:A:1673:G:H2'	1:A:1674:G:H8	1.81	0.46
1:A:2038:G:C2	1:A:2039:G:C8	3.04	0.46
1:A:2414:C:O2'	17:Q:49:ARG:CZ	2.63	0.46
1:A:2461:A:H2'	1:A:2462:A:C2	2.51	0.46
1:A:2677:G:H2'	1:A:2678:U:C6	2.51	0.46
23:W:79:ALA:O	23:W:80:MET:C	2.58	0.46
1:A:317:G:H2'	1:A:318:A:C8	2.51	0.46
1:A:429:A:N6	1:A:434:U:O4	2.48	0.46
1:A:465:U:H2'	1:A:466:C:C6	2.50	0.46
1:A:1092:A:H3'	1:A:1093:G:C8	2.51	0.46
1:A:1092:A:H3'	1:A:1093:G:H8	1.81	0.46
1:A:1094:A:C2	1:A:1159:U:H1'	2.51	0.46
1:A:1493:C:H2'	1:A:1494:G:H8	1.79	0.46
1:A:1872:C:H5''	23:W:301:LYS:HZ1	1.81	0.46
1:A:2108:U:HO2'	1:A:2109:G:P	2.38	0.46
1:A:2401:G:N2	1:A:2402:A:H61	2.13	0.46
1:A:2424:C:N4	1:A:2450:G:O2'	2.48	0.46
1:A:363:C:H2'	1:A:364:A:O4'	2.16	0.45
1:A:952:A:H2'	1:A:953:G:H8	1.81	0.45
1:A:1057:G:C4	1:A:1059:A:C8	3.03	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1873:U:H2'	1:A:1874:G:C8	2.52	0.45
1:A:2174:C:H2'	1:A:2176:A:C2	2.51	0.45
1:A:2655:C:H2'	1:A:2656:G:C8	2.46	0.45
2:B:18:A:N6	2:B:19:G:O6	2.49	0.45
2:B:35:C:H41	2:B:45:C:H5	1.64	0.45
2:B:61:U:H2'	2:B:62:U:C6	2.51	0.45
1:A:197:G:C2	1:A:205:U:O2	2.70	0.45
1:A:268:A:H2'	1:A:269:G:H4'	1.97	0.45
1:A:639:C:H2'	1:A:640:U:C6	2.51	0.45
1:A:827:G:C2	1:A:829:A:C2	3.05	0.45
1:A:1013:U:H2'	1:A:1014:A:C8	2.50	0.45
1:A:1292:G:OP2	12:L:14:ARG:NH2	2.48	0.45
1:A:1766:C:H2'	1:A:1767:A:O4'	2.16	0.45
1:A:2423:C:H5'	1:A:2424:C:H2'	1.98	0.45
1:A:97:C:H2'	1:A:98:U:C6	2.51	0.45
1:A:399:C:H2'	1:A:400:U:O4'	2.16	0.45
1:A:766:C:H2'	1:A:767:U:H6	1.82	0.45
1:A:910:A:H8	1:A:910:A:OP2	1.99	0.45
1:A:1224:A:H2'	1:A:1225:G:C8	2.52	0.45
1:A:1224:A:H2'	1:A:1225:G:H8	1.81	0.45
1:A:1629:C:H3'	1:A:1630:G:H8	1.82	0.45
1:A:1922:C:C6	1:A:1924:C:H5	2.35	0.45
1:A:2176:A:N7	1:A:2177:G:C4	2.85	0.45
1:A:2496:C:C2	1:A:2497:A:N6	2.84	0.45
10:J:74:GLU:C	10:J:76:ASN:H	2.22	0.45
23:W:210:THR:OG1	26:W:501:GNP:O1G	2.33	0.45
1:A:306:C:H2'	1:A:307:A:H8	1.82	0.45
1:A:1769:G:H2'	1:A:1770:C:C6	2.51	0.45
1:A:2688:G:C2	1:A:2690:G:H5''	2.51	0.45
1:A:2697:G:H2'	1:A:2698:G:H8	1.81	0.45
19:S:53:LEU:H	19:S:53:LEU:HD12	1.81	0.45
1:A:759:G:C5	1:A:760:G:C5	3.05	0.45
1:A:2378:G:C5	1:A:2398:A:N6	2.85	0.45
11:K:63:THR:HA	11:K:76:THR:HA	1.99	0.45
1:A:2135:G:H2'	1:A:2136:C:H6	1.82	0.45
1:A:2859:G:H1'	1:A:2904:A:N6	2.32	0.45
1:A:983:U:H2'	1:A:984:G:H8	1.80	0.45
1:A:1867:C:H5''	1:A:1928:A:C2	2.51	0.45
1:A:2366:G:O2'	1:A:2367:G:O4'	2.30	0.45
1:A:2374:G:O5'	1:A:2376:C:H5'	2.16	0.45
1:A:2685:U:C4	1:A:2694:A:C8	3.05	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2725:U:H2'	1:A:2726:G:H8	1.81	0.45
1:A:341:G:N1	1:A:383:U:OP2	2.43	0.45
1:A:421:A:C2	1:A:422:C:H1'	2.52	0.45
1:A:1025:A:H2'	1:A:1028:C:N4	2.32	0.45
1:A:1193:U:H5'	1:A:1194:A:OP2	2.17	0.45
1:A:1346:A:H2'	1:A:1347:A:H8	1.82	0.45
1:A:1461:A:N7	1:A:1631:A:N6	2.65	0.45
1:A:2039:G:H5''	14:N:42:ALA:HB2	1.99	0.45
1:A:2173:G:C2	1:A:2175:C:H4'	2.52	0.45
1:A:2199:G:H2'	1:A:2200:A:C4	2.52	0.45
1:A:2374:G:N1	1:A:2401:G:C2	2.85	0.45
1:A:2455:A:N7	1:A:2459:A:H5'	2.31	0.45
25:Y:64:VAL:HG12	25:Y:155:GLU:HB2	1.97	0.45
1:A:192:G:O6	1:A:208:G:O2'	2.31	0.45
1:A:194:A:H2'	1:A:195:C:C6	2.51	0.45
1:A:502:C:O2'	1:A:503:C:H5'	2.17	0.45
1:A:916:G:H2'	1:A:917:A:C8	2.52	0.45
1:A:1009:U:O2'	1:A:1010:C:OP1	2.25	0.45
1:A:1492:G:C2	1:A:1512:G:C2	3.05	0.45
1:A:1547:U:H2'	1:A:1548:U:C6	2.52	0.45
1:A:1553:A:O2'	1:A:1554:U:H5'	2.16	0.45
1:A:1768:A:C6	1:A:1769:G:C4	3.05	0.45
1:A:1788:A:H2'	1:A:1789:A:C8	2.52	0.45
1:A:1874:G:O6	1:A:1925:A:C6	2.69	0.45
1:A:2140:U:P	1:A:2141:A:H62	2.37	0.45
1:A:2322:C:H42	1:A:2369:A:N6	2.15	0.45
1:A:2496:C:N4	1:A:2514:G:O6	2.49	0.45
1:A:2684:G:N1	1:A:2693:G:H3'	2.30	0.45
1:A:2774:C:H2'	1:A:2775:U:H6	1.82	0.45
1:A:11:G:H2'	1:A:12:A:C8	2.51	0.45
1:A:152:C:H2'	1:A:153:C:C6	2.52	0.45
1:A:316:G:H2'	1:A:317:G:C8	2.51	0.45
1:A:358:C:H2'	1:A:359:C:C6	2.52	0.45
1:A:674:G:H2'	1:A:675:C:C6	2.51	0.45
1:A:774:A:O2'	1:A:775:G:O5'	2.34	0.45
1:A:971:A:C5	1:A:972:U:C4	3.04	0.45
1:A:1005:A:H3'	1:A:1006:A:C8	2.52	0.45
1:A:1548:U:H2'	1:A:1549:U:C6	2.52	0.45
1:A:2189:G:H2'	1:A:2190:C:C6	2.52	0.45
1:A:2491:U:H3	1:A:2518:G:N2	2.14	0.45
1:A:2831:A:H2'	1:A:2832:G:C8	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:14:ILE:O	18:R:15:GLU:C	2.60	0.45
1:A:785:C:HO2'	1:A:786:A:P	2.37	0.44
1:A:789:C:H2'	1:A:790:A:H8	1.81	0.44
1:A:1400:G:H2'	1:A:1401:C:H6	1.81	0.44
1:A:1913:A:C4	1:A:1914:A:C8	3.05	0.44
1:A:2102:C:H2'	1:A:2103:U:C2	2.53	0.44
1:A:2368:G:C6	1:A:2369:A:C6	3.05	0.44
1:A:2494:C:H42	1:A:2517:A:H61	1.65	0.44
1:A:2683:A:N6	1:A:2696:C:H42	2.15	0.44
2:B:45:C:C6	2:B:46:A:H2'	2.52	0.44
1:A:429:A:C2	1:A:440:U:C2	3.05	0.44
1:A:824:G:H2'	1:A:825:G:C8	2.52	0.44
1:A:852:G:HO2'	1:A:853:C:P	2.41	0.44
1:A:907:U:C2	1:A:2297:A:N6	2.85	0.44
1:A:919:U:H2'	1:A:920:G:O4'	2.17	0.44
1:A:1085:G:H22	1:A:1163:U:H2'	1.83	0.44
1:A:1093:G:N1	1:A:1156:G:H2'	2.32	0.44
1:A:1155:C:H2'	1:A:1156:G:C4	2.52	0.44
1:A:1181:C:H5'	1:A:1182:G:OP2	2.17	0.44
1:A:1603:U:H2'	1:A:1604:C:C6	2.52	0.44
1:A:1850:A:H2'	1:A:1851:G:H8	1.83	0.44
1:A:1877:A:N6	1:A:1922:C:N3	2.45	0.44
1:A:2727:U:H2'	1:A:2728:U:H6	1.82	0.44
8:H:93:PRO:HB3	8:H:114:ILE:CG2	2.47	0.44
1:A:448:A:C6	1:A:449:A:C6	3.06	0.44
1:A:767:U:H2'	1:A:768:G:C8	2.52	0.44
1:A:800:G:H2'	1:A:801:U:C6	2.53	0.44
1:A:807:G:H2'	1:A:808:A:O4'	2.17	0.44
1:A:981:C:H2'	1:A:982:U:C6	2.52	0.44
1:A:1768:A:H2'	1:A:1769:G:O4'	2.17	0.44
1:A:2130:G:H2'	1:A:2131:U:H6	1.82	0.44
1:A:2273:U:O4'	1:A:2463:A:N6	2.51	0.44
1:A:2625:U:O2'	1:A:2626:G:OP1	2.33	0.44
1:A:2683:A:H61	1:A:2696:C:H42	1.64	0.44
1:A:2911:G:H2'	1:A:2912:A:C8	2.52	0.44
23:W:48:TRP:CD2	23:W:156:LEU:HD13	2.53	0.44
1:A:10:A:H2'	1:A:11:G:C8	2.53	0.44
1:A:297:G:H2'	1:A:298:U:C6	2.52	0.44
1:A:391:A:H2'	1:A:392:C:H6	1.83	0.44
1:A:499:G:C2	1:A:505:G:C5	3.04	0.44
1:A:1521:G:H22	1:A:1563:G:N2	2.14	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1735:A:H2'	1:A:1736:C:O4'	2.17	0.44
1:A:2197:G:H1'	1:A:2199:G:O6	2.17	0.44
1:A:2685:U:N3	1:A:2686:A:C8	2.85	0.44
1:A:2802:U:H5''	4:D:168:GLN:HE22	1.83	0.44
23:W:192:VAL:O	23:W:193:ASN:C	2.60	0.44
1:A:304:G:N3	1:A:305:A:C8	2.86	0.44
1:A:902:G:N7	1:A:903:G:N2	2.66	0.44
1:A:917:A:C4	1:A:918:U:H1'	2.52	0.44
1:A:974:A:H2'	1:A:975:C:C6	2.53	0.44
1:A:986:G:H2'	1:A:987:A:O4'	2.17	0.44
1:A:1712:G:O6	1:A:2020:U:H3'	2.18	0.44
1:A:1866:C:H2'	1:A:1928:A:C6	2.53	0.44
1:A:2163:A:C5	1:A:2185:G:N1	2.86	0.44
1:A:2316:A:H4'	1:A:2318:G:C2	2.52	0.44
1:A:2426:G:N2	1:A:2449:C:H41	2.16	0.44
1:A:2436:A:O2'	1:A:2437:U:OP1	2.32	0.44
1:A:2591:U:O4	1:A:2595:A:N7	2.51	0.44
1:A:2802:U:H5''	4:D:168:GLN:NE2	2.33	0.44
2:B:22:G:HO2'	2:B:24:C:H41	1.58	0.44
1:A:7:G:H2'	1:A:8:U:C6	2.52	0.44
1:A:65:A:H2'	1:A:66:C:C6	2.53	0.44
1:A:317:G:H2'	1:A:318:A:H8	1.83	0.44
1:A:358:C:H2'	1:A:359:C:H6	1.83	0.44
1:A:555:C:H6	1:A:555:C:H2'	1.56	0.44
1:A:682:G:P	9:I:132:ALA:N	2.91	0.44
1:A:684:G:H2'	1:A:685:U:O4'	2.18	0.44
1:A:1170:C:C2	1:A:1171:G:C8	3.06	0.44
1:A:1271:U:C2	1:A:1272:G:C8	3.06	0.44
1:A:1520:A:N6	1:A:1564:C:H42	2.15	0.44
1:A:2317:A:C5	1:A:2319:G:C2	3.06	0.44
1:A:2325:U:N3	1:A:2366:G:O6	2.51	0.44
1:A:2332:G:C8	1:A:2333:G:H2'	2.52	0.44
1:A:2374:G:H5''	24:Z:34:LYS:HZ3	1.83	0.44
1:A:2615:C:H2'	1:A:2616:A:C8	2.52	0.44
2:B:88:C:H2'	2:B:89:C:H6	1.83	0.44
12:L:52:GLN:O	12:L:53:LYS:C	2.60	0.44
23:W:138:PHE:N	25:Y:129:ARG:HH21	2.07	0.44
25:Y:194:ASP:O	25:Y:198:LYS:HB2	2.17	0.44
1:A:232:U:H1'	1:A:233:G:O5'	2.18	0.44
1:A:437:A:H2'	1:A:437:A:N3	2.33	0.44
1:A:642:G:H2'	1:A:643:U:H6	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:682:G:N7	9:I:110:LYS:NZ	2.49	0.44
1:A:805:G:H21	1:A:2010:A:H62	1.65	0.44
1:A:970:A:C5'	17:Q:34:ALA:HB3	2.48	0.44
1:A:1521:G:H1	1:A:1563:G:H1	1.65	0.44
1:A:1870:U:H2'	1:A:1871:G:C8	2.53	0.44
1:A:2110:C:N4	1:A:2266:G:N7	2.66	0.44
1:A:2209:U:H2'	1:A:2210:G:C8	2.52	0.44
1:A:2859:G:H21	1:A:2908:A:N6	2.16	0.44
7:G:110:LEU:HB2	7:G:111:PRO:HD2	1.98	0.44
1:A:152:C:H2'	1:A:153:C:H6	1.82	0.44
1:A:423:G:H2'	1:A:424:G:C8	2.53	0.44
1:A:1507:U:H2'	1:A:1508:C:H6	1.81	0.44
1:A:1715:C:H2'	1:A:1716:U:O4'	2.17	0.44
1:A:1927:U:H3'	1:A:1928:A:H4'	1.99	0.44
1:A:2149:G:H2'	1:A:2149:G:N3	2.32	0.44
1:A:2378:G:C5	1:A:2398:A:C6	3.06	0.44
2:B:24:C:H2'	2:B:25:A:O4'	2.17	0.44
2:B:44:A:H4'	2:B:45:C:OP2	2.17	0.44
2:B:98:G:C4	2:B:99:A:C8	3.05	0.44
23:W:353:ARG:HG3	23:W:390:VAL:HG22	1.99	0.44
1:A:66:C:H2'	1:A:67:A:H8	1.83	0.44
1:A:201:C:H2'	1:A:2459:A:C5	2.52	0.44
1:A:368:G:C2	1:A:369:A:H1'	2.53	0.44
1:A:891:G:C2	1:A:981:C:C2	3.06	0.44
1:A:1002:G:C5	1:A:1004:U:H4'	2.53	0.44
1:A:1884:G:C6	1:A:1885:A:C6	3.05	0.44
1:A:2114:C:O2	1:A:2114:C:H2'	2.17	0.44
1:A:2392:U:H2'	1:A:2393:C:N1	2.33	0.44
1:A:2468:A:N7	1:A:2615:C:H4'	2.32	0.44
1:A:2565:G:H2'	1:A:2566:U:H6	1.83	0.44
1:A:89:U:H3'	1:A:90:A:C8	2.53	0.43
1:A:649:G:O2'	1:A:650:U:OP1	2.33	0.43
1:A:662:U:H2'	1:A:663:G:C8	2.51	0.43
1:A:785:C:O2'	1:A:786:A:H5'	2.18	0.43
1:A:1088:G:O6	1:A:1159:U:C4	2.71	0.43
1:A:1285:G:H4'	5:E:38:LEU:HD11	1.99	0.43
1:A:1871:G:N1	1:A:1927:U:N3	2.65	0.43
1:A:2040:U:OP2	14:N:16:LYS:NZ	2.43	0.43
1:A:2238:C:H2'	1:A:2239:U:C5	2.53	0.43
1:A:2290:C:H2'	1:A:2291:U:H5'	2.00	0.43
23:W:177:GLN:O	23:W:258:SER:HB3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:59:G:H1'	1:A:73:A:H2'	1.99	0.43
1:A:756:U:H2'	1:A:757:C:H6	1.83	0.43
1:A:1361:A:C2	1:A:1362:G:C8	3.06	0.43
1:A:1426:A:H5'	1:A:1515:C:H1'	2.00	0.43
1:A:1518:G:H4'	1:A:1519:C:OP1	2.18	0.43
1:A:1711:G:O2'	8:H:6:THR:OG1	2.33	0.43
1:A:2143:A:C2	1:A:2144:G:H1'	2.54	0.43
1:A:2191:A:H3'	1:A:2193:C:C5	2.53	0.43
1:A:2389:A:H2'	1:A:2390:A:O4'	2.19	0.43
1:A:35:G:H1'	1:A:501:A:N3	2.33	0.43
1:A:523:G:H21	1:A:527:A:H62	1.66	0.43
1:A:851:A:H2'	1:A:852:G:C8	2.53	0.43
1:A:1265:A:O3'	13:M:85:LYS:NZ	2.50	0.43
1:A:1463:C:H2'	1:A:1464:A:O4'	2.18	0.43
1:A:2145:G:H1	1:A:2164:A:C5'	2.31	0.43
1:A:2370:G:H5''	1:A:2403:C:H4'	1.99	0.43
1:A:2414:C:HO2'	17:Q:49:ARG:CZ	2.31	0.43
2:B:43:A:N3	2:B:43:A:C2'	2.81	0.43
2:B:84:G:H2'	2:B:84:G:N3	2.34	0.43
1:A:39:C:H2'	1:A:40:U:H6	1.83	0.43
1:A:198:A:N1	1:A:202:A:C8	2.86	0.43
1:A:680:G:H2'	1:A:681:C:H6	1.83	0.43
1:A:878:G:H2'	1:A:879:G:H8	1.84	0.43
1:A:887:C:H2'	1:A:888:A:C8	2.51	0.43
1:A:995:U:P	1:A:1007:G:H21	2.41	0.43
1:A:1155:C:O2'	1:A:1156:G:O4'	2.31	0.43
1:A:1411:U:H2'	1:A:1412:A:H8	1.84	0.43
1:A:1595:U:H2'	1:A:1596:U:C6	2.53	0.43
1:A:1653:A:C8	1:A:1656:C:N4	2.86	0.43
1:A:2347:G:H5'	1:A:2348:C:O5'	2.18	0.43
1:A:2793:A:C5	1:A:2795:G:C2	3.06	0.43
6:F:69:THR:O	6:F:72:LEU:HG	2.18	0.43
1:A:294:G:C4	1:A:295:G:C8	3.06	0.43
1:A:327:G:C2	1:A:400:U:O2	2.71	0.43
1:A:472:G:H2'	1:A:473:C:C6	2.53	0.43
1:A:999:A:H61	1:A:1010:C:N4	2.16	0.43
1:A:1231:G:OP1	9:I:32:GLY:CA	2.65	0.43
1:A:1329:C:H2'	1:A:1330:C:H6	1.83	0.43
1:A:1562:A:O2'	1:A:1604:C:O2'	2.29	0.43
1:A:2332:G:C5	1:A:2333:G:C5	3.05	0.43
1:A:2352:G:H21	1:A:2353:U:H3	1.63	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2397:C:O2'	1:A:2398:A:N7	2.50	0.43
1:A:2423:C:O3'	1:A:2424:C:H3'	2.18	0.43
1:A:2497:A:H2'	1:A:2498:A:C4	2.53	0.43
1:A:2873:G:N1	1:A:2892:G:N3	2.66	0.43
6:F:48:ASP:N	6:F:48:ASP:OD1	2.52	0.43
1:A:152:C:C2	1:A:178:A:H2	2.37	0.43
1:A:231:A:H3'	1:A:231:A:N3	2.34	0.43
1:A:275:A:H3'	1:A:276:C:H5''	2.01	0.43
1:A:280:G:C2	1:A:291:C:C2	3.07	0.43
1:A:425:C:O2'	1:A:426:G:O5'	2.36	0.43
1:A:462:A:N6	1:A:2438:G:N7	2.67	0.43
1:A:660:G:H2'	1:A:661:A:H8	1.83	0.43
1:A:679:A:H1'	1:A:2432:C:O3'	2.19	0.43
1:A:769:A:H2'	1:A:770:A:C8	2.50	0.43
1:A:1223:C:H2'	1:A:1224:A:C8	2.53	0.43
1:A:1916:U:O2'	1:A:1917:G:P	2.77	0.43
1:A:2084:C:H5''	1:A:2085:G:C5'	2.49	0.43
1:A:2201:U:H3'	1:A:2202:A:H8	1.84	0.43
1:A:2207:C:H2'	1:A:2208:C:H6	1.84	0.43
1:A:2369:A:O2'	1:A:2370:G:N3	2.34	0.43
2:B:69:C:H2'	2:B:70:G:O4'	2.18	0.43
2:B:97:A:C4	2:B:98:G:C8	3.07	0.43
8:H:40:VAL:HA	8:H:59:LYS:HA	1.99	0.43
1:A:903:G:O2'	1:A:904:A:H8	2.02	0.43
1:A:918:U:N3	1:A:953:G:C6	2.84	0.43
1:A:1088:G:O6	1:A:1159:U:O4	2.36	0.43
1:A:1227:G:H2'	1:A:1228:G:O4'	2.19	0.43
1:A:1354:C:O2'	1:A:1431:G:N3	2.51	0.43
1:A:1809:A:H3'	1:A:1810:G:H2'	2.00	0.43
1:A:1871:G:C6	1:A:1927:U:C4	3.06	0.43
1:A:2176:A:N6	1:A:2177:G:N3	2.67	0.43
1:A:2180:U:H1'	1:A:2181:C:C5	2.54	0.43
1:A:2321:U:OP1	1:A:2409:U:H5''	2.18	0.43
1:A:2460:U:N3	1:A:2462:A:OP2	2.48	0.43
1:A:2916:A:H2'	1:A:2917:G:C8	2.54	0.43
25:Y:194:ASP:HA	25:Y:197:LEU:CG	2.48	0.43
1:A:198:A:N1	1:A:202:A:H8	2.16	0.43
1:A:316:G:H2'	1:A:317:G:H8	1.82	0.43
1:A:415:C:H2'	1:A:416:U:C6	2.53	0.43
1:A:446:G:C2	1:A:447:G:H1'	2.53	0.43
1:A:573:C:C4	1:A:2808:U:H2'	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:910:A:C5	1:A:911:G:N7	2.86	0.43
1:A:1231:G:C2	1:A:1232:G:N7	2.86	0.43
1:A:1634:U:H2'	1:A:1635:G:C8	2.53	0.43
1:A:1819:C:H2'	1:A:1820:A:N7	2.34	0.43
1:A:2017:C:H2'	1:A:2018:A:H8	1.84	0.43
1:A:2404:G:H2'	1:A:2404:G:N3	2.33	0.43
1:A:2521:U:OP2	23:W:386:THR:OG1	2.36	0.43
1:A:2779:A:HO2'	1:A:2781:C:H41	1.54	0.43
23:W:137:GLY:C	25:Y:129:ARG:NH2	2.74	0.43
1:A:249:C:N4	1:A:250:G:C6	2.86	0.43
1:A:384:A:H2'	1:A:385:G:O4'	2.18	0.43
1:A:878:G:H2'	1:A:879:G:C8	2.53	0.43
1:A:1015:G:H2'	1:A:1016:U:H6	1.83	0.43
1:A:1247:G:O2'	1:A:1248:C:O5'	2.36	0.43
1:A:1435:U:OP1	1:A:1435:U:H3'	2.19	0.43
1:A:1681:U:H2'	1:A:1682:C:C6	2.54	0.43
1:A:1826:C:H2'	1:A:1827:U:C6	2.54	0.43
1:A:2152:A:H2'	1:A:2153:G:H5''	2.01	0.43
1:A:2193:C:H5'	1:A:2201:U:OP2	2.19	0.43
1:A:2224:U:H5'	1:A:2225:C:OP2	2.18	0.43
1:A:2317:A:C8	1:A:2318:G:N3	2.87	0.43
1:A:2367:G:H1'	1:A:2368:G:N2	2.34	0.43
1:A:2468:A:C5	1:A:2615:C:H4'	2.53	0.43
2:B:7:G:C5	2:B:110:G:C6	3.07	0.43
1:A:65:A:N1	1:A:90:A:N6	2.67	0.43
1:A:280:G:N2	1:A:292:U:C2	2.87	0.43
1:A:289:C:HO2'	1:A:290:U:H6	1.65	0.43
1:A:683:A:H5'	9:I:134:GLU:OE1	2.19	0.43
1:A:888:A:H2'	1:A:889:A:C8	2.53	0.43
1:A:891:G:N2	1:A:981:C:C2	2.87	0.43
1:A:1508:C:H2'	1:A:1509:C:C6	2.53	0.43
1:A:1529:G:C6	1:A:1553:A:N1	2.87	0.43
1:A:1571:G:C2	1:A:1572:G:C5	3.07	0.43
1:A:2272:U:H2'	1:A:2463:A:C2	2.53	0.43
1:A:2523:G:C2	1:A:2524:G:C2	3.07	0.43
1:A:2582:G:C2	1:A:2583:U:H1'	2.53	0.43
2:B:21:G:N2	2:B:59:U:C2	2.87	0.43
6:F:73:LEU:HA	6:F:76:MET:SD	2.59	0.43
16:P:77:GLU:O	16:P:79:THR:HG23	2.18	0.43
1:A:280:G:H22	1:A:291:C:H2'	1.82	0.42
1:A:564:G:H2'	1:A:565:U:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:736:A:H2'	1:A:737:C:C6	2.54	0.42
1:A:1419:G:C2	1:A:1420:G:C8	3.06	0.42
1:A:1566:G:C8	1:A:1567:U:C6	3.07	0.42
1:A:1808:U:O2	1:A:1812:A:N6	2.51	0.42
1:A:2355:U:C2	1:A:2356:A:N7	2.87	0.42
1:A:2360:G:H1'	1:A:2364:A:H61	1.81	0.42
1:A:2361:C:C5	1:A:2365:A:N6	2.86	0.42
1:A:2462:A:C8	1:A:2463:A:C2	3.06	0.42
1:A:2796:C:C2	1:A:2797:C:C5	3.07	0.42
2:B:34:C:N4	2:B:45:C:H5	2.12	0.42
2:B:37:A:O2'	2:B:42:G:N2	2.52	0.42
25:Y:58:GLN:OE1	25:Y:60:ARG:HB3	2.18	0.42
1:A:260:A:H2'	1:A:261:C:C6	2.54	0.42
1:A:625:C:H2'	1:A:626:G:H8	1.85	0.42
1:A:783:C:H2'	1:A:784:C:H6	1.84	0.42
1:A:913:A:N6	1:A:961:C:C4	2.86	0.42
1:A:917:A:C3'	1:A:918:U:H4'	2.48	0.42
1:A:1057:G:C6	1:A:1197:A:C6	3.07	0.42
1:A:1337:C:H2'	1:A:1338:G:O4'	2.19	0.42
1:A:2170:A:C5	1:A:2171:G:C5	3.07	0.42
1:A:2170:A:C6	1:A:2171:G:C6	3.07	0.42
1:A:2270:A:H2'	1:A:2271:G:O4'	2.19	0.42
1:A:2374:G:C2	1:A:2376:C:N4	2.88	0.42
1:A:2496:C:H2'	1:A:2497:A:C5	2.54	0.42
2:B:45:C:H6	2:B:46:A:H2'	1.84	0.42
5:E:104:LYS:O	5:E:105:VAL:C	2.62	0.42
23:W:184:PRO:HD3	23:W:233:MET:O	2.19	0.42
1:A:438:A:H8	1:A:438:A:OP2	2.02	0.42
1:A:1652:C:H1'	1:A:1653:A:OP2	2.19	0.42
1:A:2255:C:H2'	1:A:2256:A:O4'	2.19	0.42
1:A:2330:A:H5''	1:A:2331:U:H5	1.85	0.42
1:A:2432:C:N3	1:A:2444:G:N1	2.67	0.42
1:A:2684:G:C5	1:A:2693:G:C5	3.07	0.42
2:B:12:U:OP2	2:B:68:C:O2'	2.36	0.42
2:B:88:C:H2'	2:B:89:C:C6	2.53	0.42
23:W:138:PHE:H	25:Y:129:ARG:CZ	2.32	0.42
25:Y:197:LEU:C	25:Y:199:ALA:N	2.73	0.42
1:A:106:G:H2'	1:A:107:G:H8	1.84	0.42
1:A:143:G:C2	1:A:144:A:C8	3.07	0.42
1:A:401:C:H2'	1:A:402:U:C6	2.54	0.42
1:A:920:G:C6	1:A:921:G:N7	2.87	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:987:A:H2'	1:A:988:G:C8	2.54	0.42
1:A:1094:A:P	1:A:1097:A:H61	2.42	0.42
1:A:1210:A:H2'	1:A:1211:C:C6	2.55	0.42
1:A:1477:A:H2'	1:A:1478:G:C8	2.54	0.42
1:A:1549:U:C2	1:A:1550:C:C5	3.08	0.42
1:A:2093:C:H2'	1:A:2094:C:O4'	2.19	0.42
1:A:2180:U:O2'	1:A:2182:G:N7	2.48	0.42
1:A:2425:G:H1'	1:A:2426:G:C2	2.54	0.42
1:A:2840:C:H2'	1:A:2841:C:H6	1.83	0.42
6:F:7:LYS:HG2	6:F:8:LEU:H	1.82	0.42
1:A:132:C:H2'	1:A:133:A:H8	1.85	0.42
1:A:624:C:H2'	1:A:625:C:C6	2.55	0.42
1:A:743:U:H2'	1:A:744:C:C6	2.54	0.42
1:A:767:U:H2'	1:A:768:G:H8	1.85	0.42
1:A:956:A:N7	1:A:959:C:C4	2.87	0.42
1:A:1004:U:OP1	1:A:1005:A:H5''	2.19	0.42
1:A:1270:C:C2	1:A:1271:U:C5	3.06	0.42
1:A:1411:U:H2'	1:A:1412:A:C8	2.54	0.42
1:A:1471:G:H2'	1:A:1472:G:C8	2.53	0.42
1:A:2143:A:C8	1:A:2147:U:H5''	2.55	0.42
1:A:2294:U:N1	1:A:2295:A:H2'	2.34	0.42
1:A:2402:A:O2'	1:A:2403:C:OP1	2.32	0.42
1:A:2692:G:H2'	1:A:2693:G:C8	2.54	0.42
2:B:34:C:H2'	2:B:47:C:H5	1.84	0.42
1:A:58:G:H2'	1:A:59:G:C8	2.55	0.42
1:A:297:G:H5''	1:A:298:U:OP2	2.20	0.42
1:A:783:C:H2'	1:A:784:C:C6	2.54	0.42
1:A:800:G:H2'	1:A:801:U:H6	1.85	0.42
1:A:959:C:H2'	1:A:960:U:C6	2.54	0.42
1:A:1088:G:C6	1:A:1160:G:C6	3.07	0.42
1:A:1095:C:H5	1:A:1097:A:N6	2.18	0.42
1:A:1226:U:H5''	1:A:1227:G:OP1	2.19	0.42
1:A:1841:G:H2'	1:A:1842:C:H6	1.84	0.42
1:A:2017:C:H2'	1:A:2018:A:C8	2.54	0.42
1:A:2162:G:H1	1:A:2183:G:H3'	1.85	0.42
1:A:2310:C:H3'	1:A:2311:G:H5'	2.02	0.42
1:A:2374:G:H4'	1:A:2375:A:C5'	2.49	0.42
1:A:2439:G:C4	1:A:2440:A:C8	3.08	0.42
1:A:2797:C:H2'	1:A:2798:C:C6	2.54	0.42
25:Y:201:PRO:HG2	25:Y:208:TYR:CE1	2.44	0.42
1:A:277:C:N4	1:A:278:A:H62	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:281:A:C2	1:A:291:C:C2	3.08	0.42
1:A:789:C:H2'	1:A:790:A:C8	2.54	0.42
1:A:888:A:H2'	1:A:889:A:H8	1.85	0.42
1:A:1567:U:C4	1:A:1568:G:C5	3.07	0.42
1:A:2070:U:H2'	1:A:2071:A:H8	1.80	0.42
1:A:2111:A:C2	1:A:2112:G:H1'	2.55	0.42
1:A:2317:A:C8	1:A:2319:G:C2	3.07	0.42
1:A:2349:A:C2'	1:A:2361:C:H5	2.26	0.42
1:A:2368:G:C5	1:A:2369:A:C5	3.08	0.42
1:A:2777:A:N6	1:A:2783:U:N3	2.39	0.42
1:A:2920:C:H2'	1:A:2921:U:H6	1.83	0.42
2:B:39:A:C8	2:B:41:C:H1'	2.54	0.42
4:D:62:ASN:O	4:D:65:GLU:HB2	2.19	0.42
8:H:76:TYR:HB2	11:K:76:THR:CG2	2.49	0.42
1:A:8:U:H2'	1:A:9:U:H6	1.84	0.42
1:A:172:U:H2'	1:A:173:A:H8	1.85	0.42
1:A:177:G:C2	1:A:178:A:C2	3.07	0.42
1:A:548:A:OP2	1:A:548:A:H8	2.02	0.42
1:A:1221:A:H2'	1:A:1222:A:C8	2.54	0.42
1:A:1664:G:C2	1:A:1665:G:C8	3.08	0.42
1:A:1668:G:C2	1:A:1669:G:C8	3.07	0.42
1:A:2134:A:H2'	1:A:2135:G:C8	2.55	0.42
1:A:2315:A:O2'	1:A:2412:G:O6	2.31	0.42
1:A:2362:A:H3'	1:A:2362:A:N3	2.35	0.42
1:A:2518:G:O2'	1:A:2519:G:OP2	2.31	0.42
1:A:39:C:H2'	1:A:40:U:C6	2.55	0.42
1:A:282:G:C5	1:A:283:G:C5	3.07	0.42
1:A:324:A:H2'	1:A:325:A:H8	1.85	0.42
1:A:324:A:C6	1:A:325:A:C6	3.08	0.42
1:A:436:A:C4	1:A:437:A:C8	3.07	0.42
1:A:660:G:H2'	1:A:661:A:C8	2.55	0.42
1:A:690:A:H2'	1:A:692:A:C8	2.54	0.42
1:A:1243:A:C6	1:A:1244:A:C6	3.07	0.42
1:A:1566:G:H2'	1:A:1567:U:O4'	2.20	0.42
1:A:1798:G:C2	1:A:1799:G:C8	3.08	0.42
1:A:1861:C:H2'	1:A:1862:C:N1	2.35	0.42
1:A:1883:A:N6	1:A:1917:G:C2	2.86	0.42
1:A:2131:U:H3'	1:A:2132:A:H8	1.85	0.42
1:A:2294:U:C1'	1:A:2295:A:H2'	2.47	0.42
1:A:2300:G:H8	1:A:2301:U:O4'	2.02	0.42
1:A:2495:C:H2'	1:A:2496:C:C6	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2795:G:C5	1:A:2796:C:C5	3.08	0.42
5:E:155:VAL:HA	5:E:176:VAL:O	2.20	0.42
25:Y:194:ASP:OD1	25:Y:197:LEU:HD21	2.20	0.42
1:A:292:U:H2'	1:A:293:U:H6	1.85	0.42
1:A:366:A:OP2	5:E:169:ASN:HB2	2.20	0.42
1:A:421:A:C4	1:A:448:A:N6	2.88	0.42
1:A:511:U:C4	1:A:835:A:C5	3.08	0.42
1:A:578:A:H4'	1:A:579:G:C8	2.55	0.42
1:A:697:G:H2'	1:A:698:C:C6	2.55	0.42
1:A:724:A:O2'	1:A:2099:G:O2'	2.38	0.42
1:A:1424:A:H1'	1:A:1425:C:C6	2.54	0.42
1:A:1458:U:H1'	1:A:1460:G:C2	2.55	0.42
1:A:2111:A:H2'	1:A:2112:G:C8	2.55	0.42
1:A:2122:G:C2	1:A:2123:A:C8	3.08	0.42
1:A:2123:A:O4'	1:A:2227:A:N6	2.53	0.42
1:A:2130:G:H2'	1:A:2131:U:C6	2.55	0.42
1:A:2309:G:H3'	1:A:2310:C:C6	2.55	0.42
1:A:2433:C:N3	1:A:2443:G:N1	2.68	0.42
2:B:14:G:C6	2:B:67:G:C2	3.07	0.42
2:B:31:G:N1	2:B:48:G:C6	2.88	0.42
3:C:168:GLU:HB3	3:C:171:TYR:O	2.20	0.42
25:Y:78:PHE:O	25:Y:120:MET:CE	2.68	0.42
25:Y:202:ALA:O	25:Y:203:ALA:HB3	2.20	0.42
1:A:669:C:H2'	1:A:670:C:H6	1.84	0.41
1:A:1390:C:HO2'	1:A:1619:A:HO2'	1.63	0.41
1:A:1477:A:H2'	1:A:1478:G:H8	1.84	0.41
1:A:2119:A:C6	1:A:2259:G:O6	2.73	0.41
1:A:2172:C:H2'	1:A:2173:G:C8	2.55	0.41
1:A:2362:A:O2'	1:A:2363:C:H3'	2.21	0.41
2:B:21:G:H2'	2:B:22:G:C5	2.55	0.41
12:L:97:ASP:O	12:L:98:LEU:C	2.63	0.41
1:A:67:A:C6	1:A:68:C:C4	3.07	0.41
1:A:512:G:H2'	1:A:513:A:C8	2.56	0.41
1:A:1080:G:N2	1:A:1168:G:H1'	2.35	0.41
1:A:1490:A:H8	1:A:1490:A:O5'	2.03	0.41
1:A:1823:U:H2'	1:A:1824:C:C6	2.55	0.41
1:A:2327:A:N1	1:A:2347:G:H5''	2.36	0.41
1:A:2332:G:N2	1:A:2343:A:H1'	2.25	0.41
1:A:85:G:H2'	1:A:86:C:O4'	2.21	0.41
1:A:309:U:C2	1:A:408:G:C2	3.08	0.41
1:A:684:G:C5	1:A:685:U:C4	3.08	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:686:C:O2'	1:A:687:U:H5'	2.20	0.41
1:A:801:U:H2'	1:A:802:G:C8	2.55	0.41
1:A:1063:G:C6	1:A:1192:G:C6	3.08	0.41
1:A:1811:C:H42	1:A:2615:C:H42	1.67	0.41
1:A:1833:G:H8	1:A:1833:G:OP2	2.03	0.41
1:A:2369:A:C6	1:A:2370:G:C6	3.09	0.41
1:A:2697:G:H2'	1:A:2698:G:C8	2.54	0.41
1:A:2827:A:H2'	1:A:2828:G:O4'	2.19	0.41
3:C:205:ILE:HG23	3:C:210:ARG:HB2	2.01	0.41
25:Y:57:GLN:HE21	25:Y:57:GLN:HB2	1.64	0.41
1:A:460:C:H42	1:A:2439:G:H1	1.68	0.41
1:A:758:A:C6	1:A:768:G:C6	3.08	0.41
1:A:1027:A:H5'	1:A:1028:C:OP2	2.20	0.41
1:A:1053:C:H5'	7:G:38:ARG:HH12	1.85	0.41
1:A:1519:C:N4	1:A:1566:G:H1	2.14	0.41
1:A:1581:A:H1'	1:A:1582:U:H2'	2.02	0.41
1:A:2085:G:H2'	1:A:2086:G:C8	2.55	0.41
1:A:2129:G:O6	1:A:2218:U:C4	2.72	0.41
1:A:2213:U:H2'	1:A:2214:G:C8	2.55	0.41
1:A:2349:A:H3'	1:A:2351:A:C6	2.56	0.41
1:A:2695:C:OP2	1:A:2696:C:N4	2.53	0.41
24:Z:9:CYS:SG	24:Z:13:GLY:N	2.87	0.41
1:A:250:G:N2	1:A:253:G:N7	2.68	0.41
1:A:436:A:C4	1:A:437:A:H8	2.38	0.41
1:A:663:G:O2'	1:A:664:C:H5'	2.19	0.41
1:A:674:G:C6	1:A:682:G:C2	3.08	0.41
1:A:914:C:H2'	1:A:915:U:C6	2.56	0.41
1:A:967:G:H2'	1:A:968:C:O4'	2.21	0.41
1:A:1340:A:C5	1:A:1342:G:C8	3.08	0.41
1:A:1358:G:C2	1:A:1373:U:C2	3.09	0.41
1:A:1540:A:H2'	1:A:1541:A:C8	2.56	0.41
1:A:1574:G:H8	1:A:1574:G:O5'	2.03	0.41
1:A:1764:U:H2'	1:A:1765:G:O4'	2.20	0.41
1:A:2144:G:O6	1:A:2146:A:H3'	2.20	0.41
1:A:2293:C:C4	1:A:2305:G:C6	3.09	0.41
1:A:2370:G:C2	1:A:2371:C:N4	2.88	0.41
1:A:2770:A:C2	1:A:2771:G:H1'	2.55	0.41
6:F:60:LYS:HA	6:F:63:ARG:HD2	2.02	0.41
1:A:982:U:H2'	1:A:983:U:H6	1.85	0.41
1:A:1302:A:C4	1:A:1303:U:C5	3.09	0.41
1:A:1414:G:H2'	1:A:1415:C:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1922:C:O2'	1:A:1924:C:H3'	2.20	0.41
1:A:2086:G:H2'	1:A:2087:A:C8	2.42	0.41
1:A:2294:U:C6	1:A:2295:A:H8	2.38	0.41
1:A:2400:G:C8	1:A:2402:A:N6	2.87	0.41
1:A:2569:C:O2'	1:A:2769:A:N3	2.53	0.41
1:A:2687:C:N4	1:A:2688:G:O6	2.54	0.41
1:A:2796:C:H2'	1:A:2797:C:H6	1.85	0.41
2:B:102:A:C2	2:B:103:G:H1'	2.56	0.41
12:L:62:ILE:HG12	12:L:93:LYS:HD2	2.02	0.41
17:Q:49:ARG:O	17:Q:49:ARG:HG3	2.19	0.41
23:W:137:GLY:C	25:Y:129:ARG:HH21	2.28	0.41
1:A:37:C:H2'	1:A:38:A:C8	2.55	0.41
1:A:515:G:O6	21:U:39:ARG:NH2	2.54	0.41
1:A:684:G:O6	1:A:697:G:C6	2.74	0.41
1:A:687:U:H2'	1:A:688:G:C8	2.56	0.41
1:A:692:A:H2'	1:A:693:G:O4'	2.20	0.41
1:A:1212:U:N3	1:A:1213:G:N7	2.68	0.41
1:A:1338:G:N1	1:A:1685:A:OP2	2.40	0.41
1:A:1435:U:H3'	1:A:1435:U:P	2.60	0.41
1:A:1598:C:H2'	1:A:1599:U:H6	1.85	0.41
1:A:1884:G:HO2'	1:A:1885:A:P	2.42	0.41
1:A:2218:U:O2'	1:A:2219:G:H5'	2.20	0.41
1:A:2443:G:H5''	1:A:2444:G:OP2	2.21	0.41
1:A:2539:C:H2'	1:A:2540:U:C6	2.56	0.41
6:F:59:GLN:O	6:F:63:ARG:HG3	2.20	0.41
1:A:32:C:O2'	1:A:33:U:H5'	2.20	0.41
1:A:46:C:H2'	1:A:47:C:C6	2.55	0.41
1:A:127:C:H2'	1:A:128:C:H6	1.86	0.41
1:A:664:C:O2'	1:A:665:G:O4'	2.38	0.41
1:A:956:A:C5	1:A:959:C:C5	3.09	0.41
1:A:988:G:H2'	1:A:989:U:C6	2.55	0.41
1:A:1169:C:H2'	1:A:1170:C:H6	1.86	0.41
1:A:1249:U:O2'	1:A:1277:A:N1	2.48	0.41
1:A:1424:A:C6	1:A:1442:A:C5	3.08	0.41
1:A:2029:G:H2'	1:A:2030:A:H8	1.85	0.41
1:A:2111:A:N6	1:A:2266:G:O2'	2.54	0.41
1:A:2155:A:OP2	1:A:2202:A:H5''	2.21	0.41
1:A:2307:A:C6	1:A:2308:G:C5	3.08	0.41
1:A:2350:G:OP1	1:A:2350:G:C4	2.74	0.41
1:A:2460:U:O2	1:A:2460:U:H2'	2.20	0.41
1:A:2716:U:O2'	1:A:2717:G:OP1	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2873:G:C6	1:A:2892:G:C2	3.09	0.41
1:A:27:G:N2	1:A:558:G:H2'	2.36	0.41
1:A:78:U:H2'	1:A:79:C:H6	1.84	0.41
1:A:139:A:H1'	1:A:1449:C:O4'	2.21	0.41
1:A:290:U:HO2'	1:A:291:C:C5'	2.33	0.41
1:A:304:G:C2	1:A:415:C:N3	2.89	0.41
1:A:448:A:C6	1:A:449:A:N1	2.89	0.41
1:A:460:C:H2'	1:A:461:C:C6	2.56	0.41
1:A:1556:A:C4	1:A:1557:G:C8	3.08	0.41
1:A:1586:G:O2'	1:A:1587:U:O4'	2.27	0.41
1:A:1723:A:H2'	1:A:1724:A:C8	2.56	0.41
1:A:2109:G:C6	1:A:2270:A:N1	2.89	0.41
1:A:2162:G:H2'	1:A:2166:C:C2	2.55	0.41
1:A:2168:G:C6	1:A:2182:G:N1	2.89	0.41
1:A:2243:C:H2'	1:A:2244:G:O4'	2.20	0.41
1:A:2318:G:H2'	1:A:2373:U:C5	2.55	0.41
1:A:2404:G:H4'	1:A:2405:A:C4	2.56	0.41
1:A:2686:A:N6	1:A:2693:G:H1'	2.36	0.41
1:A:2920:C:H2'	1:A:2921:U:C6	2.55	0.41
1:A:2922:U:H2'	1:A:2923:A:C8	2.56	0.41
2:B:91:C:H2'	2:B:92:C:H6	1.85	0.41
20:T:15:LEU:O	20:T:18:THR:HG22	2.20	0.41
23:W:184:PRO:HB3	23:W:208:GLY:H	1.85	0.41
25:Y:121:MET:HG3	25:Y:145:VAL:HG11	2.02	0.41
1:A:80:G:C6	1:A:106:G:C6	3.09	0.41
1:A:177:G:H8	1:A:177:G:OP1	2.03	0.41
1:A:274:A:C6	1:A:275:A:C6	3.10	0.41
1:A:281:A:N1	1:A:291:C:C4	2.89	0.41
1:A:711:U:C2	1:A:712:C:C5	3.08	0.41
1:A:837:U:H6	1:A:837:U:H2'	1.75	0.41
1:A:1303:U:O2'	20:T:8:THR:HG22	2.21	0.41
1:A:1354:C:H2'	1:A:1355:U:H6	1.84	0.41
1:A:2182:G:H8	1:A:2182:G:OP2	2.04	0.41
1:A:2302:A:H2	1:A:2303:A:N1	2.19	0.41
1:A:2490:C:H1'	1:A:2523:G:N2	2.33	0.41
1:A:2676:U:C4	1:A:2702:G:O6	2.74	0.41
1:A:2703:G:H2'	1:A:2704:A:H8	1.84	0.41
1:A:2910:C:H42	20:T:39:SER:HB3	1.86	0.41
1:A:421:A:N3	1:A:448:A:C6	2.90	0.40
1:A:718:C:O2'	1:A:719:C:H6	2.04	0.40
1:A:902:G:H1	1:A:969:C:H5	1.63	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1030:G:H5'	1:A:1031:C:H5	1.86	0.40
1:A:1302:A:H2'	1:A:1302:A:N3	2.36	0.40
1:A:1306:G:H5''	20:T:20:PHE:CE1	2.56	0.40
1:A:1458:U:H1'	1:A:1460:G:C6	2.56	0.40
1:A:1518:G:O2'	1:A:1519:C:O5'	2.31	0.40
1:A:2327:A:C6	1:A:2328:G:C4	3.10	0.40
1:A:2411:G:O2'	1:A:2412:G:OP2	2.27	0.40
1:A:2425:G:C6	1:A:2449:C:C4	3.09	0.40
1:A:2863:G:C4	1:A:2864:G:C8	3.09	0.40
1:A:122:G:H2'	1:A:123:G:H8	1.87	0.40
1:A:206:A:C8	1:A:207:A:C8	3.10	0.40
1:A:330:A:OP2	1:A:330:A:H8	2.04	0.40
1:A:456:A:H2'	1:A:457:G:C8	2.56	0.40
1:A:461:C:N3	1:A:462:A:H8	2.20	0.40
1:A:476:A:H2'	1:A:477:A:C8	2.55	0.40
1:A:523:G:N2	1:A:525:A:O2'	2.53	0.40
1:A:812:G:H2'	1:A:813:G:H8	1.86	0.40
1:A:910:A:H2'	1:A:911:G:H5'	2.03	0.40
1:A:1317:G:H5'	10:J:20:LEU:CD2	2.51	0.40
1:A:1694:G:O2'	10:J:110:ASP:OD2	2.35	0.40
1:A:1697:A:N7	1:A:1698:G:C5	2.90	0.40
1:A:1783:C:H2'	1:A:1784:A:C8	2.56	0.40
1:A:2108:U:C2	1:A:2109:G:C8	3.09	0.40
1:A:2160:U:O5'	1:A:2186:G:N2	2.54	0.40
1:A:2399:G:H4'	24:Z:40:LYS:NZ	2.36	0.40
1:A:2628:G:H2'	1:A:2629:A:H8	1.86	0.40
1:A:2714:G:C2	1:A:2715:G:C8	3.09	0.40
1:A:2758:G:H2'	1:A:2759:C:C6	2.56	0.40
1:A:423:G:C4	1:A:446:G:C2	3.10	0.40
1:A:681:C:H2'	1:A:682:G:O4'	2.21	0.40
1:A:921:G:N7	1:A:922:A:C4	2.89	0.40
1:A:1070:G:C6	1:A:1071:G:C6	3.09	0.40
1:A:1072:A:C8	1:A:1180:C:C4	3.09	0.40
1:A:1541:A:H2'	1:A:1542:A:H8	1.84	0.40
1:A:1623:C:H2'	1:A:1624:U:H6	1.86	0.40
1:A:2092:C:H6	1:A:2092:C:H2'	1.70	0.40
1:A:2162:G:N7	1:A:2185:G:C2	2.89	0.40
2:B:47:C:OP1	22:V:104:GLY:HA3	2.21	0.40
2:B:89:C:H2'	2:B:90:C:C6	2.56	0.40
5:E:58:ARG:NH2	21:U:37:LYS:HZ3	2.19	0.40
1:A:58:G:O2'	1:A:59:G:P	2.80	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:153:C:C2	1:A:177:G:N1	2.89	0.40
1:A:201:C:N3	1:A:202:A:N6	2.69	0.40
1:A:302:A:H2'	1:A:303:G:H8	1.85	0.40
1:A:441:C:C2	1:A:442:C:C5	3.10	0.40
1:A:843:C:H2'	1:A:844:U:C6	2.57	0.40
1:A:914:C:H2'	1:A:915:U:H6	1.86	0.40
1:A:1061:A:H2'	1:A:1062:C:H6	1.85	0.40
1:A:1087:U:H2'	1:A:1160:G:H1	1.87	0.40
1:A:1211:C:H2'	1:A:1212:U:C6	2.56	0.40
1:A:1332:U:H2'	1:A:1333:C:H6	1.86	0.40
1:A:1585:A:H61	1:A:1587:U:H1'	1.86	0.40
1:A:2159:U:H1'	1:A:2187:A:C6	2.56	0.40
1:A:2406:A:H2'	1:A:2406:A:N3	2.36	0.40
1:A:2439:G:H2'	1:A:2440:A:O4'	2.21	0.40
1:A:2561:G:C5	1:A:2562:U:C4	3.10	0.40
1:A:2575:U:H1'	1:A:2594:A:H2	1.87	0.40
1:A:2575:U:H1'	1:A:2594:A:C2	2.56	0.40
3:C:61:GLN:HA	3:C:61:GLN:OE1	2.21	0.40
1:A:7:G:H5'	7:G:133:HIS:CD2	2.57	0.40
1:A:63:G:H2'	1:A:64:A:C8	2.41	0.40
1:A:117:A:OP2	1:A:118:A:H2'	2.22	0.40
1:A:2110:C:O2	1:A:2110:C:H2'	2.21	0.40
1:A:2119:A:H2'	1:A:2120:U:C6	2.57	0.40
1:A:2134:A:C6	1:A:2214:G:N1	2.89	0.40
1:A:2210:G:H2'	1:A:2211:G:O4'	2.22	0.40
1:A:2214:G:H2'	1:A:2215:U:H6	1.87	0.40
1:A:2217:U:H2'	1:A:2218:U:H6	1.84	0.40
1:A:2321:U:H1'	1:A:2403:C:N3	2.37	0.40
1:A:2660:G:H4'	1:A:2916:A:H5'	2.03	0.40
1:A:2774:C:C2	1:A:2775:U:C5	3.10	0.40
1:A:2863:G:C5	1:A:2864:G:C8	3.10	0.40
7:G:28:ARG:H	7:G:28:ARG:HG2	1.55	0.40
23:W:91:ASN:OD1	23:W:92:GLY:N	2.55	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	262/277 (95%)	238 (91%)	24 (9%)	0	100	100
4	D	180/209 (86%)	170 (94%)	10 (6%)	0	100	100
5	E	203/207 (98%)	189 (93%)	14 (7%)	0	100	100
6	F	61/179 (34%)	59 (97%)	2 (3%)	0	100	100
7	G	142/145 (98%)	130 (92%)	12 (8%)	0	100	100
8	H	119/122 (98%)	106 (89%)	13 (11%)	0	100	100
9	I	111/146 (76%)	105 (95%)	6 (5%)	0	100	100
10	J	117/120 (98%)	108 (92%)	9 (8%)	0	100	100
11	K	110/115 (96%)	103 (94%)	7 (6%)	0	100	100
12	L	115/118 (98%)	108 (94%)	7 (6%)	0	100	100
13	M	99/102 (97%)	89 (90%)	10 (10%)	0	100	100
14	N	107/113 (95%)	100 (94%)	7 (6%)	0	100	100
15	O	89/95 (94%)	81 (91%)	8 (9%)	0	100	100
16	P	89/103 (86%)	80 (90%)	9 (10%)	0	100	100
17	Q	60/94 (64%)	56 (93%)	4 (7%)	0	100	100
18	R	63/66 (96%)	58 (92%)	5 (8%)	0	100	100
19	S	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
20	T	50/59 (85%)	46 (92%)	4 (8%)	0	100	100
21	U	42/44 (96%)	40 (95%)	2 (5%)	0	100	100
22	V	102/120 (85%)	94 (92%)	8 (8%)	0	100	100
23	W	401/436 (92%)	367 (92%)	33 (8%)	1 (0%)	43	71
24	Z	45/49 (92%)	43 (96%)	2 (4%)	0	100	100
25	Y	168/232 (72%)	148 (88%)	18 (11%)	2 (1%)	10	37
All	All	2791/3210 (87%)	2572 (92%)	216 (8%)	3 (0%)	49	75

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
25	Y	66	PRO
25	Y	67	ASN
23	W	392	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	202/225 (90%)	202 (100%)	0	100	100
4	D	139/170 (82%)	139 (100%)	0	100	100
5	E	155/170 (91%)	155 (100%)	0	100	100
6	F	48/151 (32%)	48 (100%)	0	100	100
7	G	117/123 (95%)	117 (100%)	0	100	100
8	H	92/101 (91%)	92 (100%)	0	100	100
9	I	85/110 (77%)	85 (100%)	0	100	100
10	J	94/100 (94%)	94 (100%)	0	100	100
11	K	85/100 (85%)	85 (100%)	0	100	100
12	L	86/97 (89%)	86 (100%)	0	100	100
13	M	79/84 (94%)	79 (100%)	0	100	100
14	N	86/93 (92%)	86 (100%)	0	100	100
15	O	80/85 (94%)	80 (100%)	0	100	100
16	P	74/87 (85%)	74 (100%)	0	100	100
17	Q	27/74 (36%)	27 (100%)	0	100	100
18	R	48/57 (84%)	48 (100%)	0	100	100
19	S	50/53 (94%)	50 (100%)	0	100	100
20	T	44/53 (83%)	44 (100%)	0	100	100
21	U	38/39 (97%)	38 (100%)	0	100	100
22	V	64/93 (69%)	64 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	W	309/372 (83%)	308 (100%)	1 (0%)	86	86
24	Z	41/47 (87%)	41 (100%)	0	100	100
25	Y	140/185 (76%)	129 (92%)	11 (8%)	11	36
All	All	2183/2669 (82%)	2171 (100%)	12 (0%)	78	83

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
23	W	395	PHE
25	Y	56	ASP
25	Y	57	GLN
25	Y	59	ILE
25	Y	60	ARG
25	Y	65	LEU
25	Y	67	ASN
25	Y	121	MET
25	Y	198	LYS
25	Y	200	LYS
25	Y	205	LYS
25	Y	207	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	153	GLN
4	D	43	ASN
4	D	95	GLN
4	D	128	GLN
4	D	135	HIS
6	F	66	HIS
7	G	78	HIS
7	G	131	HIS
7	G	133	HIS
9	I	35	HIS
9	I	68	ASN
10	J	61	GLN
10	J	76	ASN
12	L	107	ASN
13	M	81	ASN
14	N	60	HIS

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Mol	Chain	Res	Type
14	N	61	ASN
21	U	6	GLN
21	U	16	HIS
23	W	13	ASN
23	W	312	ASN
23	W	316	HIS
23	W	349	ASN
25	Y	57	GLN
25	Y	67	ASN
25	Y	106	GLN
25	Y	188	ASN
25	Y	211	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2666/2927 (91%)	919 (34%)	75 (2%)
2	B	109/119 (91%)	55 (50%)	5 (4%)
All	All	2775/3046 (91%)	974 (35%)	80 (2%)

All (974) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	4	U
1	A	12	A
1	A	13	A
1	A	15	G
1	A	25	U
1	A	28	A
1	A	34	U
1	A	35	G
1	A	36	G
1	A	46	C
1	A	49	A
1	A	51	G
1	A	53	A
1	A	55	G
1	A	59	G
1	A	63	G
1	A	71	A
1	A	75	G

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Mol	Chain	Res	Type
1	A	76	C
1	A	87	U
1	A	88	G
1	A	91	A
1	A	92	G
1	A	99	U
1	A	101	G
1	A	117	A
1	A	119	U
1	A	130	A
1	A	145	G
1	A	157	U
1	A	158	C
1	A	159	U
1	A	163	U
1	A	164	U
1	A	166	A
1	A	175	G
1	A	176	A
1	A	178	A
1	A	184	G
1	A	198	A
1	A	199	A
1	A	200	A
1	A	201	C
1	A	202	A
1	A	203	U
1	A	204	C
1	A	207	A
1	A	208	G
1	A	216	A
1	A	219	A
1	A	224	A
1	A	225	A
1	A	226	A
1	A	227	G
1	A	229	A
1	A	231	A
1	A	232	U
1	A	233	G
1	A	236	A
1	A	242	U

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Mol	Chain	Res	Type
1	A	245	G
1	A	251	G
1	A	252	C
1	A	253	G
1	A	258	A
1	A	260	A
1	A	266	U
1	A	267	C
1	A	268	A
1	A	269	G
1	A	272	C
1	A	275	A
1	A	276	C
1	A	282	G
1	A	286	U
1	A	287	G
1	A	288	C
1	A	289	C
1	A	290	U
1	A	291	C
1	A	294	G
1	A	296	G
1	A	297	G
1	A	298	U
1	A	299	U
1	A	302	A
1	A	304	G
1	A	308	C
1	A	310	C
1	A	311	U
1	A	312	G
1	A	315	C
1	A	321	U
1	A	322	A
1	A	324	A
1	A	326	A
1	A	327	G
1	A	330	A
1	A	331	C
1	A	334	G
1	A	338	G
1	A	345	A

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Mol	Chain	Res	Type
1	A	346	G
1	A	355	A
1	A	361	G
1	A	362	C
1	A	367	G
1	A	374	A
1	A	375	C
1	A	376	A
1	A	377	G
1	A	382	G
1	A	386	U
1	A	387	C
1	A	388	A
1	A	390	A
1	A	392	C
1	A	394	U
1	A	396	G
1	A	405	U
1	A	410	G
1	A	411	G
1	A	412	A
1	A	416	U
1	A	417	G
1	A	418	A
1	A	419	G
1	A	420	U
1	A	424	G
1	A	426	G
1	A	428	A
1	A	429	A
1	A	430	C
1	A	431	A
1	A	432	C
1	A	433	G
1	A	436	A
1	A	437	A
1	A	438	A
1	A	440	U
1	A	444	U
1	A	445	C
1	A	448	A
1	A	449	A

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Mol	Chain	Res	Type
1	A	451	C
1	A	453	G
1	A	459	A
1	A	461	C
1	A	462	A
1	A	463	U
1	A	464	C
1	A	469	A
1	A	478	U
1	A	482	C
1	A	485	U
1	A	487	G
1	A	504	A
1	A	511	U
1	A	514	G
1	A	520	G
1	A	526	A
1	A	528	G
1	A	538	A
1	A	548	A
1	A	551	A
1	A	552	G
1	A	554	U
1	A	555	C
1	A	556	C
1	A	567	U
1	A	568	G
1	A	570	C
1	A	571	U
1	A	576	G
1	A	577	U
1	A	578	A
1	A	579	G
1	A	592	A
1	A	594	C
1	A	595	G
1	A	598	U
1	A	599	G
1	A	607	G
1	A	617	G
1	A	618	A
1	A	619	A

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Mol	Chain	Res	Type
1	A	647	A
1	A	648	G
1	A	650	U
1	A	651	U
1	A	658	A
1	A	659	A
1	A	665	G
1	A	666	G
1	A	673	A
1	A	683	A
1	A	684	G
1	A	687	U
1	A	688	G
1	A	689	A
1	A	690	A
1	A	691	U
1	A	692	A
1	A	701	G
1	A	716	G
1	A	718	C
1	A	719	C
1	A	722	A
1	A	733	U
1	A	761	U
1	A	763	A
1	A	765	A
1	A	766	C
1	A	771	U
1	A	773	G
1	A	774	A
1	A	775	G
1	A	777	C
1	A	783	C
1	A	785	C
1	A	786	A
1	A	787	C
1	A	792	G
1	A	794	U
1	A	795	G
1	A	799	A
1	A	809	U
1	A	811	A

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Mol	Chain	Res	Type
1	A	818	G
1	A	822	G
1	A	823	G
1	A	826	U
1	A	829	A
1	A	830	A
1	A	831	U
1	A	837	U
1	A	838	C
1	A	839	G
1	A	841	A
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	869	U
1	A	870	A
1	A	872	C
1	A	873	U
1	A	874	U
1	A	876	A
1	A	877	G
1	A	892	U
1	A	896	A
1	A	898	U
1	A	901	U
1	A	902	G
1	A	904	A
1	A	906	G
1	A	907	U
1	A	908	A
1	A	910	A
1	A	911	G
1	A	912	C
1	A	913	A
1	A	914	C
1	A	915	U
1	A	916	G

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Mol	Chain	Res	Type
1	A	917	A
1	A	918	U
1	A	919	U
1	A	922	A
1	A	948	A
1	A	950	U
1	A	951	C
1	A	952	A
1	A	953	G
1	A	954	U
1	A	957	A
1	A	958	A
1	A	959	C
1	A	961	C
1	A	964	A
1	A	966	U
1	A	970	A
1	A	971	A
1	A	972	U
1	A	973	G
1	A	975	C
1	A	978	A
1	A	981	C
1	A	987	A
1	A	989	U
1	A	991	A
1	A	992	G
1	A	1002	G
1	A	1003	A
1	A	1004	U
1	A	1005	A
1	A	1007	G
1	A	1008	A
1	A	1010	C
1	A	1011	C
1	A	1020	A
1	A	1027	A
1	A	1030	G
1	A	1031	C
1	A	1037	C
1	A	1042	A
1	A	1054	A

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Mol	Chain	Res	Type
1	A	1055	A
1	A	1058	U
1	A	1059	A
1	A	1061	A
1	A	1062	C
1	A	1065	U
1	A	1066	A
1	A	1068	G
1	A	1069	U
1	A	1071	G
1	A	1072	A
1	A	1073	A
1	A	1074	A
1	A	1076	G
1	A	1079	U
1	A	1080	G
1	A	1081	U
1	A	1082	G
1	A	1084	A
1	A	1091	U
1	A	1093	G
1	A	1094	A
1	A	1096	A
1	A	1097	A
1	A	1098	C
1	A	1155	C
1	A	1157	A
1	A	1158	G
1	A	1160	G
1	A	1161	A
1	A	1164	C
1	A	1165	U
1	A	1167	C
1	A	1173	A
1	A	1174	A
1	A	1178	U
1	A	1179	A
1	A	1181	C
1	A	1182	G
1	A	1185	G
1	A	1187	U
1	A	1188	A

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Mol	Chain	Res	Type
1	A	1194	A
1	A	1201	A
1	A	1209	G
1	A	1214	U
1	A	1215	U
1	A	1217	U
1	A	1218	U
1	A	1219	C
1	A	1220	G
1	A	1221	A
1	A	1222	A
1	A	1223	C
1	A	1246	G
1	A	1247	G
1	A	1248	C
1	A	1249	U
1	A	1251	U
1	A	1252	G
1	A	1276	G
1	A	1278	G
1	A	1289	U
1	A	1293	A
1	A	1296	G
1	A	1305	A
1	A	1311	G
1	A	1312	A
1	A	1314	A
1	A	1315	G
1	A	1327	U
1	A	1339	A
1	A	1340	A
1	A	1341	U
1	A	1344	C
1	A	1345	U
1	A	1346	A
1	A	1363	G
1	A	1364	C
1	A	1375	A
1	A	1376	G
1	A	1380	U
1	A	1384	C
1	A	1388	A

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Mol	Chain	Res	Type
1	A	1391	U
1	A	1404	A
1	A	1417	A
1	A	1418	U
1	A	1424	A
1	A	1432	A
1	A	1433	U
1	A	1434	A
1	A	1435	U
1	A	1439	U
1	A	1441	U
1	A	1449	C
1	A	1456	A
1	A	1457	U
1	A	1459	U
1	A	1460	G
1	A	1465	A
1	A	1473	A
1	A	1474	C
1	A	1495	C
1	A	1496	G
1	A	1497	G
1	A	1498	U
1	A	1499	A
1	A	1500	U
1	A	1501	U
1	A	1503	G
1	A	1504	A
1	A	1505	U
1	A	1506	A
1	A	1507	U
1	A	1513	U
1	A	1515	C
1	A	1519	C
1	A	1520	A
1	A	1521	G
1	A	1524	A
1	A	1526	G
1	A	1528	U
1	A	1529	G
1	A	1533	A
1	A	1535	U

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Mol	Chain	Res	Type
1	A	1536	A
1	A	1537	G
1	A	1539	C
1	A	1540	A
1	A	1550	C
1	A	1553	A
1	A	1554	U
1	A	1556	A
1	A	1561	G
1	A	1563	G
1	A	1567	U
1	A	1571	G
1	A	1572	G
1	A	1573	C
1	A	1578	G
1	A	1582	U
1	A	1583	A
1	A	1584	U
1	A	1596	U
1	A	1607	C
1	A	1614	A
1	A	1615	A
1	A	1617	A
1	A	1624	U
1	A	1626	U
1	A	1631	A
1	A	1632	G
1	A	1634	U
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	1660	C
1	A	1661	A
1	A	1667	A
1	A	1671	G
1	A	1691	A
1	A	1692	U
1	A	1693	C

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Mol	Chain	Res	Type
1	A	1696	G
1	A	1697	A
1	A	1712	G
1	A	1719	G
1	A	1722	A
1	A	1725	U
1	A	1727	A
1	A	1728	C
1	A	1733	U
1	A	1743	A
1	A	1745	A
1	A	1747	G
1	A	1757	G
1	A	1759	U
1	A	1773	G
1	A	1774	A
1	A	1775	G
1	A	1777	G
1	A	1778	A
1	A	1779	G
1	A	1780	C
1	A	1781	C
1	A	1782	G
1	A	1783	C
1	A	1784	A
1	A	1785	G
1	A	1789	A
1	A	1790	U
1	A	1791	A
1	A	1792	G
1	A	1793	G
1	A	1798	G
1	A	1802	A
1	A	1809	A
1	A	1810	G
1	A	1811	C
1	A	1814	A
1	A	1829	C
1	A	1830	G
1	A	1831	A
1	A	1832	A
1	A	1834	C

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Mol	Chain	Res	Type
1	A	1845	A
1	A	1848	A
1	A	1851	G
1	A	1858	A
1	A	1864	G
1	A	1867	C
1	A	1871	G
1	A	1872	C
1	A	1874	G
1	A	1878	G
1	A	1881	U
1	A	1882	A
1	A	1884	G
1	A	1885	A
1	A	1887	G
1	A	1890	C
1	A	1913	A
1	A	1915	U
1	A	1916	U
1	A	1917	G
1	A	1918	A
1	A	1922	C
1	A	1923	C
1	A	1924	C
1	A	1927	U
1	A	1928	A
1	A	1929	A
1	A	2010	A
1	A	2011	U
1	A	2023	C
1	A	2024	U
1	A	2026	A
1	A	2031	G
1	A	2049	A
1	A	2050	G
1	A	2052	A
1	A	2060	A
1	A	2062	A
1	A	2064	G
1	A	2072	C
1	A	2083	A
1	A	2085	G

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Mol	Chain	Res	Type
1	A	2086	G
1	A	2088	A
1	A	2089	A
1	A	2090	G
1	A	2091	A
1	A	2092	C
1	A	2093	C
1	A	2096	G
1	A	2097	U
1	A	2105	U
1	A	2107	C
1	A	2109	G
1	A	2110	C
1	A	2111	A
1	A	2115	U
1	A	2116	G
1	A	2121	U
1	A	2122	G
1	A	2124	A
1	A	2128	U
1	A	2129	G
1	A	2130	G
1	A	2133	C
1	A	2135	G
1	A	2139	G
1	A	2140	U
1	A	2141	A
1	A	2142	C
1	A	2143	A
1	A	2144	G
1	A	2145	G
1	A	2148	A
1	A	2149	G
1	A	2150	G
1	A	2151	U
1	A	2152	A
1	A	2153	G
1	A	2154	G
1	A	2155	A
1	A	2156	G
1	A	2157	C
1	A	2158	C

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Mol	Chain	Res	Type
1	A	2159	U
1	A	2160	U
1	A	2161	G
1	A	2162	G
1	A	2163	A
1	A	2165	A
1	A	2166	C
1	A	2167	C
1	A	2169	G
1	A	2170	A
1	A	2171	G
1	A	2172	C
1	A	2174	C
1	A	2175	C
1	A	2176	A
1	A	2180	U
1	A	2181	C
1	A	2182	G
1	A	2183	G
1	A	2184	U
1	A	2185	G
1	A	2186	G
1	A	2187	A
1	A	2188	G
1	A	2189	G
1	A	2192	U
1	A	2193	C
1	A	2194	G
1	A	2195	G
1	A	2196	U
1	A	2197	G
1	A	2198	G
1	A	2199	G
1	A	2201	U
1	A	2202	A
1	A	2203	C
1	A	2204	U
1	A	2205	A
1	A	2207	C
1	A	2208	C
1	A	2217	U
1	A	2219	G

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Mol	Chain	Res	Type
1	A	2221	C
1	A	2223	U
1	A	2224	U
1	A	2225	C
1	A	2227	A
1	A	2228	A
1	A	2231	C
1	A	2232	G
1	A	2233	C
1	A	2240	U
1	A	2241	A
1	A	2243	C
1	A	2248	G
1	A	2252	A
1	A	2253	G
1	A	2254	A
1	A	2260	U
1	A	2262	A
1	A	2263	G
1	A	2264	G
1	A	2265	U
1	A	2266	G
1	A	2267	G
1	A	2272	U
1	A	2273	U
1	A	2291	U
1	A	2292	C
1	A	2293	C
1	A	2294	U
1	A	2295	A
1	A	2296	A
1	A	2297	A
1	A	2298	A
1	A	2299	G
1	A	2301	U
1	A	2302	A
1	A	2304	C
1	A	2305	G
1	A	2306	G
1	A	2307	A
1	A	2309	G
1	A	2310	C

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Mol	Chain	Res	Type
1	A	2311	G
1	A	2313	C
1	A	2314	C
1	A	2315	A
1	A	2316	A
1	A	2317	A
1	A	2318	G
1	A	2319	G
1	A	2320	U
1	A	2321	U
1	A	2322	C
1	A	2324	C
1	A	2326	C
1	A	2327	A
1	A	2329	A
1	A	2330	A
1	A	2331	U
1	A	2332	G
1	A	2333	G
1	A	2342	C
1	A	2343	A
1	A	2345	U
1	A	2347	G
1	A	2348	C
1	A	2349	A
1	A	2350	G
1	A	2351	A
1	A	2352	G
1	A	2353	U
1	A	2354	G
1	A	2355	U
1	A	2356	A
1	A	2358	A
1	A	2359	G
1	A	2360	G
1	A	2362	A
1	A	2363	C
1	A	2364	A
1	A	2365	A
1	A	2366	G
1	A	2367	G
1	A	2368	G

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Mol	Chain	Res	Type
1	A	2369	A
1	A	2370	G
1	A	2371	C
1	A	2372	U
1	A	2373	U
1	A	2374	G
1	A	2375	A
1	A	2378	G
1	A	2379	C
1	A	2380	G
1	A	2381	A
1	A	2382	G
1	A	2384	C
1	A	2385	C
1	A	2386	U
1	A	2387	A
1	A	2391	G
1	A	2394	G
1	A	2395	A
1	A	2396	G
1	A	2398	A
1	A	2399	G
1	A	2400	G
1	A	2401	G
1	A	2402	A
1	A	2403	C
1	A	2404	G
1	A	2405	A
1	A	2406	A
1	A	2407	A
1	A	2408	G
1	A	2409	U
1	A	2410	C
1	A	2411	G
1	A	2412	G
1	A	2413	G
1	A	2414	C
1	A	2415	U
1	A	2416	U
1	A	2419	U
1	A	2421	A
1	A	2422	U

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Mol	Chain	Res	Type
1	A	2423	C
1	A	2424	C
1	A	2426	G
1	A	2428	G
1	A	2429	G
1	A	2430	U
1	A	2432	C
1	A	2435	C
1	A	2436	A
1	A	2437	U
1	A	2438	G
1	A	2443	G
1	A	2444	G
1	A	2445	C
1	A	2446	C
1	A	2449	C
1	A	2450	G
1	A	2451	C
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	2462	A
1	A	2463	A
1	A	2465	G
1	A	2468	A
1	A	2469	C
1	A	2470	C
1	A	2472	C
1	A	2489	U
1	A	2493	C
1	A	2494	C
1	A	2495	C
1	A	2496	C
1	A	2497	A
1	A	2513	G
1	A	2516	G

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Mol	Chain	Res	Type
1	A	2517	A
1	A	2518	G
1	A	2519	G
1	A	2521	U
1	A	2522	U
1	A	2523	G
1	A	2524	G
1	A	2525	C
1	A	2526	A
1	A	2538	G
1	A	2541	C
1	A	2542	A
1	A	2543	U
1	A	2546	C
1	A	2547	A
1	A	2555	G
1	A	2556	C
1	A	2557	U
1	A	2558	G
1	A	2559	U
1	A	2561	G
1	A	2564	G
1	A	2568	C
1	A	2572	G
1	A	2575	U
1	A	2576	U
1	A	2577	G
1	A	2583	U
1	A	2591	U
1	A	2595	A
1	A	2596	G
1	A	2598	G
1	A	2600	U
1	A	2624	G
1	A	2625	U
1	A	2626	G
1	A	2631	A
1	A	2632	G
1	A	2638	U
1	A	2639	C
1	A	2640	C
1	A	2642	U

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Mol	Chain	Res	Type
1	A	2648	U
1	A	2658	A
1	A	2659	G
1	A	2668	A
1	A	2675	C
1	A	2676	U
1	A	2680	C
1	A	2683	A
1	A	2684	G
1	A	2685	U
1	A	2692	G
1	A	2696	C
1	A	2711	G
1	A	2717	G
1	A	2718	U
1	A	2720	C
1	A	2731	G
1	A	2743	G
1	A	2755	U
1	A	2762	A
1	A	2764	G
1	A	2773	G
1	A	2775	U
1	A	2776	G
1	A	2780	G
1	A	2781	C
1	A	2784	C
1	A	2785	U
1	A	2786	A
1	A	2787	A
1	A	2789	C
1	A	2795	G
1	A	2797	C
1	A	2799	C
1	A	2805	A
1	A	2807	A
1	A	2808	U
1	A	2809	G
1	A	2813	U
1	A	2818	C
1	A	2819	A
1	A	2820	U

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Mol	Chain	Res	Type
1	A	2823	C
1	A	2825	C
1	A	2826	A
1	A	2845	A
1	A	2858	U
1	A	2859	G
1	A	2860	A
1	A	2866	C
1	A	2873	G
1	A	2874	G
1	A	2892	G
1	A	2897	G
1	A	2899	C
1	A	2904	A
1	A	2909	U
1	A	2918	G
1	A	2919	A
1	A	2921	U
1	A	2925	C
2	B	4	G
2	B	7	G
2	B	8	G
2	B	9	C
2	B	10	G
2	B	11	A
2	B	12	U
2	B	13	A
2	B	14	G
2	B	17	A
2	B	19	G
2	B	20	A
2	B	21	G
2	B	22	G
2	B	23	U
2	B	27	A
2	B	28	C
2	B	30	C
2	B	32	U
2	B	33	U
2	B	34	C
2	B	35	C
2	B	36	C

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Mol	Chain	Res	Type
2	B	37	A
2	B	39	A
2	B	40	C
2	B	41	C
2	B	42	G
2	B	43	A
2	B	44	A
2	B	45	C
2	B	46	A
2	B	47	C
2	B	48	G
2	B	49	G
2	B	51	A
2	B	53	U
2	B	54	U
2	B	55	A
2	B	62	U
2	B	65	G
2	B	84	G
2	B	90	C
2	B	94	G
2	B	95	U
2	B	96	G
2	B	102	A
2	B	104	G
2	B	107	G
2	B	108	C
2	B	110	G
2	B	111	C
2	B	112	C
2	B	113	A
2	B	114	A

All (80) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	12	A
1	A	58	G
1	A	175	G
1	A	200	A
1	A	201	C
1	A	230	A

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Mol	Chain	Res	Type
1	A	231	A
1	A	232	U
1	A	267	C
1	A	268	A
1	A	288	C
1	A	419	G
1	A	463	U
1	A	537	A
1	A	649	G
1	A	683	A
1	A	687	U
1	A	717	A
1	A	785	C
1	A	837	U
1	A	852	G
1	A	900	U
1	A	971	A
1	A	1009	U
1	A	1080	G
1	A	1245	G
1	A	1339	A
1	A	1362	G
1	A	1438	C
1	A	1455	C
1	A	1518	G
1	A	1555	A
1	A	1581	A
1	A	1595	U
1	A	1652	C
1	A	1779	G
1	A	1784	A
1	A	1813	A
1	A	1870	U
1	A	1877	A
1	A	1881	U
1	A	1884	G
1	A	1915	U
1	A	1916	U
1	A	1922	C
1	A	2108	U
1	A	2140	U
1	A	2155	A

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Mol	Chain	Res	Type
1	A	2183	G
1	A	2203	C
1	A	2264	G
1	A	2291	U
1	A	2298	A
1	A	2315	A
1	A	2318	G
1	A	2325	U
1	A	2361	C
1	A	2374	G
1	A	2381	A
1	A	2400	G
1	A	2401	G
1	A	2402	A
1	A	2435	C
1	A	2436	A
1	A	2444	G
1	A	2450	G
1	A	2453	C
1	A	2454	A
1	A	2524	G
1	A	2625	U
1	A	2716	U
1	A	2784	C
1	A	2785	U
1	A	2796	C
1	A	2812	A
2	B	13	A
2	B	19	G
2	B	39	A
2	B	44	A
2	B	48	G

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

2 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
26	GNP	W	502	-	34,34,34	1.26	5 (14%)	47,54,54	0.74	1 (2%)
26	GNP	W	501	-	34,34,34	1.18	5 (14%)	47,54,54	0.64	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
26	GNP	W	502	-	-	5/18/38/38	0/3/3/3
26	GNP	W	501	-	-	6/18/38/38	0/3/3/3

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
26	W	502	GNP	PB-O3A	4.36	1.64	1.59
26	W	501	GNP	PB-O3A	3.24	1.63	1.59
26	W	501	GNP	PB-O1B	3.10	1.50	1.46
26	W	502	GNP	PB-O1B	2.97	1.50	1.46
26	W	502	GNP	PG-O1G	2.64	1.50	1.46
26	W	501	GNP	PG-N3B	2.64	1.70	1.63
26	W	501	GNP	PG-O1G	2.64	1.50	1.46
26	W	502	GNP	PG-N3B	2.55	1.70	1.63
26	W	502	GNP	PB-O2B	-2.44	1.50	1.56
26	W	501	GNP	PB-O2B	-2.35	1.50	1.56

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	W	502	GNP	O1G-PG-N3B	-2.83	107.60	111.77

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
26	W	501	GNP	PG-N3B-PB-O1B
26	W	501	GNP	C5'-O5'-PA-O3A
26	W	501	GNP	C5'-O5'-PA-O2A
26	W	501	GNP	O4'-C4'-C5'-O5'
26	W	502	GNP	PB-N3B-PG-O1G
26	W	502	GNP	PA-O3A-PB-O2B
26	W	501	GNP	C3'-C4'-C5'-O5'
26	W	501	GNP	C5'-O5'-PA-O1A
26	W	502	GNP	C3'-C4'-C5'-O5'
26	W	502	GNP	PA-O3A-PB-O1B
26	W	502	GNP	O4'-C4'-C5'-O5'

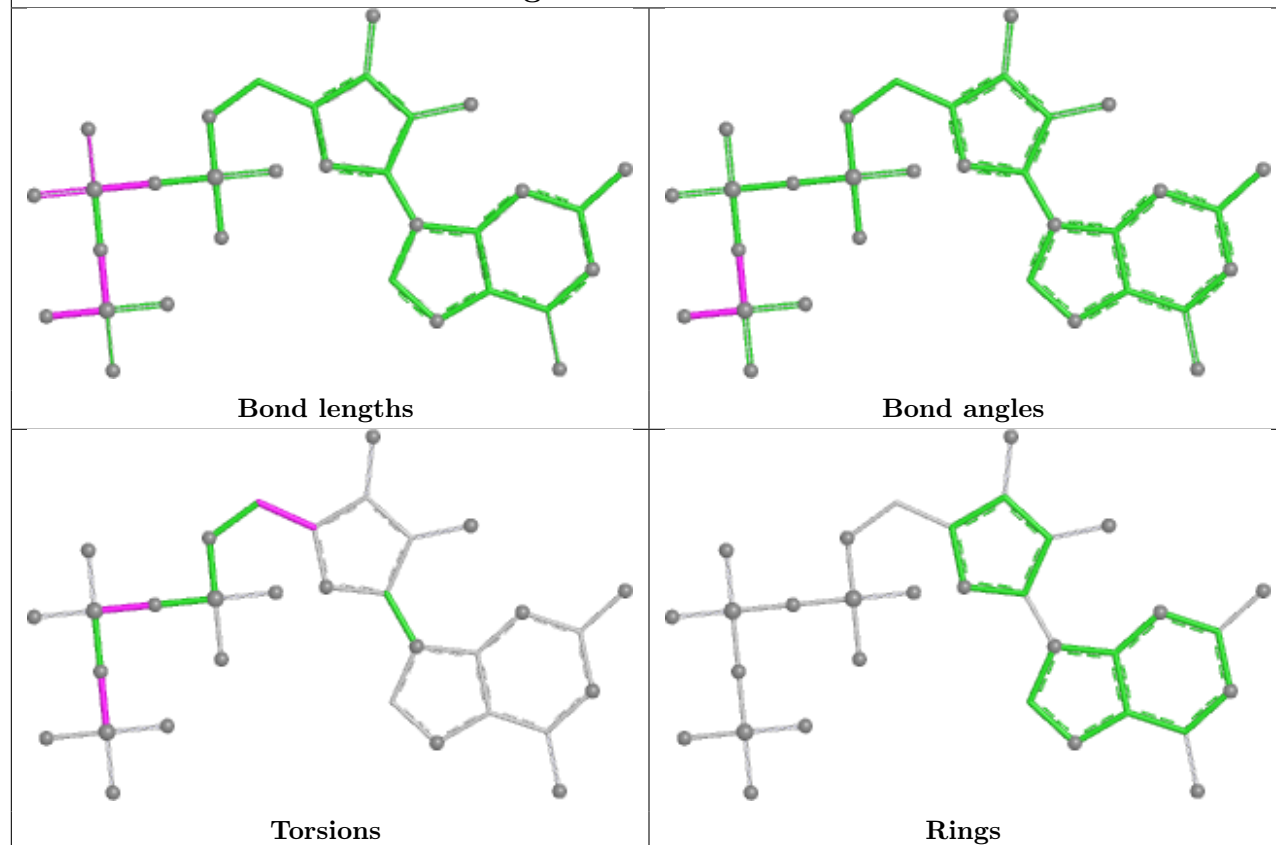
There are no ring outliers.

2 monomers are involved in 2 short contacts:

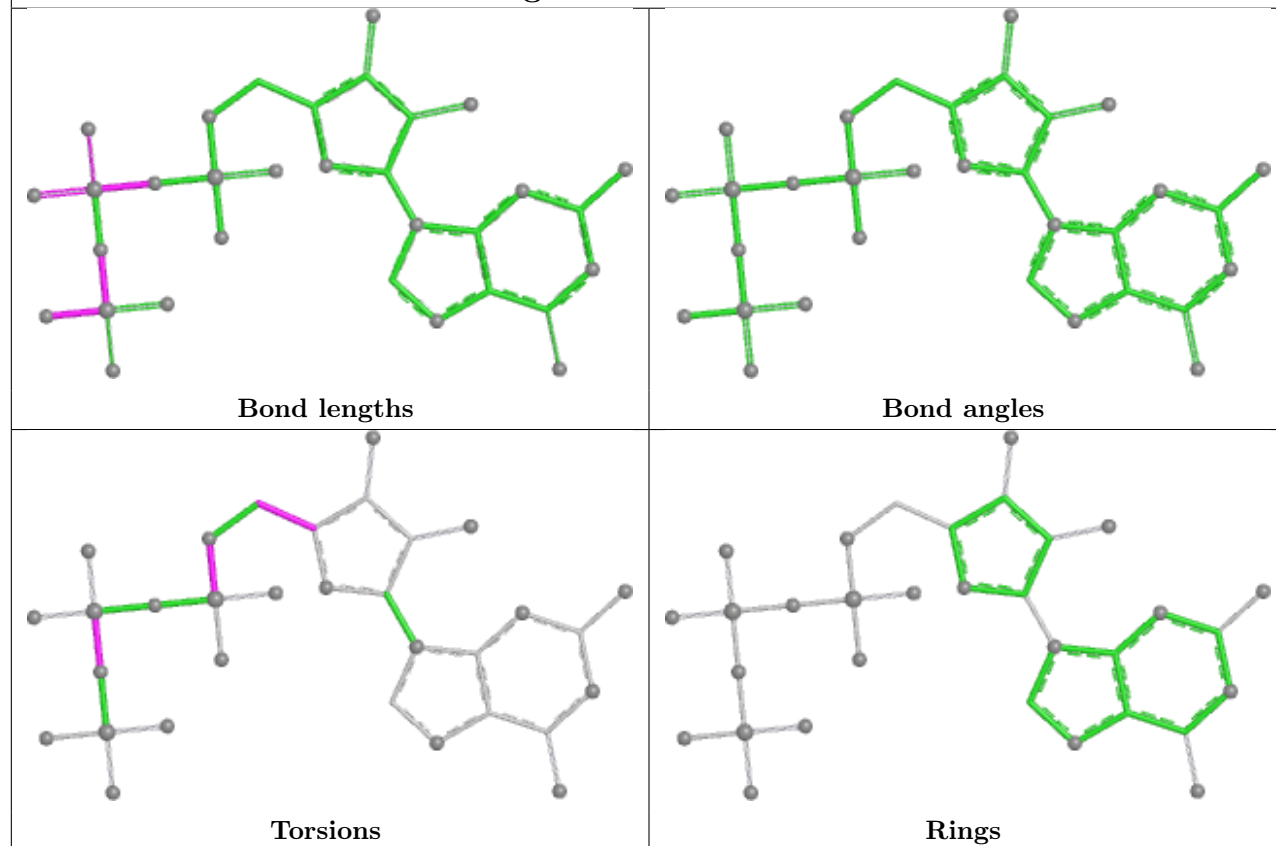
Mol	Chain	Res	Type	Clashes	Symm-Clashes
26	W	502	GNP	1	0
26	W	501	GNP	1	0

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.

Ligand GNP W 502



Ligand GNP W 501



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.

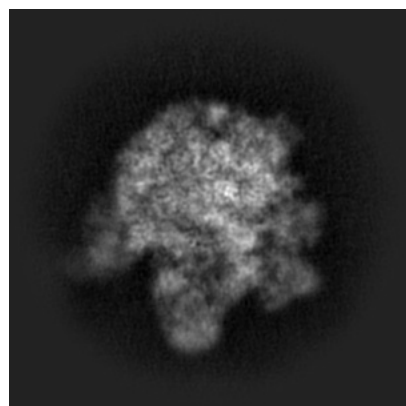
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-44849. These allow visual inspection of the internal detail of the map and identification of artifacts.

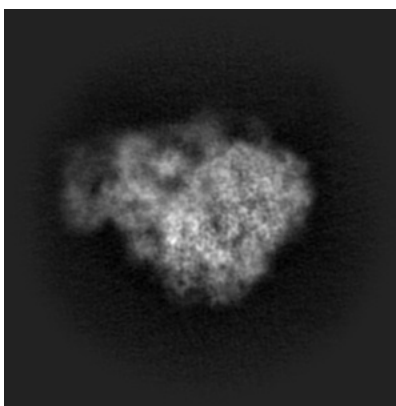
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

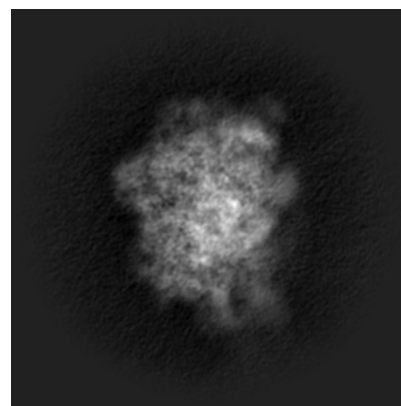
6.1.1 Primary map



X

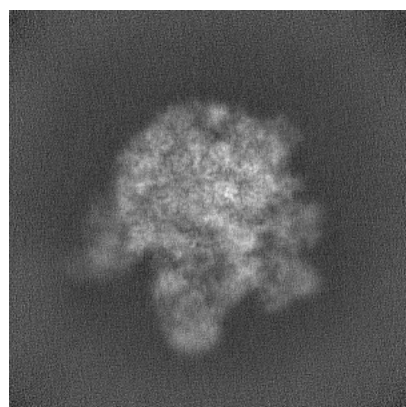


Y

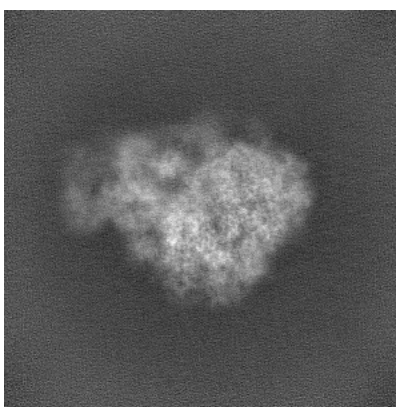


Z

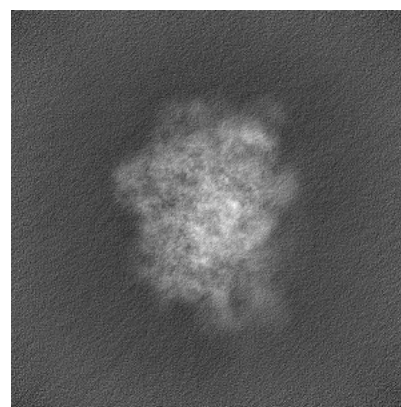
6.1.2 Raw map



X



Y

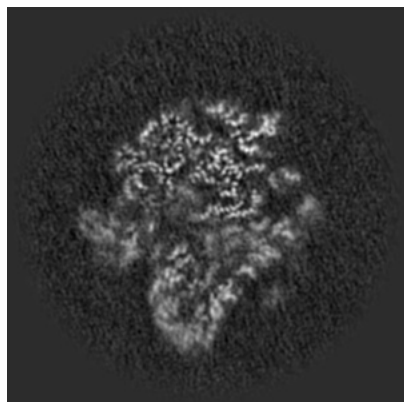


Z

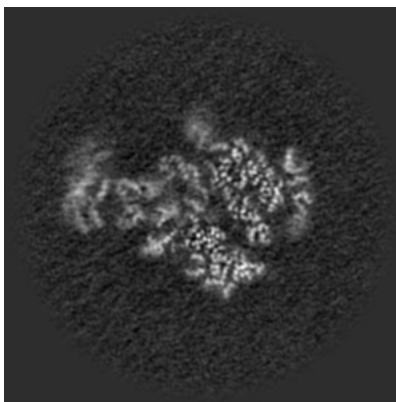
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

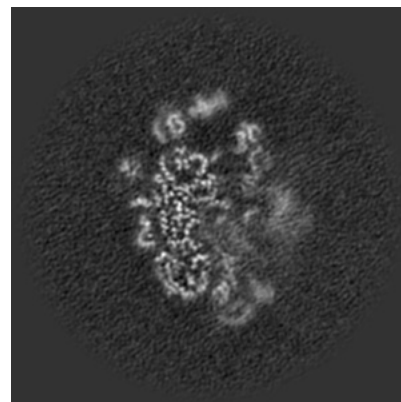
6.2.1 Primary map



X Index: 212

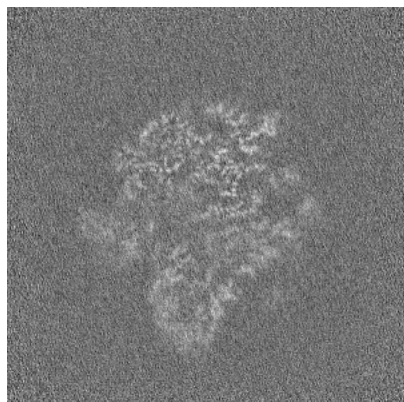


Y Index: 212

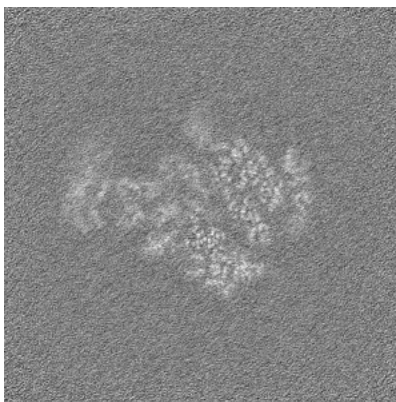


Z Index: 212

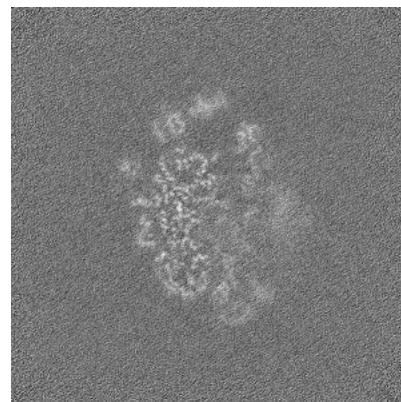
6.2.2 Raw map



X Index: 212



Y Index: 212

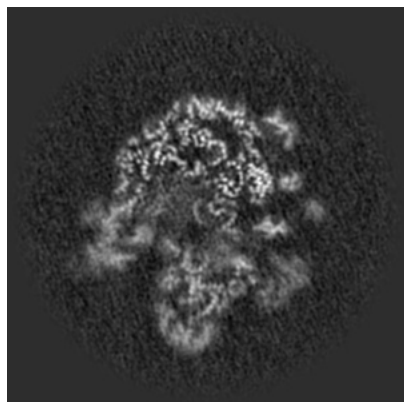


Z Index: 212

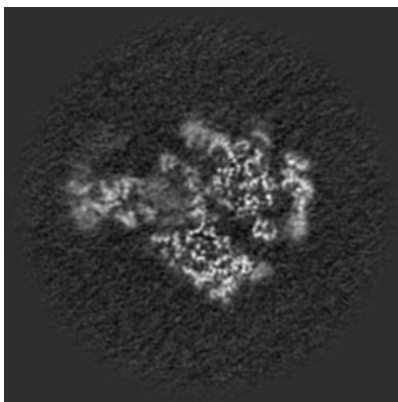
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

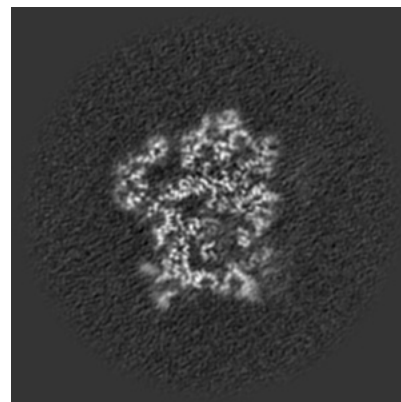
6.3.1 Primary map



X Index: 224

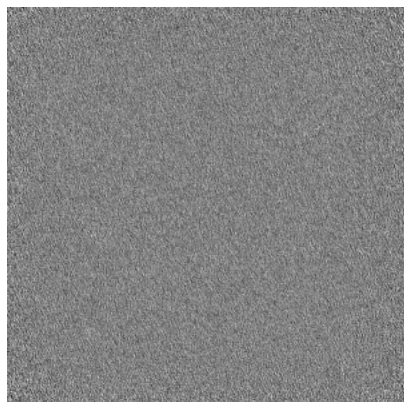


Y Index: 219

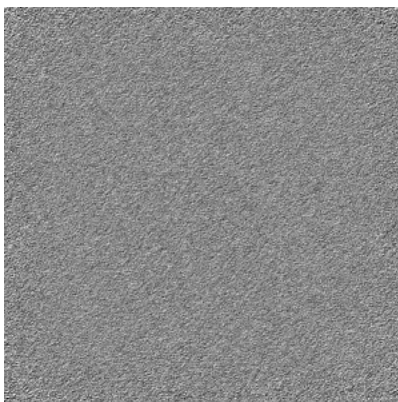


Z Index: 238

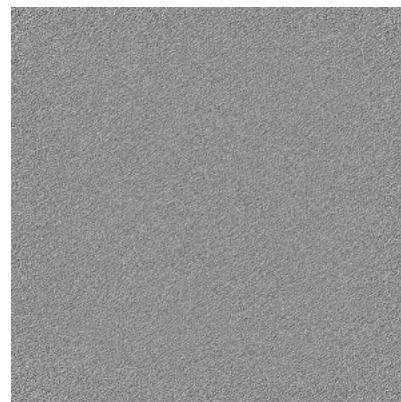
6.3.2 Raw map



X Index: 0



Y Index: 0

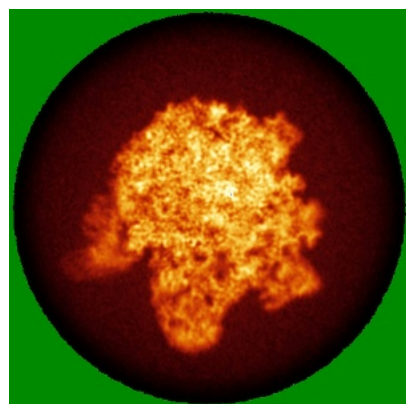


Z Index: 0

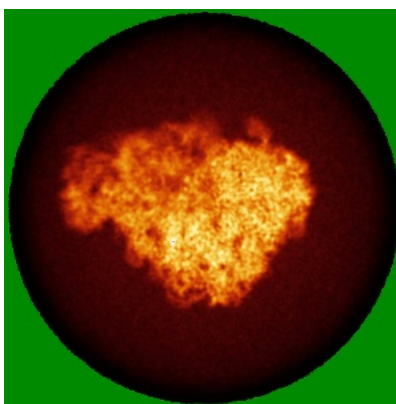
The images above show the largest variance slices of the map in three orthogonal directions.

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

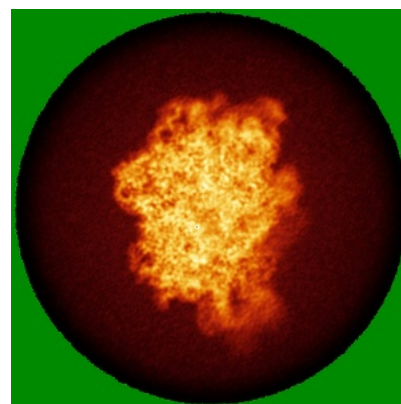
6.4.1 Primary map



X

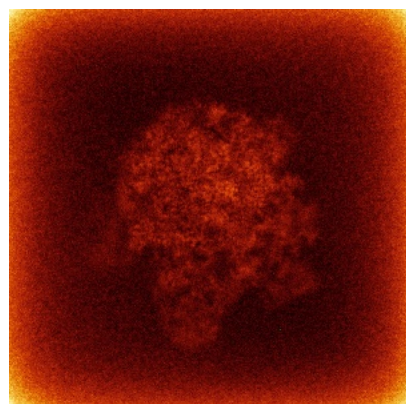


Y

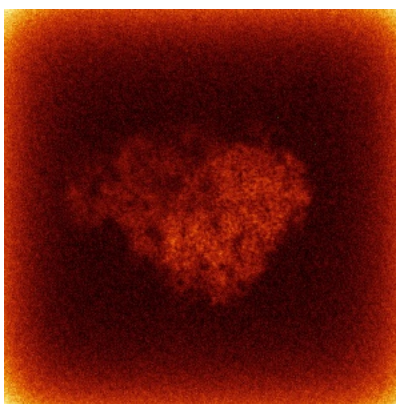


Z

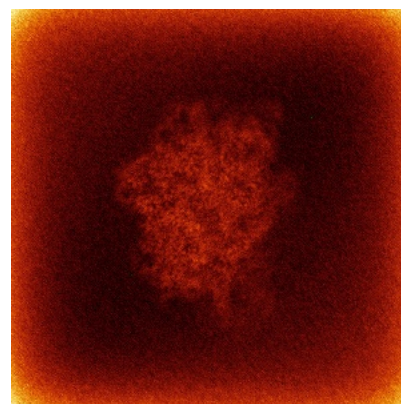
6.4.2 Raw map



X



Y



Z

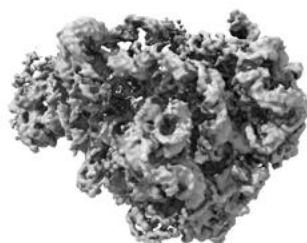
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

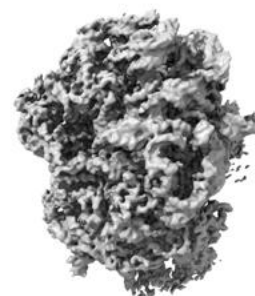
6.5.1 Primary map



X



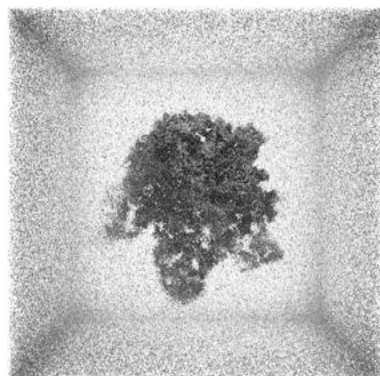
Y



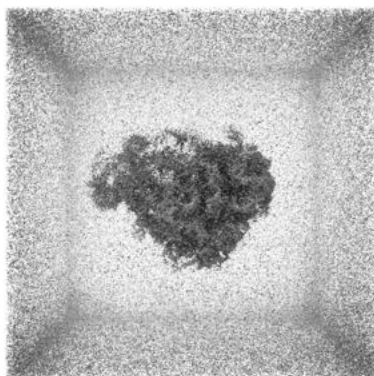
Z

The images above show the 3D surface view of the map at the recommended contour level 0.255. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

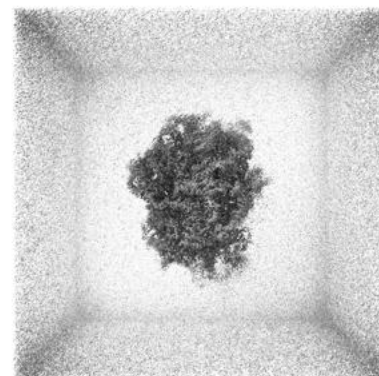
6.5.2 Raw map



X



Y



Z

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

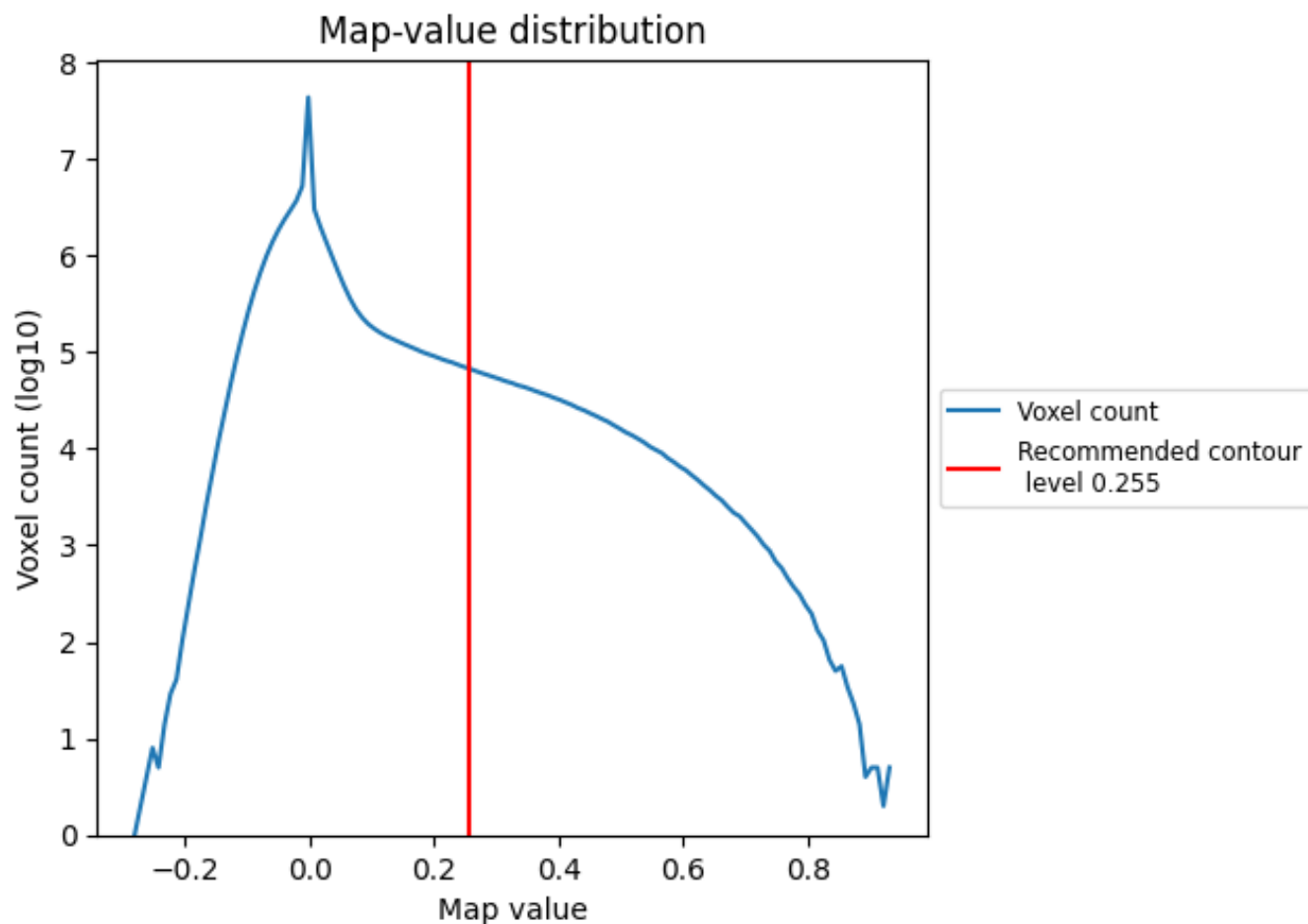
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

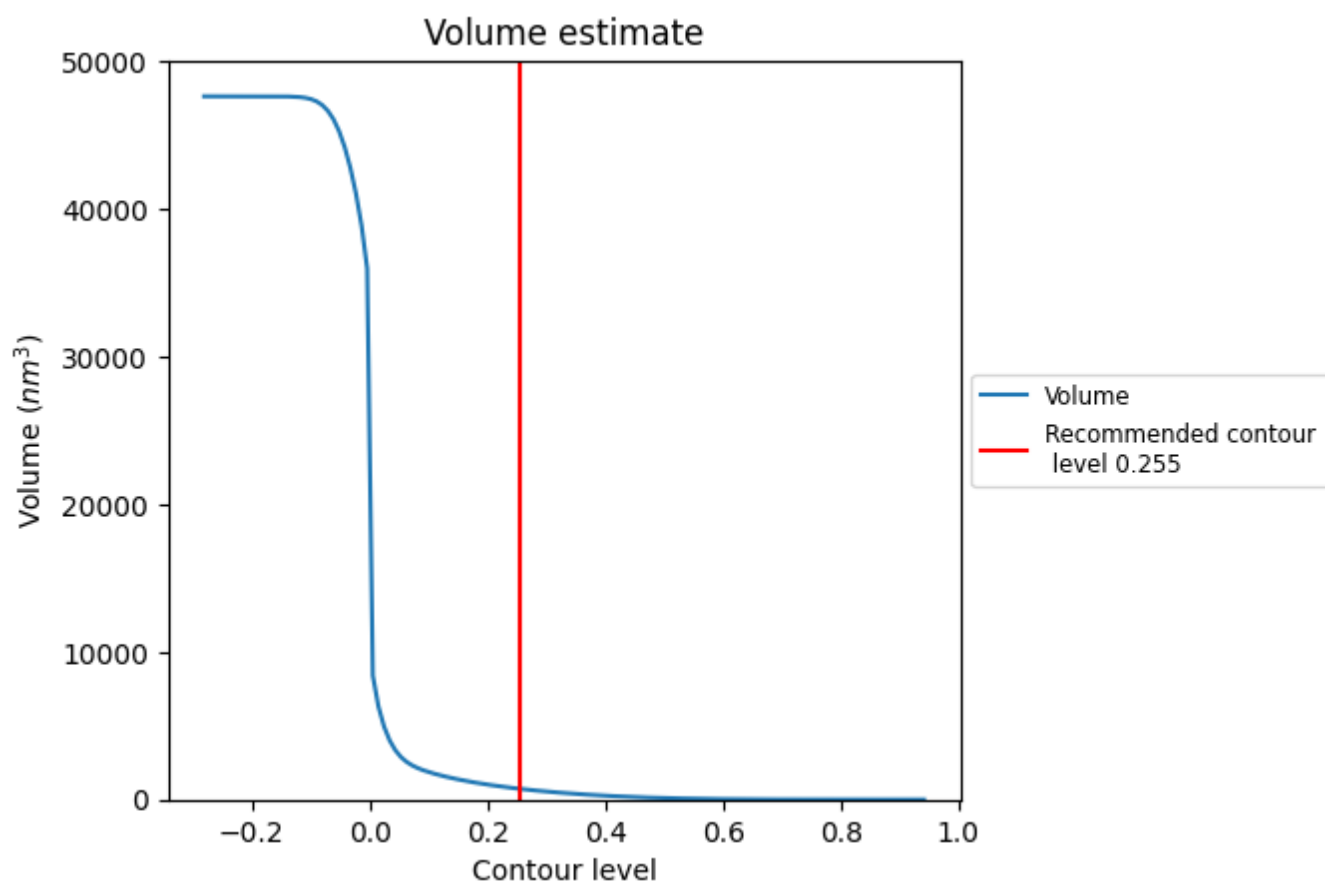
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

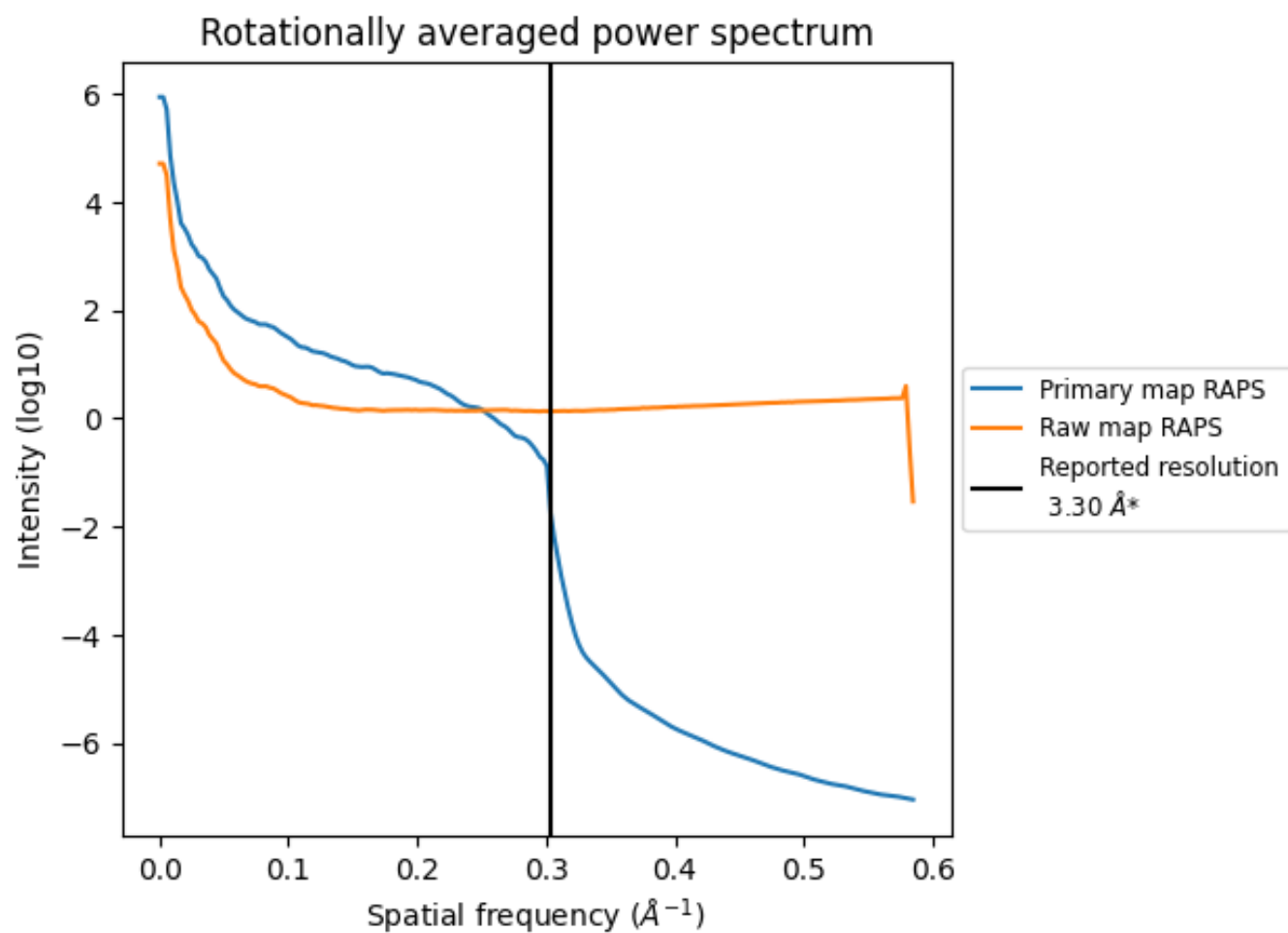
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 729 nm³; this corresponds to an approximate mass of 658 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 ⓘ

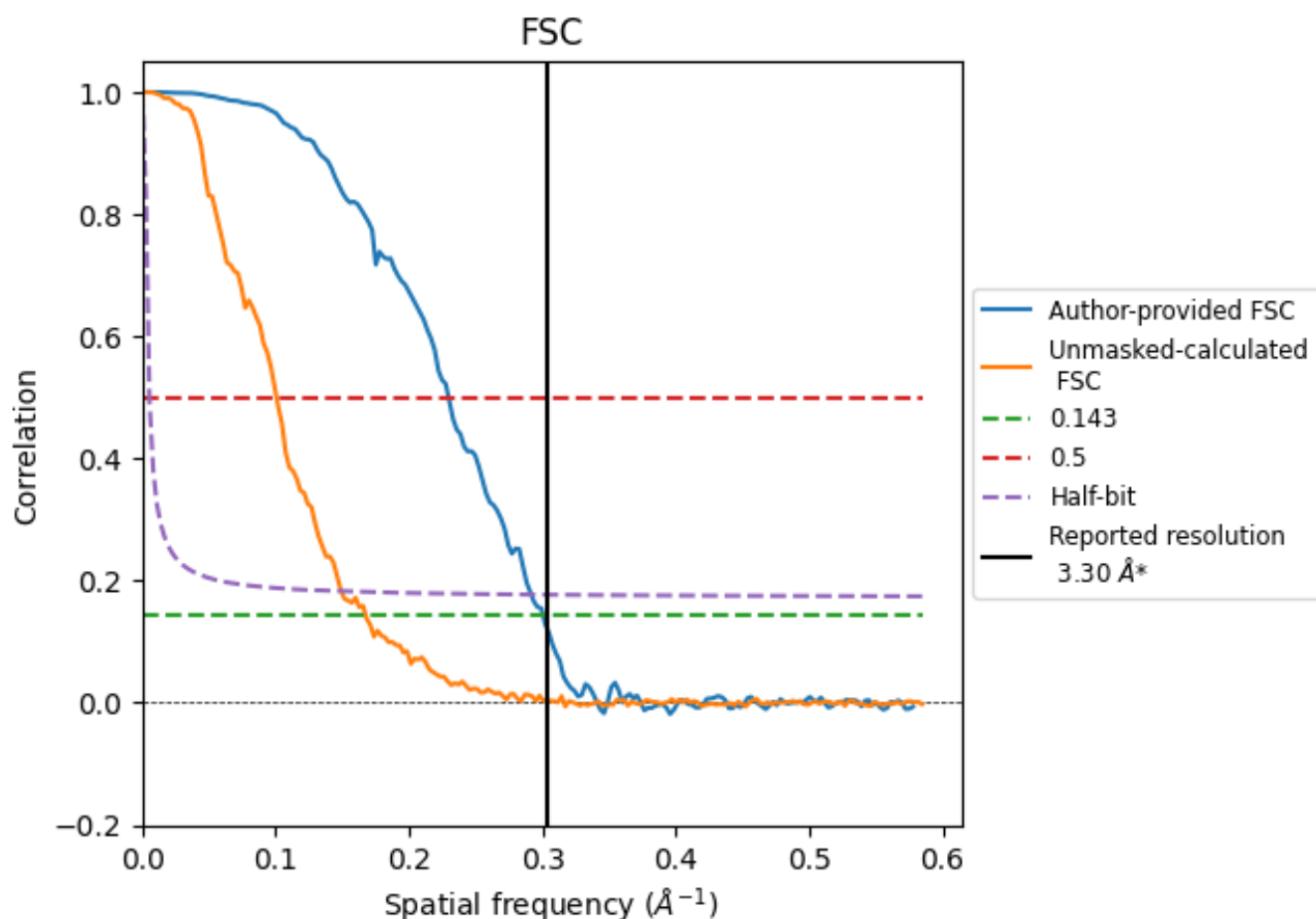


*Reported resolution corresponds to spatial frequency of 0.303 \AA^{-1}

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 0.303 \AA^{-1}

8.2 Resolution estimates

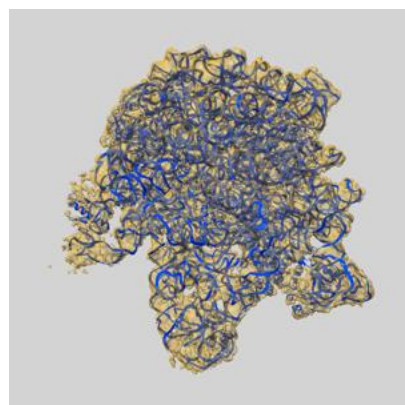
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.33	4.35	3.43
Unmasked-calculated*	5.97	9.93	6.70

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 5.97 differs from the reported value 3.3 by more than 10 %

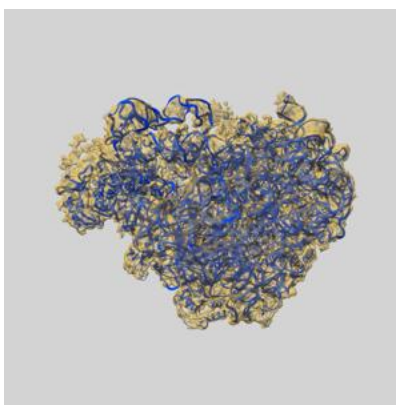
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-44849 and PDB model 9BS0. Per-residue inclusion information can be found in [section 3](#) on [page 9](#).

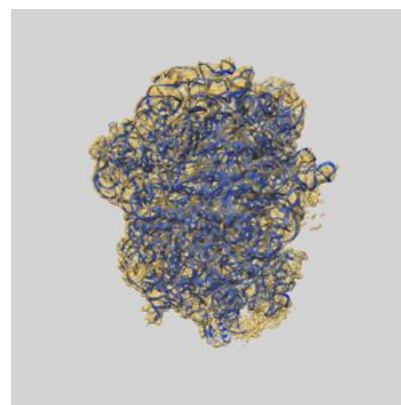
9.1 Map-model overlay [i](#)



X



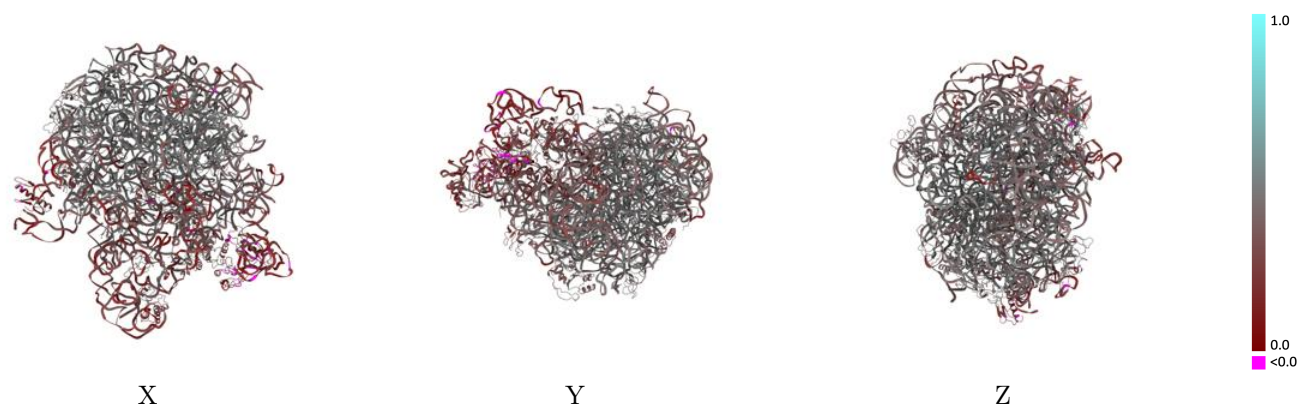
Y



Z

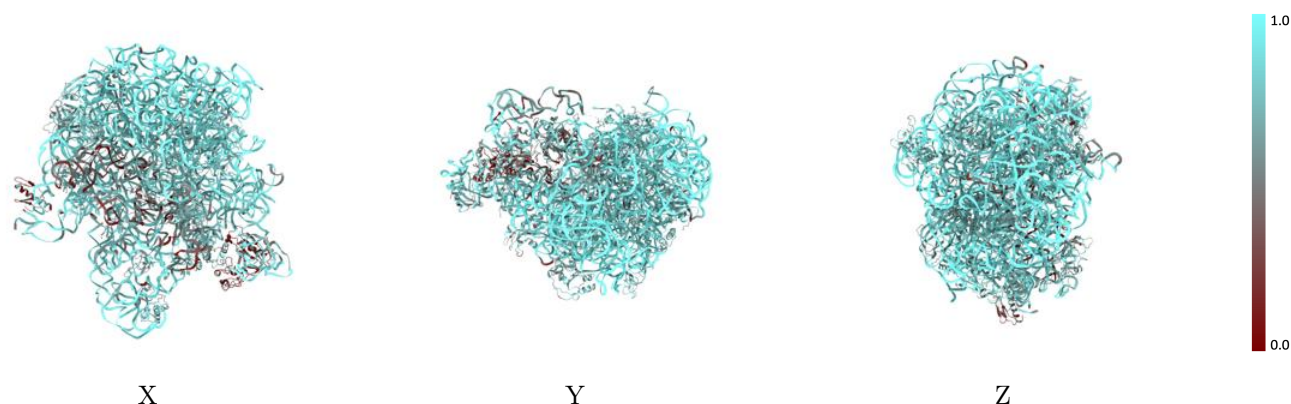
The images above show the 3D surface view of the map at the recommended contour level 0.255 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



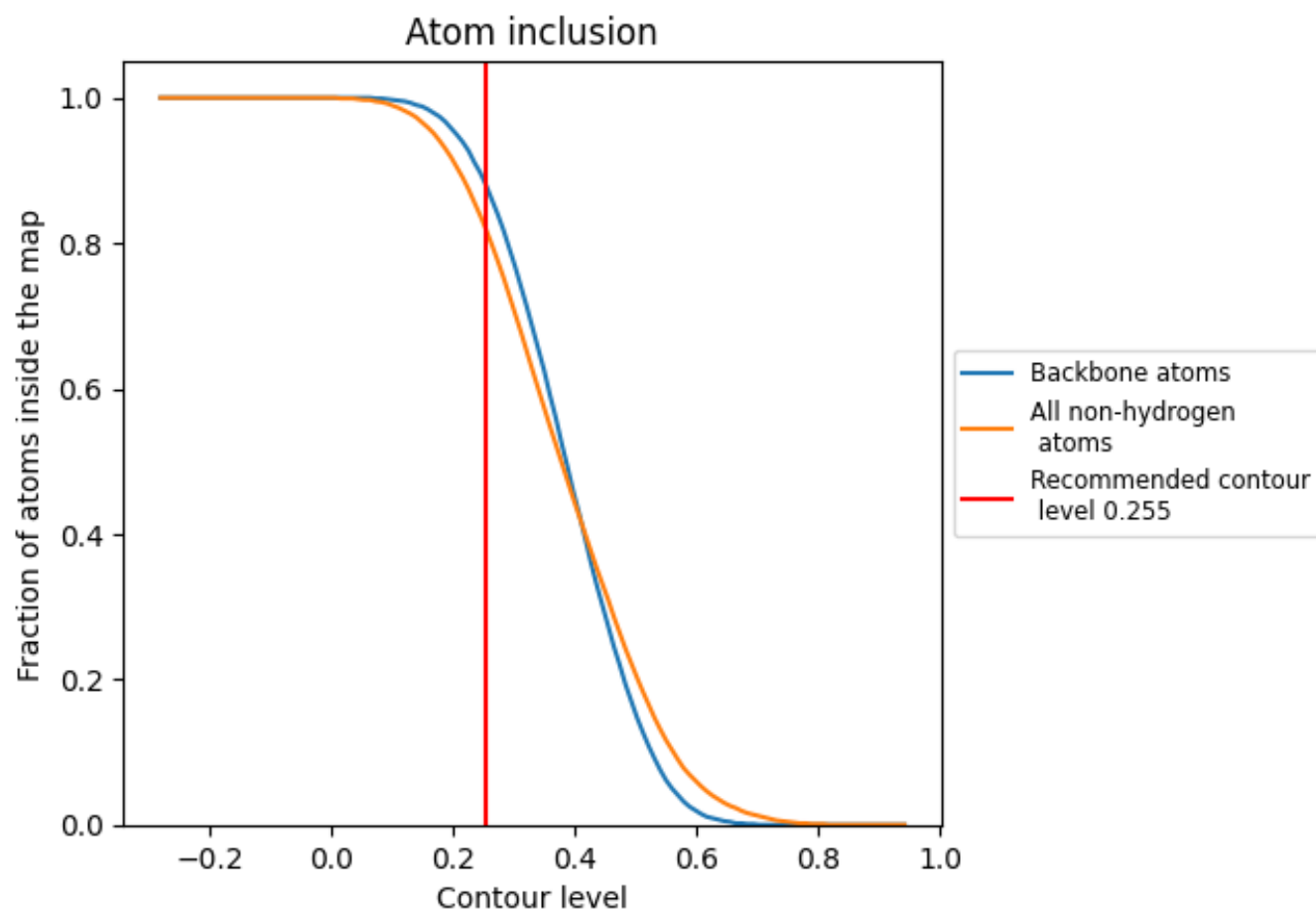
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.255).





















































9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 82% 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 (0.255) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8170	 0.3900
A	 0.8760	 0.3950
B	 0.8790	 0.2760
C	 0.7050	 0.4410
D	 0.6730	 0.4380
E	 0.7060	 0.4210
F	 0.3720	 0.2340
G	 0.7180	 0.4260
H	 0.6880	 0.4240
I	 0.6780	 0.3970
J	 0.7370	 0.4270
K	 0.7280	 0.4280
L	 0.7680	 0.4470
M	 0.7280	 0.4420
N	 0.7180	 0.4530
O	 0.7090	 0.4390
P	 0.7550	 0.4150
Q	 0.6910	 0.4120
R	 0.7090	 0.3410
S	 0.6730	 0.3920
T	 0.7280	 0.4430
U	 0.7570	 0.4790
V	 0.6720	 0.2970
W	 0.5640	 0.3520
Y	 0.2440	 0.1470
Z	 0.5950	 0.3740

