



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 07:54 AM UTC

PDB ID : 6DDG / pdb_00006ddg
EMDB ID : EMD-7870
Title : Structure of the 50S ribosomal subunit from Methicillin Resistant Staphylococcus aureus in complex with the oxazolidinone antibiotic LZD-6
Authors : Belousoff, M.J.; Venugopal, H.; Bamert, R.S.; Lithgow, T.
Deposited on : 2018-05-10
Resolution : 3.10 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

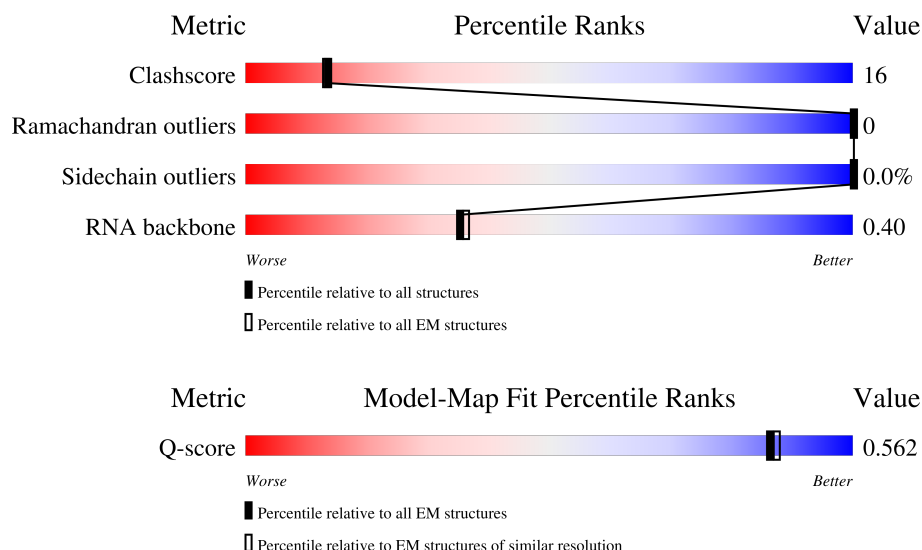
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.10 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	14724 (2.60 - 3.60)

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	116	5% 52% 46% .
2	B	276	. 60% 38% .
3	C	118	. 69% 30% .

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Mol	Chain	Length	Quality of chain
4	D	102	
5	E	116	
6	F	91	
7	G	105	
8	H	217	
9	I	85	
10	J	62	
11	K	69	
12	L	217	
13	M	59	
14	N	57	
15	O	49	
16	P	45	
17	Q	65	
18	R	37	
19	S	207	
20	V	145	
21	W	122	
22	X	146	
23	Y	144	
24	Z	122	
25	a	119	
26	1	2923	
27	2	115	

2 Entry composition

There are 28 unique types of molecules in this entry. The entry contains 79603 atoms, of which 19 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 protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	113	Total	C	N	O	0	0
			915	576	184	155		

- Molecule 2 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	270	Total	C	N	O	S	0	0
			2063	1285	410	363	5		

- Molecule 3 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	116	Total	C	N	O	S	0	0
			943	593	189	157	4		

- Molecule 4 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	100	Total	C	N	O	S	0	0
			785	499	139	146	1		

- Molecule 5 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	111	Total	C	N	O	S	0	0
			853	532	163	155	3		

- Molecule 6 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	84	Total	C	N	O	S	0	0
			684	430	125	125	4		

- Molecule 7 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	91	Total	C	N	O	S	0	0
			697	441	128	127	1		

- Molecule 8 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	93	Total	C	N	O	S	0	0
			727	465	129	132	1		

- Molecule 9 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	78	Total	C	N	O	S	0	0
			597	367	116	114			

- Molecule 10 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	57	Total	C	N	O	S	0	0
			449	278	97	73	1		

- Molecule 11 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	56	Total	C	N	O	S	0	0
			463	285	88	90			

- Molecule 12 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	215	Total	C	N	O	S	0	0
			1628	1018	299	306	5		

- Molecule 13 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	56	Total	C	N	O	S	0	0
			432	269	82	81			

- Molecule 14 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	50	Total	C	N	O	S	0	0
			397	241	83	68	5		

- Molecule 15 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	47	Total	C	N	O	S	0	0
			390	233	79	73	5		

- Molecule 16 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	44	Total	C	N	O	S	0	0
			372	228	90	53	1		

- Molecule 17 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	64	Total	C	N	O	S	0	0
			521	324	113	82	2		

- Molecule 18 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	37	Total	C	N	O	S	0	0
			296	186	60	45	5		

- Molecule 19 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	188	Total	C	N	O	S	0	0
			1441	904	267	268	2		

- Molecule 20 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	V	143	Total	C	N	O	S	0	0
			1138	710	209	217	2		

- Molecule 21 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	W	120	Total	C	N	O	S	0	0
			903	561	172	167	3		

- Molecule 22 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	X	144	Total	C	N	O		0	0
			1082	669	213	200			

- Molecule 23 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Y	135	Total	C	N	O	S	0	0
			1080	693	205	178	4		

- Molecule 24 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Z	121	Total	C	N	O	S	0	0
			955	586	183	185	1		

- Molecule 25 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	a	100	Total	C	N	O		0	0
			787	493	153	141			

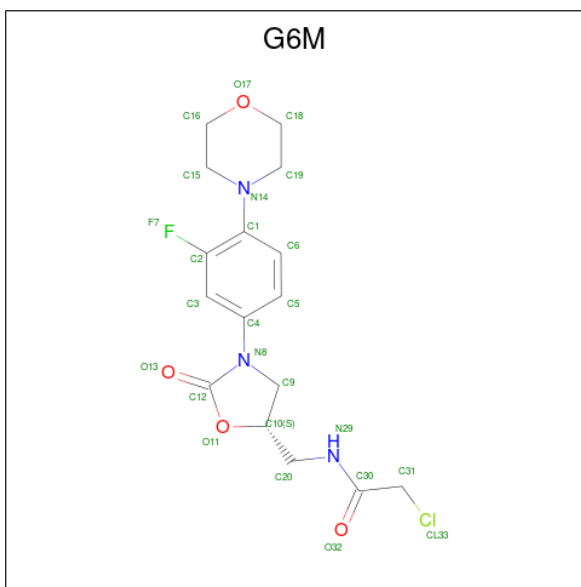
- Molecule 26 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	1	2646	Total	C	N	O	P	0	0
			56747	25338	10405	18361	2643		

- Molecule 27 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	2	104	Total	C	N	O	P	0	0
			2214	990	395	725	104		

- Molecule 28 is 2-chloro-N-({(5S)-3-[3-fluoro-4-(morpholin-4-yl)phenyl]-2-oxo-1,3-oxazolidin-5-yl}methyl)acetamide (CCD ID: G6M) (formula: C₁₆H₁₉ClFN₃O₄).

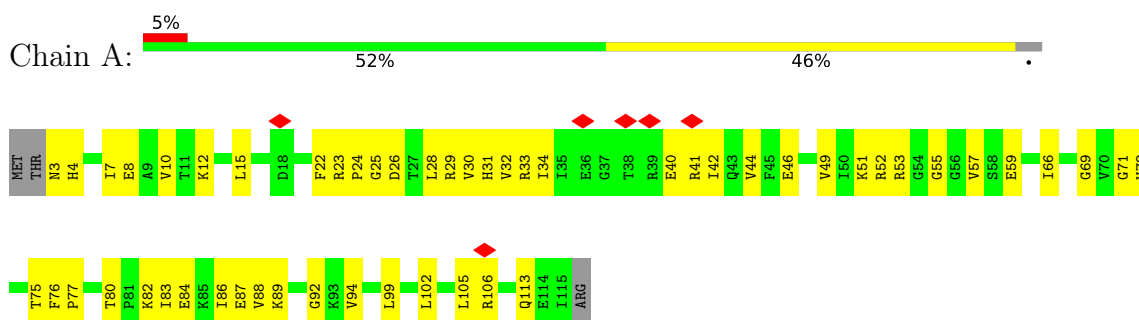


Mol	Chain	Residues	Atoms							AltConf
			Total	C	Cl	F	H	N	O	
28	1	1	44	16	1	1	19	3	4	0

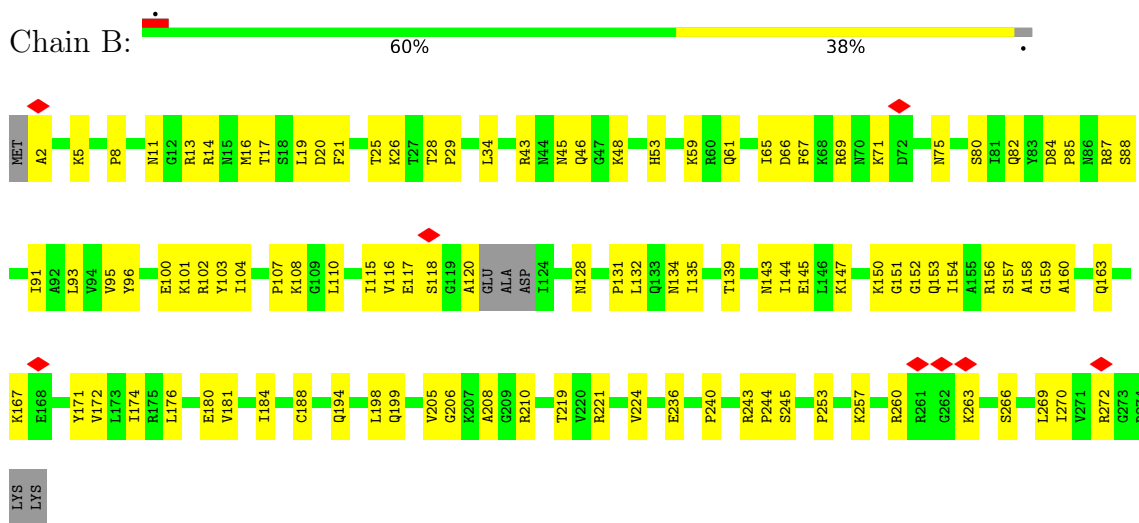
3 Residue-property plots [i](#)

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.

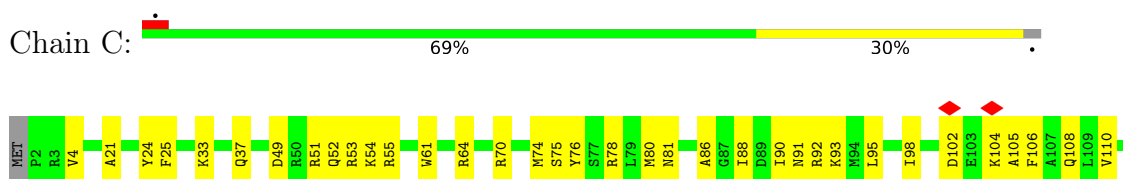
• Molecule 1: 50S ribosomal protein L19

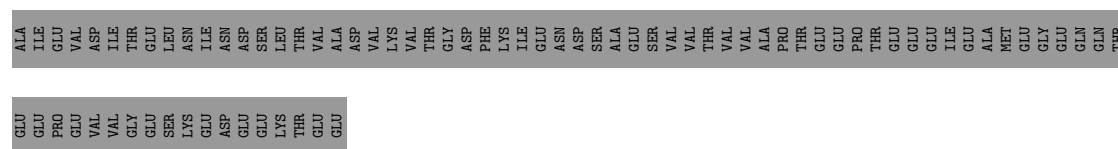


• Molecule 2: 50S ribosomal protein L2



• Molecule 3: 50S ribosomal protein L20

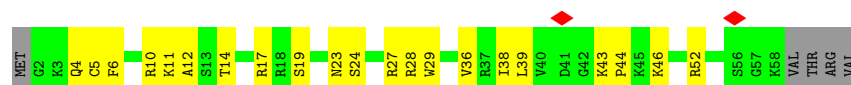




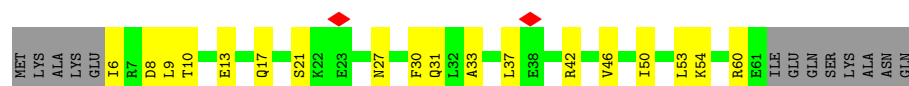
• Molecule 9: 50S ribosomal protein L27



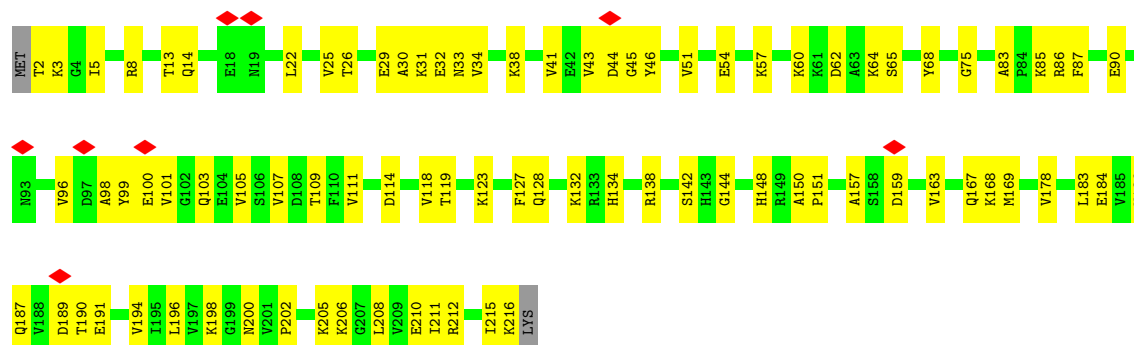
• Molecule 10: 50S ribosomal protein L28



• Molecule 11: 50S ribosomal protein L29



• Molecule 12: 50S ribosomal protein L3



• Molecule 13: 50S ribosomal protein L30



- Molecule 14: 50S ribosomal protein L32

Chain N:  68% 19% 12%



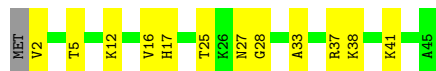
- Molecule 15: 50S ribosomal protein L33

Chain O:  49% 47%



- Molecule 16: 50S ribosomal protein L34

Chain P:  71% 27%



- Molecule 17: 50S ribosomal protein L35

Chain Q:  63% 35%



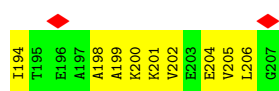
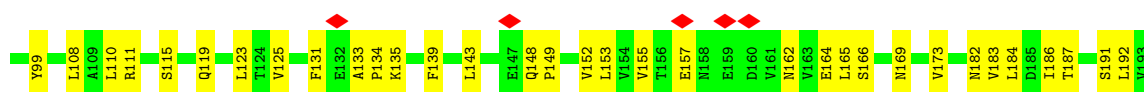
- Molecule 18: 50S ribosomal protein L36

Chain R:  46% 54%

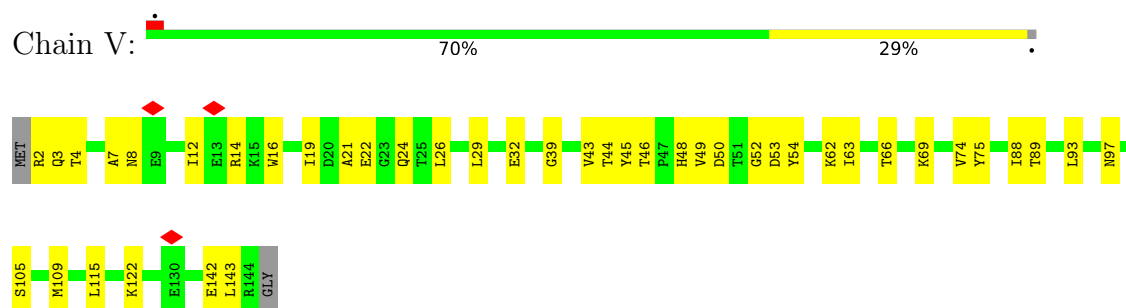


- Molecule 19: 50S ribosomal protein L4

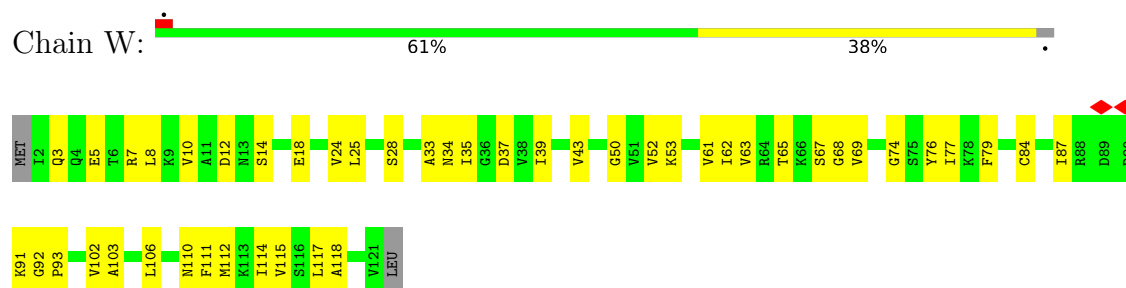
Chain S:  58% 32% 9%



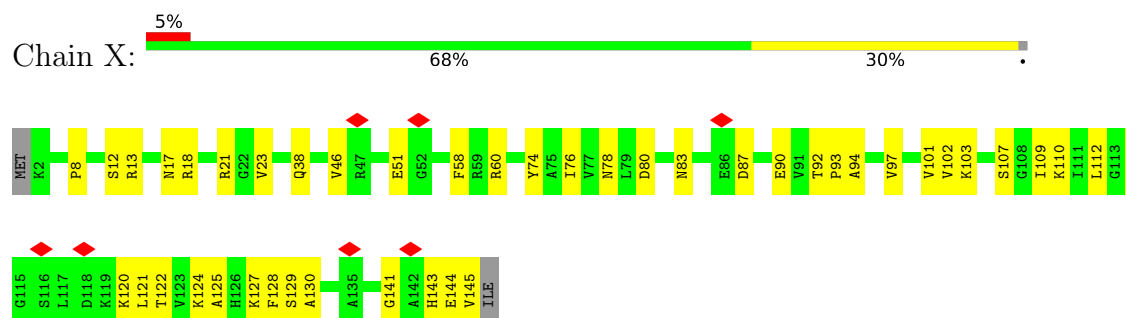
- Molecule 20: 50S ribosomal protein L13



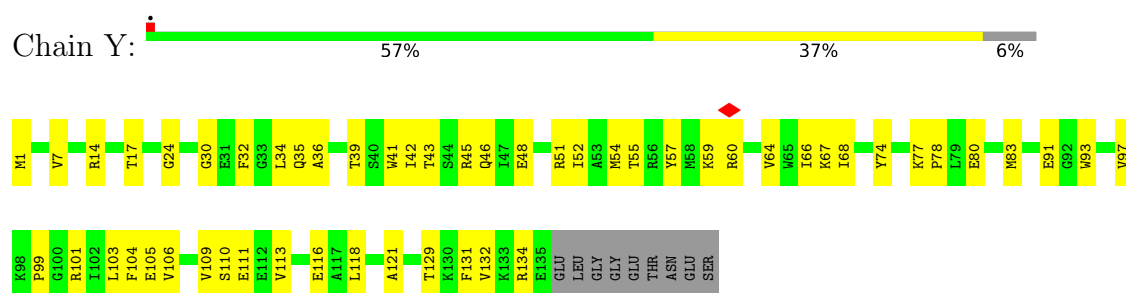
- Molecule 21: 50S ribosomal protein L14



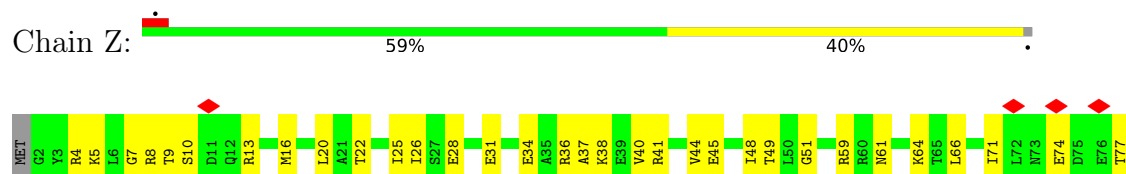
- Molecule 22: 50S ribosomal protein L15



- Molecule 23: 50S ribosomal protein L16



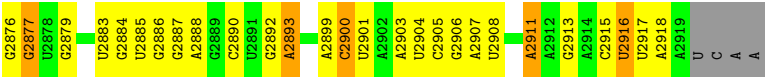
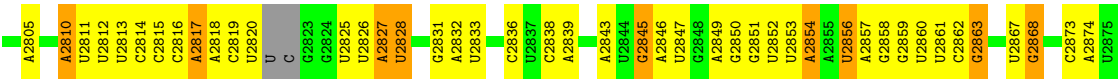
- Molecule 24: 50S ribosomal protein L17



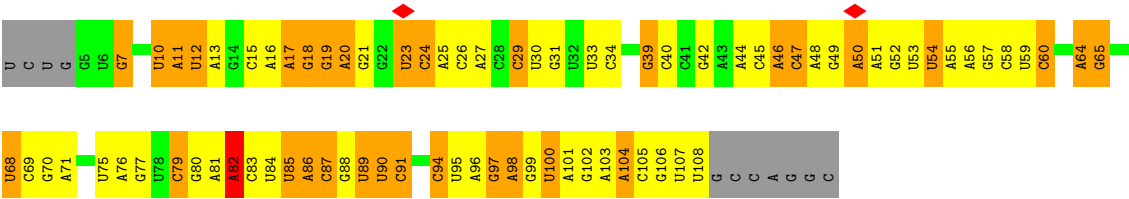
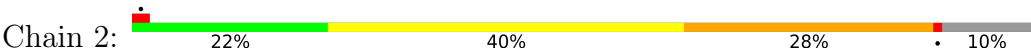


U1589	A1662	U1460	C1387	A1314	G1225	C	A1023	G876	U787	U712	A629
C1590	G1663	C1461	C1388	C1315	G1227	G	A1027	G877	A788	A713	G830
A1592	U1593	G1462	U1389	G1316	U1227	A	G1028	C878	U792	C717	U631
U1594	A1670	U1464	A1391	G1317	U1227	C	U	U879	G793	C718	U632
C1595	U1676	G1465	U1394	G1318	U1238	U1157	C1031	U884	A794	C719	A633
U1598	U1683	A1471	G1395	G1320	C1239	C1160	A1034	A885	A795	A721	C634
A1684	U1684	C1472	U1396	G1321	U1240	A1161	C1035	A886	A796	A722	U637
U1600	U1684	G1473	A1402	G1322	A1241	C1162	A1037	U887	U799	A723	U638
U1603	U1690	U1477	G1405	A1323	A1242	U1163	G1039	U888	G800	C724	U639
C1604	U1691	A1478	G1406	U1325	U1248	G1169	C1040	A891	A801	G725	G640
A1605	U1692	G1479	C1407	G1326	U1249	A1170	A1041	U890	G802	G726	A641
G1693	U1693	A1480	G1408	C1327	G1257	A1171	C1042	U891	U799	A727	U642
U1607	U1694	A1481	U1409	G1328	A1258	A1172	U1043	U892	U799	C728	A643
U1608	U1695	U1482	A1410	U1330	G1261	U1174	A1044	U893	A801	A729	U644
C1696	U1696	A1483	G1411	C1334	U1262	G1175	A1045	U894	G802	A730	A645
U1697	U1697	G1484	G1412	U1337	A1263	U1176	G1046	U895	U799	A731	A646
A1698	U1698	U1487	A1415	U1338	G1266	C1178	C1049	U896	U799	C732	U647
U1699	U1699	A1488	U1416	U1339	A1267	C1179	U1053	U897	U799	C733	U648
U1701	U1701	A1489	U1417	G1340	C1268	U1179	A1054	U898	U799	C734	U649
C1702	U1702	G1490	A1421	U1343	U1270	G1182	A1055	U899	U799	C735	U650
A1616	U1703	C1491	G1422	U1344	G1271	G1183	A1056	U900	U799	C736	A651
A1618	U1704	G1492	C1423	A1344	U1272	C1184	A1057	U901	U799	C737	A652
U1619	U1705	U1493	A1424	U1345	G1273	U1185	U1058	U902	U799	C738	U653
G1620	U1706	G1494	G1425	A1346	G1274	A1186	U1059	U903	U799	C739	U654
C1621	U1707	A1495	G1426	G1347	G1275	A1187	U1060	U904	U799	C740	U655
U1622	U1708	G1496	U1427	U1348	G1276	A1190	U1061	U905	U799	C741	U656
G1623	U1709	A1497	U1428	U1349	G1277	U1191	U1062	U906	U799	C742	U657
C1624	U1710	U1498	G1429	U1350	G1278	U1192	U1063	U907	U799	C743	U658
U1625	U1711	U1499	A1430	C1351	G1279	U1193	A1064	U908	U799	C744	U659
A1626	U1712	G1500	U1431	U1352	G1280	U1194	A1065	U909	U799	C745	U660
U1627	U1713	G1501	A1432	A1353	G1281	U1195	A1066	U910	U799	C746	U661
A1628	U1714	A1502	U1433	G1354	G1282	U1196	U1067	U911	U799	C747	U662
U1629	U1715	U1503	U1434	A1355	G1283	U1197	U1068	U912	U799	C748	U663
A1630	U1716	U1504	U1349	G1356	G1284	U1198	U1069	U913	U799	C749	U664
U1631	U1717	G1505	U1350	G1357	G1285	U1199	U1070	U914	U799	C750	U665
A1632	U1718	U1506	U1351	U1358	G1286	U1200	A1071	U915	U799	C751	U666
U1633	U1719	U1507	U1352	U1359	G1287	U1201	A1072	U916	U799	C752	U667
A1634	U1720	G1508	U1353	U1360	G1288	U1202	U1073	U917	U799	C753	U668
U1635	U1721	U1509	U1354	U1361	G1289	U1203	U1074	U918	U799	C754	U669
A1636	U1722	U1510	U1355	U1362	G1290	U1204	U1075	U919	U799	C755	U670
U1637	U1723	C1511	U1356	U1363	G1291	U1205	U1076	U920	U799	C756	U671
A1638	U1724	U1512	U1357	U1364	G1292	U1206	U1077	U921	U799	C757	U672
U1639	U1725	U1513	U1358	U1365	U1293	U1207	U1078	U922	U799	C758	U673
G1639	U1726	U1514	U1359	U1366	G1294	U1208	U1079	U923	U799	C759	U674
U1640	U1727	G1515	U1360	U1367	G1295	U1209	U1080	U924	U799	C760	U675
A1641	U1728	U1516	U1361	U1368	G1296	U1210	U1081	U925	U799	C761	U676
U1642	U1729	U1517	U1362	U1369	G1297	U1211	U1082	U926	U799	C762	U677
A1643	U1730	U1518	U1363	U1370	G1298	U1212	U1083	U927	U799	C763	U678
C1644	U1731	U1519	U1364	U1371	U1299	U1213	U1084	U928	U799	C764	U679
U1645	U1732	U1520	U1365	U1372	U1300	U1214	U1085	U929	U799	C765	U680
U1646	U1733	U1521	U1366	U1373	G1301	U1215	U1086	U930	U799	C766	U681
A1647	U1734	G1522	U1367	U1374	G1302	U1216	U1087	U931	U799	C767	U682
U1648	U1735	U1523	U1368	U1375	G1303	U1217	U1088	U932	U799	C768	U683
G1649	U1736	U1524	U1369	U1376	G1304	U1218	U1089	U933	U799	C769	U684
U1650	U1737	U1525	U1370	U1377	G1305	U1219	U1090	U934	U799	C770	U685
A1651	U1738	U1526	U1371	U1378	G1306	U1220	U1091	U935	U799	C771	U686
U1652	U1739	U1527	U1372	U1379	G1307	U1221	U1092	U936	U799	C772	U687
A1653	U1740	U1528	U1373	U1380	G1308	U1222	U1093	U937	U799	C773	U688
U1654	U1741	U1529	U1374	U1381	G1309	U1223	U1094	U938	U799	C774	U689
U1655	U1742	U1530	U1375	U1382	G1310	U1224	U1095	U939	U799	C775	U690
U1656	U1743	U1531	U1376	U1383	A1310	U1225	U1096	U940	U799	C776	U691
U1657	U1744	U1532	U1377	U1384	A1311	U1226	U1097	U941	U799	C777	U692
U1658	U1745	U1533	U1378	U1385	A1312	U1227	U1098	U942	U799	C778	U693
U1659	U1746	U1534	U1379	U1386	A1313	U1228	U1099	U943	U799	C779	U694
U1660	U1747	U1535	U1380	U1387	A1314	U1229	U1100	U944	U799	C780	U695
U1661	U1748	U1536	U1381	U1388	A1315	U1230	U1101	U945	U799	C781	U696
U1662	U1749	U1537	U1382	U1389	A1316	U1231	U1102	U946	U799	C782	U697
U1663	U1750	U1538	U1383	U1390	A1317	U1232	U1103	U947	U799	C783	U698
U1664	U1751	U1539	U1384	U1391	A1318	U1233	U1104	U948	U799	C784	U699
U1665	U1752	U1540	U1385	U1392	A1319	U1234	U1105	U949	U799	C785	U700
U1666	U1753	U1541	U1386	U1393	A1320	U1235	U1106	U950	U799	C786	U701
U1667	U1754	U1542	U1387	U1394	A1321	U1236	U1107	U951	U799	C787	U702
U1668	U1755	U1543	U1388	U1395	A1322	U1237	U1108	U952	U799	C788	U703
U1669	U1756	U1544	U1389	U1396	A1323	U1238	U1109	U953	U799	C789	U704
U1670	U1757	U1545	U1390	U1397	A1324	U1239	U1110	U954	U799	C790	U705
U1671	U1758	U1546	U1391	U1398	A1325	U1240	U1111	U955	U799	C791	U706
U1672	U1759	U1547	U1392	U1399	A1326	U1241	U1112	U956	U799	C792	U707
U1673	U1760	U1548	U1393	U1400	A1327	U1242	U1113	U957	U799	C793	U708
U1674	U1761	U1549	U1394	U1401	A1328	U1243	U1114	U958	U799	C794	U709
U1675	U1762	U1550	U1395	U1402	A1329	U1244	U1115	U959	U799	C795	U710
U1676	U1763	U1551	U1396	U1403	A1330	U1245	U1116	U960	U799	C796	U711
U1677	U1764	U1552	U1397	U1404	A1331	U1246	U1117	U961	U799	C797	U712
U1678	U1765	U1553	U1398	U1405	A1332	U1247	U1118	U962	U799	C798	U713
U1679	U1766	U1554	U1399	U1406	A1333	U1248	U1119	U963	U799	C799	U714
U1680	U1767	U1555	U1400	U1407	A1334	U1249	U1120	U964	U799	C800	U715
U1681	U1768	U1556	U1401	U1408	A1335	U1250	U1121	U965	U799	C801	U716
U1682	U1769	U1557	U1402	U1409	A1336	U1251	U1122	U966	U799	C802	U717
U1683	U1770	U1558	U1403	U1410	A1337	U1252	U1123	U967	U799	C803	U718
U1684	U1771	U1559	U1404	U1411	A1338	U1253	U1124	U968	U799	C804	U719
U1685	U1772	U1560	U1405	U1412	A1339	U1254	U1125	U969	U799	C805	U720
U1686	U1773	U1561	U1406	U1413	A1340	U1255	U1126	U970	U799	C806	U721
U1687	U1774	U1562	U1407	U1414	A1341	U1256	U1127	U971	U799	C807	U722
U1688	U1775	U1563	U1408	U1415	A1342	U1257	U1128	U972	U799	C808	U723
U1689	U1776	U1564	U1409	U1416	A1343	U1258	U1129	U973	U799	C809	U724
U1690	U1777	U1565	U1410	U1417	A1344	U1259	U1130	U974	U799	C810	U725
U1691	U1778	U1566	U1411	U1418	A1345	U1260	U1131	U975	U799	C811	U726
U1692	U1779	U1567	U1412	U1419	A1346	U1261	U1132	U976	U799	C812	U727
U1693	U1780	U1568	U1413	U1420	A1347	U1262	U1133	U977	U799	C813	U728
U1694	U1781	U1569	U1414	U1421	A1348	U1263	U1134	U978	U799	C814	U729
U1695	U1782	U1570	U1415	U1422	A1349	U1264	U1135	U979	U799	C815	U730
U1696	U1783	U1571	U1416	U1423	A1350	U1265	U1136	U980	U799	C816	U731
U1697	U1784	U1572	U1417	U1424	A1351	U1266	U1137	U981	U799	C817	U732
U1698	U1785	U1573	U1418	U1425	A1352	U1267	U1138	U982	U799	C818	U733
U1699	U1786	U1574	U1419	U1426	A1353	U1268	U1139	U983	U799	C819	U734
U1700	U1787	U1575	U1420	U1427	A1354	U1269	U1140	U984	U799	C820	U735
U1701	U1788	U1576	U1421	U							

U2725	C2639	A2558	C2483	G2399	A2327	C2241	U2118	A2040	C1961	G1894	G1820	G1747
C2726	U2640	G2559	U2484	U2400	A2328	G2244	U2119	A2041	U1962	C1895	U1821	G1748
G2727	A2641	U2560	U2485	C2401	G2329	G2244	G2120	A2042	A1963	U1896	C1822	U1750
U2728	U2642	C2561	A2486	U2404	G2330	G2244	A2121	G2045	G1964	U1897	U1823	G1751
G2729	U2646	G2562	U2487	A2404	U2487	G2250	A2122	A2046	U1965	C1898	C1824	G1752
C2737	U2649	U2564	U2488	G2406	U2488	A2252	A2123	A2047	U1899	U1825	U1753	G1753
A2740	G2650	G2570	U2489	A2407	G2407	A2260	U2124	G2048	G1900	C1827	C1828	C1754
G2741	U2657	G2571	C2494	G2410	G2410	G2261	C	U2049	U1970	U1755	U1829	U1755
C2742	G2658	G2580	A2495	A2411	A2411	G2261	G	A2050	C1974	U1756	A1830	U1757
U2743	U2658	U2581	A2496	C2412	A2412	G2262	C	C2051	G1975	A1831	A1831	A1758
G2744	U2662	U2582	G2497	G2416	U2416	C2263	C	C2052	C2052	G1904	C1832	G1759
U2745	U2663	G2583	A2498	U2417	A2417	G2264	A	U2053	G1976	G1905	C1833	G1760
G2746	U2665	C2585	U2499	C2422	C2422	G2265	C	G2054	G1977	C1906	C1833	G1761
U2747	U2665	G2585	U2500	G2423	U2423	G2266	C	U2055	U1978	U1907	A1836	U1762
A2748	U2673	U2589	U2501	U2424	U2424	G2267	G	A2056	A1979	G1910	A1836	U1763
U2753	U2674	U2590	A2499	U2425	U2425	C2268	C	C2057	U1980	A1911	G1839	A1764
G2759	U2675	U2591	U2500	U2426	U2426	C2269	C	A2058	U1981	U1912	U1840	A1765
A2760	U2676	G2592	U2501	G2427	U2427	G2270	C	U2059	U1982	U1913	U1841	C1766
G2761	U2677	G2593	A2499	U2428	U2428	U2271	C	A2060	U1983	C1914	A1842	G1767
U2762	U2678	C2594	U2502	U2429	U2429	U2272	C	C2061	C1988	G1915	U1843	C1768
G2763	U2679	G2595	A2503	C2430	U2430	U2273	C	C2062	C1989	A1916	U1844	C1769
U2764	U2680	U2596	U2504	C2431	U2431	U2274	C	C2063	C1990	G1917	U1845	C1770
A2765	U2681	U2597	U2505	C2432	U2432	U2275	C	C2070	A1993	G1918	A1846	A1771
U2766	U2682	U2598	U2506	C2433	U2433	U2276	C	G2073	C1994	U1919	U1847	G1772
G2767	U2683	U2599	U2507	C2434	U2434	G2282	C	U2074	C1994	A1848	U1848	A1773
A2768	U2684	G2600	U2508	C2435	U2435	G2283	C	G2075	G1995	A1849	U1849	A1774
U2769	U2685	C2601	U2509	C2436	U2436	U2284	C	U2076	A1996	A1856	A1856	G1775
G2770	U2686	U2602	U2510	U2437	U2437	U2285	C	A2081	A1997	U1925	G1862	A1776
U2771	U2687	U2603	U2511	U2438	U2438	U2286	C	U2082	A1998	A1926	C1863	G1777
G2772	U2688	A2604	U2512	U2439	U2439	U2287	C	C2083	G1999	U1927	U1864	G1780
U2773	U2689	G2605	U2513	A2439	U2439	U2288	C	U2084	U2003	G1930	C1865	C1781
G2774	U2690	C2606	U2514	G2440	U2440	U2289	C	A2085	C2006	C1931	C1866	A1782
U2775	U2691	U2607	U2515	U2441	U2441	A2290	C	U2086	G2007	C1932	G1867	G1783
A2776	U2692	U2608	U2516	U2442	U2442	A2291	C	A2087	A2008	U1868	U1869	G1790
U2777	U2693	G2609	U2517	U2443	U2443	A2300	C	U2088	U2009	C1870	G1791	G1791
G2778	U2694	U2610	U2518	U2444	U2444	A2301	C	C2091	U2010	A1939	G1873	C1794
U2779	U2695	U2611	U2519	U2445	U2445	G2307	C	C2092	U2011	A1940	U1874	A1795
C2782	U2696	U2612	U2520	U2446	U2446	G2308	C	C2093	G2012	C1941	A1875	A1796
U2783	U2697	G2613	U2521	U2447	U2447	G2309	C	G2094	A2016	U1942	A1876	G1797
A2784	U2700	C2614	U2522	U2448	U2448	U2310	C	U2095	C2017	U1943	G1877	A1800
U2785	G2701	U2615	U2523	U2449	U2449	U2311	C	G2096	A1945	U1944	U1878	U1804
G2786	A2702	U2620	U2524	U2450	U2450	G2312	C	U2097	U2018	A1946	U1879	U1805
U2787	C2703	C2621	U2525	U2451	U2451	A2225	C	A2098	U2020	C1947	U1880	U1806
C2788	U2708	G2622	U2526	U2452	U2452	A2314	C	C2100	G1948	G1949	A1881	U1807
A2791	U2709	A2625	U2527	U2453	U2453	A2315	C	U2101	G1949	U1950	G1882	U1808
U2792	C2710	G2626	U2528	U2454	U2454	G2316	C	U2102	A2024	U1951	A1883	C1809
G2793	U2711	A2627	U2529	U2455	U2455	G2317	C	C2103	G2027	C1952	G1884	A1810
U2794	G2712	C2628	U2530	U2456	U2456	U2318	C	C2104	A2028	U1953	G1885	A1811
C2795	U2713	A2629	U2531	U2457	U2457	A2224	C	U2105	G2029	A1954	A1886	G1887
U2796	U2714	G2630	U2532	U2458	U2458	A2225	C	G2106	C2036	A1955	C1815	C1815
G2797	U2715	U2631	U2533	U2459	U2459	A2226	C	U2107	G2037	G1956	A1816	A1816
U2798	U2716	C2632	U2534	U2460	U2460	A2227	C	A2108	U2038	G1957	C1817	C1817
C2799	A2717	U2633	U2535	U2461	U2461	A2228	C	A2109	G2039	U1958	A1818	A1818
U2800	U2718	U2634	U2536	U2462	U2462	A2229	C	G2110	A2117	U1959	A1892	A1892
C2801	C2719	G2635	U2537	U2463	U2463	A2230	C	U2111	A2117	A1893	A1893	A1893
A2802	U2720	U2636	U2538	U2464	U2464	A2231	C	C2112	A2117	A1893	A1893	A1893



• Molecule 27: 5S rRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	49223	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.284	Depositor
Minimum map value	-0.180	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.008	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	385.83997, 385.83997, 385.83997	wwPDB
Map dimensions	364, 364, 364	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: G6M

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	0.31	0/927	0.51	0/1239
2	B	0.37	0/2097	0.50	0/2814
3	C	0.37	0/955	0.52	0/1265
4	D	0.31	0/795	0.49	0/1062
5	E	0.32	0/861	0.59	0/1159
6	F	0.33	0/691	0.63	1/921 (0.1%)
7	G	0.22	0/703	0.41	0/936
8	H	0.22	0/735	0.40	0/986
9	I	0.35	0/603	0.48	0/801
10	J	0.35	0/455	0.49	0/605
11	K	0.25	0/464	0.44	0/619
12	L	0.34	0/1652	0.55	0/2216
13	M	0.35	0/434	0.63	0/585
14	N	0.33	0/404	0.54	1/537 (0.2%)
15	O	0.28	0/393	0.55	0/523
16	P	0.40	0/376	0.55	0/491
17	Q	0.36	0/526	0.50	0/690
18	R	0.33	0/299	0.45	0/393
19	S	0.31	0/1463	0.45	0/1976
20	V	0.31	0/1160	0.42	0/1563
21	W	0.32	0/910	0.46	0/1222
22	X	0.31	0/1096	0.51	0/1461
23	Y	0.30	0/1104	0.45	0/1481
24	Z	0.31	0/959	0.48	0/1282
25	a	0.23	0/794	0.44	0/1056
26	1	0.37	0/63551	0.38	9/99100 (0.0%)
27	2	0.29	1/2475 (0.0%)	0.65	9/3854 (0.2%)
All	All	0.36	1/86882 (0.0%)	0.42	20/130837 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
27	2	68	U	C1'-N1	5.39	1.56	1.48

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	2	91	C	C1'-C2'-O2'	-10.88	92.09	108.40
26	1	1924	G	C1'-C2'-O2'	-10.65	92.42	108.40
26	1	1954	A	C1'-C2'-O2'	-10.57	92.54	108.40
27	2	90	U	C1'-C2'-O2'	-9.20	94.60	108.40
26	1	1867	G	C4'-C3'-O3'	8.11	125.17	113.00
27	2	89	U	C4'-C3'-O3'	7.33	124.00	113.00
27	2	82	A	C1'-C2'-O2'	-7.13	97.71	108.40
6	F	45	ILE	N-CA-C	6.89	117.00	110.53
26	1	1867	G	N9-C1'-C2'	-6.15	102.77	112.00
27	2	89	U	C1'-C2'-O2'	-5.99	99.42	108.40
26	1	1866	G	C4'-C3'-O3'	5.91	121.86	113.00
27	2	88	G	C1'-C2'-O2'	-5.89	99.57	108.40
26	1	1867	G	C2'-C3'-O3'	-5.87	104.89	113.70
26	1	1924	G	C4'-C3'-O3'	5.84	121.76	113.00
26	1	1930	G	C4'-C3'-O3'	5.82	121.73	113.00
14	N	47	GLY	N-CA-C	5.76	119.83	111.24
27	2	88	G	C4'-C3'-O3'	5.64	121.47	113.00
27	2	82	A	C3'-C2'-O2'	5.18	118.47	110.70
27	2	91	C	C4'-C3'-O3'	5.12	120.69	113.00
26	1	1867	G	C3'-C2'-O2'	5.05	118.28	110.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	915	0	987	48	0
2	B	2063	0	2176	90	0
3	C	943	0	1014	42	0
4	D	785	0	825	39	0
5	E	853	0	914	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	F	684	0	726	31	0
7	G	697	0	754	36	0
8	H	727	0	777	38	0
9	I	597	0	607	20	0
10	J	449	0	485	14	0
11	K	463	0	487	17	0
12	L	1628	0	1667	81	0
13	M	432	0	472	17	0
14	N	397	0	407	12	0
15	O	390	0	396	20	0
16	P	372	0	420	13	0
17	Q	521	0	586	28	0
18	R	296	0	340	24	0
19	S	1441	0	1487	61	0
20	V	1138	0	1130	41	0
21	W	903	0	958	40	0
22	X	1082	0	1119	41	0
23	Y	1080	0	1149	53	0
24	Z	955	0	1002	45	0
25	a	787	0	826	49	0
26	1	56747	0	28540	1250	0
27	2	2214	0	1120	76	0
28	1	25	19	0	0	0
All	All	79584	19	51371	2044	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 16.

All (2044) 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)
26:1:1489:A:H62	26:1:1509:G:N2	1.46	1.12
26:1:1489:A:N6	26:1:1509:G:H21	1.50	1.08
19:S:40:GLN:HG2	19:S:184:LEU:HB2	1.37	1.06
19:S:125:VAL:HG22	19:S:194:ILE:HD11	1.42	1.00
1:A:29:ARG:HG2	1:A:46:GLU:HG2	1.43	0.99
12:L:60:LYS:HE3	12:L:62:ASP:HB2	1.47	0.97
26:1:591:A:H4'	26:1:592:A:H5'	1.48	0.95
26:1:699:U:H4'	26:1:700:A:H5'	1.50	0.94
19:S:131:PHE:HB2	19:S:162:ASN:HB3	1.50	0.93
15:O:4:ASN:HA	15:O:20:THR:HG22	1.51	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:107:PRO:HD2	2:B:110:LEU:HD22	1.52	0.90
9:I:73:GLY:HA3	9:I:90:TYR:O	1.71	0.90
23:Y:1:MET:HB3	23:Y:48:GLU:HG3	1.52	0.90
26:1:1728:C:H2'	26:1:1729:C:H5''	1.53	0.89
26:1:2876:G:H2'	26:1:2877:G:H5''	1.53	0.88
26:1:1489:A:H62	26:1:1509:G:H21	0.89	0.88
7:G:42:LYS:HD2	26:1:544:U:H5''	1.53	0.87
12:L:41:VAL:HA	12:L:45:GLY:HA2	1.56	0.87
9:I:81:GLY:HA2	27:2:10:U:H5'	1.57	0.86
19:S:155:VAL:HB	19:S:194:ILE:HG22	1.55	0.85
2:B:95:VAL:HG12	2:B:101:LYS:HD3	1.57	0.85
12:L:38:LYS:HE3	12:L:100:GLU:HG3	1.59	0.85
25:a:107:ALA:HA	25:a:110:GLU:HG2	1.59	0.84
3:C:91:ASN:HD21	26:1:1040:A:H4'	1.43	0.84
3:C:4:VAL:HG22	26:1:1238:U:H1'	1.57	0.83
26:1:167:U:H2'	26:1:168:A:H5''	1.60	0.83
8:H:65:VAL:HG11	8:H:70:ILE:HD13	1.60	0.83
12:L:43:VAL:HG12	26:1:2811:U:H4'	1.61	0.82
2:B:16:MET:HG3	2:B:206:GLY:HA3	1.62	0.82
8:H:44:ASP:HB2	8:H:47:GLU:HB3	1.63	0.81
24:Z:25:ILE:HD11	24:Z:66:LEU:HD11	1.62	0.81
3:C:92:ARG:NH2	3:C:95:LEU:O	2.14	0.80
16:P:25:THR:HG22	16:P:27:ASN:H	1.46	0.80
12:L:38:LYS:HB3	12:L:100:GLU:HG2	1.63	0.80
8:H:80:ASP:HB2	8:H:85:GLN:HE21	1.47	0.80
26:1:505:U:H2'	26:1:506:A:H5''	1.65	0.79
8:H:31:VAL:HG12	8:H:36:THR:HG21	1.63	0.79
24:Z:16:MET:HE1	26:1:1314:A:H4'	1.64	0.79
26:1:1521:A:H61	26:1:1559:G:H1	1.29	0.79
2:B:84:ASP:OD2	2:B:87:ARG:NH1	2.15	0.79
26:1:1084:U:H2'	26:1:1085:U:H5''	1.65	0.79
25:a:29:PRO:HG2	25:a:92:ILE:HD12	1.65	0.79
17:Q:58:VAL:HG13	17:Q:61:LEU:HB2	1.64	0.78
7:G:10:LYS:HE3	7:G:78:PRO:HG3	1.65	0.77
26:1:1620:G:H2'	26:1:1621:C:H5'	1.65	0.77
8:H:2:ALA:HB3	8:H:51:VAL:HG23	1.67	0.77
26:1:1946:A:H2'	26:1:1947:C:H5'	1.65	0.77
14:N:9:SER:HB2	26:1:2047:A:H5'	1.65	0.77
1:A:3:ASN:HD22	26:1:2863:G:H21	1.32	0.77
4:D:27:VAL:HG21	4:D:62:VAL:HG21	1.67	0.77
22:X:76:ILE:HG23	22:X:112:LEU:HD12	1.67	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:793:G:H22	26:1:796:A:H5'	1.49	0.77
2:B:118:SER:O	2:B:134:ASN:ND2	2.17	0.76
23:Y:57:TYR:OH	23:Y:116:GLU:OE1	2.04	0.76
26:1:1510:U:O2'	26:1:1511:C:O4'	2.04	0.76
26:1:1770:C:H2'	26:1:1771:A:H5''	1.68	0.76
26:1:2429:U:H2'	26:1:2430:C:H5'	1.68	0.76
3:C:78:ARG:HH12	26:1:1195:A:H1'	1.51	0.76
12:L:25:VAL:HG21	12:L:196:LEU:HB3	1.67	0.76
12:L:54:GLU:O	12:L:86:ARG:N	2.13	0.76
19:S:110:LEU:HD22	19:S:206:LEU:HD21	1.68	0.76
26:1:1320:G:N2	26:1:1323:A:OP2	2.15	0.76
7:G:91:VAL:HG11	7:G:100:GLU:HG2	1.66	0.75
13:M:15:ARG:HD2	13:M:53:LEU:HD21	1.68	0.75
21:W:65:THR:HG22	21:W:67:SER:H	1.50	0.75
26:1:1085:U:N3	26:1:1158:G:N1	2.34	0.75
12:L:128:GLN:HE21	12:L:132:LYS:HG2	1.51	0.75
22:X:125:ALA:HB3	22:X:128:PHE:HE1	1.51	0.75
26:1:1063:U:OP1	26:1:1079:U:O2'	2.04	0.75
26:1:527:G:O2'	26:1:552:A:N6	2.20	0.74
25:a:31:LEU:HD13	25:a:44:ILE:HG22	1.67	0.74
3:C:37:GLN:HE22	26:1:606:G:H21	1.33	0.74
17:Q:40:GLN:NE2	26:1:2389:G:OP1	2.21	0.74
27:2:18:G:H2'	27:2:19:G:H5'	1.70	0.74
26:1:645:A:O2'	26:1:647:G:O2'	2.04	0.74
15:O:31:GLU:HG2	15:O:46:ARG:HD2	1.70	0.74
26:1:142:G:H2'	26:1:143:U:H5'	1.70	0.74
26:1:326:A:H2'	26:1:327:G:H5''	1.69	0.73
27:2:31:G:N2	27:2:33:U:O4	2.21	0.73
25:a:44:ILE:HG12	25:a:54:ALA:HB3	1.70	0.73
9:I:57:GLU:HG2	9:I:88:SER:HB2	1.69	0.73
24:Z:31:GLU:HG2	24:Z:118:ILE:HG12	1.71	0.73
27:2:59:U:H2'	27:2:60:C:H5'	1.71	0.73
25:a:58:SER:HB3	25:a:72:LEU:HD21	1.70	0.72
26:1:2740:A:O2'	26:1:2742:C:OP2	2.05	0.72
2:B:108:LYS:HD2	2:B:198:LEU:HD11	1.70	0.72
24:Z:102:ARG:HH21	24:Z:122:VAL:HG23	1.52	0.72
26:1:308:C:O2	26:1:407:G:N2	2.19	0.72
23:Y:42:ILE:HA	23:Y:46:GLN:HE21	1.53	0.72
26:1:1780:G:N2	26:1:1783:G:OP2	2.22	0.72
2:B:5:LYS:HD2	2:B:17:THR:HG22	1.72	0.72
7:G:80:ARG:HB2	7:G:95:LYS:HG3	1.70	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:H:4:LEU:HD12	8:H:61:ILE:HG21	1.71	0.72
17:Q:35:ASN:ND2	26:1:2417:U:OP2	2.22	0.72
26:1:403:U:H2'	26:1:404:U:H5''	1.72	0.72
26:1:1337:A:H4'	26:1:1338:U:H5''	1.72	0.72
26:1:1901:C:H2'	26:1:1902:G:H5'	1.71	0.72
5:E:78:GLU:OE2	26:1:562:C:O2'	2.05	0.71
26:1:629:A:H62	26:1:1289:A:H2	1.38	0.71
4:D:64:LYS:HB3	4:D:94:LYS:HG2	1.71	0.71
23:Y:14:ARG:HD2	23:Y:41:TRP:HH2	1.55	0.71
26:1:373:A:H2	26:1:1248:U:H2'	1.55	0.71
3:C:98:ILE:HD11	4:D:4:ILE:HD11	1.73	0.71
26:1:1482:U:H3	26:1:1600:A:H2	1.37	0.71
11:K:37:LEU:HD21	11:K:42:ARG:HH11	1.56	0.71
18:R:7:VAL:HG22	18:R:37:GLY:HA2	1.71	0.71
26:1:367:A:N6	26:1:381:G:O2'	2.24	0.71
26:1:2608:G:N2	26:1:2608:G:OP2	2.23	0.71
1:A:77:PRO:HB2	1:A:80:THR:HG23	1.71	0.71
4:D:50:ALA:HB1	4:D:51:PRO:HD2	1.73	0.71
26:1:85:G:O2'	26:1:102:A:N6	2.24	0.71
26:1:1711:G:O2'	26:1:2018:U:O4	2.09	0.71
13:M:44:ARG:HD3	13:M:47:ILE:HD11	1.72	0.70
27:2:29:C:O2'	27:2:51:A:N6	2.23	0.70
18:R:23:VAL:HB	18:R:37:GLY:HA3	1.73	0.70
21:W:12:ASP:OD2	21:W:14:SER:OG	2.08	0.70
21:W:28:SER:HG	26:1:2590:U:HO2'	1.36	0.70
26:1:2343:U:H2'	26:1:2344:C:C6	2.26	0.70
26:1:2680:U:OP2	26:1:2681:A:O2'	2.07	0.70
1:A:75:THR:HB	21:W:76:TYR:HB2	1.72	0.70
9:I:55:PRO:HG3	9:I:61:ARG:HB2	1.73	0.70
26:1:1862:G:H1	26:1:1932:C:H5	1.40	0.70
26:1:758:G:H1'	26:1:763:A:H61	1.56	0.70
19:S:148:GLN:NE2	19:S:191:SER:OG	2.24	0.70
26:1:514:G:H2'	26:1:515:G:H5'	1.73	0.70
1:A:69:GLY:O	1:A:106:ARG:NH2	2.24	0.69
26:1:1515:G:H1	26:1:1565:U:H3	1.38	0.69
26:1:1633:A:OP2	26:1:1634:A:N6	2.25	0.69
26:1:1931:G:H21	26:1:1955:A:H8	1.39	0.69
19:S:82:GLN:HB2	26:1:1294:G:H21	1.57	0.69
26:1:342:A:N3	26:1:362:C:O2'	2.25	0.69
10:J:14:THR:HG22	10:J:28:ARG:HG2	1.74	0.69
26:1:1395:G:O2'	26:1:1410:A:N6	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:2355:A:H2'	26:1:2356:A:C8	2.27	0.69
12:L:38:LYS:HE3	12:L:100:GLU:CG	2.23	0.69
12:L:57:LYS:HB2	12:L:68:TYR:HD1	1.57	0.69
19:S:29:ASN:HD22	19:S:108:LEU:HD21	1.57	0.69
25:a:44:ILE:HG13	25:a:53:LEU:HB2	1.75	0.69
26:1:1512:U:H2'	26:1:1513:A:C8	2.28	0.69
26:1:1981:G:O2'	26:1:1983:U:O4	2.08	0.69
2:B:174:ILE:HG13	2:B:184:ILE:HD12	1.72	0.69
26:1:1063:U:H3	26:1:1186:A:H62	1.41	0.69
26:1:1520:A:H2'	26:1:1521:A:O4'	1.93	0.69
25:a:17:ARG:HA	26:1:2361:U:O2'	1.93	0.68
26:1:721:A:H8	26:1:2096:G:H21	1.40	0.68
26:1:2272:U:H5''	26:1:2273:G:H5'	1.76	0.68
23:Y:32:PHE:CZ	23:Y:111:GLU:HG2	2.28	0.68
26:1:350:G:H1'	26:1:373:A:H61	1.57	0.68
26:1:897:A:H61	26:1:971:U:H3	1.42	0.68
27:2:96:A:C2'	27:2:97:G:H5'	2.23	0.68
26:1:161:A:H2'	26:1:162:A:H5''	1.73	0.68
12:L:46:TYR:OH	26:1:2663:U:O2'	2.11	0.68
26:1:116:G:OP2	26:1:118:A:O2'	2.07	0.68
9:I:40:THR:HG22	9:I:41:GLY:H	1.58	0.68
13:M:52:HIS:CD2	13:M:52:HIS:H	2.10	0.68
25:a:40:ILE:N	25:a:58:SER:OG	2.26	0.68
4:D:46:VAL:O	4:D:47:LYS:HD2	1.94	0.67
26:1:753:U:H2'	26:1:754:U:C6	2.30	0.67
26:1:1017:A:H5'	26:1:1227:U:H1'	1.75	0.67
26:1:173:A:H2'	26:1:174:U:C6	2.30	0.67
26:1:1901:C:C2'	26:1:1902:G:H5'	2.24	0.67
26:1:2580:G:H8	26:1:2609:G:H21	1.42	0.67
2:B:245:SER:OG	26:1:1869:G:O2'	2.11	0.67
7:G:27:LEU:HD12	7:G:32:ARG:HB2	1.75	0.67
25:a:69:LYS:N	27:2:48:A:OP1	2.27	0.67
6:F:25:TYR:HH	6:F:86:SER:HG	1.43	0.67
26:1:10:A:O2'	26:1:11:U:OP1	2.11	0.67
26:1:2858:G:H1	26:1:2900:C:H5	1.41	0.67
27:2:104:A:H2'	27:2:105:C:C6	2.29	0.67
11:K:6:ILE:HG12	11:K:53:LEU:HD23	1.74	0.67
26:1:1943:A:H5''	26:1:1944:U:H5	1.60	0.67
7:G:43:LYS:O	7:G:56:ILE:HA	1.93	0.67
26:1:181:G:H2'	26:1:182:C:O4'	1.94	0.67
26:1:273:A:OP2	26:1:297:G:N1	2.22	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1248:U:OP1	26:1:1249:U:O2'	2.10	0.67
2:B:29:PRO:HB2	2:B:34:LEU:HD11	1.77	0.67
2:B:65:ILE:HD11	2:B:91:ILE:HG21	1.76	0.67
12:L:86:ARG:NH1	26:1:2850:G:OP2	2.28	0.67
26:1:2309:G:H4'	26:1:2416:G:O2'	1.95	0.67
26:1:2560:U:H2'	26:1:2561:C:H5'	1.77	0.67
23:Y:14:ARG:HD2	23:Y:41:TRP:CH2	2.29	0.67
26:1:1385:G:H2'	26:1:1386:U:H5'	1.77	0.67
26:1:1077:U:O2'	26:1:2777:A:N6	2.27	0.66
26:1:2340:C:H2'	26:1:2341:A:C8	2.30	0.66
12:L:3:LYS:NZ	12:L:98:ALA:HB2	2.10	0.66
26:1:2307:G:C2'	26:1:2308:C:H5'	2.25	0.66
9:I:54:TYR:OH	26:1:2359:C:OP1	2.13	0.66
25:a:40:ILE:HD11	25:a:104:ARG:HH21	1.60	0.66
26:1:2123:A:H2'	26:1:2124:U:C6	2.30	0.66
26:1:89:U:H3'	26:1:90:A:H3'	1.76	0.66
26:1:340:C:H2'	26:1:341:G:O4'	1.95	0.66
26:1:1431:U:C2'	26:1:1432:A:H5'	2.26	0.66
26:1:2817:A:O2'	26:1:2818:A:H5''	1.95	0.66
3:C:91:ASN:HB2	4:D:11:GLN:CD	2.21	0.66
26:1:788:A:O2'	26:1:1703:U:OP1	2.12	0.66
26:1:2649:U:O3'	26:1:2845:G:N2	2.21	0.66
22:X:18:ARG:NH2	26:1:1288:G:N7	2.44	0.66
26:1:1728:C:C2'	26:1:1729:C:H5''	2.26	0.66
26:1:2342:U:H2'	26:1:2343:U:C6	2.31	0.66
26:1:1880:A:H2'	26:1:1881:A:C8	2.30	0.66
26:1:2314:A:H62	26:1:2371:U:H3	1.44	0.66
17:Q:58:VAL:HG13	17:Q:61:LEU:HD12	1.77	0.66
18:R:30:PRO:HB2	26:1:2554:C:H5''	1.77	0.65
21:W:63:VAL:HG11	21:W:102:VAL:HG12	1.78	0.65
23:Y:51:ARG:HD3	23:Y:66:ILE:HD11	1.77	0.65
26:1:1588:U:H2'	26:1:1589:U:H6	1.60	0.65
26:1:901:G:H2'	26:1:902:A:C8	2.31	0.65
2:B:240:PRO:HB2	26:1:1930:G:OP1	1.95	0.65
26:1:105:C:O2'	26:1:337:A:O2'	2.14	0.65
26:1:793:G:N2	26:1:795:A:H3'	2.11	0.65
26:1:1070:A:OP2	26:1:1178:C:O2'	2.13	0.65
26:1:1212:U:H2'	26:1:1213:C:C6	2.30	0.65
26:1:1463:A:H2'	26:1:1464:U:H5''	1.79	0.65
26:1:1556:G:O2'	26:1:1557:C:OP2	2.12	0.65
4:D:81:ASN:HB3	22:X:23:VAL:HG11	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:O:9:CYS:HB3	15:O:13:GLY:O	1.96	0.65
23:Y:54:MET:CG	23:Y:121:ALA:HB2	2.27	0.65
26:1:575:G:N2	26:1:2050:A:OP1	2.29	0.65
26:1:1588:U:H2'	26:1:1589:U:C6	2.32	0.65
26:1:805:G:H2'	26:1:806:A:O4'	1.97	0.65
1:A:102:LEU:HD23	1:A:105:LEU:HD12	1.78	0.65
26:1:786:U:H2'	26:1:787:U:C6	2.32	0.65
26:1:1966:U:OP1	26:1:2631:U:O2'	2.14	0.65
6:F:13:THR:H	6:F:16:SER:HB3	1.61	0.65
26:1:1769:C:H2'	26:1:1770:C:C6	2.32	0.65
26:1:2507:C:H2'	26:1:2508:G:H5'	1.79	0.65
3:C:95:LEU:HD13	4:D:4:ILE:HD13	1.80	0.64
26:1:1185:U:H4'	26:1:1186:A:O4'	1.97	0.64
8:H:29:ALA:HB3	8:H:41:VAL:HG23	1.78	0.64
24:Z:74:GLU:HB3	24:Z:77:THR:HB	1.79	0.64
3:C:98:ILE:HD11	4:D:4:ILE:CD1	2.28	0.64
26:1:889:U:H3'	26:1:890:G:C8	2.32	0.64
10:J:39:LEU:HD23	10:J:44:PRO:HB3	1.79	0.64
26:1:1481:A:H2'	26:1:1482:U:C6	2.33	0.64
2:B:167:LYS:HG2	2:B:172:VAL:HG12	1.79	0.64
17:Q:8:ARG:NH2	26:1:247:A:OP2	2.28	0.64
26:1:1563:U:H2'	26:1:1564:G:H8	1.62	0.64
16:P:12:LYS:O	16:P:16:VAL:HG12	1.97	0.64
26:1:2038:U:H2'	26:1:2039:G:O4'	1.98	0.64
26:1:2885:U:OP2	26:1:2886:G:O2'	2.14	0.64
5:E:89:ALA:HB2	26:1:793:G:H5'	1.77	0.64
26:1:1162:C:H3'	26:1:1163:U:H5''	1.80	0.64
26:1:1519:U:O2'	26:1:1520:A:H5'	1.97	0.64
26:1:1943:A:H3'	26:1:1944:U:C6	2.33	0.64
23:Y:36:ALA:HB2	23:Y:103:LEU:HD21	1.80	0.64
26:1:2006:C:C2'	26:1:2007:G:H5'	2.28	0.64
26:1:403:U:C2'	26:1:404:U:H5''	2.28	0.63
26:1:2532:G:O2'	26:1:2533:U:H5''	1.98	0.63
1:A:10:VAL:HG11	12:L:196:LEU:HD11	1.80	0.63
23:Y:45:ARG:HD3	26:1:2511:G:OP1	1.98	0.63
26:1:748:U:H2'	26:1:749:G:O4'	1.97	0.63
26:1:1066:G:N2	26:1:1067:U:O4	2.30	0.63
26:1:2599:A:O2'	26:1:2602:C:OP1	2.09	0.63
23:Y:36:ALA:HB2	23:Y:103:LEU:CD2	2.28	0.63
26:1:156:A:H62	26:1:172:U:H3	1.46	0.63
20:V:7:ALA:H	20:V:46:THR:HG21	1.63	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:629:A:N1	26:1:854:G:O2'	2.27	0.63
26:1:2876:G:C2'	26:1:2877:G:H5''	2.25	0.63
9:I:79:ARG:HA	9:I:85:LYS:HA	1.79	0.63
21:W:61:VAL:HG11	21:W:111:PHE:CE1	2.33	0.63
26:1:963:A:H62	26:1:2295:A:H2	1.47	0.63
7:G:42:LYS:HB3	7:G:58:GLU:HG2	1.81	0.63
26:1:162:A:H8	26:1:2244:G:H21	1.46	0.63
26:1:183:A:H3'	26:1:183:A:OP2	1.99	0.63
26:1:1218:G:H2'	26:1:1219:G:C8	2.33	0.63
24:Z:13:ARG:NH2	26:1:2717:A:OP2	2.32	0.63
27:2:83:C:H42	27:2:86:A:H61	1.45	0.63
2:B:13:ARG:HD2	26:1:773:G:H4'	1.80	0.63
26:1:1072:A:N3	26:1:2513:G:O2'	2.30	0.63
25:a:93:VAL:HG23	26:1:2405:A:H1'	1.81	0.63
26:1:89:U:H3'	26:1:90:A:C3'	2.28	0.63
26:1:1085:U:O4	26:1:1158:G:O6	2.16	0.63
12:L:65:SER:OG	26:1:2851:G:OP2	2.06	0.62
12:L:157:ALA:HB3	26:1:2602:C:H5'	1.81	0.62
17:Q:31:HIS:CD2	17:Q:32:LEU:HG	2.34	0.62
7:G:24:ILE:HD11	7:G:36:GLU:HA	1.80	0.62
26:1:1797:G:H1	26:1:2009:U:H3	1.47	0.62
14:N:3:VAL:HG12	26:1:2042:A:C2	2.34	0.62
19:S:115:SER:O	19:S:119:GLN:HG2	1.99	0.62
26:1:758:G:H1'	26:1:763:A:N6	2.14	0.62
26:1:1387:C:H2'	26:1:1388:C:H5'	1.81	0.62
15:O:18:ILE:HG21	26:1:2446:U:H4'	1.80	0.62
22:X:124:LYS:HE2	22:X:144:GLU:HB2	1.79	0.62
24:Z:48:ILE:HD12	24:Z:89:ILE:HG22	1.81	0.62
26:1:1022:G:H2'	26:1:1023:A:H5'	1.80	0.62
26:1:1387:C:C2'	26:1:1388:C:H5'	2.28	0.62
27:2:45:C:H2'	27:2:46:A:H5'	1.80	0.62
27:2:59:U:C2'	27:2:60:C:H5'	2.30	0.62
4:D:41:VAL:HG22	4:D:48:VAL:CG2	2.29	0.62
8:H:9:ARG:HE	8:H:40:SER:HB3	1.63	0.62
24:Z:74:GLU:CB	24:Z:77:THR:HB	2.29	0.62
25:a:45:ILE:HG12	25:a:46:ASP:O	1.99	0.62
3:C:70:ARG:HE	3:C:75:SER:HA	1.64	0.62
7:G:44:HIS:O	7:G:54:GLY:N	2.33	0.62
23:Y:1:MET:HE3	23:Y:48:GLU:HG3	1.80	0.62
26:1:613:G:H2'	26:1:2057:A:N7	2.15	0.62
26:1:785:C:O2'	26:1:786:U:H5'	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:2331:G:H22	26:1:2339:U:H5	1.47	0.62
21:W:43:VAL:HG21	21:W:52:VAL:CG1	2.30	0.62
21:W:69:VAL:HG22	21:W:77:ILE:HG22	1.82	0.62
26:1:1169:G:OP2	26:1:1170:A:O2'	2.13	0.62
17:Q:14:VAL:CG2	17:Q:22:LEU:HB3	2.30	0.62
26:1:363:A:O2'	26:1:365:A:OP2	2.17	0.62
27:2:105:C:H2'	27:2:106:G:O4'	2.00	0.62
2:B:69:ARG:HD3	2:B:104:ILE:HD12	1.81	0.62
26:1:460:C:H2'	26:1:461:A:C8	2.35	0.62
1:A:34:ILE:O	1:A:40:GLU:HA	1.99	0.61
8:H:4:LEU:HD11	8:H:51:VAL:HG11	1.82	0.61
23:Y:77:LYS:HE2	26:1:1000:G:H5''	1.82	0.61
26:1:69:C:H4'	26:1:75:G:N7	2.15	0.61
1:A:53:ARG:NH2	26:1:2710:C:OP1	2.23	0.61
22:X:103:LYS:HE2	26:1:648:G:O6	2.00	0.61
26:1:434:G:H2'	26:1:436:A:C2	2.35	0.61
26:1:2584:G:H2'	26:1:2585:C:C6	2.35	0.61
26:1:2102:U:OP2	26:1:2265:G:O2'	2.13	0.61
25:a:37:ASN:HD21	27:2:27:A:H5''	1.65	0.61
26:1:514:G:C2'	26:1:515:G:H5'	2.30	0.61
26:1:556:U:C2'	26:1:557:G:H5'	2.30	0.61
26:1:1268:C:H2'	26:1:1269:A:C8	2.35	0.61
26:1:1771:A:H2'	26:1:1772:G:O4'	1.99	0.61
19:S:48:THR:O	26:1:488:G:N2	2.29	0.61
24:Z:74:GLU:HB2	24:Z:77:THR:O	2.00	0.61
26:1:195:C:H2'	26:1:196:U:H5'	1.82	0.61
26:1:2915:C:H2'	26:1:2916:U:C6	2.34	0.61
1:A:29:ARG:HD2	1:A:89:LYS:HE2	1.81	0.61
26:1:632:U:H2'	26:1:633:A:H8	1.66	0.61
26:1:1085:U:O2	26:1:1158:G:N2	2.33	0.61
26:1:2676:U:H2'	26:1:2677:C:C6	2.35	0.61
21:W:50:GLY:O	21:W:53:LYS:NZ	2.25	0.61
26:1:631:U:H2'	26:1:632:U:C6	2.36	0.61
26:1:1988:C:O2'	26:1:1989:C:OP1	2.13	0.61
26:1:89:U:H3'	26:1:90:A:H2'	1.81	0.61
26:1:414:C:C2'	26:1:415:U:H5'	2.31	0.61
26:1:632:U:H2'	26:1:633:A:C8	2.35	0.61
26:1:1632:A:H4'	26:1:1633:A:C4	2.34	0.61
19:S:26:ILE:HG13	19:S:111:ARG:NH1	2.15	0.61
26:1:1766:C:H2'	26:1:1767:G:H5'	1.81	0.61
26:1:2429:U:C2'	26:1:2430:C:H5'	2.30	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:117:GLU:OE2	2:B:120:ALA:HA	2.01	0.61
26:1:774:G:H5'	26:1:775:A:H5''	1.83	0.61
26:1:2594:G:H2'	26:1:2595:C:C6	2.36	0.61
8:H:65:VAL:HG21	8:H:70:ILE:HD11	1.83	0.60
17:Q:18:ALA:CB	26:1:673:G:H5''	2.31	0.60
19:S:164:GLU:HG3	19:S:165:LEU:HG	1.83	0.60
1:A:29:ARG:HB2	1:A:87:GLU:HG2	1.83	0.60
3:C:53:ARG:NH1	26:1:580:C:O3'	2.33	0.60
24:Z:45:GLU:HB3	26:1:2859:G:H4'	1.84	0.60
26:1:1176:U:O2'	26:1:1177:A:H5'	2.01	0.60
26:1:889:U:H3'	26:1:890:G:H8	1.66	0.60
26:1:1220:A:H2'	26:1:1221:C:C6	2.36	0.60
26:1:1329:G:H2'	26:1:1330:U:C6	2.36	0.60
26:1:1450:A:H3'	26:1:1451:U:C5	2.37	0.60
26:1:2317:G:O2'	26:1:2318:U:H5'	2.01	0.60
26:1:2341:A:H2'	26:1:2342:U:C6	2.36	0.60
26:1:92:G:H2'	26:1:93:U:C6	2.36	0.60
26:1:1565:U:H2'	26:1:1566:G:C8	2.35	0.60
27:2:47:C:H2'	27:2:48:A:C8	2.35	0.60
23:Y:24:GLY:N	26:1:952:A:OP1	2.32	0.60
26:1:59:U:O2'	26:1:74:U:OP2	2.20	0.60
4:D:14:VAL:CG2	4:D:97:ILE:HG13	2.31	0.60
26:1:348:C:H2'	26:1:349:U:C6	2.36	0.60
26:1:651:A:H2'	26:1:652:A:C8	2.37	0.60
26:1:2288:C:C2'	26:1:2289:U:H5'	2.32	0.60
12:L:57:LYS:HB2	12:L:68:TYR:CD1	2.36	0.60
16:P:38:LYS:NZ	26:1:514:G:OP2	2.34	0.60
20:V:54:TYR:CE1	20:V:122:LYS:HG2	2.37	0.60
26:1:2224:U:H1'	26:1:2225:A:C2	2.36	0.60
4:D:65:GLN:HG3	4:D:93:THR:HG22	1.84	0.60
9:I:76:LYS:HD3	9:I:90:TYR:CE2	2.37	0.60
26:1:1563:U:H2'	26:1:1564:G:C8	2.36	0.60
9:I:17:SER:HB3	26:1:2282:G:H21	1.65	0.60
11:K:8:ASP:O	11:K:60:ARG:NH1	2.24	0.60
15:O:31:GLU:HG2	15:O:46:ARG:CD	2.32	0.60
22:X:125:ALA:HB3	22:X:128:PHE:CE1	2.34	0.60
26:1:238:U:H2'	26:1:239:C:C6	2.37	0.60
26:1:2222:U:O2'	26:1:2223:C:H5'	2.02	0.60
16:P:2:VAL:N	26:1:1663:G:HO2'	2.00	0.60
19:S:91:GLY:HA2	26:1:1286:G:H5'	1.84	0.60
26:1:100:U:H5'	26:1:101:G:C8	2.37	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:394:U:H2'	26:1:395:U:C6	2.37	0.60
26:1:505:U:C2'	26:1:506:A:H5''	2.32	0.60
26:1:597:U:O2'	26:1:598:G:H5'	2.02	0.60
26:1:1577:G:H22	26:1:1588:U:H3	1.48	0.60
26:1:2318:U:H2'	26:1:2319:U:C6	2.37	0.60
2:B:174:ILE:CG1	2:B:184:ILE:HD12	2.32	0.59
26:1:1745:A:H2'	26:1:1746:G:H5'	1.84	0.59
21:W:39:ILE:HD13	21:W:62:ILE:HD11	1.84	0.59
22:X:128:PHE:CE2	22:X:143:HIS:HB2	2.37	0.59
26:1:64:A:H62	26:1:90:A:H61	1.50	0.59
26:1:2273:G:H2'	26:1:2274:A:C8	2.37	0.59
12:L:99:TYR:HB3	12:L:101:VAL:HG22	1.84	0.59
17:Q:14:VAL:HG21	17:Q:22:LEU:HB3	1.84	0.59
23:Y:42:ILE:HA	23:Y:46:GLN:NE2	2.17	0.59
25:a:92:ILE:HG22	25:a:118:GLU:O	2.02	0.59
25:a:100:LEU:HB2	27:2:46:A:OP1	2.02	0.59
26:1:902:A:C2'	26:1:903:G:H5'	2.32	0.59
4:D:41:VAL:HG22	4:D:48:VAL:HG22	1.85	0.59
4:D:79:ARG:NH2	26:1:615:A:OP2	2.34	0.59
26:1:1352:C:O2'	26:1:1429:G:N3	2.34	0.59
26:1:1410:A:H5'	26:1:2239:A:H1'	1.84	0.59
2:B:26:LYS:HE2	2:B:28:THR:O	2.03	0.59
24:Z:45:GLU:CB	26:1:2859:G:H4'	2.32	0.59
26:1:1494:G:H2'	26:1:1495:C:H5'	1.84	0.59
26:1:1884:G:H21	26:1:1912:A:H62	1.50	0.59
26:1:2383:C:H2'	26:1:2384:U:O4'	2.03	0.59
7:G:32:ARG:HD3	7:G:64:HIS:HA	1.84	0.59
15:O:18:ILE:HD13	26:1:2446:U:H5'	1.83	0.59
20:V:29:LEU:HD13	20:V:143:LEU:HD11	1.83	0.59
20:V:53:ASP:O	20:V:122:LYS:HD3	2.02	0.59
26:1:100:U:H3'	26:1:101:G:H5'	1.83	0.59
26:1:448:A:H2'	26:1:449:U:H5'	1.83	0.59
27:2:69:C:H2'	27:2:70:G:O4'	2.03	0.59
12:L:2:THR:HB	12:L:109:THR:HB	1.85	0.59
20:V:29:LEU:CD1	20:V:143:LEU:HD11	2.32	0.59
26:1:339:A:H2'	26:1:340:C:C6	2.38	0.59
26:1:1897:U:H3	26:1:1899:U:H5'	1.66	0.59
26:1:2688:G:H2'	26:1:2689:A:O4'	2.03	0.59
1:A:30:VAL:HG13	1:A:83:ILE:HG23	1.85	0.59
5:E:1:MET:HG2	5:E:2:GLU:H	1.68	0.59
16:P:41:LYS:HG3	26:1:505:U:H5''	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:24:MET:HG2	18:R:35:ARG:CB	2.32	0.59
6:F:10:PRO:HD3	11:K:30:PHE:CD1	2.38	0.59
8:H:16:SER:HB3	27:2:89:U:H5'	1.85	0.59
12:L:134:HIS:CD2	12:L:168:LYS:HD2	2.37	0.59
21:W:5:GLU:HG3	26:1:1713:A:C8	2.38	0.59
26:1:396:G:H2'	26:1:397:U:C6	2.37	0.59
26:1:1726:A:H2'	26:1:1727:C:C6	2.37	0.59
26:1:2221:U:H2'	26:1:2222:U:H6	1.68	0.59
26:1:2308:C:O2'	26:1:2309:G:H5'	2.03	0.59
1:A:76:PHE:HB3	1:A:83:ILE:HD11	1.84	0.59
2:B:208:ALA:HB2	26:1:1817:C:O2'	2.03	0.59
24:Z:41:ARG:O	24:Z:45:GLU:HG2	2.03	0.59
26:1:259:A:H2'	26:1:260:A:C8	2.38	0.59
26:1:2340:C:O2'	26:1:2341:A:H5'	2.03	0.59
26:1:2917:U:H2'	26:1:2918:A:C8	2.37	0.59
25:a:39:HIS:CE1	25:a:59:LYS:HB3	2.37	0.58
26:1:247:A:H2'	26:1:248:G:O4'	2.02	0.58
26:1:447:A:H2'	26:1:448:A:H8	1.68	0.58
26:1:858:U:H2'	26:1:859:C:C6	2.38	0.58
26:1:1442:C:H2'	26:1:1443:A:C8	2.38	0.58
26:1:1911:A:H2'	26:1:1912:A:C8	2.38	0.58
26:1:2746:G:O2'	26:1:2747:U:H5'	2.03	0.58
8:H:4:LEU:HD21	8:H:51:VAL:HG11	1.85	0.58
26:1:637:U:H2'	26:1:638:U:C6	2.37	0.58
26:1:642:U:O2'	26:1:643:G:H5'	2.03	0.58
26:1:1312:A:H4'	26:1:1313:G:OP1	2.02	0.58
26:1:1514:A:O2'	26:1:1515:G:H5'	2.03	0.58
26:1:1943:A:H3'	26:1:1944:U:H6	1.67	0.58
26:1:2041:A:H2'	26:1:2042:A:C8	2.38	0.58
27:2:51:A:H2'	27:2:52:G:H5'	1.84	0.58
5:E:42:ALA:HB2	26:1:2037:G:H5'	1.85	0.58
19:S:152:VAL:HG12	19:S:191:SER:HB3	1.86	0.58
26:1:397:U:H2'	26:1:398:C:C6	2.39	0.58
26:1:2224:U:H1'	26:1:2225:A:H2	1.67	0.58
2:B:118:SER:HA	2:B:131:PRO:CD	2.33	0.58
7:G:91:VAL:HG11	7:G:100:GLU:CG	2.33	0.58
22:X:46:VAL:HG13	22:X:51:GLU:HA	1.84	0.58
26:1:1219:G:O2'	26:1:1220:A:O4'	2.21	0.58
26:1:2516:G:O2'	26:1:2517:G:H5'	2.03	0.58
22:X:76:ILE:CG2	22:X:112:LEU:HD12	2.32	0.58
26:1:242:U:O2'	26:1:243:U:H5'	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1031:C:O2'	26:1:1044:A:N3	2.34	0.58
26:1:2123:A:O2'	26:1:2124:U:O4'	2.15	0.58
26:1:2270:U:H2'	26:1:2271:U:C6	2.38	0.58
27:2:33:U:H2'	27:2:34:C:C6	2.38	0.58
18:R:17:ILE:HG21	18:R:26:ILE:HD11	1.85	0.58
26:1:133:A:H2'	26:1:134:U:C6	2.39	0.58
26:1:1390:A:H2'	26:1:1391:A:C8	2.38	0.58
26:1:2058:A:N3	26:1:2482:G:O2'	2.30	0.58
6:F:4:ARG:HG2	6:F:5:ASP:H	1.69	0.58
26:1:991:A:H2'	26:1:992:A:C8	2.39	0.58
26:1:1492:G:O2'	26:1:1575:A:O2'	2.16	0.58
26:1:2300:A:H2'	26:1:2301:A:C8	2.38	0.58
15:O:12:CYS:SG	15:O:39:GLU:HG3	2.44	0.58
26:1:328:G:O6	26:1:399:U:O2	2.21	0.58
13:M:4:LEU:HB3	13:M:6:ILE:HD11	1.85	0.58
19:S:67:GLN:NE2	26:1:720:A:H4'	2.19	0.58
23:Y:54:MET:HE1	23:Y:104:PHE:CD1	2.38	0.58
15:O:7:LEU:HA	15:O:46:ARG:O	2.03	0.58
23:Y:66:ILE:HG12	23:Y:104:PHE:CE1	2.39	0.58
26:1:1355:A:H2'	26:1:1356:G:H5'	1.86	0.58
27:2:12:U:O2'	27:2:102:G:H1'	2.04	0.58
7:G:8:ASN:HA	7:G:21:GLY:O	2.03	0.57
7:G:15:LYS:NZ	26:1:546:A:OP1	2.33	0.57
19:S:22:ALA:O	19:S:111:ARG:NH1	2.36	0.57
26:1:221:G:H22	26:1:238:U:H4'	1.69	0.57
26:1:1512:U:H2'	26:1:1513:A:H8	1.66	0.57
26:1:2658:G:H4'	26:1:2911:A:H5''	1.86	0.57
27:2:47:C:H2'	27:2:48:A:H8	1.69	0.57
26:1:160:G:H21	26:1:168:A:H2	1.53	0.57
26:1:373:A:C2	26:1:1248:U:H2'	2.39	0.57
26:1:962:A:H5''	26:1:2295:A:N6	2.19	0.57
26:1:1083:G:H2'	26:1:1084:U:C6	2.39	0.57
13:M:4:LEU:O	13:M:6:ILE:HD12	2.05	0.57
26:1:1943:A:H5''	26:1:1944:U:C5	2.39	0.57
26:1:2006:C:H2'	26:1:2007:G:H5'	1.86	0.57
11:K:21:SER:HA	11:K:50:ILE:CD1	2.34	0.57
23:Y:77:LYS:HB3	23:Y:78:PRO:HD2	1.87	0.57
26:1:24:G:H2'	26:1:25:U:H6	1.69	0.57
26:1:2061:U:O2'	26:1:2062:G:H5'	2.03	0.57
26:1:2676:U:H2'	26:1:2677:C:H6	1.69	0.57
7:G:11:VAL:HA	7:G:68:VAL:HG12	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:402:C:H2'	26:1:403:U:O2	2.04	0.57
26:1:561:C:O2'	26:1:562:C:H5'	2.05	0.57
26:1:1562:C:H2'	26:1:1563:U:C6	2.40	0.57
26:1:1982:U:O4	26:1:2583:C:N4	2.37	0.57
26:1:2221:U:H2'	26:1:2222:U:C6	2.40	0.57
26:1:2543:G:O2'	26:1:2544:C:H5'	2.04	0.57
26:1:2604:A:H2'	26:1:2641:A:N6	2.20	0.57
2:B:67:PHE:HB3	2:B:152:GLY:H	1.67	0.57
6:F:58:TYR:OH	26:1:1377:U:OP2	2.23	0.57
19:S:46:GLN:NE2	26:1:487:U:O2'	2.37	0.57
21:W:91:LYS:CD	21:W:110:ASN:HB2	2.33	0.57
26:1:1385:G:C2'	26:1:1386:U:H5'	2.34	0.57
26:1:145:A:H2'	26:1:146:U:C6	2.38	0.57
26:1:481:C:H2'	26:1:482:U:H5'	1.85	0.57
26:1:1081:G:H2'	26:1:1082:C:C6	2.40	0.57
6:F:10:PRO:HD3	11:K:30:PHE:CE1	2.39	0.57
12:L:64:LYS:HE2	26:1:2851:G:C5	2.40	0.57
23:Y:34:LEU:HD11	23:Y:129:THR:OG1	2.05	0.57
23:Y:83:MET:HE1	26:1:1000:G:C1'	2.35	0.57
26:1:1160:C:H2'	26:1:1161:A:C8	2.40	0.57
26:1:1514:A:H2	26:1:1566:G:H22	1.53	0.57
2:B:205:VAL:HG23	26:1:1818:A:H4'	1.87	0.57
19:S:153:LEU:HB3	19:S:192:LEU:HD23	1.87	0.57
26:1:38:A:H2'	26:1:39:C:O4'	2.05	0.57
26:1:1558:U:H2'	26:1:1559:G:C8	2.39	0.57
2:B:67:PHE:CE1	2:B:156:ARG:HD2	2.40	0.57
2:B:180:GLU:OE2	2:B:270:ILE:HG23	2.05	0.57
26:1:1828:U:O4	26:1:2229:C:H4'	2.05	0.57
26:1:2541:U:H2'	26:1:2542:C:C6	2.39	0.57
4:D:35:PHE:O	4:D:57:THR:HB	2.05	0.56
8:H:57:ARG:HH22	8:H:77:TYR:HE1	1.53	0.56
26:1:89:U:H3'	26:1:90:A:C2'	2.34	0.56
7:G:22:LYS:O	7:G:35:VAL:HG13	2.04	0.56
26:1:1770:C:C2'	26:1:1771:A:H5''	2.35	0.56
26:1:1959:A:H2'	26:1:1960:G:O4'	2.05	0.56
1:A:22:PHE:CE2	1:A:52:ARG:HD2	2.40	0.56
1:A:28:LEU:CD2	1:A:88:VAL:HG22	2.35	0.56
1:A:92:GLY:HA2	1:A:113:GLN:O	2.05	0.56
2:B:147:LYS:HE3	26:1:2231:C:H1'	1.86	0.56
25:a:29:PRO:HG2	25:a:92:ILE:CD1	2.33	0.56
25:a:72:LEU:HD12	25:a:75:LYS:HB2	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:916:U:O2'	26:1:917:U:H5'	2.05	0.56
26:1:1988:C:O2'	26:1:1989:C:H5'	2.06	0.56
26:1:2904:U:H2'	26:1:2905:C:O4'	2.04	0.56
2:B:176:LEU:HB2	2:B:180:GLU:HB3	1.87	0.56
6:F:25:TYR:OH	6:F:86:SER:OG	2.17	0.56
11:K:50:ILE:O	11:K:54:LYS:HG2	2.06	0.56
17:Q:10:ALA:O	17:Q:14:VAL:HG12	2.06	0.56
23:Y:17:THR:O	23:Y:39:THR:HG21	2.04	0.56
26:1:753:U:H2'	26:1:754:U:H6	1.69	0.56
26:1:2496:A:H2'	26:1:2497:G:O4'	2.05	0.56
26:1:2610:G:C2'	26:1:2611:U:H5'	2.35	0.56
6:F:7:LEU:HD12	6:F:45:ILE:HD12	1.88	0.56
23:Y:54:MET:HE1	23:Y:104:PHE:CG	2.40	0.56
24:Z:16:MET:CE	26:1:1314:A:H4'	2.34	0.56
26:1:1881:A:H62	26:1:1915:G:H8	1.52	0.56
26:1:2419:A:H2	26:1:2451:C:H42	1.52	0.56
22:X:124:LYS:CD	22:X:144:GLU:HB2	2.36	0.56
23:Y:35:GLN:HB2	23:Y:132:VAL:HG21	1.88	0.56
26:1:1900:G:H2'	26:1:1901:C:C6	2.40	0.56
26:1:615:A:H61	26:1:2056:G:H8	1.54	0.56
26:1:1161:A:H2'	26:1:1162:C:C6	2.41	0.56
26:1:2761:C:H2'	26:1:2762:G:O4'	2.05	0.56
1:A:10:VAL:CG2	12:L:194:VAL:HG21	2.36	0.56
2:B:236:GLU:HG3	26:1:2627:A:H2	1.71	0.56
6:F:16:SER:O	6:F:20:MET:HG2	2.05	0.56
12:L:118:VAL:HG22	12:L:211:ILE:HD13	1.88	0.56
18:R:14:CYS:SG	18:R:32:HIS:ND1	2.78	0.56
24:Z:16:MET:HE2	24:Z:36:ARG:HD3	1.88	0.56
25:a:88:GLY:O	25:a:89:ILE:HD13	2.06	0.56
26:1:242:U:C2'	26:1:243:U:H5'	2.36	0.56
26:1:1084:U:C2'	26:1:1085:U:H5''	2.34	0.56
26:1:1464:U:H5'	26:1:1465:G:OP2	2.06	0.56
26:1:1897:U:H2'	26:1:1898:C:H4'	1.88	0.56
2:B:16:MET:CG	2:B:206:GLY:HA3	2.35	0.56
6:F:56:MET:HE2	26:1:1378:U:O4'	2.05	0.56
19:S:149:PRO:HG2	19:S:191:SER:HB2	1.88	0.56
26:1:2101:U:H2'	26:1:2102:U:C6	2.41	0.56
2:B:26:LYS:HD3	2:B:82:GLN:HE21	1.70	0.56
2:B:176:LEU:HD12	2:B:180:GLU:HG2	1.87	0.56
8:H:31:VAL:O	8:H:38:ASN:HA	2.05	0.56
12:L:189:ASP:HB3	12:L:194:VAL:CG2	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:189:ASP:HB3	12:L:194:VAL:HG23	1.87	0.56
15:O:34:LYS:HB2	15:O:45:HIS:CD2	2.41	0.56
26:1:178:A:O2'	26:1:179:A:H5'	2.06	0.56
26:1:753:U:O2'	26:1:754:U:H5'	2.06	0.56
26:1:1895:C:H2'	26:1:1896:U:O4'	2.06	0.56
2:B:159:GLY:HA2	2:B:198:LEU:CD2	2.36	0.55
7:G:10:LYS:CE	7:G:78:PRO:HG3	2.36	0.55
14:N:5:LYS:NZ	26:1:2081:A:H2'	2.21	0.55
26:1:830:U:H4'	26:1:1806:U:H4'	1.88	0.55
26:1:878:C:H2'	26:1:879:U:C6	2.41	0.55
26:1:2083:G:H1	26:1:2639:C:H5	1.54	0.55
26:1:2360:A:H5'	26:1:2362:A:H1'	1.88	0.55
26:1:2560:U:C2'	26:1:2561:C:H5'	2.35	0.55
2:B:260:ARG:HB2	26:1:1825:U:OP1	2.05	0.55
4:D:85:LYS:HD2	26:1:1263:A:H4'	1.89	0.55
6:F:62:LYS:HB3	6:F:71:TYR:CE1	2.41	0.55
12:L:138:ARG:HG2	26:1:2024:A:OP2	2.07	0.55
26:1:1472:C:C5	26:1:1616:A:H5''	2.41	0.55
27:2:19:G:H2'	27:2:20:A:C8	2.41	0.55
8:H:73:MET:O	8:H:91:PHE:HA	2.06	0.55
9:I:61:ARG:O	9:I:61:ARG:HD3	2.05	0.55
14:N:5:LYS:HZ3	26:1:2081:A:H2'	1.71	0.55
24:Z:4:ARG:NH1	26:1:1696:C:OP1	2.39	0.55
27:2:30:U:H1'	27:2:50:A:H61	1.72	0.55
26:1:1352:C:H2'	26:1:1353:A:H8	1.71	0.55
2:B:145:GLU:HG2	2:B:151:GLY:O	2.06	0.55
12:L:118:VAL:HG22	12:L:211:ILE:CD1	2.36	0.55
21:W:25:LEU:CD2	26:1:2589:U:H4'	2.36	0.55
25:a:103:GLY:HA3	27:2:47:C:OP1	2.06	0.55
26:1:446:G:C2'	26:1:447:A:H5''	2.37	0.55
26:1:699:U:C4'	26:1:700:A:H5'	2.30	0.55
26:1:1075:G:C2'	26:1:1076:A:H5'	2.37	0.55
26:1:1515:G:H22	26:1:1565:U:H3	1.54	0.55
12:L:43:VAL:CG1	26:1:2811:U:H4'	2.33	0.55
20:V:14:ARG:NH1	20:V:50:ASP:O	2.40	0.55
26:1:24:G:H2'	26:1:25:U:C6	2.42	0.55
26:1:275:A:H2'	26:1:276:C:H5'	1.88	0.55
26:1:1897:U:O2	26:1:1899:U:H5'	2.06	0.55
26:1:2495:A:N1	26:1:2508:G:O2'	2.32	0.55
2:B:205:VAL:O	2:B:210:ARG:HD3	2.06	0.55
3:C:4:VAL:HG22	26:1:1238:U:C1'	2.35	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:81:ASN:HB3	22:X:23:VAL:CG1	2.36	0.55
12:L:3:LYS:HZ1	12:L:98:ALA:HB2	1.71	0.55
18:R:32:HIS:O	18:R:34:GLN:HG3	2.07	0.55
25:a:37:ASN:ND2	27:2:27:A:H5''	2.21	0.55
2:B:150:LYS:HE3	2:B:153:GLN:NE2	2.22	0.55
8:H:21:LEU:CD1	8:H:42:LYS:HD3	2.37	0.55
26:1:268:A:H2'	26:1:269:G:O4'	2.07	0.55
26:1:393:G:O2'	26:1:394:U:H5'	2.06	0.55
26:1:1829:A:H2'	26:1:1830:A:C8	2.42	0.55
2:B:71:LYS:HG3	2:B:96:TYR:CE1	2.42	0.55
20:V:109:MET:HE2	26:1:1182:G:H21	1.72	0.55
26:1:1603:U:H2'	26:1:1604:C:C6	2.42	0.55
26:1:2770:U:H2'	26:1:2771:G:O4'	2.07	0.55
8:H:48:PHE:HA	8:H:51:VAL:HG12	1.88	0.54
16:P:38:LYS:HZ1	26:1:515:G:H22	1.54	0.54
26:1:748:U:O2'	26:1:749:G:H5'	2.07	0.54
26:1:2696:G:H3'	26:1:2697:G:H5''	1.89	0.54
27:2:39:G:H2'	27:2:39:G:N3	2.22	0.54
3:C:64:ARG:HD2	20:V:43:VAL:O	2.08	0.54
16:P:25:THR:HB	16:P:28:GLY:H	1.72	0.54
26:1:1916:A:H2'	26:1:1917:A:C8	2.42	0.54
23:Y:54:MET:HG3	23:Y:121:ALA:HB2	1.90	0.54
26:1:150:A:H61	26:1:179:A:H2	1.55	0.54
26:1:583:A:H2'	26:1:584:G:O4'	2.08	0.54
5:E:44:SER:O	5:E:48:GLU:HG3	2.07	0.54
15:O:29:ARG:HD3	15:O:46:ARG:HH21	1.71	0.54
26:1:1906:C:H2'	26:1:1907:U:O4'	2.08	0.54
6:F:35:LYS:HB2	6:F:53:VAL:HG13	1.90	0.54
19:S:169:ASN:ND2	26:1:366:G:H2'	2.21	0.54
20:V:8:ASN:OD1	26:1:583:A:H4'	2.07	0.54
24:Z:22:THR:O	24:Z:26:ILE:HG12	2.08	0.54
26:1:2326:G:H2'	26:1:2327:A:C8	2.43	0.54
5:E:29:ALA:O	5:E:33:ILE:HD12	2.08	0.54
9:I:77:PHE:CD1	9:I:87:VAL:HG22	2.42	0.54
23:Y:67:LYS:NZ	23:Y:105:GLU:OE2	2.40	0.54
26:1:1326:C:OP1	26:1:1691:G:N2	2.34	0.54
26:1:1710:G:C2'	26:1:1711:G:H5'	2.37	0.54
26:1:2270:U:O2'	26:1:2461:A:N1	2.34	0.54
26:1:2664:U:O2'	26:1:2665:G:H5'	2.08	0.54
1:A:41:ARG:O	1:A:42:ILE:HD13	2.06	0.54
13:M:21:LYS:O	13:M:24:GLU:HG3	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:28:PHE:CD1	26:1:2419:A:H4'	2.43	0.54
25:a:14:ARG:HD3	26:1:2322:C:OP2	2.08	0.54
26:1:12:U:H5''	26:1:13:A:OP2	2.07	0.54
26:1:801:A:H2'	26:1:802:G:O4'	2.08	0.54
26:1:2307:G:H2'	26:1:2308:C:H5'	1.88	0.54
27:2:79:C:H2'	27:2:80:G:C8	2.43	0.54
5:E:81:THR:HG22	5:E:99:ARG:HG2	1.89	0.54
12:L:13:THR:HG22	12:L:14:GLN:H	1.72	0.54
25:a:23:SER:HB2	25:a:47:ASP:OD2	2.07	0.54
26:1:1504:U:O4	26:1:1505:G:N1	2.41	0.54
26:1:1897:U:C2	26:1:1899:U:H5'	2.43	0.54
20:V:48:HIS:CD2	20:V:49:VAL:HG13	2.43	0.54
23:Y:32:PHE:CE2	23:Y:111:GLU:HA	2.42	0.54
24:Z:49:THR:OG1	26:1:2860:U:OP1	2.16	0.54
24:Z:51:GLY:HA2	24:Z:86:PHE:CE1	2.43	0.54
26:1:2326:G:H2'	26:1:2327:A:H8	1.73	0.54
26:1:2354:A:H2'	26:1:2355:A:C8	2.42	0.54
2:B:67:PHE:HD1	2:B:143:ASN:HD21	1.56	0.54
2:B:69:ARG:O	2:B:116:VAL:HG11	2.08	0.54
19:S:134:PRO:HB3	19:S:165:LEU:HB2	1.89	0.54
23:Y:48:GLU:O	23:Y:52:ILE:HG12	2.08	0.54
26:1:556:U:H4'	26:1:1273:G:H4'	1.89	0.54
26:1:1501:G:H22	26:1:2729:G:H22	1.56	0.54
26:1:1821:U:H2'	26:1:1822:C:C6	2.43	0.54
3:C:76:TYR:OH	3:C:93:LYS:HD2	2.08	0.53
26:1:165:C:H3'	26:1:166:A:H8	1.72	0.53
26:1:414:C:H2'	26:1:415:U:H5'	1.90	0.53
26:1:1669:C:H2'	26:1:1670:A:O4'	2.09	0.53
26:1:2262:G:H2'	26:1:2263:C:C6	2.44	0.53
26:1:2867:U:H2'	26:1:2868:G:O4'	2.07	0.53
12:L:123:LYS:HE3	26:1:2708:C:OP2	2.08	0.53
16:P:33:ALA:O	16:P:37:ARG:HG2	2.09	0.53
22:X:121:LEU:O	22:X:141:GLY:HA3	2.08	0.53
26:1:308:C:H2'	26:1:309:U:C6	2.43	0.53
26:1:390:A:H2'	26:1:391:A:C8	2.43	0.53
26:1:447:A:H2'	26:1:448:A:C8	2.43	0.53
26:1:920:A:H2'	26:1:921:C:O4'	2.08	0.53
26:1:1075:G:O2'	26:1:1076:A:H5'	2.08	0.53
26:1:1931:G:O2'	26:1:1932:C:H5'	2.08	0.53
27:2:54:U:O2'	27:2:55:A:OP2	2.23	0.53
2:B:91:ILE:HD12	2:B:103:TYR:CD1	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:78:ARG:NH2	26:1:606:G:OP2	2.40	0.53
26:1:75:G:H22	26:1:110:A:H2	1.56	0.53
26:1:506:A:H2'	26:1:507:C:H5'	1.89	0.53
26:1:2494:C:H2'	26:1:2495:A:O4'	2.07	0.53
26:1:2856:U:H2'	26:1:2857:A:C8	2.44	0.53
1:A:29:ARG:HD2	1:A:89:LYS:NZ	2.23	0.53
26:1:342:A:H2'	26:1:343:A:C8	2.44	0.53
26:1:1643:C:C2'	26:1:1644:C:H5'	2.39	0.53
26:1:2818:A:H2'	26:1:2819:C:C6	2.43	0.53
14:N:44:LYS:HA	14:N:44:LYS:HE2	1.90	0.53
21:W:43:VAL:HG21	21:W:52:VAL:HG12	1.90	0.53
26:1:404:U:H3'	26:1:404:U:OP1	2.08	0.53
26:1:421:C:H2'	26:1:422:G:H8	1.73	0.53
26:1:1446:U:H2'	26:1:1447:A:C8	2.43	0.53
26:1:2394:G:O2'	26:1:2395:C:H5'	2.08	0.53
1:A:29:ARG:HD2	1:A:89:LYS:CE	2.38	0.53
5:E:42:ALA:O	5:E:45:PRO:HD2	2.09	0.53
8:H:63:LEU:HG	8:H:64:GLY:H	1.73	0.53
24:Z:16:MET:HE3	24:Z:20:LEU:HD11	1.91	0.53
26:1:403:U:C3'	26:1:404:U:H5''	2.39	0.53
26:1:770:G:O2'	26:1:771:G:H5'	2.08	0.53
26:1:969:A:H3'	26:1:970:U:C4'	2.38	0.53
26:1:2702:A:H2'	26:1:2703:C:O4'	2.09	0.53
26:1:2831:G:O2'	26:1:2832:A:H5'	2.08	0.53
27:2:58:C:H2'	27:2:59:U:C5	2.44	0.53
7:G:86:VAL:HG21	7:G:100:GLU:OE2	2.08	0.53
9:I:77:PHE:CD2	26:1:902:A:H5'	2.44	0.53
26:1:872:U:O2'	26:1:2095:U:N3	2.42	0.53
26:1:1249:U:OP1	26:1:1249:U:H2'	2.08	0.53
26:1:2810:A:H2'	26:1:2811:U:C6	2.44	0.53
3:C:106:PHE:O	3:C:110:VAL:HG23	2.08	0.53
9:I:45:LEU:HD11	9:I:69:ALA:HB2	1.91	0.53
26:1:27:G:O2'	26:1:28:A:OP2	2.27	0.53
26:1:445:G:H2'	26:1:446:G:O4'	2.09	0.53
26:1:519:G:O2'	26:1:520:G:H5'	2.09	0.53
26:1:597:U:C2'	26:1:598:G:H5'	2.39	0.53
26:1:1326:C:H2'	26:1:1327:C:C6	2.44	0.53
26:1:2533:U:H3	26:1:2610:G:H1	1.56	0.53
2:B:266:SER:O	2:B:269:LEU:N	2.40	0.53
5:E:35:ILE:HG13	14:N:27:MET:HE1	1.90	0.53
10:J:36:VAL:O	10:J:46:LYS:HA	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:575:G:O2'	26:1:577:A:N7	2.41	0.53
26:1:597:U:H2'	26:1:598:G:O4'	2.08	0.53
26:1:1450:A:H3'	26:1:1451:U:C6	2.43	0.53
26:1:2826:U:H2'	26:1:2827:A:N9	2.24	0.53
23:Y:30:GLY:O	23:Y:134:ARG:NH2	2.42	0.53
25:a:92:ILE:HG21	25:a:119:PHE:HE1	1.74	0.53
26:1:30:G:H2'	26:1:31:C:C6	2.43	0.53
26:1:161:A:O2'	26:1:2235:A:H4'	2.08	0.53
26:1:1372:C:O2'	26:1:1373:U:H5'	2.08	0.53
26:1:1773:A:H2'	26:1:1774:A:O4'	2.09	0.53
26:1:2340:C:H2'	26:1:2341:A:H8	1.71	0.53
2:B:11:ASN:O	26:1:774:G:N2	2.41	0.52
23:Y:39:THR:OG1	23:Y:99:PRO:HD3	2.08	0.52
26:1:1462:G:H8	26:1:1626:A:H62	1.57	0.52
3:C:49:ASP:OD2	26:1:579:U:O2'	2.15	0.52
26:1:4:U:H2'	26:1:5:A:C8	2.44	0.52
26:1:544:U:H2'	26:1:545:G:O4'	2.08	0.52
26:1:1356:G:O2'	26:1:1357:G:H5'	2.08	0.52
26:1:1452:C:H3'	26:1:1453:G:H5''	1.91	0.52
26:1:1454:U:O4	26:1:1629:U:H2'	2.10	0.52
26:1:2377:C:H2'	26:1:2378:G:O4'	2.09	0.52
26:1:2619:G:H2'	26:1:2620:U:O4'	2.08	0.52
27:2:58:C:H2'	27:2:59:U:C6	2.44	0.52
3:C:105:ALA:O	3:C:108:GLN:HB2	2.08	0.52
5:E:81:THR:CG2	5:E:99:ARG:HG2	2.39	0.52
13:M:40:ASN:HB2	13:M:43:ILE:H	1.74	0.52
26:1:720:A:O2'	26:1:721:A:H5'	2.10	0.52
26:1:1459:A:N6	26:1:1630:A:O4'	2.43	0.52
26:1:1501:G:H22	26:1:2729:G:H1	1.56	0.52
26:1:2774:G:O6	26:1:2782:C:H5''	2.08	0.52
26:1:2883:U:H2'	26:1:2884:G:C8	2.44	0.52
1:A:29:ARG:HD3	1:A:87:GLU:OE2	2.10	0.52
2:B:159:GLY:HA2	2:B:198:LEU:HD23	1.91	0.52
6:F:37:GLN:HE21	26:1:144:C:H4'	1.74	0.52
17:Q:55:MET:O	17:Q:59:LYS:HB3	2.10	0.52
26:1:620:G:H2'	26:1:621:A:C8	2.45	0.52
26:1:908:A:H2'	26:1:909:G:C8	2.44	0.52
26:1:1593:G:H5''	26:1:1594:U:OP1	2.09	0.52
26:1:2240:U:H3'	26:1:2241:C:H5'	1.92	0.52
26:1:2794:C:C2'	26:1:2795:C:H5'	2.39	0.52
26:1:2818:A:H2'	26:1:2819:C:H6	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:4:ILE:HB	4:D:40:PHE:HB3	1.90	0.52
20:V:32:GLU:HG2	20:V:143:LEU:HD22	1.91	0.52
26:1:100:U:H3'	26:1:101:G:C5'	2.40	0.52
26:1:970:U:OP1	26:1:971:U:H5'	2.10	0.52
26:1:1880:A:H2'	26:1:1881:A:H8	1.72	0.52
27:2:23:U:H5'	27:2:24:C:H5	1.74	0.52
7:G:95:LYS:HA	7:G:95:LYS:HE2	1.90	0.52
26:1:389:A:H2'	26:1:390:A:H5'	1.91	0.52
26:1:448:A:C2'	26:1:449:U:H5'	2.40	0.52
26:1:712:U:H2'	26:1:713:A:O4'	2.10	0.52
26:1:749:G:H1'	26:1:772:A:N6	2.24	0.52
26:1:1753:U:O2'	26:1:1754:C:H5'	2.10	0.52
26:1:1914:C:C2'	26:1:1915:G:H5'	2.39	0.52
26:1:2098:A:H2'	26:1:2099:G:C8	2.44	0.52
26:1:2260:A:H2'	26:1:2261:G:C8	2.45	0.52
27:2:81:A:H2'	27:2:82:A:C8	2.45	0.52
20:V:54:TYR:HE1	20:V:122:LYS:HG2	1.74	0.52
26:1:194:A:H2'	26:1:195:C:C6	2.44	0.52
2:B:132:LEU:HG	2:B:188:CYS:O	2.10	0.52
10:J:36:VAL:HG13	10:J:38:ILE:HG23	1.91	0.52
12:L:159:ASP:HB2	26:1:2598:U:O3'	2.10	0.52
26:1:2313:A:H4'	26:1:2314:A:O4'	2.09	0.52
27:2:81:A:H2'	27:2:82:A:H8	1.75	0.52
2:B:243:ARG:HB3	2:B:244:PRO:HD2	1.92	0.52
11:K:10:THR:O	11:K:13:GLU:HB3	2.10	0.52
26:1:238:U:H2'	26:1:239:C:H6	1.75	0.52
26:1:1939:A:H62	26:1:1944:U:H3	1.56	0.52
5:E:59:GLU:HG3	5:E:66:THR:CG2	2.40	0.52
8:H:2:ALA:O	8:H:61:ILE:HG23	2.10	0.52
12:L:210:GLU:HG3	12:L:212:ARG:HH12	1.74	0.52
16:P:38:LYS:NZ	26:1:515:G:H22	2.09	0.52
22:X:109:ILE:HD11	22:X:125:ALA:HB2	1.92	0.52
24:Z:5:LYS:HD2	26:1:2029:G:OP1	2.09	0.52
26:1:487:U:O2'	26:1:488:G:H5'	2.10	0.52
26:1:1517:A:C2'	26:1:1518:G:H5'	2.40	0.52
26:1:2236:C:H5''	26:1:2237:U:H2'	1.92	0.52
4:D:80:LYS:O	4:D:82:SER:N	2.43	0.51
23:Y:32:PHE:HZ	23:Y:111:GLU:HG2	1.73	0.51
25:a:47:ASP:N	25:a:47:ASP:OD1	2.43	0.51
26:1:167:U:C2'	26:1:168:A:H5''	2.34	0.51
26:1:556:U:H2'	26:1:557:G:H5'	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1022:G:C2'	26:1:1023:A:H5'	2.40	0.51
26:1:1353:A:H2'	26:1:1354:G:C8	2.44	0.51
26:1:1886:A:H2'	26:1:1887:G:O4'	2.10	0.51
26:1:625:G:H2'	26:1:626:G:C8	2.45	0.51
26:1:1388:C:H2'	26:1:1389:U:C6	2.45	0.51
26:1:1865:C:O2	26:1:1865:C:H2'	2.09	0.51
12:L:127:PHE:HB2	26:1:2843:A:OP1	2.10	0.51
26:1:155:U:C2'	26:1:156:A:H5'	2.40	0.51
26:1:992:A:H2'	26:1:993:C:C6	2.45	0.51
26:1:1763:U:H2'	26:1:1765:A:OP2	2.11	0.51
26:1:1816:A:O2'	26:1:1817:C:H5'	2.10	0.51
26:1:1897:U:N3	26:1:1899:U:H5'	2.25	0.51
26:1:2391:C:H2'	26:1:2392:G:O4'	2.11	0.51
26:1:2801:C:H2'	26:1:2802:A:O4'	2.11	0.51
27:2:11:A:H2'	27:2:12:U:H5''	1.91	0.51
3:C:52:GLN:HG2	3:C:55:ARG:NH2	2.26	0.51
12:L:38:LYS:HD2	12:L:96:VAL:HB	1.91	0.51
21:W:68:GLY:HA3	21:W:77:ILE:O	2.10	0.51
22:X:110:LYS:HA	22:X:127:LYS:O	2.10	0.51
26:1:78:U:H2'	26:1:79:U:C6	2.45	0.51
26:1:593:U:O2'	26:1:594:G:OP1	2.23	0.51
26:1:1767:G:H2'	26:1:1768:C:C6	2.45	0.51
26:1:1918:G:H2'	26:1:1919:C:C6	2.45	0.51
26:1:2488:C:H2'	26:1:2489:U:C6	2.46	0.51
5:E:35:ILE:O	5:E:39:THR:HG23	2.10	0.51
7:G:80:ARG:HG3	26:1:379:C:OP1	2.10	0.51
22:X:122:THR:HG22	22:X:141:GLY:HA2	1.93	0.51
24:Z:109:ARG:HG2	24:Z:110:ARG:O	2.10	0.51
26:1:21:A:H2'	26:1:22:C:O4'	2.11	0.51
26:1:266:A:H2'	26:1:267:G:O4'	2.11	0.51
26:1:309:U:O2'	26:1:310:C:H2'	2.11	0.51
26:1:1308:C:H5''	26:1:1309:G:O5'	2.11	0.51
26:1:1848:A:H2'	26:1:1849:G:C8	2.45	0.51
26:1:2231:C:H2'	26:1:2232:A:C8	2.46	0.51
26:1:2489:U:H1'	26:1:2518:U:O4	2.11	0.51
26:1:2494:C:O2'	26:1:2495:A:H5'	2.10	0.51
1:A:8:GLU:O	1:A:12:LYS:HG2	2.11	0.51
12:L:60:LYS:HD3	12:L:68:TYR:CE2	2.46	0.51
17:Q:28:PHE:CE1	26:1:2419:A:H4'	2.46	0.51
21:W:91:LYS:HD2	21:W:110:ASN:HB2	1.93	0.51
25:a:74:THR:O	25:a:78:GLU:HG3	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:955:A:H2'	26:1:956:A:C8	2.46	0.51
26:1:2817:A:HO2'	26:1:2818:A:H5''	1.76	0.51
7:G:79:THR:HG21	7:G:96:LYS:HG3	1.93	0.51
17:Q:23:LYS:HE2	17:Q:47:ALA:HB3	1.93	0.51
21:W:7:ARG:HB3	21:W:18:GLU:OE2	2.10	0.51
26:1:1020:G:HO2'	26:1:1199:A:HO2'	1.57	0.51
26:1:1310:A:H3'	26:1:1311:A:C8	2.46	0.51
26:1:1598:U:H2'	26:1:1599:G:O4'	2.11	0.51
26:1:1804:U:O2'	26:1:1805:U:H5'	2.11	0.51
26:1:1978:U:H2'	26:1:1980:A:OP2	2.10	0.51
26:1:2679:U:H2'	26:1:2680:U:C6	2.46	0.51
27:2:19:G:H2'	27:2:20:A:H8	1.74	0.51
10:J:19:SER:HB3	26:1:2107:G:OP1	2.09	0.51
11:K:17:GLN:HG2	11:K:53:LEU:HB3	1.93	0.51
13:M:17:GLU:CD	13:M:21:LYS:HE2	2.36	0.51
22:X:90:GLU:HA	22:X:122:THR:OG1	2.10	0.51
26:1:128:C:O2'	26:1:129:C:H5'	2.11	0.51
26:1:175:C:H5''	26:1:176:A:OP1	2.11	0.51
26:1:687:G:N2	26:1:689:A:H3'	2.26	0.51
26:1:1820:G:H2'	26:1:1821:U:O4'	2.09	0.51
26:1:1996:A:H5'	26:1:1997:A:OP1	2.11	0.51
26:1:2404:A:H2'	26:1:2405:A:H8	1.75	0.51
27:2:75:U:H3	27:2:94:C:H5	1.58	0.51
19:S:133:ALA:HB1	19:S:134:PRO:HD2	1.93	0.51
25:a:107:ALA:HA	25:a:110:GLU:CG	2.38	0.51
26:1:133:A:H2'	26:1:134:U:H6	1.76	0.51
26:1:383:A:C2'	26:1:384:G:H5'	2.41	0.51
26:1:633:A:H2'	26:1:634:C:C6	2.46	0.51
27:2:15:C:H41	27:2:103:A:H2	1.58	0.51
27:2:52:G:O2'	27:2:53:U:H5'	2.11	0.51
27:2:107:U:H2'	27:2:108:U:C6	2.45	0.51
1:A:28:LEU:HD23	1:A:88:VAL:HG22	1.93	0.51
2:B:5:LYS:HD2	2:B:17:THR:CG2	2.41	0.51
2:B:66:ASP:OD2	2:B:102:ARG:HD3	2.11	0.51
22:X:80:ASP:HA	22:X:83:ASN:ND2	2.25	0.51
26:1:2329:U:H2'	26:1:2330:G:C8	2.46	0.51
26:1:2350:G:O2'	26:1:2351:U:H5'	2.11	0.51
27:2:76:A:H2'	27:2:77:G:H5'	1.92	0.51
1:A:25:GLY:HA3	1:A:94:VAL:HG11	1.93	0.50
2:B:145:GLU:HB2	2:B:188:CYS:HB3	1.93	0.50
12:L:87:PHE:CD1	12:L:208:LEU:HD22	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:167:GLN:HG2	12:L:169:MET:HE3	1.93	0.50
14:N:16:ARG:NH2	26:1:1302:G:OP1	2.34	0.50
19:S:39:LEU:HD11	19:S:99:TYR:O	2.11	0.50
22:X:93:PRO:O	22:X:97:VAL:HG23	2.11	0.50
23:Y:68:ILE:HD12	23:Y:68:ILE:O	2.10	0.50
26:1:1463:A:C2'	26:1:1464:U:H5''	2.41	0.50
26:1:1572:G:H22	26:1:1593:G:H1	1.57	0.50
26:1:1634:A:H2'	26:1:1635:A:O4'	2.10	0.50
26:1:1975:G:O2'	26:1:1976:G:H5'	2.11	0.50
2:B:75:ASN:HA	2:B:115:ILE:HG22	1.94	0.50
2:B:253:PRO:HG2	2:B:257:LYS:HE3	1.94	0.50
9:I:23:ASP:OD1	26:1:2290:C:N4	2.44	0.50
19:S:110:LEU:O	19:S:110:LEU:HD23	2.10	0.50
26:1:225:A:N6	26:1:235:G:H1'	2.26	0.50
26:1:1471:A:H4'	26:1:1472:C:O5'	2.09	0.50
26:1:2299:U:H5''	26:1:2300:A:OP1	2.11	0.50
26:1:2883:U:H2'	26:1:2884:G:H8	1.75	0.50
4:D:27:VAL:CG2	4:D:62:VAL:HG21	2.39	0.50
6:F:7:LEU:HD11	6:F:42:VAL:HG12	1.92	0.50
19:S:165:LEU:HB3	26:1:364:A:O4'	2.11	0.50
25:a:117:LEU:HG	25:a:118:GLU:H	1.76	0.50
26:1:63:U:H1'	26:1:64:A:C2	2.47	0.50
26:1:145:A:H2'	26:1:146:U:H6	1.77	0.50
26:1:206:U:OP2	26:1:207:A:O2'	2.16	0.50
26:1:858:U:H2'	26:1:859:C:H6	1.75	0.50
26:1:1491:C:H2'	26:1:1492:G:H5'	1.92	0.50
26:1:2317:G:C2'	26:1:2318:U:H5'	2.41	0.50
26:1:2341:A:O2'	26:1:2342:U:H5'	2.12	0.50
26:1:2404:A:H2'	26:1:2405:A:C8	2.46	0.50
2:B:139:THR:O	2:B:163:GLN:HA	2.12	0.50
3:C:81:ASN:ND2	26:1:1195:A:H4'	2.27	0.50
6:F:12:ILE:O	6:F:12:ILE:HG13	2.12	0.50
19:S:88:ILE:HG22	19:S:90:PHE:O	2.12	0.50
22:X:87:ASP:OD1	22:X:120:LYS:N	2.38	0.50
23:Y:39:THR:HA	23:Y:97:VAL:O	2.11	0.50
26:1:155:U:H2'	26:1:156:A:H5'	1.93	0.50
26:1:747:U:O2'	26:1:748:U:H5'	2.12	0.50
8:H:70:ILE:HG13	8:H:72:VAL:HG13	1.94	0.50
22:X:74:TYR:CD1	22:X:107:SER:HB3	2.47	0.50
24:Z:25:ILE:CD1	24:Z:85:LEU:HD12	2.42	0.50
26:1:525:A:H4'	26:1:526:A:OP1	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:900:G:H2'	26:1:901:G:O4'	2.11	0.50
26:1:1567:A:OP2	26:1:1568:U:O2'	2.19	0.50
2:B:132:LEU:HD23	2:B:135:ILE:HD12	1.93	0.50
8:H:65:VAL:HG21	8:H:70:ILE:CD1	2.42	0.50
23:Y:42:ILE:HD11	23:Y:68:ILE:HD13	1.92	0.50
26:1:44:A:O2'	26:1:45:G:OP1	2.24	0.50
26:1:884:U:O2'	26:1:885:C:H5'	2.11	0.50
26:1:1045:A:H2'	26:1:1046:G:O4'	2.11	0.50
26:1:1207:G:O2'	26:1:1208:A:H5'	2.12	0.50
26:1:1210:U:H5'	26:1:1211:G:OP2	2.12	0.50
26:1:1319:U:H2'	26:1:1320:G:O4'	2.12	0.50
26:1:1624:C:H2'	26:1:1625:U:C1'	2.42	0.50
26:1:1700:C:H2'	26:1:1701:U:C6	2.47	0.50
26:1:2092:C:H2'	26:1:2093:C:C6	2.46	0.50
27:2:64:A:H4'	27:2:65:G:OP1	2.10	0.50
8:H:61:ILE:O	8:H:72:VAL:N	2.40	0.50
13:M:40:ASN:H	13:M:43:ILE:HG22	1.77	0.50
14:N:3:VAL:HG12	26:1:2042:A:N3	2.26	0.50
19:S:139:PHE:CE2	19:S:143:LEU:HD11	2.47	0.50
26:1:741:G:O2'	26:1:742:U:H5'	2.12	0.50
26:1:1368:C:O2'	26:1:1369:G:H5'	2.11	0.50
26:1:1865:C:H4'	26:1:1866:G:H5''	1.92	0.50
7:G:69:GLN:CB	7:G:78:PRO:HB2	2.42	0.50
23:Y:66:ILE:HG12	23:Y:104:PHE:HE1	1.75	0.50
26:1:99:U:OP1	26:1:100:U:H2'	2.12	0.50
26:1:154:A:H2'	26:1:155:U:O4'	2.11	0.50
26:1:446:G:O2'	26:1:447:A:H5''	2.12	0.50
26:1:969:A:H3'	26:1:970:U:O4'	2.12	0.50
26:1:1780:G:H2'	26:1:1782:A:OP2	2.12	0.50
3:C:91:ASN:HB2	4:D:11:GLN:OE1	2.11	0.50
19:S:67:GLN:HE21	26:1:720:A:H4'	1.77	0.50
20:V:14:ARG:NH1	20:V:50:ASP:OD1	2.45	0.50
24:Z:103:ILE:HG23	24:Z:117:VAL:HB	1.93	0.50
26:1:158:G:H2'	26:1:159:U:O4'	2.12	0.50
26:1:1431:U:H2'	26:1:1432:A:H5'	1.92	0.50
26:1:1501:G:N2	26:1:2729:G:H22	2.09	0.50
26:1:1644:C:O2'	26:1:1645:G:H5'	2.11	0.50
26:1:1724:U:N3	26:1:1791:G:OP2	2.43	0.50
5:E:33:ILE:O	5:E:37:LYS:HG3	2.12	0.49
19:S:157:GLU:HA	19:S:198:ALA:HB2	1.94	0.49
26:1:877:G:H2'	26:1:878:C:C6	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1891:U:OP1	26:1:2437:G:O2'	2.29	0.49
26:1:2222:U:C2'	26:1:2223:C:H5'	2.41	0.49
3:C:37:GLN:HE21	26:1:1290:G:H1	1.59	0.49
21:W:24:VAL:HG13	21:W:33:ALA:HB2	1.94	0.49
23:Y:83:MET:HE1	26:1:1000:G:H1'	1.95	0.49
26:1:143:U:H2'	26:1:144:C:O4'	2.13	0.49
26:1:346:A:H2'	26:1:347:U:C6	2.47	0.49
26:1:523:A:H2'	26:1:524:A:C8	2.47	0.49
26:1:1727:C:H2'	26:1:1728:C:C6	2.46	0.49
26:1:2082:C:H5'	26:1:2083:G:O5'	2.12	0.49
26:1:2310:C:C6	26:1:2416:G:H2'	2.47	0.49
26:1:2400:U:H2'	26:1:2401:C:C6	2.47	0.49
2:B:176:LEU:HD12	2:B:180:GLU:CG	2.42	0.49
9:I:73:GLY:CA	9:I:90:TYR:O	2.52	0.49
12:L:30:ALA:HB3	12:L:107:VAL:CG1	2.43	0.49
23:Y:118:LEU:HD12	23:Y:131:PHE:CE1	2.47	0.49
26:1:1211:G:H5''	26:1:1212:U:OP2	2.13	0.49
26:1:1241:A:H2'	26:1:1242:A:C8	2.46	0.49
26:1:1522:G:O2'	26:1:1523:G:H5'	2.12	0.49
26:1:2420:U:H2'	26:1:2421:C:O4'	2.12	0.49
26:1:2580:G:C8	26:1:2610:G:H1'	2.47	0.49
26:1:2690:G:H2'	26:1:2691:G:C8	2.48	0.49
26:1:267:G:O2'	26:1:268:A:H5''	2.12	0.49
26:1:1734:A:H2'	26:1:1735:C:O4'	2.12	0.49
26:1:2007:G:O2'	26:1:2009:U:OP2	2.26	0.49
26:1:2484:U:O2'	26:1:2485:U:H5'	2.13	0.49
2:B:65:ILE:HD11	2:B:91:ILE:CG2	2.43	0.49
2:B:150:LYS:HD3	26:1:2231:C:H4'	1.94	0.49
10:J:43:LYS:HD2	10:J:44:PRO:HD2	1.94	0.49
11:K:9:LEU:O	11:K:13:GLU:HB2	2.12	0.49
12:L:142:SER:OG	26:1:2020:U:H4'	2.11	0.49
14:N:9:SER:CB	26:1:2047:A:H5'	2.40	0.49
26:1:61:A:H2'	26:1:62:C:C6	2.48	0.49
26:1:799:U:O2'	26:1:800:G:H5'	2.12	0.49
26:1:1575:A:O2'	26:1:1576:A:H5'	2.12	0.49
26:1:2418:G:C6	26:1:2454:C:H1'	2.47	0.49
26:1:2444:C:O2'	26:1:2445:A:H5'	2.12	0.49
26:1:2611:U:H2'	26:1:2612:U:H5''	1.93	0.49
26:1:399:U:H2'	26:1:400:C:C6	2.47	0.49
26:1:504:G:O2'	26:1:515:G:O6	2.25	0.49
26:1:1065:A:H8	26:1:1066:G:H5''	1.76	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1217:U:H1'	26:1:1218:G:C2	2.47	0.49
26:1:1481:A:O4'	26:1:1561:G:N2	2.46	0.49
26:1:1710:G:O2'	26:1:1711:G:H5'	2.13	0.49
12:L:178:VAL:HG23	12:L:202:PRO:CG	2.43	0.49
19:S:139:PHE:HE2	19:S:173:VAL:HG11	1.77	0.49
26:1:45:G:H2'	26:1:218:G:C8	2.48	0.49
26:1:793:G:N2	26:1:796:A:OP2	2.46	0.49
26:1:1215:U:H5'	26:1:1216:U:C2	2.47	0.49
26:1:1326:C:H2'	26:1:1327:C:H6	1.77	0.49
26:1:2117:A:O2'	26:1:2118:U:H5'	2.12	0.49
26:1:2322:C:O2'	26:1:2323:U:H5'	2.13	0.49
1:A:77:PRO:HB2	1:A:80:THR:CG2	2.42	0.49
2:B:263:LYS:NZ	2:B:266:SER:HB3	2.28	0.49
7:G:69:GLN:HB2	7:G:78:PRO:HB2	1.94	0.49
20:V:109:MET:HE2	26:1:1182:G:N2	2.27	0.49
26:1:248:G:O2'	26:1:249:C:H5'	2.12	0.49
26:1:785:C:C2'	26:1:786:U:H5'	2.43	0.49
4:D:1:MET:HA	4:D:42:GLY:O	2.13	0.49
18:R:30:PRO:HG2	26:1:2555:U:OP1	2.13	0.49
22:X:124:LYS:CE	22:X:144:GLU:HB2	2.41	0.49
26:1:274:A:O2'	26:1:275:A:H5'	2.13	0.49
26:1:862:C:O2'	26:1:884:U:OP1	2.28	0.49
26:1:1352:C:H2'	26:1:1353:A:C8	2.47	0.49
26:1:2356:A:H2'	26:1:2357:G:C8	2.47	0.49
20:V:19:ILE:HD13	20:V:142:GLU:HA	1.94	0.49
25:a:14:ARG:NH1	26:1:2322:C:OP1	2.46	0.49
25:a:22:LEU:HD23	25:a:23:SER:OG	2.13	0.49
1:A:31:HIS:ND1	1:A:44:VAL:HG12	2.28	0.48
4:D:11:GLN:HG3	4:D:39:LEU:HD12	1.93	0.48
8:H:21:LEU:HD11	8:H:42:LYS:HD3	1.95	0.48
10:J:17:ARG:HB2	10:J:27:ARG:HG2	1.95	0.48
21:W:5:GLU:HG3	26:1:1713:A:H8	1.78	0.48
24:Z:25:ILE:HD13	24:Z:85:LEU:HD12	1.95	0.48
24:Z:26:ILE:CD1	24:Z:71:ILE:HD11	2.42	0.48
26:1:1043:U:O2'	26:1:1044:A:H5'	2.13	0.48
26:1:2267:C:O2'	26:1:2268:A:H5'	2.12	0.48
7:G:41:MET:HE1	26:1:526:A:O5'	2.13	0.48
26:1:173:A:H2'	26:1:174:U:H6	1.75	0.48
26:1:391:A:H2'	26:1:392:U:C6	2.49	0.48
26:1:1219:G:O2'	26:1:1220:A:O5'	2.30	0.48
26:1:1407:C:H2'	26:1:1408:G:O4'	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1491:C:O2	26:1:1574:G:N2	2.25	0.48
26:1:2051:C:H2'	26:1:2052:C:C6	2.48	0.48
26:1:326:A:C2'	26:1:327:G:H5''	2.40	0.48
26:1:702:U:H2'	26:1:703:A:C8	2.49	0.48
26:1:1013:U:H2'	26:1:1014:U:C6	2.49	0.48
26:1:1298:G:H2'	26:1:1299:U:O4'	2.13	0.48
26:1:2860:U:H2'	26:1:2861:U:C6	2.48	0.48
3:C:80:MET:HE1	3:C:92:ARG:HB3	1.95	0.48
11:K:31:GLN:HB3	11:K:37:LEU:HB2	1.95	0.48
17:Q:18:ALA:HB2	26:1:673:G:H5''	1.95	0.48
22:X:124:LYS:HE2	22:X:144:GLU:OE1	2.13	0.48
25:a:83:LYS:O	25:a:87:LYS:HG2	2.13	0.48
26:1:64:A:H5'	26:1:64:A:N3	2.28	0.48
26:1:226:A:O2'	26:1:466:C:O2	2.31	0.48
26:1:509:G:N2	26:1:512:A:OP2	2.42	0.48
26:1:992:A:H2'	26:1:993:C:H6	1.78	0.48
26:1:1365:G:H2'	26:1:1367:C:C5	2.48	0.48
26:1:1918:G:H2'	26:1:1919:C:H6	1.77	0.48
26:1:2563:G:C2'	26:1:2564:U:H5'	2.42	0.48
26:1:2618:C:H2'	26:1:2619:G:C8	2.48	0.48
19:S:110:LEU:HD22	19:S:206:LEU:CD2	2.39	0.48
22:X:78:ASN:CG	22:X:114:ASN:HB3	2.39	0.48
26:1:61:A:H2'	26:1:62:C:H6	1.78	0.48
26:1:168:A:C5	26:1:169:G:H1'	2.49	0.48
26:1:1914:C:H2'	26:1:1915:G:H5'	1.95	0.48
26:1:2715:G:N1	26:1:2747:U:OP2	2.35	0.48
27:2:82:A:H61	27:2:87:C:H42	1.61	0.48
2:B:45:ASN:OD1	2:B:46:GLN:HG3	2.13	0.48
2:B:145:GLU:HG2	2:B:151:GLY:C	2.39	0.48
12:L:186:VAL:HG12	12:L:187:GLN:HG3	1.94	0.48
19:S:198:ALA:O	19:S:201:LYS:HB2	2.13	0.48
22:X:21:ARG:HA	26:1:856:U:H2'	1.95	0.48
26:1:122:G:H2'	26:1:123:G:O4'	2.13	0.48
26:1:400:C:H3'	26:1:401:U:H5''	1.95	0.48
26:1:408:U:H2'	26:1:409:G:H5'	1.96	0.48
26:1:948:U:H2'	26:1:949:C:C6	2.49	0.48
26:1:2293:A:H4'	26:1:2294:A:O5'	2.13	0.48
26:1:2329:U:H2'	26:1:2330:G:O4'	2.13	0.48
2:B:65:ILE:HD12	2:B:87:ARG:CZ	2.44	0.48
3:C:91:ASN:HB2	4:D:11:GLN:CG	2.43	0.48
10:J:12:ALA:HA	10:J:29:TRP:O	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:P:5:THR:HG22	26:1:732:C:H1'	1.95	0.48
18:R:18:LYS:NZ	18:R:21:GLY:O	2.45	0.48
19:S:34:PHE:CE2	22:X:8:PRO:HB3	2.49	0.48
20:V:24:GLN:NE2	20:V:143:LEU:HD12	2.28	0.48
25:a:69:LYS:HB2	27:2:48:A:OP2	2.14	0.48
26:1:147:G:H2'	26:1:148:U:O4'	2.14	0.48
26:1:164:A:H5'	26:1:165:C:OP2	2.13	0.48
26:1:170:C:O2'	26:1:171:A:H5'	2.14	0.48
26:1:1078:G:H2'	26:1:1079:U:C6	2.49	0.48
26:1:1080:G:O2'	26:1:1081:G:H5'	2.14	0.48
26:1:1516:C:H2'	26:1:1517:A:O4'	2.14	0.48
26:1:1712:A:H4'	26:1:1713:A:O5'	2.13	0.48
27:2:56:A:O2'	27:2:57:G:H5'	2.14	0.48
3:C:21:ALA:HB1	3:C:24:TYR:CD2	2.48	0.48
7:G:73:PRO:HG2	7:G:101:ILE:HG22	1.95	0.48
20:V:3:GLN:O	20:V:3:GLN:HG2	2.14	0.48
21:W:114:ILE:O	21:W:118:ALA:N	2.46	0.48
25:a:30:ARG:HH12	27:2:7:G:P	2.37	0.48
26:1:18:C:O2'	26:1:597:U:OP1	2.29	0.48
26:1:273:A:O2'	26:1:274:A:H5'	2.14	0.48
26:1:364:A:O2'	26:1:383:A:O2'	2.29	0.48
26:1:770:G:H2'	26:1:771:G:O4'	2.13	0.48
26:1:1707:U:O2'	26:1:2713:G:H4'	2.14	0.48
26:1:1900:G:H2'	26:1:1901:C:H6	1.79	0.48
26:1:1988:C:H2'	26:1:1989:C:O4'	2.14	0.48
26:1:2810:A:H2'	26:1:2811:U:H6	1.78	0.48
7:G:27:LEU:HD12	7:G:32:ARG:CB	2.42	0.48
12:L:142:SER:O	12:L:144:GLY:N	2.45	0.48
12:L:144:GLY:O	26:1:2607:U:H5''	2.14	0.48
24:Z:40:VAL:O	24:Z:44:VAL:HG12	2.13	0.48
26:1:686:U:H2'	26:1:687:G:O4'	2.13	0.48
26:1:1085:U:C4	26:1:1158:G:O6	2.67	0.48
2:B:8:PRO:HB3	2:B:14:ARG:HG3	1.96	0.48
8:H:51:VAL:O	8:H:55:VAL:HG22	2.14	0.48
9:I:53:ILE:O	9:I:67:LEU:HD11	2.14	0.48
17:Q:57:ARG:HG3	26:1:879:U:H5'	1.95	0.48
19:S:26:ILE:HG13	19:S:111:ARG:HH12	1.78	0.48
21:W:111:PHE:HB3	21:W:114:ILE:HD12	1.95	0.48
24:Z:7:GLY:C	24:Z:8:ARG:HD2	2.38	0.48
26:1:902:A:O2'	26:1:903:G:H5'	2.13	0.48
26:1:1053:A:N3	26:1:1197:C:O2'	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1766:C:H2'	26:1:1767:G:C5'	2.43	0.48
26:1:1864:C:H2'	26:1:1926:A:N6	2.29	0.48
27:2:23:U:O2	27:2:27:A:N6	2.46	0.48
27:2:29:C:O2	27:2:29:C:H2'	2.13	0.48
27:2:96:A:H2'	27:2:97:G:H5'	1.96	0.48
5:E:69:LEU:HA	5:E:108:SER:O	2.13	0.47
12:L:22:LEU:HD13	21:W:74:GLY:HA3	1.94	0.47
17:Q:5:LYS:NZ	26:1:256:C:OP2	2.32	0.47
21:W:35:ILE:HG21	21:W:103:ALA:HB3	1.95	0.47
23:Y:109:VAL:CG1	23:Y:113:VAL:HB	2.44	0.47
25:a:15:HIS:NE2	25:a:95:ASP:OD2	2.41	0.47
26:1:615:A:H5''	26:1:616:G:OP2	2.14	0.47
26:1:917:U:O2'	26:1:918:G:H5'	2.14	0.47
26:1:1353:A:H2'	26:1:1354:G:H8	1.77	0.47
26:1:1489:A:N6	26:1:1509:G:N2	2.25	0.47
26:1:2293:A:H4'	26:1:2294:A:N3	2.29	0.47
27:2:79:C:H42	27:2:90:U:H3	1.61	0.47
1:A:51:LYS:HE2	1:A:53:ARG:HB2	1.95	0.47
5:E:2:GLU:CD	5:E:72:LYS:HE2	2.39	0.47
5:E:4:LYS:HB3	5:E:106:VAL:HG22	1.95	0.47
12:L:99:TYR:CB	12:L:101:VAL:HG22	2.44	0.47
13:M:12:VAL:HA	13:M:15:ARG:HG3	1.97	0.47
16:P:16:VAL:HG13	16:P:17:HIS:ND1	2.29	0.47
17:Q:23:LYS:HE2	17:Q:47:ALA:CB	2.44	0.47
20:V:2:ARG:NH2	20:V:3:GLN:OE1	2.47	0.47
26:1:234:C:H2'	26:1:235:G:O4'	2.15	0.47
26:1:364:A:HO2'	26:1:383:A:HO2'	1.61	0.47
26:1:390:A:H2'	26:1:391:A:H8	1.79	0.47
26:1:1961:C:C2'	26:1:1962:G:H5'	2.45	0.47
27:2:50:A:H3'	27:2:50:A:N3	2.30	0.47
26:1:102:A:H5''	26:1:103:U:H5	1.79	0.47
26:1:859:C:O2'	26:1:860:U:H5'	2.14	0.47
26:1:1845:U:O2'	26:1:1846:A:OP2	2.23	0.47
26:1:2322:C:H2'	26:1:2323:U:O4'	2.14	0.47
2:B:96:TYR:HE2	2:B:102:ARG:HD2	1.78	0.47
4:D:16:GLU:HG2	4:D:16:GLU:O	2.13	0.47
25:a:17:ARG:HG2	26:1:2361:U:O3'	2.14	0.47
26:1:54:G:H2'	26:1:55:G:O4'	2.14	0.47
26:1:750:A:H2'	26:1:751:A:C8	2.50	0.47
26:1:1170:A:H4'	26:1:1171:A:O5'	2.14	0.47
26:1:1343:U:O2'	26:1:1344:A:H5'	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1349:U:H4'	26:1:1350:U:O5'	2.14	0.47
26:1:1884:G:H2'	26:1:1885:G:O4'	2.14	0.47
26:1:2397:G:O2'	26:1:2398:G:H5'	2.15	0.47
27:2:97:G:H2'	27:2:98:A:C8	2.50	0.47
2:B:43:ARG:HA	2:B:48:LYS:O	2.14	0.47
12:L:98:ALA:HB1	12:L:103:GLN:HE22	1.80	0.47
12:L:215:ILE:HD12	12:L:216:LYS:HG3	1.95	0.47
18:R:17:ILE:HG13	18:R:18:LYS:H	1.80	0.47
26:1:159:U:H2'	26:1:160:G:H5'	1.96	0.47
26:1:408:U:C2'	26:1:409:G:H5'	2.45	0.47
26:1:1878:U:H2'	26:1:1879:U:O4'	2.14	0.47
26:1:2016:A:H2'	26:1:2017:C:O4'	2.15	0.47
26:1:2561:C:H2'	26:1:2562:G:O4'	2.15	0.47
26:1:2873:C:H2'	26:1:2874:A:C8	2.50	0.47
27:2:76:A:C2'	27:2:77:G:H5'	2.44	0.47
1:A:33:ARG:O	1:A:34:ILE:HD13	2.15	0.47
20:V:48:HIS:O	26:1:600:U:O2'	2.30	0.47
22:X:38:GLN:OE1	26:1:876:G:O2'	2.30	0.47
26:1:114:C:H2'	26:1:115:C:C6	2.49	0.47
26:1:464:U:H2'	26:1:465:C:C6	2.50	0.47
26:1:685:C:H2'	26:1:686:U:C6	2.50	0.47
2:B:167:LYS:CG	2:B:172:VAL:HG12	2.44	0.47
12:L:190:THR:HG22	12:L:191:GLU:H	1.77	0.47
12:L:190:THR:O	12:L:191:GLU:HB2	2.15	0.47
19:S:78:ILE:HG13	19:S:79:ARG:HG2	1.95	0.47
26:1:296:G:O2'	26:1:297:G:H5'	2.15	0.47
26:1:590:U:OP1	26:1:1257:G:O2'	2.23	0.47
26:1:651:A:H2'	26:1:652:A:H8	1.78	0.47
26:1:769:U:O2'	26:1:770:G:H5'	2.13	0.47
26:1:889:U:H2'	26:1:890:G:O4'	2.14	0.47
26:1:1325:U:O2'	26:1:1326:C:OP1	2.32	0.47
26:1:1483:A:H2'	26:1:1484:G:O4'	2.14	0.47
26:1:1867:G:H2'	26:1:1868:U:C6	2.50	0.47
26:1:1959:A:H61	26:1:1995:G:H1'	1.79	0.47
26:1:2092:C:H2'	26:1:2093:C:H6	1.80	0.47
26:1:2124:U:H2'	26:1:2125:U:O4'	2.14	0.47
26:1:2325:A:N6	26:1:2345:A:H1'	2.29	0.47
26:1:2540:A:H2'	26:1:2541:U:C6	2.50	0.47
7:G:26:THR:HG23	7:G:33:VAL:HG12	1.97	0.47
7:G:40:ILE:CG2	7:G:58:GLU:HB3	2.45	0.47
8:H:16:SER:O	8:H:20:GLN:HG2	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:44:ARG:CD	13:M:47:ILE:HD11	2.42	0.47
19:S:64:PRO:HB2	19:S:65:TRP:CE3	2.49	0.47
19:S:74:ARG:NH2	26:1:2472:G:OP1	2.42	0.47
19:S:183:VAL:O	19:S:187:THR:HG22	2.15	0.47
26:1:298:U:H4'	26:1:299:U:H5'	1.97	0.47
26:1:1238:U:H2'	26:1:1239:C:C6	2.50	0.47
26:1:1497:A:H3'	26:1:1497:A:N3	2.30	0.47
26:1:1611:C:H2'	26:1:1612:C:C6	2.50	0.47
26:1:2360:A:C5'	26:1:2362:A:H1'	2.44	0.47
1:A:31:HIS:HB3	1:A:42:ILE:CG2	2.45	0.47
3:C:78:ARG:NH1	26:1:1195:A:H1'	2.24	0.47
9:I:75:VAL:HG12	9:I:89:VAL:HG22	1.96	0.47
26:1:43:A:H62	26:1:482:U:H3	1.63	0.47
26:1:341:G:H5''	26:1:342:A:OP1	2.15	0.47
26:1:417:A:H4'	26:1:418:G:OP1	2.14	0.47
26:1:625:G:H2'	26:1:626:G:H8	1.78	0.47
26:1:872:U:H5'	26:1:873:U:C5	2.49	0.47
26:1:908:A:O2'	26:1:909:G:H5'	2.15	0.47
26:1:1437:U:O2'	26:1:1438:G:H5'	2.15	0.47
26:1:1733:A:H2'	26:1:1734:A:C8	2.49	0.47
26:1:2505:A:H1'	26:1:2555:U:O2'	2.14	0.47
26:1:2826:U:H2'	26:1:2827:A:C8	2.49	0.47
1:A:30:VAL:HG12	1:A:32:VAL:HG13	1.97	0.47
9:I:53:ILE:CG2	9:I:87:VAL:HG23	2.45	0.47
13:M:17:GLU:OE2	13:M:21:LYS:HE2	2.15	0.47
20:V:69:LYS:HE2	26:1:1066:G:N7	2.30	0.47
25:a:31:LEU:HB2	25:a:92:ILE:HG12	1.97	0.47
26:1:64:A:H2'	26:1:65:A:O4'	2.15	0.47
26:1:422:G:H2'	26:1:423:A:C8	2.50	0.47
26:1:455:A:O2'	26:1:456:G:H5'	2.15	0.47
26:1:1727:C:H2'	26:1:1728:C:H6	1.78	0.47
26:1:1806:U:H5	26:1:1811:A:N7	2.12	0.47
26:1:2356:A:H2'	26:1:2357:G:H8	1.80	0.47
27:2:15:C:H2'	27:2:16:A:O4'	2.15	0.47
27:2:90:U:H2'	27:2:91:C:C6	2.50	0.47
3:C:53:ARG:HD3	26:1:580:C:O2'	2.15	0.46
5:E:42:ALA:CB	26:1:2037:G:H5''	2.44	0.46
5:E:88:ARG:HD3	26:1:793:G:OP2	2.15	0.46
6:F:17:SER:HA	6:F:20:MET:CG	2.45	0.46
7:G:71:LEU:HA	7:G:78:PRO:HA	1.97	0.46
26:1:481:C:C2'	26:1:482:U:H5'	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:578:G:H2'	26:1:579:U:C6	2.50	0.46
26:1:1334:C:OP1	26:1:2737:C:H4'	2.15	0.46
26:1:2626:G:O2'	26:1:2627:A:H5'	2.15	0.46
26:1:2812:U:H2'	26:1:2813:U:C6	2.51	0.46
26:1:163:U:H6	26:1:165:C:H41	1.63	0.46
26:1:268:A:H2'	26:1:269:G:C4'	2.45	0.46
26:1:899:U:O2'	26:1:900:G:H5'	2.14	0.46
26:1:1081:G:N2	26:1:1163:U:H1'	2.30	0.46
26:1:1617:A:H2'	26:1:1618:A:C8	2.50	0.46
26:1:2262:G:O2'	26:1:2263:C:H5'	2.15	0.46
26:1:2622:G:N2	26:1:2625:A:OP2	2.39	0.46
26:1:2748:A:H1'	26:1:2893:A:O2'	2.15	0.46
10:J:23:ASN:ND2	26:1:203:U:OP1	2.46	0.46
19:S:125:VAL:CG2	19:S:194:ILE:HD11	2.30	0.46
26:1:349:U:C2'	26:1:350:G:H5'	2.45	0.46
26:1:536:A:H2'	26:1:537:A:C8	2.50	0.46
26:1:551:G:H4'	26:1:552:A:H5''	1.97	0.46
26:1:596:G:H2'	26:1:597:U:C6	2.51	0.46
26:1:907:G:H2'	26:1:908:A:O4'	2.15	0.46
26:1:1350:U:O2'	26:1:1351:C:OP1	2.20	0.46
26:1:1517:A:H2'	26:1:1518:G:H5'	1.97	0.46
26:1:2308:C:C2'	26:1:2309:G:H5'	2.45	0.46
3:C:51:ARG:NH1	26:1:1200:A:O4'	2.48	0.46
17:Q:58:VAL:CG1	17:Q:61:LEU:HD12	2.43	0.46
25:a:31:LEU:HD13	25:a:44:ILE:CG2	2.41	0.46
26:1:486:G:O2'	26:1:487:U:H5'	2.15	0.46
26:1:646:A:H4'	26:1:647:G:OP1	2.16	0.46
26:1:1459:A:H61	26:1:1630:A:C4'	2.29	0.46
26:1:2482:G:H2'	26:1:2483:C:C6	2.50	0.46
26:1:2696:G:H5''	26:1:2697:G:OP2	2.16	0.46
26:1:2852:U:H1'	26:1:2854:A:C4	2.50	0.46
27:2:45:C:H2'	27:2:46:A:C5'	2.44	0.46
1:A:15:LEU:CD2	1:A:57:VAL:HG22	2.46	0.46
24:Z:28:GLU:OE2	24:Z:84:LYS:NZ	2.39	0.46
26:1:86:C:O2'	26:1:87:U:H5'	2.16	0.46
26:1:422:G:H2'	26:1:423:A:H8	1.81	0.46
26:1:1640:U:O2'	26:1:1641:G:H5'	2.15	0.46
26:1:2091:C:H2'	26:1:2092:C:C6	2.50	0.46
6:F:10:PRO:HD2	11:K:33:ALA:CB	2.46	0.46
6:F:26:THR:HG23	6:F:79:ILE:HG12	1.97	0.46
19:S:149:PRO:CG	19:S:191:SER:HB2	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:Y:7:VAL:HG11	23:Y:93:TRP:CH2	2.50	0.46
26:1:663:U:H2'	26:1:664:G:O4'	2.16	0.46
26:1:1003:A:H2'	26:1:1004:A:C8	2.50	0.46
26:1:1758:A:H3'	26:1:1758:A:N3	2.30	0.46
26:1:2836:C:O2	26:1:2903:A:O2'	2.28	0.46
7:G:32:ARG:HH22	26:1:524:A:H5'	1.80	0.46
12:L:41:VAL:HG12	12:L:45:GLY:HA2	1.97	0.46
20:V:66:THR:HG21	26:1:1185:U:P	2.55	0.46
24:Z:61:ASN:O	24:Z:64:LYS:HG2	2.16	0.46
25:a:7:LYS:HE3	27:2:45:C:OP1	2.15	0.46
26:1:142:G:C2'	26:1:143:U:H5'	2.42	0.46
26:1:1315:C:H2'	26:1:1316:G:C8	2.50	0.46
26:1:1869:G:H2'	26:1:1870:C:C6	2.51	0.46
26:1:2396:A:O2'	26:1:2397:G:H5'	2.15	0.46
27:2:103:A:H3'	27:2:104:A:H5'	1.96	0.46
27:2:104:A:H2'	27:2:105:C:H6	1.78	0.46
1:A:26:ASP:O	1:A:49:VAL:HG23	2.15	0.46
2:B:19:LEU:HD11	2:B:199:GLN:HB2	1.97	0.46
7:G:55:GLY:N	26:1:529:A:O2'	2.40	0.46
14:N:38:LEU:O	14:N:41:ARG:HB2	2.15	0.46
21:W:63:VAL:CG1	21:W:102:VAL:HG12	2.44	0.46
2:B:2:ALA:HA	2:B:199:GLN:HG3	1.97	0.46
11:K:17:GLN:NE2	11:K:53:LEU:O	2.49	0.46
13:M:17:GLU:OE1	13:M:21:LYS:HE2	2.16	0.46
15:O:34:LYS:NZ	26:1:2374:C:OP1	2.30	0.46
21:W:28:SER:OG	26:1:2590:U:O2'	2.12	0.46
24:Z:107:GLY:N	24:Z:115:GLU:OE2	2.47	0.46
26:1:178:A:H2'	26:1:179:A:O4'	2.16	0.46
26:1:214:G:O2'	26:1:215:G:H5'	2.16	0.46
26:1:718:C:C2'	26:1:719:G:H5'	2.45	0.46
26:1:983:G:C2'	26:1:984:G:H5'	2.46	0.46
18:R:10:ILE:HG23	26:1:2504:C:N4	2.31	0.46
20:V:46:THR:OG1	20:V:49:VAL:HG22	2.15	0.46
20:V:88:ILE:HG13	20:V:89:THR:H	1.81	0.46
24:Z:74:GLU:HB2	24:Z:77:THR:HB	1.97	0.46
26:1:215:G:H2'	26:1:216:A:O4'	2.16	0.46
26:1:1452:C:C3'	26:1:1453:G:H5''	2.46	0.46
26:1:1461:C:H5''	26:1:1462:G:OP2	2.16	0.46
26:1:2317:G:H2'	26:1:2318:U:C6	2.51	0.46
18:R:19:ARG:NE	26:1:2783:U:OP2	2.49	0.45
19:S:125:VAL:HG13	19:S:194:ILE:CD1	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:W:91:LYS:HD2	21:W:110:ASN:HD22	1.80	0.45
25:a:15:HIS:CD2	25:a:97:GLY:HA2	2.51	0.45
26:1:20:C:O2'	26:1:21:A:H5'	2.16	0.45
26:1:97:C:O2'	26:1:98:U:H5'	2.16	0.45
26:1:135:G:H2'	26:1:136:A:C8	2.51	0.45
26:1:663:U:O2'	26:1:664:G:H5'	2.16	0.45
26:1:811:C:H2'	26:1:812:U:O4'	2.16	0.45
26:1:888:G:H2'	26:1:889:U:H6	1.80	0.45
26:1:1498:U:O2	26:1:1498:U:H2'	2.16	0.45
26:1:1645:G:O2'	26:1:1646:U:H5'	2.16	0.45
26:1:1863:C:H2'	26:1:1864:C:C6	2.51	0.45
26:1:1883:A:O2'	26:1:1884:G:H5'	2.16	0.45
26:1:2570:G:H2'	26:1:2571:G:C8	2.51	0.45
2:B:61:GLN:NE2	26:1:1616:A:H4'	2.30	0.45
6:F:6:ILE:HD11	6:F:38:VAL:HA	1.98	0.45
15:O:1:MET:HG2	26:1:2311:U:OP1	2.17	0.45
19:S:157:GLU:CA	19:S:198:ALA:HB2	2.46	0.45
20:V:21:ALA:HB1	20:V:63:ILE:CG2	2.46	0.45
26:1:207:A:H4'	26:1:208:G:OP1	2.17	0.45
26:1:461:A:O2'	26:1:462:U:H5'	2.16	0.45
26:1:2321:C:O2'	26:1:2322:C:H5'	2.16	0.45
26:1:2416:G:H5'	26:1:2417:U:C5'	2.46	0.45
26:1:2664:U:H2'	26:1:2665:G:O4'	2.16	0.45
26:1:2693:C:H3'	26:1:2694:C:C6	2.51	0.45
3:C:102:ASP:OD2	4:D:47:LYS:HE2	2.17	0.45
5:E:59:GLU:HG3	5:E:66:THR:HG23	1.97	0.45
6:F:17:SER:O	6:F:20:MET:HB2	2.16	0.45
8:H:4:LEU:HD12	8:H:61:ILE:CG2	2.43	0.45
8:H:65:VAL:O	8:H:68:LYS:HG2	2.16	0.45
13:M:4:LEU:HB3	13:M:6:ILE:CD1	2.45	0.45
21:W:91:LYS:HD3	21:W:110:ASN:HB2	1.98	0.45
22:X:109:ILE:HG13	22:X:125:ALA:HB1	1.98	0.45
26:1:156:A:H2'	26:1:157:U:O4'	2.16	0.45
26:1:181:G:O2'	26:1:182:C:H5'	2.16	0.45
26:1:372:A:H4'	26:1:373:A:OP2	2.16	0.45
26:1:383:A:H2'	26:1:384:G:H5'	1.98	0.45
26:1:427:A:H2'	26:1:428:G:O4'	2.15	0.45
26:1:1322:G:N2	26:1:1366:U:OP1	2.35	0.45
26:1:1517:A:H61	26:1:1563:U:H3	1.65	0.45
26:1:1745:A:C2'	26:1:1746:G:H5'	2.45	0.45
26:1:1781:C:C5	26:1:2744:G:H5'	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1884:G:O2'	26:1:1885:G:H5'	2.16	0.45
26:1:1988:C:HO2'	26:1:1989:C:P	2.36	0.45
26:1:2509:A:H2'	26:1:2510:C:H5'	1.97	0.45
26:1:2846:A:H2'	26:1:2847:U:H5'	1.99	0.45
26:1:2873:C:H2'	26:1:2874:A:H8	1.81	0.45
12:L:75:GLY:HA3	26:1:2813:U:O2'	2.17	0.45
20:V:4:THR:OG1	26:1:1039:C:O2	2.18	0.45
26:1:183:A:H3'	26:1:183:A:P	2.56	0.45
26:1:1070:A:H2'	26:1:1071:A:H5'	1.99	0.45
26:1:1869:G:H2'	26:1:1870:C:H6	1.81	0.45
26:1:2275:C:C2'	26:1:2276:U:H5'	2.46	0.45
6:F:11:VAL:HB	6:F:26:THR:HB	1.97	0.45
8:H:85:GLN:NE2	8:H:87:THR:OG1	2.48	0.45
9:I:78:GLU:O	9:I:85:LYS:HB2	2.16	0.45
19:S:57:VAL:HG21	19:S:87:GLY:HA2	1.97	0.45
20:V:50:ASP:HB3	20:V:115:LEU:HD11	1.98	0.45
26:1:91:A:H5''	26:1:92:G:OP2	2.17	0.45
26:1:526:A:N3	26:1:544:U:O2'	2.46	0.45
26:1:1268:C:H2'	26:1:1269:A:H8	1.81	0.45
26:1:1426:G:H2'	26:1:1427:U:O4'	2.17	0.45
26:1:1479:G:O2'	26:1:1480:G:H5'	2.15	0.45
26:1:1560:A:H5''	26:1:1561:G:OP1	2.16	0.45
26:1:1955:A:H2'	26:1:1956:G:O4'	2.16	0.45
1:A:76:PHE:CB	1:A:83:ILE:HD11	2.47	0.45
2:B:171:TYR:OH	26:1:2250:A:OP1	2.31	0.45
7:G:3:ILE:HG22	7:G:23:VAL:HG21	1.99	0.45
8:H:32:TYR:HB3	8:H:38:ASN:ND2	2.31	0.45
15:O:26:ASN:HD21	26:1:2313:A:H2'	1.82	0.45
18:R:17:ILE:HG21	18:R:26:ILE:CD1	2.45	0.45
18:R:24:MET:HG2	18:R:35:ARG:HB3	1.97	0.45
20:V:22:GLU:HG2	20:V:62:LYS:CB	2.47	0.45
25:a:17:ARG:HB3	26:1:2362:A:OP2	2.15	0.45
26:1:136:A:H2'	26:1:137:G:C8	2.50	0.45
26:1:153:G:O2'	26:1:154:A:H5'	2.16	0.45
26:1:268:A:N6	26:1:473:U:O2'	2.50	0.45
26:1:356:A:O2'	26:1:357:U:H5'	2.17	0.45
26:1:483:C:O2'	26:1:484:U:H5'	2.16	0.45
26:1:2084:G:O2'	26:1:2085:A:H5'	2.16	0.45
27:2:16:A:H2'	27:2:17:A:O4'	2.17	0.45
1:A:32:VAL:O	1:A:42:ILE:HA	2.17	0.45
24:Z:9:THR:HG22	24:Z:10:SER:H	1.79	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:161:A:H1'	26:1:2235:A:O2'	2.17	0.45
26:1:341:G:O6	26:1:381:G:H5''	2.17	0.45
26:1:872:U:H5'	26:1:873:U:C4	2.52	0.45
26:1:1426:G:O2'	26:1:1427:U:H5'	2.16	0.45
26:1:2268:A:H2'	26:1:2269:G:C8	2.51	0.45
26:1:2786:G:O2'	26:1:2787:C:H5'	2.17	0.45
27:2:57:G:H3'	27:2:58:C:H6	1.80	0.45
5:E:66:THR:HG22	5:E:69:LEU:HD11	1.98	0.45
12:L:13:THR:HG22	12:L:14:GLN:N	2.32	0.45
19:S:157:GLU:N	19:S:198:ALA:HB2	2.32	0.45
21:W:87:ILE:HG13	21:W:92:GLY:O	2.17	0.45
25:a:113:ARG:HE	25:a:119:PHE:HD2	1.65	0.45
26:1:159:U:H2'	26:1:160:G:C5'	2.47	0.45
26:1:221:G:N2	26:1:238:U:H4'	2.31	0.45
26:1:222:A:H2'	26:1:223:G:O4'	2.17	0.45
26:1:747:U:H2'	26:1:748:U:C6	2.52	0.45
26:1:747:U:H2'	26:1:748:U:H6	1.82	0.45
26:1:1085:U:N3	26:1:1158:G:C6	2.85	0.45
26:1:1355:A:C2'	26:1:1356:G:H5'	2.46	0.45
1:A:77:PRO:HD3	21:W:74:GLY:O	2.16	0.45
2:B:118:SER:HA	2:B:131:PRO:HD3	1.99	0.45
12:L:83:ALA:O	12:L:85:LYS:HE3	2.17	0.45
25:a:44:ILE:HG13	25:a:44:ILE:O	2.16	0.45
26:1:310:C:H3'	26:1:310:C:OP2	2.17	0.45
26:1:461:A:H2'	26:1:462:U:C6	2.52	0.45
26:1:464:U:H2'	26:1:465:C:H6	1.81	0.45
26:1:864:A:H5''	26:1:1017:A:N1	2.32	0.45
26:1:1315:C:H2'	26:1:1316:G:H8	1.81	0.45
26:1:1325:U:HO2'	26:1:1326:C:P	2.40	0.45
3:C:54:LYS:NZ	26:1:1038:C:OP2	2.43	0.45
8:H:9:ARG:NH1	8:H:28:PRO:HB3	2.32	0.45
15:O:5:VAL:HG11	15:O:21:LYS:HD3	1.98	0.45
17:Q:31:HIS:HD2	17:Q:32:LEU:HG	1.79	0.45
24:Z:37:ALA:CB	24:Z:117:VAL:HG21	2.47	0.45
26:1:405:G:H2'	26:1:406:A:C4'	2.46	0.45
26:1:1592:A:H3'	26:1:1593:G:C8	2.52	0.45
26:1:1767:G:H2'	26:1:1768:C:H6	1.82	0.45
26:1:1823:U:H2'	26:1:1824:C:C6	2.51	0.45
26:1:1994:C:C2'	26:1:1995:G:H5'	2.47	0.45
26:1:2777:A:H1'	26:1:2779:C:N4	2.32	0.45
2:B:53:HIS:CD2	2:B:219:THR:HA	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:154:ILE:HG21	2:B:176:LEU:HD22	1.99	0.44
10:J:10:ARG:HH21	10:J:52:ARG:HG2	1.82	0.44
12:L:163:VAL:O	26:1:2646:U:H5'	2.17	0.44
19:S:47:GLY:HA2	19:S:49:HIS:CD2	2.52	0.44
19:S:74:ARG:O	19:S:74:ARG:HG2	2.17	0.44
19:S:152:VAL:HA	19:S:191:SER:O	2.17	0.44
21:W:106:LEU:HG	21:W:111:PHE:HB2	1.99	0.44
25:a:113:ARG:HE	25:a:119:PHE:HB2	1.82	0.44
26:1:720:A:C2'	26:1:721:A:H5'	2.46	0.44
26:1:2713:G:H2'	26:1:2714:U:C6	2.51	0.44
12:L:25:VAL:CG2	12:L:196:LEU:HB3	2.45	0.44
12:L:41:VAL:HA	12:L:45:GLY:CA	2.39	0.44
16:P:41:LYS:CG	26:1:505:U:H5''	2.46	0.44
18:R:24:MET:HG2	18:R:35:ARG:HB2	1.98	0.44
21:W:35:ILE:HD12	21:W:69:VAL:HG13	1.98	0.44
26:1:91:A:H3'	26:1:92:G:C8	2.53	0.44
26:1:191:A:H2	26:1:211:C:H42	1.63	0.44
26:1:325:A:O2'	26:1:326:A:H5'	2.17	0.44
26:1:362:C:O2'	26:1:363:A:H5'	2.17	0.44
26:1:793:G:H2'	26:1:793:G:N3	2.33	0.44
26:1:1637:A:H2'	26:1:1638:G:C8	2.52	0.44
26:1:1683:U:H2'	26:1:1684:A:H5'	1.99	0.44
26:1:1771:A:N3	26:1:1771:A:H5'	2.32	0.44
26:1:2342:U:O2'	26:1:2343:U:H5'	2.18	0.44
19:S:125:VAL:HG13	19:S:194:ILE:HD12	1.98	0.44
26:1:135:G:H2'	26:1:136:A:H8	1.82	0.44
26:1:1794:C:H2'	26:1:1795:A:O4'	2.17	0.44
26:1:2543:G:C2'	26:1:2544:C:H5'	2.47	0.44
27:2:85:U:H6	27:2:85:U:H5''	1.82	0.44
14:N:30:CYS:HB3	14:N:33:CYS:HB2	1.99	0.44
16:P:16:VAL:HG13	16:P:17:HIS:CE1	2.52	0.44
20:V:26:LEU:HD21	20:V:105:SER:OG	2.16	0.44
26:1:210:A:H2'	26:1:211:C:O4'	2.17	0.44
26:1:698:U:H2'	26:1:699:U:H5'	2.00	0.44
26:1:898:U:O2'	26:1:899:U:H5'	2.17	0.44
26:1:1161:A:H2'	26:1:1162:C:H6	1.81	0.44
26:1:1700:C:H2'	26:1:1701:U:H6	1.82	0.44
26:1:2521:G:C2'	26:1:2522:G:H5'	2.48	0.44
8:H:31:VAL:CG1	8:H:36:THR:HG21	2.41	0.44
15:O:3:VAL:HG23	15:O:23:LYS:HB2	1.99	0.44
19:S:49:HIS:ND1	19:S:92:PRO:HB3	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:X:125:ALA:O	22:X:145:VAL:HA	2.17	0.44
26:1:569:U:H2'	26:1:570:U:C6	2.53	0.44
26:1:841:C:H2'	26:1:842:U:C6	2.53	0.44
26:1:1218:G:H2'	26:1:1219:G:O4'	2.17	0.44
26:1:1450:A:H2'	26:1:1450:A:N3	2.33	0.44
26:1:1710:G:H2'	26:1:1711:G:O4'	2.18	0.44
26:1:2262:G:H2'	26:1:2263:C:H6	1.82	0.44
27:2:79:C:N4	27:2:91:C:N3	2.66	0.44
3:C:33:LYS:HE2	26:1:624:C:OP2	2.16	0.44
12:L:90:GLU:OE1	26:1:2662:U:O2'	2.30	0.44
19:S:135:LYS:O	19:S:166:SER:HB2	2.18	0.44
21:W:35:ILE:HG21	21:W:103:ALA:CB	2.47	0.44
22:X:74:TYR:CE2	22:X:127:LYS:HD3	2.52	0.44
23:Y:83:MET:HE2	26:1:1004:A:H61	1.82	0.44
24:Z:34:GLU:O	24:Z:38:LYS:HG2	2.17	0.44
24:Z:48:ILE:CD1	24:Z:89:ILE:HG22	2.47	0.44
25:a:57:SER:O	25:a:76:VAL:HG22	2.18	0.44
26:1:5:A:O2'	26:1:6:A:H5'	2.17	0.44
26:1:2045:A:O2'	26:1:2046:U:H5'	2.18	0.44
26:1:2350:G:H2'	26:1:2351:U:O4'	2.18	0.44
26:1:2455:G:H5''	26:1:2456:G:O5'	2.18	0.44
26:1:2501:U:H3'	26:1:2502:C:C6	2.52	0.44
26:1:2516:G:C2'	26:1:2517:G:H5'	2.48	0.44
11:K:21:SER:HA	11:K:50:ILE:HD13	1.99	0.44
20:V:32:GLU:CG	20:V:143:LEU:HD22	2.47	0.44
22:X:128:PHE:HE2	22:X:143:HIS:HB2	1.81	0.44
26:1:1390:A:H2'	26:1:1391:A:H8	1.80	0.44
26:1:2439:A:H2'	26:1:2440:G:H5'	1.99	0.44
5:E:72:LYS:HG2	5:E:73:GLU:HG3	2.00	0.44
7:G:82:GLY:O	7:G:93:ILE:HG22	2.17	0.44
12:L:31:LYS:HG3	12:L:32:GLU:OE1	2.17	0.44
23:Y:59:LYS:HE2	23:Y:59:LYS:HA	1.99	0.44
24:Z:36:ARG:O	24:Z:40:VAL:HG23	2.18	0.44
26:1:421:C:H2'	26:1:422:G:C8	2.53	0.44
26:1:1283:G:C2'	26:1:1284:A:H5'	2.47	0.44
26:1:1631:G:O2'	26:1:1632:A:O5'	2.20	0.44
26:1:1877:G:H2'	26:1:1878:U:C6	2.53	0.44
26:1:2109:A:H2'	26:1:2110:G:O4'	2.17	0.44
26:1:2347:A:H5'	26:1:2348:G:C5	2.53	0.44
27:2:89:U:H2'	27:2:90:U:H6	1.83	0.44
2:B:95:VAL:HA	2:B:100:GLU:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:J:17:ARG:O	10:J:24:SER:HA	2.17	0.44
11:K:27:ASN:O	11:K:31:GLN:HG3	2.18	0.44
12:L:215:ILE:HD11	26:1:2798:C:H4'	2.00	0.44
26:1:52:A:H2'	26:1:53:A:C8	2.53	0.44
26:1:140:A:H1'	26:1:1445:C:O2'	2.18	0.44
26:1:153:G:H2'	26:1:154:A:H8	1.83	0.44
26:1:302:A:O2'	26:1:303:G:OP2	2.30	0.44
26:1:474:A:O2'	26:1:475:A:H5'	2.18	0.44
26:1:763:A:H2'	26:1:764:C:O4'	2.17	0.44
26:1:1388:C:O2'	26:1:1618:A:H1'	2.18	0.44
26:1:1651:C:H4'	26:1:1652:A:C5'	2.48	0.44
26:1:2098:A:H2'	26:1:2099:G:H8	1.82	0.44
26:1:2289:U:H4'	26:1:2355:A:H2	1.83	0.44
26:1:2662:U:H2'	26:1:2663:U:O4'	2.18	0.44
5:E:14:PRO:O	5:E:18:ARG:HG3	2.18	0.43
12:L:138:ARG:HB2	12:L:148:HIS:O	2.18	0.43
19:S:199:ALA:O	19:S:202:VAL:HG22	2.19	0.43
26:1:108:A:H2'	26:1:109:G:O4'	2.18	0.43
26:1:174:U:O2'	26:1:175:C:H5'	2.18	0.43
26:1:268:A:O2'	26:1:269:G:H4'	2.17	0.43
26:1:609:U:O2'	26:1:610:U:H5'	2.17	0.43
26:1:1297:G:O2'	26:1:1298:G:H5'	2.17	0.43
26:1:1572:G:C2'	26:1:1573:A:H5'	2.48	0.43
26:1:2814:C:H2'	26:1:2815:C:C6	2.53	0.43
2:B:25:THR:HB	2:B:80:SER:HB3	1.99	0.43
3:C:61:TRP:HB3	3:C:93:LYS:O	2.17	0.43
3:C:104:LYS:HB2	4:D:47:LYS:NZ	2.32	0.43
6:F:62:LYS:HA	6:F:71:TYR:HA	2.00	0.43
20:V:75:TYR:HB2	20:V:88:ILE:HG22	2.00	0.43
22:X:60:ARG:NH1	26:1:2455:G:H21	2.16	0.43
22:X:80:ASP:HA	22:X:83:ASN:HD22	1.83	0.43
26:1:44:A:HO2'	26:1:45:G:P	2.40	0.43
26:1:98:U:C2'	26:1:99:U:H5''	2.47	0.43
26:1:303:G:H2'	26:1:304:G:O4'	2.17	0.43
26:1:640:G:O2'	26:1:641:A:H5'	2.18	0.43
26:1:1356:G:H2'	26:1:1357:G:N3	2.34	0.43
27:2:99:G:C5	27:2:100:U:H1'	2.53	0.43
3:C:90:ILE:HD11	3:C:92:ARG:NE	2.33	0.43
7:G:80:ARG:HH22	26:1:343:A:H3'	1.83	0.43
8:H:79:PHE:CZ	8:H:84:ASN:HA	2.54	0.43
12:L:43:VAL:HG23	12:L:43:VAL:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:111:VAL:N	12:L:114:ASP:OD2	2.28	0.43
18:R:1:MET:CE	26:1:2769:G:H5'	2.47	0.43
19:S:58:SER:O	19:S:79:ARG:NE	2.43	0.43
23:Y:55:THR:CG2	23:Y:60:ARG:HG3	2.48	0.43
26:1:78:U:O2'	26:1:79:U:H5'	2.18	0.43
26:1:515:G:O2'	26:1:516:A:O4'	2.32	0.43
26:1:1028:G:H2'	26:1:1028:G:N3	2.33	0.43
26:1:1816:A:H2'	26:1:1817:C:O4'	2.18	0.43
26:1:2500:U:H2'	26:1:2501:U:O2	2.18	0.43
26:1:2597:G:H2'	26:1:2598:U:O4'	2.18	0.43
26:1:2714:U:H2'	26:1:2715:G:O4'	2.18	0.43
26:1:2907:A:H2'	26:1:2908:U:C6	2.54	0.43
2:B:115:ILE:H	2:B:128:ASN:ND2	2.16	0.43
18:R:2:LYS:HE2	18:R:31:LYS:O	2.18	0.43
26:1:4:U:H2'	26:1:5:A:H8	1.83	0.43
26:1:74:U:H4'	26:1:75:G:O5'	2.19	0.43
26:1:442:G:C2'	26:1:443:U:H5'	2.48	0.43
26:1:908:A:H2'	26:1:909:G:H8	1.84	0.43
26:1:1651:C:H4'	26:1:1652:A:H5'	2.01	0.43
26:1:1865:C:H4'	26:1:1866:G:C5'	2.48	0.43
26:1:1950:U:H2'	26:1:1951:C:C6	2.53	0.43
26:1:2052:C:H2'	26:1:2053:U:C6	2.54	0.43
26:1:2827:A:H2'	26:1:2828:U:C6	2.53	0.43
2:B:93:LEU:HD12	2:B:102:ARG:O	2.18	0.43
22:X:92:THR:HG22	22:X:94:ALA:H	1.83	0.43
23:Y:55:THR:HG22	23:Y:60:ARG:HG3	1.99	0.43
23:Y:80:GLU:HG3	23:Y:80:GLU:O	2.19	0.43
26:1:674:C:O2	26:1:684:U:O2'	2.37	0.43
26:1:700:A:H4'	26:1:701:G:OP1	2.18	0.43
26:1:862:C:C2'	26:1:863:G:H5'	2.49	0.43
26:1:1350:U:HO2'	26:1:1351:C:P	2.37	0.43
26:1:2764:G:O2'	26:1:2765:A:H5'	2.19	0.43
4:D:38:VAL:HG13	4:D:53:VAL:HB	2.00	0.43
5:E:14:PRO:HG3	5:E:78:GLU:HG3	2.00	0.43
18:R:29:ASN:HD22	18:R:32:HIS:CE1	2.36	0.43
19:S:200:LYS:O	19:S:204:GLU:HG3	2.17	0.43
23:Y:101:ARG:NH2	26:1:953:C:OP1	2.50	0.43
26:1:216:A:H4'	26:1:216:A:OP1	2.17	0.43
26:1:310:C:H1'	26:1:311:U:C6	2.54	0.43
26:1:565:G:H2'	26:1:566:U:O4'	2.18	0.43
26:1:702:U:H2'	26:1:703:A:H8	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:766:G:O2'	26:1:767:A:H5'	2.18	0.43
26:1:1240:U:H2'	26:1:1241:A:C8	2.53	0.43
26:1:1962:G:N1	26:1:1989:C:O2'	2.50	0.43
26:1:2011:U:H2'	26:1:2012:G:C8	2.53	0.43
26:1:2690:G:H2'	26:1:2691:G:H8	1.82	0.43
2:B:132:LEU:HD13	2:B:172:VAL:HG21	2.01	0.43
4:D:79:ARG:C	4:D:80:LYS:HD2	2.43	0.43
15:O:29:ARG:HG3	15:O:47:GLU:HA	2.01	0.43
17:Q:21:GLN:CD	17:Q:49:LEU:HD13	2.44	0.43
21:W:112:MET:HA	21:W:115:VAL:HG22	2.00	0.43
22:X:17:ASN:HD22	22:X:18:ARG:H	1.67	0.43
22:X:124:LYS:HD3	22:X:144:GLU:HB2	2.01	0.43
23:Y:74:TYR:CE2	23:Y:91:GLU:HB3	2.53	0.43
25:a:91:GLU:HA	25:a:118:GLU:HB2	1.99	0.43
26:1:114:C:H2'	26:1:115:C:H6	1.84	0.43
26:1:577:A:H4'	26:1:578:G:C8	2.54	0.43
26:1:587:C:O2'	26:1:588:G:H5'	2.18	0.43
26:1:899:U:H2'	26:1:900:G:H8	1.83	0.43
26:1:901:G:H2'	26:1:902:A:H8	1.78	0.43
26:1:1182:G:H2'	26:1:1183:G:O4'	2.18	0.43
26:1:1225:G:H2'	26:1:1226:G:O4'	2.18	0.43
26:1:1757:U:O2'	26:1:1758:A:H5'	2.19	0.43
26:1:1904:A:H2'	26:1:1905:G:C8	2.53	0.43
27:2:96:A:O2'	27:2:97:G:H5'	2.18	0.43
2:B:205:VAL:CG2	26:1:1818:A:H5''	2.48	0.43
3:C:86:ALA:HB3	3:C:88:ILE:HG22	2.01	0.43
3:C:90:ILE:HD11	3:C:92:ARG:HE	1.84	0.43
5:E:37:LYS:HA	5:E:48:GLU:OE2	2.19	0.43
6:F:60:PRO:HB2	6:F:71:TYR:HB3	2.01	0.43
8:H:62:GLU:HB3	8:H:69:THR:HB	2.01	0.43
9:I:27:LYS:O	9:I:29:LEU:HB2	2.19	0.43
11:K:13:GLU:O	11:K:17:GLN:HG3	2.19	0.43
12:L:99:TYR:H	12:L:103:GLN:HE22	1.67	0.43
12:L:150:ALA:HB1	12:L:151:PRO:HD2	2.00	0.43
17:Q:58:VAL:CG1	17:Q:61:LEU:HB2	2.40	0.43
22:X:101:VAL:HG12	22:X:102:VAL:HG23	2.01	0.43
26:1:2055:U:O2'	26:1:2056:G:H5'	2.19	0.43
26:1:2263:C:H2'	26:1:2264:G:O4'	2.19	0.43
26:1:2431:C:H2'	26:1:2432:G:O4'	2.18	0.43
2:B:263:LYS:NZ	26:1:1827:C:OP2	2.52	0.43
19:S:164:GLU:HG3	19:S:165:LEU:N	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:V:74:VAL:HG13	20:V:88:ILE:O	2.19	0.43
22:X:12:SER:O	22:X:13:ARG:HD3	2.18	0.43
24:Z:100:TYR:O	24:Z:122:VAL:HG12	2.18	0.43
26:1:40:U:H3	26:1:485:A:H61	1.67	0.43
26:1:176:A:OP2	26:1:176:A:H4'	2.18	0.43
26:1:181:G:C2'	26:1:182:C:H5'	2.49	0.43
26:1:725:A:H2'	26:1:726:G:C8	2.54	0.43
26:1:887:A:H2'	26:1:888:G:O4'	2.18	0.43
26:1:1749:G:O2'	26:1:1750:U:H5'	2.19	0.43
26:1:2406:G:H2'	26:1:2407:A:C8	2.53	0.43
26:1:2495:A:O2'	26:1:2508:G:N2	2.52	0.43
26:1:2772:C:H2'	26:1:2773:U:C6	2.54	0.43
27:2:57:G:C2	27:2:58:C:H1'	2.54	0.43
12:L:34:VAL:O	12:L:51:VAL:HA	2.18	0.43
26:1:57:C:H2'	26:1:58:G:O4'	2.19	0.43
26:1:717:C:O2'	26:1:718:C:H5'	2.19	0.43
26:1:1443:A:H2'	26:1:1444:C:C6	2.54	0.43
26:1:1669:C:O2'	26:1:1670:A:H5'	2.19	0.43
26:1:1817:C:H2'	26:1:1818:A:C8	2.53	0.43
26:1:1904:A:H2'	26:1:1905:G:H8	1.84	0.43
26:1:2767:A:H2'	26:1:2768:A:C8	2.54	0.43
26:1:391:A:H2'	26:1:392:U:O4'	2.19	0.42
26:1:768:A:H2'	26:1:769:U:C6	2.53	0.42
26:1:909:G:H2'	26:1:910:C:C6	2.54	0.42
26:1:1215:U:H5'	26:1:1216:U:N3	2.34	0.42
26:1:2388:A:C2'	26:1:2389:G:H5'	2.49	0.42
1:A:10:VAL:HG22	12:L:194:VAL:HG21	2.00	0.42
2:B:176:LEU:HD12	2:B:180:GLU:HB3	1.99	0.42
3:C:105:ALA:HB1	4:D:40:PHE:HZ	1.84	0.42
13:M:2:ALA:HA	13:M:38:GLU:HG2	2.01	0.42
18:R:19:ARG:HG2	26:1:2783:U:OP2	2.19	0.42
20:V:19:ILE:CD1	20:V:142:GLU:HA	2.49	0.42
26:1:825:G:H2'	26:1:827:A:N7	2.34	0.42
26:1:1487:G:H1	26:1:1595:C:H42	1.67	0.42
1:A:33:ARG:NH2	1:A:82:LYS:HA	2.34	0.42
3:C:91:ASN:HB2	4:D:11:GLN:HB2	2.00	0.42
5:E:4:LYS:CB	5:E:106:VAL:HG22	2.49	0.42
11:K:42:ARG:O	11:K:46:VAL:HG23	2.19	0.42
12:L:157:ALA:HB2	26:1:2602:C:H4'	2.00	0.42
20:V:8:ASN:O	20:V:12:ILE:HG13	2.20	0.42
23:Y:118:LEU:HD12	23:Y:131:PHE:HE1	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:89:U:H2'	26:1:90:A:H2'	2.01	0.42
26:1:793:G:H1	26:1:796:A:H5'	1.84	0.42
26:1:896:U:H2'	26:1:897:A:H8	1.83	0.42
26:1:1724:U:H2'	26:1:1725:G:O4'	2.19	0.42
26:1:1776:A:H2'	26:1:1777:G:O4'	2.19	0.42
26:1:1832:C:O2'	26:1:1833:C:H5'	2.18	0.42
26:1:1924:G:H2'	26:1:1925:U:C6	2.55	0.42
1:A:23:ARG:HA	1:A:24:PRO:HD3	1.91	0.42
1:A:29:ARG:CG	1:A:89:LYS:HE2	2.49	0.42
1:A:72:VAL:HG12	21:W:79:PHE:CD1	2.54	0.42
2:B:20:ASP:OD1	2:B:21:PHE:N	2.52	0.42
4:D:67:ARG:NH2	26:1:1261:G:OP1	2.52	0.42
8:H:48:PHE:O	8:H:52:ILE:HG22	2.19	0.42
8:H:79:PHE:O	8:H:81:PRO:HD3	2.19	0.42
18:R:7:VAL:CG2	18:R:37:GLY:HA2	2.45	0.42
26:1:269:G:H21	26:1:323:C:H6	1.66	0.42
26:1:1044:A:H2'	26:1:1045:A:C8	2.55	0.42
26:1:1445:C:O2'	26:1:1446:U:H5'	2.20	0.42
26:1:1863:C:H2'	26:1:1864:C:H6	1.85	0.42
6:F:55:ILE:HD12	6:F:76:ARG:HH11	1.84	0.42
12:L:8:ARG:HB3	12:L:29:GLU:HG2	2.01	0.42
24:Z:20:LEU:HD13	24:Z:40:VAL:HG21	2.01	0.42
26:1:197:G:H2'	26:1:198:A:O4'	2.20	0.42
26:1:752:G:C2'	26:1:753:U:H5'	2.49	0.42
26:1:2051:C:H2'	26:1:2052:C:H6	1.83	0.42
26:1:2388:A:H2'	26:1:2389:G:H5'	2.01	0.42
2:B:53:HIS:NE2	2:B:219:THR:HA	2.35	0.42
2:B:59:LYS:HB2	26:1:1615:G:H4'	2.01	0.42
3:C:64:ARG:HD3	20:V:45:TYR:O	2.19	0.42
4:D:63:ASN:HB3	4:D:94:LYS:HG3	2.01	0.42
6:F:4:ARG:HH21	6:F:6:ILE:HG22	1.83	0.42
21:W:8:LEU:HD13	21:W:84:CYS:HB3	2.01	0.42
21:W:34:ASN:N	21:W:37:ASP:OD2	2.33	0.42
26:1:101:G:O2'	26:1:102:A:OP2	2.32	0.42
26:1:437:A:N3	26:1:437:A:H2'	2.33	0.42
26:1:565:G:H2'	26:1:566:U:C6	2.54	0.42
26:1:575:G:N3	26:1:575:G:H2'	2.33	0.42
26:1:750:A:H2'	26:1:751:A:O4'	2.19	0.42
27:2:56:A:H2'	27:2:57:G:H8	1.84	0.42
27:2:90:U:H2'	27:2:91:C:H6	1.84	0.42
5:E:17:VAL:HG13	5:E:47:ILE:HD11	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:M:23:VAL:HG23	13:M:28:LEU:HD12	2.01	0.42
26:1:94:A:H2'	26:1:95:A:O4'	2.20	0.42
26:1:389:A:H2'	26:1:390:A:C5'	2.49	0.42
26:1:559:A:H2'	26:1:560:A:O4'	2.19	0.42
26:1:561:C:C2'	26:1:562:C:H5'	2.49	0.42
26:1:1034:A:O2'	26:1:1036:C:OP2	2.32	0.42
26:1:1428:U:H2'	26:1:1430:A:OP2	2.20	0.42
26:1:2618:C:H2'	26:1:2619:G:H8	1.84	0.42
7:G:85:PHE:HD1	7:G:90:LYS:HD2	1.85	0.42
12:L:5:ILE:HG22	12:L:105:VAL:HG12	2.01	0.42
12:L:119:THR:HB	12:L:210:GLU:HG2	2.02	0.42
17:Q:57:ARG:HD3	26:1:878:C:O2'	2.20	0.42
18:R:36:GLN:NE2	26:1:1169:G:H5'	2.34	0.42
20:V:39:GLY:HA3	20:V:52:GLY:HA2	2.01	0.42
24:Z:59:ARG:HG3	24:Z:86:PHE:CE2	2.55	0.42
26:1:89:U:C2'	26:1:90:A:H2'	2.50	0.42
26:1:491:C:O2'	26:1:492:G:H5'	2.20	0.42
26:1:1215:U:H3'	26:1:1216:U:O4'	2.20	0.42
26:1:1425:G:O2'	26:1:1426:G:H5'	2.20	0.42
26:1:1463:A:H5'	26:1:1463:A:N3	2.35	0.42
26:1:1499:U:H2'	26:1:1500:G:O4'	2.20	0.42
26:1:1696:C:H2'	26:1:1697:G:O4'	2.20	0.42
26:1:2620:U:H2'	26:1:2621:C:C6	2.55	0.42
1:A:66:ILE:HA	1:A:71:GLY:HA2	2.01	0.42
6:F:35:LYS:HB3	6:F:55:ILE:HD13	2.02	0.42
10:J:5:CYS:SG	10:J:6:PHE:N	2.93	0.42
13:M:2:ALA:N	13:M:38:GLU:HG2	2.35	0.42
17:Q:58:VAL:HG11	22:X:58:PHE:CE2	2.55	0.42
22:X:129:SER:OG	22:X:130:ALA:N	2.53	0.42
24:Z:74:GLU:HB2	24:Z:77:THR:C	2.44	0.42
26:1:726:G:H2'	26:1:727:G:O4'	2.20	0.42
26:1:1269:A:H2'	26:1:1270:U:C6	2.55	0.42
26:1:1459:A:N3	26:1:1459:A:H2'	2.34	0.42
26:1:1822:C:H2'	26:1:1823:U:O4'	2.19	0.42
26:1:1917:A:H2'	26:1:1918:G:H5'	2.02	0.42
26:1:2605:G:OP2	26:1:2605:G:H4'	2.19	0.42
27:2:68:U:O2'	27:2:69:C:H5'	2.20	0.42
4:D:11:GLN:OE1	4:D:11:GLN:N	2.53	0.42
8:H:76:ASP:H	8:H:90:ASP:HB2	1.84	0.42
17:Q:35:ASN:HB3	26:1:2417:U:H5''	2.02	0.42
19:S:123:LEU:HA	19:S:192:LEU:HB2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:32:C:N4	26:1:493:A:OP2	2.53	0.42
26:1:69:C:H4'	26:1:75:G:C8	2.55	0.42
26:1:217:G:H2'	26:1:218:G:O4'	2.20	0.42
26:1:630:G:N3	26:1:630:G:H5'	2.34	0.42
26:1:1217:U:H1'	26:1:1218:G:N1	2.35	0.42
26:1:1491:C:C2'	26:1:1492:G:H5'	2.50	0.42
26:1:2231:C:H2'	26:1:2232:A:H8	1.84	0.42
26:1:2348:G:H5''	26:1:2349:A:OP2	2.19	0.42
26:1:2825:U:H2'	26:1:2826:U:C6	2.54	0.42
1:A:99:LEU:HD23	1:A:102:LEU:CD1	2.50	0.41
6:F:62:LYS:HB3	6:F:71:TYR:HE1	1.83	0.41
7:G:9:VAL:HG12	7:G:70:LEU:HD13	2.01	0.41
17:Q:58:VAL:HG22	17:Q:61:LEU:HD12	2.02	0.41
18:R:17:ILE:HG13	18:R:18:LYS:N	2.34	0.41
19:S:57:VAL:CG1	19:S:79:ARG:HD2	2.50	0.41
21:W:93:PRO:HG3	21:W:117:LEU:HD12	2.02	0.41
25:a:77:GLY:O	25:a:80:ILE:HG22	2.20	0.41
26:1:1314:A:H2'	26:1:1315:C:C6	2.56	0.41
26:1:1465:G:H5'	26:1:2238:U:H6	1.84	0.41
26:1:1562:C:H2'	26:1:1563:U:H6	1.85	0.41
26:1:1571:G:H2'	26:1:1572:G:H8	1.85	0.41
26:1:1632:A:H4'	26:1:1633:A:N3	2.35	0.41
26:1:1651:C:H5''	26:1:1652:A:H5'	2.01	0.41
26:1:1752:C:O2'	26:1:1753:U:H5'	2.20	0.41
26:1:1893:A:C6	26:1:1894:G:H1'	2.55	0.41
26:1:2725:U:H2'	26:1:2726:C:C6	2.55	0.41
27:2:39:G:O2'	27:2:40:C:OP1	2.36	0.41
6:F:7:LEU:HD23	6:F:29:VAL:HG12	2.02	0.41
12:L:60:LYS:NZ	12:L:62:ASP:OD2	2.26	0.41
26:1:151:U:H2'	26:1:152:C:C6	2.54	0.41
26:1:161:A:C2'	26:1:162:A:H5''	2.44	0.41
26:1:905:U:H1'	26:1:2295:A:H5'	2.01	0.41
26:1:1520:A:C2'	26:1:1521:A:H5'	2.50	0.41
26:1:2422:C:H2'	26:1:2423:G:C8	2.54	0.41
26:1:2626:G:C2'	26:1:2627:A:H5'	2.50	0.41
26:1:2860:U:H2'	26:1:2861:U:H6	1.85	0.41
1:A:33:ARG:HD3	1:A:84:GLU:OE2	2.20	0.41
2:B:84:ASP:OD1	2:B:85:PRO:HD2	2.20	0.41
2:B:160:ALA:O	2:B:194:GLN:HG3	2.20	0.41
5:E:78:GLU:O	26:1:24:G:O2'	2.39	0.41
5:E:89:ALA:HB1	26:1:793:G:N2	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:L:184:GLU:HB2	12:L:198:LYS:HD2	2.02	0.41
14:N:9:SER:HB2	26:1:2047:A:C5'	2.42	0.41
19:S:201:LYS:O	19:S:205:VAL:HG23	2.20	0.41
20:V:44:THR:O	20:V:44:THR:HG22	2.20	0.41
26:1:56:A:H2'	26:1:57:C:O4'	2.20	0.41
26:1:111:U:H2'	26:1:112:U:H5'	2.02	0.41
26:1:207:A:H5'	26:1:209:U:O4'	2.20	0.41
26:1:830:U:H2'	26:1:831:C:C6	2.55	0.41
26:1:970:U:H4'	26:1:971:U:O5'	2.20	0.41
26:1:1283:G:O2'	26:1:1284:A:H5'	2.21	0.41
26:1:1621:C:H2'	26:1:1622:C:C6	2.55	0.41
26:1:1976:G:H2'	26:1:1977:G:O4'	2.19	0.41
26:1:2223:C:H2'	26:1:2224:U:C6	2.56	0.41
26:1:2288:C:O2'	26:1:2289:U:H5'	2.21	0.41
26:1:2794:C:H2'	26:1:2795:C:H5'	2.02	0.41
26:1:2799:C:H2'	26:1:2800:U:C6	2.55	0.41
1:A:4:HIS:HB3	1:A:7:ILE:HD12	2.02	0.41
1:A:55:GLY:HA2	1:A:59:GLU:HG2	2.00	0.41
2:B:144:ILE:HG22	2:B:145:GLU:O	2.21	0.41
6:F:82:LEU:HD23	6:F:82:LEU:HA	1.84	0.41
12:L:215:ILE:HD13	26:1:2798:C:H5''	2.02	0.41
19:S:182:ASN:O	19:S:186:ILE:HG13	2.19	0.41
20:V:39:GLY:CA	20:V:52:GLY:HA2	2.50	0.41
24:Z:16:MET:HE3	24:Z:20:LEU:CD1	2.50	0.41
26:1:266:A:H1'	26:1:476:A:N3	2.36	0.41
26:1:1041:G:O2'	26:1:1042:C:H5'	2.20	0.41
26:1:1409:U:O2'	26:1:2239:A:H8	2.04	0.41
26:1:2541:U:H2'	26:1:2542:C:H6	1.84	0.41
1:A:33:ARG:HH21	1:A:82:LYS:HA	1.86	0.41
2:B:65:ILE:HD12	2:B:87:ARG:NH1	2.35	0.41
12:L:26:THR:OG1	12:L:200:ASN:HA	2.21	0.41
15:O:7:LEU:HB3	15:O:45:HIS:HB3	2.03	0.41
17:Q:7:HIS:HD2	17:Q:10:ALA:HB2	1.85	0.41
23:Y:32:PHE:HE2	23:Y:111:GLU:HA	1.82	0.41
24:Z:102:ARG:NH2	24:Z:122:VAL:HG23	2.25	0.41
25:a:8:ASN:HA	25:a:11:ARG:HB3	2.03	0.41
26:1:402:C:H2'	26:1:403:U:C2	2.55	0.41
26:1:730:A:H5'	26:1:819:A:N6	2.35	0.41
26:1:1059:A:O2'	26:1:1060:U:H5'	2.20	0.41
26:1:1081:G:H22	26:1:1163:U:H1'	1.84	0.41
26:1:1266:G:H2'	26:1:1267:A:O4'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1903:A:H2'	26:1:1904:A:C8	2.55	0.41
26:1:2027:G:O2'	26:1:2028:A:H5'	2.21	0.41
26:1:2519:U:H2'	26:1:2520:U:C6	2.55	0.41
26:1:2799:C:H2'	26:1:2800:U:H6	1.85	0.41
26:1:2815:C:C2'	26:1:2816:C:H5'	2.51	0.41
26:1:2838:C:O2'	26:1:2839:A:H5'	2.20	0.41
1:A:28:LEU:HD22	1:A:86:ILE:CG2	2.51	0.41
4:D:11:GLN:HE21	4:D:39:LEU:CD1	2.33	0.41
6:F:35:LYS:O	6:F:53:VAL:HG11	2.20	0.41
15:O:9:CYS:HB2	15:O:45:HIS:CE1	2.55	0.41
25:a:19:ARG:O	25:a:19:ARG:HG2	2.21	0.41
26:1:92:G:H2'	26:1:93:U:H6	1.81	0.41
26:1:349:U:H2'	26:1:350:G:H5'	2.03	0.41
26:1:888:G:H2'	26:1:889:U:C6	2.54	0.41
26:1:1737:U:H4'	26:1:1738:C:OP2	2.20	0.41
26:1:2271:U:H2'	26:1:2272:U:O4'	2.21	0.41
26:1:2427:G:H2'	26:1:2428:U:C6	2.56	0.41
26:1:2555:U:H2'	26:1:2557:U:O5'	2.21	0.41
26:1:2617:A:H2'	26:1:2618:C:H6	1.85	0.41
6:F:17:SER:HA	6:F:20:MET:HG3	2.02	0.41
20:V:75:TYR:HB2	20:V:88:ILE:CG2	2.51	0.41
20:V:88:ILE:HG13	20:V:89:THR:N	2.36	0.41
23:Y:43:THR:H	23:Y:46:GLN:NE2	2.18	0.41
24:Z:84:LYS:HA	24:Z:88:GLU:OE1	2.21	0.41
24:Z:112:ASP:O	26:1:2036:G:H1'	2.21	0.41
26:1:356:A:H2'	26:1:357:U:C6	2.56	0.41
26:1:679:G:H2'	26:1:680:C:C6	2.56	0.41
26:1:691:A:H2'	26:1:692:G:O4'	2.20	0.41
26:1:894:A:H2'	26:1:895:U:O2	2.20	0.41
26:1:1238:U:H2'	26:1:1239:C:H6	1.84	0.41
26:1:1350:U:H5	26:1:1647:A:N1	2.19	0.41
26:1:1411:G:O2'	26:1:1412:G:H5'	2.20	0.41
26:1:1916:A:H2'	26:1:1917:A:O4'	2.19	0.41
26:1:1951:C:O2'	26:1:1952:C:H5'	2.21	0.41
26:1:1994:C:H2'	26:1:1995:G:H5'	2.03	0.41
2:B:221:ARG:O	2:B:224:VAL:HG22	2.21	0.41
7:G:69:GLN:OE1	7:G:78:PRO:HB2	2.21	0.41
8:H:2:ALA:HB3	8:H:51:VAL:CG2	2.44	0.41
19:S:54:ARG:HD2	26:1:718:C:OP1	2.21	0.41
21:W:3:GLN:O	21:W:3:GLN:HG3	2.21	0.41
21:W:69:VAL:HG22	21:W:77:ILE:CG2	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:a:44:ILE:HG12	25:a:54:ALA:CB	2.47	0.41
26:1:1203:U:O2'	26:1:1204:G:H5'	2.20	0.41
26:1:1772:G:C2'	26:1:1773:A:H5'	2.51	0.41
26:1:2250:A:H2'	26:1:2251:G:O4'	2.21	0.41
26:1:2581:U:H2'	26:1:2582:U:C6	2.56	0.41
2:B:205:VAL:HG21	26:1:1818:A:H5''	2.02	0.41
2:B:260:ARG:HD3	2:B:260:ARG:O	2.21	0.41
4:D:11:GLN:HE21	4:D:39:LEU:HD11	1.86	0.41
4:D:98:ASP:O	4:D:99:LYS:HD2	2.21	0.41
15:O:7:LEU:HD21	15:O:32:MET:HG3	2.01	0.41
26:1:165:C:H5'	26:1:166:A:OP2	2.21	0.41
26:1:470:G:H2'	26:1:471:G:O4'	2.21	0.41
26:1:526:A:H3'	26:1:527:G:H5''	2.03	0.41
26:1:1316:G:C2'	26:1:1317:G:H5'	2.50	0.41
26:1:1347:G:H2'	26:1:1348:U:H5'	2.03	0.41
26:1:1514:A:C2'	26:1:1515:G:H5'	2.51	0.41
26:1:1576:A:H2'	26:1:1577:G:O4'	2.21	0.41
26:1:1605:A:H4'	26:1:1606:C:OP1	2.21	0.41
26:1:1756:U:O2	26:1:1756:U:H2'	2.21	0.41
26:1:1875:A:H61	26:1:1921:C:H1'	1.85	0.41
26:1:1904:A:O2'	26:1:1905:G:H5'	2.20	0.41
26:1:1939:A:N7	26:1:1944:U:O4	2.54	0.41
26:1:2529:G:H5''	26:1:2530:A:H5''	2.03	0.41
26:1:2793:G:H2'	26:1:2793:G:N3	2.36	0.41
27:2:46:A:O2'	27:2:47:C:OP2	2.32	0.41
3:C:25:PHE:N	26:1:578:G:OP1	2.42	0.41
3:C:70:ARG:HD3	3:C:74:MET:O	2.20	0.41
3:C:76:TYR:CZ	3:C:80:MET:HG3	2.56	0.41
8:H:92:LEU:HD13	27:2:99:G:H4'	2.03	0.41
19:S:40:GLN:NE2	26:1:660:A:O2'	2.54	0.41
19:S:169:ASN:HB2	26:1:365:A:OP2	2.20	0.41
22:X:109:ILE:CG1	22:X:125:ALA:HB1	2.50	0.41
24:Z:79:GLN:NE2	24:Z:88:GLU:OE2	2.34	0.41
26:1:89:U:C3'	26:1:90:A:H2'	2.47	0.41
26:1:229:A:H4'	26:1:230:A:OP1	2.20	0.41
26:1:262:G:H1'	26:1:666:A:O2'	2.21	0.41
26:1:525:A:H1'	26:1:526:A:H5''	2.03	0.41
26:1:1513:A:H3'	26:1:1514:A:H8	1.85	0.41
26:1:1781:C:H5	26:1:2743:U:O2'	2.04	0.41
26:1:2260:A:H2'	26:1:2261:G:H8	1.85	0.41
1:A:15:LEU:HD21	1:A:57:VAL:HG22	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:54:LYS:HE2	26:1:1038:C:C5	2.56	0.40
4:D:42:GLY:HA2	4:D:46:VAL:O	2.21	0.40
12:L:33:ASN:HB3	12:L:105:VAL:HB	2.03	0.40
12:L:57:LYS:HG3	12:L:68:TYR:HE1	1.85	0.40
23:Y:1:MET:HE3	23:Y:48:GLU:CG	2.46	0.40
23:Y:64:VAL:HG22	23:Y:106:VAL:HG12	2.03	0.40
23:Y:109:VAL:HG12	23:Y:110:SER:O	2.21	0.40
26:1:523:A:O2'	26:1:524:A:H5'	2.20	0.40
26:1:603:C:H2'	26:1:604:G:O4'	2.21	0.40
26:1:793:G:N2	26:1:796:A:H5'	2.27	0.40
26:1:2288:C:H2'	26:1:2289:U:H5'	2.03	0.40
26:1:2367:A:H2'	26:1:2368:G:C8	2.56	0.40
27:2:23:U:H4'	27:2:24:C:C5	2.56	0.40
27:2:44:A:H2'	27:2:45:C:C6	2.56	0.40
18:R:1:MET:N	26:1:2553:G:O2'	2.45	0.40
26:1:2610:G:H2'	26:1:2611:U:H5'	2.02	0.40
26:1:2686:G:C3'	26:1:2687:A:H5''	2.51	0.40
2:B:181:VAL:HB	2:B:272:ARG:HB2	2.03	0.40
15:O:36:CYS:HB2	15:O:43:THR:CG2	2.51	0.40
17:Q:39:LYS:O	17:Q:43:GLN:HB2	2.21	0.40
20:V:93:LEU:CD1	20:V:97:ASN:HB3	2.51	0.40
26:1:442:G:O2'	26:1:443:U:H5'	2.21	0.40
26:1:895:U:H5	26:1:973:A:N1	2.19	0.40
26:1:1478:A:O2'	26:1:1479:G:H5'	2.20	0.40
26:1:2105:C:H2'	26:1:2106:U:C6	2.56	0.40
26:1:2400:U:H2'	26:1:2401:C:H6	1.86	0.40
26:1:2507:C:C2'	26:1:2508:G:H5'	2.50	0.40
26:1:2559:G:N2	26:1:2690:G:O2'	2.54	0.40
26:1:2610:G:O2'	26:1:2611:U:H5'	2.21	0.40
26:1:2683:U:O2	26:1:2692:A:N7	2.55	0.40
26:1:2832:A:H2'	26:1:2833:U:O4'	2.22	0.40
27:2:33:U:H3	27:2:48:A:H1'	1.85	0.40
2:B:88:SER:C	2:B:158:ALA:HB2	2.46	0.40
2:B:157:SER:OG	2:B:158:ALA:N	2.55	0.40
12:L:44:ASP:HB3	12:L:46:TYR:CE1	2.57	0.40
12:L:64:LYS:HE2	26:1:2851:G:C6	2.56	0.40
12:L:205:LYS:O	12:L:206:LYS:HB2	2.20	0.40
26:1:50:U:H4'	26:1:51:G:OP2	2.22	0.40
26:1:386:C:O2'	26:1:387:G:H5'	2.22	0.40
26:1:683:G:H2'	26:1:684:U:O4'	2.22	0.40
26:1:1085:U:C2	26:1:1158:G:N1	2.88	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:1:1423:C:H2'	26:1:1424:A:H8	1.86	0.40
26:1:1759:G:H3'	26:1:1760:G:H5''	2.03	0.40
26:1:1772:G:H2'	26:1:1773:A:H5'	2.02	0.40
26:1:2563:G:O2'	26:1:2564:U:H5'	2.21	0.40
10:J:4:GLN:HG3	10:J:5:CYS:O	2.21	0.40
10:J:4:GLN:OE1	10:J:11:LYS:HE2	2.22	0.40
12:L:183:LEU:HD22	12:L:198:LYS:O	2.22	0.40
18:R:24:MET:HA	18:R:35:ARG:HA	2.02	0.40
20:V:16:TRP:HA	20:V:54:TYR:O	2.22	0.40
21:W:10:VAL:HG22	21:W:84:CYS:SG	2.62	0.40
23:Y:42:ILE:CD1	23:Y:68:ILE:HD13	2.51	0.40
23:Y:83:MET:HE1	26:1:1000:G:O4'	2.22	0.40
26:1:155:U:O2'	26:1:156:A:H5'	2.21	0.40
26:1:162:A:H5'	26:1:163:U:H2'	2.04	0.40
26:1:222:A:N3	26:1:237:U:O2'	2.51	0.40
26:1:262:G:H21	26:1:666:A:H8	1.68	0.40
26:1:423:A:H2'	26:1:424:C:C6	2.56	0.40
26:1:1301:U:H2'	26:1:1302:G:C8	2.56	0.40
26:1:1394:U:H2'	26:1:1395:G:O4'	2.22	0.40
26:1:1479:G:H2'	26:1:1480:G:H8	1.86	0.40
26:1:1494:G:C2'	26:1:1495:C:H5'	2.50	0.40
26:1:1756:U:H3	26:1:1773:A:H62	1.69	0.40
26:1:1873:G:O2'	26:1:1874:A:H5'	2.22	0.40
26:1:2439:A:C2'	26:1:2440:G:H5'	2.52	0.40
27:2:15:C:N4	27:2:103:A:H2	2.18	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	
1	A	111/116 (96%)	98 (88%)	13 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	266/276 (96%)	237 (89%)	29 (11%)	0	100	100
3	C	114/118 (97%)	106 (93%)	8 (7%)	0	100	100
4	D	98/102 (96%)	91 (93%)	7 (7%)	0	100	100
5	E	109/116 (94%)	102 (94%)	7 (6%)	0	100	100
6	F	82/91 (90%)	75 (92%)	7 (8%)	0	100	100
7	G	87/105 (83%)	76 (87%)	11 (13%)	0	100	100
8	H	91/217 (42%)	81 (89%)	10 (11%)	0	100	100
9	I	76/85 (89%)	67 (88%)	9 (12%)	0	100	100
10	J	55/62 (89%)	47 (86%)	8 (14%)	0	100	100
11	K	54/69 (78%)	50 (93%)	4 (7%)	0	100	100
12	L	213/217 (98%)	188 (88%)	25 (12%)	0	100	100
13	M	54/59 (92%)	47 (87%)	7 (13%)	0	100	100
14	N	48/57 (84%)	45 (94%)	3 (6%)	0	100	100
15	O	45/49 (92%)	41 (91%)	4 (9%)	0	100	100
16	P	42/45 (93%)	42 (100%)	0	0	100	100
17	Q	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
18	R	35/37 (95%)	30 (86%)	5 (14%)	0	100	100
19	S	186/207 (90%)	173 (93%)	13 (7%)	0	100	100
20	V	141/145 (97%)	131 (93%)	10 (7%)	0	100	100
21	W	118/122 (97%)	108 (92%)	10 (8%)	0	100	100
22	X	142/146 (97%)	121 (85%)	21 (15%)	0	100	100
23	Y	133/144 (92%)	127 (96%)	6 (4%)	0	100	100
24	Z	119/122 (98%)	107 (90%)	12 (10%)	0	100	100
25	a	94/119 (79%)	85 (90%)	9 (10%)	0	100	100
All	All	2575/2891 (89%)	2334 (91%)	241 (9%)	0	100	100

There are no Ramachandran outliers to report.

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	
1	A	99/102 (97%)	99 (100%)	0	100	100
2	B	218/223 (98%)	218 (100%)	0	100	100
3	C	96/98 (98%)	96 (100%)	0	100	100
4	D	85/86 (99%)	85 (100%)	0	100	100
5	E	90/94 (96%)	90 (100%)	0	100	100
6	F	76/82 (93%)	76 (100%)	0	100	100
7	G	76/90 (84%)	76 (100%)	0	100	100
8	H	81/190 (43%)	81 (100%)	0	100	100
9	I	61/66 (92%)	61 (100%)	0	100	100
10	J	47/52 (90%)	47 (100%)	0	100	100
11	K	51/62 (82%)	51 (100%)	0	100	100
12	L	173/175 (99%)	173 (100%)	0	100	100
13	M	50/53 (94%)	49 (98%)	1 (2%)	48	72
14	N	45/50 (90%)	45 (100%)	0	100	100
15	O	45/47 (96%)	45 (100%)	0	100	100
16	P	39/40 (98%)	39 (100%)	0	100	100
17	Q	55/56 (98%)	55 (100%)	0	100	100
18	R	35/35 (100%)	35 (100%)	0	100	100
19	S	154/170 (91%)	154 (100%)	0	100	100
20	V	122/123 (99%)	122 (100%)	0	100	100
21	W	98/100 (98%)	98 (100%)	0	100	100
22	X	110/112 (98%)	110 (100%)	0	100	100
23	Y	112/119 (94%)	112 (100%)	0	100	100
24	Z	101/102 (99%)	101 (100%)	0	100	100
25	a	80/95 (84%)	80 (100%)	0	100	100
All	All	2199/2422 (91%)	2198 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
13	M	52	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (49) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3	ASN
1	A	4	HIS
2	B	82	GLN
2	B	153	GLN
3	C	37	GLN
3	C	38	GLN
3	C	91	ASN
5	E	28	ASN
5	E	65	ASN
6	F	37	GLN
6	F	54	ASN
6	F	57	ASN
8	H	85	GLN
8	H	88	HIS
11	K	31	GLN
12	L	128	GLN
12	L	134	HIS
12	L	146	HIS
12	L	181	GLN
13	M	52	HIS
15	O	25	ASN
16	P	9	ASN
17	Q	7	HIS
17	Q	31	HIS
17	Q	35	ASN
18	R	29	ASN
19	S	29	ASN
19	S	38	ASN
19	S	40	GLN
19	S	46	GLN
19	S	67	GLN
19	S	141	ASN
19	S	148	GLN
19	S	169	ASN
19	S	188	ASN
20	V	24	GLN
20	V	48	HIS
20	V	59	ASN
20	V	81	HIS
20	V	119	GLN
21	W	110	ASN

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Mol	Chain	Res	Type
22	X	4	HIS
22	X	17	ASN
22	X	126	HIS
23	Y	25	ASN
23	Y	46	GLN
23	Y	71	HIS
25	a	37	ASN
25	a	39	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
26	1	2634/2923 (90%)	649 (24%)	18 (0%)
27	2	103/115 (89%)	38 (36%)	1 (0%)
All	All	2737/3038 (90%)	687 (25%)	19 (0%)

All (687) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
26	1	10	A
26	1	11	U
26	1	12	U
26	1	15	G
26	1	25	U
26	1	34	U
26	1	44	A
26	1	45	G
26	1	58	G
26	1	62	C
26	1	63	U
26	1	64	A
26	1	71	A
26	1	72	U
26	1	73	A
26	1	75	G
26	1	83	G
26	1	89	U
26	1	90	A
26	1	91	A
26	1	95	A
26	1	96	G

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Mol	Chain	Res	Type
26	1	97	C
26	1	99	U
26	1	100	U
26	1	101	G
26	1	102	A
26	1	115	C
26	1	116	G
26	1	117	A
26	1	118	A
26	1	119	U
26	1	130	A
26	1	150	A
26	1	156	A
26	1	160	G
26	1	162	A
26	1	163	U
26	1	164	A
26	1	165	C
26	1	168	A
26	1	169	G
26	1	176	A
26	1	177	G
26	1	180	G
26	1	183	A
26	1	184	C
26	1	185	A
26	1	191	A
26	1	199	A
26	1	202	A
26	1	216	A
26	1	218	G
26	1	219	A
26	1	224	A
26	1	225	A
26	1	227	G
26	1	228	A
26	1	230	A
26	1	233	U
26	1	236	A
26	1	242	U
26	1	243	U
26	1	244	A

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Mol	Chain	Res	Type
26	1	250	G
26	1	251	G
26	1	253	G
26	1	255	G
26	1	258	A
26	1	268	A
26	1	269	G
26	1	277	C
26	1	294	G
26	1	296	G
26	1	299	U
26	1	301	U
26	1	302	A
26	1	303	G
26	1	308	C
26	1	310	C
26	1	311	U
26	1	327	G
26	1	331	G
26	1	332	A
26	1	333	C
26	1	338	G
26	1	345	C
26	1	351	G
26	1	354	A
26	1	356	A
26	1	359	A
26	1	366	G
26	1	372	A
26	1	373	A
26	1	381	G
26	1	384	G
26	1	397	U
26	1	398	C
26	1	401	U
26	1	402	C
26	1	404	U
26	1	406	A
26	1	407	G
26	1	410	G
26	1	411	A
26	1	415	U

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Mol	Chain	Res	Type
26	1	432	G
26	1	434	G
26	1	439	U
26	1	443	U
26	1	447	A
26	1	448	A
26	1	452	G
26	1	457	G
26	1	458	A
26	1	459	C
26	1	460	C
26	1	463	C
26	1	464	U
26	1	466	C
26	1	471	G
26	1	489	A
26	1	501	C
26	1	502	C
26	1	503	A
26	1	506	A
26	1	507	C
26	1	526	A
26	1	527	G
26	1	540	G
26	1	547	A
26	1	548	A
26	1	550	A
26	1	552	A
26	1	553	A
26	1	554	C
26	1	555	C
26	1	558	A
26	1	563	G
26	1	566	U
26	1	567	G
26	1	575	G
26	1	576	U
26	1	577	A
26	1	578	G
26	1	590	U
26	1	592	A
26	1	593	U

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Mol	Chain	Res	Type
26	1	594	G
26	1	598	G
26	1	606	G
26	1	616	G
26	1	617	A
26	1	618	A
26	1	620	G
26	1	621	A
26	1	622	A
26	1	630	G
26	1	646	A
26	1	647	G
26	1	650	U
26	1	657	U
26	1	658	A
26	1	659	A
26	1	660	A
26	1	665	G
26	1	667	G
26	1	679	G
26	1	680	C
26	1	682	A
26	1	683	G
26	1	689	A
26	1	690	U
26	1	691	A
26	1	698	U
26	1	699	U
26	1	700	A
26	1	723	C
26	1	727	G
26	1	730	A
26	1	731	U
26	1	735	C
26	1	740	G
26	1	744	A
26	1	754	U
26	1	756	A
26	1	757	G
26	1	765	U
26	1	771	G
26	1	775	A

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Mol	Chain	Res	Type
26	1	785	C
26	1	786	U
26	1	792	U
26	1	793	G
26	1	796	A
26	1	802	G
26	1	809	A
26	1	810	A
26	1	819	A
26	1	820	G
26	1	821	C
26	1	822	G
26	1	823	G
26	1	827	A
26	1	829	U
26	1	830	U
26	1	834	A
26	1	837	G
26	1	838	A
26	1	850	G
26	1	857	C
26	1	891	A
26	1	903	G
26	1	904	G
26	1	911	A
26	1	912	C
26	1	914	G
26	1	917	U
26	1	920	A
26	1	921	C
26	1	954	A
26	1	955	A
26	1	960	C
26	1	969	A
26	1	970	U
26	1	971	U
26	1	972	A
26	1	977	A
26	1	982	G
26	1	985	A
26	1	989	A
26	1	990	G

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Mol	Chain	Res	Type
26	1	997	G
26	1	1002	U
26	1	1005	G
26	1	1018	A
26	1	1020	G
26	1	1027	A
26	1	1040	A
26	1	1045	A
26	1	1049	C
26	1	1054	A
26	1	1055	A
26	1	1056	U
26	1	1057	A
26	1	1065	A
26	1	1066	G
26	1	1070	A
26	1	1072	A
26	1	1076	A
26	1	1077	U
26	1	1085	U
26	1	1158	G
26	1	1161	A
26	1	1162	C
26	1	1163	U
26	1	1173	A
26	1	1174	U
26	1	1176	U
26	1	1177	A
26	1	1179	C
26	1	1183	G
26	1	1186	A
26	1	1187	A
26	1	1190	A
26	1	1193	U
26	1	1195	A
26	1	1210	U
26	1	1211	G
26	1	1213	C
26	1	1214	C
26	1	1215	U
26	1	1216	U
26	1	1217	U

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Mol	Chain	Res	Type
26	1	1218	G
26	1	1220	A
26	1	1248	U
26	1	1249	U
26	1	1258	A
26	1	1267	A
26	1	1271	G
26	1	1276	G
26	1	1278	G
26	1	1284	A
26	1	1288	G
26	1	1291	A
26	1	1293	U
26	1	1294	G
26	1	1309	G
26	1	1310	A
26	1	1311	A
26	1	1312	A
26	1	1313	G
26	1	1317	G
26	1	1321	A
26	1	1323	A
26	1	1326	C
26	1	1337	A
26	1	1338	U
26	1	1339	U
26	1	1340	G
26	1	1344	A
26	1	1345	A
26	1	1349	U
26	1	1351	C
26	1	1358	A
26	1	1366	U
26	1	1375	G
26	1	1378	U
26	1	1382	C
26	1	1386	U
26	1	1388	C
26	1	1389	U
26	1	1396	A
26	1	1402	A
26	1	1405	G

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Mol	Chain	Res	Type
26	1	1415	A
26	1	1416	U
26	1	1421	A
26	1	1423	C
26	1	1430	A
26	1	1432	A
26	1	1433	U
26	1	1436	C
26	1	1447	A
26	1	1448	U
26	1	1449	A
26	1	1450	A
26	1	1451	U
26	1	1452	C
26	1	1453	G
26	1	1454	U
26	1	1462	G
26	1	1463	A
26	1	1464	U
26	1	1465	G
26	1	1471	A
26	1	1472	C
26	1	1473	G
26	1	1477	U
26	1	1496	G
26	1	1497	A
26	1	1499	U
26	1	1502	A
26	1	1503	U
26	1	1504	U
26	1	1509	G
26	1	1510	U
26	1	1511	C
26	1	1512	U
26	1	1516	C
26	1	1517	A
26	1	1519	U
26	1	1520	A
26	1	1557	C
26	1	1561	G
26	1	1563	U
26	1	1566	G

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Mol	Chain	Res	Type
26	1	1570	G
26	1	1572	G
26	1	1575	A
26	1	1590	C
26	1	1591	G
26	1	1592	A
26	1	1594	U
26	1	1595	C
26	1	1600	A
26	1	1606	C
26	1	1607	A
26	1	1613	G
26	1	1616	A
26	1	1623	U
26	1	1625	U
26	1	1627	G
26	1	1628	A
26	1	1629	U
26	1	1631	G
26	1	1632	A
26	1	1634	A
26	1	1636	U
26	1	1644	C
26	1	1652	A
26	1	1653	A
26	1	1654	A
26	1	1662	A
26	1	1663	G
26	1	1676	A
26	1	1683	U
26	1	1690	A
26	1	1691	G
26	1	1692	C
26	1	1693	G
26	1	1698	A
26	1	1708	A
26	1	1711	G
26	1	1716	C
26	1	1718	G
26	1	1720	A
26	1	1722	A
26	1	1729	C

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Mol	Chain	Res	Type
26	1	1739	G
26	1	1740	G
26	1	1747	G
26	1	1756	U
26	1	1758	A
26	1	1759	G
26	1	1760	G
26	1	1761	G
26	1	1765	A
26	1	1767	G
26	1	1771	A
26	1	1772	G
26	1	1790	G
26	1	1791	G
26	1	1795	A
26	1	1800	A
26	1	1809	C
26	1	1811	A
26	1	1815	C
26	1	1826	G
26	1	1827	C
26	1	1828	U
26	1	1836	A
26	1	1839	G
26	1	1841	G
26	1	1842	A
26	1	1843	U
26	1	1846	A
26	1	1856	A
26	1	1865	C
26	1	1866	G
26	1	1875	A
26	1	1881	A
26	1	1886	A
26	1	1887	G
26	1	1893	A
26	1	1894	G
26	1	1898	C
26	1	1900	G
26	1	1901	C
26	1	1902	G
26	1	1910	G

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Mol	Chain	Res	Type
26	1	1911	A
26	1	1913	U
26	1	1924	G
26	1	1926	A
26	1	1927	A
26	1	1933	G
26	1	1939	A
26	1	1940	A
26	1	1941	C
26	1	1942	U
26	1	1943	A
26	1	1944	U
26	1	1946	A
26	1	1949	G
26	1	1954	A
26	1	1956	G
26	1	1957	G
26	1	1959	A
26	1	1962	G
26	1	1963	A
26	1	1965	A
26	1	1967	U
26	1	1970	U
26	1	1974	C
26	1	1982	U
26	1	1989	C
26	1	1990	C
26	1	1993	A
26	1	1994	C
26	1	1997	A
26	1	1998	A
26	1	1999	G
26	1	2003	U
26	1	2007	G
26	1	2008	A
26	1	2009	U
26	1	2018	U
26	1	2023	C
26	1	2046	U
26	1	2049	U
26	1	2050	A
26	1	2058	A

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Mol	Chain	Res	Type
26	1	2059	G
26	1	2060	A
26	1	2063	C
26	1	2070	C
26	1	2073	G
26	1	2079	G
26	1	2082	C
26	1	2083	G
26	1	2087	A
26	1	2088	G
26	1	2091	C
26	1	2093	C
26	1	2095	U
26	1	2096	G
26	1	2107	G
26	1	2108	U
26	1	2120	G
26	1	2122	A
26	1	2223	C
26	1	2226	A
26	1	2231	C
26	1	2235	A
26	1	2237	U
26	1	2238	U
26	1	2239	A
26	1	2241	C
26	1	2252	A
26	1	2265	G
26	1	2266	G
26	1	2289	U
26	1	2295	A
26	1	2300	A
26	1	2307	G
26	1	2308	C
26	1	2310	C
26	1	2313	A
26	1	2314	A
26	1	2315	A
26	1	2318	U
26	1	2329	U
26	1	2330	G
26	1	2331	G

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Mol	Chain	Res	Type
26	1	2341	A
26	1	2346	U
26	1	2347	A
26	1	2349	A
26	1	2362	A
26	1	2374	C
26	1	2377	C
26	1	2410	G
26	1	2412	C
26	1	2416	G
26	1	2417	U
26	1	2429	U
26	1	2432	G
26	1	2433	C
26	1	2450	U
26	1	2452	A
26	1	2453	A
26	1	2456	G
26	1	2468	C
26	1	2474	G
26	1	2475	A
26	1	2479	C
26	1	2480	A
26	1	2486	A
26	1	2499	G
26	1	2500	U
26	1	2501	U
26	1	2502	C
26	1	2505	A
26	1	2514	G
26	1	2521	G
26	1	2523	C
26	1	2525	C
26	1	2529	G
26	1	2532	G
26	1	2533	U
26	1	2540	A
26	1	2544	C
26	1	2545	A
26	1	2546	U
26	1	2556	G
26	1	2560	U

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Mol	Chain	Res	Type
26	1	2562	G
26	1	2564	U
26	1	2581	U
26	1	2585	C
26	1	2593	A
26	1	2594	G
26	1	2600	C
26	1	2609	G
26	1	2611	U
26	1	2612	U
26	1	2629	A
26	1	2630	G
26	1	2636	U
26	1	2637	C
26	1	2640	U
26	1	2642	U
26	1	2650	G
26	1	2657	G
26	1	2663	U
26	1	2673	C
26	1	2675	G
26	1	2677	C
26	1	2683	U
26	1	2687	A
26	1	2688	G
26	1	2693	C
26	1	2694	C
26	1	2696	G
26	1	2697	G
26	1	2700	G
26	1	2712	G
26	1	2716	U
26	1	2717	A
26	1	2718	C
26	1	2727	G
26	1	2741	G
26	1	2747	U
26	1	2753	U
26	1	2759	G
26	1	2760	A
26	1	2762	G
26	1	2769	G

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Mol	Chain	Res	Type
26	1	2771	G
26	1	2772	C
26	1	2775	A
26	1	2777	A
26	1	2778	G
26	1	2784	A
26	1	2791	A
26	1	2792	A
26	1	2793	G
26	1	2795	C
26	1	2799	C
26	1	2805	A
26	1	2810	A
26	1	2817	A
26	1	2820	U
26	1	2827	A
26	1	2828	U
26	1	2845	G
26	1	2849	A
26	1	2853	U
26	1	2854	A
26	1	2856	U
26	1	2862	C
26	1	2863	G
26	1	2868	G
26	1	2877	G
26	1	2879	G
26	1	2887	G
26	1	2888	A
26	1	2890	C
26	1	2892	G
26	1	2893	A
26	1	2899	A
26	1	2900	C
26	1	2901	U
26	1	2906	G
26	1	2911	A
26	1	2913	G
26	1	2916	U
27	2	7	G
27	2	10	U
27	2	11	A

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Mol	Chain	Res	Type
27	2	12	U
27	2	13	A
27	2	17	A
27	2	18	G
27	2	19	G
27	2	20	A
27	2	21	G
27	2	23	U
27	2	24	C
27	2	25	A
27	2	26	C
27	2	29	C
27	2	39	G
27	2	42	G
27	2	46	A
27	2	47	C
27	2	49	G
27	2	50	A
27	2	54	U
27	2	60	C
27	2	64	A
27	2	65	G
27	2	71	A
27	2	79	C
27	2	82	A
27	2	85	U
27	2	86	A
27	2	87	C
27	2	94	C
27	2	95	U
27	2	97	G
27	2	98	A
27	2	100	U
27	2	101	A
27	2	104	A

All (19) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
26	1	10	A
26	1	44	A
26	1	90	A

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Mol	Chain	Res	Type
26	1	229	A
26	1	276	C
26	1	433	U
26	1	525	A
26	1	1350	U
26	1	1510	U
26	1	1631	G
26	1	1845	U
26	1	1865	C
26	1	1926	A
26	1	1988	C
26	1	2330	G
26	1	2783	U
26	1	2827	A
26	1	2887	G
27	2	84	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
28	G6M	1	3001	-	27,27,27	1.81	2 (7%)	37,37,37	1.96	9 (24%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
28	G6M	1	3001	-	-	8/15/35/35	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
28	1	3001	G6M	O11-C12	6.97	1.45	1.35
28	1	3001	G6M	C12-N8	-4.76	1.31	1.36

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
28	1	3001	G6M	C10-O11-C12	-5.56	105.66	110.10
28	1	3001	G6M	C19-N14-C15	4.70	122.14	111.57
28	1	3001	G6M	C9-N8-C12	3.96	114.10	111.17
28	1	3001	G6M	C3-C2-C1	-3.93	119.88	123.35
28	1	3001	G6M	C18-C19-N14	-2.99	104.27	109.93
28	1	3001	G6M	O11-C10-C9	2.91	107.32	104.50
28	1	3001	G6M	C10-C9-N8	-2.31	99.67	101.85
28	1	3001	G6M	C4-N8-C12	-2.11	123.77	125.98
28	1	3001	G6M	C10-C20-N29	2.05	116.06	111.98

There are no chirality outliers.

All (8) torsion outliers are listed below:

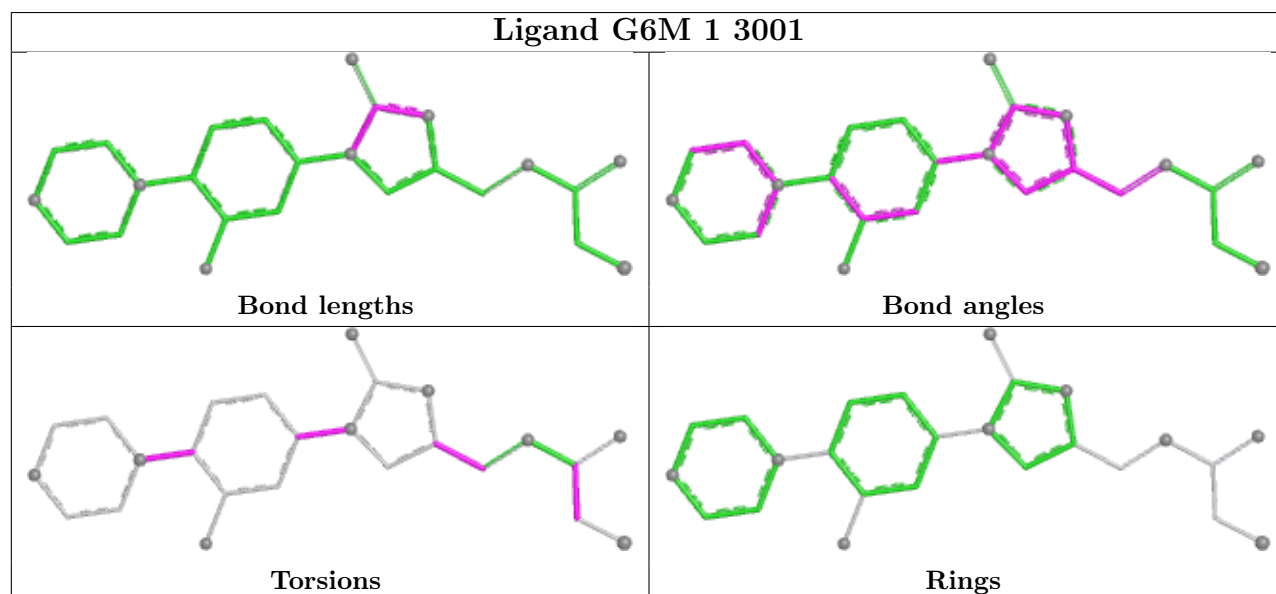
Mol	Chain	Res	Type	Atoms
28	1	3001	G6M	C2-C1-N14-C15
28	1	3001	G6M	N29-C30-C31-CL33
28	1	3001	G6M	O32-C30-C31-CL33
28	1	3001	G6M	C3-C4-N8-C12
28	1	3001	G6M	C6-C1-N14-C15
28	1	3001	G6M	C5-C4-N8-C12
28	1	3001	G6M	C9-C10-C20-N29
28	1	3001	G6M	C2-C1-N14-C19

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths,

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



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

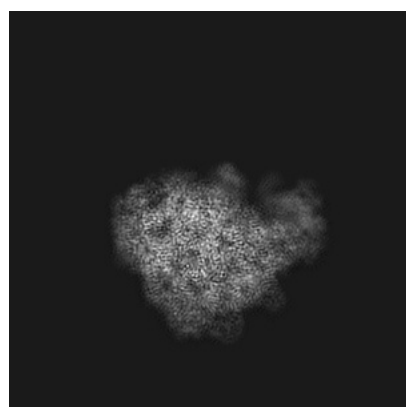
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7870. These allow visual inspection of the internal detail of the map and identification of artifacts.

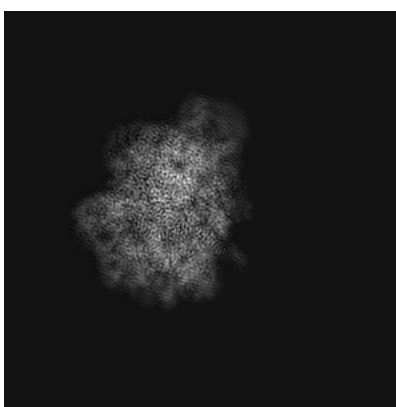
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

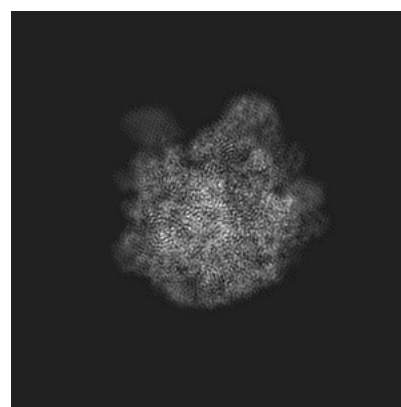
6.1.1 Primary map



X



Y



Z

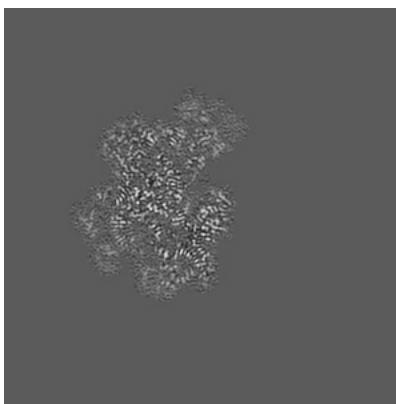
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

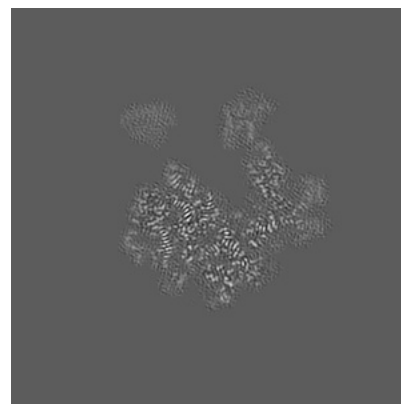
6.2.1 Primary map



X Index: 182



Y Index: 182



Z Index: 182

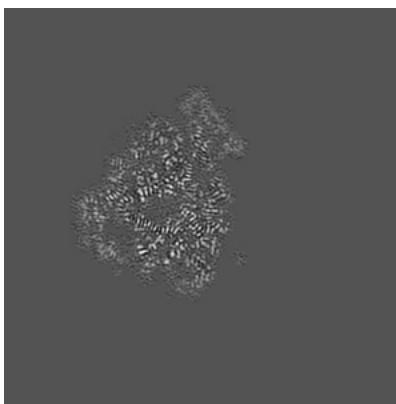
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

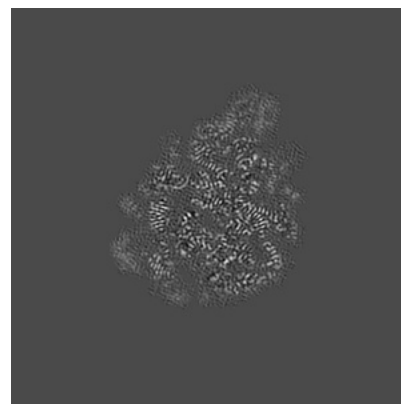
6.3.1 Primary map



X Index: 190



Y Index: 165

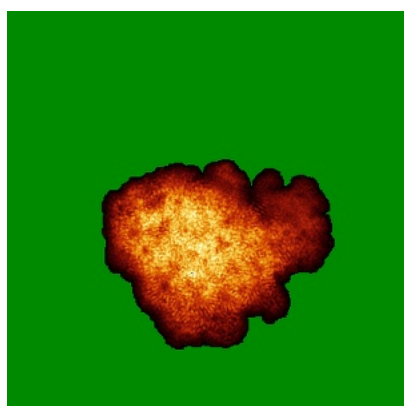


Z Index: 147

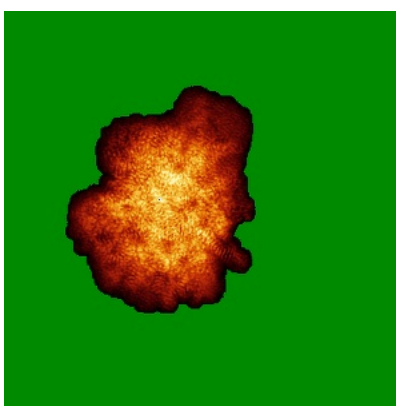
The images above show the largest variance slices of the map in three orthogonal directions.

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

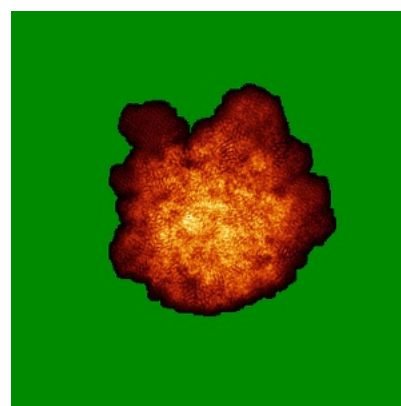
6.4.1 Primary map



X



Y

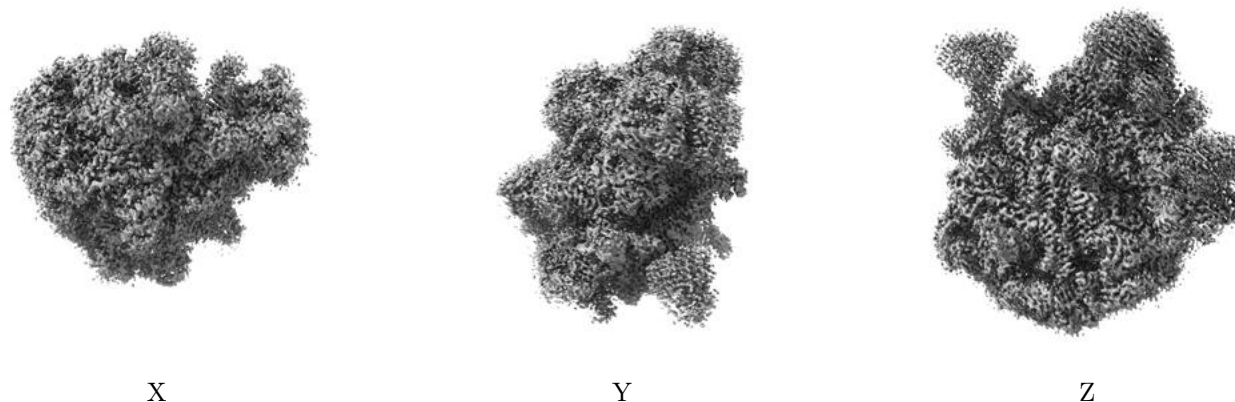


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.03. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

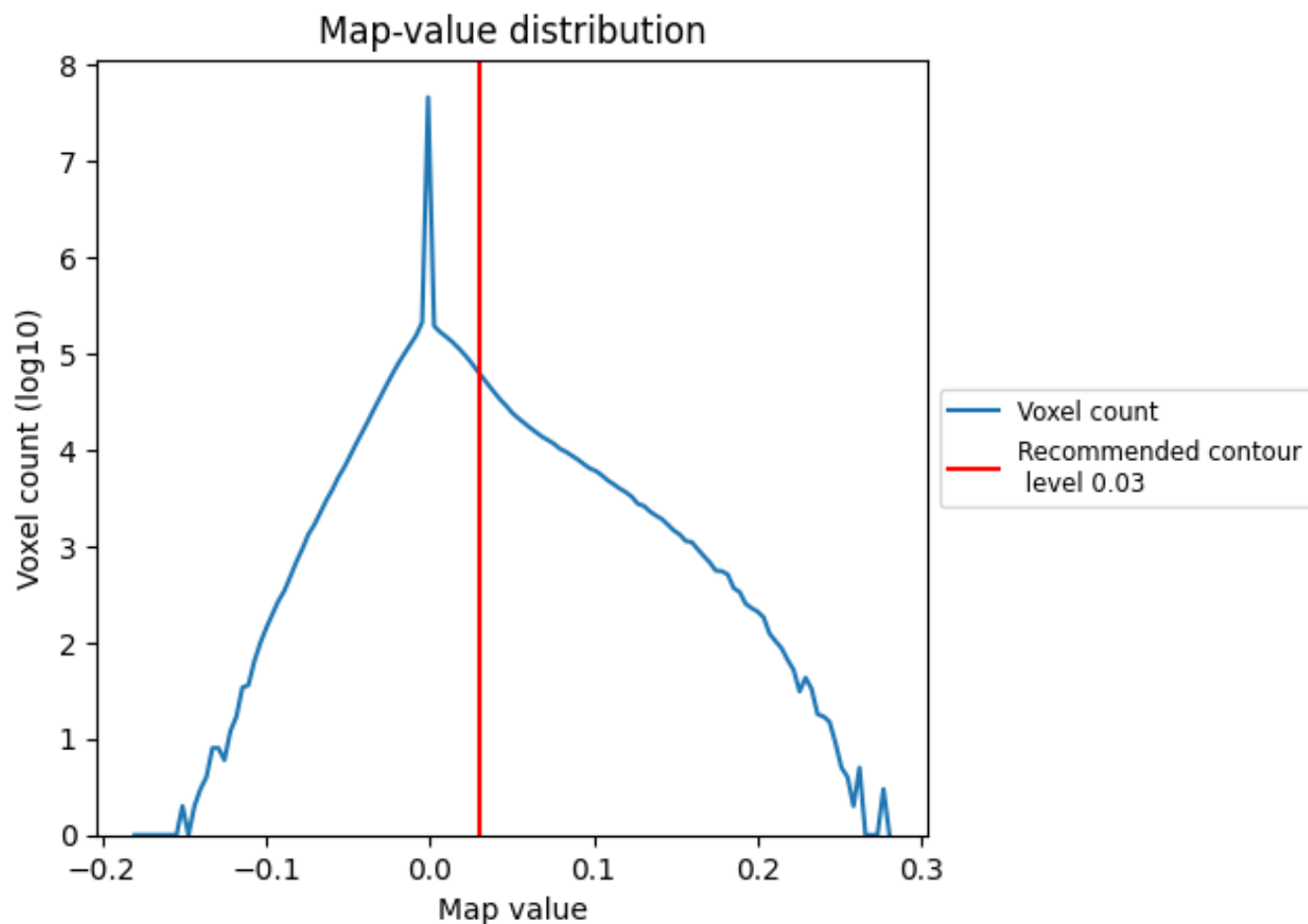
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

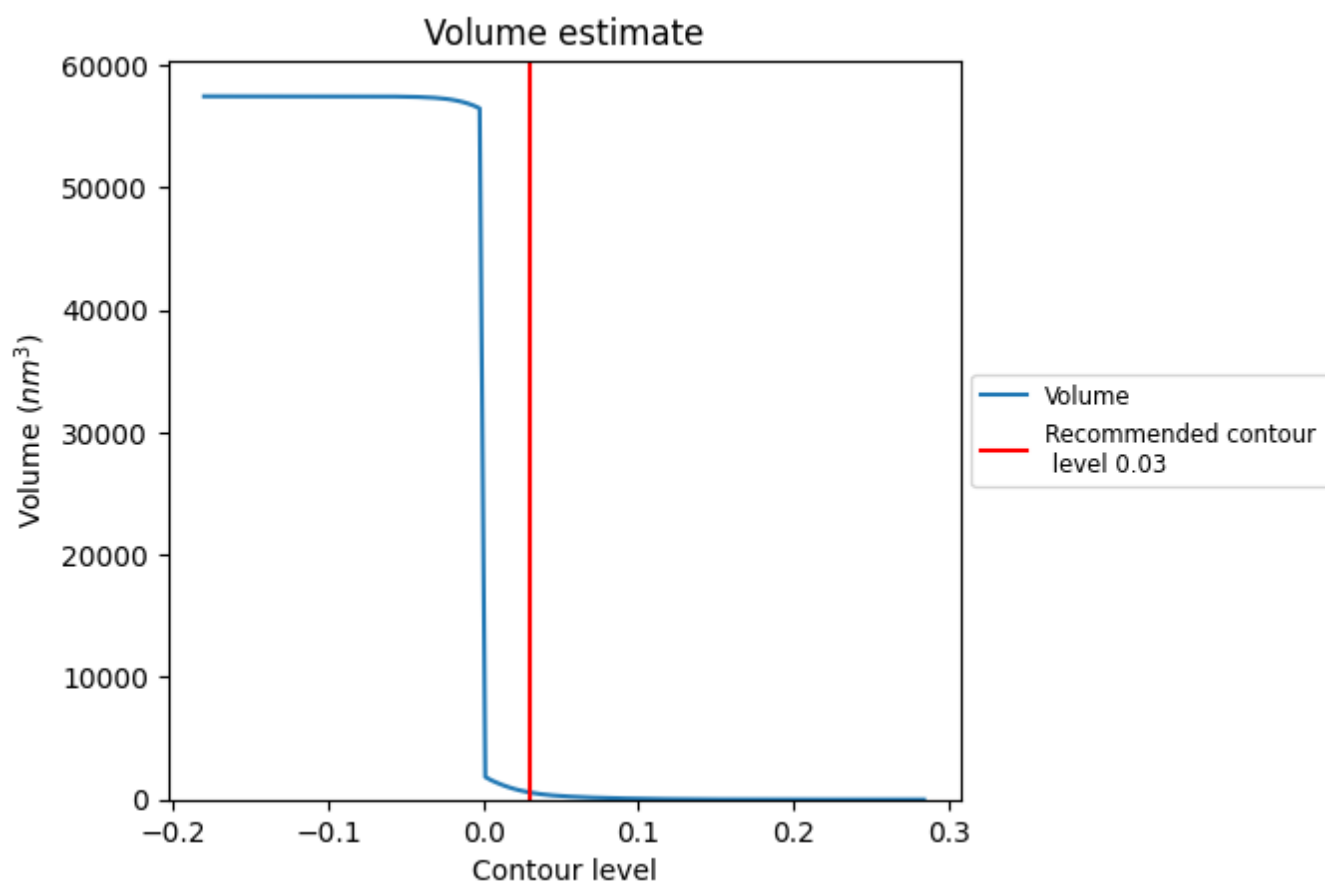
This section contains the results of statistical analysis of the map.

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.

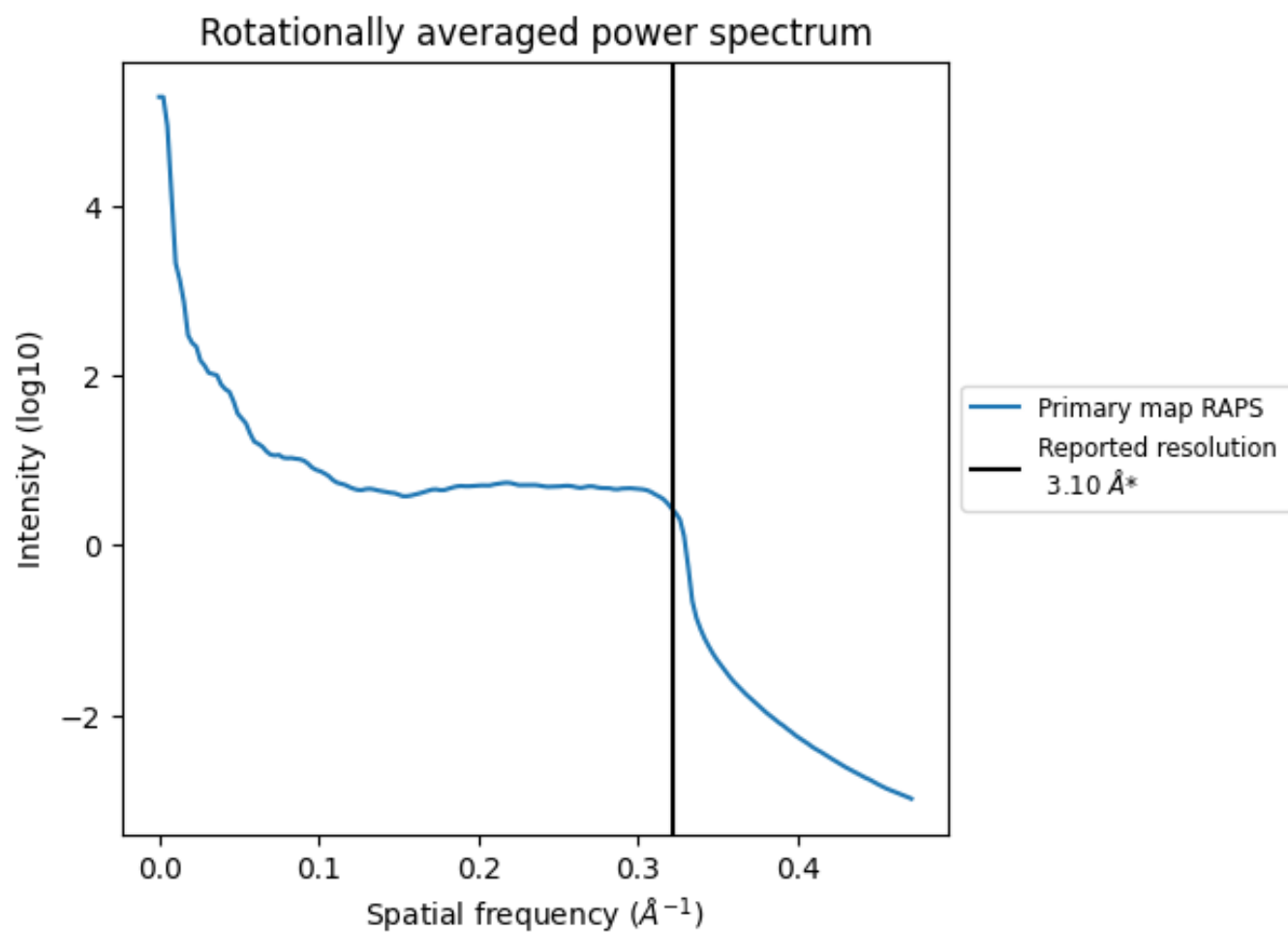
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 573 nm³; this corresponds to an approximate mass of 518 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 0.323 Å⁻¹

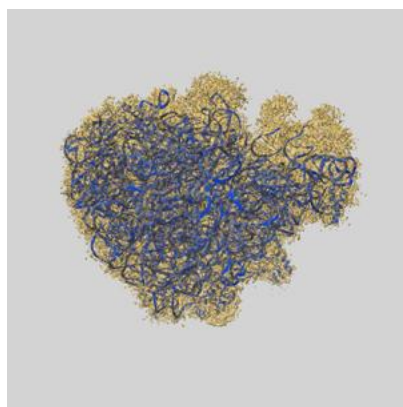
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

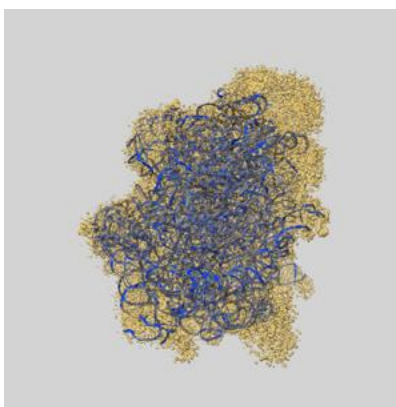
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-7870 and PDB model 6DDG. Per-residue inclusion information can be found in section [3](#) on page [9](#).

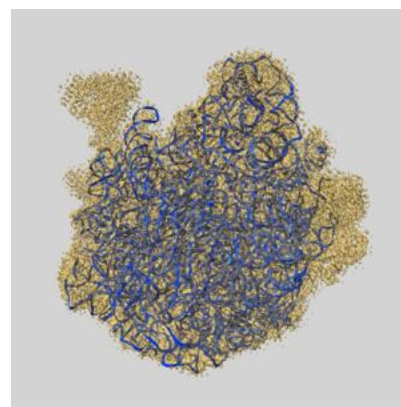
9.1 Map-model overlay [i](#)



X



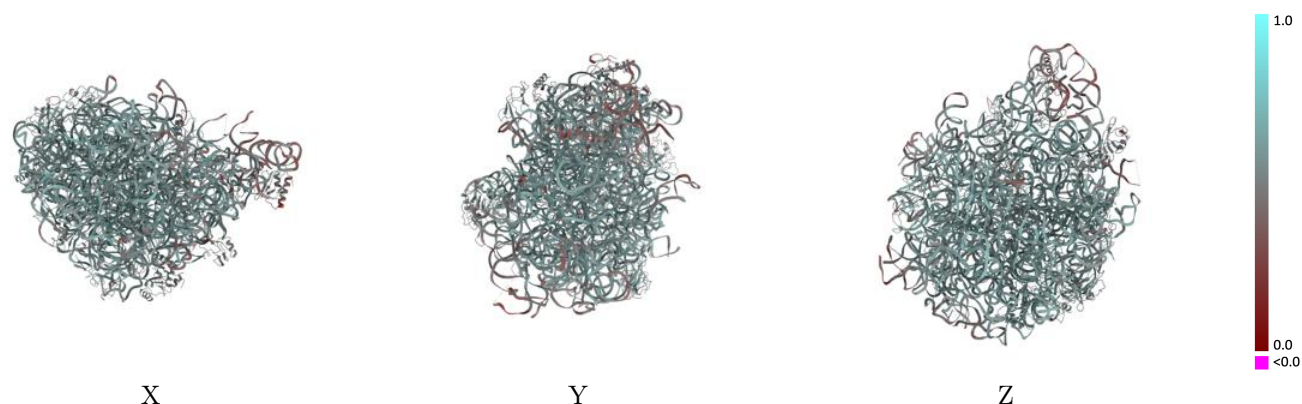
Y



Z

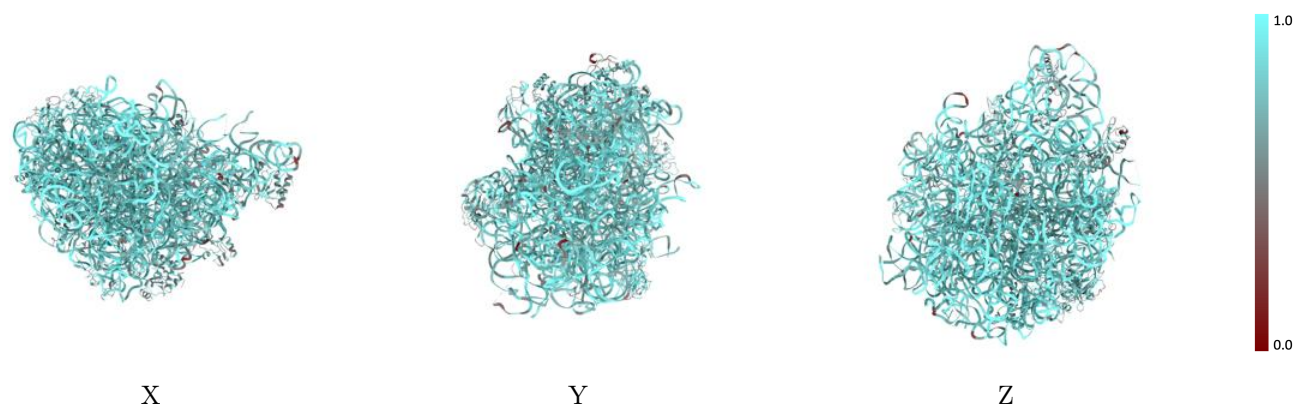
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



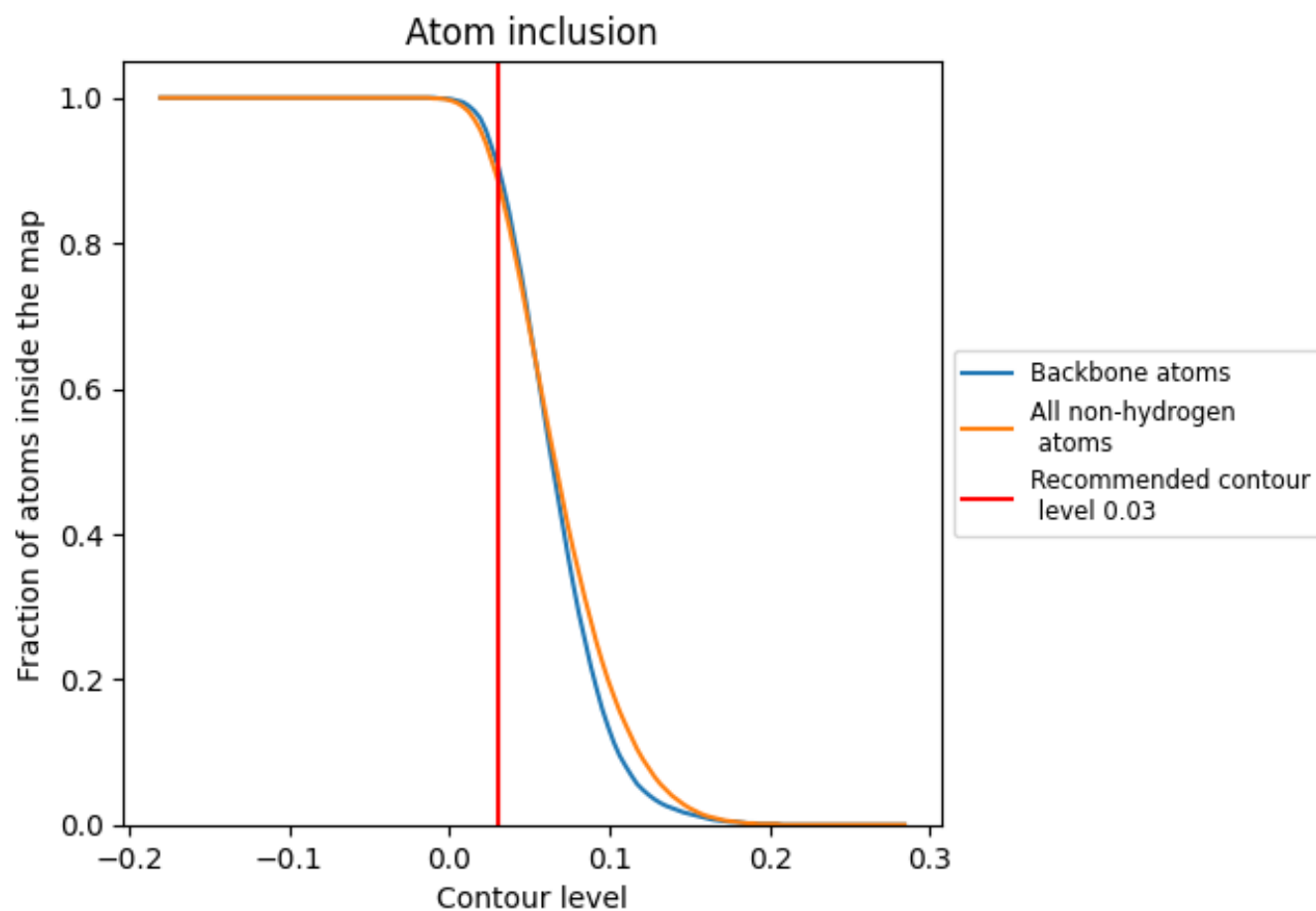
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 89% 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 (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8890	 0.5620
1	 0.9260	 0.5750
2	 0.7980	 0.4590
A	 0.7610	 0.5240
B	 0.8470	 0.5660
C	 0.8500	 0.5520
D	 0.7850	 0.5340
E	 0.8290	 0.5570
F	 0.7810	 0.5300
G	 0.6840	 0.4880
H	 0.6180	 0.4720
I	 0.8220	 0.5510
J	 0.7690	 0.5420
K	 0.7290	 0.4980
L	 0.8300	 0.5530
M	 0.8280	 0.5520
N	 0.8560	 0.5690
O	 0.7530	 0.5010
P	 0.8830	 0.6010
Q	 0.8800	 0.5810
R	 0.8280	 0.5470
S	 0.7750	 0.5310
V	 0.8390	 0.5560
W	 0.7950	 0.5410
X	 0.7900	 0.5270
Y	 0.8120	 0.5460
Z	 0.8070	 0.5440
a	 0.6630	 0.4430

