



Full wwPDB EM Validation Report ⓘ

Mar 2, 2024 – 07:50 pm GMT

PDB ID : 8CDV
EMDB ID : EMD-16596
Title : Rnase R bound to a 30S degradation intermediate (state II)
Authors : Paternoga, H.; Dimitrova-Paternoga, L.; Wilson, D.N.
Deposited on : 2023-02-01
Resolution : 4.73 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:

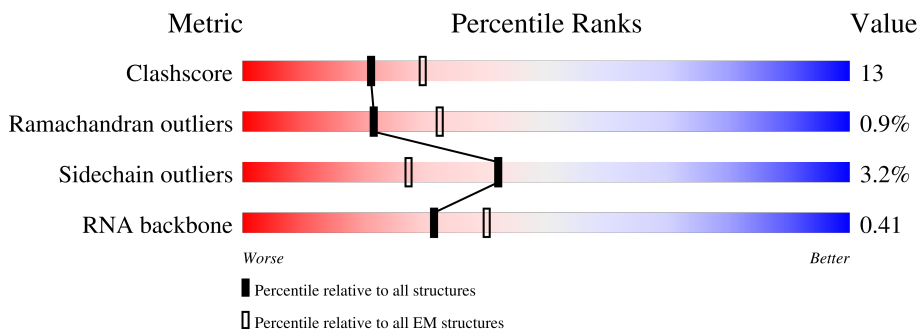
EMDB validation analysis : 0.0.1.dev70
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance i

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

The reported resolution of this entry is 4.73 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	1554	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;"> <p>26%</p> <p>22%</p> </div> <div style="flex-grow: 1;"> </div> </div>
2	B	11	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;"> <p>100%</p> <p>9%</p> </div> <div style="flex-grow: 1;"> </div> </div>
3	C	779	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;"> <p>58%</p> <p>55%</p> </div> <div style="flex-grow: 1;"> </div> </div>
4	F	200	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;"> <p>54%</p> <p>78%</p> </div> <div style="flex-grow: 1;"> </div> </div>
5	G	166	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;"> <p>66%</p> <p>77%</p> </div> <div style="flex-grow: 1;"> </div> </div>
6	H	156	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;"> <p>56%</p> <p>51%</p> </div> <div style="flex-grow: 1;"> </div> </div>
7	I	132	<div style="display: flex; justify-content: space-between; align-items: center;"> <div style="text-align: center;"> <p>33%</p> <p>82%</p> </div> <div style="flex-grow: 1;"> </div> </div>

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Mol	Chain	Length	Quality of chain
8	J	130	<p>75% 63% 12% 22%</p>
9	K	102	<p>59% 36% 22% 39%</p>
10	L	138	<p>30% 82% 14%</p>
11	M	121	<p>85% 64% 20% 5% 11%</p>
12	O	89	<p>30% 87% 9%</p>
13	P	90	<p>20% 78% 18%</p>
14	Q	87	<p>25% 84% 10%</p>
15	R	92	<p>85% 63% 20% 15%</p>
16	S	88	<p>36% 80% 14% 6%</p>
17	T	95	<p>74% 84% 11%</p>
18	U	79	<p>49% 57% 22% 19%</p>
19	V	131	<p>69% 60% 11% 30%</p>

2 Entry composition

There are 19 unique types of molecules in this entry. The entry contains 43593 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	A	1247	26755	11934	4917	8657	1247	0	0

- Molecule 2 is a RNA chain called RNA Substrate.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	B	11	242	110	55	66	11	0	0

- Molecule 3 is a protein called Ribonuclease R.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	C	457	3687	2316	629	724	18	0	0

- Molecule 4 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	F	185	1490	942	276	270	2	0	0

- Molecule 5 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	G	158	1170	736	216	216	2	0	0

- Molecule 6 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	H	89	727	456	134	133	4	0	0

- Molecule 7 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	I	131	1036	655	191	187	3	0	0

- Molecule 8 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
8	J	102	776	481	150	145	0	0

- Molecule 9 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	K	62	489	306	91	91	1	0	0

- Molecule 10 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	L	136	1052	653	211	186	2	0	0

- Molecule 11 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
11	M	108	868	534	176	158	0	0

- Molecule 12 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	O	85	710	436	144	129	1	0	0

- Molecule 13 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
13	P	88	695	441	128	124	2	0	0

- Molecule 14 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	Q	84	Total	C	N	O	S	0	0
			691	435	128	126	2		

- Molecule 15 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	R	78	Total	C	N	O	S	0	0
			633	409	112	110	2		

- Molecule 16 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	S	83	Total	C	N	O	S	0	0
			637	390	130	116	1		

- Molecule 17 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	T	92	Total	C	N	O	S	0	0
			755	476	132	146	1		

- Molecule 18 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	U	64	Total	C	N	O	S	0	0
			518	332	96	88	2		

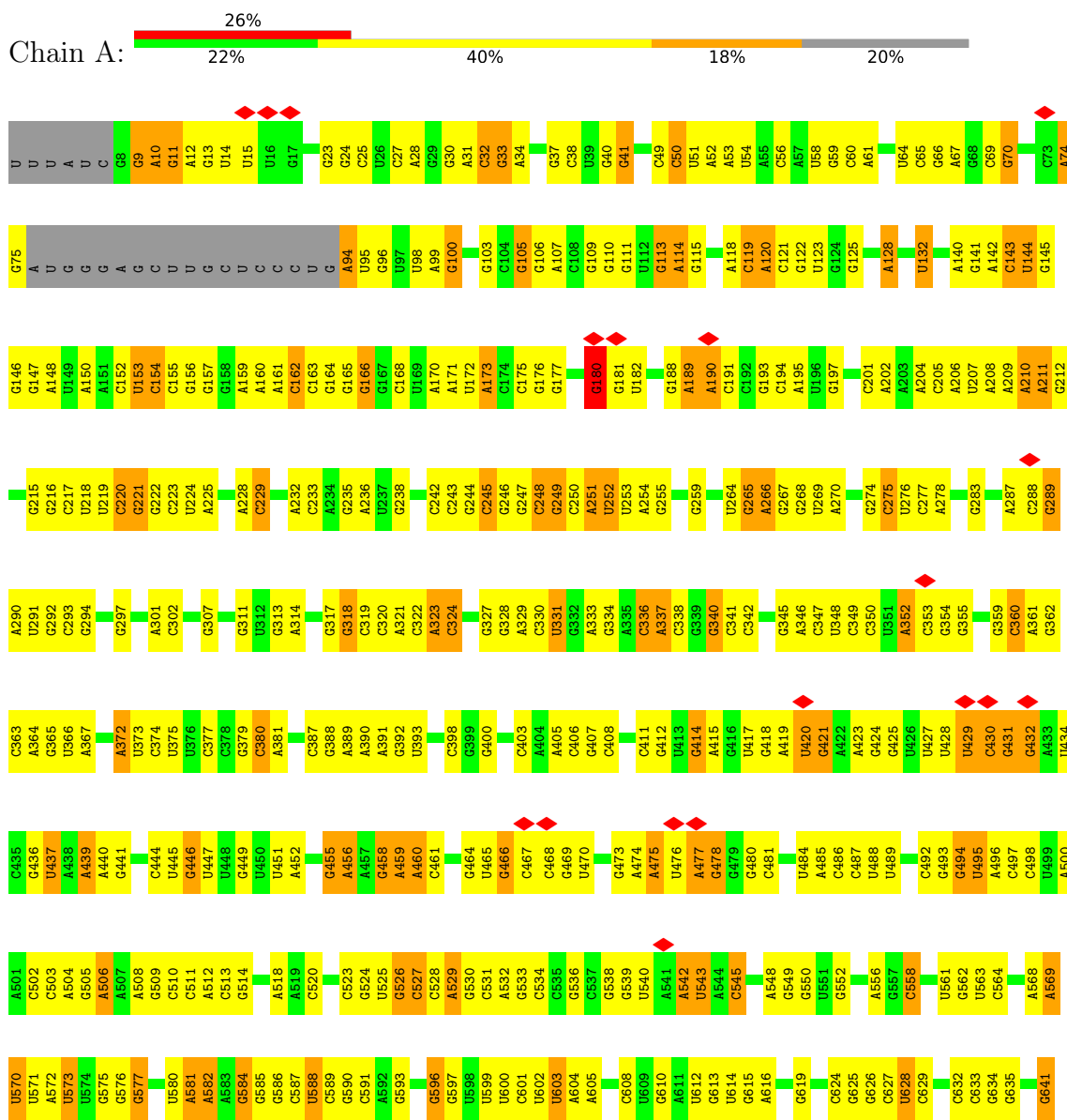
- Molecule 19 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	V	92	Total	C	N	O	S	0	0
			662	409	123	129	1		

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: 16S rRNA

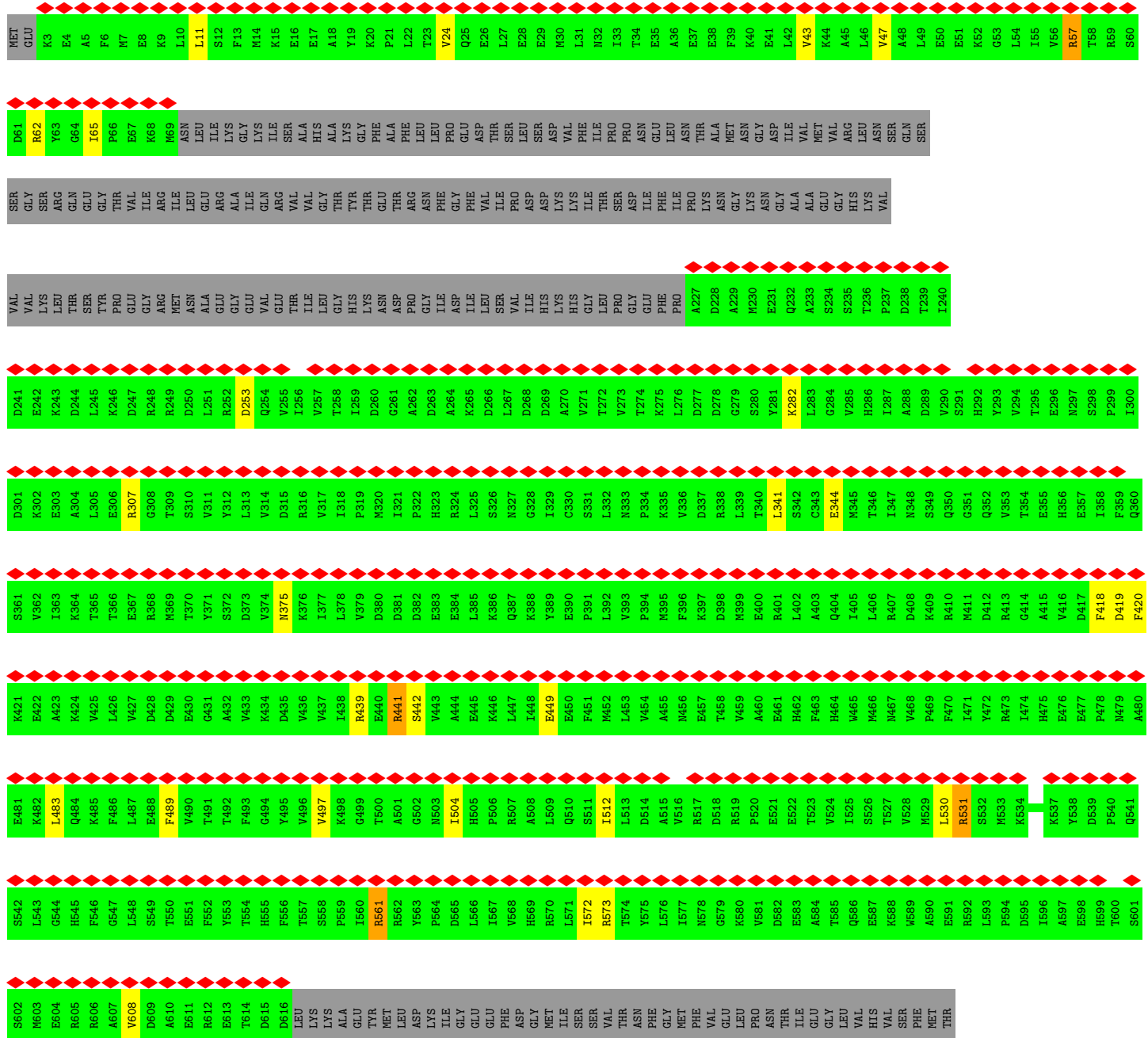


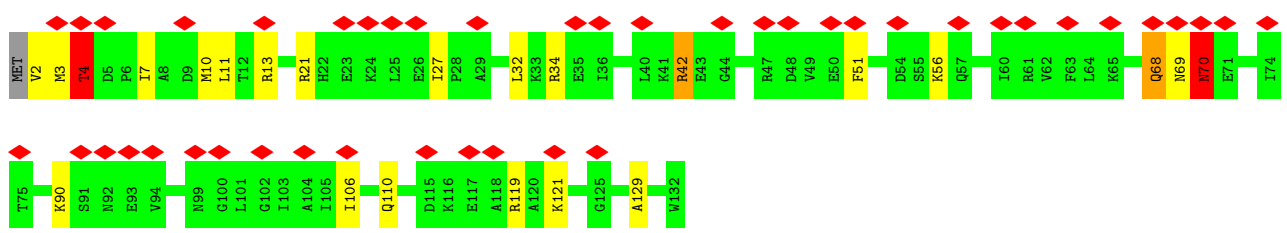
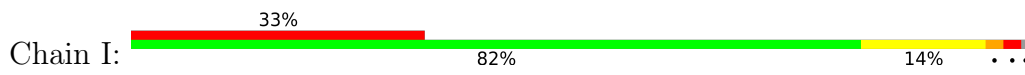
U842	U843	U844	U845	U846	U847	U848	U849	U850	U851	U852	U853	U854	U855	U856	U857	U858	U859	U860	U861	U862	U863	U864	U865	U866	U867	U868	U869	U870	U871	U872	U873	U874	U875	U876	U877	U878	U879	U880	U881	U882	U883	U884	U885	U886	U887	U888	U889	U890	U891	U892	U893	U894	U895	U896	U897	U898	U899	U900	U901	U902	U903	U904	U905	U906	U907	U908	U909	U910	U911	U912	U913	U914	U915	U916	U917	U918	U919	U920	U921	U922	U923	U924	U925	U926	U927	U928	U929	U930	U931	U932	U933	U934	U935	U936	U937	U938	U939	U940	U941	U942	U943	U944	U945	U946	U947	U948	U949	U950	U951	U952	U953	U954	U955	U956	U957	U958	U959	U960	U961	U962	U963	U964	U965	U966	U967	U968	U969	U970	U971	U972	U973	U974	U975	U976	U977	U978	U979	U980	U981	U982	U983	U984	U985	U986	U987	U988	U989	U990	U991	U992	U993	U994	U995	U996	U997	U998	U999	U1000	U1001	U1002	U1003	U1004	U1005	U1006	U1007	U1008	U1009	U1010	U1011	U1012	U1013	U1014	U1015	U1016	U1017	U1018	U1019	U1020	U1021	U1022	U1023	U1024	U1025	U1026	U1027	U1028	U1029	U1030	U1031	U1032	U1033	U1034	U1035	U1036	U1037	U1038																																																																																																																																																																																
U1039	U1040	C1041	G1042	G1043	G1044	G1045	G1046	C1047	A1048	G1049	A1050	G1051	U1052	G1053	A1054	C1055	G1056	G1057	U1058	U1059	U1060	U1061	U1062	U1063	U1064	U1065	U1066	U1067	U1068	U1069	U1070	U1071	U1072	U1073	U1074	U1075	U1076	U1077	U1078	U1079	U1080	U1081	U1082	U1083	U1084	U1085	U1086	U1087	U1088	U1089	U1090	U1091	U1092	U1093	U1094	U1095	U1096	U1097	U1098	U1099	U1100	U1101	U1102	U1103	U1104	U1105	U1106	U1107	U1108	U1109	U1110	U1111	U1112	U1113	U1114	U1115	U1116	U1117	U1118	U1119	U1120	U1121	U1122	U1123	U1124	U1125	U1126	U1127	U1128	U1129	U1130	U1131	U1132	U1133	U1134	U1135	U1136	U1137	U1138	U1139	U1140	U1141	U1142	U1143	U1144	U1145	U1146	U1147	U1148	U1149	U1150	U1151	U1152	U1153	U1154	U1155	U1156	U1157	U1158	U1159	U1160	U1161	U1162	U1163	U1164	U1165	U1166	U1167	U1168	U1169	U1170	U1171	U1172	U1173	U1174	U1175	U1176	U1177	U1178	U1179	U1180	U1181	U1182	U1183	U1184	U1185	U1186	U1187	U1188	U1189	U1190	U1191	U1192	U1193	U1194	U1195	U1196	U1197	U1198	U1199	U1200	U1201	U1202	U1203	U1204	U1205	U1206	U1207	U1208	U1209	U1210	U1211	U1212	U1213	U1214	U1215	U1216	U1217	U1218																																																																																																																																																																																																	
C1219	U1220	U1221	A1222	U1223	A1224	U1225	C1226	C1227	U1228	G1229	U1230	G1231	C1232	U1233	A1234	C1235	A1236	C1237	A1238	C1239	G1240	U1241	G1242	C1243	U1244	A1245	C1246	U1247	A1248	U1249	G1250	U1251	A1252	C1253	U1254	A1255	U1256	A1257	C1258	U1259	A1260	U1261	G1262	U1263	G1264	C1265	U1266	G1267	C1268	U1269	A1270	G1271	C1272	U1273	C1274	G1275	U1276	G1277	A1278																																																																																																																																																																																																																																																																																																																									
G1279	G1280	U1281	U1282	A1283	A1284	G1285	C1286	U1287	A1288	U1289	A1290	C1291	U1292	C1293	U1294	A1295	A1296	U1297	A1298	U1299	C1300	U1301	G1302	U1303	U1304	C1305	U1306	C1307	A1308	U1309	U1310	U1311	C1312	U1313	G1314	U1315	A1316	C1317	U1318	C1319	U1320	G1321	U1322	C1323	U1324	C1325	U1326	G1327	C1328	U1329	G1330	C1331	U1332	A1333	C1334	U1335	G1336	U1337	G1338																																																																																																																																																																																																																																																																																																																									
U1339	G1340	A1341	A1342	C1343	G1344	U1345	G1346	A1347	A1348	U1349	C1350	G1351	U1352	C1353	U1354	A1355	G1356	U1357	A1358	U1359	C1360	C1361	G1362	C1363	G1364	C1365	U1366	U1367	C1368	U1369	G1370	C1371	U1372	U1373	G1374	C1375	G1376	U1377	C1378	U1379	U1380	U1381	U1382	U1383	U1384	U1385	U1386	U1387	U1388	U1389	U1390	U1391	U1392	U1393	U1394	U1395	U1396	U1397	U1398	U1399	U1400	U1401	U1402	U1403	U1404	U1405	U1406	U1407	U1408	U1409	U1410	U1411	U1412	U1413	U1414	U1415	U1416	U1417	U1418	U1419	U1420	U1421	U1422	U1423	U1424	U1425	U1426	U1427	U1428	U1429	U1430	U1431	U1432	U1433	U1434	U1435	U1436	U1437	U1438	U1439	U1440	U1441	U1442	U1443	U1444	U1445	U1446	U1447	U1448	U1449	U1450	U1451	U1452	U1453	U1454	U1455	U1456	U1457	U1458	U1459	U1460	U1461	U1462	U1463	U1464	U1465	U1466	U1467	U1468	U1469	U1470	U1471	U1472	U1473	U1474	U1475	U1476	U1477	U1478	U1479	U1480	U1481	U1482	U1483	U1484	U1485	U1486	U1487	U1488	U1489	U1490	U1491	U1492	U1493	U1494	U1495	U1496	U1497	U1498	U1499	U1500	U1501	U1502	U1503	U1504	U1505	U1506	U1507	U1508	U1509	U1510	U1511	U1512	U1513	U1514	U1515	U1516	U1517	U1518	U1519	U1520	U1521	U1522	U1523	U1524	U1525	U1526	U1527	U1528	U1529	U1530	U1531	U1532	U1533	U1534	U1535	U1536	U1537	U1538	U1539	U1540	U1541	U1542	U1543	U1544	U1545	U1546	U1547	U1548	U1549	U1550	U1551	U1552	U1553	U1554	U1555	U1556	U1557	U1558	U1559	U1560	U1561	U1562	U1563	U1564	U1565	U1566	U1567	U1568	U1569	U1570	U1571	U1572	U1573	U1574	U1575	U1576	U1577	U1578	U1579	U1580	U1581	U1582	U1583	U1584	U1585	U1586	U1587	U1588	U1589	U1590	U1591	U1592	U1593	U1594	U1595	U1596	U1597	U1598	U1599	U1600	U1601	U1602	U1603	U1604	U1605	U1606	U1607	U1608	U1609	U1610	U1611	U1612	U1613	U1614	U1615	U1616	U1617	U1618	U1619	U1620	U1621	U1622	U1623	U1624	U1625	U1626	U1627	U1628	U1629	U1630	U1631	U1632	U1633	U1634	U1635	U1636	U1637	U1638	U1639	U1640	U1641	U1642	U1643	U1644	U1645	U1646	U1647	U1648	U1649	U1650	U1651	U1652	U1653	U1654	U1655	U1656	U1657	U1658	U1659	U1660	U1661	U1662	U1663	U1664	U1665	U1666	U1667	U1668	U1669	U1670	U1671	U1672	U1673	U1674	U1675	U1676	U1677	U1678	U1679	U1680	U1681	U1682	U1683	U1684	U1685	U1686	U1687	U1688	U1689	U1690	U1691	U1692	U1693	U1694	U1695	U1696	U1697	U1698	U1699	U1700	U1701	U1702	U1703	U1704	U1705	U1706	U1707	U1708	U1709	U1710	U1711

● Molecule 2: RNA Substrate

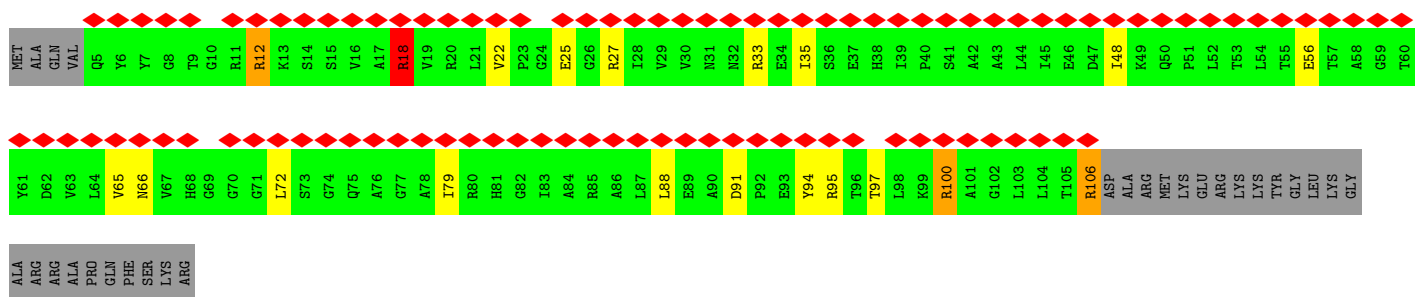
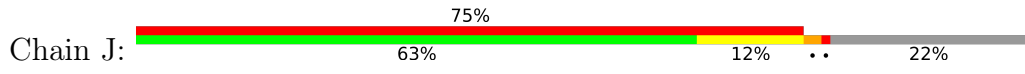


● Molecule 3: Ribonuclease R

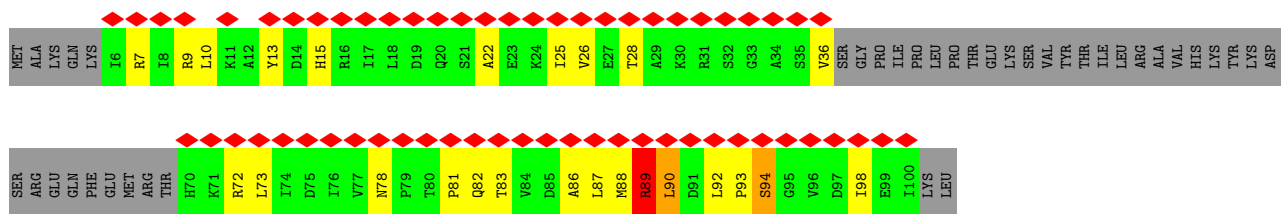




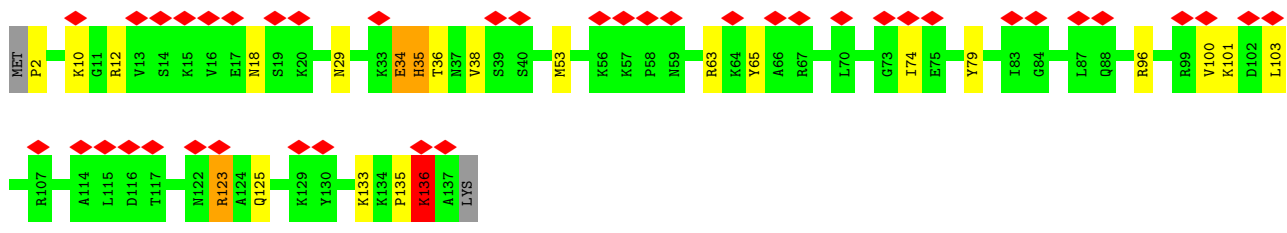
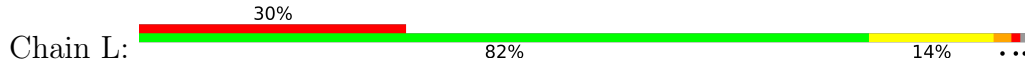
• Molecule 8: 30S ribosomal protein S9



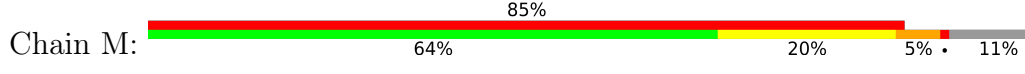
• Molecule 9: 30S ribosomal protein S10

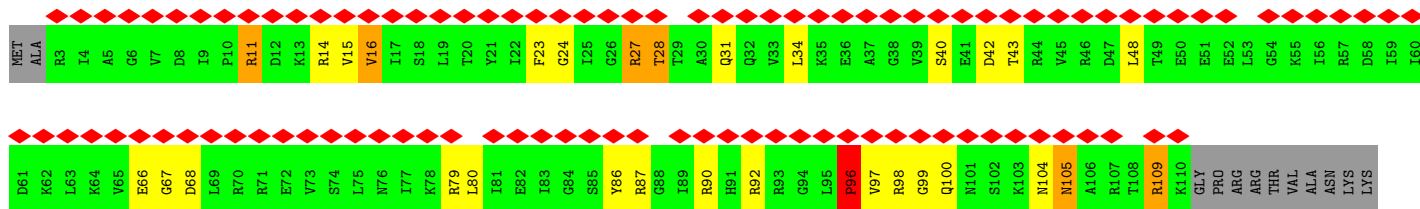


• Molecule 10: 30S ribosomal protein S12



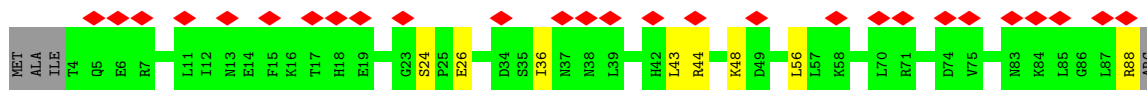
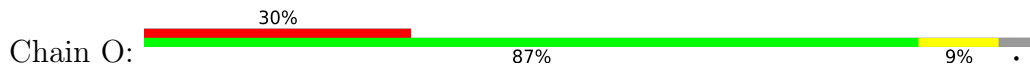
• Molecule 11: 30S ribosomal protein S13



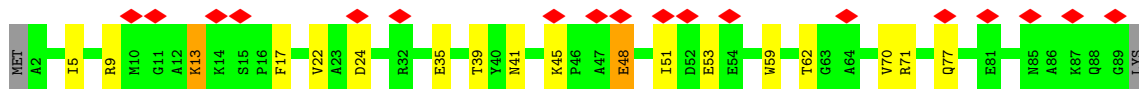
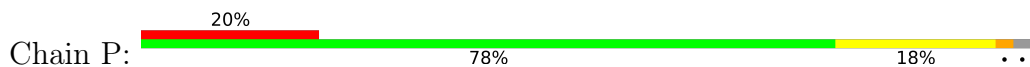


LYS

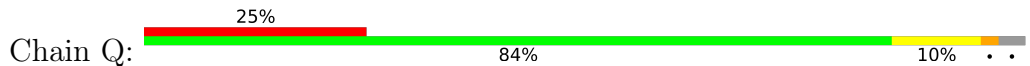
• Molecule 12: 30S ribosomal protein S15



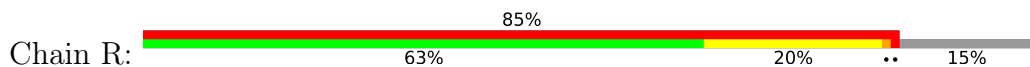
• Molecule 13: 30S ribosomal protein S16



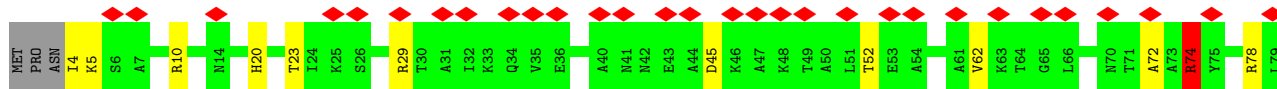
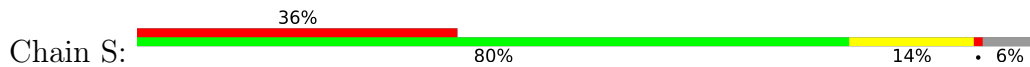
• Molecule 14: 30S ribosomal protein S17

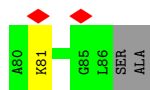


• Molecule 15: 30S ribosomal protein S19

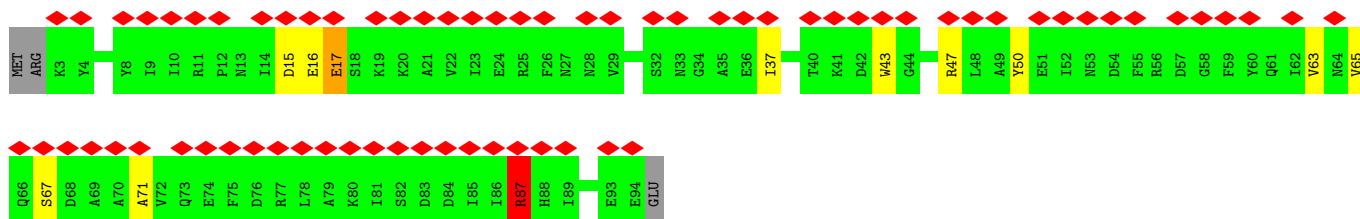
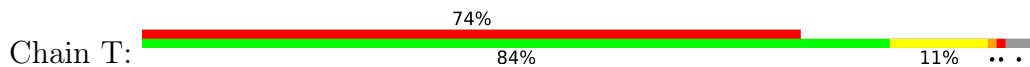


• Molecule 16: 30S ribosomal protein S20

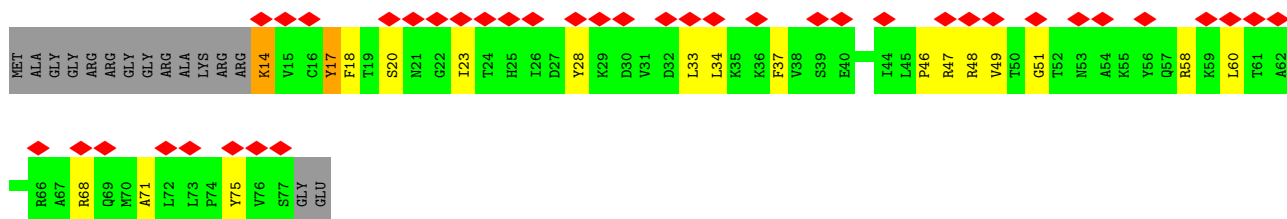




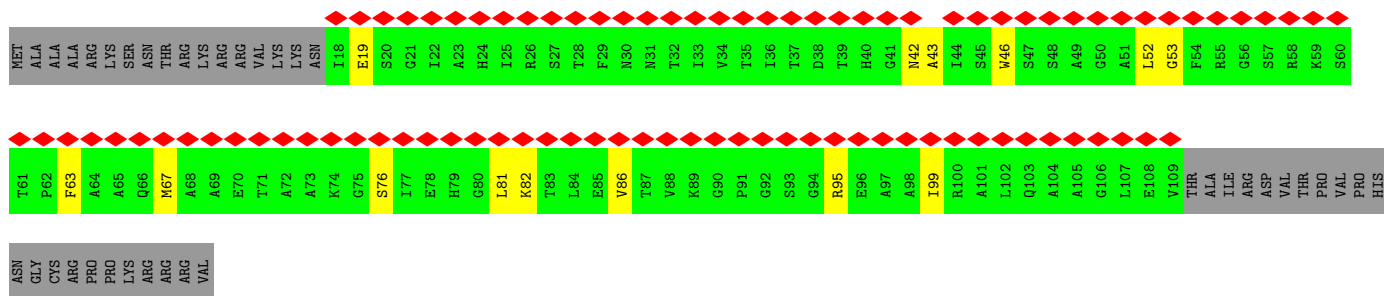
• Molecule 17: 30S ribosomal protein S6



• Molecule 18: 30S ribosomal protein S18



• Molecule 19: 30S ribosomal protein S11



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	4011	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)	400	Depositor
Maximum defocus (nm)	900	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	0.052	Depositor
Minimum map value	-0.027	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0125	Depositor
Map size (\AA)	307.2, 307.2, 307.2	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	0.8, 0.8, 0.8	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.60	0/29955	0.98	16/46719 (0.0%)
2	B	0.65	0/274	1.08	0/425
3	C	0.38	0/3747	0.62	3/5058 (0.1%)
4	F	0.38	0/1517	0.64	0/2036
5	G	0.38	0/1182	0.70	0/1591
6	H	0.36	0/733	0.62	0/976
7	I	0.39	0/1048	0.76	2/1407 (0.1%)
8	J	0.33	0/786	0.67	1/1063 (0.1%)
9	K	0.40	0/493	0.79	1/664 (0.2%)
10	L	0.37	0/1069	0.71	0/1435
11	M	0.33	0/873	0.68	1/1166 (0.1%)
12	O	0.37	0/718	0.65	0/960
13	P	0.44	0/708	0.79	1/950 (0.1%)
14	Q	0.38	0/699	0.69	0/933
15	R	0.35	0/649	0.70	1/872 (0.1%)
16	S	0.37	0/639	0.95	3/852 (0.4%)
17	T	0.32	0/766	0.64	2/1031 (0.2%)
18	U	0.37	0/526	1.01	4/705 (0.6%)
19	V	0.36	0/671	0.56	0/906
All	All	0.53	0/47053	0.90	35/69749 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
3	C	0	6
4	F	0	3
5	G	0	4
7	I	0	2
8	J	0	6
9	K	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
10	L	0	1
11	M	0	4
12	O	0	2
13	P	0	2
14	Q	0	2
15	R	0	2
16	S	0	3
17	T	0	1
18	U	0	2
All	All	0	42

There are no bond length outliers.

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	U	17	TYR	CB-CG-CD2	13.84	129.31	121.00
16	S	74	ARG	NE-CZ-NH1	-13.35	113.62	120.30
18	U	17	TYR	CB-CG-CD1	-11.44	114.14	121.00
16	S	74	ARG	NE-CZ-NH2	10.46	125.53	120.30
1	A	319	C	O5'-P-OP1	-9.13	97.48	105.70
7	I	42	ARG	NE-CZ-NH2	8.76	124.68	120.30
1	A	1287	C	O4'-C1'-N1	7.24	113.99	108.20
1	A	890	C	O5'-P-OP1	-6.76	99.61	105.70
8	J	18	ARG	NE-CZ-NH2	6.49	123.55	120.30
16	S	81	LYS	CB-CG-CD	6.41	128.27	111.60
1	A	826	C	C1'-O4'-C4'	-6.36	104.81	109.90
17	T	87	ARG	CG-CD-NE	6.19	124.80	111.80
18	U	17	TYR	OH-CZ-CE2	6.10	136.56	120.10
3	C	561	ARG	NE-CZ-NH2	-5.98	117.31	120.30
1	A	318	G	OP1-P-O3'	5.96	118.31	105.20
1	A	320	C	O5'-P-OP1	-5.94	100.36	105.70
9	K	94	SER	CA-C-N	5.84	127.88	116.20
7	I	4	THR	N-CA-CB	5.82	121.36	110.30
1	A	188	G	C3'-C2'-C1'	-5.81	96.86	101.50
1	A	180	G	C3'-C2'-C1'	-5.80	96.86	101.50
3	C	561	ARG	NE-CZ-NH1	5.67	123.14	120.30
1	A	1153	G	C3'-C2'-C1'	-5.65	96.98	101.50
13	P	13	LYS	CA-C-N	5.63	129.59	117.20
1	A	753	C	O5'-P-OP1	-5.63	100.63	105.70
3	C	531	ARG	NE-CZ-NH2	-5.62	117.49	120.30
1	A	662	U	O5'-P-OP1	5.51	117.31	110.70
17	T	87	ARG	NE-CZ-NH1	5.50	123.05	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	M	11	ARG	NE-CZ-NH1	-5.44	117.58	120.30
1	A	1211	U	C1'-O4'-C4'	-5.34	105.63	109.90
1	A	372	A	P-O3'-C3'	5.27	126.03	119.70
1	A	815	C	OP1-P-OP2	-5.11	111.93	119.60
15	R	78	ARG	NE-CZ-NH2	-5.10	117.75	120.30
1	A	94	A	OP1-P-OP2	-5.07	112.00	119.60
1	A	1148	G	P-O3'-C3'	5.05	125.76	119.70
18	U	17	TYR	CE1-CZ-OH	-5.01	106.58	120.10

There are no chirality outliers.

All (42) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	307	ARG	Sidechain
3	C	439	ARG	Sidechain
3	C	441	ARG	Sidechain
3	C	57	ARG	Sidechain
3	C	573	ARG	Sidechain
3	C	62	ARG	Sidechain
4	F	14	ARG	Sidechain
4	F	146	ARG	Sidechain
4	F	182	ARG	Sidechain
5	G	14	ARG	Sidechain
5	G	149	ARG	Sidechain
5	G	5	ASP	Peptide
5	G	88	ARG	Sidechain
7	I	119	ARG	Sidechain
7	I	42	ARG	Sidechain
8	J	100	ARG	Sidechain
8	J	106	ARG	Sidechain
8	J	12	ARG	Sidechain
8	J	18	ARG	Sidechain
8	J	27	ARG	Sidechain
8	J	33	ARG	Sidechain
9	K	89	ARG	Sidechain
9	K	93	PRO	Peptide
10	L	123	ARG	Sidechain
11	M	109	ARG	Sidechain
11	M	11	ARG	Sidechain
11	M	27	ARG	Sidechain
11	M	98	ARG	Sidechain
12	O	44	ARG	Sidechain

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Mol	Chain	Res	Type	Group
12	O	88	ARG	Sidechain
13	P	71	ARG	Sidechain
13	P	9	ARG	Sidechain
14	Q	39	ARG	Sidechain
14	Q	4	ARG	Sidechain
15	R	28	LYS	Peptide
15	R	78	ARG	Sidechain
16	S	10	ARG	Sidechain
16	S	29	ARG	Sidechain
16	S	74	ARG	Sidechain
17	T	47	ARG	Sidechain
18	U	47	ARG	Sidechain
18	U	68	ARG	Sidechain

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	26755	0	13475	767	0
2	B	242	0	122	19	0
3	C	3687	0	3670	29	0
4	F	1490	0	1518	20	0
5	G	1170	0	1245	19	0
6	H	727	0	760	7	0
7	I	1036	0	1095	18	0
8	J	776	0	799	10	0
9	K	489	0	516	18	0
10	L	1052	0	1112	16	0
11	M	868	0	925	20	0
12	O	710	0	735	3	0
13	P	695	0	721	5	0
14	Q	691	0	728	5	0
15	R	633	0	649	13	0
16	S	637	0	696	9	0
17	T	755	0	746	8	0
18	U	518	0	555	14	0
19	V	662	0	666	16	0
All	All	43593	0	30733	943	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 13.

All (943) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:70:G:H1	1:A:99:A:H61	1.07	0.98
1:A:458:G:H5'	1:A:459:A:H3'	1.50	0.92
13:P:41:ASN:HB3	13:P:48:GLU:HG3	1.53	0.91
1:A:224:U:H1'	1:A:475:A:N6	1.87	0.90
1:A:1296:A:H2'	1:A:1297:A:C8	2.07	0.90
1:A:1141:G:H1	1:A:1152:G:H21	1.18	0.89
1:A:906:U:C6	1:A:907:C:C5	2.62	0.87
1:A:683:G:H1	1:A:725:A:H61	1.18	0.87
1:A:474:A:O5'	1:A:474:A:H8	1.57	0.87
1:A:672:A:H61	1:A:751:G:H1	1.21	0.87
1:A:215:G:H2'	1:A:216:G:C8	2.09	0.86
1:A:94:A:OP1	1:A:95:U:H5	1.57	0.86
1:A:1198:U:O2'	1:A:1199:G:OP1	1.92	0.86
1:A:1168:U:H5''	1:A:1191:G:H1'	1.59	0.85
1:A:960:U:H3	1:A:1240:G:H1	1.25	0.84
1:A:13:G:N2	1:A:25:C:O2	2.10	0.84
1:A:1319:C:H2'	1:A:1320:A:H8	1.43	0.83
1:A:527:C:H4'	1:A:528:C:H5''	1.58	0.83
1:A:955:G:H1	1:A:1245:A:H61	1.26	0.83
1:A:682:G:N2	1:A:743:A:C5	2.47	0.82
1:A:242:C:O2'	1:A:243:C:H5'	1.80	0.82
1:A:698:C:H4'	1:A:714:G:H1'	1.61	0.81
1:A:64:U:OP1	1:A:393:U:O2'	1.97	0.81
1:A:222:G:C6	1:A:223:C:C4	2.69	0.81
1:A:495:U:H2'	1:A:496:A:H8	1.46	0.81
1:A:222:G:C6	1:A:223:C:N4	2.50	0.80
1:A:253:U:C2	1:A:292:G:C2	2.68	0.80
1:A:775:A:H2'	1:A:776:A:H5'	1.63	0.79
1:A:13:G:N2	1:A:25:C:C2	2.48	0.79
1:A:365:G:O2'	1:A:366:U:H5'	1.82	0.78
1:A:955:G:H1	1:A:1245:A:N6	1.81	0.78
1:A:670:G:H2'	1:A:671:A:H4'	1.66	0.78
1:A:1024:A:H5''	15:R:14:HIS:CD2	2.18	0.78
1:A:64:U:H5''	1:A:393:U:O2'	1.83	0.77
1:A:105:G:H3'	1:A:106:G:H8	1.48	0.77
1:A:600:U:O2'	1:A:601:C:H5'	1.84	0.77
1:A:70:G:H1	1:A:99:A:N6	1.83	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:906:U:C6	1:A:907:C:H5	2.03	0.77
1:A:30:G:H2'	1:A:31:A:H8	1.49	0.76
1:A:244:G:C6	1:A:245:C:N3	2.54	0.76
11:M:96:PRO:HB3	11:M:100:GLN:HB2	1.67	0.76
1:A:328:G:H1	1:A:341:C:H42	1.32	0.76
1:A:775:A:C2'	1:A:776:A:H5'	2.16	0.75
1:A:1250:G:H2'	1:A:1251:G:H8	1.50	0.75
1:A:682:G:N2	1:A:743:A:C4	2.54	0.75
1:A:1314:G:H22	1:A:1340:G:H2'	1.52	0.75
16:S:62:VAL:CG2	16:S:72:ALA:HB2	2.16	0.75
1:A:673:G:H22	1:A:750:G:H1	1.35	0.74
1:A:698:C:H2'	1:A:699:G:C8	2.23	0.74
1:A:962:U:H5'	1:A:982:C:H41	1.52	0.74
1:A:693:U:H4'	19:V:42:ASN:HD22	1.53	0.74
1:A:290:A:C6	1:A:291:U:C2	2.76	0.74
3:C:43:VAL:HG22	19:V:67:MET:CE	2.17	0.73
3:C:420:PHE:CE2	3:C:530:LEU:HD11	2.24	0.73
1:A:74:A:H1'	1:A:95:U:N3	2.03	0.73
1:A:141:G:H2'	1:A:142:A:H8	1.54	0.73
1:A:215:G:H2'	1:A:216:G:H8	1.54	0.73
1:A:94:A:OP1	1:A:95:U:C5	2.40	0.73
1:A:224:U:H1'	1:A:475:A:H62	1.52	0.72
1:A:954:G:H1'	1:A:1348:A:H61	1.54	0.72
1:A:1039:U:H2'	1:A:1041:C:H1'	1.70	0.72
15:R:22:LEU:HD22	15:R:28:LYS:HB2	1.71	0.72
1:A:1009:C:H42	1:A:1051:G:H1	1.37	0.72
2:B:-1:A:O3'	2:B:0:A:C8	2.42	0.72
1:A:1170:C:N4	1:A:1184:G:H1	1.87	0.71
1:A:74:A:H1'	1:A:95:U:H3	1.55	0.71
1:A:523:C:H2'	1:A:524:G:H8	1.54	0.71
1:A:1194:G:O2'	1:A:1195:G:O4'	2.07	0.71
1:A:1139:C:H42	1:A:1152:G:H1	1.39	0.71
11:M:15:VAL:HG23	11:M:43:THR:O	1.90	0.71
1:A:1016:A:H61	1:A:1033:G:H2'	1.56	0.71
1:A:1172:G:H1	1:A:1182:C:H42	1.38	0.70
1:A:1125:U:H1'	1:A:1194:G:H1	1.56	0.70
1:A:1141:G:O5'	1:A:1141:G:H8	1.74	0.70
1:A:421:G:H21	1:A:436:G:H1'	1.57	0.70
1:A:1326:C:O5'	1:A:1326:C:H6	1.74	0.70
1:A:474:A:O5'	1:A:474:A:C8	2.42	0.70
8:J:65:VAL:HG11	8:J:79:ILE:HG12	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:851:U:H1'	1:A:855:G:H1	1.56	0.69
1:A:13:G:O2'	1:A:14:U:H5'	1.93	0.69
1:A:141:G:H1	1:A:229:C:H42	1.40	0.69
1:A:147:G:H1	1:A:173:A:H61	1.40	0.69
1:A:1037:C:H42	1:A:1044:G:H1	1.39	0.69
1:A:1250:G:H2'	1:A:1251:G:C8	2.27	0.69
1:A:1290:U:O4	9:K:9:ARG:NH1	2.27	0.68
1:A:265:G:O2'	1:A:266:A:O5'	2.12	0.68
1:A:1043:G:H2'	1:A:1044:G:C8	2.28	0.67
1:A:526:G:O2'	1:A:539:G:H4'	1.94	0.67
7:I:21:ARG:NH1	7:I:70:ASN:O	2.26	0.67
1:A:586:G:H4'	1:A:826:C:H5'	1.76	0.67
3:C:531:ARG:O	6:H:93:PRO:HG2	1.93	0.67
1:A:1001:U:H1'	1:A:1003:G:H1'	1.76	0.67
1:A:1134:G:H1'	1:A:1135:U:H5	1.60	0.66
1:A:33:G:H1	1:A:50:C:H5'	1.61	0.66
1:A:40:G:O2'	1:A:41:G:C5'	2.43	0.66
16:S:62:VAL:HG21	16:S:72:ALA:CB	2.25	0.66
3:C:24:VAL:HG11	19:V:67:MET:CE	2.25	0.65
3:C:24:VAL:HG11	19:V:67:MET:HE3	1.77	0.65
1:A:121:C:O2	1:A:247:G:N2	2.27	0.65
1:A:217:C:H1'	1:A:475:A:H2	1.61	0.65
1:A:1038:C:H1'	1:A:1044:G:H22	1.62	0.65
1:A:1277:G:H2'	1:A:1278:A:C8	2.31	0.65
1:A:737:A:H2'	1:A:738:A:C8	2.32	0.64
1:A:1008:C:H3'	1:A:1009:C:O4'	1.97	0.64
1:A:957:G:H4'	1:A:1341:A:H2	1.61	0.64
1:A:1142:C:OP2	1:A:1142:C:H6	1.80	0.64
3:C:43:VAL:HG22	19:V:67:MET:HE2	1.79	0.64
1:A:960:U:H2'	1:A:961:G:C8	2.33	0.64
1:A:995:C:H2'	1:A:996:A:C8	2.32	0.64
1:A:989:C:H1'	1:A:1326:C:H42	1.62	0.64
1:A:1278:A:H2	1:A:1321:G:H2'	1.63	0.64
18:U:17:TYR:CE2	18:U:33:LEU:HD11	2.32	0.64
1:A:955:G:H1'	1:A:1346:G:H1'	1.80	0.64
1:A:1170:C:H42	1:A:1184:G:H1	1.43	0.64
3:C:43:VAL:HG11	19:V:52:LEU:HB3	1.80	0.64
1:A:60:C:H2'	1:A:61:A:H8	1.62	0.64
1:A:822:U:H2'	1:A:823:A:H8	1.62	0.63
1:A:277:C:H2'	1:A:278:A:C8	2.33	0.63
1:A:989:C:N4	1:A:1370:G:H1	1.95	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:523:C:H2'	1:A:524:G:C8	2.32	0.63
1:A:269:U:OP2	16:S:74:ARG:NH2	2.28	0.63
1:A:869:C:O2'	1:A:870:A:H5'	1.99	0.63
1:A:95:U:H2'	1:A:96:G:C8	2.34	0.63
1:A:290:A:C6	1:A:291:U:O2	2.52	0.63
5:G:79:THR:HB	5:G:121:ALA:HB3	1.80	0.63
1:A:251:A:N6	1:A:289:G:O2'	2.32	0.62
1:A:1313:G:H2'	1:A:1314:G:C8	2.34	0.62
17:T:87:ARG:HG3	17:T:87:ARG:HH11	1.64	0.62
1:A:683:G:H1	1:A:725:A:N6	1.94	0.62
1:A:713:A:H3'	1:A:714:G:H8	1.65	0.62
1:A:1162:G:H2'	1:A:1163:G:C8	2.34	0.62
1:A:244:G:C2	1:A:245:C:O2	2.53	0.62
4:F:63:VAL:HG21	4:F:68:PHE:HD1	1.63	0.62
1:A:690:A:H61	1:A:718:U:H3	1.47	0.62
1:A:906:U:H6	1:A:907:C:H5	1.46	0.62
1:A:265:G:H2'	1:A:266:A:C8	2.35	0.62
4:F:66:ARG:HB3	4:F:66:ARG:HH21	1.63	0.62
3:C:43:VAL:CG2	19:V:67:MET:HE2	2.30	0.62
1:A:957:G:H4'	1:A:1341:A:C2	2.35	0.62
1:A:1139:C:N4	1:A:1152:G:H1	1.97	0.62
1:A:1129:U:H2'	1:A:1130:C:C6	2.35	0.62
1:A:1314:G:N2	1:A:1340:G:H2'	2.14	0.62
1:A:672:A:N6	1:A:751:G:H1	1.94	0.61
1:A:144:U:H2'	1:A:145:G:H8	1.65	0.61
1:A:954:G:H1'	1:A:1348:A:N6	2.14	0.61
1:A:1156:C:H2'	1:A:1157:U:H4'	1.83	0.61
1:A:601:C:C4	1:A:602:U:C4	2.89	0.61
1:A:960:U:H2'	1:A:961:G:H8	1.64	0.61
1:A:527:C:H2'	1:A:539:G:C8	2.36	0.61
1:A:1182:C:H2'	1:A:1183:G:H4'	1.83	0.61
1:A:968:A:H1'	1:A:996:A:H5'	1.83	0.60
1:A:1378:C:H2'	1:A:1379:G:H8	1.66	0.60
1:A:474:A:H8	1:A:474:A:P	2.24	0.60
1:A:1130:C:N3	1:A:1163:G:N2	2.49	0.60
1:A:222:G:C2	1:A:223:C:C2	2.90	0.60
1:A:1141:G:H1	1:A:1152:G:N2	1.96	0.60
1:A:242:C:C2'	1:A:243:C:H5'	2.31	0.60
1:A:1018:U:H3	1:A:1031:A:H61	1.50	0.60
1:A:1316:U:H2'	1:A:1317:C:C6	2.37	0.60
8:J:35:ILE:HD11	8:J:48:ILE:HD13	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:M:96:PRO:HA	11:M:109:ARG:HG3	1.83	0.60
1:A:345:G:H2'	1:A:346:A:C8	2.37	0.59
1:A:1037:C:N4	1:A:1044:G:H1	2.00	0.59
1:A:903:C:H2'	1:A:904:G:C8	2.38	0.59
1:A:996:A:H1'	15:R:55:ARG:HA	1.84	0.59
1:A:1003:G:H2'	1:A:1005:C:H5	1.68	0.59
1:A:1008:C:H5'	1:A:1009:C:OP2	2.03	0.59
2:B:5:A:H2'	2:B:6:A:H5''	1.83	0.59
1:A:682:G:C2	1:A:743:A:C6	2.91	0.59
11:M:40:SER:HB3	11:M:43:THR:HG23	1.84	0.59
10:L:123:ARG:HD2	10:L:125:GLN:O	2.03	0.58
1:A:477:A:H5'	1:A:478:G:C8	2.37	0.58
1:A:655:G:H3'	1:A:656:G:H8	1.68	0.58
1:A:689:C:H2'	1:A:690:A:C8	2.37	0.58
1:A:1120:A:H2'	1:A:1121:A:H8	1.68	0.58
1:A:531:C:H1'	1:A:545:C:H5''	1.84	0.58
1:A:1248:A:H62	1:A:1308:A:H62	1.52	0.58
15:R:36:ARG:NH2	15:R:75:ALA:O	2.36	0.58
1:A:290:A:C5	1:A:291:U:C2	2.92	0.58
1:A:589:C:H42	1:A:770:G:H1	1.50	0.58
1:A:1335:U:H2'	1:A:1336:G:H8	1.69	0.58
3:C:418:PHE:HB3	3:C:420:PHE:CE2	2.39	0.58
3:C:43:VAL:HG22	19:V:67:MET:HE1	1.86	0.58
1:A:144:U:H3	1:A:176:G:H1	1.52	0.58
1:A:1172:G:H1	1:A:1182:C:N4	2.00	0.58
1:A:1317:C:H5'	11:M:109:ARG:HD3	1.86	0.58
17:T:63:VAL:HG12	17:T:65:VAL:HG13	1.86	0.58
1:A:120:A:H61	1:A:247:G:H1	1.50	0.58
1:A:224:U:H4'	1:A:473:G:H4'	1.85	0.58
1:A:708:C:H2'	1:A:709:G:C8	2.37	0.58
5:G:36:LEU:HD21	5:G:137:ILE:HD12	1.86	0.58
1:A:222:G:O6	1:A:223:C:N4	2.37	0.57
2:B:-1:A:O3'	2:B:0:A:N7	2.36	0.57
1:A:1296:A:C8	1:A:1297:A:N7	2.72	0.57
1:A:1194:G:H2'	1:A:1195:G:C8	2.39	0.57
1:A:533:G:H2'	1:A:534:C:C6	2.39	0.57
1:A:580:U:O5'	1:A:580:U:H6	1.87	0.57
1:A:909:C:H2'	1:A:910:A:C8	2.39	0.57
1:A:1319:C:H2'	1:A:1320:A:C8	2.34	0.57
1:A:1329:C:H2'	1:A:1330:U:C6	2.40	0.57
1:A:317:G:H2'	1:A:318:G:H8	1.69	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1151:G:H3'	1:A:1152:G:C8	2.38	0.57
1:A:722:G:H2'	1:A:723:G:C8	2.39	0.57
1:A:527:C:H5	1:A:539:G:O5'	1.88	0.57
1:A:686:U:H3	1:A:722:G:H1	1.53	0.57
1:A:1363:C:H2'	1:A:1364:G:C8	2.39	0.57
9:K:26:VAL:HG13	9:K:36:VAL:HG11	1.87	0.57
1:A:1231:G:H2'	1:A:1232:C:C6	2.39	0.57
1:A:1255:G:H1	1:A:1300:C:H42	1.52	0.57
1:A:27:C:H2'	1:A:28:A:C8	2.39	0.57
1:A:957:G:H5'	1:A:1342:A:H1'	1.87	0.57
1:A:513:C:H42	1:A:550:G:H1	1.53	0.56
1:A:244:G:C2	1:A:245:C:C2	2.93	0.56
1:A:267:G:H1	1:A:275:C:H42	1.52	0.56
1:A:458:G:H1	1:A:492:C:H42	1.52	0.56
1:A:972:C:H2'	1:A:973:G:C8	2.40	0.56
5:G:30:ARG:HH12	6:H:110:LEU:HD13	1.69	0.56
1:A:591:C:H41	1:A:767:G:H2'	1.71	0.56
1:A:1326:C:O5'	1:A:1326:C:C6	2.56	0.56
1:A:572:A:N3	1:A:572:A:H2'	2.20	0.56
1:A:1122:C:H3'	1:A:1124:C:H41	1.70	0.56
1:A:13:G:N1	1:A:25:C:N3	2.53	0.56
1:A:626:G:H1	1:A:632:C:H42	1.52	0.56
1:A:699:G:H2'	1:A:700:G:O4'	2.06	0.56
1:A:420:U:H2'	1:A:421:G:H4'	1.86	0.56
1:A:411:C:H5''	4:F:129:PRO:HD2	1.88	0.56
9:K:10:LEU:HD11	9:K:25:ILE:HD12	1.88	0.56
1:A:779:C:N3	1:A:780:G:N7	2.54	0.55
1:A:1313:G:H21	1:A:1342:A:H62	1.53	0.55
11:M:23:PHE:N	11:M:66:GLU:OE1	2.38	0.55
1:A:69:C:H2'	1:A:70:G:C8	2.42	0.55
1:A:685:A:H2	1:A:723:G:H1	1.54	0.55
18:U:37:PHE:CG	18:U:60:LEU:HD21	2.41	0.55
1:A:495:U:H2'	1:A:496:A:C8	2.35	0.55
1:A:906:U:C5	1:A:907:C:N4	2.74	0.55
1:A:1239:C:H2'	1:A:1240:G:C8	2.42	0.55
1:A:1360:U:H4'	6:H:33:ASP:HB3	1.87	0.55
1:A:23:G:H2'	1:A:24:G:C8	2.42	0.55
1:A:246:G:H2'	1:A:247:G:C8	2.41	0.55
1:A:1013:G:H22	1:A:1048:A:H1'	1.71	0.55
1:A:327:G:H1	1:A:342:C:H42	1.54	0.55
1:A:527:C:C5	1:A:539:G:O5'	2.59	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1271:A:H2'	1:A:1272:A:C8	2.41	0.55
1:A:40:G:O2'	1:A:41:G:H5'	2.07	0.55
1:A:1153:G:H8	1:A:1154:C:H3'	1.71	0.55
5:G:48:PHE:CD1	5:G:141:LEU:CD1	2.90	0.55
1:A:157:G:H1	1:A:162:C:H42	1.54	0.55
1:A:1158:C:H5'	8:J:18:ARG:HH12	1.72	0.55
1:A:58:U:H2'	1:A:59:G:C8	2.41	0.55
1:A:602:U:H3	1:A:655:G:H1	1.54	0.55
1:A:775:A:H2'	1:A:776:A:C5'	2.35	0.55
1:A:1159:U:H2'	1:A:1160:A:C8	2.41	0.55
1:A:1198:U:HO2'	1:A:1199:G:P	2.25	0.55
1:A:128:A:H2'	14:Q:4:ARG:HH22	1.71	0.55
1:A:504:A:H61	4:F:116:HIS:HE1	1.54	0.55
1:A:625:G:H1	1:A:633:C:H42	1.55	0.55
2:B:9:A:C4	3:C:561:ARG:NH2	2.70	0.55
1:A:999:U:H2'	1:A:1000:C:C6	2.42	0.54
1:A:1042:G:C2	1:A:1043:G:H1'	2.41	0.54
1:A:674:A:H62	1:A:733:G:H1	1.55	0.54
1:A:901:U:H2'	1:A:902:A:H8	1.72	0.54
1:A:967:U:H4'	15:R:79:THR:HB	1.88	0.54
1:A:225:A:H4'	1:A:478:G:N2	2.22	0.54
2:B:-1:A:H4'	2:B:0:A:C8	2.43	0.54
18:U:17:TYR:CE2	18:U:23:ILE:HD12	2.42	0.54
1:A:470:U:H3	1:A:480:G:H1	1.55	0.54
1:A:1324:U:O2'	1:A:1369:A:N3	2.40	0.54
1:A:1032:C:H2'	1:A:1033:G:O4'	2.08	0.54
1:A:217:C:H1'	1:A:475:A:C2	2.41	0.54
1:A:1139:C:N3	1:A:1152:G:N2	2.56	0.54
1:A:1308:A:H2'	1:A:1310:U:C6	2.43	0.54
1:A:113:G:H4'	1:A:114:A:O5'	2.08	0.54
1:A:224:U:C1'	1:A:475:A:N6	2.66	0.54
1:A:687:U:H2'	1:A:688:C:C6	2.43	0.54
16:S:62:VAL:HG21	16:S:72:ALA:HB2	1.83	0.54
1:A:510:C:H1'	1:A:558:C:H1'	1.89	0.54
1:A:986:G:N7	1:A:1371:C:N4	2.56	0.54
16:S:20:HIS:O	16:S:23:THR:HB	2.08	0.54
1:A:155:C:H42	1:A:164:G:H1	1.55	0.53
5:G:48:PHE:HD1	5:G:141:LEU:HD13	1.73	0.53
1:A:701:U:H1'	1:A:704:A:C8	2.43	0.53
1:A:374:C:H1'	1:A:403:C:O2	2.08	0.53
1:A:624:C:H42	1:A:634:G:H1	1.55	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1157:U:H3'	1:A:1158:C:C6	2.43	0.53
1:A:153:U:H3	1:A:166:G:H1	1.56	0.53
1:A:330:C:H2'	1:A:331:U:C6	2.43	0.53
1:A:715:A:H3'	1:A:716:U:O4'	2.08	0.53
1:A:749:U:C2'	1:A:750:G:O5'	2.57	0.53
2:B:4:A:H3'	2:B:5:A:H8	1.73	0.53
1:A:494:G:H1'	1:A:495:U:H5	1.73	0.53
1:A:1008:C:OP1	1:A:1009:C:OP2	2.27	0.53
8:J:91:ASP:HB3	8:J:94:TYR:CD2	2.43	0.53
1:A:835:C:H4'	7:I:13:ARG:HG2	1.90	0.53
1:A:965:U:H2'	1:A:966:U:C6	2.44	0.53
5:G:110:PRO:HG2	5:G:136:MET:HE3	1.89	0.53
1:A:145:G:H1	1:A:175:C:H42	1.56	0.53
1:A:301:A:H5'	1:A:619:G:C2	2.43	0.53
1:A:634:G:H2'	1:A:635:G:H8	1.73	0.53
1:A:840:U:H3	1:A:865:G:H1	1.56	0.53
1:A:1003:G:H2'	1:A:1005:C:C5	2.43	0.53
1:A:854:C:H3'	1:A:855:G:C8	2.44	0.53
3:C:282:LYS:HE2	3:C:344:GLU:CD	2.29	0.53
7:I:10:MET:HG3	7:I:27:ILE:HD13	1.91	0.53
1:A:360:C:O2	1:A:363:C:N4	2.40	0.53
1:A:527:C:H4'	1:A:528:C:C5'	2.35	0.53
1:A:328:G:H1	1:A:341:C:N4	2.02	0.52
1:A:1179:A:H2'	1:A:1180:A:O4'	2.09	0.52
5:G:89:PHE:O	5:G:90:GLY:O	2.27	0.52
5:G:90:GLY:O	5:G:92:GLY:N	2.39	0.52
1:A:153:U:H2'	1:A:154:C:H5'	1.91	0.52
1:A:254:A:H62	1:A:289:G:H1'	1.74	0.52
1:A:779:C:O2'	1:A:909:C:N3	2.42	0.52
1:A:1133:A:H2'	1:A:1133:A:N3	2.25	0.52
1:A:1142:C:C2	1:A:1143:A:C5	2.97	0.52
1:A:1174:U:H3	1:A:1180:A:H62	1.55	0.52
7:I:11:LEU:HD11	7:I:129:ALA:HB2	1.92	0.52
8:J:91:ASP:HB3	8:J:94:TYR:CE2	2.44	0.52
17:T:87:ARG:HH11	17:T:87:ARG:CG	2.22	0.52
1:A:468:C:H2'	1:A:469:G:C8	2.44	0.52
1:A:1310:U:O2'	1:A:1311:U:H3'	2.10	0.52
5:G:115:LEU:HD13	5:G:123:ILE:HG21	1.91	0.52
1:A:906:U:H2'	1:A:907:C:C6	2.45	0.52
1:A:1216:C:H2'	1:A:1217:C:H4'	1.92	0.52
1:A:32:C:H42	1:A:562:G:H1	1.56	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:323:A:H4'	1:A:324:C:OP1	2.10	0.52
1:A:906:U:H5	1:A:907:C:H41	1.56	0.52
1:A:1136:U:C5	9:K:73:LEU:HD22	2.45	0.52
3:C:341:LEU:HD21	3:C:572:ILE:HG21	1.91	0.52
3:C:419:ASP:HA	3:C:441:ARG:NH2	2.24	0.52
1:A:994:C:H2'	1:A:995:C:C6	2.45	0.52
1:A:1142:C:OP2	1:A:1142:C:C6	2.61	0.52
1:A:1263:G:H2'	1:A:1264:G:C8	2.44	0.52
1:A:1299:U:H2'	1:A:1300:C:C6	2.44	0.52
1:A:163:C:H2'	1:A:164:G:C8	2.44	0.52
1:A:700:G:H22	1:A:704:A:H5''	1.75	0.52
1:A:857:C:H2'	1:A:858:C:C6	2.45	0.52
1:A:1342:A:H3'	1:A:1343:G:C8	2.45	0.52
1:A:222:G:N1	1:A:223:C:C4	2.77	0.52
1:A:290:A:N6	1:A:291:U:O2	2.43	0.52
1:A:423:A:N6	1:A:436:G:H1	2.07	0.52
1:A:959:A:H1'	1:A:1373:U:N3	2.25	0.52
1:A:1127:G:H2'	1:A:1128:A:C8	2.45	0.52
1:A:1176:A:H2'	1:A:1178:A:C8	2.45	0.52
8:J:35:ILE:HD11	8:J:48:ILE:CD1	2.39	0.52
1:A:329:A:H61	1:A:340:G:H1	1.58	0.52
1:A:1297:A:H2'	1:A:1298:A:C8	2.45	0.52
1:A:906:U:O2'	1:A:907:C:H6	1.93	0.51
1:A:1249:U:H4'	6:H:38:LYS:HD2	1.90	0.51
9:K:92:LEU:HD12	9:K:98:ILE:HG12	1.92	0.51
1:A:593:G:H1	1:A:766:U:H3	1.57	0.51
1:A:826:C:H4'	1:A:827:G:O5'	2.10	0.51
1:A:1191:G:H5'	1:A:1194:G:OP1	2.09	0.51
1:A:918:A:H2'	1:A:919:A:C8	2.45	0.51
1:A:1254:A:H2'	1:A:1255:G:C8	2.46	0.51
15:R:50:ALA:HB1	15:R:57:HIS:HB3	1.91	0.51
1:A:439:A:H3'	1:A:440:A:H8	1.76	0.51
1:A:511:C:H42	1:A:552:G:H1	1.58	0.51
9:K:86:ALA:O	9:K:90:LEU:HB2	2.10	0.51
1:A:390:A:H2'	1:A:391:A:C8	2.45	0.51
1:A:600:U:HO2'	1:A:601:C:H5'	1.75	0.51
1:A:1375:C:H2'	1:A:1376:C:C6	2.44	0.51
1:A:497:C:H2'	1:A:498:C:C6	2.46	0.51
1:A:648:G:N3	1:A:648:G:H2'	2.25	0.51
1:A:771:A:H2'	1:A:772:G:C8	2.46	0.51
1:A:972:C:H2'	1:A:973:G:H8	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1326:C:H2'	1:A:1327:A:C8	2.46	0.51
1:A:222:G:N1	1:A:223:C:N3	2.59	0.51
1:A:1235:C:H1'	1:A:1236:A:H8	1.74	0.51
1:A:225:A:H4'	1:A:478:G:H21	1.75	0.51
1:A:427:U:H3	1:A:432:G:H1	1.59	0.51
1:A:469:G:H1	1:A:481:C:H42	1.58	0.51
1:A:1142:C:N3	1:A:1143:A:N6	2.59	0.51
1:A:147:G:H1	1:A:173:A:N6	2.07	0.51
1:A:170:A:H2'	1:A:171:A:C8	2.46	0.51
1:A:825:A:H3'	1:A:827:G:OP1	2.11	0.51
1:A:451:U:H2'	1:A:452:A:C8	2.46	0.51
1:A:1342:A:H3'	1:A:1343:G:H8	1.76	0.51
1:A:1367:U:H2'	1:A:1368:C:O4'	2.10	0.51
1:A:163:C:H2'	1:A:164:G:H8	1.76	0.50
1:A:114:A:H61	1:A:321:A:H1'	1.77	0.50
1:A:1157:U:H3'	1:A:1158:C:H6	1.76	0.50
1:A:1199:G:H1	1:A:1202:G:H21	1.59	0.50
7:I:106:ILE:HD12	7:I:106:ILE:N	2.26	0.50
9:K:81:PRO:O	9:K:83:THR:N	2.44	0.50
1:A:475:A:H2'	1:A:477:A:H1'	1.93	0.50
1:A:1180:A:H2'	1:A:1181:C:C6	2.46	0.50
1:A:1195:G:C2	1:A:1196:G:H1'	2.46	0.50
1:A:634:G:H2'	1:A:635:G:C8	2.46	0.50
1:A:1029:G:H2'	1:A:1030:G:H5''	1.93	0.50
1:A:683:G:N2	1:A:725:A:N1	2.58	0.50
1:A:845:G:H1	1:A:860:U:H3	1.59	0.50
1:A:923:A:H1'	1:A:924:A:H1'	1.93	0.50
1:A:1160:A:H2'	1:A:1161:A:C8	2.45	0.50
1:A:1327:A:H2'	1:A:1328:A:H5''	1.93	0.50
1:A:1332:G:H2'	1:A:1333:A:C8	2.46	0.50
1:A:391:A:C5	1:A:392:G:H1'	2.46	0.50
1:A:714:G:C5	1:A:715:A:H1'	2.46	0.50
1:A:987:A:H1'	1:A:991:U:H3	1.76	0.50
1:A:998:G:H1'	1:A:1025:G:H1	1.77	0.50
1:A:244:G:N1	1:A:245:C:C2	2.80	0.50
1:A:455:G:H3'	1:A:494:G:N1	2.27	0.50
1:A:815:C:H2'	1:A:816:A:C8	2.47	0.50
1:A:928:A:H2'	1:A:929:A:C8	2.47	0.50
1:A:987:A:H4'	1:A:990:C:N4	2.26	0.50
1:A:1122:C:H2'	1:A:1123:C:C6	2.47	0.50
1:A:1146:C:H2'	1:A:1147:A:C8	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1363:C:H2'	1:A:1364:G:H8	1.77	0.50
1:A:37:G:H1	1:A:558:C:H42	1.58	0.49
1:A:610:G:H1	1:A:646:U:H3	1.58	0.49
1:A:723:G:H2'	1:A:724:A:C8	2.47	0.49
1:A:778:G:H1	1:A:819:C:H42	1.59	0.49
1:A:1181:C:H2'	1:A:1182:C:C6	2.47	0.49
4:F:29:ARG:HB3	4:F:31:TYR:CZ	2.47	0.49
1:A:10:A:H62	4:F:199:SER:HG	1.60	0.49
1:A:601:C:C4	1:A:602:U:O4	2.65	0.49
1:A:1232:C:C5	1:A:1233:U:H5	2.30	0.49
1:A:1278:A:C2	1:A:1321:G:H2'	2.47	0.49
1:A:11:G:H5'	5:G:108:GLY:HA3	1.93	0.49
1:A:745:U:H2'	1:A:746:C:C6	2.48	0.49
1:A:897:G:H1	1:A:920:C:H42	1.60	0.49
1:A:906:U:H2'	1:A:907:C:C5	2.47	0.49
2:B:5:A:H3'	2:B:6:A:C2	2.47	0.49
4:F:72:PHE:CZ	4:F:82:HIS:CE1	3.00	0.49
11:M:14:ARG:HD2	11:M:42:ASP:HA	1.94	0.49
1:A:64:U:H5''	1:A:393:U:C2'	2.42	0.49
1:A:156:G:H2'	1:A:157:G:H8	1.78	0.49
1:A:228:A:H2'	1:A:229:C:H5''	1.94	0.49
1:A:505:G:H2'	1:A:506:A:H8	1.77	0.49
1:A:922:C:H2'	1:A:923:A:C8	2.47	0.49
1:A:1315:A:H1'	1:A:1341:A:C2	2.47	0.49
1:A:655:G:H3'	1:A:656:G:C8	2.47	0.49
1:A:1277:G:H1'	1:A:1336:G:H5'	1.95	0.49
5:G:48:PHE:CD1	5:G:141:LEU:HD13	2.48	0.49
1:A:587:C:H2'	1:A:588:U:C6	2.47	0.49
1:A:739:G:H5'	1:A:825:A:H4'	1.94	0.49
1:A:224:U:H1'	1:A:475:A:H61	1.72	0.49
1:A:484:U:H2'	1:A:485:A:C8	2.48	0.49
1:A:548:A:H2'	1:A:549:G:C8	2.47	0.49
1:A:613:G:H2'	1:A:614:U:O4'	2.12	0.49
1:A:661:U:H1'	1:A:662:U:C6	2.47	0.49
19:V:19:GLU:HG3	19:V:82:LYS:HE2	1.94	0.49
1:A:430:C:O2'	1:A:431:G:N2	2.46	0.49
1:A:477:A:H5'	1:A:478:G:H8	1.78	0.49
1:A:673:G:OP1	18:U:58:ARG:NH1	2.45	0.49
1:A:1014:A:H1'	1:A:1046:G:H1	1.78	0.49
2:B:5:A:H3'	2:B:6:A:H2	1.77	0.49
1:A:37:G:H2'	1:A:38:C:C6	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:989:C:N3	1:A:1369:A:N6	2.61	0.48
1:A:1166:A:N7	1:A:1186:G:N2	2.61	0.48
5:G:15:LEU:HD11	5:G:18:VAL:CG2	2.43	0.48
1:A:123:U:H3	1:A:244:G:H1	1.61	0.48
1:A:693:U:H3	1:A:715:A:H61	1.61	0.48
1:A:973:G:H3'	1:A:974:A:C8	2.48	0.48
1:A:1309:G:O3'	1:A:1312:C:N4	2.46	0.48
1:A:110:G:H2'	1:A:111:G:H5'	1.95	0.48
1:A:466:G:H1	1:A:484:U:H3	1.60	0.48
1:A:584:G:H3'	1:A:826:C:N4	2.27	0.48
7:I:7:ILE:HD11	7:I:32:LEU:HD23	1.95	0.48
1:A:569:A:H5''	1:A:570:U:H3'	1.95	0.48
1:A:984:A:O3'	1:A:985:A:H3'	2.13	0.48
1:A:1276:C:N3	1:A:1336:G:H4'	2.29	0.48
1:A:1324:U:C5	15:R:7:LYS:HE3	2.48	0.48
3:C:57:ARG:NH1	19:V:63:PHE:CD2	2.82	0.48
1:A:206:A:H4'	16:S:52:THR:HG22	1.95	0.48
1:A:317:G:O2'	1:A:616:A:N1	2.47	0.48
1:A:336:C:H4'	1:A:337:A:H5''	1.96	0.48
1:A:1357:U:H2'	1:A:1357:U:O2	2.14	0.48
1:A:30:G:C4	1:A:31:A:C8	3.01	0.48
1:A:99:A:H5''	1:A:100:G:C8	2.49	0.48
1:A:141:G:N3	1:A:210:A:H2	2.11	0.48
1:A:224:U:H2'	1:A:225:A:C8	2.48	0.48
1:A:629:C:C2	4:F:128:ILE:HD13	2.48	0.48
1:A:712:G:H4'	1:A:713:A:H8	1.79	0.48
1:A:1163:G:H2'	1:A:1164:U:C6	2.49	0.48
1:A:1324:U:H5	15:R:7:LYS:HE3	1.78	0.48
1:A:1158:C:H5'	8:J:18:ARG:NH1	2.29	0.48
4:F:139:ILE:N	4:F:139:ILE:HD12	2.29	0.48
17:T:37:ILE:HG23	17:T:63:VAL:HG13	1.95	0.48
1:A:563:U:H2'	1:A:564:C:C6	2.49	0.48
1:A:1026:A:H3'	1:A:1027:U:C6	2.49	0.48
13:P:17:PHE:CZ	13:P:39:THR:HB	2.48	0.48
1:A:253:U:N1	1:A:292:G:N2	2.62	0.48
1:A:780:G:H2'	1:A:781:U:C6	2.48	0.48
1:A:961:G:H2'	1:A:962:U:C6	2.49	0.48
1:A:1140:A:N1	1:A:1154:C:H5'	2.28	0.48
1:A:1296:A:C5	1:A:1297:A:C6	3.02	0.48
1:A:1355:A:O3'	1:A:1356:G:H4'	2.14	0.48
1:A:317:G:H2'	1:A:318:G:C8	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:347:C:H2'	1:A:348:U:C6	2.49	0.48
1:A:1056:A:H5''	1:A:1057:G:N7	2.29	0.48
1:A:1166:A:H4'	1:A:1167:C:O5'	2.14	0.48
1:A:146:G:H2'	1:A:147:G:C8	2.49	0.47
1:A:340:G:H5'	1:A:340:G:H8	1.78	0.47
1:A:573:U:OP1	10:L:12:ARG:NE	2.31	0.47
1:A:776:A:H2'	1:A:777:A:O4'	2.13	0.47
1:A:1141:G:N2	1:A:1154:C:OP1	2.47	0.47
1:A:1258:C:H2'	1:A:1259:A:H5''	1.95	0.47
4:F:66:ARG:HH21	4:F:66:ARG:CB	2.27	0.47
1:A:267:G:H1	1:A:275:C:N4	2.12	0.47
1:A:379:G:H1	1:A:398:C:H42	1.61	0.47
1:A:429:U:O2'	1:A:431:G:C5	2.64	0.47
1:A:696:A:H5''	19:V:46:TRP:CZ2	2.48	0.47
1:A:718:U:H2'	1:A:719:G:H4'	1.96	0.47
1:A:1038:C:H1'	1:A:1044:G:N2	2.27	0.47
1:A:1133:A:N1	1:A:1158:C:N4	2.55	0.47
1:A:302:C:H42	1:A:311:G:H1	1.61	0.47
1:A:717:G:H2'	1:A:718:U:C6	2.49	0.47
1:A:815:C:H2'	1:A:816:A:H8	1.79	0.47
1:A:968:A:H2'	1:A:969:A:C8	2.50	0.47
1:A:1278:A:N1	1:A:1322:U:H5'	2.30	0.47
1:A:1328:A:N6	1:A:1370:G:H1'	2.30	0.47
1:A:141:G:H1	1:A:229:C:N4	2.08	0.47
1:A:682:G:C2	1:A:743:A:C5	3.02	0.47
1:A:691:C:O2	1:A:717:G:N2	2.47	0.47
3:C:497:VAL:HG21	3:C:512:ILE:HD11	1.96	0.47
18:U:17:TYR:CE2	18:U:33:LEU:CD1	2.97	0.47
1:A:64:U:H3	1:A:103:G:H1	1.61	0.47
1:A:531:C:H1'	1:A:545:C:C5'	2.44	0.47
1:A:843:U:C2	1:A:863:G:C2	3.03	0.47
2:B:3:A:H2'	2:B:4:A:O4'	2.15	0.47
10:L:36:THR:HG22	10:L:38:VAL:HG23	1.96	0.47
1:A:27:C:C5'	1:A:533:G:H1'	2.45	0.47
1:A:111:G:N3	1:A:361:A:O2'	2.47	0.47
1:A:156:G:H2'	1:A:157:G:C8	2.49	0.47
1:A:414:G:H2'	1:A:415:A:C8	2.49	0.47
1:A:663:G:H1	1:A:763:C:H5	1.63	0.47
1:A:965:U:H2'	1:A:966:U:H6	1.79	0.47
1:A:1012:U:H2'	1:A:1013:G:C8	2.50	0.47
1:A:1229:G:H2'	1:A:1230:G:O4'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1315:A:H2'	1:A:1316:U:O4'	2.14	0.47
1:A:1365:G:H2'	1:A:1366:A:C8	2.49	0.47
5:G:61:ARG:NH1	5:G:65:GLU:OE1	2.48	0.47
1:A:120:A:N6	1:A:247:G:H1	2.13	0.47
1:A:189:A:H4'	1:A:190:A:OP1	2.14	0.47
1:A:1247:A:C4	1:A:1312:C:H4'	2.49	0.47
1:A:1305:C:H4'	1:A:1311:U:N3	2.29	0.47
4:F:95:ASP:OD1	4:F:96:ASN:N	2.48	0.47
1:A:74:A:C1'	1:A:95:U:H3	2.27	0.47
1:A:1261:A:H4'	1:A:1378:C:H4'	1.97	0.47
1:A:1369:A:H3'	1:A:1370:G:C8	2.50	0.47
3:C:420:PHE:CZ	3:C:530:LEU:HD11	2.50	0.47
3:C:483:LEU:HD21	3:C:504:ILE:HG21	1.96	0.47
10:L:29:ASN:HB3	10:L:34:GLU:HG3	1.96	0.47
12:O:24:SER:OG	12:O:26:GLU:OE2	2.33	0.47
1:A:869:C:H2'	1:A:870:A:C8	2.50	0.47
1:A:890:C:H2'	1:A:891:G:H8	1.79	0.47
1:A:1142:C:O2	1:A:1143:A:C5	2.68	0.47
1:A:1224:G:O2'	1:A:1225:A:O4'	2.31	0.47
1:A:276:U:H2'	1:A:277:C:C6	2.50	0.46
1:A:700:G:H2'	1:A:701:U:C6	2.49	0.46
1:A:113:G:H1'	1:A:114:A:N7	2.30	0.46
1:A:1155:A:H2'	1:A:1155:A:N3	2.30	0.46
1:A:1199:G:H1	1:A:1202:G:N2	2.12	0.46
1:A:1211:U:H6	1:A:1212:C:C5	2.32	0.46
1:A:107:A:H2'	1:A:334:G:N2	2.30	0.46
1:A:380:C:H4'	1:A:381:A:OP1	2.16	0.46
1:A:561:U:H5'	10:L:96:ARG:NH1	2.30	0.46
1:A:576:G:H2'	1:A:577:G:O4'	2.15	0.46
11:M:16:VAL:HG13	11:M:34:LEU:HD12	1.98	0.46
1:A:115:G:O5'	1:A:115:G:H8	1.98	0.46
1:A:212:G:N2	1:A:228:A:H1'	2.30	0.46
1:A:244:G:C6	1:A:245:C:C4	3.04	0.46
1:A:475:A:H8	1:A:475:A:H5''	1.81	0.46
1:A:832:G:O2'	7:I:2:VAL:HG13	2.15	0.46
1:A:840:U:OP1	11:M:92:ARG:NH1	2.48	0.46
1:A:915:U:H2'	1:A:916:G:O4'	2.16	0.46
1:A:961:G:N2	1:A:980:C:O2'	2.48	0.46
1:A:1004:A:C4	1:A:1225:A:H4'	2.50	0.46
1:A:1232:C:H5	1:A:1233:U:H5	1.63	0.46
5:G:16:VAL:HG21	5:G:137:ILE:HD11	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:H:29:LYS:NZ	6:H:98:THR:HG23	2.30	0.46
11:M:86:TYR:O	11:M:90:ARG:HG2	2.15	0.46
1:A:132:U:C2	1:A:238:G:N1	2.83	0.46
1:A:205:C:H2'	1:A:206:A:C8	2.51	0.46
1:A:254:A:N6	1:A:289:G:H1'	2.30	0.46
1:A:455:G:H3'	1:A:494:G:H1	1.80	0.46
1:A:691:C:H2'	1:A:692:G:H8	1.81	0.46
1:A:692:G:H1'	1:A:717:G:O2'	2.16	0.46
1:A:779:C:C4	1:A:780:G:N7	2.83	0.46
2:B:0:A:H62	3:C:489:PHE:HE1	1.63	0.46
4:F:75:ALA:HA	4:F:78:LEU:HD13	1.97	0.46
4:F:181:GLU:O	4:F:182:ARG:HB3	2.16	0.46
8:J:18:ARG:HH21	8:J:66:ASN:ND2	2.13	0.46
13:P:51:ILE:HD12	13:P:77:GLN:HG3	1.98	0.46
1:A:159:A:H1'	1:A:352:A:C5	2.50	0.46
1:A:919:A:H2'	1:A:920:C:O4'	2.16	0.46
1:A:15:U:H1'	1:A:924:A:H5''	1.97	0.46
1:A:220:C:H1'	1:A:221:G:C2	2.49	0.46
1:A:222:G:C5	1:A:223:C:C4	3.04	0.46
2:B:7:A:C4	2:B:8:A:C8	3.04	0.46
9:K:22:ALA:O	9:K:26:VAL:HG23	2.16	0.46
18:U:17:TYR:HD2	18:U:18:PHE:CD1	2.33	0.46
1:A:417:U:H2'	1:A:418:G:O4'	2.15	0.46
1:A:418:G:H2'	1:A:437:U:C5	2.51	0.46
1:A:525:U:O2'	1:A:528:C:N3	2.47	0.46
1:A:529:A:H61	1:A:542:A:H61	1.64	0.46
1:A:896:G:H1	1:A:921:U:H3	1.64	0.46
1:A:907:C:H2'	1:A:908:G:C8	2.51	0.46
1:A:1056:A:C2	1:A:1224:G:H4'	2.50	0.46
19:V:76:SER:HB3	19:V:81:LEU:HD13	1.97	0.46
1:A:159:A:H2'	1:A:160:A:O4'	2.16	0.46
1:A:468:C:H2'	1:A:469:G:H8	1.80	0.46
1:A:1259:A:H2	1:A:1362:G:H21	1.64	0.46
1:A:1270:A:N6	1:A:1283:A:O2'	2.49	0.46
18:U:46:PRO:O	18:U:49:VAL:HG12	2.16	0.46
1:A:456:A:H2	1:A:495:U:H3	1.63	0.46
1:A:763:C:H3'	1:A:764:G:H5'	1.98	0.46
1:A:974:A:H2'	1:A:979:A:H1'	1.97	0.46
1:A:1161:A:H4'	9:K:15:HIS:CE1	2.51	0.46
1:A:1178:A:H2'	1:A:1179:A:O4'	2.15	0.46
1:A:1265:C:H4'	1:A:1266:A:C5'	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1302:G:H2'	1:A:1303:U:C6	2.52	0.46
10:L:79:TYR:CG	10:L:100:VAL:HG21	2.51	0.46
11:M:79:ARG:NH1	15:R:65:ASP:O	2.48	0.46
1:A:159:A:H1'	1:A:352:A:C4	2.51	0.45
1:A:366:U:H2'	1:A:367:A:C8	2.50	0.45
1:A:601:C:N4	1:A:602:U:O4	2.49	0.45
1:A:1160:A:O2'	9:K:72:ARG:NH2	2.49	0.45
1:A:1360:U:H2'	1:A:1361:C:O4'	2.16	0.45
18:U:14:LYS:HG2	18:U:51:GLY:HA3	1.97	0.45
1:A:684:A:H2'	1:A:685:A:C8	2.52	0.45
1:A:1158:C:H2'	1:A:1159:U:C6	2.52	0.45
1:A:1314:G:H1'	1:A:1341:A:H62	1.80	0.45
1:A:1354:U:H4'	1:A:1355:A:O5'	2.17	0.45
1:A:532:A:C2	10:L:101:LYS:HB3	2.51	0.45
1:A:596:G:H4'	7:I:4:THR:HA	1.99	0.45
1:A:721:A:N3	1:A:721:A:H2'	2.30	0.45
1:A:769:G:H3'	1:A:770:G:H8	1.81	0.45
1:A:910:A:H2'	1:A:911:A:C8	2.51	0.45
1:A:912:G:H2'	1:A:913:A:C8	2.51	0.45
1:A:1161:A:H4'	9:K:15:HIS:NE2	2.31	0.45
1:A:1296:A:H2'	1:A:1297:A:H8	1.75	0.45
1:A:224:U:C1'	1:A:475:A:H62	2.25	0.45
1:A:904:G:H2'	1:A:905:G:O4'	2.16	0.45
1:A:1123:C:C4	1:A:1197:A:H1'	2.51	0.45
1:A:1227:C:H2'	1:A:1228:U:C6	2.51	0.45
1:A:1243:C:H1'	1:A:1373:U:C2	2.50	0.45
3:C:24:VAL:HG11	19:V:67:MET:HE1	1.99	0.45
9:K:10:LEU:HD22	9:K:98:ILE:HG13	1.98	0.45
18:U:17:TYR:HD2	18:U:18:PHE:CE1	2.34	0.45
1:A:675:G:H1	1:A:749:U:H3	1.63	0.45
1:A:1273:C:HO2'	1:A:1280:G:H1	1.61	0.45
1:A:1296:A:H1'	1:A:1363:C:H5'	1.98	0.45
3:C:420:PHE:CE2	3:C:530:LEU:HD21	2.52	0.45
14:Q:25:VAL:HG21	14:Q:63:ILE:HG21	1.99	0.45
1:A:1187:G:N2	1:A:1189:A:H3'	2.32	0.45
1:A:1236:A:H2'	1:A:1236:A:N3	2.31	0.45
9:K:7:ARG:HG3	9:K:73:LEU:HD11	1.97	0.45
1:A:1034:U:O2'	1:A:1035:C:H2'	2.17	0.45
1:A:1259:A:H61	1:A:1363:C:H4'	1.82	0.45
15:R:27:LYS:HD2	15:R:27:LYS:HA	1.65	0.45
1:A:122:G:C6	1:A:246:G:C6	3.05	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:459:A:H4'	1:A:460:A:O5'	2.17	0.45
1:A:1286:C:C3'	1:A:1287:C:H4'	2.47	0.45
1:A:1296:A:C2'	1:A:1297:A:O5'	2.65	0.45
2:B:7:A:O3'	3:C:449:GLU:HG3	2.17	0.45
7:I:110:GLN:HB3	7:I:121:LYS:NZ	2.32	0.45
1:A:204:A:H2'	1:A:205:C:C6	2.52	0.45
1:A:222:G:C5	1:A:223:C:C5	3.05	0.45
1:A:242:C:H4'	14:Q:68:PRO:HG3	1.97	0.45
1:A:1310:U:H2'	1:A:1312:C:C5	2.52	0.45
1:A:1331:C:H5''	11:M:99:GLY:HA3	1.98	0.45
1:A:56:C:H2'	1:A:360:C:H41	1.82	0.45
1:A:243:C:H2'	1:A:244:G:C8	2.51	0.45
1:A:649:A:H2'	1:A:650:A:C8	2.51	0.45
1:A:1379:G:N3	1:A:1379:G:H2'	2.32	0.45
6:H:27:ILE:HG13	6:H:43:LEU:HD13	1.99	0.45
10:L:35:HIS:CE1	10:L:74:ILE:HD11	2.52	0.45
1:A:412:G:N7	4:F:2:ALA:HA	2.33	0.44
1:A:601:C:N3	1:A:602:U:C4	2.85	0.44
1:A:956:A:H1'	1:A:1245:A:C2	2.51	0.44
1:A:963:G:N1	1:A:1236:A:N6	2.65	0.44
1:A:1141:G:H5''	1:A:1142:C:OP1	2.17	0.44
1:A:1214:U:H4'	1:A:1215:G:O5'	2.16	0.44
1:A:1219:C:H2'	1:A:1220:U:H4'	1.99	0.44
1:A:1307:C:H1'	1:A:1308:A:C6	2.52	0.44
1:A:1353:C:H4'	1:A:1357:U:O2	2.17	0.44
1:A:222:G:C2	1:A:223:C:N3	2.85	0.44
1:A:528:C:H2'	1:A:529:A:C8	2.52	0.44
1:A:1019:C:H2'	1:A:1020:C:C6	2.51	0.44
14:Q:52:ASN:C	14:Q:53:ASN:HD22	2.20	0.44
1:A:141:G:H1'	1:A:180:G:O6	2.16	0.44
1:A:548:A:H2'	1:A:549:G:H8	1.81	0.44
1:A:718:U:C2	1:A:719:G:H1'	2.52	0.44
1:A:1236:A:C5	1:A:1237:C:H1'	2.53	0.44
1:A:1263:G:H2'	1:A:1264:G:H8	1.81	0.44
9:K:83:THR:O	9:K:87:LEU:N	2.48	0.44
13:P:22:VAL:HG21	13:P:59:TRP:CD1	2.51	0.44
1:A:248:C:N4	1:A:294:G:H1	2.15	0.44
1:A:518:A:H5'	4:F:47:TYR:HD2	1.81	0.44
1:A:824:A:H5''	1:A:824:A:H8	1.82	0.44
10:L:79:TYR:HB2	10:L:100:VAL:HG21	2.00	0.44
11:M:27:ARG:HG2	11:M:31:GLN:HG3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:407:G:H2'	1:A:408:C:C6	2.52	0.44
1:A:425:G:H1	1:A:434:U:H3	1.64	0.44
1:A:514:G:H5'	1:A:543:U:H2'	1.99	0.44
1:A:1123:C:H6	1:A:1124:C:H5	1.66	0.44
1:A:1284:A:N1	1:A:1292:C:H5'	2.33	0.44
1:A:1285:G:H2'	1:A:1286:C:C6	2.53	0.44
1:A:1378:C:H2'	1:A:1379:G:C8	2.50	0.44
1:A:466:G:N3	1:A:466:G:H2'	2.33	0.44
1:A:512:A:H2'	1:A:513:C:C6	2.53	0.44
1:A:1286:C:H1'	1:A:1291:C:C2	2.53	0.44
10:L:35:HIS:HE1	10:L:74:ILE:HD11	1.82	0.44
17:T:67:SER:HB2	17:T:71:ALA:HB3	1.99	0.44
1:A:113:G:H21	1:A:115:G:H1	1.66	0.44
1:A:253:U:C2	1:A:292:G:N1	2.86	0.44
1:A:581:A:N3	1:A:927:G:H1'	2.33	0.44
2:B:6:A:C4	2:B:6:A:C3'	3.01	0.44
15:R:23:ASN:OD1	15:R:47:HIS:HE1	2.00	0.44
1:A:819:C:H2'	1:A:820:C:O4'	2.17	0.44
1:A:822:U:H3'	1:A:825:A:H62	1.83	0.44
1:A:835:C:H5'	7:I:13:ARG:CZ	2.48	0.44
1:A:1030:G:H2'	1:A:1031:A:C8	2.52	0.44
3:C:375:ASN:HD21	3:C:442:SER:CB	2.31	0.44
5:G:15:LEU:HD11	5:G:18:VAL:HG23	2.00	0.44
7:I:68:GLN:O	7:I:69:ASN:C	2.56	0.44
15:R:22:LEU:HD22	15:R:28:LYS:CB	2.45	0.44
19:V:86:VAL:HG11	19:V:99:ILE:HG12	2.00	0.44
1:A:109:G:H2'	1:A:110:G:H8	1.83	0.43
1:A:327:G:H1	1:A:342:C:N4	2.16	0.43
1:A:689:C:N3	1:A:719:G:N2	2.65	0.43
1:A:719:G:C2	1:A:720:G:H1'	2.53	0.43
1:A:1231:G:OP2	1:A:1331:C:N4	2.51	0.43
1:A:302:C:N4	1:A:311:G:H1	2.16	0.43
1:A:698:C:H5'	1:A:714:G:N3	2.33	0.43
1:A:731:G:N3	1:A:731:G:H2'	2.33	0.43
1:A:1041:C:H4'	1:A:1042:G:C2	2.53	0.43
1:A:74:A:H2'	1:A:75:G:C8	2.53	0.43
1:A:1151:G:C2	1:A:1152:G:H1'	2.53	0.43
1:A:1369:A:H3'	1:A:1370:G:H8	1.83	0.43
4:F:180:PRO:O	4:F:181:GLU:CB	2.65	0.43
9:K:89:ARG:HA	9:K:89:ARG:HD3	1.84	0.43
1:A:216:G:H2'	1:A:217:C:C6	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1365:G:H2'	1:A:1366:A:H8	1.82	0.43
9:K:28:THR:OG1	9:K:86:ALA:HB1	2.18	0.43
1:A:892:C:H2'	1:A:893:C:C6	2.53	0.43
1:A:1008:C:H42	1:A:1052:U:H3	1.66	0.43
1:A:1119:C:H3'	1:A:1120:A:C8	2.53	0.43
1:A:1143:A:H2'	1:A:1144:U:O4'	2.18	0.43
1:A:1261:A:O5'	1:A:1261:A:H8	2.01	0.43
1:A:1282:U:H2'	1:A:1283:A:C8	2.54	0.43
17:T:15:ASP:OD2	17:T:17:GLU:HB3	2.17	0.43
1:A:144:U:H2'	1:A:145:G:C8	2.48	0.43
1:A:211:A:C6	1:A:229:C:H4'	2.54	0.43
1:A:1252:A:H2'	1:A:1252:A:N3	2.33	0.43
2:B:5:A:P	3:C:608:VAL:HG11	2.59	0.43
14:Q:9:VAL:HG11	14:Q:62:LYS:HE3	2.01	0.43
1:A:1015:C:OP1	1:A:1049:G:H1'	2.17	0.43
1:A:1039:U:H1'	1:A:1043:G:C2	2.54	0.43
1:A:1146:C:H5'	1:A:1146:C:H6	1.82	0.43
1:A:1157:U:O3'	8:J:18:ARG:HD3	2.19	0.43
1:A:1243:C:H2'	1:A:1244:U:C6	2.53	0.43
1:A:1286:C:O3'	1:A:1287:C:H4'	2.18	0.43
7:I:69:ASN:O	7:I:70:ASN:C	2.57	0.43
1:A:906:U:C5	1:A:907:C:C5	3.05	0.43
1:A:985:A:H2	1:A:1375:C:H1'	1.84	0.43
1:A:1260:A:H2'	1:A:1261:A:C8	2.54	0.43
1:A:1264:G:H1	1:A:1291:C:H42	1.66	0.43
16:S:4:ILE:O	16:S:5:LYS:C	2.57	0.43
1:A:110:G:H2'	1:A:110:G:N3	2.34	0.43
1:A:387:C:O2'	1:A:388:G:H5'	2.19	0.43
1:A:776:A:O2'	1:A:777:A:H5'	2.19	0.43
1:A:995:C:H2'	1:A:996:A:H8	1.78	0.43
1:A:1053:G:H2'	1:A:1054:A:C8	2.54	0.43
1:A:1167:C:H3'	1:A:1190:G:N2	2.34	0.43
1:A:70:G:H1'	1:A:170:A:N3	2.34	0.43
1:A:364:A:N6	1:A:365:G:C4	2.87	0.43
1:A:744:C:H2'	1:A:745:U:C6	2.54	0.43
1:A:962:U:H2'	1:A:963:G:H4'	2.01	0.43
3:C:47:VAL:HG11	19:V:53:GLY:O	2.19	0.43
1:A:464:G:H2'	1:A:465:U:C6	2.54	0.42
1:A:822:U:H2'	1:A:823:A:C8	2.48	0.42
3:C:497:VAL:CG2	3:C:512:ILE:HD11	2.49	0.42
7:I:34:ARG:HG3	7:I:51:PHE:CE1	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:L:53:MET:HG3	10:L:65:TYR:CE1	2.54	0.42
12:O:43:LEU:HD12	12:O:56:LEU:HD22	2.00	0.42
1:A:265:G:H8	1:A:265:G:H5''	1.84	0.42
1:A:612:U:H2'	1:A:613:G:C8	2.54	0.42
1:A:746:C:H2'	1:A:747:U:C6	2.54	0.42
1:A:833:U:C1'	7:I:2:VAL:HG22	2.49	0.42
1:A:1056:A:H2'	1:A:1056:A:N3	2.33	0.42
10:L:79:TYR:CB	10:L:100:VAL:HG21	2.49	0.42
11:M:15:VAL:HG21	11:M:48:LEU:HD21	2.01	0.42
11:M:27:ARG:O	11:M:28:THR:C	2.58	0.42
1:A:307:G:O5'	1:A:307:G:H8	2.01	0.42
1:A:389:A:H2'	1:A:390:A:C8	2.53	0.42
1:A:588:U:H2'	1:A:589:C:C6	2.54	0.42
1:A:691:C:H2'	1:A:692:G:C8	2.54	0.42
1:A:824:A:H4'	1:A:827:G:OP2	2.18	0.42
1:A:1219:C:H2'	1:A:1220:U:C4'	2.50	0.42
2:B:4:A:H5''	2:B:5:A:N7	2.34	0.42
1:A:473:G:N3	1:A:477:A:H2	2.17	0.42
1:A:511:C:N4	1:A:552:G:H1	2.17	0.42
1:A:718:U:H2'	1:A:719:G:C4'	2.49	0.42
3:C:419:ASP:HA	3:C:441:ARG:HH21	1.85	0.42
4:F:180:PRO:O	4:F:181:GLU:HG2	2.19	0.42
11:M:80:LEU:HD11	11:M:87:ARG:NH1	2.35	0.42
18:U:28:TYR:HA	18:U:34:LEU:HD11	2.01	0.42
1:A:10:A:H5'	5:G:106:ILE:HG22	2.01	0.42
1:A:232:A:H2'	1:A:233:C:O4'	2.19	0.42
1:A:474:A:H2'	1:A:475:A:O4'	2.19	0.42
1:A:987:A:H2'	1:A:988:A:H5''	2.00	0.42
1:A:1182:C:C2	1:A:1183:G:H1'	2.55	0.42
1:A:1304:U:H2'	1:A:1305:C:C6	2.54	0.42
10:L:135:PRO:O	10:L:136:LYS:C	2.58	0.42
1:A:119:C:H4'	1:A:120:A:OP1	2.18	0.42
1:A:251:A:H4'	1:A:252:U:H3'	2.02	0.42
1:A:538:G:H4'	1:A:542:A:C5	2.55	0.42
1:A:643:C:H2'	1:A:644:A:C8	2.55	0.42
1:A:1039:U:H1'	1:A:1043:G:N2	2.33	0.42
1:A:1228:U:H2'	1:A:1229:G:H8	1.84	0.42
1:A:1312:C:H3'	1:A:1313:G:C8	2.54	0.42
1:A:1355:A:H2	1:A:1357:U:C6	2.37	0.42
1:A:381:A:H2'	1:A:381:A:N3	2.35	0.42
1:A:449:G:O6	1:A:502:C:N3	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1228:U:H2'	1:A:1229:G:C8	2.55	0.42
1:A:1250:G:N2	1:A:1305:C:N3	2.67	0.42
1:A:1254:A:H2'	1:A:1255:G:H8	1.84	0.42
1:A:1338:G:O2'	11:M:24:GLY:HA2	2.20	0.42
1:A:14:U:H3	1:A:24:G:H1	1.67	0.42
1:A:235:G:H2'	1:A:236:A:O4'	2.20	0.42
1:A:251:A:C2	1:A:253:U:H2'	2.55	0.42
1:A:531:C:H41	10:L:63:ARG:NH2	2.18	0.42
1:A:715:A:H5''	1:A:715:A:C8	2.54	0.42
1:A:989:C:N4	1:A:1370:G:N1	2.65	0.42
2:B:5:A:C2	2:B:6:A:H5'	2.55	0.42
17:T:37:ILE:HD13	17:T:65:VAL:HG12	2.01	0.42
1:A:216:G:N2	1:A:224:U:C2	2.87	0.42
1:A:417:U:H3	1:A:441:G:H1	1.68	0.42
1:A:615:G:H21	1:A:641:G:H5'	1.83	0.42
1:A:702:G:H2'	1:A:703:A:C8	2.55	0.42
1:A:708:C:H2'	1:A:709:G:H8	1.81	0.42
1:A:829:U:H4'	1:A:830:G:OP2	2.19	0.42
1:A:1056:A:H2	1:A:1224:G:H4'	1.85	0.42
4:F:13:ARG:O	4:F:14:ARG:C	2.58	0.42
12:O:36:ILE:HG23	12:O:56:LEU:HD11	2.02	0.42
1:A:9:G:H2'	5:G:124:LEU:HD22	2.01	0.41
1:A:474:A:C8	1:A:474:A:P	3.08	0.41
1:A:906:U:O2'	1:A:907:C:C6	2.68	0.41
2:B:-1:A:H4'	2:B:0:A:H8	1.84	0.41
1:A:249:G:H2'	1:A:250:C:C6	2.55	0.41
1:A:333:A:H2'	1:A:334:G:C8	2.55	0.41
1:A:446:G:O6	1:A:503:C:H2'	2.20	0.41
1:A:765:C:H4'	7:I:2:VAL:HG12	2.01	0.41
1:A:766:U:H2'	1:A:767:G:O4'	2.19	0.41
1:A:842:U:O2	1:A:863:G:N2	2.53	0.41
1:A:955:G:H2'	1:A:955:G:N3	2.35	0.41
1:A:1188:A:H2'	1:A:1189:A:C8	2.54	0.41
1:A:224:U:H2'	1:A:225:A:H8	1.86	0.41
1:A:475:A:C4	1:A:477:A:H1'	2.55	0.41
1:A:781:U:H2'	1:A:782:G:C8	2.56	0.41
1:A:906:U:C2'	1:A:907:C:C6	3.04	0.41
1:A:1370:G:N7	1:A:1371:C:N4	2.67	0.41
5:G:48:PHE:HD1	5:G:141:LEU:CD1	2.31	0.41
9:K:83:THR:O	9:K:87:LEU:HG	2.20	0.41
1:A:418:G:H2'	1:A:437:U:C4	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:844:A:OP1	18:U:58:ARG:NH2	2.54	0.41
1:A:854:C:O3'	18:U:20:SER:HA	2.21	0.41
1:A:992:U:H4'	1:A:993:A:O5'	2.20	0.41
1:A:1199:G:H2'	1:A:1199:G:N3	2.35	0.41
1:A:1215:G:N3	1:A:1215:G:H2'	2.35	0.41
1:A:602:U:H2'	1:A:603:U:C6	2.55	0.41
1:A:833:U:H1'	7:I:2:VAL:HG22	2.01	0.41
1:A:1006:A:C2	1:A:1056:A:H4'	2.56	0.41
1:A:1291:C:H2'	1:A:1292:C:C6	2.55	0.41
1:A:321:A:H2'	1:A:322:C:C6	2.55	0.41
1:A:749:U:H2'	1:A:750:G:O5'	2.20	0.41
2:B:4:A:H62	3:C:530:LEU:HD22	1.85	0.41
15:R:15:LEU:HD21	15:R:71:LEU:HD11	2.02	0.41
16:S:62:VAL:HG22	16:S:72:ALA:HB2	2.01	0.41
1:A:1056:A:H5''	1:A:1057:G:C8	2.56	0.41
1:A:1356:G:H2'	1:A:1359:A:N1	2.36	0.41
3:C:341:LEU:HD21	3:C:572:ILE:CG2	2.51	0.41
17:T:50:TYR:CZ	18:U:71:ALA:HB2	2.56	0.41
1:A:686:U:H2'	1:A:687:U:O4'	2.20	0.41
1:A:719:G:H2'	1:A:720:G:H8	1.86	0.41
1:A:952:G:H22	1:A:1350:U:H1'	1.85	0.41
1:A:1027:U:H2'	1:A:1028:A:H4'	2.03	0.41
1:A:1142:C:N3	1:A:1143:A:C6	2.88	0.41
10:L:53:MET:HG3	10:L:65:TYR:CD1	2.56	0.41
16:S:45:ASP:N	16:S:45:ASP:OD1	2.53	0.41
1:A:13:G:H1	1:A:25:C:N4	2.19	0.41
1:A:64:U:H2'	1:A:65:C:C6	2.55	0.41
1:A:292:G:H2'	1:A:293:C:C6	2.55	0.41
1:A:337:A:H8	1:A:337:A:H5'	1.86	0.41
1:A:365:G:O2'	1:A:366:U:C5'	2.63	0.41
1:A:414:G:H1	1:A:444:C:N4	2.18	0.41
1:A:599:U:H2'	1:A:600:U:C6	2.56	0.41
1:A:624:C:N4	1:A:634:G:H1	2.18	0.41
1:A:626:G:H1	1:A:632:C:N4	2.19	0.41
1:A:628:U:C2	4:F:128:ILE:HD12	2.55	0.41
1:A:691:C:H6	1:A:691:C:O5'	2.03	0.41
1:A:694:G:N2	1:A:713:A:OP1	2.54	0.41
1:A:744:C:H2'	1:A:745:U:H6	1.86	0.41
1:A:900:G:N2	1:A:916:G:H2'	2.36	0.41
1:A:998:G:H4'	1:A:1024:A:H61	1.86	0.41
1:A:1003:G:N2	1:A:1056:A:O2'	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1256:A:H2'	1:A:1257:A:O4'	2.20	0.41
11:M:104:ASN:O	11:M:105:ASN:C	2.58	0.41
1:A:54:U:H6	1:A:54:U:H5''	1.86	0.41
1:A:349:C:H2'	1:A:350:C:C6	2.56	0.41
1:A:719:G:H2'	1:A:720:G:C8	2.56	0.41
1:A:931:U:H4'	5:G:24:VAL:HB	2.03	0.41
1:A:1288:A:H1'	1:A:1291:C:N4	2.36	0.41
1:A:1354:U:O5'	1:A:1357:U:H1'	2.21	0.41
6:H:30:MET:SD	6:H:120:LEU:HD22	2.61	0.41
11:M:67:GLY:O	11:M:68:ASP:C	2.60	0.41
11:M:109:ARG:HA	11:M:109:ARG:HD2	1.76	0.41
13:P:5:ILE:HG22	13:P:70:VAL:HG11	2.02	0.41
1:A:107:A:C6	1:A:334:G:C6	3.10	0.40
1:A:122:G:C6	1:A:246:G:N1	2.89	0.40
1:A:458:G:H1	1:A:492:C:N4	2.19	0.40
1:A:694:G:H4'	19:V:43:ALA:O	2.21	0.40
1:A:1210:A:H5''	1:A:1214:U:H3	1.86	0.40
1:A:1376:C:H2'	1:A:1377:G:C8	2.55	0.40
2:B:3:A:C2	2:B:4:A:H1'	2.55	0.40
4:F:32:ALA:O	4:F:37:GLY:HA3	2.21	0.40
8:J:88:LEU:HD21	8:J:95:ARG:HA	2.04	0.40
1:A:161:A:C5	1:A:162:C:H1'	2.56	0.40
1:A:496:A:H3'	1:A:497:C:C6	2.57	0.40
1:A:504:A:H4'	1:A:505:G:O5'	2.22	0.40
1:A:625:G:H1	1:A:633:C:N4	2.20	0.40
1:A:1305:C:H4'	1:A:1311:U:C2	2.56	0.40
1:A:1313:G:N2	1:A:1342:A:H62	2.18	0.40
1:A:1314:G:HO2'	1:A:1315:A:H8	1.66	0.40
9:K:90:LEU:HD23	9:K:90:LEU:HA	1.89	0.40
10:L:63:ARG:CB	10:L:103:LEU:HD11	2.51	0.40
1:A:143:C:H2'	1:A:144:U:C6	2.57	0.40
1:A:484:U:H2'	1:A:485:A:H8	1.86	0.40
1:A:683:G:H4'	18:U:75:TYR:CE2	2.56	0.40
1:A:264:U:H2'	1:A:265:G:C8	2.56	0.40
1:A:582:A:H8	1:A:582:A:H5'	1.86	0.40
1:A:608:C:OP1	7:I:90:LYS:HD2	2.22	0.40
1:A:743:A:N3	1:A:743:A:H2'	2.37	0.40
1:A:832:G:N3	7:I:2:VAL:HG21	2.36	0.40
1:A:991:U:H2'	1:A:992:U:C5	2.57	0.40
1:A:1003:G:O2'	1:A:1222:A:N6	2.54	0.40
1:A:1332:G:H5'	1:A:1332:G:H8	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:105:G:H3'	1:A:106:G:C8	2.40	0.40
1:A:268:G:H2'	1:A:269:U:C6	2.57	0.40
1:A:1194:G:H2'	1:A:1195:G:H8	1.83	0.40
1:A:1198:U:O2'	1:A:1199:G:P	2.75	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	453/779 (58%)	449 (99%)	4 (1%)	0	100	100
4	F	179/200 (90%)	167 (93%)	7 (4%)	5 (3%)	5	33
5	G	156/166 (94%)	150 (96%)	3 (2%)	3 (2%)	8	40
6	H	85/156 (54%)	85 (100%)	0	0	100	100
7	I	129/132 (98%)	122 (95%)	3 (2%)	4 (3%)	4	30
8	J	100/130 (77%)	96 (96%)	4 (4%)	0	100	100
9	K	58/102 (57%)	52 (90%)	4 (7%)	2 (3%)	3	29
10	L	134/138 (97%)	129 (96%)	4 (3%)	1 (1%)	22	62
11	M	106/121 (88%)	94 (89%)	11 (10%)	1 (1%)	17	56
12	O	83/89 (93%)	81 (98%)	2 (2%)	0	100	100
13	P	86/90 (96%)	82 (95%)	3 (4%)	1 (1%)	13	50
14	Q	82/87 (94%)	79 (96%)	3 (4%)	0	100	100
15	R	76/92 (83%)	72 (95%)	2 (3%)	2 (3%)	5	34
16	S	81/88 (92%)	77 (95%)	4 (5%)	0	100	100
17	T	90/95 (95%)	85 (94%)	5 (6%)	0	100	100
18	U	62/79 (78%)	60 (97%)	2 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	V	90/131 (69%)	89 (99%)	1 (1%)	0	100	100
All	All	2050/2675 (77%)	1969 (96%)	62 (3%)	19 (1%)	21	56

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	F	181	GLU
4	F	182	ARG
5	G	26	LYS
5	G	90	GLY
5	G	91	ALA
7	I	3	MET
9	K	94	SER
15	R	28	LYS
4	F	24	LYS
7	I	4	THR
7	I	70	ASN
9	K	82	GLN
10	L	136	LYS
4	F	28	LYS
7	I	56	LYS
4	F	180	PRO
11	M	96	PRO
13	P	13	LYS
15	R	25	THR

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	411/692 (59%)	408 (99%)	3 (1%)	84	90
4	F	159/173 (92%)	155 (98%)	4 (2%)	47	68
5	G	123/130 (95%)	120 (98%)	3 (2%)	49	69
6	H	78/132 (59%)	78 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
7	I	111/112 (99%)	109 (98%)	2 (2%)	59	77
8	J	80/102 (78%)	72 (90%)	8 (10%)	7	28
9	K	55/92 (60%)	50 (91%)	5 (9%)	9	32
10	L	114/116 (98%)	107 (94%)	7 (6%)	18	46
11	M	94/104 (90%)	89 (95%)	5 (5%)	22	49
12	O	80/83 (96%)	79 (99%)	1 (1%)	69	82
13	P	74/76 (97%)	68 (92%)	6 (8%)	11	37
14	Q	77/80 (96%)	74 (96%)	3 (4%)	32	57
15	R	70/81 (86%)	68 (97%)	2 (3%)	42	64
16	S	66/70 (94%)	65 (98%)	1 (2%)	65	80
17	T	81/84 (96%)	77 (95%)	4 (5%)	25	51
18	U	56/64 (88%)	54 (96%)	2 (4%)	35	59
19	V	66/100 (66%)	65 (98%)	1 (2%)	65	80
All	All	1795/2291 (78%)	1738 (97%)	57 (3%)	42	62

All (57) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	11	LEU
3	C	65	ILE
3	C	253	ASP
4	F	66	ARG
4	F	71	LEU
4	F	146	ARG
4	F	178	ARG
5	G	5	ASP
5	G	58	GLU
5	G	157	ARG
7	I	68	GLN
7	I	70	ASN
8	J	12	ARG
8	J	22	VAL
8	J	25	GLU
8	J	56	GLU
8	J	72	LEU
8	J	97	THR
8	J	100	ARG

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Mol	Chain	Res	Type
8	J	106	ARG
9	K	13	TYR
9	K	78	ASN
9	K	88	MET
9	K	89	ARG
9	K	90	LEU
10	L	2	PRO
10	L	10	LYS
10	L	18	ASN
10	L	34	GLU
10	L	35	HIS
10	L	133	LYS
10	L	136	LYS
11	M	16	VAL
11	M	28	THR
11	M	96	PRO
11	M	97	VAL
11	M	105	ASN
12	O	48	LYS
13	P	24	ASP
13	P	35	GLU
13	P	45	LYS
13	P	48	GLU
13	P	53	GLU
13	P	62	THR
14	Q	50	ASP
14	Q	53	ASN
14	Q	85	VAL
15	R	20	GLU
15	R	81	LYS
16	S	78	ARG
17	T	16	GLU
17	T	17	GLU
17	T	43	TRP
17	T	87	ARG
18	U	14	LYS
18	U	48	ARG
19	V	95	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	360	GLN
3	C	464	HIS
3	C	535	GLN
4	F	112	GLN
5	G	70	ASN
6	H	56	ASN
7	I	57	GLN
8	J	5	GLN
8	J	66	ASN
8	J	81	HIS
12	O	72	ASN
13	P	41	ASN
14	Q	53	ASN
15	R	29	GLN
15	R	47	HIS
17	T	61	GLN
19	V	42	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	1243/1554 (79%)	421 (33%)	97 (7%)
2	B	10/11 (90%)	7 (70%)	2 (20%)
All	All	1253/1565 (80%)	428 (34%)	99 (7%)

All (428) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	9	G
1	A	10	A
1	A	11	G
1	A	12	A
1	A	32	C
1	A	33	G
1	A	34	A
1	A	41	G
1	A	49	C
1	A	50	C
1	A	51	U
1	A	52	A
1	A	53	A
1	A	67	A

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Mol	Chain	Res	Type
1	A	70	G
1	A	74	A
1	A	98	U
1	A	100	G
1	A	105	G
1	A	114	A
1	A	118	A
1	A	119	C
1	A	120	A
1	A	125	G
1	A	128	A
1	A	132	U
1	A	140	A
1	A	143	C
1	A	144	U
1	A	148	A
1	A	150	A
1	A	152	C
1	A	153	U
1	A	154	C
1	A	162	C
1	A	165	G
1	A	166	G
1	A	168	C
1	A	172	U
1	A	173	A
1	A	177	G
1	A	180	G
1	A	181	G
1	A	182	U
1	A	189	A
1	A	190	A
1	A	191	C
1	A	194	C
1	A	195	A
1	A	197	G
1	A	201	C
1	A	202	A
1	A	208	A
1	A	209	A
1	A	210	A
1	A	211	A

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Mol	Chain	Res	Type
1	A	218	U
1	A	219	U
1	A	220	C
1	A	221	G
1	A	229	C
1	A	245	C
1	A	248	C
1	A	249	G
1	A	251	A
1	A	252	U
1	A	255	G
1	A	259	G
1	A	265	G
1	A	266	A
1	A	270	A
1	A	274	G
1	A	275	C
1	A	283	G
1	A	287	A
1	A	288	C
1	A	289	G
1	A	297	G
1	A	314	A
1	A	323	A
1	A	324	C
1	A	331	U
1	A	336	C
1	A	337	A
1	A	338	C
1	A	340	G
1	A	352	A
1	A	353	C
1	A	354	G
1	A	355	G
1	A	359	G
1	A	360	C
1	A	362	G
1	A	373	U
1	A	375	U
1	A	377	C
1	A	380	C
1	A	400	G

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Mol	Chain	Res	Type
1	A	405	A
1	A	406	C
1	A	414	G
1	A	419	A
1	A	420	U
1	A	421	G
1	A	424	G
1	A	428	U
1	A	429	U
1	A	430	C
1	A	431	G
1	A	432	G
1	A	437	U
1	A	439	A
1	A	445	U
1	A	447	U
1	A	456	A
1	A	458	G
1	A	459	A
1	A	460	A
1	A	461	C
1	A	466	G
1	A	467	C
1	A	475	A
1	A	476	U
1	A	477	A
1	A	478	G
1	A	487	C
1	A	488	U
1	A	489	U
1	A	493	G
1	A	494	G
1	A	495	U
1	A	500	A
1	A	506	A
1	A	508	A
1	A	509	G
1	A	520	C
1	A	526	G
1	A	527	C
1	A	529	A
1	A	530	G

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Mol	Chain	Res	Type
1	A	536	G
1	A	540	U
1	A	542	A
1	A	543	U
1	A	545	C
1	A	556	A
1	A	558	C
1	A	568	A
1	A	569	A
1	A	570	U
1	A	571	U
1	A	573	U
1	A	577	G
1	A	581	A
1	A	582	A
1	A	585	G
1	A	588	U
1	A	597	G
1	A	603	U
1	A	604	A
1	A	605	A
1	A	627	C
1	A	628	U
1	A	641	G
1	A	642	U
1	A	643	C
1	A	648	G
1	A	651	A
1	A	655	G
1	A	656	G
1	A	659	A
1	A	661	U
1	A	662	U
1	A	663	G
1	A	667	G
1	A	668	C
1	A	669	A
1	A	671	A
1	A	672	A
1	A	674	A
1	A	675	G
1	A	684	A

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Mol	Chain	Res	Type
1	A	693	U
1	A	694	G
1	A	695	U
1	A	696	A
1	A	697	G
1	A	698	C
1	A	702	G
1	A	704	A
1	A	708	C
1	A	711	A
1	A	712	G
1	A	713	A
1	A	714	G
1	A	715	A
1	A	716	U
1	A	717	G
1	A	718	U
1	A	725	A
1	A	731	G
1	A	732	U
1	A	733	G
1	A	738	A
1	A	739	G
1	A	740	G
1	A	755	G
1	A	756	U
1	A	757	A
1	A	758	A
1	A	764	G
1	A	768	A
1	A	775	A
1	A	821	G
1	A	824	A
1	A	825	A
1	A	826	C
1	A	827	G
1	A	828	A
1	A	829	U
1	A	830	G
1	A	839	G
1	A	849	G
1	A	853	C

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Mol	Chain	Res	Type
1	A	855	G
1	A	856	C
1	A	881	U
1	A	883	A
1	A	886	A
1	A	894	U
1	A	895	G
1	A	901	U
1	A	906	U
1	A	909	C
1	A	923	A
1	A	924	A
1	A	931	U
1	A	932	G
1	A	953	U
1	A	954	G
1	A	956	A
1	A	958	C
1	A	962	U
1	A	963	G
1	A	966	U
1	A	970	U
1	A	971	U
1	A	972	C
1	A	975	A
1	A	976	G
1	A	977	C
1	A	978	A
1	A	979	A
1	A	980	C
1	A	981	G
1	A	982	C
1	A	983	G
1	A	984	A
1	A	985	A
1	A	986	G
1	A	987	A
1	A	988	A
1	A	992	U
1	A	993	A
1	A	994	C
1	A	996	A

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Mol	Chain	Res	Type
1	A	999	U
1	A	1002	U
1	A	1003	G
1	A	1008	C
1	A	1009	C
1	A	1010	U
1	A	1012	U
1	A	1013	G
1	A	1014	A
1	A	1017	A
1	A	1019	C
1	A	1022	A
1	A	1023	G
1	A	1024	A
1	A	1025	G
1	A	1027	U
1	A	1028	A
1	A	1030	G
1	A	1033	G
1	A	1034	U
1	A	1036	C
1	A	1039	U
1	A	1040	U
1	A	1041	C
1	A	1042	G
1	A	1043	G
1	A	1046	G
1	A	1047	C
1	A	1048	A
1	A	1051	G
1	A	1053	G
1	A	1054	A
1	A	1057	G
1	A	1124	C
1	A	1125	U
1	A	1129	U
1	A	1134	G
1	A	1135	U
1	A	1137	G
1	A	1139	C
1	A	1140	A
1	A	1142	C

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Mol	Chain	Res	Type
1	A	1145	U
1	A	1147	A
1	A	1148	G
1	A	1149	U
1	A	1150	U
1	A	1151	G
1	A	1152	G
1	A	1153	G
1	A	1154	C
1	A	1155	A
1	A	1157	U
1	A	1162	G
1	A	1163	G
1	A	1166	A
1	A	1167	C
1	A	1168	U
1	A	1169	G
1	A	1171	C
1	A	1172	G
1	A	1173	G
1	A	1176	A
1	A	1177	C
1	A	1178	A
1	A	1183	G
1	A	1190	G
1	A	1191	G
1	A	1193	G
1	A	1194	G
1	A	1197	A
1	A	1198	U
1	A	1199	G
1	A	1200	A
1	A	1202	G
1	A	1205	A
1	A	1206	A
1	A	1208	U
1	A	1209	C
1	A	1210	A
1	A	1211	U
1	A	1212	C
1	A	1213	A
1	A	1214	U

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Mol	Chain	Res	Type
1	A	1215	G
1	A	1216	C
1	A	1221	U
1	A	1222	A
1	A	1223	U
1	A	1224	G
1	A	1225	A
1	A	1233	U
1	A	1234	A
1	A	1235	C
1	A	1236	A
1	A	1237	C
1	A	1244	U
1	A	1245	A
1	A	1246	C
1	A	1247	A
1	A	1249	U
1	A	1250	G
1	A	1252	A
1	A	1253	C
1	A	1259	A
1	A	1265	C
1	A	1266	A
1	A	1267	G
1	A	1270	A
1	A	1271	A
1	A	1272	A
1	A	1273	C
1	A	1274	C
1	A	1279	G
1	A	1280	G
1	A	1282	U
1	A	1287	C
1	A	1288	A
1	A	1289	A
1	A	1291	C
1	A	1294	A
1	A	1295	C
1	A	1296	A
1	A	1297	A
1	A	1302	G
1	A	1304	U

Continued on next page...

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Mol	Chain	Res	Type
1	A	1305	C
1	A	1307	C
1	A	1308	A
1	A	1309	G
1	A	1310	U
1	A	1311	U
1	A	1312	C
1	A	1313	G
1	A	1321	G
1	A	1325	G
1	A	1326	C
1	A	1327	A
1	A	1328	A
1	A	1332	G
1	A	1340	G
1	A	1345	U
1	A	1347	G
1	A	1350	U
1	A	1352	G
1	A	1354	U
1	A	1355	A
1	A	1356	G
1	A	1357	U
1	A	1359	A
1	A	1362	G
1	A	1369	A
1	A	1371	C
1	A	1377	G
1	A	1379	G
2	B	0	A
2	B	1	A
2	B	3	A
2	B	5	A
2	B	6	A
2	B	7	A
2	B	9	A

All (99) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	9	G
1	A	10	A

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Mol	Chain	Res	Type
1	A	66	G
1	A	113	G
1	A	128	A
1	A	189	A
1	A	190	A
1	A	193	G
1	A	207	U
1	A	209	A
1	A	220	C
1	A	251	A
1	A	287	A
1	A	313	G
1	A	323	A
1	A	352	A
1	A	359	G
1	A	372	A
1	A	419	A
1	A	420	U
1	A	429	U
1	A	446	G
1	A	455	G
1	A	459	A
1	A	475	A
1	A	486	C
1	A	487	C
1	A	494	G
1	A	508	A
1	A	568	A
1	A	569	A
1	A	570	U
1	A	575	G
1	A	584	G
1	A	585	G
1	A	590	G
1	A	596	G
1	A	603	U
1	A	604	A
1	A	641	G
1	A	661	U
1	A	662	U
1	A	667	G
1	A	671	A

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Mol	Chain	Res	Type
1	A	707	G
1	A	710	U
1	A	713	A
1	A	715	A
1	A	727	A
1	A	762	A
1	A	824	A
1	A	826	C
1	A	827	G
1	A	828	A
1	A	848	G
1	A	855	G
1	A	894	U
1	A	899	A
1	A	952	G
1	A	965	U
1	A	970	U
1	A	976	G
1	A	977	C
1	A	992	U
1	A	1016	A
1	A	1018	U
1	A	1032	C
1	A	1041	C
1	A	1056	A
1	A	1134	G
1	A	1148	G
1	A	1151	G
1	A	1154	C
1	A	1157	U
1	A	1161	A
1	A	1162	G
1	A	1166	A
1	A	1170	C
1	A	1176	A
1	A	1198	U
1	A	1214	U
1	A	1223	U
1	A	1234	A
1	A	1235	C
1	A	1246	C
1	A	1252	A

Continued on next page...

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Mol	Chain	Res	Type
1	A	1266	A
1	A	1271	A
1	A	1279	G
1	A	1294	A
1	A	1304	U
1	A	1307	C
1	A	1309	G
1	A	1310	U
1	A	1311	U
1	A	1326	C
1	A	1354	U
2	B	0	A
2	B	6	A

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.

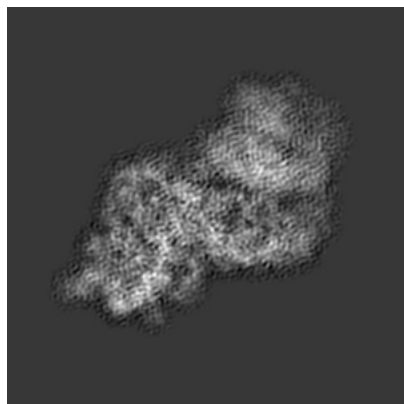
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-16596. These allow visual inspection of the internal detail of the map and identification of artifacts.

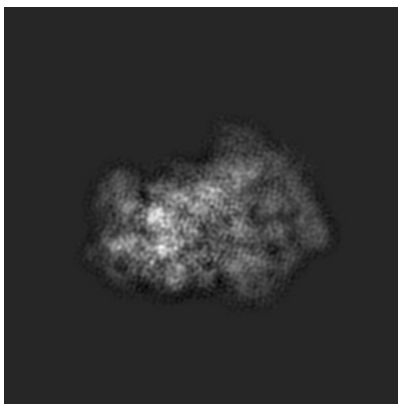
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

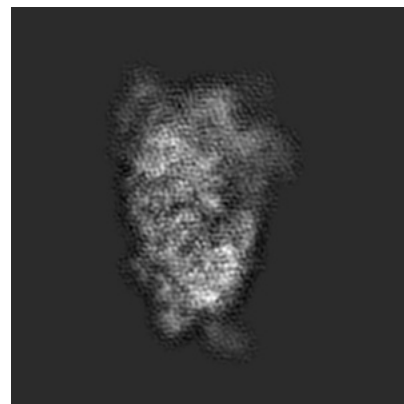
6.1.1 Primary map



X

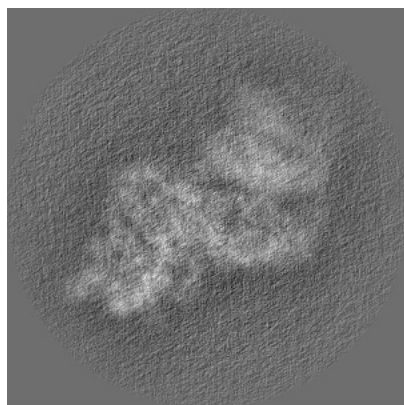


Y

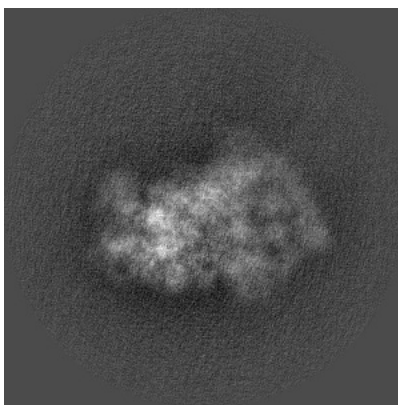


Z

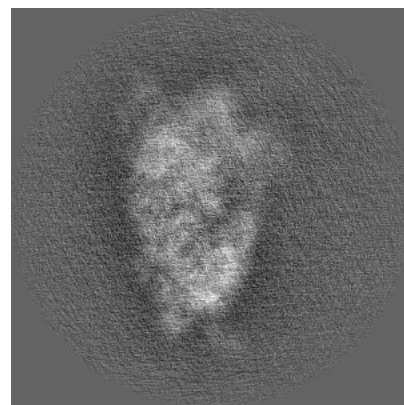
6.1.2 Raw map



X



Y

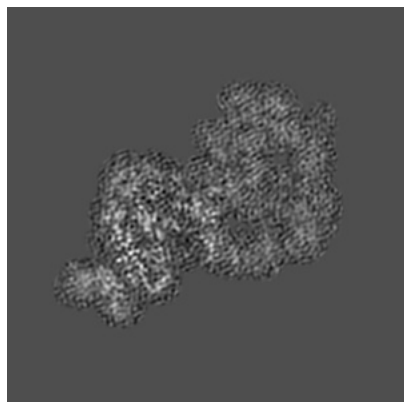


Z

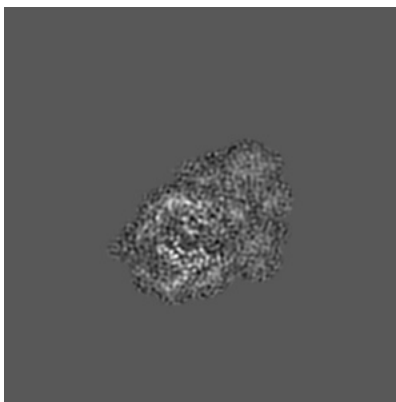
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

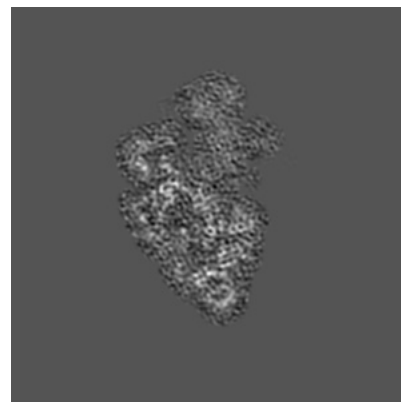
6.2.1 Primary map



X Index: 192

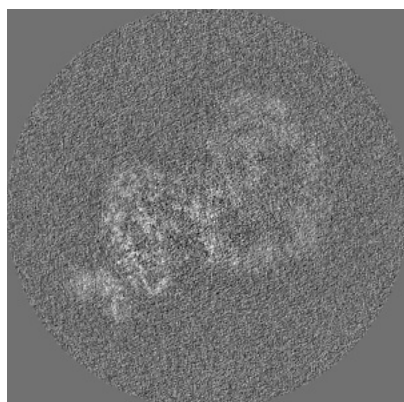


Y Index: 192

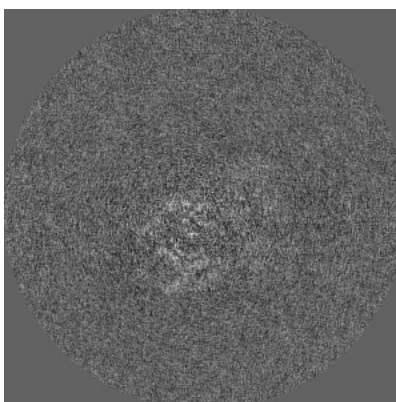


Z Index: 192

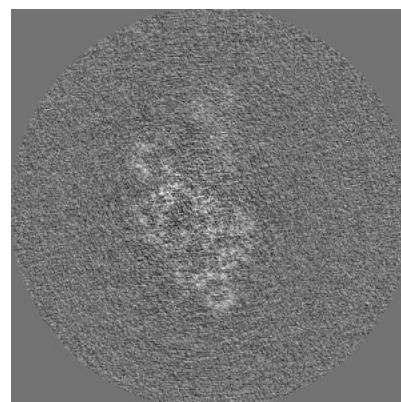
6.2.2 Raw map



X Index: 192



Y Index: 192

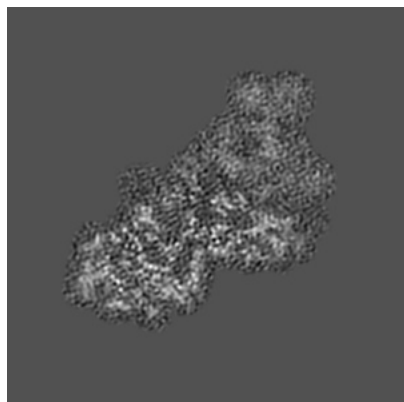


Z Index: 192

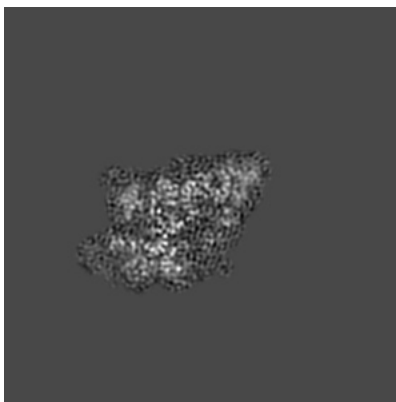
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

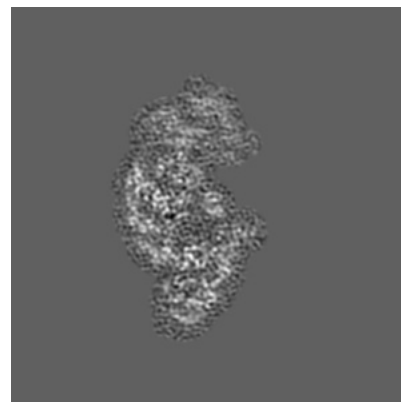
6.3.1 Primary map



X Index: 159

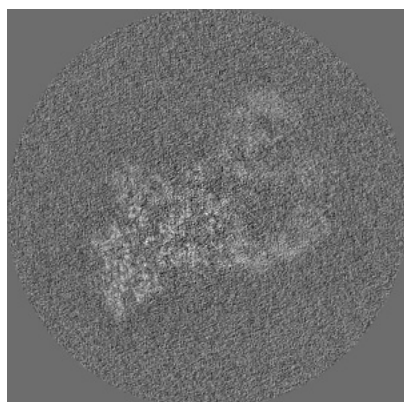


Y Index: 151

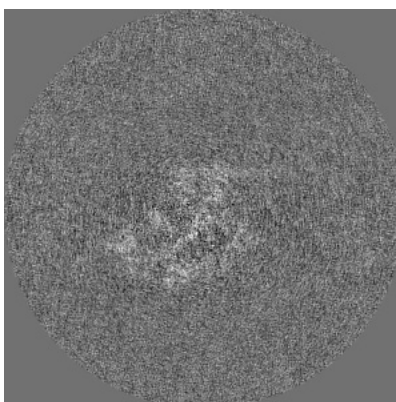


Z Index: 162

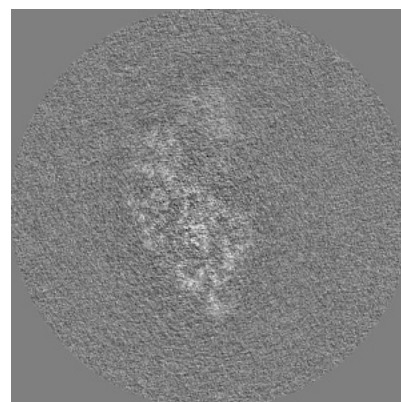
6.3.2 Raw map



X Index: 178



Y Index: 173

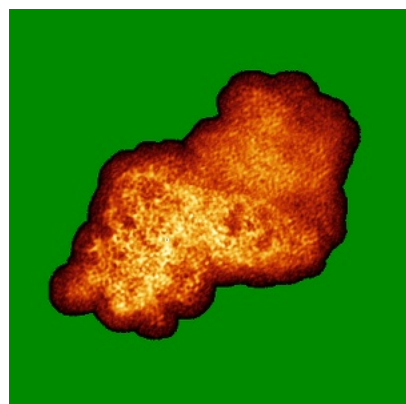


Z Index: 185

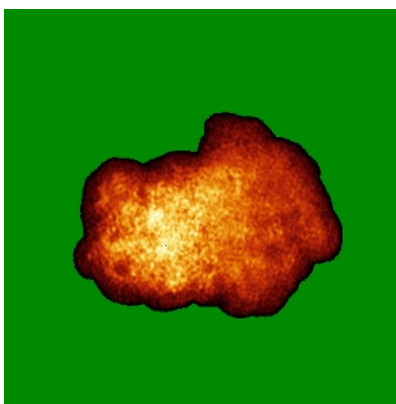
The images above show the largest variance slices of the map in three orthogonal directions.

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

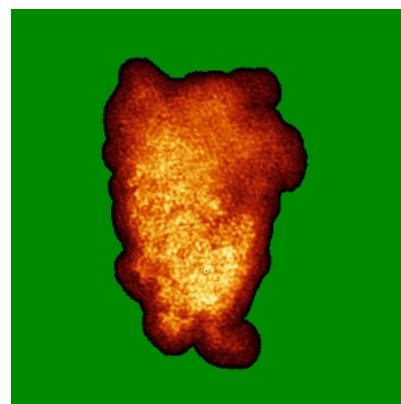
6.4.1 Primary map



X

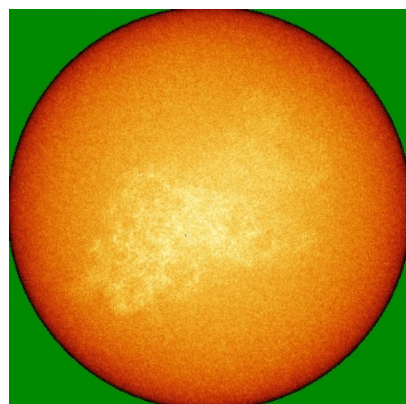


Y

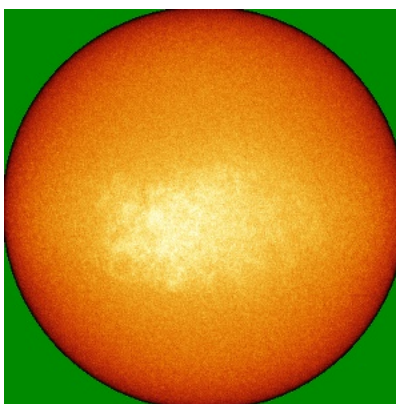


Z

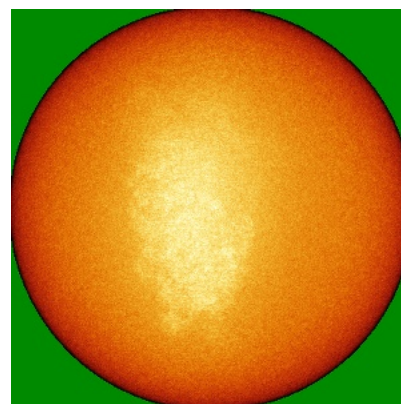
6.4.2 Raw map



X



Y

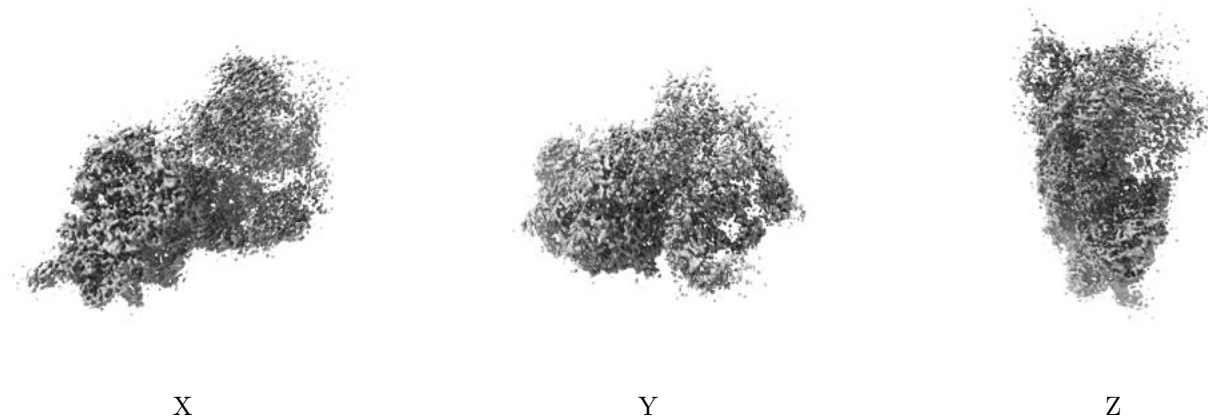


Z

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

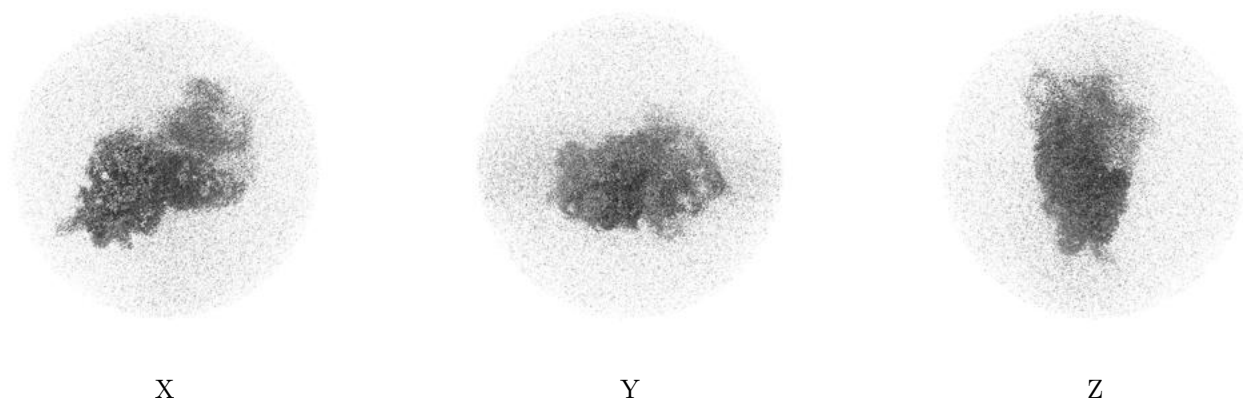
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0125. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

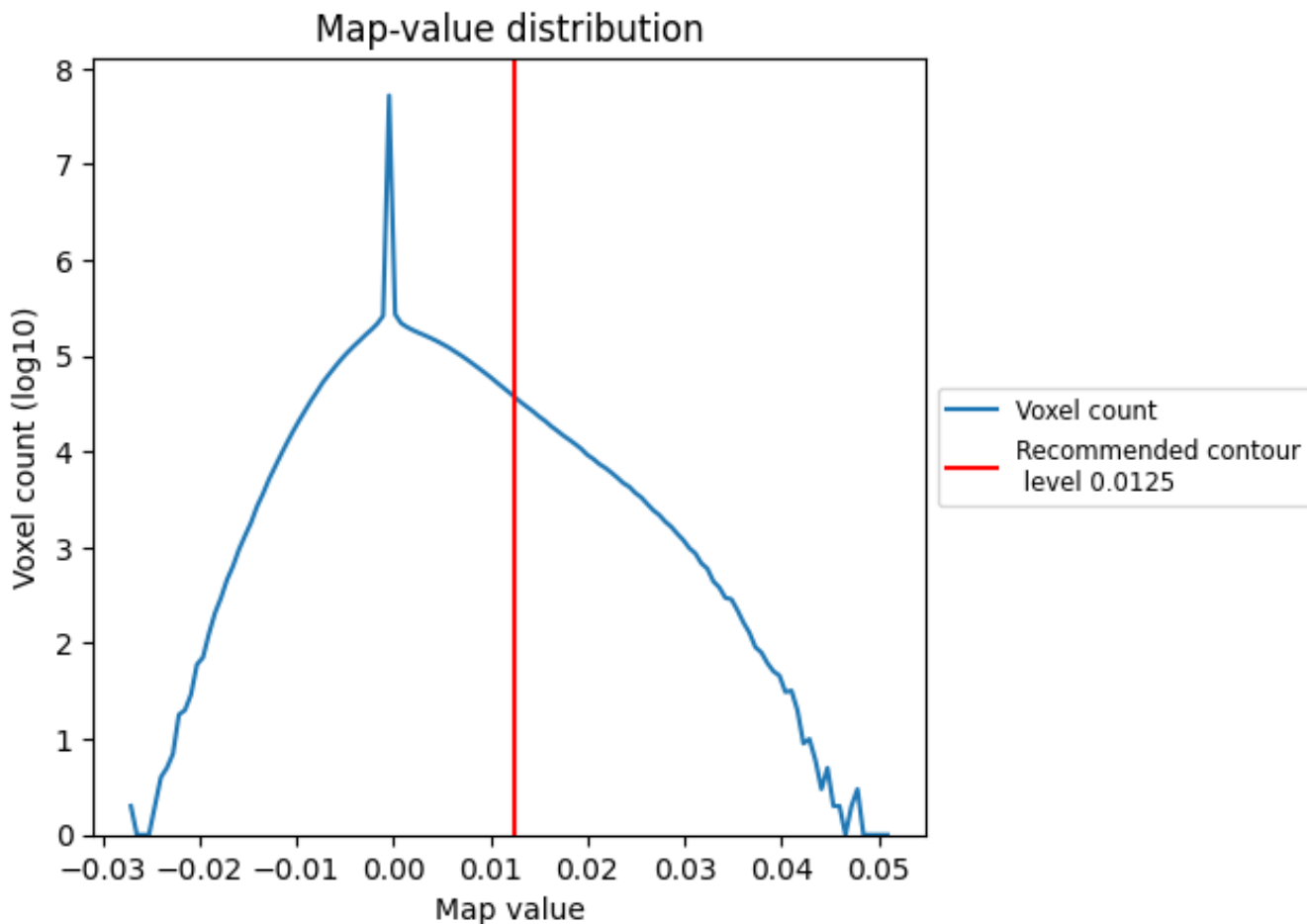
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

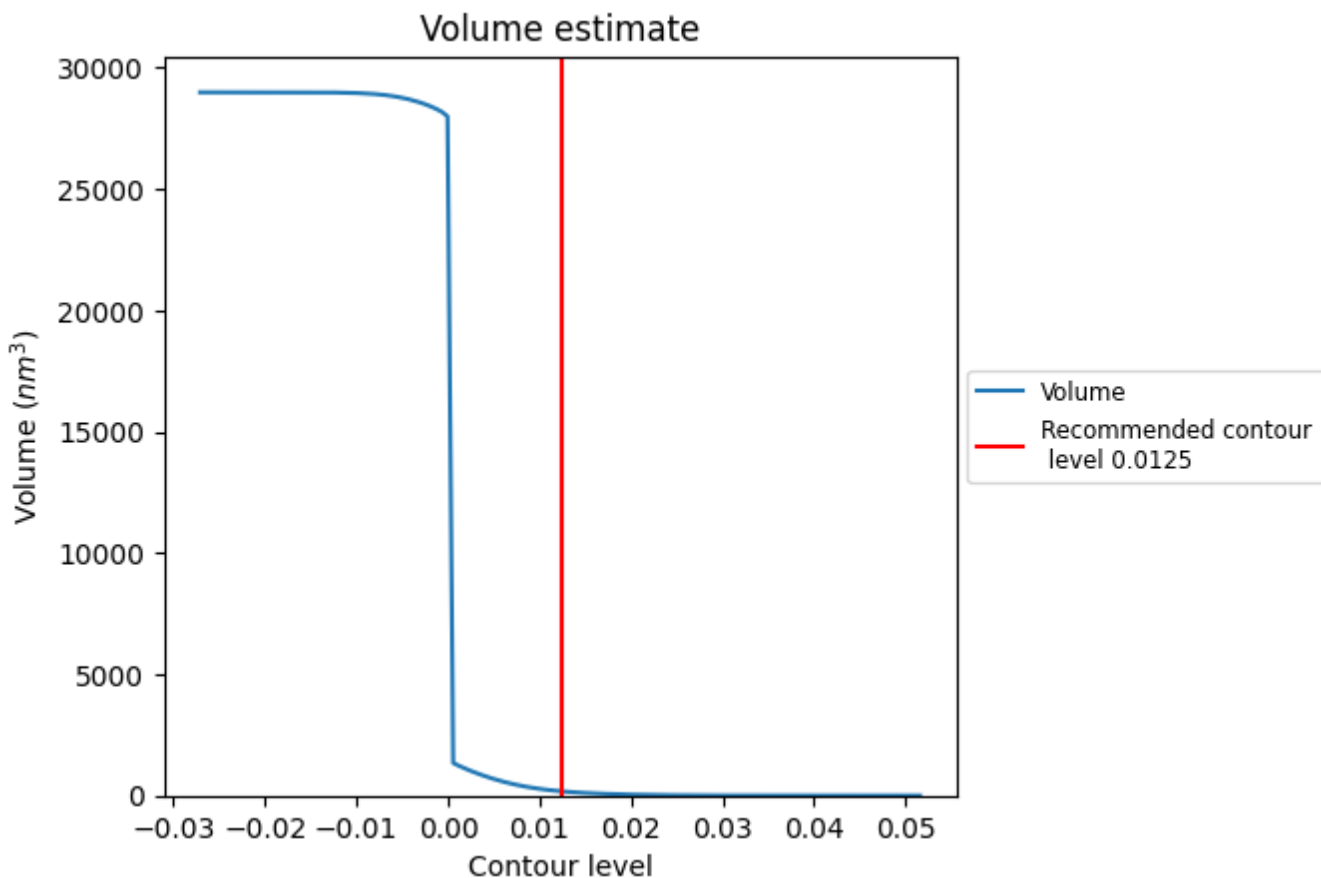
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

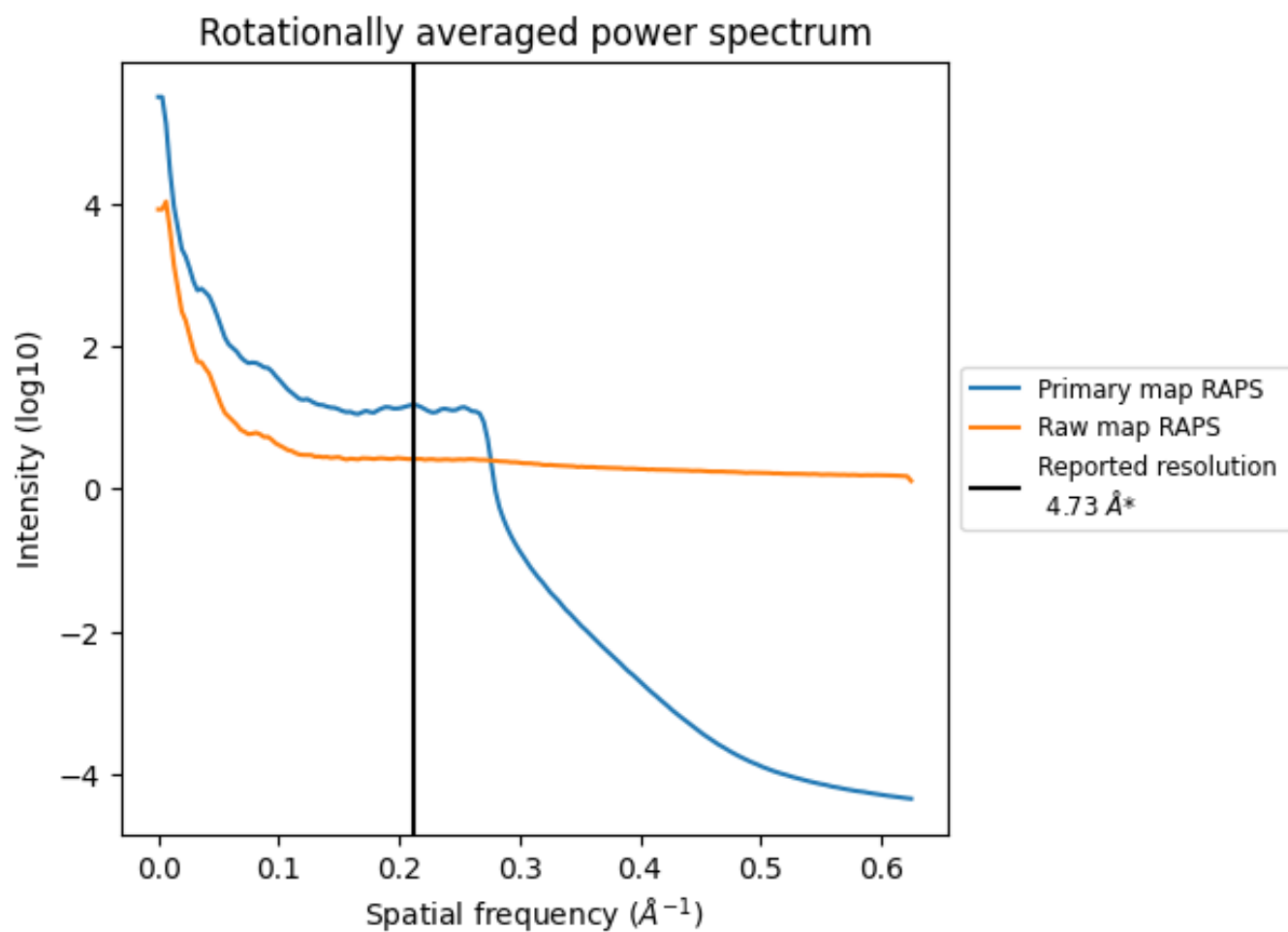
7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 173 nm³; this corresponds to an approximate mass of 156 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 i

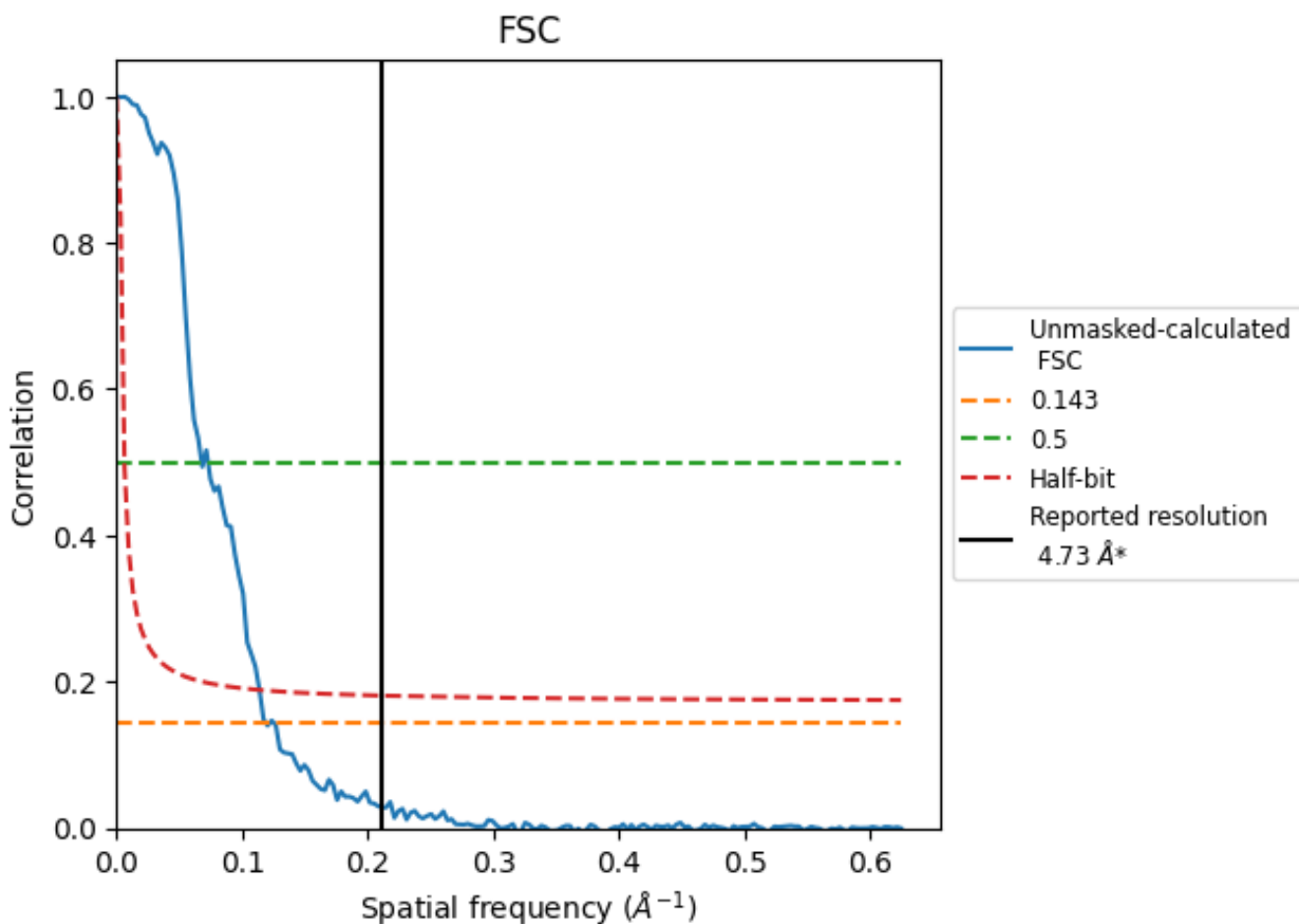


*Reported resolution corresponds to spatial frequency of 0.211 \AA^{-1}

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.211 Å⁻¹

8.2 Resolution estimates [i](#)

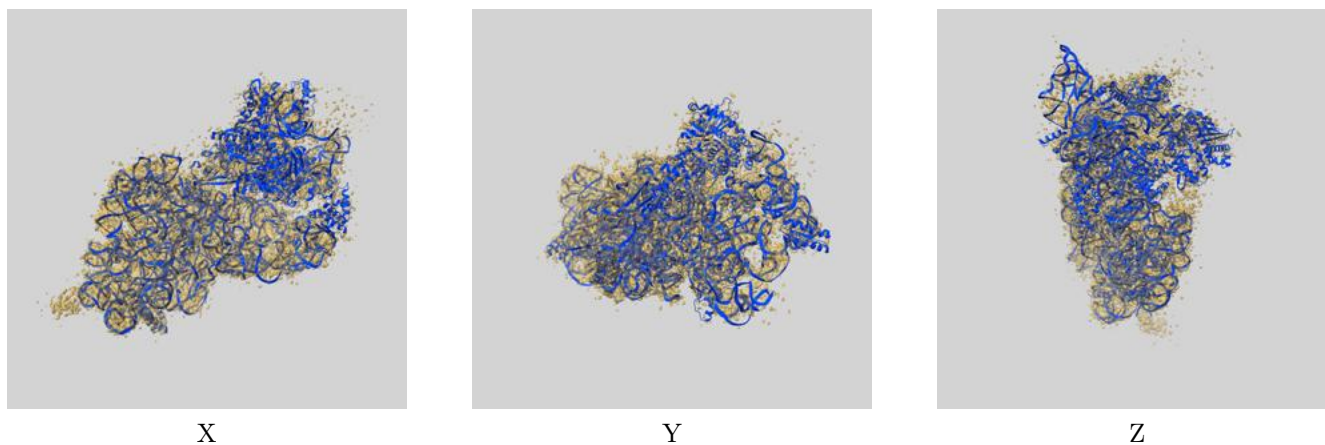
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.73	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	8.39	14.75	8.77

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 8.39 differs from the reported value 4.73 by more than 10 %

9 Map-model fit [i](#)

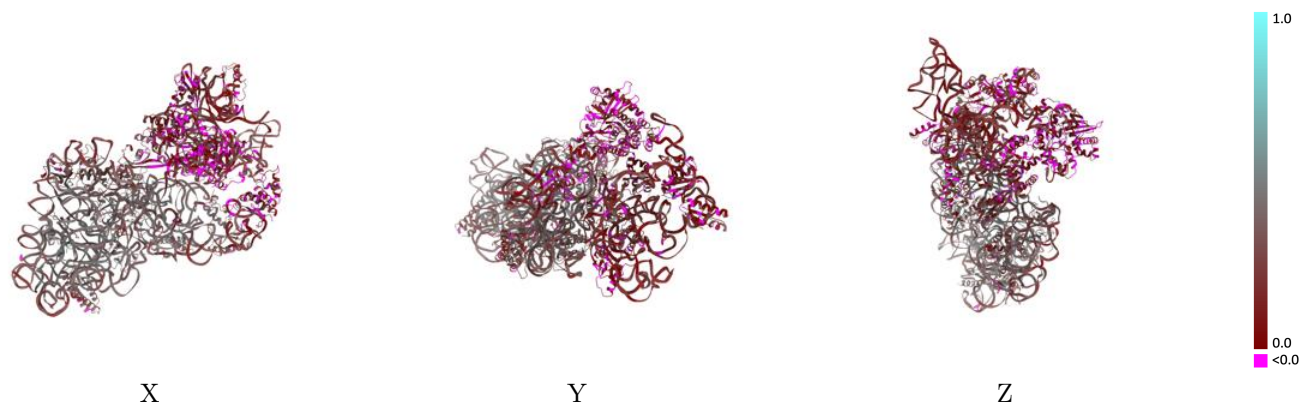
This section contains information regarding the fit between EMDB map EMD-16596 and PDB model 8CDV. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)



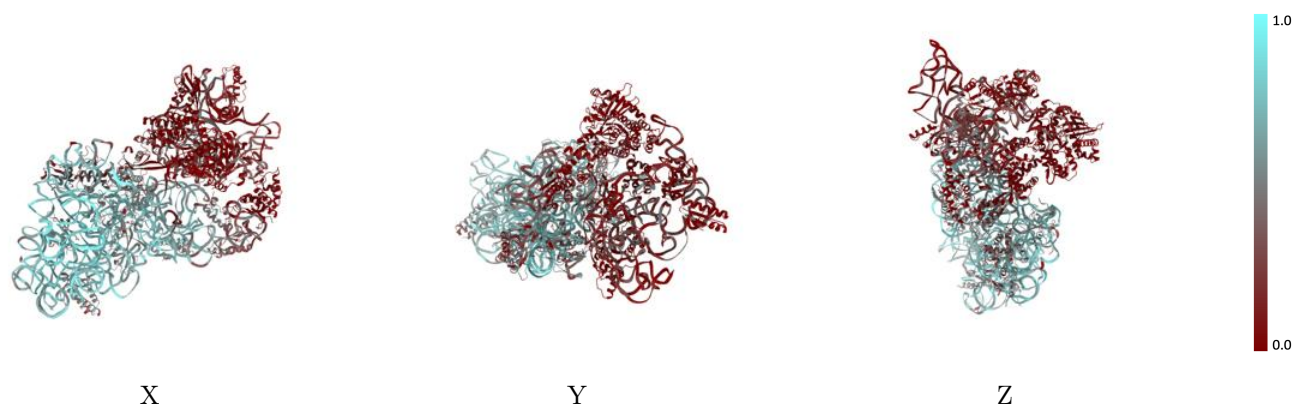
The images above show the 3D surface view of the map at the recommended contour level 0.0125 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



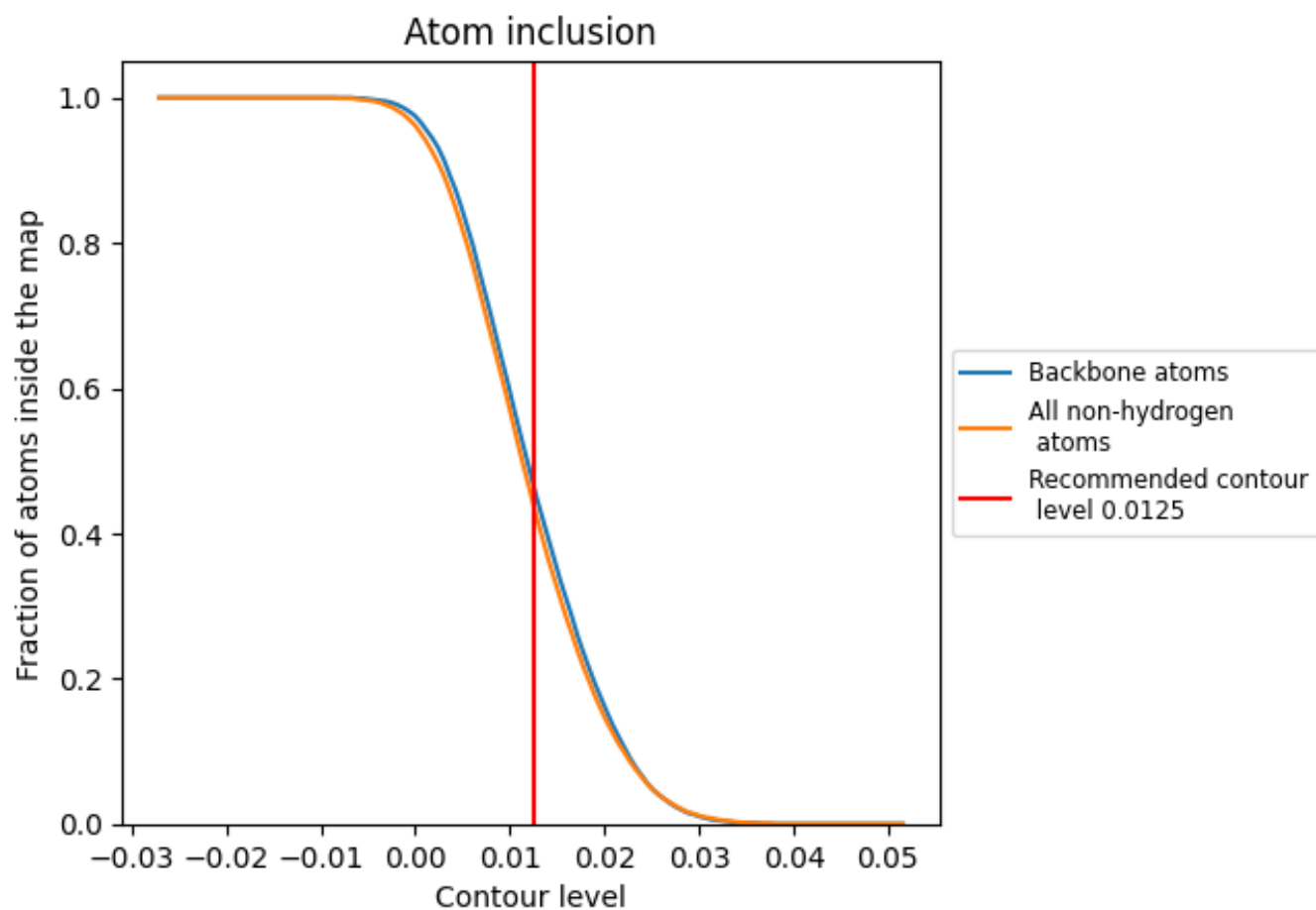
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0125).









































9.4 Atom inclusion [i](#)



At the recommended contour level, 47% of all backbone atoms, 44% 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 (0.0125) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.4390	 0.2720
A	 0.5530	 0.3090
B	 0.0950	 0.1610
C	 0.0540	 0.0690
F	 0.3860	 0.2940
G	 0.2880	 0.2500
H	 0.0880	 0.1180
I	 0.4750	 0.3680
J	 0.0770	 0.1020
K	 0.0480	 0.1180
L	 0.5260	 0.3790
M	 0.0720	 0.1270
O	 0.5120	 0.3410
P	 0.5590	 0.3950
Q	 0.5070	 0.3860
R	 0.0590	 0.0790
S	 0.4730	 0.3120
T	 0.2840	 0.2430
U	 0.3370	 0.2770
V	 0.0690	 0.1010

