



## Full wwPDB EM Validation Report ⓘ

Jul 2, 2026 – 06:13 PM JST

PDB ID : 9L96 / pdb\_00009196  
EMDB ID : EMD-62895  
Title : State D of archaeal pre-50S ribosome  
Authors : Li, Z.Q.; Yang, X.Y.  
Deposited on : 2024-12-29  
Resolution : 2.97 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](mailto: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>.

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

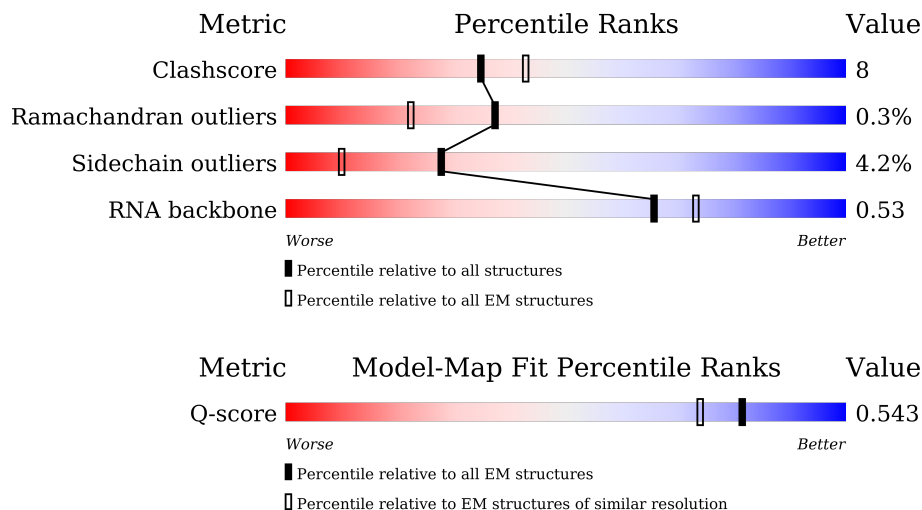
EMDB validation analysis : 0.0.1.dev133  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
MolProbity : 4-5-2 with Phenix2.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (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) : 2.50

# 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 2.97 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	13205 ( 2.47 - 3.47 )

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  $\geq 3$ , 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	0	2916	
2	9	122	
3	a	406	



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Mol	Chain	Length	Quality of chain
4	E	120	63% 28% 8% ..
5	F	176	80% 18% ..
6	G	196	76% 19% ..
7	H	116	78% 21% .
8	I	184	77% 22% .
9	J	151	71% 26% .
10	K	96	83% 16% .
11	L	153	80% 18% ..
12	M	67	67% 19% 13%
13	N	118	67% 27% ..
14	O	154	80% 19% .
15	P	92	77% 18% ..
16	Q	234	48% 12% . 39%
17	R	89	69% 21% 10%
18	S	58	83% 16% .
19	T	93	73% 26% .
20	U	241	76% 21% .
21	V	338	83% 16% .
22	W	248	82% 17% .
23	X	172	5% 74% 24% .
24	Y	178	70% 27% ..
25	b	145	78% 21% .
26	f	132	77% 22% .
27	d	70	7% 70% 29% .
28	c	83	81% 19%

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Mol	Chain	Length	Quality of chain
29	A	50	
30	e	58	

## 2 Entry composition

There are 33 unique types of molecules in this entry. The entry contains 93108 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	0	2801	60043	26800	11056	19386	2801	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	9	120	2551	1138	453	840	120	0	0

- Molecule 3 is a protein called CBS domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
3	a	281	2081	1306	358	413	4	0	0

- Molecule 4 is a protein called Large ribosomal subunit protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	E	119	859	531	139	188	1	0	0

- Molecule 5 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
5	F	174	1348	836	247	257	8	0	0

- Molecule 6 is a protein called Large ribosomal subunit protein eL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
6	G	192	1564	955	333	274	2	0	0

- Molecule 7 is a protein called Large ribosomal subunit protein eL18.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
7	H	115	880	541	167	172	0	0

- Molecule 8 is a protein called Large ribosomal subunit protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
8	I	183	1417	880	258	278	1	0	0

- Molecule 9 is a protein called Large ribosomal subunit protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
9	J	147	1179	712	243	223	1	0	0

- Molecule 10 is a protein called Large ribosomal subunit protein eL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
10	K	95	736	451	150	133	2	0	0

- Molecule 11 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
11	L	151	1170	728	214	224	4	0	0

- Molecule 12 is a protein called Large ribosomal subunit protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
12	M	58	466	287	83	94	2	0	0

- Molecule 13 is a protein called Large ribosomal subunit protein uL24.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
13	N	114	903	545	171	187	0	0

- Molecule 14 is a protein called Large ribosomal subunit protein uL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	154	Total	C	N	O	S	0	0
			1200	731	220	245	4		

- Molecule 15 is a protein called Large ribosomal subunit protein eL31.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	89	Total	C	N	O	S	0	0
			708	439	135	133	1		

- Molecule 16 is a protein called Large ribosomal subunit protein eL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Q	142	Total	C	N	O	S	0	0
			1146	698	231	216	1		

- Molecule 17 is a protein called Large ribosomal subunit protein eL43.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	80	Total	C	N	O	S	0	0
			617	374	125	117	1		

- Molecule 18 is a protein called Large ribosomal subunit protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	57	Total	C	N	O	S	0	0
			439	265	90	80	4		

- Molecule 19 is a protein called Large ribosomal subunit protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	93	Total	C	N	O	S	0	0
			746	457	152	129	8		

- Molecule 20 is a protein called Large ribosomal subunit protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	U	235	Total	C	N	O	S	0	0
			1737	1073	344	315	5		

- Molecule 21 is a protein called Large ribosomal subunit protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
21	V	337	2615	1621	484	500	10	0	0

- Molecule 22 is a protein called Large ribosomal subunit protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
22	W	248	1884	1157	354	371	2	0	0

- Molecule 23 is a protein called Large ribosomal subunit protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
23	X	169	1279	790	226	261	2	0	0

- Molecule 24 is a protein called Large ribosomal subunit protein uL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
24	Y	174	1329	823	224	279	3	0	0

- Molecule 25 is a protein called Large ribosomal subunit protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
25	b	144	1127	701	201	220	5	0	0

- Molecule 26 is a protein called Large ribosomal subunit protein uL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
26	f	132	973	599	187	183	4	0	0

- Molecule 27 is a protein called Large ribosomal subunit protein uL29.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
27	d	69	491	302	87	102	0	0

- Molecule 28 is a protein called Large ribosomal subunit protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
28	c	83	640	395	110	132	3	0	0

- Molecule 29 is a protein called Large ribosomal subunit protein eL39.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
29	A	31	252	159	51	40	2	0	0

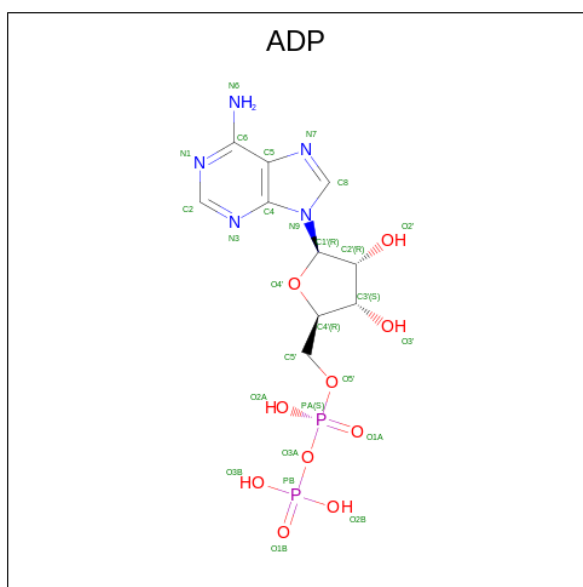
- Molecule 30 is a protein called Large ribosomal subunit protein eL20.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
30	e	58	440	272	77	91	0	0

- Molecule 31 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
31	0	212	Total	Mg	0
			212	212	
31	9	5	Total	Mg	0
			5	5	
31	F	1	Total	Mg	0
			1	1	
31	G	4	Total	Mg	0
			4	4	
31	J	1	Total	Mg	0
			1	1	
31	L	1	Total	Mg	0
			1	1	
31	O	1	Total	Mg	0
			1	1	
31	P	1	Total	Mg	0
			1	1	
31	U	1	Total	Mg	0
			1	1	
31	V	5	Total	Mg	0
			5	5	

- Molecule 32 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>10</sub>P<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
32	a	1	27	10	5	10	2	0
32	a	1	27	10	5	10	2	0

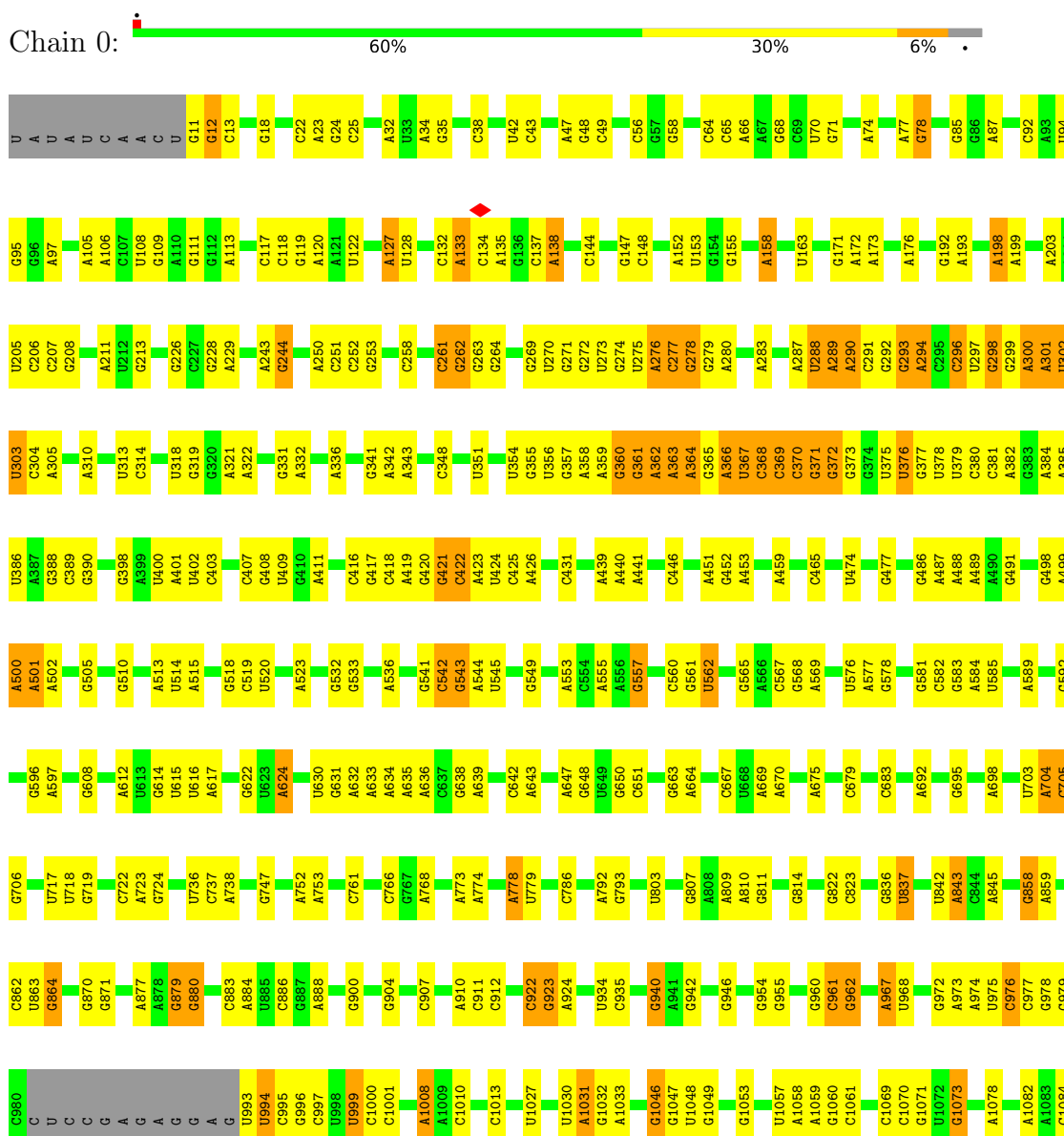
- Molecule 33 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
33	S	1	1	1	0
33	T	1	1	1	0

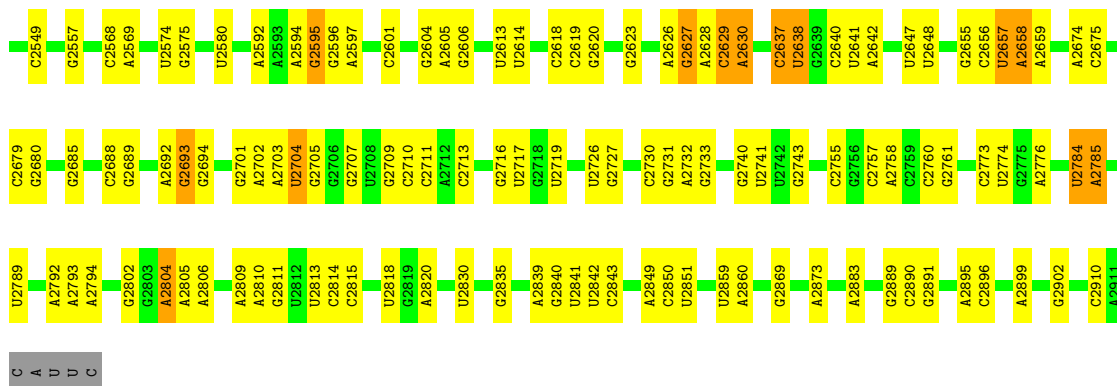
### 3 Residue-property plots

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

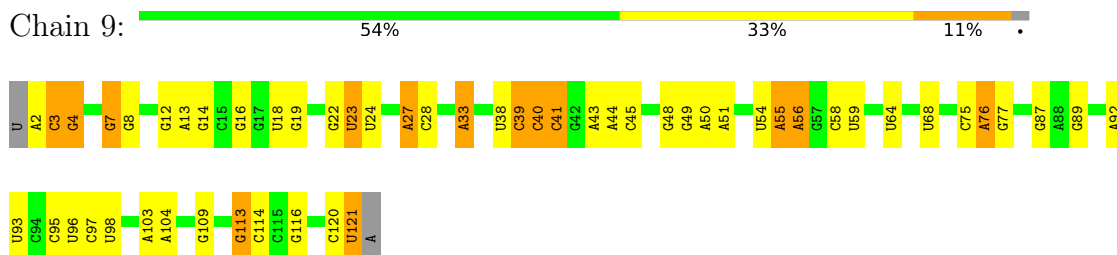
#### • Molecule 1: 23S RNA



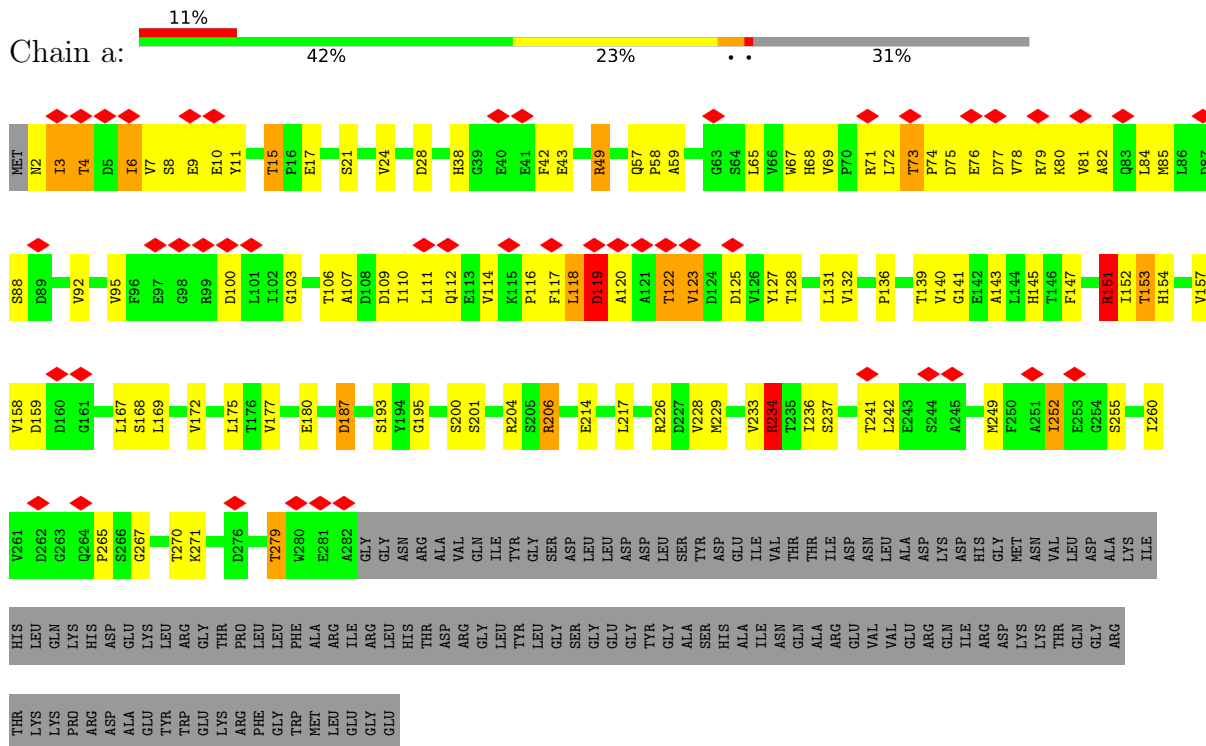
U2441	U2318	U2062	G1942	A1840	G1717	G1596	U498	G1360	A1233	G1169	C1085
G2442	U2319	G2063	G1943	U1843	U1718	C1597	A1499	A1354	U1234	A1170	C1086
G2455	U2320	C2064	G1944	U1844	C1719	G1600	U1500	A1355	C1235	A1171	C1087
A2458	U2321	G2065	G1945	C1849	U1724	A1602	C1509	C1356	G1236	A1172	G1088
G2459	C2321	G2066	A1946	C1849	C1725	A1603	U1510	A1365	A1239	G1173	A1089
A2460	G	A2067	C1948	A1858	G1739	A1608	U1511	G1366	C1240	A1174	A1093
A2463	U	G2076	U1949	U1864	G1746	A1609	U1512	A1382	U1242	C1176	G1094
G2469	A	A2076	A1950	C1865	C1747	G1612	C1516	A1391	A1243	A1178	A1098
A2325	G	C2077	U1951	G1866	A1748	A1621	A1517	C1251	C1180	C1179	A1099
A2326	U	C2078	A1952	C1867	A1749	A1622	A1518	U1252	C1181	C1181	C1103
A2327	U	C2079	A1953	C1868	G1750	A1623	U1519	U1261	U1182	U1182	A1107
A2328	U	C2080	C1954	A1869	U1751	A1624	A1520	G1262	C1183	C1183	A1108
A2329	U	A2082	C1955	C1870	U1752	A1625	A1521	A1402	U1184	U1184	G1109
A2330	U	G2084	C1956	U1872	U1753	A1626	A1522	A1403	G1185	G1185	U1110
A2331	U	A2089	U1959	C1875	A1762	U1636	A1523	A1410	G1270	A1186	G1111
A2332	U	A2093	U1960	U1876	G1763	A1637	C1529	A1411	C1271	A1187	A1115
A2333	U	A2094	A1961	C1877	C1766	C1647	G1530	U1414	U1272	A1188	U1116
A2334	U	G2096	A1962	U1878	C1767	A1651	C1531	U1415	U1273	A1189	U1117
A2335	U	A2098	G1963	C1878	C1768	A1652	U1534	U1415	U1274	A1190	A1125
A2336	U	C2097	G1964	C1882	U1772	A1653	C1535	U1442	U1275	A1191	U1126
A2337	U	C2098	U1969	C1887	A1772	A1654	A1539	U1443	U1276	A1192	G1127
A2338	U	C2099	G1970	A1888	C1784	A1655	A1540	U1444	C1277	A1193	G1128
A2339	U	U2100	A1971	G1889	C1784	A1656	C1541	U1445	U1278	A1194	G1129
A2340	U	C2103	G1972	G1895	U1787	A1657	C1542	U1446	C1279	A1195	G1130
A2341	U	G2104	U1973	U1896	U1788	A1658	A1542	U1447	U1285	A1196	A1130
A2342	U	A2105	C1974	A1897	C1789	A1659	C1543	C1447	C1286	A1197	A1134
A2343	U	G2106	C1975	A1901	U1791	A1660	C1544	U1453	U1299	C1198	G1135
A2344	U	U1989	U1989	A1902	U1791	A1661	A1545	A1454	U1299	A1199	U1136
A2345	U	C1992	C1992	A1903	C1796	A1662	A1546	A1455	A1300	G1200	G1140
A2346	U	U1997	U1997	A1904	A1797	A1663	A1547	A1456	A1309	C1201	G1141
A2347	U	G1998	G1998	A1905	C1803	A1664	C1553	A1457	U1202	G1201	G1142
A2348	U	C1999	C1999	A1906	C1803	A1665	C1554	A1458	U1203	A1204	C1143
A2349	U	A2000	A2000	A1907	C1809	A1666	C1555	A1459	A1204	A1204	C1144
A2350	U	U2001	U2001	A1908	C1809	A1667	C1556	A1460	C1205	C1205	G1145
A2351	U	G2135	A2004	A1909	G1812	A1668	C1557	U1464	C1206	G1207	U1146
A2352	U	U2136	U2005	A1910	G1813	A1669	C1558	A1464	C1207	G1207	U1147
A2353	U	C	G2006	A1911	G1813	A1670	C1559	A1466	C1208	G1208	A1148
A2354	U	G	G2007	A1912	U1818	A1671	C1560	A1467	G1211	G1211	C1154
A2355	U	C	G2007	A1913	C1819	A1682	C1561	A1468	A1212	A1212	G1155
A2356	U	U	U2025	A1914	C1820	A1683	C1562	A1473	G1213	G1213	G1156
A2357	U	A	G2026	G1917	G1821	A1684	C1563	A1481	G1214	G1214	G1157
A2358	U	U	G2027	G1918	A1822	A1685	C1564	A1482	A1218	A1218	A1158
A2359	U	C	U2027	A1923	G1825	A1686	C1565	A1483	G1219	G1219	G1159
A2360	U	C	G2046	A1924	U1828	A1687	C1566	A1484	G1220	G1220	G1160
A2361	U	C	G2046	A1924	G1829	A1688	C1567	A1485	A1326	A1326	G1161
A2362	U	C	G2046	A1924	U1829	A1689	C1568	A1486	A1327	A1327	G1162
A2363	U	C	G2046	A1924	G1830	A1690	C1569	A1487	G1331	G1331	G1163
A2364	U	C	G2046	A1924	G1831	A1691	C1570	A1488	U1332	U1332	G1164
A2365	U	C	G2046	A1924	G1832	A1692	C1571	A1489	G1333	G1333	G1165
A2366	U	C	G2046	A1924	G1833	A1693	C1572	A1490	U1334	U1334	G1166
A2367	U	C	G2046	A1924	G1834	A1694	C1573	A1491	G1335	G1335	G1167
A2368	U	C	G2046	A1924	G1835	A1695	C1574	A1492	G1336	G1336	U1168
A2369	U	C	G2046	A1924	G1836	A1696	C1575	A1493	G1337	G1337	U1169
A2370	U	C	G2046	A1924	G1837	A1697	C1576	A1494	G1338	G1338	U1170
A2371	U	C	G2046	A1924	G1838	A1698	C1577	A1495	A1348	A1348	U1171
A2372	U	C	G2046	A1924	G1839	A1699	C1578	A1496	A1349	A1349	U1172
A2373	U	C	G2046	A1924	G1840	A1700	C1579	A1497	A1350	A1350	U1173
A2374	U	C	G2046	A1924	G1841	A1701	C1580	A1498	A1351	A1351	U1174
A2375	U	C	G2046	A1924	G1842	A1702	C1581	A1499	A1352	A1352	U1175
A2376	U	C	G2046	A1924	G1843	A1703	C1582	A1500	A1353	A1353	U1176
A2377	U	C	G2046	A1924	G1844	A1704	C1583	A1501	A1354	A1354	U1177
A2378	U	C	G2046	A1924	G1845	A1705	C1584	A1502	A1355	A1355	U1178
A2379	U	C	G2046	A1924	G1846	A1706	C1585	A1503	A1356	A1356	U1179
A2380	U	C	G2046	A1924	G1847	A1707	C1586	A1504	A1357	A1357	U1180
A2381	U	C	G2046	A1924	G1848	A1708	C1587	A1505	A1358	A1358	U1181
A2382	U	C	G2046	A1924	G1849	A1709	C1588	A1506	A1359	A1359	U1182
A2383	U	C	G2046	A1924	G1850	A1710	C1589	A1507	A1360	A1360	U1183
A2384	U	C	G2046	A1924	G1851	A1711	C1590	A1508	A1361	A1361	U1184
A2385	U	C	G2046	A1924	G1852	A1712	C1591	A1509	A1362	A1362	U1185
A2386	U	C	G2046	A1924	G1853	A1713	C1592	A1510	A1363	A1363	U1186
A2387	U	C	G2046	A1924	G1854	A1714	C1593	A1511	A1364	A1364	U1187
A2388	U	C	G2046	A1924	G1855	A1715	C1594	A1512	A1365	A1365	U1188
A2389	U	C	G2046	A1924	G1856	A1716	C1595	A1513	A1366	A1366	U1189
A2390	U	C	G2046	A1924	G1857	A1717	C1596	A1514	A1367	A1367	U1190
A2391	U	C	G2046	A1924	G1858	A1718	C1597	A1515	A1368	A1368	U1191
A2392	U	C	G2046	A1924	G1859	A1719	C1598	A1516	A1369	A1369	U1192
A2393	U	C	G2046	A1924	G1860	A1720	C1599	A1517	A1370	A1370	U1193
A2394	U	C	G2046	A1924	G1861	A1721	C1600	A1518	A1371	A1371	U1194
A2395	U	C	G2046	A1924	G1862	A1722	C1601	A1519	A1372	A1372	U1195
A2396	U	C	G2046	A1924	G1863	A1723	C1602	A1520	A1373	A1373	U1196
A2397	U	C	G2046	A1924	G1864	A1724	C1603	A1521	A1374	A1374	U1197
A2398	U	C	G2046	A1924	G1865	A1725	C1604	A1522	A1375	A1375	U1198
A2399	U	C	G2046	A1924	G1866	A1726	C1605	A1523	A1376	A1376	U1199
A2400	U	C	G2046	A1924	G1867	A1727	C1606	A1524	A1377	A1377	U1200
A2401	U	C	G2046	A1924	G1868	A1728	C1607	A1525	A1378	A1378	U1201
A2402	U	C	G2046	A1924	G1869	A1729	C1608	A1526	A1379	A1379	U1202
A2403	U	C	G2046	A1924	G1870	A1730	C1609	A1527	A1380	A1380	U1203
A2404	U	C	G2046	A1924	G1871	A1731	C1610	A1528	A1381	A1381	U1204
A2405	U	C	G2046	A1924	G1872	A1732	C1611	A1529	A1382	A1382	U1205
A2406	U	C	G2046	A1924	G1873	A1733	C1612	A1530	A1383	A1383	U1206
A2407	U	C	G2046	A1924	G1874	A1734	C1613	A1531	A1384	A1384	U1207
A2408	U	C	G2046	A1924	G1875	A1735	C1614	A1532	A1385	A1385	U1208
A2409	U	C	G2046	A1924	G1876	A1736	C1615	A1533	A1386	A1386	U1209
A2410	U	C	G2046	A1924	G1877	A1737	C1616	A1534	A1387	A1387	U1210
A2411	U	C	G2046	A1924	G1878	A1738	C1617	A1535	A1388	A1388	U1211
A2412	U	C	G2046	A1924	G1879	A1739	C1618	A1536	A1389	A1389	U1212
A2413	U	C	G2046	A1924	G1880	A1740	C1619	A1537	A1390	A1390	U1213
A2414	U	C	G2046	A1924	G1881	A1741	C1620	A1538	A1391	A1391	U1214
A2415	U	C	G2046	A1924	G1882	A1742	C1621	A1539	A1392	A1392	U1215
A2416	U	C	G2046	A1924							



• Molecule 2: 5S RNA

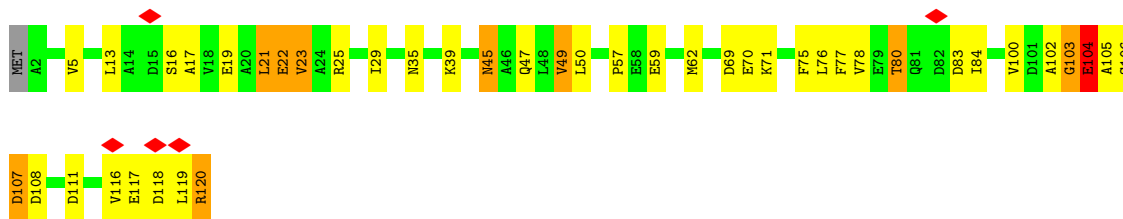


• Molecule 3: CBS domain-containing protein



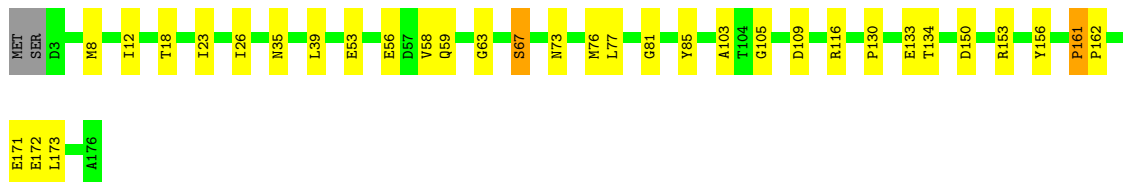
• Molecule 4: Large ribosomal subunit protein eL8





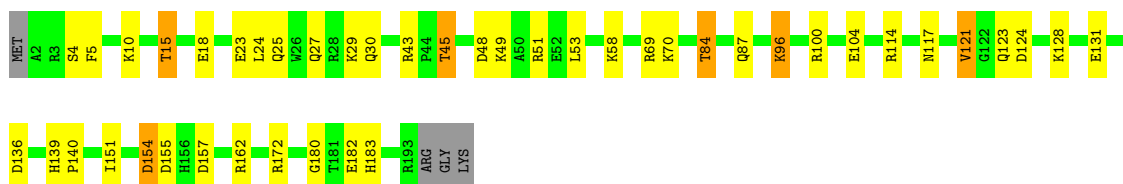
- Molecule 5: Large ribosomal subunit protein uL16

Chain F: 80% 18%



- Molecule 6: Large ribosomal subunit protein eL15

Chain G: 76% 19%



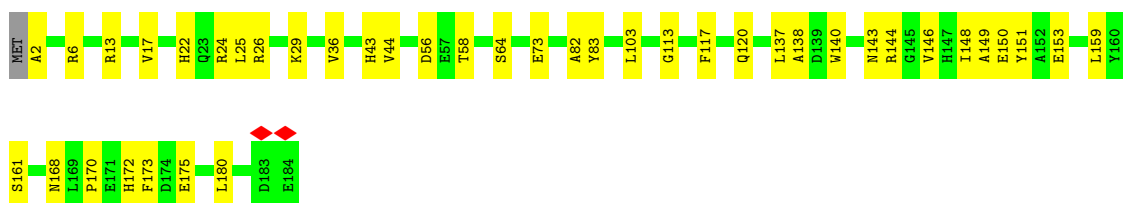
- Molecule 7: Large ribosomal subunit protein eL18

Chain H: 78% 21%



- Molecule 8: Large ribosomal subunit protein uL18

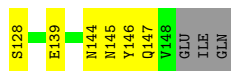
Chain I: 77% 22%



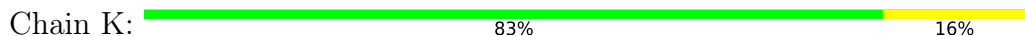
- Molecule 9: Large ribosomal subunit protein eL19

Chain J: 71% 26%

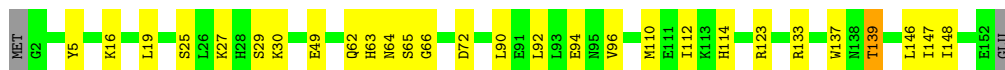
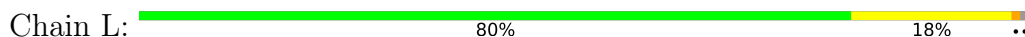




• Molecule 10: Large ribosomal subunit protein eL21



• Molecule 11: Large ribosomal subunit protein uL22



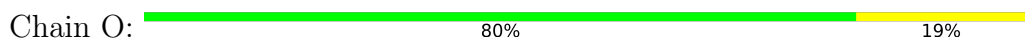
• Molecule 12: Large ribosomal subunit protein eL24



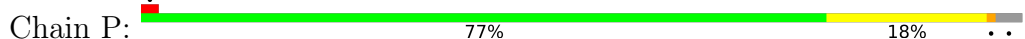
• Molecule 13: Large ribosomal subunit protein uL24




• Molecule 14: Large ribosomal subunit protein uL30

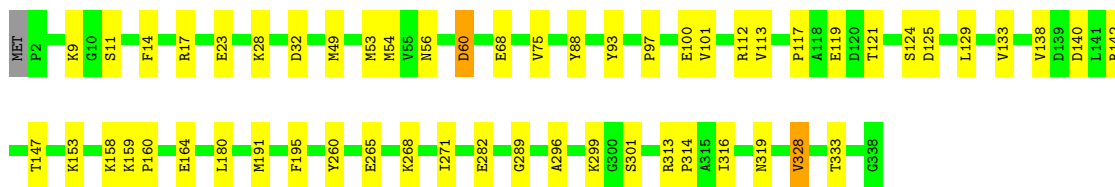


• Molecule 15: Large ribosomal subunit protein eL31




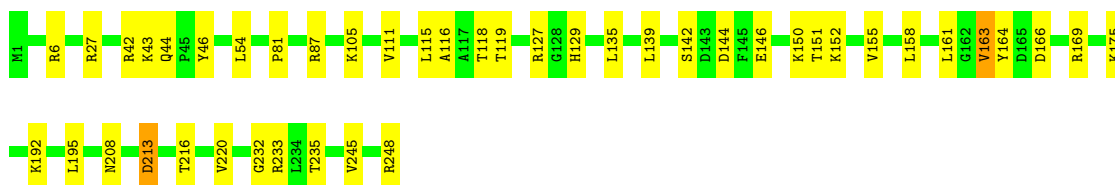


Chain V:  83% 16%




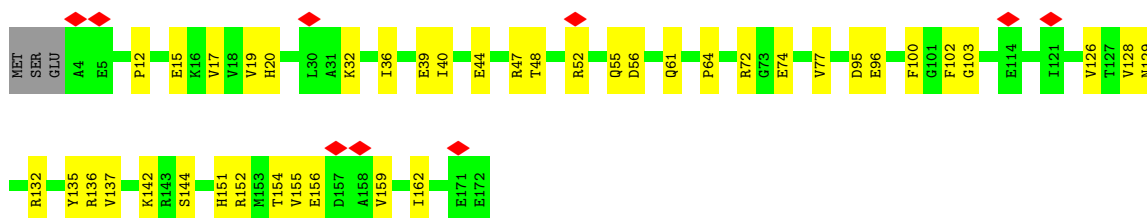
• Molecule 22: Large ribosomal subunit protein uL4

Chain W:  82% 17%



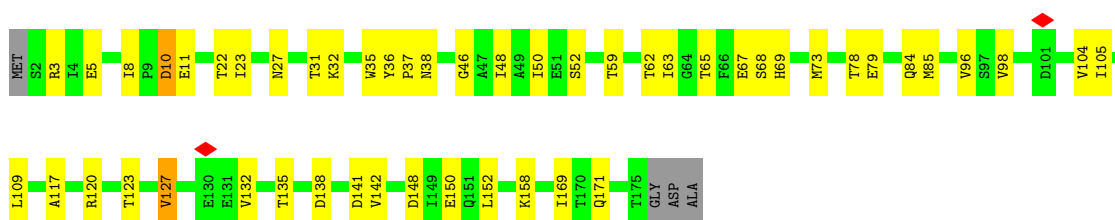
• Molecule 23: Large ribosomal subunit protein uL5

Chain X:  5% 74% 24%




• Molecule 24: Large ribosomal subunit protein uL6

Chain Y:  70% 27%




• Molecule 25: Large ribosomal subunit protein uL13

Chain b:  78% 21%



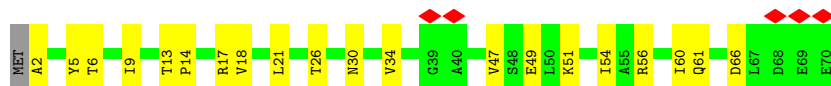
• Molecule 26: Large ribosomal subunit protein uL14

Chain f:  77% 22%




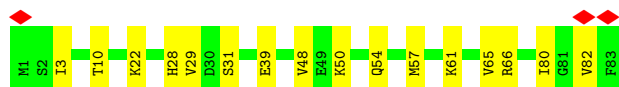
- Molecule 27: Large ribosomal subunit protein uL29

Chain d:  7% 70% 29%



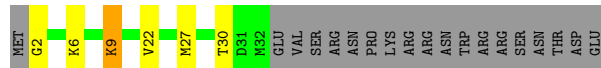
- Molecule 28: Large ribosomal subunit protein uL23

Chain c:  81% 19%




- Molecule 29: Large ribosomal subunit protein eL39

Chain A:  50% 10% 38%



- Molecule 30: Large ribosomal subunit protein eL20

Chain e:  7% 86% 14%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	918876	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.341	Depositor
Minimum map value	-0.170	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.012	Depositor
Recommended contour level	0.034	Depositor
Map size (Å)	427.52, 427.52, 427.52	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.668, 0.668, 0.668	Depositor

## 5 Model quality i

### 5.1 Standard geometry i

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

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	0	0.25	0/67233	0.32	1/104859 (0.0%)
2	9	0.23	0/2848	0.32	0/4436
3	a	0.61	0/2116	0.78	1/2886 (0.0%)
4	E	0.72	1/868 (0.1%)	0.85	4/1184 (0.3%)
5	F	0.22	0/1371	0.41	1/1849 (0.1%)
6	G	0.26	0/1591	0.35	0/2126
7	H	0.23	0/888	0.45	0/1201
8	I	0.19	0/1447	0.32	0/1969
9	J	0.22	0/1191	0.36	0/1587
10	K	0.25	0/750	0.36	0/1001
11	L	0.22	0/1195	0.41	0/1614
12	M	0.23	0/474	0.41	0/634
13	N	0.24	0/911	0.43	0/1232
14	O	0.23	0/1218	0.37	0/1651
15	P	0.24	0/723	0.40	0/976
16	Q	0.23	0/1165	0.34	0/1561
17	R	0.22	0/624	0.37	0/835
18	S	0.25	0/446	0.33	0/586
19	T	0.21	0/764	0.33	0/1015
20	U	0.28	0/1771	0.44	0/2386
21	V	0.23	0/2673	0.35	0/3612
22	W	0.21	0/1911	0.34	0/2581
23	X	0.26	0/1300	0.52	0/1757
24	Y	0.22	0/1351	0.44	0/1839
25	b	0.23	0/1144	0.39	0/1541
26	f	0.41	0/981	0.57	2/1320 (0.2%)
27	d	0.16	0/494	0.30	0/670
28	c	0.18	0/645	0.35	0/867
29	A	0.26	0/254	0.42	0/333
30	e	0.19	0/446	0.32	0/601
All	All	0.26	1/100793 (0.0%)	0.36	9/150709 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
3	a	0	6
4	E	0	2
26	f	0	2
All	All	0	10

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	104	GLU	C-O	9.61	1.36	1.24

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
26	f	62	PRO	CA-N-CD	-7.37	101.68	112.00
4	E	103	GLY	O-C-N	-7.00	113.60	122.70
26	f	62	PRO	N-CD-CG	-6.68	93.18	103.20
3	a	153	THR	N-CA-C	-5.96	105.25	113.18
5	F	161	PRO	CA-N-CD	-5.92	103.71	112.00
4	E	107	ASP	CA-C-N	-5.55	113.07	120.79
4	E	107	ASP	C-N-CA	-5.55	113.07	120.79
4	E	104	GLU	CA-C-O	5.49	126.27	119.79
1	0	294	A	N9-C1'-C2'	5.12	119.68	112.00

There are no chirality outliers.

All (10) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	E	103	GLY	Mainchain
4	E	120	ARG	Sidechain
3	a	151	ARG	Sidechain
3	a	204	ARG	Sidechain
3	a	206	ARG	Sidechain
3	a	234	ARG	Sidechain
3	a	49	ARG	Sidechain
3	a	79	ARG	Sidechain
26	f	105	ARG	Sidechain
26	f	77	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	0	60043	0	30284	678	0
2	9	2551	0	1298	43	0
3	a	2081	0	2046	73	0
4	E	859	0	806	36	0
5	F	1348	0	1319	20	0
6	G	1564	0	1590	35	0
7	H	880	0	901	13	0
8	I	1417	0	1365	29	0
9	J	1179	0	1183	23	0
10	K	736	0	745	13	0
11	L	1170	0	1142	18	0
12	M	466	0	443	10	0
13	N	903	0	886	22	0
14	O	1200	0	1159	19	0
15	P	708	0	680	11	0
16	Q	1146	0	1146	22	0
17	R	617	0	618	15	0
18	S	439	0	445	9	0
19	T	746	0	736	18	0
20	U	1737	0	1752	34	0
21	V	2615	0	2568	39	0
22	W	1884	0	1878	36	0
23	X	1279	0	1198	30	0
24	Y	1329	0	1264	30	0
25	b	1127	0	1118	22	0
26	f	973	0	1012	19	0
27	d	491	0	468	20	0
28	c	640	0	635	14	0
29	A	252	0	287	5	0
30	e	440	0	431	5	0
31	0	212	0	0	0	0
31	9	5	0	0	0	0
31	F	1	0	0	0	0
31	G	4	0	0	0	0
31	J	1	0	0	0	0
31	L	1	0	0	0	0
31	O	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	P	1	0	0	0	0
31	U	1	0	0	0	0
31	V	5	0	0	0	0
32	a	54	0	24	7	0
33	S	1	0	0	0	0
33	T	1	0	0	0	0
All	All	93108	0	61427	1215	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 8.

All (1215) 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)
27:d:2:ALA:HB1	27:d:5:TYR:CZ	1.69	1.27
27:d:2:ALA:CB	27:d:5:TYR:CZ	2.17	1.25
13:N:82:LYS:HD2	13:N:86:GLU:HB3	1.42	0.99
1:0:300:A:N6	1:0:360:G:H21	1.58	0.99
27:d:2:ALA:CB	27:d:5:TYR:OH	2.10	0.98
27:d:2:ALA:HB1	27:d:5:TYR:CE2	2.02	0.95
1:0:300:A:H62	1:0:360:G:H21	1.12	0.94
1:0:300:A:H62	1:0:360:G:N2	1.68	0.92
23:X:12:PRO:HB3	23:X:154:THR:HG21	1.52	0.89
3:a:136:PRO:HB2	3:a:226:ARG:HE	1.38	0.87
3:a:2:ASN:HA	3:a:77:ASP:HA	1.56	0.87
19:T:14:CYS:HB3	19:T:75:CYS:SG	2.15	0.86
1:0:1876:U:O2'	1:0:2006:G:N2	2.09	0.85
6:G:70:LYS:NZ	6:G:123:GLN:OE1	2.11	0.84
7:H:7:ARG:HH21	22:W:27:ARG:HH11	1.21	0.83
1:0:163:U:H5''	6:G:172:ARG:HD3	1.61	0.82
21:V:88:TYR:HB2	21:V:140:ASP:HB2	1.59	0.82
27:d:2:ALA:HB3	27:d:5:TYR:OH	1.82	0.80
25:b:30:VAL:HG11	25:b:101:VAL:HG22	1.63	0.80
3:a:270:THR:HG21	32:a:502:ADP:O2A	1.82	0.79
1:0:1902:A:H2'	1:0:1903:A:H8	1.46	0.78
1:0:2134:G:O2'	1:0:2229:C:N4	2.15	0.78
1:0:1941:G:H2'	1:0:1942:G:H8	1.49	0.77
1:0:1161:U:H1'	1:0:1162:G:H3'	1.66	0.77
2:9:8:G:H5''	10:K:28:GLN:HG3	1.67	0.77
4:E:17:ALA:HB1	4:E:50:LEU:HD21	1.67	0.77
1:0:1166:U:O2	1:0:1174:A:N6	2.18	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1171:A:H5'	1:0:1172:G:H5''	1.66	0.76
1:0:155:G:H5''	18:S:45:LYS:HG3	1.67	0.76
2:9:3:C:H3'	2:9:4:G:H5'	1.67	0.76
3:a:270:THR:CB	32:a:502:ADP:O2A	2.34	0.75
13:N:39:ARG:O	13:N:40:ASN:ND2	2.19	0.75
4:E:5:VAL:HG22	4:E:77:PHE:HE2	1.52	0.74
1:0:1941:G:H2'	1:0:1942:G:C8	2.22	0.74
24:Y:32:LYS:HB3	24:Y:73:MET:HE1	1.69	0.74
1:0:85:G:H21	1:0:106:A:H62	1.35	0.74
1:0:1896:U:O2'	1:0:1897:A:N7	2.21	0.74
16:Q:208:ARG:NH2	16:Q:224:ASN:O	2.21	0.74
1:0:542:C:OP1	1:0:622:G:N2	2.19	0.74
1:0:1366:G:OP1	11:L:65:SER:OG	2.04	0.74
1:0:137:C:O2'	1:0:138:A:N7	2.21	0.74
4:E:105:ALA:HA	4:E:108:ASP:HB2	1.69	0.74
20:U:93:THR:OG1	20:U:155:THR:OG1	2.05	0.74
1:0:348:C:OP1	13:N:40:ASN:ND2	2.20	0.74
7:H:45:ASN:OD1	7:H:68:SER:OG	2.05	0.73
11:L:112:ILE:HA	11:L:148:ILE:HG22	1.69	0.73
13:N:48:THR:HB	13:N:101:GLU:HB2	1.68	0.73
1:0:2134:G:N2	1:0:2228:G:O2'	2.22	0.72
1:0:976:C:H42	1:0:995:C:H42	1.37	0.72
2:9:45:C:OP2	23:X:136:ARG:NH1	2.22	0.72
22:W:213:ASP:OD1	22:W:233:ARG:NH2	2.18	0.72
1:0:2899:A:OP1	15:P:43:LYS:NZ	2.20	0.72
1:0:2487:G:N2	5:F:103:ALA:O	2.24	0.71
6:G:114:ARG:NH1	6:G:151:ILE:O	2.23	0.71
1:0:421:G:OP2	1:0:2436:A:O2'	2.09	0.71
23:X:12:PRO:HB3	23:X:154:THR:CG2	2.19	0.71
3:a:270:THR:CG2	32:a:502:ADP:O2A	2.38	0.71
27:d:17:ARG:NH1	27:d:66:ASP:OD2	2.24	0.71
1:0:1156:G:H3'	1:0:1157:G:H8	1.54	0.70
7:H:7:ARG:NH2	22:W:27:ARG:HH11	1.89	0.70
1:0:2083:A:H2'	1:0:2084:G:C8	2.26	0.70
27:d:2:ALA:HB1	27:d:5:TYR:CE1	2.25	0.70
1:0:1517:A:H1'	1:0:1518:A:H5'	1.72	0.70
1:0:375:U:C4	1:0:376:U:O4	2.45	0.69
1:0:973:A:H2'	1:0:974:A:H8	1.55	0.69
19:T:61:LYS:HG3	19:T:62:PRO:HD2	1.73	0.69
25:b:21:ARG:HB2	25:b:119:THR:HG22	1.75	0.69
17:R:34:MET:HE1	17:R:46:ARG:HD3	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1969:G:N1	1:0:1997:U:OP2	2.20	0.69
3:a:78:VAL:C	3:a:80:LYS:H	2.00	0.69
24:Y:22:THR:HG22	24:Y:31:THR:HG23	1.75	0.69
1:0:370:C:O2'	1:0:371:G:O4'	2.10	0.69
2:9:40:C:H4'	23:X:44:GLU:HB2	1.74	0.69
3:a:123:VAL:HA	3:a:241:THR:HA	1.74	0.69
1:0:2236:C:O2	1:0:2251:A:N6	2.26	0.68
1:0:2804:A:O2'	1:0:2810:A:N7	2.22	0.68
1:0:583:G:H2'	1:0:584:A:C8	2.29	0.68
1:0:1752:U:N3	1:0:1813:G:OP2	2.26	0.68
7:H:7:ARG:HH21	22:W:27:ARG:NH1	1.88	0.68
1:0:1902:A:H2'	1:0:1903:A:C8	2.28	0.68
27:d:2:ALA:HB2	27:d:5:TYR:CZ	2.24	0.68
1:0:582:C:OP1	30:e:27:ASN:ND2	2.26	0.68
1:0:2713:C:O2	26:f:87:ARG:NH2	2.27	0.68
1:0:1084:C:O2'	1:0:1125:A:N1	2.26	0.67
1:0:1221:G:OP1	30:e:13:ARG:NH2	2.26	0.67
3:a:270:THR:HB	32:a:502:ADP:O2A	1.92	0.67
1:0:2237:A:N1	1:0:2252:C:N4	2.43	0.67
23:X:17:VAL:HG22	23:X:128:VAL:HG12	1.76	0.67
1:0:1048:U:H2'	1:0:1049:G:H8	1.59	0.67
3:a:136:PRO:O	3:a:226:ARG:HG3	1.94	0.67
1:0:298:G:N2	1:0:362:A:O4'	2.27	0.66
1:0:293:G:H1	1:0:294:A:H62	1.43	0.66
1:0:384:A:H2'	6:G:10:LYS:HE2	1.77	0.66
23:X:102:PHE:HB2	23:X:126:VAL:HB	1.77	0.66
1:0:1156:G:H21	1:0:1186:A:H8	1.43	0.66
2:9:38:U:O2'	2:9:43:A:N6	2.27	0.66
6:G:157:ASP:O	6:G:162:ARG:NH1	2.28	0.66
11:L:114:HIS:HB3	11:L:147:ILE:HG12	1.76	0.66
1:0:332:A:N3	22:W:208:ASN:ND2	2.42	0.66
3:a:255:SER:HB3	3:a:271:LYS:CG	2.24	0.66
11:L:16:LYS:HB3	11:L:147:ILE:HG22	1.77	0.66
9:J:13:ASP:OD2	9:J:38:ARG:NH1	2.24	0.66
1:0:279:G:H2'	1:0:280:A:H8	1.61	0.65
3:a:153:THR:O	3:a:168:SER:HA	1.95	0.65
1:0:1951:U:H2'	1:0:1952:G:C8	2.32	0.65
15:P:79:ASP:HA	15:P:84:SER:HA	1.76	0.65
1:0:85:G:N2	1:0:106:A:H62	1.94	0.65
2:9:12:G:OP2	10:K:20:ARG:NH2	2.29	0.65
4:E:102:ALA:HB1	4:E:105:ALA:HB3	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:d:6:THR:HG22	27:d:56:ARG:HD3	1.77	0.65
28:c:31:SER:O	28:c:61:LYS:NZ	2.30	0.65
22:W:213:ASP:OD1	22:W:213:ASP:N	2.29	0.65
24:Y:78:THR:HG22	24:Y:79:GLU:HG3	1.79	0.65
3:a:255:SER:HB3	3:a:271:LYS:HG3	1.77	0.65
26:f:75:ARG:NH2	26:f:110:LYS:O	2.29	0.65
1:0:639:A:OP1	1:0:1355:U:O2'	2.14	0.65
1:0:1163:A:H2'	1:0:1164:G:H8	1.61	0.65
26:f:2:GLU:OE1	26:f:2:GLU:N	2.29	0.65
1:0:1489:A:O2'	1:0:1500:U:O2	2.13	0.64
7:H:19:SER:HB2	7:H:27:TRP:HB2	1.77	0.64
1:0:1591:U:OP2	9:J:124:TYR:OH	2.16	0.64
1:0:1739:G:O2'	1:0:2025:U:O4	2.13	0.64
27:d:2:ALA:HB2	27:d:5:TYR:OH	1.96	0.64
1:0:2421:G:N7	19:T:61:LYS:NZ	2.45	0.64
1:0:1073:G:OP2	16:Q:148:ARG:NH2	2.30	0.64
1:0:1843:U:O3'	20:U:235:ARG:NH1	2.30	0.64
20:U:2:GLY:HA2	20:U:197:VAL:HG23	1.80	0.64
4:E:102:ALA:HB1	4:E:105:ALA:C	2.23	0.64
1:0:300:A:H3'	1:0:301:A:H5''	1.80	0.64
1:0:1940:G:H2'	1:0:1941:G:C8	2.32	0.63
1:0:2620:G:N7	20:U:206:ARG:NH2	2.38	0.63
3:a:236:ILE:HD12	3:a:237:SER:H	1.63	0.63
1:0:1945:U:H5'	1:0:1946:A:C5	2.33	0.63
25:b:54:MET:HE3	25:b:54:MET:HA	1.81	0.63
1:0:300:A:O2'	1:0:301:A:OP1	2.17	0.63
3:a:92:VAL:HG23	3:a:106:THR:HG22	1.79	0.63
1:0:1517:A:HO2'	1:0:1518:A:H8	1.46	0.62
1:0:510:G:N1	1:0:513:A:OP2	2.33	0.62
3:a:270:THR:HG21	32:a:502:ADP:PA	2.40	0.62
4:E:23:VAL:HG23	4:E:105:ALA:HB2	1.80	0.62
1:0:1229:A:N3	1:0:2544:C:O2'	2.31	0.62
17:R:34:MET:HE1	17:R:46:ARG:HH11	1.63	0.62
24:Y:59:THR:O	24:Y:63:ILE:HG12	1.98	0.62
28:c:50:LYS:HB3	28:c:66:ARG:HB3	1.82	0.62
1:0:1184:U:H4'	1:0:1186:A:H2	1.63	0.62
22:W:129:HIS:ND1	22:W:166:ASP:OD2	2.27	0.62
28:c:29:VAL:HG12	29:A:6:LYS:HD2	1.82	0.62
14:O:126:ARG:H	14:O:137:GLN:HG3	1.63	0.62
12:M:24:LYS:HB2	12:M:28:THR:HB	1.81	0.62
1:0:1510:U:H2'	1:0:1511:U:C6	2.35	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:9:98:U:OP1	14:O:133:LYS:NZ	2.28	0.62
27:d:2:ALA:CB	27:d:5:TYR:CE1	2.81	0.61
9:J:115:LEU:HD22	9:J:119:GLN:HB2	1.81	0.61
1:0:1700:A:OP1	9:J:66:ARG:NH1	2.34	0.61
3:a:57:GLN:O	3:a:59:ALA:N	2.26	0.61
17:R:47:VAL:HG12	17:R:48:GLU:HG3	1.82	0.61
1:0:2081:C:OP1	11:L:66:GLY:N	2.30	0.61
5:F:23:ILE:HG13	5:F:26:ILE:HD11	1.82	0.61
1:0:144:C:OP1	1:0:264:G:O2'	2.15	0.61
1:0:360:G:H4'	1:0:361:G:OP1	1.99	0.61
14:O:17:VAL:HG13	14:O:48:VAL:HG12	1.83	0.61
21:V:133:VAL:HG22	21:V:138:VAL:HG21	1.82	0.61
18:S:14:LYS:HG2	18:S:15:THR:H	1.66	0.60
1:0:863:U:O2'	1:0:1483:A:N6	2.34	0.60
1:0:1167:U:N3	1:0:1170:A:OP2	2.34	0.60
1:0:1947:A:H2'	1:0:1948:C:C6	2.36	0.60
2:9:39:C:H5'	2:9:40:C:H5'	1.84	0.60
13:N:50:GLU:HB2	13:N:60:GLU:HG2	1.84	0.60
1:0:1519:U:H2'	1:0:1520:A:C8	2.37	0.60
1:0:1567:A:H2'	1:0:1568:A:C8	2.36	0.60
1:0:1887:C:H4'	1:0:1888:A:H5'	1.84	0.60
1:0:2354:A:H2'	1:0:2355:A:C8	2.37	0.59
3:a:140:VAL:HG11	3:a:175:LEU:HD11	1.82	0.59
2:9:28:C:H1'	2:9:55:A:H61	1.67	0.59
8:I:144:ARG:HG3	8:I:173:PHE:HD2	1.66	0.59
1:0:1185:A:O2'	1:0:1186:A:N3	2.32	0.59
1:0:1239:A:OP2	25:b:60:ARG:NH2	2.26	0.59
1:0:1911:U:O2'	1:0:1914:A:N6	2.30	0.59
1:0:1945:U:H5'	1:0:1946:A:N7	2.18	0.59
20:U:212:PRO:O	20:U:213:LYS:HB2	2.01	0.59
1:0:1946:A:H2	1:0:1953:A:H61	1.50	0.59
1:0:2335:G:H5''	1:0:2336:G:H21	1.68	0.59
6:G:136:ASP:OD2	6:G:139:HIS:N	2.34	0.59
26:f:31:ILE:HD12	26:f:53:VAL:HG11	1.85	0.59
16:Q:99:LYS:HB3	16:Q:221:ARG:HG3	1.85	0.59
24:Y:3:ARG:NH2	24:Y:5:GLU:OE2	2.36	0.59
27:d:30:ASN:O	27:d:34:VAL:HG23	2.03	0.59
1:0:440:A:H2'	1:0:441:A:C8	2.38	0.59
1:0:555:A:N3	1:0:1331:G:O2'	2.31	0.59
4:E:5:VAL:HG22	4:E:77:PHE:CE2	2.36	0.59
20:U:176:TYR:CE1	20:U:180:LYS:HE3	2.38	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:417:G:H2'	1:0:418:C:C6	2.38	0.59
14:O:63:GLU:OE2	14:O:67:ARG:NH1	2.34	0.59
25:b:104:TYR:CD2	25:b:108:PRO:HG3	2.37	0.59
1:0:356:U:H2'	1:0:357:G:C8	2.38	0.58
1:0:1299:U:H2'	1:0:1300:A:H8	1.68	0.58
1:0:1522:A:H1'	1:0:1523:A:C8	2.38	0.58
20:U:109:GLU:OE1	20:U:113:GLY:N	2.30	0.58
1:0:647:A:N1	1:0:904:G:O2'	2.32	0.58
1:0:2337:A:H4'	1:0:2338:A:OP2	2.03	0.58
8:I:6:ARG:O	10:K:22:ARG:NH2	2.36	0.58
1:0:1944:G:H1'	1:0:1956:C:N4	2.17	0.58
1:0:2355:A:H2'	1:0:2356:G:C8	2.38	0.58
3:a:167:LEU:HD21	3:a:228:VAL:HG13	1.85	0.58
10:K:6:GLY:O	10:K:9:LYS:HG2	2.03	0.58
14:O:130:HIS:HB3	14:O:134:GLU:HG3	1.83	0.58
27:d:2:ALA:CB	27:d:5:TYR:CE2	2.73	0.58
1:0:1279:C:H2'	1:0:1280:A:H8	1.67	0.58
1:0:2595:G:H2'	1:0:2596:G:H8	1.69	0.58
1:0:2841:U:OP2	21:V:112:ARG:NH2	2.36	0.58
1:0:576:U:H2'	1:0:577:A:C8	2.38	0.58
1:0:1194:G:N2	1:0:1200:G:O6	2.37	0.58
1:0:2259:A:H2'	1:0:2260:G:H8	1.69	0.58
1:0:1098:A:H2'	1:0:1099:A:C8	2.39	0.58
20:U:176:TYR:CZ	20:U:180:LYS:HE3	2.38	0.58
1:0:2339:C:O2'	23:X:20:HIS:NE2	2.32	0.58
24:Y:36:TYR:CD2	24:Y:62:THR:HG21	2.39	0.58
6:G:114:ARG:NH2	6:G:157:ASP:OD1	2.36	0.57
24:Y:120:ARG:NH1	24:Y:148:ASP:OD2	2.37	0.57
25:b:102:ARG:HB3	25:b:104:TYR:HE1	1.68	0.57
1:0:1875:C:O2'	1:0:2005:U:OP2	2.22	0.57
1:0:2105:A:H2'	1:0:2106:G:H8	1.69	0.57
1:0:2705:G:OP1	26:f:43:ARG:NH1	2.37	0.57
15:P:23:SER:HA	15:P:26:ARG:HG3	1.85	0.57
1:0:2065:G:N3	1:0:2483:A:O2'	2.34	0.57
3:a:28:ASP:OD1	3:a:28:ASP:N	2.37	0.57
24:Y:69:HIS:O	24:Y:73:MET:HG2	2.03	0.57
1:0:642:C:H2'	1:0:643:A:H8	1.69	0.57
1:0:1942:G:H2'	1:0:1943:G:C8	2.40	0.57
1:0:2489:C:H2'	1:0:2490:A:C8	2.40	0.57
2:9:49:G:H2'	2:9:50:A:C8	2.40	0.57
1:0:1509:C:H2'	1:0:1510:U:C6	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:2496:A:H5''	1:O:2504:A:C6	2.40	0.57
4:E:47:GLN:NE2	4:E:100:VAL:O	2.36	0.57
20:U:101:GLU:OE2	20:U:131:HIS:NE2	2.37	0.57
24:Y:123:THR:HG23	24:Y:142:VAL:HG12	1.87	0.57
1:O:576:U:H2'	1:O:577:A:H8	1.68	0.57
13:N:106:ASP:OD1	13:N:106:ASP:N	2.25	0.57
1:O:1466:A:OP2	6:G:69:ARG:NH2	2.35	0.57
1:O:1520:A:H1'	1:O:1521:A:O5'	2.04	0.57
4:E:59:GLU:HA	4:E:62:MET:HE3	1.87	0.57
1:O:560:C:H2'	1:O:561:G:H8	1.70	0.56
24:Y:117:ALA:HB2	24:Y:152:LEU:HD22	1.87	0.56
19:T:74:ASP:OD1	19:T:74:ASP:N	2.28	0.56
1:O:1193:C:H2'	1:O:1194:G:O4'	2.05	0.56
9:J:80:SER:O	9:J:80:SER:OG	2.23	0.56
28:c:48:VAL:HG13	28:c:65:VAL:HG13	1.86	0.56
1:O:1226:G:OP2	1:O:1227:A:O2'	2.21	0.56
1:O:453:A:C5	22:W:43:LYS:HE3	2.39	0.56
1:O:2789:U:O3'	24:Y:120:ARG:NH2	2.39	0.56
1:O:2835:G:OP2	1:O:2835:G:N2	2.29	0.56
11:L:19:LEU:HG	11:L:92:LEU:HD13	1.88	0.56
20:U:71:PRO:HA	20:U:159:VAL:HA	1.86	0.56
1:O:1172:G:H1'	1:O:1189:A:H4'	1.88	0.56
1:O:2685:G:O2'	1:O:2694:G:O6	2.19	0.56
26:f:4:LEU:HA	26:f:119:GLU:OE1	2.05	0.56
1:O:1672:U:OP2	29:A:9:LYS:NZ	2.38	0.56
1:O:2259:A:H2'	1:O:2260:G:C8	2.41	0.56
1:O:1411:G:N7	29:A:2:GLY:N	2.54	0.56
1:O:1582:U:H3	1:O:1603:G:H1	1.53	0.56
1:O:2426:U:H2'	1:O:2427:A:C8	2.40	0.56
4:E:19:GLU:O	4:E:23:VAL:HG22	2.06	0.56
1:O:381:C:H2'	1:O:382:A:C8	2.42	0.55
1:O:1163:A:H2'	1:O:1164:G:C8	2.40	0.55
1:O:488:A:H1'	13:N:90:ARG:HE	1.69	0.55
2:9:14:G:H21	8:I:2:ALA:HA	1.71	0.55
1:O:1590:G:OP2	9:J:120:TYR:OH	2.24	0.55
1:O:1647:C:OP1	20:U:174:LYS:NZ	2.31	0.55
7:H:58:THR:HG23	7:H:76:THR:HG22	1.86	0.55
1:O:1943:G:H2'	1:O:1944:G:C4	2.41	0.55
3:a:38:HIS:HA	3:a:42:PHE:HA	1.88	0.55
21:V:60:ASP:OD1	21:V:60:ASP:N	2.37	0.55
26:f:32:ILE:HD11	26:f:54:THR:HG22	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2839:A:H5'	21:V:159:LYS:HD3	1.87	0.55
1:0:56:C:O2	18:S:46:ARG:NH1	2.39	0.55
1:0:423:A:H1'	1:0:1914:A:H2	1.72	0.55
1:0:486:G:N1	1:0:489:A:OP2	2.35	0.55
20:U:123:GLY:H	20:U:159:VAL:HG23	1.70	0.55
1:0:2237:A:H5''	6:G:30:GLN:OE1	2.07	0.55
3:a:234:ARG:HG2	3:a:252:ILE:HG21	1.88	0.55
9:J:119:GLN:HG2	9:J:146:TYR:HE2	1.72	0.55
23:X:36:ILE:O	23:X:40:ILE:HD12	2.06	0.55
1:0:581:G:N2	1:0:584:A:OP2	2.39	0.55
1:0:2489:C:H2'	1:0:2490:A:H8	1.72	0.55
3:a:58:PRO:HB3	3:a:177:VAL:HG12	1.89	0.55
4:E:102:ALA:HB3	4:E:106:SER:HA	1.88	0.55
24:Y:85:MET:HE3	24:Y:169:ILE:HG12	1.89	0.55
17:R:72:ALA:HB1	20:U:158:VAL:HG21	1.89	0.55
24:Y:36:TYR:CD1	24:Y:37:PRO:HD2	2.42	0.55
1:0:11:G:N2	1:0:11:G:OP1	2.36	0.55
1:0:1895:G:H2'	1:0:1896:U:O4'	2.07	0.55
1:0:2439:C:H2'	1:0:2440:A:H8	1.72	0.55
5:F:58:VAL:HG21	5:F:161:PRO:HG3	1.88	0.55
17:R:71:PRO:HA	17:R:74:LYS:HG3	1.89	0.55
25:b:42:GLU:HB3	25:b:105:VAL:HG13	1.89	0.55
30:e:19:PHE:HE1	30:e:21:LYS:HB2	1.72	0.55
1:0:369:C:H1'	1:0:370:C:H5''	1.89	0.54
1:0:1442:U:H2'	28:c:54:GLN:NE2	2.22	0.54
1:0:2318:U:H2'	1:0:2319:U:C6	2.41	0.54
13:N:9:ARG:O	13:N:12:THR:HG22	2.06	0.54
24:Y:27:ASN:ND2	24:Y:79:GLU:O	2.40	0.54
1:0:1510:U:H2'	1:0:1511:U:H6	1.71	0.54
6:G:96:LYS:HG2	6:G:100:ARG:HB2	1.89	0.54
1:0:277:C:H5''	1:0:278:G:O5'	2.07	0.54
1:0:451:A:O2'	22:W:44:GLN:NE2	2.41	0.54
1:0:642:C:H2'	1:0:643:A:C8	2.41	0.54
1:0:1048:U:H2'	1:0:1049:G:C8	2.42	0.54
1:0:2334:G:H5''	1:0:2335:G:N7	2.21	0.54
2:9:23:U:H3'	2:9:24:U:O2	2.08	0.54
1:0:2099:C:H2'	1:0:2100:U:H6	1.72	0.54
4:E:57:PRO:HG2	6:G:45:THR:HA	1.89	0.54
12:M:5:ARG:NH1	12:M:14:ILE:HG21	2.22	0.54
21:V:313:ARG:HH21	21:V:316:ILE:HD11	1.72	0.54
1:0:1830:G:H1'	3:a:201:SER:OG	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Y:127:VAL:HG13	24:Y:132:VAL:HG22	1.89	0.54
1:0:1567:A:H2'	1:0:1568:A:H8	1.71	0.54
1:0:117:C:HO2'	1:0:128:U:HO2'	1.54	0.54
2:9:103:A:H2'	2:9:104:A:H8	1.72	0.54
23:X:52:ARG:HA	23:X:61:GLN:HG2	1.90	0.54
1:0:2006:G:H2'	1:0:2007:G:H8	1.73	0.54
1:0:2105:A:H2'	1:0:2106:G:C8	2.43	0.54
1:0:2134:G:H2'	1:0:2135:G:O4'	2.08	0.54
2:9:7:G:OP2	8:I:13:ARG:NH2	2.40	0.54
2:9:89:G:N2	2:9:92:A:OP2	2.36	0.54
6:G:25:GLN:HB3	6:G:29:LYS:HZ1	1.72	0.54
1:0:228:G:H2'	1:0:229:A:C8	2.43	0.54
1:0:1154:C:H2'	1:0:1155:G:H8	1.72	0.54
1:0:2760:C:OP1	21:V:319:ASN:ND2	2.39	0.54
2:9:75:C:H3'	2:9:76:A:H5''	1.89	0.54
1:0:1490:C:H2'	1:0:1491:U:C6	2.43	0.53
1:0:1509:C:H2'	1:0:1510:U:H6	1.74	0.53
1:0:1511:U:H2'	1:0:1512:C:C6	2.43	0.53
1:0:1789:G:OP1	9:J:104:ARG:NH2	2.37	0.53
1:0:1950:A:H2'	1:0:1951:U:O4'	2.08	0.53
1:0:2679:C:H2'	1:0:2680:G:H8	1.72	0.53
8:I:29:LYS:HB3	10:K:70:ARG:NH1	2.22	0.53
20:U:224:LYS:HD2	20:U:228:ILE:HG23	1.90	0.53
1:0:822:G:O2'	1:0:858:G:H4'	2.08	0.53
1:0:994:U:H2'	1:0:995:C:C6	2.42	0.53
1:0:1204:A:N6	1:0:1205:C:O2	2.42	0.53
1:0:2891:G:H4'	21:V:289:GLY:HA2	1.89	0.53
21:V:32:ASP:N	21:V:32:ASP:OD1	2.41	0.53
25:b:125:SER:O	25:b:125:SER:OG	2.24	0.53
1:0:488:A:H4'	13:N:91:PRO:HG2	1.90	0.53
1:0:1154:C:H2'	1:0:1155:G:C8	2.44	0.53
1:0:1161:U:C2	1:0:1163:A:H5''	2.43	0.53
1:0:2093:A:H2'	1:0:2531:A:N1	2.23	0.53
4:E:102:ALA:HB1	4:E:105:ALA:CB	2.37	0.53
1:0:252:C:H2'	1:0:253:G:H5'	1.90	0.53
1:0:2630:A:OP2	3:a:180:GLU:HB3	2.08	0.53
11:L:123:ARG:HB2	11:L:139:THR:HG23	1.91	0.53
1:0:1544:C:OP1	9:J:64:ARG:NH1	2.42	0.53
2:9:28:C:O2'	2:9:55:A:N1	2.41	0.53
20:U:82:ILE:HD12	20:U:93:THR:HB	1.89	0.53
22:W:142:SER:OG	22:W:144:ASP:OD1	2.20	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1876:U:HO2'	1:0:2006:G:H21	1.54	0.53
11:L:30:LYS:HE2	11:L:62:GLN:HG3	1.89	0.53
1:0:738:A:N3	1:0:2399:U:O2'	2.33	0.53
1:0:1155:G:H2'	1:0:1156:G:C8	2.44	0.53
1:0:1299:U:H2'	1:0:1300:A:C8	2.44	0.53
6:G:23:GLU:O	6:G:27:GLN:HG2	2.08	0.53
14:O:36:PRO:HD2	14:O:41:TYR:CE2	2.43	0.53
1:0:1948:C:O2'	1:0:1950:A:N7	2.41	0.53
4:E:21:LEU:HD12	4:E:50:LEU:HD13	1.91	0.53
17:R:69:GLU:OE1	17:R:74:LYS:NZ	2.42	0.53
20:U:200:PRO:HG2	20:U:225:VAL:HG21	1.90	0.53
1:0:1117:U:H3	1:0:1243:A:H62	1.55	0.53
21:V:119:GLU:N	21:V:119:GLU:OE1	2.42	0.53
1:0:300:A:N6	1:0:360:G:N2	2.34	0.53
1:0:1818:U:O2'	1:0:1992:C:OP1	2.26	0.53
1:0:1944:G:H2'	1:0:1945:U:C4'	2.39	0.53
6:G:121:VAL:HG21	6:G:131:GLU:OE2	2.08	0.53
9:J:21:ARG:NH1	9:J:53:LYS:O	2.38	0.53
16:Q:111:LEU:HD23	16:Q:168:ALA:HB1	1.91	0.53
1:0:612:A:O2'	1:0:1320:G:OP1	2.20	0.52
1:0:1047:G:H2'	1:0:1048:U:C6	2.43	0.52
3:a:78:VAL:C	3:a:80:LYS:N	2.64	0.52
8:I:73:GLU:OE2	8:I:73:GLU:N	2.42	0.52
19:T:71:ILE:HD13	19:T:78:ALA:HB2	1.90	0.52
1:0:809:A:H2'	1:0:810:A:C8	2.44	0.52
1:0:2425:C:H2'	1:0:2426:U:C6	2.45	0.52
1:0:2441:U:H2'	1:0:2442:G:H8	1.74	0.52
1:0:423:A:H1'	1:0:1914:A:C2	2.44	0.52
1:0:993:U:O2	1:0:994:U:N3	2.42	0.52
3:a:152:ILE:HG23	32:a:502:ADP:N7	2.25	0.52
9:J:144:ASN:OD1	9:J:145:ASN:ND2	2.42	0.52
20:U:5:ILE:HG22	20:U:8:GLN:HG3	1.91	0.52
1:0:118:C:O2'	18:S:21:ARG:O	2.23	0.52
1:0:1940:G:O6	1:0:1963:G:N2	2.43	0.52
2:9:95:C:H2'	2:9:96:U:C6	2.45	0.52
4:E:104:GLU:C	4:E:106:SER:N	2.65	0.52
8:I:25:LEU:O	8:I:29:LYS:HG3	2.09	0.52
1:0:973:A:H2	1:0:1000:C:N4	2.07	0.52
1:0:1261:U:H2'	1:0:1262:G:H8	1.74	0.52
1:0:1944:G:H1'	1:0:1956:C:H42	1.73	0.52
6:G:53:LEU:HD13	6:G:117:ASN:HB3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:398:G:N1	6:G:182:GLU:OE1	2.22	0.52
1:0:2859:U:H4'	1:0:2860:A:H5'	1.91	0.52
23:X:74:GLU:HA	23:X:77:VAL:HG12	1.91	0.52
1:0:70:U:C2	1:0:71:G:C8	2.98	0.52
1:0:667:C:OP2	22:W:105:LYS:NZ	2.43	0.52
1:0:1534:U:H2'	1:0:1535:A:C8	2.44	0.52
1:0:1671:G:OP1	29:A:9:LYS:NZ	2.34	0.52
1:0:2426:U:H2'	1:0:2427:A:H8	1.75	0.52
3:a:3:ILE:O	3:a:4:THR:C	2.51	0.52
27:d:2:ALA:HB3	27:d:5:TYR:CZ	2.28	0.52
1:0:879:G:H5'	1:0:880:G:OP1	2.10	0.52
1:0:1146:U:H4'	1:0:1147:A:H5''	1.91	0.52
3:a:11:TYR:HE2	3:a:103:GLY:HA2	1.75	0.52
21:V:56:ASN:ND2	21:V:68:GLU:OE1	2.40	0.52
1:0:11:G:O2'	1:0:12:G:O5'	2.28	0.52
1:0:1520:A:H4'	1:0:1521:A:OP1	2.09	0.52
1:0:803:U:H3	1:0:814:G:H1	1.58	0.51
1:0:1803:C:OP1	12:M:45:ARG:HD3	2.09	0.51
6:G:15:THR:O	6:G:15:THR:OG1	2.24	0.51
19:T:9:THR:HB	19:T:81:ARG:HH22	1.75	0.51
1:0:301:A:C4	1:0:302:U:H1'	2.46	0.51
1:0:310:A:N3	1:0:331:G:O2'	2.41	0.51
1:0:375:U:O4	1:0:376:U:O4	2.28	0.51
1:0:961:C:O2'	1:0:962:G:O5'	2.29	0.51
1:0:1541:C:H2'	1:0:1542:A:C8	2.45	0.51
11:L:96:VAL:HG21	11:L:146:LEU:HD23	1.92	0.51
1:0:1030:U:OP1	1:0:1031:A:O2'	2.22	0.51
1:0:1950:A:H3'	1:0:1950:A:N3	2.26	0.51
1:0:2258:U:H2'	1:0:2259:A:H8	1.75	0.51
2:9:3:C:C3'	2:9:4:G:H5'	2.39	0.51
4:E:104:GLU:C	4:E:106:SER:H	2.18	0.51
22:W:220:VAL:O	22:W:248:ARG:NH2	2.43	0.51
23:X:132:ARG:HH22	23:X:159:VAL:HG21	1.75	0.51
1:0:2258:U:H2'	1:0:2259:A:C8	2.45	0.51
16:Q:139:ARG:HH21	16:Q:141:ARG:HD2	1.76	0.51
30:e:6:ILE:HG12	30:e:55:VAL:HG13	1.92	0.51
1:0:569:A:OP2	1:0:596:G:N1	2.30	0.51
1:0:1190:U:O2	1:0:1191:A:N6	2.27	0.51
1:0:1612:U:C2	1:0:1637:A:H2	2.29	0.51
2:9:95:C:H2'	2:9:96:U:H6	1.75	0.51
4:E:45:ASN:OD1	4:E:45:ASN:N	2.42	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:85:G:H21	1:0:106:A:N6	2.06	0.51
1:0:279:G:H2'	1:0:280:A:C8	2.45	0.51
10:K:17:ASN:OD1	10:K:46:PRO:HB2	2.11	0.51
23:X:19:VAL:HG12	23:X:126:VAL:HG22	1.93	0.51
1:0:1608:A:H2'	1:0:1609:G:O4'	2.10	0.51
1:0:1701:G:N1	1:0:1704:U:OP2	2.44	0.51
1:0:960:G:H2'	1:0:961:C:C6	2.45	0.51
1:0:999:U:O2	1:0:1000:C:N4	2.44	0.51
1:0:1129:A:H2'	1:0:1130:A:C8	2.46	0.51
1:0:1331:G:OP2	16:Q:201:SER:OG	2.19	0.51
1:0:1961:A:H2'	1:0:1962:A:C8	2.46	0.51
15:P:27:ALA:O	15:P:30:SER:HB2	2.10	0.51
1:0:38:C:H5'	13:N:13:ARG:HH12	1.76	0.50
1:0:42:U:H2'	1:0:43:C:H6	1.77	0.50
1:0:946:G:C4	14:O:23:MET:HE1	2.46	0.50
1:0:977:C:H2'	1:0:978:G:C8	2.46	0.50
1:0:1058:A:H2'	1:0:1059:A:C8	2.45	0.50
1:0:1140:G:H2'	1:0:1141:A:C8	2.46	0.50
3:a:136:PRO:HB2	3:a:226:ARG:NE	2.18	0.50
3:a:255:SER:HB3	3:a:271:LYS:HG2	1.91	0.50
22:W:111:VAL:HG11	22:W:248:ARG:HH12	1.76	0.50
1:0:365:G:H1'	1:0:366:A:N1	2.26	0.50
1:0:2595:G:H2'	1:0:2596:G:C8	2.46	0.50
3:a:132:VAL:HG21	3:a:152:ILE:HD11	1.91	0.50
4:E:69:ASP:OD1	4:E:70:GLU:N	2.44	0.50
1:0:1951:U:H2'	1:0:1952:G:H8	1.77	0.50
3:a:73:THR:O	3:a:74:PRO:C	2.55	0.50
3:a:81:VAL:O	3:a:85:MET:HG2	2.10	0.50
12:M:4:LYS:HB3	12:M:14:ILE:O	2.11	0.50
1:0:11:G:HO2'	1:0:12:G:H8	1.55	0.50
1:0:2289:C:H2'	1:0:2290:U:H6	1.75	0.50
9:J:105:ARG:NE	9:J:139:GLU:OE2	2.41	0.50
1:0:624:A:O2'	16:Q:126:ASP:OD2	2.28	0.50
1:0:768:A:N3	1:0:2471:U:O2'	2.44	0.50
1:0:773:A:H2'	1:0:774:A:C8	2.45	0.50
1:0:1046:G:O6	1:0:1071:G:N2	2.45	0.50
1:0:1955:C:H3'	1:0:1956:C:H2'	1.94	0.50
25:b:19:MET:HE3	25:b:82:ALA:HB2	1.93	0.50
1:0:298:G:N1	1:0:361:G:O2'	2.44	0.50
1:0:1117:U:OP1	1:0:1136:U:O2'	2.24	0.50
1:0:1182:U:H2'	1:0:1183:C:O4'	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2637:C:O2'	1:0:2638:U:O5'	2.29	0.50
4:E:102:ALA:CB	4:E:105:ALA:C	2.84	0.50
17:R:11:SER:OG	17:R:31:GLU:OE2	2.24	0.50
21:V:142:ARG:HD2	21:V:164:GLU:OE1	2.11	0.50
1:0:1522:A:N6	1:0:1658:A:H2'	2.26	0.50
8:I:172:HIS:O	8:I:175:GLU:HB3	2.12	0.50
22:W:169:ARG:NH2	22:W:192:LYS:O	2.44	0.50
22:W:216:THR:O	22:W:220:VAL:HG13	2.11	0.50
24:Y:38:ASN:O	24:Y:52:SER:OG	2.28	0.50
1:0:973:A:H2'	1:0:974:A:C8	2.41	0.50
13:N:84:ASP:OD1	13:N:85:GLY:N	2.45	0.50
22:W:144:ASP:OD1	22:W:144:ASP:N	2.44	0.50
1:0:117:C:O2'	1:0:128:U:O2'	2.27	0.49
1:0:283:A:N1	1:0:376:U:C4	2.80	0.49
1:0:1129:A:N3	1:0:2514:G:O2'	2.39	0.49
1:0:1140:G:H2'	1:0:1141:A:H8	1.76	0.49
1:0:1831:U:O2'	1:0:2637:C:H5''	2.12	0.49
1:0:2366:A:H2'	1:0:2367:A:H8	1.77	0.49
5:F:35:ASN:HB3	5:F:39:LEU:HD21	1.94	0.49
6:G:48:ASP:OD1	6:G:49:LYS:N	2.45	0.49
1:0:384:A:OP2	6:G:10:LYS:HE3	2.12	0.49
1:0:577:A:H2'	1:0:578:G:H8	1.77	0.49
1:0:1194:G:H21	1:0:1199:A:H62	1.60	0.49
14:O:107:LEU:HD22	14:O:112:VAL:HG21	1.94	0.49
1:0:296:C:N4	1:0:367:U:H5	2.10	0.49
1:0:453:A:C4	22:W:43:LYS:HE3	2.46	0.49
1:0:704:A:H5''	1:0:705:C:H5'	1.93	0.49
1:0:723:A:C2	7:H:116:ARG:HB3	2.47	0.49
1:0:1534:U:H2'	1:0:1535:A:H8	1.78	0.49
1:0:1749:A:H2'	1:0:1750:G:O4'	2.11	0.49
1:0:2000:A:N3	1:0:2620:G:O2'	2.39	0.49
9:J:113:GLY:O	9:J:115:LEU:N	2.40	0.49
14:O:149:LEU:O	14:O:153:MET:HG2	2.12	0.49
17:R:34:MET:CE	17:R:46:ARG:HD3	2.40	0.49
26:f:5:LYS:HG3	26:f:119:GLU:OE2	2.12	0.49
1:0:542:C:N3	1:0:2053:A:O2'	2.44	0.49
1:0:995:C:H2'	1:0:996:G:C8	2.47	0.49
1:0:2483:A:N6	1:0:2484:G:O6	2.45	0.49
5:F:73:ASN:OD1	5:F:85:TYR:OH	2.18	0.49
1:0:290:A:N6	1:0:370:C:O2	2.45	0.49
1:0:1454:A:H2'	1:0:1455:A:C8	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2533:G:C8	3:a:206:ARG:HD2	2.47	0.49
3:a:154:HIS:O	32:a:502:ADP:N6	2.45	0.49
1:0:1178:A:C2	1:0:1189:A:H8	2.30	0.49
1:0:1459:U:H2'	1:0:1460:A:H8	1.76	0.49
1:0:1511:U:H2'	1:0:1512:C:H6	1.78	0.49
3:a:109:ASP:HA	3:a:112:GLN:HB2	1.94	0.49
6:G:154:ASP:OD1	6:G:154:ASP:N	2.28	0.49
12:M:23:VAL:HG11	26:f:132:VAL:HG21	1.94	0.49
28:c:31:SER:HB2	28:c:61:LYS:HD2	1.93	0.49
1:0:127:A:H4'	18:S:21:ARG:HD3	1.94	0.49
1:0:650:G:H2'	1:0:651:C:C6	2.47	0.49
1:0:1093:A:H2'	1:0:1094:G:H8	1.77	0.49
1:0:1270:G:C6	1:0:1271:C:N4	2.81	0.49
1:0:1273:A:H1'	1:0:1275:U:C5	2.48	0.49
1:0:1839:U:H2'	1:0:1840:A:C8	2.47	0.49
1:0:2574:U:H5''	1:0:2575:G:H5'	1.94	0.49
1:0:2811:G:N3	21:V:97:PRO:HG2	2.28	0.49
1:0:369:C:H4'	1:0:370:C:OP1	2.11	0.49
1:0:2269:U:H2'	1:0:2270:U:C6	2.48	0.49
1:0:2539:U:OP2	26:f:41:LYS:NZ	2.36	0.49
1:0:766:C:OP1	22:W:87:ARG:NH2	2.42	0.49
1:0:1592:A:OP2	9:J:103:ARG:NH1	2.46	0.49
1:0:1828:U:H5	1:0:1833:A:N7	2.11	0.49
8:I:161:SER:O	8:I:161:SER:OG	2.28	0.49
13:N:82:LYS:CD	13:N:86:GLU:HB3	2.30	0.49
26:f:31:ILE:HG23	26:f:53:VAL:HG11	1.95	0.49
1:0:38:C:OP2	13:N:9:ARG:NH1	2.46	0.48
1:0:543:G:H2'	1:0:544:A:C8	2.48	0.48
1:0:1027:U:OP1	14:O:108:ARG:NH1	2.46	0.48
1:0:1490:C:H2'	1:0:1491:U:H6	1.78	0.48
1:0:2099:C:H2'	1:0:2100:U:C6	2.48	0.48
2:9:33:A:H61	2:9:48:G:H1'	1.77	0.48
1:0:119:G:OP1	18:S:21:ARG:NH1	2.46	0.48
1:0:418:C:H2'	1:0:419:A:H8	1.77	0.48
1:0:942:G:O2'	1:0:1033:A:N3	2.46	0.48
1:0:1520:A:O2'	1:0:1521:A:H2'	2.13	0.48
1:0:2619:C:H2'	1:0:2620:G:C8	2.46	0.48
20:U:24:TYR:OH	20:U:181:ALA:O	2.30	0.48
1:0:638:G:O2'	1:0:1354:A:OP1	2.30	0.48
20:U:82:ILE:HG23	20:U:93:THR:HB	1.96	0.48
24:Y:48:ILE:HD12	24:Y:48:ILE:H	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2623:G:N2	1:0:2626:A:OP2	2.34	0.48
1:0:2840:G:H5''	21:V:158:LYS:HE3	1.94	0.48
3:a:158:VAL:HG12	3:a:159:ASP:O	2.13	0.48
7:H:42:ALA:HB2	7:H:116:ARG:HD2	1.94	0.48
23:X:36:ILE:HA	23:X:39:GLU:OE2	2.14	0.48
1:0:1198:C:H3'	1:0:1199:A:H8	1.79	0.48
1:0:2129:G:H2'	1:0:2130:A:C8	2.49	0.48
3:a:43:GLU:OE1	3:a:43:GLU:N	2.46	0.48
19:T:70:TYR:O	19:T:78:ALA:HA	2.12	0.48
1:0:294:A:H61	1:0:368:C:H6	1.62	0.48
1:0:615:U:H2'	1:0:616:U:C6	2.48	0.48
4:E:76:LEU:HD13	4:E:116:VAL:HG22	1.95	0.48
5:F:172:GLU:HG2	5:F:173:LEU:HD23	1.95	0.48
20:U:227:ASP:OD1	20:U:227:ASP:N	2.46	0.48
24:Y:84:GLN:HB2	24:Y:171:GLN:HB3	1.94	0.48
1:0:778:A:H5''	1:0:883:C:H41	1.78	0.48
1:0:2132:G:C2	1:0:2230:G:C2	3.02	0.48
18:S:5:GLY:O	18:S:9:GLN:HG2	2.13	0.48
1:0:298:G:N2	1:0:361:G:H1'	2.29	0.48
1:0:568:G:O2'	1:0:597:A:N6	2.47	0.48
1:0:1046:G:H2'	1:0:1047:G:H8	1.79	0.48
1:0:2236:C:O2'	1:0:2251:A:N6	2.47	0.48
1:0:2784:U:H1'	1:0:2785:A:H5''	1.95	0.48
3:a:75:ASP:O	3:a:76:GLU:C	2.56	0.48
21:V:147:THR:O	21:V:160:PRO:HB3	2.14	0.48
1:0:152:A:H2'	1:0:153:U:C6	2.48	0.47
1:0:272:G:C6	1:0:273:U:C4	3.01	0.47
1:0:1178:A:H2	1:0:1189:A:H8	1.62	0.47
1:0:2269:U:H2'	1:0:2270:U:H6	1.79	0.47
8:I:44:VAL:HG21	8:I:82:ALA:HA	1.96	0.47
1:0:1587:G:H2'	1:0:1588:C:C6	2.49	0.47
21:V:93:TYR:CE2	25:b:3:PHE:HD2	2.31	0.47
24:Y:150:GLU:OE1	24:Y:169:ILE:HG13	2.14	0.47
1:0:994:U:O2'	1:0:995:C:O4'	2.30	0.47
1:0:1309:A:H5'	16:Q:202:SER:O	2.15	0.47
1:0:1945:U:O2'	1:0:1955:C:N4	2.47	0.47
1:0:2814:C:H4'	21:V:117:PRO:HG3	1.96	0.47
2:9:41:C:O2	23:X:72:ARG:NE	2.29	0.47
21:V:14:PHE:O	21:V:17:ARG:HG2	2.14	0.47
21:V:268:LYS:NZ	21:V:301:SER:O	2.39	0.47
1:0:425:C:H2'	1:0:426:A:H8	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1186:A:O4'	1:0:1206:C:O2'	2.29	0.47
1:0:1790:A:H2'	1:0:1791:U:C6	2.50	0.47
24:Y:10:ASP:OD1	24:Y:11:GLU:N	2.35	0.47
1:0:163:U:OP1	6:G:172:ARG:NH1	2.42	0.47
1:0:1867:U:O4	20:U:117:LYS:NZ	2.46	0.47
1:0:1942:G:C2	1:0:1943:G:C6	3.02	0.47
1:0:2813:U:H2'	1:0:2814:C:C6	2.49	0.47
16:Q:90:GLU:N	16:Q:229:GLU:OE2	2.47	0.47
16:Q:184:THR:O	16:Q:187:LEU:HB2	2.15	0.47
20:U:129:LEU:HB2	20:U:137:ILE:HG22	1.96	0.47
28:c:80:ILE:HG13	28:c:82:VAL:HG23	1.97	0.47
1:0:363:A:H1'	1:0:364:A:C8	2.49	0.47
1:0:1316:U:H2'	1:0:1317:A:H8	1.80	0.47
1:0:1796:C:H2'	1:0:1797:A:H8	1.79	0.47
1:0:2707:G:H4'	21:V:11:SER:HB2	1.97	0.47
8:I:170:PRO:O	8:I:173:PHE:HB3	2.15	0.47
9:J:81:ARG:HG2	9:J:88:ARG:CZ	2.45	0.47
10:K:8:MET:HE3	10:K:8:MET:HB3	1.73	0.47
20:U:93:THR:HG1	20:U:155:THR:HG1	1.45	0.47
23:X:154:THR:HB	23:X:159:VAL:HG23	1.95	0.47
27:d:2:ALA:N	27:d:49:GLU:OE2	2.48	0.47
1:0:64:C:H2'	1:0:65:C:C6	2.49	0.47
1:0:289:A:N6	1:0:372:G:O2'	2.48	0.47
1:0:1235:C:H5'	1:0:1236:G:OP2	2.14	0.47
1:0:1279:C:H2'	1:0:1280:A:C8	2.47	0.47
1:0:1467:A:H2'	1:0:1468:U:C6	2.50	0.47
3:a:119:ASP:O	3:a:120:ALA:C	2.57	0.47
3:a:153:THR:HG23	3:a:169:LEU:H	1.79	0.47
9:J:10:MET:HE3	9:J:41:ILE:HG13	1.97	0.47
16:Q:185:ASP:N	16:Q:185:ASP:OD1	2.47	0.47
21:V:75:VAL:HG23	21:V:296:ALA:HB3	1.95	0.47
23:X:151:HIS:O	23:X:151:HIS:ND1	2.48	0.47
28:c:57:MET:O	28:c:57:MET:HG3	2.13	0.47
1:0:258:C:O3'	6:G:140:PRO:HB2	2.14	0.47
1:0:1684:A:N6	11:L:133:ARG:O	2.48	0.47
25:b:102:ARG:HB3	25:b:104:TYR:CE1	2.50	0.47
1:0:2522:G:H5'	5:F:109:ASP:OD1	2.15	0.47
4:E:49:VAL:HG22	4:E:75:PHE:HB2	1.97	0.47
1:0:402:U:O2'	6:G:180:GLY:O	2.33	0.47
1:0:418:C:H2'	1:0:419:A:C8	2.49	0.47
1:0:1678:G:HO2'	1:0:1717:G:HO2'	1.56	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:N:28:LEU:HD22	13:N:32:LEU:HB3	1.97	0.47
20:U:232:ARG:NH1	20:U:234:GLY:O	2.39	0.47
26:f:31:ILE:HG23	26:f:53:VAL:CG1	2.45	0.47
1:0:42:U:H2'	1:0:43:C:C6	2.50	0.46
1:0:1975:C:O2	3:a:145:HIS:HB2	2.15	0.46
3:a:169:LEU:HA	3:a:172:VAL:HG22	1.97	0.46
9:J:36:ILE:HG13	9:J:37:THR:HG23	1.96	0.46
23:X:159:VAL:O	23:X:162:ILE:HG13	2.16	0.46
2:9:7:G:O5'	8:I:24:ARG:NH1	2.48	0.46
5:F:171:GLU:H	5:F:171:GLU:CD	2.22	0.46
22:W:155:VAL:HG13	22:W:164:TYR:CE1	2.49	0.46
1:0:836:G:H3'	1:0:837:U:H4'	1.97	0.46
1:0:2627:G:H2'	1:0:2628:A:H8	1.79	0.46
1:0:1517:A:O2'	1:0:1518:A:H8	1.98	0.46
1:0:2385:C:O2'	10:K:78:ASP:OD2	2.34	0.46
1:0:2496:A:H5''	1:0:2504:A:N1	2.30	0.46
3:a:78:VAL:O	3:a:80:LYS:N	2.48	0.46
22:W:6:ARG:HD2	22:W:6:ARG:N	2.31	0.46
23:X:95:ASP:OD1	23:X:96:GLU:N	2.48	0.46
1:0:1159:G:O2'	1:0:1160:G:O5'	2.30	0.46
1:0:2332:U:H5''	23:X:103:GLY:O	2.16	0.46
2:9:48:G:H5'	8:I:148:ILE:HD11	1.97	0.46
2:9:103:A:H2'	2:9:104:A:C8	2.49	0.46
4:E:80:THR:HG22	4:E:83:ASP:OD2	2.15	0.46
13:N:31:ASP:OD1	13:N:31:ASP:N	2.48	0.46
16:Q:139:ARG:NH2	16:Q:141:ARG:HD2	2.31	0.46
25:b:6:PHE:O	25:b:109:TYR:OH	2.22	0.46
1:0:1490:C:OP2	1:0:1500:U:N3	2.41	0.46
1:0:1762:A:H2'	1:0:1763:G:O4'	2.16	0.46
1:0:2131:C:H2'	1:0:2132:G:C8	2.51	0.46
1:0:2320:U:H2'	1:0:2321:C:C6	2.51	0.46
3:a:82:ALA:HB3	3:a:279:THR:HG23	1.97	0.46
11:L:64:ASN:N	11:L:64:ASN:OD1	2.49	0.46
1:0:250:A:C8	1:0:251:C:C5	3.04	0.46
1:0:1158:A:O2'	1:0:1159:G:O5'	2.34	0.46
1:0:2490:A:H2'	1:0:2491:C:C6	2.51	0.46
5:F:63:GLY:O	5:F:67:SER:OG	2.33	0.46
14:O:54:HIS:CE1	14:O:140:LYS:HB2	2.50	0.46
1:0:158:A:H1'	1:0:446:C:H5'	1.98	0.46
1:0:1169:G:N2	1:0:1197:A:O4'	2.49	0.46
1:0:1186:A:H4'	1:0:1205:C:O2'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2098:C:H2'	1:0:2099:C:C6	2.51	0.46
1:0:2757:C:H2'	1:0:2758:A:H8	1.80	0.46
3:a:110:ILE:O	3:a:114:VAL:HG23	2.15	0.46
14:O:4:ILE:O	14:O:32:ALA:HA	2.16	0.46
16:Q:207:LYS:HB2	16:Q:207:LYS:HE3	1.77	0.46
20:U:173:GLY:O	20:U:177:HIS:ND1	2.49	0.46
1:0:376:U:H2'	1:0:377:G:C8	2.51	0.46
1:0:420:G:OP1	1:0:421:G:H5'	2.16	0.46
1:0:1093:A:H2'	1:0:1094:G:C8	2.50	0.46
1:0:1242:C:H5''	1:0:1243:A:H8	1.81	0.46
1:0:2077:C:H2'	1:0:2078:C:C6	2.51	0.46
1:0:2441:U:H2'	1:0:2442:G:C8	2.50	0.46
11:L:90:LEU:HD23	11:L:90:LEU:HA	1.81	0.46
13:N:47:ASP:O	13:N:63:VAL:HG23	2.16	0.46
26:f:68:VAL:O	26:f:69:LEU:HD13	2.16	0.46
1:0:301:A:H3'	1:0:302:U:O4'	2.16	0.46
1:0:408:G:H2'	1:0:409:U:O4'	2.16	0.46
1:0:1521:A:OP2	1:0:1521:A:H3'	2.15	0.46
1:0:2568:C:H2'	1:0:2569:A:O4'	2.16	0.46
2:9:68:U:H4'	10:K:20:ARG:HH12	1.81	0.46
2:9:96:U:H2'	2:9:97:C:C6	2.50	0.46
2:9:96:U:H2'	2:9:97:C:H6	1.80	0.46
23:X:32:LYS:O	23:X:36:ILE:HD12	2.15	0.46
24:Y:8:ILE:HG12	24:Y:46:GLY:C	2.40	0.46
1:0:616:U:H2'	1:0:617:A:H8	1.80	0.45
1:0:1155:G:H2'	1:0:1156:G:H8	1.80	0.45
1:0:1270:G:H2'	1:0:1271:C:C6	2.51	0.45
1:0:1665:A:H2'	1:0:1666:A:C8	2.51	0.45
1:0:1820:C:H2'	1:0:1821:G:H8	1.81	0.45
9:J:40:ASP:OD1	9:J:40:ASP:N	2.49	0.45
1:0:11:G:O2'	1:0:12:G:C8	2.68	0.45
1:0:451:A:H2'	1:0:452:G:C8	2.51	0.45
1:0:1109:G:C5	1:0:1111:G:C8	3.04	0.45
1:0:1931:G:H2'	1:0:1932:U:O4'	2.16	0.45
1:0:336:A:N6	1:0:351:U:O4'	2.49	0.45
1:0:549:G:H1	1:0:615:U:H3	1.64	0.45
1:0:786:C:O2'	1:0:1454:A:N3	2.41	0.45
1:0:2320:U:H2'	1:0:2321:C:H6	1.81	0.45
2:9:113:G:H2'	2:9:114:C:C6	2.51	0.45
17:R:11:SER:HB3	17:R:35:ARG:HH22	1.81	0.45
1:0:274:G:H2'	1:0:275:U:C6	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:663:G:N1	7:H:43:GLU:OE2	2.35	0.45
6:G:70:LYS:HE3	6:G:124:ASP:O	2.17	0.45
8:I:43:HIS:ND1	8:I:64:SER:OG	2.37	0.45
25:b:59:LYS:HD2	25:b:59:LYS:C	2.42	0.45
1:0:1497:A:OP1	9:J:38:ARG:NH2	2.49	0.45
1:0:1904:C:C2	1:0:1905:A:C8	3.05	0.45
1:0:2133:U:H2'	1:0:2134:G:C8	2.52	0.45
3:a:127:TYR:CD2	3:a:267:GLY:HA3	2.51	0.45
4:E:39:LYS:HE3	6:G:4:SER:HA	1.98	0.45
23:X:55:GLN:HG2	23:X:56:ASP:OD1	2.17	0.45
1:0:366:A:H1'	1:0:367:U:O4'	2.17	0.45
1:0:1013:C:OP2	10:K:18:LYS:NZ	2.45	0.45
1:0:1174:A:C4	1:0:1175:G:C8	3.05	0.45
1:0:1666:A:H2'	1:0:1667:G:C8	2.52	0.45
1:0:2440:A:H2'	1:0:2441:U:C6	2.51	0.45
1:0:561:G:H2'	1:0:562:U:C6	2.51	0.45
1:0:1636:U:C2	1:0:1637:A:C8	3.05	0.45
1:0:1803:C:H1'	12:M:43:LEU:HD22	1.99	0.45
16:Q:228:VAL:HG12	16:Q:230:VAL:HG23	1.98	0.45
1:0:354:U:H2'	1:0:355:G:H8	1.82	0.45
1:0:1348:A:OP1	22:W:46:TYR:OH	2.23	0.45
1:0:1918:G:OP1	19:T:29:ARG:NH2	2.50	0.45
1:0:2490:A:H2'	1:0:2491:C:H6	1.82	0.45
1:0:2713:C:H4'	12:M:18:THR:HG22	1.99	0.45
1:0:2850:C:H2'	1:0:2851:U:C6	2.52	0.45
15:P:13:VAL:HG11	15:P:34:ILE:HD12	1.98	0.45
1:0:198:A:C4	1:0:244:G:N7	2.85	0.45
1:0:863:U:H2'	1:0:864:G:N7	2.32	0.45
1:0:1414:U:C4	28:c:57:MET:HE2	2.51	0.45
1:0:2521:U:O2'	5:F:105:GLY:O	2.33	0.45
4:E:105:ALA:CA	4:E:108:ASP:HB2	2.42	0.45
8:I:140:TRP:HZ3	8:I:143:ASN:HD22	1.63	0.45
14:O:16:ASP:OD1	14:O:16:ASP:C	2.60	0.45
19:T:3:MET:HE3	19:T:22:VAL:HG21	1.99	0.45
21:V:191:MET:HE3	21:V:195:PHE:CD2	2.52	0.45
1:0:752:A:H2'	1:0:753:A:C8	2.52	0.45
1:0:954:G:N3	1:0:2295:A:H2'	2.31	0.45
1:0:1180:C:N4	1:0:1189:A:C8	2.85	0.45
1:0:1232:G:C8	1:0:2059:C:H4'	2.52	0.45
1:0:2544:C:O2'	1:0:2545:C:H5'	2.17	0.45
2:9:120:C:H2'	2:9:121:U:O4'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:a:122:THR:HB	3:a:242:LEU:HD12	1.99	0.45
14:O:38:ASN:O	14:O:42:ARG:HB2	2.17	0.45
16:Q:140:PRO:HB2	16:Q:148:ARG:HB2	1.97	0.45
16:Q:187:LEU:HD23	16:Q:187:LEU:HA	1.84	0.45
21:V:282:GLU:HG3	21:V:333:THR:O	2.17	0.45
1:0:356:U:H2'	1:0:357:G:H8	1.81	0.44
1:0:669:A:H2'	1:0:670:A:C8	2.51	0.44
1:0:1086:C:H2'	1:0:1087:A:O4'	2.17	0.44
1:0:1278:G:H2'	1:0:1279:C:H6	1.82	0.44
1:0:1869:C:N4	20:U:123:GLY:O	2.50	0.44
1:0:2133:U:C4	1:0:2134:G:C6	3.05	0.44
1:0:2493:C:H2'	1:0:2494:G:H8	1.83	0.44
1:0:2773:C:H2'	1:0:2774:U:C6	2.52	0.44
16:Q:172:HIS:CG	16:Q:173:PRO:HD2	2.52	0.44
17:R:31:GLU:O	17:R:34:MET:HB3	2.17	0.44
1:0:78:G:H22	1:0:113:A:H2	1.65	0.44
1:0:542:C:H5''	1:0:543:G:C8	2.52	0.44
1:0:1157:G:H5'	1:0:1158:A:H5'	2.00	0.44
1:0:1273:A:H1'	1:0:1275:U:C4	2.53	0.44
1:0:1948:C:H2'	1:0:1949:U:C6	2.52	0.44
4:E:78:VAL:HG11	4:E:84:ILE:HD11	1.98	0.44
17:R:25:ARG:HG3	17:R:29:GLU:OE1	2.17	0.44
21:V:53:MET:HE3	21:V:53:MET:HB3	1.75	0.44
1:0:1652:A:H2'	1:0:1653:A:C8	2.52	0.44
1:0:1787:U:H2'	1:0:1788:U:C6	2.51	0.44
1:0:1952:G:H2'	1:0:1953:A:C8	2.52	0.44
1:0:2004:A:C4	1:0:2006:G:C2	3.05	0.44
3:a:260:ILE:HA	3:a:265:PRO:HA	2.00	0.44
4:E:102:ALA:HB3	4:E:106:SER:CA	2.46	0.44
19:T:11:CYS:HB3	19:T:14:CYS:SG	2.56	0.44
24:Y:35:TRP:CE2	25:b:127:ILE:HG22	2.53	0.44
1:0:1160:G:C8	1:0:1161:U:C4	3.05	0.44
2:9:58:C:H2'	2:9:59:U:C6	2.52	0.44
3:a:143:ALA:C	3:a:145:HIS:H	2.25	0.44
10:K:27:PRO:O	10:K:31:ILE:HG13	2.17	0.44
11:L:72:ASP:OD1	11:L:72:ASP:N	2.50	0.44
1:0:22:C:H2'	1:0:23:A:H8	1.82	0.44
1:0:1162:G:C4	1:0:1171:A:H1'	2.52	0.44
1:0:1179:C:H4'	1:0:1180:C:C6	2.52	0.44
1:0:1530:G:H2'	1:0:1531:C:H6	1.82	0.44
1:0:1820:C:H2'	1:0:1821:G:C8	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:25:LEU:HD13	10:K:27:PRO:CB	2.48	0.44
13:N:33:ARG:HD2	13:N:39:ARG:HA	1.98	0.44
1:0:87:A:C2	1:0:105:A:C5	3.06	0.44
1:0:1141:A:H2'	1:0:1142:G:H8	1.82	0.44
1:0:1555:U:O2'	1:0:1556:U:H5'	2.17	0.44
1:0:2134:G:H8	1:0:2134:G:OP2	2.01	0.44
1:0:2540:C:OP1	21:V:9:LYS:HE3	2.17	0.44
1:0:2726:U:H2'	1:0:2727:G:H8	1.82	0.44
5:F:130:PRO:HD2	5:F:133:GLU:HG3	1.99	0.44
14:O:13:ILE:HG22	14:O:18:ARG:HG3	1.98	0.44
17:R:54:ASN:HB2	17:R:59:GLU:HG2	1.99	0.44
1:0:68:G:H1	1:0:92:C:H5	1.66	0.44
1:0:679:C:H1'	22:W:42:ARG:HD3	1.99	0.44
1:0:1239:A:H2'	1:0:1240:C:C6	2.53	0.44
1:0:1530:G:H2'	1:0:1531:C:C6	2.53	0.44
1:0:2710:C:O2'	1:0:2711:C:H5'	2.18	0.44
7:H:72:GLN:HA	7:H:72:GLN:OE1	2.18	0.44
21:V:23:GLU:OE1	21:V:260:TYR:OH	2.27	0.44
1:0:24:G:H2'	1:0:25:C:H6	1.83	0.44
1:0:47:A:H2'	1:0:48:G:C8	2.53	0.44
1:0:171:G:H2'	1:0:172:A:O4'	2.17	0.44
1:0:417:G:H2'	1:0:418:C:H6	1.81	0.44
1:0:976:C:N4	1:0:995:C:H42	2.12	0.44
1:0:1276:U:H4'	1:0:1277:A:OP1	2.18	0.44
1:0:2289:C:H2'	1:0:2290:U:C6	2.51	0.44
1:0:2313:A:H4'	1:0:2314:A:O4'	2.18	0.44
4:E:29:ILE:HG22	4:E:100:VAL:HB	1.99	0.44
8:I:113:GLY:HA2	8:I:138:ALA:HB2	2.00	0.44
21:V:121:THR:O	21:V:121:THR:OG1	2.35	0.44
22:W:151:THR:O	22:W:155:VAL:HG23	2.18	0.44
23:X:40:ILE:HD12	23:X:40:ILE:H	1.83	0.44
1:0:996:G:H2'	1:0:997:C:C6	2.53	0.44
1:0:1410:A:H2'	1:0:1411:G:O4'	2.18	0.44
1:0:2403:G:H2'	1:0:2404:C:C6	2.53	0.44
1:0:2802:G:OP2	21:V:28:LYS:NZ	2.50	0.44
2:9:56:A:H8	23:X:137:VAL:HG21	1.83	0.44
3:a:85:MET:HE3	3:a:107:ALA:HB2	1.99	0.44
8:I:83:TYR:HD2	8:I:143:ASN:HD21	1.59	0.44
8:I:140:TRP:HZ3	8:I:143:ASN:ND2	2.15	0.44
20:U:74:ILE:HD11	20:U:91:GLY:HA3	2.00	0.44
21:V:54:MET:HB2	21:V:328:VAL:HA	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:W:139:LEU:HD22	22:W:161:LEU:HD13	1.99	0.44
22:W:150:LYS:HD3	22:W:152:LYS:HE2	2.00	0.44
26:f:72:VAL:HG23	26:f:98:ILE:HG12	1.99	0.44
27:d:47:VAL:HG12	27:d:51:LYS:HE3	2.00	0.44
1:0:288:U:H1'	1:0:289:A:C2	2.53	0.43
1:0:675:A:H2	1:0:679:C:H41	1.65	0.43
1:0:978:G:C2	1:0:979:G:N7	2.86	0.43
1:0:1047:G:H2'	1:0:1048:U:H6	1.81	0.43
1:0:1156:G:C4	1:0:1157:G:C8	3.06	0.43
1:0:1396:C:H4'	15:P:57:GLU:HG2	2.00	0.43
1:0:1653:A:H2'	1:0:1654:A:C8	2.53	0.43
1:0:1706:A:N3	1:0:1809:C:O2'	2.49	0.43
1:0:1901:G:N1	1:0:1923:A:OP2	2.34	0.43
1:0:2252:C:C2	1:0:2253:A:C8	3.06	0.43
1:0:2701:G:H2'	1:0:2702:A:C8	2.53	0.43
3:a:236:ILE:HD12	3:a:237:SER:N	2.31	0.43
14:O:82:GLU:CD	14:O:82:GLU:H	2.26	0.43
1:0:1170:A:H1'	1:0:1197:A:H4'	2.00	0.43
1:0:1178:A:H2	1:0:1189:A:C8	2.37	0.43
1:0:1516:C:H2'	1:0:1517:A:H8	1.83	0.43
3:a:111:LEU:HD23	3:a:111:LEU:HA	1.81	0.43
3:a:127:TYR:HD2	3:a:267:GLY:HA3	1.83	0.43
4:E:71:LYS:HD3	4:E:71:LYS:HA	1.86	0.43
8:I:168:ASN:OD1	8:I:168:ASN:N	2.42	0.43
9:J:70:ARG:HA	9:J:74:HIS:O	2.18	0.43
20:U:67:MET:HE3	20:U:67:MET:HB2	1.74	0.43
1:0:296:C:H42	1:0:366:A:N6	2.16	0.43
1:0:1184:U:O2'	1:0:1186:A:OP2	2.35	0.43
1:0:2814:C:H2'	1:0:2815:C:H6	1.83	0.43
27:d:21:LEU:HD11	27:d:54:ILE:HG23	2.00	0.43
1:0:300:A:C3'	1:0:301:A:H5''	2.48	0.43
1:0:1162:G:O4'	1:0:1171:A:O2'	2.26	0.43
1:0:1220:G:H5''	30:e:13:ARG:NH1	2.33	0.43
1:0:1272:U:O2'	1:0:1273:A:H5'	2.18	0.43
1:0:2053:A:H2'	1:0:2054:C:C6	2.52	0.43
1:0:2260:G:H2'	1:0:2261:C:C6	2.54	0.43
1:0:2371:U:P	19:T:8:ASN:HD22	2.41	0.43
2:9:116:G:H21	8:I:56:ASP:H	1.66	0.43
3:a:100:ASP:OD1	3:a:100:ASP:N	2.52	0.43
13:N:29:SER:HA	13:N:98:ARG:HD2	1.98	0.43
25:b:51:GLU:OE1	25:b:51:GLU:N	2.41	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:303:U:H2'	1:0:304:C:O4'	2.18	0.43
1:0:1589:C:H4'	1:0:1602:A:H4'	2.00	0.43
1:0:2501:C:O2'	1:0:2502:A:H8	2.02	0.43
3:a:116:PRO:O	3:a:117:PHE:C	2.62	0.43
5:F:153:ARG:HA	5:F:156:TYR:CE2	2.53	0.43
22:W:115:LEU:HD21	22:W:245:VAL:HG22	1.99	0.43
1:0:32:A:H1'	1:0:523:A:C2	2.53	0.43
1:0:276:A:O4'	1:0:278:G:H1'	2.19	0.43
1:0:1557:C:H3'	1:0:1558:G:C8	2.54	0.43
1:0:2439:C:H2'	1:0:2440:A:C8	2.51	0.43
1:0:2655:G:O2'	1:0:2809:A:N1	2.49	0.43
8:I:117:PHE:HB3	8:I:137:LEU:HD23	2.01	0.43
21:V:265:GLU:HB3	21:V:268:LYS:HE3	2.01	0.43
26:f:84:ASP:OD1	26:f:86:THR:HG23	2.18	0.43
1:0:108:U:H2'	1:0:109:G:H8	1.83	0.43
1:0:318:U:H2'	1:0:319:G:O4'	2.19	0.43
1:0:362:A:N3	1:0:364:A:N6	2.67	0.43
1:0:1459:U:H2'	1:0:1460:A:C8	2.52	0.43
1:0:2692:A:O5'	1:0:2692:A:H8	2.01	0.43
1:0:2726:U:H2'	1:0:2727:G:C8	2.54	0.43
8:I:149:ALA:O	8:I:153:GLU:HG3	2.18	0.43
1:0:407:C:OP1	6:G:70:LYS:HG3	2.19	0.43
1:0:614:G:H2'	1:0:615:U:C6	2.54	0.43
1:0:843:A:O2'	1:0:845:A:OP2	2.36	0.43
1:0:946:G:N3	14:O:23:MET:HE1	2.34	0.43
1:0:1553:C:O2	1:0:1558:G:N2	2.41	0.43
1:0:1975:C:O2'	3:a:141:GLY:O	2.32	0.43
1:0:2335:G:O2'	1:0:2336:G:H4'	2.18	0.43
10:K:21:GLU:HG3	10:K:21:GLU:O	2.18	0.43
14:O:76:ASP:OD1	14:O:76:ASP:N	2.51	0.43
1:0:152:A:H2'	1:0:153:U:H6	1.83	0.43
1:0:300:A:H3'	1:0:301:A:C5'	2.47	0.43
1:0:498:G:N2	1:0:501:A:OP2	2.47	0.43
1:0:557:G:P	16:Q:198:ARG:HH22	2.42	0.43
1:0:2135:G:H2'	1:0:2136:U:C5	2.53	0.43
1:0:2324:C:OP2	1:0:2345:G:N1	2.44	0.43
1:0:2366:A:H2'	1:0:2367:A:C8	2.54	0.43
8:I:103:LEU:HD22	8:I:120:GLN:HB2	2.01	0.43
8:I:146:VAL:O	8:I:150:GLU:HG2	2.19	0.43
1:0:108:U:H2'	1:0:109:G:C8	2.52	0.43
1:0:424:U:H2'	1:0:425:C:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1173:C:H2'	1:0:1194:G:O6	2.19	0.43
1:0:1587:G:H2'	1:0:1588:C:H6	1.84	0.43
1:0:1917:G:H4'	19:T:29:ARG:HH12	1.84	0.43
1:0:2331:G:O2'	23:X:102:PHE:O	2.34	0.43
1:0:2701:G:H2'	1:0:2702:A:H8	1.84	0.43
5:F:77:LEU:HA	5:F:81:GLY:O	2.19	0.43
28:c:22:LYS:HG2	28:c:66:ARG:HB2	2.01	0.43
1:0:792:A:H2'	1:0:793:G:O4'	2.18	0.42
1:0:1458:C:H2'	1:0:1459:U:C6	2.54	0.42
1:0:2128:A:H2'	1:0:2129:G:C8	2.54	0.42
1:0:2656:C:OP2	1:0:2657:U:O2'	2.23	0.42
1:0:2849:A:H4'	15:P:12:THR:HB	2.00	0.42
3:a:21:SER:O	3:a:24:VAL:HG12	2.18	0.42
27:d:9:ILE:HG22	27:d:60:ILE:HG21	2.01	0.42
1:0:273:U:C4	1:0:274:G:C6	3.07	0.42
1:0:297:U:O2	1:0:365:G:N1	2.52	0.42
1:0:423:A:H2'	1:0:424:U:C6	2.54	0.42
1:0:1103:C:H1'	1:0:1110:U:H3	1.83	0.42
1:0:1202:U:H2'	1:0:1203:U:O4'	2.20	0.42
1:0:1232:G:N2	1:0:1233:A:C2	2.88	0.42
1:0:1961:A:C6	1:0:1962:A:C6	3.07	0.42
1:0:2814:C:H2'	1:0:2815:C:C6	2.54	0.42
2:9:43:A:C4	2:9:44:A:C8	3.06	0.42
4:E:84:ILE:N	4:E:84:ILE:HD13	2.34	0.42
6:G:123:GLN:HB2	6:G:128:LYS:HG2	2.01	0.42
13:N:114:LYS:HA	13:N:114:LYS:HD2	1.93	0.42
20:U:50:PRO:O	20:U:182:ARG:NH1	2.52	0.42
22:W:81:PRO:HA	22:W:87:ARG:O	2.19	0.42
24:Y:105:ILE:HD13	24:Y:105:ILE:HA	1.87	0.42
1:0:389:C:H2'	1:0:390:G:H8	1.83	0.42
1:0:1070:C:H2'	1:0:1071:G:O4'	2.19	0.42
1:0:1464:G:O2'	1:0:1858:A:N3	2.42	0.42
1:0:2425:C:H2'	1:0:2426:U:H6	1.83	0.42
1:0:2628:A:C2'	1:0:2629:C:H5'	2.49	0.42
1:0:2647:U:H2'	1:0:2648:U:C6	2.55	0.42
3:a:84:LEU:HD12	3:a:84:LEU:H	1.84	0.42
22:W:54:LEU:HD21	22:W:87:ARG:HD3	2.02	0.42
23:X:100:PHE:CE1	23:X:128:VAL:HG21	2.55	0.42
24:Y:35:TRP:CZ2	25:b:127:ILE:HG22	2.54	0.42
1:0:1117:U:H3	1:0:1243:A:N6	2.17	0.42
1:0:1194:G:H2'	1:0:1195:U:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2318:U:H2'	1:0:2319:U:H6	1.80	0.42
1:0:2688:C:H2'	1:0:2689:G:O4'	2.20	0.42
1:0:2732:A:C4	1:0:2733:G:C8	3.07	0.42
2:9:27:A:H2'	2:9:28:C:C6	2.54	0.42
11:L:49:GLU:HG3	11:L:90:LEU:HD11	2.01	0.42
13:N:15:ALA:HB1	13:N:19:GLU:HB2	2.01	0.42
20:U:31:LYS:HG3	20:U:66:ARG:NE	2.34	0.42
21:V:101:VAL:HG13	21:V:125:ASP:HB2	2.01	0.42
23:X:52:ARG:HG2	23:X:61:GLN:OE1	2.20	0.42
27:d:61:GLN:HG2	27:d:66:ASP:HB2	2.01	0.42
28:c:3:ILE:HG22	28:c:39:GLU:CD	2.44	0.42
1:0:132:C:O2'	1:0:133:A:O5'	2.27	0.42
1:0:505:G:OP1	11:L:5:TYR:OH	2.26	0.42
2:9:13:A:O2'	2:9:14:G:H5'	2.20	0.42
6:G:96:LYS:NZ	6:G:104:GLU:OE1	2.34	0.42
19:T:11:CYS:HB2	19:T:20:HIS:CE1	2.54	0.42
21:V:180:LEU:HD23	21:V:180:LEU:HA	1.81	0.42
1:0:1242:C:H5''	1:0:1243:A:C8	2.54	0.42
2:9:33:A:C2	8:I:151:TYR:HB2	2.54	0.42
4:E:107:ASP:O	4:E:108:ASP:C	2.63	0.42
21:V:153:LYS:HB2	21:V:153:LYS:HE3	1.79	0.42
29:A:27:MET:HA	29:A:30:THR:HG22	2.01	0.42
1:0:270:U:OP1	6:G:51:ARG:NH1	2.52	0.42
1:0:301:A:C5	1:0:302:U:H1'	2.55	0.42
1:0:425:C:HO2'	1:0:1912:A:H62	1.66	0.42
1:0:973:A:H2	1:0:1000:C:H42	1.67	0.42
1:0:1212:A:N3	1:0:1213:G:H1'	2.34	0.42
1:0:1332:U:C2	1:0:1333:A:C8	3.08	0.42
1:0:1512:C:H2'	1:0:1513:U:C6	2.54	0.42
1:0:1512:C:H2'	1:0:1513:U:H6	1.85	0.42
1:0:1596:G:H2'	1:0:1597:C:C6	2.54	0.42
1:0:1636:U:H2'	1:0:1637:A:H8	1.84	0.42
1:0:1923:A:H2'	1:0:1924:A:C8	2.54	0.42
1:0:2325:A:H2'	1:0:2326:C:O4'	2.19	0.42
4:E:102:ALA:HB3	4:E:106:SER:N	2.35	0.42
17:R:42:ASP:OD1	17:R:42:ASP:N	2.53	0.42
21:V:121:THR:OG1	21:V:124:SER:OG	2.37	0.42
1:0:34:A:H2'	1:0:35:G:H8	1.84	0.42
1:0:967:A:H5'	1:0:968:U:OP2	2.19	0.42
1:0:1962:A:H2'	1:0:1963:G:O4'	2.20	0.42
3:a:114:VAL:HG13	3:a:117:PHE:HD2	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:12:ILE:HG12	5:F:59:GLN:HG3	2.01	0.42
12:M:13:GLU:OE2	12:M:13:GLU:HA	2.20	0.42
13:N:56:PHE:HE2	13:N:90:ARG:HD3	1.85	0.42
16:Q:105:ASP:N	16:Q:105:ASP:OD1	2.53	0.42
16:Q:164:THR:O	16:Q:169:ARG:NH2	2.42	0.42
19:T:2:GLN:HB3	19:T:92:GLN:HG3	2.00	0.42
24:Y:109:LEU:HD21	24:Y:158:LYS:NZ	2.35	0.42
1:0:367:U:H3'	1:0:367:U:O2	2.19	0.42
1:0:976:C:H2'	1:0:977:C:O4'	2.20	0.42
1:0:1154:C:N4	1:0:1155:G:O6	2.53	0.42
1:0:1157:G:H21	1:0:1204:A:H62	1.66	0.42
1:0:1658:A:OP2	1:0:1659:A:O2'	2.28	0.42
1:0:2046:G:H4'	11:L:137:TRP:CE2	2.55	0.42
1:0:2628:A:O2'	1:0:2629:C:H5'	2.20	0.42
1:0:2658:A:OP2	1:0:2658:A:H4'	2.20	0.42
4:E:35:ASN:OD1	6:G:5:PHE:HD1	2.03	0.42
4:E:117:GLU:O	4:E:118:ASP:C	2.63	0.42
5:F:76:MET:HE3	5:F:76:MET:HB3	1.85	0.42
6:G:182:GLU:O	6:G:183:HIS:ND1	2.53	0.42
9:J:11:ALA:O	9:J:15:LEU:HB2	2.19	0.42
22:W:233:ARG:O	22:W:235:THR:HG23	2.20	0.42
23:X:47:ARG:HG2	23:X:64:PRO:HB3	2.00	0.42
1:0:300:A:O2'	1:0:301:A:C8	2.73	0.42
1:0:1184:U:H4'	1:0:1186:A:C2	2.48	0.42
3:a:106:THR:O	3:a:110:ILE:HD13	2.20	0.42
4:E:13:LEU:HD23	4:E:13:LEU:HA	1.87	0.42
22:W:116:ALA:O	22:W:119:THR:HG22	2.20	0.42
25:b:79:PHE:HB3	25:b:103:VAL:HG11	2.01	0.42
1:0:34:A:H2'	1:0:35:G:C8	2.55	0.41
1:0:369:C:O2	1:0:370:C:H6	2.03	0.41
1:0:545:U:OP1	16:Q:121:GLN:HG2	2.21	0.41
1:0:724:G:H22	1:0:940:G:P	2.43	0.41
1:0:976:C:H2'	1:0:977:C:C6	2.55	0.41
1:0:1251:C:H2'	1:0:1252:U:C6	2.55	0.41
1:0:1940:G:H2'	1:0:1941:G:N7	2.34	0.41
1:0:2062:U:H2'	1:0:2063:G:C8	2.55	0.41
1:0:2135:G:O5'	1:0:2135:G:H8	2.03	0.41
1:0:2679:C:C2	1:0:2680:G:C8	3.08	0.41
3:a:84:LEU:O	3:a:88:SER:OG	2.29	0.41
5:F:53:GLU:N	5:F:53:GLU:OE1	2.53	0.41
22:W:158:LEU:HG	22:W:163:VAL:HG23	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:d:14:PRO:O	27:d:18:VAL:HG12	2.20	0.41
1:0:934:U:H2'	1:0:935:C:C6	2.55	0.41
1:0:2336:G:H1'	1:0:2337:A:C8	2.55	0.41
2:9:3:C:H4'	2:9:4:G:OP2	2.20	0.41
3:a:15:THR:OG1	3:a:17:GLU:HG3	2.20	0.41
3:a:71:ARG:NH1	3:a:71:ARG:HB2	2.35	0.41
3:a:147:PHE:HA	3:a:152:ILE:HB	2.01	0.41
11:L:25:SER:O	11:L:29:SER:OG	2.33	0.41
11:L:27:LYS:HD3	11:L:63:HIS:CG	2.55	0.41
14:O:84:VAL:HG11	14:O:92:ASP:O	2.20	0.41
22:W:135:LEU:HD23	22:W:135:LEU:HA	1.83	0.41
24:Y:5:GLU:HA	24:Y:48:ILE:O	2.20	0.41
24:Y:138:ASP:HB3	24:Y:141:ASP:HB2	2.01	0.41
1:0:11:G:O2'	1:0:12:G:H8	2.01	0.41
1:0:1143:C:H2'	1:0:1144:C:H6	1.85	0.41
1:0:1160:G:H2'	1:0:1161:U:C5	2.55	0.41
1:0:1170:A:C4	1:0:1174:A:C8	3.08	0.41
1:0:1414:U:O4	28:c:57:MET:HE2	2.21	0.41
1:0:1521:A:H1'	1:0:1522:A:C5	2.55	0.41
1:0:2098:C:H2'	1:0:2099:C:H6	1.85	0.41
2:9:7:G:H1'	8:I:56:ASP:HB2	2.02	0.41
19:T:25:VAL:HG23	19:T:67:HIS:O	2.20	0.41
23:X:15:GLU:HB3	23:X:129:ASN:HB3	2.02	0.41
25:b:128:LYS:HB3	25:b:128:LYS:HE2	1.50	0.41
28:c:28:HIS:HD2	28:c:29:VAL:H	1.67	0.41
1:0:1073:G:C6	1:0:1088:G:C5	3.09	0.41
1:0:1157:G:N1	1:0:1203:U:OP2	2.47	0.41
1:0:1669:U:H2'	1:0:1670:C:C6	2.55	0.41
1:0:2422:A:H2'	1:0:2423:A:H8	1.85	0.41
1:0:2731:G:C2	1:0:2732:A:C8	3.09	0.41
6:G:43:ARG:HD3	6:G:43:ARG:HA	1.77	0.41
12:M:25:THR:O	26:f:112:PRO:HD3	2.20	0.41
1:0:270:U:P	6:G:51:ARG:HH12	2.42	0.41
1:0:577:A:N6	1:0:589:A:N6	2.68	0.41
1:0:614:G:H2'	1:0:615:U:H6	1.86	0.41
1:0:1457:U:H2'	1:0:1458:C:H6	1.85	0.41
1:0:2232:C:H2'	1:0:2233:U:C6	2.56	0.41
1:0:2656:C:O2'	1:0:2810:A:OP1	2.30	0.41
2:9:58:C:H2'	2:9:59:U:H6	1.86	0.41
7:H:50:GLU:OE2	7:H:73:LYS:HG3	2.20	0.41
15:P:18:VAL:O	15:P:21:VAL:HG22	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:b:19:MET:HE3	25:b:82:ALA:CB	2.51	0.41
26:f:82:ARG:CZ	26:f:115:ARG:HH11	2.33	0.41
1:0:922:C:H5''	1:0:923:G:OP1	2.20	0.41
1:0:999:U:H2'	1:0:1000:C:C5	2.55	0.41
1:0:1057:U:O4'	5:F:8:MET:HE3	2.21	0.41
1:0:1103:C:H1'	1:0:1110:U:N3	2.35	0.41
1:0:1126:U:H6	1:0:1126:U:H2'	1.68	0.41
1:0:1323:G:N2	1:0:1326:A:OP2	2.50	0.41
1:0:1414:U:H4'	1:0:1415:U:O5'	2.21	0.41
1:0:1944:G:H2'	1:0:1945:U:O4'	2.20	0.41
1:0:2275:U:O2'	5:F:116:ARG:NH2	2.53	0.41
1:0:2421:G:OP2	19:T:85:ARG:NH2	2.50	0.41
1:0:2440:A:H2'	1:0:2441:U:H6	1.85	0.41
3:a:118:LEU:HB3	3:a:119:ASP:H	1.64	0.41
17:R:51:ILE:HD13	20:U:46:ILE:HG22	2.01	0.41
21:V:313:ARG:HG3	21:V:314:PRO:O	2.20	0.41
23:X:132:ARG:NH2	23:X:154:THR:HA	2.35	0.41
1:0:577:A:H2'	1:0:578:G:C8	2.55	0.41
1:0:975:U:H2'	1:0:976:C:C6	2.55	0.41
1:0:1070:C:O2'	1:0:1082:A:N3	2.49	0.41
1:0:1179:C:H4'	1:0:1180:C:C5	2.55	0.41
1:0:2006:G:H2'	1:0:2007:G:C8	2.54	0.41
2:9:76:A:H8	2:9:76:A:OP1	2.04	0.41
19:T:19:GLU:O	19:T:73:SER:OG	2.38	0.41
20:U:106:CYS:N	20:U:155:THR:O	2.54	0.41
21:V:313:ARG:NH2	21:V:316:ILE:HD11	2.36	0.41
22:W:127:ARG:HD3	22:W:232:GLY:C	2.45	0.41
26:f:34:VAL:HB	26:f:37:TYR:HB2	2.00	0.41
1:0:293:G:C6	1:0:294:A:N7	2.89	0.41
1:0:695:G:N2	1:0:698:A:OP2	2.43	0.41
1:0:2077:C:H2'	1:0:2078:C:H6	1.85	0.41
1:0:2658:A:H2'	1:0:2658:A:N3	2.36	0.41
15:P:29:ARG:HA	15:P:29:ARG:HD3	1.85	0.41
17:R:31:GLU:HA	17:R:34:MET:HB3	2.03	0.41
22:W:115:LEU:O	22:W:118:THR:HG22	2.19	0.41
1:0:289:A:N3	1:0:289:A:H3'	2.36	0.41
1:0:364:A:H1'	1:0:365:G:C5	2.56	0.41
1:0:416:C:H2'	1:0:417:G:H8	1.85	0.41
1:0:912:C:O2'	1:0:934:U:H5''	2.21	0.41
1:0:923:G:H2'	1:0:924:A:C8	2.55	0.41
1:0:1457:U:H2'	1:0:1458:C:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:2065:G:C6	1:0:2526:C:H1'	2.55	0.41
1:0:2126:U:H4'	1:0:2127:G:O5'	2.20	0.41
1:0:2549:C:O2'	1:0:2592:A:N3	2.46	0.41
1:0:2692:A:H2'	1:0:2693:G:O4'	2.21	0.41
1:0:2730:C:OP2	9:J:62:ARG:NH2	2.46	0.41
3:a:65:LEU:HD23	3:a:65:LEU:HA	1.87	0.41
5:F:56:GLU:OE2	5:F:162:PRO:HD2	2.21	0.41
6:G:24:LEU:HA	6:G:24:LEU:HD12	1.87	0.41
8:I:22:HIS:O	8:I:26:ARG:HG3	2.20	0.41
15:P:80:GLU:HG2	15:P:81:ASP:H	1.86	0.41
18:S:17:HIS:HA	18:S:28:TYR:O	2.19	0.41
21:V:101:VAL:HG22	21:V:125:ASP:HB3	2.03	0.41
21:V:271:ILE:HD11	21:V:299:LYS:HB2	2.02	0.41
1:0:422:C:H2'	1:0:423:A:H8	1.86	0.41
1:0:536:A:O2'	1:0:2077:C:O2	2.38	0.41
1:0:567:C:H2'	1:0:568:G:O4'	2.20	0.41
1:0:862:C:H2'	1:0:863:U:O4'	2.20	0.41
1:0:1008:A:N3	1:0:2291:C:O2'	2.45	0.41
1:0:1046:G:H2'	1:0:1047:G:C8	2.55	0.41
1:0:1317:A:H2'	1:0:1318:C:C6	2.56	0.41
1:0:1908:C:H2'	1:0:1909:A:H8	1.86	0.41
3:a:151:ARG:HD3	3:a:151:ARG:HA	1.91	0.41
4:E:22:GLU:HG3	4:E:23:VAL:N	2.35	0.41
4:E:119:LEU:O	4:E:120:ARG:C	2.63	0.41
7:H:21:GLU:C	7:H:21:GLU:OE2	2.63	0.41
12:M:50:LEU:O	12:M:56:GLY:HA3	2.21	0.41
26:f:67:GLN:HB3	26:f:69:LEU:HD21	2.03	0.41
1:0:243:A:O2'	1:0:439:A:N6	2.54	0.40
1:0:498:G:N2	1:0:500:A:H3'	2.36	0.40
1:0:532:G:H2'	1:0:533:G:H8	1.86	0.40
1:0:561:G:O2'	1:0:562:U:H5'	2.20	0.40
1:0:1159:G:N2	1:0:1182:U:N3	2.69	0.40
1:0:1174:A:H3'	1:0:1175:G:H8	1.87	0.40
2:9:4:G:OP2	2:9:4:G:H8	2.03	0.40
2:9:27:A:H2'	2:9:28:C:H6	1.85	0.40
5:F:150:ASP:O	5:F:153:ARG:HB3	2.20	0.40
25:b:64:GLY:HA2	25:b:69:PRO:HD2	2.02	0.40
1:0:252:C:N4	1:0:272:G:O6	2.54	0.40
1:0:279:G:N3	1:0:280:A:C8	2.89	0.40
1:0:615:U:H2'	1:0:616:U:H6	1.85	0.40
1:0:635:A:N3	1:0:2066:G:O2'	2.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:0:1906:C:H2'	1:0:1907:C:C6	2.56	0.40
3:a:11:TYR:CE2	3:a:103:GLY:HA2	2.54	0.40
3:a:74:PRO:O	3:a:75:ASP:C	2.64	0.40
3:a:80:LYS:O	3:a:84:LEU:HD12	2.21	0.40
6:G:84:THR:HA	6:G:87:GLN:HG3	2.03	0.40
8:I:159:LEU:HD23	8:I:159:LEU:HA	1.83	0.40
20:U:175:LYS:HD2	20:U:179:MET:HE2	2.02	0.40
20:U:217:ARG:O	20:U:217:ARG:HG3	2.19	0.40
22:W:175:LYS:HE3	22:W:175:LYS:HB2	1.88	0.40
23:X:48:THR:O	23:X:64:PRO:HA	2.21	0.40
1:0:972:G:H2'	1:0:973:A:H8	1.85	0.40
1:0:1277:A:O2'	1:0:1278:G:H8	2.04	0.40
1:0:2716:G:H2'	1:0:2717:U:C6	2.57	0.40
24:Y:67:GLU:C	24:Y:67:GLU:OE2	2.65	0.40
25:b:139:LEU:HD23	25:b:139:LEU:HA	1.87	0.40
1:0:474:U:O2'	18:S:17:HIS:ND1	2.48	0.40
1:0:1167:U:O2	1:0:1169:G:H3'	2.22	0.40
1:0:1271:C:N4	1:0:1272:U:O4	2.54	0.40
1:0:1923:A:H2'	1:0:1924:A:H8	1.86	0.40
1:0:2004:A:N3	1:0:2006:G:N2	2.69	0.40
1:0:2517:G:H2'	1:0:2518:G:C8	2.56	0.40
1:0:2711:C:H4'	21:V:49:MET:SD	2.61	0.40
9:J:122:THR:O	9:J:126:LYS:HG3	2.21	0.40
15:P:4:ASN:HA	15:P:79:ASP:HB3	2.03	0.40
16:Q:191:ASP:OD1	16:Q:191:ASP:C	2.64	0.40
24:Y:22:THR:C	24:Y:23:ILE:HD12	2.46	0.40
25:b:91:LYS:HD3	25:b:91:LYS:HA	1.97	0.40
1:0:38:C:OP1	13:N:13:ARG:NH2	2.45	0.40
1:0:261:C:H4'	1:0:262:G:O5'	2.22	0.40
1:0:1272:U:H4'	1:0:1273:A:OP1	2.21	0.40
1:0:1440:G:O3'	28:c:10:THR:HG21	2.22	0.40
1:0:1582:U:C4	1:0:1583:G:C5	3.10	0.40
1:0:2605:A:O4'	1:0:2640:C:N4	2.55	0.40
1:0:2613:U:O4	3:a:214:GLU:N	2.51	0.40
1:0:2703:A:H2'	1:0:2704:U:C6	2.57	0.40
3:a:217:LEU:HD12	3:a:217:LEU:HA	1.78	0.40
7:H:88:THR:O	7:H:91:GLU:HG2	2.20	0.40
19:T:88:ARG:HD3	19:T:90:GLU:OE1	2.21	0.40
22:W:111:VAL:HG11	22:W:248:ARG:NH1	2.34	0.40
24:Y:65:THR:O	24:Y:68:SER:OG	2.40	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	a	279/406 (69%)	221 (79%)	51 (18%)	7 (2%)	4	21
4	E	117/120 (98%)	111 (95%)	6 (5%)	0	100	100
5	F	172/176 (98%)	161 (94%)	11 (6%)	0	100	100
6	G	190/196 (97%)	184 (97%)	6 (3%)	0	100	100
7	H	113/116 (97%)	111 (98%)	2 (2%)	0	100	100
8	I	181/184 (98%)	178 (98%)	3 (2%)	0	100	100
9	J	145/151 (96%)	141 (97%)	4 (3%)	0	100	100
10	K	93/96 (97%)	91 (98%)	2 (2%)	0	100	100
11	L	149/153 (97%)	146 (98%)	3 (2%)	0	100	100
12	M	56/67 (84%)	54 (96%)	2 (4%)	0	100	100
13	N	112/118 (95%)	106 (95%)	6 (5%)	0	100	100
14	O	152/154 (99%)	144 (95%)	8 (5%)	0	100	100
15	P	87/92 (95%)	82 (94%)	5 (6%)	0	100	100
16	Q	140/234 (60%)	136 (97%)	4 (3%)	0	100	100
17	R	78/89 (88%)	72 (92%)	6 (8%)	0	100	100
18	S	55/58 (95%)	52 (94%)	3 (6%)	0	100	100
19	T	91/93 (98%)	89 (98%)	2 (2%)	0	100	100
20	U	233/241 (97%)	222 (95%)	9 (4%)	2 (1%)	14	45
21	V	335/338 (99%)	321 (96%)	14 (4%)	0	100	100
22	W	246/248 (99%)	240 (98%)	6 (2%)	0	100	100
23	X	167/172 (97%)	152 (91%)	14 (8%)	1 (1%)	21	53
24	Y	172/178 (97%)	163 (95%)	8 (5%)	1 (1%)	21	53
25	b	142/145 (98%)	140 (99%)	2 (1%)	0	100	100
26	f	130/132 (98%)	124 (95%)	6 (5%)	0	100	100
27	d	67/70 (96%)	67 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	c	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
29	A	29/50 (58%)	29 (100%)	0	0	100	100
30	e	56/58 (97%)	56 (100%)	0	0	100	100
All	All	3868/4218 (92%)	3671 (95%)	186 (5%)	11 (0%)	37	67

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	a	6	ILE
3	a	10	GLU
20	U	213	LYS
23	X	152	ARG
3	a	4	THR
20	U	229	ALA
24	Y	10	ASP
3	a	9	GLU
3	a	119	ASP
3	a	195	GLY
3	a	187	ASP

### 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	a	227/344 (66%)	196 (86%)	31 (14%)	3	16
4	E	87/94 (93%)	77 (88%)	10 (12%)	5	22
5	F	139/147 (95%)	136 (98%)	3 (2%)	45	73
6	G	160/163 (98%)	151 (94%)	9 (6%)	19	50
7	H	96/99 (97%)	88 (92%)	8 (8%)	10	35
8	I	144/145 (99%)	140 (97%)	4 (3%)	38	69
9	J	117/121 (97%)	110 (94%)	7 (6%)	17	48
10	K	77/78 (99%)	76 (99%)	1 (1%)	61	81

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
11	L	121/124 (98%)	118 (98%)	3 (2%)	42	71
12	M	48/55 (87%)	48 (100%)	0	100	100
13	N	98/102 (96%)	88 (90%)	10 (10%)	7	27
14	O	132/132 (100%)	129 (98%)	3 (2%)	44	72
15	P	74/80 (92%)	72 (97%)	2 (3%)	39	70
16	Q	120/191 (63%)	117 (98%)	3 (2%)	42	71
17	R	61/68 (90%)	59 (97%)	2 (3%)	33	65
18	S	48/49 (98%)	48 (100%)	0	100	100
19	T	77/77 (100%)	76 (99%)	1 (1%)	61	81
20	U	176/186 (95%)	173 (98%)	3 (2%)	53	77
21	V	276/278 (99%)	271 (98%)	5 (2%)	51	76
22	W	194/198 (98%)	190 (98%)	4 (2%)	47	74
23	X	133/147 (90%)	128 (96%)	5 (4%)	29	61
24	Y	145/151 (96%)	139 (96%)	6 (4%)	27	60
25	b	122/123 (99%)	118 (97%)	4 (3%)	33	65
26	f	100/106 (94%)	96 (96%)	4 (4%)	28	60
27	d	45/56 (80%)	43 (96%)	2 (4%)	25	58
28	c	72/76 (95%)	72 (100%)	0	100	100
29	A	27/46 (59%)	25 (93%)	2 (7%)	13	40
30	e	48/49 (98%)	46 (96%)	2 (4%)	26	59
All	All	3164/3485 (91%)	3030 (96%)	134 (4%)	28	59

All (134) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	a	3	ILE
3	a	6	ILE
3	a	7	VAL
3	a	8	SER
3	a	15	THR
3	a	49	ARG
3	a	67	TRP
3	a	68	HIS
3	a	69	VAL
3	a	72	LEU

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
3	a	73	THR
3	a	95	VAL
3	a	118	LEU
3	a	119	ASP
3	a	122	THR
3	a	123	VAL
3	a	125	ASP
3	a	128	THR
3	a	131	LEU
3	a	139	THR
3	a	151	ARG
3	a	157	VAL
3	a	187	ASP
3	a	193	SER
3	a	200	SER
3	a	229	MET
3	a	233	VAL
3	a	234	ARG
3	a	249	MET
3	a	252	ILE
3	a	279	THR
4	E	16	SER
4	E	21	LEU
4	E	22	GLU
4	E	23	VAL
4	E	25	ARG
4	E	45	ASN
4	E	49	VAL
4	E	80	THR
4	E	104	GLU
4	E	111	ASP
5	F	18	THR
5	F	67	SER
5	F	134	THR
6	G	15	THR
6	G	18	GLU
6	G	45	THR
6	G	58	LYS
6	G	84	THR
6	G	96	LYS
6	G	121	VAL
6	G	154	ASP

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
6	G	155	ASP
7	H	10	SER
7	H	15	LEU
7	H	75	VAL
7	H	83	SER
7	H	93	VAL
7	H	97	VAL
7	H	110	SER
7	H	114	VAL
8	I	17	VAL
8	I	36	VAL
8	I	58	THR
8	I	180	LEU
9	J	3	ASP
9	J	30	SER
9	J	45	VAL
9	J	89	GLN
9	J	118	THR
9	J	128	SER
9	J	147	GLN
10	K	76	ILE
11	L	94	GLU
11	L	110	MET
11	L	139	THR
13	N	12	THR
13	N	31	ASP
13	N	49	VAL
13	N	51	VAL
13	N	72	VAL
13	N	77	ASP
13	N	93	GLN
13	N	95	SER
13	N	106	ASP
13	N	108	VAL
14	O	109	GLU
14	O	112	VAL
14	O	140	LYS
15	P	13	VAL
15	P	44	VAL
16	Q	103	LEU
16	Q	111	LEU
16	Q	202	SER

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
17	R	30	ILE
17	R	84	LEU
19	T	74	ASP
20	U	39	ILE
20	U	65	GLN
20	U	148	LEU
21	V	60	ASP
21	V	100	GLU
21	V	113	VAL
21	V	129	LEU
21	V	328	VAL
22	W	146	GLU
22	W	163	VAL
22	W	195	LEU
22	W	213	ASP
23	X	135	TYR
23	X	142	LYS
23	X	144	SER
23	X	155	VAL
23	X	156	GLU
24	Y	50	ILE
24	Y	96	VAL
24	Y	98	VAL
24	Y	104	VAL
24	Y	127	VAL
24	Y	135	THR
25	b	10	VAL
25	b	24	SER
25	b	124	LEU
25	b	143	VAL
26	f	79	SER
26	f	97	ILE
26	f	98	ILE
26	f	105	ARG
27	d	13	THR
27	d	26	THR
29	A	9	LYS
29	A	22	VAL
30	e	42	GLU
30	e	46	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
3	a	30	HIS
3	a	56	HIS
3	a	83	GLN
5	F	14	ASN
5	F	84	GLN
6	G	8	HIS
6	G	90	ASN
6	G	138	ASN
7	H	28	GLN
8	I	47	GLN
8	I	120	GLN
9	J	74	HIS
9	J	143	GLN
9	J	144	ASN
9	J	145	ASN
11	L	98	ASN
16	Q	195	GLN
17	R	36	ASN
19	T	13	ASN
19	T	18	HIS
19	T	20	HIS
21	V	231	GLN
22	W	73	GLN
23	X	7	HIS
28	c	28	HIS

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	0	2798/2916 (95%)	480 (17%)	22 (0%)
2	9	120/122 (98%)	24 (20%)	2 (1%)
All	All	2918/3038 (96%)	504 (17%)	24 (0%)

All (504) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	0	12	G
1	0	13	C
1	0	18	G
1	0	49	C
1	0	58	G
1	0	66	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	0	74	A
1	0	77	A
1	0	78	G
1	0	94	U
1	0	95	G
1	0	97	A
1	0	111	G
1	0	120	A
1	0	122	U
1	0	127	A
1	0	133	A
1	0	134	C
1	0	135	A
1	0	138	A
1	0	147	G
1	0	148	C
1	0	158	A
1	0	173	A
1	0	176	A
1	0	192	G
1	0	193	A
1	0	198	A
1	0	199	A
1	0	203	A
1	0	205	U
1	0	206	C
1	0	207	C
1	0	208	G
1	0	211	A
1	0	213	G
1	0	226	G
1	0	244	G
1	0	261	C
1	0	262	G
1	0	263	G
1	0	269	G
1	0	271	G
1	0	276	A
1	0	277	C
1	0	278	G
1	0	287	A
1	0	288	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	0	289	A
1	0	290	A
1	0	291	C
1	0	292	G
1	0	293	G
1	0	296	C
1	0	298	G
1	0	299	G
1	0	300	A
1	0	301	A
1	0	302	U
1	0	303	U
1	0	305	A
1	0	313	U
1	0	314	C
1	0	321	A
1	0	322	A
1	0	341	G
1	0	342	A
1	0	343	A
1	0	358	A
1	0	359	A
1	0	360	G
1	0	361	G
1	0	362	A
1	0	363	A
1	0	364	A
1	0	366	A
1	0	367	U
1	0	368	C
1	0	369	C
1	0	370	C
1	0	371	G
1	0	372	G
1	0	373	G
1	0	376	U
1	0	378	U
1	0	379	U
1	0	380	C
1	0	385	A
1	0	386	U
1	0	388	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	0	400	U
1	0	401	A
1	0	403	C
1	0	411	A
1	0	421	G
1	0	422	C
1	0	431	C
1	0	459	A
1	0	465	C
1	0	477	G
1	0	487	A
1	0	491	G
1	0	500	A
1	0	501	A
1	0	502	A
1	0	514	U
1	0	515	A
1	0	518	G
1	0	519	C
1	0	520	U
1	0	541	G
1	0	542	C
1	0	543	G
1	0	553	A
1	0	557	G
1	0	562	U
1	0	565	G
1	0	585	U
1	0	592	G
1	0	608	G
1	0	624	A
1	0	630	U
1	0	631	G
1	0	632	A
1	0	633	A
1	0	634	A
1	0	636	A
1	0	648	G
1	0	664	A
1	0	683	C
1	0	692	A
1	0	703	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	0	704	A
1	0	705	C
1	0	706	G
1	0	717	U
1	0	718	U
1	0	719	G
1	0	722	C
1	0	736	U
1	0	737	C
1	0	747	G
1	0	761	C
1	0	778	A
1	0	779	U
1	0	807	G
1	0	811	G
1	0	823	C
1	0	837	U
1	0	842	U
1	0	843	A
1	0	858	G
1	0	859	A
1	0	864	G
1	0	870	G
1	0	871	G
1	0	877	A
1	0	879	G
1	0	880	G
1	0	884	A
1	0	886	C
1	0	888	A
1	0	900	G
1	0	907	C
1	0	910	A
1	0	911	C
1	0	922	C
1	0	923	G
1	0	940	G
1	0	955	G
1	0	962	G
1	0	967	A
1	0	976	C
1	0	994	U

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	0	999	U
1	0	1001	C
1	0	1008	A
1	0	1010	C
1	0	1031	A
1	0	1032	G
1	0	1046	G
1	0	1053	G
1	0	1060	G
1	0	1061	C
1	0	1069	C
1	0	1073	G
1	0	1078	A
1	0	1089	A
1	0	1107	A
1	0	1110	U
1	0	1111	G
1	0	1115	A
1	0	1125	A
1	0	1126	U
1	0	1127	C
1	0	1128	G
1	0	1134	U
1	0	1148	A
1	0	1156	G
1	0	1157	G
1	0	1158	A
1	0	1159	G
1	0	1160	G
1	0	1161	U
1	0	1162	G
1	0	1163	A
1	0	1168	A
1	0	1172	G
1	0	1174	A
1	0	1176	C
1	0	1180	C
1	0	1181	C
1	0	1182	U
1	0	1185	A
1	0	1186	A
1	0	1188	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	0	1189	A
1	0	1190	U
1	0	1191	A
1	0	1192	G
1	0	1193	C
1	0	1196	A
1	0	1197	A
1	0	1202	U
1	0	1205	C
1	0	1206	C
1	0	1207	G
1	0	1208	G
1	0	1211	G
1	0	1212	A
1	0	1213	G
1	0	1214	G
1	0	1218	G
1	0	1223	G
1	0	1231	U
1	0	1233	A
1	0	1235	C
1	0	1236	G
1	0	1239	A
1	0	1243	A
1	0	1271	C
1	0	1272	U
1	0	1273	A
1	0	1274	U
1	0	1275	U
1	0	1276	U
1	0	1277	A
1	0	1278	G
1	0	1285	U
1	0	1286	C
1	0	1312	G
1	0	1327	A
1	0	1336	G
1	0	1338	C
1	0	1349	C
1	0	1350	G
1	0	1356	C
1	0	1365	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	0	1382	G
1	0	1391	C
1	0	1402	U
1	0	1403	A
1	0	1443	U
1	0	1447	C
1	0	1453	U
1	0	1456	G
1	0	1473	A
1	0	1481	A
1	0	1483	A
1	0	1487	A
1	0	1492	G
1	0	1499	A
1	0	1500	U
1	0	1517	A
1	0	1518	A
1	0	1519	U
1	0	1520	A
1	0	1521	A
1	0	1522	A
1	0	1523	A
1	0	1529	C
1	0	1539	A
1	0	1550	G
1	0	1554	C
1	0	1556	U
1	0	1565	C
1	0	1575	A
1	0	1581	G
1	0	1582	U
1	0	1587	G
1	0	1600	G
1	0	1612	U
1	0	1621	A
1	0	1628	C
1	0	1629	U
1	0	1636	U
1	0	1651	A
1	0	1660	G
1	0	1677	A
1	0	1679	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	0	1680	U
1	0	1686	A
1	0	1687	C
1	0	1688	A
1	0	1704	U
1	0	1705	A
1	0	1716	U
1	0	1718	U
1	0	1719	C
1	0	1724	U
1	0	1725	C
1	0	1746	G
1	0	1747	C
1	0	1750	G
1	0	1766	C
1	0	1768	C
1	0	1772	A
1	0	1784	C
1	0	1812	G
1	0	1813	G
1	0	1822	A
1	0	1825	G
1	0	1849	C
1	0	1864	U
1	0	1866	G
1	0	1872	U
1	0	1878	A
1	0	1882	C
1	0	1887	C
1	0	1889	G
1	0	1912	A
1	0	1914	A
1	0	1918	G
1	0	1935	A
1	0	1940	G
1	0	1941	G
1	0	1942	G
1	0	1943	G
1	0	1944	G
1	0	1945	U
1	0	1946	A
1	0	1947	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	0	1948	C
1	0	1949	U
1	0	1950	A
1	0	1951	U
1	0	1954	C
1	0	1955	C
1	0	1956	C
1	0	1957	U
1	0	1958	C
1	0	1959	U
1	0	1960	U
1	0	1963	G
1	0	1964	G
1	0	1971	A
1	0	1973	U
1	0	1974	A
1	0	1989	U
1	0	1997	U
1	0	1999	C
1	0	2001	U
1	0	2004	A
1	0	2006	G
1	0	2027	U
1	0	2057	U
1	0	2065	G
1	0	2066	G
1	0	2067	A
1	0	2075	G
1	0	2089	A
1	0	2094	A
1	0	2095	G
1	0	2096	A
1	0	2103	A
1	0	2127	G
1	0	2130	A
1	0	2131	C
1	0	2132	G
1	0	2226	C
1	0	2227	U
1	0	2228	G
1	0	2229	C
1	0	2230	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	0	2231	A
1	0	2236	C
1	0	2246	G
1	0	2251	A
1	0	2264	G
1	0	2265	G
1	0	2284	A
1	0	2285	C
1	0	2306	C
1	0	2310	C
1	0	2314	A
1	0	2315	A
1	0	2331	G
1	0	2332	U
1	0	2333	C
1	0	2334	G
1	0	2335	G
1	0	2336	G
1	0	2337	A
1	0	2338	A
1	0	2339	C
1	0	2347	A
1	0	2354	A
1	0	2362	A
1	0	2388	A
1	0	2413	G
1	0	2415	U
1	0	2455	G
1	0	2458	A
1	0	2459	G
1	0	2460	A
1	0	2463	A
1	0	2469	C
1	0	2475	G
1	0	2476	A
1	0	2487	G
1	0	2496	A
1	0	2497	A
1	0	2498	G
1	0	2504	A
1	0	2531	A
1	0	2533	G

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	0	2534	U
1	0	2546	A
1	0	2557	G
1	0	2580	U
1	0	2594	A
1	0	2595	G
1	0	2597	A
1	0	2601	C
1	0	2604	G
1	0	2606	G
1	0	2614	U
1	0	2618	C
1	0	2627	G
1	0	2629	C
1	0	2630	A
1	0	2637	C
1	0	2638	U
1	0	2641	U
1	0	2642	A
1	0	2658	A
1	0	2659	A
1	0	2674	A
1	0	2675	C
1	0	2693	G
1	0	2704	U
1	0	2709	G
1	0	2719	U
1	0	2740	G
1	0	2741	U
1	0	2743	G
1	0	2755	C
1	0	2761	G
1	0	2776	A
1	0	2785	A
1	0	2792	A
1	0	2793	A
1	0	2794	A
1	0	2804	A
1	0	2805	A
1	0	2806	A
1	0	2818	U
1	0	2820	A

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	0	2830	U
1	0	2842	U
1	0	2843	C
1	0	2869	G
1	0	2873	A
1	0	2883	A
1	0	2889	G
1	0	2890	C
1	0	2895	A
1	0	2896	C
1	0	2902	G
1	0	2910	C
2	9	3	C
2	9	4	G
2	9	7	G
2	9	16	G
2	9	18	U
2	9	19	G
2	9	23	U
2	9	27	A
2	9	33	A
2	9	39	C
2	9	40	C
2	9	41	C
2	9	51	A
2	9	54	U
2	9	55	A
2	9	56	A
2	9	64	U
2	9	76	A
2	9	77	G
2	9	87	G
2	9	93	U
2	9	109	G
2	9	113	G
2	9	121	U

All (24) RNA pucker outliers are listed below:

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	0	206	C
1	0	261	C

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Mol	Chain	Res	Type
1	0	360	G
1	0	366	A
1	0	369	C
1	0	379	U
1	0	499	A
1	0	879	G
1	0	961	C
1	0	1127	C
1	0	1159	G
1	0	1180	C
1	0	1272	U
1	0	1276	U
1	0	1520	A
1	0	1659	A
1	0	1941	G
1	0	1956	C
1	0	2337	A
1	0	2657	U
1	0	2784	U
1	0	2842	U
2	9	2	A
2	9	22	G

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 236 ligands modelled in this entry, 234 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the

expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
32	ADP	a	502	-	27,29,29	0.41	0	42,45,45	0.42	0
32	ADP	a	501	-	27,29,29	0.43	0	42,45,45	0.51	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
32	ADP	a	502	-	-	4/16/32/32	0/3/3/3
32	ADP	a	501	-	-	6/16/32/32	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
32	a	501	ADP	C5'-O5'-PA-O3A
32	a	501	ADP	O4'-C4'-C5'-O5'
32	a	502	ADP	PB-O3A-PA-O5'
32	a	502	ADP	O4'-C4'-C5'-O5'
32	a	501	ADP	C3'-C4'-C5'-O5'
32	a	502	ADP	C3'-C4'-C5'-O5'
32	a	501	ADP	C5'-O5'-PA-O1A
32	a	501	ADP	C5'-O5'-PA-O2A
32	a	501	ADP	C4'-C5'-O5'-PA
32	a	502	ADP	C4'-C5'-O5'-PA

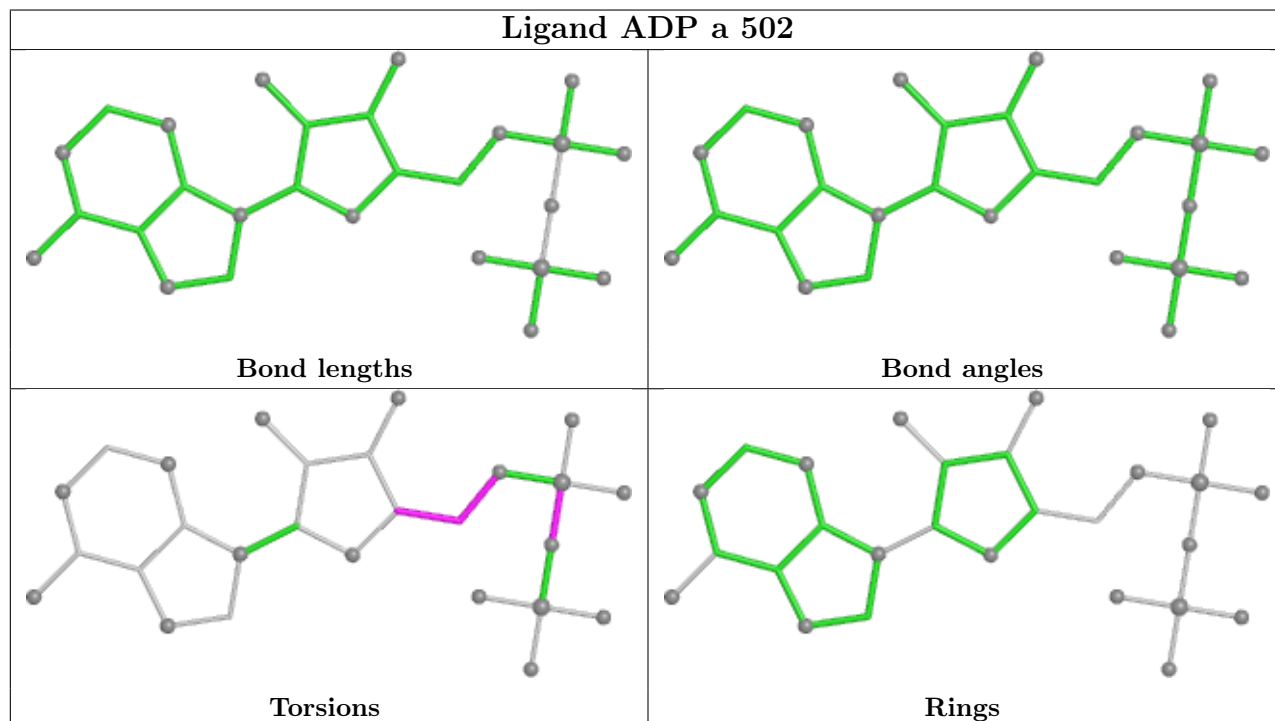
There are no ring outliers.

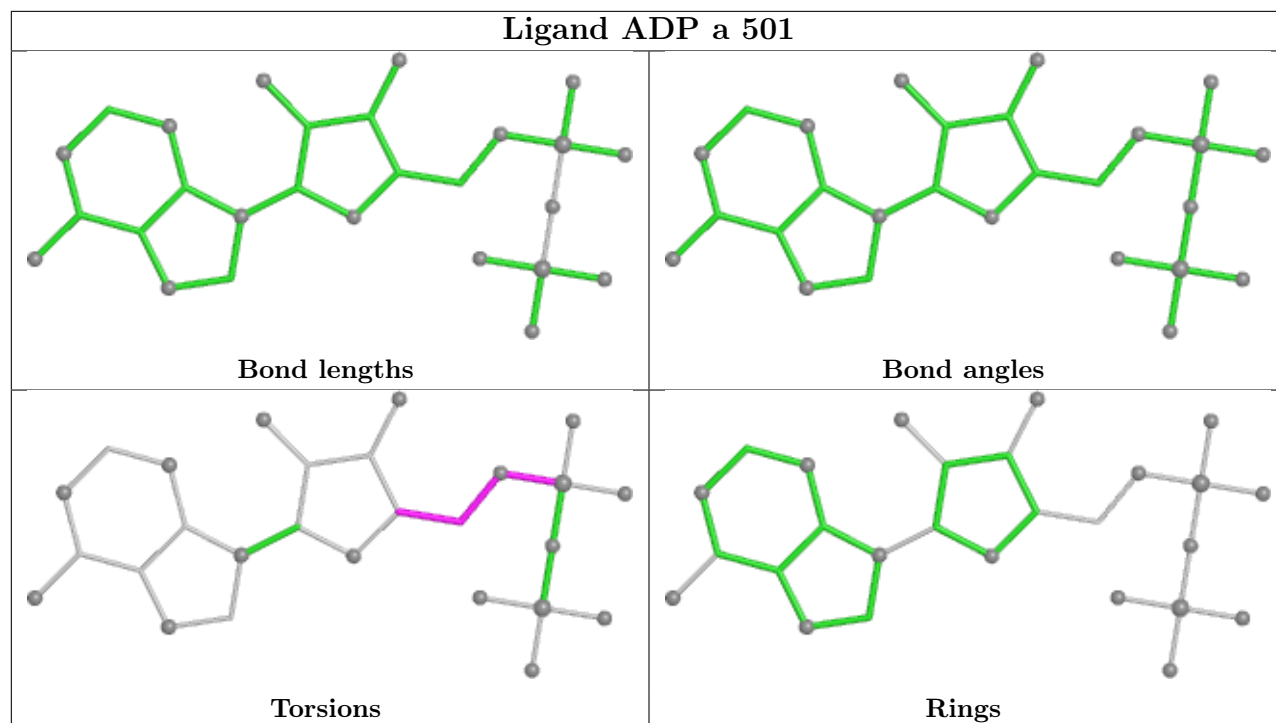
1 monomer is involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
32	a	502	ADP	7	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In

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





## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

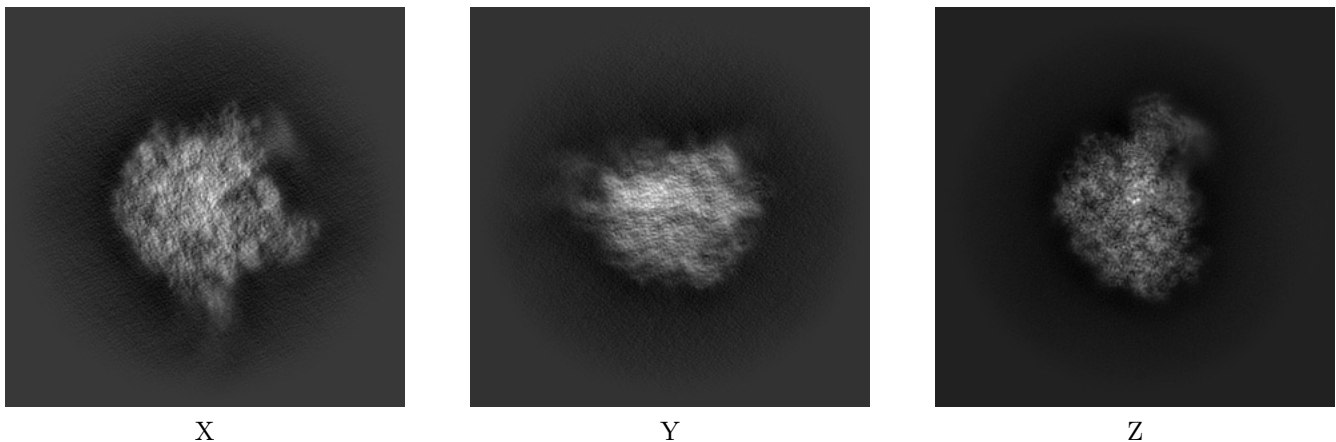
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-62895. These allow visual inspection of the internal detail of the map and identification of artifacts.

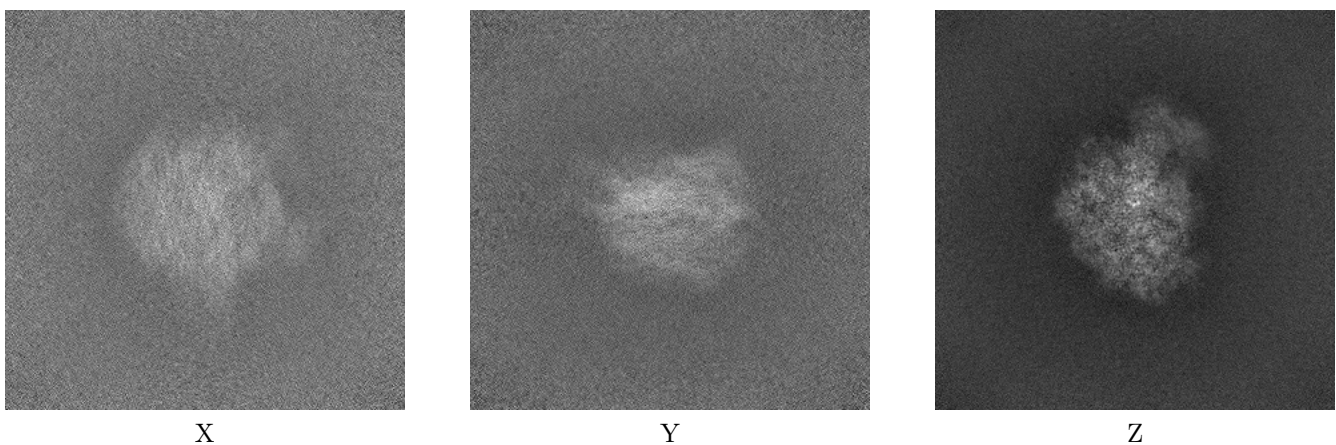
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

#### 6.1.1 Primary map



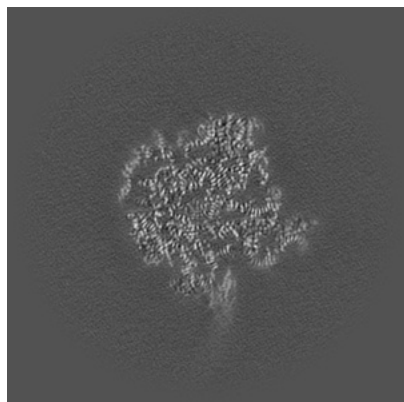
#### 6.1.2 Raw map



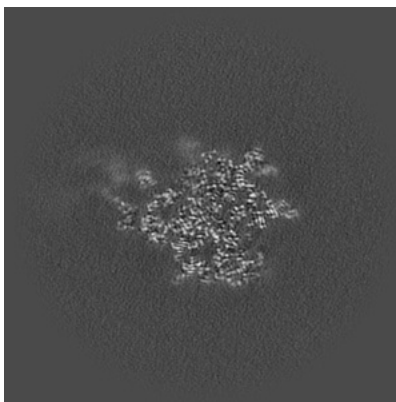
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

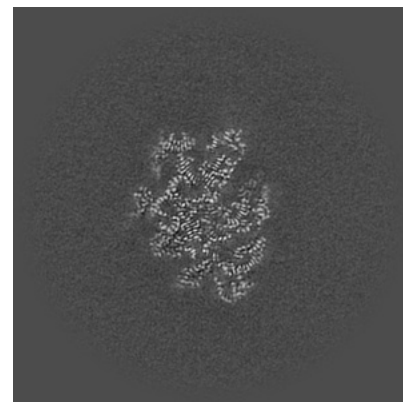
### 6.2.1 Primary map



X Index: 320

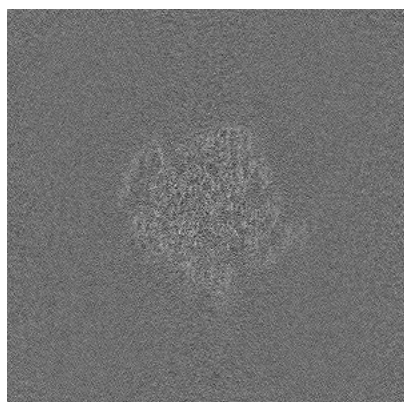


Y Index: 320

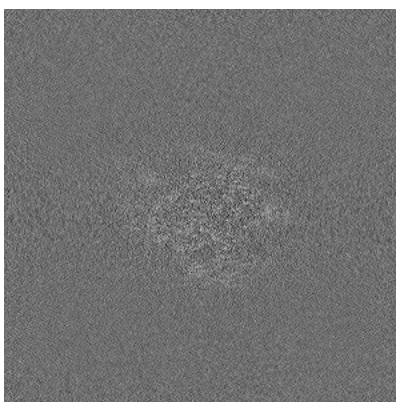


Z Index: 320

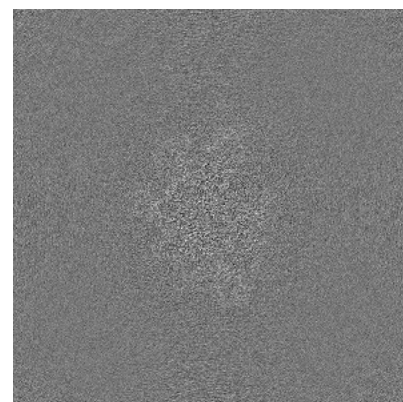
### 6.2.2 Raw map



X Index: 320



Y Index: 320

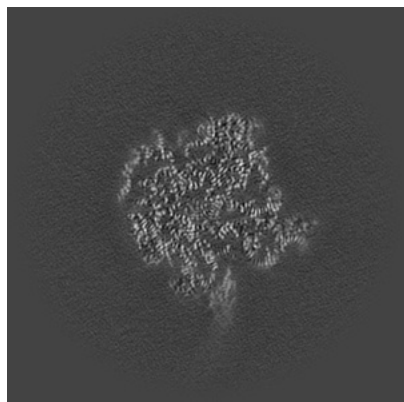


Z Index: 320

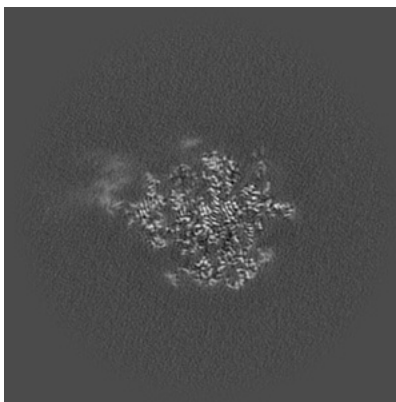
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

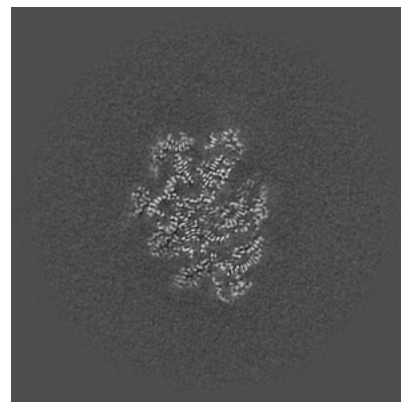
### 6.3.1 Primary map



X Index: 321

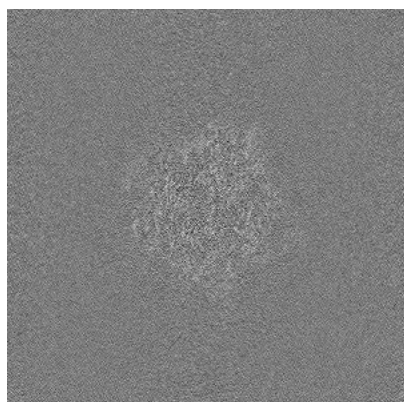


Y Index: 330

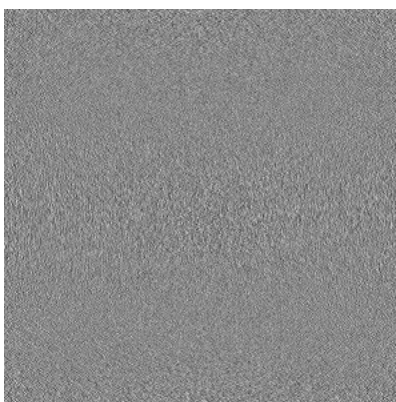


Z Index: 321

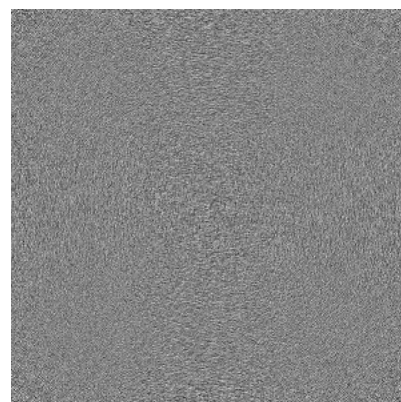
### 6.3.2 Raw map



X Index: 316



Y Index: 0

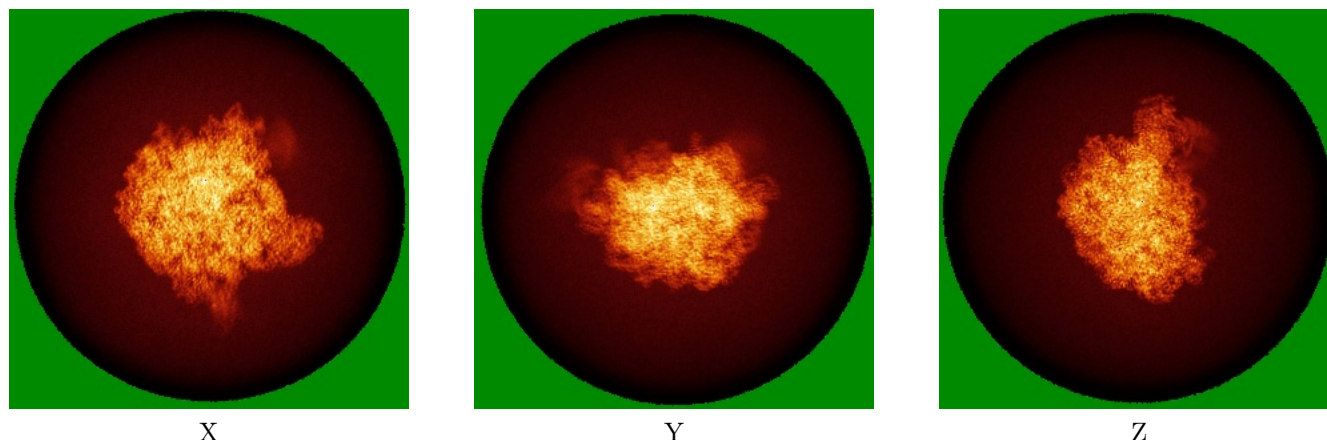


Z Index: 0

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

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

### 6.4.1 Primary map

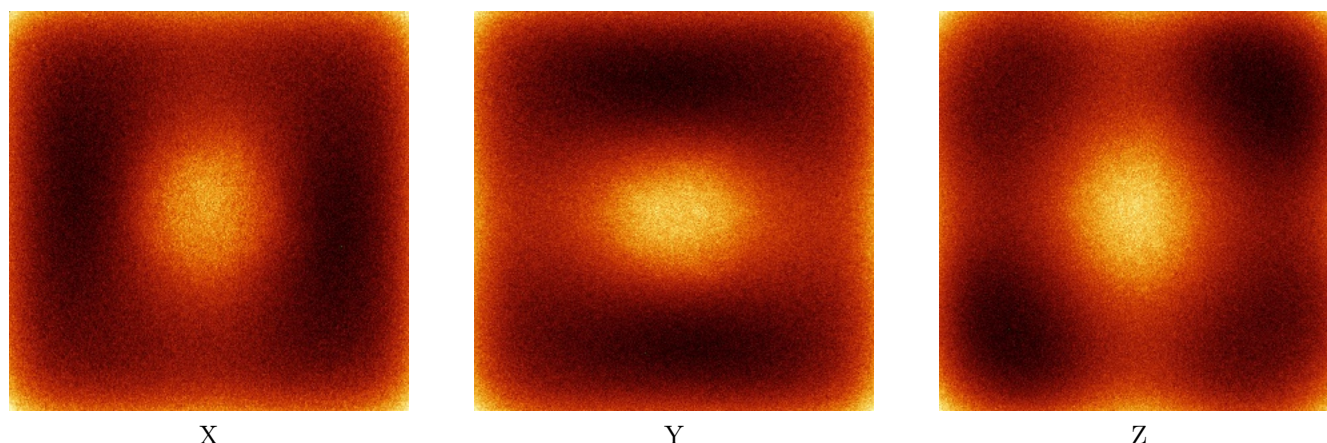


X

Y

Z

### 6.4.2 Raw map



X

Y

Z

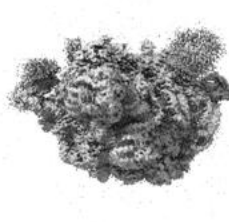
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



X



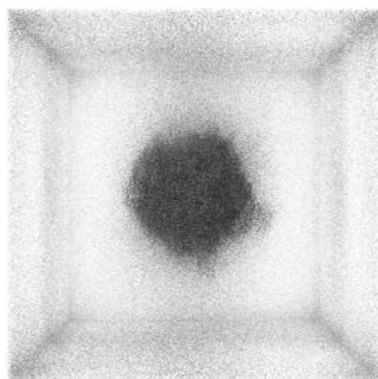
Y



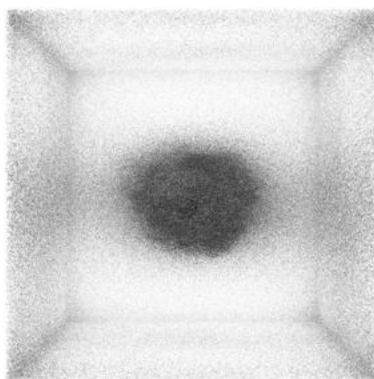
Z

The images above show the 3D surface view of the map at the recommended contour level 0.034. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

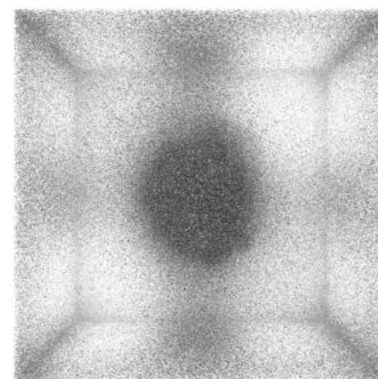
### 6.5.2 Raw map



X



Y



Z

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

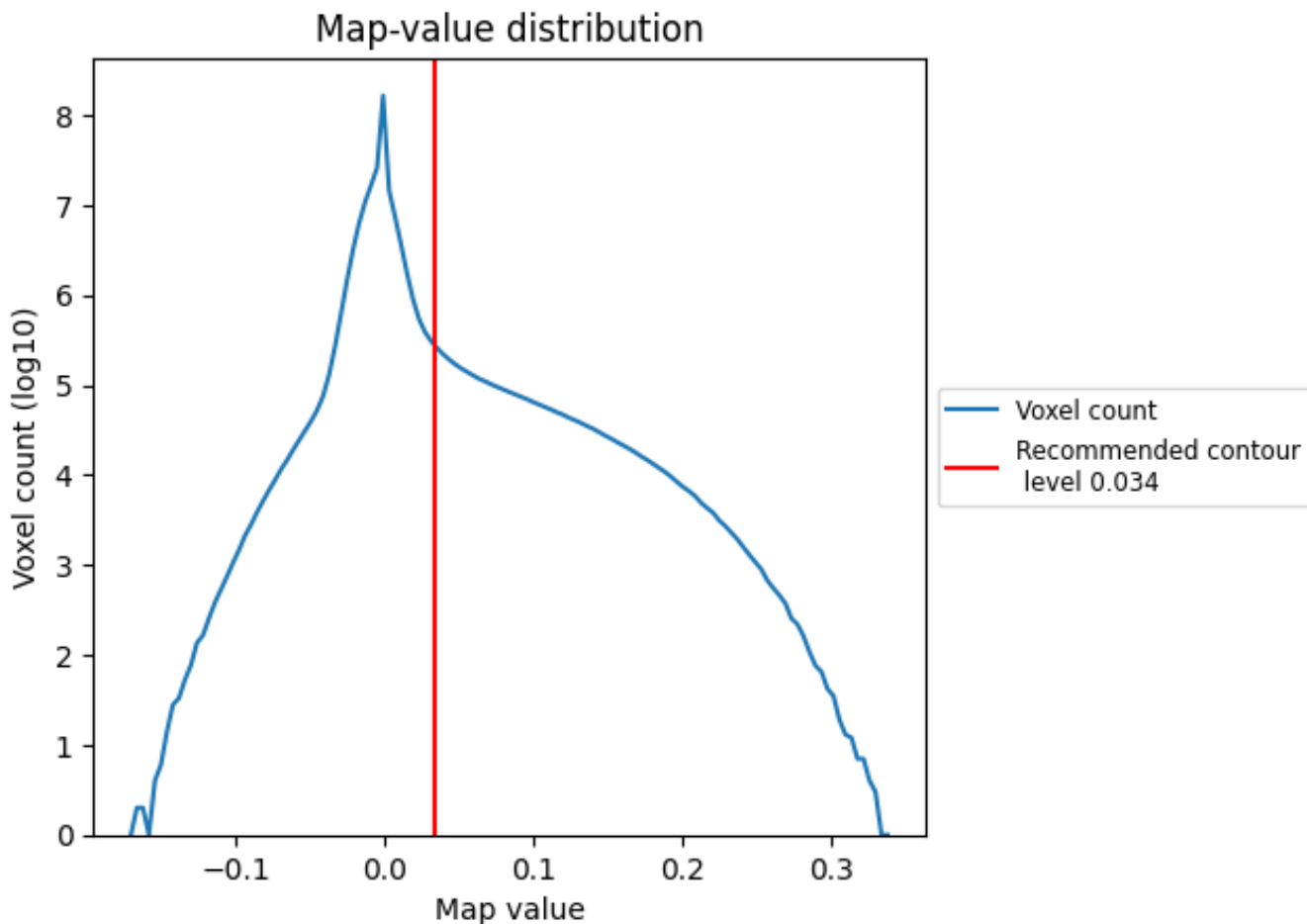
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

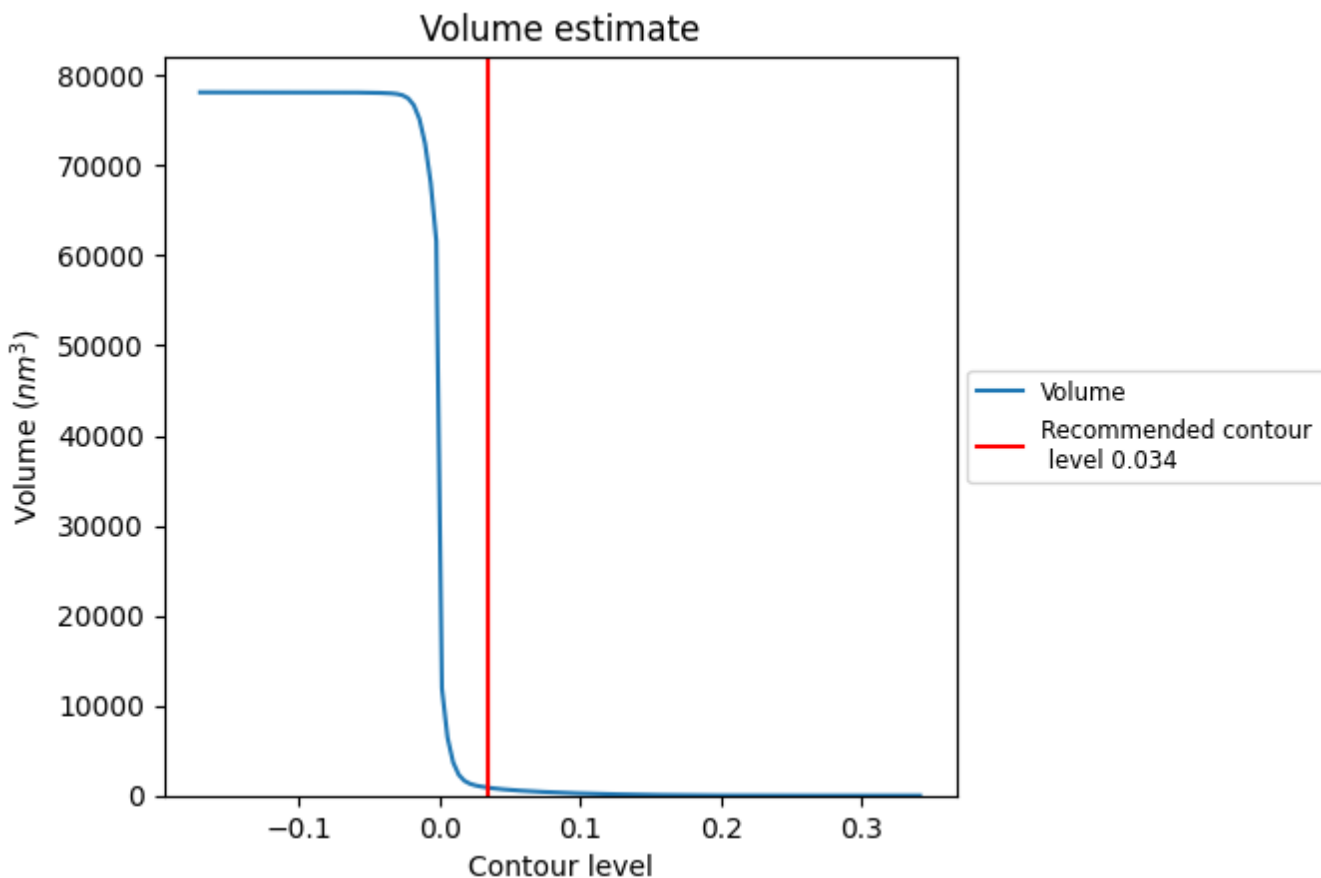
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



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

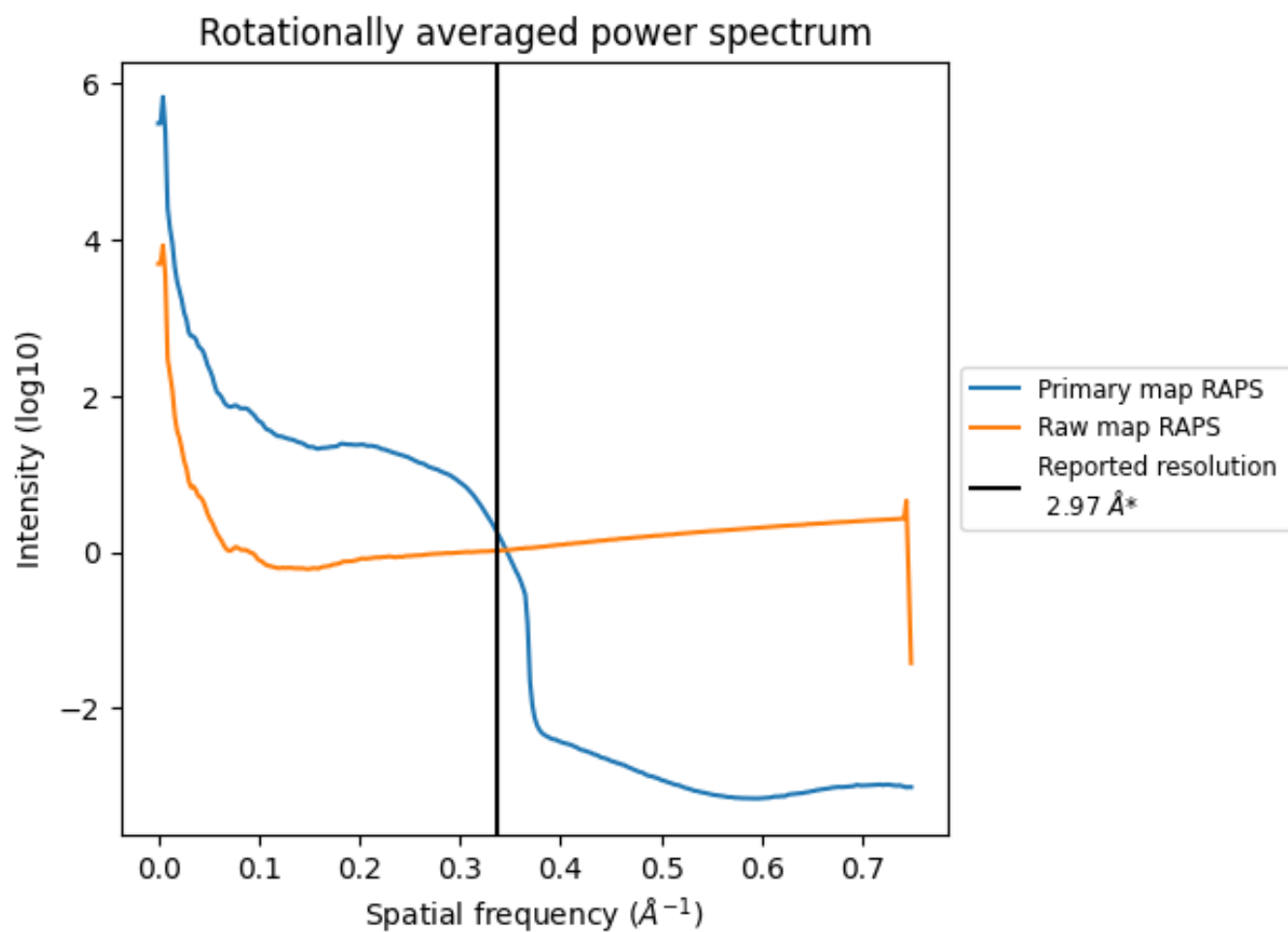
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 888 nm<sup>3</sup>; this corresponds to an approximate mass of 802 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

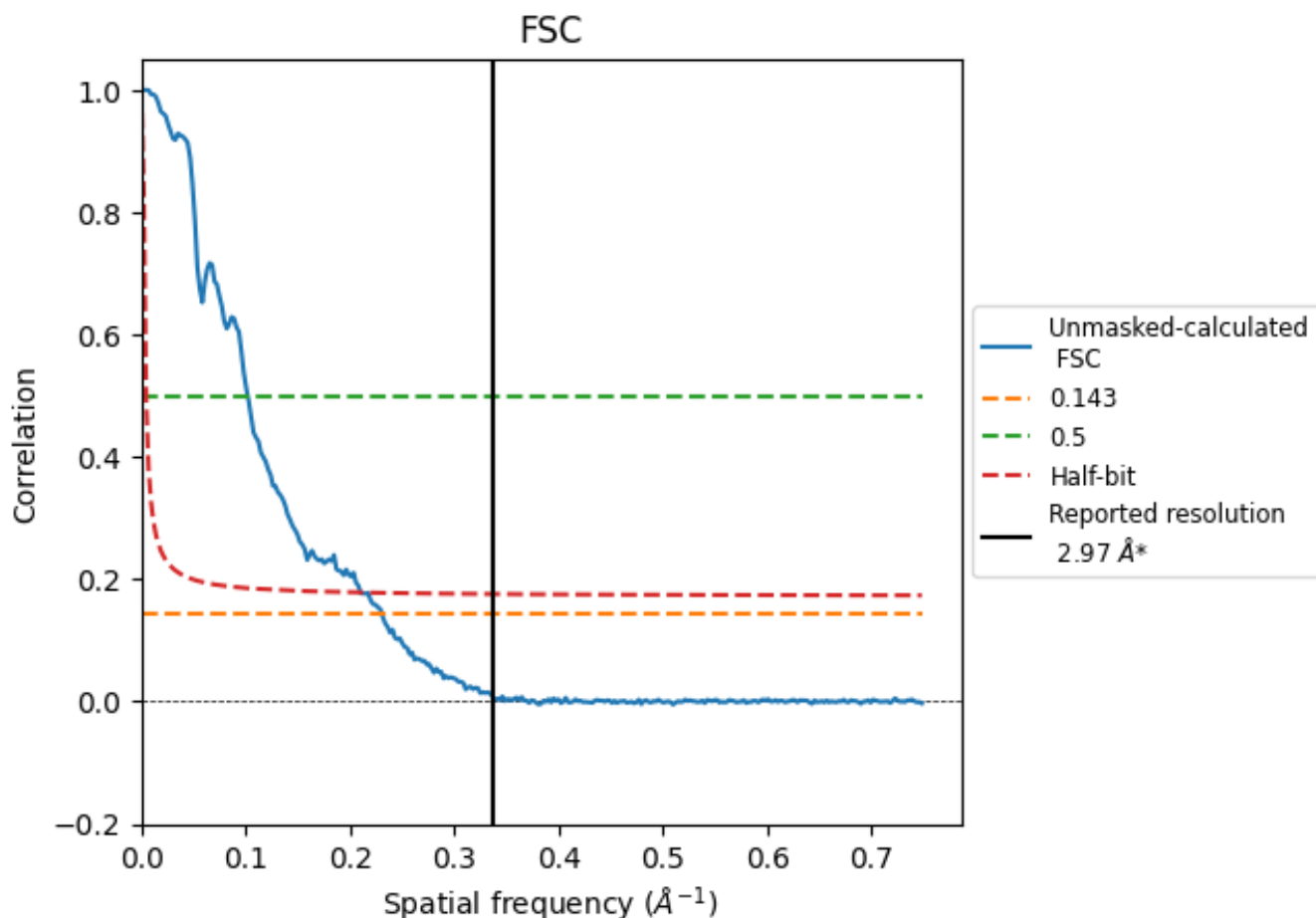


\*Reported resolution corresponds to spatial frequency of  $0.337 \text{ \AA}^{-1}$

## 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 0.337 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

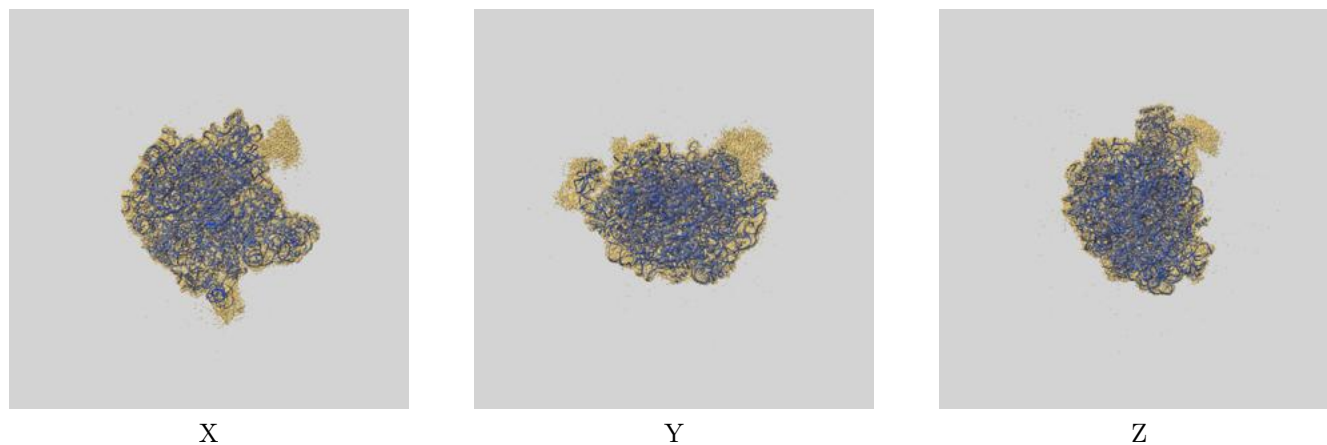
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.97	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.34	9.80	4.76

\*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 4.34 differs from the reported value 2.97 by more than 10 %

## 9 Map-model fit [i](#)

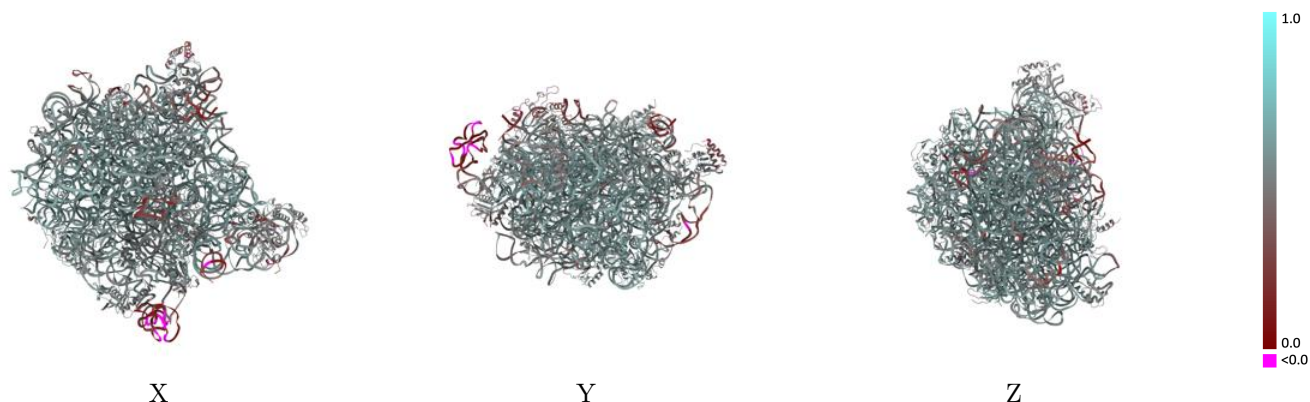
This section contains information regarding the fit between EMDB map EMD-62895 and PDB model 9L96. Per-residue inclusion information can be found in section 3 on page 11.

### 9.1 Map-model overlay [i](#)



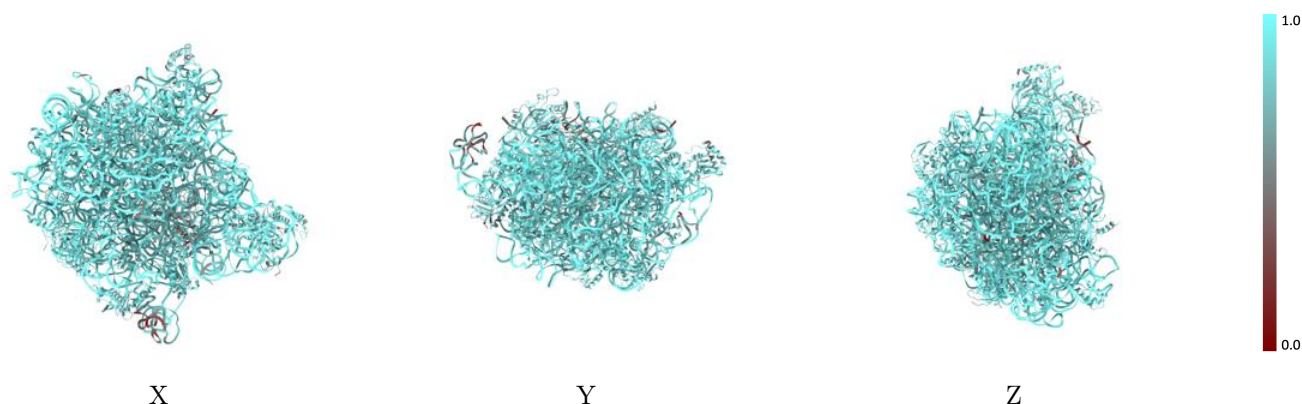
The images above show the 3D surface view of the map at the recommended contour level 0.034 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



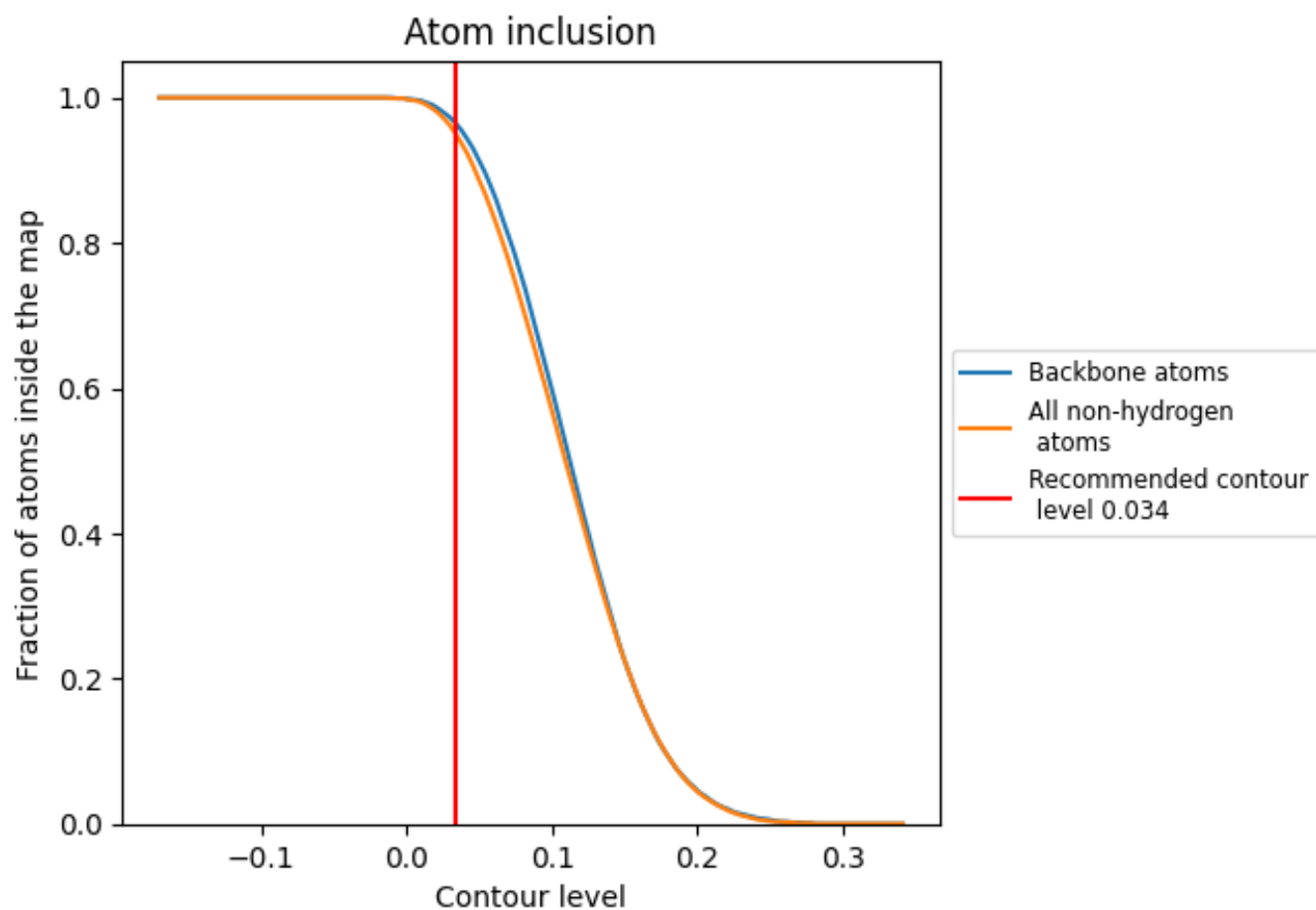
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.034).































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 95% 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 (0.034) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9490	 0.5430
0	 0.9710	 0.5450
9	 0.9790	 0.5420
A	 0.9510	 0.5450
E	 0.8460	 0.4540
F	 0.9390	 0.5580
G	 0.9750	 0.5760
H	 0.9350	 0.5540
I	 0.9200	 0.5250
J	 0.9370	 0.5480
K	 0.9550	 0.5910
L	 0.9430	 0.5790
M	 0.9250	 0.5330
N	 0.9280	 0.5590
O	 0.9300	 0.5530
P	 0.9190	 0.5500
Q	 0.9380	 0.5610
R	 0.8880	 0.5190
S	 0.9790	 0.5990
T	 0.9610	 0.5770
U	 0.9430	 0.5530
V	 0.9430	 0.5690
W	 0.9330	 0.5730
X	 0.7920	 0.4190
Y	 0.8510	 0.4970
a	 0.6660	 0.4890
b	 0.9260	 0.5460
c	 0.8570	 0.5130
d	 0.7990	 0.4560
e	 0.7600	 0.4700
f	 0.9440	 0.5620

