



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 02:40 PM UTC

PDB ID : 8VK7 / pdb_00008vk7
EMDB ID : EMD-43305
Title : Structure of Mycobacterium smegmatis 50S ribosomal subunit bound to HflX:50S-HflX-B
Authors : Majumdar, S.; Koripella, R.K.; Sharma, M.R.; Manjari, S.R.; Banavali, N.K.; Agrawal, R.K.
Deposited on : 2024-01-08
Resolution : 3.09 Å (reported)
Based on initial models : 6DZI, 5O61

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

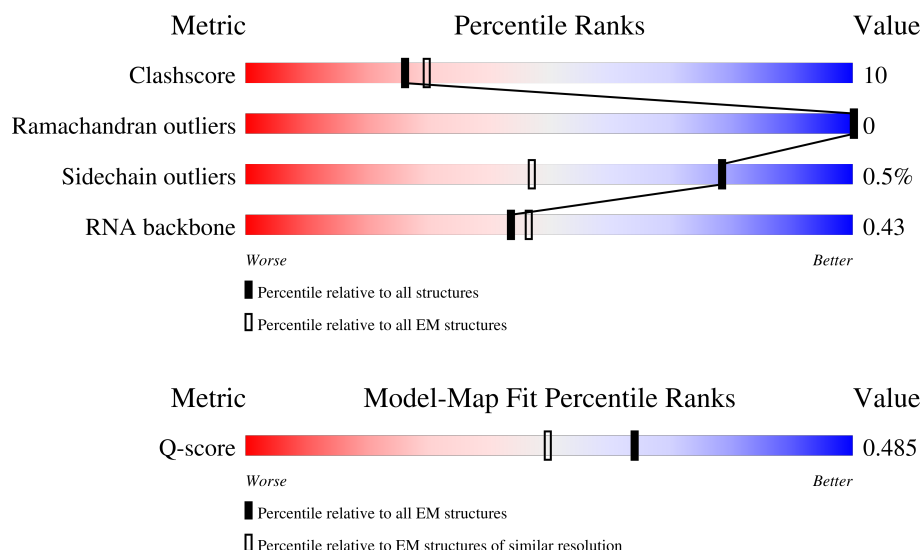
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.09 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.



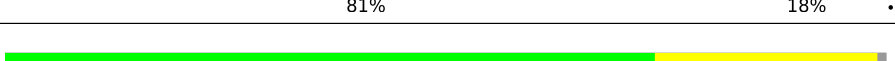
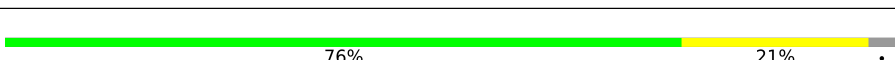
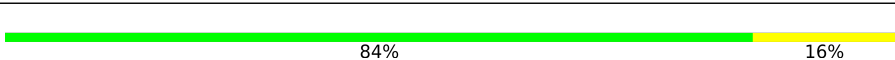
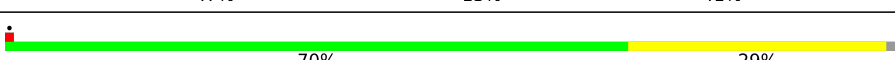
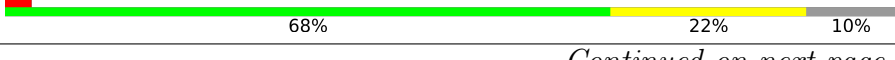
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14003 (2.59 - 3.59)

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

Mol	Chain	Length	Quality of chain
1	2	61	
2	3	24	

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Mol	Chain	Length	Quality of chain
3	4	470	
4	A	3120	
5	B	118	
6	C	278	
7	D	217	
8	E	215	
9	F	187	
10	G	179	
11	H	151	
12	I	175	
13	J	142	
14	K	147	
15	L	122	
16	M	147	
17	N	138	
18	O	199	
19	P	127	
20	Q	113	
21	R	129	
22	S	103	
23	T	153	
24	U	100	
25	V	105	
26	W	215	
27	X	88	

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Mol	Chain	Length	Quality of chain
28	Y	64	
29	Z	77	
30	b	57	
31	c	55	
32	d	47	
33	e	64	
34	f	37	
35	g	75	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
36	GCP	4	501	-	-	X	-

2 Entry composition

There are 36 unique types of molecules in this entry. The entry contains 96832 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 protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	2	59	Total	C	N	O	0	0
			474	292	95	87		

- Molecule 2 is a protein called 50S Ribosomal Protein L37.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	3	23	Total	C	N	O	0	0
			189	111	50	28		

- Molecule 3 is a protein called GTPase HflX.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	4	468	Total	C	N	O	S	0	0
			3539	2187	651	694	7		

- Molecule 4 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	2950	Total	C	N	O	P	0	0
			63364	28241	11658	20515	2950		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	114	Total	C	N	O	P	0	0
			2438	1088	452	784	114		

- Molecule 6 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	275	Total	C	N	O	S	0	0
			2110	1298	438	370	4		

- Molecule 7 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	214	Total	C	N	O	S	0	0
			1587	982	310	290	5		

- Molecule 8 is a protein called 50S Ribosomal Protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	209	Total	C	N	O	S	0	0
			1569	969	295	303	2		

- Molecule 9 is a protein called 50S Ribosomal Protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	182	Total	C	N	O	S	0	0
			1445	907	271	261	6		

- Molecule 10 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	176	Total	C	N	O	S	0	0
			1348	845	249	253	1		

- Molecule 11 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	H	151	Total	C	N	O	S	0	0
			1018	635	188	194	1		

- Molecule 12 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	I	126	Total	C	N	O	S	0	0
			918	580	156	180	2		

- Molecule 13 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	J	133	Total	C	N	O	S	0	0
			990	625	175	187	3		

- Molecule 14 is a protein called 50S Ribosomal Protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	K	146	Total	C	N	O	S	0	0
			1130	722	207	200	1		

- Molecule 15 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	L	122	Total	C	N	O	S	0	0
			938	586	179	170	3		

- Molecule 16 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	M	145	Total	C	N	O	S	0	0
			1078	676	205	194	3		

- Molecule 17 is a protein called Large ribosomal subunit protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	N	136	Total	C	N	O	S	0	0
			1092	690	213	187	2		

- Molecule 18 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	O	118	Total	C	N	O	S	0	0
			928	583	180	163	2		

- Molecule 19 is a protein called 50S Ribosomal Protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	P	126	Total	C	N	O	S	0	0
			956	586	199	171			

- Molecule 20 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Q	113	Total	C	N	O	S	0	0
			907	570	171	165	1		

- Molecule 21 is a protein called 50S Ribosomal Protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	R	124	Total	C	N	O	0	0
			988	613	203	172		

- Molecule 22 is a protein called 50S Ribosomal Protein L21.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	S	100	Total	C	N	O	0	0
			754	478	137	139		

- Molecule 23 is a protein called 50S Ribosomal Protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	T	114	Total	C	N	O	0	0
			873	543	171	159		

- Molecule 24 is a protein called 50S Ribosomal Protein L23.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	U	97	Total	C	N	O	0	0
			756	479	138	139		

- Molecule 25 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	V	95	Total	C	N	O	S	0	0
			719	448	135	134	2		

- Molecule 26 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	W	95	Total	C	N	O	0	0
			735	452	149	134		

- Molecule 27 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	X	79	Total	C	N	O	0	0
			586	361	123	102		

- Molecule 28 is a protein called 50S Ribosomal Protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Y	63	Total	C	N	O	S	0	0
			470	283	103	80	4		

- Molecule 29 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Z	64	Total	C	N	O	S	0	0
			531	324	103	103	1		

- Molecule 30 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	b	54	Total	C	N	O	S	0	0
			423	260	93	69	1		

- Molecule 31 is a protein called 50S Ribosomal Protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	c	49	Total	C	N	O	S	0	0
			405	248	82	71	4		

- Molecule 32 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	d	46	Total	C	N	O	S	0	0
			377	225	97	54	1		

- Molecule 33 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	e	63	Total	C	N	O	0	0
			502	302	115	85		

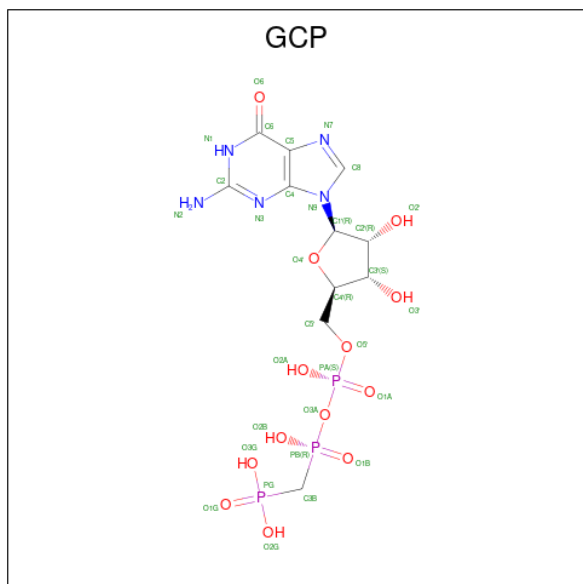
- Molecule 34 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	f	37	Total	C	N	O	S	0	0
			299	181	66	47	5		

- Molecule 35 is a protein called 50S Ribosomal Protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	g	48	Total	C	N	O	S	0	0
			364	225	63	71	5		

- Molecule 36 is PHOSPHOMETHYLPHOSPHONIC ACID GUANYLATE ESTER (CCD ID: GCP) (formula: $C_{11}H_{18}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).

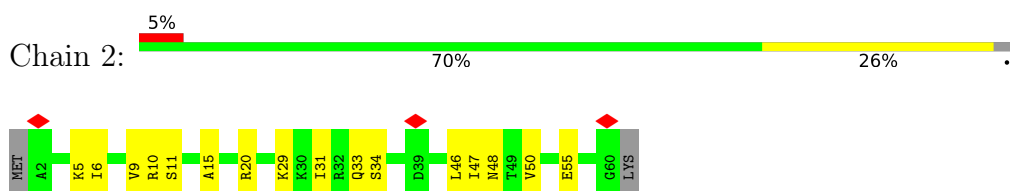


Mol	Chain	Residues	Atoms					AltConf
36	4	1	Total	C	N	O	P	0
			32	11	5	13	3	

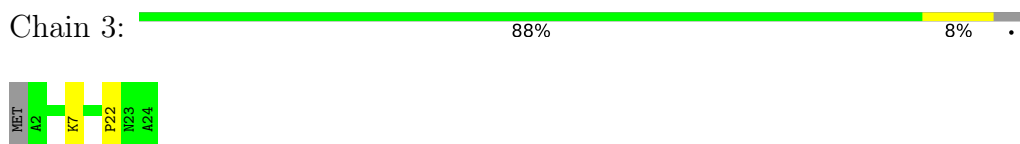
3 Residue-property plots

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

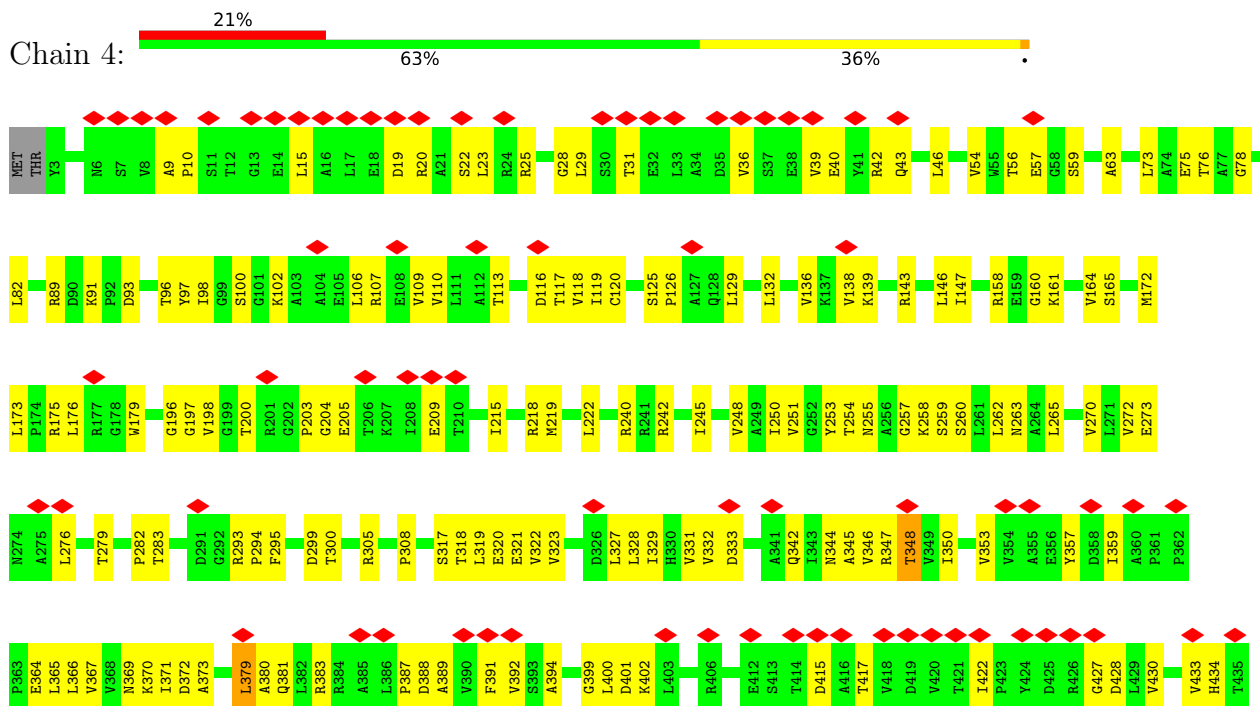
- Molecule 1: 50S ribosomal protein L30

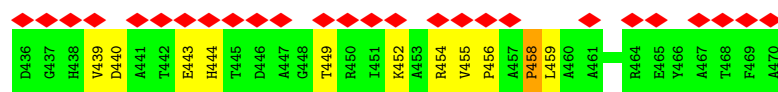


- Molecule 2: 50S Ribosomal Protein L37



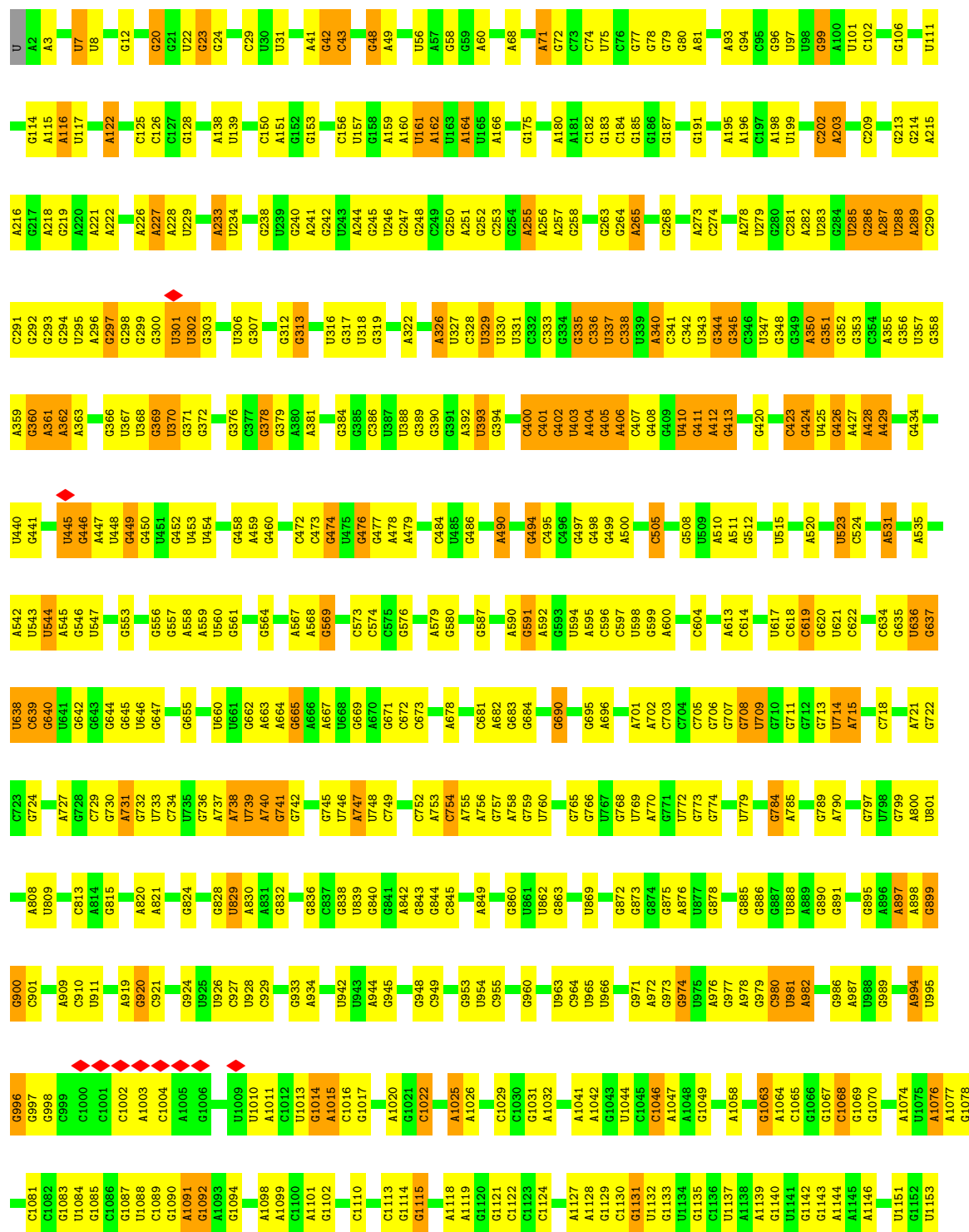
- Molecule 3: GTPase HflX



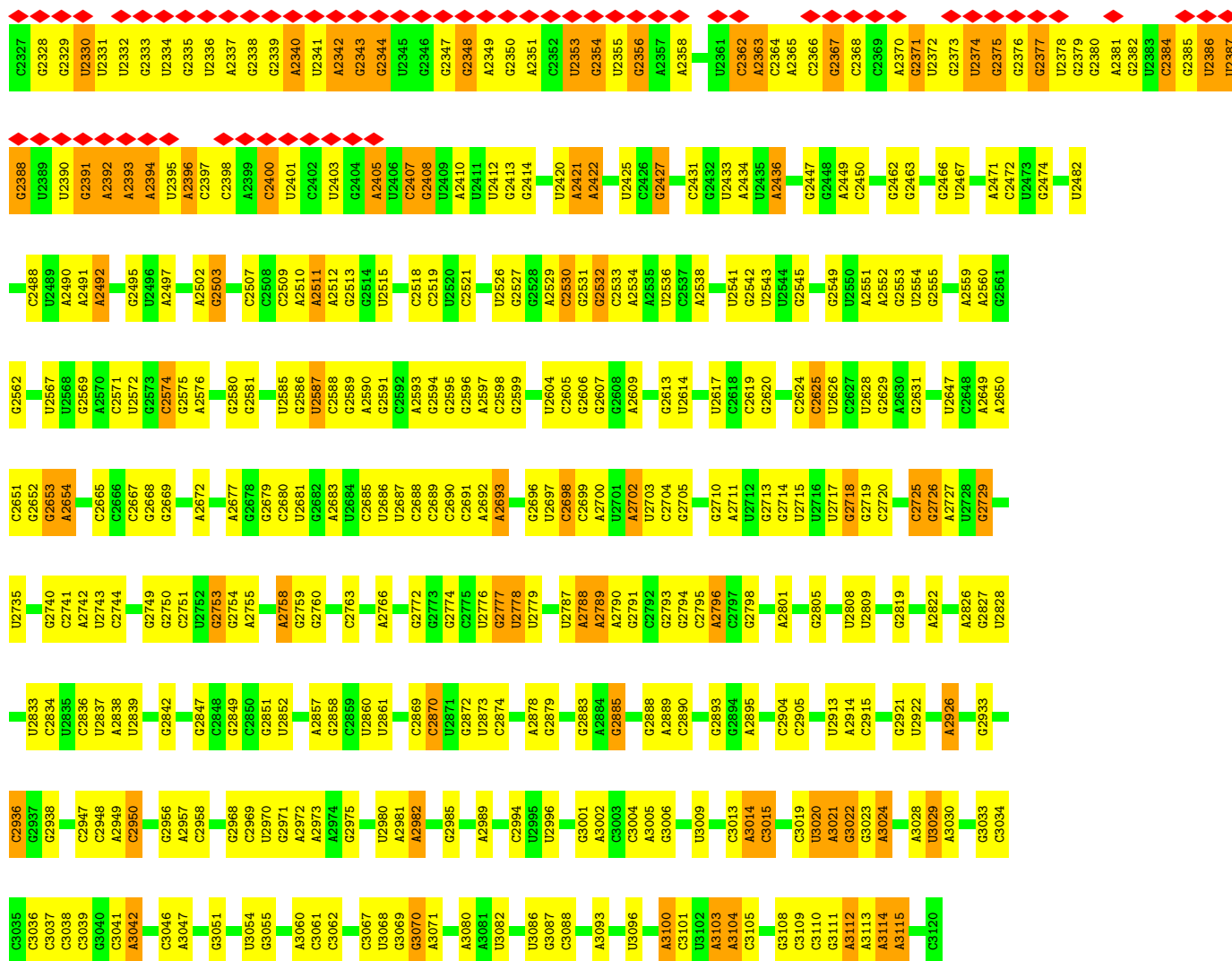


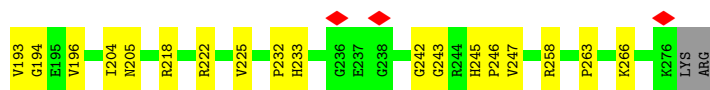
• Molecule 4: 23S ribosomal RNA

Chain A: 49% 35% 10% 5%



C2224	A2151	C2023	G1917	A1832	G1726	U1641	G1507	G1411	C1321	U1223	G1154
A2225	A2152	G2024	G1917	C1833	A1727	G1642	G1510	A1415	C1322	G1224	C1155
G2228	G2153	C2025	G1921	C1834	U1728	G1643	A1511	A1416	G1323	G1225	A1156
G2234	G2154	A2026	G1921	C1835	A1729	G1644	U1512	A1417	G1324	U1226	G1157
G2235	G2155	G2031	C1927	G1837	U1731	G1645	C1513	A1418	G1326	G1227	U1158
G2236	A2156	A2032	C1930	G1845	U1732	A1648	C1514	A1419	A1327	G1228	G1159
C2243	G2157	U2033	C1930	G1846	U1735	C1649	G1515	G1425	A1328	A1229	G1160
A2244	G2158	G2034	U1931	G1847	G1736	G1650	G1516	A1426	G1329	A1230	C1161
C2245	G2159	A2035	U1932	A1848	A1737	C1651	A1517	U1427	C1330	G1230	G1162
U2246	A2160	G2036	G1933	A1849	U1737	G1652	A1518	G1428	C1331	U1235	G1165
G2251	A2161	U2037	U1937	G1850	G1743	G1653	G1522	A1429	U1335	G1236	A1166
A2254	A2162	A2038	G1938	G1851	A1744	A1655	G1529	C1430	A1336	U1237	C1167
A2255	U2163	C2043	U1945	A1852	C1753	G1656	U1530	G1434	G1337	G1238	A1168
G2256	U2164	U2044	U1946	A1853	G1754	A1657	G1531	A1435	U1338	G1239	A1169
A2257	C2165	G2045	U1947	U1854	A1755	U1665	G1532	G1436	G1339	G1240	A1172
U2261	C2166	A2046	U1947	C1855	G1756	U1669	G1533	A1437	A1340	G1243	G1173
G2262	U2167	G1950	G1950	U1857	U1757	G1670	C1534	G1438	U1341	U1244	G1174
G2263	U2168	C2049	C1954	A1858	G1758	A1673	C1535	A1442	G1342	U1245	A1175
C2267	G2169	U2051	A1955	A1859	A1759	U1674	U1536	G1443	A1344	U1246	G1176
A2274	U2170	C2052	A1956	G1860	G1762	U1675	U1537	G1444	G1350	U1247	U1177
C2279	C2171	C2053	A1957	G1861	G1763	G1676	G1538	U1449	A1351	U1248	U1178
G2280	U2175	C2054	G1957	U1864	U1767	A1677	G1541	C1449	A1352	U1250	U1179
A2284	A2176	G2055	A1972	A1865	U1768	A1679	A1542	G1453	G1357	U1251	G1180
G2285	C2177	C2056	C1973	C1866	C1768	A1680	A1543	G1454	U1358	G1252	C1181
A2286	U2178	C2057	A1974	G1867	G1769	U1681	U1544	G1455	G1362	G1253	U1183
C2287	U2180	C2058	A1975	U1870	G1770	G1682	C1545	G1456	A1363	G1254	U1184
G2288	C2181	C2059	A1976	A1871	U1771	A1683	A	A1457	U1364	G1256	A1187
C2289	U2182	C2060	A1977	A1872	G1772	C1687	G	G1458	G1365	U1259	A1188
C2290	G2183	C2061	C1977	A1873	U1773	U1687	C	U1459	G1366	G1260	G1189
A2294	A2184	C2062	U1981	U1875	G1780	A1691	G	A1464	A1367	A1261	A1191
C2295	C2185	C2063	G1986	U1876	U1786	G1692	G	G1465	G1368	G1192	G1192
U2301	U2186	C2064	A1987	U1877	A1787	C1693	U	G1466	A1369	G1268	C1193
G2302	G2187	C2065	A1988	G1878	G1788	C1694	U	U1467	U1370	C1269	C1194
U2314	C2188	C2066	C1988	G1879	A1789	U1695	C	A1468	G1371	G1270	A1195
U2315	A2190	C2067	A1989	U1880	C1797	G1696	U	A1473	G1379	C1271	C1196
G2316	C2191	C2068	A1990	U1881	U1798	U1697	A	G1478	A1380	G1272	C1197
U2317	U2192	C2069	C1991	A1882	G1799	G1703	C	G1479	G1381	A1275	G1198
G2318	A2193	C2070	U1996	G1883	A1803	U1704	C	A1480	A1386	G1287	A1202
U2319	C2194	C2071	A1997	G1884	G1804	C1705	A	C1481	U1387	C1287	A1203
U2320	U2195	C2072	A2001	G1885	G1805	A1706	U	G1485	C1393	G1291	G1205
U2321	G2196	C2073	A2002	A1886	A1806	A1707	C	U1486	A1394	U1292	A1206
A2324	C2197	C2074	A2003	A1887	C1807	A1710	C	U1487	G1400	G1293	G1207
U2325	G2198	C2075	G1892	G1889	G1808	G1711	A	G1488	C1403	U1295	U1208
A2326	U2199	C2076	C1893	G1890	C1809	U1712	A	U1489	U1406	G1296	G1209
	C2200	C2077	C1894	U1891	A1831	U1713	C	A1493	U1407	C1210	C1211
	A2221	C2078	U1911	U1911	G1831	U1714	C	U1494	G1408	A1304	U1212
		C2079	U1911	U1911	G1832	U1715	C	U1499	U1409	G1305	A1213
		C2080	U1911	U1911	G1833	U1716	C	A1500	U1410	C1314	A1214
		C2081	U1911	U1911	G1834	U1717	C		U1411	G1315	U1215
		C2082	U1911	U1911	G1835	U1718	C		U1412		G1217
		C2083	U1911	U1911	G1836	U1719	C		U1413		
		C2084	U1911	U1911	G1837	U1720	C		U1414		
		C2085	U1911	U1911	G1838	U1721	C		U1415		
		C2086	U1911	U1911	G1839	U1722	C		U1416		
		C2087	U1911	U1911	G1840	U1723	C		U1417		
		C2088	U1911	U1911	G1841	U1724	C		U1418		
		C2089	U1911	U1911	G1842	U1725	C		U1419		
		C2090	U1911	U1911	G1843	U1726	C		U1420		
		C2091	U1911	U1911	G1844	U1727	C		U1421		
		C2092	U1911	U1911	G1845	U1728	C		U1422		
		C2093	U1911	U1911	G1846	U1729	C		U1423		
		C2094	U1911	U1911	G1847	U1730	C		U1424		
		C2095	U1911	U1911	G1848	U1731	C		U1425		
		C2096	U1911	U1911	G1849	U1732	C		U1426		
		C2097	U1911	U1911	G1850	U1733	C		U1427		
		C2098	U1911	U1911	G1851	U1734	C		U1428		
		C2099	U1911	U1911	G1852	U1735	C		U1429		
		C2100	U1911	U1911	G1853	U1736	C		U1430		
		C2101	U1911	U1911	G1854	U1737	C		U1431		
		C2102	U1911	U1911	G1855	U1738	C		U1432		
		C2103	U1911	U1911	G1856	U1739	C		U1433		
		C2104	U1911	U1911	G1857	U1740	C		U1434		
		C2105	U1911	U1911	G1858	U1741	C		U1435		
		C2106	U1911	U1911	G1859	U1742	C		U1436		
		C2107	U1911	U1911	G1860	U1743	C		U1437		
		C2108	U1911	U1911	G1861	U1744	C		U1438		
		C2109	U1911	U1911	G1862	U1745	C		U1439		
		C2110	U1911	U1911	G1863	U1746	C		U1440		
		C2111	U1911	U1911	G1864	U1747	C		U1441		
		C2112	U1911	U1911	G1865	U1748	C		U1442		
		C2113	U1911	U1911	G1866	U1749	C		U1443		
		C2114	U1911	U1911	G1867	U1750	C		U1444		
		C2115	U1911	U1911	G1868	U1751	C		U1445		
		C2116	U1911	U1911	G1869	U1752	C		U1446		
		C2117	U1911	U1911	G1870	U1753	C		U1447		
		C2118	U1911	U1911	G1871	U1754	C		U1448		
		C2119	U1911	U1911	G1872	U1755	C		U1449		
		C2120	U1911	U1911	G1873	U1756	C		U1450		
		C2121	U1911	U1911	G1874	U1757	C		U1451		
		C2122	U1911	U1911	G1875	U1758	C		U1452		
		C2123	U1911	U1911	G1876	U1759	C		U1453		
		C2124	U1911	U1911	G1877	U1760	C		U1454		
		C2125	U1911	U1911	G1878	U1761	C		U1455		
		C2126	U1911	U1911	G1879	U1762	C		U1456		
		C2127	U1911	U1911	G1880	U1763	C		U1457		
		C2128	U1911	U1911	G1881	U1764	C		U1458		
		C2129	U1911	U1911	G1882	U1765	C		U1459		
		C2130	U1911	U1911	G1883	U1766	C		U1460		
		C2131	U1911	U1911	G1884	U1767	C		U1461		
		C2132	U1911	U1911	G1885	U1768	C		U1462		
		C2133	U1911	U1911	G1886	U1769	C		U1463		
		C2134	U1911	U1911	G1887	U1770	C		U1464		
		C2135	U1911	U1911	G1888	U1771	C		U1465		
		C2136	U1911	U1911	G1889	U1772	C		U1466		
		C2137	U1911	U1911	G1890	U1773	C		U1467		
		C2138	U1911	U1911	G1891	U1774	C		U1468		
		C2139	U1911	U1911	G1892	U1775	C		U1469		
		C2140	U1911	U1911	G1893	U1776	C		U1470		
		C2141	U1911	U1911	G1894	U1777	C		U1471		
		C2142	U1911	U1911	G1895	U1778	C		U1472		
		C2143	U1911	U1911	G1896	U1779	C		U1473		
		C2144	U1911	U1911	G1897	U1780	C		U1474		
		C2145	U1911	U1911	G1898	U1781	C		U1475		
		C2146	U1911	U1911	G1899	U1782	C		U1476		
		C2147	U1911	U1911	G1900	U1783	C		U1477		
		C2148	U1911	U1911	G1901	U1784	C		U1478		
		C2149	U1911	U1911	G1902	U1785	C		U1479		
		C2150	U1911	U1911	G1903	U1786	C		U1480		
		C2151	U1911	U1911	G1904	U1787	C		U1481		
		C2152	U1911	U1911	G1905	U1788	C		U1482		
		C2153	U1911	U1911	G1906	U1789	C		U1483		
		C2154	U1911	U1911	G1907	U1790	C		U1484		
		C2155	U1911	U1911	G1908	U1791	C		U1485		
		C2156	U1911	U1911	G1909	U1792	C		U1486		
		C2157	U1911	U1911	G1910	U1793	C		U1487		
		C2158	U1911	U1911	G1911	U1794	C		U1488		
		C2159	U1911	U1911	G1912	U1795					





• Molecule 7: 50S ribosomal protein L3

Chain D: 73% 25%



• Molecule 8: 50S Ribosomal Protein L4

Chain E: 76% 21%



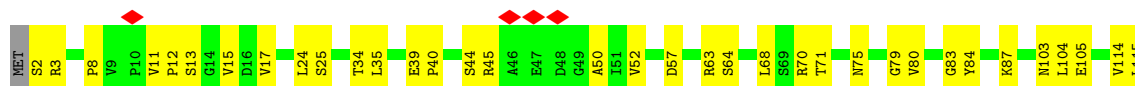
• Molecule 9: 50S Ribosomal Protein L5

Chain F: 10% 68% 29%

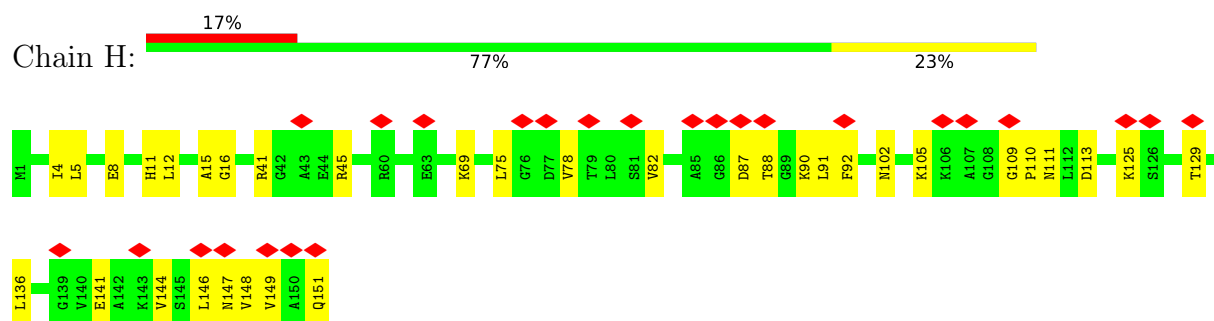


• Molecule 10: 50S ribosomal protein L6

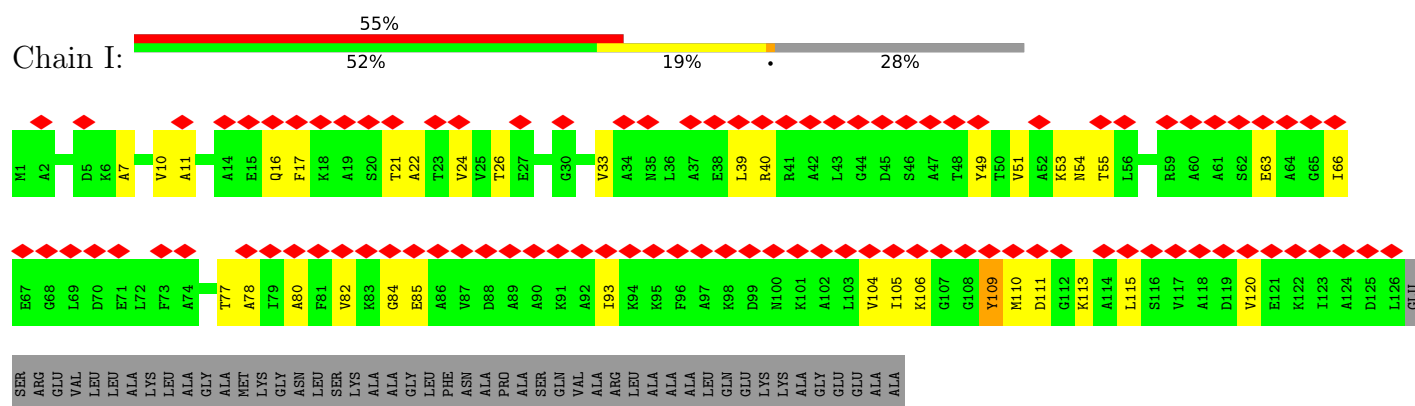
Chain G: 72% 27%



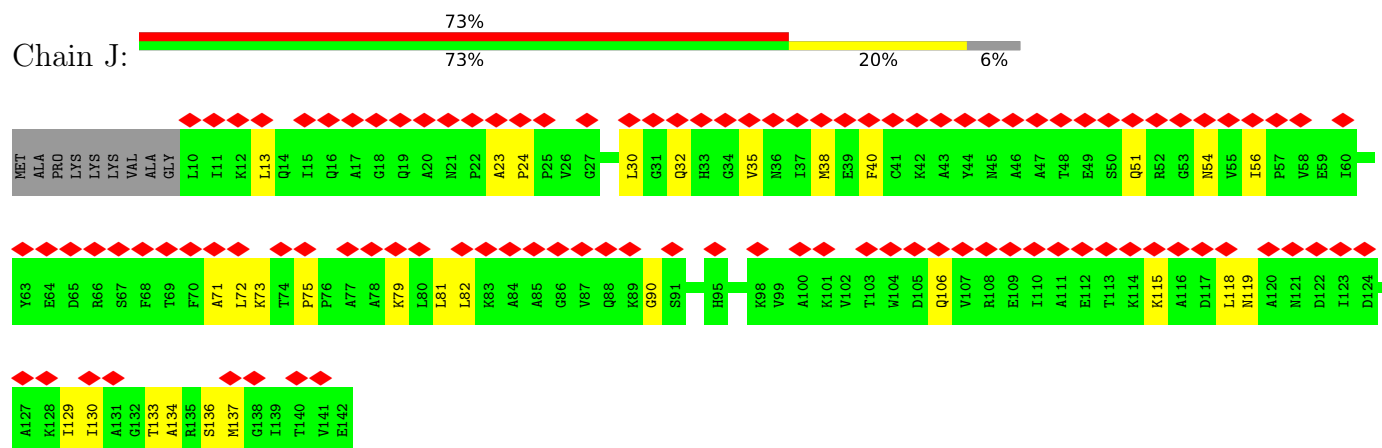
- Molecule 11: 50S ribosomal protein L9



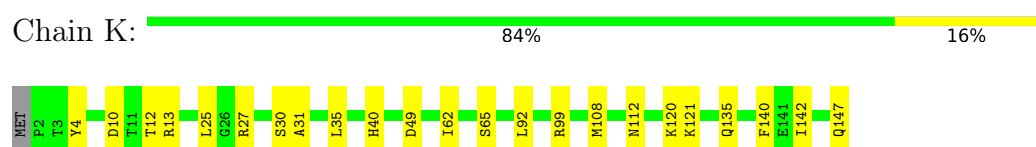
- Molecule 12: 50S ribosomal protein L10



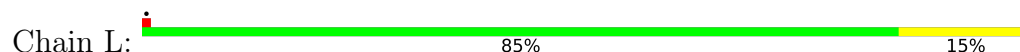
- Molecule 13: 50S ribosomal protein L11



- Molecule 14: 50S Ribosomal Protein L13



- Molecule 15: 50S ribosomal protein L14





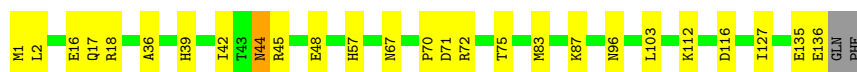
- Molecule 16: 50S ribosomal protein L15

Chain M: 77% 22%



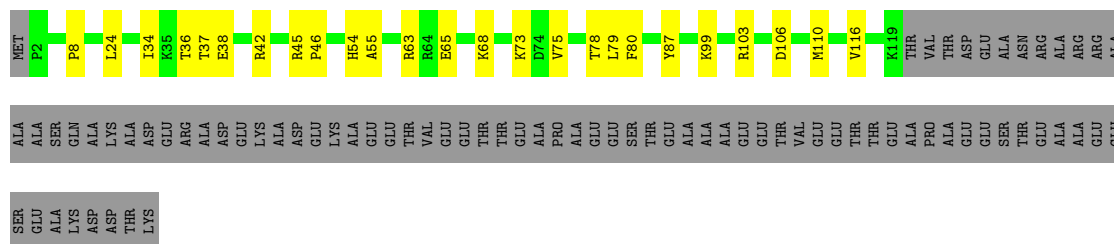
- Molecule 17: Large ribosomal subunit protein uL16

Chain N: 80% 18%



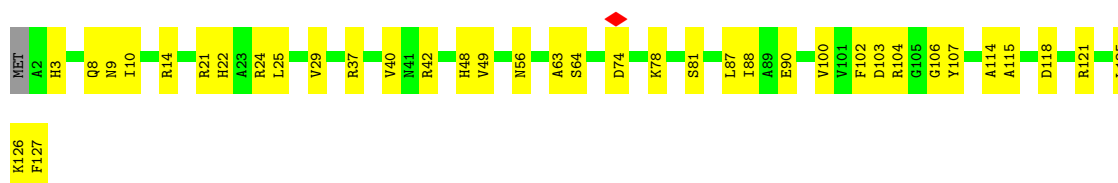
- Molecule 18: 50S ribosomal protein L17

Chain O: 47% 13% 41%



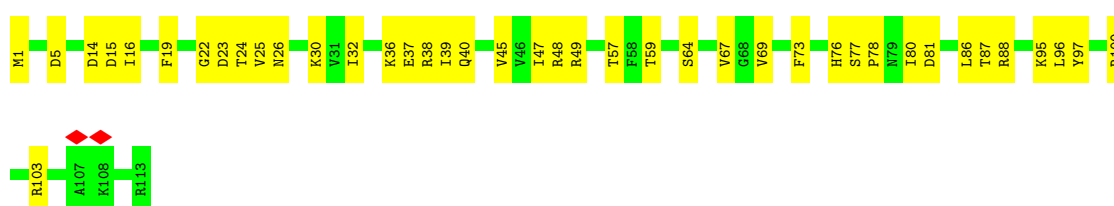
- Molecule 19: 50S Ribosomal Protein L18

Chain P: 70% 29%

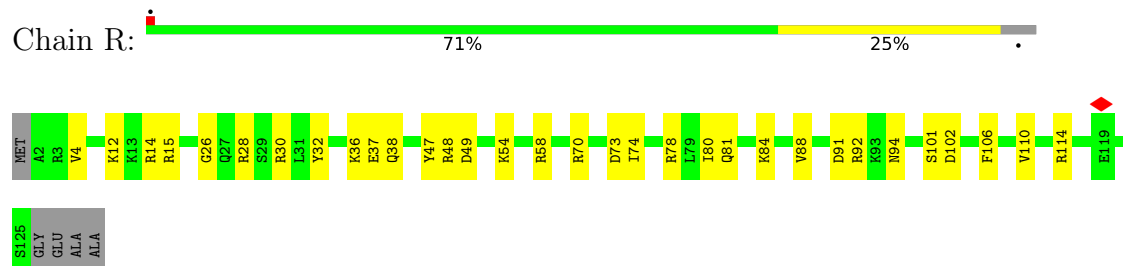


- Molecule 20: 50S ribosomal protein L19

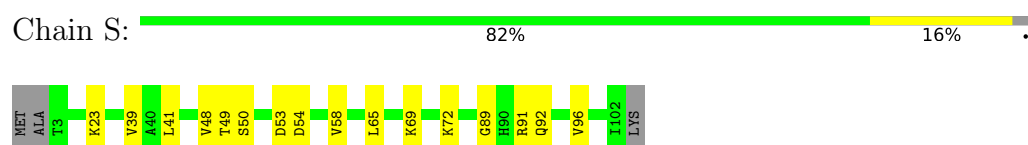
Chain Q: 64% 36%



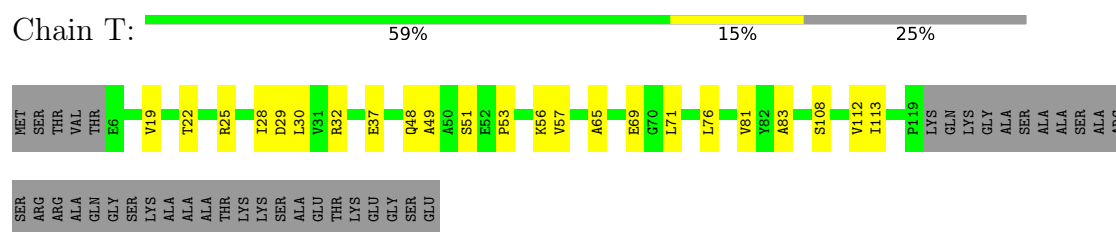
- Molecule 21: 50S Ribosomal Protein L20



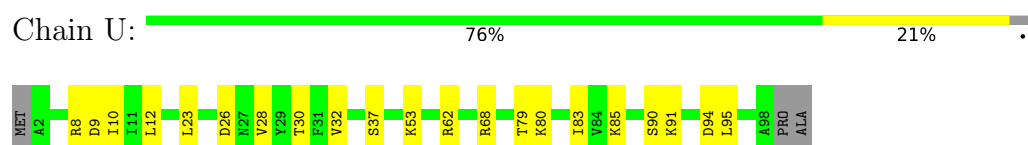
- Molecule 22: 50S Ribosomal Protein L21



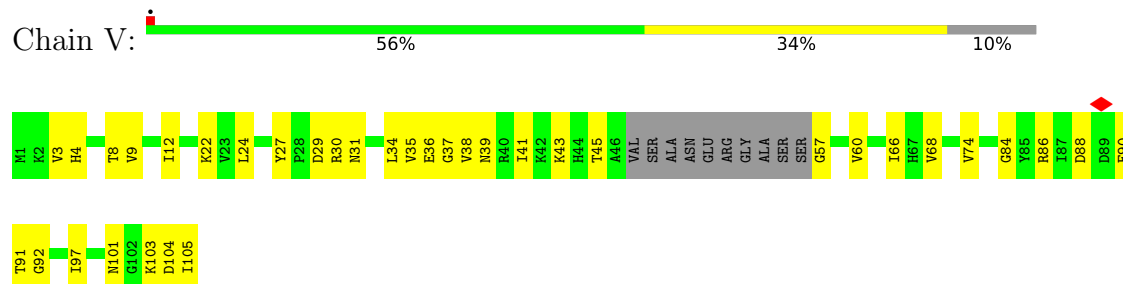
- Molecule 23: 50S Ribosomal Protein L22



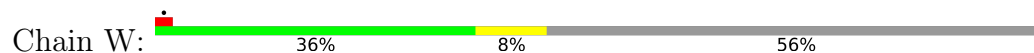
- Molecule 24: 50S Ribosomal Protein L23



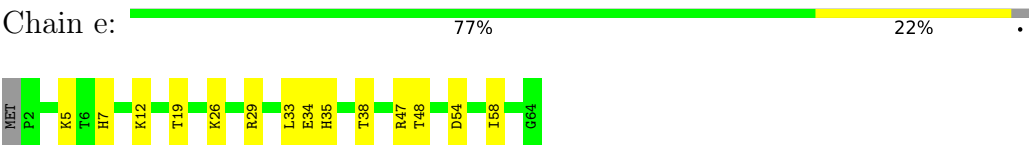
- Molecule 25: 50S ribosomal protein L24



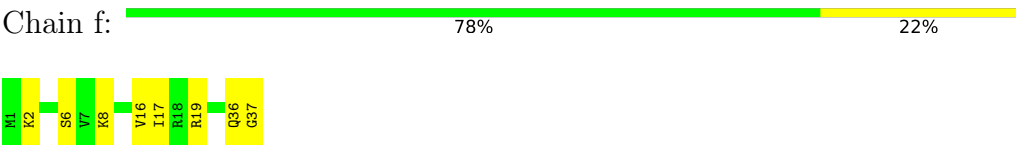
- Molecule 26: 50S ribosomal protein L25



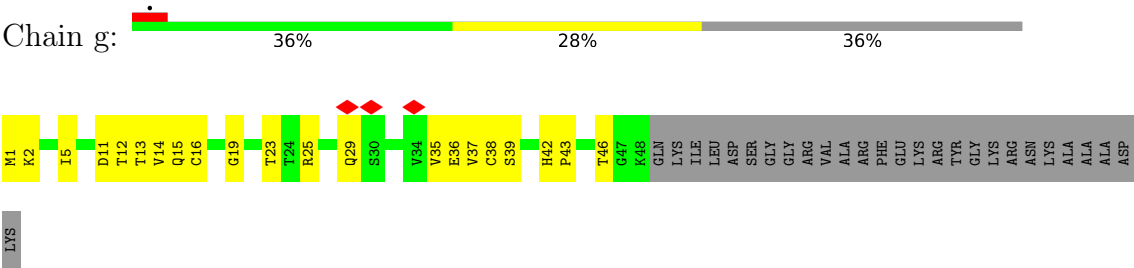
• Molecule 33: 50S ribosomal protein L35



• Molecule 34: 50S ribosomal protein L36



• Molecule 35: 50S Ribosomal Protein L31



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	84008	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	51.85	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	64000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	2.755	Depositor
Minimum map value	-0.985	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.102	Depositor
Recommended contour level	0.35	Depositor
Map size (Å)	430.4, 430.4, 430.4	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.076, 1.076, 1.076	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	2	0.26	0/477	0.36	0/640
2	3	0.29	0/191	0.34	0/247
3	4	0.46	2/3583 (0.1%)	0.59	5/4857 (0.1%)
4	A	0.34	0/70952	0.32	0/110707
5	B	0.26	0/2727	0.32	0/4250
6	C	0.29	0/2153	0.43	0/2895
7	D	0.30	0/1609	0.41	0/2165
8	E	0.29	0/1592	0.38	0/2153
9	F	0.24	0/1467	0.49	2/1973 (0.1%)
10	G	0.22	0/1369	0.38	0/1848
11	H	0.21	0/1027	0.42	0/1398
12	I	0.17	0/925	0.38	0/1246
13	J	0.17	0/1006	0.39	0/1364
14	K	0.29	0/1157	0.39	0/1567
15	L	0.28	0/946	0.41	0/1268
16	M	0.28	0/1091	0.43	0/1457
17	N	0.30	0/1118	0.39	0/1506
18	O	0.30	0/945	0.38	0/1267
19	P	0.23	0/966	0.38	0/1298
20	Q	0.27	0/921	0.40	0/1236
21	R	0.31	0/1000	0.37	0/1341
22	S	0.27	0/764	0.36	0/1030
23	T	0.28	0/887	0.39	0/1204
24	U	0.27	0/766	0.38	0/1030
25	V	0.25	0/725	0.39	0/969
26	W	0.22	0/745	0.39	0/1008
27	X	0.31	0/595	0.40	0/798
28	Y	0.29	0/478	0.38	0/641
29	Z	0.24	0/534	0.34	0/713
30	b	0.28	0/427	0.34	0/572
31	c	0.26	0/413	0.35	0/553
32	d	0.33	0/380	0.36	0/500

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	e	0.32	0/507	0.40	0/672
34	f	0.28	0/303	0.37	0/401
35	g	0.17	0/372	0.32	0/503
All	All	0.32	2/105118 (0.0%)	0.35	7/157277 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	4	458	PRO	CG-CD	-21.28	0.78	1.50
3	4	458	PRO	N-CD	9.82	1.61	1.47

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	4	458	PRO	N-CD-CG	-20.42	72.57	103.20
3	4	458	PRO	CA-CB-CG	-11.04	83.52	104.50
3	4	458	PRO	CA-N-CD	-9.32	98.95	112.00
9	F	9	PRO	N-CD-CG	-7.30	92.24	103.20
9	F	9	PRO	CA-CB-CG	-6.87	91.45	104.50
3	4	458	PRO	CB-CG-CD	6.10	125.62	106.10
3	4	359	ILE	N-CA-C	-5.28	107.45	111.62

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2	474	0	500	8	0
2	3	189	0	205	2	0
3	4	3539	0	3584	147	0
4	A	63364	0	31879	899	0
5	B	2438	0	1241	38	0
6	C	2110	0	2165	41	0
7	D	1587	0	1630	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	E	1569	0	1607	37	0
9	F	1445	0	1476	50	0
10	G	1348	0	1399	42	0
11	H	1018	0	988	29	0
12	I	918	0	959	30	0
13	J	990	0	1021	28	0
14	K	1130	0	1167	20	0
15	L	938	0	1000	14	0
16	M	1078	0	1151	27	0
17	N	1092	0	1128	20	0
18	O	928	0	972	16	0
19	P	956	0	991	32	0
20	Q	907	0	938	32	0
21	R	988	0	1038	26	0
22	S	754	0	802	12	0
23	T	873	0	909	20	0
24	U	756	0	802	17	0
25	V	719	0	768	30	0
26	W	735	0	756	11	0
27	X	586	0	601	17	0
28	Y	470	0	484	9	0
29	Z	531	0	541	11	0
30	b	423	0	463	7	0
31	c	405	0	411	8	0
32	d	377	0	411	10	0
33	e	502	0	541	18	0
34	f	299	0	324	7	0
35	g	364	0	350	13	0
36	4	32	0	14	15	0
All	All	96832	0	65216	1602	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 10.

All (1602) 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)
4:A:287:A:O2'	4:A:288:U:O5'	1.81	0.97
4:A:1543:A:N7	4:A:1627:U:O2	1.98	0.95
5:B:10:G:O2'	5:B:11:U:O5'	1.84	0.94
4:A:1211:G:N2	4:A:1217:G:O6	1.99	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4:143:ARG:NH2	3:4:305:ARG:O	2.01	0.93
7:D:10:LYS:NZ	7:D:200:GLY:O	2.02	0.93
4:A:1756:G:OP2	4:A:1758:G:N2	2.01	0.93
4:A:2362:C:O2'	4:A:2363:A:O5'	1.87	0.93
26:W:11:LEU:HD12	26:W:67:LEU:HD11	1.51	0.92
16:M:31:LYS:O	16:M:32:THR:OG1	1.88	0.92
4:A:2400:C:O2'	4:A:2401:U:O4'	1.88	0.91
4:A:1541:G:O6	4:A:1631:A:N1	2.04	0.91
4:A:2958:C:N4	4:A:2994:C:O2	2.03	0.90
9:F:20:ARG:NH2	9:F:32:VAL:O	2.05	0.90
4:A:2321:U:O2	4:A:2414:G:O6	1.90	0.90
4:A:3020:U:O2'	4:A:3022:G:O6	1.91	0.88
2:3:7:LYS:NZ	4:A:1252:G:O4'	2.07	0.88
4:A:287:A:N6	4:A:299:G:C2	2.41	0.88
4:A:242:G:N2	4:A:255:A:OP2	2.06	0.88
4:A:1996:U:OP2	4:A:2001:A:N6	2.07	0.88
23:T:25:ARG:NH1	23:T:83:ALA:O	2.06	0.87
4:A:199:U:O2	4:A:474:G:N2	2.08	0.87
4:A:2567:U:HO2'	4:A:2597:A:HO2'	1.17	0.86
4:A:1243:G:OP2	4:A:1244:A:O2'	1.94	0.86
3:4:96:THR:OG1	3:4:132:LEU:HD21	1.74	0.85
4:A:378:G:O2'	4:A:424:G:N2	2.09	0.85
3:4:383:ARG:O	3:4:383:ARG:NE	2.09	0.84
15:L:30:ARG:NH2	15:L:37:ASP:OD2	2.11	0.84
4:A:1456:G:HO2'	4:A:1512:U:HO2'	1.26	0.84
4:A:3086:U:OP2	4:A:3087:G:O2'	1.96	0.84
4:A:1533:U:O2	4:A:1803:A:O2'	1.95	0.84
4:A:361:A:N6	4:A:440:U:O2	2.11	0.84
4:A:2340:A:N6	4:A:2388:G:O6	2.11	0.84
4:A:1411:G:OP1	4:A:2933:G:O2'	1.95	0.83
7:D:36:VAL:HG13	7:D:101:LEU:HD11	1.61	0.83
4:A:1213:A:O2'	4:A:1214:A:O5'	1.95	0.83
5:B:31:C:OP1	19:P:14:ARG:NH1	2.12	0.82
14:K:4:TYR:OH	14:K:10:ASP:OD1	1.97	0.82
35:g:43:PRO:O	35:g:46:THR:OG1	1.97	0.82
4:A:1927:C:O2'	4:A:3080:A:N3	2.12	0.81
3:4:96:THR:HG23	3:4:98:ILE:HG22	1.62	0.81
3:4:370:LYS:HG3	36:4:501:GCP:HN22	1.45	0.81
4:A:1146:A:N3	4:A:2710:G:O2'	2.13	0.81
4:A:745:G:OP1	33:e:19:THR:OG1	1.97	0.81
23:T:29:ASP:OD1	23:T:30:LEU:N	2.14	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:2279:C:OP1	30:b:5:LYS:NZ	2.12	0.81
13:J:82:LEU:HD11	13:J:137:MET:HE2	1.61	0.81
4:A:392:A:O2'	4:A:393:U:OP2	1.97	0.80
4:A:724:G:N2	4:A:727:A:OP2	2.12	0.80
4:A:1272:C:OP1	21:R:92:ARG:NH2	2.13	0.80
4:A:479:A:O2'	4:A:498:G:OP1	1.99	0.80
15:L:64:ARG:NH1	15:L:101:PRO:O	2.14	0.80
4:A:191:G:O6	4:A:202:C:O2'	1.99	0.80
4:A:1203:A:O2'	4:A:1204:A:O4'	1.98	0.80
4:A:808:A:O2'	4:A:1468:A:N3	2.15	0.79
4:A:2384:C:O2'	4:A:2396:A:OP1	2.00	0.79
4:A:1531:C:N3	4:A:1805:G:N2	2.31	0.79
24:U:37:SER:O	24:U:80:LYS:NZ	2.15	0.79
4:A:295:U:O2	4:A:340:A:N6	2.14	0.79
8:E:23:GLU:OE1	8:E:23:GLU:N	2.14	0.79
4:A:724:G:OP1	33:e:47:ARG:NH2	2.16	0.79
3:4:9:ALA:HB3	3:4:10:PRO:HD2	1.65	0.78
4:A:234:U:O4	4:A:263:G:N2	2.16	0.78
4:A:1077:A:H61	17:N:83:MET:HE2	1.48	0.78
4:A:1813:C:OP1	24:U:53:LYS:NZ	2.17	0.78
7:D:94:GLU:OE2	7:D:94:GLU:N	2.17	0.78
3:4:428:ASP:OD2	4:A:1214:A:N6	2.16	0.78
9:F:14:ARG:NH2	9:F:179:ALA:O	2.17	0.78
6:C:85:ASP:OD2	6:C:88:ARG:NH1	2.17	0.77
4:A:246:U:O4	33:e:12:LYS:NZ	2.17	0.77
4:A:980:C:O2'	4:A:981:U:O5'	2.01	0.77
4:A:388:U:O2'	4:A:1325:U:OP2	2.01	0.77
4:A:2474:G:O2'	4:A:2720:C:OP1	2.01	0.77
19:P:100:VAL:HG22	19:P:125:LEU:HD11	1.65	0.77
3:4:344:ASN:OD1	3:4:347:ARG:NH2	2.18	0.77
3:4:440:ASP:OD2	3:4:454:ARG:NH2	2.18	0.76
4:A:289:A:N1	4:A:338:C:N3	2.33	0.76
4:A:1326:G:O2'	4:A:1327:A:OP2	2.03	0.76
12:I:54:ASN:ND2	12:I:77:THR:OG1	2.18	0.76
20:Q:19:PHE:O	20:Q:49:ARG:NH1	2.18	0.76
4:A:1379:G:OP1	30:b:16:ARG:NH2	2.18	0.76
4:A:2727:A:O2'	4:A:2729:G:OP2	2.03	0.76
3:4:73:LEU:O	3:4:76:THR:OG1	2.03	0.76
4:A:2702:A:OP2	34:f:2:LYS:NZ	2.13	0.75
4:A:2788:A:O2'	4:A:2789:A:O5'	2.01	0.75
3:4:196:GLY:N	3:4:204:GLY:O	2.20	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1323:G:O2'	4:A:1352:A:N1	2.16	0.75
9:F:68:THR:HG23	9:F:70:GLN:H	1.51	0.75
11:H:75:LEU:HD11	11:H:78:VAL:HG22	1.67	0.75
4:A:2375:G:O2'	4:A:2376:G:O4'	2.03	0.75
4:A:1063:G:O6	4:A:1090:G:N2	2.20	0.75
25:V:38:VAL:HB	25:V:66:ILE:HD11	1.69	0.75
4:A:587:G:N1	4:A:590:A:OP2	2.20	0.74
4:A:731:A:OP1	16:M:132:SER:OG	2.04	0.74
4:A:3022:G:O2'	4:A:3023:G:O4'	2.05	0.74
4:A:660:U:O2	4:A:2254:A:N6	2.20	0.74
29:Z:11:ARG:NH1	29:Z:63:GLU:OE2	2.21	0.74
4:A:2016:G:O2'	6:C:181:GLU:OE2	2.01	0.74
13:J:82:LEU:HD11	13:J:137:MET:CE	2.18	0.74
4:A:49:A:OP2	4:A:114:G:N1	2.20	0.73
4:A:742:G:O2'	4:A:2575:G:OP1	2.05	0.73
10:G:8:PRO:O	10:G:70:ARG:NH2	2.20	0.73
3:4:89:ARG:NH2	3:4:91:LYS:O	2.21	0.73
4:A:2971:G:OP1	10:G:75:ASN:ND2	2.21	0.73
10:G:150:ARG:NH1	10:G:163:VAL:O	2.21	0.73
4:A:58:G:OP2	29:Z:51:ARG:NH2	2.21	0.73
3:4:253:TYR:O	3:4:254:THR:HG23	1.89	0.73
4:A:1115:G:OP2	21:R:58:ARG:NH1	2.21	0.73
4:A:2366:C:O2'	4:A:2368:C:N4	2.22	0.73
5:B:43:C:O3'	35:g:2:LYS:NZ	2.22	0.73
10:G:75:ASN:O	10:G:84:TYR:OH	2.06	0.73
23:T:19:VAL:O	23:T:108:SER:OG	2.04	0.73
4:A:288:U:O2'	4:A:289:A:OP2	2.05	0.72
27:X:11:ARG:O	27:X:14:ARG:NH2	2.21	0.72
4:A:1137:U:O2'	4:A:1139:A:N7	2.20	0.72
4:A:2255:A:N3	4:A:2679:G:O2'	2.20	0.72
4:A:2358:A:N6	4:A:2379:G:O2'	2.21	0.72
17:N:16:GLU:OE1	17:N:17:GLN:N	2.21	0.72
19:P:49:VAL:HG21	19:P:88:ILE:HG21	1.71	0.72
3:4:106:LEU:HD12	3:4:107:ARG:N	2.05	0.72
7:D:188:GLU:N	7:D:188:GLU:OE1	2.23	0.72
4:A:1083:G:O4'	4:A:2491:A:N6	2.23	0.72
4:A:1756:G:O2'	4:A:1758:G:O4'	2.07	0.72
9:F:78:ARG:NH1	9:F:88:GLU:OE2	2.23	0.72
4:A:1640:A:OP2	4:A:1797:C:N4	2.23	0.72
19:P:49:VAL:CG2	19:P:88:ILE:HG21	2.20	0.72
20:Q:73:PHE:HB3	20:Q:80:ILE:HD11	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:T:53:PRO:O	23:T:57:VAL:HG23	1.90	0.71
3:4:158:ARG:NH1	4:A:2705:G:OP1	2.23	0.71
4:A:2044:U:OP2	6:C:222:ARG:NE	2.24	0.71
7:D:19:GLU:N	7:D:19:GLU:OE1	2.23	0.71
4:A:2219:U:O2	15:L:3:GLN:NE2	2.23	0.71
3:4:245:ILE:HD11	3:4:294:PRO:O	1.90	0.71
8:E:118:ARG:NH2	8:E:189:LEU:O	2.24	0.71
4:A:2515:U:OP1	4:A:2604:U:O2'	2.07	0.71
4:A:289:A:N6	4:A:338:C:O2	2.23	0.71
4:A:2164:U:O2	4:A:2166:C:N4	2.22	0.71
4:A:1183:U:O4	4:A:1187:A:O2'	2.07	0.71
4:A:2691:C:OP1	34:f:8:LYS:NZ	2.24	0.71
4:A:2883:G:O2'	4:A:2885:G:N7	2.22	0.71
4:A:1259:U:OP2	14:K:65:SER:OG	2.07	0.70
4:A:2796:A:OP2	7:D:156:THR:OG1	2.09	0.70
4:A:790:A:O2'	8:E:68:GLN:OE1	2.08	0.70
4:A:1426:G:OP2	4:A:1426:G:N2	2.22	0.70
4:A:544:U:O2	4:A:547:U:O2'	2.05	0.70
4:A:286:G:N2	4:A:300:G:N7	2.40	0.70
4:A:287:A:N6	4:A:299:G:N2	2.40	0.70
4:A:1090:G:OP2	4:A:1091:A:O2'	2.02	0.69
6:C:175:LEU:O	6:C:175:LEU:HD12	1.92	0.69
4:A:815:G:O2'	4:A:1850:A:N3	2.24	0.69
6:C:135:ASN:O	6:C:135:ASN:ND2	2.25	0.69
35:g:36:GLU:OE1	35:g:36:GLU:N	2.25	0.69
4:A:2204:G:O2'	4:A:2206:C:OP2	2.07	0.69
4:A:3068:U:OP1	20:Q:95:LYS:NZ	2.26	0.69
4:A:1867:G:O2'	18:O:106:ASP:OD2	2.04	0.69
4:A:369:G:O2'	4:A:370:U:OP2	2.10	0.69
22:S:39:VAL:HG11	22:S:58:VAL:HG13	1.75	0.69
4:A:568:A:OP2	25:V:43:LYS:NZ	2.26	0.69
4:A:2554:U:O2'	27:X:41:ARG:O	2.05	0.69
4:A:287:A:HO2'	4:A:288:U:P	2.14	0.69
4:A:2054:C:O2'	4:A:2153:G:O2'	2.09	0.69
23:T:37:GLU:OE1	23:T:37:GLU:N	2.22	0.69
3:4:364:GLU:OE2	3:4:364:GLU:N	2.25	0.68
4:A:2777:G:N2	4:A:2779:U:OP1	2.25	0.68
4:A:1337:G:N2	4:A:1340:A:OP2	2.25	0.68
4:A:690:G:N2	16:M:15:GLU:O	2.26	0.68
3:4:265:LEU:HD23	3:4:265:LEU:O	1.94	0.68
4:A:1205:G:O6	4:A:1207:G:N2	2.27	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1696:G:O2'	4:A:1736:G:O6	2.11	0.68
32:d:18:VAL:O	32:d:23:LEU:HD23	1.94	0.68
4:A:80:G:O2'	4:A:99:G:N2	2.22	0.68
4:A:637:G:O2'	4:A:638:U:OP2	2.11	0.68
4:A:285:U:O2'	4:A:287:A:OP1	2.12	0.68
4:A:1976:A:HO2'	4:A:2938:G:HO2'	1.33	0.68
4:A:2362:C:N3	4:A:2376:G:N2	2.41	0.67
4:A:2980:U:OP2	34:f:19:ARG:NE	2.27	0.67
9:F:57:ILE:HD13	9:F:91:PRO:HB2	1.74	0.67
9:F:100:GLY:N	9:F:103:MET:SD	2.68	0.67
3:4:370:LYS:HG3	36:4:501:GCP:N2	2.09	0.67
4:A:1911:U:O2'	6:C:14:ARG:NH1	2.27	0.67
23:T:30:LEU:HD21	30:b:22:ALA:O	1.94	0.67
4:A:1900:C:OP2	4:A:1917:G:N2	2.24	0.67
4:A:3019:C:N4	4:A:3024:A:N1	2.42	0.67
25:V:97:ILE:HD12	25:V:104:ASP:HA	1.77	0.67
1:2:15:ALA:O	1:2:20:ARG:NH1	2.27	0.67
3:4:327:LEU:HD23	3:4:328:LEU:N	2.08	0.67
4:A:227:A:N6	4:A:2631:G:N3	2.42	0.67
4:A:1854:U:O2'	4:A:1977:C:O2'	2.03	0.67
4:A:2275:A:OP2	7:D:147:ARG:NH1	2.27	0.67
4:A:2314:U:OP2	4:A:2315:U:O2'	2.09	0.67
4:A:2691:C:OP1	34:f:6:SER:OG	2.12	0.67
25:V:86:ARG:HD3	25:V:97:ILE:HD13	1.76	0.67
4:A:403:U:O2'	8:E:138:THR:OG1	2.09	0.67
4:A:2034:G:OP1	6:C:88:ARG:NH2	2.27	0.67
4:A:2175:U:O2'	4:A:2176:A:O5'	2.12	0.67
9:F:142:GLN:OE1	9:F:157:ARG:N	2.28	0.67
8:E:2:THR:N	8:E:119:ALA:O	2.27	0.67
35:g:16:CYS:SG	35:g:19:GLY:N	2.68	0.67
5:B:31:C:O2'	5:B:58:A:N6	2.28	0.67
4:A:1175:A:H1'	12:I:33:VAL:HG21	1.77	0.67
4:A:2693:A:N6	4:A:2705:G:O2'	2.24	0.66
7:D:135:GLN:OE1	7:D:135:GLN:N	2.28	0.66
3:4:251:VAL:CG2	3:4:328:LEU:HD11	2.25	0.66
3:4:93:ASP:O	3:4:97:TYR:N	2.28	0.66
9:F:19:ILE:HD12	9:F:179:ALA:HB1	1.77	0.66
4:A:604:C:OP2	30:b:10:ARG:NH2	2.29	0.66
4:A:1121:G:O2'	4:A:1128:A:N1	2.26	0.66
16:M:89:GLN:N	16:M:89:GLN:OE1	2.29	0.66
6:C:23:GLU:OE1	6:C:23:GLU:N	2.29	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4:242:ARG:NH1	4:A:2755:A:OP1	2.29	0.66
4:A:413:G:H22	4:A:1324:G:N2	1.93	0.66
10:G:103:ASN:HB2	10:G:115:LEU:HD11	1.77	0.66
31:c:11:ILE:HD13	31:c:53:GLU:HG3	1.76	0.66
4:A:737:A:N1	4:A:2593:A:O2'	2.27	0.66
4:A:2179:U:O2'	4:A:2776:U:OP1	2.08	0.66
4:A:1669:G:O2'	4:A:1670:G:OP1	2.13	0.65
4:A:3041:C:OP2	4:A:3042:A:N6	2.27	0.65
10:G:103:ASN:CB	10:G:115:LEU:HD11	2.26	0.65
7:D:96:GLU:N	7:D:96:GLU:OE1	2.30	0.65
11:H:105:LYS:NZ	11:H:111:ASN:OD1	2.24	0.65
9:F:64:LEU:O	9:F:68:THR:HG22	1.96	0.65
3:4:383:ARG:NH1	3:4:389:ALA:O	2.30	0.65
4:A:1743:G:OP2	4:A:1744:A:O2'	2.06	0.65
4:A:2168:U:O4	4:A:2187:U:O2'	2.10	0.65
4:A:2176:A:OP1	15:L:44:LYS:NZ	2.29	0.65
4:A:2244:A:O2'	4:A:2246:U:OP2	2.15	0.65
4:A:1449:C:OP1	24:U:68:ARG:NH2	2.29	0.64
25:V:45:THR:OG1	25:V:57:GLY:O	2.15	0.64
3:4:22:SER:O	3:4:22:SER:OG	2.13	0.64
4:A:1532:G:O2'	4:A:1533:U:O5'	2.13	0.64
4:A:1758:G:O2'	4:A:1759:A:O5'	2.14	0.64
4:A:2050:C:H42	4:A:2196:G:H1	1.45	0.64
6:C:232:PRO:O	6:C:233:HIS:CD2	2.51	0.64
3:4:57:GLU:N	3:4:57:GLU:OE2	2.30	0.64
4:A:328:C:N3	4:A:448:U:O4	2.31	0.64
4:A:335:G:O2'	4:A:336:C:OP1	2.15	0.64
5:B:54:A:N6	5:B:56:C:N3	2.46	0.64
20:Q:24:THR:HG22	20:Q:86:LEU:HD21	1.79	0.64
4:A:344:G:O2'	4:A:345:G:OP1	2.14	0.64
4:A:1130:C:OP1	21:R:70:ARG:NH2	2.30	0.64
19:P:21:ARG:NH1	19:P:106:GLY:O	2.31	0.64
3:4:19:ASP:O	3:4:20:ARG:NE	2.31	0.64
3:4:401:ASP:OD2	3:4:402:LYS:NZ	2.29	0.64
4:A:2391:G:O2'	4:A:2392:A:O5'	2.16	0.64
11:H:141:GLU:N	11:H:141:GLU:OE1	2.30	0.64
3:4:116:ASP:O	3:4:117:THR:OG1	2.12	0.63
23:T:65:ALA:HB3	23:T:76:LEU:HD11	1.80	0.63
4:A:701:A:OP2	4:A:713:G:N1	2.23	0.63
4:A:1455:U:OP2	24:U:62:ARG:NH2	2.31	0.63
6:C:155:LEU:HD13	6:C:177:MET:HE1	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:121:LYS:HG3	7:D:170:MET:HE2	1.80	0.63
18:O:55:ALA:HB2	18:O:79:LEU:HD21	1.78	0.63
4:A:1362:A:OP1	8:E:96:ARG:NH2	2.32	0.63
6:C:263:PRO:O	6:C:266:LYS:NZ	2.19	0.63
4:A:1256:G:N2	14:K:108:MET:SD	2.72	0.63
4:A:1770:G:OP1	4:A:1937:U:O2'	2.08	0.63
5:B:49:C:OP1	19:P:42:ARG:NH1	2.32	0.63
27:X:56:ASP:OD1	27:X:58:THR:OG1	2.16	0.63
10:G:44:SER:OG	10:G:52:VAL:O	2.13	0.62
4:A:218:A:N3	4:A:234:U:O2'	2.28	0.62
4:A:337:U:O2'	4:A:344:G:O6	2.15	0.62
3:4:240:ARG:NH1	4:A:2697:U:O4'	2.32	0.62
4:A:678:A:N1	4:A:924:G:O2'	2.32	0.62
3:4:379:LEU:HD23	3:4:381:GLN:OE1	1.99	0.62
3:4:82:LEU:HD13	3:4:113:THR:HB	1.81	0.62
4:A:1350:G:H4'	4:A:1351:G:OP1	1.98	0.62
25:V:88:ASP:OD2	25:V:91:THR:OG1	2.17	0.62
33:e:34:GLU:O	33:e:35:HIS:CD2	2.53	0.62
3:4:323:VAL:HG21	3:4:357:TYR:HB2	1.81	0.62
3:4:132:LEU:O	3:4:136:VAL:HG22	2.00	0.62
3:4:422:ILE:HG21	3:4:430:VAL:HG23	1.81	0.62
4:A:1137:U:OP1	4:A:1153:U:O2'	2.12	0.62
4:A:1493:A:O2'	4:A:1494:U:OP2	2.18	0.62
5:B:61:C:O2'	5:B:62:C:OP1	2.17	0.62
3:4:106:LEU:HA	3:4:109:VAL:HG22	1.81	0.62
4:A:159:A:N3	4:A:2431:C:O2'	2.29	0.62
4:A:1541:G:O6	4:A:1631:A:C6	2.53	0.62
4:A:2343:G:O2'	4:A:2344:G:O5'	2.17	0.62
15:L:10:VAL:HG12	15:L:12:ASP:OD2	2.00	0.62
4:A:1177:G:H5'	13:J:118:LEU:HD22	1.81	0.61
19:P:49:VAL:HG21	19:P:88:ILE:HD13	1.80	0.61
4:A:1162:G:O2'	4:A:1229:A:N6	2.33	0.61
4:A:2982:A:C4	10:G:68:LEU:HD21	2.35	0.61
15:L:107:ARG:O	15:L:110:LYS:NZ	2.31	0.61
19:P:104:ARG:NH1	19:P:107:TYR:O	2.33	0.61
4:A:287:A:H61	4:A:298:G:H1	1.48	0.61
7:D:118:SER:OG	7:D:173:ASP:OD1	2.16	0.61
4:A:2879:G:O2'	4:A:2888:G:O6	2.08	0.61
16:M:125:THR:HG23	16:M:145:THR:HG23	1.83	0.61
25:V:22:LYS:C	25:V:35:VAL:HG23	2.25	0.61
31:c:12:THR:O	31:c:54:SER:N	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4:215:ILE:O	3:4:219:MET:HG3	2.01	0.61
4:A:202:C:OP2	4:A:203:A:O2'	2.12	0.61
4:A:2503:G:N7	27:X:14:ARG:NH1	2.48	0.61
4:A:209:C:O2'	4:A:1481:C:O2	2.19	0.61
4:A:81:A:N1	4:A:96:G:O2'	2.31	0.61
4:A:406:A:N6	4:A:420:G:O2'	2.34	0.61
3:4:251:VAL:HG23	3:4:328:LEU:HD11	1.83	0.60
4:A:1127:A:N3	4:A:1272:C:O2'	2.34	0.60
4:A:1631:A:H3'	4:A:1632:G:O4'	2.01	0.60
4:A:2482:U:O2'	4:A:2651:C:OP2	2.19	0.60
4:A:885:G:OP2	32:d:14:ARG:NH2	2.33	0.60
4:A:251:A:OP1	33:e:7:HIS:NE2	2.32	0.60
4:A:1099:A:N1	4:A:2251:G:O2'	2.27	0.60
4:A:2338:G:N1	4:A:2342:A:OP1	2.35	0.60
4:A:1213:A:HO2'	4:A:1214:A:C5'	2.13	0.60
4:A:2158:C:H1'	4:A:2159:G:H2'	1.84	0.60
4:A:2587:U:O2	27:X:39:ARG:NH2	2.35	0.60
26:W:47:LEU:N	26:W:47:LEU:HD23	2.17	0.60
4:A:413:G:H22	4:A:1324:G:H22	1.49	0.60
9:F:100:GLY:O	9:F:103:MET:SD	2.59	0.60
10:G:11:VAL:O	10:G:11:VAL:HG13	2.01	0.60
21:R:73:ASP:OD1	21:R:73:ASP:O	2.20	0.60
4:A:159:A:OP2	4:A:164:A:N6	2.29	0.60
4:A:895:G:OP1	6:C:218:ARG:NH2	2.33	0.60
4:A:1726:C:H2'	4:A:1727:A:C8	2.36	0.60
4:A:2805:G:N2	4:A:2805:G:OP2	2.34	0.59
4:A:1025:A:N3	4:A:2488:C:O2'	2.33	0.59
18:O:54:HIS:NE2	18:O:65:GLU:OE2	2.35	0.59
4:A:376:G:H22	4:A:426:G:H5''	1.65	0.59
1:2:46:LEU:O	1:2:50:VAL:HG22	2.02	0.59
35:g:13:THR:HG22	35:g:14:VAL:H	1.65	0.59
4:A:740:A:O2'	4:A:741:G:OP2	2.19	0.59
4:A:979:G:H2'	4:A:980:C:H6	1.68	0.59
11:H:91:LEU:HD12	11:H:125:LYS:HA	1.85	0.59
4:A:960:G:OP2	4:A:960:G:N2	2.19	0.59
17:N:75:THR:HG21	17:N:87:LYS:HE3	1.85	0.59
3:4:250:ILE:HG23	3:4:329:ILE:HD11	1.84	0.59
4:A:736:G:N1	4:A:739:U:OP2	2.34	0.59
4:A:2509:C:OP2	31:c:28:ASN:ND2	2.35	0.59
4:A:3041:C:O2'	7:D:201:ARG:NE	2.35	0.59
4:A:122:A:OP2	32:d:22:ARG:NH1	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1425:G:N2	4:A:1428:U:C4	2.72	0.58
4:A:2754:G:N7	10:G:173:LYS:NZ	2.44	0.58
4:A:3038:C:OP1	18:O:99:LYS:NZ	2.32	0.58
7:D:43:GLU:OE1	7:D:43:GLU:N	2.34	0.58
13:J:56:ILE:O	13:J:56:ILE:HG23	2.01	0.58
4:A:1532:G:O2'	4:A:1533:U:O4'	2.21	0.58
4:A:2393:A:O2'	4:A:2394:A:OP2	2.17	0.58
26:W:76:GLN:NE2	26:W:77:LEU:O	2.34	0.58
4:A:402:G:N2	4:A:405:G:N7	2.51	0.58
4:A:2321:U:O2	4:A:2414:G:C6	2.56	0.58
8:E:189:LEU:CD2	16:M:9:LEU:HD11	2.33	0.58
8:E:199:GLU:OE1	8:E:199:GLU:N	2.36	0.58
4:A:1675:U:O2'	4:A:1676:G:N7	2.36	0.58
4:A:48:G:O2'	4:A:116:A:N1	2.37	0.58
4:A:1938:G:H21	4:A:1956:A:H62	1.50	0.58
17:N:17:GLN:O	17:N:39:HIS:ND1	2.36	0.58
3:4:371:ILE:HD12	3:4:391:PHE:O	2.04	0.58
13:J:106:GLN:N	13:J:106:GLN:OE1	2.37	0.58
4:A:944:A:N7	4:A:2471:A:O2'	2.36	0.58
10:G:25:SER:HB3	10:G:34:THR:HG22	1.84	0.58
4:A:639:C:O2'	4:A:640:G:O5'	2.21	0.58
4:A:1696:G:O2'	4:A:1697:U:OP2	2.21	0.58
4:A:1403:C:OP1	4:A:1404:C:N4	2.36	0.58
16:M:31:LYS:HG2	16:M:32:THR:HG23	1.86	0.58
4:A:2050:C:O2	4:A:2197:G:N2	2.37	0.58
9:F:172:GLU:N	9:F:172:GLU:OE1	2.37	0.58
3:4:455:VAL:HG12	3:4:459:LEU:HD23	1.86	0.57
4:A:2696:G:N2	4:A:2703:U:O4	2.37	0.57
12:I:16:GLN:OE1	12:I:16:GLN:N	2.34	0.57
4:A:2425:U:O2'	4:A:2427:G:OP1	2.20	0.57
7:D:27:THR:OG1	7:D:196:GLY:O	2.22	0.57
11:H:113:ASP:OD1	11:H:113:ASP:N	2.37	0.57
4:A:1175:A:C1'	12:I:33:VAL:HG21	2.33	0.57
4:A:2015:U:O2'	4:A:2019:A:N3	2.35	0.57
20:Q:32:ILE:HD12	20:Q:32:ILE:N	2.20	0.57
4:A:79:G:O2'	4:A:80:G:O4'	2.22	0.57
4:A:2905:C:OP2	7:D:119:LYS:NZ	2.35	0.57
22:S:53:ASP:OD1	22:S:54:ASP:N	2.36	0.57
29:Z:22:LEU:HD11	29:Z:58:TYR:CE2	2.39	0.57
5:B:81:U:OP1	17:N:18:ARG:NH2	2.37	0.57
8:E:207:ALA:O	8:E:210:LYS:NZ	2.36	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4:369:ASN:HB3	36:4:501:GCP:HN21	1.70	0.57
4:A:2515:U:O2'	4:A:2598:C:O2	2.23	0.57
5:B:10:G:O2'	5:B:11:U:P	2.62	0.57
4:A:1081:C:O2'	4:A:2497:A:N3	2.33	0.57
4:A:1533:U:OP1	4:A:1536:A:N6	2.37	0.57
11:H:146:LEU:O	11:H:146:LEU:HD23	2.04	0.56
33:e:34:GLU:OE1	33:e:35:HIS:N	2.36	0.56
4:A:240:G:OP2	4:A:241:A:O2'	2.13	0.56
4:A:1366:A:O2'	4:A:1368:A:OP2	2.24	0.56
4:A:1425:G:N2	4:A:1428:U:O4	2.38	0.56
9:F:74:VAL:O	9:F:74:VAL:HG23	2.04	0.56
17:N:2:LEU:HD23	17:N:70:PRO:CD	2.35	0.56
18:O:87:TYR:OH	18:O:116:VAL:O	2.18	0.56
18:O:38:GLU:OE1	18:O:42:ARG:NH2	2.37	0.56
4:A:718:C:O2'	4:A:772:U:OP1	2.24	0.56
4:A:1338:U:H4'	22:S:89:GLY:O	2.06	0.56
4:A:3096:U:O2	20:Q:1:MET:N	2.39	0.56
33:e:54:ASP:O	33:e:58:ILE:HD12	2.06	0.56
4:A:402:G:N3	4:A:405:G:C6	2.73	0.56
4:A:1199:U:O2	13:J:119:ASN:ND2	2.38	0.56
4:A:2055:C:C4'	4:A:2154:G:H22	2.19	0.56
4:A:1113:C:OP2	21:R:54:LYS:NZ	2.39	0.56
11:H:75:LEU:CD1	11:H:78:VAL:HG22	2.34	0.56
31:c:17:VAL:HG21	31:c:49:GLN:OE1	2.05	0.56
11:H:8:GLU:OE2	11:H:15:ALA:N	2.32	0.56
3:4:96:THR:CG2	3:4:98:ILE:HG22	2.35	0.56
4:A:2735:U:O2'	7:D:148:PRO:O	2.22	0.56
21:R:91:ASP:OD1	21:R:94:ASN:ND2	2.37	0.56
3:4:119:ILE:HG22	3:4:120:CYS:H	1.71	0.56
4:A:287:A:C6	4:A:299:G:N2	2.74	0.56
4:A:669:G:O2'	4:A:1369:A:OP1	2.24	0.56
4:A:2343:G:N2	4:A:2401:U:O2	2.39	0.56
4:A:3108:G:OP1	30:b:29:THR:HG22	2.06	0.56
12:I:82:VAL:HG21	12:I:85:GLU:O	2.06	0.56
3:4:96:THR:OG1	3:4:132:LEU:HD11	2.06	0.55
9:F:118:ILE:HG21	9:F:121:PHE:HB2	1.87	0.55
4:A:268:G:O2'	4:A:360:G:O2'	2.21	0.55
4:A:2518:C:OP1	19:P:104:ARG:NH2	2.37	0.55
4:A:74:C:O3'	29:Z:11:ARG:NH2	2.39	0.55
4:A:1032:A:H5''	4:A:2492:A:H61	1.70	0.55
10:G:57:ASP:OD1	10:G:57:ASP:C	2.50	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:326:A:H2	4:A:449:G:H22	1.53	0.55
4:A:340:A:C2	4:A:341:C:C5	2.94	0.55
4:A:389:G:H21	4:A:412:A:H61	1.52	0.55
4:A:974:G:O2'	4:A:1031:G:O6	2.24	0.55
4:A:1991:C:H2'	4:A:1991:C:O2	2.05	0.55
21:R:48:ARG:NH1	21:R:49:ASP:OD1	2.39	0.55
25:V:24:LEU:N	25:V:34:LEU:O	2.39	0.55
4:A:3029:U:O2	4:A:3030:A:C8	2.60	0.55
3:4:129:LEU:HD11	3:4:179:TRP:HB3	1.89	0.55
4:A:1172:A:N6	4:A:1224:G:O6	2.39	0.55
4:A:2007:C:H2'	4:A:2008:A:C8	2.41	0.55
4:A:2519:C:OP2	19:P:24:ARG:NH2	2.40	0.55
12:I:10:VAL:HG13	12:I:11:ALA:H	1.70	0.55
3:4:250:ILE:HD12	3:4:329:ILE:HD11	1.87	0.55
3:4:293:ARG:O	3:4:295:PHE:N	2.40	0.55
4:A:183:G:O2'	4:A:216:A:N3	2.35	0.55
4:A:326:A:N6	4:A:450:G:C6	2.75	0.55
4:A:1487:U:O2'	4:A:2436:A:N3	2.38	0.55
4:A:1623:U:O2'	4:A:1624:U:O4'	2.12	0.55
16:M:84:ASN:ND2	16:M:117:LYS:O	2.36	0.55
4:A:3022:G:C2'	4:A:3023:G:O4'	2.55	0.55
5:B:47:A:C5	5:B:48:C:C5	2.95	0.55
10:G:13:SER:C	10:G:15:VAL:H	2.15	0.55
4:A:1131:G:O4'	14:K:147:GLN:NE2	2.39	0.55
20:Q:73:PHE:CB	20:Q:80:ILE:HD11	2.37	0.55
21:R:74:ILE:HG21	21:R:110:VAL:HG13	1.88	0.55
23:T:48:GLN:O	23:T:51:SER:OG	2.14	0.55
26:W:47:LEU:HD23	26:W:47:LEU:H	1.72	0.55
4:A:971:G:H2'	4:A:972:A:C8	2.41	0.54
4:A:2580:G:H4'	27:X:20:ARG:HB2	1.89	0.54
4:A:1442:A:H2'	4:A:1443:G:O4'	2.07	0.54
11:H:129:THR:HG22	11:H:147:ASN:OD1	2.07	0.54
4:A:255:A:H2'	4:A:256:A:O4'	2.07	0.54
29:Z:61:LEU:C	29:Z:61:LEU:HD23	2.33	0.54
4:A:662:G:H2'	4:A:2254:A:N7	2.22	0.54
10:G:160:GLY:O	10:G:164:ARG:NH2	2.41	0.54
4:A:1342:C:OP1	21:R:12:LYS:NZ	2.37	0.54
3:4:119:ILE:HD12	3:4:146:LEU:HD21	1.90	0.54
3:4:198:VAL:O	3:4:200:THR:N	2.39	0.54
3:4:331:VAL:HA	3:4:367:VAL:HG23	1.90	0.54
4:A:29:C:N4	4:A:535:A:OP2	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:351:G:H2'	4:A:352:G:O4'	2.06	0.54
4:A:428:A:O2'	4:A:429:A:OP1	2.22	0.54
4:A:980:C:HO2'	4:A:981:U:P	2.30	0.54
4:A:1381:G:OP2	30:b:17:ARG:NE	2.32	0.54
3:4:372:ASP:OD1	3:4:373:ALA:N	2.41	0.54
4:A:2049:C:H2'	4:A:2050:C:O4'	2.08	0.54
10:G:2:SER:OG	10:G:3:ARG:N	2.37	0.54
13:J:129:ILE:O	13:J:133:THR:HG23	2.07	0.54
4:A:1110:C:OP1	21:R:47:TYR:OH	2.25	0.54
4:A:1168:A:N1	10:G:3:ARG:NH2	2.56	0.54
4:A:1630:U:H2'	4:A:1631:A:O4'	2.07	0.54
17:N:71:ASP:OD2	17:N:72:ARG:N	2.41	0.54
4:A:681:C:H2'	4:A:682:A:C8	2.42	0.54
4:A:2165:C:N4	4:A:2191:C:OP2	2.41	0.54
3:4:319:LEU:HG	3:4:353:VAL:HG22	1.90	0.53
4:A:1165:G:OP2	12:I:53:LYS:NZ	2.40	0.53
4:A:1456:G:C2	24:U:83:ILE:HG21	2.43	0.53
8:E:163:GLU:OE1	8:E:163:GLU:N	2.40	0.53
16:M:49:MET:SD	16:M:49:MET:N	2.77	0.53
17:N:71:ASP:OD2	17:N:71:ASP:C	2.51	0.53
20:Q:22:GLY:HA2	20:Q:96:LEU:HD11	1.90	0.53
4:A:1457:A:O2'	4:A:1459:U:OP2	2.14	0.53
4:A:2668:G:OP2	8:E:69:LYS:NZ	2.36	0.53
3:4:39:VAL:HG13	3:4:46:LEU:HD22	1.89	0.53
3:4:251:VAL:HG21	3:4:328:LEU:HD11	1.90	0.53
4:A:388:U:H2'	4:A:389:G:O4'	2.09	0.53
3:4:218:ARG:O	3:4:222:LEU:HD23	2.08	0.53
4:A:246:U:N3	4:A:247:G:N7	2.57	0.53
4:A:1769:G:O3'	4:A:1957:G:N2	2.41	0.53
8:E:197:SER:OG	8:E:199:GLU:OE1	2.25	0.53
9:F:132:THR:O	9:F:134:ASN:N	2.38	0.53
19:P:114:ALA:O	19:P:118:ASP:OD2	2.26	0.53
8:E:150:GLU:N	8:E:150:GLU:OE1	2.41	0.53
24:U:95:LEU:O	24:U:95:LEU:HD23	2.09	0.53
4:A:56:U:O2'	4:A:71:A:OP2	2.25	0.53
4:A:2407:C:N4	4:A:2408:G:O6	2.41	0.53
25:V:9:VAL:HG12	25:V:35:VAL:HG21	1.91	0.53
29:Z:5:THR:HG21	29:Z:53:GLU:CD	2.34	0.53
3:4:209:GLU:HB2	3:4:215:ILE:HD11	1.90	0.53
3:4:415:ASP:N	3:4:415:ASP:OD1	2.40	0.53
4:A:1165:G:N2	4:A:1228:A:N7	2.57	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:2286:A:N6	4:A:2727:A:N7	2.55	0.53
18:O:103:ARG:HE	18:O:110:MET:HE2	1.73	0.53
3:4:394:ALA:O	36:4:501:GCP:N1	2.42	0.53
4:A:293:G:H2'	4:A:294:G:C8	2.44	0.53
4:A:2006:A:H2'	4:A:2007:C:O4'	2.09	0.53
12:I:109:TYR:C	12:I:110:MET:HE2	2.34	0.53
25:V:90:GLU:OE1	25:V:90:GLU:N	2.41	0.53
3:4:392:VAL:HG13	3:4:399:GLY:O	2.09	0.53
4:A:273:A:H2	4:A:322:A:O4'	1.91	0.53
4:A:2367:G:O2'	4:A:2371:G:N1	2.42	0.53
7:D:52:LEU:HD11	7:D:84:LEU:HD22	1.91	0.53
4:A:556:G:N7	32:d:42:ARG:NH2	2.53	0.52
4:A:2165:C:H42	4:A:2191:C:P	2.32	0.52
10:G:17:VAL:O	10:G:45:ARG:NH2	2.42	0.52
3:4:40:GLU:HB2	3:4:43:GLN:O	2.10	0.52
4:A:1180:G:C2	4:A:1181:G:C8	2.97	0.52
4:A:1731:A:H2'	4:A:1732:U:O4'	2.10	0.52
3:4:345:ALA:O	3:4:348:THR:HG22	2.09	0.52
4:A:860:G:HO2'	4:A:863:G:HO2'	1.54	0.52
4:A:1673:A:H2'	4:A:1673:A:N3	2.23	0.52
16:M:78:VAL:HG13	16:M:78:VAL:O	2.08	0.52
3:4:422:ILE:HD11	3:4:433:VAL:HG11	1.92	0.52
4:A:446:G:O2'	4:A:447:A:O4'	2.25	0.52
9:F:101:ASP:OD1	9:F:101:ASP:N	2.43	0.52
3:4:161:LYS:O	3:4:165:SER:OG	2.19	0.52
4:A:2330:U:O2'	4:A:2405:A:N6	2.43	0.52
1:2:6:ILE:HD13	1:2:47:ILE:HD11	1.90	0.52
4:A:1500:A:O2'	4:A:1511:U:O2	2.27	0.52
11:H:149:VAL:HG23	11:H:149:VAL:O	2.08	0.52
4:A:2851:G:O2'	4:A:3005:A:N1	2.38	0.52
17:N:1:MET:HE2	17:N:44:ASN:HB2	1.92	0.52
6:C:97:TYR:O	6:C:100:GLY:N	2.39	0.52
4:A:2031:G:OP2	4:A:2032:A:O2'	2.18	0.52
4:A:2055:C:OP1	4:A:2154:G:N1	2.43	0.52
4:A:2690:C:N4	4:A:2691:C:N4	2.58	0.52
4:A:2936:C:OP1	4:A:2938:G:H4'	2.10	0.52
15:L:10:VAL:HG12	15:L:12:ASP:CG	2.35	0.52
23:T:71:LEU:HB3	23:T:76:LEU:HD21	1.92	0.51
5:B:10:G:H2'	5:B:11:U:C6	2.44	0.51
1:2:11:SER:HB3	1:2:31:ILE:HD11	1.92	0.51
3:4:347:ARG:O	3:4:350:ILE:HG13	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1691:A:N6	4:A:1743:G:O2'	2.42	0.51
10:G:15:VAL:HG23	10:G:17:VAL:HG23	1.92	0.51
20:Q:64:SER:O	20:Q:67:VAL:N	2.40	0.51
4:A:448:U:H2'	4:A:449:G:C8	2.45	0.51
4:A:1161:C:N4	4:A:1162:G:O6	2.44	0.51
4:A:2687:U:H2'	4:A:2688:C:O4'	2.10	0.51
25:V:35:VAL:O	25:V:38:VAL:HG22	2.10	0.51
34:f:16:VAL:O	34:f:17:ILE:HG23	2.11	0.51
4:A:732:G:C5	4:A:745:G:N2	2.78	0.51
5:B:25:G:N7	5:B:57:U:O2'	2.37	0.51
12:I:21:THR:O	12:I:111:ASP:N	2.43	0.51
17:N:2:LEU:HD23	17:N:70:PRO:HD2	1.93	0.51
3:4:262:LEU:HD23	3:4:270:VAL:HG11	1.93	0.51
4:A:995:U:H3'	4:A:996:G:O4'	2.10	0.51
20:Q:57:THR:OG1	20:Q:73:PHE:O	2.16	0.51
22:S:23:LYS:HG2	22:S:96:VAL:HG12	1.93	0.51
3:4:428:ASP:HB3	4:A:1213:A:H62	1.76	0.51
4:A:219:G:O2'	4:A:233:A:N3	2.38	0.51
4:A:1532:G:N2	4:A:1804:G:C4	2.79	0.51
4:A:2170:U:O2'	4:A:2185:C:O2	2.16	0.51
24:U:12:LEU:HD12	24:U:32:VAL:HG12	1.92	0.51
4:A:329:U:O2'	4:A:447:A:N1	2.34	0.51
4:A:989:G:O6	4:A:1020:A:N6	2.44	0.51
19:P:78:LYS:O	19:P:81:SER:OG	2.21	0.51
4:A:2052:G:O2'	4:A:2055:C:N4	2.30	0.51
12:I:93:ILE:HD12	12:I:105:ILE:HG13	1.93	0.51
35:g:11:ASP:HA	35:g:25:ARG:HA	1.93	0.51
4:A:2555:G:OP1	27:X:44:HIS:ND1	2.44	0.50
6:C:245:HIS:O	6:C:247:VAL:HG23	2.11	0.50
7:D:5:GLY:HA3	7:D:84:LEU:HD21	1.93	0.50
12:I:40:ARG:HA	12:I:49:TYR:HB3	1.93	0.50
4:A:2510:A:OP1	31:c:31:ASN:ND2	2.40	0.50
9:F:106:PHE:C	9:F:106:PHE:CD2	2.89	0.50
3:4:439:VAL:O	3:4:439:VAL:HG13	2.10	0.50
4:A:1269:C:O2	21:R:78:ARG:NH2	2.44	0.50
4:A:1331:C:OP2	21:R:15:ARG:NH1	2.41	0.50
4:A:1393:C:H2'	4:A:1394:A:H8	1.77	0.50
4:A:2008:A:C2	4:A:2046:A:H4'	2.46	0.50
10:G:71:THR:O	10:G:75:ASN:OD1	2.29	0.50
4:A:544:U:O4	4:A:558:A:N6	2.45	0.50
4:A:3014:A:H62	4:A:3113:A:H2	1.59	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:Q:86:LEU:H	20:Q:86:LEU:HD23	1.76	0.50
4:A:273:A:H62	4:A:313:G:H21	1.59	0.50
4:A:546:G:O2'	4:A:557:G:O6	2.18	0.50
4:A:1532:G:HO2'	4:A:1533:U:C4'	2.24	0.50
5:B:80:C:H2'	5:B:81:U:O4'	2.12	0.50
6:C:222:ARG:O	6:C:225:VAL:HG22	2.12	0.50
26:W:64:ASN:OD1	26:W:64:ASN:O	2.29	0.50
3:4:25:ARG:HB3	3:4:102:LYS:HZ2	1.77	0.50
3:4:263:ASN:OD1	3:4:270:VAL:N	2.44	0.50
4:A:256:A:C5	4:A:257:A:N7	2.80	0.50
4:A:292:G:N1	4:A:343:U:O2	2.45	0.50
4:A:547:U:OP2	4:A:557:G:N1	2.38	0.50
4:A:1988:C:O2'	4:A:2003:A:O4'	2.24	0.50
4:A:2972:A:N3	10:G:64:SER:OG	2.44	0.50
23:T:30:LEU:HD22	30:b:24:ALA:HB2	1.92	0.50
4:A:356:G:H21	4:A:362:A:N6	2.10	0.50
4:A:1711:G:O2'	4:A:1712:G:C8	2.60	0.50
4:A:2294:A:H2'	4:A:2295:C:C6	2.47	0.50
4:A:2533:C:H2'	4:A:2534:A:O4'	2.12	0.50
4:A:1674:G:OP1	18:O:73:LYS:NZ	2.44	0.50
6:C:143:HIS:ND1	6:C:194:GLY:O	2.36	0.50
7:D:103:ALA:HB1	7:D:192:LEU:HD21	1.94	0.50
16:M:80:VAL:HG22	16:M:114:GLY:HA2	1.94	0.50
19:P:56:ASN:OD1	19:P:56:ASN:N	2.44	0.50
20:Q:100:ARG:O	20:Q:103:ARG:NH2	2.43	0.50
4:A:1189:G:H2'	4:A:1190:C:C6	2.47	0.49
5:B:45:G:OP2	35:g:1:MET:N	2.44	0.49
7:D:14:THR:OG1	7:D:15:GLN:N	2.45	0.49
4:A:636:U:O2'	4:A:637:G:O4'	2.29	0.49
4:A:733:U:C2	4:A:734:C:C5	3.00	0.49
4:A:2801:A:O4'	4:A:2836:C:N4	2.45	0.49
14:K:25:LEU:O	14:K:27:ARG:N	2.40	0.49
17:N:103:LEU:HD11	17:N:127:ILE:HD11	1.93	0.49
20:Q:37:GLU:OE2	20:Q:37:GLU:HA	2.12	0.49
4:A:328:C:O2	4:A:448:U:N3	2.45	0.49
4:A:1473:G:O2'	4:A:1488:A:N6	2.45	0.49
11:H:151:GLN:N	11:H:151:GLN:OE1	2.43	0.49
18:O:36:THR:OG1	18:O:37:THR:N	2.45	0.49
19:P:118:ASP:OD2	19:P:118:ASP:N	2.39	0.49
20:Q:77:SER:HB3	20:Q:80:ILE:HD12	1.93	0.49
3:4:259:SER:N	36:4:501:GCP:O2B	2.37	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4:427:GLY:N	13:J:32:GLN:OE1	2.45	0.49
4:A:241:A:N6	4:A:255:A:C8	2.80	0.49
4:A:2532:G:N3	4:A:2532:G:H2'	2.27	0.49
4:A:2889:A:C2	4:A:2890:C:C6	3.01	0.49
6:C:156:ALA:HA	6:C:161:VAL:HG11	1.93	0.49
7:D:28:VAL:O	7:D:28:VAL:HG13	2.13	0.49
21:R:28:ARG:NH1	21:R:38:GLN:OE1	2.45	0.49
25:V:36:GLU:OE2	25:V:37:GLY:N	2.45	0.49
1:2:29:LYS:N	1:2:33:GLN:OE1	2.42	0.49
4:A:244:A:C2	4:A:255:A:C2	3.01	0.49
4:A:2613:G:H5''	4:A:2614:U:O4'	2.12	0.49
12:I:40:ARG:NE	12:I:49:TYR:O	2.41	0.49
19:P:3:HIS:O	19:P:3:HIS:ND1	2.39	0.49
3:4:205:GLU:OE1	17:N:45:ARG:NH2	2.44	0.49
4:A:1229:A:O2'	4:A:1230:G:OP2	2.31	0.49
3:4:160:GLY:O	3:4:164:VAL:HG12	2.12	0.49
3:4:273:GLU:O	36:4:501:GCP:H5'1	2.11	0.49
4:A:291:C:C2'	4:A:344:G:H1	2.25	0.49
4:A:1173:G:H2'	4:A:1174:G:O4'	2.12	0.49
4:A:2749:G:C2	4:A:2763:C:C2	3.01	0.49
12:I:51:VAL:HG12	12:I:78:ALA:HA	1.95	0.49
14:K:31:ALA:O	14:K:35:LEU:HD23	2.13	0.49
17:N:16:GLU:O	17:N:96:ASN:ND2	2.46	0.49
32:d:2:ALA:O	32:d:4:GLY:N	2.44	0.49
3:4:329:ILE:HG22	3:4:365:LEU:HD22	1.94	0.49
4:A:199:U:O4	4:A:250:G:N2	2.46	0.49
8:E:8:LYS:HE2	8:E:14:THR:HG22	1.94	0.49
9:F:142:GLN:O	9:F:142:GLN:HG3	2.12	0.49
24:U:30:THR:HG23	24:U:83:ILE:HD13	1.95	0.49
28:Y:7:ILE:HD11	28:Y:49:ILE:HD12	1.94	0.49
4:A:773:G:H21	8:E:106:MET:CE	2.26	0.49
4:A:829:U:O2'	4:A:830:A:OP1	2.26	0.49
4:A:1314:C:H2'	4:A:1315:C:H6	1.77	0.49
4:A:1712:G:O2'	4:A:1713:U:OP1	2.22	0.49
8:E:154:VAL:CG2	8:E:175:VAL:HG22	2.42	0.49
20:Q:36:LYS:HG3	20:Q:36:LYS:O	2.13	0.49
3:4:370:LYS:N	36:4:501:GCP:HN21	2.11	0.49
4:A:289:A:N6	4:A:338:C:C2	2.78	0.49
24:U:90:SER:O	24:U:91:LYS:C	2.56	0.49
3:4:22:SER:O	3:4:23:LEU:HB3	2.12	0.48
3:4:379:LEU:HG	3:4:380:ALA:H	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1118:A:OP2	4:A:1273:G:N1	2.30	0.48
4:A:1403:C:C2	4:A:1442:A:C2	3.01	0.48
4:A:3037:C:O2	4:A:3104:A:O2'	2.30	0.48
8:E:79:THR:HG22	8:E:79:THR:O	2.13	0.48
16:M:57:ILE:HG23	16:M:58:HIS:N	2.28	0.48
21:R:73:ASP:O	21:R:114:ARG:NH1	2.38	0.48
29:Z:5:THR:HG21	29:Z:53:GLU:OE2	2.13	0.48
4:A:722:G:C6	4:A:730:G:C2	3.00	0.48
4:A:1069:G:C6	4:A:1083:G:C6	3.02	0.48
4:A:1168:A:N6	4:A:2975:G:O6	2.46	0.48
4:A:1849:G:N2	4:A:1852:A:OP2	2.42	0.48
4:A:2256:G:O6	4:A:2677:A:O2'	2.22	0.48
4:A:2772:G:O2'	15:L:4:GLN:OE1	2.30	0.48
3:4:327:LEU:HD23	3:4:327:LEU:C	2.38	0.48
4:A:20:G:OP1	4:A:591:G:N2	2.47	0.48
4:A:247:G:O6	33:e:12:LYS:NZ	2.46	0.48
4:A:2562:G:O3'	9:F:78:ARG:NH2	2.46	0.48
5:B:2:U:H4'	5:B:3:U:OP1	2.13	0.48
12:I:10:VAL:HG13	12:I:11:ALA:N	2.27	0.48
20:Q:57:THR:HG1	20:Q:73:PHE:C	2.17	0.48
3:4:147:ILE:HG21	3:4:308:PRO:HG2	1.95	0.48
4:A:2872:G:H2'	4:A:2873:U:C6	2.49	0.48
29:Z:20:ASP:C	29:Z:20:ASP:OD1	2.55	0.48
2:3:22:PRO:HB3	4:A:1102:G:H2'	1.96	0.48
4:A:356:G:H4'	4:A:358:G:C4	2.49	0.48
4:A:730:G:C2	16:M:113:LEU:HD11	2.48	0.48
4:A:1140:G:H1'	4:A:1142:G:O6	2.14	0.48
4:A:1314:C:H1'	21:R:4:VAL:HG22	1.95	0.48
4:A:2007:C:H2'	4:A:2008:A:N7	2.28	0.48
4:A:2585:U:H2'	4:A:2586:G:H5'	1.94	0.48
4:A:2588:C:H2'	4:A:2589:G:O4'	2.14	0.48
4:A:2717:U:C4	4:A:2718:G:C8	3.01	0.48
21:R:26:GLY:O	21:R:30:ARG:NH1	2.47	0.48
25:V:35:VAL:CG1	25:V:38:VAL:HG11	2.44	0.48
3:4:259:SER:HB2	3:4:272:VAL:HG12	1.94	0.48
4:A:1172:A:C6	4:A:1224:G:C6	3.01	0.48
4:A:1704:U:H2'	4:A:1705:C:C6	2.49	0.48
4:A:2393:A:O2'	4:A:2394:A:P	2.72	0.48
5:B:46:A:C4	5:B:47:A:C8	3.02	0.48
17:N:36:ALA:HB1	17:N:127:ILE:HD12	1.95	0.48
21:R:78:ARG:NH1	21:R:81:GLN:OE1	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4:458:PRO:HD2	3:4:459:LEU:H	1.79	0.48
4:A:22:U:C2'	4:A:23:G:O5'	2.61	0.48
4:A:273:A:H62	4:A:313:G:N2	2.12	0.48
4:A:1543:A:N7	4:A:1627:U:C2	2.79	0.48
4:A:2619:C:H2'	4:A:2620:G:O4'	2.14	0.48
13:J:56:ILE:CG1	13:J:72:LEU:HD22	2.44	0.48
19:P:40:VAL:HG23	19:P:49:VAL:HG12	1.96	0.48
22:S:54:ASP:O	22:S:58:VAL:HG12	2.14	0.48
3:4:283:THR:N	3:4:299:ASP:OD1	2.44	0.48
4:A:759:G:H22	27:X:64:PRO:HB3	1.78	0.48
4:A:2743:U:O4'	4:A:2766:A:N6	2.45	0.48
4:A:3014:A:N6	4:A:3113:A:OP2	2.33	0.48
5:B:10:G:HO2'	5:B:11:U:P	2.35	0.48
8:E:129:GLU:HA	8:E:129:GLU:OE1	2.13	0.48
14:K:10:ASP:O	14:K:12:THR:HG23	2.14	0.48
25:V:22:LYS:O	25:V:35:VAL:HG23	2.13	0.48
25:V:29:ASP:OD1	25:V:30:ARG:N	2.46	0.48
35:g:13:THR:HG22	35:g:14:VAL:N	2.29	0.48
4:A:813:C:O2'	4:A:849:A:N6	2.43	0.48
5:B:44:C:O2	9:F:99:ARG:NE	2.46	0.48
15:L:15:GLY:HA2	15:L:47:ILE:HD12	1.95	0.48
23:T:29:ASP:OD1	23:T:29:ASP:C	2.57	0.48
24:U:23:LEU:O	24:U:26:ASP:N	2.46	0.48
3:4:106:LEU:O	3:4:110:VAL:HG22	2.14	0.47
4:A:636:U:HO2'	4:A:637:G:C1'	2.26	0.47
4:A:842:A:P	4:A:1652:A:HO2'	2.37	0.47
4:A:2163:U:O2	4:A:2164:U:O2	2.32	0.47
6:C:108:PRO:HD2	6:C:111:LEU:HD22	1.95	0.47
7:D:6:ILE:HG13	7:D:34:ASN:OD1	2.13	0.47
19:P:22:HIS:NE2	19:P:103:ASP:OD2	2.47	0.47
20:Q:48:ARG:NH2	20:Q:59:THR:OG1	2.46	0.47
4:A:535:A:N1	4:A:542:A:O2'	2.28	0.47
4:A:1329:G:O6	4:A:1350:G:C2	2.68	0.47
4:A:1350:G:H2'	4:A:1351:G:C4	2.50	0.47
4:A:1485:C:H2'	4:A:1486:G:O4'	2.14	0.47
4:A:1532:G:HO2'	4:A:1533:U:C5'	2.25	0.47
4:A:2527:G:C6	4:A:2538:A:C6	3.02	0.47
9:F:67:ILE:HD11	9:F:145:PHE:CB	2.45	0.47
9:F:68:THR:HG21	9:F:96:VAL:HG21	1.97	0.47
19:P:100:VAL:CG2	19:P:125:LEU:HD11	2.39	0.47
3:4:250:ILE:O	3:4:300:THR:OG1	2.24	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1202:A:C8	12:I:51:VAL:HG21	2.50	0.47
4:A:1224:G:C5	4:A:1225:G:N7	2.82	0.47
4:A:1845:G:C6	4:A:1858:A:N7	2.82	0.47
4:A:2510:A:H4'	4:A:2511:A:O4'	2.14	0.47
4:A:2617:U:H4'	16:M:61:LEU:O	2.15	0.47
4:A:2798:G:O2'	7:D:154:CYS:N	2.44	0.47
4:A:3051:G:OP1	7:D:61:LYS:NZ	2.29	0.47
9:F:51:ALA:O	9:F:90:MET:SD	2.72	0.47
11:H:69:LYS:CB	11:H:136:LEU:HD22	2.43	0.47
3:4:258:LYS:N	36:4:501:GCP:O2B	2.47	0.47
4:A:296:A:H3'	4:A:297:G:H5''	1.97	0.47
4:A:1213:A:O2'	4:A:1214:A:P	2.71	0.47
4:A:1381:G:O2'	4:A:2236:G:O6	2.22	0.47
12:I:115:LEU:HD11	12:I:120:VAL:HG12	1.95	0.47
18:O:63:ARG:HA	18:O:80:PHE:CZ	2.49	0.47
3:4:29:LEU:O	3:4:31:THR:HG23	2.15	0.47
4:A:227:A:N1	4:A:505:C:O2'	2.40	0.47
4:A:1197:C:N4	4:A:1206:A:C5	2.82	0.47
4:A:1206:A:N6	13:J:136:SER:OG	2.47	0.47
4:A:1954:C:O2'	4:A:1955:A:O5'	2.27	0.47
4:A:2777:G:H3'	4:A:2778:U:C4'	2.44	0.47
6:C:19:SER:HB2	6:C:204:ILE:HD11	1.97	0.47
9:F:27:PHE:N	9:F:27:PHE:CD1	2.80	0.47
35:g:29:GLN:N	35:g:29:GLN:OE1	2.47	0.47
3:4:198:VAL:O	3:4:198:VAL:HG12	2.15	0.47
3:4:282:PRO:HG3	3:4:318:THR:HG22	1.95	0.47
3:4:369:ASN:CB	36:4:501:GCP:HN21	2.28	0.47
3:4:430:VAL:HG22	3:4:434:HIS:HD2	1.79	0.47
4:A:350:A:H3'	4:A:351:G:H21	1.80	0.47
4:A:665:G:N2	4:A:2255:A:OP1	2.43	0.47
4:A:929:C:H1'	4:A:1339:G:N2	2.30	0.47
4:A:1210:C:H3'	4:A:1211:G:C8	2.50	0.47
4:A:1878:G:C6	4:A:1879:G:N7	2.83	0.47
4:A:1930:C:OP2	4:A:1931:A:O2'	2.27	0.47
4:A:3033:G:H2'	4:A:3034:C:C6	2.50	0.47
7:D:40:ARG:N	7:D:49:ALA:O	2.45	0.47
8:E:118:ARG:NH2	8:E:191:ALA:O	2.44	0.47
9:F:161:ILE:HD12	9:F:162:THR:H	1.80	0.47
16:M:57:ILE:HD13	33:e:58:ILE:HD11	1.97	0.47
16:M:84:ASN:C	16:M:84:ASN:OD1	2.57	0.47
17:N:112:LYS:O	17:N:116:ASP:OD2	2.32	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4:119:ILE:HG22	3:4:120:CYS:N	2.29	0.47
4:A:368:U:O2'	4:A:369:G:O5'	2.21	0.47
4:A:2697:U:HO2'	4:A:2698:C:H6	1.61	0.47
4:A:2743:U:C6	4:A:2766:A:N6	2.82	0.47
7:D:161:PHE:O	7:D:164:THR:OG1	2.33	0.47
13:J:13:LEU:HD12	13:J:40:PHE:CE2	2.50	0.47
4:A:977:G:H2'	4:A:978:A:O4'	2.14	0.47
4:A:1122:C:H2'	4:A:1129:G:H2'	1.96	0.47
4:A:1156:A:C2	4:A:1236:G:C2	3.02	0.47
4:A:2624:C:C2'	4:A:2625:C:O5'	2.63	0.47
4:A:58:G:OP1	29:Z:48:ARG:NE	2.40	0.47
4:A:81:A:OP2	25:V:4:HIS:NE2	2.48	0.47
4:A:1530:G:H22	4:A:1805:G:H1	1.63	0.47
4:A:1640:A:H2'	4:A:1642:G:N7	2.30	0.47
5:B:9:G:OP1	19:P:37:ARG:NH2	2.48	0.47
8:E:119:ALA:HB2	8:E:124:ILE:HD12	1.96	0.47
13:J:13:LEU:HD12	13:J:40:PHE:CZ	2.50	0.47
19:P:25:LEU:O	19:P:29:VAL:HG12	2.15	0.47
24:U:9:ASP:OD1	24:U:10:ILE:N	2.48	0.47
4:A:253:C:OP2	33:e:5:LYS:NZ	2.46	0.46
4:A:1189:G:OP1	4:A:1189:G:C8	2.68	0.46
4:A:1516:G:H2'	4:A:1517:U:O4'	2.15	0.46
4:A:1729:A:C6	4:A:1731:A:N6	2.83	0.46
4:A:2162:A:N3	4:A:2162:A:H2'	2.30	0.46
4:A:2420:U:H1'	4:A:2421:A:C8	2.49	0.46
4:A:2702:A:C8	4:A:2753:G:N7	2.83	0.46
5:B:107:A:H2'	5:B:108:C:C6	2.49	0.46
13:J:81:LEU:CD1	13:J:134:ALA:HB2	2.45	0.46
3:4:342:GLN:O	3:4:346:VAL:HG12	2.16	0.46
4:A:1453:G:H2'	4:A:1454:G:O4'	2.15	0.46
4:A:2400:C:H2'	4:A:2401:U:C6	2.50	0.46
4:A:2697:U:H2'	4:A:2699:C:N4	2.30	0.46
5:B:47:A:C4	5:B:48:C:C6	3.03	0.46
5:B:107:A:H2'	5:B:108:C:O4'	2.15	0.46
6:C:15:GLY:O	6:C:205:ASN:ND2	2.49	0.46
3:4:257:GLY:HA2	36:4:501:GCP:PA	2.56	0.46
3:4:370:LYS:CG	36:4:501:GCP:HN22	2.22	0.46
4:A:161:U:O2'	4:A:162:A:OP2	2.31	0.46
4:A:265:A:N6	4:A:515:U:O2'	2.39	0.46
4:A:564:G:H22	4:A:567:A:C5'	2.28	0.46
4:A:752:C:C2	4:A:753:A:C8	3.03	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:979:G:H2'	4:A:980:C:C6	2.48	0.46
4:A:1083:G:O2'	4:A:1084:U:H5'	2.15	0.46
4:A:2155:U:H4'	4:A:2156:A:OP1	2.15	0.46
4:A:2531:G:H5'	4:A:2532:G:N7	2.31	0.46
4:A:2581:G:OP1	27:X:20:ARG:NE	2.48	0.46
4:A:2718:G:C5	4:A:2719:G:N7	2.83	0.46
4:A:2852:U:O2'	4:A:3006:G:OP1	2.23	0.46
9:F:26:GLU:C	9:F:27:PHE:HD1	2.22	0.46
10:G:105:GLU:OE2	10:G:115:LEU:HB2	2.16	0.46
11:H:82:VAL:HG11	11:H:91:LEU:HD21	1.97	0.46
16:M:28:SER:O	16:M:30:GLY:N	2.49	0.46
19:P:48:HIS:ND1	19:P:64:SER:OG	2.25	0.46
20:Q:39:ILE:HD11	20:Q:81:ASP:HB3	1.97	0.46
25:V:104:ASP:O	25:V:105:ILE:OXT	2.34	0.46
4:A:1178:U:O4	13:J:133:THR:HG22	2.15	0.46
4:A:1434:G:O2'	4:A:1435:C:H5'	2.15	0.46
4:A:1691:A:H2'	4:A:1692:G:O4'	2.16	0.46
9:F:149:ASP:OD1	9:F:149:ASP:N	2.48	0.46
10:G:44:SER:HG	10:G:52:VAL:C	2.19	0.46
11:H:78:VAL:HG23	11:H:144:VAL:HG21	1.97	0.46
14:K:13:ARG:NH2	14:K:49:ASP:O	2.43	0.46
3:4:388:ASP:OD2	3:4:388:ASP:C	2.59	0.46
3:4:422:ILE:HG12	3:4:433:VAL:HG21	1.98	0.46
4:A:741:G:H2'	4:A:742:G:O4'	2.16	0.46
4:A:773:G:H21	8:E:106:MET:HE2	1.80	0.46
4:A:933:G:O2'	4:A:934:A:O4'	2.33	0.46
4:A:996:G:H2'	4:A:997:G:N9	2.30	0.46
4:A:1536:A:H2'	4:A:1537:U:O4'	2.16	0.46
4:A:2008:A:C2	4:A:2046:A:C4'	2.99	0.46
16:M:57:ILE:CD1	33:e:58:ILE:HD11	2.44	0.46
4:A:598:U:H5'	4:A:1351:G:OP1	2.16	0.46
4:A:2016:G:C4	6:C:177:MET:HE3	2.51	0.46
4:A:2151:A:O2'	4:A:2152:A:OP1	2.32	0.46
4:A:2166:C:H4'	4:A:2168:U:P	2.55	0.46
4:A:2169:G:H4'	4:A:2170:U:H5'	1.98	0.46
4:A:2363:A:O2'	4:A:2364:C:O4'	2.24	0.46
4:A:2400:C:HO2'	4:A:2401:U:C4'	2.21	0.46
4:A:2851:G:N2	4:A:3001:G:OP2	2.48	0.46
4:A:3060:A:C5	4:A:3061:C:C5	3.04	0.46
6:C:245:HIS:ND1	6:C:246:PRO:HD2	2.31	0.46
16:M:23:GLY:HA2	16:M:30:GLY:O	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:W:37:LEU:HD11	26:W:99:VAL:HG12	1.98	0.46
4:A:389:G:N2	4:A:412:A:H61	2.14	0.46
4:A:1074:A:C6	4:A:1076:A:C4	3.03	0.46
4:A:2921:G:H2'	4:A:2922:U:O4'	2.16	0.46
6:C:193:VAL:HG12	6:C:194:GLY:N	2.30	0.46
12:I:53:LYS:NZ	12:I:55:THR:OG1	2.42	0.46
22:S:65:LEU:HB2	22:S:96:VAL:HG23	1.98	0.46
25:V:84:GLY:O	25:V:97:ILE:N	2.49	0.46
4:A:333:C:N4	4:A:445:U:O4	2.48	0.46
4:A:568:A:H1'	25:V:41:ILE:HD11	1.97	0.46
4:A:1514:C:OP1	24:U:85:LYS:NZ	2.33	0.46
4:A:1541:G:OP2	4:A:1629:G:N2	2.48	0.46
4:A:2301:C:H2'	4:A:2302:U:O4'	2.16	0.46
4:A:2973:A:O3'	10:G:63:ARG:HD2	2.15	0.46
6:C:131:LEU:N	6:C:131:LEU:HD23	2.31	0.46
20:Q:87:THR:OG1	20:Q:88:ARG:N	2.49	0.46
21:R:14:ARG:HA	21:R:32:TYR:CE1	2.51	0.46
3:4:39:VAL:HG21	3:4:46:LEU:HD13	1.98	0.46
3:4:197:GLY:N	3:4:204:GLY:HA3	2.31	0.46
3:4:257:GLY:HA2	36:4:501:GCP:O2A	2.16	0.46
4:A:222:A:O2'	4:A:508:G:N3	2.46	0.46
4:A:954:U:H2'	4:A:955:C:C6	2.50	0.46
4:A:1434:G:H2'	4:A:1435:C:C6	2.50	0.46
4:A:1728:U:H4'	4:A:1729:A:O5'	2.15	0.46
4:A:2502:A:H3'	4:A:2503:G:H5''	1.96	0.46
4:A:2788:A:C2'	4:A:2789:A:O5'	2.63	0.46
9:F:87:ARG:H	9:F:90:MET:HE3	1.81	0.46
9:F:109:ARG:O	9:F:113:ILE:HG22	2.16	0.46
10:G:104:LEU:O	10:G:115:LEU:HD12	2.16	0.46
14:K:31:ALA:CB	14:K:142:ILE:HG22	2.46	0.46
16:M:124:VAL:HG21	16:M:137:ILE:HD11	1.97	0.46
21:R:48:ARG:CZ	21:R:49:ASP:OD1	2.64	0.46
4:A:226:A:C2	4:A:2631:G:H1'	2.51	0.46
4:A:695:G:O2'	4:A:770:A:N1	2.44	0.46
4:A:1087:G:H2'	4:A:1088:U:C6	2.51	0.46
4:A:2969:C:H2'	4:A:2970:U:O4'	2.16	0.46
7:D:6:ILE:HD13	7:D:31:ALA:HB1	1.98	0.46
13:J:79:LYS:HA	13:J:82:LEU:HD12	1.98	0.46
18:O:24:LEU:HD23	18:O:34:ILE:HD12	1.98	0.46
22:S:69:LYS:O	22:S:92:GLN:O	2.34	0.46
26:W:84:ASP:OD1	26:W:84:ASP:C	2.58	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4:371:ILE:HG22	3:4:394:ALA:H	1.80	0.45
4:A:2349:A:N6	4:A:2386:U:O4'	2.46	0.45
4:A:2551:A:H2'	4:A:2552:A:C8	2.50	0.45
9:F:144:MET:HE2	9:F:144:MET:HA	1.98	0.45
21:R:101:SER:O	21:R:102:ASP:C	2.58	0.45
35:g:38:CYS:SG	35:g:39:SER:N	2.88	0.45
35:g:42:HIS:O	35:g:46:THR:HG23	2.16	0.45
4:A:1629:G:O2'	4:A:1632:G:O6	2.20	0.45
4:A:184:C:C2	4:A:185:G:C8	3.04	0.45
4:A:378:G:OP2	4:A:378:G:N3	2.50	0.45
4:A:774:G:N2	8:E:36:GLN:OE1	2.22	0.45
4:A:1132:U:C2	4:A:1133:G:C8	3.04	0.45
4:A:1180:G:O6	4:A:1195:A:N6	2.49	0.45
4:A:2422:A:O3'	28:Y:63:ARG:NH2	2.49	0.45
4:A:3021:A:O4'	4:A:3022:G:C5	2.69	0.45
13:J:38:MET:HE3	13:J:38:MET:HA	1.98	0.45
13:J:71:ALA:O	13:J:72:LEU:HD23	2.17	0.45
4:A:425:U:H6	4:A:425:U:OP2	1.99	0.45
4:A:428:A:HO2'	4:A:429:A:P	2.37	0.45
4:A:637:G:C2	4:A:638:U:C4	3.05	0.45
4:A:708:G:N3	4:A:709:U:C5	2.84	0.45
4:A:1156:A:C6	4:A:1157:G:N7	2.85	0.45
4:A:1177:G:H4'	13:J:118:LEU:HD13	1.97	0.45
4:A:2552:A:H2'	4:A:2553:G:C8	2.52	0.45
9:F:51:ALA:HA	9:F:90:MET:SD	2.57	0.45
17:N:57:HIS:HE1	17:N:116:ASP:HB3	1.82	0.45
17:N:135:GLU:O	17:N:136:GLU:HB2	2.14	0.45
19:P:115:ALA:O	19:P:118:ASP:OD2	2.34	0.45
33:e:34:GLU:OE1	33:e:34:GLU:HA	2.17	0.45
3:4:399:GLY:C	3:4:400:LEU:HD22	2.41	0.45
4:A:621:U:H2'	4:A:622:C:C6	2.51	0.45
4:A:899:G:H5'	4:A:900:G:OP1	2.17	0.45
4:A:2050:C:H3'	4:A:2051:U:H5	1.82	0.45
4:A:2353:U:O2'	4:A:2356:G:O2'	2.31	0.45
4:A:2374:U:H4'	4:A:2375:G:OP1	2.17	0.45
4:A:2375:G:C2'	4:A:2376:G:O4'	2.64	0.45
4:A:3061:C:O2'	4:A:3062:C:H5'	2.15	0.45
5:B:51:G:O2'	5:B:52:G:O5'	2.30	0.45
12:I:104:VAL:HG22	12:I:105:ILE:N	2.31	0.45
3:4:443:GLU:OE1	3:4:452:LYS:N	2.50	0.45
4:A:1124:C:C2	4:A:1256:G:N2	2.85	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1706:A:C6	4:A:1724:G:C6	3.04	0.45
4:A:2175:U:O2'	4:A:2176:A:P	2.74	0.45
4:A:2713:G:O2'	4:A:2714:G:H5'	2.17	0.45
8:E:58:VAL:HG21	8:E:80:ARG:HB3	1.99	0.45
23:T:69:GLU:OE1	23:T:69:GLU:N	2.50	0.45
4:A:682:A:O2'	4:A:683:G:H5'	2.16	0.45
4:A:784:G:O2'	4:A:785:A:C8	2.66	0.45
4:A:944:A:N7	4:A:2472:C:H5'	2.32	0.45
4:A:986:G:O2'	4:A:987:A:H5'	2.17	0.45
4:A:1878:G:C2	4:A:1879:G:C8	3.05	0.45
6:C:177:MET:HB3	6:C:178:PRO:HD2	1.99	0.45
7:D:50:VAL:HG21	7:D:95:TYR:HD2	1.81	0.45
10:G:103:ASN:HB3	10:G:115:LEU:HD11	1.95	0.45
12:I:10:VAL:HG23	12:I:63:GLU:HG2	1.99	0.45
3:4:126:PRO:HG3	3:4:175:ARG:HA	1.99	0.45
4:A:1879:G:O6	4:A:2224:C:N4	2.50	0.45
4:A:2869:C:H4'	4:A:2956:G:O2'	2.17	0.45
4:A:3022:G:H2'	4:A:3023:G:O4'	2.17	0.45
5:B:61:C:HO2'	5:B:62:C:P	2.37	0.45
12:I:104:VAL:HG22	12:I:105:ILE:H	1.82	0.45
19:P:121:ARG:NE	19:P:127:PHE:OXT	2.50	0.45
35:g:15:GLN:HG3	35:g:35:VAL:O	2.16	0.45
4:A:306:U:H5''	11:H:41:ARG:HD3	1.99	0.45
4:A:413:G:H1	4:A:1324:G:N2	2.15	0.45
4:A:740:A:O2'	4:A:741:G:P	2.75	0.45
4:A:860:G:O2'	4:A:863:G:O2'	2.25	0.45
4:A:978:A:H2'	4:A:979:G:H8	1.80	0.45
4:A:1855:A:O2'	4:A:1856:C:H5'	2.17	0.45
4:A:2037:U:H4'	4:A:2038:A:OP2	2.17	0.45
4:A:2511:A:C5	4:A:2513:G:C8	3.05	0.45
10:G:8:PRO:HB3	10:G:52:VAL:HG22	1.98	0.45
10:G:134:VAL:HG23	10:G:134:VAL:O	2.17	0.45
12:I:39:LEU:O	12:I:39:LEU:HD23	2.16	0.45
3:4:248:VAL:HG22	3:4:327:LEU:HB3	1.99	0.45
3:4:260:SER:CA	3:4:272:VAL:HG11	2.47	0.45
4:A:361:A:N1	4:A:441:G:O4'	2.50	0.45
4:A:400:C:C3'	4:A:401:C:O4'	2.65	0.45
4:A:576:G:O3'	23:T:56:LYS:NZ	2.50	0.45
4:A:613:A:N1	4:A:2849:G:O2'	2.46	0.45
4:A:790:A:N3	4:A:2667:C:O2'	2.48	0.45
4:A:1875:U:OP1	7:D:146:ARG:N	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:2750:G:OP2	10:G:154:ARG:NH2	2.44	0.45
15:L:122:LEU:CD2	20:Q:69:VAL:HG11	2.47	0.45
1:2:55:GLU:OE2	1:2:55:GLU:HA	2.17	0.44
4:A:1325:U:C3'	4:A:1326:G:H5'	2.46	0.44
4:A:1735:U:H2'	4:A:1736:G:O4'	2.17	0.44
4:A:2560:A:N6	27:X:43:THR:OG1	2.46	0.44
4:A:3020:U:H2'	4:A:3021:A:C2	2.53	0.44
10:G:149:ILE:HG22	10:G:163:VAL:HG11	1.99	0.44
14:K:49:ASP:OD2	14:K:49:ASP:C	2.61	0.44
32:d:46:THR:OG1	32:d:47:ALA:N	2.50	0.44
4:A:251:A:C5	4:A:252:G:H1'	2.52	0.44
4:A:301:U:H3'	4:A:302:U:H4'	1.99	0.44
4:A:886:G:OP1	32:d:17:ARG:HD2	2.17	0.44
4:A:920:G:N2	4:A:944:A:OP1	2.47	0.44
4:A:1118:A:C2	4:A:1274:A:C2	3.05	0.44
4:A:1196:C:O2'	4:A:1206:A:O5'	2.34	0.44
4:A:1235:U:H2'	4:A:1236:G:O4'	2.17	0.44
4:A:1260:C:O2'	14:K:27:ARG:NH2	2.41	0.44
4:A:1529:U:H2'	4:A:1530:G:O4'	2.16	0.44
4:A:2178:G:H21	4:A:2774:G:H4'	1.81	0.44
4:A:2808:U:H2'	4:A:2809:U:H2'	1.99	0.44
4:A:2869:C:H3'	4:A:2870:C:H5'	1.98	0.44
4:A:3004:C:OP2	14:K:120:LYS:NZ	2.38	0.44
12:I:110:MET:O	12:I:113:LYS:N	2.46	0.44
19:P:63:ALA:HB3	19:P:88:ILE:CG2	2.48	0.44
20:Q:26:ASN:OD1	20:Q:26:ASN:O	2.35	0.44
25:V:38:VAL:O	25:V:39:ASN:C	2.60	0.44
4:A:497:G:O2'	4:A:498:G:H5'	2.18	0.44
4:A:820:A:H2'	4:A:821:A:O4'	2.18	0.44
4:A:1130:C:P	21:R:70:ARG:NH2	2.91	0.44
4:A:1534:C:O2	4:A:1534:C:O4'	2.36	0.44
4:A:3046:C:H2'	4:A:3047:A:O4'	2.17	0.44
18:O:75:VAL:HA	18:O:78:THR:HG22	1.99	0.44
3:4:75:GLU:O	3:4:78:GLY:N	2.50	0.44
3:4:392:VAL:HG13	3:4:392:VAL:O	2.17	0.44
4:A:646:U:H2'	4:A:647:G:O4'	2.17	0.44
4:A:1025:A:H2	4:A:2488:C:O2	1.99	0.44
4:A:1065:C:H1'	4:A:1102:G:C8	2.52	0.44
4:A:2567:U:O2'	4:A:2597:A:O2'	2.06	0.44
5:B:40:A:H2'	5:B:41:U:C6	2.53	0.44
10:G:13:SER:O	10:G:15:VAL:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:329:U:H2'	4:A:447:A:H61	1.82	0.44
4:A:635:G:OP2	4:A:635:G:N2	2.49	0.44
4:A:1132:U:N3	4:A:1133:G:N7	2.66	0.44
4:A:1172:A:C2	4:A:1173:G:C5	3.06	0.44
4:A:1177:G:H2'	4:A:1178:U:C4	2.52	0.44
4:A:3022:G:H2'	4:A:3023:G:C8	2.53	0.44
25:V:104:ASP:OD2	25:V:104:ASP:N	2.50	0.44
4:A:1168:A:H8	4:A:1169:A:C8	2.36	0.44
4:A:1182:C:C4	4:A:1183:U:C4	3.06	0.44
4:A:1823:C:H2'	4:A:1824:C:O4'	2.17	0.44
4:A:2167:U:O3'	4:A:2170:U:O4	2.36	0.44
4:A:2690:C:C4	4:A:2691:C:N4	2.86	0.44
7:D:74:GLY:O	7:D:75:VAL:HG13	2.17	0.44
13:J:56:ILE:HD11	13:J:72:LEU:HB3	2.00	0.44
4:A:821:A:N6	4:A:840:G:H1'	2.33	0.44
4:A:824:G:C6	4:A:838:G:C6	3.05	0.44
4:A:1247:A:N1	4:A:2793:G:O2'	2.25	0.44
4:A:1253:C:N4	4:A:1256:G:N7	2.66	0.44
4:A:1882:A:H61	4:A:2220:C:H42	1.66	0.44
4:A:2007:C:C3'	4:A:2008:A:C8	3.01	0.44
4:A:2007:C:C2'	4:A:2008:A:C8	3.00	0.44
4:A:2049:C:H2'	4:A:2050:C:C1'	2.48	0.44
4:A:2285:G:O2'	4:A:2287:C:N4	2.47	0.44
4:A:2750:G:C6	4:A:2751:C:C4	3.05	0.44
4:A:3046:C:O2	4:A:3046:C:O4'	2.36	0.44
6:C:25:THR:OG1	6:C:82:ILE:N	2.34	0.44
6:C:141:VAL:HG13	6:C:162:SER:HB2	1.99	0.44
9:F:141:GLU:O	9:F:143:SER:N	2.49	0.44
11:H:109:GLY:N	11:H:110:PRO:HD2	2.33	0.44
13:J:73:LYS:NZ	13:J:75:PRO:O	2.46	0.44
33:e:34:GLU:OE1	33:e:34:GLU:CA	2.66	0.44
4:A:1473:G:N1	4:A:1487:U:OP2	2.36	0.44
4:A:1530:G:N2	4:A:1805:G:H1	2.14	0.44
4:A:1797:C:O3'	4:A:1798:U:O4'	2.36	0.44
4:A:2022:U:C2	4:A:2023:C:C5	3.05	0.44
4:A:2598:C:N4	4:A:2599:G:O6	2.51	0.44
4:A:2653:G:N7	16:M:55:MET:HG3	2.33	0.44
4:A:2725:C:O2'	4:A:2726:G:OP2	2.31	0.44
13:J:23:ALA:HB3	13:J:24:PRO:HD3	2.00	0.44
14:K:112:ASN:OD1	14:K:112:ASN:N	2.50	0.44
17:N:2:LEU:HD23	17:N:70:PRO:HD3	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:P:125:LEU:HD12	19:P:126:LYS:N	2.32	0.44
3:4:107:ARG:NH1	3:4:136:VAL:O	2.49	0.44
4:A:1367:G:N2	21:R:37:GLU:OE2	2.40	0.44
4:A:2860:U:H2'	4:A:2861:U:C6	2.53	0.44
3:4:176:LEU:HD22	3:4:215:ILE:HD13	2.00	0.43
4:A:389:G:H21	4:A:412:A:N6	2.14	0.43
4:A:1203:A:H2'	4:A:1204:A:C4	2.53	0.43
4:A:1683:C:HO2'	4:A:2926:A:HO2'	1.58	0.43
4:A:2348:G:H22	4:A:2393:A:H5''	1.83	0.43
4:A:2787:U:C2	4:A:2789:A:OP2	2.71	0.43
5:B:33:C:C2	5:B:52:G:N2	2.86	0.43
10:G:79:GLY:O	10:G:83:GLY:N	2.50	0.43
3:4:15:LEU:HD22	3:4:100:SER:N	2.33	0.43
4:A:328:C:N3	4:A:448:U:C4	2.87	0.43
4:A:490:A:H61	4:A:510:A:H61	1.66	0.43
4:A:965:U:H2'	4:A:966:U:C6	2.53	0.43
4:A:2378:U:H2'	4:A:2379:G:O4'	2.19	0.43
11:H:11:HIS:O	11:H:12:LEU:HD22	2.18	0.43
11:H:105:LYS:CE	11:H:111:ASN:OD1	2.66	0.43
18:O:79:LEU:HD23	18:O:80:PHE:CD2	2.53	0.43
20:Q:23:ASP:O	20:Q:25:VAL:HG13	2.18	0.43
20:Q:97:TYR:O	20:Q:100:ARG:HG2	2.18	0.43
25:V:3:VAL:HG21	25:V:68:VAL:CG2	2.48	0.43
3:4:456:PRO:HB2	3:4:458:PRO:HD3	2.00	0.43
4:A:326:A:C6	4:A:327:U:C4	3.06	0.43
4:A:510:A:H2'	4:A:511:A:O4'	2.17	0.43
4:A:664:A:H5''	4:A:665:G:OP2	2.18	0.43
4:A:672:C:H2'	4:A:673:C:C6	2.54	0.43
4:A:898:A:O2'	4:A:900:G:OP1	2.31	0.43
4:A:1543:A:C5	4:A:1627:U:O2	2.70	0.43
4:A:1806:A:H2'	4:A:1807:C:C6	2.54	0.43
4:A:2164:U:C2	4:A:2166:C:N4	2.86	0.43
4:A:2376:G:O2'	4:A:2377:G:H5'	2.18	0.43
10:G:15:VAL:HG23	10:G:17:VAL:CG2	2.48	0.43
13:J:56:ILE:HG13	13:J:72:LEU:HD22	2.00	0.43
17:N:48:GLU:C	17:N:48:GLU:OE1	2.61	0.43
20:Q:38:ARG:NH2	20:Q:40:GLN:OE1	2.51	0.43
25:V:27:TYR:O	25:V:31:ASN:N	2.51	0.43
4:A:296:A:C2	4:A:297:G:H1'	2.53	0.43
4:A:638:U:HO2'	4:A:639:C:H6	1.63	0.43
4:A:895:G:OP1	6:C:218:ARG:NH1	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1248:U:OP2	4:A:2794:G:N2	2.46	0.43
4:A:1833:C:H2'	4:A:1835:C:C5	2.54	0.43
4:A:1870:U:C4	18:O:8:PRO:HG2	2.54	0.43
4:A:1878:G:N1	4:A:1879:G:C5	2.86	0.43
4:A:2154:G:H1'	4:A:2155:U:N3	2.34	0.43
4:A:2530:C:H5''	4:A:2531:G:H2'	2.00	0.43
7:D:156:THR:HB	7:D:157:PRO:CD	2.48	0.43
9:F:80:SER:OG	9:F:88:GLU:N	2.46	0.43
20:Q:100:ARG:O	20:Q:103:ARG:NE	2.48	0.43
27:X:51:VAL:HG21	27:X:78:VAL:O	2.18	0.43
3:4:118:VAL:O	3:4:119:ILE:HD13	2.18	0.43
3:4:387:PRO:O	3:4:388:ASP:C	2.61	0.43
4:A:42:G:H5'	4:A:43:C:OP1	2.18	0.43
4:A:156:C:H2'	4:A:157:U:O4'	2.19	0.43
4:A:410:U:C2'	4:A:411:G:OP1	2.67	0.43
4:A:741:G:N3	4:A:2574:C:O2'	2.51	0.43
4:A:919:A:H5''	4:A:920:G:OP1	2.18	0.43
4:A:2376:G:H2'	4:A:2377:G:C8	2.54	0.43
4:A:2576:A:N6	4:A:2589:G:O2'	2.50	0.43
4:A:2698:C:H3'	4:A:2699:C:C6	2.53	0.43
4:A:3041:C:O2'	4:A:3042:A:OP1	2.30	0.43
5:B:81:U:H2'	5:B:82:A:C8	2.53	0.43
12:I:22:ALA:HA	12:I:109:TYR:O	2.19	0.43
12:I:66:ILE:HG22	12:I:109:TYR:CE2	2.53	0.43
19:P:9:ASN:OD1	19:P:10:ILE:N	2.51	0.43
22:S:49:THR:O	22:S:49:THR:HG23	2.17	0.43
23:T:65:ALA:O	23:T:69:GLU:HG2	2.18	0.43
24:U:79:THR:HG22	24:U:80:LYS:N	2.34	0.43
26:W:10:LYS:HD3	26:W:10:LYS:C	2.43	0.43
28:Y:18:VAL:HG22	28:Y:24:ARG:HG2	2.00	0.43
4:A:768:G:HO2'	4:A:769:U:H5	1.64	0.43
4:A:809:U:OP1	6:C:59:LYS:NZ	2.42	0.43
4:A:1176:G:H22	13:J:129:ILE:HG12	1.83	0.43
4:A:1225:G:C6	4:A:1226:U:C4	3.07	0.43
4:A:1650:G:H2'	4:A:1651:C:C6	2.54	0.43
4:A:1693:C:N3	4:A:1694:C:C5	2.86	0.43
4:A:1831:A:C2	4:A:1837:G:C6	3.07	0.43
4:A:1847:U:O4	4:A:1848:A:N6	2.51	0.43
4:A:2220:C:H4'	4:A:2221:A:OP1	2.18	0.43
6:C:233:HIS:HB2	6:C:242:GLY:HA2	2.00	0.43
14:K:30:SER:N	14:K:108:MET:HE1	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:K:92:LEU:HD22	14:K:99:ARG:HB3	2.00	0.43
27:X:26:PHE:N	27:X:29:GLN:OE1	2.38	0.43
3:4:394:ALA:O	36:4:501:GCP:C6	2.67	0.43
4:A:934:A:C4	4:A:1304:A:C2	3.06	0.43
4:A:1129:G:C5	4:A:1131:G:C8	3.06	0.43
4:A:1430:C:O2'	4:A:1507:G:H1'	2.18	0.43
6:C:135:ASN:O	6:C:135:ASN:CG	2.62	0.43
7:D:5:GLY:CA	7:D:84:LEU:HD21	2.48	0.43
8:E:14:THR:O	8:E:14:THR:OG1	2.34	0.43
18:O:65:GLU:O	18:O:68:LYS:HG2	2.18	0.43
22:S:69:LYS:HB3	22:S:91:ARG:HG2	2.01	0.43
3:4:255:ASN:HB2	3:4:276:LEU:HD13	2.01	0.43
4:A:1013:U:O3'	4:A:1014:G:O4'	2.36	0.43
4:A:1644:G:H4'	4:A:1712:G:H21	1.84	0.43
4:A:1758:G:HO2'	4:A:1759:A:C5'	2.31	0.43
4:A:2819:G:N2	4:A:2822:A:OP2	2.38	0.43
11:H:4:ILE:HD12	11:H:45:ARG:CB	2.49	0.43
12:I:17:PHE:HE2	12:I:109:TYR:HB3	1.83	0.43
16:M:32:THR:O	16:M:33:ALA:C	2.62	0.43
20:Q:5:ASP:OD1	20:Q:5:ASP:O	2.36	0.43
31:c:15:CYS:SG	31:c:16:GLU:N	2.92	0.43
32:d:16:ALA:O	32:d:20:GLY:HA3	2.19	0.43
4:A:378:G:C8	4:A:424:G:O6	2.72	0.43
4:A:797:G:H5'	32:d:29:ALA:HB2	2.00	0.43
4:A:1154:G:C6	4:A:1238:G:C6	3.06	0.43
5:B:58:A:O4'	9:F:31:ASN:OD1	2.37	0.43
9:F:57:ILE:HA	9:F:60:ALA:HB3	2.00	0.43
11:H:88:THR:HG23	11:H:90:LYS:H	1.84	0.43
12:I:21:THR:HG22	12:I:84:GLY:HA2	2.01	0.43
15:L:37:ASP:OD1	15:L:37:ASP:N	2.52	0.43
20:Q:30:LYS:NZ	20:Q:78:PRO:O	2.50	0.43
1:2:9:VAL:HG23	1:2:10:ARG:H	1.84	0.43
4:A:150:C:H2'	4:A:151:A:H8	1.84	0.43
4:A:285:U:H3'	4:A:286:G:C5'	2.48	0.43
4:A:476:G:C8	4:A:478:A:C8	3.06	0.43
4:A:663:A:N3	4:A:663:A:H2'	2.34	0.43
4:A:736:G:N2	4:A:739:U:OP2	2.49	0.43
4:A:1367:G:N7	21:R:36:LYS:NZ	2.60	0.43
4:A:1886:A:H4'	4:A:1887:A:O5'	2.19	0.43
4:A:2531:G:O6	9:F:47:VAL:O	2.37	0.43
4:A:2857:A:C2	4:A:2858:G:C5	3.07	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:3014:A:H1'	4:A:3112:A:N6	2.34	0.43
9:F:100:GLY:O	9:F:101:ASP:C	2.61	0.43
10:G:80:VAL:HA	10:G:137:ILE:HD11	2.01	0.43
20:Q:32:ILE:HD12	20:Q:32:ILE:H	1.82	0.43
21:R:106:PHE:O	21:R:110:VAL:HG23	2.19	0.43
29:Z:5:THR:HG23	29:Z:5:THR:O	2.19	0.43
29:Z:7:PRO:HA	29:Z:10:LEU:HB3	2.01	0.43
4:A:24:G:C2	4:A:599:G:N3	2.87	0.42
4:A:114:G:OP2	4:A:116:A:O2'	2.23	0.42
4:A:182:C:O2'	4:A:520:A:N3	2.45	0.42
4:A:335:G:N2	4:A:347:U:H1'	2.34	0.42
4:A:406:A:OP1	8:E:171:ASN:ND2	2.51	0.42
4:A:579:A:C2'	4:A:580:G:H5'	2.49	0.42
4:A:1213:A:O2'	4:A:1214:A:H8	2.01	0.42
4:A:1665:U:C4	4:A:1687:G:C2	3.07	0.42
4:A:1754:G:C6	4:A:1759:A:N6	2.86	0.42
4:A:2698:C:H2'	4:A:2698:C:O2	2.19	0.42
4:A:2869:C:H3'	4:A:2870:C:C5'	2.47	0.42
6:C:233:HIS:HB2	6:C:242:GLY:CA	2.49	0.42
8:E:30:ASN:O	8:E:34:MET:HG3	2.19	0.42
8:E:135:THR:O	8:E:136:PRO:C	2.60	0.42
9:F:130:ASP:OD1	9:F:130:ASP:N	2.50	0.42
23:T:69:GLU:CG	23:T:71:LEU:HD13	2.48	0.42
3:4:54:VAL:HG21	3:4:97:TYR:CD2	2.53	0.42
4:A:402:G:H1'	4:A:405:G:C6	2.53	0.42
4:A:800:A:C8	4:A:888:U:O4	2.71	0.42
4:A:976:A:H2'	4:A:977:G:O4'	2.19	0.42
4:A:1189:G:N2	4:A:1207:G:N3	2.67	0.42
4:A:1418:G:O2'	4:A:1419:A:H5'	2.19	0.42
4:A:2034:G:N3	4:A:2034:G:H2'	2.33	0.42
4:A:2152:A:O2'	4:A:2153:G:N2	2.52	0.42
4:A:2872:G:H2'	4:A:2873:U:H6	1.84	0.42
4:A:2874:C:C2	4:A:2895:A:C2	3.06	0.42
4:A:3037:C:O2	4:A:3037:C:H2'	2.19	0.42
4:A:3114:A:C8	4:A:3115:A:O4'	2.72	0.42
5:B:46:A:C6	5:B:47:A:C4	3.06	0.42
15:L:9:LYS:CG	15:L:10:VAL:N	2.82	0.42
25:V:101:ASN:O	25:V:103:LYS:NZ	2.52	0.42
34:f:36:GLN:O	34:f:37:GLY:OXT	2.37	0.42
3:4:56:THR:O	3:4:57:GLU:C	2.61	0.42
4:A:900:G:C4	4:A:901:C:C5	3.07	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1381:G:N7	23:T:22:THR:OG1	2.51	0.42
4:A:1762:C:H2'	4:A:1763:G:O4'	2.19	0.42
4:A:2175:U:O2'	4:A:2177:A:OP2	2.24	0.42
4:A:2274:C:H2'	4:A:2275:A:O4'	2.18	0.42
4:A:2842:G:H21	7:D:160:VAL:HG21	1.84	0.42
4:A:3028:A:H2'	4:A:3029:U:O4'	2.19	0.42
6:C:155:LEU:HD13	6:C:177:MET:CE	2.47	0.42
9:F:115:LEU:O	9:F:118:ILE:CG2	2.67	0.42
11:H:5:LEU:O	11:H:16:GLY:N	2.52	0.42
14:K:35:LEU:HD13	14:K:40:HIS:CE1	2.54	0.42
3:4:9:ALA:CB	3:4:10:PRO:HD2	2.43	0.42
3:4:126:PRO:O	3:4:129:LEU:HG	2.19	0.42
3:4:417:THR:O	3:4:417:THR:HG22	2.20	0.42
4:A:196:A:N6	4:A:2654:A:O2'	2.52	0.42
4:A:294:G:C8	4:A:295:U:C5	3.08	0.42
4:A:569:G:H4'	4:A:569:G:OP1	2.20	0.42
4:A:2795:C:O2'	7:D:157:PRO:HD3	2.19	0.42
4:A:3028:A:C6	4:A:3029:U:C5	3.07	0.42
15:L:75:SER:OG	15:L:76:TYR:N	2.53	0.42
24:U:28:VAL:HG13	24:U:83:ILE:HG22	2.01	0.42
33:e:26:LYS:CE	33:e:48:THR:HG23	2.50	0.42
3:4:129:LEU:C	3:4:129:LEU:HD12	2.44	0.42
4:A:246:U:C2	4:A:247:G:C8	3.08	0.42
4:A:301:U:O2'	4:A:302:U:OP1	2.31	0.42
4:A:423:C:O2	4:A:424:G:N7	2.52	0.42
4:A:994:A:C5	4:A:1015:A:C8	3.07	0.42
4:A:2151:A:O2'	4:A:2152:A:P	2.77	0.42
4:A:2234:G:H5''	23:T:49:ALA:HB3	2.00	0.42
4:A:2235:C:H2'	4:A:2236:G:O4'	2.19	0.42
9:F:129:PHE:CE2	9:F:132:THR:O	2.72	0.42
11:H:146:LEU:HD23	11:H:146:LEU:C	2.45	0.42
19:P:125:LEU:HD12	19:P:125:LEU:C	2.45	0.42
4:A:257:A:C5	4:A:258:G:C8	3.07	0.42
4:A:1176:G:C6	4:A:1199:U:O4	2.72	0.42
4:A:2025:C:O2	4:A:2025:C:O4'	2.36	0.42
4:A:2595:G:C2'	4:A:2596:G:O5'	2.68	0.42
4:A:2758:A:C5	4:A:2759:G:C8	3.08	0.42
7:D:54:TYR:CG	7:D:55:GLY:N	2.88	0.42
21:R:88:VAL:HG12	22:S:50:SER:HB2	2.01	0.42
28:Y:36:VAL:O	28:Y:36:VAL:HG23	2.20	0.42
3:4:59:SER:O	3:4:63:ALA:N	2.38	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4:116:ASP:C	3:4:117:THR:HG1	2.20	0.42
3:4:198:VAL:HB	3:4:203:PRO:O	2.18	0.42
4:A:101:U:C5	4:A:102:C:C5	3.08	0.42
4:A:403:U:O5'	4:A:404:A:OP2	2.37	0.42
4:A:458:G:O5'	4:A:511:A:N6	2.51	0.42
4:A:895:G:C2	4:A:897:A:C2	3.08	0.42
4:A:910:C:H2'	4:A:911:U:C6	2.55	0.42
4:A:1177:G:OP2	4:A:1178:U:H3'	2.19	0.42
4:A:1214:A:H2'	4:A:1215:U:C4'	2.49	0.42
4:A:2161:A:N1	4:A:2193:A:C2	2.87	0.42
4:A:2362:C:HO2'	4:A:2363:A:P	2.30	0.42
4:A:2680:C:N3	4:A:2681:U:C5	2.87	0.42
4:A:2883:G:N3	4:A:2885:G:OP2	2.53	0.42
8:E:164:VAL:O	8:E:169:VAL:HG23	2.19	0.42
9:F:113:ILE:HD12	35:g:37:VAL:O	2.19	0.42
10:G:105:GLU:OE2	10:G:114:VAL:O	2.38	0.42
16:M:75:TYR:OH	16:M:128:LYS:NZ	2.49	0.42
19:P:74:ASP:C	19:P:74:ASP:OD2	2.62	0.42
23:T:81:VAL:HG23	23:T:112:VAL:HG22	2.01	0.42
26:W:33:VAL:HG11	26:W:54:PHE:HD2	1.84	0.42
3:4:28:GLY:O	3:4:29:LEU:C	2.63	0.42
3:4:279:THR:O	3:4:279:THR:HG23	2.19	0.42
36:4:501:GCP:H8	36:4:501:GCP:H2'	1.75	0.42
4:A:159:A:C5	4:A:166:A:C2	3.08	0.42
4:A:872:G:H2'	4:A:873:G:H5'	2.01	0.42
4:A:1089:C:OP1	4:A:1092:G:C8	2.73	0.42
4:A:1877:U:C2	4:A:1878:G:C8	3.08	0.42
4:A:1886:A:O2'	4:A:1892:G:N7	2.46	0.42
4:A:2363:A:C2'	4:A:2364:C:O4'	2.67	0.42
8:E:33:LEU:CD1	8:E:106:MET:HG2	2.49	0.42
33:e:29:ARG:O	33:e:33:LEU:HD21	2.20	0.42
4:A:7:U:O4	4:A:3114:A:C8	2.73	0.42
4:A:619:C:O2	4:A:619:C:H2'	2.20	0.42
4:A:963:U:C2	4:A:964:C:C6	3.07	0.42
4:A:3036:C:C4	4:A:3037:C:C5	3.08	0.42
4:A:3055:G:H2'	4:A:3100:A:H61	1.85	0.42
5:B:10:G:H2'	5:B:11:U:C5	2.55	0.42
16:M:51:GLU:OE2	16:M:57:ILE:N	2.45	0.42
3:4:319:LEU:HA	3:4:322:VAL:HG12	2.02	0.42
4:A:3:A:N3	14:K:135:GLN:NE2	2.67	0.42
4:A:390:G:O2'	4:A:411:G:N2	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:573:C:N3	4:A:574:C:C5	2.88	0.42
4:A:1094:G:H4'	4:A:1275:A:N7	2.34	0.42
4:A:1753:C:H2'	4:A:1754:G:C1'	2.50	0.42
4:A:3110:C:H2'	4:A:3111:G:O4'	2.20	0.42
6:C:65:ILE:HG21	6:C:106:ILE:HD11	2.01	0.42
12:I:26:THR:HA	12:I:106:LYS:HB3	2.02	0.42
13:J:115:LYS:HE3	13:J:130:ILE:HD11	2.01	0.42
20:Q:16:ILE:HD11	20:Q:76:HIS:CD2	2.55	0.42
3:4:36:VAL:O	3:4:36:VAL:HG22	2.19	0.41
3:4:42:ARG:O	3:4:43:GLN:NE2	2.53	0.41
4:A:402:G:N2	4:A:405:G:C8	2.87	0.41
4:A:405:G:OP2	4:A:406:A:H8	2.03	0.41
4:A:579:A:H2'	4:A:580:G:H5'	2.01	0.41
4:A:747:A:H2	4:A:768:G:H21	1.67	0.41
4:A:1067:G:C2'	4:A:1068:C:O5'	2.68	0.41
4:A:1407:G:H2'	4:A:1408:C:C6	2.55	0.41
4:A:1899:G:OP2	4:A:1974:A:N6	2.51	0.41
4:A:2628:U:H2'	4:A:2629:G:O4'	2.20	0.41
9:F:64:LEU:O	9:F:67:ILE:HG22	2.19	0.41
10:G:39:GLU:N	10:G:40:PRO:CD	2.83	0.41
11:H:146:LEU:HD21	11:H:148:VAL:HG22	2.02	0.41
16:M:93:VAL:HG23	16:M:94:GLY:H	1.85	0.41
19:P:115:ALA:HA	19:P:118:ASP:OD2	2.20	0.41
26:W:24:SER:OG	26:W:28:ARG:NH1	2.44	0.41
4:A:75:U:C2	4:A:106:G:N2	2.88	0.41
4:A:367:U:H2'	4:A:368:U:O4'	2.20	0.41
4:A:754:C:C2	4:A:755:A:C8	3.09	0.41
4:A:1064:A:H2'	4:A:1065:C:O4'	2.20	0.41
4:A:1757:U:H3'	4:A:1758:G:C5'	2.50	0.41
4:A:2050:C:H4'	4:A:2051:U:OP1	2.20	0.41
4:A:2193:A:H4'	4:A:2196:G:H1'	2.03	0.41
4:A:2947:C:H2'	4:A:2948:C:O4'	2.20	0.41
4:A:2969:C:O2	10:G:140:GLN:NE2	2.46	0.41
4:A:3022:G:O2'	4:A:3023:G:O5'	2.39	0.41
5:B:27:A:C2	5:B:28:A:H1'	2.55	0.41
9:F:118:ILE:HG21	9:F:121:PHE:CB	2.50	0.41
11:H:91:LEU:HD12	11:H:125:LYS:CA	2.48	0.41
14:K:49:ASP:OD2	14:K:121:LYS:NZ	2.38	0.41
19:P:87:LEU:O	19:P:90:GLU:HG2	2.20	0.41
23:T:28:ILE:HG23	23:T:81:VAL:HG13	2.02	0.41
24:U:8:ARG:NH1	24:U:8:ARG:HB2	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4:46:LEU:HD23	3:4:46:LEU:H	1.85	0.41
4:A:246:U:C4	4:A:247:G:N7	2.89	0.41
4:A:473:C:O2	4:A:478:A:H2	2.03	0.41
4:A:531:A:C5	8:E:46:ARG:HD2	2.56	0.41
4:A:875:G:H2'	4:A:876:A:O4'	2.19	0.41
4:A:1016:C:H2'	4:A:1017:G:O4'	2.20	0.41
4:A:1756:G:O2'	4:A:1758:G:C1'	2.68	0.41
4:A:1771:U:H2'	4:A:1772:G:O4'	2.20	0.41
4:A:1878:G:C6	4:A:2225:A:C6	3.07	0.41
4:A:1879:G:H2'	4:A:1880:U:C6	2.55	0.41
4:A:2190:A:H4'	4:A:2191:C:OP1	2.19	0.41
4:A:3103:A:H3'	4:A:3104:A:H5''	2.01	0.41
6:C:232:PRO:O	6:C:233:HIS:HD2	1.99	0.41
9:F:111:ILE:HD11	9:F:181:GLY:O	2.21	0.41
12:I:7:ALA:O	12:I:10:VAL:HG12	2.20	0.41
17:N:42:ILE:N	17:N:42:ILE:HD13	2.35	0.41
18:O:45:ARG:HB3	18:O:46:PRO:HD3	2.01	0.41
20:Q:45:VAL:O	20:Q:47:ILE:HG23	2.19	0.41
25:V:8:THR:O	25:V:74:VAL:HG22	2.19	0.41
25:V:88:ASP:HB2	25:V:92:GLY:H	1.85	0.41
31:c:32:ASP:OD2	31:c:32:ASP:N	2.52	0.41
3:4:15:LEU:H	3:4:22:SER:HB2	1.86	0.41
4:A:159:A:C6	4:A:160:A:C6	3.08	0.41
4:A:544:U:H2'	4:A:545:A:H5'	2.03	0.41
4:A:559:A:H2'	4:A:560:U:O4'	2.19	0.41
4:A:709:U:O2	4:A:709:U:O4'	2.36	0.41
4:A:733:U:H2'	4:A:734:C:C6	2.55	0.41
4:A:1878:G:C6	4:A:2225:A:N1	2.89	0.41
4:A:1908:A:H2'	4:A:1909:C:O4'	2.20	0.41
4:A:2054:C:N4	4:A:2156:A:H5'	2.35	0.41
4:A:2860:U:O2'	7:D:47:TYR:OH	2.26	0.41
4:A:2949:A:O2'	4:A:2950:C:OP2	2.31	0.41
7:D:11:LEU:HB3	7:D:28:VAL:HG13	2.01	0.41
9:F:33:MET:SD	9:F:33:MET:N	2.93	0.41
9:F:68:THR:OG1	9:F:96:VAL:HG11	2.20	0.41
10:G:24:LEU:HD23	10:G:35:LEU:O	2.20	0.41
10:G:79:GLY:HA3	10:G:84:TYR:CE2	2.55	0.41
14:K:35:LEU:HD21	14:K:140:PHE:CE2	2.56	0.41
15:L:122:LEU:HD21	20:Q:69:VAL:HG11	2.02	0.41
33:e:34:GLU:CD	33:e:35:HIS:N	2.78	0.41
3:4:332:VAL:HG12	3:4:333:ASP:H	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:4:370:LYS:CG	36:4:501:GCP:N2	2.79	0.41
4:A:400:C:H2'	4:A:401:C:O4'	2.21	0.41
4:A:729:C:H2'	4:A:730:G:O4'	2.21	0.41
4:A:799:G:OP1	32:d:24:ARG:NH2	2.54	0.41
4:A:981:U:C4'	4:A:982:A:OP2	2.68	0.41
4:A:1191:A:C4	4:A:1192:G:C8	3.09	0.41
4:A:1860:G:O2'	4:A:1861:G:H5'	2.19	0.41
4:A:2590:A:H2'	4:A:2591:G:O4'	2.19	0.41
4:A:2980:U:H4'	4:A:2981:A:OP1	2.20	0.41
4:A:3067:C:H2'	4:A:3068:U:O4'	2.19	0.41
5:B:48:C:C4	5:B:49:C:C4	3.09	0.41
9:F:135:TYR:O	9:F:162:THR:OG1	2.37	0.41
10:G:87:LYS:HB2	10:G:166:GLU:HB3	2.02	0.41
10:G:119:PRO:O	10:G:120:GLU:HG3	2.21	0.41
11:H:102:ASN:O	11:H:105:LYS:HG2	2.20	0.41
13:J:51:GLN:HG3	13:J:54:ASN:HB2	2.03	0.41
22:S:41:LEU:HD11	22:S:48:VAL:HG13	2.01	0.41
3:4:260:SER:HA	3:4:272:VAL:HG11	2.02	0.41
4:A:579:A:H2'	4:A:580:G:O4'	2.20	0.41
4:A:789:G:OP1	8:E:55:ARG:NH2	2.53	0.41
4:A:1535:C:O2	4:A:1535:C:O4'	2.38	0.41
4:A:1541:G:C6	4:A:1631:A:N1	2.83	0.41
4:A:2171:C:O4'	4:A:2171:C:OP2	2.39	0.41
4:A:2490:A:H4'	4:A:2491:A:N3	2.36	0.41
4:A:3046:C:O2	4:A:3046:C:O5'	2.38	0.41
4:A:3108:G:O2'	4:A:3109:C:H5'	2.20	0.41
5:B:34:G:C2	5:B:51:G:N1	2.89	0.41
5:B:46:A:C2	5:B:47:A:H1'	2.56	0.41
6:C:233:HIS:HB2	6:C:243:GLY:N	2.35	0.41
9:F:86:LEU:HD23	9:F:87:ARG:N	2.35	0.41
19:P:102:PHE:HB2	19:P:127:PHE:CD2	2.56	0.41
31:c:46:GLY:O	31:c:47:THR:HG23	2.21	0.41
4:A:402:G:H1'	4:A:405:G:N1	2.35	0.41
4:A:645:G:H2'	4:A:646:U:C6	2.55	0.41
4:A:898:A:C2	4:A:900:G:C8	3.08	0.41
4:A:1173:G:O2'	12:I:33:VAL:HG13	2.21	0.41
4:A:1175:A:N6	4:A:1176:G:O6	2.54	0.41
4:A:1243:G:H5'	34:f:37:GLY:OXT	2.21	0.41
4:A:1343:G:H5''	4:A:1344:A:OP1	2.20	0.41
4:A:1464:A:H3'	4:A:1465:C:C5'	2.51	0.41
4:A:1711:G:O4'	6:C:99:ASP:OD1	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:1804:G:H2'	4:A:1805:G:C8	2.56	0.41
4:A:1858:A:C4	4:A:1859:A:C8	3.08	0.41
4:A:2007:C:O3'	4:A:2008:A:H8	2.04	0.41
4:A:2515:U:H4'	4:A:2604:U:O2	2.20	0.41
11:H:87:ASP:OD1	11:H:88:THR:N	2.52	0.41
13:J:30:LEU:O	13:J:35:VAL:O	2.39	0.41
33:e:34:GLU:O	33:e:35:HIS:CG	2.72	0.41
4:A:1181:G:C6	4:A:1194:C:N4	2.89	0.41
4:A:1400:G:H22	4:A:1443:G:H5''	1.86	0.41
4:A:1532:G:N2	4:A:1804:G:C5	2.89	0.41
4:A:2155:U:H1'	4:A:2156:A:H2'	2.02	0.41
5:B:54:A:C4	5:B:55:G:H1'	2.55	0.41
5:B:57:U:O2'	5:B:58:A:OP2	2.38	0.41
6:C:158:SER:O	6:C:196:VAL:HG11	2.21	0.41
8:E:162:ASP:OD1	8:E:164:VAL:HG13	2.20	0.41
21:R:80:ILE:O	21:R:84:LYS:HG2	2.21	0.41
27:X:53:ARG:NH2	27:X:57:ASP:OD2	2.53	0.41
27:X:68:GLU:OE1	27:X:68:GLU:C	2.63	0.41
3:4:9:ALA:HB3	3:4:10:PRO:CD	2.43	0.41
3:4:317:SER:O	3:4:321:GLU:HG2	2.21	0.41
4:A:252:G:H2'	4:A:253:C:H6	1.86	0.41
4:A:256:A:C4	4:A:257:A:C8	3.09	0.41
4:A:278:A:H2'	4:A:279:U:C6	2.56	0.41
4:A:381:A:O2'	4:A:400:C:O2	2.38	0.41
4:A:523:U:H2'	4:A:524:C:H5'	2.03	0.41
4:A:564:G:H22	4:A:567:A:H5'	1.85	0.41
4:A:737:A:C2'	4:A:738:A:O5'	2.69	0.41
4:A:987:A:H2	4:A:1022:C:C4	2.39	0.41
4:A:1046:C:O2'	4:A:1287:C:H1'	2.21	0.41
4:A:1176:G:C6	4:A:1177:G:C6	3.09	0.41
4:A:1268:C:O2'	4:A:1269:C:H5'	2.21	0.41
4:A:1295:U:C2	4:A:1296:G:C8	3.09	0.41
4:A:1437:A:N7	4:A:1438:G:N7	2.68	0.41
4:A:1625:G:HO2'	4:A:1626:G:C5'	2.33	0.41
4:A:1724:G:C2	4:A:1725:G:N7	2.89	0.41
4:A:1938:G:N1	4:A:1955:A:OP2	2.33	0.41
4:A:2362:C:C2'	4:A:2363:A:O5'	2.69	0.41
4:A:2400:C:HO2'	4:A:2401:U:C5'	2.34	0.41
4:A:2466:G:H2'	4:A:2467:U:O4'	2.20	0.41
4:A:2490:A:H4'	4:A:2491:A:O5'	2.21	0.41
4:A:2536:U:O2	9:F:44:ASN:ND2	2.39	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:2749:G:N1	4:A:2763:C:N3	2.68	0.41
4:A:2749:G:N2	4:A:2763:C:C2	2.89	0.41
4:A:3069:G:O2'	4:A:3070:G:OP2	2.31	0.41
7:D:36:VAL:HG12	7:D:52:LEU:CD2	2.50	0.41
7:D:112:VAL:HG22	7:D:180:LEU:O	2.21	0.41
10:G:105:GLU:OE2	10:G:114:VAL:C	2.63	0.41
13:J:90:GLY:HA3	13:J:137:MET:HE3	2.03	0.41
16:M:54:GLN:O	16:M:55:MET:C	2.63	0.41
23:T:32:ARG:NH2	23:T:81:VAL:O	2.53	0.41
28:Y:6:ASP:OD1	28:Y:6:ASP:N	2.53	0.41
28:Y:61:VAL:O	28:Y:61:VAL:HG23	2.21	0.41
3:4:138:VAL:HG22	3:4:139:LYS:N	2.35	0.41
3:4:366:LEU:HB2	3:4:388:ASP:O	2.21	0.41
3:4:434:HIS:CE1	3:4:439:VAL:HG21	2.56	0.41
4:A:410:U:H2'	4:A:411:G:OP1	2.21	0.41
4:A:644:G:H2'	4:A:645:G:H8	1.85	0.41
4:A:844:G:O2'	4:A:878:G:H4'	2.21	0.41
4:A:928:U:H2'	4:A:929:C:C6	2.56	0.41
4:A:928:U:O2'	4:A:1339:G:H1'	2.21	0.41
4:A:948:G:H2'	4:A:949:C:C6	2.55	0.41
4:A:1098:A:O2'	4:A:2261:U:O2'	2.17	0.41
4:A:1129:G:C6	4:A:1270:G:C6	3.09	0.41
4:A:1182:C:H2'	4:A:1183:U:O4'	2.21	0.41
4:A:1327:A:H2'	4:A:1328:A:O4'	2.21	0.41
4:A:1656:A:O2'	4:A:1657:G:H5'	2.21	0.41
4:A:1875:U:H2'	4:A:1876:A:H8	1.86	0.41
4:A:2686:U:H2'	4:A:2687:U:C6	2.56	0.41
22:S:72:LYS:HD2	22:S:91:ARG:HD2	2.03	0.41
1:2:5:LYS:NZ	1:2:34:SER:OG	2.48	0.40
3:4:172:MET:O	3:4:173:LEU:C	2.64	0.40
3:4:332:VAL:HG12	3:4:333:ASP:N	2.35	0.40
3:4:444:HIS:HA	3:4:449:THR:HG23	2.04	0.40
4:A:402:G:H2'	8:E:139:LYS:NZ	2.35	0.40
4:A:671:G:O2'	4:A:2243:C:OP1	2.37	0.40
4:A:702:A:H2'	4:A:703:C:O4'	2.21	0.40
4:A:953:G:C5	4:A:1058:A:N6	2.89	0.40
4:A:978:A:O2'	4:A:979:G:H5'	2.20	0.40
4:A:2289:C:H2'	4:A:2290:C:H6	1.86	0.40
4:A:2353:U:N3	4:A:2354:G:O6	2.55	0.40
4:A:2526:U:O2'	4:A:2527:G:H5'	2.21	0.40
8:E:3:LEU:O	8:E:4:LYS:C	2.63	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:E:167:LYS:HA	8:E:171:ASN:N	2.36	0.40
12:I:24:VAL:HG22	12:I:80:ALA:HB3	2.02	0.40
26:W:65:ALA:O	26:W:79:LEU:HD12	2.21	0.40
27:X:56:ASP:O	27:X:57:ASP:HB2	2.21	0.40
4:A:7:U:O2'	4:A:8:U:O4'	2.32	0.40
4:A:7:U:N3	4:A:3114:A:C4	2.89	0.40
4:A:360:G:H5''	4:A:361:A:H5'	2.02	0.40
4:A:636:U:O2	4:A:637:G:C6	2.74	0.40
4:A:714:U:O2'	4:A:715:A:OP2	2.32	0.40
4:A:899:G:H4'	4:A:900:G:O5'	2.20	0.40
4:A:997:G:C8	4:A:998:G:N7	2.89	0.40
4:A:1118:A:H2'	4:A:1119:A:C8	2.56	0.40
4:A:1357:G:H2'	4:A:1358:U:O4'	2.22	0.40
4:A:1406:U:O2'	4:A:1407:G:H5'	2.21	0.40
4:A:1630:U:H2'	4:A:1631:A:C8	2.56	0.40
4:A:2016:G:OP1	6:C:258:ARG:NE	2.42	0.40
4:A:2347:G:H3'	4:A:2348:G:H4'	2.03	0.40
4:A:2363:A:H2'	4:A:2364:C:N1	2.36	0.40
4:A:2495:G:H5''	27:X:18:ALA:HB1	2.04	0.40
4:A:2541:U:H2'	4:A:2542:G:O4'	2.21	0.40
4:A:2685:C:H2'	4:A:2686:U:C6	2.56	0.40
4:A:2740:G:O2'	4:A:2741:C:H5'	2.21	0.40
4:A:2759:G:C2	4:A:2760:G:C8	3.09	0.40
5:B:106:C:H4'	5:B:107:A:H5''	2.03	0.40
9:F:142:GLN:O	9:F:142:GLN:CG	2.69	0.40
25:V:45:THR:CG2	25:V:60:VAL:HG22	2.51	0.40
3:4:125:SER:OG	3:4:126:PRO:HD2	2.20	0.40
4:A:425:U:OP2	4:A:425:U:C6	2.74	0.40
4:A:494:G:H2'	4:A:495:C:O4'	2.21	0.40
4:A:842:A:O2'	4:A:843:G:H5'	2.20	0.40
4:A:971:G:C2	4:A:972:A:C6	3.09	0.40
4:A:972:A:C6	4:A:973:G:C6	3.09	0.40
4:A:1205:G:H2'	4:A:1207:G:O4'	2.22	0.40
4:A:1478:C:O2'	4:A:2026:A:O2'	2.39	0.40
4:A:1991:C:O2	4:A:1991:C:C2'	2.66	0.40
4:A:2053:C:H3'	4:A:2054:C:H5''	2.04	0.40
4:A:2412:U:H2'	4:A:2413:G:H8	1.86	0.40
4:A:2883:G:C2	4:A:2885:G:OP2	2.74	0.40
4:A:3014:A:C2	4:A:3015:C:C5	3.10	0.40
5:B:47:A:C6	5:B:48:C:C4	3.09	0.40
6:C:155:LEU:HD13	6:C:177:MET:SD	2.61	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:56:GLU:HA	7:D:56:GLU:OE2	2.21	0.40
7:D:64:LYS:HB2	7:D:65:PRO:HD3	2.03	0.40
8:E:161:THR:O	8:E:161:THR:OG1	2.38	0.40
10:G:12:PRO:HG2	10:G:50:ALA:HA	2.02	0.40
16:M:79:ASN:HA	16:M:113:LEU:O	2.21	0.40
19:P:8:GLN:N	19:P:8:GLN:CD	2.79	0.40
25:V:35:VAL:HG13	25:V:38:VAL:HG11	2.04	0.40
28:Y:37:ARG:HE	28:Y:48:ARG:NH2	2.19	0.40
28:Y:41:ARG:O	28:Y:43:GLY:N	2.53	0.40
3:4:28:GLY:O	3:4:29:LEU:HG	2.21	0.40
4:A:869:U:O2'	4:A:1387:A:N1	2.55	0.40
4:A:1291:G:N3	4:A:1292:U:O3'	2.55	0.40
4:A:1304:A:H2'	4:A:1305:G:H5'	2.04	0.40
4:A:2572:U:OP2	33:e:38:THR:HG21	2.22	0.40
4:A:2654:A:N3	4:A:2654:A:H2'	2.36	0.40
4:A:2904:C:O2'	4:A:2905:C:H5'	2.22	0.40
9:F:87:ARG:H	9:F:90:MET:CE	2.35	0.40
11:H:102:ASN:HA	11:H:105:LYS:CD	2.51	0.40
13:J:56:ILE:HG12	13:J:72:LEU:HD22	2.04	0.40
24:U:94:ASP:N	24:U:94:ASP:OD1	2.54	0.40
25:V:35:VAL:HG13	25:V:38:VAL:CG1	2.51	0.40
28:Y:14:PHE:CE2	28:Y:28:ARG:HD3	2.56	0.40
3:4:320:GLU:HA	3:4:323:VAL:HG12	2.03	0.40
4:A:139:U:O5'	4:A:139:U:O2	2.40	0.40
4:A:926:U:O2'	4:A:1365:G:O2'	2.12	0.40
4:A:1015:A:H2'	4:A:1016:C:O4'	2.21	0.40
4:A:1167:C:N3	4:A:1168:A:C6	2.89	0.40
4:A:1400:G:N2	4:A:1443:G:H5''	2.36	0.40
4:A:2318:U:H4'	11:H:11:HIS:ND1	2.36	0.40
4:A:2385:G:H2'	4:A:2387:U:C2	2.57	0.40
4:A:2427:G:OP1	6:C:148:ARG:NH1	2.54	0.40
4:A:2569:G:N3	4:A:2605:C:H2'	2.36	0.40
4:A:3023:G:H2'	4:A:3024:A:O4'	2.22	0.40
8:E:198:VAL:HG23	8:E:199:GLU:N	2.37	0.40
11:H:102:ASN:HA	11:H:105:LYS:HD3	2.04	0.40
14:K:25:LEU:HD13	14:K:62:ILE:HG12	2.03	0.40
20:Q:14:ASP:O	20:Q:15:ASP:HB3	2.22	0.40
24:U:28:VAL:O	24:U:28:VAL:HG12	2.20	0.40
25:V:3:VAL:HG21	25:V:68:VAL:HG23	2.02	0.40
27:X:30:VAL:O	27:X:30:VAL:HG23	2.20	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	2	57/61 (93%)	54 (95%)	3 (5%)	0	100	100
2	3	21/24 (88%)	20 (95%)	1 (5%)	0	100	100
3	4	466/470 (99%)	369 (79%)	97 (21%)	0	100	100
6	C	273/278 (98%)	248 (91%)	25 (9%)	0	100	100
7	D	212/217 (98%)	200 (94%)	12 (6%)	0	100	100
8	E	207/215 (96%)	185 (89%)	22 (11%)	0	100	100
9	F	180/187 (96%)	156 (87%)	24 (13%)	0	100	100
10	G	174/179 (97%)	160 (92%)	14 (8%)	0	100	100
11	H	149/151 (99%)	126 (85%)	23 (15%)	0	100	100
12	I	124/175 (71%)	110 (89%)	14 (11%)	0	100	100
13	J	131/142 (92%)	113 (86%)	18 (14%)	0	100	100
14	K	144/147 (98%)	127 (88%)	17 (12%)	0	100	100
15	L	120/122 (98%)	108 (90%)	12 (10%)	0	100	100
16	M	143/147 (97%)	127 (89%)	16 (11%)	0	100	100
17	N	134/138 (97%)	120 (90%)	14 (10%)	0	100	100
18	O	116/199 (58%)	109 (94%)	7 (6%)	0	100	100
19	P	124/127 (98%)	115 (93%)	9 (7%)	0	100	100
20	Q	111/113 (98%)	98 (88%)	13 (12%)	0	100	100
21	R	122/129 (95%)	114 (93%)	8 (7%)	0	100	100
22	S	98/103 (95%)	92 (94%)	6 (6%)	0	100	100
23	T	112/153 (73%)	109 (97%)	3 (3%)	0	100	100
24	U	95/100 (95%)	86 (90%)	9 (10%)	0	100	100
25	V	91/105 (87%)	80 (88%)	11 (12%)	0	100	100
26	W	93/215 (43%)	87 (94%)	6 (6%)	0	100	100
27	X	77/88 (88%)	74 (96%)	3 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	Y	61/64 (95%)	56 (92%)	5 (8%)	0	100	100
29	Z	62/77 (80%)	60 (97%)	2 (3%)	0	100	100
30	b	52/57 (91%)	46 (88%)	6 (12%)	0	100	100
31	c	47/55 (86%)	44 (94%)	3 (6%)	0	100	100
32	d	44/47 (94%)	42 (96%)	2 (4%)	0	100	100
33	e	61/64 (95%)	58 (95%)	3 (5%)	0	100	100
34	f	35/37 (95%)	33 (94%)	2 (6%)	0	100	100
35	g	46/75 (61%)	33 (72%)	13 (28%)	0	100	100
All	All	3982/4461 (89%)	3559 (89%)	423 (11%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	2	52/54 (96%)	51 (98%)	1 (2%)	50	73
2	3	18/19 (95%)	18 (100%)	0	100	100
3	4	370/372 (100%)	368 (100%)	2 (0%)	81	85
6	C	215/218 (99%)	214 (100%)	1 (0%)	81	85
7	D	160/163 (98%)	159 (99%)	1 (1%)	78	83
8	E	169/173 (98%)	168 (99%)	1 (1%)	78	83
9	F	151/156 (97%)	151 (100%)	0	100	100
10	G	148/150 (99%)	148 (100%)	0	100	100
11	H	90/116 (78%)	89 (99%)	1 (1%)	65	78
12	I	89/120 (74%)	88 (99%)	1 (1%)	65	78
13	J	102/108 (94%)	102 (100%)	0	100	100
14	K	119/120 (99%)	119 (100%)	0	100	100
15	L	100/100 (100%)	99 (99%)	1 (1%)	68	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	M	112/114 (98%)	112 (100%)	0	100	100
17	N	114/116 (98%)	112 (98%)	2 (2%)	51	73
18	O	97/158 (61%)	97 (100%)	0	100	100
19	P	93/94 (99%)	93 (100%)	0	100	100
20	Q	100/100 (100%)	100 (100%)	0	100	100
21	R	97/99 (98%)	97 (100%)	0	100	100
22	S	81/83 (98%)	81 (100%)	0	100	100
23	T	90/117 (77%)	89 (99%)	1 (1%)	65	78
24	U	83/85 (98%)	83 (100%)	0	100	100
25	V	79/86 (92%)	78 (99%)	1 (1%)	61	77
26	W	77/168 (46%)	76 (99%)	1 (1%)	61	77
27	X	58/63 (92%)	58 (100%)	0	100	100
28	Y	50/51 (98%)	50 (100%)	0	100	100
29	Z	58/66 (88%)	58 (100%)	0	100	100
30	b	43/46 (94%)	43 (100%)	0	100	100
31	c	47/52 (90%)	47 (100%)	0	100	100
32	d	35/36 (97%)	35 (100%)	0	100	100
33	e	53/54 (98%)	53 (100%)	0	100	100
34	f	35/35 (100%)	35 (100%)	0	100	100
35	g	43/63 (68%)	40 (93%)	3 (7%)	14	41
All	All	3228/3555 (91%)	3211 (100%)	17 (0%)	78	85

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	2	48	ASN
3	4	348	THR
3	4	379	LEU
6	C	53	HIS
7	D	37	THR
8	E	42	LEU
11	H	92	PHE
12	I	109	TYR
15	L	28	SER
17	N	44	ASN

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Mol	Chain	Res	Type
17	N	67	ASN
23	T	113	ILE
25	V	12	ILE
26	W	40	HIS
35	g	5	ILE
35	g	12	THR
35	g	23	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	2	8	GLN
1	2	19	GLN
3	4	434	HIS
6	C	135	ASN
6	C	201	GLN
7	D	183	HIS
8	E	100	GLN
8	E	171	ASN
8	E	202	ASN
9	F	24	GLN
12	I	54	ASN
12	I	100	ASN
14	K	130	HIS
18	O	31	HIS
19	P	50	GLN
20	Q	2	ASN
21	R	122	ASN
22	S	13	GLN
23	T	67	ASN
23	T	68	ASN
26	W	64	ASN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	A	2947/3120 (94%)	675 (22%)	20 (0%)
5	B	113/118 (95%)	32 (28%)	6 (5%)
All	All	3060/3238 (94%)	707 (23%)	26 (0%)

All (707) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
4	A	7	U
4	A	12	G
4	A	20	G
4	A	23	G
4	A	31	U
4	A	41	A
4	A	42	G
4	A	43	C
4	A	48	G
4	A	60	A
4	A	68	A
4	A	71	A
4	A	72	G
4	A	77	G
4	A	78	G
4	A	93	A
4	A	94	G
4	A	97	U
4	A	99	G
4	A	111	U
4	A	115	A
4	A	116	A
4	A	117	U
4	A	122	A
4	A	125	C
4	A	126	C
4	A	128	G
4	A	138	A
4	A	153	G
4	A	161	U
4	A	162	A
4	A	164	A
4	A	175	G
4	A	180	A
4	A	187	G
4	A	195	A
4	A	198	A
4	A	202	C
4	A	203	A
4	A	213	G
4	A	214	G
4	A	215	A

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Mol	Chain	Res	Type
4	A	221	A
4	A	227	A
4	A	228	A
4	A	229	U
4	A	233	A
4	A	238	G
4	A	245	G
4	A	248	G
4	A	255	A
4	A	264	G
4	A	265	A
4	A	274	C
4	A	281	C
4	A	282	A
4	A	283	U
4	A	285	U
4	A	286	G
4	A	287	A
4	A	288	U
4	A	289	A
4	A	290	C
4	A	297	G
4	A	301	U
4	A	302	U
4	A	303	G
4	A	307	G
4	A	312	G
4	A	313	G
4	A	316	U
4	A	317	G
4	A	318	U
4	A	319	G
4	A	326	A
4	A	329	U
4	A	330	U
4	A	331	U
4	A	336	C
4	A	337	U
4	A	338	C
4	A	340	A
4	A	342	C
4	A	344	G

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Mol	Chain	Res	Type
4	A	345	G
4	A	348	G
4	A	350	A
4	A	351	G
4	A	353	G
4	A	355	A
4	A	357	U
4	A	359	A
4	A	360	G
4	A	361	A
4	A	362	A
4	A	363	A
4	A	366	G
4	A	369	G
4	A	370	U
4	A	371	G
4	A	372	G
4	A	378	G
4	A	379	G
4	A	384	G
4	A	386	C
4	A	393	U
4	A	394	G
4	A	400	C
4	A	401	C
4	A	402	G
4	A	403	U
4	A	404	A
4	A	405	G
4	A	406	A
4	A	407	C
4	A	408	G
4	A	411	G
4	A	412	A
4	A	413	G
4	A	423	C
4	A	424	G
4	A	426	G
4	A	427	A
4	A	429	A
4	A	434	G
4	A	445	U

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Mol	Chain	Res	Type
4	A	446	G
4	A	449	G
4	A	452	G
4	A	453	U
4	A	454	U
4	A	459	A
4	A	460	G
4	A	472	C
4	A	474	G
4	A	476	G
4	A	477	G
4	A	484	C
4	A	486	G
4	A	490	A
4	A	494	G
4	A	499	G
4	A	500	A
4	A	505	C
4	A	512	G
4	A	523	U
4	A	531	A
4	A	543	U
4	A	544	U
4	A	553	G
4	A	561	G
4	A	569	G
4	A	591	G
4	A	592	A
4	A	594	U
4	A	595	A
4	A	596	C
4	A	597	C
4	A	600	A
4	A	614	C
4	A	617	U
4	A	618	C
4	A	619	C
4	A	620	G
4	A	634	C
4	A	636	U
4	A	637	G
4	A	638	U

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Mol	Chain	Res	Type
4	A	639	C
4	A	640	G
4	A	642	G
4	A	655	G
4	A	665	G
4	A	667	A
4	A	684	G
4	A	690	G
4	A	696	A
4	A	705	C
4	A	706	G
4	A	707	G
4	A	708	G
4	A	709	U
4	A	711	G
4	A	714	U
4	A	715	A
4	A	721	A
4	A	731	A
4	A	738	A
4	A	739	U
4	A	740	A
4	A	741	G
4	A	746	U
4	A	747	A
4	A	748	U
4	A	749	C
4	A	754	C
4	A	756	A
4	A	757	G
4	A	758	A
4	A	760	U
4	A	765	G
4	A	766	G
4	A	779	U
4	A	784	G
4	A	801	U
4	A	828	G
4	A	829	U
4	A	832	G
4	A	836	G
4	A	839	U

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Mol	Chain	Res	Type
4	A	845	C
4	A	862	U
4	A	890	G
4	A	891	G
4	A	897	A
4	A	899	G
4	A	900	G
4	A	909	A
4	A	920	G
4	A	921	C
4	A	927	C
4	A	942	U
4	A	945	G
4	A	974	G
4	A	981	U
4	A	982	A
4	A	994	A
4	A	996	G
4	A	1002	C
4	A	1003	A
4	A	1004	C
4	A	1010	U
4	A	1011	A
4	A	1014	G
4	A	1015	A
4	A	1022	C
4	A	1025	A
4	A	1026	A
4	A	1029	C
4	A	1041	A
4	A	1042	A
4	A	1044	U
4	A	1046	C
4	A	1047	A
4	A	1049	G
4	A	1063	G
4	A	1068	C
4	A	1070	G
4	A	1076	A
4	A	1078	G
4	A	1085	G
4	A	1091	A

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Mol	Chain	Res	Type
4	A	1092	G
4	A	1101	A
4	A	1114	G
4	A	1115	G
4	A	1131	G
4	A	1135	G
4	A	1143	G
4	A	1144	A
4	A	1151	U
4	A	1157	G
4	A	1159	C
4	A	1162	G
4	A	1165	G
4	A	1167	C
4	A	1175	A
4	A	1178	U
4	A	1179	U
4	A	1181	G
4	A	1182	C
4	A	1184	U
4	A	1187	A
4	A	1188	A
4	A	1189	G
4	A	1191	A
4	A	1202	A
4	A	1203	A
4	A	1205	G
4	A	1206	A
4	A	1208	U
4	A	1211	G
4	A	1212	U
4	A	1213	A
4	A	1214	A
4	A	1215	U
4	A	1223	U
4	A	1228	A
4	A	1229	A
4	A	1230	G
4	A	1235	U
4	A	1237	U
4	A	1240	G
4	A	1245	U

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Mol	Chain	Res	Type
4	A	1246	A
4	A	1247	A
4	A	1248	U
4	A	1250	U
4	A	1251	A
4	A	1253	C
4	A	1254	G
4	A	1260	C
4	A	1261	A
4	A	1292	U
4	A	1294	U
4	A	1295	U
4	A	1321	C
4	A	1326	G
4	A	1335	G
4	A	1343	G
4	A	1344	A
4	A	1351	G
4	A	1352	A
4	A	1362	A
4	A	1364	U
4	A	1368	A
4	A	1371	G
4	A	1380	A
4	A	1386	G
4	A	1387	A
4	A	1408	C
4	A	1415	A
4	A	1416	A
4	A	1427	U
4	A	1444	U
4	A	1465	C
4	A	1467	U
4	A	1480	A
4	A	1489	G
4	A	1493	A
4	A	1494	U
4	A	1499	A
4	A	1507	G
4	A	1510	A
4	A	1511	U
4	A	1517	U

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Mol	Chain	Res	Type
4	A	1518	A
4	A	1522	G
4	A	1531	C
4	A	1534	C
4	A	1538	G
4	A	1542	A
4	A	1543	A
4	A	1624	U
4	A	1625	G
4	A	1626	G
4	A	1628	A
4	A	1629	G
4	A	1630	U
4	A	1632	G
4	A	1639	G
4	A	1640	A
4	A	1641	U
4	A	1642	G
4	A	1645	G
4	A	1648	A
4	A	1649	C
4	A	1654	G
4	A	1670	G
4	A	1674	G
4	A	1676	G
4	A	1679	A
4	A	1680	A
4	A	1681	U
4	A	1703	G
4	A	1710	A
4	A	1711	G
4	A	1712	G
4	A	1714	A
4	A	1716	A
4	A	1717	U
4	A	1718	C
4	A	1727	A
4	A	1728	U
4	A	1729	A
4	A	1730	U
4	A	1731	A
4	A	1737	A

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Mol	Chain	Res	Type
4	A	1744	A
4	A	1753	C
4	A	1754	G
4	A	1755	A
4	A	1756	G
4	A	1757	U
4	A	1758	G
4	A	1767	U
4	A	1769	G
4	A	1780	G
4	A	1786	G
4	A	1788	G
4	A	1789	A
4	A	1798	U
4	A	1803	A
4	A	1825	C
4	A	1826	A
4	A	1827	A
4	A	1828	A
4	A	1829	C
4	A	1831	A
4	A	1832	A
4	A	1836	A
4	A	1837	G
4	A	1845	G
4	A	1851	G
4	A	1852	A
4	A	1864	U
4	A	1866	C
4	A	1871	G
4	A	1872	A
4	A	1883	A
4	A	1884	G
4	A	1892	G
4	A	1893	C
4	A	1903	C
4	A	1911	U
4	A	1921	G
4	A	1933	G
4	A	1938	G
4	A	1945	U
4	A	1946	U

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Mol	Chain	Res	Type
4	A	1947	U
4	A	1950	G
4	A	1955	A
4	A	1972	A
4	A	1974	A
4	A	1975	A
4	A	1981	U
4	A	1984	G
4	A	1985	A
4	A	1990	A
4	A	2001	A
4	A	2017	C
4	A	2018	G
4	A	2026	A
4	A	2031	G
4	A	2033	U
4	A	2036	A
4	A	2038	A
4	A	2043	C
4	A	2046	A
4	A	2050	C
4	A	2051	U
4	A	2052	G
4	A	2053	C
4	A	2054	C
4	A	2055	C
4	A	2152	A
4	A	2153	G
4	A	2154	G
4	A	2156	A
4	A	2158	C
4	A	2159	G
4	A	2160	A
4	A	2162	A
4	A	2163	U
4	A	2164	U
4	A	2165	C
4	A	2166	C
4	A	2167	U
4	A	2168	U
4	A	2169	G
4	A	2170	U

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Mol	Chain	Res	Type
4	A	2171	C
4	A	2176	A
4	A	2178	G
4	A	2179	U
4	A	2181	C
4	A	2183	G
4	A	2184	A
4	A	2186	C
4	A	2187	U
4	A	2188	G
4	A	2189	C
4	A	2190	A
4	A	2191	C
4	A	2192	G
4	A	2193	A
4	A	2197	G
4	A	2198	C
4	A	2199	G
4	A	2215	U
4	A	2217	U
4	A	2220	C
4	A	2221	A
4	A	2228	G
4	A	2244	A
4	A	2245	C
4	A	2246	U
4	A	2254	A
4	A	2255	A
4	A	2256	G
4	A	2257	A
4	A	2263	G
4	A	2267	C
4	A	2279	C
4	A	2280	G
4	A	2284	A
4	A	2285	G
4	A	2286	A
4	A	2316	G
4	A	2320	C
4	A	2324	A
4	A	2325	U
4	A	2328	G

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Mol	Chain	Res	Type
4	A	2329	G
4	A	2330	U
4	A	2331	U
4	A	2332	U
4	A	2333	G
4	A	2334	U
4	A	2335	G
4	A	2336	U
4	A	2337	A
4	A	2339	G
4	A	2340	A
4	A	2341	U
4	A	2342	A
4	A	2343	G
4	A	2344	G
4	A	2348	G
4	A	2350	G
4	A	2351	A
4	A	2353	U
4	A	2354	G
4	A	2355	U
4	A	2356	G
4	A	2362	C
4	A	2363	A
4	A	2365	A
4	A	2367	G
4	A	2370	A
4	A	2371	G
4	A	2372	U
4	A	2373	G
4	A	2375	G
4	A	2377	G
4	A	2380	G
4	A	2382	G
4	A	2384	C
4	A	2386	U
4	A	2387	U
4	A	2388	G
4	A	2390	U
4	A	2391	G
4	A	2392	A
4	A	2393	A

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Mol	Chain	Res	Type
4	A	2394	A
4	A	2395	U
4	A	2396	A
4	A	2397	C
4	A	2398	C
4	A	2400	C
4	A	2403	U
4	A	2405	A
4	A	2407	C
4	A	2408	G
4	A	2410	A
4	A	2421	A
4	A	2422	A
4	A	2427	G
4	A	2433	U
4	A	2434	A
4	A	2436	A
4	A	2447	G
4	A	2449	A
4	A	2450	C
4	A	2462	G
4	A	2463	G
4	A	2492	A
4	A	2503	G
4	A	2507	C
4	A	2511	A
4	A	2512	A
4	A	2521	C
4	A	2529	A
4	A	2530	C
4	A	2532	G
4	A	2543	U
4	A	2545	G
4	A	2549	G
4	A	2559	A
4	A	2571	C
4	A	2574	C
4	A	2587	U
4	A	2594	G
4	A	2606	G
4	A	2607	G
4	A	2609	A

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Mol	Chain	Res	Type
4	A	2625	C
4	A	2626	U
4	A	2647	U
4	A	2649	A
4	A	2650	A
4	A	2652	G
4	A	2653	G
4	A	2654	A
4	A	2665	C
4	A	2669	G
4	A	2672	A
4	A	2683	A
4	A	2689	C
4	A	2692	A
4	A	2693	A
4	A	2698	C
4	A	2700	A
4	A	2702	A
4	A	2704	C
4	A	2711	A
4	A	2715	U
4	A	2718	G
4	A	2725	C
4	A	2726	G
4	A	2729	G
4	A	2742	A
4	A	2744	C
4	A	2753	G
4	A	2758	A
4	A	2777	G
4	A	2778	U
4	A	2788	A
4	A	2789	A
4	A	2790	A
4	A	2791	G
4	A	2796	A
4	A	2826	A
4	A	2827	G
4	A	2828	U
4	A	2833	U
4	A	2834	C
4	A	2837	U

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Mol	Chain	Res	Type
4	A	2838	A
4	A	2839	U
4	A	2847	G
4	A	2870	C
4	A	2878	A
4	A	2885	G
4	A	2893	G
4	A	2913	U
4	A	2914	A
4	A	2915	C
4	A	2926	A
4	A	2936	C
4	A	2950	C
4	A	2957	A
4	A	2968	G
4	A	2982	A
4	A	2985	G
4	A	2989	A
4	A	2996	U
4	A	3002	A
4	A	3009	U
4	A	3013	C
4	A	3014	A
4	A	3015	C
4	A	3020	U
4	A	3021	A
4	A	3022	G
4	A	3024	A
4	A	3029	U
4	A	3039	C
4	A	3042	A
4	A	3054	U
4	A	3070	G
4	A	3071	A
4	A	3082	U
4	A	3088	C
4	A	3093	A
4	A	3100	A
4	A	3101	C
4	A	3103	A
4	A	3104	A
4	A	3105	C

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Mol	Chain	Res	Type
4	A	3112	A
4	A	3114	A
4	A	3115	A
5	B	3	U
5	B	4	A
5	B	5	C
5	B	6	G
5	B	10	G
5	B	11	U
5	B	13	C
5	B	14	A
5	B	23	G
5	B	24	G
5	B	26	A
5	B	31	C
5	B	33	C
5	B	37	C
5	B	43	C
5	B	46	A
5	B	47	A
5	B	51	G
5	B	52	G
5	B	54	A
5	B	55	G
5	B	56	C
5	B	57	U
5	B	58	A
5	B	62	C
5	B	67	A
5	B	68	G
5	B	82	A
5	B	88	C
5	B	89	C
5	B	107	A
5	B	114	A

All (26) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	A	335	G
4	A	344	G
4	A	369	G

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Mol	Chain	Res	Type
4	A	410	U
4	A	428	A
4	A	899	G
4	A	980	C
4	A	981	U
4	A	1350	G
4	A	1625	G
4	A	1669	G
4	A	1728	U
4	A	1954	C
4	A	2050	C
4	A	2155	U
4	A	2192	G
4	A	2343	G
4	A	2362	C
4	A	2374	U
4	A	2381	A
5	B	2	U
5	B	4	A
5	B	10	G
5	B	22	A
5	B	57	U
5	B	61	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
36	GCP	4	501	-	32,34,34	1.39	7 (21%)	49,54,54	1.80	8 (16%)

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
36	GCP	4	501	-	-	1/19/38/38	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	4	501	GCP	C5-C4	2.88	1.46	1.38
36	4	501	GCP	C6-N1	-2.71	1.33	1.38
36	4	501	GCP	PG-O3G	2.70	1.61	1.55
36	4	501	GCP	PG-O2G	2.61	1.60	1.55
36	4	501	GCP	C5-N7	-2.16	1.34	1.39
36	4	501	GCP	C4-N9	-2.15	1.32	1.38
36	4	501	GCP	PB-O3A	2.09	1.60	1.58

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	4	501	GCP	C5-C4-N3	-5.66	119.38	128.39
36	4	501	GCP	PB-O3A-PA	-4.62	117.30	132.37
36	4	501	GCP	C2-N3-C4	4.39	119.86	112.30
36	4	501	GCP	N9-C4-N3	4.30	134.55	125.95
36	4	501	GCP	C6-C5-N7	3.09	135.92	130.29
36	4	501	GCP	C4-C5-N7	-2.45	106.80	110.67
36	4	501	GCP	C2'-C1'-N9	-2.26	106.97	113.25
36	4	501	GCP	C3'-C2'-C1'	2.14	105.50	101.46

There are no chirality outliers.

All (1) torsion outliers are listed below:

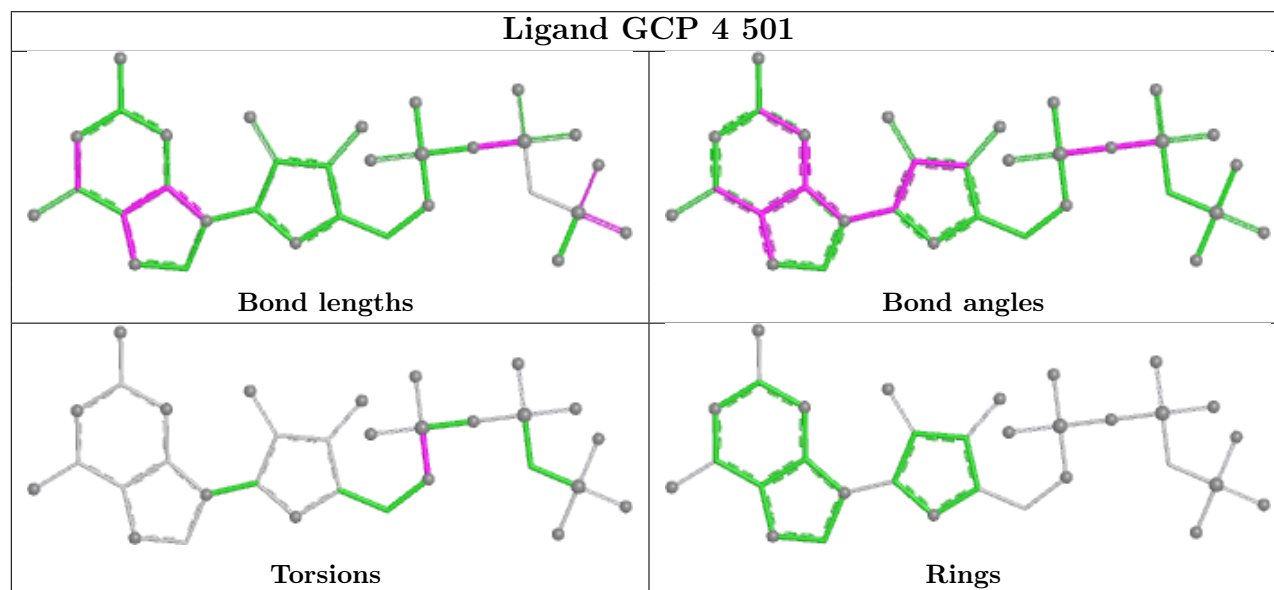
Mol	Chain	Res	Type	Atoms
36	4	501	GCP	C5'-O5'-PA-O1A

There are no ring outliers.

1 monomer is involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
36	4	501	GCP	15	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.

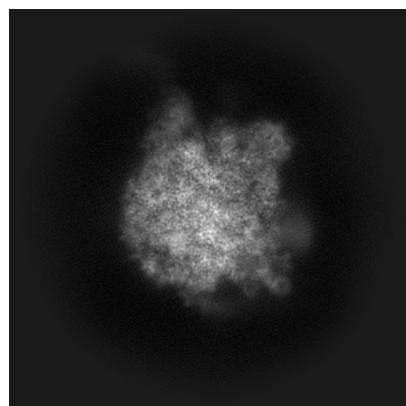
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-43305. These allow visual inspection of the internal detail of the map and identification of artifacts.

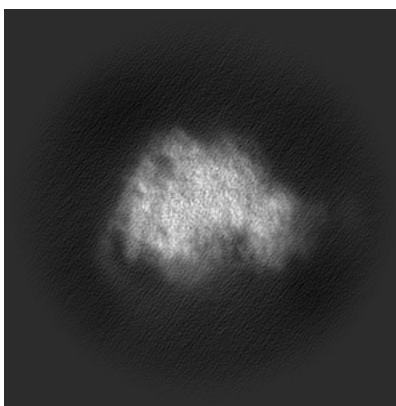
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

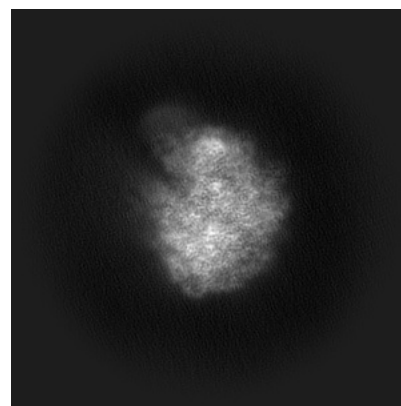
6.1.1 Primary map



X

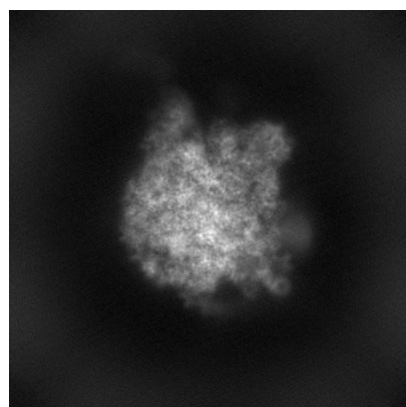


Y

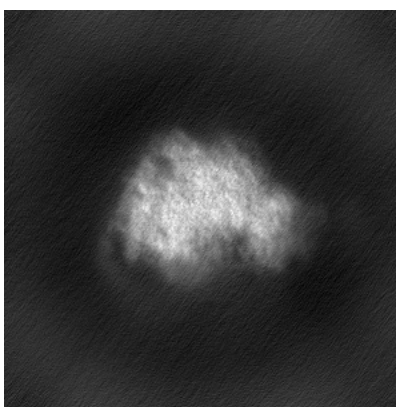


Z

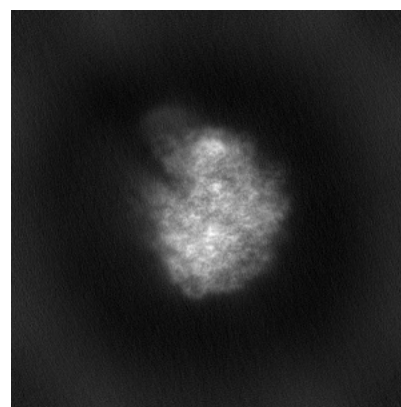
6.1.2 Raw map



X



Y

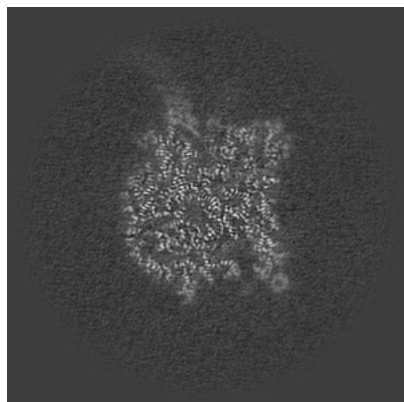


Z

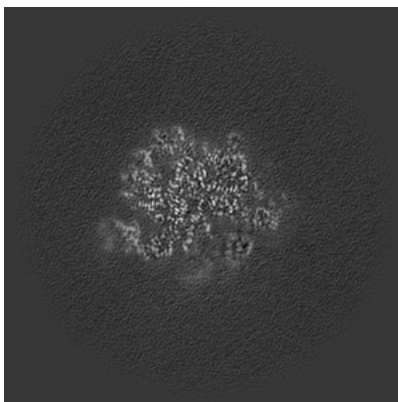
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

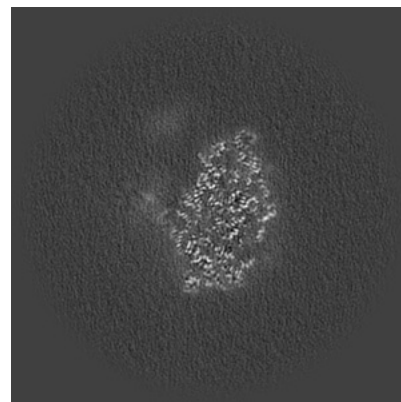
6.2.1 Primary map



X Index: 200

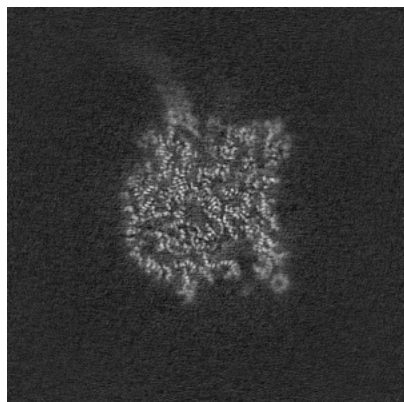


Y Index: 200

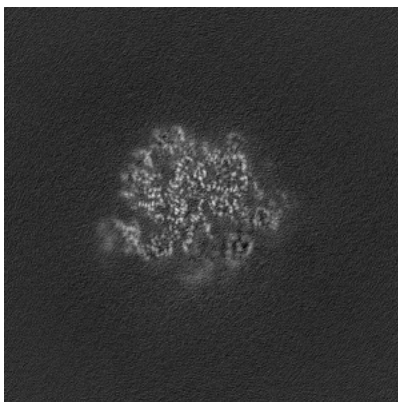


Z Index: 200

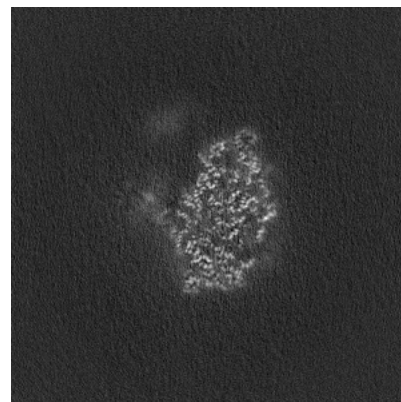
6.2.2 Raw map



X Index: 200



Y Index: 200

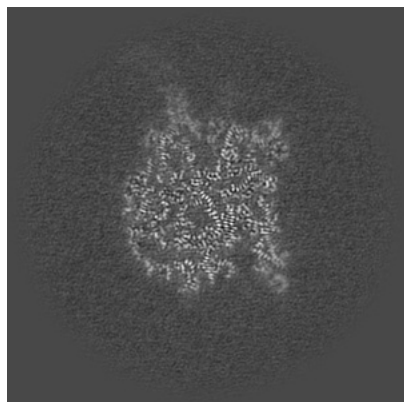


Z Index: 200

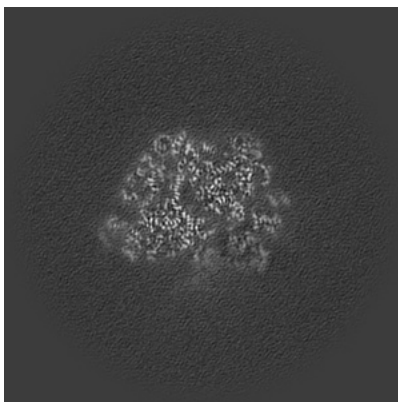
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

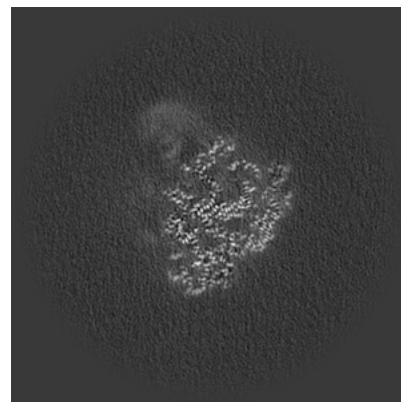
6.3.1 Primary map



X Index: 203

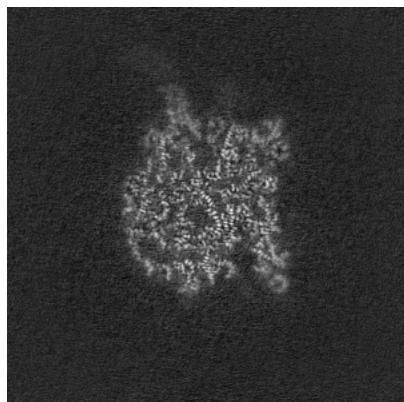


Y Index: 192

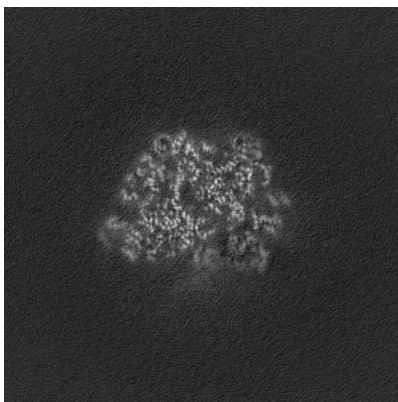


Z Index: 173

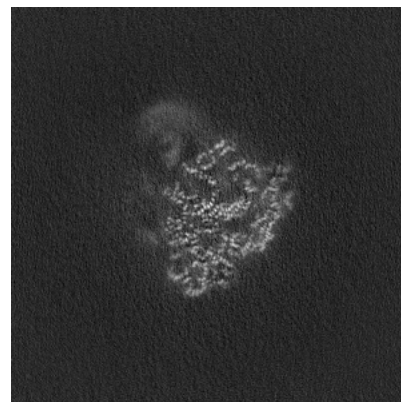
6.3.2 Raw map



X Index: 203



Y Index: 192

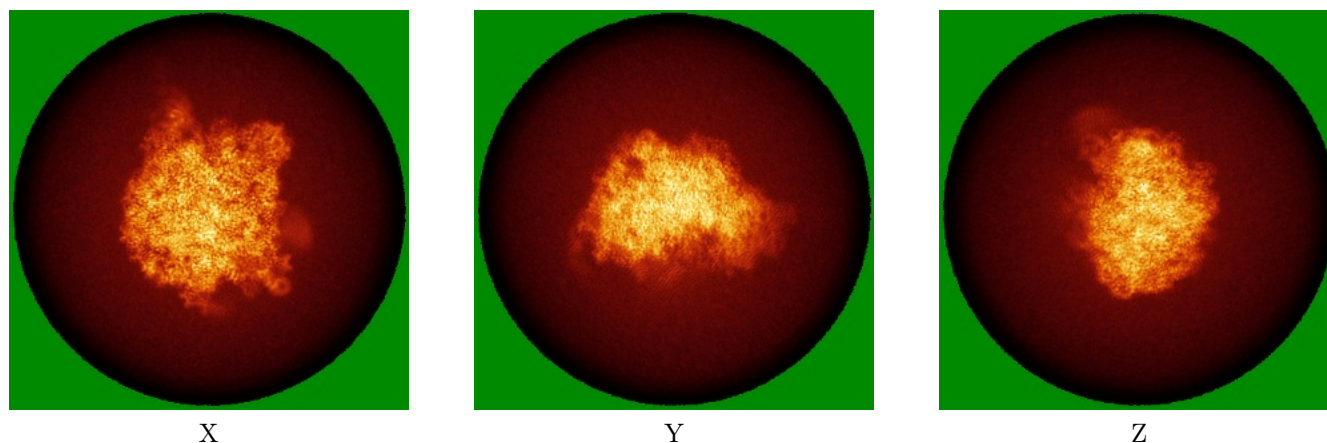


Z Index: 172

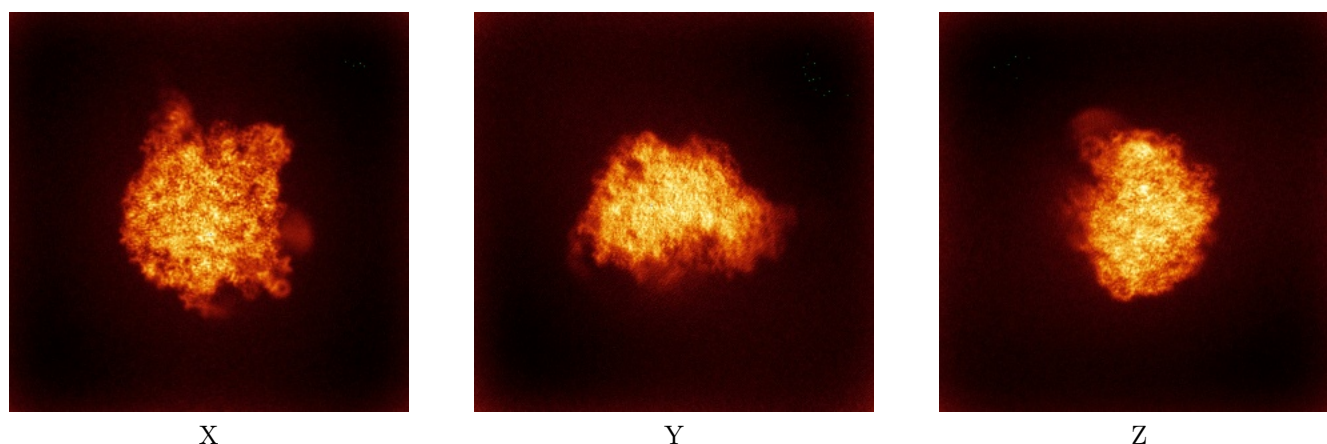
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

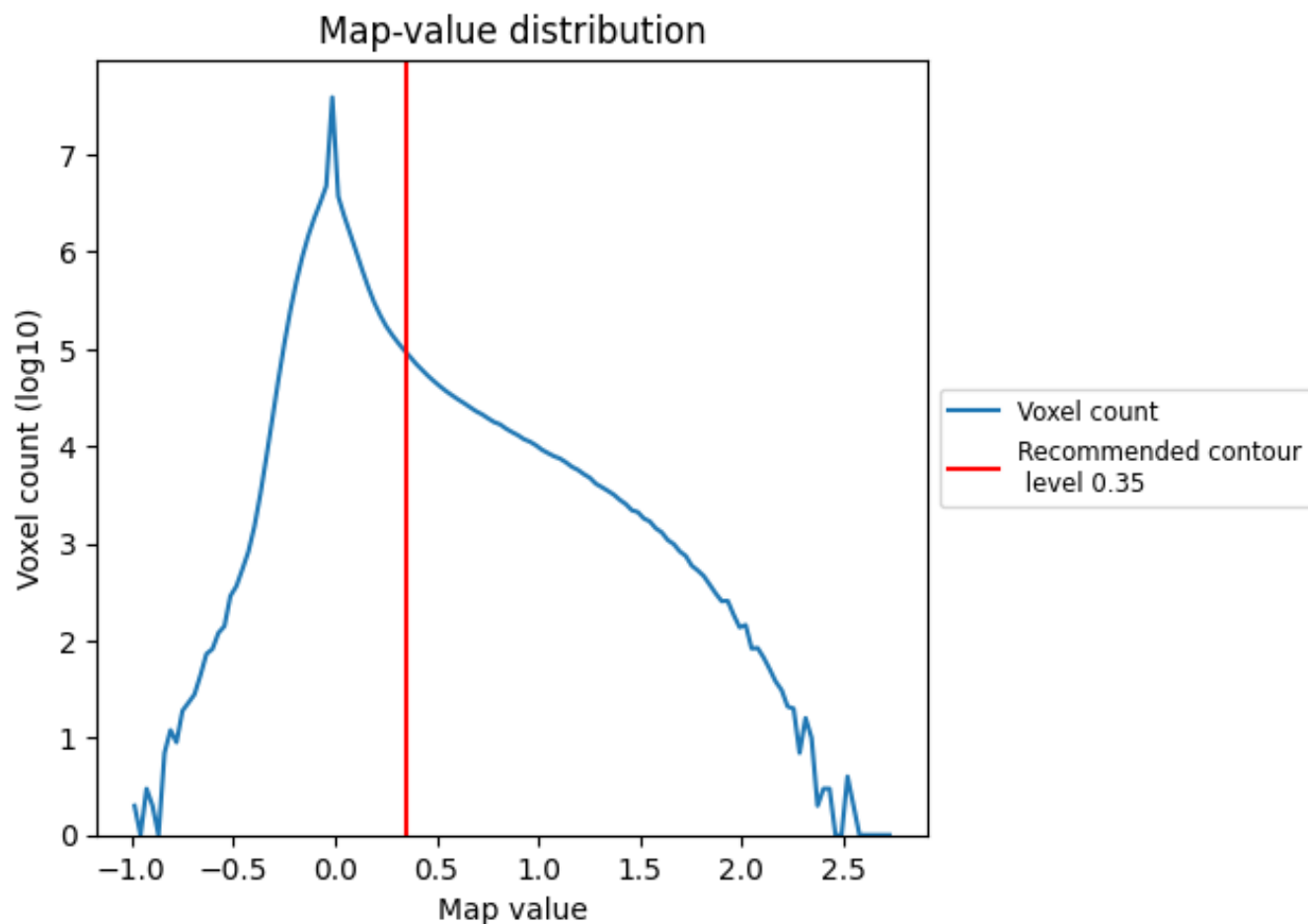
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

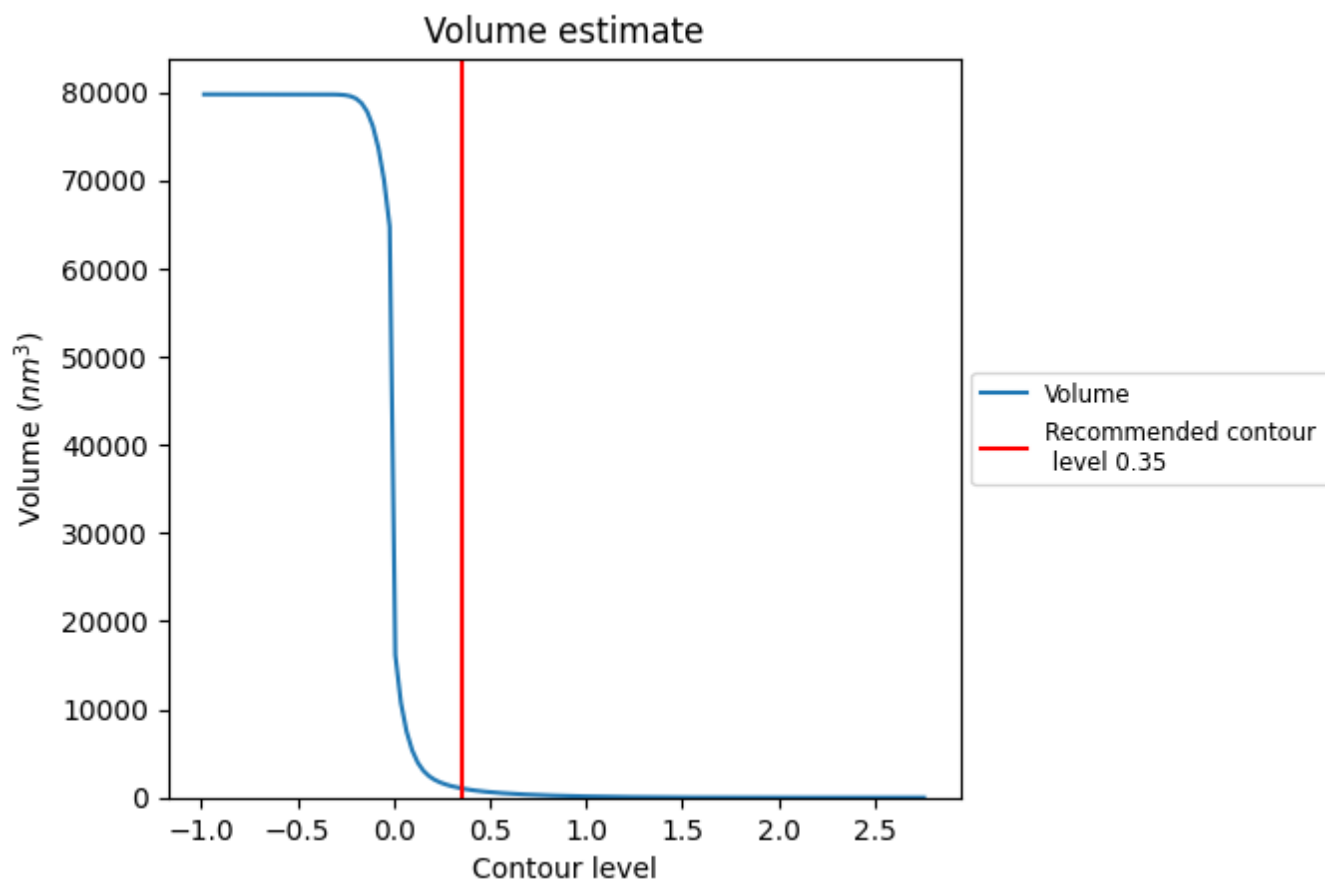
This section contains the results of statistical analysis of the map.

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.

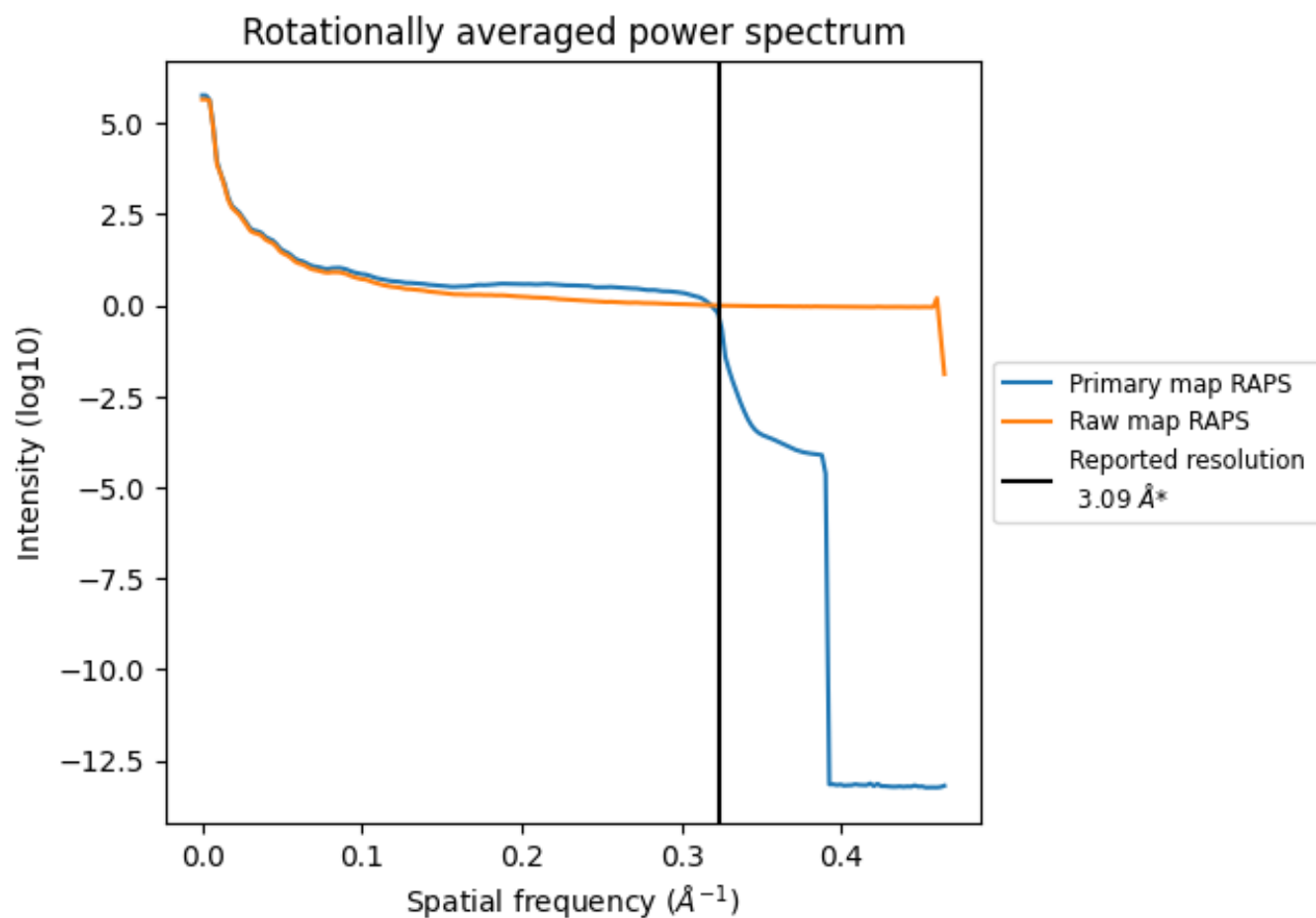
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1055 nm³; this corresponds to an approximate mass of 953 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

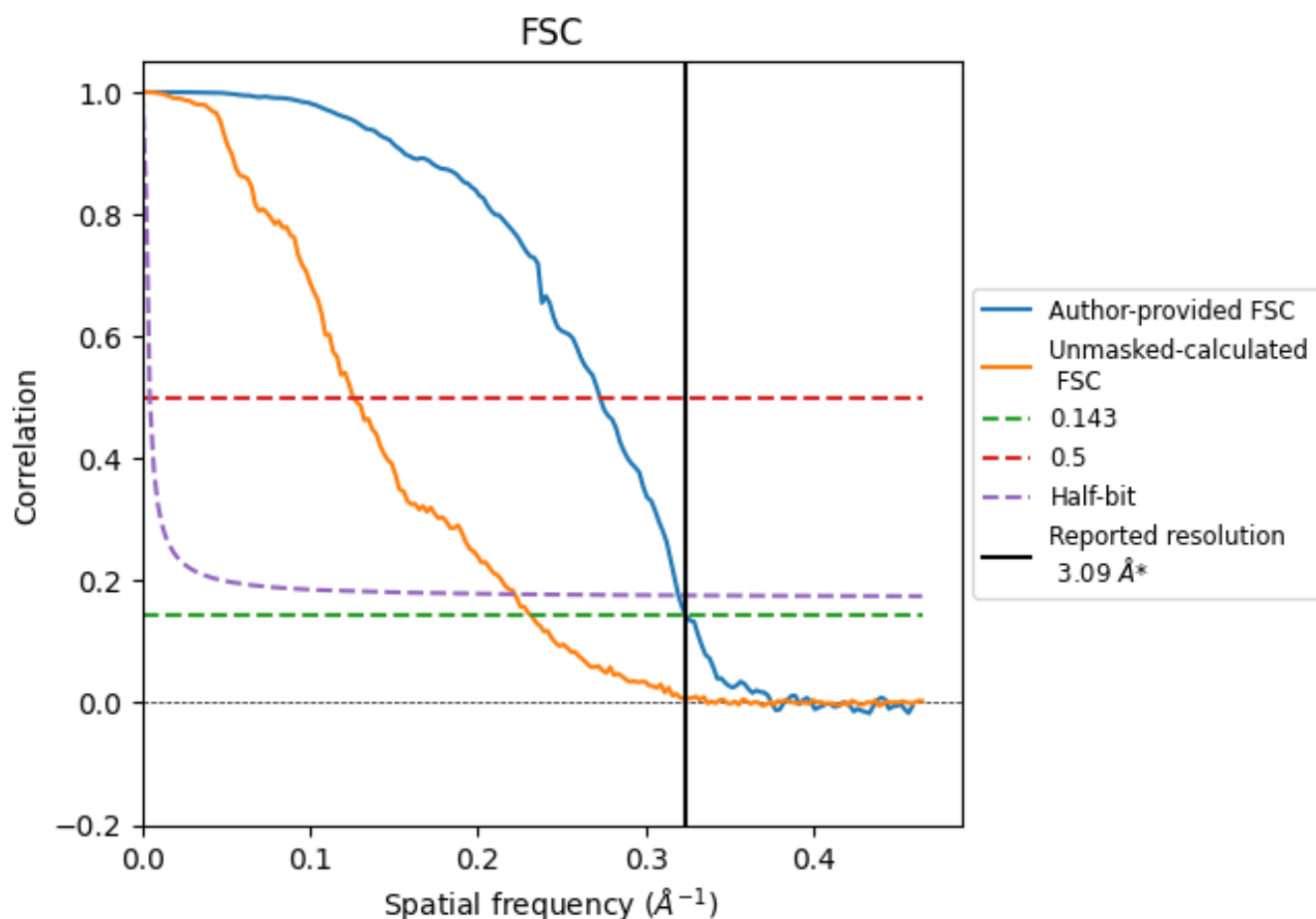


*Reported resolution corresponds to spatial frequency of 0.324 $\text{\AA}^{-1}$

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 0.324 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.09	-	-
Author-provided FSC curve	3.09	3.67	3.13
Unmasked-calculated*	4.32	7.95	4.50

*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 4.32 differs from the reported value 3.09 by more than 10 %

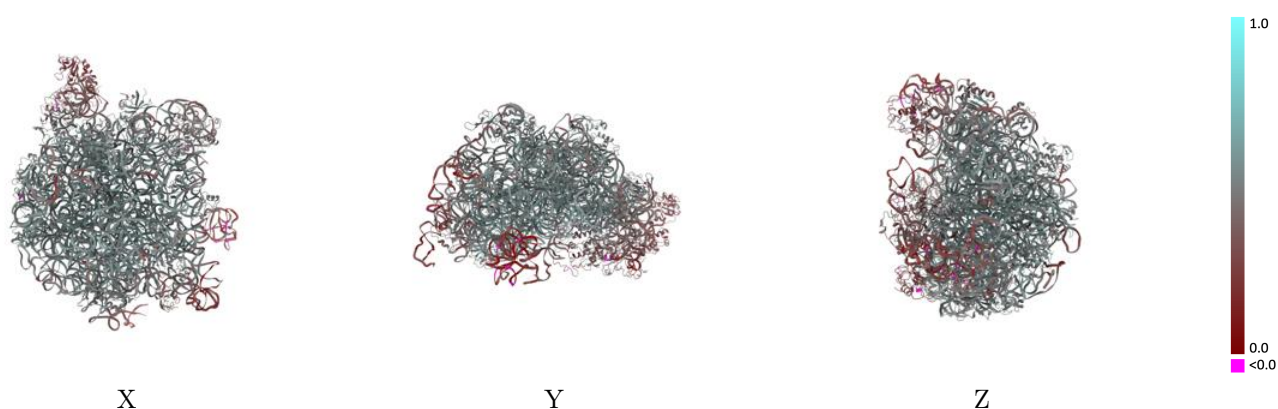
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-43305 and PDB model 8VK7. Per-residue inclusion information can be found in section 3 on page 11.

9.1 Map-model overlay [i](#)

This section was not generated.

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

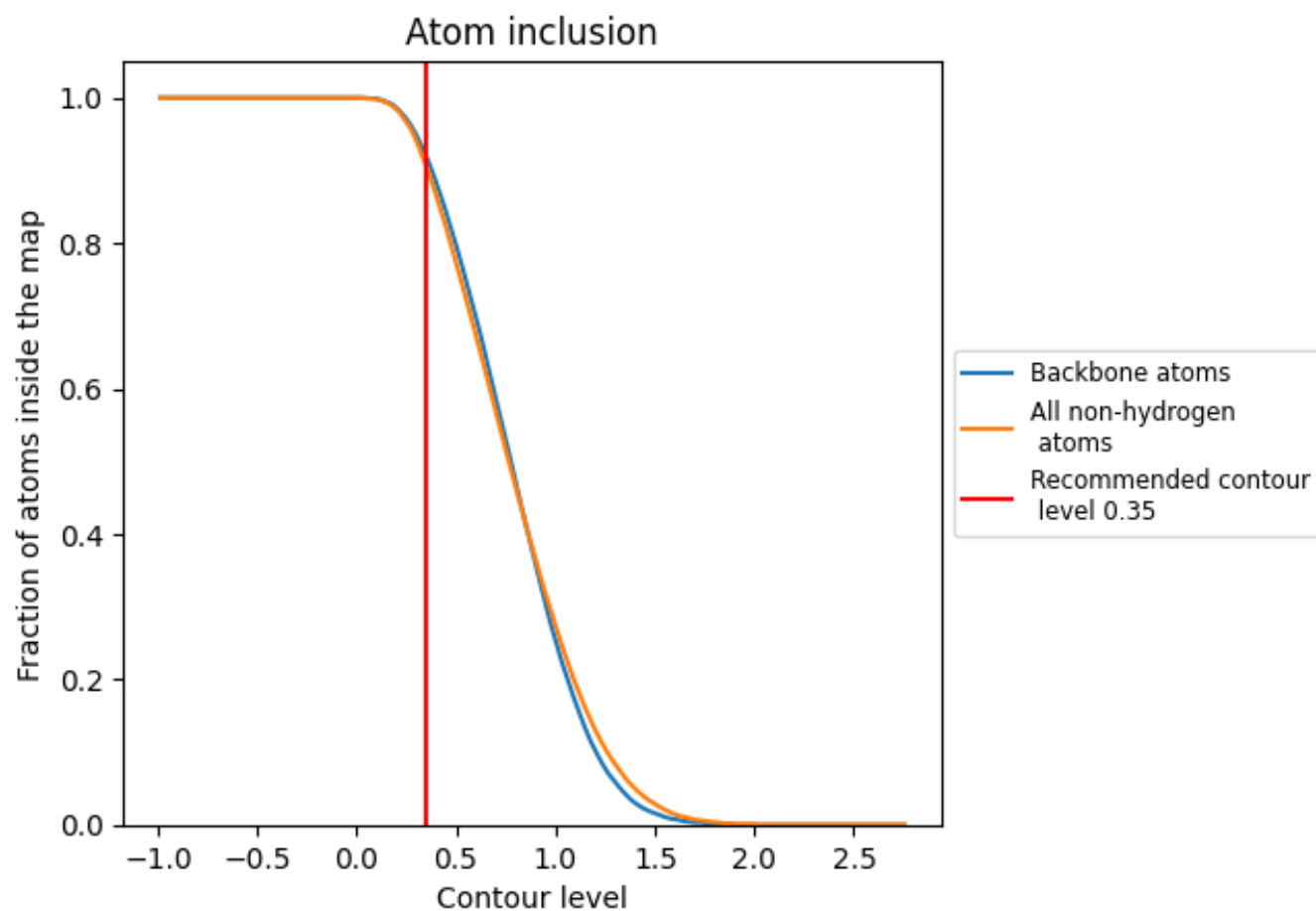


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion ⓘ



At the recommended contour level, 92% of all backbone atoms, 91% 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 (0.35) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9070	 0.4850
2	 0.8950	 0.5340
3	 0.9890	 0.5670
4	 0.6310	 0.3740
A	 0.9420	 0.4910
B	 0.9730	 0.4640
C	 0.9250	 0.5360
D	 0.9450	 0.5340
E	 0.9220	 0.5180
F	 0.7480	 0.3540
G	 0.8360	 0.4420
H	 0.6990	 0.4140
I	 0.2450	 0.2810
J	 0.2290	 0.2680
K	 0.9490	 0.5390
L	 0.9330	 0.5200
M	 0.9310	 0.5280
N	 0.9350	 0.5170
O	 0.9390	 0.5360
P	 0.8950	 0.4620
Q	 0.9100	 0.5010
R	 0.9440	 0.5360
S	 0.9100	 0.5370
T	 0.9530	 0.5390
U	 0.9410	 0.5140
V	 0.8980	 0.4800
W	 0.8110	 0.4810
X	 0.9440	 0.5450
Y	 0.9630	 0.5500
Z	 0.9040	 0.4950
b	 0.9400	 0.5490
c	 0.9520	 0.5440
d	 0.9660	 0.5650
e	 0.9670	 0.5480
f	 0.9620	 0.5510
g	 0.6610	 0.3260

