



Full wwPDB EM Validation Report ⓘ

Mar 10, 2026 – 01:34 AM UTC

PDB ID : 7S9U / pdb_00007s9u
EMDB ID : EMD-24937
Title : 44SR3C ribosomal particle
Authors : Ortega, J.; Seffouh, A.
Deposited on : 2021-09-21
Resolution : 3.20 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

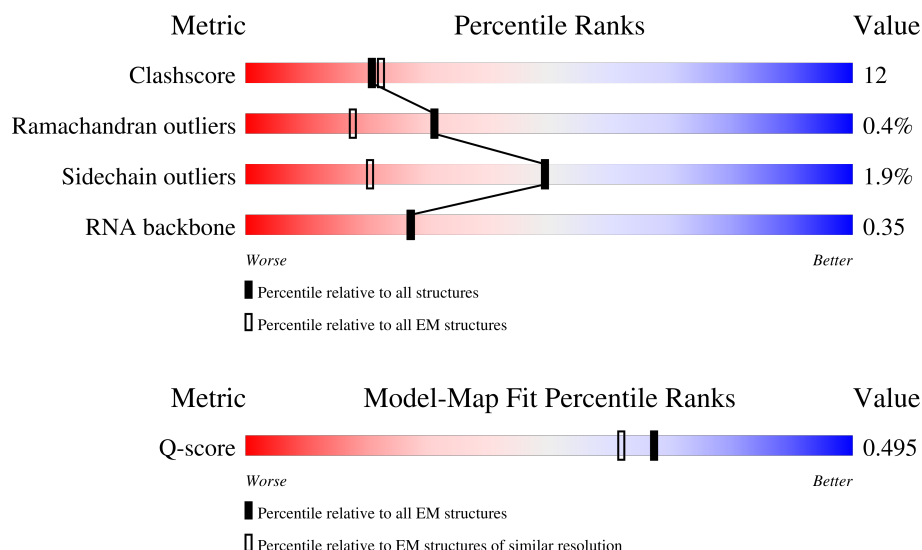
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.20 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	15020 (2.70 - 3.70)

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

Mol	Chain	Length	Quality of chain
1	A	2928	
2	C	277	
3	D	209	

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Mol	Chain	Length	Quality of chain
4	E	207	
5	J	145	
6	K	122	
7	L	146	
8	N	120	
9	P	115	
10	Q	119	
11	R	102	
12	S	113	
13	T	95	
14	U	103	
15	V	94	
16	Z	59	
17	b	59	
18	Y	66	
19	d	44	

2 Entry composition

There are 19 unique types of molecules in this entry. The entry contains 68620 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called RNA (2436-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2436	Total	C	N	O	P	0	0
			52346	23355	9704	16851	2436		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1558	C	G	conflict	GB 1864548803

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	267	Total	C	N	O	S	0	0
			2052	1277	402	367	6		

- Molecule 3 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	179	Total	C	N	O	S	0	0
			1354	854	241	256	3		

- Molecule 4 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	205	Total	C	N	O	S	0	0
			1561	980	289	290	2		

- Molecule 5 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	J	142	Total	C	N	O	S	0	0
			1123	710	206	202	5		

- Molecule 6 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	K	122	Total	C	N	O	S	0	0
			920	571	173	172	4		

- Molecule 7 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L	130	Total	C	N	O	S	0	0
			973	608	183	180	2		

- Molecule 8 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	N	119	Total	C	N	O	S	0	0
			953	583	186	180	4		

- Molecule 9 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	P	114	Total	C	N	O	S	0	0
			936	595	184	157			

- Molecule 10 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	Q	117	Total	C	N	O	S	0	0
			940	591	189	156	4		

- Molecule 11 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	R	101	Total	C	N	O	S	0	0
			786	501	139	146			

- Molecule 12 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	S	109	Total	C	N	O	S	0	0
			842	525	164	150	3		

- Molecule 13 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	T	92	Total	C	N	O	S	0	0
			741	463	136	138	4		

- Molecule 14 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	U	100	Total	C	N	O	S	0	0
			754	473	141	137	3		

- Molecule 15 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	V	72	Total	C	N	O	S	0	0
			561	349	109	103			

- Molecule 16 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Z	58	Total	C	N	O	S	0	0
			455	281	89	84	1		

- Molecule 17 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	b	54	Total	C	N	O	S	0	0
			426	262	86	71	7		

- Molecule 18 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	Y	65	Total	C	N	O	S	0	0
			530	328	102	98	2		

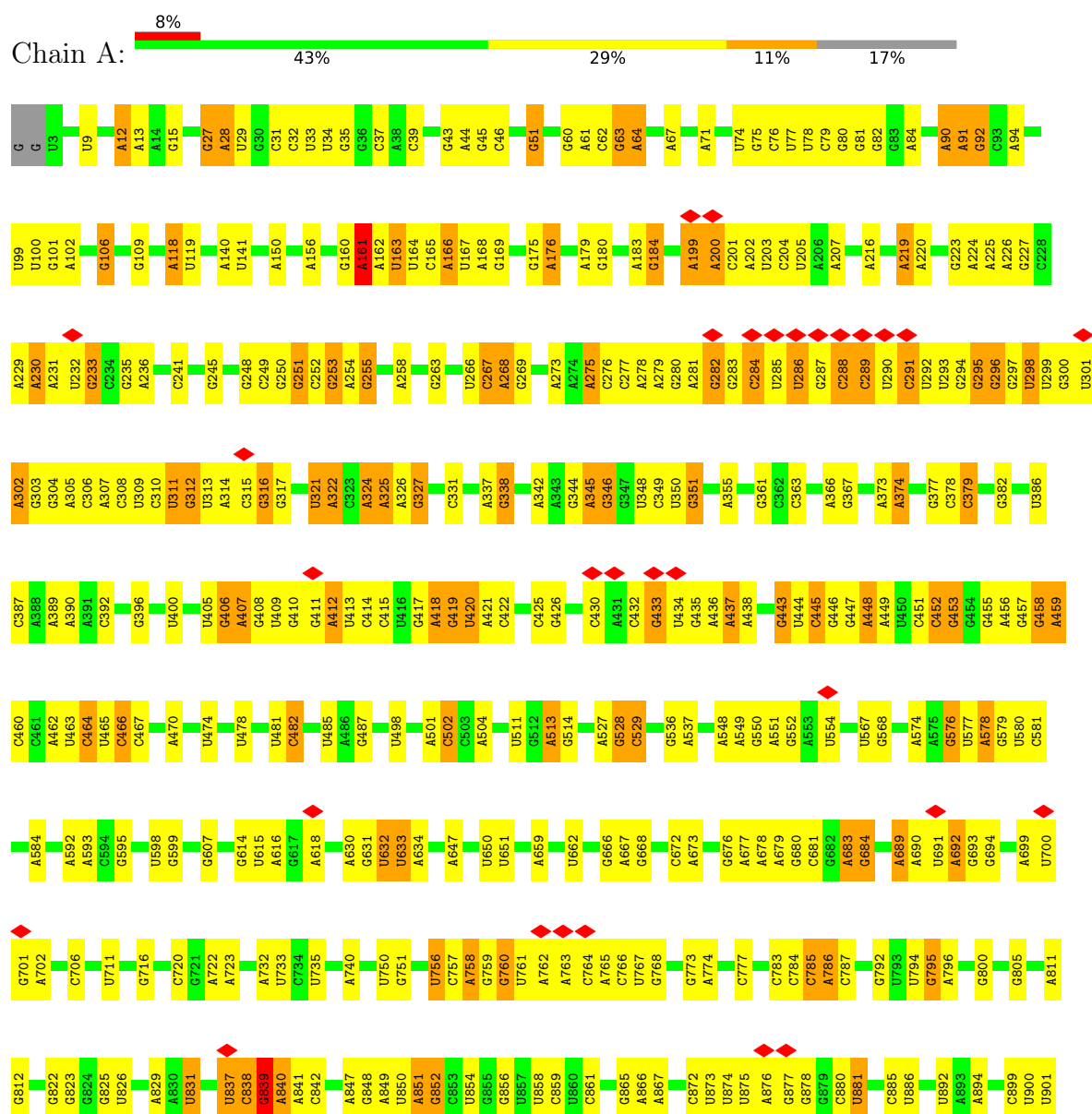
- Molecule 19 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	d	44	Total	C	N	O	S	0	0
			367	222	89	54	2		

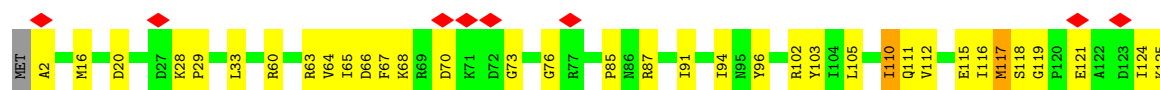
3 Residue-property plots

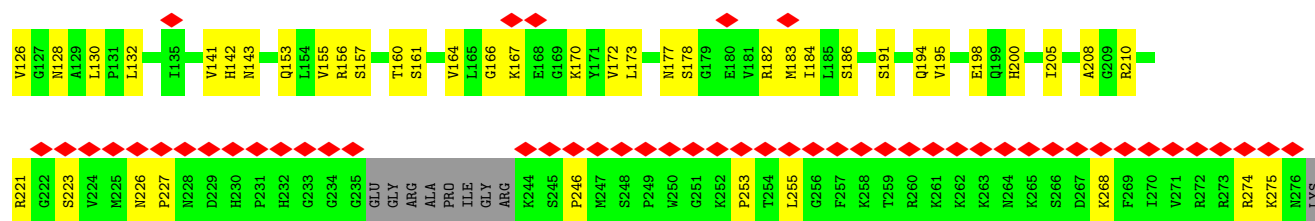
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: RNA (2436-MER)

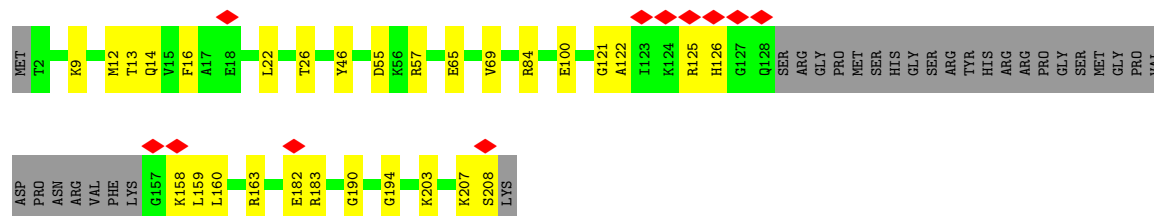


A2009	G2009	U1808	G1706	G1633	G1546	A1480	U1380	U1289	C1181	C	C	G902
A2010	G2010	U1809	U1707	A1638	U1547	G1481	U1381	G1290	G1184	A	A	G903
U2011	U2011	G1810	G1712	G1639	U1548	G1482	U1382	G1291	G1185	G	G	A904
C2012	C2012	C1811	A1713	A1648	U1549	A1483	U1383	G1292	C1186	C	C	G905
A2017	A2017	A1812	A1714	C1650	C1550	G1488	G1387	A1294	U1187	A	A	G906
C2018	C2018	U1813	G1719	C1651	C1551	G1489	A1388	U1295	A1188	C	C	U907
U2019	U2019	A1814	C1720	C1652	C1552	A1491	U1391	G1296	A1189	C	C	G911
G2021	G2021	A1815	A1723	A1653	U1553	G1492	A1392	A1201	A1067	A	A	G912
A2022	A2022	C1819	A1724	A1654	U1554	C1493	A1404	A1302	U1068	U	U	A913
C2023	C2023	G1820	G1725	A1655	A1555	G1494	A1405	U1303	U1069	U	U	C914
U2024	U2024	A1821	U1726	G1656	G1556	C1495	A1406	G1304	U1070	U	U	U915
A2025	A2025	U1822	G1727	G1657	U1557	G1496	A1409	A1305	G1071	A	A	G916
C2026	C2026	G1823	A1728	C1558	C1558	G1497	U1409	U1216	A1072	A	A	A917
G2027	G2027	A1831	A1734	C1559	U1560	U1498	U1412	C1217	A1073	G	G	U918
C2028	C2028	U1832	A1735	C1560	G1561	U1499	A1413	U1218	A1074	A	A	U919
G2038	G2038	A1833	A1736	C1561	U1562	U1500	G1414	C1219	A1075	G	G	G920
C2039	C2039	G1834	U1737	C1562	G1563	U1501	A1417	A1222	G1076	U	U	G921
U2040	U2040	U1835	U1738	C1563	C1564	G1502	U1418	G1223	A1077	C	C	A922
G2041	G2041	A1839	C1739	C1564	G1565	G1503	U1424	U1321	U1079	G	G	C923
A2044	A2044	G1840	G1740	C1565	G1566	U1504	C1425	G1322	U1080	U	U	U924
C2045	C2045	U1841	A1741	C1566	U1567	U1505	U1433	A1323	G1081	A	A	G925
U2046	U2046	A1842	A1742	C1567	U1568	U1506	A1434	G1324	G1082	A	A	G926
G2047	G2047	U1843	C1743	C1568	U1569	U1507	U1435	U1327	A1083	U	U	U927
C2048	C2048	G1844	A1744	C1569	U1570	C1508	U1436	U1328	U1084	U	U	G
G2038	G2038	A1845	G1745	C1570	G1571	C1511	U1437	G1238	A1085	U	U	C
C2039	C2039	U1846	A1746	C1571	G1572	C1512	U1438	U1239	U1086	U	U	C
U2040	U2040	A1847	C1747	C1572	G1573	C1513	U1439	U1240	U1087	U	U	C
G2041	G2041	U1848	A1748	C1573	G1574	C1514	U1440	G1241	U1088	U	U	C
A2044	A2044	G1849	C1749	C1574	U1575	C1515	U1441	A1242	U1089	U	U	C
C2045	C2045	U1850	G1750	C1575	G1576	C1516	U1442	U1243	C1010	U	U	C
U2046	U2046	A1851	C1751	C1576	G1577	C1517	U1443	G1244	U1013	U	U	C
G2047	G2047	U1852	C1752	C1577	G1578	C1518	U1444	U1245	A1014	U	U	C
C2048	C2048	G1853	C1753	C1578	U1579	C1519	U1445	G1246	G1015	U	U	C
G2038	G2038	A1854	C1754	C1579	A1580	C1520	U1446	G1247	U1016	U	U	C
C2039	C2039	U1855	A1755	C1580	U1581	C1521	U1447	U1248	C1017	U	U	C
U2040	U2040	G1856	C1756	C1581	U1582	C1522	U1448	C1249	U1017	U	U	C
G2041	G2041	U1857	C1757	C1582	U1583	C1523	U1449	U1250	A1020	U	U	C
A2044	A2044	A1858	C1758	C1583	U1584	C1524	U1450	U1251	A1027	U	U	C
C2045	C2045	U1859	C1759	C1584	U1585	C1525	U1451	U1252	C1028	U	U	C
U2046	U2046	G1860	C1760	C1585	U1586	C1526	U1452	G1257	A1036	U	U	C
G2047	G2047	A1861	C1761	C1586	U1587	C1527	U1453	A1258	C1037	U	U	C
C2048	C2048	U1862	C1762	C1587	U1588	C1528	U1454	G1259	C1041	U	U	C
G2038	G2038	G1863	C1763	C1588	U1589	C1529	U1455	U1260	A1042	U	U	C
C2039	C2039	A1864	C1764	C1589	U1590	C1530	U1456	A1269	A1043	U	U	C
U2040	U2040	U1865	A1765	C1590	U1591	C1531	U1457	C1270	C1044	U	U	C
G2041	G2041	G1866	C1766	C1591	U1592	C1532	U1458	U1271	U1045	U	U	C
A2044	A2044	A1867	C1767	C1592	U1593	C1533	U1459	U1272	A1046	U	U	C
C2045	C2045	U1868	C1768	C1593	U1594	C1534	U1460	G1273	G1171	U	U	C
U2046	U2046	G1869	C1769	C1594	U1595	C1535	U1461	U1274	A1172	U	U	C
G2047	G2047	A1870	C1770	C1595	U1596	C1536	U1462	A1269	A1173	U	U	C
C2048	C2048	U1871	C1771	C1596	U1597	C1537	U1463	C1270	A1174	U	U	C
G2038	G2038	G1872	C1772	C1597	U1598	C1538	U1464	U1271	A1175	U	U	C
C2039	C2039	A1873	C1773	C1598	U1599	C1539	U1465	U1272	G1176	U	U	C
U2040	U2040	U1874	C1774	C1599	U1600	C1540	U1466	U1273	U1177	U	U	C
G2041	G2041	G1875	C1775	C1600	U1601	C1541	U1467	G1274	U1178	U	U	C
A2044	A2044	A1876	C1776	C1601	U1602	C1542	U1468	U1275	A1179	U	U	C
C2045	C2045	U1877	C1777	C1602	U1603	C1543	U1469	U1276	C1180	U	U	C
U2046	U2046	G1878	C1778	C1603	U1604	C1544	U1470	U1277				
G2047	G2047	A1879	C1779	C1604	U1605	C1545	U1471	U1278				
C2048	C2048	U1880	C1780	C1605	U1606	C1546	U1472	U1279				
G2038	G2038	G1881	C1781	C1606	U1607	C1547	U1473	U1280				
C2039	C2039	A1882	C1782	C1607	U1608	C1548	U1474	U1281				
U2040	U2040	U1883	C1783	C1608	U1609	C1549	U1475					
G2041	G2041	G1884	C1784	C1609	U1610	C1550	U1476					
A2044	A2044	A1885	C1785	C1610	U1611	C1551	U1477					
C2045	C2045	U1886	C1786	C1611	U1612	C1552	U1478					
U2046	U2046	G1887	C1787	C1612	U1613	C1553	U1479					
G2047	G2047	A1888	C1788	C1613	U1614	C1554						
C2048	C2048	U1889	C1789	C1614	U1615	C1555						
G2038	G2038	G1890	C1790	C1615	U1616	C1556						
C2039	C2039	A1891	C1791	C1616	U1617	C1557						
U2040	U2040	U1892	C1792	C1617	U1618	C1558						
G2041	G2041	G1893	C1793	C1618	U1619	C1559						
A2044	A2044	A1894	C1794	C1619	U1620	C1560						
C2045	C2045	U1895	C1795	C1620	U1621	C1561						
U2046	U2046	G1896	C1796	C1621	U1622	C1562						
G2047	G2047	A1897	C1797	C1622	U1623	C1563						
C2048	C2048	U1898	C1798	C1623	U1624	C1564						
G2038	G2038	G1899	C1799	C1624	U1625	C1565						
C2039	C2039	A1899	C1800	C1625	U1626	C1566						
U2040	U2040	U1900	C1801	C1626	U1627	C1567						
G2041	G2041	G1901	C1802	C1627	U1628	C1568						
A2044	A2044	A1902	C1803	C1628	U1629	C1569						
C2045	C2045	U1903	C1804	C1629	U1630	C1570						
U2046	U2046	G1904	C1805	C1630	U1631	C1571						
G2047	G2047	A1905	C1806	C1631	U1632	C1572						
C2048	C2048	U1906	C1807	C1632	U1633	C1573						
G2038	G2038	G1907	C1808	C1633	U1634	C1574						
C2039	C2039	A1908	C1809	C1634	U1635	C1575						
U2040	U2040	U1909	C1810	C1635	U1636	C1576						
G2041	G2041	G1910	C1811	C1636	U1637	C1577						
A2044	A2044	A1911	C1812	C1637	U1638	C1578						
C2045	C2045	U1912	C1813	C1638	U1639	C1579						
U2046	U2046	G1913	C1814	C1639	U1640	C1580						
G2047	G2047	A1914	C1815	C1640	U1641	C1581						
C2048	C2048	U1915	C1816	C1641	U1642	C1582						
G2038	G2038	G1916	C1817	C1642	U1643	C1583						
C2039	C2039	A1917	C1818	C1643	U1644	C1584						
U2040	U2040	U1918	C1819	C1644	U1645	C1585						
G2041	G2041	G1919	C1820	C1645	U1646	C1586						
A2044	A2044	A1920	C1821	C1646	U1647	C1587						
C2045	C2045	U1921	C1822	C1647	U1648	C1588						
U2046	U2046	G1922	C1823	C1648	U1649	C1589						
G2047	G2047	A1923	C1824	C1649	U1650	C1590						
C2048	C2048	U1924	C1825	C1650	U1651	C1591						
G2038	G2038	G1925	C1826	C1651	U1652	C1592						
C2039	C2039	A1926	C1827	C1652	U1653	C1593						
U2040	U2040	U1927	C1828	C1653	U1654	C1594						
G2041	G2041	G1928	C1829	C1654	U1655	C1595						
A2044	A2044	A1929	C1830	C1655	U1656	C1596						
C2045	C2045	U1930	C1831	C1656	U1657	C1597						
U2046	U2046	G1931	C1832	C1657	U1658	C1598						
G2047	G2047	A1932	C1833	C1658	U1659	C1599						
C2048	C2048	U1933	C1834	C1659	U1660	C1600						
G2038	G2038	G1934	C1835	C1660	U1661	C1601						
C2039	C2039	A1935	C1836	C1661	U1662	C1602						
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G2041	G2041	G1937	C1838	C1								

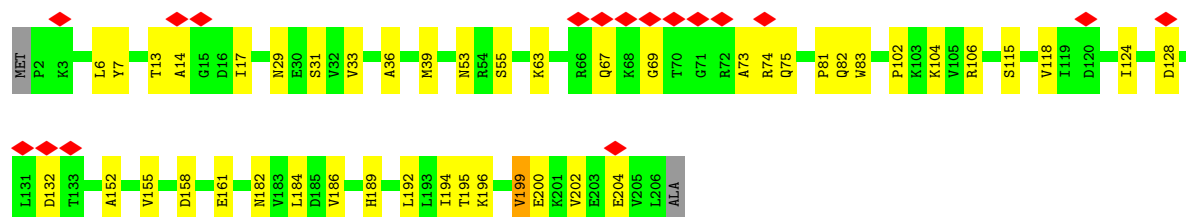
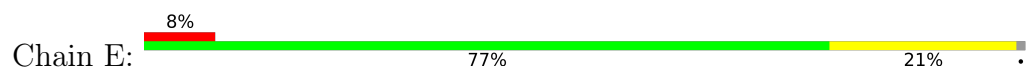




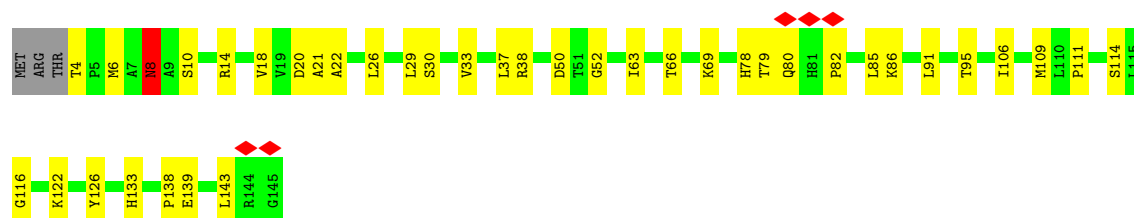
• Molecule 3: 50S ribosomal protein L3



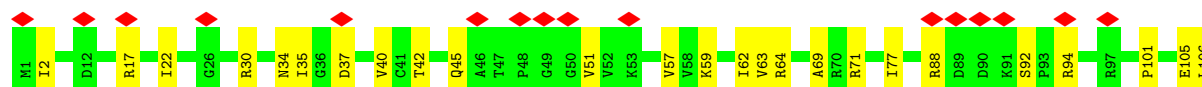
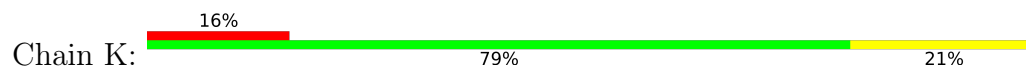
• Molecule 4: 50S ribosomal protein L4

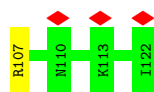


• Molecule 5: 50S ribosomal protein L13

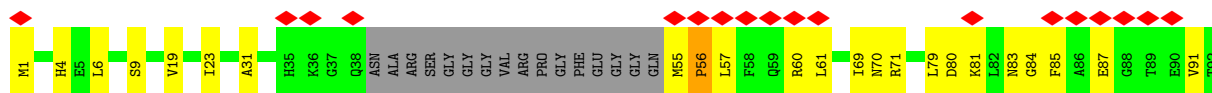


• Molecule 6: 50S ribosomal protein L14

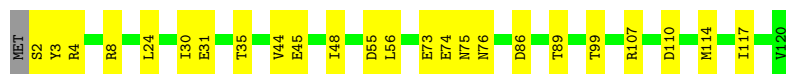
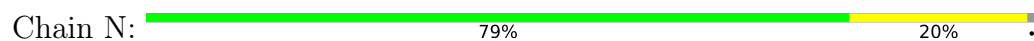




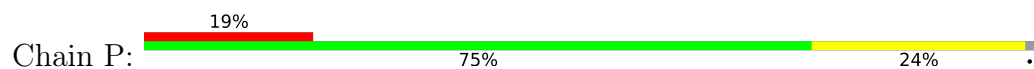
- Molecule 7: 50S ribosomal protein L15



- Molecule 8: 50S ribosomal protein L17



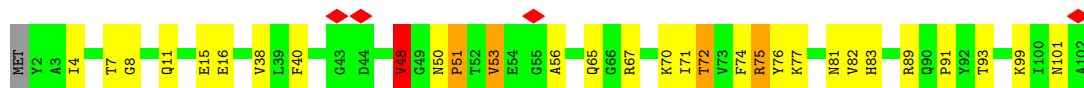
- Molecule 9: 50S ribosomal protein L19



- Molecule 10: 50S ribosomal protein L20



- Molecule 11: 50S ribosomal protein L21



- Molecule 12: 50S ribosomal protein L22

Chain S:  75% 20% ..



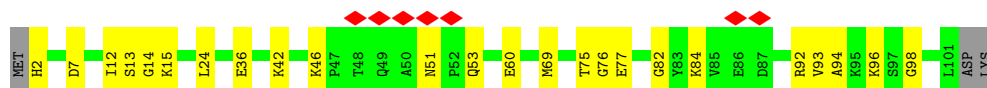
- Molecule 13: 50S ribosomal protein L23

Chain T:  75% 21% ..



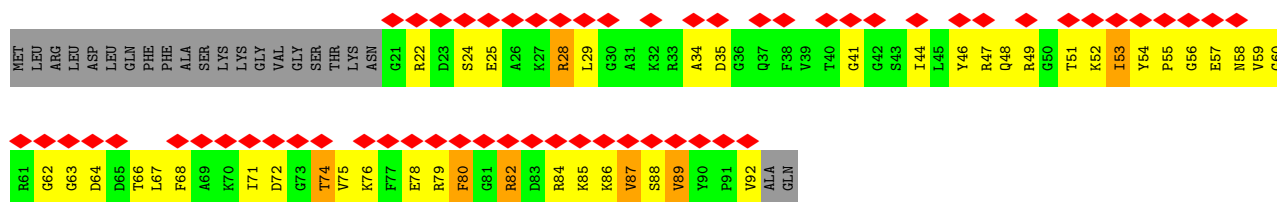
- Molecule 14: 50S ribosomal protein L24

Chain U:  7% 74% 23% .



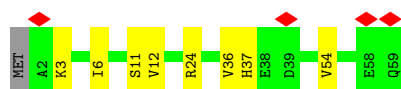
- Molecule 15: 50S ribosomal protein L27

Chain V:  29% 63% 40% 7% 23%



- Molecule 16: 50S ribosomal protein L30

Chain Z:  7% 85% 14% .

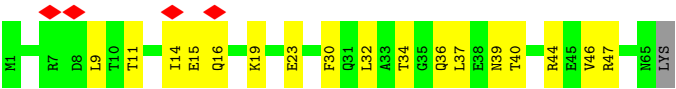


- Molecule 17: 50S ribosomal protein L32

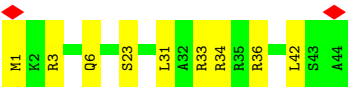
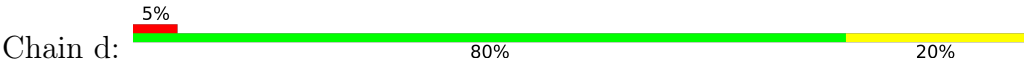
Chain b:  69% 22% 8%



- Molecule 18: 50S ribosomal protein L29



• Molecule 19: 50S ribosomal protein L34



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	121252	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1250	Depositor
Maximum defocus (nm)	3250	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.040	Depositor
Minimum map value	-0.010	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.00983	Depositor
Map size (Å)	287.28, 287.28, 287.28	wwPDB
Map dimensions	336, 336, 336	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.855, 0.855, 0.855	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.56	0/58643	0.50	12/91483 (0.0%)
2	C	0.40	0/2087	0.53	0/2798
3	D	0.54	0/1367	0.54	0/1830
4	E	0.60	0/1580	0.59	0/2132
5	J	0.59	1/1146 (0.1%)	0.52	0/1542
6	K	0.42	0/927	0.51	0/1245
7	L	0.44	0/982	0.52	0/1308
8	N	0.64	0/960	0.60	0/1284
9	P	0.46	0/949	0.48	0/1269
10	Q	0.76	0/952	0.80	3/1266 (0.2%)
11	R	0.55	0/797	0.65	0/1070
12	S	0.59	0/851	0.58	0/1146
13	T	0.57	0/747	0.60	0/995
14	U	0.50	0/764	0.51	0/1022
15	V	0.35	0/569	0.81	0/757
16	Z	0.48	0/457	0.46	0/613
17	b	0.59	0/433	0.58	0/574
18	Y	0.51	0/531	0.62	1/707 (0.1%)
19	d	0.68	0/370	0.57	0/483
All	All	0.56	1/75112 (0.0%)	0.51	16/113524 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	J	8	ASN	CA-CB	-5.21	1.40	1.53

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1511	C	P-O3'-C3'	10.44	135.86	120.20
1	A	160	G	P-O3'-C3'	8.70	133.25	120.20
1	A	839	G	C2'-C3'-O3'	7.88	121.32	109.50
10	Q	90	VAL	N-CA-C	-7.63	97.90	108.12

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	161	A	C2'-C3'-O3'	-7.50	102.44	113.70
1	A	1595	U	C2'-C3'-O3'	6.97	124.16	113.70
1	A	161	A	O5'-P-OP2	-6.93	87.21	108.00
1	A	2774	C	C2'-C3'-O3'	-6.84	103.44	113.70
10	Q	93	LYS	N-CA-C	-6.41	101.95	111.81
1	A	1512	G	C2'-C3'-O3'	-6.36	104.17	113.70
1	A	1512	G	C4'-C3'-O3'	5.63	121.44	113.00
10	Q	98	LEU	N-CA-C	-5.49	106.09	112.89
1	A	880	C	O3'-P-O5'	5.29	111.94	104.00
1	A	27	G	C4'-C3'-O3'	5.24	117.27	109.40
1	A	161	A	C5'-C4'-C3'	5.20	123.80	116.00
18	Y	46	VAL	N-CA-C	-5.18	107.78	112.96

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	52346	0	26332	892	0
2	C	2052	0	2138	79	0
3	D	1354	0	1425	22	0
4	E	1561	0	1647	36	0
5	J	1123	0	1162	28	0
6	K	920	0	977	14	0
7	L	973	0	1032	33	0
8	N	953	0	983	15	0
9	P	936	0	1008	20	0
10	Q	940	0	1005	53	0
11	R	786	0	826	40	0
12	S	842	0	899	18	0
13	T	741	0	793	17	0
14	U	754	0	809	18	0
15	V	561	0	567	89	0
16	Z	455	0	491	5	0
17	b	426	0	443	18	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	Y	530	0	568	13	0
19	d	367	0	410	8	0
All	All	68620	0	43515	1314	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 12.

All (1314) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2351:A:N6	1:A:2362:A:N6	1.62	1.42
1:A:2434:G:N2	1:A:2442:G:C6	1.94	1.35
1:A:2292:C:N4	1:A:2307:A:C6	1.96	1.34
1:A:1525:G:C2	1:A:1560:U:O2	1.81	1.33
1:A:2328:G:O6	1:A:2347:G:N2	1.63	1.32
1:A:251:G:O2'	1:A:2461:A:OP1	1.57	1.20
1:A:2434:G:N2	1:A:2442:G:O6	1.74	1.19
1:A:2292:C:N4	1:A:2307:A:N1	1.89	1.18
10:Q:61:TRP:CH2	10:Q:94:MET:HG3	1.80	1.16
2:C:33:LEU:O	2:C:64:VAL:HG23	1.42	1.15
1:A:1525:G:N2	1:A:1560:U:O2	1.79	1.15
15:V:53:ILE:HG21	15:V:87:VAL:CG2	1.78	1.14
15:V:53:ILE:HG21	15:V:87:VAL:HG23	1.31	1.12
1:A:2774:C:N4	1:A:2788:G:H1	1.47	1.11
1:A:839:G:H22	1:A:2101:G:C4'	1.64	1.09
15:V:54:TYR:O	15:V:86:LYS:HG3	1.54	1.08
2:C:94:ILE:HD13	2:C:116:ILE:CD1	1.84	1.07
1:A:2292:C:C4	1:A:2307:A:C2	2.43	1.06
7:L:57:LEU:HD13	7:L:61:LEU:HD12	1.36	1.06
1:A:1579:A:N7	1:A:1588:A:C6	2.24	1.05
1:A:2328:G:O6	1:A:2347:G:C2	2.09	1.05
10:Q:61:TRP:CZ2	10:Q:94:MET:HG2	1.90	1.05
2:C:94:ILE:HD13	2:C:116:ILE:HD13	1.34	1.05
1:A:2351:A:C6	1:A:2362:A:N6	2.24	1.04
15:V:28:ARG:H	15:V:28:ARG:HD2	1.21	1.03
1:A:2328:G:C6	1:A:2347:G:N2	2.20	1.03
1:A:2352:G:H5''	1:A:2352:G:H8	1.21	1.03
15:V:78:GLU:HG3	15:V:79:ARG:H	0.87	1.01
7:L:55:MET:N	7:L:56:PRO:HD3	1.75	1.00
1:A:199:A:N6	1:A:878:G:N3	2.10	1.00
1:A:2094:C:H5'	1:A:2280:G:H21	1.23	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:Q:61:TRP:CZ2	10:Q:94:MET:CG	2.46	0.99
10:Q:61:TRP:CH2	10:Q:94:MET:CG	2.46	0.98
15:V:78:GLU:CG	15:V:79:ARG:H	1.74	0.98
1:A:2099:G:N1	1:A:2471:C:N3	1.75	0.98
1:A:1433:U:H4'	1:A:1648:A:H4'	1.45	0.98
15:V:53:ILE:CG2	15:V:87:VAL:HG23	1.93	0.97
15:V:56:GLY:HA2	15:V:86:LYS:HE2	1.44	0.97
7:L:55:MET:N	7:L:56:PRO:CD	2.27	0.97
1:A:1492:G:H1	1:A:1511:C:H42	1.13	0.97
15:V:78:GLU:HG3	15:V:79:ARG:N	1.70	0.97
1:A:1496:G:H1	1:A:1507:U:H3	1.10	0.95
15:V:56:GLY:HA2	15:V:86:LYS:CE	1.96	0.95
15:V:35:ASP:OD1	15:V:76:LYS:HA	1.66	0.94
1:A:2292:C:C4	1:A:2307:A:N1	2.36	0.91
1:A:2352:G:H5''	1:A:2352:G:C8	2.06	0.91
1:A:2328:G:O6	1:A:2347:G:N1	2.03	0.91
1:A:2351:A:H62	1:A:2362:A:N6	1.68	0.91
1:A:2779:A:HO2'	1:A:2782:A:H2	0.98	0.90
1:A:2324:C:N3	1:A:2367:G:N1	2.20	0.90
2:C:94:ILE:CD1	2:C:116:ILE:HD13	2.02	0.89
15:V:58:ASN:HB3	15:V:71:ILE:HG22	1.53	0.89
1:A:839:G:H22	1:A:2101:G:H4'	1.39	0.88
1:A:1579:A:C5	1:A:1588:A:N1	2.42	0.87
1:A:2348:C:H4'	1:A:2349:A:H5''	1.57	0.87
1:A:2774:C:H42	1:A:2788:G:H1	1.14	0.87
1:A:2096:G:C8	1:A:2098:G:N7	2.43	0.87
1:A:2309:G:H4'	1:A:2356:A:H5'	1.57	0.87
1:A:2360:G:O2'	15:V:51:THR:HG22	1.76	0.86
15:V:56:GLY:CA	15:V:86:LYS:HE2	2.04	0.86
1:A:2287:C:C5'	15:V:22:ARG:HH22	1.88	0.86
1:A:2085:G:H22	17:b:2:ALA:HB1	1.41	0.85
1:A:2290:C:H2'	15:V:24:SER:OG	1.76	0.84
7:L:136:VAL:HG22	7:L:141:GLY:HA3	1.60	0.84
10:Q:86:SER:HB3	10:Q:116:GLN:HG3	1.59	0.84
1:A:1036:A:H8	11:R:75:ARG:HH12	1.23	0.84
10:Q:61:TRP:CZ3	10:Q:94:MET:HB2	2.12	0.84
5:J:6:MET:SD	5:J:6:MET:N	2.51	0.83
1:A:2324:C:C4	1:A:2367:G:N1	2.47	0.83
1:A:2328:G:N1	1:A:2347:G:N2	2.25	0.83
1:A:411:G:O2'	1:A:412:A:N7	2.11	0.83
10:Q:61:TRP:CE3	10:Q:94:MET:HB2	2.13	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2774:C:N4	1:A:2788:G:N1	2.19	0.82
1:A:1579:A:N6	1:A:1588:A:C4	2.47	0.82
1:A:2415:U:O2'	15:V:49:ARG:NH1	2.12	0.81
1:A:1579:A:C6	1:A:1588:A:C2	2.69	0.81
1:A:2287:C:H5''	15:V:22:ARG:HH22	1.45	0.81
10:Q:61:TRP:CE2	10:Q:94:MET:HG2	2.16	0.81
1:A:255:G:H8	1:A:255:G:H5''	1.45	0.81
1:A:2090:G:O2'	1:A:2092:C:H5'	1.80	0.80
11:R:50:ASN:HB2	11:R:51:PRO:HD2	1.62	0.80
1:A:805:G:H21	1:A:2010:A:H62	1.29	0.80
1:A:2094:C:H5'	1:A:2280:G:N2	1.97	0.80
1:A:1579:A:C5	1:A:1588:A:C2	2.69	0.79
1:A:839:G:N2	1:A:2101:G:H4'	1.97	0.79
1:A:2328:G:H1	1:A:2347:G:N2	1.80	0.79
1:A:2773:G:H5''	1:A:2784:C:C2	2.18	0.79
2:C:63:ARG:HH21	2:C:63:ARG:HG3	1.47	0.79
1:A:419:G:H22	1:A:447:G:H2'	1.47	0.79
1:A:1380:U:H5''	1:A:1436:U:O2	1.83	0.79
1:A:1579:A:C5	1:A:1588:A:C6	2.71	0.79
7:L:57:LEU:CD1	7:L:61:LEU:HD12	2.12	0.79
1:A:2434:G:N2	1:A:2442:G:N1	2.32	0.78
1:A:690:A:H61	1:A:2378:G:H21	1.31	0.78
10:Q:61:TRP:HB3	10:Q:93:LYS:O	1.83	0.77
1:A:90:A:H4'	1:A:91:A:H5'	1.67	0.77
2:C:67:PHE:CZ	2:C:156:ARG:HD2	2.19	0.77
11:R:50:ASN:OD1	11:R:50:ASN:O	2.03	0.77
1:A:2312:C:C5	1:A:2418:G:C4	2.73	0.77
2:C:66:ASP:OD2	2:C:102:ARG:NH1	2.18	0.77
2:C:94:ILE:HD13	2:C:116:ILE:HD11	1.67	0.76
10:Q:95:LEU:HD13	10:Q:95:LEU:O	1.85	0.76
1:A:311:U:O2'	1:A:312:G:O5'	2.03	0.76
1:A:2794:A:N3	1:A:2794:A:H2'	2.00	0.76
1:A:2773:G:H3'	1:A:2784:C:O2	1.85	0.76
5:J:8:ASN:OD1	5:J:8:ASN:N	2.15	0.76
1:A:200:A:C5	1:A:2459:A:C5	2.65	0.76
1:A:2776:G:H21	1:A:2786:A:H62	1.33	0.76
1:A:2779:A:O2'	1:A:2782:A:H2	1.68	0.75
1:A:2386:U:H5''	1:A:2386:U:C6	2.21	0.75
2:C:143:ASN:H	2:C:155:VAL:HG23	1.52	0.75
15:V:55:PRO:HB3	15:V:59:VAL:HG12	1.67	0.74
1:A:2765:G:H5''	1:A:2765:G:H8	1.52	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:V:29:LEU:HD22	15:V:48:GLN:O	1.87	0.74
1:A:2099:G:H1	1:A:2471:C:N4	1.83	0.74
1:A:1247:G:N1	1:A:1280:G:C2	2.55	0.74
1:A:2440:A:H2'	1:A:2441:A:H8	1.52	0.74
6:K:2:ILE:HD13	6:K:62:ILE:HD13	1.69	0.74
15:V:58:ASN:CB	15:V:71:ILE:HG22	2.17	0.74
1:A:1244:A:H8	7:L:4:HIS:HB3	1.52	0.74
1:A:840:A:N6	1:A:2102:C:OP1	2.21	0.74
1:A:287:G:OP2	1:A:288:C:N4	2.19	0.74
1:A:2351:A:H5''	1:A:2351:A:H8	1.53	0.74
1:A:2773:G:H5''	1:A:2784:C:O2	1.87	0.74
4:E:152:ALA:O	4:E:189:HIS:ND1	2.20	0.74
1:A:2324:C:C2	1:A:2367:G:C2	2.76	0.73
1:A:2459:A:N3	1:A:2459:A:H3'	2.03	0.73
14:U:51:ASN:OD1	14:U:53:GLN:NE2	2.21	0.73
1:A:680:G:H2'	1:A:681:C:C6	2.24	0.73
1:A:630:A:H62	1:A:1291:A:H2	1.36	0.73
1:A:960:U:O2	1:A:961:C:N4	2.21	0.73
11:R:99:LYS:HE3	11:R:101:ASN:HB3	1.71	0.73
1:A:678:A:H2'	1:A:679:A:H8	1.53	0.73
1:A:1579:A:N7	1:A:1588:A:N6	2.37	0.73
1:A:1516:A:H62	1:A:1568:G:H8	1.38	0.72
1:A:1696:G:HO2'	1:A:1697:A:H8	1.35	0.72
1:A:2113:C:H2'	1:A:2114:C:C6	2.24	0.72
1:A:2470:C:OP1	1:A:2470:C:H4'	1.90	0.72
2:C:105:LEU:HD21	2:C:156:ARG:HG3	1.70	0.72
2:C:157:SER:O	2:C:195:VAL:HG21	1.90	0.72
1:A:275:A:H62	1:A:296:G:H21	1.38	0.72
1:A:2857:U:O2	1:A:2859:G:N1	2.22	0.72
1:A:1579:A:C8	1:A:1588:A:N6	2.58	0.72
1:A:417:G:OP2	1:A:470:A:N6	2.22	0.72
1:A:513:A:OP1	19:d:34:ARG:NH1	2.23	0.71
1:A:2049:A:OP2	17:b:6:ARG:NH1	2.23	0.71
1:A:839:G:H1	1:A:2101:G:H1'	1.55	0.71
2:C:94:ILE:CD1	2:C:116:ILE:CD1	2.65	0.71
1:A:1808:U:H5	1:A:1812:A:H62	1.39	0.71
1:A:311:U:H2'	1:A:312:G:C4	2.26	0.71
2:C:115:GLU:OE2	2:C:115:GLU:N	2.16	0.71
1:A:1847:U:OP2	2:C:156:ARG:NE	2.22	0.71
6:K:22:ILE:HD11	6:K:42:THR:HG23	1.71	0.70
1:A:425:C:N4	1:A:426:G:O6	2.24	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:911:G:HO2'	1:A:912:C:H6	1.38	0.70
3:D:13:THR:HG22	3:D:14:GLN:H	1.56	0.70
1:A:2352:G:H8	1:A:2352:G:C5'	2.02	0.70
1:A:865:G:N1	1:A:1228:G:O2'	2.18	0.69
1:A:1053:C:OP1	5:J:38:ARG:NH1	2.26	0.69
1:A:200:A:N6	1:A:2459:A:C4	2.61	0.69
1:A:1359:G:H22	1:A:1370:C:N4	1.90	0.69
15:V:28:ARG:H	15:V:28:ARG:CD	1.98	0.69
1:A:250:G:O2'	1:A:253:G:O6	2.11	0.69
1:A:650:U:OP2	4:E:104:LYS:NZ	2.26	0.69
1:A:2360:G:O2'	15:V:51:THR:CG2	2.41	0.69
1:A:1652:C:H4'	1:A:1653:A:O5'	1.91	0.69
1:A:2689:A:H3'	1:A:2690:G:H8	1.57	0.69
1:A:277:C:H2'	1:A:278:A:C8	2.28	0.69
1:A:784:C:H2'	1:A:785:C:H5''	1.74	0.68
1:A:200:A:H62	1:A:2459:A:H2'	1.56	0.68
1:A:337:A:O2'	1:A:338:G:O4'	2.10	0.68
1:A:732:A:H8	1:A:735:U:H3	1.40	0.68
1:A:1497:G:H22	1:A:1505:U:H3	1.41	0.68
1:A:200:A:H62	1:A:2459:A:C2'	2.06	0.68
15:V:56:GLY:HA2	15:V:86:LYS:HE3	1.76	0.68
1:A:2767:A:O5'	1:A:2767:A:H8	1.77	0.68
1:A:2769:A:C8	1:A:2792:G:N2	2.62	0.68
1:A:456:A:H2'	1:A:457:G:C8	2.29	0.68
1:A:2096:G:N1	1:A:2473:G:N2	2.40	0.67
1:A:2362:A:N7	1:A:2364:A:N1	2.42	0.67
1:A:2909:U:H5	17:b:40:HIS:CD2	2.11	0.67
1:A:1579:A:H4'	1:A:1579:A:OP1	1.93	0.67
1:A:2415:U:HO2'	15:V:49:ARG:HH11	1.41	0.67
10:Q:86:SER:CB	10:Q:116:GLN:HG3	2.24	0.67
15:V:53:ILE:HG21	15:V:87:VAL:HG22	1.74	0.67
1:A:831:U:O4'	2:C:226:ASN:ND2	2.27	0.67
1:A:1532:A:H2'	1:A:1533:A:H8	1.58	0.67
1:A:2114:C:O2	1:A:2264:G:N2	2.28	0.67
1:A:2688:G:N1	1:A:2691:A:OP2	2.19	0.67
1:A:678:A:H2'	1:A:679:A:C8	2.30	0.67
1:A:1387:G:H2'	1:A:1388:A:H5''	1.74	0.67
1:A:1529:G:H2'	1:A:1530:G:C8	2.29	0.67
1:A:200:A:N6	1:A:2459:A:N3	2.43	0.67
9:P:30:ARG:NH1	9:P:88:GLU:OE2	2.28	0.67
1:A:839:G:N2	1:A:2101:G:O4'	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1583:A:N3	1:A:1583:A:H2'	2.08	0.67
1:A:2292:C:N4	1:A:2307:A:C2	2.51	0.67
1:A:266:U:H2'	1:A:267:C:O4'	1.94	0.66
1:A:711:U:O3'	1:A:987:A:OP1	2.13	0.66
1:A:839:G:N2	1:A:2101:G:C4'	2.46	0.66
1:A:1380:U:OP2	1:A:1380:U:H6	1.78	0.66
15:V:41:GLY:H	15:V:72:ASP:HB3	1.60	0.66
1:A:1482:G:H21	1:A:1562:A:H8	1.42	0.66
4:E:6:LEU:HD21	4:E:17:ILE:HB	1.77	0.66
1:A:1828:G:O2'	2:C:182:ARG:NH1	2.29	0.66
1:A:922:A:O2'	1:A:949:U:N3	2.28	0.66
1:A:2440:A:H2'	1:A:2441:A:C8	2.30	0.66
2:C:198:GLU:OE1	2:C:198:GLU:N	2.29	0.66
1:A:894:A:H62	1:A:979:U:H3	1.44	0.66
1:A:199:A:H61	1:A:878:G:H1'	1.59	0.66
3:D:100:GLU:N	3:D:100:GLU:OE1	2.26	0.66
11:R:76:TYR:HB2	11:R:83:HIS:HD2	1.60	0.66
1:A:2362:A:C8	1:A:2364:A:N1	2.64	0.65
1:A:2357:A:H2'	1:A:2358:A:H8	1.62	0.65
1:A:1512:G:H8	1:A:1512:G:H5''	1.61	0.65
1:A:2678:U:H6	1:A:2678:U:O5'	1.80	0.65
1:A:288:C:O2'	1:A:289:C:OP1	2.12	0.65
2:C:115:GLU:H	2:C:115:GLU:CD	2.04	0.65
2:C:226:ASN:OD1	2:C:227:PRO:HD2	1.96	0.65
13:T:90:ILE:HG22	13:T:91:GLU:H	1.60	0.65
1:A:1631:A:H4'	1:A:1632:G:H4'	1.78	0.65
1:A:2086:G:H2'	1:A:2087:A:C8	2.32	0.65
2:C:65:ILE:HD12	2:C:87:ARG:HH21	1.62	0.65
1:A:1517:A:H61	1:A:1567:U:H3	1.44	0.65
10:Q:109:LEU:CD2	11:R:48:VAL:HG21	2.26	0.65
14:U:7:ASP:OD2	14:U:92:ARG:NH2	2.30	0.65
18:Y:37:LEU:HD23	18:Y:40:THR:HG22	1.79	0.65
1:A:875:U:H4'	1:A:878:G:C6	2.32	0.64
1:A:1496:G:N2	1:A:1508:C:C2	2.65	0.64
1:A:1831:A:H2'	1:A:1832:A:C8	2.32	0.64
3:D:125:ARG:NH1	3:D:160:LEU:O	2.30	0.64
15:V:46:TYR:CG	15:V:53:ILE:CD1	2.80	0.64
2:C:28:LYS:NZ	2:C:29:PRO:O	2.24	0.64
2:C:200:HIS:O	2:C:200:HIS:ND1	2.29	0.64
7:L:23:ILE:HD12	11:R:81:ASN:HB3	1.79	0.64
1:A:276:C:O2	1:A:295:G:N2	2.21	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:33:LEU:O	2:C:64:VAL:CG2	2.35	0.64
3:D:9:LYS:NZ	3:D:194:GLY:O	2.27	0.64
8:N:2:SER:OG	8:N:3:TYR:N	2.30	0.64
15:V:58:ASN:CG	15:V:71:ILE:CG2	2.71	0.64
1:A:1304:G:OP1	17:b:16:ARG:NH2	2.20	0.64
1:A:1540:A:H2'	1:A:1541:A:H8	1.63	0.64
1:A:1726:G:O2'	1:A:1727:A:OP1	2.15	0.64
1:A:2253:G:OP1	2:C:268:LYS:NZ	2.29	0.64
1:A:2323:C:N3	1:A:2324:C:N4	2.45	0.64
1:A:457:G:N2	1:A:465:U:O2	2.31	0.64
1:A:969:C:O2'	15:V:34:ALA:HB2	1.97	0.64
15:V:29:LEU:CD2	15:V:48:GLN:O	2.45	0.64
1:A:2383:A:O2'	15:V:44:ILE:HG22	1.96	0.64
1:A:1532:A:H2'	1:A:1533:A:C8	2.33	0.64
1:A:2354:G:H8	1:A:2354:G:OP1	1.80	0.64
15:V:74:THR:HG23	15:V:92:VAL:CG2	2.28	0.64
2:C:117:MET:HE3	2:C:119:GLY:H	1.63	0.64
14:U:2:HIS:O	14:U:92:ARG:NH1	2.30	0.64
1:A:905:G:OP1	15:V:52:LYS:HE3	1.97	0.63
1:A:1433:U:C4'	1:A:1648:A:H4'	2.24	0.63
1:A:1579:A:C8	1:A:1588:A:C6	2.86	0.63
1:A:1492:G:H1	1:A:1511:C:N4	1.93	0.63
3:D:208:SER:OG	3:D:208:SER:O	2.16	0.63
1:A:1526:G:O5'	1:A:1526:G:H8	1.82	0.63
2:C:161:SER:HB3	2:C:194:GLN:HG3	1.80	0.63
13:T:88:LYS:HB2	13:T:90:ILE:HD11	1.79	0.63
1:A:2324:C:N3	1:A:2367:G:C2	2.67	0.63
1:A:2467:U:H2'	1:A:2470:C:C5	2.34	0.63
1:A:1579:A:C6	1:A:1588:A:N3	2.67	0.63
1:A:283:G:O6	1:A:288:C:N4	2.32	0.63
1:A:1847:U:C6	2:C:156:ARG:NH2	2.66	0.63
8:N:55:ASP:OD1	8:N:56:LEU:N	2.32	0.63
9:P:56:GLY:H	9:P:60:GLU:HG2	1.64	0.63
7:L:83:ASN:HD22	7:L:117:LEU:HA	1.63	0.63
10:Q:61:TRP:CZ2	10:Q:94:MET:HG3	2.19	0.63
1:A:312:G:O2'	1:A:313:U:O4'	2.17	0.62
13:T:86:ASP:OD1	13:T:86:ASP:N	2.31	0.62
1:A:2666:U:OP1	3:D:84:ARG:NH1	2.33	0.62
1:A:2789:C:H6	1:A:2789:C:OP2	1.81	0.62
1:A:1585:A:H3'	1:A:1585:A:H8	1.65	0.62
15:V:78:GLU:CG	15:V:79:ARG:N	2.45	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:200:A:C5	1:A:2459:A:C4	2.86	0.62
1:A:277:C:H2'	1:A:278:A:H8	1.64	0.62
1:A:2362:A:C8	1:A:2364:A:C6	2.88	0.62
4:E:182:ASN:OD1	4:E:182:ASN:N	2.30	0.62
1:A:2112:G:N7	1:A:2266:G:N2	2.47	0.62
2:C:117:MET:N	2:C:128:ASN:OD1	2.29	0.62
1:A:304:G:N2	1:A:415:C:O2	2.33	0.62
1:A:852:G:H22	1:A:2473:G:H1'	1.65	0.62
1:A:881:U:OP1	1:A:881:U:H6	1.83	0.62
1:A:1691:A:H5''	1:A:1692:U:H5''	1.81	0.62
2:C:33:LEU:C	2:C:64:VAL:HG23	2.23	0.61
12:S:10:VAL:HG11	12:S:46:ILE:HG21	1.81	0.61
15:V:80:PHE:HB3	15:V:84:ARG:HB2	1.81	0.61
1:A:250:G:N2	1:A:254:A:OP2	2.31	0.61
1:A:351:G:H21	1:A:374:A:N6	1.98	0.61
1:A:1560:U:C5'	1:A:1560:U:H6	2.13	0.61
15:V:58:ASN:CG	15:V:71:ILE:HG22	2.25	0.61
1:A:231:A:O2'	1:A:233:G:OP2	2.18	0.61
1:A:2324:C:N4	1:A:2367:G:H1	1.99	0.61
1:A:689:A:N6	1:A:2398:A:O2'	2.31	0.61
1:A:1247:G:C2	1:A:1280:G:N2	2.68	0.61
1:A:2292:C:H41	1:A:2307:A:N6	1.98	0.61
7:L:144:GLU:OE2	7:L:144:GLU:N	2.31	0.61
8:N:73:GLU:O	8:N:76:ASN:ND2	2.33	0.61
12:S:65:ASP:OD2	12:S:66:ALA:N	2.33	0.61
1:A:1005:A:H2'	1:A:1006:A:N3	2.16	0.61
15:V:57:GLU:HB2	15:V:88:SER:OG	2.00	0.61
1:A:2386:U:H5''	1:A:2386:U:H6	1.66	0.61
1:A:2909:U:C5	17:b:40:HIS:HD2	2.18	0.61
10:Q:92:ARG:HD3	11:R:11:GLN:HE21	1.66	0.61
1:A:576:G:O2'	1:A:578:A:N7	2.33	0.61
1:A:1245:G:HO2'	1:A:1246:G:P	2.23	0.61
1:A:1696:G:O2'	1:A:1697:A:H8	1.84	0.61
1:A:2273:U:H4'	1:A:2463:A:N6	2.15	0.61
1:A:1345:U:O2'	1:A:1346:A:O5'	2.18	0.61
1:A:1529:G:H1'	1:A:1555:A:H61	1.66	0.61
1:A:2386:U:O2	1:A:2388:C:OP2	2.18	0.61
2:C:167:LYS:HA	2:C:172:VAL:HA	1.83	0.61
10:Q:66:ASN:OD1	10:Q:70:ARG:NH1	2.33	0.61
15:V:28:ARG:HD2	15:V:28:ARG:N	2.04	0.61
1:A:1555:A:HO2'	1:A:1556:A:H8	1.47	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:Q:61:TRP:CB	10:Q:93:LYS:O	2.48	0.60
15:V:51:THR:HG23	15:V:51:THR:O	2.01	0.60
1:A:632:U:O2'	1:A:633:U:OP1	2.18	0.60
1:A:2317:A:H2	1:A:2413:G:H21	1.50	0.60
1:A:2824:G:O2'	1:A:2827:A:N6	2.34	0.60
10:Q:90:VAL:HG23	10:Q:90:VAL:O	2.01	0.60
15:V:74:THR:CG2	15:V:92:VAL:CG2	2.79	0.60
1:A:960:U:H1'	1:A:961:C:H5	1.66	0.60
1:A:60:G:O6	1:A:63:G:N1	2.26	0.60
1:A:200:A:N3	1:A:200:A:H2'	2.15	0.60
1:A:1579:A:C6	1:A:1588:A:C4	2.90	0.60
4:E:161:GLU:OE1	4:E:161:GLU:N	2.28	0.60
1:A:1814:A:O2'	1:A:1815:A:OP2	2.16	0.60
5:J:80:GLN:C	5:J:82:PRO:HD3	2.27	0.60
1:A:1460:G:O2'	1:A:1631:A:N6	2.30	0.60
1:A:1497:G:H8	1:A:1497:G:OP2	1.85	0.60
1:A:2287:C:C5'	15:V:22:ARG:NH2	2.62	0.60
2:C:105:LEU:CD2	2:C:156:ARG:HG3	2.32	0.60
1:A:1461:A:H62	1:A:1630:G:H21	1.49	0.60
1:A:331:C:H6	1:A:331:C:O5'	1.84	0.60
1:A:692:A:H2'	1:A:693:G:O4'	2.02	0.60
1:A:902:G:H2'	1:A:903:G:H8	1.67	0.60
1:A:2462:A:H3'	1:A:2462:A:H8	1.65	0.60
11:R:72:THR:HG22	11:R:72:THR:O	2.00	0.60
14:U:75:THR:OG1	14:U:76:GLY:N	2.34	0.60
1:A:907:U:O2	1:A:964:A:N7	2.35	0.60
10:Q:100:VAL:HG23	10:Q:100:VAL:O	2.01	0.60
1:A:760:G:O2'	1:A:765:A:N1	2.33	0.59
1:A:2099:G:N1	1:A:2471:C:C4	2.47	0.59
10:Q:92:ARG:HB2	11:R:11:GLN:HE21	1.66	0.59
15:V:29:LEU:HD22	15:V:48:GLN:C	2.27	0.59
15:V:46:TYR:CD1	15:V:53:ILE:HD11	2.37	0.59
1:A:1695:A:H2'	1:A:1696:G:H5'	1.84	0.59
2:C:155:VAL:HG23	2:C:155:VAL:O	2.01	0.59
14:U:77:GLU:OE2	14:U:96:LYS:NZ	2.31	0.59
1:A:760:G:H2'	1:A:761:U:C4	2.37	0.59
1:A:1492:G:N2	1:A:1511:C:N3	2.36	0.59
2:C:67:PHE:HZ	2:C:156:ARG:HD2	1.66	0.59
2:C:246:PRO:HG2	2:C:255:LEU:HB2	1.85	0.59
10:Q:92:ARG:HB3	10:Q:95:LEU:H	1.68	0.59
1:A:2765:G:H5''	1:A:2765:G:C8	2.34	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:117:MET:HE3	2:C:118:SER:H	1.68	0.59
3:D:122:ALA:O	3:D:126:HIS:N	2.29	0.59
11:R:48:VAL:O	11:R:48:VAL:HG22	2.02	0.59
1:A:452:C:O2'	1:A:453:G:O5'	2.20	0.59
1:A:2312:C:C4	1:A:2418:G:C5	2.90	0.59
1:A:1540:A:H2'	1:A:1541:A:C8	2.38	0.59
1:A:2296:A:N6	1:A:2301:U:H3	2.00	0.59
6:K:30:ARG:NH2	6:K:37:ASP:OD2	2.36	0.59
7:L:85:PHE:O	7:L:119:LYS:NZ	2.35	0.59
10:Q:83:LEU:HD23	10:Q:113:ALA:HB2	1.85	0.59
1:A:2094:C:H3'	1:A:2094:C:H6	1.67	0.59
1:A:2795:G:H5''	1:A:2795:G:N3	2.18	0.59
1:A:1548:U:H2'	1:A:1549:U:C6	2.38	0.58
1:A:2357:A:H2'	1:A:2358:A:C8	2.37	0.58
1:A:276:C:O2'	1:A:306:C:OP1	2.20	0.58
1:A:839:G:H1	1:A:2101:G:C1'	2.16	0.58
1:A:1551:C:H2'	1:A:1552:C:C6	2.38	0.58
15:V:55:PRO:HG3	15:V:67:LEU:CD2	2.33	0.58
1:A:1322:G:H1'	1:A:1368:U:H5	1.69	0.58
1:A:1520:A:H2	1:A:1565:U:H3	1.50	0.58
1:A:2039:G:H5''	12:S:42:ALA:HB2	1.86	0.58
1:A:2786:A:H3'	1:A:2787:A:H5''	1.85	0.58
1:A:2776:G:C6	1:A:2783:U:C5	2.91	0.58
1:A:2118:U:O2	1:A:2259:G:O6	2.21	0.58
9:P:78:PRO:HG2	9:P:81:THR:HB	1.86	0.58
1:A:254:A:O5'	1:A:254:A:H8	1.87	0.58
1:A:881:U:H1'	1:A:2387:A:N3	2.18	0.58
1:A:1247:G:C2	1:A:1280:G:C2	2.92	0.58
1:A:1292:G:OP2	10:Q:13:ARG:NH2	2.33	0.58
2:C:63:ARG:HG3	2:C:63:ARG:NH2	2.13	0.58
2:C:156:ARG:O	2:C:156:ARG:HG2	2.03	0.58
19:d:3:ARG:O	19:d:6:GLN:NE2	2.36	0.58
1:A:1313:A:HO2'	1:A:1691:A:H2	1.47	0.58
1:A:412:A:H2'	1:A:413:U:C6	2.39	0.58
1:A:2665:U:O2'	3:D:46:TYR:OH	2.21	0.58
2:C:221:ARG:HE	2:C:223:SER:HG	1.51	0.58
1:A:1518:G:N2	1:A:1566:G:H22	2.00	0.58
1:A:291:C:H2'	1:A:292:U:C6	2.39	0.57
1:A:307:A:H2'	1:A:308:C:H6	1.68	0.57
1:A:2087:A:H3'	1:A:2088:A:H5''	1.87	0.57
9:P:30:ARG:HG2	9:P:47:GLU:HG2	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:V:57:GLU:H	15:V:88:SER:HB2	1.69	0.57
1:A:618:A:N1	1:A:2083:A:H5''	2.19	0.57
10:Q:83:LEU:CD2	10:Q:113:ALA:HB2	2.34	0.57
1:A:306:C:H2'	1:A:307:A:H8	1.68	0.57
1:A:973:G:H2'	1:A:974:A:H8	1.69	0.57
1:A:2312:C:C5	1:A:2418:G:N9	2.72	0.57
15:V:46:TYR:CG	15:V:53:ILE:HD11	2.40	0.57
1:A:455:G:H2'	1:A:456:A:C8	2.40	0.57
1:A:1515:C:H2'	1:A:1516:A:C8	2.39	0.57
1:A:2312:C:N4	1:A:2418:G:C5	2.72	0.57
1:A:2360:G:O3'	15:V:51:THR:CG2	2.52	0.57
1:A:307:A:H2'	1:A:308:C:C6	2.40	0.57
1:A:2085:G:N2	17:b:2:ALA:HB1	2.18	0.57
1:A:2267:G:H4'	1:A:2268:G:H5'	1.85	0.57
12:S:18:ARG:NH1	12:S:76:VAL:O	2.37	0.57
14:U:12:ILE:HG13	14:U:69:MET:HE3	1.87	0.57
1:A:321:U:O2'	1:A:322:A:OP2	2.21	0.57
1:A:1541:A:H2'	1:A:1542:A:C8	2.39	0.57
10:Q:88:ILE:HB	11:R:51:PRO:HD3	1.86	0.57
15:V:46:TYR:CD2	15:V:53:ILE:HD12	2.40	0.57
19:d:31:LEU:HD22	19:d:42:LEU:HD23	1.86	0.57
1:A:200:A:N6	1:A:2459:A:H2'	2.20	0.57
1:A:1512:G:C8	1:A:1512:G:H3'	2.40	0.57
1:A:2776:G:N2	1:A:2786:A:H62	2.03	0.57
1:A:2005:C:O2'	1:A:2006:A:O5'	2.23	0.56
7:L:91:VAL:HG23	7:L:123:VAL:HA	1.85	0.56
12:S:108:SER:OG	12:S:109:GLU:N	2.34	0.56
1:A:268:A:H2'	1:A:269:G:H4'	1.87	0.56
1:A:2328:G:H1	1:A:2347:G:H21	1.49	0.56
10:Q:95:LEU:HD11	11:R:4:ILE:CG2	2.35	0.56
15:V:60:GLY:O	15:V:68:PHE:CD2	2.58	0.56
1:A:255:G:H5''	1:A:255:G:C8	2.35	0.56
1:A:800:G:H5''	19:d:1:MET:HE2	1.86	0.56
1:A:1343:C:O2'	1:A:1344:C:O5'	2.24	0.56
1:A:2351:A:H5''	1:A:2351:A:C8	2.36	0.56
2:C:73:GLY:H	2:C:117:MET:HE1	1.70	0.56
10:Q:50:ARG:NH1	11:R:71:ILE:HG21	2.21	0.56
1:A:275:A:H2	1:A:304:G:H21	1.52	0.56
3:D:182:GLU:OE2	3:D:183:ARG:NH2	2.38	0.56
12:S:73:GLN:HB2	12:S:106:VAL:HB	1.88	0.56
1:A:90:A:H4'	1:A:91:A:C5'	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:200:A:C6	1:A:2459:A:C4	2.93	0.56
10:Q:92:ARG:HG2	10:Q:94:MET:HB3	1.87	0.56
11:R:7:THR:OG1	11:R:8:GLY:N	2.39	0.56
1:A:1525:G:N2	1:A:1560:U:C2	2.67	0.56
1:A:2049:A:P	17:b:6:ARG:HH12	2.28	0.56
1:A:2312:C:N4	1:A:2418:G:C6	2.74	0.56
1:A:2324:C:C6	1:A:2367:G:N2	2.74	0.56
15:V:29:LEU:HD23	15:V:47:ARG:HG2	1.88	0.56
1:A:379:C:H4'	14:U:69:MET:HE2	1.87	0.56
1:A:1522:U:O2'	1:A:1523:U:O5'	2.23	0.56
1:A:1578:G:O5'	1:A:1578:G:H8	1.88	0.56
1:A:2254:A:H4'	1:A:2255:C:O5'	2.04	0.56
1:A:1613:C:O2'	1:A:1614:A:H2'	2.06	0.56
1:A:2462:A:H3'	1:A:2462:A:C8	2.40	0.56
1:A:1083:G:C6	1:A:1165:U:O2	2.59	0.56
1:A:1187:U:OP2	5:J:66:THR:OG1	2.24	0.56
1:A:1545:C:H2'	1:A:1546:G:H8	1.71	0.56
15:V:75:VAL:HG12	15:V:76:LYS:N	2.19	0.56
1:A:63:G:P	1:A:63:G:H3'	2.46	0.56
1:A:1585:A:H3'	1:A:1585:A:C8	2.40	0.56
1:A:2909:U:C5	17:b:40:HIS:CD2	2.93	0.56
1:A:2099:G:N1	1:A:2471:C:N4	2.51	0.55
3:D:121:GLY:O	3:D:125:ARG:N	2.37	0.55
1:A:419:G:N2	1:A:447:G:H2'	2.18	0.55
5:J:78:HIS:CD2	5:J:85:LEU:HB3	2.41	0.55
1:A:911:G:O2'	1:A:912:C:H5'	2.07	0.55
15:V:74:THR:HG23	15:V:92:VAL:HG23	1.87	0.55
1:A:293:U:H2'	1:A:294:G:C8	2.42	0.55
1:A:1228:G:O2'	1:A:1229:U:OP2	2.24	0.55
5:J:20:ASP:OD1	5:J:21:ALA:N	2.40	0.55
1:A:873:U:O2	1:A:878:G:O6	2.25	0.55
1:A:998:G:H21	1:A:2296:A:H2	1.53	0.55
1:A:2280:G:H2'	1:A:2281:G:O4'	2.07	0.55
1:A:2875:A:N7	1:A:2893:A:O2'	2.37	0.55
1:A:2105:U:OP2	1:A:2267:G:N2	2.38	0.55
2:C:110:ILE:HD12	2:C:111:GLN:H	1.71	0.55
7:L:69:ILE:HG13	7:L:70:ASN:H	1.72	0.55
11:R:15:GLU:OE2	11:R:16:GLU:N	2.34	0.55
1:A:913:A:H2	1:A:914:C:H5	1.55	0.55
1:A:2110:C:N4	1:A:2268:G:O6	2.40	0.55
1:A:1820:A:N6	1:A:1857:G:O2'	2.38	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:S:11:ARG:HH21	12:S:98:LYS:HD2	1.72	0.55
1:A:2126:G:H22	1:A:2221:C:H1'	1.72	0.55
7:L:57:LEU:O	7:L:61:LEU:HB2	2.06	0.55
13:T:44:GLU:OE2	13:T:51:VAL:N	2.40	0.55
15:V:46:TYR:CD2	15:V:53:ILE:CD1	2.90	0.55
1:A:2351:A:H61	1:A:2362:A:N6	1.89	0.54
1:A:2415:U:H3'	1:A:2415:U:H6	1.72	0.54
6:K:64:ARG:NH1	6:K:101:PRO:O	2.40	0.54
7:L:79:LEU:HB2	7:L:114:ASN:O	2.07	0.54
15:V:75:VAL:O	15:V:76:LYS:HD3	2.07	0.54
1:A:711:U:H4'	1:A:987:A:P	2.46	0.54
1:A:2086:G:H5'	17:b:3:VAL:HG21	1.88	0.54
1:A:920:G:H5''	1:A:922:A:H62	1.71	0.54
1:A:1362:G:H2'	1:A:1363:G:H5''	1.89	0.54
7:L:1:MET:HE2	7:L:6:LEU:HA	1.88	0.54
1:A:351:G:H21	1:A:374:A:H62	1.54	0.54
1:A:1533:A:H2'	1:A:1534:A:H8	1.73	0.54
1:A:2360:G:O3'	15:V:51:THR:HG23	2.07	0.54
10:Q:61:TRP:CZ3	10:Q:94:MET:CB	2.89	0.54
12:S:88:ARG:HB2	12:S:92:ARG:HB2	1.89	0.54
1:A:1578:G:H21	1:A:1588:A:H62	1.53	0.54
1:A:2909:U:H5	17:b:40:HIS:HD2	1.49	0.54
13:T:39:VAL:O	13:T:43:VAL:HG23	2.08	0.54
1:A:1848:A:H5''	2:C:160:THR:HG21	1.90	0.54
1:A:2290:C:H2'	15:V:24:SER:CB	2.37	0.54
1:A:2389:A:H8	1:A:2389:A:OP2	1.90	0.54
2:C:64:VAL:O	2:C:103:TYR:HB2	2.08	0.54
1:A:926:G:N1	1:A:945:C:O2'	2.38	0.54
1:A:954:U:H2'	1:A:955:C:C6	2.42	0.54
1:A:1499:A:O2'	1:A:1500:U:H5''	2.07	0.54
1:A:2292:C:H2'	1:A:2292:C:O2	2.08	0.54
1:A:2696:C:H2'	1:A:2697:G:O4'	2.06	0.54
1:A:433:G:OP2	1:A:435:G:N2	2.34	0.54
1:A:1560:U:H6	1:A:1560:U:H5''	1.72	0.54
1:A:1815:A:H61	1:A:2012:C:H5'	1.72	0.54
13:T:2:LYS:NZ	13:T:38:GLU:OE1	2.35	0.54
1:A:1359:G:H22	1:A:1370:C:H41	1.54	0.54
1:A:2318:G:O6	1:A:2372:U:O2	2.25	0.54
1:A:1257:C:H2'	1:A:1258:A:H5''	1.88	0.53
1:A:1571:G:H2'	1:A:1572:G:H5'	1.90	0.53
1:A:1075:A:N6	1:A:1171:G:H1'	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1244:A:C8	7:L:4:HIS:HB3	2.38	0.53
1:A:1245:G:O2'	1:A:1246:G:O5'	2.11	0.53
1:A:2692:G:H2'	1:A:2693:G:C8	2.43	0.53
6:K:51:VAL:HG11	6:K:94:ARG:HH21	1.74	0.53
15:V:56:GLY:HA3	15:V:86:LYS:HE2	1.88	0.53
15:V:58:ASN:CG	15:V:71:ILE:HG21	2.34	0.53
1:A:291:C:H2'	1:A:292:U:H6	1.73	0.53
1:A:759:G:H3'	1:A:760:G:C8	2.44	0.53
1:A:1042:A:H4'	10:Q:92:ARG:HD2	1.90	0.53
9:P:74:GLU:OE1	9:P:74:GLU:N	2.41	0.53
1:A:458:G:H8	1:A:458:G:H5''	1.73	0.53
1:A:916:G:H3'	1:A:917:A:H8	1.73	0.53
1:A:2362:A:C8	1:A:2364:A:C2	2.96	0.53
1:A:2776:G:H21	1:A:2786:A:N6	2.04	0.53
11:R:50:ASN:CB	11:R:51:PRO:HD2	2.30	0.53
11:R:74:PHE:C	11:R:74:PHE:CD2	2.85	0.53
2:C:2:ALA:N	2:C:20:ASP:OD2	2.42	0.53
9:P:25:PRO:HA	9:P:50:VAL:HG23	1.91	0.53
1:A:325:A:H2'	1:A:326:A:H8	1.74	0.53
1:A:373:A:N6	14:U:15:LYS:H	2.06	0.53
1:A:2780:G:H4'	1:A:2780:G:OP2	2.08	0.53
15:V:62:GLY:N	15:V:66:THR:O	2.39	0.53
1:A:302:A:N6	1:A:451:C:O2	2.42	0.53
1:A:2875:A:OP2	1:A:2891:G:N2	2.32	0.53
2:C:126:VAL:O	2:C:126:VAL:HG13	2.09	0.53
1:A:78:U:H2'	1:A:79:C:C6	2.44	0.53
1:A:954:U:O2'	1:A:955:C:H5'	2.09	0.53
1:A:1008:A:H2'	1:A:1009:U:C6	2.44	0.53
1:A:1525:G:C2	1:A:1560:U:C2	2.85	0.53
1:A:1585:A:C8	1:A:1585:A:C3'	2.92	0.53
4:E:158:ASP:N	4:E:158:ASP:OD1	2.39	0.53
9:P:29:LEU:HD21	9:P:50:VAL:HG13	1.91	0.53
13:T:11:PRO:HD3	18:Y:30:PHE:CE1	2.43	0.53
1:A:345:A:O2'	1:A:346:G:O5'	2.17	0.52
1:A:1526:G:H2'	1:A:1527:C:H5'	1.89	0.52
1:A:2099:G:H4'	1:A:2099:G:OP1	2.07	0.52
8:N:110:ASP:OD1	8:N:110:ASP:N	2.39	0.52
15:V:56:GLY:CA	15:V:86:LYS:CE	2.75	0.52
1:A:325:A:C6	1:A:326:A:C5	2.97	0.52
1:A:850:U:O2'	1:A:851:A:H5'	2.09	0.52
4:E:128:ASP:OD1	4:E:128:ASP:N	2.38	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:481:U:O2'	1:A:482:C:O2	2.27	0.52
1:A:952:A:H2'	1:A:954:U:C6	2.45	0.52
1:A:1579:A:C4	1:A:1588:A:N1	2.76	0.52
4:E:192:LEU:HD21	4:E:194:ILE:HG13	1.91	0.52
1:A:199:A:H61	1:A:878:G:C1'	2.23	0.52
1:A:2114:C:H2'	1:A:2115:U:H6	1.75	0.52
1:A:2318:G:N3	1:A:2319:G:C8	2.78	0.52
4:E:13:THR:OG1	4:E:14:ALA:N	2.43	0.52
14:U:13:SER:OG	14:U:14:GLY:N	2.42	0.52
1:A:1512:G:C8	1:A:1512:G:C3'	2.92	0.52
6:K:17:ARG:NH1	6:K:45:GLN:OE1	2.42	0.52
1:A:2292:C:N4	1:A:2307:A:C5	2.66	0.52
1:A:2457:G:H21	7:L:60:ARG:HH22	1.58	0.52
1:A:248:G:H2'	1:A:249:C:C6	2.44	0.52
1:A:1463:C:H2'	1:A:1464:A:O4'	2.10	0.52
1:A:1495:C:H42	1:A:1508:C:H42	1.56	0.52
1:A:1581:A:N3	1:A:1581:A:H2'	2.24	0.52
1:A:2779:A:H1'	1:A:2781:C:H41	1.74	0.52
8:N:86:ASP:O	8:N:89:THR:HG22	2.10	0.52
11:R:53:VAL:HG12	11:R:53:VAL:O	2.09	0.52
1:A:1184:G:N3	5:J:109:MET:HE2	2.24	0.52
1:A:2459:A:N3	1:A:2459:A:C3'	2.73	0.52
1:A:2678:U:H2'	1:A:2679:C:H6	1.74	0.52
11:R:50:ASN:OD1	11:R:50:ASN:C	2.53	0.52
1:A:766:C:H2'	1:A:767:U:C6	2.45	0.52
1:A:2470:C:H2'	1:A:2470:C:O2	2.09	0.52
5:J:10:SER:O	5:J:10:SER:OG	2.28	0.52
1:A:74:U:OP1	18:Y:47:ARG:NH2	2.43	0.52
1:A:2085:G:H21	17:b:3:VAL:HG22	1.73	0.52
1:A:298:U:H4'	1:A:298:U:OP1	2.09	0.51
1:A:2096:G:N9	1:A:2098:G:N7	2.58	0.51
1:A:219:A:N7	1:A:478:U:H5	2.08	0.51
1:A:418:A:H1'	1:A:420:U:C6	2.45	0.51
1:A:796:A:H4'	1:A:1311:G:N3	2.26	0.51
10:Q:94:MET:SD	10:Q:94:MET:C	2.94	0.51
1:A:163:U:O2'	1:A:166:A:N1	2.36	0.51
1:A:1527:C:O2'	1:A:1528:U:OP1	2.29	0.51
6:K:40:VAL:HG12	6:K:59:LYS:HG2	1.91	0.51
10:Q:58:ARG:O	10:Q:62:ILE:HG12	2.10	0.51
10:Q:109:LEU:HD21	11:R:48:VAL:CG2	2.41	0.51
1:A:1815:A:N1	1:A:2011:U:O2'	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2666:U:H5''	3:D:84:ARG:NH1	2.25	0.51
1:A:1505:U:H2'	1:A:1506:A:H5''	1.93	0.51
1:A:2315:A:H4'	1:A:2316:A:O4'	2.11	0.51
15:V:53:ILE:HG22	15:V:87:VAL:HG23	1.88	0.51
1:A:229:A:O2'	1:A:230:A:OP1	2.28	0.51
1:A:899:C:N4	1:A:900:U:O4	2.44	0.51
1:A:1075:A:H61	1:A:1171:G:H1'	1.76	0.51
1:A:1187:U:H4'	1:A:1188:A:O4'	2.10	0.51
1:A:1518:G:N2	1:A:1566:G:H1	2.09	0.51
1:A:2094:C:C5'	1:A:2280:G:N2	2.72	0.51
1:A:2794:A:N3	1:A:2794:A:C2'	2.73	0.51
10:Q:109:LEU:HD21	11:R:48:VAL:HG21	1.93	0.51
15:V:46:TYR:CG	15:V:53:ILE:HD12	2.46	0.51
1:A:306:C:C2	1:A:307:A:C8	2.99	0.51
1:A:1000:G:O6	1:A:1010:C:N4	2.44	0.51
1:A:2044:A:C2	17:b:3:VAL:HG12	2.45	0.51
1:A:168:A:H3'	1:A:169:G:H8	1.76	0.51
1:A:275:A:H62	1:A:296:G:N2	2.09	0.51
1:A:2099:G:H1	1:A:2471:C:H42	1.58	0.51
1:A:2414:C:H2'	1:A:2414:C:O2	2.10	0.51
2:C:274:ARG:HG3	2:C:275:LYS:H	1.75	0.51
4:E:31:SER:HG	7:L:9:SER:HG	1.59	0.51
1:A:740:A:O2'	1:A:1392:A:N3	2.42	0.50
1:A:1179:A:O2'	1:A:2055:U:O2'	2.27	0.50
1:A:1310:C:H5''	1:A:1311:G:H5'	1.92	0.50
1:A:2777:A:C2	1:A:2778:A:H2'	2.47	0.50
5:J:126:TYR:OH	5:J:133:HIS:NE2	2.40	0.50
10:Q:14:ARG:HG2	10:Q:32:TYR:CE1	2.45	0.50
1:A:973:G:H2'	1:A:974:A:C8	2.44	0.50
1:A:1087:U:H4'	1:A:1161:A:N1	2.26	0.50
1:A:1549:U:H2'	1:A:1550:C:C6	2.46	0.50
1:A:2441:A:H2'	1:A:2442:G:O4'	2.10	0.50
1:A:2462:A:C8	1:A:2462:A:C3'	2.94	0.50
14:U:24:LEU:HD11	14:U:36:GLU:HB3	1.92	0.50
1:A:1246:G:H1'	1:A:1247:G:H5'	1.93	0.50
1:A:1322:G:H1'	1:A:1368:U:C5	2.45	0.50
1:A:1555:A:O2'	1:A:1556:A:H8	1.94	0.50
9:P:35:VAL:HG13	9:P:42:ARG:HG3	1.93	0.50
1:A:2111:A:H3'	1:A:2112:G:H8	1.75	0.50
1:A:2394:G:OP1	15:V:63:GLY:N	2.45	0.50
3:D:26:THR:OG1	3:D:190:GLY:O	2.29	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:J:18:VAL:HG23	5:J:138:PRO:HB2	1.93	0.50
7:L:93:PRO:HA	7:L:96:LEU:HD12	1.94	0.50
12:S:11:ARG:HD2	12:S:99:ARG:O	2.11	0.50
13:T:11:PRO:HD3	18:Y:30:PHE:CD1	2.46	0.50
18:Y:34:THR:HG23	18:Y:36:GLN:HG2	1.93	0.50
1:A:311:U:H2'	1:A:312:G:N3	2.27	0.50
1:A:785:C:O2'	1:A:786:A:OP1	2.29	0.50
1:A:901:U:H2'	1:A:902:G:H8	1.77	0.50
1:A:902:G:H2'	1:A:903:G:C8	2.46	0.50
1:A:2096:G:HO2'	1:A:2098:G:H8	1.57	0.50
14:U:82:GLY:O	14:U:93:VAL:HG22	2.11	0.50
18:Y:19:LYS:O	18:Y:23:GLU:HG2	2.11	0.50
1:A:304:G:N7	1:A:411:G:N2	2.59	0.50
1:A:693:G:H2'	1:A:694:G:O4'	2.12	0.50
1:A:913:A:C2	1:A:914:C:H5	2.29	0.50
1:A:1351:U:H6	1:A:1351:U:H5'	1.76	0.50
1:A:2874:G:O2'	1:A:2891:G:N2	2.45	0.50
1:A:2119:A:H2'	1:A:2120:U:C6	2.47	0.50
4:E:155:VAL:CG2	4:E:194:ILE:HG12	2.42	0.50
5:J:66:THR:O	5:J:69:LYS:NZ	2.42	0.50
10:Q:50:ARG:O	10:Q:54:LYS:NZ	2.45	0.50
10:Q:80:MET:HE2	10:Q:93:LYS:NZ	2.26	0.50
1:A:37:C:H4'	1:A:498:U:OP1	2.11	0.50
1:A:902:G:C6	1:A:970:A:N1	2.79	0.50
1:A:1504:A:H4'	1:A:1505:U:H5'	1.93	0.50
2:C:67:PHE:CE1	2:C:105:LEU:HD13	2.47	0.50
4:E:63:LYS:NZ	4:E:75:GLN:HG3	2.27	0.50
1:A:881:U:P	1:A:881:U:O4'	2.70	0.50
1:A:1726:G:HO2'	1:A:1727:A:P	2.33	0.50
1:A:2292:C:N4	1:A:2307:A:N6	2.53	0.50
1:A:1072:A:C4	1:A:1073:A:H2	2.30	0.49
1:A:2096:G:C5	1:A:2098:G:C5	2.93	0.49
1:A:2678:U:H2'	1:A:2679:C:C6	2.47	0.49
18:Y:9:LEU:O	18:Y:11:THR:N	2.45	0.49
1:A:919:U:C4	1:A:920:G:C8	3.00	0.49
1:A:1545:C:H2'	1:A:1546:G:C8	2.47	0.49
1:A:1861:C:O2'	1:A:1862:C:OP1	2.28	0.49
1:A:2687:C:N4	1:A:2688:G:O6	2.45	0.49
2:C:76:GLY:HA3	2:C:96:TYR:HD2	1.76	0.49
5:J:78:HIS:HD2	5:J:85:LEU:HB3	1.75	0.49
13:T:17:SER:O	13:T:17:SER:OG	2.25	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:683:A:H4'	1:A:684:G:O5'	2.12	0.49
1:A:2294:U:H2'	1:A:2295:A:C8	2.48	0.49
1:A:850:U:C2'	1:A:851:A:H5'	2.42	0.49
1:A:1171:G:O6	1:A:1172:A:N6	2.45	0.49
1:A:2104:U:H3'	1:A:2267:G:N2	2.28	0.49
1:A:2310:C:H2'	1:A:2311:G:C8	2.47	0.49
1:A:953:G:H3'	1:A:954:U:C5'	2.43	0.49
1:A:1819:C:H2'	1:A:1820:A:C8	2.47	0.49
1:A:2345:U:H2'	1:A:2346:C:C6	2.48	0.49
1:A:2819:A:H4'	1:A:2820:U:H5''	1.94	0.49
9:P:52:LYS:HG2	9:P:63:THR:HG23	1.94	0.49
16:Z:36:VAL:O	16:Z:37:HIS:ND1	2.45	0.49
1:A:164:U:H2'	1:A:165:C:C6	2.48	0.49
1:A:1296:G:H21	4:E:82:GLN:HB2	1.78	0.49
1:A:1547:U:H2'	1:A:1548:U:C6	2.48	0.49
9:P:26:GLY:H	9:P:50:VAL:HG23	1.76	0.49
1:A:183:A:H5''	1:A:482:C:H1'	1.93	0.49
1:A:2352:G:C8	1:A:2352:G:C5'	2.85	0.49
7:L:79:LEU:O	7:L:83:ASN:N	2.38	0.49
1:A:61:A:OP1	18:Y:44:ARG:NH1	2.46	0.48
1:A:948:A:H3'	1:A:948:A:N3	2.28	0.48
1:A:953:G:H2'	1:A:953:G:N3	2.26	0.48
1:A:977:U:O2'	1:A:978:A:H5'	2.13	0.48
1:A:1000:G:N1	1:A:1010:C:N3	2.61	0.48
1:A:1077:G:H2'	1:A:1078:A:O4'	2.13	0.48
1:A:2094:C:C3'	1:A:2094:C:C6	2.96	0.48
1:A:805:G:N2	1:A:2010:A:H62	2.05	0.48
1:A:2009:G:H3'	1:A:2010:A:H5''	1.95	0.48
1:A:2312:C:C5	1:A:2418:G:C8	3.02	0.48
13:T:88:LYS:HB2	13:T:90:ILE:CD1	2.42	0.48
1:A:12:A:OP2	1:A:12:A:H8	1.97	0.48
1:A:292:U:H2'	1:A:293:U:H6	1.77	0.48
1:A:1041:C:N3	5:J:4:THR:HG22	2.28	0.48
4:E:196:LYS:O	4:E:199:VAL:HG12	2.13	0.48
1:A:1217:U:O2'	1:A:1218:U:H3'	2.14	0.48
1:A:1512:G:H1'	1:A:1593:A:C2	2.49	0.48
1:A:2245:G:HO2'	1:A:2246:G:H8	1.59	0.48
1:A:2273:U:H2'	1:A:2274:U:H6	1.78	0.48
1:A:2334:U:O2'	1:A:2335:U:OP1	2.25	0.48
1:A:2768:U:H5''	1:A:2792:G:O6	2.13	0.48
2:C:67:PHE:CZ	2:C:156:ARG:CD	2.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:K:63:VAL:HG23	6:K:106:LEU:HD11	1.94	0.48
15:V:75:VAL:CG1	15:V:76:LYS:N	2.76	0.48
1:A:63:G:H1'	1:A:64:A:C5'	2.44	0.48
1:A:64:A:OP1	13:T:73:THR:HB	2.13	0.48
1:A:527:A:O2'	14:U:42:LYS:O	2.30	0.48
1:A:1280:G:H2'	1:A:1281:C:O2	2.13	0.48
1:A:1506:A:N3	1:A:1506:A:H2'	2.28	0.48
1:A:2284:G:H2'	1:A:2285:G:H8	1.79	0.48
2:C:124:ILE:O	2:C:124:ILE:HG13	2.12	0.48
2:C:177:ASN:OD1	2:C:178:SER:N	2.47	0.48
1:A:2415:U:HO2'	15:V:49:ARG:NH1	2.05	0.48
2:C:132:LEU:HB3	2:C:172:VAL:HG11	1.96	0.48
11:R:77:LYS:HB2	11:R:82:VAL:HB	1.96	0.48
1:A:275:A:O2'	1:A:414:C:O2'	2.29	0.48
1:A:2702:G:H2'	1:A:2703:G:C8	2.48	0.48
1:A:2769:A:H2'	1:A:2770:A:C8	2.49	0.48
1:A:268:A:H2'	1:A:269:G:C4'	2.43	0.48
1:A:419:G:N2	1:A:447:G:N3	2.62	0.48
1:A:1358:G:H2'	1:A:1359:G:C8	2.48	0.48
15:V:79:ARG:NH1	15:V:82:ARG:HD3	2.28	0.48
1:A:760:G:H2'	1:A:761:U:C5	2.49	0.48
1:A:1658:G:O2'	19:d:3:ARG:HD2	2.14	0.48
1:A:2353:U:H5'	1:A:2354:G:H5'	1.94	0.48
1:A:306:C:H2'	1:A:307:A:C8	2.48	0.48
1:A:2312:C:C5	1:A:2418:G:C5	3.02	0.48
8:N:45:GLU:OE1	8:N:99:THR:OG1	2.30	0.48
14:U:46:LYS:HE3	14:U:46:LYS:HB2	1.63	0.48
1:A:711:U:H4'	1:A:986:G:O3'	2.14	0.47
1:A:1073:A:N6	1:A:1172:A:N3	2.62	0.47
1:A:2702:G:H2'	1:A:2703:G:H8	1.79	0.47
1:A:2789:C:O2	1:A:2789:C:H2'	2.13	0.47
1:A:325:A:C4	1:A:326:A:C8	3.02	0.47
1:A:1083:G:C6	1:A:1165:U:C2	3.01	0.47
1:A:1083:G:O6	1:A:1165:U:C2	2.66	0.47
1:A:1405:A:O5'	1:A:1405:A:H8	1.98	0.47
2:C:246:PRO:O	2:C:253:PRO:HA	2.14	0.47
1:A:1491:A:H62	1:A:1512:G:H22	1.62	0.47
2:C:67:PHE:HE1	2:C:105:LEU:HD13	1.79	0.47
13:T:83:LEU:HD11	13:T:89:GLU:HB2	1.96	0.47
1:A:911:G:O2'	1:A:912:C:H6	1.97	0.47
1:A:1572:G:OP2	1:A:1572:G:H2'	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:140:A:H2'	1:A:141:U:C6	2.50	0.47
1:A:906:G:O2'	1:A:907:U:OP2	2.32	0.47
1:A:2292:C:N3	1:A:2307:A:C2	2.81	0.47
1:A:2320:U:H2'	1:A:2321:U:C6	2.50	0.47
1:A:2350:G:H3'	1:A:2350:G:N3	2.30	0.47
1:A:2374:G:H4'	1:A:2375:A:H5''	1.96	0.47
1:A:1478:G:H2'	1:A:1479:G:C8	2.49	0.47
1:A:1525:G:N1	1:A:1560:U:C2	2.82	0.47
1:A:2284:G:H1	1:A:2304:C:H42	1.62	0.47
1:A:2394:G:H5'	1:A:2395:A:OP1	2.15	0.47
2:C:205:ILE:HG22	2:C:210:ARG:HB3	1.97	0.47
1:A:795:G:H5''	12:S:89:ALA:HB2	1.96	0.47
1:A:872:C:H4'	1:A:2457:G:C5	2.50	0.47
1:A:2096:G:C2	1:A:2473:G:N2	2.82	0.47
1:A:2273:U:H2'	1:A:2274:U:C6	2.50	0.47
1:A:2324:C:C2	1:A:2367:G:N2	2.83	0.47
1:A:2688:G:H22	1:A:2691:A:P	2.37	0.47
1:A:2691:A:N3	1:A:2691:A:H2'	2.30	0.47
3:D:14:GLN:NE2	3:D:22:LEU:HD11	2.30	0.47
10:Q:61:TRP:CZ3	10:Q:94:MET:CG	2.96	0.47
10:Q:91:ASN:O	10:Q:96:ALA:HB2	2.15	0.47
15:V:64:ASP:OD1	15:V:66:THR:OG1	2.30	0.47
19:d:33:ARG:O	19:d:36:ARG:N	2.48	0.47
1:A:451:C:O2'	1:A:452:C:OP2	2.32	0.47
1:A:720:C:H5''	4:E:81:PRO:HD2	1.95	0.47
1:A:756:U:H2'	1:A:757:C:C6	2.50	0.47
1:A:926:G:O6	1:A:946:G:H4'	2.15	0.47
1:A:2287:C:H5'	15:V:22:ARG:NH2	2.29	0.47
5:J:14:ARG:NH2	5:J:50:ASP:O	2.48	0.47
1:A:78:U:H2'	1:A:79:C:H6	1.80	0.47
1:A:293:U:H2'	1:A:294:G:H8	1.77	0.47
1:A:302:A:H2'	1:A:303:G:C8	2.50	0.47
1:A:1533:A:H2'	1:A:1534:A:C8	2.50	0.47
1:A:2096:G:C6	1:A:2098:G:C6	2.99	0.47
1:A:2872:U:H2'	1:A:2873:G:O4'	2.14	0.47
2:C:141:VAL:CG2	2:C:191:SER:O	2.63	0.47
9:P:55:GLY:HA3	9:P:60:GLU:HA	1.97	0.47
1:A:311:U:HO2'	1:A:312:G:P	2.34	0.47
1:A:325:A:H2'	1:A:326:A:C8	2.50	0.47
1:A:1659:A:C2	12:S:93:ALA:HB2	2.50	0.47
1:A:2113:C:H2'	1:A:2114:C:H6	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:D:163:ARG:HE	3:D:163:ARG:HB2	1.54	0.47
4:E:194:ILE:HG22	4:E:195:THR:O	2.15	0.47
1:A:916:G:H2'	1:A:917:A:C8	2.50	0.46
1:A:2224:U:H2'	1:A:2225:C:C6	2.49	0.46
1:A:408:G:C6	1:A:409:U:C4	3.03	0.46
1:A:1349:G:N2	1:A:1352:U:C4	2.84	0.46
1:A:1360:A:C4	1:A:1361:A:C8	3.03	0.46
1:A:1458:U:H4'	1:A:1459:U:H5''	1.96	0.46
15:V:29:LEU:HD22	15:V:48:GLN:CA	2.46	0.46
1:A:166:A:H2'	1:A:167:U:N1	2.31	0.46
1:A:166:A:H2'	1:A:167:U:C2	2.50	0.46
1:A:1725:U:O2'	1:A:1726:G:H5'	2.15	0.46
2:C:170:LYS:O	2:C:186:SER:HB2	2.16	0.46
5:J:30:SER:HB2	5:J:106:ILE:HG12	1.98	0.46
8:N:75:ASN:C	8:N:75:ASN:OD1	2.58	0.46
1:A:278:A:H2'	1:A:279:A:H8	1.81	0.46
1:A:699:A:O5'	1:A:699:A:H8	1.99	0.46
1:A:732:A:H8	1:A:735:U:N3	2.10	0.46
1:A:848:G:H8	4:E:55:SER:HB3	1.81	0.46
1:A:1320:G:H2'	1:A:1321:U:C6	2.51	0.46
1:A:2083:A:H2	17:b:5:PHE:HB2	1.81	0.46
1:A:2098:G:N2	1:A:2472:C:C2	2.84	0.46
1:A:2112:G:N3	1:A:2112:G:H2'	2.31	0.46
1:A:2439:G:C5	1:A:2440:A:C8	3.04	0.46
2:C:116:ILE:O	2:C:116:ILE:HG13	2.15	0.46
1:A:63:G:H1'	1:A:64:A:H5''	1.96	0.46
1:A:278:A:H2'	1:A:279:A:C8	2.51	0.46
1:A:1565:U:C2	1:A:1566:G:C8	3.03	0.46
6:K:34:ASN:OD1	6:K:35:ILE:N	2.42	0.46
8:N:30:ILE:HG22	8:N:117:ILE:HG23	1.97	0.46
11:R:53:VAL:HG12	11:R:56:ALA:HB3	1.97	0.46
1:A:852:G:N2	1:A:2473:G:H1'	2.30	0.46
1:A:1240:U:H1'	10:Q:4:VAL:HG22	1.98	0.46
5:J:26:LEU:HA	5:J:63:ILE:HD11	1.97	0.46
5:J:29:LEU:O	5:J:33:VAL:HG23	2.16	0.46
6:K:42:THR:HG22	6:K:57:VAL:HG22	1.96	0.46
13:T:66:VAL:O	13:T:68:ARG:N	2.48	0.46
1:A:305:A:C5	1:A:306:C:C5	3.03	0.46
1:A:1313:A:O2'	1:A:1691:A:H2	1.98	0.46
1:A:2090:G:O3'	1:A:2091:A:H3'	2.16	0.46
1:A:2312:C:C4	1:A:2418:G:C4	3.03	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2432:C:OP2	1:A:2432:C:H6	1.99	0.46
1:A:2775:U:O4	1:A:2784:C:H5''	2.16	0.46
1:A:459:A:OP1	1:A:460:C:N4	2.49	0.46
1:A:758:A:H2'	1:A:759:G:C8	2.51	0.46
4:E:155:VAL:HG22	4:E:194:ILE:HG12	1.98	0.46
1:A:345:A:HO2'	1:A:346:G:C5'	2.25	0.46
1:A:580:U:H2'	1:A:581:C:C6	2.51	0.46
1:A:680:G:H2'	1:A:681:C:H6	1.79	0.46
1:A:1246:G:H2'	1:A:1246:G:N3	2.31	0.46
1:A:2224:U:H2'	1:A:2225:C:C5	2.51	0.46
2:C:70:ASP:OD1	2:C:70:ASP:O	2.33	0.46
3:D:12:MET:HE2	3:D:12:MET:HB3	1.77	0.46
11:R:74:PHE:HD2	11:R:74:PHE:O	1.99	0.46
15:V:74:THR:O	15:V:89:VAL:HA	2.16	0.46
1:A:1495:C:N4	1:A:1508:C:H42	2.14	0.45
1:A:2096:G:C8	1:A:2098:G:C5	3.03	0.45
7:L:19:VAL:HB	7:L:31:ALA:HB1	1.98	0.45
7:L:57:LEU:HD13	7:L:61:LEU:CD1	2.27	0.45
1:A:1554:U:H4'	1:A:1555:A:C8	2.52	0.45
1:A:2425:G:C2	1:A:2450:G:C2	3.04	0.45
1:A:2783:U:H6	1:A:2783:U:O5'	1.99	0.45
14:U:60:GLU:N	14:U:60:GLU:OE2	2.49	0.45
19:d:23:SER:O	19:d:23:SER:OG	2.30	0.45
1:A:1015:G:H2'	1:A:1016:U:C6	2.50	0.45
4:E:102:PRO:O	4:E:106:ARG:HG3	2.17	0.45
4:E:200:GLU:O	4:E:204:GLU:HG2	2.16	0.45
6:K:69:ALA:HB1	6:K:105:GLU:OE2	2.17	0.45
15:V:75:VAL:O	15:V:76:LYS:CD	2.65	0.45
1:A:419:G:H4'	1:A:420:U:O5'	2.15	0.45
1:A:750:U:H2'	1:A:751:G:O4'	2.17	0.45
1:A:881:U:O2	1:A:2387:A:H1'	2.17	0.45
1:A:953:G:OP2	1:A:954:U:H5'	2.17	0.45
1:A:1363:G:H4'	1:A:1363:G:OP1	2.15	0.45
1:A:1630:G:H4'	1:A:1631:A:OP1	2.15	0.45
4:E:39:MET:HE2	4:E:39:MET:HB2	1.90	0.45
7:L:69:ILE:HG13	7:L:70:ASN:N	2.31	0.45
8:N:44:VAL:O	8:N:48:ILE:HG13	2.16	0.45
11:R:4:ILE:HG12	11:R:40:PHE:HB3	1.98	0.45
1:A:161:A:OP2	1:A:166:A:N6	2.49	0.45
1:A:580:U:H5'	10:Q:42:SER:HB2	1.98	0.45
1:A:1444:C:H2'	1:A:1445:A:H8	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1557:G:C2'	1:A:1558:C:H5'	2.47	0.45
1:A:1819:C:O2'	2:C:208:ALA:HB2	2.17	0.45
1:A:2101:G:HO2'	1:A:2102:C:H6	1.63	0.45
1:A:2320:U:H2'	1:A:2321:U:H6	1.81	0.45
1:A:2324:C:N1	1:A:2367:G:N2	2.65	0.45
10:Q:95:LEU:CD1	11:R:4:ILE:HB	2.47	0.45
15:V:75:VAL:O	15:V:76:LYS:HG2	2.17	0.45
1:A:200:A:H62	1:A:2459:A:C3'	2.29	0.45
1:A:308:C:C2	1:A:309:U:C5	3.05	0.45
1:A:464:C:H1'	1:A:2436:A:H2	1.82	0.45
1:A:1345:U:O2'	1:A:1346:A:P	2.75	0.45
1:A:2096:G:H1	1:A:2473:G:H1	1.63	0.45
1:A:2099:G:C8	1:A:2099:G:H5''	2.51	0.45
1:A:2100:A:H2	1:A:2470:C:N3	2.15	0.45
13:T:73:THR:OG1	13:T:74:SER:N	2.50	0.45
1:A:308:C:H2'	1:A:309:U:C6	2.52	0.45
1:A:762:A:H2'	1:A:763:A:N9	2.32	0.45
1:A:957:A:O2'	1:A:958:A:O5'	2.34	0.45
1:A:2428:G:C6	1:A:2429:G:N7	2.84	0.45
1:A:2790:A:C2'	1:A:2791:U:H5'	2.47	0.45
3:D:203:LYS:HE2	3:D:203:LYS:HB3	1.79	0.45
8:N:30:ILE:HG12	8:N:31:GLU:H	1.81	0.45
10:Q:74:LEU:HG	10:Q:114:LYS:HE2	1.99	0.45
1:A:437:A:O2'	1:A:459:A:H4'	2.17	0.45
1:A:2415:U:C3'	1:A:2415:U:C6	3.00	0.45
1:A:2681:U:O2	1:A:2698:G:C2	2.70	0.45
2:C:132:LEU:HD11	2:C:184:ILE:HD11	1.98	0.45
4:E:182:ASN:O	4:E:186:VAL:HG23	2.17	0.45
1:A:448:A:H2'	1:A:449:A:C8	2.51	0.45
1:A:1046:A:H2'	1:A:1047:A:C8	2.51	0.45
1:A:1542:A:H2'	1:A:1544:C:N4	2.31	0.45
1:A:2680:C:N4	1:A:2699:G:N1	2.64	0.45
1:A:2692:G:H2'	1:A:2693:G:H8	1.80	0.45
1:A:2778:A:H3'	1:A:2779:A:H3'	1.98	0.45
16:Z:24:ARG:O	16:Z:24:ARG:NH1	2.50	0.45
1:A:51:G:O2'	1:A:118:A:N6	2.43	0.45
1:A:229:A:H1'	1:A:231:A:H61	1.82	0.45
1:A:349:C:H2'	1:A:350:U:C6	2.52	0.45
1:A:759:G:C5	1:A:760:G:C4	3.05	0.45
1:A:1008:A:H2'	1:A:1009:U:H6	1.80	0.45
1:A:1433:U:C5'	1:A:1648:A:H4'	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1438:C:HO2'	1:A:1439:U:P	2.39	0.45
1:A:2097:U:C2	1:A:2097:U:OP2	2.70	0.45
1:A:2376:C:C2	1:A:2377:U:C5	3.05	0.45
2:C:182:ARG:HG2	2:C:183:MET:H	1.82	0.45
8:N:24:LEU:HD23	8:N:44:VAL:HG21	1.99	0.45
1:A:293:U:C2	1:A:294:G:C8	3.05	0.44
1:A:672:C:O2	7:L:81:LYS:NZ	2.29	0.44
1:A:711:U:H1'	1:A:986:G:OP1	2.17	0.44
1:A:751:G:H1'	1:A:774:A:N6	2.32	0.44
1:A:903:G:H2'	1:A:904:A:C8	2.51	0.44
1:A:1579:A:N7	1:A:1588:A:N1	2.55	0.44
14:U:84:LYS:HD3	14:U:93:VAL:HG11	1.97	0.44
15:V:75:VAL:C	15:V:76:LYS:HG2	2.42	0.44
1:A:91:A:H8	1:A:92:G:H1'	1.81	0.44
1:A:1579:A:C4	1:A:1588:A:C2	3.04	0.44
1:A:2094:C:H3'	1:A:2094:C:C6	2.49	0.44
1:A:2228:A:N7	1:A:2254:A:N6	2.65	0.44
1:A:2327:A:H2'	1:A:2328:G:C8	2.53	0.44
1:A:2457:G:N2	7:L:60:ARG:HH22	2.14	0.44
1:A:2779:A:H1'	1:A:2781:C:N4	2.32	0.44
4:E:67:GLN:NE2	4:E:69:GLY:O	2.50	0.44
10:Q:80:MET:HE2	10:Q:93:LYS:HZ3	1.82	0.44
1:A:414:C:H2'	1:A:415:C:C6	2.53	0.44
1:A:1359:G:H8	1:A:1359:G:OP2	2.00	0.44
1:A:2094:C:C6	1:A:2094:C:O5'	2.70	0.44
10:Q:89:GLU:H	11:R:51:PRO:HD3	1.81	0.44
1:A:150:A:H61	1:A:179:A:H2	1.65	0.44
1:A:407:A:H2'	1:A:408:G:H8	1.83	0.44
1:A:662:U:OP1	4:E:106:ARG:HD2	2.17	0.44
1:A:920:G:N3	1:A:920:G:H2'	2.32	0.44
1:A:973:G:C4	1:A:974:A:C8	3.05	0.44
1:A:2106:A:OP1	1:A:2267:G:N1	2.40	0.44
1:A:2326:C:C5	1:A:2326:C:OP2	2.70	0.44
15:V:60:GLY:O	15:V:68:PHE:CE2	2.70	0.44
1:A:407:A:H2'	1:A:408:G:C8	2.52	0.44
1:A:792:G:O2'	1:A:795:G:O2'	2.24	0.44
1:A:1555:A:C4	1:A:1556:A:N7	2.86	0.44
1:A:1810:G:OP2	1:A:1811:C:H5'	2.18	0.44
2:C:60:ARG:HD3	2:C:85:PRO:HB2	1.99	0.44
1:A:446:G:C6	1:A:447:G:C5	3.05	0.44
1:A:1244:A:O2'	1:A:1245:G:H5'	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2318:G:C2	1:A:2319:G:C8	3.06	0.44
1:A:2356:A:H1'	1:A:2357:A:C8	2.52	0.44
1:A:2389:A:OP2	1:A:2389:A:C8	2.69	0.44
1:A:2467:U:H3'	1:A:2467:U:C6	2.53	0.44
1:A:2791:U:H2'	1:A:2792:G:C8	2.53	0.44
2:C:65:ILE:HD11	2:C:91:ILE:HG21	1.99	0.44
6:K:107:ARG:HD3	9:P:37:GLU:OE2	2.18	0.44
1:A:63:G:H1'	1:A:64:A:P	2.58	0.44
1:A:84:A:C2	1:A:102:A:C5	3.06	0.44
1:A:325:A:C6	1:A:326:A:C6	3.06	0.44
1:A:432:C:O2'	1:A:435:G:N2	2.50	0.44
1:A:732:A:N6	1:A:825:G:H21	2.15	0.44
1:A:762:A:H2'	1:A:763:A:C8	2.53	0.44
1:A:839:G:N1	1:A:2101:G:H1'	2.27	0.44
1:A:1444:C:H2'	1:A:1445:A:C8	2.52	0.44
1:A:2318:G:N3	1:A:2318:G:H2'	2.33	0.44
1:A:2319:G:H2'	1:A:2320:U:C6	2.53	0.44
1:A:2415:U:H3'	1:A:2415:U:C6	2.53	0.44
2:C:115:GLU:N	2:C:115:GLU:CD	2.73	0.44
18:Y:15:GLU:OE2	18:Y:16:GLN:HG2	2.18	0.44
1:A:465:U:H2'	1:A:466:C:C6	2.52	0.44
1:A:1082:G:C6	1:A:1166:G:C6	3.05	0.44
1:A:1526:G:H8	1:A:1526:G:P	2.41	0.44
1:A:1560:U:H5''	1:A:1560:U:C6	2.52	0.44
1:A:2361:C:OP1	15:V:84:ARG:NH2	2.33	0.44
2:C:94:ILE:HG21	2:C:116:ILE:HD11	2.00	0.44
5:J:50:ASP:OD1	5:J:122:LYS:NZ	2.47	0.44
1:A:28:A:H2'	1:A:29:U:H5'	2.00	0.44
1:A:241:C:N3	1:A:263:G:N1	2.66	0.44
1:A:759:G:H3'	1:A:760:G:H8	1.82	0.44
1:A:922:A:H8	1:A:922:A:OP2	2.01	0.44
1:A:1314:A:H4'	1:A:1315:G:OP1	2.16	0.44
1:A:2103:U:H2'	1:A:2104:U:H6	1.83	0.44
1:A:62:C:H5'	1:A:63:G:OP2	2.18	0.43
1:A:316:G:H2'	1:A:317:G:C8	2.53	0.43
1:A:421:A:H1'	1:A:448:A:N6	2.33	0.43
1:A:690:A:N6	1:A:2378:G:H21	2.07	0.43
1:A:1497:G:N2	1:A:1505:U:H3	2.13	0.43
1:A:2416:U:H3'	1:A:2416:U:O2	2.18	0.43
4:E:7:TYR:CD2	4:E:124:ILE:HG23	2.53	0.43
1:A:288:C:H2'	1:A:289:C:C2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:598:U:H2'	1:A:599:G:O4'	2.18	0.43
4:E:199:VAL:HA	4:E:202:VAL:HG12	1.99	0.43
9:P:42:ARG:NH1	9:P:44:GLN:HE21	2.15	0.43
9:P:106:LEU:O	9:P:111:ALA:HB2	2.18	0.43
16:Z:3:LYS:HE2	16:Z:3:LYS:HB3	1.63	0.43
1:A:2271:G:H2'	1:A:2272:U:O4'	2.17	0.43
1:A:2321:U:OP1	1:A:2407:A:N6	2.42	0.43
11:R:74:PHE:CD2	11:R:74:PHE:O	2.70	0.43
15:V:55:PRO:HG3	15:V:67:LEU:HG	1.99	0.43
1:A:885:C:H2'	1:A:886:U:C6	2.54	0.43
1:A:1242:U:H2'	1:A:1243:A:H8	1.83	0.43
1:A:1755:C:H2'	1:A:1756:U:C6	2.54	0.43
2:C:65:ILE:CD1	2:C:87:ARG:HE	2.31	0.43
5:J:37:LEU:O	5:J:52:GLY:HA3	2.18	0.43
1:A:751:G:H2'	1:A:773:G:H22	1.83	0.43
1:A:1461:A:H62	1:A:1630:G:N2	2.15	0.43
1:A:2010:A:N3	1:A:2010:A:H2'	2.33	0.43
1:A:2096:G:C4	1:A:2098:G:N7	2.86	0.43
3:D:16:PHE:CE1	3:D:22:LEU:HD12	2.53	0.43
10:Q:92:ARG:HD3	11:R:11:GLN:NE2	2.30	0.43
17:b:39:SER:O	17:b:40:HIS:HB2	2.18	0.43
1:A:683:A:OP2	7:L:113:GLY:N	2.48	0.43
1:A:786:A:N3	1:A:787:C:N4	2.55	0.43
1:A:1456:A:C2	1:A:1632:G:C6	3.06	0.43
1:A:1498:U:O2	1:A:1498:U:H2'	2.19	0.43
1:A:1695:A:C2'	1:A:1696:G:H5'	2.49	0.43
1:A:2312:C:H5	1:A:2418:G:C8	2.36	0.43
1:A:2697:G:C2	1:A:2698:G:C8	3.07	0.43
2:C:132:LEU:CD1	2:C:184:ILE:HD11	2.48	0.43
15:V:72:ASP:OD1	15:V:72:ASP:O	2.36	0.43
1:A:839:G:H1'	1:A:840:A:H5''	2.01	0.43
1:A:1067:A:C2	1:A:1069:U:C2	3.06	0.43
1:A:1579:A:C8	1:A:1588:A:N1	2.86	0.43
1:A:1613:C:O2'	1:A:1614:A:H8	2.02	0.43
1:A:2090:G:O2'	1:A:2092:C:OP2	2.23	0.43
1:A:2292:C:C5	1:A:2307:A:C2	3.01	0.43
1:A:175:G:H5'	1:A:176:A:OP2	2.19	0.43
1:A:501:A:H3'	1:A:502:C:H5''	2.01	0.43
1:A:758:A:C6	1:A:768:G:C6	3.07	0.43
1:A:914:C:H2'	1:A:915:U:O4'	2.19	0.43
1:A:1053:C:H5''	5:J:38:ARG:NH1	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1863:U:O2	1:A:1863:U:H2'	2.19	0.43
1:A:2686:A:H3'	1:A:2687:C:H6	1.83	0.43
1:A:2776:G:H1'	1:A:2787:A:N6	2.34	0.43
1:A:2791:U:OP2	1:A:2791:U:C5	2.71	0.43
18:Y:11:THR:HA	18:Y:14:ILE:HG22	2.00	0.43
1:A:632:U:H5''	1:A:632:U:H6	1.83	0.43
1:A:1517:A:C6	1:A:1518:G:C6	3.06	0.43
1:A:2324:C:N3	1:A:2367:G:C6	2.87	0.43
1:A:2333:G:H1	1:A:2337:G:P	2.41	0.43
1:A:2703:G:H2'	1:A:2704:A:C8	2.53	0.43
2:C:126:VAL:O	2:C:126:VAL:HG22	2.18	0.43
2:C:142:HIS:HA	2:C:155:VAL:HG21	2.00	0.43
11:R:76:TYR:CB	11:R:83:HIS:HD2	2.30	0.43
1:A:106:G:H1'	1:A:337:A:H8	1.83	0.43
1:A:267:C:H2'	1:A:268:A:H5''	2.00	0.43
1:A:292:U:H2'	1:A:293:U:C6	2.53	0.43
1:A:618:A:C2	1:A:2083:A:H5''	2.54	0.43
1:A:899:C:C4	1:A:900:U:C5	3.07	0.43
1:A:923:C:O5'	1:A:946:G:N2	2.52	0.43
1:A:2094:C:H2'	1:A:2095:C:C2	2.54	0.43
2:C:153:GLN:HA	2:C:156:ARG:HH12	1.84	0.43
7:L:80:ASP:N	7:L:80:ASP:OD1	2.50	0.43
7:L:87:GLU:HA	7:L:121:LEU:HD21	2.00	0.43
11:R:76:TYR:HB2	11:R:82:VAL:O	2.18	0.43
1:A:711:U:H4'	1:A:987:A:OP1	2.19	0.42
1:A:1352:U:OP2	1:A:1353:C:N4	2.49	0.42
2:C:105:LEU:HD21	2:C:156:ARG:CG	2.42	0.42
9:P:42:ARG:HH12	9:P:44:GLN:HE21	1.66	0.42
11:R:99:LYS:HD2	11:R:99:LYS:HA	1.65	0.42
14:U:94:ALA:O	14:U:98:GLY:HA2	2.19	0.42
16:Z:11:SER:OG	16:Z:12:VAL:N	2.52	0.42
1:A:184:G:H2'	1:A:184:G:OP1	2.20	0.42
1:A:275:A:H5''	1:A:276:C:H5	1.84	0.42
1:A:278:A:C4	1:A:279:A:C8	3.08	0.42
1:A:417:G:H4'	1:A:418:A:OP2	2.18	0.42
1:A:632:U:HO2'	1:A:633:U:P	2.39	0.42
15:V:71:ILE:HG12	15:V:72:ASP:N	2.34	0.42
1:A:91:A:C8	1:A:92:G:H1'	2.54	0.42
1:A:307:A:C6	1:A:410:G:C6	3.07	0.42
1:A:327:G:O6	1:A:400:U:O2	2.37	0.42
1:A:1303:U:H5''	17:b:13:LYS:HD2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1380:U:C5'	1:A:1436:U:O2	2.60	0.42
1:A:1539:C:O2'	1:A:1540:A:H5'	2.19	0.42
1:A:1578:G:O5'	1:A:1578:G:C8	2.70	0.42
1:A:2096:G:C5	1:A:2098:G:N7	2.87	0.42
1:A:2235:G:H2'	1:A:2236:C:C6	2.55	0.42
1:A:2356:A:O2'	1:A:2357:A:OP2	2.38	0.42
1:A:2402:A:H2'	1:A:2403:C:O4'	2.19	0.42
1:A:2683:A:H62	1:A:2695:C:H41	1.66	0.42
2:C:117:MET:CB	2:C:128:ASN:OD1	2.68	0.42
2:C:183:MET:O	2:C:183:MET:HG3	2.19	0.42
4:E:132:ASP:N	4:E:132:ASP:OD1	2.52	0.42
9:P:27:ASP:N	9:P:27:ASP:OD1	2.52	0.42
17:b:33:CYS:HB3	17:b:46:CYS:HB3	1.71	0.42
1:A:273:A:OP2	1:A:297:G:N2	2.48	0.42
1:A:1161:A:H2'	1:A:1162:C:O4'	2.19	0.42
1:A:2415:U:H4'	15:V:64:ASP:HA	2.00	0.42
1:A:2434:G:H2'	1:A:2440:A:N6	2.35	0.42
5:J:91:LEU:O	5:J:95:THR:HG22	2.20	0.42
10:Q:20:LEU:HD23	10:Q:20:LEU:HA	1.83	0.42
1:A:311:U:N3	1:A:406:G:C2	2.88	0.42
1:A:765:A:H5''	1:A:766:C:H5	1.84	0.42
1:A:1557:G:O5'	1:A:1557:G:H8	2.02	0.42
1:A:1689:U:H2'	1:A:1690:G:H5'	2.01	0.42
5:J:143:LEU:HD23	5:J:143:LEU:HA	1.90	0.42
15:V:46:TYR:CE1	15:V:53:ILE:HD11	2.54	0.42
1:A:1000:G:H1	1:A:1009:U:H3	1.66	0.42
1:A:1202:A:O4'	10:Q:51:ARG:NH1	2.53	0.42
1:A:1515:C:H2'	1:A:1516:A:H8	1.83	0.42
1:A:1527:C:H6	1:A:1527:C:H2'	1.68	0.42
1:A:1812:A:C2'	1:A:1813:A:H5'	2.49	0.42
1:A:2292:C:C5	1:A:2307:A:N1	2.85	0.42
1:A:2338:A:H2'	1:A:2338:A:N3	2.34	0.42
1:A:2467:U:C6	1:A:2467:U:C3'	3.02	0.42
7:L:57:LEU:C	7:L:57:LEU:HD12	2.44	0.42
9:P:17:ARG:HD3	9:P:80:HIS:HA	2.01	0.42
11:R:70:LYS:HB2	11:R:89:ARG:HD3	2.01	0.42
15:V:55:PRO:HG3	15:V:67:LEU:HD23	2.02	0.42
1:A:2439:G:C2	1:A:2440:A:H1'	2.54	0.42
1:A:2771:G:OP2	1:A:2771:G:H8	2.03	0.42
1:A:2781:C:C4	1:A:2782:A:H1'	2.55	0.42
10:Q:35:ALA:O	10:Q:39:VAL:HG23	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:Q:92:ARG:HB3	10:Q:94:MET:H	1.85	0.42
11:R:48:VAL:O	11:R:48:VAL:HG13	2.20	0.42
1:A:253:G:H2'	1:A:254:A:C8	2.55	0.42
1:A:1028:C:O2	1:A:1028:C:H2'	2.18	0.42
1:A:1080:G:H2'	1:A:1081:U:C6	2.55	0.42
1:A:1519:C:N4	1:A:1520:A:N1	2.68	0.42
1:A:1572:G:O2'	1:A:1573:C:P	2.77	0.42
1:A:2395:A:H5'	1:A:2396:G:OP2	2.20	0.42
1:A:2401:G:H2'	1:A:2402:A:H8	1.85	0.42
1:A:2780:G:H5'	1:A:2781:C:C6	2.55	0.42
1:A:2826:A:H2'	1:A:2827:A:O4'	2.20	0.42
1:A:2847:G:H2'	1:A:2848:A:H5''	2.01	0.42
3:D:65:GLU:O	3:D:69:VAL:HG22	2.20	0.42
6:K:88:ARG:HE	6:K:92:SER:HG	1.62	0.42
1:A:80:G:O2'	1:A:337:A:N6	2.52	0.42
1:A:205:U:H6	1:A:205:U:O5'	2.03	0.42
1:A:901:U:H2'	1:A:902:G:C8	2.55	0.42
1:A:1723:A:N3	1:A:2019:C:O2'	2.49	0.42
1:A:2126:G:N2	1:A:2221:C:O2	2.49	0.42
1:A:2777:A:H2	1:A:2778:A:H2'	1.85	0.42
5:J:111:PRO:O	5:J:116:GLY:HA3	2.20	0.42
11:R:38:VAL:HG12	11:R:38:VAL:O	2.19	0.42
1:A:2323:C:H1'	1:A:2368:G:N2	2.35	0.42
2:C:117:MET:CA	2:C:128:ASN:OD1	2.68	0.42
4:E:73:ALA:O	4:E:74:ARG:NE	2.37	0.42
5:J:86:LYS:HB2	5:J:86:LYS:HE2	1.88	0.42
8:N:4:ARG:HD3	8:N:35:THR:HG23	2.01	0.42
15:V:41:GLY:H	15:V:72:ASP:CB	2.29	0.42
15:V:75:VAL:O	15:V:76:LYS:CG	2.68	0.42
19:d:31:LEU:HD23	19:d:31:LEU:HA	1.86	0.42
1:A:267:C:H2'	1:A:268:A:C5'	2.50	0.41
1:A:1526:G:O5'	1:A:1526:G:C8	2.69	0.41
1:A:2669:G:C6	1:A:2804:A:C2	3.09	0.41
1:A:528:G:H1'	1:A:552:G:H21	1.85	0.41
1:A:2334:U:H2'	1:A:2335:U:C5	2.54	0.41
1:A:2467:U:H3'	1:A:2467:U:H6	1.85	0.41
4:E:36:ALA:O	4:E:39:MET:HG3	2.20	0.41
7:L:83:ASN:OD1	7:L:84:GLY:N	2.53	0.41
8:N:8:ARG:HD3	8:N:8:ARG:HA	1.71	0.41
10:Q:95:LEU:CD1	11:R:4:ILE:CG2	2.97	0.41
1:A:32:C:O2'	1:A:33:U:H5'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:61:A:N1	1:A:94:A:C2	2.89	0.41
1:A:406:G:C2	1:A:407:A:C4	3.08	0.41
1:A:2323:C:O2	1:A:2368:G:C6	2.73	0.41
4:E:82:GLN:HG2	4:E:83:TRP:N	2.34	0.41
1:A:81:G:H2'	1:A:82:G:O4'	2.21	0.41
1:A:84:A:N7	1:A:99:U:N3	2.68	0.41
1:A:251:G:N7	1:A:253:G:C2	2.88	0.41
1:A:325:A:C5	1:A:326:A:N7	2.88	0.41
1:A:1565:U:N3	1:A:1566:G:N7	2.69	0.41
1:A:1757:G:O4'	1:A:1759:U:H5'	2.20	0.41
1:A:2666:U:H5''	3:D:84:ARG:HH12	1.85	0.41
5:J:139:GLU:N	5:J:139:GLU:OE1	2.54	0.41
12:S:21:MET:HE2	12:S:76:VAL:HG23	2.02	0.41
12:S:55:ILE:O	12:S:59:GLU:HG3	2.20	0.41
15:V:46:TYR:CD2	15:V:53:ILE:HD11	2.55	0.41
1:A:241:C:C2	1:A:263:G:C2	3.09	0.41
1:A:444:U:H2'	1:A:445:C:C6	2.55	0.41
1:A:458:G:H5''	1:A:458:G:C8	2.55	0.41
1:A:676:G:O6	7:L:71:ARG:NH2	2.53	0.41
1:A:1177:G:O2'	1:A:2055:U:H5'	2.20	0.41
1:A:1638:A:H2'	1:A:1639:G:O4'	2.21	0.41
1:A:2374:G:H5'	1:A:2376:C:H5'	2.02	0.41
5:J:114:SER:O	5:J:114:SER:OG	2.38	0.41
8:N:74:GLU:C	8:N:76:ASN:H	2.29	0.41
8:N:107:ARG:HG3	8:N:114:MET:SD	2.60	0.41
13:T:54:VAL:HG22	13:T:81:VAL:HG22	2.01	0.41
1:A:632:U:H5''	1:A:632:U:C6	2.56	0.41
1:A:676:G:N2	1:A:679:A:OP2	2.50	0.41
1:A:732:A:H62	1:A:825:G:H21	1.68	0.41
1:A:756:U:H2'	1:A:757:C:H6	1.85	0.41
1:A:1659:A:N1	12:S:93:ALA:HB2	2.36	0.41
1:A:2115:U:C2	1:A:2116:G:C8	3.09	0.41
1:A:2360:G:H4'	15:V:51:THR:CG2	2.50	0.41
1:A:2644:U:H1'	17:b:4:PRO:HB3	2.02	0.41
1:A:2676:U:H2'	1:A:2677:G:H8	1.86	0.41
11:R:67:ARG:HA	11:R:91:PRO:HA	2.03	0.41
1:A:676:G:C2	1:A:680:G:C6	3.09	0.41
1:A:972:U:C2	1:A:973:G:C8	3.09	0.41
1:A:2126:G:N1	1:A:2221:C:O2	2.53	0.41
1:A:2315:A:H1'	1:A:2316:A:C5	2.55	0.41
1:A:2444:G:H2'	1:A:2445:C:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:Q:111:ASP:OD2	10:Q:112:ALA:N	2.54	0.41
1:A:690:A:H61	1:A:2378:G:N2	2.08	0.41
1:A:875:U:H4'	1:A:878:G:O6	2.20	0.41
1:A:1518:G:O5'	1:A:1518:G:H8	2.03	0.41
1:A:1784:A:O2'	1:A:1785:G:OP1	2.36	0.41
1:A:2038:G:OP1	12:S:41:ARG:NH1	2.52	0.41
1:A:2100:A:C2	1:A:2470:C:N3	2.88	0.41
1:A:2337:G:H21	1:A:2339:A:H5''	1.86	0.41
2:C:65:ILE:HD12	2:C:87:ARG:HE	1.86	0.41
2:C:166:GLY:O	2:C:173:LEU:N	2.52	0.41
9:P:94:LYS:HB3	9:P:114:LYS:HB2	2.02	0.41
11:R:65:GLN:NE2	11:R:93:THR:OG1	2.54	0.41
1:A:342:A:N3	1:A:363:C:O2'	2.54	0.41
1:A:443:G:C6	1:A:444:U:C4	3.09	0.41
1:A:528:G:O2'	1:A:529:C:OP2	2.35	0.41
1:A:1280:G:O5'	1:A:1280:G:H8	2.03	0.41
1:A:1493:C:H2'	1:A:1494:G:C8	2.56	0.41
1:A:1613:C:HO2'	1:A:1614:A:P	2.44	0.41
1:A:1648:A:H2'	1:A:1649:C:H5'	2.02	0.41
1:A:1696:G:O2'	1:A:1697:A:P	2.79	0.41
1:A:2041:G:OP1	12:S:11:ARG:NH2	2.49	0.41
1:A:2096:G:N7	1:A:2098:G:N7	2.65	0.41
1:A:2372:U:H2'	1:A:2373:U:C6	2.55	0.41
2:C:16:MET:HE2	2:C:210:ARG:HD2	2.03	0.41
2:C:173:LEU:HA	2:C:183:MET:HA	2.03	0.41
4:E:53:ASN:OD1	4:E:53:ASN:N	2.52	0.41
4:E:75:GLN:OE1	4:E:75:GLN:N	2.50	0.41
5:J:20:ASP:OD1	5:J:22:ALA:N	2.53	0.41
10:Q:19:LYS:HA	10:Q:19:LYS:HD3	1.64	0.41
11:R:76:TYR:HB2	11:R:83:HIS:CD2	2.48	0.41
14:U:12:ILE:HA	14:U:12:ILE:HD13	1.85	0.41
14:U:75:THR:OG1	14:U:77:GLU:HG2	2.21	0.41
15:V:59:VAL:HG23	15:V:89:VAL:HG23	2.02	0.41
1:A:309:U:H2'	1:A:310:C:H6	1.86	0.41
1:A:751:G:H1'	1:A:774:A:H61	1.86	0.41
1:A:837:U:O2'	1:A:838:C:OP1	2.34	0.41
1:A:2122:G:C6	1:A:2123:A:C6	3.09	0.41
1:A:2273:U:H4'	1:A:2463:A:C6	2.56	0.41
4:E:115:SER:O	4:E:118:VAL:HG12	2.20	0.41
4:E:192:LEU:CD2	4:E:194:ILE:HG13	2.51	0.41
1:A:282:G:H1	1:A:290:U:H3	1.68	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:284:C:H2'	1:A:286:U:OP2	2.21	0.40
1:A:901:U:C2	1:A:971:A:C2	3.08	0.40
1:A:1178:U:OP2	1:A:1179:A:H8	2.04	0.40
1:A:1220:G:C2	1:A:1221:A:C5	3.09	0.40
1:A:1595:U:H6	1:A:1595:U:H5''	1.86	0.40
1:A:1706:G:H2'	1:A:1707:U:H6	1.87	0.40
1:A:2275:G:H2'	1:A:2276:A:C8	2.57	0.40
1:A:2672:G:H2'	1:A:2673:A:H8	1.85	0.40
4:E:184:LEU:HD12	4:E:184:LEU:HA	1.89	0.40
9:P:14:GLU:OE1	9:P:14:GLU:N	2.55	0.40
13:T:5:ARG:NH2	18:Y:23:GLU:OE1	2.54	0.40
16:Z:6:ILE:HG23	16:Z:54:VAL:CG1	2.52	0.40
18:Y:32:LEU:HB2	18:Y:37:LEU:HD22	2.03	0.40
1:A:406:G:N1	1:A:407:A:C5	2.89	0.40
1:A:455:G:C6	1:A:467:C:N3	2.89	0.40
1:A:2090:G:O2'	1:A:2092:C:C5'	2.62	0.40
1:A:2442:G:C2	1:A:2443:G:C8	3.09	0.40
3:D:158:LYS:HG2	3:D:159:LEU:H	1.86	0.40
4:E:29:ASN:O	4:E:33:VAL:HG23	2.21	0.40
6:K:71:ARG:HH21	6:K:77:ILE:HD12	1.85	0.40
7:L:56:PRO:HB2	7:L:57:LEU:H	1.70	0.40
12:S:2:GLN:N	12:S:107:VAL:O	2.54	0.40
15:V:71:ILE:HG12	15:V:72:ASP:H	1.86	0.40
17:b:43:CYS:SG	17:b:44:LYS:N	2.94	0.40
18:Y:15:GLU:CD	18:Y:16:GLN:HG2	2.46	0.40
1:A:165:C:O2'	1:A:166:A:OP1	2.35	0.40
1:A:324:A:N1	1:A:325:A:C6	2.89	0.40
1:A:430:C:H5''	1:A:432:C:OP2	2.22	0.40
1:A:633:U:H2'	1:A:634:A:H8	1.87	0.40
1:A:1523:U:H3'	1:A:1524:A:H5''	2.03	0.40
1:A:2346:C:O5'	1:A:2346:C:H6	2.05	0.40
1:A:2762:A:N1	3:D:207:LYS:O	2.54	0.40
1:A:2774:C:N3	1:A:2788:G:N2	2.69	0.40
9:P:64:VAL:O	9:P:74:GLU:HA	2.21	0.40
12:S:46:ILE:H	12:S:46:ILE:HG13	1.75	0.40
1:A:91:A:C4	1:A:91:A:OP2	2.75	0.40
1:A:223:G:C6	1:A:474:U:C5	3.09	0.40
1:A:867:A:N3	1:A:989:U:O2'	2.51	0.40
1:A:964:A:H5'	1:A:2297:A:N6	2.37	0.40
1:A:1327:U:O2	1:A:1327:U:H2'	2.20	0.40
1:A:2284:G:H2'	1:A:2285:G:C8	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:226:ASN:O	2:C:227:PRO:C	2.65	0.40
1:A:278:A:C6	1:A:294:G:N1	2.90	0.40
1:A:446:G:C4	1:A:447:G:C8	3.10	0.40
1:A:455:G:H2'	1:A:456:A:H8	1.85	0.40
1:A:1085:G:C5	1:A:1086:U:N3	2.89	0.40
1:A:1595:U:H2'	1:A:1596:U:C6	2.56	0.40
1:A:2360:G:H4'	15:V:51:THR:HG22	2.02	0.40
1:A:2402:A:C5	1:A:2403:C:C5	3.09	0.40
3:D:57:ARG:HH11	3:D:57:ARG:HD2	1.76	0.40
7:L:110:LYS:HE2	7:L:112:LEU:HD21	2.03	0.40
10:Q:25:PHE:CD2	10:Q:25:PHE:C	3.00	0.40
13:T:2:LYS:HD2	13:T:2:LYS:HA	1.92	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	
2	C	263/277 (95%)	219 (83%)	44 (17%)	0	100	100
3	D	175/209 (84%)	155 (89%)	20 (11%)	0	100	100
4	E	203/207 (98%)	165 (81%)	38 (19%)	0	100	100
5	J	140/145 (97%)	124 (89%)	16 (11%)	0	100	100
6	K	120/122 (98%)	101 (84%)	19 (16%)	0	100	100
7	L	126/146 (86%)	107 (85%)	18 (14%)	1 (1%)	16	50
8	N	117/120 (98%)	101 (86%)	16 (14%)	0	100	100
9	P	112/115 (97%)	101 (90%)	11 (10%)	0	100	100
10	Q	115/119 (97%)	94 (82%)	18 (16%)	3 (3%)	4	26
11	R	99/102 (97%)	81 (82%)	16 (16%)	2 (2%)	6	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	S	107/113 (95%)	97 (91%)	9 (8%)	1 (1%)	14	47
13	T	90/95 (95%)	74 (82%)	16 (18%)	0	100	100
14	U	98/103 (95%)	75 (76%)	23 (24%)	0	100	100
15	V	70/94 (74%)	48 (69%)	21 (30%)	1 (1%)	9	39
16	Z	56/59 (95%)	50 (89%)	6 (11%)	0	100	100
17	b	52/59 (88%)	45 (86%)	7 (14%)	0	100	100
18	Y	63/66 (96%)	52 (82%)	10 (16%)	1 (2%)	7	36
19	d	42/44 (96%)	38 (90%)	4 (10%)	0	100	100
All	All	2048/2195 (93%)	1727 (84%)	312 (15%)	9 (0%)	31	62

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	L	56	PRO
10	Q	86	SER
11	R	51	PRO
10	Q	88	ILE
12	S	11	ARG
15	V	82	ARG
18	Y	39	ASN
10	Q	85	LEU
11	R	48	VAL

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	
2	C	218/225 (97%)	210 (96%)	8 (4%)	30	63
3	D	144/170 (85%)	143 (99%)	1 (1%)	76	83
4	E	169/170 (99%)	168 (99%)	1 (1%)	78	84
5	J	120/123 (98%)	118 (98%)	2 (2%)	53	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	K	101/101 (100%)	101 (100%)	0	100	100
7	L	101/110 (92%)	100 (99%)	1 (1%)	68	80
8	N	99/100 (99%)	99 (100%)	0	100	100
9	P	99/100 (99%)	99 (100%)	0	100	100
10	Q	96/98 (98%)	89 (93%)	7 (7%)	13	43
11	R	83/84 (99%)	79 (95%)	4 (5%)	23	56
12	S	90/93 (97%)	90 (100%)	0	100	100
13	T	83/85 (98%)	82 (99%)	1 (1%)	63	79
14	U	84/87 (97%)	84 (100%)	0	100	100
15	V	56/74 (76%)	48 (86%)	8 (14%)	3	16
16	Z	52/53 (98%)	52 (100%)	0	100	100
17	b	48/53 (91%)	48 (100%)	0	100	100
18	Y	56/57 (98%)	56 (100%)	0	100	100
19	d	39/39 (100%)	39 (100%)	0	100	100
All	All	1738/1822 (95%)	1705 (98%)	33 (2%)	49	73

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	68	LYS
2	C	110	ILE
2	C	112	VAL
2	C	117	MET
2	C	121	GLU
2	C	125	LYS
2	C	130	LEU
2	C	164	VAL
3	D	55	ASP
4	E	199	VAL
5	J	8	ASN
5	J	79	THR
7	L	122	THR
10	Q	83	LEU
10	Q	84	LYS
10	Q	88	ILE
10	Q	92	ARG
10	Q	93	LYS

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Mol	Chain	Res	Type
10	Q	95	LEU
10	Q	100	VAL
11	R	48	VAL
11	R	53	VAL
11	R	72	THR
11	R	75	ARG
13	T	39	VAL
15	V	25	GLU
15	V	28	ARG
15	V	53	ILE
15	V	74	THR
15	V	80	PHE
15	V	85	LYS
15	V	87	VAL
15	V	89	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
2	C	38	HIS
2	C	53	HIS
2	C	86	ASN
2	C	143	ASN
2	C	204	ASN
3	D	33	ASN
3	D	50	GLN
3	D	128	GLN
6	K	82	ASN
8	N	76	ASN
9	P	44	GLN
10	Q	81	HIS
11	R	11	GLN
11	R	65	GLN
11	R	83	HIS
11	R	101	ASN
12	S	97	ASN
14	U	53	GLN
14	U	99	GLN
17	b	19	HIS
17	b	40	HIS
19	d	16	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2430/2928 (82%)	730 (30%)	40 (1%)

All (730) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	9	U
1	A	12	A
1	A	13	A
1	A	15	G
1	A	28	A
1	A	31	C
1	A	34	U
1	A	35	G
1	A	39	C
1	A	43	G
1	A	44	A
1	A	45	G
1	A	46	C
1	A	51	G
1	A	63	G
1	A	64	A
1	A	67	A
1	A	71	A
1	A	75	G
1	A	76	C
1	A	77	U
1	A	91	A
1	A	92	G
1	A	100	U
1	A	101	G
1	A	106	G
1	A	109	G
1	A	118	A
1	A	119	U
1	A	156	A
1	A	161	A
1	A	162	A
1	A	163	U
1	A	166	A
1	A	176	A
1	A	180	G

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Mol	Chain	Res	Type
1	A	184	G
1	A	199	A
1	A	200	A
1	A	201	C
1	A	202	A
1	A	203	U
1	A	204	C
1	A	207	A
1	A	216	A
1	A	219	A
1	A	220	A
1	A	224	A
1	A	225	A
1	A	226	A
1	A	227	G
1	A	230	A
1	A	232	U
1	A	233	G
1	A	235	G
1	A	236	A
1	A	245	G
1	A	251	G
1	A	252	C
1	A	253	G
1	A	255	G
1	A	258	A
1	A	267	C
1	A	268	A
1	A	275	A
1	A	280	G
1	A	281	A
1	A	282	G
1	A	284	C
1	A	285	U
1	A	286	U
1	A	288	C
1	A	289	C
1	A	291	C
1	A	295	G
1	A	296	G
1	A	298	U
1	A	299	U

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Mol	Chain	Res	Type
1	A	300	G
1	A	301	U
1	A	302	A
1	A	311	U
1	A	312	G
1	A	314	A
1	A	315	C
1	A	316	G
1	A	321	U
1	A	322	A
1	A	324	A
1	A	325	A
1	A	327	G
1	A	338	G
1	A	344	G
1	A	345	A
1	A	346	G
1	A	348	U
1	A	351	G
1	A	355	A
1	A	361	G
1	A	366	A
1	A	367	G
1	A	374	A
1	A	377	G
1	A	378	C
1	A	379	C
1	A	382	G
1	A	386	U
1	A	387	C
1	A	389	A
1	A	390	A
1	A	392	C
1	A	396	G
1	A	405	U
1	A	406	G
1	A	407	A
1	A	412	A
1	A	418	A
1	A	419	G
1	A	420	U
1	A	422	C

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Mol	Chain	Res	Type
1	A	433	G
1	A	434	U
1	A	436	A
1	A	437	A
1	A	438	A
1	A	443	G
1	A	445	C
1	A	448	A
1	A	452	C
1	A	453	G
1	A	458	G
1	A	459	A
1	A	462	A
1	A	463	U
1	A	464	C
1	A	466	C
1	A	482	C
1	A	485	U
1	A	487	G
1	A	502	C
1	A	504	A
1	A	511	U
1	A	513	A
1	A	514	G
1	A	528	G
1	A	529	C
1	A	536	G
1	A	537	A
1	A	548	A
1	A	550	G
1	A	551	A
1	A	554	U
1	A	567	U
1	A	568	G
1	A	574	A
1	A	576	G
1	A	577	U
1	A	578	A
1	A	579	G
1	A	584	A
1	A	592	A
1	A	593	A

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Mol	Chain	Res	Type
1	A	595	G
1	A	607	G
1	A	614	G
1	A	615	U
1	A	616	A
1	A	631	G
1	A	632	U
1	A	633	U
1	A	647	A
1	A	651	U
1	A	659	A
1	A	666	G
1	A	667	A
1	A	668	G
1	A	673	A
1	A	677	A
1	A	683	A
1	A	684	G
1	A	689	A
1	A	691	U
1	A	692	A
1	A	700	U
1	A	701	G
1	A	702	A
1	A	706	C
1	A	716	G
1	A	722	A
1	A	723	A
1	A	733	U
1	A	756	U
1	A	758	A
1	A	760	G
1	A	764	C
1	A	777	C
1	A	783	C
1	A	785	C
1	A	786	A
1	A	794	U
1	A	795	G
1	A	811	A
1	A	812	G
1	A	822	G

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Mol	Chain	Res	Type
1	A	823	G
1	A	826	U
1	A	829	A
1	A	831	U
1	A	837	U
1	A	838	C
1	A	839	G
1	A	840	A
1	A	841	A
1	A	842	C
1	A	847	A
1	A	849	A
1	A	851	A
1	A	852	G
1	A	854	U
1	A	856	G
1	A	858	U
1	A	859	C
1	A	861	C
1	A	866	A
1	A	874	U
1	A	876	A
1	A	877	G
1	A	881	U
1	A	892	U
1	A	906	G
1	A	912	C
1	A	916	G
1	A	917	A
1	A	918	U
1	A	919	U
1	A	920	G
1	A	921	G
1	A	924	U
1	A	925	A
1	A	926	G
1	A	927	G
1	A	947	A
1	A	948	A
1	A	950	U
1	A	951	C
1	A	953	G

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Mol	Chain	Res	Type
1	A	954	U
1	A	955	C
1	A	957	A
1	A	958	A
1	A	961	C
1	A	963	G
1	A	964	A
1	A	970	A
1	A	972	U
1	A	973	G
1	A	974	A
1	A	975	C
1	A	976	U
1	A	980	C
1	A	984	G
1	A	987	A
1	A	991	A
1	A	992	G
1	A	999	A
1	A	1000	G
1	A	1004	U
1	A	1006	A
1	A	1007	G
1	A	1008	A
1	A	1013	U
1	A	1017	C
1	A	1020	A
1	A	1027	A
1	A	1036	A
1	A	1037	C
1	A	1042	A
1	A	1043	G
1	A	1045	U
1	A	1051	C
1	A	1058	U
1	A	1059	A
1	A	1063	G
1	A	1067	A
1	A	1068	G
1	A	1069	U
1	A	1070	G
1	A	1072	A

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Mol	Chain	Res	Type
1	A	1073	A
1	A	1075	A
1	A	1076	G
1	A	1077	G
1	A	1078	A
1	A	1079	U
1	A	1083	G
1	A	1086	U
1	A	1087	U
1	A	1161	A
1	A	1173	A
1	A	1174	A
1	A	1175	A
1	A	1176	U
1	A	1177	G
1	A	1178	U
1	A	1179	A
1	A	1180	C
1	A	1181	C
1	A	1185	G
1	A	1188	A
1	A	1189	A
1	A	1201	A
1	A	1202	A
1	A	1214	U
1	A	1216	C
1	A	1217	U
1	A	1218	U
1	A	1219	C
1	A	1220	G
1	A	1221	A
1	A	1223	C
1	A	1229	U
1	A	1231	G
1	A	1238	G
1	A	1246	G
1	A	1247	G
1	A	1248	C
1	A	1250	G
1	A	1251	U
1	A	1252	G
1	A	1258	A

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Mol	Chain	Res	Type
1	A	1260	A
1	A	1269	A
1	A	1271	U
1	A	1273	G
1	A	1278	G
1	A	1280	G
1	A	1289	U
1	A	1290	G
1	A	1293	A
1	A	1295	U
1	A	1296	G
1	A	1297	C
1	A	1302	A
1	A	1305	A
1	A	1312	A
1	A	1315	G
1	A	1324	G
1	A	1335	A
1	A	1339	A
1	A	1340	A
1	A	1344	C
1	A	1345	U
1	A	1346	A
1	A	1351	U
1	A	1352	U
1	A	1359	G
1	A	1360	A
1	A	1363	G
1	A	1364	C
1	A	1376	G
1	A	1380	U
1	A	1383	U
1	A	1384	C
1	A	1388	A
1	A	1391	U
1	A	1404	A
1	A	1409	C
1	A	1412	A
1	A	1414	G
1	A	1417	A
1	A	1418	U
1	A	1424	A

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Mol	Chain	Res	Type
1	A	1425	C
1	A	1434	A
1	A	1435	U
1	A	1439	U
1	A	1441	U
1	A	1450	C
1	A	1458	U
1	A	1459	U
1	A	1460	G
1	A	1461	A
1	A	1465	A
1	A	1466	U
1	A	1472	G
1	A	1473	A
1	A	1474	C
1	A	1475	G
1	A	1480	A
1	A	1483	A
1	A	1488	G
1	A	1495	C
1	A	1496	G
1	A	1497	G
1	A	1498	U
1	A	1499	A
1	A	1500	U
1	A	1501	U
1	A	1503	G
1	A	1504	A
1	A	1505	U
1	A	1506	A
1	A	1507	U
1	A	1512	G
1	A	1513	U
1	A	1516	A
1	A	1519	C
1	A	1521	G
1	A	1523	U
1	A	1524	A
1	A	1527	C
1	A	1528	U
1	A	1537	G
1	A	1539	C

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Mol	Chain	Res	Type
1	A	1540	A
1	A	1550	C
1	A	1551	C
1	A	1553	A
1	A	1554	U
1	A	1555	A
1	A	1556	A
1	A	1558	C
1	A	1560	U
1	A	1561	G
1	A	1562	A
1	A	1563	G
1	A	1570	U
1	A	1571	G
1	A	1572	G
1	A	1573	C
1	A	1580	A
1	A	1581	A
1	A	1582	U
1	A	1584	U
1	A	1585	A
1	A	1586	G
1	A	1587	U
1	A	1596	U
1	A	1607	C
1	A	1615	A
1	A	1617	A
1	A	1626	U
1	A	1629	C
1	A	1630	G
1	A	1631	A
1	A	1632	G
1	A	1633	G
1	A	1652	C
1	A	1653	A
1	A	1655	A
1	A	1690	G
1	A	1692	U
1	A	1693	C
1	A	1695	A
1	A	1697	A
1	A	1698	G

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Mol	Chain	Res	Type
1	A	1712	G
1	A	1714	A
1	A	1719	G
1	A	1720	C
1	A	1723	A
1	A	1727	A
1	A	1728	C
1	A	1734	A
1	A	1736	C
1	A	1738	U
1	A	1739	C
1	A	1740	G
1	A	1743	A
1	A	1744	G
1	A	1745	A
1	A	1746	A
1	A	1752	G
1	A	1756	U
1	A	1757	G
1	A	1758	U
1	A	1767	A
1	A	1774	A
1	A	1777	G
1	A	1778	A
1	A	1779	G
1	A	1780	C
1	A	1781	C
1	A	1782	G
1	A	1785	G
1	A	1791	A
1	A	1792	G
1	A	1793	G
1	A	1802	A
1	A	1805	G
1	A	1808	U
1	A	1809	A
1	A	1810	G
1	A	1811	C
1	A	1813	A
1	A	1814	A
1	A	1815	A
1	A	1829	C

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Mol	Chain	Res	Type
1	A	1831	A
1	A	1835	C
1	A	1839	A
1	A	1845	A
1	A	1848	A
1	A	1850	A
1	A	1856	U
1	A	1858	A
1	A	1862	C
1	A	1863	U
1	A	2001	G
1	A	2004	G
1	A	2005	C
1	A	2006	A
1	A	2010	A
1	A	2011	U
1	A	2017	C
1	A	2020	U
1	A	2022	U
1	A	2023	C
1	A	2025	C
1	A	2026	A
1	A	2028	C
1	A	2060	A
1	A	2061	G
1	A	2068	G
1	A	2072	C
1	A	2081	G
1	A	2082	G
1	A	2084	C
1	A	2085	G
1	A	2086	G
1	A	2088	A
1	A	2089	A
1	A	2090	G
1	A	2091	A
1	A	2092	C
1	A	2093	C
1	A	2096	G
1	A	2097	U
1	A	2098	G
1	A	2099	G

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Mol	Chain	Res	Type
1	A	2100	A
1	A	2101	G
1	A	2102	C
1	A	2109	G
1	A	2110	C
1	A	2112	G
1	A	2113	C
1	A	2116	G
1	A	2122	G
1	A	2123	A
1	A	2124	A
1	A	2222	C
1	A	2227	A
1	A	2232	G
1	A	2233	C
1	A	2241	A
1	A	2243	C
1	A	2246	G
1	A	2252	A
1	A	2254	A
1	A	2255	C
1	A	2264	G
1	A	2266	G
1	A	2267	G
1	A	2272	U
1	A	2275	G
1	A	2278	U
1	A	2279	G
1	A	2284	G
1	A	2285	G
1	A	2288	G
1	A	2289	C
1	A	2290	C
1	A	2291	U
1	A	2292	C
1	A	2293	C
1	A	2305	G
1	A	2308	G
1	A	2312	C
1	A	2313	C
1	A	2315	A
1	A	2323	C

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Mol	Chain	Res	Type
1	A	2325	U
1	A	2326	C
1	A	2329	A
1	A	2331	U
1	A	2333	G
1	A	2334	U
1	A	2335	U
1	A	2336	G
1	A	2337	G
1	A	2338	A
1	A	2339	A
1	A	2340	A
1	A	2341	U
1	A	2342	C
1	A	2343	A
1	A	2344	U
1	A	2345	U
1	A	2346	C
1	A	2348	C
1	A	2349	A
1	A	2351	A
1	A	2352	G
1	A	2353	U
1	A	2354	G
1	A	2356	A
1	A	2359	G
1	A	2362	A
1	A	2363	C
1	A	2364	A
1	A	2366	G
1	A	2369	A
1	A	2372	U
1	A	2373	U
1	A	2374	G
1	A	2376	C
1	A	2377	U
1	A	2379	C
1	A	2383	A
1	A	2387	A
1	A	2389	A
1	A	2390	A
1	A	2392	U

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Mol	Chain	Res	Type
1	A	2395	A
1	A	2400	G
1	A	2402	A
1	A	2408	G
1	A	2411	G
1	A	2412	G
1	A	2414	C
1	A	2417	A
1	A	2418	G
1	A	2424	C
1	A	2425	G
1	A	2430	U
1	A	2431	U
1	A	2432	C
1	A	2435	C
1	A	2436	A
1	A	2451	C
1	A	2454	A
1	A	2455	A
1	A	2456	C
1	A	2457	G
1	A	2458	G
1	A	2459	A
1	A	2460	U
1	A	2461	A
1	A	2462	A
1	A	2463	A
1	A	2464	A
1	A	2468	A
1	A	2469	C
1	A	2470	C
1	A	2474	G
1	A	2648	U
1	A	2649	C
1	A	2653	G
1	A	2658	A
1	A	2659	G
1	A	2668	A
1	A	2675	C
1	A	2677	G
1	A	2681	U
1	A	2683	A

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Mol	Chain	Res	Type
1	A	2684	G
1	A	2689	A
1	A	2690	G
1	A	2692	G
1	A	2693	G
1	A	2698	G
1	A	2702	G
1	A	2711	G
1	A	2714	G
1	A	2718	U
1	A	2720	C
1	A	2731	G
1	A	2743	G
1	A	2748	G
1	A	2755	U
1	A	2756	G
1	A	2762	A
1	A	2770	A
1	A	2773	G
1	A	2775	U
1	A	2778	A
1	A	2779	A
1	A	2780	G
1	A	2781	C
1	A	2782	A
1	A	2784	C
1	A	2785	U
1	A	2786	A
1	A	2787	A
1	A	2789	C
1	A	2790	A
1	A	2791	U
1	A	2793	A
1	A	2794	A
1	A	2795	G
1	A	2797	C
1	A	2807	A
1	A	2808	U
1	A	2813	U
1	A	2818	C
1	A	2819	A
1	A	2820	U

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Mol	Chain	Res	Type
1	A	2823	C
1	A	2825	C
1	A	2826	A
1	A	2828	G
1	A	2837	A
1	A	2845	A
1	A	2846	A
1	A	2858	U
1	A	2859	G
1	A	2860	A
1	A	2861	U
1	A	2874	G
1	A	2884	G
1	A	2892	G
1	A	2897	G
1	A	2898	A
1	A	2899	C
1	A	2905	C
1	A	2908	A
1	A	2916	A
1	A	2918	G
1	A	2921	U

All (40) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	27	G
1	A	43	G
1	A	63	G
1	A	90	A
1	A	458	G
1	A	549	A
1	A	632	U
1	A	683	A
1	A	785	C
1	A	837	U
1	A	839	G
1	A	1245	G
1	A	1339	A
1	A	1351	U
1	A	1438	C
1	A	1497	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1511	C
1	A	1518	G
1	A	1522	U
1	A	1527	C
1	A	1560	U
1	A	1595	U
1	A	1630	G
1	A	1652	C
1	A	1726	G
1	A	1755	C
1	A	1779	G
1	A	1784	A
1	A	1861	C
1	A	2005	C
1	A	2099	G
1	A	2254	A
1	A	2292	C
1	A	2334	U
1	A	2338	A
1	A	2352	G
1	A	2454	A
1	A	2784	C
1	A	2812	A
1	A	2858	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

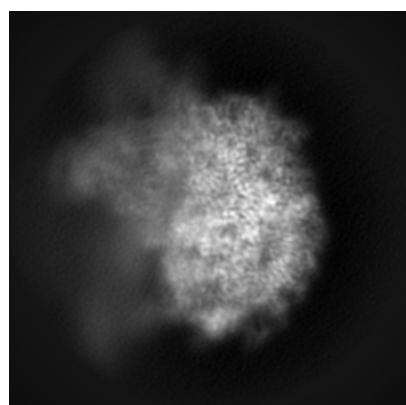
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24937. These allow visual inspection of the internal detail of the map and identification of artifacts.

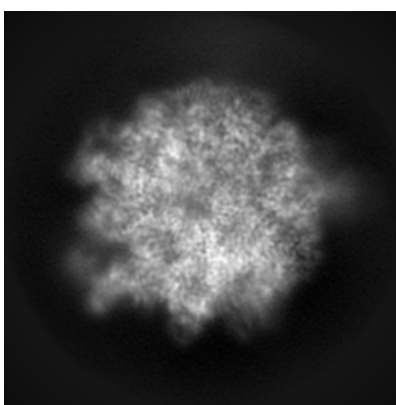
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

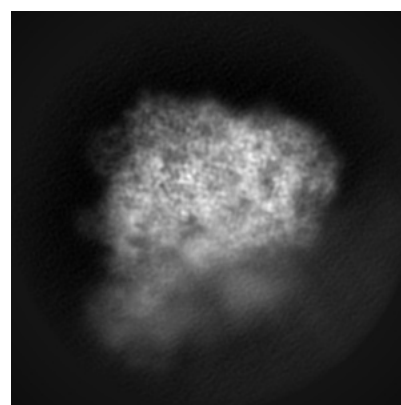
6.1.1 Primary map



X



Y

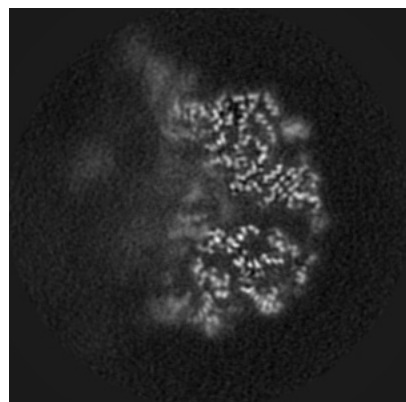


Z

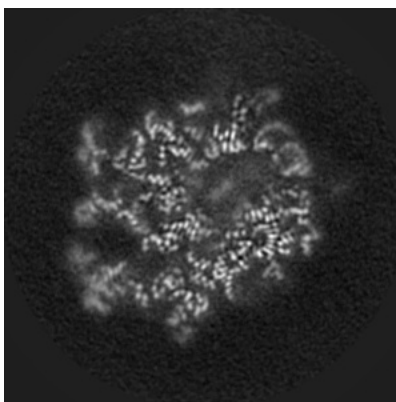
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

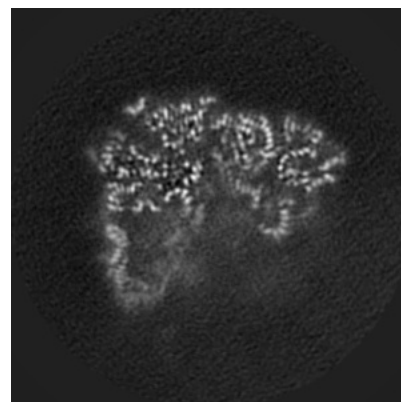
6.2.1 Primary map



X Index: 168



Y Index: 168

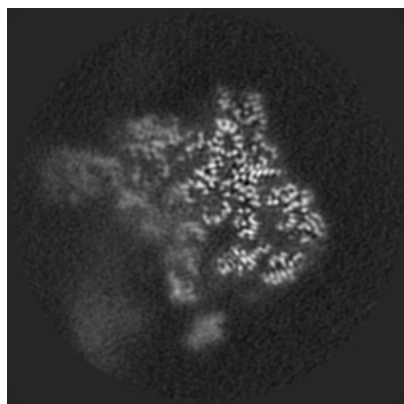


Z Index: 168

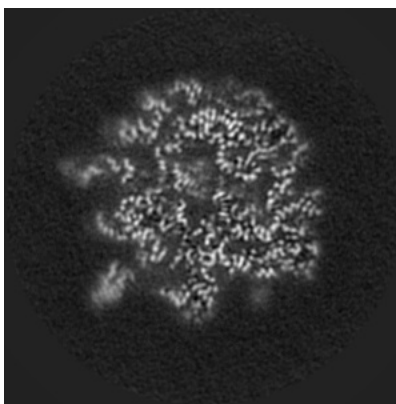
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

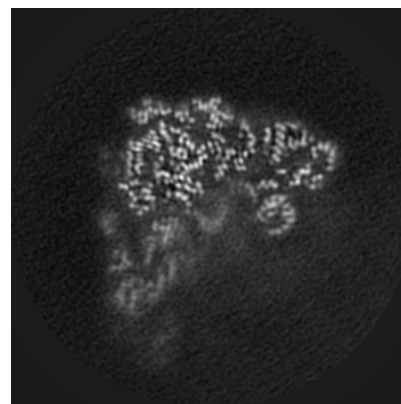
6.3.1 Primary map



X Index: 125



Y Index: 197

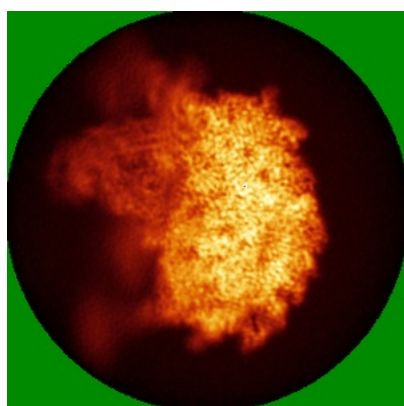


Z Index: 176

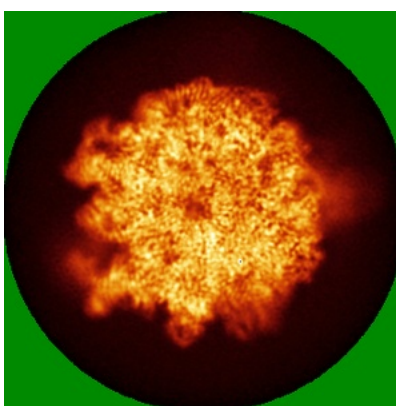
The images above show the largest variance slices of the map in three orthogonal directions.

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

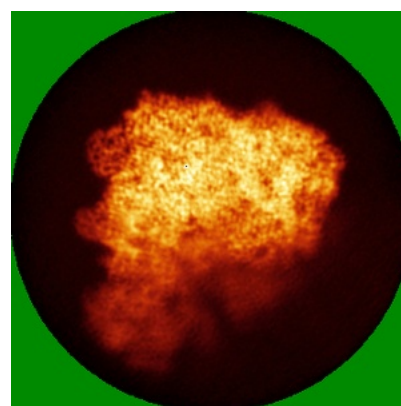
6.4.1 Primary map



X



Y

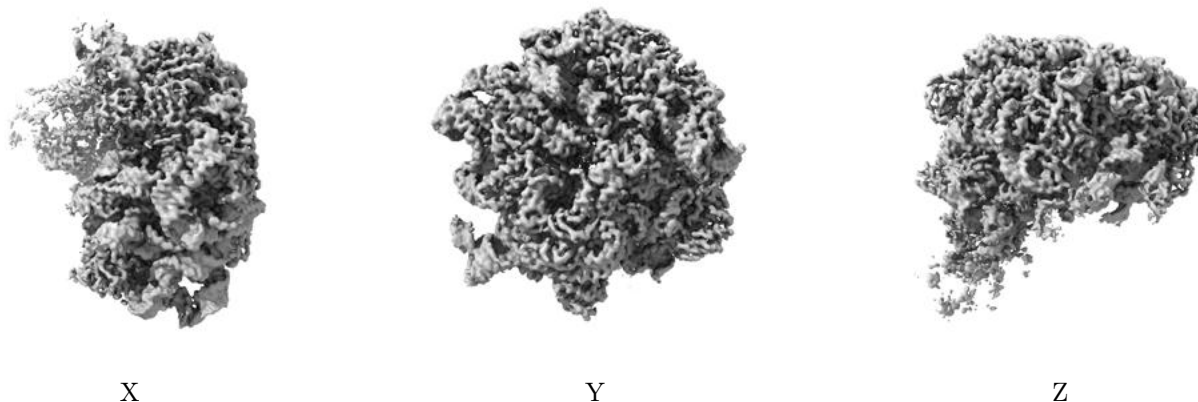


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.00983. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

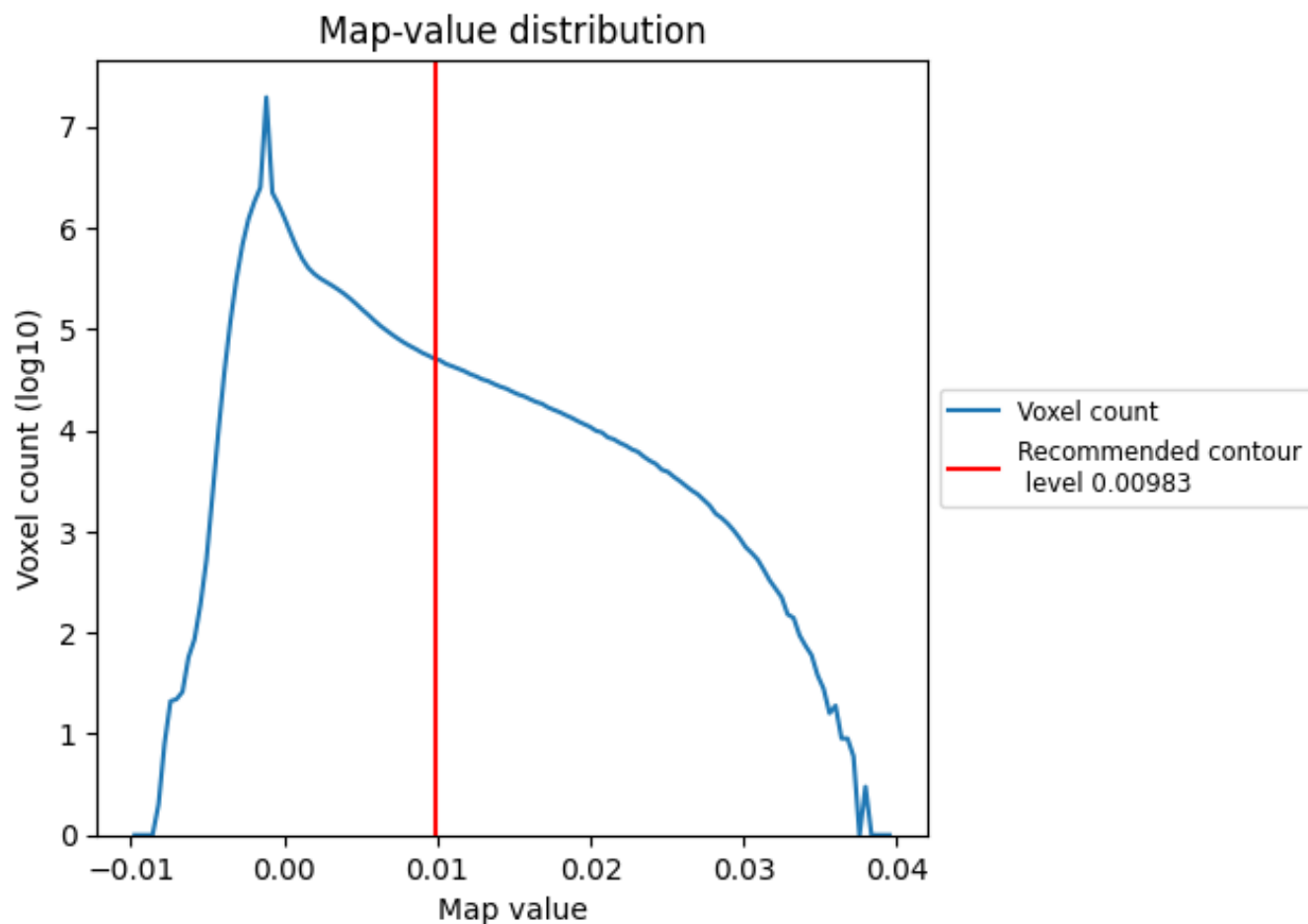
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

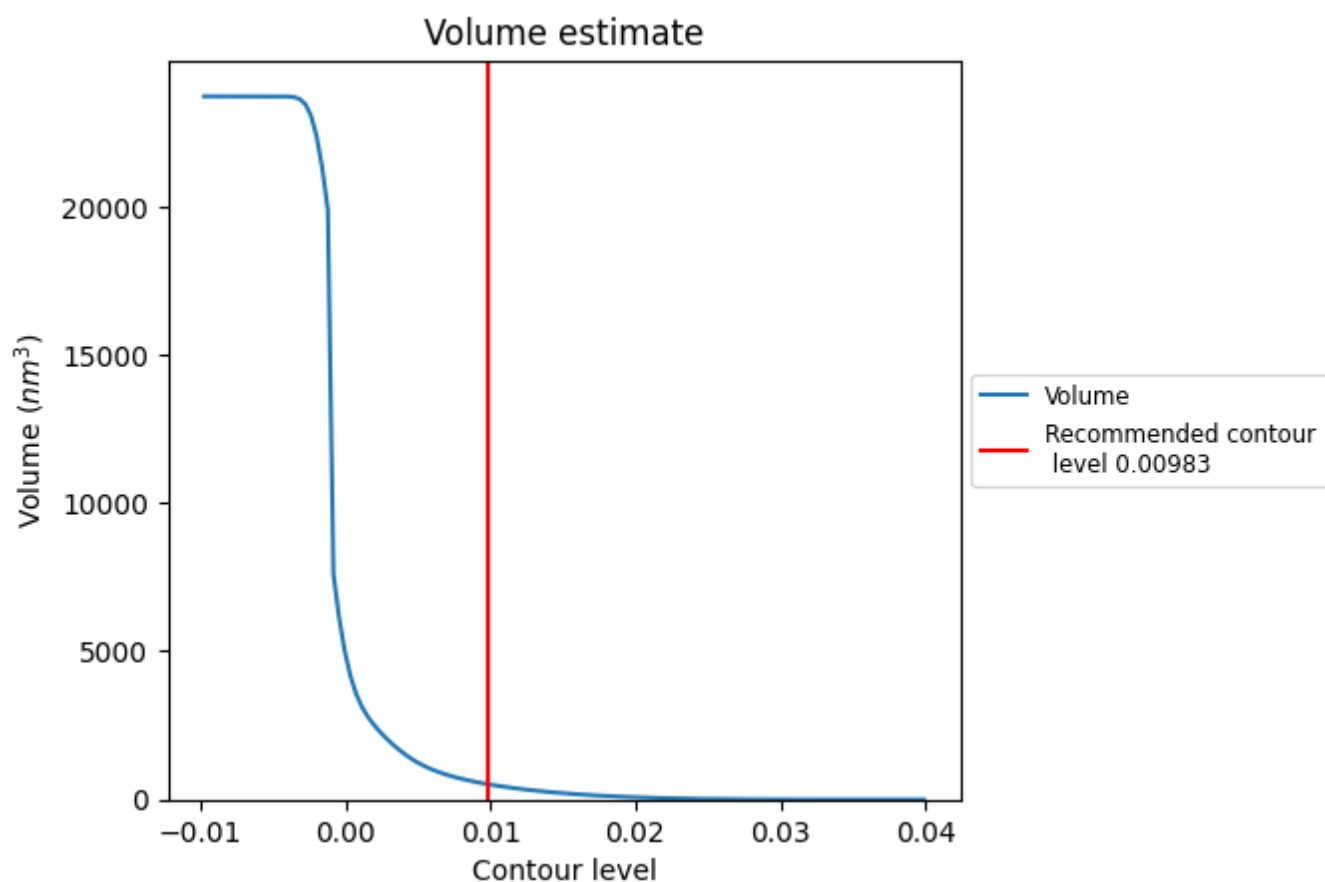
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

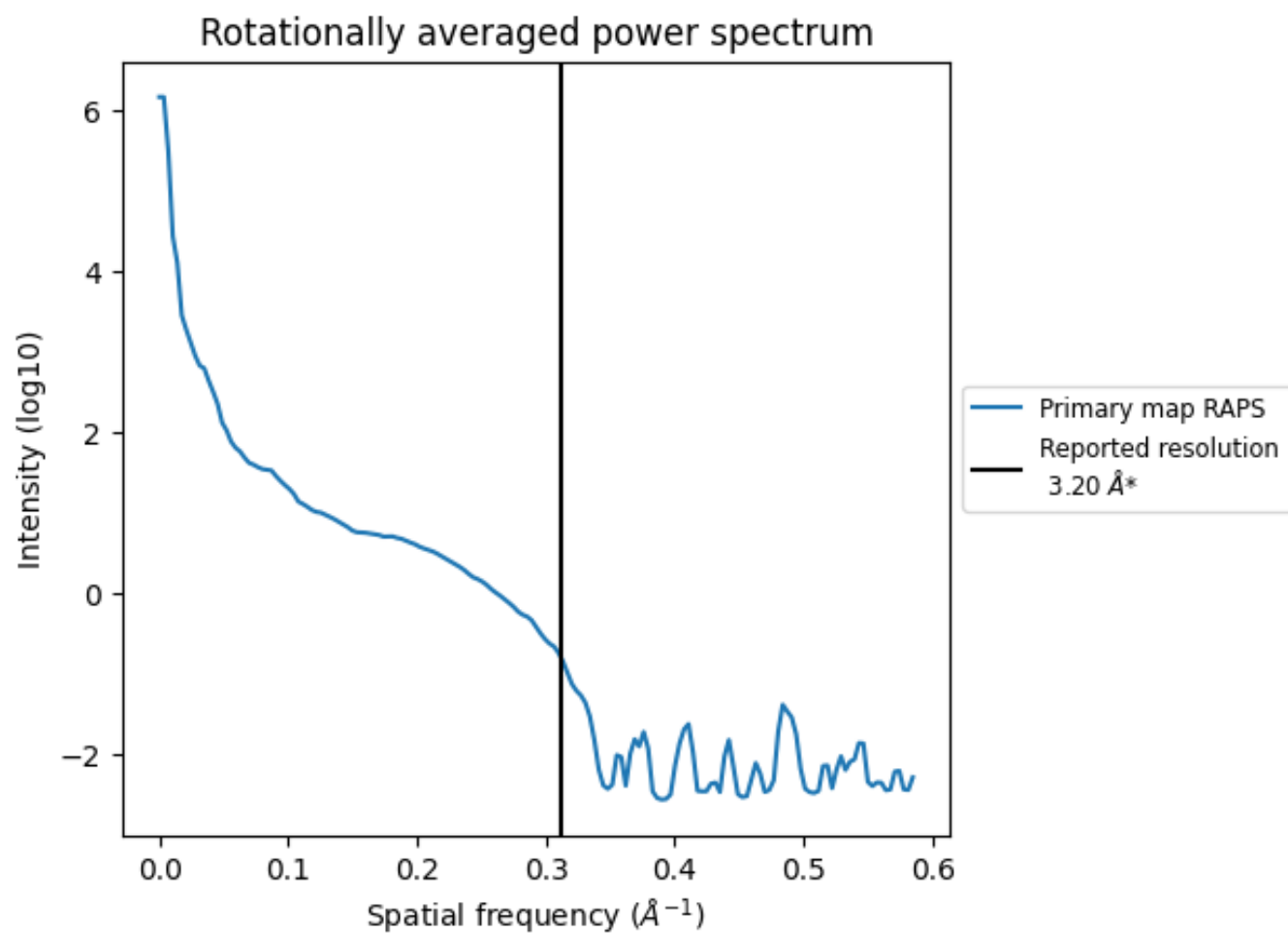
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 518 nm³; this corresponds to an approximate mass of 468 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 ⓘ

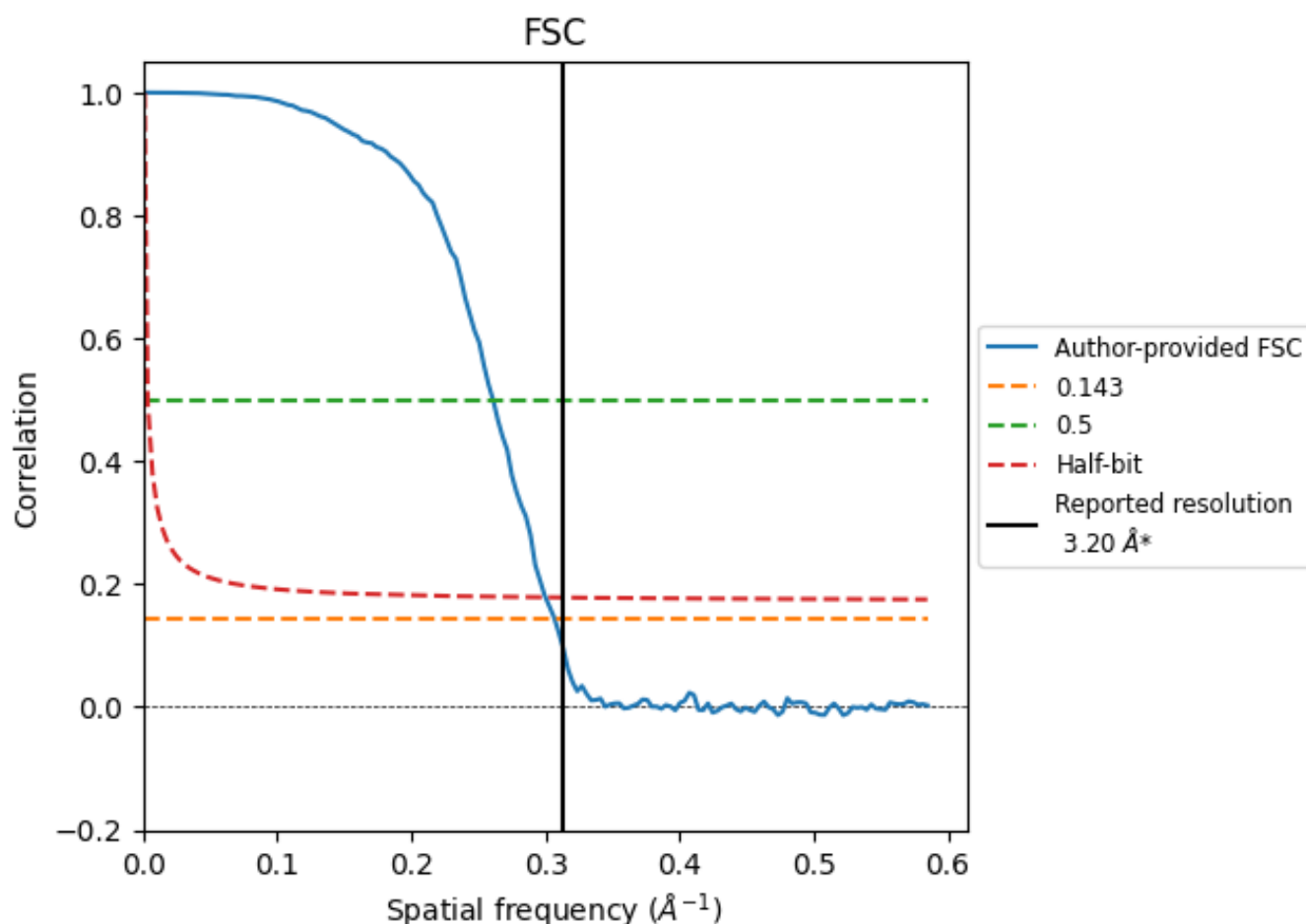


*Reported resolution corresponds to spatial frequency of 0.312 Å⁻¹

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 0.312 Å⁻¹

8.2 Resolution estimates [i](#)

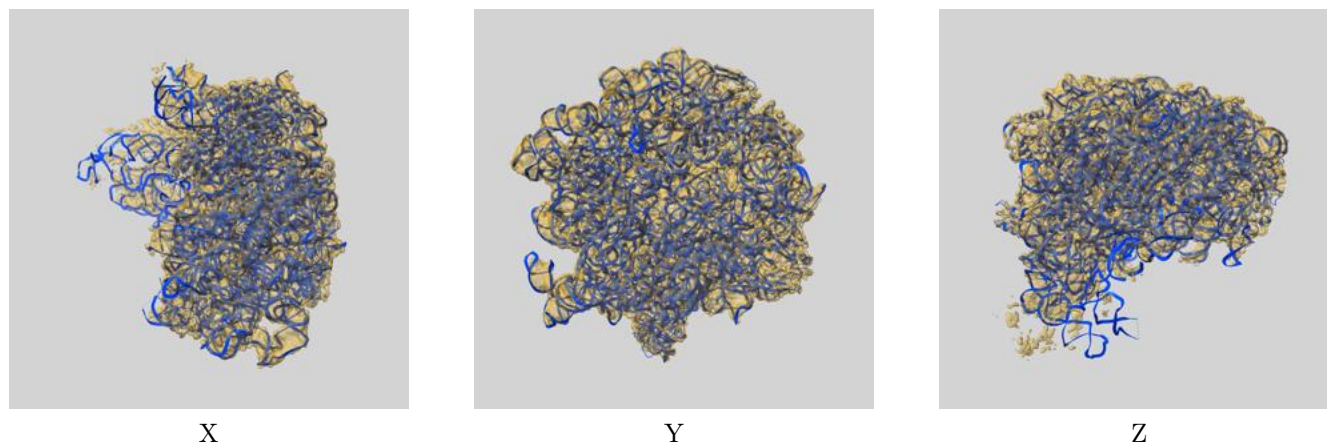
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.20	-	-
Author-provided FSC curve	3.26	3.83	3.33
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

9 Map-model fit [i](#)

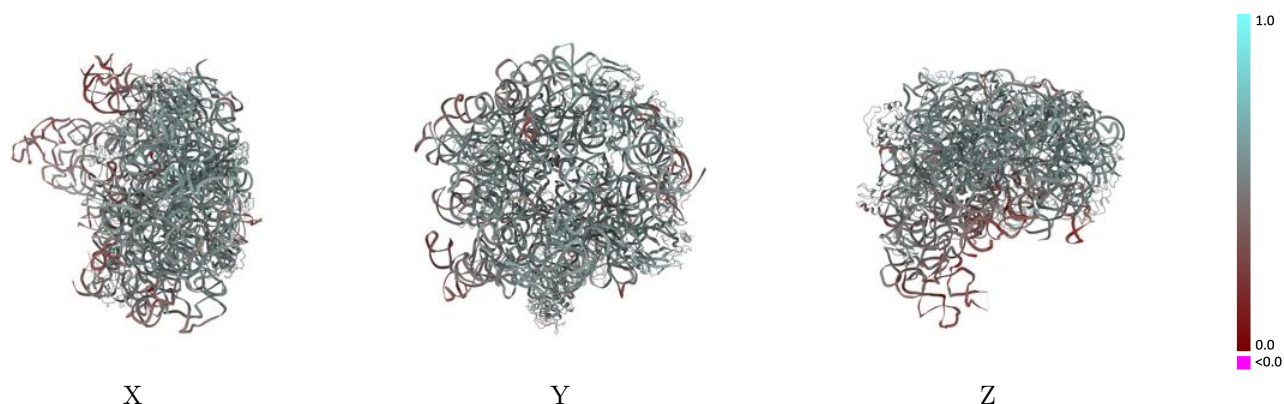
This section contains information regarding the fit between EMDB map EMD-24937 and PDB model 7S9U. Per-residue inclusion information can be found in section [3](#) on page [7](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 0.00983 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

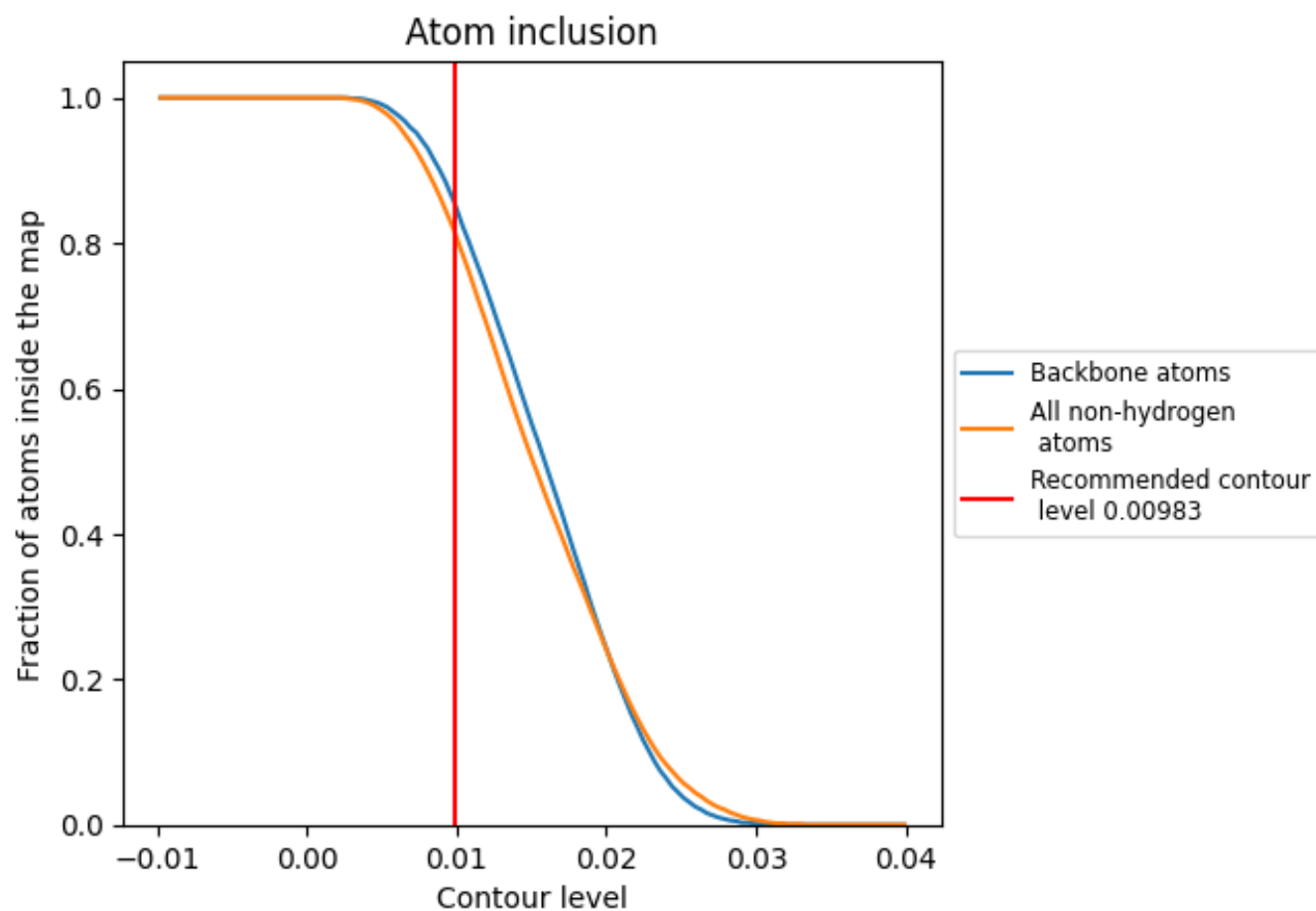


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 82% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.00983) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8180	 0.4950
A	 0.8500	 0.4870
C	 0.5970	 0.5060
D	 0.7440	 0.5350
E	 0.7530	 0.5240
J	 0.8090	 0.5250
K	 0.5740	 0.5140
L	 0.5870	 0.4750
N	 0.8590	 0.5480
P	 0.6080	 0.5190
Q	 0.8610	 0.5380
R	 0.7800	 0.5400
S	 0.8220	 0.5440
T	 0.7970	 0.5300
U	 0.7390	 0.5360
V	 0.2440	 0.4800
Y	 0.7340	 0.4860
Z	 0.6990	 0.5280
b	 0.8330	 0.5480
d	 0.8580	 0.5580

