



## Full wwPDB EM Validation Report ⓘ

May 25, 2025 – 01:11 PM EDT

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](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev118  
MolProbity : 4-5-2 with Phenix2.0rc1  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.43.1

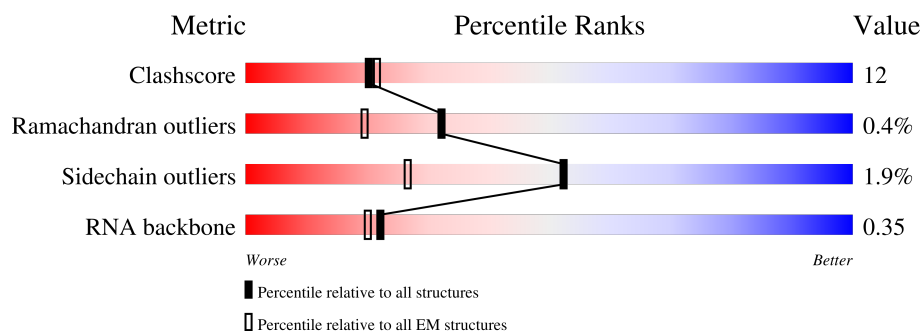
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.20 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.










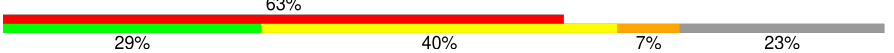




Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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

Mol	Chain	Length	Quality of chain
1	A	2928	
2	C	277	
3	D	209	
4	E	207	
5	J	145	
6	K	122	
7	L	146	

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Mol	Chain	Length	Quality of chain
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		

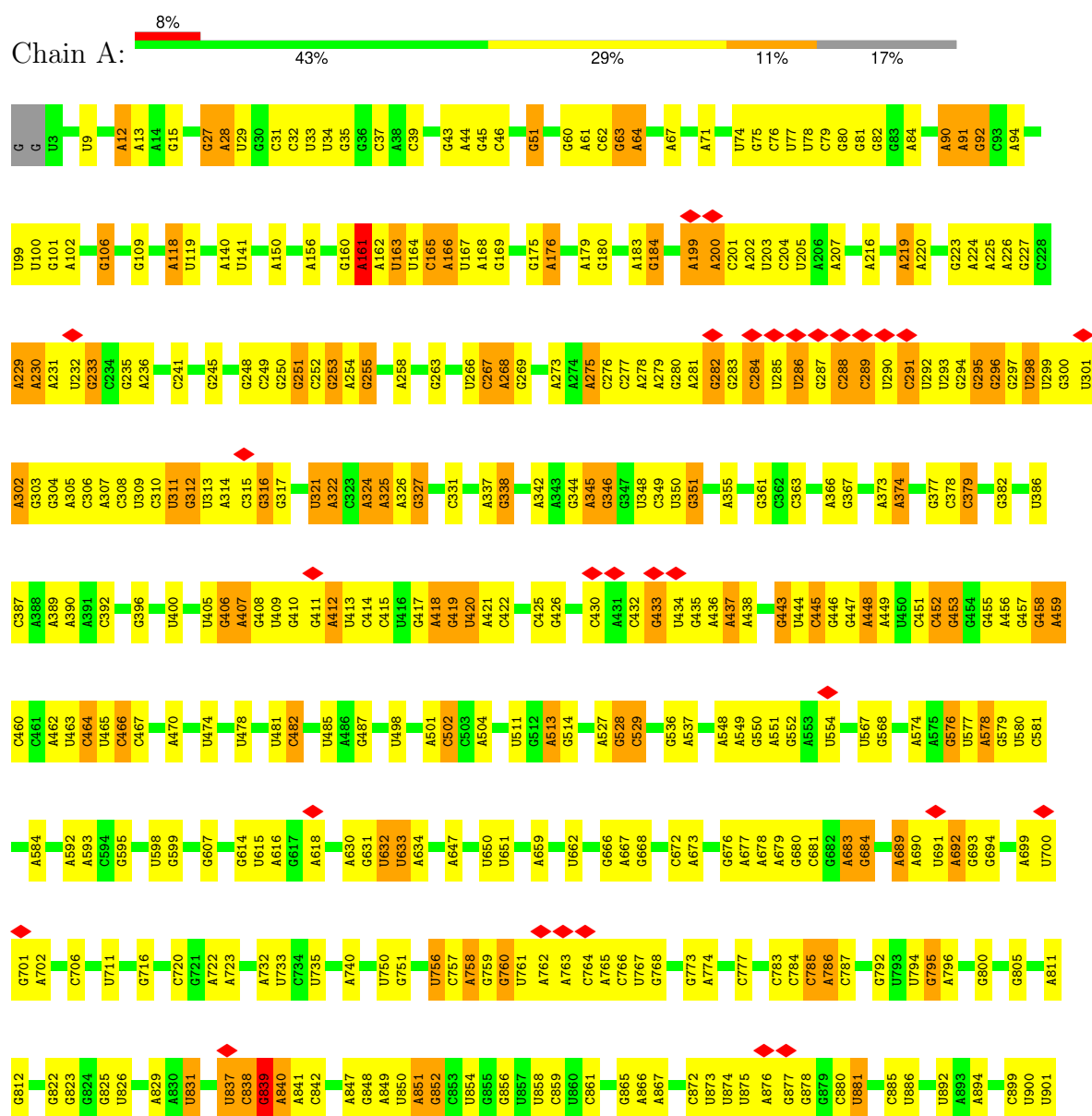
- Molecule 19 is a protein called 50S ribosomal protein L34.

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

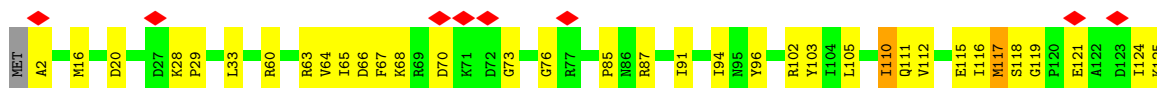
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

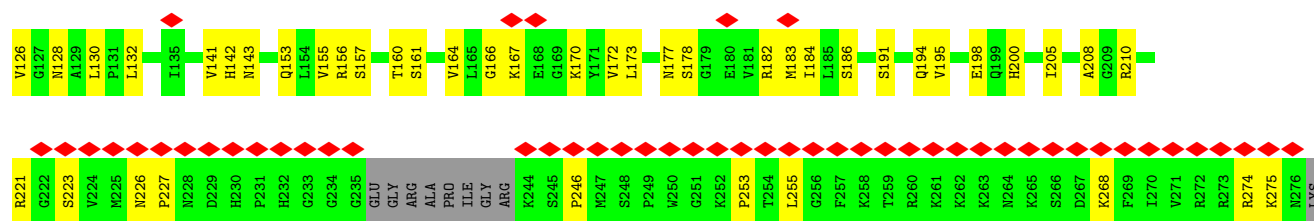
#### • Molecule 1: RNA (2436-MER)



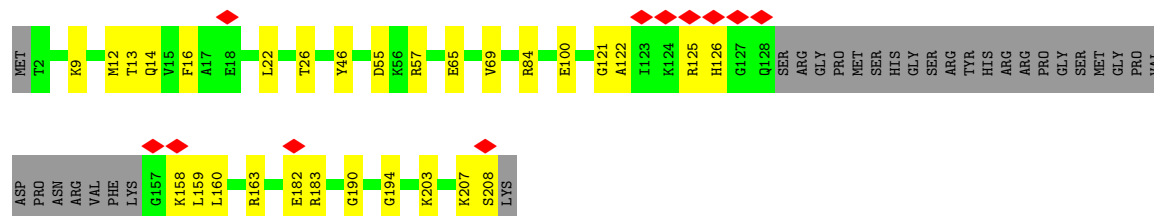
A2009	G2009	U1756	G1633	G1546	A1480	U1380	U1289	C1181	C	C	G902
A2010	G2010	G1757	A1638	U1547	G1481	U1380	G1290	G1184	A	G	G903
U2011	G2011	U1758	A1639	U1548	A1482	U1384	G1291	G1185	G	C	A904
C2012	G2012	U1759	A1640	U1549	A1483	C1384	G1292	C1186	C	C	G905
A2017	G2017	A1767	A1648	C1550	G1488	G1387	A1294	U1187	A	A	G906
C2018	G2018	A1774	C1649	C1552	G1491	A1388	U1295	A1188	C	C	U907
A2019	G2019	G1777	C1652	U1553	A1492	U1391	G1296	A1189	C	C	G911
C2020	G2020	A1778	A1653	U1554	C1493	A1392	A1302	A1201	A	A	G912
A2021	G2021	G1779	A1654	A1555	G1494	A1404	U1303	A1067	U	U	A913
C2022	G2022	C1780	A1655	G1557	C1495	A1405	G1304	U1069	U	U	C914
A2023	G2023	C1781	G1658	C1558	G1497	A1406	A1305	U1070	A	A	U915
C2024	G2024	G1782	A1659	U1560	U1498	C1409	U1305	G1071	A	A	G916
A2025	G2025	C1783	G1660	G1561	A1499	U1412	C1310	A1072	A	A	A917
C2026	G2026	A1784	A1662	U1562	U1500	G1413	G1311	A1073	G	G	U918
A2027	G2027	G1785	A1663	G1563	U1501	G1414	A1312	A1074	A	A	U919
C2028	G2028	A1791	U1664	C1564	G1502	G1417	A1313	G1075	U	U	G920
A2029	G2029	G1792	G1665	U1565	G1503	U1418	A1221	G1076	U	U	G921
C2030	G2030	C1793	G1666	U1566	U1504	U1418	A1222	A1077	C	C	A922
A2031	G2031	A1802	G1667	U1567	U1505	A1424	G1322	U1079	G	G	C923
C2032	G2032	G1805	A1668	C1568	U1506	C1425	U1321	U1080	A	A	U924
A2033	G2033	U1808	G1697	U1570	U1507	A1433	A1323	G1081	A	A	G925
C2034	G2034	A1809	A1698	G1571	C1508	U1434	G1324	G1082	U	U	G926
A2035	G2035	G1706	G1707	C1572	C1511	U1435	U1327	A1083	G	G	A927
C2036	G2036	U1712	G1713	U1573	C1512	U1436	A1335	G1084	A	A	G928
A2037	G2037	A1714	A1715	C1513	C1514	C1437	U1339	U1085	U	U	G929
C2038	G2038	G1719	U1720	C1515	C1516	U1438	A1340	U1086	C	C	G930
A2039	G2039	C1721	A1722	C1517	C1518	U1439	U1341	U1087	U	U	A931
C2040	G2040	G1723	A1724	C1519	C1520	G1444	U1342	U1088	A	A	U932
A2041	G2041	U1725	G1726	C1521	C1522	A1445	U1343	U1089	U	U	G933
C2042	G2042	A1727	A1728	C1523	C1524	U1450	U1344	U1090	C	C	G934
A2043	G2043	C1729	U1730	C1525	C1526	A1456	U1345	U1091	A	A	U935
C2044	G2044	G1731	A1732	C1527	C1528	U1457	U1351	U1092	U	U	A936
A2045	G2045	A1733	U1734	C1529	C1530	U1458	U1352	U1093	C	C	A937
C2046	G2046	C1735	A1736	C1531	C1532	G1460	C1353	U1094	A	A	U938
A2047	G2047	U1737	U1738	C1533	C1534	A1461	G1354	U1095	U	U	A939
C2048	G2048	C1739	C1740	C1535	C1536	G1462	A1355	U1096	U	U	U940
A2049	G2049	A1741	A1742	C1607	C1537	C1463	A1356	U1097	A	A	A941
C2050	G2050	G1743	U1744	C1613	G1538	A1464	G1357	U1098	U	U	U942
A2051	G2051	A1745	A1746	A1614	C1539	U1465	A1358	U1099	C	C	A943
C2052	G2052	U1747	U1748	A1615	A1540	U1466	A1359	U1100	U	U	U944
A2053	G2053	G1749	G1750	G1616	A1541	A1467	A1360	U1101	U	U	U945
C2054	G2054	A1751	A1752	A1617	A1542	U1468	A1361	U1102	A	A	A946
A2055	G2055	U1753	U1754	U1626	A1543	U1469	G1362	U1103	U	U	U947
C2056	G2056	C1755	C1756	C1629	U1544	G1472	A1363	U1104	U	U	A948
A2057	G2057	A1757	A1758	G1630	C1545	A1473	C1364	G1171	G	G	U949
C2058	G2058	U1857	U1858	A1631	C1546	U1474	A1365	A1172	C	C	C951
A2059	G2059	G1859	G1860	G1632	C1547	C1475	G1366	A1173	U	U	A952
C2060	G2060	A1861	A1862	C1862	C1863	U1476	A1367	A1174	U	U	G953
A2061	G2061	U1863	U1864	U1865	U1866	A1477	A1368	A1175	A	A	U954
C2062	G2062	G1867	G1868	G1869	G1870	U1478	C1369	U1176	G	G	C955
A2063	G2063	A1869	A1870	A1871	A1872	G1479	G1370	U1177	A	A	A956
C2064	G2064	C1871	C1872	C1873	C1874	U1480	G1371	U1178	U	U	A957
A2065	G2065	U1873	U1874	U1875	U1876	U1481	G1372	A1179	C	C	A958
C2066	G2066	A1877	A1878	A1879	A1880	U1482	G1373	C1180	U	U	U959
A2067	G2067	G1879	G1880	G1881	G1882	U1483	G1374				A960
C2068	G2068	U1881	U1882	U1883	U1884	U1484	G1375				C961
A2069	G2069	A1883	A1884	A1885	A1886	U1485	G1376				G963
C2070	G2070	C1887	C1888	C1889	C1890	U1486	G1377				
A2071	G2071	U1889	U1890	U1891	U1892	U1487	G1378				
C2072	G2072	A1891	A1892	A1893	A1894	U1488	G1379				
A2073	G2073	G1891	G1892	G1893	G1894	U1489	G1380				
C2074	G2074	U1895	U1896	U1897	U1898	U1490	G1381				
A2075	G2075	A1899	A1900	A1901	A1902	U1491	G1382				
C2076	G2076	C1901	C1902	C1903	C1904	U1492	G1383				
A2077	G2077	U1901	U1902	U1903	U1904	U1493	G1384				
C2078	G2078	A1905	A1906	A1907	A1908	U1494	G1385				
A2079	G2079	G1905	G1906	G1907	G1908	U1495	G1386				
C2080	G2080	U1909	U1910	U1911	U1912	U1496	G1387				
A2081	G2081	A1911	A1912	A1913	A1914	U1497	G1388				
C2082	G2082	C1911	C1912	C1913	C1914	U1498	G1389				
A2083	G2083	U1915	U1916	U1917	U1918	U1499	G1390				
C2084	G2084	A1919	A1920	A1921	A1922	U1500	G1391				
A2085	G2085	G1919	G1920	G1921	G1922	U1501	G1392				
C2086	G2086	U1921	U1922	U1923	U1924	U1502	G1393				
A2087	G2087	A1925	A1926	A1927	A1928	U1503	G1394				
C2088	G2088	U1929	U1930	U1931	U1932	U1504	G1395				
A2089	G2089	A1931	A1932	A1933	A1934	U1505	G1396				
C2090	G2090	C1931	C1932	C1933	C1934	U1506	G1397				
A2091	G2091	U1935	U1936	U1937	U1938	U1507	G1398				
C2092	G2092	A1939	A1940	A1941	A1942	U1508	G1399				
A2093	G2093	G1939	G1940	G1941	G1942	U1509	G1400				
C2094	G2094	U1941	U1942	U1943	U1944	U1510	G1401				
A2095	G2095	A1945	A1946	A1947	A1948	U1511	G1402				
C2096	G2096	C1945	C1946	C1947	C1948	U1512	G1403				
A2097	G2097	U1949	U1950	U1951	U1952	U1513	G1404				
C2098	G2098	A1951	A1952	A1953	A1954	U1514	G1405				
A2099	G2099	G1951	G1952	G1953	G1954	U1515	G1406				
C2100	G2100	U1955	U1956	U1957	U1958	U1516	G1407				
A2101	G2101	A1959	A1960	A1961	A1962	U1517	G1408				
C2102	G2102	C1959	C1960	C1961	C1962	U1518	G1409				
A2103	G2103	U1961	U1962	U1963	U1964	U1519	G1410				
C2104	G2104	A1965	A1966	A1967	A1968	U1520	G1411				
A2105	G2105	G1965	G1966	G1967	G1968	U1521	G1412				
C2106	G2106	U1969	U1970	U1971	U1972	U1522	G1413				
A2107	G2107	A1971	A1972	A1973	A1974	U1523	G1414				
C2108	G2108	C1969	C1970	C1971	C1972	U1524	G1415				
A2109	G2109	U1973	U1974	U1975	U1976	U1525	G1416				
C2110	G2110	A1975	A1976	A1977	A1978	U1526	G1417				
A2111	G2111	G1975	G1976	G1977	G1978	U1527	G1418				
C2112	G2112	U1979	U1980	U1981	U1982	U1528	G1419				
A2113	G2113	A1981	A1982	A1983	A1984	U1529	G1420				
C2114	G2114	C1979	C1980	C1981	C1982	U1530	G1421				
A2115	G2115	U1983	U1984	U1985	U1986	G1531	G1422				
C2116	G2116	A1985	A1986	A1987	A1988	U1532	G1423				
A2117	G2117	G1985	G1986	G1987	G1988	U1533	G1424				
C2118	G2118	U1989	U1990	U1991	U1992	G1534	G1425				
A2119	G2119	A1991	A1992	A1993	A1994	U1535	G1426				
C2120	G2120	C1989	C1990	C1991	C1992	U1536	G1427				
A2121	G2121	U1993	U1994	U1995	U1996	U1537	G1428				
C2122	G2122	A1995	A1996	A1997	A1998	U1538	G1429				
A2123	G2123	G1995	G1996	G1997	G1998	U1539	G1430				
C2124	G2124	U1999	U2000	U2001	U2002	U1540	G1431				
A2125	G2125	A1999	A2000	A2001	A2002	U1541	G1432				
C2126	G2126	C1999	C2000	C2001	C2002	U1542	G1433				
A2127	G2127	U2003	U2004	U2005	U2006	U1543	G1434				
C2128	G2128	A2003	A2004	A2005	A2006	U1544	G1435				
A2129	G2129	G2003	G2004	G2005	G2006	U1545	G1436				
C2130	G2130	U2007	U2008	U2009	U2010	U1546	G1437				
A2131	G2131	A2007	A2008	A2009	A2010	U1547	G1438				
C2132	G2132	C2007	C2008	C2009	C2010	U1548	G1439				
A2133	G2133	U2011	U2012	U2013	U2014	U1549	G1440				
C2134	G2134	A2011	A2012	A2013	A2014	U1550	G1441				
A2135	G2135	G2011	G2012	G2013	G2014	U1551	G1442				



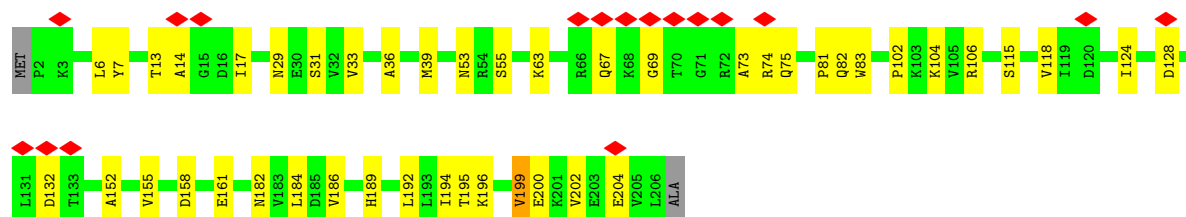
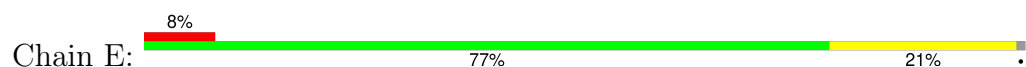




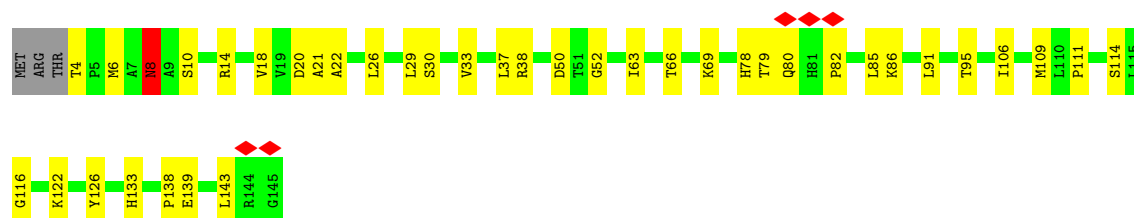
• Molecule 3: 50S ribosomal protein L3



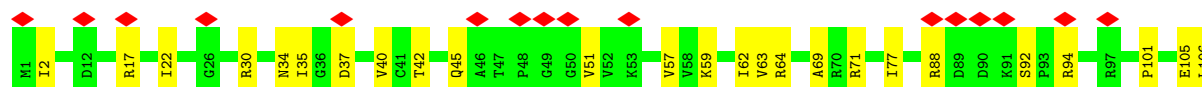
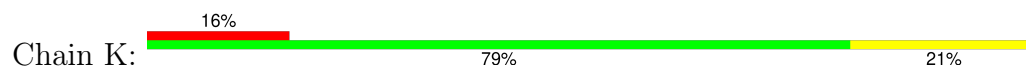
• Molecule 4: 50S ribosomal protein L4

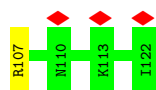


• Molecule 5: 50S ribosomal protein L13

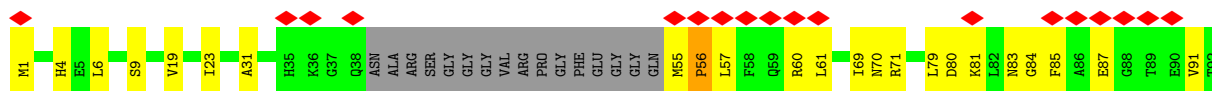


• Molecule 6: 50S ribosomal protein L14

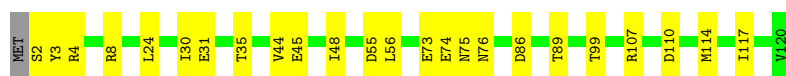
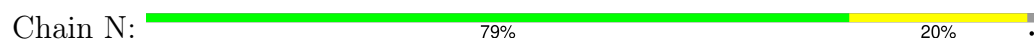




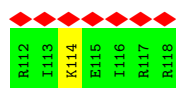
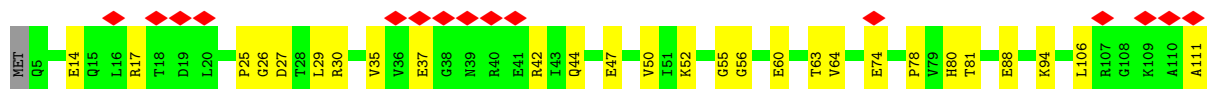
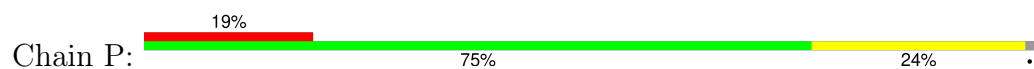
- Molecule 7: 50S ribosomal protein L15



- Molecule 8: 50S ribosomal protein L17



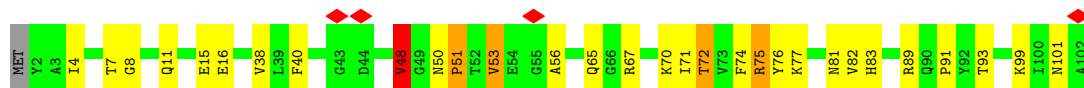
- Molecule 9: 50S ribosomal protein L19




- Molecule 10: 50S ribosomal protein L20



- Molecule 11: 50S ribosomal protein L21




- Molecule 12: 50S ribosomal protein L22

Chain S: 




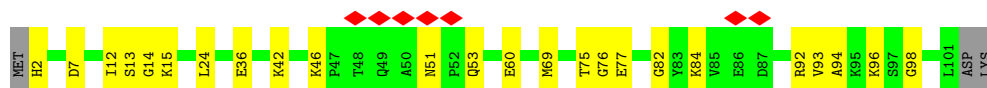
- Molecule 13: 50S ribosomal protein L23

Chain T: 



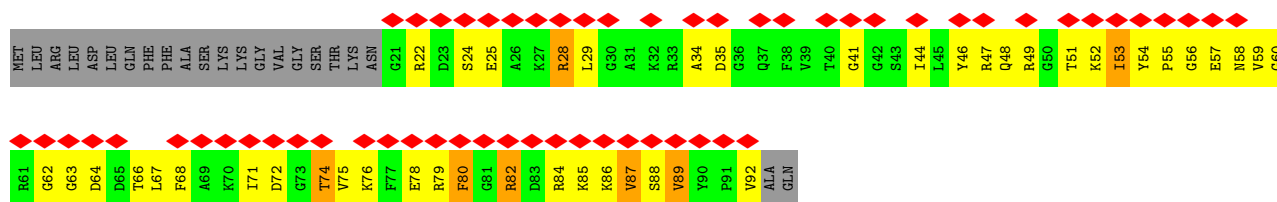
- Molecule 14: 50S ribosomal protein L24

Chain U: 




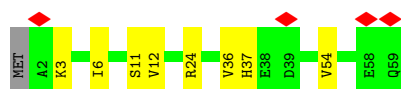
- Molecule 15: 50S ribosomal protein L27

Chain V: 



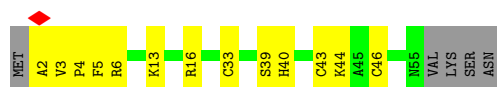
- Molecule 16: 50S ribosomal protein L30

Chain Z: 

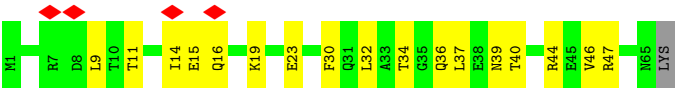


- Molecule 17: 50S ribosomal protein L32

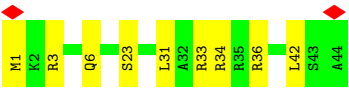
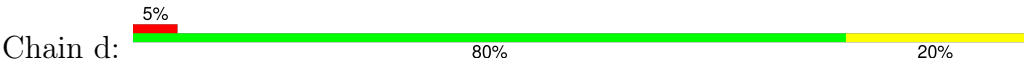
Chain b: 



- 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	51
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	27
11	R	99/102 (97%)	81 (82%)	16 (16%)	2 (2%)	6	32

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	S	107/113 (95%)	97 (91%)	9 (8%)	1 (1%)	14	49
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	40
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%)	8	37
19	d	42/44 (96%)	38 (90%)	4 (10%)	0	100	100
All	All	2048/2195 (93%)	1727 (84%)	312 (15%)	9 (0%)	32	64

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%)	29	62
3	D	144/170 (85%)	143 (99%)	1 (1%)	81	92
4	E	169/170 (99%)	168 (99%)	1 (1%)	84	92
5	J	120/123 (98%)	118 (98%)	2 (2%)	56	78

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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%)	73	87
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%)	11	41
11	R	83/84 (99%)	79 (95%)	4 (5%)	21	55
12	S	90/93 (97%)	90 (100%)	0	100	100
13	T	83/85 (98%)	82 (99%)	1 (1%)	67	85
14	U	84/87 (97%)	84 (100%)	0	100	100
15	V	56/74 (76%)	48 (86%)	8 (14%)	2	13
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%)	52	76

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%)	47 (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

*Continued on next page...*

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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

*Continued on next page...*

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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 (47) 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	165	C
1	A	229	A
1	A	267	C
1	A	288	C
1	A	311	U
1	A	377	G
1	A	419	G
1	A	458	G
1	A	549	A
1	A	632	U
1	A	683	A
1	A	785	C

*Continued on next page...*

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Mol	Chain	Res	Type
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
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

There are no ligands in this entry.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.



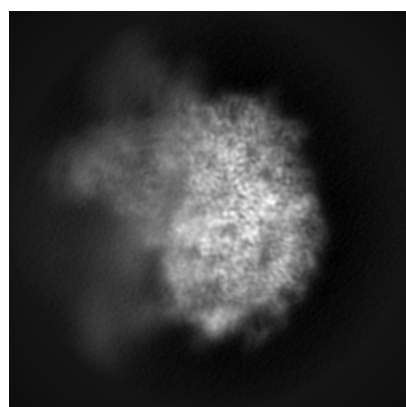
## 6 Map visualisation [i](#)

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.

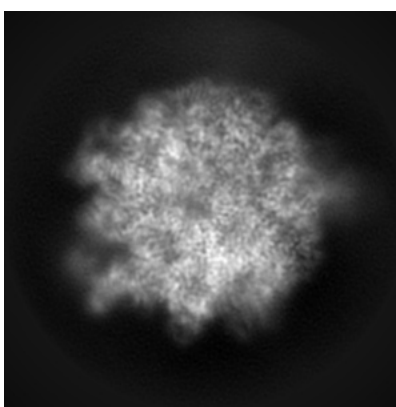
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

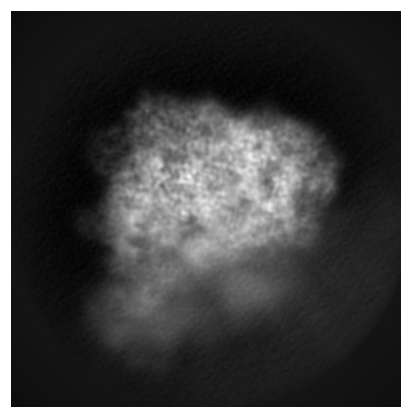
#### 6.1.1 Primary map



X



Y

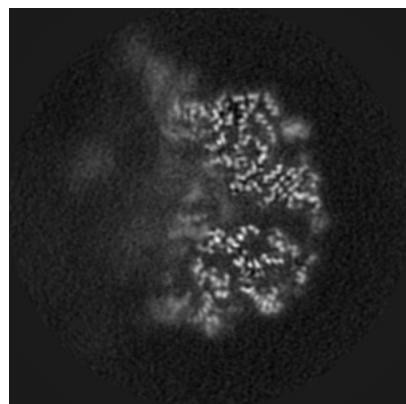


Z

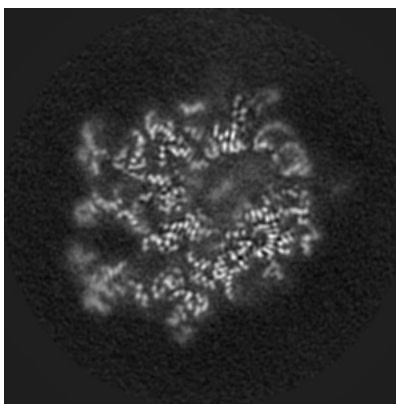
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

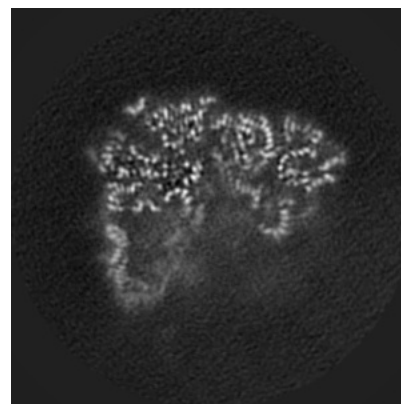
#### 6.2.1 Primary map



X Index: 168



Y Index: 168

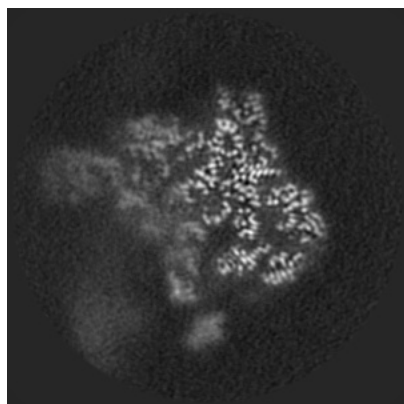


Z Index: 168

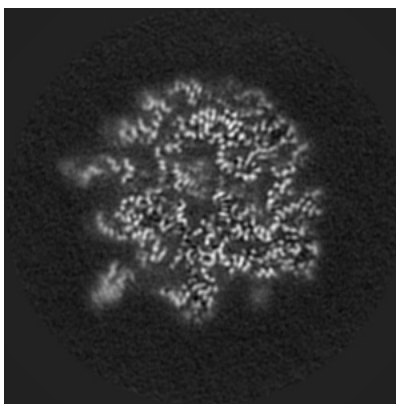
The images above show central slices of the map in three orthogonal directions.

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

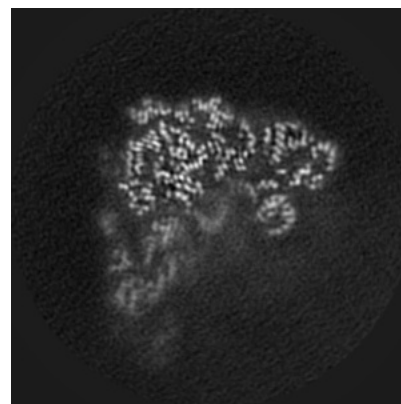
### 6.3.1 Primary map



X Index: 125



Y Index: 197

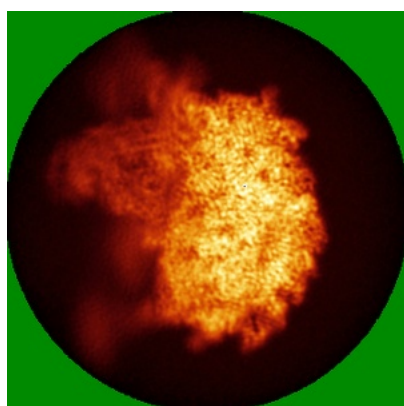


Z Index: 176

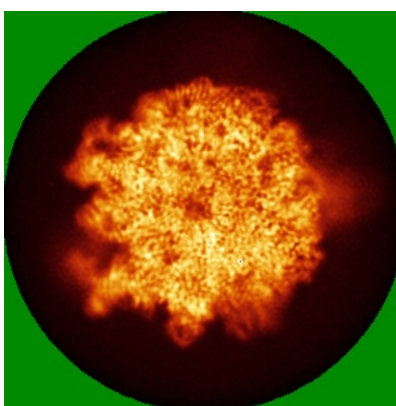
The images above show the largest variance slices of the map in three orthogonal directions.

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

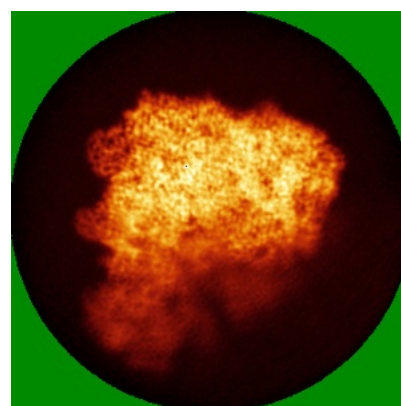
### 6.4.1 Primary map



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.

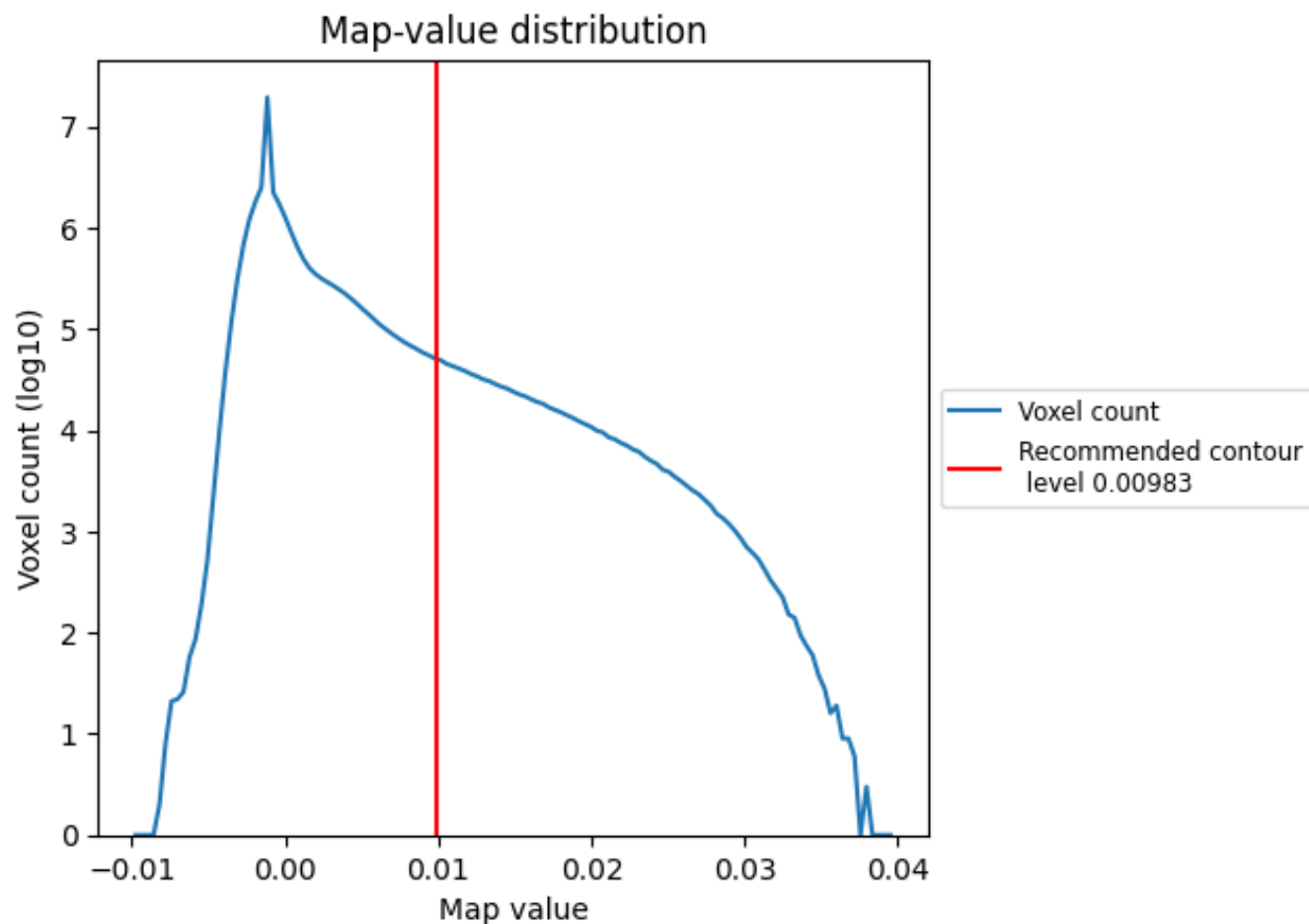
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

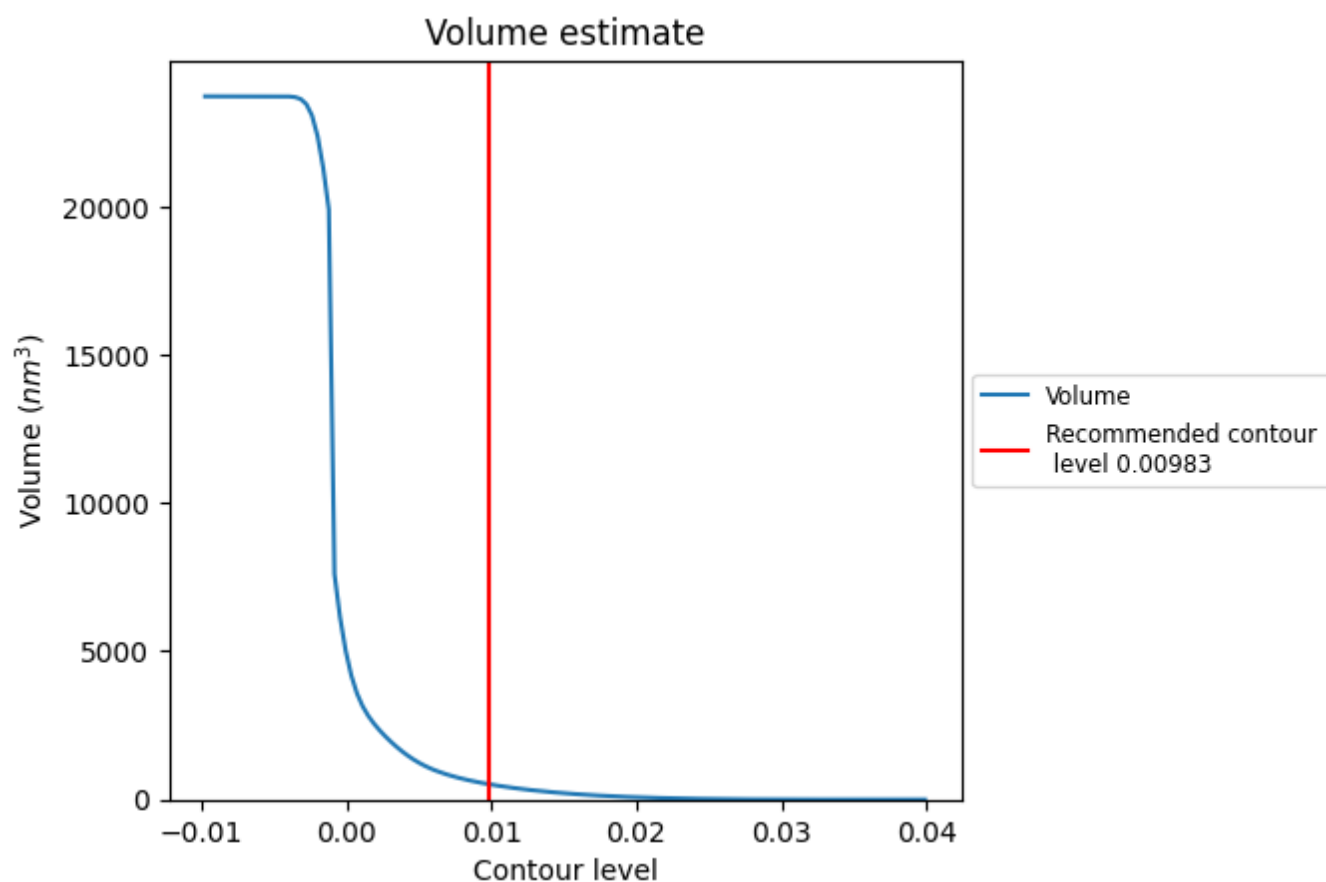
This section contains the results of statistical analysis of the map.

### 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.

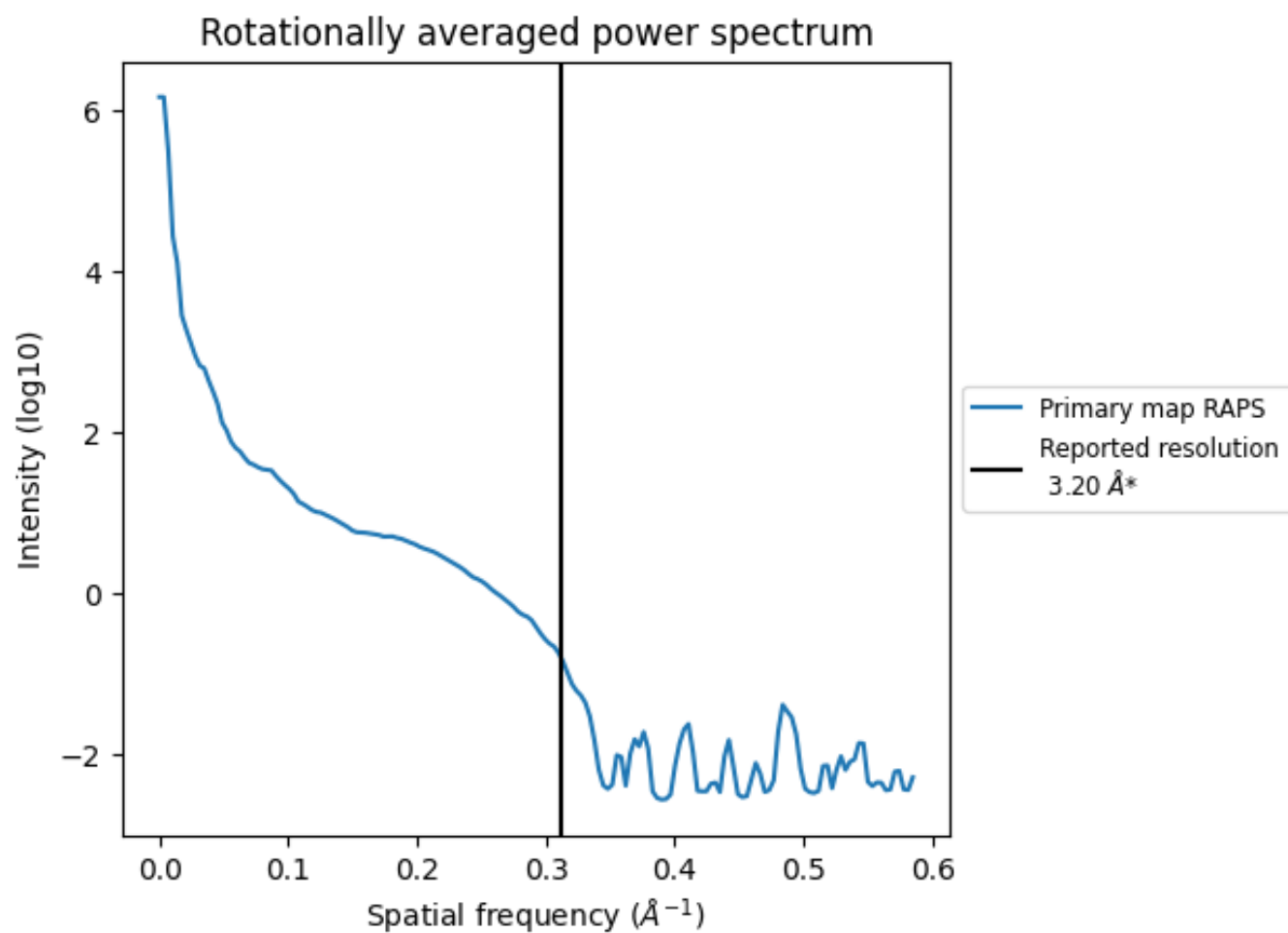
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 518 nm<sup>3</sup>; 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 ⓘ

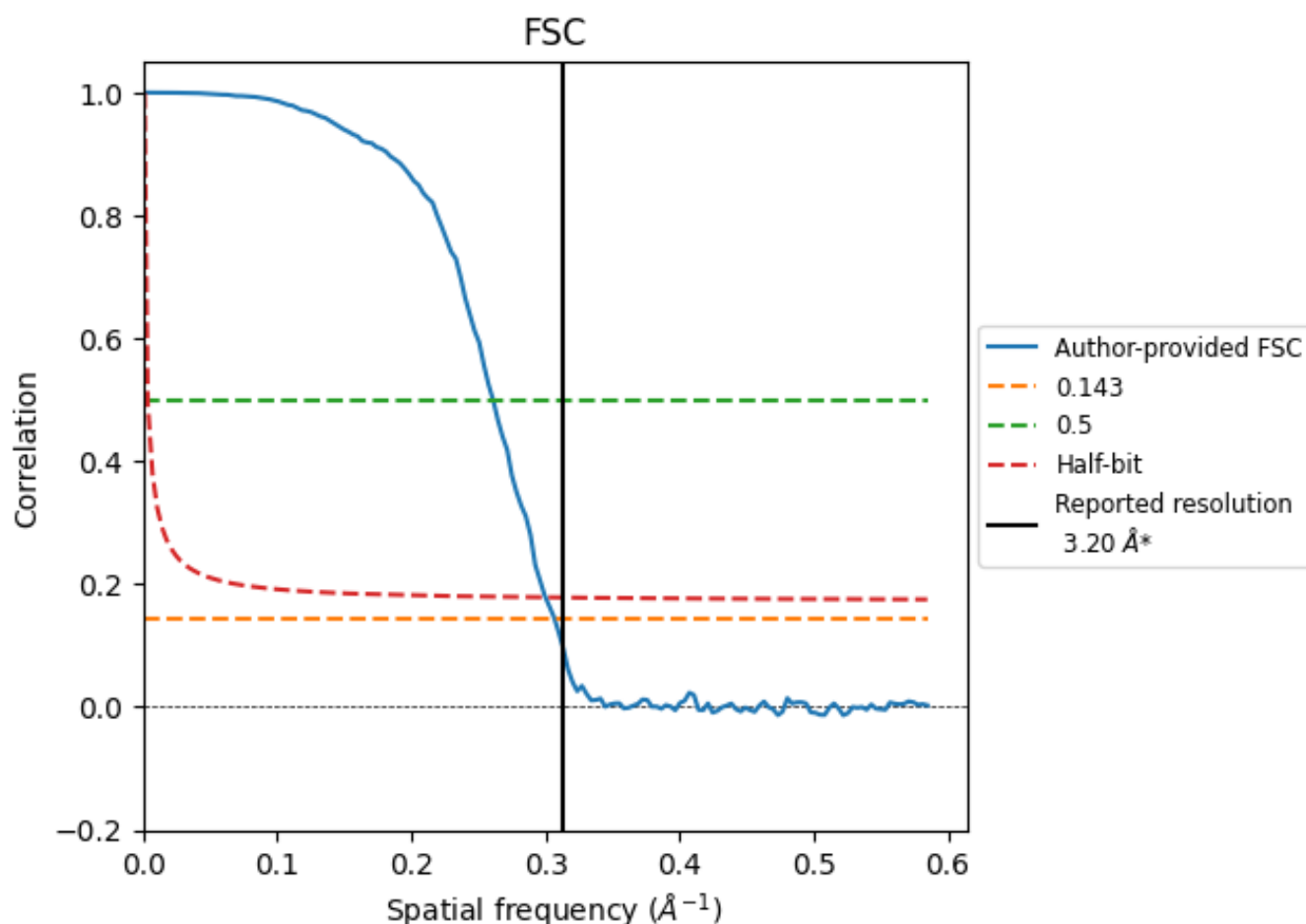


\*Reported resolution corresponds to spatial frequency of 0.312 Å<sup>-1</sup>

## 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<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

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

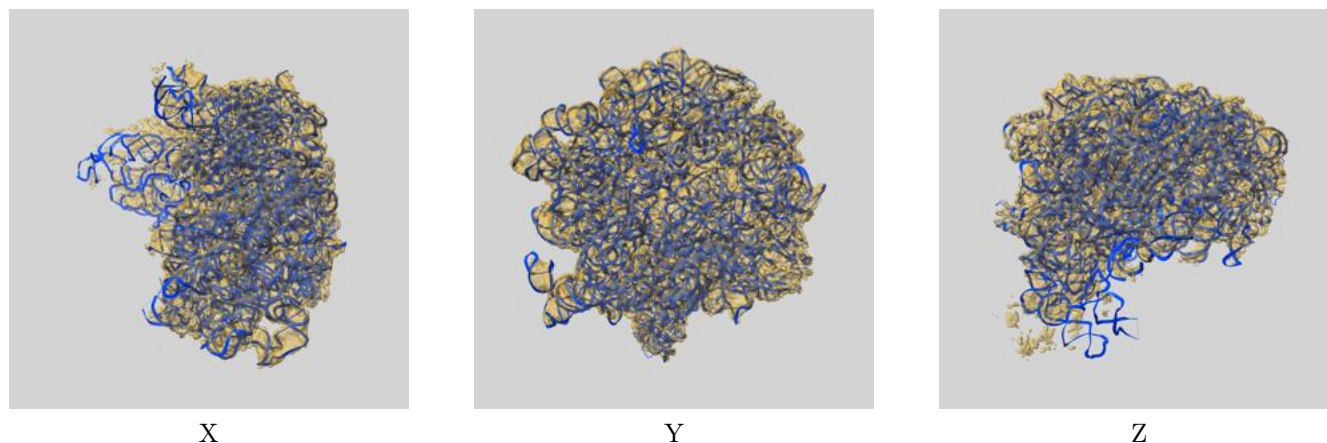
\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.



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

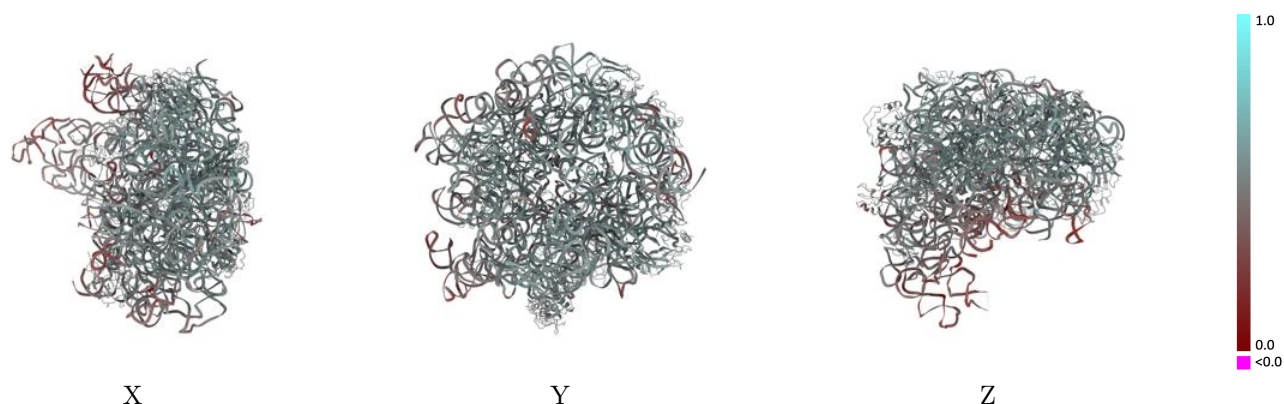
This section contains information regarding the fit between EMDB map EMD-24937 and PDB model 7S9U. Per-residue inclusion information can be found in section [3](#) on page [7](#).

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



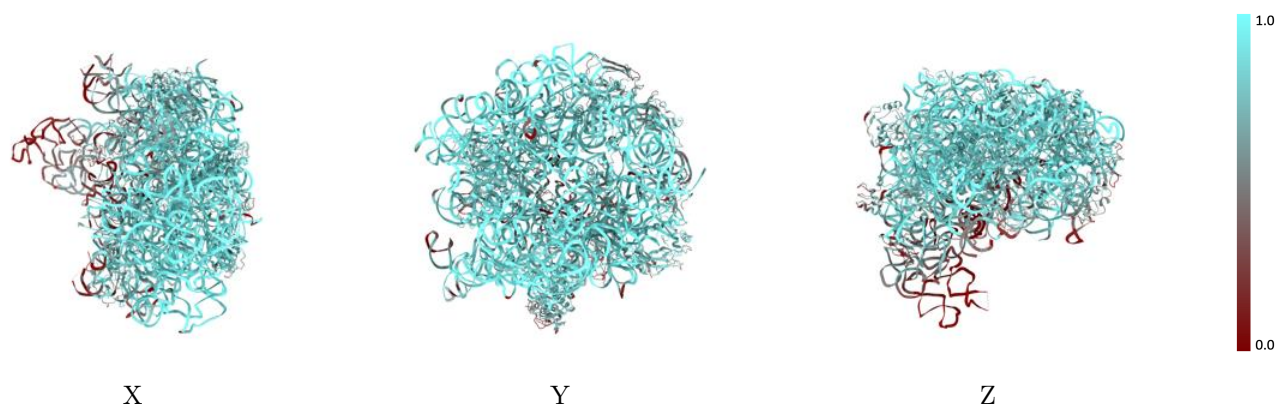
The images above show the 3D surface view of the map at the recommended contour level 0.00983 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



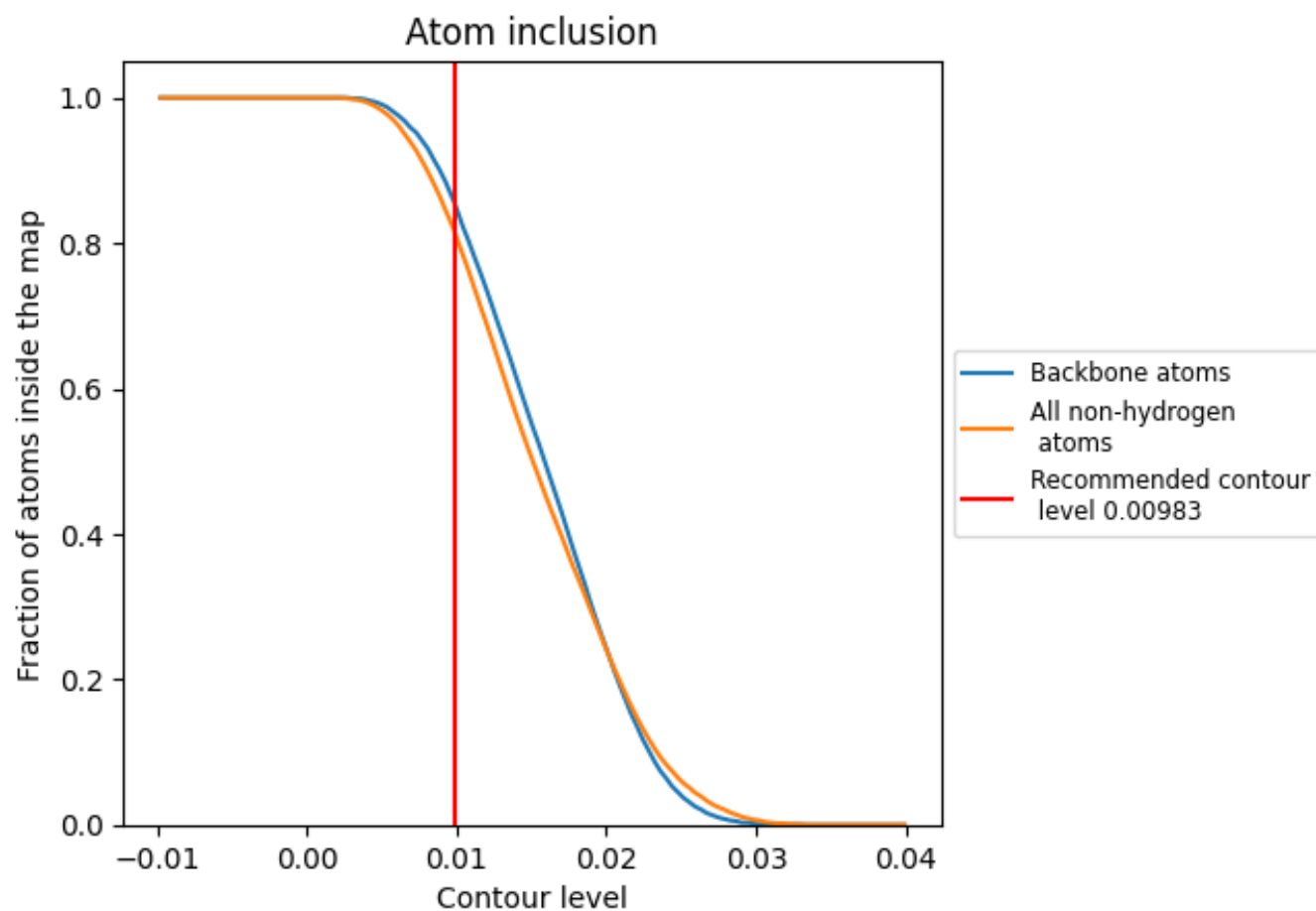
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.00983).









































## 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

