



Full wwPDB EM Validation Report ⓘ

Mar 22, 2026 – 05:42 PM UTC

PDB ID : 7ASN / pdb_00007asn
EMDB ID : EMD-11901
Title : Staphylococcus aureus 50S after 30 minutes incubation a 37C
Authors : Camicata, G.; Bashan, A.; Yonath, A.
Deposited on : 2020-10-27
Resolution : 2.73 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

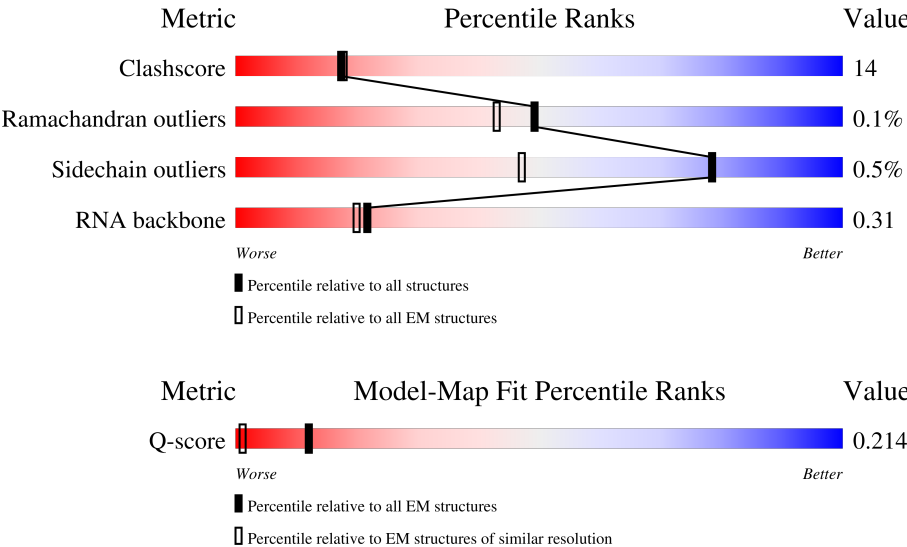
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13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

1 Overall quality at a glance

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

The reported resolution of this entry is 2.73 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10432 (2.23 - 3.23)

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

Mol	Chain	Length	Quality of chain
1	A	2742	
2	B	106	
3	1	47	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	2	43	
5	3	64	
6	F	274	
7	D	215	
8	E	206	
9	H	144	
10	L	146	
11	Y	137	
12	G	122	
13	M	117	
14	N	114	
15	O	116	
16	P	102	
17	Q	112	
18	R	89	
19	S	103	
20	T	94	
21	a	79	
22	V	49	
23	W	67	
24	X	58	
25	b	48	

2 Entry composition

There are 25 unique types of molecules in this entry. The entry contains 80694 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 23S.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2742	Total	C	N	O	P	0	0
			58787	26244	10755	19046	2742		

- Molecule 2 is a RNA chain called 5S.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	106	Total	C	N	O	P	0	0
			2260	1010	407	737	106		

- Molecule 3 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	1	47	Total	C	N	O	S	0	0
			390	238	78	70	4		

- Molecule 4 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	2	43	Total	C	N	O	S	0	0
			367	225	89	52	1		

- Molecule 5 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	3	64	Total	C	N	O	S	0	0
			521	324	113	82	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	274	Total	C	N	O	S	0	0
			2094	1303	415	371	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	215	Total	C	N	O	S	0	0
			1627	1018	299	305	5		

- Molecule 8 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	206	Total	C	N	O	S	0	0
			1572	986	288	296	2		

- Molecule 9 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	144	Total	C	N	O	S	0	0
			1132	708	204	217	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	1	MET	-	initiating methionine	UNP W8TUE6

- Molecule 10 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	146	Total	C	N	O	S	0	0
			1086	674	214	197	1		

- Molecule 11 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	Y	137	Total	C	N	O	S	0	0
			1071	689	203	175	4		

- Molecule 12 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	122	Total	C	N	O	S	0	0
			918	572	174	168	4		

- Molecule 13 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	M	117	Total	C	N	O	0	0
			872	543	172	157		

- Molecule 14 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
14	N	113	Total	C	N	O	0	0
			878	557	171	150		

- Molecule 15 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	116	Total	C	N	O	S	0	0
			942	593	189	156	4		

- Molecule 16 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	102	Total	C	N	O	S	0	0
			790	503	142	144	1		

- Molecule 17 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	Q	112	Total	C	N	O	S	0	0
			854	534	164	153	3		

- Molecule 18 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	89	Total	C	N	O	S	0	0
			715	453	127	131	4		

- Molecule 19 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	103	Total	C	N	O	S	0	0
			770	486	142	141	1		

- Molecule 20 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	T	94	Total	C	N	O	0	0
			722	463	130	129		

- Molecule 21 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	a	79	Total	C	N	O	0	0
			597	369	117	111		

- Molecule 22 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	V	49	Total	C	N	O	0	0
			379	234	82	63		

- Molecule 23 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	W	67	Total	C	N	O	0	0
			541	333	102	106		

- Molecule 24 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	X	58	Total	C	N	O	0	0
			449	280	85	84		

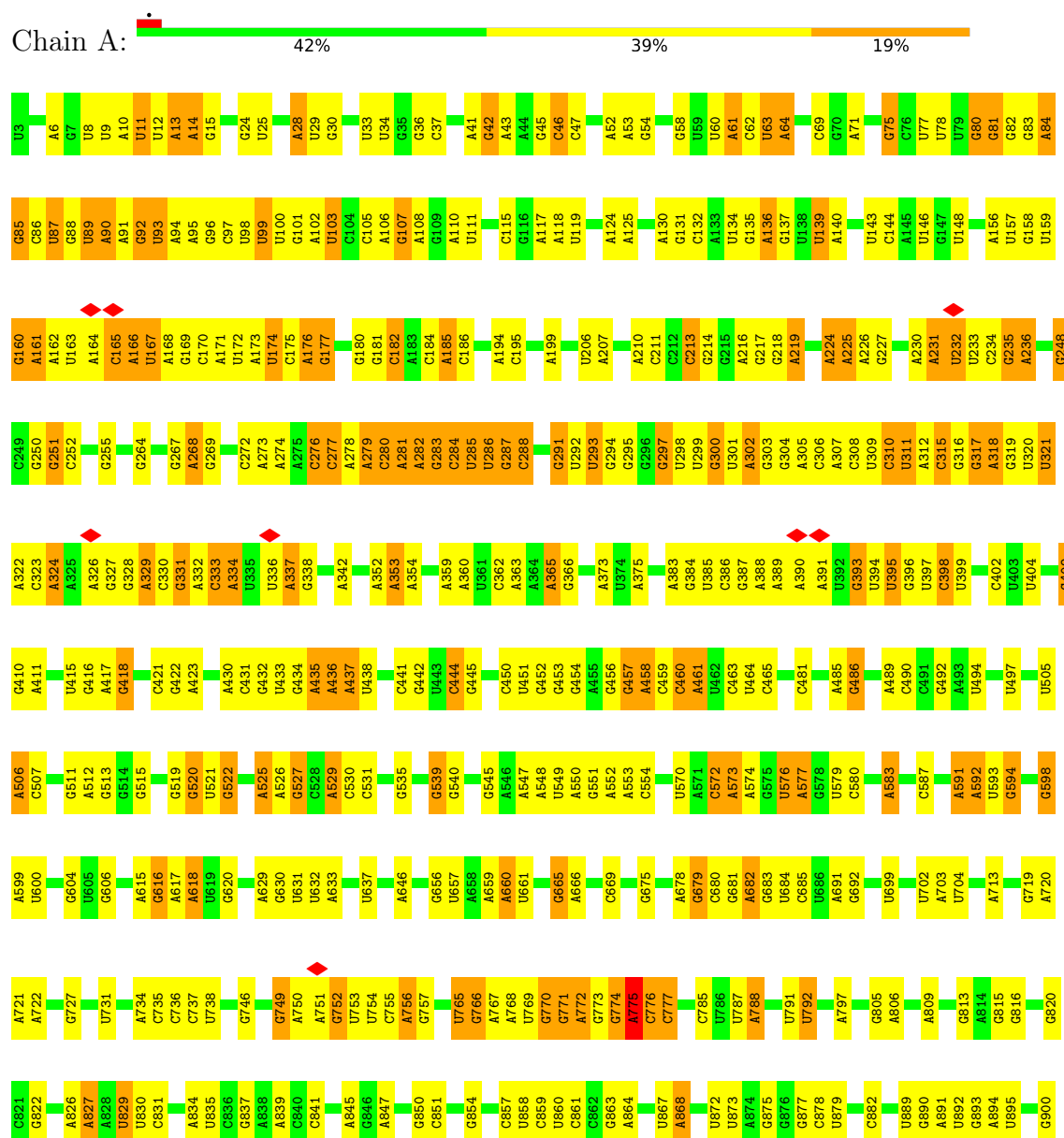
- Molecule 25 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	b	48	Total	C	N	O	S	0	0
			360	222	77	59	2		

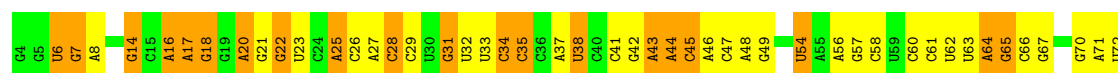
3 Residue-property plots

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: 23S

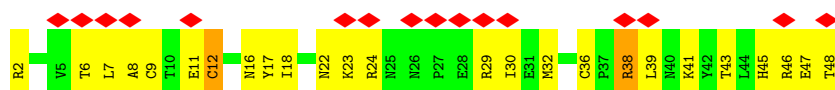


A2008	C1947	U1879	U1804	G1731	U1640	C1486	G1408	A1312	C1197	U1079	A973	G901
G2012	G1948	A1880	U1805	U1732	G1641	G1487	U1409	G1313	G1198	G1080	A977	A902
G2013	G1949	A1881	U1806	A1733	C1642	A1488	A1410	C1314	A1199	C1081	A977	G903
C2017	U1950	G1882	U1807	U1734		A1489		C1315	G1201	C1082	G986	G904
U2018	U1953	G1883	U1808	U1735	U1645	G1490	U1416	G1316	G1202	U1084		A908
G2019	A1954	A1884	A1810	U1736	A1647	C1491	G1417	A1321	U1203	U1085	A989	G909
G2020	A1955	G1885	A1811	U1737		U1493	A1421	A1324	G1204	U1086	A990	C910
C2021	A1956	G1886	A1812	C1738	G1650	G1494	G1425	G1336	A1208	C1087	A991	A911
U2022	G1957	A1887	A1813	G1739	C1651	C1495	G1496	A1337	U1209	C1088	A992	C912
G2023	U1958	G1888	A1814	G1740	A1652	U1497		U1338	C1201	C1089	U995	U913
A2024	A1959	A1888	C1815	G1741	A1653	U1498	G1429	A1339	U1210	A1090		A908
G2025	G1960	G1889	A1816	A1742	A1654	U1499	A1430	U1343	G1211	U1091	A1003	G918
C2026	C1961	A1890	C1817	A1744		G1500	U1431	A1344	U1212	A1092	A1004	A919
G2027	G1962	G1891	A1818	A1745	G1663	G1501	U1440	U1345	C1214	C1093	G1005	A920
A2032	A1963	U1891	G1820	G1746	A1666	A1502	G1441	G1347	U1215	A1095	C1008	C921
C2033	A1964	U1892	U1823	G1747	C1669	U1503	G1442	U1348	U1216	C1096		G922
U2034	A1965	A1893	C1824	G1748	A1670	U1504	A1443	U1349	G1217	C1097	C1015	A923
G2037	U1966	G1894	U1750	G1749	A1671	G1505	A1444	U1350	U1218	U1152		G924
C2041	C1967	C1895	G1751	U1750	A1672	A1506	U1445	C1351	G1219	C1153		G925
A2042	U1968	U1896	C1752	C1752	G1675	A1507	U1446	C1352	A1220	G1154	A1018	G926
G2044	U1970	A1897	U1753	U1753	A1676	U1508	U1447		C1221	A1155	A1019	G927
A2042	U1971	C1898	A1830	G1754	G1677	G1509	A1448	A1355	A1222	U1157	A1027	C928
A2045	U1972	U1899		U1755	G1678	U1598	U1449	G1356	G1225	G1158		C929
U2046	C1973	G1900	A1837	U1756	A1679	G1599	A1450	G1357	U1227		G1033	G937
A2047	G1974	C1901	U1840	U1757	U1680	A1600	A1451	A1358	A1228		C1038	G938
G2048	G1975	G1902	U1843	U1758	U1681	U1603	U1452	A1359			C1039	U939
U2049	U1976	A1903	U1844	G1759		C1604	G1453	U1366	U1238		A1040	U940
A2050	A1977	U1904	U1845	G1761	A1685	A1605	U1454	C1367	U1240		A1041	A941
C2052	U1980	G1905	U1846	U1762	C1686	C1606	U1455	C1368			G1041	C942
U2053	U1981	C1906	A1946	U1763	G1687	A1607		G1369	U1241		C1042	C943
G2054	U1982	U1907	G1852	A1764	A1690	C1608	A1458	C1370	G1245		U1043	A944
A2058	U1983	A1908	C1853	U1765	G1691	U1609	U1459				A1044	A945
G2059	C1984	C1909	U1854	U1766	C1692	G1610	U1460	U1373	G1250		A1045	A946
A2060	C1985	G1910	G1855	G1767		G1613	C1461	G1374	A1258		A1046	U947
U2061	G1986	A1911	A1856	C1768	A1698		C1462			A1171		U948
G2062	A1987	A1912	C1857	C1769	A1699	A1616	U1463	U1381		C1050	C1050	C949
C2063	C1988	U1913	C1857	A1771	C1700	A1617	U1464	C1382	G1261	C1051	C1051	A950
C2070	C1990	U1913	C1860	G1772	U1701	A1618	G1465	G1383	A1275	A1052	A1052	G951
G2075	G1991	C1914	G1862	C1781	U1703	U1623	G1467	G1384		A1053	A1053	A952
A2076	C1992	G1915	C1863	A1782	G1704	C1624	G1468	G1385	A1285	A1054	A1054	C953
C2077	A1993	A1916	C1864	G1785	U1706	U1625	G1469	U1386	G1286	A1055	A1055	A954
G2078	G1994		G1866	A1786	U1707	U1626		C1387	U1287	U1056	U1056	A955
A2078	G1995	C1921	G1867			G1627	C1472	U1388	G1288	U1058	U1058	C957
G2079	A1997	A1922	U1868	G1790	G1710	U1628	G1473	U1389	A1289	A1059	A1059	U958
C2080	A1998	G1923	G1869	G1791	G1711	A1630	A1475		G1182	G1183	G1183	C960
A2081	G1999	C1870	G1870	G1717	G1717	A1631	U1476	G1395	C1184	C1184	C1061	G961
C2082	G2000	U1871	C1792	G1718	G1718	A1632	U1477	A1396	U1291	U1185	U1062	A962
G2083	C2001	G1872	C1793			A1633	A1478		G1294	A1186	A1062	A962
A2087	G2002	G1873	U1874	U1724	U1724	A1634	G1479	A1402	C1189	A1065	A1065	G965
G2088	U2003	A1874	A1726	G1725	G1725	A1635	A1481	C1403			G1074	C966
A2089	A2004	A1875	C1798	A1726	A1726	A1636	U1482	A1404	G1302		G1075	C967
C2090	C2005	G1876	G1799	C1727	C1727	A1637	U1483	G1405	G1309		G1076	A968
	G2006	U1877	A1800			A1638	G1484	G1406	A1311		U1077	A969
		U1878	G1803			G1638	G1485				U1077	U970
						G1639					G1078	A972

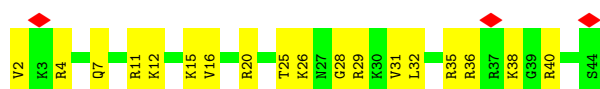




• Molecule 3: 50S ribosomal protein L33



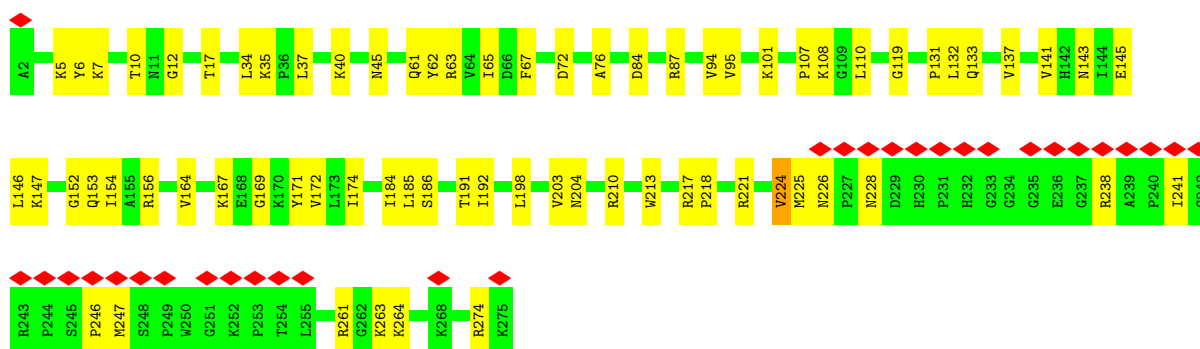
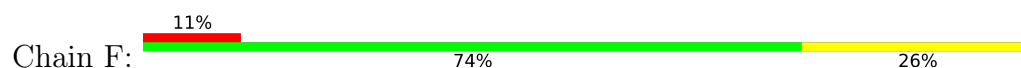
• Molecule 4: 50S ribosomal protein L34



• Molecule 5: 50S ribosomal protein L35

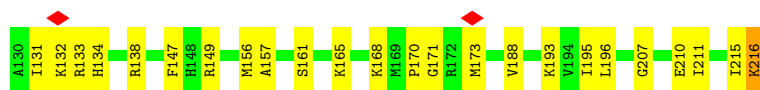


• Molecule 6: 50S ribosomal protein L2

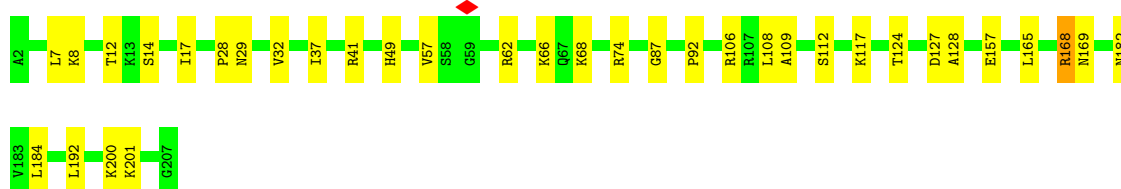
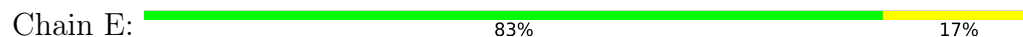


• Molecule 7: 50S ribosomal protein L3

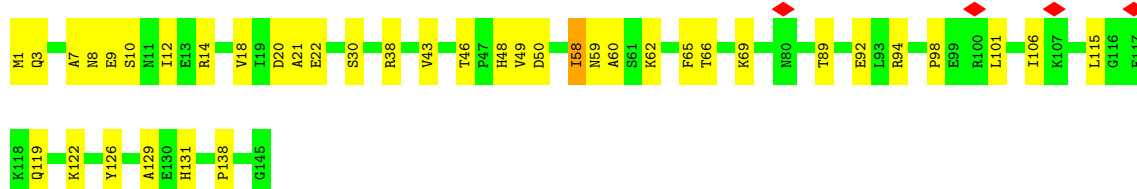




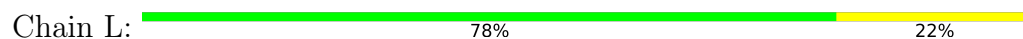
- Molecule 8: 50S ribosomal protein L4



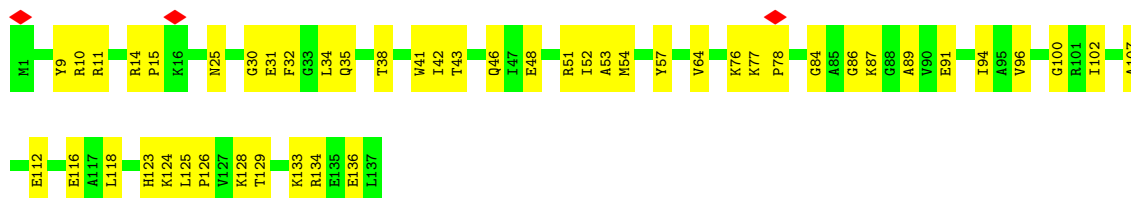
- Molecule 9: 50S ribosomal protein L13



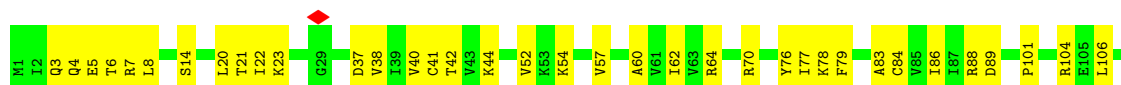
- Molecule 10: 50S ribosomal protein L15

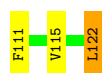


- Molecule 11: 50S ribosomal protein L16



- Molecule 12: 50S ribosomal protein L14





- Molecule 13: 50S ribosomal protein L18



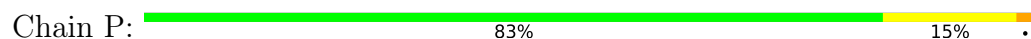
- Molecule 14: 50S ribosomal protein L19



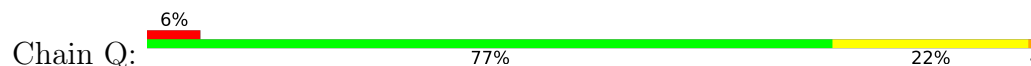
- Molecule 15: 50S ribosomal protein L20



- Molecule 16: 50S ribosomal protein L21

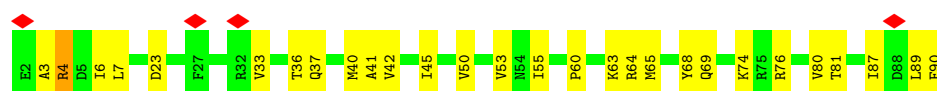


- Molecule 17: 50S ribosomal protein L22



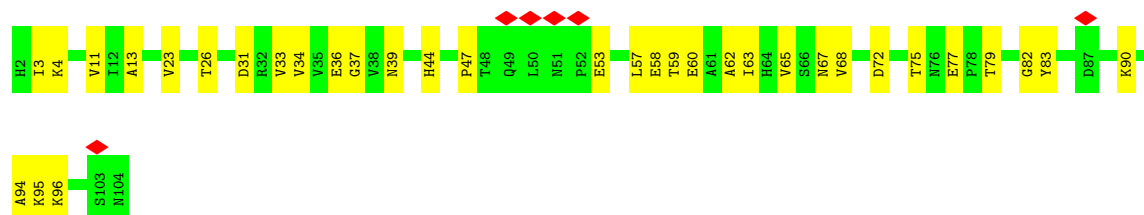
- Molecule 18: 50S ribosomal protein L23

Chain R:  69% 30%



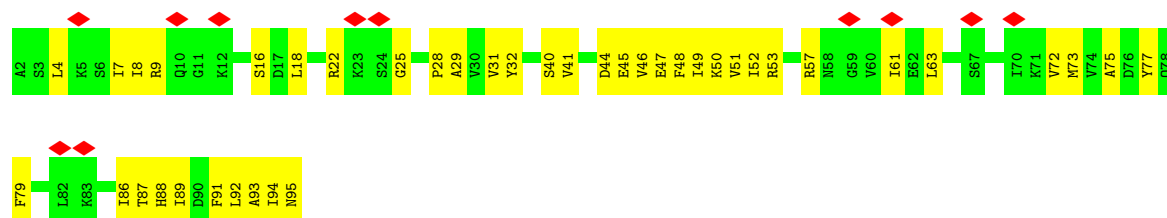
- Molecule 19: 50S ribosomal protein L24

Chain S:  67% 33%



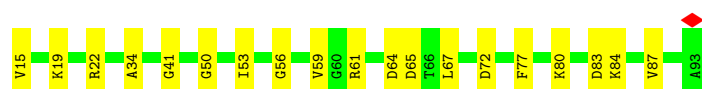
- Molecule 20: 50S ribosomal protein L25

Chain T:  56% 44%



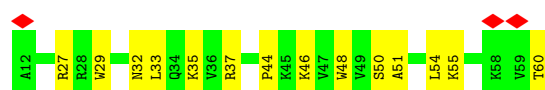
- Molecule 21: 50S ribosomal protein L27

Chain a:  76% 24%



- Molecule 22: 50S ribosomal protein L28

Chain V:  71% 29%

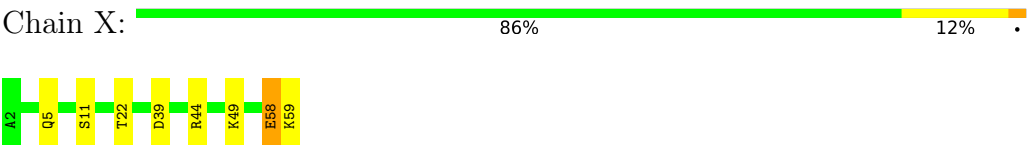


- Molecule 23: 50S ribosomal protein L29

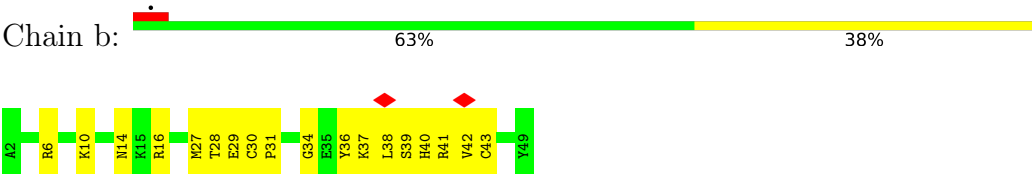
Chain W:  67% 33%



● Molecule 24: 50S ribosomal protein L30



● Molecule 25: 50S ribosomal protein L32



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	175844	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	47	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.029	Depositor
Minimum map value	-0.011	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.0026	Depositor
Map size ($\text{\AA}$)	281.42398, 281.42398, 281.42398	wwPDB
Map dimensions	328, 328, 328	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.8579999, 0.8579999, 0.8579999	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 2MA, 5MU

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	0.38	0/65753	0.50	3/102527 (0.0%)
2	B	0.22	0/2523	0.44	0/3920
3	1	0.33	0/395	0.87	2/530 (0.4%)
4	2	0.47	0/371	0.96	0/484
5	3	0.36	0/526	0.73	0/690
6	F	0.38	0/2129	0.73	1/2858 (0.0%)
7	D	0.40	0/1651	0.78	1/2215 (0.0%)
8	E	0.40	0/1595	0.73	1/2154 (0.0%)
9	H	0.42	0/1153	0.69	0/1553
10	L	0.38	0/1100	0.80	1/1467 (0.1%)
11	Y	0.30	0/1095	0.65	0/1472
12	G	0.43	0/925	0.74	0/1242
13	M	0.24	0/881	0.67	1/1180 (0.1%)
14	N	0.40	0/889	0.73	0/1192
15	O	0.48	0/954	0.81	0/1264
16	P	0.47	0/800	0.79	0/1070
17	Q	0.40	0/862	0.69	0/1161
18	R	0.33	0/723	0.65	1/966 (0.1%)
19	S	0.33	0/779	0.71	0/1043
20	T	0.26	0/730	0.65	0/981
21	a	0.34	0/603	0.57	0/802
22	V	0.28	0/384	0.64	0/515
23	W	0.29	0/542	0.67	0/722
24	X	0.35	0/451	0.62	0/606
25	b	0.38	0/366	0.91	0/489
All	All	0.38	0/88180	0.55	11/133103 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
3	1	0	1
7	D	0	2
8	E	0	1
9	H	0	1
All	All	0	5

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	1	12	CYS	CA-CB-SG	6.89	130.24	114.40
6	F	224	VAL	N-CA-C	-6.73	106.17	112.83
8	E	168	ARG	N-CA-C	-5.80	107.45	114.75
3	1	38	ARG	N-CA-C	-5.71	106.96	114.04
18	R	4	ARG	N-CA-C	-5.63	107.41	114.56
1	A	775	A	C2'-C3'-O3'	5.40	117.60	109.50
13	M	27	GLU	N-CA-C	-5.39	107.36	114.31
10	L	59	ARG	CB-CG-CD	5.20	123.27	111.30
1	A	1706	U	C2'-C3'-O3'	5.06	121.29	113.70
7	D	133	ARG	CB-CG-CD	5.01	122.83	111.30
1	A	2075	G	C2'-C3'-O3'	5.01	121.22	113.70

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	1	11	GLU	Peptide
7	D	53	PHE	Peptide
7	D	6	LEU	Peptide
8	E	12	THR	Peptide
9	H	58	ILE	Peptide

5.2 Too-close contacts ⓘ

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	58787	0	29564	1175	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	2260	0	1148	59	0
3	1	390	0	394	23	0
4	2	367	0	415	16	0
5	3	521	0	586	13	0
6	F	2094	0	2205	57	0
7	D	1627	0	1667	47	0
8	E	1572	0	1619	23	0
9	H	1132	0	1120	32	0
10	L	1086	0	1125	22	0
11	Y	1071	0	1123	39	0
12	G	918	0	981	36	0
13	M	872	0	893	33	0
14	N	878	0	923	34	0
15	O	942	0	1014	34	0
16	P	790	0	830	13	0
17	Q	854	0	914	20	0
18	R	715	0	748	23	0
19	S	770	0	809	32	0
20	T	722	0	766	32	0
21	a	597	0	604	15	0
22	V	379	0	400	10	0
23	W	541	0	563	18	0
24	X	449	0	491	5	0
25	b	360	0	358	25	0
All	All	80694	0	51260	1700	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 14.

All (1700) 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:2432:G:H21	1:A:2439:A:N6	1.39	1.21
1:A:2432:G:N2	1:A:2439:A:H62	1.44	1.14
1:A:2171:G:H21	1:A:2174:A:N6	1.50	1.09
1:A:2852:U:H1'	1:A:2853:U:H5'	1.38	1.05
1:A:307:A:N6	1:A:409:G:C6	2.26	1.04
1:A:959:C:H1'	1:A:960:C:H5'	1.41	1.02
1:A:2552:G:H21	1:A:2768:A:H2	1.08	1.00
1:A:2834:C:H1'	25:b:40:HIS:HB2	1.41	1.00
1:A:87:U:H3	1:A:95:A:H61	1.09	0.99

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:656:G:H21	1:A:660:A:H2	1.12	0.98
1:A:2724:G:N2	1:A:2738:A:N7	2.11	0.97
1:A:2109:A:N7	1:A:2264:G:N2	2.13	0.97
1:A:2724:G:H1	1:A:2738:A:N6	1.63	0.96
1:A:2855:A:H61	1:A:2902:A:H2	1.02	0.95
1:A:2769:G:H1	1:A:2789:U:H3	1.15	0.95
1:A:2675:G:H1	1:A:2700:G:H22	1.05	0.95
1:A:2494:C:HO2'	11:Y:123:HIS:HD1	1.15	0.94
13:M:90:LYS:HG3	13:M:91:GLU:H	1.33	0.94
1:A:1663:G:HO2'	4:2:2:VAL:N	1.65	0.94
1:A:2831:G:H1	1:A:2908:U:H3	0.96	0.93
1:A:1218:G:C6	1:A:1219:G:O6	2.21	0.93
20:T:72:VAL:HG21	20:T:91:PHE:HB3	1.51	0.92
1:A:2866:G:N2	1:A:2889:G:O6	2.02	0.91
1:A:2171:G:N2	1:A:2174:A:C6	2.38	0.91
1:A:919:G:N2	1:A:949:C:N3	2.18	0.91
1:A:2853:U:H4'	1:A:2854:A:H5'	1.53	0.90
1:A:2859:G:H22	1:A:2897:A:H2	1.14	0.90
1:A:2861:U:H3	1:A:2895:G:H1	1.04	0.90
11:Y:38:THR:HG23	11:Y:128:LYS:HE2	1.53	0.90
1:A:2706:A:H2	1:A:2756:G:H1	1.21	0.89
1:A:2727:G:H22	1:A:2735:G:H1	1.14	0.89
6:F:67:PHE:HE1	6:F:156:ARG:HD2	1.37	0.89
1:A:1705:G:H1	1:A:2026:C:H5	1.20	0.89
1:A:1459:A:H61	1:A:1631:G:H5'	1.36	0.89
1:A:1453:G:H4'	1:A:1455:U:H3	1.38	0.88
1:A:156:A:H61	1:A:172:U:H3	1.22	0.88
1:A:2818:A:N6	1:A:2826:U:O2	2.05	0.88
1:A:1052:A:N3	1:A:1053:A:N6	2.19	0.87
6:F:5:LYS:HD2	6:F:6:TYR:H	1.38	0.87
1:A:2171:G:N2	1:A:2174:A:N6	2.23	0.86
1:A:1179:C:N4	1:A:1182:G:OP2	2.09	0.86
12:G:104:ARG:HH12	14:N:34:ILE:HG12	1.40	0.86
1:A:1240:U:O2'	8:E:41:ARG:NH2	2.09	0.86
5:3:21:GLN:HB3	5:3:49:LEU:HD11	1.58	0.86
1:A:1781:C:H5	14:N:96:ARG:HH21	1.21	0.86
1:A:2111:C:N3	1:A:2262:G:N1	2.23	0.86
17:Q:51:LEU:HA	17:Q:105:ILE:HD11	1.58	0.85
1:A:1092:A:N7	1:A:1155:A:N6	2.25	0.84
1:A:1497:A:H4'	1:A:1498:U:H2'	1.59	0.84
1:A:2502:C:H42	1:A:2556:G:H1	1.23	0.84

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2684:A:H62	1:A:2691:G:H21	1.25	0.84
2:B:18:G:H1	2:B:61:C:H42	1.25	0.84
1:A:163:U:O4	1:A:2244:G:O2'	1.95	0.84
2:B:26:C:H2'	2:B:27:A:C8	2.12	0.84
1:A:1199:A:H5''	15:O:55:ARG:HH21	1.42	0.83
11:Y:43:THR:HG22	11:Y:94:ILE:HG22	1.61	0.83
1:A:1061:G:H22	1:A:1189:C:H5	1.25	0.83
1:A:577:A:OP1	1:A:604:G:N2	2.12	0.82
1:A:2712:G:H4'	12:G:76:TYR:HE2	1.44	0.82
18:R:53:VAL:HG22	18:R:80:VAL:HG12	1.61	0.82
1:A:2729:G:O6	1:A:2733:A:N6	2.10	0.82
1:A:1079:U:O2	1:A:1164:G:N2	2.11	0.82
19:S:39:ASN:HD22	19:S:63:ILE:HG22	1.45	0.81
1:A:2189:G:H21	1:A:2191:U:H3	1.25	0.81
1:A:273:A:N7	1:A:298:U:O2	2.13	0.81
1:A:1085:U:H3	1:A:1158:G:H22	1.25	0.81
1:A:1718:G:H1	1:A:2017:C:H5	1.24	0.81
1:A:2432:G:H21	1:A:2439:A:H62	0.81	0.81
1:A:2895:G:H1'	14:N:2:THR:HB	1.62	0.81
1:A:1675:G:H1	1:A:1725:G:HO2'	1.28	0.81
13:M:39:HIS:HD2	13:M:59:LYS:HB2	1.46	0.80
1:A:579:U:H5'	15:O:42:SER:HB2	1.63	0.80
1:A:1745:A:O2'	1:A:1793:C:OP1	2.00	0.80
7:D:129:GLY:HA2	7:D:170:PRO:HB3	1.61	0.80
1:A:1261:G:OP1	16:P:67:ARG:NH1	2.15	0.79
1:A:868:A:N6	1:A:879:U:O4	2.14	0.79
6:F:107:PRO:HD2	6:F:110:LEU:HD22	1.64	0.79
11:Y:30:GLY:O	11:Y:134:ARG:NH2	2.15	0.79
11:Y:77:LYS:HG3	11:Y:78:PRO:HD2	1.64	0.79
1:A:882:C:H5	1:A:986:G:H1	1.31	0.79
1:A:1741:G:C6	1:A:1742:A:H2'	2.18	0.79
1:A:927:G:N2	1:A:927:G:OP2	2.15	0.78
1:A:2866:G:H21	1:A:2889:G:H1	1.31	0.78
6:F:132:LEU:HD23	6:F:172:VAL:HB	1.65	0.78
1:A:250:G:OP2	1:A:252:C:N4	2.17	0.78
1:A:307:A:C6	1:A:409:G:C6	2.71	0.78
1:A:2675:G:H1	1:A:2700:G:N2	1.80	0.78
1:A:2672:G:H1'	1:A:2760:A:H4'	1.64	0.78
11:Y:35:GLN:HB3	11:Y:102:ILE:HD13	1.66	0.77
19:S:72:ASP:HB2	19:S:79:THR:HG21	1.65	0.77
1:A:1757:U:O2	1:A:1772:G:N2	2.16	0.77

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2711:U:H3'	1:A:2712:G:H21	1.48	0.77
1:A:2728:U:H3	1:A:2734:C:H42	1.30	0.77
1:A:944:G:H2'	1:A:945:A:C8	2.19	0.77
19:S:59:THR:HG22	19:S:60:GLU:H	1.48	0.77
1:A:2554:C:O2	1:A:2563:G:N1	2.15	0.77
25:b:10:LYS:O	25:b:14:ASN:ND2	2.14	0.77
14:N:92:GLY:HA2	14:N:115:ILE:HG12	1.66	0.77
1:A:2553:G:N2	1:A:2564:U:O2	2.18	0.76
1:A:1818:A:N6	1:A:1855:G:O2'	2.16	0.76
17:Q:2:GLU:OE2	17:Q:72:LYS:NZ	2.13	0.76
1:A:660:A:H8	8:E:182:ASN:HB3	1.48	0.76
11:Y:77:LYS:NZ	11:Y:86:GLY:O	2.19	0.76
13:M:19:ARG:NH2	13:M:47:ASP:OD2	2.19	0.76
1:A:2726:C:H2'	1:A:2727:G:C8	2.21	0.76
4:2:25:THR:HG23	4:2:28:GLY:H	1.50	0.76
1:A:2715:G:N2	1:A:2749:G:H1	1.84	0.76
22:V:33:LEU:HD12	22:V:48:TRP:HB3	1.68	0.76
1:A:161:A:H62	1:A:167:U:H3	1.33	0.76
1:A:80:G:O2'	1:A:389:A:N7	2.19	0.76
1:A:1741:G:O3'	1:A:2005:A:H4'	1.86	0.76
1:A:1798:C:N3	1:A:1799:G:N1	2.34	0.76
15:O:98:ILE:HD11	16:P:4:ILE:HD11	1.67	0.76
12:G:70:ARG:HG3	12:G:76:TYR:HE1	1.49	0.75
1:A:2686:G:N2	1:A:2689:A:OP2	2.19	0.75
1:A:1455:U:O4	1:A:1631:G:N1	2.20	0.74
1:A:1976:G:N2	1:A:1985:C:O2	2.16	0.74
1:A:928:C:N4	1:A:938:G:OP2	2.20	0.74
1:A:1742:A:H4'	1:A:1743:G:C8	2.21	0.74
7:D:2:THR:OG1	7:D:93:ASN:O	2.05	0.74
1:A:1063:U:O2'	1:A:1065:A:N7	2.19	0.74
1:A:2712:G:H4'	12:G:76:TYR:CE2	2.22	0.74
1:A:234:C:H3'	1:A:235:G:H8	1.52	0.74
8:E:17:ILE:HD11	8:E:200:LYS:HE3	1.68	0.74
1:A:1490:G:O2'	1:A:1491:C:OP2	2.04	0.74
1:A:2121:A:H2'	1:A:2122:A:C8	2.23	0.74
6:F:67:PHE:CE1	6:F:156:ARG:HD2	2.20	0.74
1:A:2727:G:N2	1:A:2735:G:H1	1.86	0.73
10:L:71:ARG:NH1	10:L:72:LYS:O	2.21	0.73
1:A:2727:G:N2	1:A:2735:G:H22	1.86	0.73
1:A:2720:A:H2	1:A:2744:G:H22	1.36	0.73
1:A:775:A:O2'	1:A:776:C:OP1	2.06	0.73

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:131:G:N2	1:A:148:U:O2	2.20	0.73
1:A:1799:G:N2	1:A:2007:G:H22	1.85	0.73
1:A:2490:C:H42	1:A:2515:A:H61	1.36	0.73
1:A:159:U:O4	1:A:160:G:N2	2.22	0.72
1:A:136:A:H2'	1:A:137:G:O4'	1.88	0.72
1:A:1737:U:N3	1:A:1857:C:O2'	2.20	0.72
11:Y:42:ILE:HA	11:Y:46:GLN:HE21	1.54	0.72
25:b:30:CYS:HB3	25:b:34:GLY:HA3	1.71	0.72
2:B:73:G:H3'	2:B:74:G:H8	1.51	0.72
1:A:722:A:O2'	1:A:2098:A:OP1	2.06	0.72
1:A:1336:G:H21	1:A:1685:A:H62	1.37	0.72
1:A:1465:G:O6	1:A:1624:C:N4	2.18	0.72
1:A:2147:G:N2	1:A:2205:C:N3	2.36	0.72
2:B:70:G:H21	2:B:101:A:H62	1.38	0.72
1:A:1963:A:OP2	1:A:1989:C:N4	2.15	0.72
1:A:319:G:H1'	1:A:324:A:H62	1.55	0.71
1:A:78:U:H3	1:A:107:G:H1	1.37	0.71
1:A:826:A:OP1	6:F:217:ARG:NH2	2.23	0.71
17:Q:11:ARG:NH1	17:Q:98:LYS:HD2	2.05	0.71
1:A:1218:G:H2'	1:A:1219:G:C8	2.25	0.71
1:A:2496:A:N6	1:A:2508:G:N2	2.37	0.71
1:A:2552:G:N2	1:A:2768:A:C2	2.53	0.71
1:A:572:C:OP2	1:A:2807:G:N1	2.22	0.71
1:A:1675:G:N1	1:A:1725:G:O2'	2.21	0.71
3:1:8:ALA:O	3:1:46:ARG:N	2.20	0.71
1:A:1734:A:H61	1:A:1741:G:H22	1.36	0.71
1:A:2673:C:O2'	1:A:2674:U:O5'	2.09	0.71
1:A:2657:G:O2'	1:A:2658:G:OP1	2.09	0.70
1:A:2712:G:C4'	12:G:76:TYR:HE2	2.04	0.70
20:T:4:LEU:HD21	20:T:51:VAL:HG21	1.72	0.70
12:G:104:ARG:NH1	14:N:34:ILE:HG12	2.04	0.70
1:A:1482:U:OP2	1:A:1600:A:N6	2.24	0.70
12:G:104:ARG:NH2	14:N:43:GLN:OE1	2.25	0.70
14:N:8:GLU:O	14:N:12:LYS:HB2	1.91	0.70
1:A:2831:G:O6	1:A:2908:U:O4	2.09	0.70
2:B:26:C:H2'	2:B:27:A:H8	1.56	0.69
1:A:283:G:H2'	1:A:284:C:H4'	1.74	0.69
1:A:944:G:H2'	1:A:945:A:H8	1.57	0.69
1:A:2819:C:N4	1:A:2824:G:O6	2.25	0.69
1:A:2024:A:H5''	7:D:138:ARG:HD3	1.72	0.69
1:A:2510:C:H3'	1:A:2511:G:H5''	1.75	0.69

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:7:LEU:HD21	18:R:42:VAL:HG12	1.74	0.69
10:L:73:GLU:O	10:L:107:SER:OG	2.08	0.69
1:A:675:G:OP1	5:3:23:LYS:NZ	2.16	0.69
1:A:2703:C:H42	1:A:2759:G:H1	1.41	0.69
11:Y:76:LYS:HG2	11:Y:77:LYS:H	1.57	0.69
1:A:2872:G:N2	1:A:2883:U:O4	2.19	0.69
17:Q:11:ARG:O	17:Q:11:ARG:HD3	1.93	0.69
1:A:176:A:H1'	1:A:177:G:N7	2.08	0.68
21:a:41:GLY:N	21:a:72:ASP:OD1	2.25	0.68
13:M:19:ARG:NH1	13:M:22:LEU:O	2.27	0.68
1:A:2829:A:N7	1:A:2911:A:N6	2.41	0.68
1:A:2673:C:H42	1:A:2702:A:H61	1.39	0.68
1:A:80:G:H1'	1:A:389:A:C6	2.29	0.68
1:A:2347:A:O2'	1:A:2360:A:N6	2.22	0.68
21:a:19:LYS:O	21:a:22:ARG:NH1	2.27	0.68
1:A:2186:G:H2'	1:A:2187:G:H8	1.59	0.68
1:A:2187:G:C2	1:A:2188:C:H1'	2.28	0.68
1:A:2820:U:O2'	1:A:2823:G:N7	2.27	0.68
12:G:42:THR:HG22	12:G:57:VAL:HG22	1.75	0.68
1:A:1732:U:O2'	1:A:1744:A:N7	2.22	0.67
1:A:1899:U:H1'	1:A:1900:G:N7	2.08	0.67
2:B:16:A:O2'	2:B:17:A:OP1	2.12	0.67
13:M:15:HIS:O	13:M:19:ARG:HB2	1.94	0.67
1:A:1210:U:H3	1:A:1222:A:H61	1.41	0.67
1:A:2675:G:H22	1:A:2700:G:N2	1.92	0.67
1:A:2111:C:N4	1:A:2262:G:O6	2.19	0.67
1:A:2667:G:H22	1:A:2802:A:H2	1.41	0.67
1:A:2894:C:O2	14:N:2:THR:N	2.28	0.67
8:E:32:VAL:HG12	8:E:109:ALA:HB2	1.77	0.67
13:M:15:HIS:O	13:M:19:ARG:CB	2.43	0.67
20:T:32:TYR:O	20:T:93:ALA:N	2.27	0.67
1:A:2161:A:H61	1:A:2184:G:H1'	1.59	0.67
1:A:2768:A:H62	1:A:2790:G:H21	1.43	0.67
13:M:14:ARG:HH12	13:M:17:ARG:HH11	1.43	0.67
1:A:946:A:H2'	1:A:947:U:C6	2.30	0.67
1:A:1156:G:H2'	1:A:1157:U:C6	2.30	0.67
1:A:1451:U:N3	1:A:1633:A:N7	2.43	0.67
17:Q:21:LEU:HD22	17:Q:74:ALA:HB1	1.76	0.67
1:A:2111:C:O2	1:A:2262:G:N2	2.16	0.66
1:A:2567:C:O2'	1:A:2767:A:N3	2.28	0.66
1:A:2684:A:H62	1:A:2691:G:N2	1.93	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1033:G:OP2	24:X:11:SER:OG	2.13	0.66
1:A:2226:A:H62	1:A:2251:G:H21	1.42	0.66
1:A:328:G:N2	1:A:399:U:O2'	2.28	0.66
1:A:2719:C:H2'	1:A:2720:A:C8	2.31	0.66
11:Y:53:ALA:HB2	11:Y:124:LYS:HE2	1.75	0.66
1:A:1387:C:H5	1:A:1418:G:H1	1.42	0.66
1:A:1215:U:O2'	1:A:1218:G:N1	2.28	0.66
1:A:2121:A:H2'	1:A:2122:A:H8	1.60	0.66
1:A:1959:A:C2	1:A:1960:G:H1'	2.31	0.66
9:H:58:ILE:HG22	9:H:126:TYR:HB2	1.78	0.66
1:A:940:U:H2'	1:A:941:A:C8	2.31	0.65
18:R:6:ILE:HD13	18:R:41:ALA:HB2	1.78	0.65
19:S:39:ASN:ND2	19:S:63:ILE:HG22	2.11	0.65
1:A:165:C:H3'	1:A:166:A:H8	1.60	0.65
1:A:162:A:H1'	1:A:2235:A:N3	2.11	0.65
1:A:766:G:H2'	1:A:767:A:H8	1.61	0.65
1:A:1287:U:H4'	15:O:4:VAL:HG21	1.79	0.65
1:A:139:U:H3'	1:A:140:A:C8	2.31	0.65
1:A:721:A:H8	1:A:2096:G:H21	1.43	0.65
1:A:2496:A:H62	1:A:2508:G:N2	1.95	0.65
24:X:5:GLN:HB2	24:X:59:LYS:HG3	1.78	0.65
3:1:12:CYS:SG	3:1:43:THR:OG1	2.54	0.65
20:T:18:LEU:O	20:T:22:ARG:HG3	1.97	0.65
1:A:765:U:HO2'	1:A:766:G:H8	1.43	0.64
1:A:1745:A:H3'	1:A:1746:G:H8	1.62	0.64
1:A:2697:G:C4	1:A:2698:A:H1'	2.32	0.64
1:A:227:G:N7	1:A:465:C:O2'	2.31	0.64
3:1:23:LYS:HG3	3:1:24:ARG:HD3	1.78	0.64
15:O:27:SER:HA	15:O:30:THR:HG22	1.79	0.64
1:A:2669:G:H1	1:A:2800:U:H3	1.45	0.64
1:A:2704:A:H2	1:A:2758:G:H22	1.45	0.64
6:F:63:ARG:HD2	6:F:84:ASP:OD2	1.98	0.64
1:A:160:G:O2'	1:A:169:G:N2	2.31	0.64
1:A:165:C:H3'	1:A:166:A:C8	2.33	0.64
1:A:302:A:H2'	1:A:303:G:C8	2.33	0.64
1:A:1482:U:H2'	1:A:1483:A:H8	1.63	0.64
1:A:2551:G:O3'	1:A:2790:G:O2'	2.15	0.64
1:A:2859:G:N2	1:A:2897:A:H2	1.91	0.64
6:F:95:VAL:HG12	6:F:101:LYS:HG2	1.80	0.64
1:A:829:U:O4	6:F:228:ASN:ND2	2.30	0.64
20:T:9:ARG:HE	20:T:40:SER:HB3	1.63	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:331:G:H1	1:A:395:U:H3	1.44	0.63
1:A:2646:U:H5''	7:D:165:LYS:HD3	1.80	0.63
1:A:80:G:H1'	1:A:389:A:C5	2.33	0.63
1:A:2234:C:H42	1:A:2244:G:H1	1.43	0.63
1:A:2513:G:O2'	1:A:2514:G:OP1	2.15	0.63
1:A:2552:G:H1'	1:A:2768:A:H61	1.61	0.63
8:E:8:LYS:HD2	8:E:14:SER:HB2	1.79	0.63
1:A:2850:G:C5	7:D:64:LYS:HE2	2.33	0.63
1:A:460:C:H2'	1:A:461:A:H8	1.63	0.63
1:A:1724:U:N3	1:A:1791:G:OP2	2.28	0.63
1:A:1954:A:H2'	1:A:1955:A:H8	1.64	0.63
1:A:2186:G:H2'	1:A:2187:G:C8	2.33	0.63
1:A:2677:C:H2'	1:A:2678:C:C6	2.32	0.63
1:A:2760:A:O2'	1:A:2793:G:O6	2.17	0.63
2:B:22:G:N7	2:B:54:U:H2'	2.13	0.63
11:Y:42:ILE:HA	11:Y:46:GLN:NE2	2.13	0.63
1:A:91:A:H3'	1:A:92:G:H8	1.64	0.63
1:A:2851:G:N2	1:A:2899:A:H61	1.96	0.63
23:W:37:LEU:HG	23:W:39:GLU:H	1.64	0.63
1:A:307:A:N6	1:A:409:G:O6	2.30	0.63
1:A:527:G:O2'	1:A:552:A:N6	2.31	0.63
1:A:2515:A:H2'	1:A:2516:G:H8	1.63	0.63
18:R:6:ILE:HG13	18:R:33:VAL:HG21	1.80	0.63
1:A:13:A:O2'	1:A:14:A:N7	2.32	0.62
1:A:2856:U:N3	1:A:2857:A:C6	2.66	0.62
6:F:10:THR:HG22	6:F:12:GLY:H	1.64	0.62
1:A:1933:G:H8	1:A:1956:G:H2'	1.63	0.62
1:A:2855:A:N6	1:A:2902:A:H2	1.86	0.62
6:F:143:ASN:OD1	6:F:152:GLY:HA3	1.99	0.62
19:S:79:THR:HG22	19:S:96:LYS:NZ	2.14	0.62
20:T:48:PHE:O	20:T:52:ILE:HG12	1.99	0.62
1:A:1352:C:O2'	1:A:1429:G:N3	2.32	0.62
3:1:9:CYS:HB2	3:1:45:HIS:CD2	2.34	0.62
1:A:776:C:O2'	1:A:777:C:OP2	2.16	0.62
1:A:1213:C:O2	1:A:1214:C:N4	2.30	0.62
1:A:1446:U:H2'	1:A:1447:A:C8	2.34	0.62
2:B:42:G:O4'	2:B:45:C:N4	2.31	0.62
1:A:2216:U:H2'	1:A:2217:G:C8	2.34	0.62
1:A:2699:U:H5'	1:A:2700:G:OP2	1.99	0.62
1:A:279:A:H62	1:A:281:A:H62	1.47	0.62
1:A:2769:G:O6	1:A:2789:U:O4	2.17	0.62

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:80:G:H2'	1:A:81:G:C8	2.35	0.62
1:A:213:C:O2'	1:A:1403:C:O2	2.18	0.62
1:A:307:A:C6	1:A:409:G:N1	2.68	0.62
1:A:2060:A:O2'	1:A:2062:G:OP2	2.16	0.62
5:3:48:ARG:HG2	5:3:49:LEU:H	1.64	0.62
10:L:76:ILE:HG23	10:L:112:LEU:HD12	1.80	0.62
14:N:76:PHE:CE2	14:N:83:ILE:HD11	2.35	0.62
1:A:82:G:H2'	1:A:83:G:C8	2.35	0.62
1:A:1804:U:H5	1:A:1814:A:N1	1.98	0.62
1:A:2254:A:H4'	6:F:263:LYS:HD2	1.82	0.62
1:A:1977:G:P	1:A:1977:G:H8	2.23	0.61
1:A:2873:C:H2'	1:A:2874:A:C8	2.35	0.61
1:A:1060:U:H3	1:A:1190:A:H61	1.47	0.61
1:A:2360:A:H5''	1:A:2362:A:H1'	1.82	0.61
1:A:279:A:N6	1:A:281:A:N7	2.49	0.61
1:A:1878:U:OP2	1:A:1915:G:N2	2.33	0.61
1:A:1904:A:H2'	1:A:1905:G:C8	2.35	0.61
1:A:2682:G:N1	1:A:2692:A:OP2	2.32	0.61
1:A:2866:G:N2	1:A:2889:G:C6	2.67	0.61
1:A:2856:U:O4	1:A:2857:A:N6	2.34	0.61
11:Y:51:ARG:HA	11:Y:54:MET:HE2	1.83	0.61
1:A:943:C:H2'	1:A:944:G:C8	2.36	0.61
1:A:1084:U:H2'	1:A:1085:U:O4'	2.00	0.61
1:A:1734:A:H61	1:A:1741:G:N2	1.99	0.61
1:A:1885:G:N2	1:A:1911:A:OP2	2.30	0.61
1:A:2182:U:H3'	1:A:2183:G:C8	2.35	0.61
1:A:1448:U:O4	1:A:1449:A:N6	2.33	0.61
2:B:74:G:N2	2:B:75:U:O4	2.32	0.61
1:A:943:C:H2'	1:A:944:G:H8	1.65	0.61
1:A:513:G:OP2	4:2:35:ARG:HD3	2.01	0.61
1:A:766:G:H2'	1:A:767:A:C8	2.36	0.61
1:A:1482:U:H2'	1:A:1483:A:C8	2.36	0.61
1:A:1921:C:O2'	1:A:1923:A:OP2	2.16	0.61
1:A:2851:G:H4'	1:A:2852:U:O5'	2.01	0.61
13:M:48:ASN:OD1	13:M:49:LYS:N	2.34	0.61
1:A:1061:G:H1	1:A:1189:C:H41	1.46	0.60
1:A:1155:A:H4'	1:A:1156:G:OP1	1.99	0.60
1:A:1906:C:H2'	1:A:1907:U:O4'	2.01	0.60
2:B:97:G:H2'	2:B:98:A:O4'	2.01	0.60
3:1:30:ILE:H	3:1:47:GLU:HG2	1.66	0.60
1:A:115:C:HO2'	1:A:125:A:H8	1.49	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:291:G:H2'	1:A:292:U:C6	2.36	0.60
1:A:1085:U:H2'	1:A:1086:G:C8	2.36	0.60
1:A:1177:A:N6	1:A:2052:C:O2'	2.35	0.60
1:A:1732:U:O2	1:A:1744:A:H8	1.84	0.60
1:A:2259:C:OP2	22:V:27:ARG:NH2	2.32	0.60
1:A:2857:A:N1	1:A:2901:U:H5	1.98	0.60
2:B:18:G:H1	2:B:61:C:N4	1.97	0.60
9:H:7:ALA:O	9:H:9:GLU:N	2.35	0.60
1:A:276:C:H3'	1:A:277:C:H5''	1.82	0.60
3:1:6:THR:O	3:1:48:THR:OG1	2.16	0.60
1:A:684:U:H2'	1:A:685:C:C6	2.36	0.60
1:A:2807:G:H4'	1:A:2808:A:O5'	2.01	0.60
14:N:59:GLU:HG2	14:N:78:LEU:HD22	1.84	0.60
1:A:393:G:H2'	1:A:394:U:C6	2.36	0.60
1:A:2715:G:N2	1:A:2749:G:N1	2.48	0.60
1:A:353:A:O2'	1:A:354:A:H2'	2.01	0.60
1:A:389:A:H3'	1:A:390:A:C8	2.37	0.60
1:A:512:A:OP1	4:2:35:ARG:NH1	2.33	0.60
1:A:1757:U:H3	1:A:1772:G:H1	1.48	0.60
19:S:57:LEU:HD12	19:S:58:GLU:H	1.65	0.60
1:A:827:A:C2	6:F:225:MET:HG2	2.37	0.60
1:A:2343:U:H2'	1:A:2344:C:O4'	2.02	0.60
18:R:64:ARG:NH2	18:R:69:GLN:HA	2.17	0.60
25:b:30:CYS:HA	25:b:37:LYS:HZ2	1.66	0.60
1:A:1818:A:H61	1:A:1855:G:HO2'	1.44	0.60
1:A:2896:A:H2'	1:A:2897:A:C8	2.37	0.60
9:H:58:ILE:HG13	9:H:58:ILE:O	2.01	0.60
1:A:274:A:H62	1:A:297:G:H21	1.50	0.60
1:A:366:G:H2'	8:E:169:ASN:OD1	2.00	0.60
1:A:2189:G:N2	1:A:2191:U:H3	1.98	0.60
1:A:218:G:H4'	1:A:219:A:H4'	1.82	0.60
1:A:774:G:H3'	1:A:774:G:N3	2.17	0.60
1:A:1904:A:H2'	1:A:1905:G:H8	1.66	0.60
1:A:1336:G:N2	1:A:1685:A:H62	2.00	0.59
7:D:25:VAL:HG21	7:D:196:LEU:HB3	1.82	0.59
8:E:127:ASP:OD1	8:E:128:ALA:N	2.34	0.59
13:M:90:LYS:HG3	13:M:91:GLU:N	2.12	0.59
23:W:11:THR:HA	23:W:14:ILE:HD12	1.84	0.59
1:A:75:G:OP1	23:W:44:ARG:NH1	2.34	0.59
3:1:23:LYS:HE2	3:1:24:ARG:HH21	1.66	0.59
7:D:88:ILE:O	7:D:89:ARG:HD3	2.02	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:b:28:THR:O	25:b:36:TYR:HA	2.01	0.59
15:O:30:THR:HG23	15:O:31:LEU:HG	1.83	0.59
12:G:8:LEU:HG	12:G:84:CYS:HB2	1.85	0.59
1:A:2162:A:H62	1:A:2183:G:H21	1.51	0.59
1:A:2715:G:H21	1:A:2749:G:H1	1.48	0.59
12:G:22:ILE:HB	12:G:40:VAL:HG13	1.84	0.59
1:A:1466:G:H1	1:A:1623:U:H3	1.50	0.59
10:L:112:LEU:HD23	10:L:129:SER:HB3	1.83	0.59
1:A:2171:G:O6	1:A:2173:U:H1'	2.01	0.59
13:M:30:ARG:NH2	13:M:45:ILE:HD11	2.18	0.59
1:A:1741:G:H2'	1:A:1742:A:H5'	1.85	0.59
1:A:2374:C:O2'	3:1:17:TYR:OH	2.20	0.59
1:A:2553:G:O2'	1:A:2554:C:OP1	2.18	0.59
2:B:72:U:C2	2:B:73:G:C8	2.91	0.59
9:H:58:ILE:HD13	9:H:131:HIS:HD2	1.67	0.59
1:A:1599:G:H2'	1:A:1600:A:O4'	2.03	0.59
3:1:16:ASN:OD1	3:1:17:TYR:N	2.36	0.59
1:A:157:U:H2'	1:A:158:G:C8	2.38	0.59
1:A:1815:C:H5''	6:F:224:VAL:HG11	1.84	0.59
1:A:660:A:C8	8:E:182:ASN:HB3	2.33	0.58
1:A:1075:G:H2'	1:A:1076:A:C8	2.38	0.58
1:A:1979:A:H2	1:A:1981:G:H3'	1.68	0.58
23:W:12:SER:HA	23:W:15:GLU:HG3	1.85	0.58
1:A:2606:C:H1'	7:D:147:PHE:CD1	2.39	0.58
12:G:70:ARG:HG3	12:G:76:TYR:CE1	2.34	0.58
19:S:59:THR:HG22	19:S:60:GLU:N	2.18	0.58
20:T:44:ASP:OD1	20:T:45:GLU:N	2.36	0.58
1:A:572:C:O2'	1:A:573:A:OP2	2.21	0.58
1:A:1676:A:N1	1:A:1726:A:H4'	2.17	0.58
1:A:2302:C:O2'	11:Y:84:GLY:O	2.17	0.58
1:A:2496:A:N6	1:A:2508:G:C2	2.71	0.58
18:R:64:ARG:HH22	18:R:69:GLN:HA	1.68	0.58
1:A:2629:A:O2'	1:A:2630:G:OP2	2.19	0.58
1:A:2796:C:H2'	1:A:2797:C:O4'	2.02	0.58
7:D:52:GLY:HA3	7:D:85:LYS:HG3	1.85	0.58
1:A:1854:U:O2'	1:A:1997:A:N3	2.36	0.58
1:A:2256:U:H2'	1:A:2257:G:H8	1.69	0.58
7:D:215:ILE:HG13	7:D:216:LYS:HG2	1.86	0.58
13:M:29:PRO:HD2	13:M:92:ILE:HG22	1.85	0.58
25:b:27:MET:N	25:b:37:LYS:O	2.37	0.58
1:A:1494:G:H22	1:A:1504:U:H3	1.51	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1798:C:N4	1:A:1799:G:O6	2.36	0.58
1:A:2727:G:H22	1:A:2735:G:H22	1.49	0.58
1:A:458:A:H3'	1:A:459:C:H6	1.69	0.58
1:A:2253:C:H3'	1:A:2254:A:C8	2.38	0.58
1:A:2515:A:H2'	1:A:2516:G:C8	2.39	0.58
1:A:2900:C:O2'	1:A:2901:U:OP1	2.22	0.58
13:M:102:HIS:HA	13:M:106:LYS:HD2	1.84	0.58
1:A:418:G:N7	22:V:55:LYS:HE2	2.18	0.58
1:A:1075:G:OP1	11:Y:123:HIS:NE2	2.37	0.58
18:R:55:ILE:HD12	18:R:76:ARG:HH11	1.68	0.58
1:A:2499:G:H2'	1:A:2502:C:H41	1.68	0.58
1:A:2727:G:H22	1:A:2735:G:N2	2.02	0.58
1:A:1075:G:H2'	1:A:1076:A:H8	1.68	0.58
1:A:1238:U:H1'	15:O:4:VAL:HG12	1.86	0.58
1:A:2564:U:H2'	1:A:2565:C:H6	1.69	0.58
2:B:88:G:H2'	2:B:89:U:H6	1.69	0.58
1:A:6:A:H61	1:A:2915:C:H42	1.52	0.57
1:A:1474:C:H2'	1:A:1475:A:C8	2.38	0.57
1:A:2402:G:N2	1:A:2405:A:OP2	2.36	0.57
1:A:2906:G:H1'	25:b:31:PRO:HG3	1.86	0.57
15:O:90:ILE:HG22	15:O:91:ASN:H	1.67	0.57
1:A:98:U:O2'	1:A:99:U:H5'	2.05	0.57
1:A:2432:G:N2	1:A:2439:A:N6	2.19	0.57
1:A:2788:A:H2'	1:A:2789:U:O4'	2.04	0.57
6:F:108:LYS:NZ	6:F:198:LEU:HD11	2.18	0.57
1:A:60:U:O2'	1:A:61:A:O5'	2.19	0.57
1:A:86:C:H4'	1:A:103:U:H1'	1.85	0.57
1:A:302:A:H2'	1:A:303:G:H8	1.69	0.57
1:A:1731:G:N2	1:A:1745:A:OP2	2.37	0.57
1:A:1823:U:H2'	1:A:1824:C:C6	2.39	0.57
1:A:1980:A:O2'	1:A:1981:G:O4'	2.22	0.57
1:A:1907:U:H2'	1:A:1908:A:C8	2.39	0.57
1:A:2774:G:N2	1:A:2783:U:OP1	2.31	0.57
19:S:13:ALA:HB3	19:S:67:ASN:OD1	2.03	0.57
1:A:1964:A:H1'	1:A:1966:5MU:C4	2.38	0.57
1:A:1977:G:C8	1:A:1977:G:OP2	2.58	0.57
1:A:2715:G:N2	1:A:2749:G:C6	2.69	0.57
6:F:5:LYS:HD2	6:F:6:TYR:N	2.16	0.57
1:A:1477:U:H2'	1:A:1478:A:C8	2.40	0.57
1:A:2552:G:N3	1:A:2768:A:N1	2.53	0.57
8:E:66:LYS:HE3	8:E:68:LYS:O	2.04	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:60:PRO:HG3	18:R:74:LYS:HB3	1.86	0.57
20:T:49:ILE:HG22	20:T:53:ARG:HD2	1.86	0.57
1:A:276:C:O2	1:A:306:C:H5'	2.05	0.57
1:A:434:G:O2'	1:A:435:A:O5'	2.15	0.57
1:A:2564:U:H2'	1:A:2565:C:C6	2.40	0.57
1:A:2653:C:H42	1:A:2805:A:H61	1.51	0.57
6:F:143:ASN:HB3	6:F:191:THR:HG22	1.86	0.57
5:3:21:GLN:HG2	5:3:49:LEU:HD21	1.84	0.57
1:A:1732:U:H3	1:A:1744:A:H5''	1.70	0.57
1:A:2144:A:O2'	1:A:2174:A:N3	2.37	0.57
2:B:64:A:H1'	2:B:66:C:H41	1.70	0.57
3:1:39:LEU:HB2	3:1:41:LYS:HG2	1.86	0.57
8:E:49:HIS:HD2	8:E:92:PRO:CB	2.17	0.57
1:A:972:A:H3'	1:A:972:A:N3	2.20	0.57
1:A:1935:C:H2'	1:A:1936:C:O4'	2.05	0.57
13:M:30:ARG:O	13:M:44:ILE:HG13	2.04	0.57
25:b:28:THR:O	25:b:37:LYS:HG2	2.04	0.57
2:B:27:A:H2'	2:B:28:C:C6	2.40	0.56
9:H:94:ARG:HB2	9:H:101:LEU:HD22	1.86	0.56
1:A:1453:G:H4'	1:A:1455:U:N3	2.16	0.56
7:D:99:TYR:HA	7:D:103:GLN:OE1	2.05	0.56
17:Q:72:LYS:HB2	17:Q:108:SER:HB2	1.87	0.56
1:A:631:U:H2'	1:A:632:U:C6	2.40	0.56
1:A:775:A:HO2'	1:A:776:C:P	2.27	0.56
1:A:858:U:H2'	1:A:859:C:C6	2.40	0.56
1:A:959:C:O2'	1:A:960:C:OP2	2.16	0.56
1:A:1051:C:H5''	9:H:38:ARG:NH1	2.21	0.56
1:A:1608:C:H2'	1:A:1609:U:C6	2.41	0.56
2:B:88:G:H2'	2:B:89:U:C6	2.40	0.56
3:1:29:ARG:HB3	3:1:47:GLU:HB3	1.88	0.56
1:A:139:U:H3'	1:A:140:A:H8	1.70	0.56
1:A:1213:C:H2'	1:A:1214:C:H5	1.70	0.56
1:A:1816:A:OP2	6:F:221:ARG:NH2	2.37	0.56
1:A:2169:G:H22	1:A:2176:C:H42	1.53	0.56
1:A:1680:U:H2'	1:A:1681:U:C6	2.41	0.56
1:A:632:U:H2'	1:A:633:A:C8	2.41	0.56
1:A:1058:U:O4	1:A:1059:A:N6	2.39	0.56
1:A:1079:U:O2	1:A:1164:G:C2	2.59	0.56
1:A:2766:U:H3	1:A:2767:A:H62	1.54	0.56
1:A:316:G:H3'	1:A:317:G:H8	1.71	0.56
1:A:1086:G:O6	1:A:1158:G:N2	2.39	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:8:U:H2'	1:A:9:U:O4'	2.06	0.56
9:H:12:ILE:HD11	9:H:14:ARG:CZ	2.36	0.56
1:A:841:C:H5''	8:E:62:ARG:HH12	1.71	0.56
1:A:460:C:H2'	1:A:461:A:C8	2.41	0.55
1:A:1986:G:H1'	1:A:1987:A:C8	2.41	0.55
1:A:2565:C:H2'	1:A:2566:C:C6	2.41	0.55
12:G:44:LYS:O	12:G:54:LYS:NZ	2.37	0.55
1:A:910:C:H5	1:A:954:A:H62	1.53	0.55
1:A:1003:A:H2'	1:A:1004:A:C8	2.40	0.55
1:A:1892:U:N3	1:A:1893:A:H1'	2.21	0.55
3:1:22:ASN:OD1	3:1:24:ARG:N	2.39	0.55
8:E:28:PRO:HA	8:E:112:SER:HB2	1.88	0.55
25:b:41:ARG:CZ	25:b:43:CYS:HA	2.37	0.55
1:A:1178:C:H41	1:A:2054:G:H4'	1.70	0.55
3:1:9:CYS:SG	3:1:43:THR:OG1	2.62	0.55
1:A:941:A:H2'	1:A:942:C:O4'	2.06	0.55
13:M:14:ARG:O	13:M:18:VAL:HG22	2.06	0.55
1:A:583:A:N6	1:A:598:G:O2'	2.39	0.55
1:A:1870:C:H5''	1:A:1922:C:O2'	2.07	0.55
1:A:2282:G:H1	1:A:2302:C:H42	1.54	0.55
1:A:10:A:H2'	1:A:11:U:C2	2.42	0.55
1:A:1929:C:H5'	6:F:241:ILE:HG12	1.89	0.55
1:A:2560:U:H3'	1:A:2561:C:H5''	1.87	0.55
1:A:529:A:O4'	19:S:44:HIS:NE2	2.40	0.55
1:A:2818:A:N7	1:A:2827:A:N6	2.53	0.55
1:A:2853:U:H1'	1:A:2854:A:C8	2.42	0.55
1:A:2862:C:H41	1:A:2894:C:H42	1.53	0.55
8:E:49:HIS:HD2	8:E:92:PRO:HB2	1.72	0.55
10:L:117:LEU:HG	10:L:119:LYS:H	1.72	0.55
11:Y:34:LEU:HD12	11:Y:118:LEU:HB3	1.87	0.55
12:G:64:ARG:HB2	12:G:79:PHE:CG	2.42	0.55
14:N:76:PHE:CD2	14:N:83:ILE:HD11	2.41	0.55
1:A:1486:C:H2'	1:A:1487:G:N7	2.22	0.55
1:A:1973:U:H2'	1:A:1974:C:C6	2.42	0.55
15:O:91:ASN:HB2	16:P:11:GLN:OE1	2.06	0.55
19:S:47:PRO:HA	19:S:53:GLU:HA	1.89	0.55
1:A:234:C:H3'	1:A:235:G:C8	2.39	0.55
1:A:1210:U:HO2'	1:A:1211:G:P	2.30	0.55
1:A:1957:G:O2'	1:A:1958:U:OP2	2.25	0.55
1:A:1982:U:O2'	1:A:1983:U:OP2	2.22	0.55
1:A:2830:A:H61	1:A:2909:C:H42	1.55	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:G:76:TYR:O	14:N:74:ARG:HD2	2.07	0.55
12:G:78:LYS:HB2	14:N:73:GLU:HB2	1.88	0.55
1:A:291:G:H2'	1:A:292:U:N1	2.22	0.55
1:A:353:A:O2'	1:A:354:A:O5'	2.23	0.55
1:A:1698:A:N6	1:A:2076:A:OP1	2.37	0.55
7:D:107:VAL:HG11	7:D:193:LYS:HA	1.89	0.55
9:H:58:ILE:HD13	9:H:131:HIS:CD2	2.42	0.55
1:A:2905:C:N3	25:b:31:PRO:HG2	2.22	0.54
1:A:124:A:OP2	4:2:20:ARG:NE	2.39	0.54
1:A:968:A:H2'	1:A:969:A:C8	2.42	0.54
1:A:1637:A:H2'	1:A:1638:G:O4'	2.06	0.54
1:A:2235:A:H2'	1:A:2236:C:C6	2.43	0.54
6:F:137:VAL:HG13	6:F:167:LYS:HE3	1.88	0.54
1:A:1089:C:H4'	1:A:1091:G:H1'	1.89	0.54
1:A:2696:G:H2'	1:A:2697:G:O4'	2.08	0.54
1:A:33:U:O4	1:A:492:G:O2'	2.22	0.54
22:V:51:ALA:HA	22:V:54:LEU:HG	1.89	0.54
1:A:1737:U:H3'	1:A:1738:C:C6	2.42	0.54
1:A:1977:G:H8	1:A:1977:G:OP2	1.90	0.54
6:F:17:THR:HB	6:F:204:ASN:H	1.72	0.54
1:A:115:C:O2'	1:A:125:A:C8	2.59	0.54
1:A:280:C:O2'	1:A:281:A:H5''	2.08	0.54
1:A:421:C:H2'	1:A:422:G:H8	1.73	0.54
1:A:459:C:H2'	1:A:460:C:C5	2.41	0.54
1:A:1891:U:N3	1:A:1892:U:O4	2.40	0.54
1:A:2126:C:H2'	1:A:2127:G:C8	2.42	0.54
1:A:2706:A:H2	1:A:2756:G:N1	1.99	0.54
1:A:2801:C:H2'	1:A:2802:A:C8	2.43	0.54
16:P:14:VAL:HA	16:P:18:GLN:HE21	1.71	0.54
1:A:105:C:H2'	1:A:106:A:H8	1.72	0.54
1:A:576:U:H5	1:A:2045:A:N1	2.06	0.54
1:A:702:U:H2'	1:A:703:A:C8	2.42	0.54
1:A:924:G:H1	1:A:943:C:H42	1.56	0.54
1:A:2046:U:OP2	25:b:6:ARG:NH1	2.38	0.54
1:A:2677:C:H42	1:A:2698:A:N6	2.06	0.54
1:A:1455:U:H3'	1:A:1629:U:OP2	2.08	0.54
1:A:1986:G:H1'	1:A:1987:A:H8	1.73	0.54
1:A:2155:C:H2'	1:A:2156:C:C6	2.42	0.54
13:M:23:SER:HA	13:M:30:ARG:HD3	1.90	0.54
14:N:84:GLU:OE1	14:N:85:LYS:HG2	2.07	0.54
1:A:115:C:O2'	1:A:125:A:H8	1.91	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:159:U:H3	1:A:169:G:H1	1.54	0.54
1:A:2489:U:H3	1:A:2516:G:H1	1.55	0.54
5:3:24:ARG:HD2	10:L:61:LEU:HD21	1.89	0.54
1:A:620:G:O2'	1:A:1292:A:OP1	2.26	0.54
1:A:1151:G:H2'	1:A:1152:U:H6	1.72	0.54
1:A:1404:A:O3'	4:2:26:LYS:NZ	2.32	0.54
1:A:2559:G:H2'	1:A:2560:U:C6	2.42	0.54
1:A:2852:U:C1'	1:A:2853:U:H5'	2.27	0.54
2:B:6:U:H2'	2:B:7:G:C8	2.43	0.54
17:Q:14:PRO:HG3	17:Q:101:SER:HB3	1.88	0.54
1:A:1676:A:H61	1:A:1726:A:H4'	1.73	0.53
1:A:1932:C:N4	1:A:1996:A:OP1	2.33	0.53
1:A:2192:G:H3'	1:A:2193:G:H8	1.73	0.53
12:G:7:ARG:HE	12:G:20:LEU:HD12	1.72	0.53
15:O:88:ILE:HG22	15:O:90:ILE:HG12	1.90	0.53
1:A:1954:A:H2'	1:A:1955:A:C8	2.43	0.53
23:W:27:ASN:O	23:W:31:GLN:HG3	2.09	0.53
1:A:181:G:H2'	1:A:182:C:O4'	2.09	0.53
1:A:1966:5MU:H1'	1:A:2619:G:H4'	1.91	0.53
1:A:2393:A:H2'	1:A:2394:G:O4'	2.08	0.53
6:F:108:LYS:HZ2	6:F:198:LEU:HD11	1.71	0.53
11:Y:125:LEU:HD12	11:Y:126:PRO:HD2	1.90	0.53
21:a:53:ILE:HG21	21:a:87:VAL:HG23	1.88	0.53
1:A:530:C:H2'	1:A:531:C:C6	2.44	0.53
1:A:1699:A:H1'	7:D:127:PHE:CE2	2.44	0.53
1:A:1806:U:H5	1:A:1811:A:N7	2.07	0.53
1:A:2155:C:H2'	1:A:2156:C:H6	1.74	0.53
1:A:2864:A:H61	1:A:2891:U:H3	1.54	0.53
7:D:107:VAL:HG22	7:D:195:ILE:HD11	1.90	0.53
20:T:22:ARG:HH12	20:T:87:THR:HA	1.73	0.53
23:W:62:ILE:O	23:W:65:SER:OG	2.25	0.53
1:A:1669:C:H2'	1:A:1670:A:C8	2.44	0.53
1:A:2179:A:H2'	1:A:2180:C:C2	2.43	0.53
1:A:2862:C:N3	14:N:2:THR:OG1	2.42	0.53
2:B:73:G:H3'	2:B:74:G:C8	2.38	0.53
1:A:80:G:H2'	1:A:81:G:H8	1.72	0.53
1:A:393:G:H2'	1:A:394:U:H6	1.74	0.53
1:A:2112:C:H2'	1:A:2113:U:O4'	2.09	0.53
1:A:2367:A:H2'	1:A:2368:G:H8	1.73	0.53
11:Y:76:LYS:HB3	11:Y:91:GLU:HG3	1.89	0.53
1:A:545:G:N1	1:A:548:A:OP2	2.40	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2509:A:OP2	1:A:2510:C:N4	2.38	0.53
1:A:69:C:H4'	1:A:75:G:N7	2.25	0.53
1:A:281:A:H4'	1:A:282:A:H5'	1.91	0.53
1:A:287:G:H2'	1:A:288:C:C6	2.44	0.53
1:A:2485:U:O2'	1:A:2487:U:O4	2.22	0.53
21:a:56:GLY:H	21:a:59:VAL:HB	1.74	0.53
1:A:719:G:O2'	8:E:74:ARG:HD2	2.09	0.52
1:A:1169:G:H3'	1:A:1170:A:C8	2.44	0.52
2:B:38:U:N3	2:B:42:G:OP2	2.42	0.52
19:S:83:TYR:CE1	19:S:90:LYS:HE3	2.45	0.52
1:A:1095:A:N1	1:A:1152:U:N3	2.53	0.52
1:A:1480:G:H2'	1:A:1481:A:C8	2.43	0.52
3:1:7:LEU:HB3	3:1:45:HIS:HB3	1.91	0.52
1:A:1626:A:H3'	1:A:1627:G:H8	1.74	0.52
1:A:1731:G:N1	1:A:1745:A:OP2	2.43	0.52
1:A:1884:G:O2'	1:A:1912:A:N6	2.43	0.52
5:3:9:GLY:O	5:3:13:ARG:NH1	2.42	0.52
6:F:153:GLN:C	6:F:154:ILE:HD13	2.35	0.52
6:F:217:ARG:HG3	6:F:218:PRO:HD2	1.90	0.52
13:M:96:ARG:NH2	13:M:99:TYR:O	2.42	0.52
1:A:901:G:H2'	1:A:902:A:C8	2.45	0.52
1:A:1506:C:H2'	1:A:1507:A:C4	2.44	0.52
1:A:2857:A:C2	1:A:2901:U:H5	2.27	0.52
1:A:2873:C:H42	1:A:2882:A:H61	1.58	0.52
2:B:25:A:H3'	2:B:26:C:C6	2.45	0.52
1:A:1700:C:H5'	7:D:149:ARG:HB2	1.91	0.52
1:A:1978:U:C2	1:A:1984:C:N3	2.78	0.52
1:A:2162:A:H62	1:A:2183:G:N2	2.07	0.52
1:A:2716:U:OP1	1:A:2740:A:N6	2.40	0.52
1:A:2728:U:H2'	1:A:2729:G:C8	2.45	0.52
11:Y:48:GLU:O	11:Y:52:ILE:HG12	2.10	0.52
12:G:77:ILE:HG13	12:G:77:ILE:O	2.10	0.52
13:M:19:ARG:O	13:M:19:ARG:HD3	2.09	0.52
13:M:90:LYS:CG	13:M:91:GLU:H	2.15	0.52
1:A:1731:G:H2'	1:A:1732:U:O4'	2.10	0.52
1:A:1739:G:H2'	1:A:1740:G:O4'	2.10	0.52
11:Y:76:LYS:CB	11:Y:91:GLU:HG3	2.39	0.52
1:A:572:C:H4'	1:A:573:A:O5'	2.10	0.52
1:A:951:G:O2'	1:A:952:A:OP1	2.22	0.52
1:A:1199:A:H5''	15:O:55:ARG:NH2	2.20	0.52
1:A:1734:A:H2'	1:A:1735:C:O4'	2.09	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2253:C:H3'	1:A:2254:A:H8	1.73	0.52
1:A:2499:G:N2	1:A:2506:U:O4	2.42	0.52
1:A:2884:G:H2'	1:A:2886:G:H2'	1.91	0.52
1:A:2907:A:H1'	25:b:29:GLU:H	1.75	0.52
19:S:26:THR:HA	19:S:33:VAL:HG12	1.92	0.52
19:S:59:THR:CG2	19:S:60:GLU:H	2.18	0.52
19:S:79:THR:HG22	19:S:96:LYS:HZ1	1.74	0.52
20:T:25:GLY:O	20:T:45:GLU:HG2	2.09	0.52
1:A:757:G:N2	1:A:765:U:H3	2.08	0.52
1:A:864:A:N7	1:A:1227:U:H5	2.07	0.52
1:A:1628:A:H2'	1:A:1629:U:C6	2.45	0.52
1:A:1710:G:O2'	12:G:6:THR:HG22	2.10	0.52
1:A:2171:G:N2	1:A:2174:A:C5	2.77	0.52
17:Q:14:PRO:O	17:Q:18:ARG:HG3	2.10	0.52
1:A:422:G:H2'	1:A:423:A:C8	2.45	0.52
1:A:1463:A:H5''	1:A:1465:G:N7	2.25	0.52
9:H:14:ARG:NH1	9:H:50:ASP:O	2.43	0.52
1:A:452:G:H2'	1:A:453:G:O4'	2.09	0.51
1:A:830:U:H2'	1:A:831:C:C6	2.45	0.51
1:A:1736:U:H2'	1:A:1738:C:N3	2.25	0.51
1:A:1873:G:H2'	1:A:1874:A:O4'	2.11	0.51
1:A:2091:C:H2'	1:A:2092:C:C6	2.45	0.51
1:A:2325:A:H3'	1:A:2326:G:C8	2.45	0.51
1:A:2866:G:O5'	1:A:2866:G:H8	1.93	0.51
2:B:16:A:HO2'	2:B:17:A:P	2.32	0.51
10:L:83:ASN:ND2	10:L:117:LEU:O	2.43	0.51
12:G:3:GLN:O	12:G:21:THR:HG21	2.11	0.51
1:A:908:A:H2'	1:A:909:G:H8	1.75	0.51
1:A:1699:A:H1'	7:D:127:PHE:HE2	1.74	0.51
1:A:1880:A:H2'	1:A:1881:A:O4'	2.10	0.51
1:A:2133:G:H2'	1:A:2134:C:C5	2.45	0.51
1:A:11:U:N3	1:A:2655:U:OP1	2.43	0.51
1:A:1761:G:H2'	1:A:1763:U:N3	2.25	0.51
1:A:1798:C:N3	1:A:1799:G:C6	2.78	0.51
12:G:111:PHE:O	12:G:115:VAL:HG23	2.11	0.51
1:A:435:A:H2	1:A:437:A:C8	2.29	0.51
1:A:2081:A:H5'	1:A:2082:C:H4'	1.93	0.51
1:A:2180:C:H2'	1:A:2181:G:C8	2.46	0.51
1:A:2851:G:H21	1:A:2899:A:H61	1.56	0.51
12:G:14:SER:HB3	12:G:52:VAL:HG22	1.92	0.51
1:A:28:A:H2	15:O:11:ARG:HH12	1.58	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:60:U:HO2'	1:A:61:A:P	2.33	0.51
1:A:1505:G:H4'	1:A:2730:C:O2'	2.10	0.51
1:A:1823:U:H2'	1:A:1824:C:H6	1.75	0.51
1:A:2728:U:H3	1:A:2734:C:N4	2.05	0.51
2:B:73:G:H2'	2:B:74:G:H5'	1.93	0.51
9:H:66:THR:O	9:H:69:LYS:HG2	2.11	0.51
22:V:37:ARG:HB3	22:V:46:LYS:HG2	1.92	0.51
7:D:8:ARG:HA	7:D:207:GLY:O	2.11	0.51
1:A:457:G:H4'	1:A:458:A:H5''	1.93	0.51
1:A:959:C:C2	1:A:960:C:H2'	2.46	0.51
1:A:1343:U:H5	1:A:1666:A:H61	1.58	0.51
8:E:165:LEU:HA	8:E:168:ARG:HD2	1.92	0.51
11:Y:32:PHE:CE2	11:Y:133:LYS:HG2	2.45	0.51
1:A:949:C:H2'	1:A:950:A:C8	2.45	0.51
1:A:1742:A:H4'	1:A:1743:G:H8	1.70	0.51
1:A:1960:G:H2'	1:A:1961:C:O4'	2.11	0.51
1:A:2189:G:N3	1:A:2191:U:O4	2.44	0.51
1:A:2355:A:H2'	1:A:2356:A:C8	2.46	0.51
1:A:137:G:H8	1:A:137:G:O5'	1.94	0.51
1:A:749:G:N2	1:A:772:A:N7	2.59	0.51
1:A:1350:U:H5	1:A:1647:A:N1	2.09	0.51
1:A:1458:A:N1	1:A:1459:A:N6	2.57	0.51
1:A:1989:C:O2'	1:A:1991:G:OP2	2.19	0.51
2:B:16:A:H2'	2:B:17:A:C8	2.45	0.51
1:A:161:A:N6	1:A:167:U:H3	2.05	0.51
1:A:1897:U:H4'	1:A:1898:C:H3'	1.93	0.51
1:A:2190:C:H3'	1:A:2191:U:C5	2.45	0.51
1:A:2758:G:H2'	1:A:2759:G:C8	2.46	0.51
1:A:2905:C:N4	25:b:40:HIS:HA	2.26	0.51
6:F:217:ARG:CG	6:F:218:PRO:HD2	2.41	0.51
13:M:54:ALA:HB1	13:M:80:ILE:HD11	1.92	0.51
19:S:3:ILE:HD11	19:S:33:VAL:HG11	1.92	0.51
1:A:1167:C:H2'	1:A:1168:C:N1	2.26	0.50
16:P:14:VAL:HA	16:P:18:GLN:NE2	2.26	0.50
16:P:32:THR:HG22	16:P:61:THR:HG22	1.92	0.50
19:S:31:ASP:OD2	19:S:65:VAL:HB	2.12	0.50
25:b:38:LEU:O	25:b:41:ARG:HB2	2.11	0.50
1:A:2161:A:N3	1:A:2186:G:H1'	2.26	0.50
1:A:2591:A:O2'	1:A:2592:A:OP1	2.27	0.50
2:B:64:A:H4'	2:B:65:G:O5'	2.11	0.50
7:D:60:LYS:HB3	7:D:63:ALA:HB2	1.92	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:284:C:H3'	1:A:285:U:H5''	1.93	0.50
1:A:316:G:H2'	1:A:317:G:O4'	2.11	0.50
1:A:956:A:H2'	11:Y:9:TYR:OH	2.12	0.50
1:A:2826:U:N3	1:A:2827:A:N7	2.58	0.50
7:D:14:GLN:NE2	14:N:58:SER:HA	2.26	0.50
23:W:58:ARG:O	23:W:62:ILE:HG12	2.11	0.50
1:A:80:G:N3	1:A:389:A:N6	2.60	0.50
1:A:385:U:H2'	1:A:386:C:C6	2.47	0.50
1:A:765:U:O2'	1:A:766:G:H8	1.94	0.50
1:A:925:G:H2'	1:A:925:G:N3	2.26	0.50
1:A:2110:G:H2'	1:A:2111:C:C6	2.46	0.50
1:A:2679:U:O2'	1:A:2695:G:N2	2.39	0.50
1:A:61:A:H2'	1:A:62:C:C6	2.47	0.50
19:S:36:GLU:OE1	19:S:60:GLU:HG3	2.12	0.50
1:A:2346:U:H4'	1:A:2348:G:N7	2.26	0.50
7:D:129:GLY:CA	7:D:170:PRO:HB3	2.38	0.50
1:A:168:A:C2	1:A:169:G:H1'	2.46	0.50
1:A:337:A:H2	1:A:389:A:H62	1.58	0.50
6:F:76:ALA:HB1	6:F:94:VAL:HB	1.94	0.50
6:F:87:ARG:HB3	6:F:87:ARG:NH1	2.27	0.50
10:L:87:ASP:OD1	10:L:119:LYS:HD3	2.12	0.50
1:A:615:A:H5''	1:A:616:G:OP2	2.11	0.50
1:A:2215:U:H2'	1:A:2216:U:O4'	2.11	0.50
1:A:2907:A:H1'	25:b:28:THR:HG23	1.93	0.50
2:B:70:G:N2	2:B:101:A:H62	2.06	0.50
3:1:36:CYS:O	3:1:38:ARG:N	2.44	0.50
20:T:29:ALA:HB3	20:T:41:VAL:HG23	1.94	0.50
1:A:175:C:C4	1:A:176:A:C8	3.00	0.50
1:A:749:G:H21	1:A:772:A:H62	1.59	0.50
1:A:1053:A:H5'	15:O:59:LYS:HE3	1.92	0.50
7:D:129:GLY:O	7:D:131:ILE:HG22	2.11	0.50
7:D:131:ILE:HG23	7:D:132:LYS:H	1.77	0.50
9:H:22:GLU:HG2	9:H:62:LYS:HG2	1.93	0.50
1:A:274:A:H62	1:A:297:G:N2	2.10	0.49
1:A:422:G:H2'	1:A:423:A:H8	1.77	0.49
1:A:525:A:N3	1:A:527:G:H5''	2.27	0.49
1:A:986:G:HO2'	1:A:1228:A:H8	1.60	0.49
1:A:1053:A:H3'	1:A:1053:A:C8	2.46	0.49
1:A:1488:A:H3'	1:A:1489:A:H8	1.77	0.49
1:A:1844:G:H5''	6:F:87:ARG:HH12	1.77	0.49
1:A:2673:C:N4	1:A:2702:A:H61	2.10	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:3:54:ASP:O	5:3:58:VAL:HG22	2.12	0.49
19:S:3:ILE:HD11	19:S:33:VAL:HG21	1.94	0.49
23:W:28:LEU:HA	23:W:31:GLN:HE21	1.77	0.49
1:A:298:U:H5'	1:A:299:U:H5'	1.95	0.49
1:A:908:A:H2'	1:A:909:G:C8	2.47	0.49
1:A:1488:A:H2'	1:A:1489:A:O4'	2.12	0.49
1:A:2371:U:H2'	3:1:32:MET:SD	2.52	0.49
6:F:133:GLN:HB3	6:F:186:SER:OG	2.11	0.49
7:D:5:ILE:O	7:D:6:LEU:HB2	2.12	0.49
1:A:991:A:H2'	1:A:992:A:C8	2.47	0.49
1:A:1210:U:O2'	1:A:1211:G:OP1	2.21	0.49
1:A:1735:C:H2'	1:A:1736:U:O4'	2.12	0.49
1:A:1983:U:H5'	1:A:1984:C:OP1	2.13	0.49
6:F:210:ARG:HG3	6:F:213:TRP:CE3	2.47	0.49
1:A:2249:G:H2'	1:A:2250:A:C8	2.46	0.49
1:A:2437:G:H3'	1:A:2438:A:H8	1.77	0.49
1:A:2775:A:C2	1:A:2784:A:C4	3.00	0.49
9:H:43:VAL:HG12	15:O:100:ILE:HG13	1.94	0.49
1:A:735:C:H4'	6:F:217:ARG:HH22	1.76	0.49
1:A:1091:G:H5''	1:A:1092:A:OP1	2.13	0.49
13:M:31:LEU:HD23	13:M:93:VAL:O	2.13	0.49
1:A:734:A:H2'	1:A:735:C:C6	2.47	0.49
1:A:1079:U:N3	1:A:1080:G:N7	2.61	0.49
1:A:2192:G:H3'	1:A:2193:G:C8	2.48	0.49
1:A:2884:G:O2'	1:A:2886:G:H5''	2.13	0.49
1:A:2916:U:H2'	1:A:2917:U:C6	2.48	0.49
2:B:14:G:C2	2:B:67:G:H1'	2.48	0.49
9:H:9:GLU:HB2	9:H:49:VAL:HG11	1.95	0.49
24:X:39:ASP:OD2	24:X:44:ARG:NH2	2.44	0.49
1:A:749:G:N1	1:A:771:G:O2'	2.46	0.49
1:A:1490:G:H1'	1:A:1491:C:C5'	2.42	0.49
1:A:1603:U:H2'	1:A:1604:C:O4'	2.13	0.49
1:A:1627:G:C2	1:A:1628:A:C8	3.01	0.49
9:H:1:MET:N	9:H:3:GLN:HG2	2.28	0.49
9:H:46:THR:OG1	9:H:49:VAL:HG12	2.12	0.49
13:M:15:HIS:O	13:M:19:ARG:HB3	2.12	0.49
14:N:65:LYS:NZ	14:N:67:SER:OG	2.44	0.49
23:W:31:GLN:HE22	23:W:37:LEU:HD13	1.76	0.49
1:A:1197:C:OP1	15:O:92:ARG:NH2	2.41	0.49
1:A:1211:G:C2	1:A:1212:U:H1'	2.48	0.49
1:A:1494:G:O2'	1:A:1495:C:OP2	2.25	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2490:C:H42	1:A:2515:A:N6	2.09	0.49
1:A:2552:G:C1'	1:A:2768:A:H61	2.25	0.49
1:A:2697:G:H5'	1:A:2698:A:OP2	2.12	0.49
1:A:2902:A:H5''	1:A:2902:A:H8	1.77	0.49
1:A:2905:C:C2	25:b:31:PRO:HG2	2.48	0.49
13:M:43:GLN:HG2	13:M:55:GLN:HG2	1.93	0.49
1:A:174:U:H2'	1:A:175:C:H6	1.78	0.49
1:A:1799:G:N2	1:A:2007:G:H1	2.11	0.49
1:A:1963:A:H4'	1:A:1964:A:H5''	1.94	0.49
1:A:1969:C:H3'	1:A:1970:U:H2'	1.94	0.49
1:A:2565:C:H2'	1:A:2566:C:H6	1.76	0.49
1:A:2618:C:OP2	6:F:238:ARG:HG2	2.13	0.49
1:A:2825:U:H2'	1:A:2826:U:C6	2.47	0.49
4:2:4:ARG:O	4:2:7:GLN:NE2	2.45	0.49
18:R:3:ALA:O	18:R:45:ILE:HD11	2.13	0.49
1:A:1218:G:H2'	1:A:1219:G:H8	1.76	0.49
1:A:1698:A:O2'	7:D:127:PHE:O	2.24	0.49
1:A:1741:G:N1	1:A:1742:A:H2'	2.28	0.49
6:F:17:THR:O	6:F:203:VAL:HG13	2.13	0.49
1:A:986:G:O2'	1:A:1228:A:H8	1.96	0.48
1:A:1040:A:H1'	16:P:9:GLY:O	2.13	0.48
1:A:1760:G:H3'	1:A:1761:G:H4'	1.95	0.48
1:A:2200:A:OP1	1:A:2201:C:N4	2.45	0.48
2:B:43:A:N1	2:B:44:A:H1'	2.28	0.48
5:3:55:MET:O	5:3:59:LYS:HB3	2.13	0.48
1:A:320:U:H1'	1:A:326:A:H2	1.77	0.48
1:A:1167:C:H2'	1:A:1168:C:C6	2.48	0.48
1:A:1733:A:H2'	1:A:1734:A:C8	2.48	0.48
1:A:2185:A:O2'	1:A:2186:G:H5''	2.12	0.48
1:A:2209:G:H2'	1:A:2210:C:C6	2.48	0.48
1:A:2685:C:H3'	1:A:2686:G:H5''	1.95	0.48
3:1:23:LYS:HE2	3:1:24:ARG:NH2	2.28	0.48
1:A:768:A:H2'	1:A:768:A:N3	2.27	0.48
1:A:890:G:H8	1:A:892:U:O4	1.96	0.48
1:A:1315:C:H2'	1:A:1316:G:C8	2.48	0.48
1:A:1454:U:H3'	1:A:1455:U:C6	2.48	0.48
1:A:1932:C:HO2'	1:A:1956:G:HO2'	1.58	0.48
1:A:2699:U:H3'	1:A:2700:G:C8	2.47	0.48
1:A:2865:G:H2'	1:A:2866:G:C8	2.49	0.48
4:2:31:VAL:O	4:2:35:ARG:HG2	2.13	0.48
6:F:131:PRO:HB2	6:F:133:GLN:HG2	1.95	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:Q:82:LEU:HB2	17:Q:98:LYS:HB2	1.96	0.48
1:A:1701:U:H2'	1:A:1702:C:H6	1.78	0.48
1:A:2189:G:C6	1:A:2192:G:N2	2.82	0.48
1:A:2552:G:N2	1:A:2768:A:H2	1.92	0.48
1:A:2681:A:N6	1:A:2693:C:OP2	2.28	0.48
7:D:5:ILE:HG23	7:D:6:LEU:H	1.77	0.48
1:A:224:A:N1	1:A:268:A:O2'	2.45	0.48
1:A:1168:C:H2'	1:A:1169:G:O4'	2.14	0.48
1:A:1757:U:H2'	1:A:1758:A:O4'	2.14	0.48
1:A:2126:C:H2'	1:A:2127:G:H8	1.78	0.48
9:H:65:PHE:HB3	9:H:69:LYS:HB2	1.94	0.48
11:Y:54:MET:HE3	11:Y:64:VAL:HG11	1.94	0.48
1:A:1740:G:H8	1:A:1740:G:O5'	1.96	0.48
1:A:2012:G:HO2'	1:A:2013:G:P	2.37	0.48
1:A:2027:G:H21	1:A:2717:A:N6	2.11	0.48
1:A:2079:G:H4'	7:D:156:MET:O	2.13	0.48
14:N:102:LEU:HD22	14:N:112:ILE:HD12	1.95	0.48
1:A:889:U:H2'	1:A:890:G:O4'	2.14	0.48
1:A:1368:C:H2'	1:A:1370:C:C5	2.49	0.48
1:A:1443:A:H2'	1:A:1444:C:C6	2.49	0.48
1:A:1478:A:H2'	1:A:1479:G:H1'	1.94	0.48
1:A:2242:G:H2'	1:A:2243:U:C6	2.49	0.48
19:S:37:GLY:H	19:S:60:GLU:CD	2.21	0.48
1:A:342:A:N3	1:A:362:C:O2'	2.43	0.48
1:A:1887:G:C6	1:A:1910:G:C2	3.02	0.48
13:M:29:PRO:HB2	13:M:44:ILE:HD11	1.96	0.48
1:A:54:G:H1'	4:2:36:ARG:HH12	1.79	0.48
1:A:944:G:C2	1:A:945:A:C5	3.02	0.48
1:A:1605:A:H2'	1:A:1607:A:C8	2.49	0.48
24:X:22:THR:OG1	24:X:49:LYS:HD3	2.14	0.48
1:A:317:G:H2'	1:A:318:A:C8	2.49	0.48
1:A:892:U:H5	1:A:977:A:N1	2.11	0.48
1:A:1999:G:O2'	1:A:2000:G:OP1	2.28	0.48
1:A:2250:A:H2'	1:A:2251:G:O4'	2.14	0.48
1:A:2318:U:H2'	1:A:2319:U:C6	2.49	0.48
1:A:2676:U:C4	1:A:2677:C:N4	2.82	0.48
1:A:2684:A:N6	1:A:2691:G:H21	2.03	0.48
7:D:53:PHE:CG	7:D:54:GLU:N	2.82	0.48
9:H:50:ASP:OD1	9:H:122:LYS:NZ	2.46	0.48
13:M:77:GLY:O	13:M:80:ILE:HG22	2.14	0.48
1:A:185:A:H2'	1:A:186:C:H6	1.79	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:293:U:H2'	1:A:294:G:C8	2.49	0.47
1:A:1497:A:C4'	1:A:1498:U:H2'	2.37	0.47
1:A:2673:C:H42	1:A:2702:A:N6	2.10	0.47
1:A:2680:U:H3'	1:A:2681:A:H2'	1.94	0.47
1:A:2720:A:H2	1:A:2744:G:N2	2.09	0.47
3:1:9:CYS:HA	3:1:45:HIS:HA	1.96	0.47
10:L:119:LYS:HG3	10:L:121:LEU:HG	1.94	0.47
22:V:35:LYS:HD2	22:V:46:LYS:HB3	1.96	0.47
1:A:13:A:H5'	1:A:14:A:OP1	2.14	0.47
1:A:682:A:H4'	1:A:683:G:O5'	2.14	0.47
1:A:767:A:N1	1:A:768:A:H1'	2.29	0.47
1:A:1474:C:OP2	1:A:1606:C:N4	2.45	0.47
1:A:1642:C:H4'	18:R:36:THR:HG23	1.96	0.47
1:A:2211:U:H3'	1:A:2212:G:C8	2.49	0.47
1:A:2231:C:H4'	6:F:147:LYS:HD2	1.96	0.47
1:A:2511:G:H2'	1:A:2512:G:C8	2.49	0.47
2:B:20:A:H2'	2:B:21:G:C8	2.49	0.47
8:E:117:LYS:HD3	8:E:192:LEU:HB2	1.96	0.47
21:a:53:ILE:CG2	21:a:87:VAL:HG23	2.44	0.47
1:A:305:A:H3'	1:A:306:C:C6	2.50	0.47
1:A:1203:U:H2'	1:A:1204:G:H5''	1.96	0.47
1:A:1953:U:N3	1:A:1955:A:OP1	2.46	0.47
1:A:2682:G:C2	1:A:2691:G:C2	3.02	0.47
1:A:2878:U:H2'	1:A:2879:G:C8	2.49	0.47
1:A:2906:G:H21	25:b:28:THR:HG21	1.79	0.47
2:B:64:A:H5''	2:B:65:G:OP1	2.13	0.47
12:G:22:ILE:HD11	12:G:42:THR:HG23	1.95	0.47
1:A:1219:G:C2	1:A:1220:A:C4	3.02	0.47
1:A:1238:U:C1'	15:O:4:VAL:HG12	2.45	0.47
1:A:1628:A:O2'	1:A:1629:U:H5'	2.15	0.47
12:G:106:LEU:HB3	12:G:111:PHE:HB2	1.97	0.47
15:O:60:LEU:O	15:O:63:THR:HG22	2.14	0.47
17:Q:64:MET:HE3	17:Q:69:LEU:HD21	1.96	0.47
19:S:82:GLY:C	19:S:83:TYR:HD2	2.23	0.47
21:a:77:PHE:CD2	21:a:87:VAL:HG22	2.48	0.47
1:A:967:C:O2'	21:a:34:ALA:HB2	2.14	0.47
1:A:1055:A:OP1	15:O:75:SER:OG	2.32	0.47
1:A:1083:G:C2	1:A:1161:A:C2	3.02	0.47
1:A:1798:C:C2	1:A:1799:G:C2	3.02	0.47
1:A:2656:A:C6	1:A:2914:A:H2	2.33	0.47
2:B:35:C:N3	2:B:46:A:O2'	2.41	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:N:101:TYR:CD2	14:N:112:ILE:HA	2.49	0.47
1:A:1314:A:H2'	1:A:1315:C:C6	2.49	0.47
1:A:1460:U:H2'	1:A:1461:C:C6	2.49	0.47
1:A:1609:U:H2'	1:A:1610:G:C8	2.49	0.47
1:A:1731:G:N2	1:A:1745:A:C8	2.82	0.47
1:A:1937:G:C6	1:A:1948:G:C6	3.03	0.47
1:A:1978:U:O2	1:A:1984:C:C2	2.67	0.47
2:B:37:A:O2'	2:B:44:A:N6	2.47	0.47
9:H:9:GLU:HG3	9:H:46:THR:OG1	2.14	0.47
18:R:23:ASP:O	18:R:81:THR:HA	2.15	0.47
1:A:174:U:C2	1:A:175:C:C5	3.02	0.47
1:A:770:G:H5'	1:A:771:G:C5	2.49	0.47
1:A:911:A:H2'	1:A:911:A:N3	2.28	0.47
1:A:955:A:H2'	1:A:956:A:C8	2.50	0.47
1:A:1982:U:O2'	1:A:2578:C:O2'	2.26	0.47
1:A:2189:G:H5'	1:A:2200:A:OP2	2.15	0.47
1:A:2826:U:H3	1:A:2827:A:H62	1.63	0.47
1:A:2861:U:O4	1:A:2895:G:O6	2.33	0.47
7:D:14:GLN:HE21	14:N:58:SER:HA	1.79	0.47
8:E:7:LEU:HD12	8:E:124:THR:HG23	1.96	0.47
9:H:59:ASN:ND2	9:H:129:ALA:HB2	2.30	0.47
11:Y:11:ARG:HH21	11:Y:89:ALA:HA	1.79	0.47
12:G:64:ARG:HH21	14:N:70:VAL:HG21	1.80	0.47
22:V:32:ASN:O	22:V:50:SER:HA	2.15	0.47
1:A:332:A:H8	1:A:332:A:O5'	1.98	0.47
1:A:1961:C:C2	1:A:1962:G:C8	3.03	0.47
1:A:1991:G:N7	1:A:1994:C:N4	2.63	0.47
1:A:2135:U:H5'	1:A:2177:U:C2	2.49	0.47
1:A:2226:A:N6	1:A:2251:G:H21	2.12	0.47
1:A:2367:A:H2'	1:A:2368:G:C8	2.50	0.47
1:A:2541:U:H2'	1:A:2542:C:H6	1.79	0.47
2:B:113:G:H2'	2:B:114:G:O4'	2.15	0.47
21:a:61:ARG:NH2	21:a:65:ASP:OD1	2.42	0.47
1:A:2144:A:O2'	1:A:2174:A:H2'	2.14	0.47
1:A:2188:C:N3	1:A:2189:G:N7	2.62	0.47
1:A:2725:U:H2'	1:A:2726:C:O4'	2.15	0.47
1:A:2828:U:C6	1:A:2911:A:N6	2.83	0.47
20:T:9:ARG:N	20:T:40:SER:O	2.39	0.47
23:W:49:THR:HG22	23:W:52:ARG:NH2	2.30	0.47
25:b:28:THR:OG1	25:b:39:SER:OG	2.28	0.47
1:A:1408:G:C2	1:A:1409:U:C4	3.03	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1475:A:H2'	1:A:1476:G:O4'	2.15	0.47
1:A:1725:G:H21	1:A:1790:G:H5'	1.81	0.47
1:A:1959:A:C6	1:A:1960:G:C4	3.03	0.47
1:A:2097:G:O2'	1:A:2098:A:OP1	2.21	0.47
1:A:2629:A:H1'	1:A:2630:G:H5''	1.97	0.47
1:A:328:G:H22	1:A:399:U:H1'	1.81	0.46
1:A:458:A:H3'	1:A:459:C:C6	2.48	0.46
1:A:1627:G:C2	1:A:1628:A:N7	2.83	0.46
11:Y:112:GLU:O	11:Y:116:GLU:OE1	2.33	0.46
19:S:75:THR:HG23	19:S:77:GLU:HB2	1.97	0.46
20:T:9:ARG:NH2	20:T:28:PRO:HB3	2.30	0.46
1:A:64:A:H4'	18:R:63:LYS:NZ	2.30	0.46
1:A:169:G:H2'	1:A:170:C:C6	2.50	0.46
1:A:194:A:H2'	1:A:195:C:C6	2.49	0.46
1:A:579:U:H2'	1:A:580:C:C6	2.50	0.46
1:A:1480:G:H2'	1:A:1481:A:H8	1.81	0.46
1:A:1813:A:OP1	1:A:2007:G:N2	2.48	0.46
1:A:1829:A:H2'	1:A:1830:A:C8	2.51	0.46
1:A:2714:U:H2'	1:A:2715:G:C8	2.50	0.46
4:2:32:LEU:O	4:2:36:ARG:HG3	2.15	0.46
1:A:1212:U:H2'	1:A:1213:C:C1'	2.45	0.46
1:A:1686:G:H2'	1:A:1687:G:O4'	2.14	0.46
1:A:2142:G:H2'	1:A:2143:G:N7	2.30	0.46
1:A:2507:C:H2'	1:A:2508:G:C8	2.50	0.46
17:Q:72:LYS:HE3	17:Q:108:SER:HB2	1.98	0.46
20:T:29:ALA:HA	20:T:89:ILE:O	2.16	0.46
1:A:273:A:OP2	1:A:297:G:N1	2.46	0.46
1:A:736:C:H2'	1:A:737:C:H6	1.81	0.46
1:A:877:G:H2'	1:A:878:C:C6	2.51	0.46
1:A:1038:C:OP1	15:O:53:ARG:NH2	2.49	0.46
1:A:1736:U:O3'	1:A:1737:U:H2'	2.15	0.46
11:Y:41:TRP:CD1	11:Y:96:VAL:HG22	2.51	0.46
15:O:52:GLN:O	15:O:55:ARG:HG2	2.15	0.46
21:a:83:ASP:OD1	21:a:83:ASP:N	2.49	0.46
1:A:309:U:O2	1:A:310:C:N4	2.43	0.46
1:A:835:U:O2	1:A:835:U:H2'	2.15	0.46
1:A:918:G:H2'	1:A:919:G:O4'	2.16	0.46
1:A:1798:C:O2	1:A:1799:G:C2	2.68	0.46
1:A:1946:A:H2'	1:A:1947:C:N1	2.30	0.46
11:Y:32:PHE:HE2	11:Y:133:LYS:HG2	1.79	0.46
1:A:84:A:C8	1:A:99:U:C2	3.04	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:942:C:C2	1:A:943:C:H5	2.34	0.46
1:A:958:U:O2	1:A:959:C:H5	1.99	0.46
1:A:1087:C:O2'	1:A:1092:A:O2'	2.24	0.46
1:A:1458:A:H2'	1:A:1459:A:H8	1.81	0.46
1:A:1767:G:P	1:A:1768:C:H41	2.39	0.46
1:A:2799:C:H5''	7:D:215:ILE:HD12	1.96	0.46
2:B:27:A:H2	2:B:56:A:H61	1.64	0.46
23:W:49:THR:HG22	23:W:52:ARG:HH22	1.79	0.46
1:A:320:U:OP1	1:A:321:U:H5''	2.16	0.46
1:A:947:U:H2'	1:A:948:U:O4'	2.15	0.46
1:A:1092:A:C2	1:A:1157:U:H4'	2.50	0.46
1:A:1302:G:OP1	25:b:16:ARG:NH2	2.40	0.46
1:A:1450:A:N1	1:A:1634:A:N1	2.63	0.46
1:A:2161:A:H2'	1:A:2162:A:O4'	2.16	0.46
1:A:2777:A:O2'	1:A:2780:A:N6	2.49	0.46
1:A:2884:G:O2'	1:A:2885:U:O5'	2.34	0.46
1:A:29:U:H2'	1:A:30:G:C8	2.50	0.46
1:A:166:A:H2'	1:A:167:U:C6	2.50	0.46
1:A:282:A:H5''	1:A:283:G:OP2	2.15	0.46
1:A:770:G:H2'	1:A:770:G:N3	2.30	0.46
1:A:1044:A:H2'	1:A:1045:A:C8	2.50	0.46
1:A:1218:G:H2'	1:A:1219:G:N7	2.30	0.46
1:A:2130:A:H2'	1:A:2131:C:C6	2.51	0.46
1:A:2325:A:H3'	1:A:2326:G:H8	1.81	0.46
1:A:2681:A:H62	1:A:2694:C:H41	1.62	0.46
2:B:67:G:O6	2:B:104:A:H2	1.99	0.46
3:1:30:ILE:HG13	3:1:30:ILE:O	2.15	0.46
11:Y:31:GLU:HG2	11:Y:107:ALA:HA	1.97	0.46
1:A:1080:G:N1	1:A:1163:U:C2	2.83	0.46
1:A:1169:G:C8	1:A:1170:A:C8	3.04	0.46
1:A:1481:A:H2'	1:A:1482:U:O4'	2.16	0.46
1:A:1882:G:H2'	1:A:1883:A:H8	1.81	0.46
1:A:2027:G:O2'	1:A:2717:A:OP2	2.26	0.46
1:A:2256:U:H2'	1:A:2257:G:C8	2.51	0.46
1:A:2494:C:HO2'	11:Y:123:HIS:CE1	2.28	0.46
1:A:2835:C:H42	1:A:2849:A:H61	1.63	0.46
20:T:7:ILE:HG22	20:T:8:ILE:N	2.31	0.46
25:b:37:LYS:HG3	25:b:38:LEU:O	2.16	0.46
1:A:522:G:N1	1:A:525:A:OP2	2.43	0.46
1:A:1447:A:OP2	1:A:1447:A:H8	1.98	0.46
1:A:2187:G:N3	1:A:2188:C:H1'	2.31	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2433:C:H42	10:L:69:ILE:HD13	1.80	0.46
9:H:20:ASP:N	9:H:20:ASP:OD1	2.47	0.46
24:X:58:GLU:H	24:X:58:GLU:HG2	1.42	0.46
25:b:41:ARG:HH21	25:b:42:VAL:HG23	1.81	0.46
1:A:37:C:H4'	1:A:497:U:OP1	2.16	0.45
1:A:329:A:H2'	1:A:330:C:C6	2.51	0.45
1:A:332:A:H2'	1:A:333:C:C6	2.51	0.45
1:A:1290:G:O4'	15:O:33:LYS:HE2	2.16	0.45
1:A:1483:A:H3'	1:A:1484:G:C8	2.51	0.45
1:A:1840:U:H5''	6:F:40:LYS:HE3	1.97	0.45
1:A:1978:U:N3	1:A:1984:C:C4	2.84	0.45
1:A:2496:A:C6	1:A:2508:G:N2	2.84	0.45
1:A:2874:A:H2'	1:A:2875:U:O4'	2.16	0.45
6:F:169:GLY:O	6:F:171:TYR:HD2	2.00	0.45
14:N:46:GLU:O	14:N:65:LYS:HD3	2.16	0.45
19:S:72:ASP:HB3	19:S:75:THR:HG22	1.98	0.45
1:A:456:G:O2'	1:A:2434:A:OP2	2.28	0.45
1:A:894:A:H2'	1:A:895:U:C6	2.51	0.45
1:A:1770:C:H3'	1:A:1771:A:H4'	1.98	0.45
1:A:2397:G:H2'	1:A:2398:G:C8	2.51	0.45
1:A:2883:U:H4'	1:A:2884:G:O5'	2.16	0.45
2:B:76:A:N6	2:B:94:C:O2	2.49	0.45
12:G:4:GLN:O	12:G:5:GLU:HB2	2.16	0.45
1:A:286:U:H5'	1:A:287:G:C5	2.52	0.45
1:A:383:A:H2'	1:A:384:G:O4'	2.17	0.45
1:A:436:A:O2'	1:A:438:U:O4	2.34	0.45
1:A:592:A:H1'	1:A:594:G:OP2	2.17	0.45
1:A:1846:A:N1	6:F:274:ARG:NH1	2.65	0.45
1:A:2187:G:N2	1:A:2200:A:O2'	2.50	0.45
1:A:2189:G:H2'	1:A:2191:U:O4	2.16	0.45
1:A:2724:G:H1	1:A:2738:A:H62	0.78	0.45
2:B:72:U:N3	2:B:73:G:N7	2.65	0.45
17:Q:6:VAL:HA	17:Q:103:ILE:O	2.17	0.45
1:A:83:G:N2	1:A:101:G:H1'	2.32	0.45
1:A:300:G:N3	1:A:302:A:H1'	2.32	0.45
1:A:1798:C:N3	1:A:1799:G:C2	2.83	0.45
1:A:2152:G:H1'	1:A:2200:A:H61	1.81	0.45
1:A:2324:C:N3	1:A:2345:A:H2'	2.31	0.45
1:A:2791:A:H3'	1:A:2793:G:H21	1.82	0.45
5:3:10:ALA:O	5:3:14:VAL:HG12	2.17	0.45
6:F:164:VAL:HA	6:F:174:ILE:HG22	1.99	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:L:110:LYS:HD2	10:L:127:LYS:HG3	1.97	0.45
20:T:75:ALA:HB2	20:T:92:LEU:HD22	1.99	0.45
1:A:1452:C:H1'	1:A:1459:A:C2	2.51	0.45
1:A:1975:G:OP1	1:A:1975:G:H4'	2.15	0.45
1:A:2848:G:H21	1:A:2855:A:H1'	1.80	0.45
2:B:31:G:H21	2:B:34:C:N4	2.15	0.45
6:F:7:LYS:HD3	6:F:7:LYS:HA	1.79	0.45
6:F:65:ILE:HG13	6:F:67:PHE:CE2	2.51	0.45
7:D:6:LEU:HD23	7:D:53:PHE:HB2	1.97	0.45
12:G:104:ARG:HG3	12:G:122:LEU:C	2.42	0.45
14:N:102:LEU:CD2	14:N:112:ILE:HD12	2.46	0.45
16:P:78:ARG:HD2	16:P:79:ARG:NH1	2.31	0.45
18:R:42:VAL:HG23	18:R:50:VAL:HG21	1.97	0.45
19:S:65:VAL:C	19:S:67:ASN:H	2.24	0.45
21:a:53:ILE:O	21:a:67:LEU:HD11	2.16	0.45
1:A:600:U:O2'	9:H:48:HIS:O	2.25	0.45
2:B:83:C:H2'	2:B:84:U:O4'	2.17	0.45
6:F:108:LYS:HB2	6:F:108:LYS:HE2	1.67	0.45
14:N:102:LEU:HD13	14:N:112:ILE:HB	1.98	0.45
1:A:64:A:H8	18:R:65:MET:HG2	1.82	0.45
1:A:669:C:O2'	1:A:702:U:OP1	2.32	0.45
1:A:949:C:H2'	1:A:950:A:O4'	2.17	0.45
1:A:1171:A:N6	1:A:2515:A:H2	2.15	0.45
1:A:1490:G:HO2'	1:A:1491:C:P	2.34	0.45
1:A:1804:U:C5	1:A:1814:A:N1	2.82	0.45
1:A:2165:G:H2'	1:A:2166:U:O4'	2.16	0.45
1:A:2223:C:O2'	1:A:2224:U:H5'	2.16	0.45
1:A:2333:U:H2'	1:A:2334:G:H4'	1.99	0.45
5:3:29:THR:HG22	5:3:30:SER:N	2.31	0.45
6:F:210:ARG:HA	6:F:213:TRP:CD2	2.51	0.45
10:L:91:VAL:HG13	10:L:95:LEU:HD23	1.99	0.45
1:A:312:A:H8	1:A:315:C:N4	2.13	0.45
1:A:579:U:O2'	15:O:49:ASP:OD2	2.25	0.45
1:A:908:A:HO2'	1:A:909:G:P	2.39	0.45
1:A:1197:C:H5''	15:O:62:ILE:HD13	1.99	0.45
1:A:1315:C:H2'	1:A:1316:G:H8	1.82	0.45
1:A:1488:A:H3'	1:A:1489:A:C8	2.50	0.45
1:A:1626:A:N6	1:A:1627:G:C2	2.85	0.45
1:A:1953:U:H6	1:A:1956:G:H1	1.65	0.45
1:A:2695:G:H8	1:A:2695:G:O5'	2.00	0.45
1:A:2852:U:O2'	1:A:2853:U:OP2	2.29	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1926:A:O2'	1:A:1928:A:H5''	2.17	0.45
1:A:2254:A:H2'	1:A:2255:G:H8	1.82	0.45
1:A:2406:G:H2'	1:A:2407:A:C8	2.52	0.45
1:A:2434:A:H2'	1:A:2435:U:C6	2.52	0.45
1:A:2496:A:N6	1:A:2508:G:H21	2.15	0.45
7:D:71:LYS:HB2	7:D:72:PRO:HD3	1.98	0.45
13:M:45:ILE:HD12	13:M:47:ASP:OD1	2.17	0.45
16:P:27:VAL:HG11	16:P:62:VAL:HG21	1.98	0.45
1:A:172:U:H2'	1:A:173:A:C8	2.52	0.45
1:A:506:A:H2	1:A:515:G:H21	1.60	0.45
1:A:616:G:O2'	1:A:618:A:OP1	2.32	0.45
1:A:1092:A:H2'	1:A:1092:A:N3	2.31	0.45
1:A:1461:C:C4	1:A:1462:G:C5	3.05	0.45
1:A:1923:A:H8	1:A:1923:A:OP1	2.00	0.45
1:A:2041:A:H2'	1:A:2042:A:C8	2.52	0.45
1:A:2241:C:H2'	1:A:2242:G:O4'	2.17	0.45
2:B:7:G:H8	2:B:7:G:OP2	2.00	0.45
11:Y:57:TYR:HE1	11:Y:116:GLU:HG2	1.82	0.45
13:M:32:ASN:HA	13:M:95:ASP:O	2.16	0.45
1:A:225:A:N1	1:A:236:A:H5'	2.31	0.44
1:A:328:G:C6	1:A:329:A:N6	2.85	0.44
1:A:927:G:O6	1:A:938:G:H3'	2.17	0.44
1:A:1745:A:H3'	1:A:1746:G:C8	2.46	0.44
1:A:2120:G:N7	1:A:2252:A:H2'	2.32	0.44
1:A:2174:A:N3	1:A:2174:A:H2'	2.30	0.44
1:A:2509:A:N3	1:A:2509:A:H2'	2.32	0.44
1:A:2884:G:O2'	1:A:2886:G:OP1	2.27	0.44
11:Y:25:ASN:HB2	11:Y:100:GLY:O	2.17	0.44
12:G:70:ARG:CG	12:G:76:TYR:HE1	2.23	0.44
18:R:37:GLN:HA	18:R:40:MET:HG3	1.99	0.44
1:A:485:A:H2'	1:A:486:G:O4'	2.17	0.44
1:A:736:C:H2'	1:A:737:C:C6	2.52	0.44
1:A:1865:C:H4'	1:A:1866:G:C8	2.51	0.44
1:A:1884:G:N2	1:A:1913:U:O4	2.49	0.44
1:A:2123:A:H2	1:A:2220:U:O2	2.01	0.44
1:A:2560:U:O2	1:A:2691:G:H4'	2.16	0.44
1:A:2764:G:H2'	1:A:2765:A:O4'	2.17	0.44
1:A:2794:C:H2'	1:A:2795:C:C6	2.52	0.44
1:A:2857:A:N6	1:A:2901:U:O4	2.50	0.44
12:G:101:PRO:HB2	12:G:122:LEU:HD11	1.98	0.44
1:A:12:U:H2'	1:A:13:A:O4'	2.17	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:75:G:H22	1:A:110:A:H2	1.65	0.44
1:A:1078:G:H2'	1:A:1079:U:O4'	2.18	0.44
1:A:1085:U:H3	1:A:1158:G:N2	2.03	0.44
1:A:1210:U:H3	1:A:1222:A:N6	2.12	0.44
1:A:1975:G:H22	1:A:1986:G:N2	2.16	0.44
1:A:2226:A:H62	1:A:2251:G:N2	2.11	0.44
1:A:2696:G:C6	1:A:2697:G:C6	3.05	0.44
1:A:2766:U:O4	1:A:2790:G:H3'	2.17	0.44
2:B:27:A:H2'	2:B:28:C:C5	2.53	0.44
11:Y:34:LEU:HD21	11:Y:129:THR:CG2	2.47	0.44
12:G:4:GLN:HA	12:G:21:THR:HG23	1.99	0.44
1:A:131:G:H2'	1:A:132:C:C6	2.52	0.44
1:A:307:A:N1	1:A:409:G:C4	2.86	0.44
1:A:787:U:H2'	1:A:788:A:C8	2.53	0.44
1:A:1476:G:H2'	1:A:1477:U:C6	2.52	0.44
1:A:1617:A:H2'	1:A:1618:A:C8	2.52	0.44
1:A:1761:G:H2'	1:A:1763:U:C4	2.52	0.44
1:A:2340:C:H2'	1:A:2341:A:C8	2.53	0.44
1:A:2434:A:H2'	1:A:2435:U:H6	1.83	0.44
1:A:2677:C:H42	1:A:2698:A:H61	1.66	0.44
1:A:2849:A:H5'	7:D:67:LYS:HD3	2.00	0.44
10:L:109:ILE:O	10:L:126:HIS:HB2	2.18	0.44
20:T:72:VAL:HG22	20:T:73:MET:N	2.32	0.44
1:A:64:A:N6	1:A:90:A:H2'	2.32	0.44
1:A:293:U:H2'	1:A:294:G:H8	1.82	0.44
1:A:322:A:H2'	1:A:323:C:O4'	2.18	0.44
1:A:1959:A:C5	1:A:1960:G:C8	3.05	0.44
1:A:2351:U:O2'	1:A:2364:G:H5'	2.17	0.44
7:D:131:ILE:HG23	7:D:132:LYS:N	2.32	0.44
1:A:91:A:H3'	1:A:92:G:C8	2.48	0.44
1:A:530:C:H2'	1:A:531:C:H6	1.81	0.44
1:A:703:A:H2'	1:A:704:U:C6	2.53	0.44
1:A:1337:A:OP2	1:A:1671:A:N6	2.50	0.44
1:A:2510:C:H3'	1:A:2511:G:C5'	2.44	0.44
2:B:27:A:P	13:M:36:SER:HB3	2.58	0.44
1:A:92:G:H3'	1:A:93:U:H6	1.82	0.44
1:A:398:C:H2'	1:A:399:U:H6	1.83	0.44
1:A:436:A:H4'	1:A:437:A:OP1	2.18	0.44
1:A:912:C:H2'	1:A:913:U:H6	1.83	0.44
1:A:2034:U:OP1	1:A:2842:G:N2	2.50	0.44
1:A:2051:C:H2'	1:A:2052:C:C6	2.52	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2312:C:OP2	3:1:2:ARG:NH1	2.49	0.44
3:1:38:ARG:HA	3:1:38:ARG:HD3	1.82	0.44
6:F:246:PRO:O	6:F:247:MET:HE2	2.18	0.44
8:E:37:ILE:HG23	8:E:184:LEU:HD12	1.99	0.44
11:Y:10:ARG:HD3	11:Y:11:ARG:NH1	2.33	0.44
16:P:27:VAL:HG21	16:P:62:VAL:HG21	2.00	0.44
1:A:577:A:H2'	1:A:577:A:N3	2.32	0.44
1:A:1781:C:H2'	1:A:1782:A:O4'	2.16	0.44
1:A:1798:C:C4	1:A:1799:G:C6	3.05	0.44
1:A:1809:C:H1'	1:A:2636:U:H5'	1.99	0.44
1:A:2448:G:H2'	1:A:2449:C:C6	2.53	0.44
1:A:2730:C:O2'	1:A:2731:C:P	2.76	0.44
1:A:2882:A:H3'	1:A:2883:U:H3'	2.00	0.44
2:B:25:A:H3'	2:B:26:C:C5	2.53	0.44
13:M:10:VAL:O	13:M:14:ARG:HG2	2.18	0.44
13:M:14:ARG:HH12	13:M:17:ARG:NH1	2.12	0.44
13:M:39:HIS:CD2	13:M:59:LYS:HB2	2.38	0.44
20:T:31:VAL:HG12	20:T:91:PHE:HB2	1.99	0.44
1:A:41:A:H2'	1:A:42:G:O4'	2.17	0.44
1:A:169:G:H2'	1:A:170:C:H6	1.83	0.44
1:A:279:A:H62	1:A:281:A:N6	2.13	0.44
1:A:1051:C:H5''	9:H:38:ARG:HH12	1.83	0.44
1:A:1636:U:O4	1:A:1637:A:N6	2.51	0.44
1:A:1701:U:H2'	1:A:1702:C:C6	2.51	0.44
1:A:1731:G:H8	1:A:1731:G:OP2	2.01	0.44
1:A:2032:A:HO2'	1:A:2033:C:P	2.39	0.44
1:A:2684:A:C5	1:A:2692:A:C8	3.06	0.44
2:B:48:A:OP1	13:M:69:LYS:HB2	2.18	0.44
7:D:110:PHE:O	7:D:188:VAL:HG21	2.18	0.44
9:H:18:VAL:CG2	9:H:138:PRO:HB2	2.48	0.44
14:N:101:TYR:CE2	14:N:112:ILE:HG13	2.53	0.44
20:T:31:VAL:HA	20:T:91:PHE:O	2.18	0.44
20:T:61:ILE:HG22	20:T:63:LEU:H	1.83	0.44
1:A:299:U:O4	1:A:415:U:H1'	2.18	0.43
1:A:519:G:C2'	1:A:520:G:H5'	2.48	0.43
1:A:752:G:H2'	1:A:753:U:O4'	2.18	0.43
1:A:845:A:H8	1:A:845:A:OP1	2.01	0.43
1:A:1626:A:H3'	1:A:1627:G:C8	2.53	0.43
1:A:1946:A:H8	1:A:1946:A:OP2	2.00	0.43
1:A:2497:G:N7	1:A:2503:A:H1'	2.33	0.43
2:B:31:G:C6	2:B:48:A:C6	3.06	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:73:G:C2'	2:B:74:G:H5'	2.47	0.43
6:F:72:ASP:OD1	6:F:119:GLY:HA2	2.18	0.43
13:M:31:LEU:HD22	13:M:92:ILE:HD12	1.99	0.43
1:A:111:U:OP1	23:W:58:ARG:NE	2.49	0.43
1:A:168:A:C4	1:A:169:G:H1'	2.53	0.43
1:A:1219:G:H2'	1:A:1220:A:O4'	2.18	0.43
1:A:2682:G:HO2'	1:A:2683:U:P	2.41	0.43
1:A:2808:A:O2'	1:A:2809:G:H5''	2.18	0.43
10:L:57:LEU:HA	10:L:60:ARG:NH1	2.34	0.43
12:G:38:VAL:HG13	12:G:60:ALA:O	2.19	0.43
15:O:61:TRP:O	15:O:65:ILE:HG13	2.18	0.43
20:T:72:VAL:HG23	20:T:92:LEU:O	2.17	0.43
1:A:13:A:H61	1:A:570:U:H3'	1.83	0.43
1:A:665:G:H2'	1:A:665:G:N3	2.33	0.43
1:A:1862:G:H22	1:A:1957:G:H4'	1.83	0.43
1:A:2080:G:H4'	7:D:161:SER:HB2	2.00	0.43
1:A:2683:U:H2'	1:A:2684:A:O4'	2.18	0.43
1:A:2812:U:H2'	1:A:2813:U:C6	2.53	0.43
19:S:77:GLU:O	19:S:79:THR:HG23	2.18	0.43
1:A:134:U:H2'	1:A:135:G:O4'	2.19	0.43
1:A:231:A:O2'	1:A:232:U:H2'	2.18	0.43
1:A:1221:C:H2'	1:A:1222:A:O4'	2.18	0.43
1:A:1463:A:H2'	1:A:1465:G:H8	1.82	0.43
1:A:1958:U:O2	1:A:1958:U:H2'	2.18	0.43
1:A:1980:A:O2'	1:A:1981:G:O5'	2.36	0.43
1:A:2118:U:H3'	1:A:2119:U:H2'	1.99	0.43
1:A:2541:U:H2'	1:A:2542:C:C6	2.53	0.43
1:A:2857:A:C6	1:A:2901:U:H5	2.36	0.43
1:A:2906:G:O2'	25:b:29:GLU:O	2.32	0.43
23:W:51:ALA:O	23:W:55:THR:HG23	2.18	0.43
1:A:629:A:N1	1:A:854:G:O2'	2.49	0.43
1:A:1166:G:H2'	1:A:1167:C:H5'	2.00	0.43
1:A:1769:C:H2'	1:A:1770:C:C6	2.53	0.43
1:A:2180:C:H2'	1:A:2181:G:N7	2.34	0.43
1:A:2494:C:O2'	11:Y:123:HIS:ND1	2.17	0.43
1:A:2768:A:H62	1:A:2790:G:N2	2.13	0.43
7:D:125:LYS:HG3	7:D:173:MET:HG2	1.99	0.43
9:H:115:LEU:O	9:H:119:GLN:HG3	2.18	0.43
1:A:515:G:O6	4:2:38:LYS:HE2	2.18	0.43
1:A:1639:G:H3'	1:A:1640:U:H6	1.83	0.43
1:A:1738:C:O2	1:A:1739:G:N1	2.51	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1743:G:H2'	1:A:1744:A:O3'	2.19	0.43
1:A:2223:C:C2	1:A:2224:U:C5	3.06	0.43
1:A:2552:G:C2'	1:A:2768:A:H61	2.32	0.43
1:A:2562:G:C2	1:A:2563:G:C8	3.06	0.43
1:A:2584:G:H2'	1:A:2585:C:C6	2.53	0.43
7:D:60:LYS:HG2	7:D:61:LYS:N	2.34	0.43
15:O:91:ASN:OD1	15:O:92:ARG:N	2.52	0.43
23:W:49:THR:HA	23:W:52:ARG:HG2	1.99	0.43
1:A:46:C:N4	1:A:217:G:N7	2.67	0.43
1:A:460:C:C2	1:A:461:A:C8	3.07	0.43
1:A:681:G:H2'	10:L:112:LEU:HD22	2.01	0.43
1:A:1358:A:H2'	1:A:1359:A:H8	1.84	0.43
1:A:1663:G:O2'	4:2:2:VAL:N	2.41	0.43
1:A:1946:A:N7	1:A:1947:C:N4	2.67	0.43
1:A:2037:G:H5''	17:Q:42:ALA:HB2	2.01	0.43
1:A:2127:G:O2'	1:A:2128:G:H5'	2.19	0.43
1:A:2231:C:H2'	1:A:2232:A:H8	1.83	0.43
1:A:2834:C:C1'	25:b:40:HIS:HB2	2.30	0.43
4:2:11:ARG:HE	4:2:15:LYS:HE3	1.84	0.43
6:F:34:LEU:HD22	6:F:61:GLN:HG3	2.00	0.43
6:F:184:ILE:HG22	6:F:185:LEU:N	2.34	0.43
8:E:57:VAL:HG21	8:E:87:GLY:H	1.83	0.43
9:H:18:VAL:HG23	9:H:138:PRO:HB2	2.00	0.43
15:O:52:GLN:HA	15:O:55:ARG:HD3	2.00	0.43
20:T:46:VAL:O	20:T:50:LYS:HG3	2.18	0.43
23:W:45:THR:O	23:W:49:THR:HG23	2.19	0.43
1:A:159:U:O2	1:A:169:G:N2	2.48	0.43
1:A:863:G:H21	1:A:1228:A:H2	1.62	0.43
1:A:1086:G:H2'	1:A:1087:C:O4'	2.19	0.43
1:A:1963:A:N7	1:A:1967:U:C2	2.87	0.43
1:A:1986:G:O2'	1:A:1987:A:O5'	2.33	0.43
1:A:2179:A:H2'	1:A:2180:C:N1	2.33	0.43
2:B:64:A:C5	2:B:105:C:C5	3.07	0.43
14:N:77:PRO:HB2	14:N:80:THR:HB	2.00	0.43
14:N:90:ARG:HG2	14:N:91:ARG:H	1.82	0.43
16:P:50:ALA:HB3	16:P:51:PRO:HD3	2.01	0.43
1:A:165:C:OP2	1:A:166:A:N6	2.51	0.43
1:A:363:A:O2'	1:A:365:A:OP2	2.30	0.43
1:A:955:A:N6	11:Y:11:ARG:O	2.52	0.43
1:A:1008:C:O2'	1:A:2300:A:N3	2.45	0.43
1:A:1642:C:H4'	18:R:36:THR:CG2	2.49	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1882:G:H2'	1:A:1883:A:C8	2.53	0.43
1:A:2368:G:H2'	1:A:2369:C:C6	2.54	0.43
1:A:2783:U:H1'	1:A:2784:A:H5''	2.01	0.43
1:A:2791:A:H3'	1:A:2793:G:N2	2.34	0.43
2:B:72:U:C4	2:B:73:G:N7	2.86	0.43
2:B:91:C:OP1	20:T:16:SER:HB2	2.17	0.43
10:L:80:ASP:N	10:L:115:GLY:HA3	2.33	0.43
11:Y:11:ARG:HB3	11:Y:87:LYS:HD2	2.00	0.43
17:Q:11:ARG:C	17:Q:12:ILE:HG13	2.43	0.43
17:Q:51:LEU:HA	17:Q:105:ILE:CD1	2.39	0.43
20:T:77:TYR:HA	20:T:88:HIS:O	2.19	0.43
21:a:64:ASP:O	21:a:65:ASP:HB2	2.19	0.43
1:A:143:U:H2'	1:A:144:C:H6	1.82	0.43
1:A:206:U:H3'	1:A:207:A:H2'	2.00	0.43
1:A:397:U:H2'	1:A:398:C:H6	1.83	0.43
1:A:511:G:H2'	1:A:512:A:C8	2.54	0.43
1:A:591:A:H4'	1:A:592:A:H5'	2.00	0.43
1:A:1395:G:O2'	1:A:1410:A:N6	2.51	0.43
1:A:1508:C:O2'	1:A:1509:G:OP1	2.33	0.43
1:A:1753:U:O2'	1:A:2878:U:O2	2.25	0.43
1:A:1771:A:H1'	1:A:1772:G:N7	2.34	0.43
1:A:2731:C:H3'	1:A:2732:A:C8	2.54	0.43
1:A:2791:A:H5'	1:A:2793:G:H21	1.82	0.43
3:1:9:CYS:HB2	3:1:45:HIS:CG	2.53	0.43
4:2:25:THR:O	4:2:29:ARG:HG3	2.18	0.43
5:3:8:ARG:HA	5:3:8:ARG:HD2	1.78	0.43
6:F:141:VAL:HG12	6:F:192:ILE:HD13	2.00	0.43
6:F:261:ARG:HE	6:F:264:LYS:HG3	1.84	0.43
14:N:66:ILE:O	14:N:68:SER:N	2.52	0.43
14:N:101:TYR:O	14:N:102:LEU:HB3	2.17	0.43
20:T:4:LEU:HB2	20:T:63:LEU:HB3	1.99	0.43
20:T:72:VAL:CG2	20:T:91:PHE:HB3	2.37	0.43
1:A:64:A:C8	18:R:68:TYR:HE2	2.37	0.42
1:A:173:A:C6	1:A:174:U:C5	3.07	0.42
1:A:353:A:HO2'	1:A:354:A:P	2.42	0.42
1:A:444:C:OP1	22:V:32:ASN:ND2	2.38	0.42
1:A:1862:G:N2	1:A:1957:G:H4'	2.34	0.42
1:A:2098:A:H2'	1:A:2099:G:C8	2.54	0.42
1:A:2300:A:H2'	1:A:2301:A:C8	2.53	0.42
1:A:2488:C:H2'	1:A:2489:U:C6	2.54	0.42
1:A:2818:A:H2'	1:A:2819:C:O4'	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2900:C:HO2'	1:A:2901:U:P	2.41	0.42
14:N:22:PHE:CZ	14:N:86:ILE:HG21	2.54	0.42
15:O:104:LYS:HE2	15:O:104:LYS:HA	2.00	0.42
1:A:227:G:H1	1:A:234:C:H42	1.66	0.42
1:A:315:C:H1'	1:A:316:G:C8	2.54	0.42
1:A:942:C:C2	1:A:943:C:C5	3.07	0.42
1:A:2154:G:H2'	1:A:2155:C:C6	2.54	0.42
1:A:2848:G:H21	1:A:2855:A:C2'	2.31	0.42
3:1:16:ASN:O	3:1:18:ILE:HG12	2.19	0.42
9:H:30:SER:HA	9:H:106:ILE:CD1	2.48	0.42
12:G:23:LYS:HB3	12:G:40:VAL:HG12	2.01	0.42
1:A:88:G:C6	1:A:89:U:H1'	2.53	0.42
1:A:310:C:O2'	1:A:311:U:O5'	2.32	0.42
1:A:867:U:H2'	1:A:868:A:H5''	2.00	0.42
1:A:1872:G:O4'	1:A:1923:A:O2'	2.37	0.42
1:A:1980:A:N3	1:A:2587:C:O2'	2.47	0.42
1:A:2078:A:H2'	1:A:2605:G:OP1	2.18	0.42
1:A:2188:C:O2	1:A:2188:C:H2'	2.20	0.42
1:A:2281:C:H42	21:a:15:VAL:N	2.17	0.42
12:G:60:ALA:HB2	12:G:86:ILE:HD13	2.00	0.42
1:A:949:C:H6	1:A:949:C:O5'	2.02	0.42
1:A:1408:G:H2'	1:A:1409:U:C6	2.55	0.42
1:A:1449:A:H3'	1:A:1449:A:N3	2.34	0.42
1:A:1913:U:H2'	1:A:1914:C:O4'	2.18	0.42
1:A:2574:U:O2'	1:A:2575:G:O5'	2.36	0.42
1:A:2834:C:O2'	25:b:40:HIS:O	2.35	0.42
6:F:35:LYS:HD3	6:F:35:LYS:HA	1.81	0.42
18:R:87:ILE:HG22	18:R:89:LEU:HG	2.01	0.42
1:A:421:C:H2'	1:A:422:G:C8	2.52	0.42
1:A:434:G:N7	1:A:436:A:C8	2.87	0.42
1:A:756:A:H2'	1:A:757:G:C8	2.55	0.42
1:A:1074:G:OP1	11:Y:123:HIS:HA	2.20	0.42
1:A:2047:A:O2'	1:A:2048:G:H5'	2.18	0.42
1:A:2616:A:H2'	1:A:2617:A:C8	2.54	0.42
17:Q:112:GLU:H	17:Q:112:GLU:HG3	1.55	0.42
19:S:34:VAL:HG22	19:S:62:ALA:HA	2.00	0.42
1:A:92:G:H3'	1:A:93:U:C6	2.54	0.42
1:A:156:A:C6	1:A:173:A:C2	3.08	0.42
1:A:167:U:H2'	1:A:168:A:O4'	2.19	0.42
1:A:333:C:N4	1:A:334:A:N6	2.67	0.42
1:A:451:U:H4'	1:A:452:G:OP2	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:923:A:H2'	1:A:924:G:O4'	2.19	0.42
1:A:1167:C:H2'	1:A:1168:C:C2	2.54	0.42
1:A:2005:A:H8	1:A:2005:A:H5''	1.84	0.42
1:A:2196:G:H2'	1:A:2197:G:C8	2.55	0.42
1:A:2277:G:N2	11:Y:84:GLY:HA3	2.35	0.42
1:A:2627:A:H2'	1:A:2628:C:C6	2.55	0.42
1:A:2675:G:N2	1:A:2700:G:N2	2.63	0.42
1:A:2693:C:H2'	1:A:2694:C:C6	2.55	0.42
19:S:83:TYR:HE1	19:S:90:LYS:HE3	1.84	0.42
1:A:679:G:H2'	1:A:680:C:C6	2.54	0.42
1:A:1489:A:N6	1:A:1507:A:H62	2.17	0.42
1:A:1866:G:O5'	1:A:1869:G:O2'	2.37	0.42
1:A:2773:U:H3	1:A:2783:U:H5	1.68	0.42
16:P:63:ASN:O	16:P:94:LYS:HB3	2.20	0.42
21:a:50:GLY:O	21:a:65:ASP:HB3	2.20	0.42
1:A:92:G:H8	1:A:92:G:OP2	2.02	0.42
1:A:272:C:H41	1:A:298:U:H2'	1.85	0.42
1:A:307:A:C6	1:A:409:G:C5	3.07	0.42
1:A:572:C:HO2'	1:A:573:A:P	2.41	0.42
1:A:661:U:C5'	8:E:106:ARG:HD3	2.50	0.42
1:A:909:G:O2'	1:A:960:C:N4	2.52	0.42
1:A:1053:A:H3'	1:A:1053:A:H8	1.85	0.42
1:A:1053:A:C8	1:A:1053:A:C3'	3.03	0.42
1:A:1485:G:N2	1:A:1599:G:N2	2.67	0.42
1:A:1886:A:H62	1:A:1910:G:H21	1.67	0.42
1:A:2027:G:H21	1:A:2717:A:H62	1.68	0.42
1:A:2704:A:H2	1:A:2758:G:H1	1.57	0.42
1:A:2778:G:H5'	1:A:2779:C:H5	1.84	0.42
5:3:29:THR:HG22	5:3:30:SER:H	1.85	0.42
7:D:4:GLY:HA2	7:D:211:ILE:O	2.20	0.42
12:G:88:ARG:O	12:G:89:ASP:HB2	2.19	0.42
17:Q:83:LYS:O	17:Q:84:ARG:NH1	2.49	0.42
1:A:158:G:H1	1:A:170:C:H42	1.67	0.42
1:A:442:G:H1'	22:V:29:TRP:CD1	2.55	0.42
1:A:1080:G:N1	1:A:1163:U:N3	2.68	0.42
1:A:1169:G:H3'	1:A:1170:A:H8	1.84	0.42
1:A:1480:G:N1	1:A:1604:C:O2	2.34	0.42
1:A:1500:G:H2'	1:A:1501:G:H8	1.85	0.42
1:A:2241:C:H3'	1:A:2242:G:H8	1.85	0.42
1:A:251:G:O5'	1:A:252:C:H5''	2.20	0.42
1:A:441:C:H2'	1:A:442:G:H8	1.85	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1631:G:H4'	1:A:1632:A:O4'	2.20	0.42
1:A:1982:U:H4'	1:A:1984:C:N4	2.35	0.42
1:A:2719:C:H2'	1:A:2720:A:H8	1.79	0.42
1:A:2745:G:OP1	14:N:100:TYR:HD2	2.03	0.42
2:B:71:A:H3'	2:B:72:U:H6	1.85	0.42
2:B:112:A:H2'	2:B:113:G:O4'	2.20	0.42
9:H:21:ALA:HB3	9:H:60:ALA:H	1.84	0.42
12:G:37:ASP:O	12:G:62:ILE:HD12	2.20	0.42
19:S:94:ALA:O	19:S:95:LYS:HB2	2.20	0.42
20:T:44:ASP:CG	20:T:47:GLU:HG3	2.44	0.42
1:A:160:G:N2	1:A:169:G:O6	2.53	0.41
1:A:303:G:H2'	1:A:304:G:C8	2.55	0.41
1:A:305:A:H3'	1:A:306:C:C5	2.55	0.41
1:A:592:A:N3	1:A:592:A:O2'	2.45	0.41
1:A:632:U:H2'	1:A:633:A:H8	1.84	0.41
1:A:2783:U:C1'	1:A:2784:A:H5''	2.50	0.41
2:B:71:A:H3'	2:B:72:U:C6	2.55	0.41
21:a:80:LYS:HB3	21:a:84:LYS:HB2	2.01	0.41
1:A:143:U:H2'	1:A:144:C:C6	2.55	0.41
1:A:431:C:O2	1:A:436:A:N6	2.49	0.41
1:A:2776:A:C8	1:A:2777:A:H2'	2.54	0.41
1:A:2811:U:H2'	1:A:2812:U:C6	2.55	0.41
1:A:2868:G:O6	1:A:2887:G:H1'	2.20	0.41
6:F:145:GLU:C	6:F:146:LEU:HD12	2.46	0.41
7:D:127:PHE:CE1	7:D:171:GLY:HA2	2.56	0.41
15:O:95:LEU:HD23	15:O:95:LEU:HA	1.89	0.41
1:A:97:C:H2'	1:A:98:U:H6	1.86	0.41
1:A:231:A:H2'	1:A:232:U:H5''	2.02	0.41
1:A:1702:C:H2'	1:A:1703:U:C6	2.55	0.41
1:A:2226:A:OP2	1:A:2227:C:H5	2.04	0.41
1:A:2314:A:C8	1:A:2316:G:C8	3.08	0.41
1:A:2558:A:C2	1:A:2685:C:H2'	2.54	0.41
1:A:2628:C:O2'	1:A:2629:A:O4'	2.27	0.41
1:A:2677:C:N4	1:A:2698:A:H61	2.18	0.41
1:A:2684:A:C2	1:A:2685:C:H1'	2.55	0.41
1:A:2684:A:OP2	1:A:2685:C:H5	2.04	0.41
1:A:2856:U:C4	1:A:2857:A:C6	3.08	0.41
9:H:9:GLU:O	9:H:10:SER:C	2.63	0.41
14:N:50:ILE:HG22	14:N:99:LEU:HB2	2.01	0.41
15:O:88:ILE:HA	16:P:50:ALA:HA	2.00	0.41
18:R:4:ARG:HH12	18:R:45:ILE:HG23	1.85	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:84:A:N3	1:A:85:G:H1'	2.34	0.41
1:A:105:C:H2'	1:A:106:A:C8	2.54	0.41
1:A:161:A:C6	1:A:168:A:C2	3.09	0.41
1:A:302:A:H3'	1:A:411:A:H61	1.85	0.41
1:A:540:G:H21	17:Q:61:ASN:HD21	1.68	0.41
1:A:805:G:H2'	1:A:806:A:O4'	2.20	0.41
1:A:1336:G:H21	1:A:1685:A:N6	2.11	0.41
1:A:1701:U:O2'	1:A:1702:C:H5'	2.21	0.41
1:A:2223:C:H2'	1:A:2224:U:C6	2.54	0.41
1:A:2906:G:H8	1:A:2906:G:O5'	2.03	0.41
1:A:2919:A:H2'	1:A:2920:U:O4'	2.20	0.41
2:B:57:G:C2	2:B:58:C:H1'	2.55	0.41
7:D:131:ILE:HG21	7:D:149:ARG:NH1	2.35	0.41
15:O:48:ARG:O	15:O:52:GLN:HG3	2.20	0.41
1:A:210:A:H2'	1:A:211:C:O4'	2.20	0.41
1:A:225:A:C2	1:A:236:A:H4'	2.55	0.41
1:A:316:G:C2	1:A:317:G:H1'	2.55	0.41
1:A:1451:U:N3	1:A:1633:A:C8	2.88	0.41
1:A:1979:A:C2	1:A:1981:G:H3'	2.52	0.41
1:A:2768:A:H2'	1:A:2769:G:H5'	2.03	0.41
7:D:42:GLU:OE2	7:D:42:GLU:N	2.52	0.41
12:G:22:ILE:HG12	12:G:41:CYS:HA	2.02	0.41
13:M:111:ALA:O	13:M:115:SER:HB3	2.21	0.41
1:A:307:A:N6	1:A:409:G:C5	2.85	0.41
1:A:691:A:H3'	1:A:692:G:H8	1.86	0.41
1:A:1061:G:N2	1:A:1189:C:H5	2.05	0.41
1:A:1386:U:H3'	1:A:1387:C:C5'	2.51	0.41
1:A:1458:A:H2'	1:A:1459:A:C8	2.55	0.41
1:A:1700:C:O2'	1:A:1701:U:P	2.78	0.41
1:A:2855:A:H5'	1:A:2856:U:OP2	2.20	0.41
6:F:35:LYS:N	6:F:62:TYR:O	2.45	0.41
10:L:46:VAL:HG21	10:L:50:PHE:HD2	1.85	0.41
1:A:389:A:C6	1:A:390:A:C2	3.09	0.41
1:A:506:A:H2'	1:A:507:C:O4'	2.20	0.41
1:A:770:G:H2'	1:A:771:G:H5'	2.03	0.41
1:A:860:U:H2'	1:A:861:C:H6	1.86	0.41
1:A:1977:G:OP2	1:A:1977:G:O4'	2.39	0.41
1:A:2502:C:N4	1:A:2556:G:H1	2.03	0.41
1:A:2546:U:H5'	1:A:2594:G:N2	2.36	0.41
1:A:2703:C:H3'	1:A:2704:A:C8	2.54	0.41
2:B:47:C:H2'	2:B:48:A:H8	1.85	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:167:LYS:HG2	6:F:172:VAL:HG22	2.03	0.41
10:L:95:LEU:HD12	10:L:98:GLU:OE2	2.21	0.41
14:N:114:GLU:O	14:N:114:GLU:HG2	2.20	0.41
1:A:63:U:H3'	1:A:63:U:OP2	2.20	0.41
1:A:331:G:C2	1:A:332:A:C5	3.08	0.41
1:A:434:G:O2'	1:A:435:A:H3'	2.21	0.41
1:A:775:A:O2'	1:A:776:C:H5'	2.20	0.41
1:A:918:G:H22	1:A:950:A:H2'	1.85	0.41
1:A:1219:G:C4	1:A:1220:A:C8	3.09	0.41
2:B:33:U:H2'	2:B:34:C:C2	2.56	0.41
7:D:125:LYS:HB2	7:D:173:MET:HB3	2.03	0.41
7:D:134:HIS:CE1	7:D:168:LYS:HG2	2.56	0.41
10:L:28:GLY:O	10:L:29:LYS:C	2.63	0.41
15:O:28:LYS:HD3	15:O:34:VAL:CG1	2.51	0.41
19:S:11:VAL:HG22	19:S:68:VAL:HG12	2.02	0.41
20:T:79:PHE:HD1	20:T:86:ILE:HD13	1.86	0.41
1:A:11:U:C2	1:A:2655:U:OP1	2.74	0.41
1:A:84:A:N6	1:A:99:U:O4'	2.53	0.41
1:A:752:G:C2	1:A:770:G:H5''	2.56	0.41
1:A:1196:C:H2'	1:A:1197:C:H6	1.86	0.41
1:A:1357:G:C2	1:A:1366:U:H5''	2.56	0.41
1:A:1948:G:H2'	1:A:1949:G:C8	2.56	0.41
1:A:2052:C:H2'	1:A:2053:U:C6	2.56	0.41
1:A:2306:G:N7	21:a:22:ARG:NH2	2.69	0.41
1:A:2432:G:H4'	1:A:2433:C:C4	2.56	0.41
1:A:2606:C:H2'	1:A:2607:U:C6	2.56	0.41
1:A:2752:A:H1'	1:A:2753:U:H2'	2.02	0.41
1:A:2777:A:C2	1:A:2780:A:H2	2.38	0.41
2:B:31:G:H21	2:B:34:C:H41	1.69	0.41
2:B:43:A:N3	2:B:43:A:H2'	2.36	0.41
2:B:91:C:P	20:T:16:SER:HB2	2.61	0.41
4:2:12:LYS:NZ	4:2:16:VAL:HG21	2.36	0.41
4:2:35:ARG:HE	4:2:40:ARG:HG2	1.86	0.41
6:F:37:LEU:HB2	6:F:62:TYR:HB2	2.03	0.41
6:F:226:ASN:O	6:F:228:ASN:N	2.48	0.41
7:D:76:HIS:C	7:D:78:LYS:H	2.29	0.41
9:H:7:ALA:O	9:H:46:THR:HG21	2.21	0.41
10:L:85:PHE:O	10:L:119:LYS:NZ	2.46	0.41
11:Y:136:GLU:HA	20:T:57:ARG:HH12	1.86	0.41
15:O:46:ALA:O	15:O:50:ARG:HG3	2.20	0.41
15:O:48:ARG:HE	15:O:48:ARG:HB3	1.76	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:R:65:MET:HG3	18:R:65:MET:O	2.21	0.41
19:S:4:LYS:O	19:S:23:VAL:HG11	2.21	0.41
20:T:94:ILE:HG13	20:T:95:ASN:N	2.36	0.41
1:A:64:A:H4'	18:R:63:LYS:HZ3	1.85	0.41
1:A:156:A:H2'	1:A:157:U:O4'	2.21	0.41
1:A:248:G:O2'	1:A:430:A:N1	2.50	0.41
1:A:680:C:O2'	1:A:684:U:OP1	2.39	0.41
1:A:776:C:HO2'	1:A:777:C:P	2.41	0.41
1:A:1385:G:H2'	1:A:1386:U:O4'	2.20	0.41
1:A:1504:U:H3'	1:A:1504:U:OP2	2.21	0.41
1:A:1736:U:H2'	1:A:1738:C:C2	2.56	0.41
1:A:1741:G:H2'	1:A:1742:A:C5'	2.49	0.41
1:A:2243:U:O2'	1:A:2244:G:H5'	2.21	0.41
1:A:2439:A:P	1:A:2439:A:H8	2.44	0.41
1:A:2679:U:N3	1:A:2696:G:C6	2.89	0.41
10:L:57:LEU:HD12	10:L:60:ARG:HH11	1.85	0.41
1:A:1092:A:N1	1:A:1157:U:H4'	2.36	0.40
1:A:1094:A:H2'	1:A:1095:A:N7	2.36	0.40
1:A:1208:A:H2'	1:A:1209:U:C6	2.55	0.40
1:A:1373:U:H2'	1:A:1374:G:O4'	2.20	0.40
1:A:1786:A:H1'	1:A:2724:G:N2	2.36	0.40
1:A:1799:G:N2	1:A:2007:G:N2	2.61	0.40
1:A:1893:A:C2'	1:A:1894:G:H21	2.34	0.40
1:A:2338:A:OP2	1:A:2339:U:H5	2.03	0.40
1:A:2705:U:H2'	1:A:2706:A:C8	2.56	0.40
1:A:2764:G:H2'	1:A:2765:A:C8	2.56	0.40
1:A:2914:A:H2'	1:A:2915:C:C6	2.56	0.40
10:L:92:THR:OG1	10:L:95:LEU:N	2.50	0.40
1:A:84:A:C2	1:A:102:A:C6	3.10	0.40
1:A:539:G:OP1	17:Q:8:ARG:HD2	2.21	0.40
1:A:737:C:H2'	1:A:738:U:C6	2.56	0.40
1:A:1461:C:H2'	1:A:1462:G:O4'	2.21	0.40
1:A:1974:C:N3	1:A:1987:A:N1	2.69	0.40
1:A:2127:G:C2	1:A:2128:G:C8	3.10	0.40
1:A:2289:U:O2'	1:A:2290:C:H5'	2.21	0.40
1:A:2552:G:O2'	1:A:2768:A:N6	2.53	0.40
1:A:2602:C:H5'	7:D:157:ALA:HB2	2.03	0.40
1:A:2721:G:H1	1:A:2743:U:H3	1.70	0.40
1:A:2774:G:O5'	1:A:2774:G:H8	2.04	0.40
1:A:2873:C:H2'	1:A:2874:A:H8	1.84	0.40
8:E:49:HIS:CD2	8:E:92:PRO:HB2	2.55	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:G:64:ARG:HG2	12:G:83:ALA:HB3	2.03	0.40
19:S:79:THR:HG22	19:S:96:LYS:HZ3	1.83	0.40
23:W:6:ILE:HD12	23:W:53:LEU:CD2	2.52	0.40
25:b:29:GLU:C	25:b:37:LYS:HZ2	2.29	0.40
1:A:90:A:N6	18:R:68:TYR:OH	2.54	0.40
1:A:398:C:C2	1:A:399:U:C5	3.09	0.40
1:A:912:C:H2'	1:A:913:U:C6	2.56	0.40
1:A:1479:G:C6	1:A:1480:G:C6	3.09	0.40
1:A:1742:A:H4'	1:A:1743:G:N7	2.34	0.40
1:A:1965:A:N7	1:A:2617:A:O2'	2.52	0.40
1:A:1990:C:H5''	1:A:1991:G:OP1	2.22	0.40
1:A:2142:G:H2'	1:A:2143:G:C8	2.57	0.40
1:A:2704:A:H2	1:A:2758:G:N2	2.17	0.40
1:A:2816:C:H4'	1:A:2828:U:O2	2.21	0.40
1:A:2832:A:H3'	1:A:2833:U:H5''	2.02	0.40
5:3:48:ARG:HG2	5:3:49:LEU:N	2.32	0.40
6:F:45:ASN:OD1	6:F:45:ASN:N	2.53	0.40
8:E:32:VAL:HG21	8:E:108:LEU:HD23	2.03	0.40
8:E:157:GLU:HG3	8:E:201:LYS:HD2	2.03	0.40
9:H:89:THR:HG22	9:H:92:GLU:HG2	2.03	0.40
9:H:94:ARG:O	9:H:98:PRO:HB3	2.20	0.40
14:N:59:GLU:HG2	14:N:78:LEU:CD2	2.50	0.40
19:S:63:ILE:HD13	19:S:63:ILE:HG21	1.92	0.40
20:T:44:ASP:OD1	20:T:47:GLU:HG3	2.21	0.40
22:V:37:ARG:HD2	22:V:44:PRO:HB2	2.03	0.40
1:A:10:A:H2'	1:A:11:U:N3	2.37	0.40
1:A:52:A:H2'	1:A:53:A:C8	2.56	0.40
1:A:318:A:H2'	1:A:319:G:C8	2.57	0.40
1:A:576:U:H4'	1:A:577:A:H5''	2.03	0.40
1:A:959:C:O2'	1:A:959:C:O2	2.38	0.40
1:A:1762:U:C4	1:A:1768:C:C4	3.09	0.40
1:A:1872:G:O6	1:A:1921:C:H5	2.04	0.40
1:A:2032:A:H2'	1:A:2033:C:C6	2.57	0.40
1:A:2831:G:H2'	1:A:2832:A:C8	2.56	0.40
6:F:34:LEU:HD23	6:F:63:ARG:HG2	2.03	0.40
7:D:119:THR:CG2	7:D:210:GLU:HB2	2.51	0.40
11:Y:14:ARG:HA	11:Y:15:PRO:HD3	1.96	0.40
18:R:64:ARG:HH22	18:R:69:GLN:CD	2.28	0.40
23:W:28:LEU:HD11	23:W:42:ARG:HB3	2.02	0.40
1:A:1757:U:H3'	1:A:1758:A:H8	1.86	0.40
1:A:2163:A:OP2	1:A:2179:A:N6	2.54	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2667:G:N2	1:A:2802:A:H2	2.12	0.40
1:A:2827:A:H2'	1:A:2828:U:O4'	2.21	0.40
2:B:7:G:C8	2:B:7:G:OP2	2.75	0.40
2:B:90:U:H2'	2:B:91:C:C6	2.56	0.40
7:D:41:VAL:HA	7:D:46:TYR:N	2.36	0.40
9:H:8:ASN:ND2	9:H:10:SER:OG	2.54	0.40
15:O:58:ARG:HA	15:O:61:TRP:CE3	2.56	0.40
17:Q:4:LYS:HB3	17:Q:106:VAL:HG22	2.03	0.40
19:S:57:LEU:HD12	19:S:58:GLU:N	2.35	0.40
23:W:52:ARG:O	23:W:56:VAL:HG23	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	1	45/47 (96%)	41 (91%)	4 (9%)	0	100	100
4	2	41/43 (95%)	40 (98%)	1 (2%)	0	100	100
5	3	62/64 (97%)	59 (95%)	3 (5%)	0	100	100
6	F	272/274 (99%)	247 (91%)	25 (9%)	0	100	100
7	D	213/215 (99%)	172 (81%)	40 (19%)	1 (0%)	24	40
8	E	204/206 (99%)	188 (92%)	16 (8%)	0	100	100
9	H	141/144 (98%)	124 (88%)	17 (12%)	0	100	100
10	L	144/146 (99%)	128 (89%)	16 (11%)	0	100	100
11	Y	135/137 (98%)	119 (88%)	16 (12%)	0	100	100
12	G	120/122 (98%)	105 (88%)	15 (12%)	0	100	100
13	M	115/117 (98%)	101 (88%)	14 (12%)	0	100	100
14	N	109/114 (96%)	91 (84%)	18 (16%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	O	114/116 (98%)	111 (97%)	3 (3%)	0	100	100
16	P	100/102 (98%)	88 (88%)	10 (10%)	2 (2%)	6	10
17	Q	110/112 (98%)	104 (94%)	6 (6%)	0	100	100
18	R	87/89 (98%)	77 (88%)	10 (12%)	0	100	100
19	S	101/103 (98%)	82 (81%)	19 (19%)	0	100	100
20	T	92/94 (98%)	76 (83%)	16 (17%)	0	100	100
21	a	77/79 (98%)	70 (91%)	7 (9%)	0	100	100
22	V	47/49 (96%)	44 (94%)	3 (6%)	0	100	100
23	W	65/67 (97%)	58 (89%)	7 (11%)	0	100	100
24	X	56/58 (97%)	52 (93%)	4 (7%)	0	100	100
25	b	46/48 (96%)	35 (76%)	11 (24%)	0	100	100
All	All	2496/2546 (98%)	2212 (89%)	281 (11%)	3 (0%)	49	69

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	P	51	PRO
7	D	6	LEU
16	P	78	ARG

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	
3	1	44/45 (98%)	44 (100%)	0	100	100
4	2	39/39 (100%)	39 (100%)	0	100	100
5	3	55/55 (100%)	55 (100%)	0	100	100
6	F	221/221 (100%)	221 (100%)	0	100	100
7	D	173/173 (100%)	172 (99%)	1 (1%)	78	87
8	E	168/168 (100%)	167 (99%)	1 (1%)	78	87

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	H	121/122 (99%)	121 (100%)	0	100	100
10	L	109/112 (97%)	109 (100%)	0	100	100
11	Y	108/114 (95%)	108 (100%)	0	100	100
12	G	100/100 (100%)	99 (99%)	1 (1%)	68	80
13	M	83/93 (89%)	83 (100%)	0	100	100
14	N	92/100 (92%)	91 (99%)	1 (1%)	65	79
15	O	96/96 (100%)	95 (99%)	1 (1%)	68	80
16	P	84/86 (98%)	83 (99%)	1 (1%)	63	77
17	Q	89/91 (98%)	88 (99%)	1 (1%)	65	79
18	R	78/80 (98%)	77 (99%)	1 (1%)	61	75
19	S	81/88 (92%)	81 (100%)	0	100	100
20	T	78/82 (95%)	78 (100%)	0	100	100
21	a	59/62 (95%)	59 (100%)	0	100	100
22	V	39/41 (95%)	38 (97%)	1 (3%)	40	62
23	W	58/60 (97%)	58 (100%)	0	100	100
24	X	52/52 (100%)	51 (98%)	1 (2%)	50	68
25	b	35/44 (80%)	35 (100%)	0	100	100
All	All	2062/2124 (97%)	2052 (100%)	10 (0%)	78	88

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	D	216	LYS
8	E	29	ASN
12	G	122	LEU
14	N	113	GLN
15	O	88	ILE
16	P	52	THR
17	Q	112	GLU
18	R	90	PHE
22	V	60	THR
24	X	58	GLU

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

Mol	Chain	Res	Type
5	3	31	HIS
7	D	47	ASN
7	D	134	HIS
7	D	167	GLN
7	D	200	ASN
8	E	49	HIS
8	E	148	GLN
8	E	179	GLN
8	E	188	ASN
9	H	3	GLN
9	H	59	ASN
9	H	131	HIS
10	L	4	HIS
10	L	17	ASN
10	L	38	GLN
10	L	83	ASN
11	Y	12	GLN
11	Y	46	GLN
13	M	15	HIS
16	P	63	ASN
16	P	101	ASN
17	Q	97	ASN
19	S	39	ASN
21	a	37	GLN
23	W	31	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2728/2742 (99%)	948 (34%)	51 (1%)
2	B	101/106 (95%)	44 (43%)	3 (2%)
All	All	2829/2848 (99%)	992 (35%)	54 (1%)

All (992) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	11	U
1	A	14	A
1	A	15	G
1	A	24	G
1	A	25	U
1	A	28	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	34	U
1	A	36	G
1	A	42	G
1	A	43	A
1	A	45	G
1	A	46	C
1	A	47	C
1	A	58	G
1	A	61	A
1	A	63	U
1	A	64	A
1	A	71	A
1	A	75	G
1	A	77	U
1	A	80	G
1	A	81	G
1	A	84	A
1	A	85	G
1	A	87	U
1	A	89	U
1	A	90	A
1	A	92	G
1	A	93	U
1	A	94	A
1	A	96	G
1	A	99	U
1	A	100	U
1	A	103	U
1	A	107	G
1	A	108	A
1	A	117	A
1	A	118	A
1	A	119	U
1	A	130	A
1	A	136	A
1	A	139	U
1	A	146	U
1	A	160	G
1	A	161	A
1	A	164	A
1	A	165	C
1	A	166	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	167	U
1	A	171	A
1	A	174	U
1	A	176	A
1	A	177	G
1	A	180	G
1	A	182	C
1	A	184	C
1	A	185	A
1	A	199	A
1	A	213	C
1	A	214	G
1	A	216	A
1	A	219	A
1	A	224	A
1	A	225	A
1	A	226	A
1	A	230	A
1	A	231	A
1	A	232	U
1	A	233	U
1	A	235	G
1	A	236	A
1	A	248	G
1	A	251	G
1	A	255	G
1	A	264	G
1	A	267	G
1	A	268	A
1	A	269	G
1	A	276	C
1	A	277	C
1	A	278	A
1	A	279	A
1	A	280	C
1	A	281	A
1	A	282	A
1	A	283	G
1	A	284	C
1	A	285	U
1	A	286	U
1	A	287	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	288	C
1	A	291	G
1	A	293	U
1	A	295	G
1	A	297	G
1	A	300	G
1	A	301	U
1	A	302	A
1	A	308	C
1	A	310	C
1	A	311	U
1	A	315	C
1	A	317	G
1	A	318	A
1	A	321	U
1	A	324	A
1	A	327	G
1	A	329	A
1	A	331	G
1	A	333	C
1	A	334	A
1	A	336	U
1	A	337	A
1	A	338	G
1	A	353	A
1	A	359	A
1	A	360	A
1	A	365	A
1	A	373	A
1	A	375	A
1	A	387	G
1	A	388	A
1	A	391	A
1	A	393	G
1	A	395	U
1	A	396	G
1	A	398	C
1	A	402	C
1	A	404	U
1	A	409	G
1	A	410	G
1	A	416	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	417	A
1	A	418	G
1	A	432	G
1	A	433	U
1	A	435	A
1	A	436	A
1	A	437	A
1	A	444	C
1	A	445	G
1	A	450	C
1	A	454	G
1	A	457	G
1	A	458	A
1	A	460	C
1	A	461	A
1	A	463	C
1	A	464	U
1	A	481	C
1	A	486	G
1	A	489	A
1	A	490	C
1	A	494	U
1	A	505	U
1	A	506	A
1	A	520	G
1	A	521	U
1	A	522	G
1	A	526	A
1	A	527	G
1	A	529	A
1	A	535	G
1	A	539	G
1	A	547	A
1	A	549	U
1	A	550	A
1	A	551	G
1	A	553	A
1	A	554	C
1	A	573	A
1	A	574	A
1	A	576	U
1	A	577	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	583	A
1	A	587	C
1	A	591	A
1	A	592	A
1	A	593	U
1	A	594	G
1	A	598	G
1	A	599	A
1	A	606	G
1	A	616	G
1	A	617	A
1	A	618	A
1	A	630	G
1	A	637	U
1	A	646	A
1	A	657	U
1	A	659	A
1	A	660	A
1	A	665	G
1	A	666	A
1	A	678	A
1	A	679	G
1	A	682	A
1	A	699	U
1	A	713	A
1	A	720	A
1	A	727	G
1	A	731	U
1	A	746	G
1	A	749	G
1	A	750	A
1	A	751	A
1	A	752	G
1	A	754	U
1	A	755	C
1	A	756	A
1	A	765	U
1	A	766	G
1	A	769	U
1	A	770	G
1	A	771	G
1	A	772	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	773	G
1	A	775	A
1	A	776	C
1	A	777	C
1	A	785	C
1	A	788	A
1	A	791	U
1	A	792	5MU
1	A	797	A
1	A	809	A
1	A	813	G
1	A	815	G
1	A	816	G
1	A	820	G
1	A	822	G
1	A	827	A
1	A	829	U
1	A	834	A
1	A	837	G
1	A	839	A
1	A	847	A
1	A	850	G
1	A	851	C
1	A	857	C
1	A	868	A
1	A	872	U
1	A	873	U
1	A	875	G
1	A	891	A
1	A	893	G
1	A	900	G
1	A	901	G
1	A	903	G
1	A	904	G
1	A	909	G
1	A	910	C
1	A	911	A
1	A	917	U
1	A	921	C
1	A	922	G
1	A	925	G
1	A	926	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	928	C
1	A	938	G
1	A	940	U
1	A	947	U
1	A	949	C
1	A	950	A
1	A	951	G
1	A	952	A
1	A	955	A
1	A	959	C
1	A	960	C
1	A	962	A
1	A	965	G
1	A	971	U
1	A	973	A
1	A	977	A
1	A	989	A
1	A	990	G
1	A	995	U
1	A	1003	A
1	A	1005	G
1	A	1015	C
1	A	1018	A
1	A	1019	A
1	A	1027	A
1	A	1040	A
1	A	1042	C
1	A	1043	U
1	A	1046	G
1	A	1050	C
1	A	1051	C
1	A	1056	U
1	A	1057	A
1	A	1058	U
1	A	1065	A
1	A	1075	G
1	A	1077	U
1	A	1078	G
1	A	1081	G
1	A	1083	G
1	A	1085	U
1	A	1086	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1088	C
1	A	1089	C
1	A	1090	A
1	A	1091	G
1	A	1095	A
1	A	1154	G
1	A	1155	A
1	A	1156	G
1	A	1162	C
1	A	1164	G
1	A	1166	G
1	A	1169	G
1	A	1170	A
1	A	1171	A
1	A	1172	A
1	A	1173	A
1	A	1174	U
1	A	1176	U
1	A	1177	A
1	A	1178	C
1	A	1179	C
1	A	1183	G
1	A	1185	U
1	A	1186	A
1	A	1190	A
1	A	1193	U
1	A	1194	U
1	A	1201	G
1	A	1204	G
1	A	1211	G
1	A	1212	U
1	A	1213	C
1	A	1214	C
1	A	1215	U
1	A	1216	U
1	A	1217	U
1	A	1218	G
1	A	1219	G
1	A	1220	A
1	A	1221	C
1	A	1222	A
1	A	1225	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1245	G
1	A	1250	G
1	A	1258	A
1	A	1275	A
1	A	1285	A
1	A	1286	G
1	A	1289	A
1	A	1291	A
1	A	1294	G
1	A	1309	G
1	A	1310	A
1	A	1311	A
1	A	1312	A
1	A	1313	G
1	A	1321	A
1	A	1324	A
1	A	1336	G
1	A	1337	A
1	A	1338	U
1	A	1344	A
1	A	1347	G
1	A	1348	U
1	A	1350	U
1	A	1355	A
1	A	1357	G
1	A	1370	C
1	A	1381	U
1	A	1383	G
1	A	1387	C
1	A	1389	U
1	A	1392	G
1	A	1396	A
1	A	1402	A
1	A	1403	C
1	A	1405	G
1	A	1407	C
1	A	1410	A
1	A	1416	U
1	A	1421	A
1	A	1425	G
1	A	1429	G
1	A	1431	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1440	A
1	A	1442	C
1	A	1444	C
1	A	1447	A
1	A	1449	A
1	A	1450	A
1	A	1452	C
1	A	1453	G
1	A	1454	U
1	A	1455	U
1	A	1459	A
1	A	1460	U
1	A	1463	A
1	A	1464	U
1	A	1465	G
1	A	1466	G
1	A	1467	G
1	A	1469	G
1	A	1472	C
1	A	1473	G
1	A	1474	C
1	A	1479	G
1	A	1480	G
1	A	1486	C
1	A	1487	G
1	A	1490	G
1	A	1491	C
1	A	1492	G
1	A	1494	G
1	A	1495	C
1	A	1496	G
1	A	1497	A
1	A	1498	U
1	A	1499	U
1	A	1503	U
1	A	1504	U
1	A	1505	G
1	A	1506	C
1	A	1508	C
1	A	1509	G
1	A	1599	G
1	A	1600	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1604	C
1	A	1605	A
1	A	1606	C
1	A	1613	G
1	A	1616	A
1	A	1625	U
1	A	1626	A
1	A	1627	G
1	A	1629	U
1	A	1630	A
1	A	1632	A
1	A	1635	A
1	A	1638	G
1	A	1639	G
1	A	1640	U
1	A	1645	G
1	A	1650	G
1	A	1651	C
1	A	1652	A
1	A	1653	A
1	A	1654	A
1	A	1675	G
1	A	1677	G
1	A	1678	A
1	A	1679	A
1	A	1690	A
1	A	1691	G
1	A	1692	C
1	A	1698	A
1	A	1701	U
1	A	1703	U
1	A	1707	U
1	A	1717	G
1	A	1718	G
1	A	1725	G
1	A	1726	A
1	A	1727	C
1	A	1730	C
1	A	1731	G
1	A	1732	U
1	A	1734	A
1	A	1735	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1737	U
1	A	1738	C
1	A	1739	G
1	A	1740	G
1	A	1741	G
1	A	1742	A
1	A	1743	G
1	A	1744	A
1	A	1747	G
1	A	1748	G
1	A	1749	G
1	A	1750	U
1	A	1751	G
1	A	1752	C
1	A	1755	U
1	A	1759	G
1	A	1761	G
1	A	1762	U
1	A	1763	U
1	A	1764	A
1	A	1765	A
1	A	1766	C
1	A	1767	G
1	A	1768	C
1	A	1769	C
1	A	1770	C
1	A	1771	A
1	A	1772	G
1	A	1782	A
1	A	1785	G
1	A	1790	G
1	A	1791	G
1	A	1793	C
1	A	1797	G
1	A	1800	A
1	A	1803	G
1	A	1806	U
1	A	1808	U
1	A	1811	A
1	A	1813	A
1	A	1816	A
1	A	1820	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1827	C
1	A	1828	U
1	A	1837	A
1	A	1843	U
1	A	1852	G
1	A	1856	A
1	A	1860	C
1	A	1864	C
1	A	1865	C
1	A	1866	G
1	A	1867	G
1	A	1868	U
1	A	1870	C
1	A	1872	G
1	A	1874	A
1	A	1877	G
1	A	1879	U
1	A	1880	A
1	A	1882	G
1	A	1883	A
1	A	1884	G
1	A	1885	G
1	A	1887	G
1	A	1888	U
1	A	1889	G
1	A	1890	G
1	A	1891	U
1	A	1892	U
1	A	1893	A
1	A	1894	G
1	A	1895	C
1	A	1897	U
1	A	1899	U
1	A	1901	C
1	A	1904	A
1	A	1905	G
1	A	1908	A
1	A	1910	G
1	A	1912	A
1	A	1913	U
1	A	1915	G
1	A	1916	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1922	C
1	A	1923	A
1	A	1924	G
1	A	1925	U
1	A	1926	A
1	A	1929	C
1	A	1933	G
1	A	1935	C
1	A	1938	U
1	A	1939	A
1	A	1945	A
1	A	1946	A
1	A	1950	U
1	A	1953	U
1	A	1956	G
1	A	1957	G
1	A	1958	U
1	A	1961	C
1	A	1963	A
1	A	1964	A
1	A	1965	A
1	A	1968	C
1	A	1971	U
1	A	1973	U
1	A	1975	G
1	A	1976	G
1	A	1977	G
1	A	1981	G
1	A	1982	U
1	A	1983	U
1	A	1984	C
1	A	1985	C
1	A	1986	G
1	A	1987	A
1	A	1988	C
1	A	1989	C
1	A	1991	G
1	A	1992	C
1	A	1993	A
1	A	1994	C
1	A	1995	G
1	A	1996	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1997	A
1	A	1998	A
1	A	1999	G
1	A	2000	G
1	A	2002	G
1	A	2003	U
1	A	2004	A
1	A	2005	A
1	A	2006	C
1	A	2007	G
1	A	2008	A
1	A	2012	G
1	A	2013	G
1	A	2018	U
1	A	2019	G
1	A	2020	U
1	A	2021	C
1	A	2023	C
1	A	2032	A
1	A	2033	C
1	A	2034	U
1	A	2047	A
1	A	2048	G
1	A	2050	A
1	A	2054	G
1	A	2058	A
1	A	2059	G
1	A	2060	A
1	A	2063	C
1	A	2070	C
1	A	2076	A
1	A	2079	G
1	A	2082	C
1	A	2083	G
1	A	2087	A
1	A	2088	G
1	A	2089	A
1	A	2096	G
1	A	2097	G
1	A	2098	A
1	A	2111	C
1	A	2114	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	2115	A
1	A	2116	U
1	A	2118	U
1	A	2120	G
1	A	2122	A
1	A	2123	A
1	A	2129	C
1	A	2130	A
1	A	2133	G
1	A	2134	C
1	A	2135	U
1	A	2137	G
1	A	2138	U
1	A	2139	A
1	A	2140	C
1	A	2141	A
1	A	2142	G
1	A	2143	G
1	A	2145	U
1	A	2146	A
1	A	2147	G
1	A	2153	A
1	A	2154	G
1	A	2155	C
1	A	2158	U
1	A	2160	G
1	A	2162	A
1	A	2163	A
1	A	2165	G
1	A	2167	G
1	A	2170	C
1	A	2171	G
1	A	2172	C
1	A	2173	U
1	A	2174	A
1	A	2179	A
1	A	2183	G
1	A	2185	A
1	A	2186	G
1	A	2190	C
1	A	2193	G
1	A	2194	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	2195	G
1	A	2196	G
1	A	2198	A
1	A	2201	C
1	A	2203	A
1	A	2204	C
1	A	2205	C
1	A	2209	G
1	A	2210	C
1	A	2211	U
1	A	2214	G
1	A	2219	C
1	A	2221	U
1	A	2225	A
1	A	2226	A
1	A	2230	G
1	A	2231	C
1	A	2235	A
1	A	2236	C
1	A	2238	U
1	A	2239	A
1	A	2241	C
1	A	2243	U
1	A	2244	G
1	A	2245	G
1	A	2247	G
1	A	2251	G
1	A	2252	A
1	A	2253	C
1	A	2254	A
1	A	2256	U
1	A	2262	G
1	A	2263	C
1	A	2265	G
1	A	2266	G
1	A	2291	C
1	A	2295	A
1	A	2306	G
1	A	2310	C
1	A	2314	A
1	A	2319	U
1	A	2320	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	2321	C
1	A	2322	C
1	A	2324	C
1	A	2328	A
1	A	2330	G
1	A	2332	U
1	A	2334	G
1	A	2335	G
1	A	2336	A
1	A	2338	A
1	A	2342	U
1	A	2344	C
1	A	2345	A
1	A	2346	U
1	A	2347	A
1	A	2348	G
1	A	2352	G
1	A	2354	A
1	A	2358	G
1	A	2362	A
1	A	2363	A
1	A	2364	G
1	A	2371	U
1	A	2372	G
1	A	2374	C
1	A	2377	C
1	A	2388	A
1	A	2394	G
1	A	2397	G
1	A	2399	G
1	A	2400	U
1	A	2410	G
1	A	2412	C
1	A	2417	U
1	A	2418	G
1	A	2419	A
1	A	2425	U
1	A	2426	G
1	A	2427	G
1	A	2429	U
1	A	2430	C
1	A	2433	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	2434	A
1	A	2438	A
1	A	2441	G
1	A	2445	A
1	A	2453	A
1	A	2455	G
1	A	2456	G
1	A	2457	A
1	A	2459	A
1	A	2460	A
1	A	2462	A
1	A	2466	A
1	A	2467	C
1	A	2468	C
1	A	2469	C
1	A	2472	G
1	A	2474	G
1	A	2475	A
1	A	2476	U
1	A	2490	C
1	A	2494	C
1	A	2495	A
1	A	2496	A
1	A	2499	G
1	A	2502	C
1	A	2503	A
1	A	2505	A
1	A	2508	G
1	A	2509	A
1	A	2511	G
1	A	2514	G
1	A	2516	G
1	A	2519	U
1	A	2520	U
1	A	2529	G
1	A	2530	2MA
1	A	2531	U
1	A	2532	G
1	A	2535	G
1	A	2545	A
1	A	2547	C
1	A	2551	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	2552	G
1	A	2553	G
1	A	2554	C
1	A	2556	G
1	A	2558	A
1	A	2559	G
1	A	2561	C
1	A	2562	G
1	A	2566	C
1	A	2569	A
1	A	2570	G
1	A	2574	U
1	A	2575	G
1	A	2578	C
1	A	2579	U
1	A	2589	U
1	A	2591	A
1	A	2592	A
1	A	2593	A
1	A	2594	G
1	A	2600	C
1	A	2601	G
1	A	2603	G
1	A	2604	A
1	A	2605	G
1	A	2609	G
1	A	2613	C
1	A	2621	C
1	A	2629	A
1	A	2630	G
1	A	2631	U
1	A	2636	U
1	A	2637	C
1	A	2640	U
1	A	2642	U
1	A	2655	U
1	A	2656	A
1	A	2657	G
1	A	2658	G
1	A	2663	U
1	A	2672	G
1	A	2673	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	2674	U
1	A	2675	G
1	A	2677	C
1	A	2679	U
1	A	2680	U
1	A	2682	G
1	A	2683	U
1	A	2685	C
1	A	2686	G
1	A	2687	A
1	A	2689	A
1	A	2690	G
1	A	2692	A
1	A	2695	G
1	A	2697	G
1	A	2698	A
1	A	2699	U
1	A	2710	C
1	A	2717	A
1	A	2719	C
1	A	2720	A
1	A	2723	U
1	A	2729	G
1	A	2730	C
1	A	2731	C
1	A	2734	C
1	A	2735	G
1	A	2741	G
1	A	2745	G
1	A	2747	U
1	A	2748	A
1	A	2749	G
1	A	2750	C
1	A	2753	U
1	A	2759	G
1	A	2760	A
1	A	2761	C
1	A	2763	G
1	A	2764	G
1	A	2766	U
1	A	2769	G
1	A	2775	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	2777	A
1	A	2778	G
1	A	2779	C
1	A	2784	A
1	A	2786	G
1	A	2788	A
1	A	2789	U
1	A	2791	A
1	A	2794	C
1	A	2796	C
1	A	2797	C
1	A	2798	C
1	A	2804	G
1	A	2806	U
1	A	2807	G
1	A	2808	A
1	A	2809	G
1	A	2810	A
1	A	2815	C
1	A	2817	A
1	A	2818	A
1	A	2823	G
1	A	2829	A
1	A	2831	G
1	A	2832	A
1	A	2833	U
1	A	2836	C
1	A	2837	U
1	A	2839	A
1	A	2852	U
1	A	2853	U
1	A	2854	A
1	A	2855	A
1	A	2857	A
1	A	2858	G
1	A	2860	U
1	A	2862	C
1	A	2866	G
1	A	2867	U
1	A	2868	G
1	A	2875	U
1	A	2877	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	2882	A
1	A	2883	U
1	A	2884	G
1	A	2885	U
1	A	2886	G
1	A	2887	G
1	A	2892	G
1	A	2893	A
1	A	2894	C
1	A	2899	A
1	A	2901	U
1	A	2904	U
1	A	2905	C
1	A	2907	A
1	A	2911	A
1	A	2917	U
1	A	2919	A
1	A	2920	U
2	B	6	U
2	B	7	G
2	B	8	A
2	B	14	G
2	B	16	A
2	B	17	A
2	B	18	G
2	B	20	A
2	B	22	G
2	B	23	U
2	B	25	A
2	B	28	C
2	B	29	C
2	B	31	G
2	B	32	U
2	B	34	C
2	B	35	C
2	B	38	U
2	B	41	C
2	B	43	A
2	B	44	A
2	B	45	C
2	B	49	G
2	B	54	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	B	60	C
2	B	62	U
2	B	63	U
2	B	64	A
2	B	65	G
2	B	73	G
2	B	74	G
2	B	75	U
2	B	76	A
2	B	79	C
2	B	82	A
2	B	92	C
2	B	97	G
2	B	98	A
2	B	100	U
2	B	106	G
2	B	108	U
2	B	113	G
2	B	114	G
2	B	115	C

All (54) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	13	A
1	A	99	U
1	A	281	A
1	A	352	A
1	A	416	G
1	A	525	A
1	A	572	C
1	A	749	G
1	A	774	G
1	A	775	A
1	A	809	A
1	A	815	G
1	A	908	A
1	A	951	G
1	A	1155	A
1	A	1210	U
1	A	1490	G
1	A	1508	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	1676	A
1	A	1678	A
1	A	1706	U
1	A	1739	G
1	A	1742	A
1	A	1922	C
1	A	1980	A
1	A	1982	U
1	A	1989	C
1	A	1999	G
1	A	2003	U
1	A	2006	C
1	A	2007	G
1	A	2012	G
1	A	2020	U
1	A	2032	A
1	A	2075	G
1	A	2081	A
1	A	2097	G
1	A	2513	G
1	A	2515	A
1	A	2553	G
1	A	2574	U
1	A	2591	A
1	A	2603	G
1	A	2657	G
1	A	2746	G
1	A	2783	U
1	A	2851	G
1	A	2854	A
1	A	2866	G
1	A	2883	U
1	A	2900	C
2	B	16	A
2	B	64	A
2	B	97	G

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

3 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	5MU	A	792	1	19,22,23	4.96	7 (36%)	27,32,35	3.86	12 (44%)
1	2MA	A	2530	1	22,25,26	3.80	10 (45%)	32,37,40	2.71	11 (34%)
1	5MU	A	1966	1	19,22,23	5.18	7 (36%)	27,32,35	3.57	12 (44%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	5MU	A	792	1	-	0/7/25/26	0/2/2/2
1	2MA	A	2530	1	-	3/7/25/26	0/3/3/3
1	5MU	A	1966	1	-	2/7/25/26	0/2/2/2

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1966	5MU	C2-N1	12.85	1.58	1.38
1	A	792	5MU	C2-N1	11.90	1.57	1.38
1	A	2530	2MA	C4-N3	11.28	1.48	1.34
1	A	1966	5MU	C6-N1	10.81	1.56	1.38
1	A	1966	5MU	C4-C5	10.67	1.62	1.44
1	A	792	5MU	C4-C5	10.26	1.61	1.44
1	A	792	5MU	C6-N1	10.22	1.55	1.38
1	A	792	5MU	C4-N3	-7.35	1.25	1.38
1	A	1966	5MU	C4-N3	-7.18	1.25	1.38
1	A	2530	2MA	C6-N1	7.09	1.44	1.35
1	A	1966	5MU	C6-C5	6.66	1.45	1.34
1	A	792	5MU	C6-C5	6.23	1.44	1.34
1	A	2530	2MA	C2-N3	6.23	1.44	1.34
1	A	2530	2MA	C2-N1	5.51	1.43	1.34
1	A	2530	2MA	C5-C6	4.57	1.53	1.41
1	A	2530	2MA	C6-N6	-3.45	1.25	1.34
1	A	792	5MU	O4-C4	-3.36	1.17	1.23
1	A	792	5MU	O2-C2	-3.19	1.17	1.23

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	2530	2MA	C4-N9	-3.08	1.31	1.37
1	A	2530	2MA	C5-C4	-2.99	1.33	1.39
1	A	2530	2MA	C5-N7	-2.88	1.33	1.39
1	A	1966	5MU	O4-C4	-2.73	1.18	1.23
1	A	1966	5MU	O2-C2	-2.43	1.18	1.23
1	A	2530	2MA	C8-N9	-2.29	1.33	1.37

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	792	5MU	C5-C4-N3	12.26	125.98	115.32
1	A	1966	5MU	C5-C4-N3	11.38	125.21	115.32
1	A	792	5MU	C5-C6-N1	-9.84	112.62	123.31
1	A	1966	5MU	C5-C6-N1	-8.82	113.73	123.31
1	A	2530	2MA	N9-C8-N7	-6.85	104.21	113.94
1	A	2530	2MA	C1'-N9-C8	-6.42	112.85	127.09
1	A	2530	2MA	C4-N9-C8	5.69	111.71	105.74
1	A	792	5MU	C4-N3-C2	-5.45	120.20	127.34
1	A	792	5MU	O4-C4-C5	-5.05	119.14	124.92
1	A	792	5MU	N3-C2-N1	4.72	121.04	114.89
1	A	792	5MU	C5M-C5-C6	-4.71	116.47	122.85
1	A	792	5MU	C5M-C5-C4	4.59	123.69	118.78
1	A	2530	2MA	C5-C4-N3	-4.58	122.35	127.18
1	A	1966	5MU	N3-C2-N1	4.50	120.75	114.89
1	A	1966	5MU	C4-N3-C2	-4.50	121.44	127.34
1	A	1966	5MU	C5M-C5-C6	-4.28	117.06	122.85
1	A	1966	5MU	C5M-C5-C4	4.27	123.34	118.78
1	A	1966	5MU	O4-C4-C5	-4.08	120.25	124.92
1	A	2530	2MA	C5-N7-C8	3.91	109.60	103.45
1	A	2530	2MA	CM2-C2-N1	3.84	122.88	117.13
1	A	2530	2MA	C4-N9-C1'	3.76	135.43	126.63
1	A	2530	2MA	N3-C2-N1	-3.72	119.20	125.77
1	A	1966	5MU	C1'-N1-C2	3.01	122.99	117.59
1	A	1966	5MU	O4-C4-N3	-2.97	114.52	120.11
1	A	2530	2MA	N3-C4-N9	2.83	130.58	126.99
1	A	792	5MU	O4-C4-N3	-2.78	114.88	120.11
1	A	2530	2MA	C4-C5-N7	-2.77	107.41	110.58
1	A	792	5MU	C1'-N1-C2	2.67	122.38	117.59
1	A	1966	5MU	O2-C2-N3	-2.48	116.91	121.49
1	A	792	5MU	C1'-N1-C6	-2.34	117.30	121.15
1	A	2530	2MA	N6-C6-N1	2.27	120.08	117.03
1	A	792	5MU	C6-C5-C4	2.20	119.84	118.02

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1966	5MU	C6-N1-C2	-2.08	119.24	121.30
1	A	1966	5MU	C1'-N1-C6	-2.07	117.75	121.15
1	A	792	5MU	O2-C2-N1	-2.02	120.17	122.80

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	2530	2MA	O4'-C4'-C5'-O5'
1	A	1966	5MU	C2'-C1'-N1-C2
1	A	1966	5MU	C2'-C1'-N1-C6
1	A	2530	2MA	C3'-C4'-C5'-O5'
1	A	2530	2MA	C4'-C5'-O5'-P

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1966	5MU	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	11

Continued on next page...

Continued from previous page...

Mol	Chain	Number of breaks
2	B	4
9	H	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	1067:U	O3'	1074:G	P	32.56
1	A	1509:G	O3'	1598:U	P	17.87
1	A	2911:A	O3'	2914:A	P	16.95
1	A	1096:C	O3'	1151:G	P	15.42
1	A	758:G	O3'	764:C	P	14.44
1	B	9:C	O3'	13:A	P	14.19
1	A	686:U	O3'	691:A	P	14.11
1	A	1939:A	O3'	1944:U	P	13.86
1	A	929:C	O3'	937:G	P	12.60
1	A	1860:C	O3'	1862:G	P	10.14
1	A	2206:C	O3'	2208:A	P	9.45
1	A	2791:A	O3'	2793:G	P	8.08
1	B	76:A	O3'	78:U	P	7.15
1	B	86:A	O3'	88:G	P	5.72
1	B	38:U	O3'	40:C	P	5.39
1	H	1:MET	C	3:GLN	N	4.35

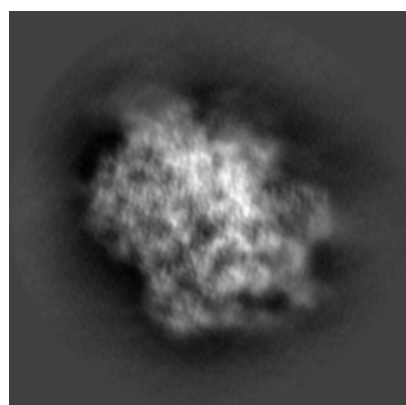
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11901. These allow visual inspection of the internal detail of the map and identification of artifacts.

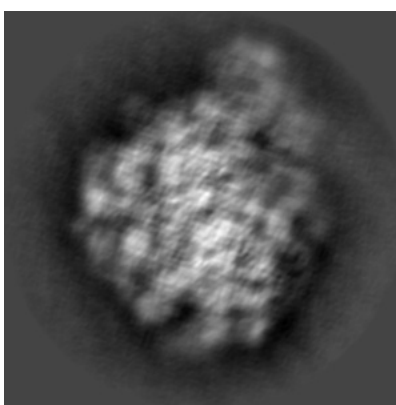
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

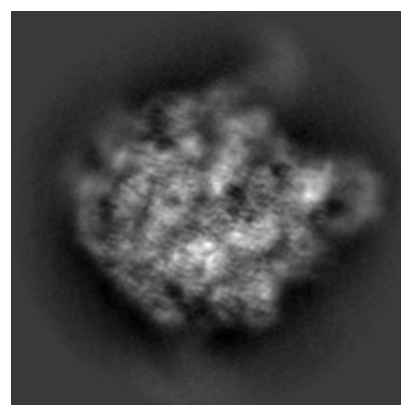
6.1.1 Primary map



X



Y

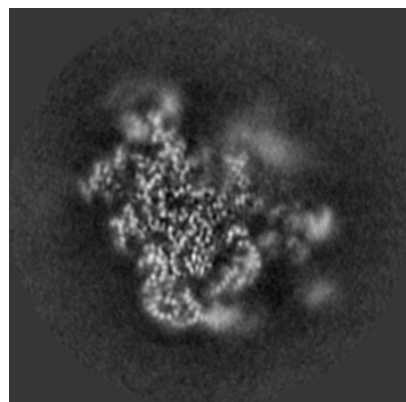


Z

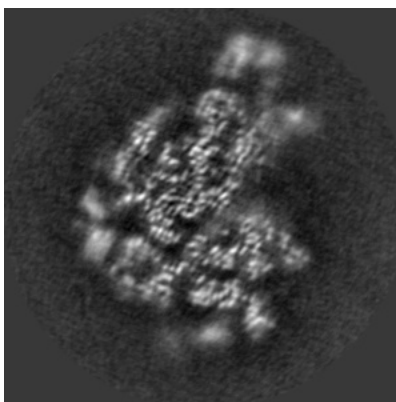
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

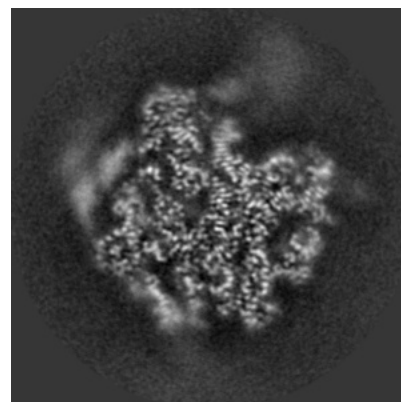
6.2.1 Primary map



X Index: 164



Y Index: 164

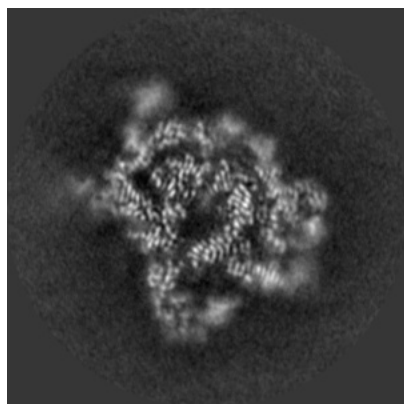


Z Index: 164

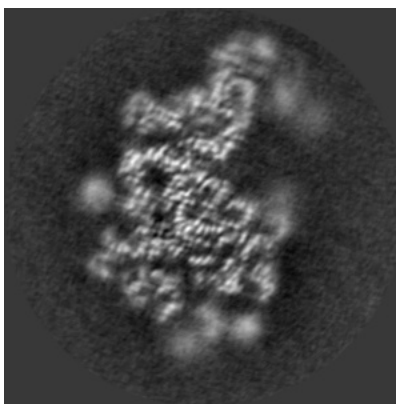
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

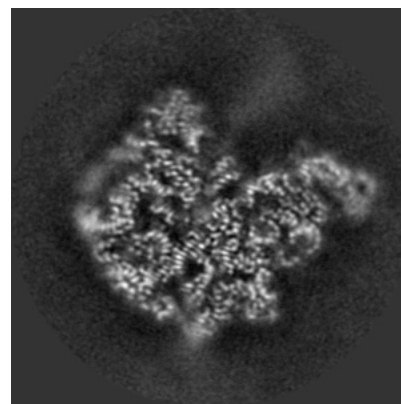
6.3.1 Primary map



X Index: 146



Y Index: 188

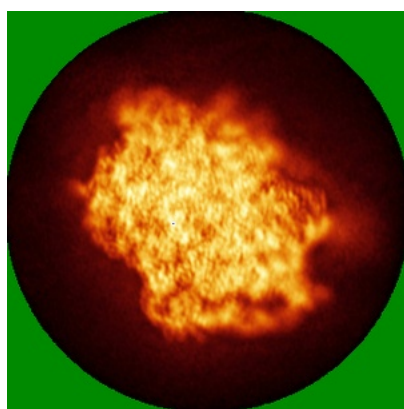


Z Index: 180

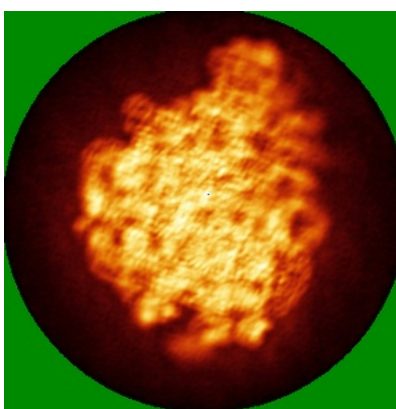
The images above show the largest variance slices of the map in three orthogonal directions.

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

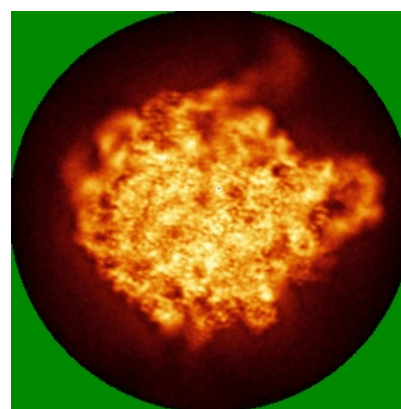
6.4.1 Primary map



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



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0026. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

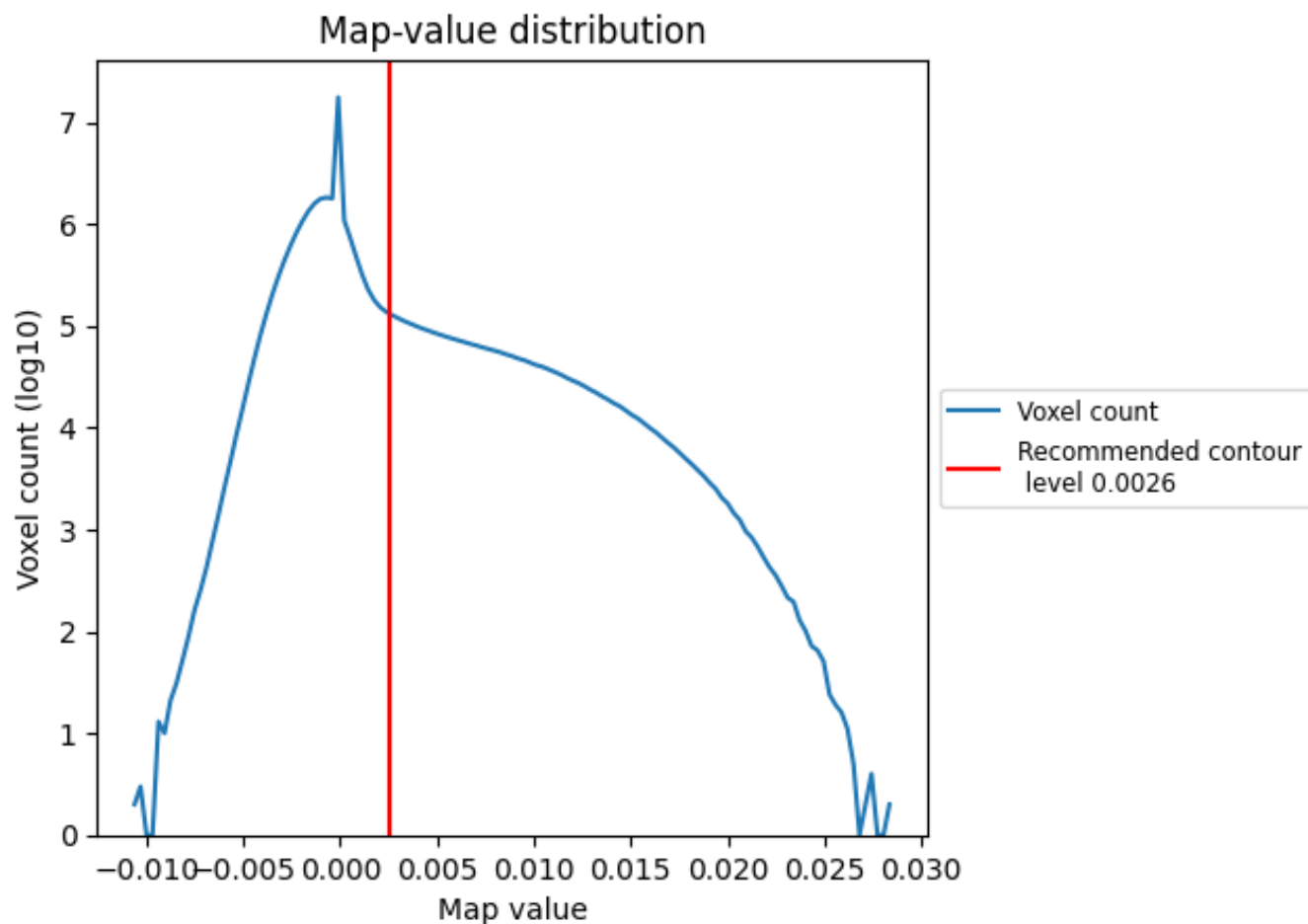
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

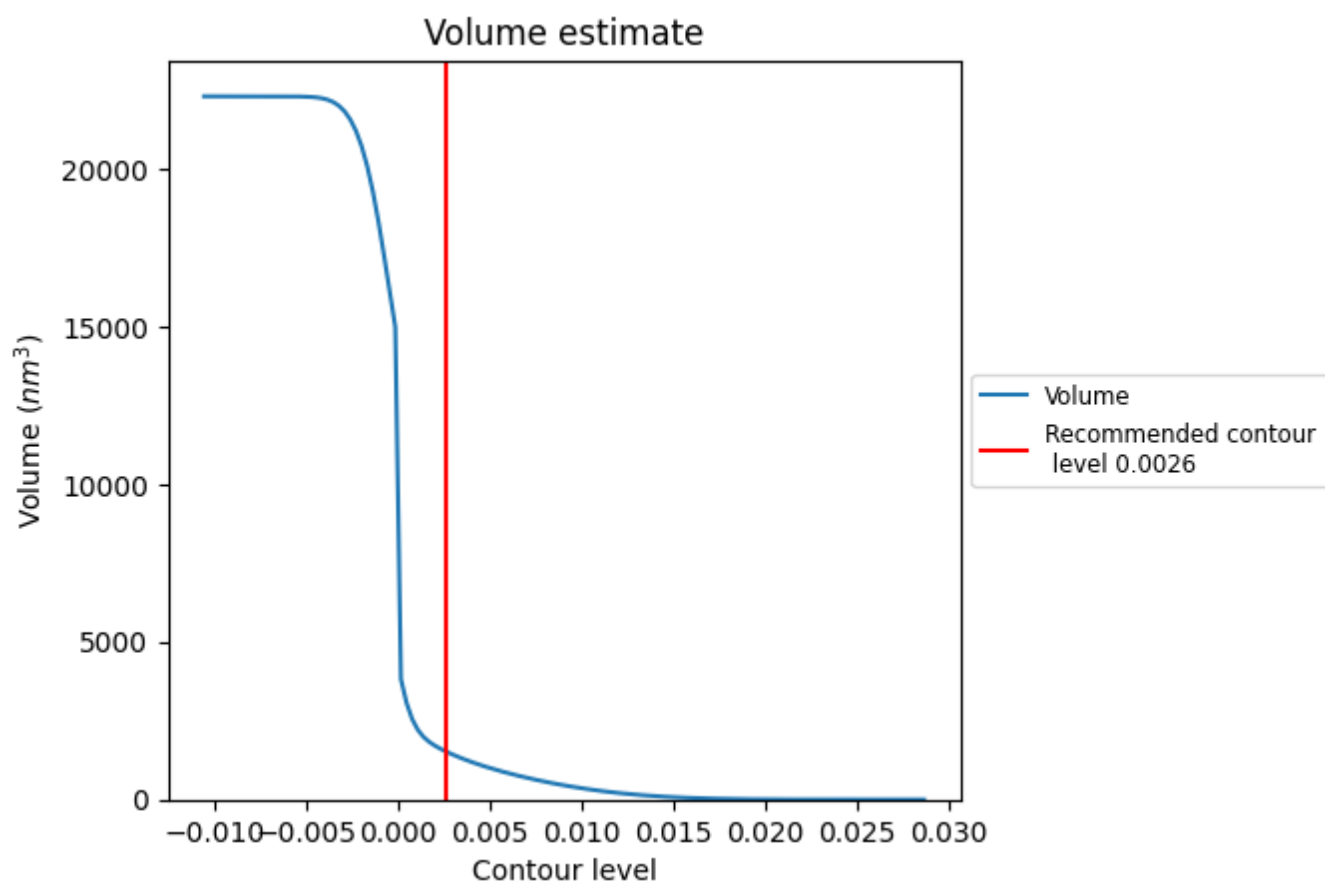
This section contains the results of statistical analysis of the map.

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.

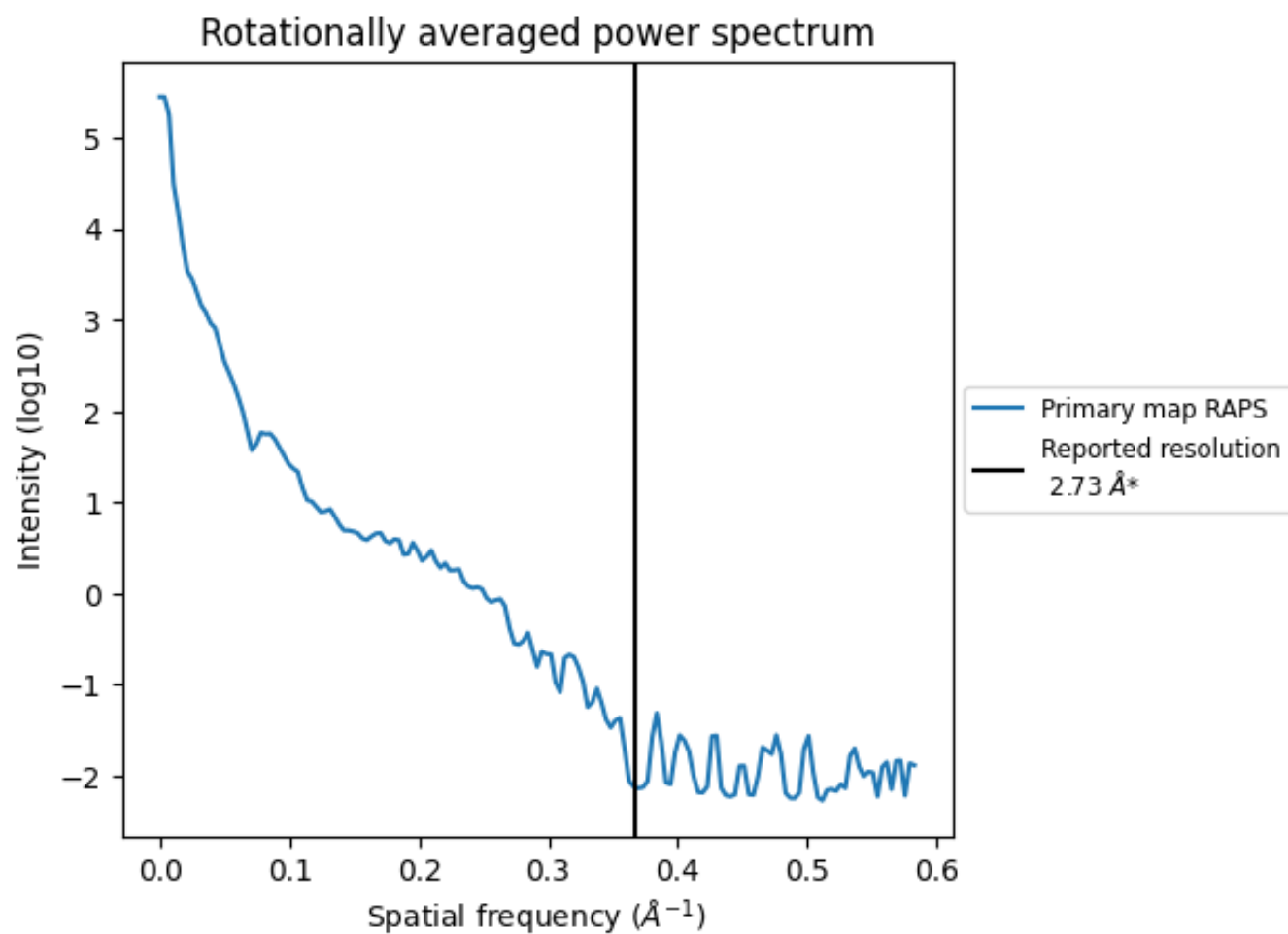
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1520 nm³; this corresponds to an approximate mass of 1373 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 0.366 Å⁻¹

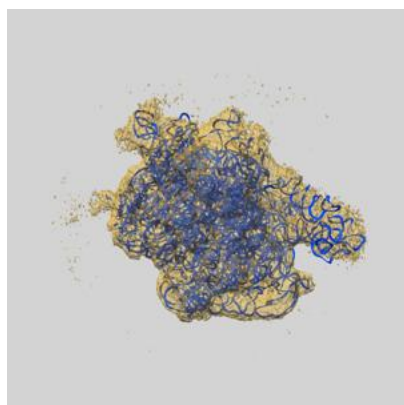
8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

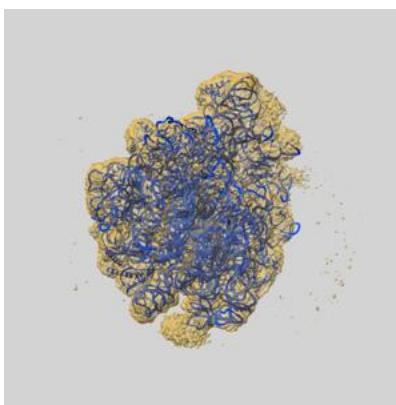
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11901 and PDB model 7ASN. Per-residue inclusion information can be found in section [3](#) on page [8](#).

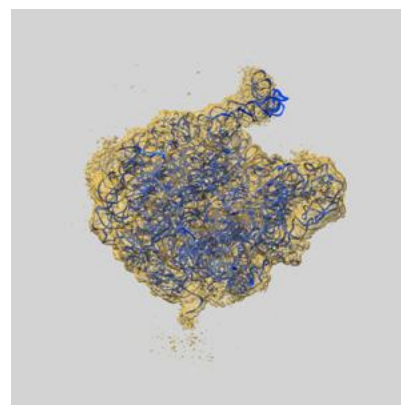
9.1 Map-model overlay [i](#)



X



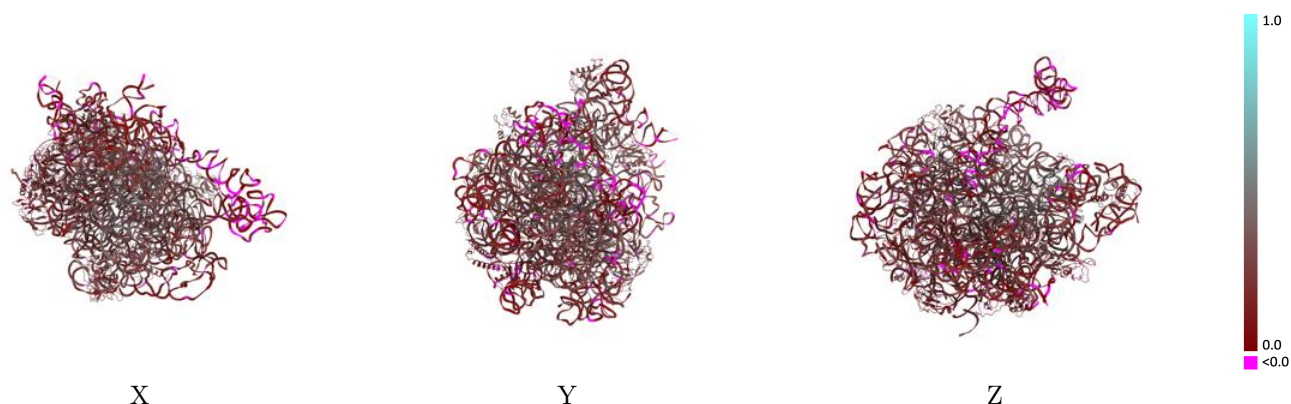
Y



Z

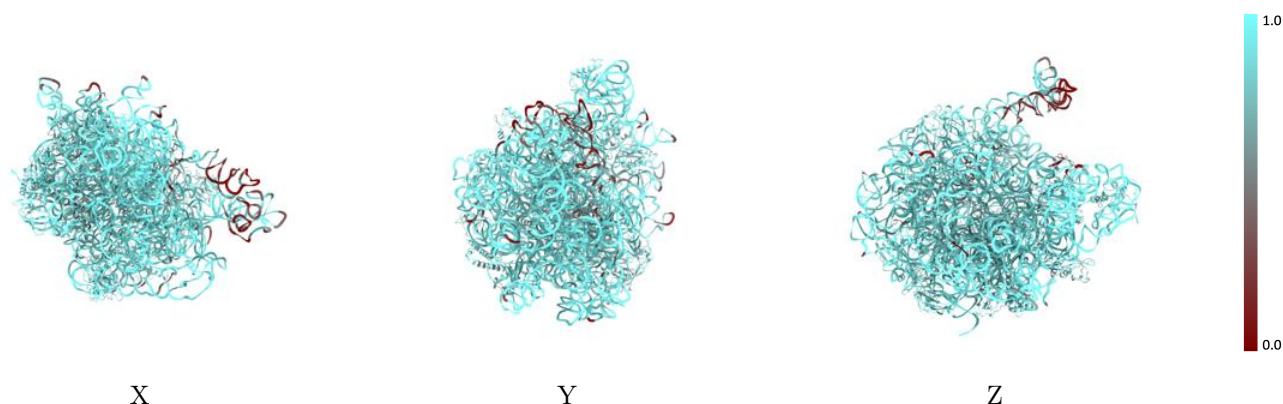
The images above show the 3D surface view of the map at the recommended contour level 0.0026 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



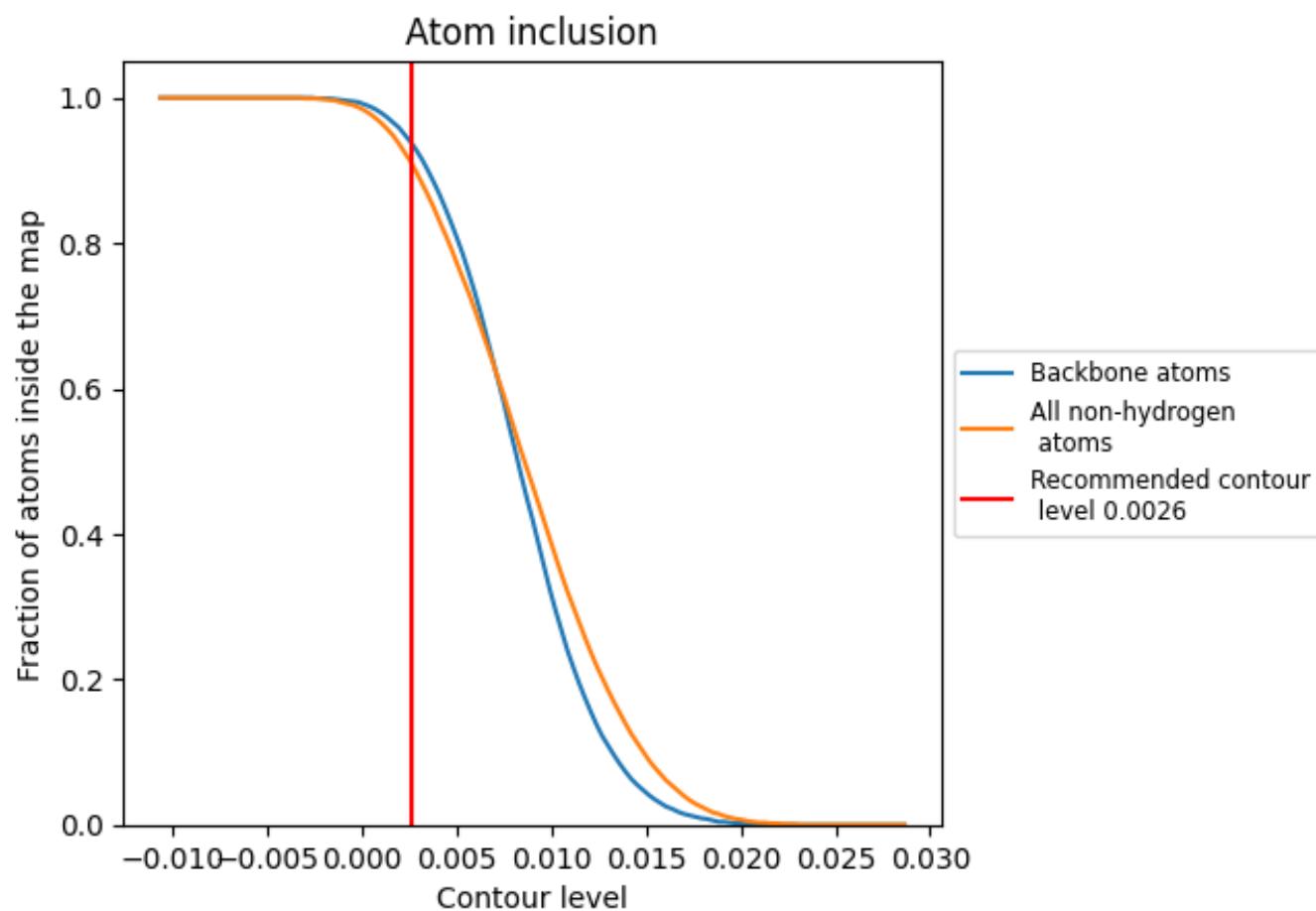
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0026).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 91% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.0026) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9120	 0.2140
1	 0.5330	 0.1980
2	 0.8090	 0.2330
3	 0.8650	 0.2920
A	 0.9330	 0.2160
B	 0.9850	 0.1650
D	 0.8370	 0.1770
E	 0.8880	 0.2570
F	 0.7900	 0.2430
G	 0.8560	 0.2280
H	 0.8290	 0.1950
L	 0.8880	 0.2940
M	 0.9230	 0.2080
N	 0.7810	 0.1890
O	 0.8310	 0.2050
P	 0.8680	 0.2180
Q	 0.8000	 0.1710
R	 0.8200	 0.1170
S	 0.8400	 0.1490
T	 0.7420	 0.1570
V	 0.8190	 0.2360
W	 0.8630	 0.1370
X	 0.8800	 0.2830
Y	 0.8820	 0.2480
a	 0.9270	 0.3170
b	 0.8100	 0.1200

