



Full wwPDB EM Validation Report ⓘ

Jun 26, 2026 – 05:44 AM EDT

PDB ID : 6OUO / pdb_00006ouo
EMDB ID : EMD-20204
Title : RF2 accommodated state bound 70S complex at long incubation time
Authors : Fu, Z.; Indrisiunaite, G.; Kaledhonkar, S.; Shah, B.; Sun, M.; Chen, B.; Grassucci, R.A.; Ehrenberg, M.; Frank, J.
Deposited on : 2019-05-05
Resolution : 3.70 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:

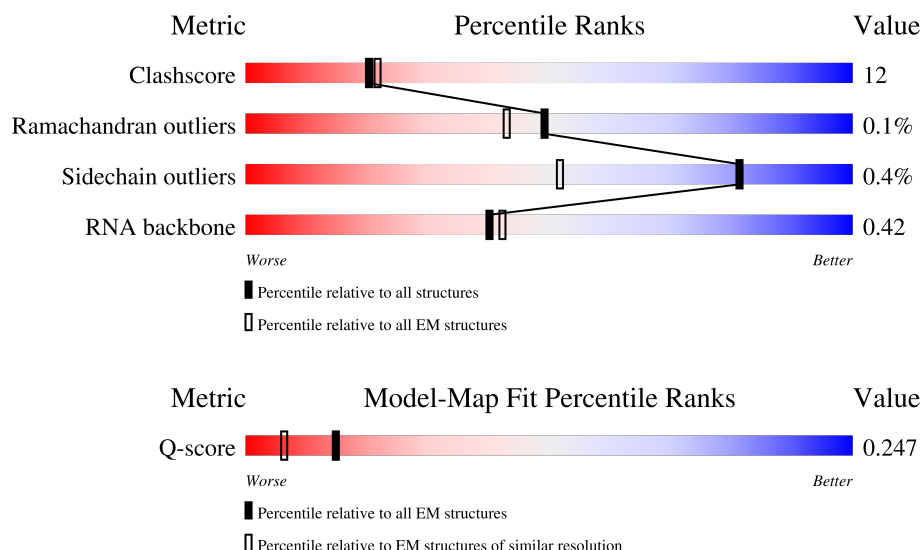
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 3.70 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.



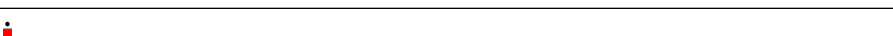
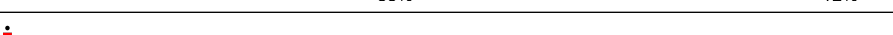
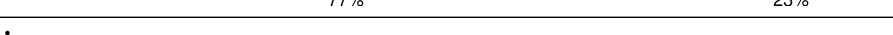
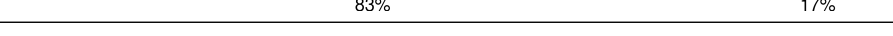
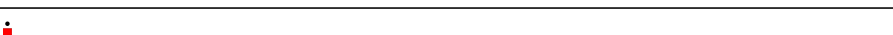
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11569 (3.20 - 4.20)

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	1	2903	
2	2	1534	
3	3	120	

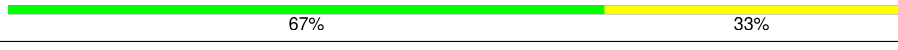
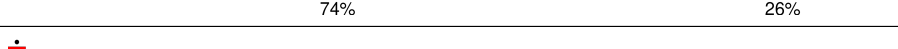
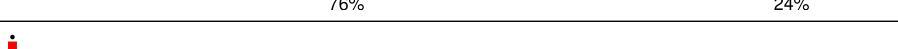
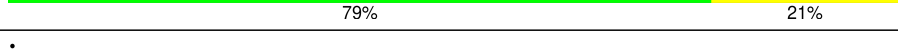
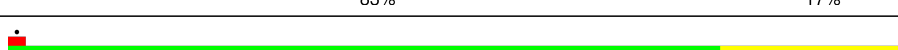
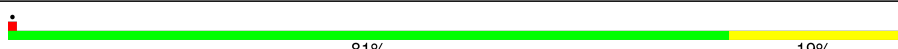
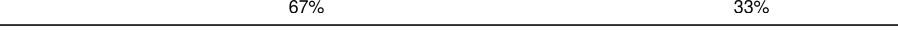
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	4	9	
5	B	271	
6	C	209	
7	D	201	
8	E	177	
9	F	175	
10	G	149	
11	J	142	
12	K	123	
13	L	144	
14	M	136	
15	N	119	
16	O	116	
17	P	114	
18	Q	117	
19	R	103	
20	S	110	
21	T	94	
22	U	103	
23	V	94	
24	W	76	
25	X	77	
26	Y	62	
27	Z	58	
28	a	66	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
29	b	56	
30	c	52	
31	d	46	
32	e	64	
33	f	38	
34	g	225	
35	h	208	
36	i	205	
37	j	156	
38	k	104	
39	l	151	
40	m	129	
41	n	127	
42	o	99	
43	p	117	
44	q	87	
45	r	116	
46	s	100	
47	t	88	
48	u	82	
49	v	80	
50	w	66	
51	x	83	
52	y	86	
53	z	70	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	5	76	46% 36% 14%
55	A	357	9% 69% 31%

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 146867 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 ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2903	Total	C	N	O	P	0	0
			62336	27816	11470	20147	2903		

- Molecule 2 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	1534	Total	C	N	O	P	0	0
			32929	14693	6041	10661	1534		

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	120	Total	C	N	O	P	0	0
			2569	1144	468	837	120		

- Molecule 4 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	9	Total	C	N	O	P	0	0
			184	83	26	66	9		

- Molecule 5 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 6 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 7 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 8 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 9 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	F	175	Total	C	N	O	S	0	0
			1313	826	241	244	2		

- Molecule 10 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 11 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	K	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 13 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	L	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 14 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	M	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 15 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	N	119	Total	C	N	O	S	0	0
			951	588	195	163	5		

- Molecule 16 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	O	116	Total	C	N	O	0	0
			892	552	178	162		

- Molecule 17 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	P	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 18 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
18	Q	117	Total	C	N	O	0	0
			947	604	192	151		

- Molecule 19 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	R	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 20 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	S	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 21 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	T	94	Total	C	N	O	S	0	0
			746	470	140	134	2		

- Molecule 22 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	U	103	Total	C	N	O	S	0	0
			788	498	148	142			

- Molecule 23 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	V	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 24 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	W	76	Total	C	N	O	S	0	0
			582	360	117	104	1		

- Molecule 25 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	X	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 26 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Y	62	Total	C	N	O	S	0	0
			501	308	98	94	1		

- Molecule 27 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Z	58	Total	C	N	O	S	0	0
			448	281	87	78	2		

- Molecule 28 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	a	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 29 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	b	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 30 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	c	52	Total	C	N	O	S	0	0
			426	275	78	73			

- Molecule 31 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	d	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 32 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 33 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	f	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 34 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	g	225	Total	C	N	O	S	0	0
			1760	1113	316	323	8		

- Molecule 35 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	h	208	Total	C	N	O	S	0	0
			1636	1036	307	290	3		

- Molecule 36 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	i	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 37 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	j	156	Total	C	N	O	S	0	0
			1152	717	217	212	6		

- Molecule 38 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	k	104	Total	C	N	O	S	0	0
			848	536	153	152	7		

- Molecule 39 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	l	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 40 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	m	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 41 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	n	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 42 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	o	99	Total	C	N	O	S	0	0
			790	495	151	143	1		

- Molecule 43 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	p	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 44 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	q	87	Total	C	N	O	S	0	0
			673	417	137	116	3		

- Molecule 45 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	r	116	Total	C	N	O	S	0	0
			900	558	181	158	3		

- Molecule 46 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	s	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 47 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	t	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 48 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	u	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 49 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	v	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 50 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	w	66	Total	C	N	O	S	0	0
			544	344	102	97	1		

- Molecule 51 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	x	83	Total	C	N	O	S	0	0
			663	424	126	111	2		

- Molecule 52 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	y	86	Total	C	N	O	S	0	0
			669	414	138	114	3		

- Molecule 53 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	z	70	Total	C	N	O	S	0	0
			589	366	125	97	1		

- Molecule 54 is a RNA chain called P-tRNA.

Mol	Chain	Residues	Atoms						AltConf	Trace
54	5	76	Total	C	N	O	P	S	0	0
			1627	727	296	527	76	1		

- Molecule 55 is a protein called Peptide chain release factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	A	357	Total	C	N	O	S	0	0
			2833	1742	498	583	10		

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
56	1	2	Total 2	Mg 2	0
56	2	1	Total 1	Mg 1	0
56	3	8	Total 8	Mg 8	0
56	i	1	Total 1	Mg 1	0

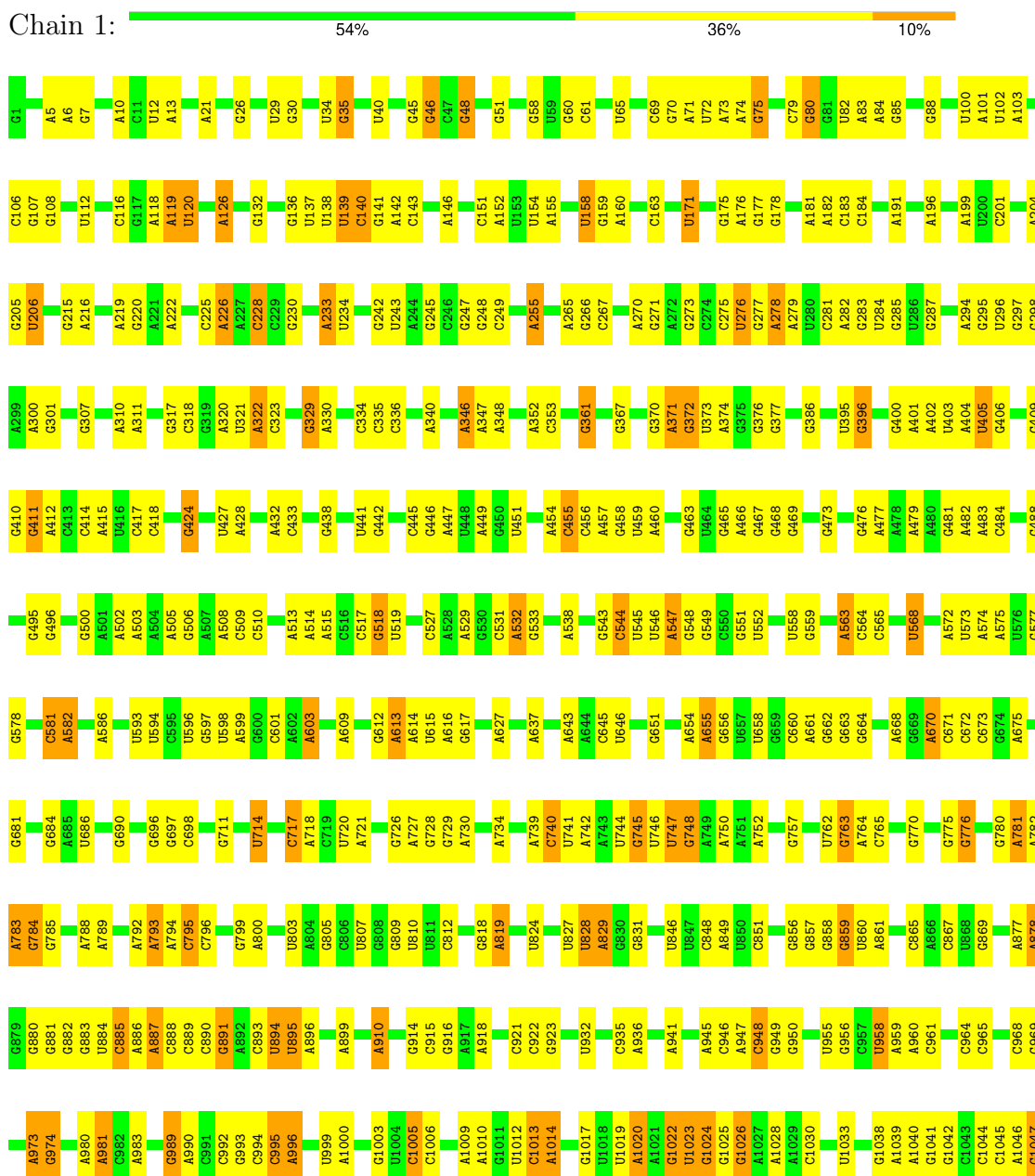
- Molecule 57 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
57	a	1	Total 1	Zn 1	0
57	f	1	Total 1	Zn 1	0

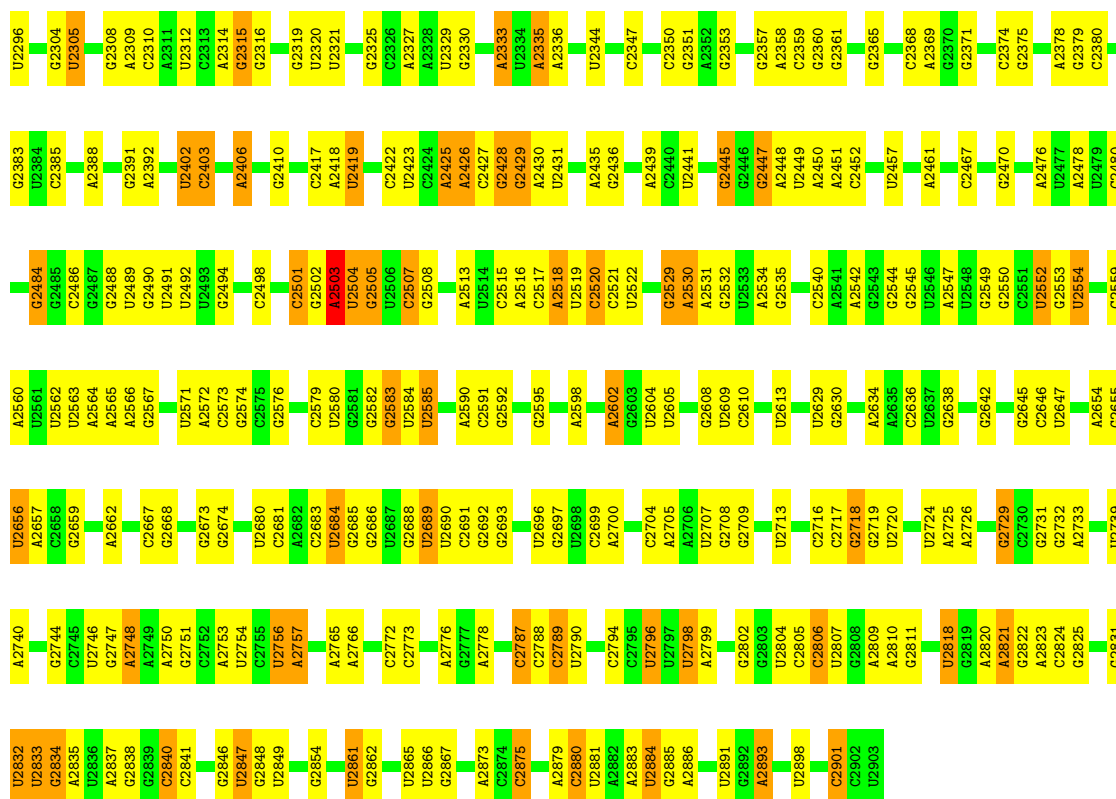
3 Residue-property plots

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

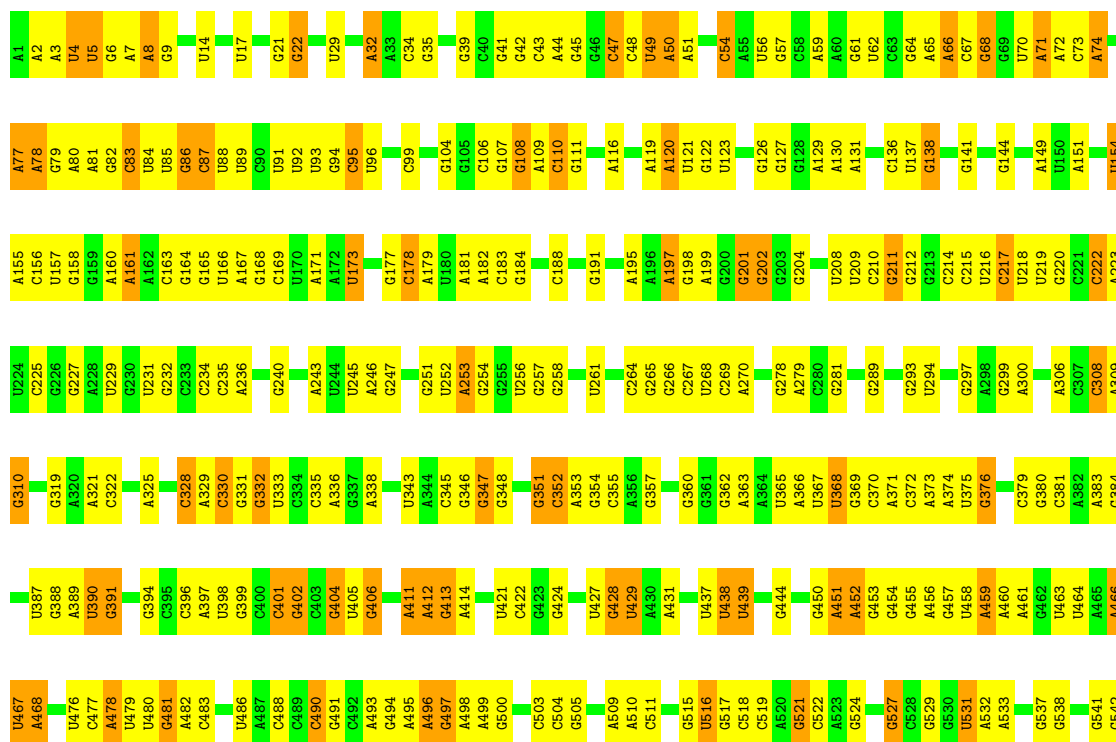
• Molecule 1: 23S ribosomal RNA



U2210	U2137	A2054	G1797	A1701	A1593	G1501	U1411	U1312	G1218	A1126	G1056
A2211	G2138	C2055	U1798	U1712	U1602	A1502	A1412	G1324	U1222	A1127	U1057
A2212	G2056	G2057	G1799	A1713	C1607	A1504	A1413	U1325	G1223	G1128	U1058
U2213	G2140	G1884	A1801	U1714	C1608	U1508	U1414	U1326	U1226	G1129	U1059
C2214	A2142	A1981	A1802	G1715	A1609	A1509	G1415	U1329	G1227	G1131	U1060
G2215	G2061	G1888	G1807	U1716	A1610	A1508	C1417	U1328	U1227	U1132	U1061
G2216	U1982	A1889	A1808	G1721	C1611	A1509	G1418	A1133	G1062	U1133	U1062
G2217	A1987	A1899	A1809	A1722	G1612	A1515	A1419	A1134	G1063	A1134	G1063
G2223	G1988	A1900	A1810	G1723	C1613	A1516	A1420	G1135	U1223	G1135	C1064
A2225	U1991	A1901	G1846	U1724	C1614	A1522	G1421	G1136	G1232	G1136	U1065
C2226	G1992	C1902	G1817	U1725	C1615	A1523	G1422	G1137	G1236	G1137	U1066
A2227	U1993	G1903	G1820	C1726	A1616	A1524	G1426	G1138	G1237	G1138	U1067
G2228	C1994	U1906	U1821	C1727	C1617	A1525	C1427	G1139	G1238	G1139	G1068
U2229	U1995	G1906	A1822	U1728	G1619	A1528	C1428	U1140	A1246	G1140	A1069
U2233	C1996	U1911	G1823	U1729	G1626	A1529	G1437	U1141	A1247	U1141	A1070
G2234	A1998	A1912	G1824	G1730	A1631	A1530	U1438	A1142	G1248	A1142	G1071
A2237	G2002	A1913	G1826	C1732	G1631	A1531	A1439	A1144	U1249	A1144	A1073
G2238	U2002	C1914	U1827	G1733	A1634	A1532	U1443	A1151	G1250	A1151	G1074
G2239	C2006	A1916	G1828	G1738	A1634	A1533	U1444	G1152	G1251	G1152	C1075
U2240	U1917	U1917	U1829	A1744	C1639	U1534	G1449	G1153	U1252	C1153	A1077
A2241	G2010	A1918	A1830	A1744	C1639	U1535	G1449	G1154	A1254	G1154	U1078
G2242	U2011	A1919	C1833	U1751	C1646	A1536	G1455	A1155	G1256	A1155	C1079
U2243	G2012	U1923	C1834	U1752	U1647	C1536	G1458	C1158	U1263	C1158	U1082
G2250	A2013	C1924	G1835	G1753	U1648	G1537	U1458	C1161	U1263	C1161	U1083
G2251	U2022	G1925	U1836	A1754	G1649	G1543	U1461	G1162	G1266	G1162	A1084
G2252	C2023	U1926	G1837	A1755	A1650	C1543	C1462	A1085	U1267	A1085	A1086
G2253	G2024	A1927	C1837	G1756	G1651	C1550	C1462	G1168	A1268	G1168	G1087
U2262	U2025	A1928	C1844	A1757	G1652	C1559	G1464	A1169	A1269	A1169	A1088
C2263	U2026	G1929	G1845	U1758	G1653	G1560	G1465	G1170	C1270	A1089	A1089
C2264	G2027	G1930	G1846	A1759	U1657	U1567	U1466	G1171	G1271	G1171	A1090
U2265	U2028	G1934	A1847	C1760	C1658	C1564	U1467	U1172	A1272	U1172	U1094
A2266	G2029	G1935	A1848	U1761	G1659	C1565	U1468	U1173	U1273	U1173	U1094
A2267	A2031	A1936	G1849	C1764	G1660	A1569	U1469	U1174	A1274	U1174	A1095
G2268	G2032	A1937	G1850	U1765	G1667	A1570	A1476	A1175	A1275	A1175	A1096
A2270	A2033	A1938	A1854	A1773	G1667	A1571	G1475	G1176	G1278	G1176	U1097
G2271	U2034	U1939	G1857	C1774	A1668	U1572	A1476	C1279	G1279	C1279	U1101
A2183	G2035	U1940	A1858	U1775	C1670	A1578	A1477	A1383	G1279	A1383	C1102
A2184	C2036	C1941	G1859	G1776	U1671	A1579	G1478	A1385	A1287	A1385	A1103
G2272	A2037	C1942	U1859	U1777	U1671	A1579	G1479	C1386	G1182	G1182	G1105
A2273	G2038	U1943	G1860	U1778	G1674	U1578	G1482	U1294	U1294	U1294	U1105
G2277	U2039	G1954	G1861	U1779	G1674	A1579	G1483	C1295	C1295	C1295	G1110
A2278	G2040	U1955	G1862	A1780	G1682	A1580	U1484	G1297	G1297	G1297	A1111
G2279	G2043	U1956	G1863	U1781	U1688	A1581	G1489	A1390	G1300	A1390	G1112
C2283	C2044	A1960	U1864	A1784	C1691	A1582	C1489	A1395	G1300	G1300	U1113
A2284	G2045	C1961	U1865	A1785	U1691	A1583	A1490	C1396	A1301	A1301	G1114
G2285	C2046	C1962	G1869	U1786	U1691	A1584	G1491	C1397	A1302	G1115	G1115
G2286	G2047	U1963	G1870	A1787	C1691	C1585	G1492	C1399	G1195	G1195	G1116
A2287	G2048	U1963	A1871	C1788	U1693	A1586	C1493	C1305	G1206	G1206	U1119
U2291	G2049	A1966	A1872	A1789	C1694	A1587	A1494	C1306	A1307	C1306	U1119
U2292	C2050	C1967	G1873	C1790	G1695	A1588	A1495	A1307	A1307	A1307	C1123
G2293	A2051	G1968	G1873	A1791	G1695	A1589	U1496	G1408	G1310	G1310	U1409
A2135	G2053	A1969	G1878	U1796	G1699	A1590	U1497	G1410	G1311	G1311	G1125



• Molecule 2: 16S ribosomal RNA



Chain 4:  78% 11% 11%



- Molecule 5: 50S ribosomal protein L2

Chain B:  75% 25%



- Molecule 6: 50S ribosomal protein L3

Chain C:  76% 23%



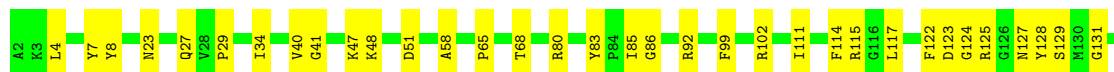
- Molecule 7: 50S ribosomal protein L4

Chain D:  79% 21%



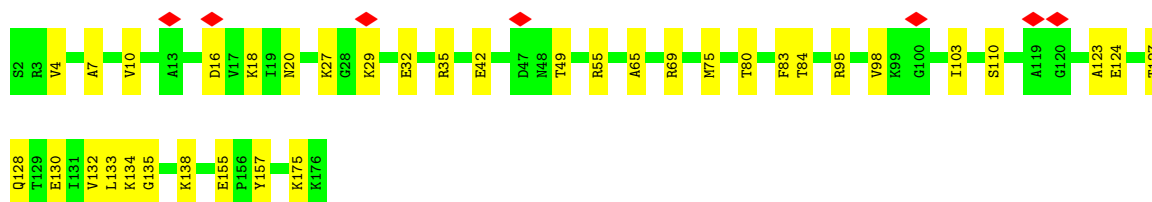
- Molecule 8: 50S ribosomal protein L5

Chain E:  75% 25%



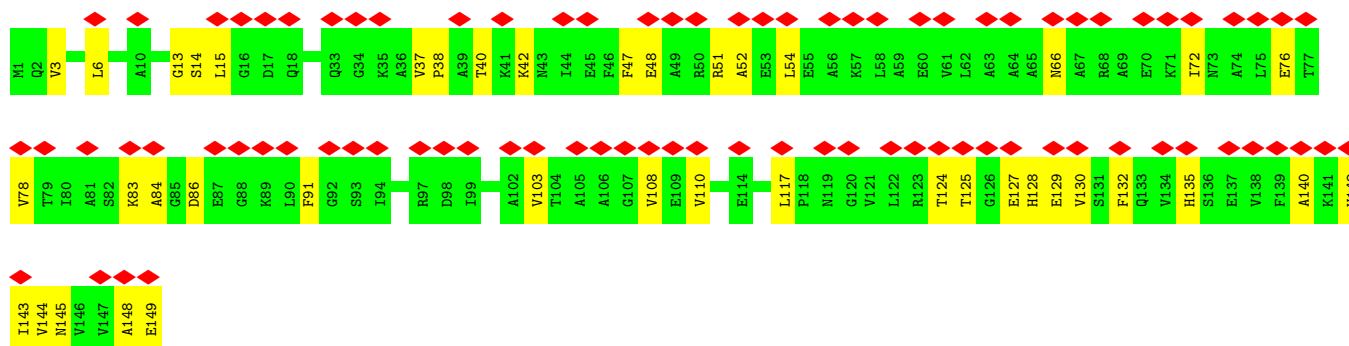
- Molecule 9: 50S ribosomal protein L6

Chain F:  79% 21%



- Molecule 10: 50S ribosomal protein L9

Chain G:  56% 72% 28%



- Molecule 11: 50S ribosomal protein L13

Chain J:  88% 12%



- Molecule 12: 50S ribosomal protein L14

Chain K:  77% 23%



- Molecule 13: 50S ribosomal protein L15

Chain L:  83% 17%



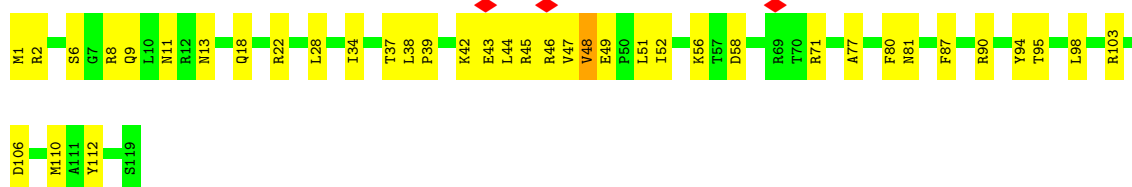
- Molecule 14: 50S ribosomal protein L16

Chain M:  82% 18%



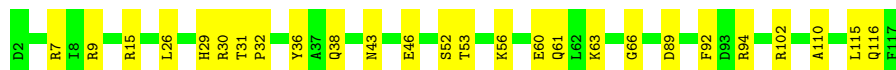
- Molecule 15: 50S ribosomal protein L17

Chain N: 67% 32%



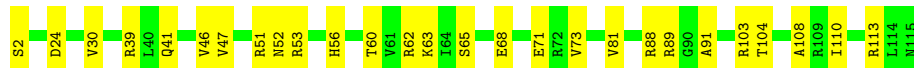
- Molecule 16: 50S ribosomal protein L18

Chain O: 78% 22%



- Molecule 17: 50S ribosomal protein L19

Chain P: 76% 24%



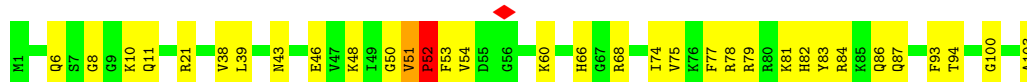
- Molecule 18: 50S ribosomal protein L20

Chain Q: 76% 24%



- Molecule 19: 50S ribosomal protein L21

Chain R: 68% 30%



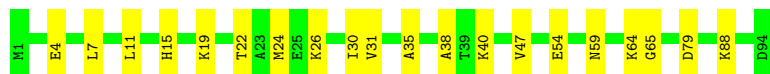
- Molecule 20: 50S ribosomal protein L22

Chain S: 79% 21%



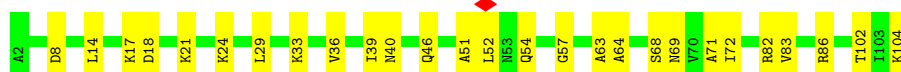
- Molecule 21: 50S ribosomal protein L23

Chain T:  79% 21%



- Molecule 22: 50S ribosomal protein L24

Chain U:  74% 26%



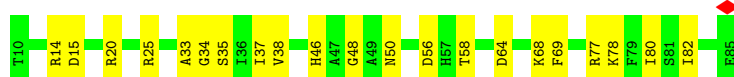
- Molecule 23: 50S ribosomal protein L25

Chain V:  72% 28%



- Molecule 24: 50S ribosomal protein L27

Chain W:  72% 28%



- Molecule 25: 50S ribosomal protein L28

Chain X:  77% 23%



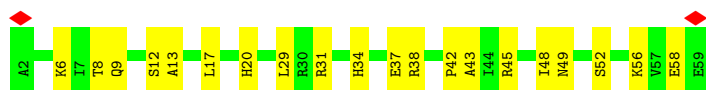
- Molecule 26: 50S ribosomal protein L29

Chain Y:  74% 26%

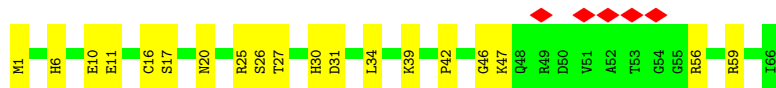


- Molecule 27: 50S ribosomal protein L30

Chain Z:  66% 34%



- Molecule 28: 50S ribosomal protein L31



- Molecule 29: 50S ribosomal protein L32



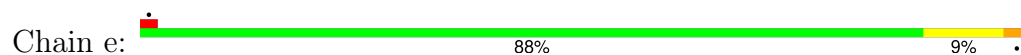
- Molecule 30: 50S ribosomal protein L33



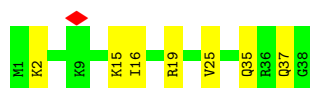
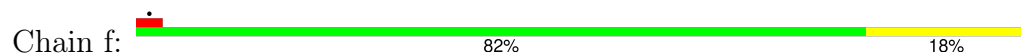
- Molecule 31: 50S ribosomal protein L34



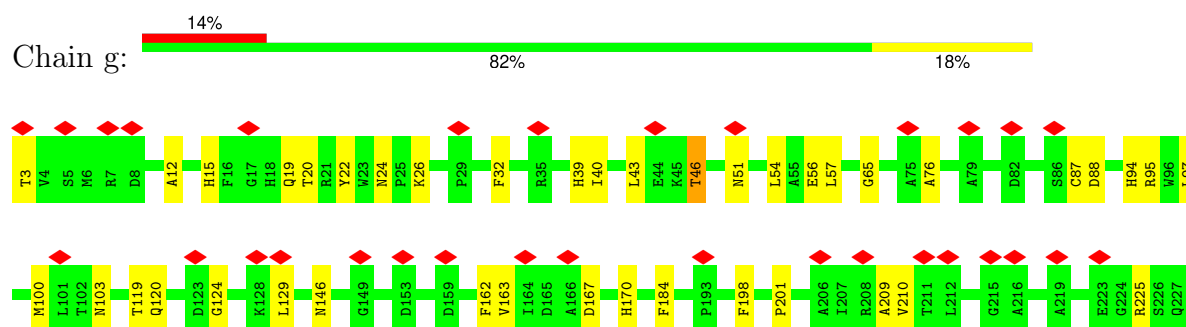
- Molecule 32: 50S ribosomal protein L35



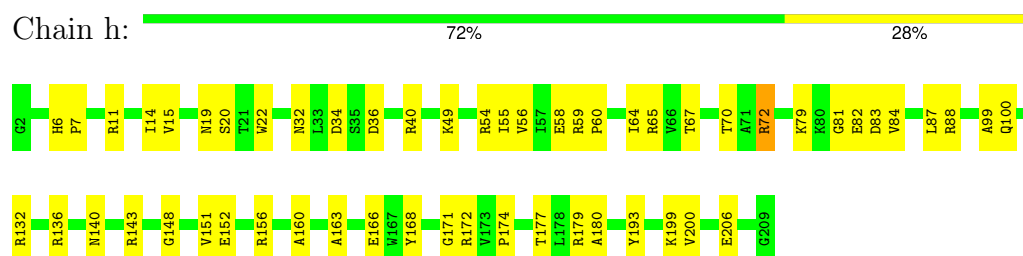
- Molecule 33: 50S ribosomal protein L36



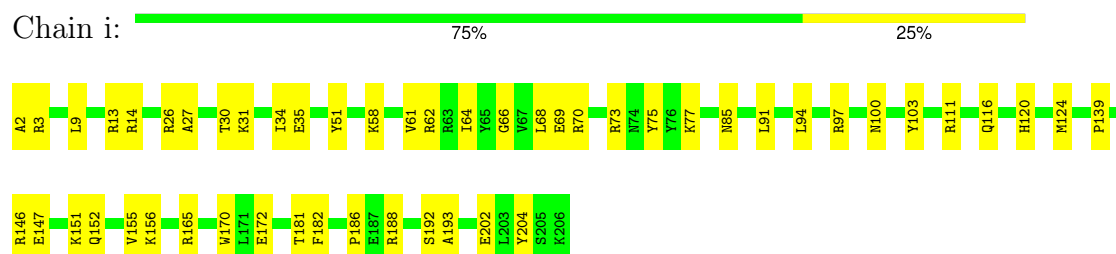
- Molecule 34: 30S ribosomal protein S2



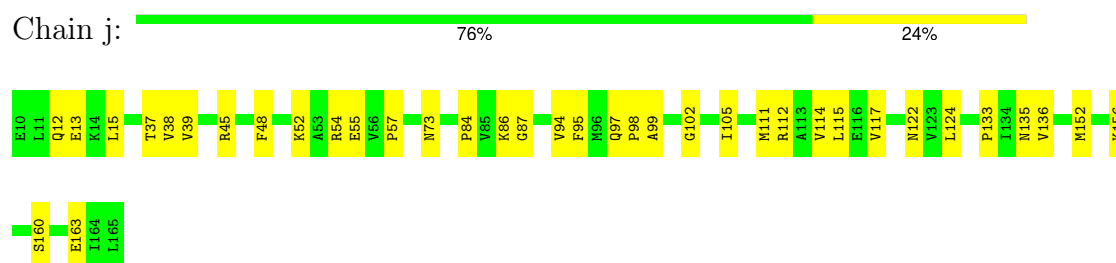
• Molecule 35: 30S ribosomal protein S3



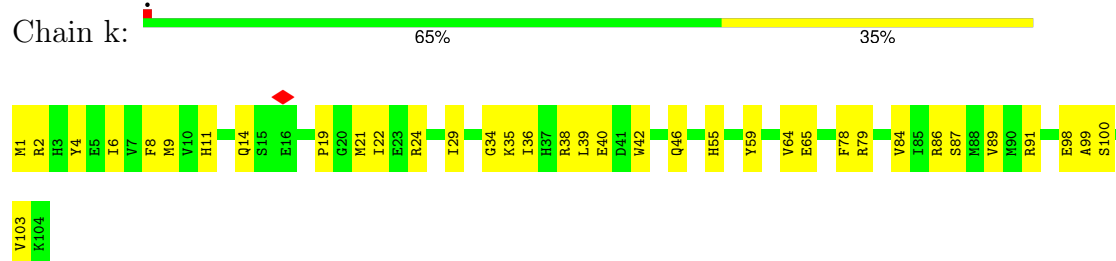
• Molecule 36: 30S ribosomal protein S4



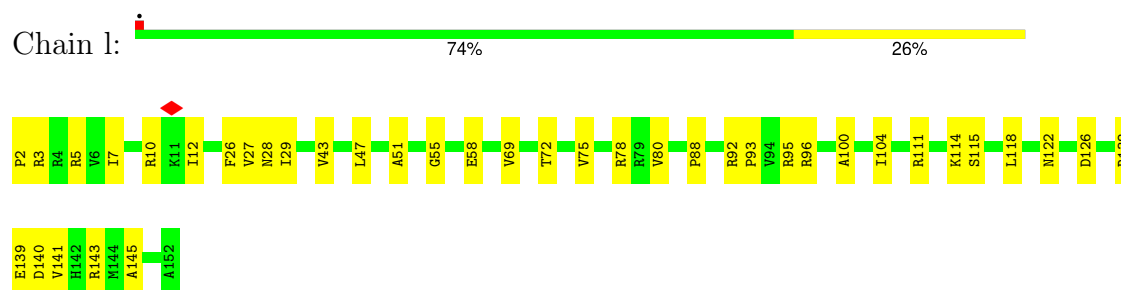
• Molecule 37: 30S ribosomal protein S5



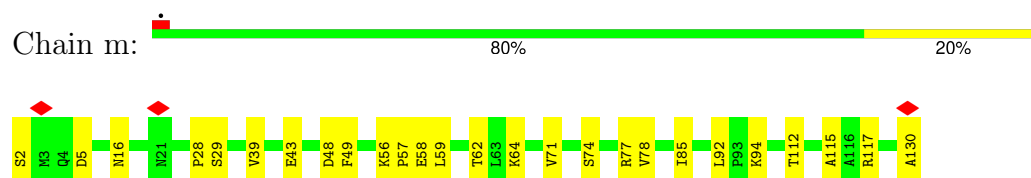
• Molecule 38: 30S ribosomal protein S6



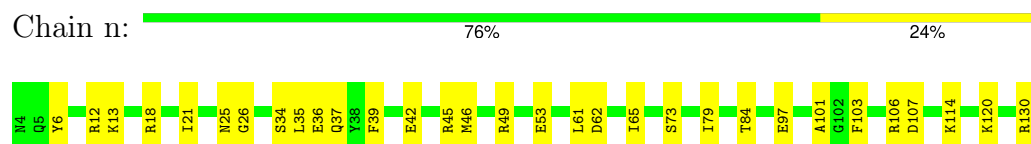
- Molecule 39: 30S ribosomal protein S7



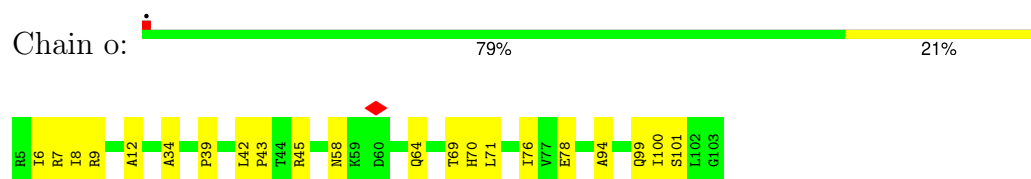
- Molecule 40: 30S ribosomal protein S8



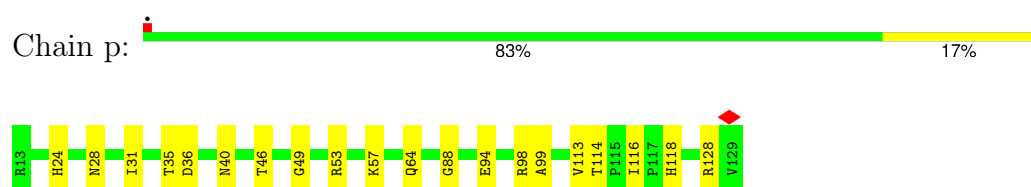
- Molecule 41: 30S ribosomal protein S9



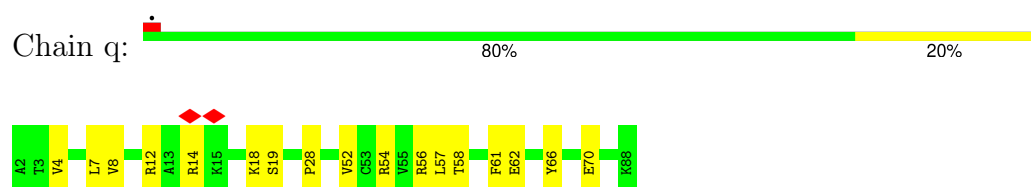
- Molecule 42: 30S ribosomal protein S10



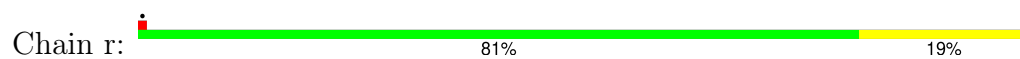
- Molecule 43: 30S ribosomal protein S11



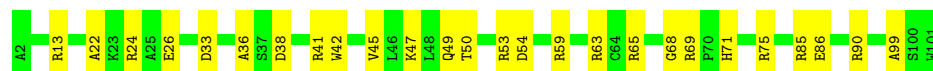
- Molecule 44: 30S ribosomal protein S12



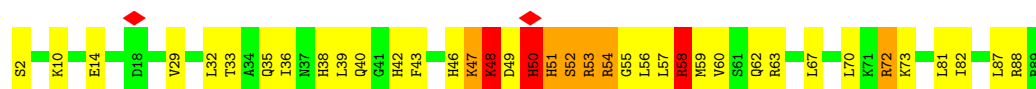
- Molecule 45: 30S ribosomal protein S13



- Molecule 46: 30S ribosomal protein S14



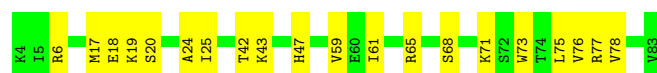
- Molecule 47: 30S ribosomal protein S15



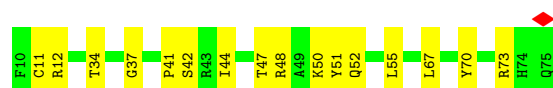
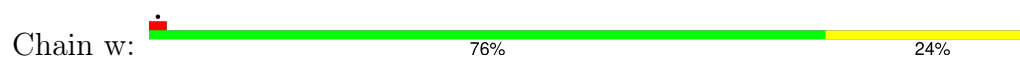
- Molecule 48: 30S ribosomal protein S16



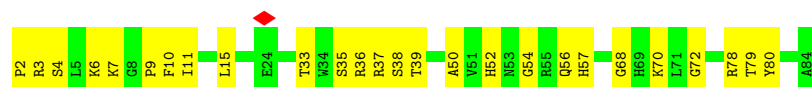
- Molecule 49: 30S ribosomal protein S17



- Molecule 50: 30S ribosomal protein S18



- Molecule 51: 30S ribosomal protein S19



- Molecule 52: 30S ribosomal protein S20

Chain y:  86% 14%

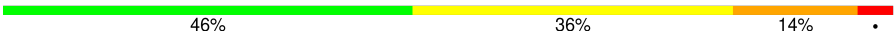


- Molecule 53: 30S ribosomal protein S21

Chain z:  9% 89% 11%



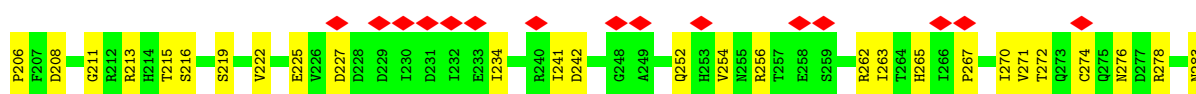
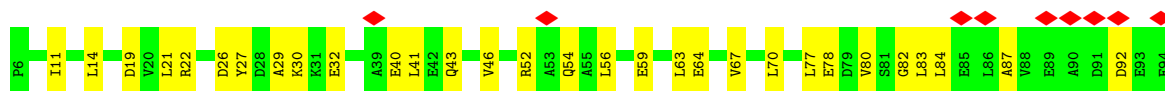
- Molecule 54: P-tRNA

Chain 5:  46% 36% 14%



- Molecule 55: Peptide chain release factor 2

Chain A:  9% 69% 31%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	94709	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	41.6	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	0.089	Depositor
Minimum map value	-0.029	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	526.4, 526.4, 526.4	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.6450001, 1.6450001, 1.6450001	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: PSU, OMU, UR3, 5MC, 2MG, OMG, MG, OMC, ZN, 5MU, 6MZ, G7M, 4OC, 1MG, 3TD, H2U, 2MA, MA6, 4SU

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	1	0.37	0/69286	0.37	2/108087 (0.0%)
2	2	0.35	0/36590	0.37	0/57074
3	3	0.33	0/2872	0.34	0/4478
4	4	0.29	0/203	0.36	0/312
5	B	0.36	0/2121	0.60	0/2852
6	C	0.38	0/1586	0.65	1/2134 (0.0%)
7	D	0.34	0/1571	0.56	0/2113
8	E	0.33	0/1434	0.57	0/1926
9	F	0.31	0/1333	0.52	0/1805
10	G	0.28	0/1122	0.62	1/1515 (0.1%)
11	J	0.35	0/1152	0.57	0/1551
12	K	0.34	0/955	0.61	0/1279
13	L	0.33	0/1062	0.59	0/1413
14	M	0.34	0/1093	0.57	0/1460
15	N	0.38	0/964	0.79	0/1289
16	O	0.30	0/902	0.56	0/1209
17	P	0.38	0/929	0.66	0/1242
18	Q	0.35	0/960	0.57	0/1278
19	R	0.43	1/829 (0.1%)	0.65	1/1107 (0.1%)
20	S	0.35	0/864	0.58	0/1156
21	T	0.33	0/752	0.57	0/1005
22	U	0.36	0/796	0.63	0/1062
23	V	0.32	0/766	0.51	0/1025
24	W	0.33	0/589	0.51	0/779
25	X	0.39	0/635	0.56	0/848
26	Y	0.32	0/502	0.57	0/667
27	Z	0.30	0/452	0.55	0/605
28	a	0.31	0/531	0.57	0/709
29	b	0.34	0/450	0.57	0/599
30	c	0.30	0/433	0.56	0/576
31	d	0.38	0/380	0.62	0/498

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	e	0.41	0/513	0.67	1/676 (0.1%)
33	f	0.30	0/303	0.60	0/397
34	g	0.32	0/1791	0.66	2/2413 (0.1%)
35	h	0.33	0/1663	0.59	0/2241
36	i	0.30	0/1665	0.55	0/2227
37	j	0.35	0/1165	0.61	0/1568
38	k	0.33	0/867	0.63	0/1171
39	l	0.29	0/1195	0.56	0/1602
40	m	0.32	0/989	0.55	0/1326
41	n	0.30	0/1034	0.61	0/1375
42	o	0.29	0/800	0.59	0/1082
43	p	0.31	0/893	0.52	0/1205
44	q	0.33	0/682	0.57	0/918
45	r	0.31	0/909	0.63	0/1215
46	s	0.30	0/817	0.53	0/1088
47	t	0.48	0/722	0.84	1/964 (0.1%)
48	u	0.33	0/659	0.66	0/884
49	v	0.32	0/657	0.64	0/881
50	w	0.30	0/553	0.54	0/743
51	x	0.30	0/680	0.55	0/915
52	y	0.34	0/675	0.54	0/895
53	z	0.29	0/597	0.56	0/792
54	5	0.33	0/1704	0.37	0/2654
55	A	0.32	0/2873	0.64	4/3870 (0.1%)
All	All	0.35	1/158520 (0.0%)	0.45	13/236755 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
19	R	52	PRO	N-CA	-6.14	1.39	1.47

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	784	G	C4'-C3'-O3'	6.65	122.97	113.00
32	e	31	HIS	O-C-N	6.46	130.62	123.25
34	g	46	THR	CA-C-N	5.84	126.04	120.43
34	g	46	THR	C-N-CA	5.84	126.04	120.43
55	A	338	THR	CA-C-N	5.50	131.60	121.70
55	A	338	THR	C-N-CA	5.50	131.60	121.70
1	1	2847	U	C4'-C3'-O3'	-5.45	104.82	113.00
6	C	152	PRO	N-CA-C	-5.33	101.38	112.36

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
19	R	52	PRO	N-CA-C	-5.25	101.65	112.47
47	t	58	ARG	N-CA-C	-5.25	105.52	112.34
10	G	13	GLY	N-CA-C	5.24	117.50	110.43
55	A	227	ASP	CA-C-N	5.02	131.13	121.54
55	A	227	ASP	C-N-CA	5.02	131.13	121.54

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	62336	0	31370	662	0
2	2	32929	0	16587	410	0
3	3	2569	0	1301	34	0
4	4	184	0	95	1	0
5	B	2082	0	2154	50	0
6	C	1565	0	1616	48	0
7	D	1552	0	1619	31	0
8	E	1410	0	1444	32	0
9	F	1313	0	1358	22	0
10	G	1111	0	1148	28	0
11	J	1129	0	1162	13	0
12	K	946	0	1023	20	0
13	L	1053	0	1129	20	0
14	M	1074	0	1157	16	0
15	N	951	0	994	34	0
16	O	892	0	923	20	0
17	P	917	0	962	24	0
18	Q	947	0	1019	22	0
19	R	816	0	839	36	0
20	S	857	0	922	19	0
21	T	746	0	811	13	0
22	U	788	0	844	20	0
23	V	753	0	780	17	0
24	W	582	0	599	13	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
25	X	625	0	652	17	0
26	Y	501	0	531	10	0
27	Z	448	0	488	11	0
28	a	522	0	520	14	0
29	b	444	0	458	14	0
30	c	426	0	464	13	0
31	d	377	0	418	8	0
32	e	504	0	572	11	0
33	f	302	0	340	6	0
34	g	1760	0	1787	24	0
35	h	1636	0	1710	35	0
36	i	1643	0	1707	38	0
37	j	1152	0	1196	28	0
38	k	848	0	846	25	0
39	l	1181	0	1238	27	0
40	m	979	0	1031	17	0
41	n	1022	0	1070	22	0
42	o	790	0	831	16	0
43	p	877	0	887	13	0
44	q	673	0	720	14	0
45	r	900	0	965	17	0
46	s	805	0	844	21	0
47	t	714	0	734	90	0
48	u	649	0	666	22	0
49	v	648	0	691	14	0
50	w	544	0	560	10	0
51	x	663	0	688	23	0
52	y	669	0	719	8	0
53	z	589	0	629	5	0
54	5	1627	0	832	25	0
55	A	2833	0	2729	79	0
56	1	2	0	0	0	0
56	2	1	0	0	0	0
56	3	8	0	0	0	0
56	i	1	0	0	0	0
57	a	1	0	0	0	0
57	f	1	0	0	0	0
All	All	146867	0	99379	1926	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 12.

All (1926) 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)
19:R:51:VAL:HG13	19:R:52:PRO:CD	1.51	1.38
19:R:51:VAL:CG1	19:R:52:PRO:HD3	1.55	1.35
2:2:764:C:C5'	47:t:53:ARG:HH11	1.40	1.35
2:2:764:C:H5'	47:t:53:ARG:NH1	1.51	1.23
6:C:151:THR:OG1	6:C:152:PRO:HD3	1.34	1.22
6:C:151:THR:HG23	6:C:152:PRO:CD	1.76	1.13
19:R:52:PRO:HD2	19:R:53:PHE:H	1.13	1.12
2:2:727:G:O2'	47:t:51:HIS:HE1	1.31	1.10
6:C:151:THR:CG2	6:C:152:PRO:HD2	1.81	1.09
47:t:46:HIS:HB3	47:t:49:ASP:OD2	1.51	1.08
47:t:57:LEU:CD2	47:t:60:VAL:HG21	1.81	1.08
47:t:57:LEU:HD22	47:t:60:VAL:HG21	1.31	1.06
2:2:727:G:O2'	47:t:51:HIS:CE1	2.09	1.05
47:t:43:PHE:CD1	47:t:56:LEU:HD13	1.96	1.01
47:t:43:PHE:CG	47:t:56:LEU:HD13	1.95	1.00
2:2:764:C:H4'	47:t:53:ARG:HD2	1.45	0.97
6:C:151:THR:CG2	6:C:152:PRO:CD	2.40	0.97
2:2:4:U:H3'	2:2:5:U:H5''	1.49	0.95
6:C:151:THR:OG1	6:C:152:PRO:CD	2.14	0.95
19:R:52:PRO:CD	19:R:53:PHE:H	1.76	0.95
47:t:51:HIS:CE1	47:t:54:ARG:HG2	2.04	0.93
6:C:151:THR:CB	6:C:152:PRO:CD	2.48	0.91
47:t:58:ARG:O	47:t:62:GLN:HB2	1.69	0.91
2:2:764:C:C5'	47:t:53:ARG:NH1	2.17	0.91
2:2:764:C:H5'	47:t:53:ARG:HH11	0.75	0.90
6:C:151:THR:HG23	6:C:152:PRO:HD2	0.94	0.90
1:1:139:U:H5'	1:1:140:C:O5'	1.73	0.89
6:C:151:THR:HG1	6:C:152:PRO:HD3	1.15	0.89
2:2:357:G:H4'	2:2:368:U:H5''	1.55	0.88
1:1:2061:G:OP1	1:1:2503:2MA:CM2	2.21	0.88
1:1:2875:C:HO2'	17:P:2:SER:N	1.72	0.86
1:1:1065:U:O2'	1:1:1066:U:O4'	1.94	0.85
47:t:52:SER:OG	47:t:56:LEU:HD23	1.76	0.85
6:C:151:THR:CB	6:C:152:PRO:HD3	2.06	0.85
1:1:578:G:H21	1:1:1252:G:H22	1.25	0.83
2:2:728:A:N7	47:t:54:ARG:HD3	1.92	0.83
2:2:742:G:C5'	47:t:58:ARG:HD3	2.09	0.82
19:R:52:PRO:CD	19:R:53:PHE:N	2.41	0.82
47:t:57:LEU:CD2	47:t:60:VAL:CG2	2.59	0.81
47:t:51:HIS:NE2	47:t:54:ARG:HG2	1.96	0.81
1:1:2061:G:OP1	1:1:2503:2MA:HM21	1.81	0.81
19:R:51:VAL:CB	19:R:52:PRO:HD3	2.10	0.81

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:R:52:PRO:HD2	19:R:53:PHE:N	1.94	0.79
1:1:729:G:N3	1:1:729:G:H2'	1.98	0.78
1:1:783:A:H2'	1:1:783:A:N3	1.97	0.78
8:E:122:PHE:O	8:E:123:ASP:OD1	2.00	0.78
54:5:13:A:C2'	54:5:14:G:H5'	2.13	0.78
19:R:51:VAL:HG13	19:R:52:PRO:HD3	0.78	0.77
47:t:57:LEU:HD23	47:t:60:VAL:CG2	2.14	0.77
2:2:467:U:H3'	2:2:467:U:OP2	1.84	0.77
47:t:57:LEU:HD23	47:t:60:VAL:HG21	1.67	0.76
8:E:123:ASP:OD2	8:E:127:ASN:HB2	1.83	0.76
1:1:881:G:H1	1:1:895:U:H3	1.33	0.75
19:R:51:VAL:HG13	19:R:52:PRO:HD2	1.65	0.75
15:N:48:VAL:HA	15:N:51:LEU:HB2	1.67	0.75
47:t:43:PHE:CG	47:t:56:LEU:CD1	2.70	0.75
2:2:136:C:H42	2:2:227:G:H1	1.31	0.75
1:1:2402:U:O2'	1:1:2403:C:H5''	1.87	0.74
2:2:590:U:H3	2:2:649:A:H61	1.34	0.74
54:5:13:A:H2'	54:5:14:G:H5'	1.69	0.73
1:1:228:C:N3	1:1:417:C:O2'	2.22	0.73
2:2:958:A:N3	2:2:985:C:O2'	2.22	0.73
47:t:43:PHE:CD2	47:t:56:LEU:HD13	2.24	0.73
2:2:158:G:H1	2:2:163:C:H42	1.34	0.72
22:U:46:GLN:HB3	22:U:57:GLY:H	1.52	0.72
2:2:376:G:H1	2:2:387:U:H3	1.38	0.72
1:1:2171:A:H5'	1:1:2174:C:H41	1.55	0.72
15:N:8:ARG:HD2	15:N:43:GLU:HB2	1.72	0.72
34:g:87:CYS:O	34:g:88:ASP:OD1	2.07	0.71
2:2:764:C:H5''	47:t:53:ARG:NH1	2.06	0.71
27:Z:31:ARG:HD2	27:Z:34:HIS:HB2	1.72	0.71
38:k:35:LYS:HB2	38:k:65:GLU:HB3	1.72	0.70
19:R:51:VAL:CG1	19:R:52:PRO:CD	2.38	0.70
1:1:2709:G:OP1	15:N:18:GLN:NE2	2.25	0.69
7:D:150:THR:HG22	7:D:152:GLU:H	1.57	0.69
1:1:2756:U:OP2	33:f:19:ARG:HG2	1.92	0.69
51:x:33:THR:HG22	51:x:35:SER:H	1.57	0.69
2:2:563:A:H3'	44:q:12:ARG:HH12	1.58	0.69
24:W:50:ASN:HB2	24:W:82:ILE:HB	1.74	0.69
1:1:245:G:N7	32:e:8:ARG:NH2	2.40	0.68
1:1:729:G:H2'	1:1:1775:U:H1'	1.75	0.68
1:1:2358:A:H61	13:L:54:GLN:HE22	1.40	0.68
1:1:748:G:OP1	20:S:88:ARG:NE	2.25	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1915:3TD:H3'	1:1:1916:A:H8	1.58	0.68
47:t:43:PHE:CE1	47:t:56:LEU:HD13	2.29	0.68
55:A:26:ASP:HB3	55:A:29:ALA:HB3	1.75	0.68
54:5:8:4SU:HN3	54:5:23:C:H41	1.40	0.68
2:2:452:A:N3	48:u:70:ARG:NH1	2.42	0.68
47:t:58:ARG:O	47:t:62:GLN:CB	2.41	0.68
2:2:450:G:H1	2:2:483:C:H42	1.41	0.68
2:2:809:G:OP2	47:t:48:LYS:HE3	1.94	0.68
1:1:465:G:H5''	31:d:44:VAL:HG21	1.76	0.67
35:h:58:GLU:HG2	35:h:60:PRO:HD3	1.75	0.67
1:1:538:A:H5''	11:J:7:LYS:HE2	1.76	0.67
12:K:78:ARG:HB2	17:P:71:GLU:HB2	1.77	0.67
2:2:742:G:H5'	47:t:58:ARG:HD3	1.76	0.66
35:h:156:ARG:HD3	35:h:193:TYR:HB3	1.78	0.66
39:l:115:SER:H	39:l:118:LEU:HD12	1.61	0.66
48:u:12:LYS:HG2	48:u:13:LYS:HG2	1.76	0.66
2:2:891:U:H2'	2:2:892:A:H8	1.60	0.66
1:1:2880:C:O2'	15:N:90:ARG:NH2	2.30	0.65
2:2:451:A:H61	2:2:481:G:H5'	1.60	0.65
9:F:155:GLU:HG2	9:F:157:TYR:H	1.60	0.65
1:1:468:G:N7	31:d:39:ARG:NH2	2.43	0.65
2:2:201:G:H1	2:2:216:U:H3	1.44	0.65
1:1:1817:G:H3'	5:B:156:ARG:HH21	1.62	0.65
2:2:668:G:OP1	47:t:50:HIS:HB2	1.96	0.65
2:2:401:C:OP2	36:i:70:ARG:NH1	2.29	0.65
35:h:88:ARG:HG2	35:h:99:ALA:HB3	1.78	0.65
25:X:33:LEU:HD23	25:X:50:ARG:HG2	1.79	0.65
16:O:29:HIS:HB3	16:O:36:TYR:HB2	1.79	0.64
2:2:107:G:OP1	2:2:325:A:N6	2.30	0.64
2:2:4:U:C3'	2:2:5:U:H5''	2.26	0.64
2:2:390:U:H2'	2:2:391:G:C8	2.32	0.64
1:1:72:U:O4	26:Y:58:ASN:ND2	2.31	0.64
1:1:1124:G:N3	33:f:37:GLN:NE2	2.44	0.64
3:3:43:C:O2	8:E:92:ARG:NH2	2.30	0.64
1:1:2692:G:H1'	1:1:2847:U:H1'	1.79	0.64
2:2:49:U:H3	2:2:362:G:H1'	1.63	0.64
47:t:54:ARG:HA	47:t:54:ARG:CZ	2.27	0.64
47:t:36:ILE:HA	47:t:39:LEU:HB2	1.80	0.64
41:n:6:TYR:HB2	41:n:21:ILE:HB	1.80	0.64
2:2:376:G:H4'	48:u:5:ARG:HD3	1.80	0.64
2:2:742:G:H5''	47:t:58:ARG:HD3	1.77	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1081:A:N7	37:j:52:LYS:NZ	2.46	0.64
35:h:14:ILE:HG22	35:h:15:VAL:HG13	1.80	0.64
47:t:43:PHE:CD1	47:t:56:LEU:CD1	2.79	0.63
2:2:979:C:O2	46:s:59:ARG:NH1	2.32	0.63
5:B:258:ARG:NH2	5:B:263:THR:OG1	2.32	0.63
47:t:51:HIS:CG	47:t:54:ARG:HB2	2.33	0.63
1:1:2134:A:N6	1:1:2157:G:O2'	2.32	0.63
6:C:6:GLY:N	6:C:201:LEU:O	2.31	0.63
1:1:1652:A:OP1	15:N:8:ARG:NH2	2.31	0.63
2:2:346:G:OP1	17:P:39:ARG:NH2	2.32	0.63
19:R:74:ILE:HB	19:R:87:GLN:HB3	1.80	0.63
1:1:2117:A:N1	1:1:2165:C:N4	2.47	0.63
38:k:29:ILE:HG22	38:k:34:GLY:HA3	1.78	0.63
47:t:43:PHE:CD1	47:t:56:LEU:HD22	2.34	0.63
1:1:1754:A:O2'	17:P:103:ARG:NH2	2.32	0.63
1:1:2579:C:O2'	6:C:136:ASN:ND2	2.32	0.63
2:2:1013:G:N2	2:2:1016:A:OP2	2.32	0.63
2:2:1106:G:H5''	35:h:172:ARG:HB3	1.81	0.63
29:b:9:THR:HG22	29:b:11:SER:H	1.64	0.63
47:t:54:ARG:HA	47:t:54:ARG:NE	2.14	0.63
1:1:1326:U:HO2'	1:1:2010:G:HO2'	1.47	0.62
47:t:53:ARG:HA	47:t:57:LEU:H	1.63	0.62
36:i:172:GLU:HB3	36:i:181:THR:HB	1.80	0.62
35:h:49:LYS:O	35:h:72:ARG:NH1	2.33	0.62
55:A:141:ALA:HA	55:A:144:TRP:HB3	1.80	0.62
1:1:2881:U:H5'	15:N:90:ARG:HH22	1.63	0.62
2:2:844:G:N3	2:2:844:G:H5''	2.13	0.62
2:2:59:A:H3'	2:2:331:G:H22	1.65	0.62
13:L:74:THR:HG22	13:L:107:PHE:HB2	1.81	0.62
18:Q:44:GLN:HE21	19:R:77:PHE:HB3	1.65	0.62
19:R:52:PRO:O	19:R:53:PHE:CG	2.52	0.62
27:Z:9:GLN:HB2	27:Z:29:LEU:HD13	1.81	0.62
43:p:113:VAL:HG12	50:w:73:ARG:HD2	1.81	0.62
2:2:764:C:H5''	47:t:53:ARG:HH11	1.53	0.62
16:O:32:PRO:HA	16:O:102:ARG:HH22	1.64	0.61
33:f:16:ILE:HG12	33:f:25:VAL:HG22	1.81	0.61
41:n:106:ARG:NH1	41:n:107:ASP:O	2.33	0.61
1:1:2425:A:H5''	1:1:2427:C:O4'	2.00	0.61
38:k:1:MET:N	38:k:1:MET:SD	2.73	0.61
1:1:65:U:O2'	1:1:456:C:N3	2.32	0.61
1:1:860:U:H2'	1:1:861:A:H8	1.65	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:380:G:N2	2:2:383:A:OP2	2.32	0.61
2:2:890:G:O2'	2:2:906:A:N6	2.34	0.61
2:2:933:G:O6	39:l:3:ARG:NH2	2.33	0.61
3:3:90:C:H5'	14:M:18:ARG:HB3	1.81	0.61
15:N:103:ARG:NH2	15:N:106:ASP:OD2	2.33	0.61
54:5:15:C:H5''	54:5:15:C:O2	2.00	0.61
2:2:563:A:OP1	44:q:14:ARG:NH1	2.33	0.61
2:2:1033:G:H2'	2:2:1034:G:H8	1.66	0.61
2:2:1328:C:O2'	45:r:29:ARG:NH1	2.30	0.61
10:G:76:GLU:HG3	10:G:142:VAL:HA	1.81	0.61
22:U:86:ARG:NH2	22:U:102:THR:OG1	2.33	0.61
1:1:2010:G:H5''	20:S:42:LYS:HB2	1.81	0.61
1:1:2188:U:H3'	1:1:2189:U:H5''	1.82	0.61
6:C:111:GLY:HA2	6:C:201:LEU:HD22	1.83	0.61
38:k:38:ARG:NH1	38:k:98:GLU:O	2.33	0.61
12:K:1:MET:SD	12:K:67:LYS:NZ	2.73	0.61
2:2:844:G:N3	2:2:844:G:H3'	2.16	0.61
20:S:7:HIS:HB3	20:S:103:ILE:HB	1.81	0.61
28:a:16:CYS:SG	28:a:17:SER:N	2.74	0.61
55:A:21:LEU:HD23	55:A:70:LEU:HD21	1.82	0.61
1:1:1715:G:N2	1:1:1744:A:OP2	2.34	0.61
1:1:2200:C:H42	1:1:2223:G:H1	1.48	0.61
22:U:52:LEU:HD23	22:U:52:LEU:O	2.01	0.61
38:k:99:ALA:HB1	38:k:103:VAL:HG21	1.81	0.61
47:t:57:LEU:HA	47:t:60:VAL:HG23	1.83	0.61
28:a:11:GLU:HA	28:a:25:ARG:HA	1.82	0.61
30:c:37:LYS:HA	30:c:48:ILE:HA	1.83	0.61
1:1:796:C:OP1	7:D:57:LYS:NZ	2.34	0.60
10:G:47:PHE:HA	10:G:51:ARG:HB2	1.82	0.60
33:f:25:VAL:HB	33:f:35:GLN:HB2	1.83	0.60
9:F:98:VAL:HG22	9:F:103:ILE:HG12	1.82	0.60
23:V:77:VAL:HG23	23:V:89:ILE:HG12	1.83	0.60
38:k:2:ARG:HB3	38:k:91:ARG:HH12	1.66	0.60
49:v:24:ALA:HA	49:v:43:LYS:HA	1.83	0.60
1:1:698:C:O2'	1:1:734:A:N6	2.33	0.60
1:1:2788:C:O2'	1:1:2809:A:N3	2.33	0.60
2:2:45:G:H1	2:2:396:C:H42	1.49	0.60
18:Q:76:TYR:OH	18:Q:92:ARG:NH1	2.34	0.60
1:1:1263:U:OP1	29:b:13:ARG:NH1	2.34	0.60
1:1:1266:G:OP1	29:b:16:ARG:NE	2.27	0.60
2:2:764:C:H4'	47:t:53:ARG:CD	2.27	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2772:C:H5'	6:C:173:GLN:HE21	1.67	0.60
32:e:31:HIS:HD2	32:e:32:ILE:HG12	1.67	0.60
1:1:1305:C:N4	1:1:1607:C:OP1	2.34	0.60
2:2:1031:C:O5'	2:2:1032:G:N2	2.34	0.60
25:X:17:ASN:OD1	25:X:27:ARG:NH1	2.35	0.60
21:T:54:GLU:HB3	21:T:88:LYS:HD2	1.84	0.60
1:1:1079:C:H41	1:1:1088:A:H5'	1.67	0.60
2:2:664:G:H22	2:2:741:G:H1	1.50	0.60
1:1:340:A:O2'	7:D:162:ARG:NH1	2.35	0.60
13:L:55:MET:O	13:L:60:ARG:NH2	2.35	0.60
30:c:17:THR:HG22	30:c:19:HIS:H	1.67	0.59
2:2:1150:A:H4'	42:o:43:PRO:HG3	1.84	0.59
18:Q:58:ARG:HE	18:Q:62:ILE:HD11	1.66	0.59
47:t:52:SER:OG	47:t:56:LEU:CD2	2.48	0.59
9:F:35:ARG:NH1	9:F:75:MET:SD	2.75	0.59
10:G:86:ASP:OD2	38:k:24:ARG:NH1	2.35	0.59
13:L:58:TYR:O	32:e:13:ARG:NH2	2.35	0.59
55:A:140:GLU:OE2	55:A:203:ARG:NH2	2.36	0.59
1:1:1417:C:N4	1:1:1581:G:O6	2.36	0.59
1:1:2061:G:N7	1:1:2501:C:O2'	2.35	0.59
2:2:4:U:H3'	2:2:5:U:C5'	2.27	0.59
3:3:9:G:OP2	16:O:15:ARG:NH1	2.35	0.59
1:1:885:C:H2'	1:1:886:A:H8	1.66	0.59
1:1:1365:A:O2'	25:X:11:ARG:NH1	2.35	0.59
1:1:2747:G:H1	1:1:2754:U:H2'	1.68	0.59
1:1:2885:G:N1	29:b:30:VAL:O	2.36	0.59
15:N:6:SER:OG	15:N:46:ARG:NE	2.34	0.59
1:1:2134:A:H1'	1:1:2159:G:H1'	1.85	0.59
2:2:1073:U:O2	34:g:103:ASN:ND2	2.35	0.59
2:2:1377:A:OP1	39:l:92:ARG:NH1	2.36	0.59
2:2:1414:U:H2'	2:2:1415:G:H8	1.68	0.59
1:1:878:A:N6	1:1:899:A:O2'	2.35	0.59
1:1:1266:G:O2'	1:1:2012:G:O6	2.21	0.59
37:j:133:PRO:HA	37:j:136:VAL:HG12	1.85	0.59
1:1:1693:U:O2	5:B:14:ARG:NH1	2.35	0.59
1:1:819:A:OP2	1:1:1187:G:N2	2.34	0.59
37:j:13:GLU:HG2	37:j:39:VAL:HG12	1.85	0.59
55:A:124:ASP:OD1	55:A:193:ARG:NH1	2.36	0.59
55:A:334:LYS:HG2	55:A:341:GLU:HG2	1.85	0.59
1:1:1246:A:HO2'	7:D:40:ARG:HH22	1.51	0.59
2:2:811:C:H4'	2:2:901:A:H61	1.67	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1368:A:OP1	42:o:64:GLN:NE2	2.35	0.59
39:l:27:VAL:HG12	39:l:43:VAL:HG21	1.85	0.59
1:1:1287:A:H5'	15:N:103:ARG:HD2	1.85	0.58
2:2:1055:A:O2'	35:h:156:ARG:NH2	2.36	0.58
8:E:48:LYS:HA	8:E:51:ASP:HB3	1.83	0.58
2:2:73:C:N3	2:2:74:A:N6	2.52	0.58
2:2:626:G:O3'	48:u:51:ARG:NH1	2.36	0.58
35:h:11:ARG:NH2	35:h:177:THR:O	2.32	0.58
1:1:2107:G:N1	1:1:2183:A:N1	2.51	0.58
1:1:2163:A:H3'	1:1:2164:C:H4'	1.86	0.58
2:2:333:U:OP1	52:y:2:ALA:N	2.36	0.58
2:2:373:A:H61	2:2:391:G:H1'	1.68	0.58
2:2:1071:C:OP1	37:j:54:ARG:NH2	2.35	0.58
20:S:83:LYS:HB3	20:S:97:LEU:HD13	1.85	0.58
43:p:28:ASN:O	43:p:57:LYS:NZ	2.34	0.58
1:1:517:C:OP2	29:b:10:ARG:NH2	2.36	0.58
2:2:300:A:O2'	2:2:564:C:N3	2.35	0.58
2:2:1318:A:N3	51:x:37:ARG:NH1	2.51	0.58
1:1:276:U:O2	1:1:278:A:N6	2.37	0.58
3:3:36:C:N4	3:3:49:C:O2	2.35	0.58
14:M:34:LYS:HA	14:M:101:VAL:HA	1.86	0.58
9:F:16:ASP:HB3	9:F:27:LYS:HB2	1.85	0.58
12:K:21:CYS:HA	12:K:41:ILE:HG22	1.85	0.58
38:k:6:ILE:HG12	38:k:89:VAL:HG22	1.84	0.58
49:v:61:ILE:HA	49:v:75:LEU:HA	1.86	0.58
1:1:119:A:H4'	1:1:120:U:H5'	1.84	0.58
1:1:1364:G:N2	1:1:1367:A:OP2	2.34	0.58
1:1:2279:G:N7	24:W:14:ARG:NH2	2.50	0.58
1:1:2293:G:H5''	16:O:94:ARG:HH22	1.68	0.58
6:C:151:THR:CG2	6:C:152:PRO:HD3	2.23	0.58
1:1:2484:G:OP1	14:M:44:ARG:NH1	2.35	0.58
6:C:181:ASP:OD2	6:C:184:ARG:NH2	2.37	0.58
23:V:36:ALA:O	23:V:93:ARG:NH2	2.35	0.58
45:r:11:ASP:HA	45:r:45:ILE:HB	1.86	0.58
6:C:179:ARG:HB3	6:C:188:LEU:HD12	1.84	0.58
17:P:60:THR:HG23	17:P:73:VAL:HG22	1.85	0.58
51:x:3:ARG:HE	51:x:7:LYS:HB3	1.68	0.58
1:1:477:A:N6	1:1:500:G:O3'	2.37	0.57
1:1:2204:G:OP2	5:B:147:LYS:NZ	2.37	0.57
1:1:2425:A:C5'	1:1:2427:C:O4'	2.51	0.57
2:2:254:G:N2	49:v:18:GLU:OE2	2.32	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:390:U:H2'	2:2:391:G:H8	1.68	0.57
2:2:1516:2MG:N2	2:2:1519:MA6:OP2	2.37	0.57
35:h:34:ASP:HB2	46:s:65:ARG:HH21	1.69	0.57
36:i:85:ASN:HA	37:j:102:GLY:HA3	1.86	0.57
55:A:126:ALA:HB1	55:A:225:GLU:HB3	1.86	0.57
1:1:2305:U:H5''	8:E:131:GLY:HA3	1.85	0.57
2:2:467:U:O2	2:2:467:U:H2'	2.04	0.57
10:G:51:ARG:HA	10:G:54:LEU:HB3	1.85	0.57
47:t:51:HIS:CD2	47:t:54:ARG:HG2	2.38	0.57
2:2:264:C:O3'	49:v:65:ARG:NH2	2.37	0.57
2:2:1136:C:H5'	2:2:1137:C:C6	2.39	0.57
49:v:76:VAL:HG23	49:v:77:ARG:HG2	1.85	0.57
2:2:1048:G:N1	2:2:1210:C:N3	2.52	0.57
18:Q:47:TYR:OH	18:Q:51:ARG:NH2	2.34	0.57
1:1:601:C:O2'	7:D:99:LYS:NZ	2.37	0.57
1:1:2746:U:H5'	9:F:138:LYS:HG2	1.87	0.57
2:2:1149:C:O2'	2:2:1280:A:N1	2.37	0.57
1:1:799:G:H3'	1:1:800:A:H2'	1.86	0.57
2:2:229:U:O2'	48:u:25:ARG:NH2	2.37	0.57
2:2:980:C:O2'	46:s:13:ARG:NH1	2.38	0.57
3:3:48:U:OP1	16:O:30:ARG:NH2	2.38	0.57
55:A:162:LYS:HB3	55:A:184:SER:HB3	1.87	0.57
1:1:1935:G:H3'	1:1:1962:5MC:HN41	1.69	0.57
1:1:2831:G:OP2	6:C:59:ARG:NH1	2.37	0.57
2:2:374:A:N1	2:2:390:U:O2'	2.38	0.57
2:2:1297:G:O2'	39:l:114:LYS:NZ	2.35	0.57
1:1:1871:A:N7	1:1:1872:A:N6	2.52	0.57
2:2:923:A:N6	2:2:1392:G:O6	2.37	0.57
10:G:6:LEU:HD11	10:G:37:VAL:HG23	1.87	0.57
1:1:1428:C:N4	1:1:1570:A:OP2	2.33	0.56
1:1:2036:C:H2'	1:1:2037:A:H8	1.70	0.56
2:2:668:G:HO2'	47:t:46:HIS:HD1	1.53	0.56
2:2:1033:G:H2'	2:2:1034:G:C8	2.39	0.56
5:B:258:ARG:NH1	5:B:264:ASP:OD1	2.38	0.56
37:j:87:GLY:N	37:j:94:VAL:O	2.37	0.56
54:5:33:U:N3	54:5:36:A:OP2	2.33	0.56
1:1:226:A:N1	1:1:418:C:O2'	2.35	0.56
1:1:243:U:OP2	32:e:8:ARG:NH1	2.38	0.56
1:1:329:G:OP2	22:U:69:ASN:ND2	2.38	0.56
1:1:643:A:N1	1:1:2369:A:O2'	2.35	0.56
1:1:2114:A:N6	1:1:2167:U:O2'	2.38	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:626:G:OP1	48:u:35:ARG:NH2	2.38	0.56
2:2:691:G:O6	43:p:53:ARG:NH2	2.36	0.56
2:2:1072:G:O6	2:2:1102:A:N6	2.38	0.56
2:2:1101:A:OP2	34:g:95:ARG:NH1	2.37	0.56
1:1:563:A:OP2	19:R:79:ARG:NH2	2.37	0.56
1:1:1170:C:H6	1:1:1170:C:H5''	1.70	0.56
1:1:1414:C:O2	1:1:1588:G:N2	2.39	0.56
1:1:2351:G:O6	32:e:42:ARG:NH1	2.39	0.56
2:2:674:G:OP1	38:k:86:ARG:NH2	2.39	0.56
2:2:1178:G:N2	2:2:1181:G:OP2	2.38	0.56
8:E:29:PRO:HB2	8:E:169:LEU:HD22	1.88	0.56
10:G:72:ILE:HD11	10:G:108:VAL:HG23	1.86	0.56
19:R:6:GLN:HG2	19:R:11:GLN:HG2	1.88	0.56
39:l:72:THR:HA	39:l:96:ARG:HH12	1.71	0.56
1:1:918:A:OP2	1:1:2268:A:N6	2.38	0.56
1:1:1040:A:OP1	23:V:46:LYS:NZ	2.39	0.56
2:2:297:G:N2	2:2:300:A:OP2	2.36	0.56
2:2:405:U:O4	36:i:2:ALA:N	2.38	0.56
10:G:127:GLU:HA	10:G:145:ASN:HA	1.86	0.56
25:X:36:HIS:ND1	25:X:37:ARG:O	2.38	0.56
47:t:57:LEU:HD22	47:t:60:VAL:CG2	2.22	0.56
1:1:323:C:H5'	7:D:163:ASN:HD21	1.69	0.56
13:L:23:ILE:HB	19:R:84:ARG:HH22	1.70	0.56
55:A:11:ILE:HD11	55:A:84:LEU:HD12	1.86	0.56
2:2:2:A:N3	2:2:613:C:O2'	2.34	0.56
2:2:151:A:OP2	2:2:169:C:N4	2.38	0.56
2:2:376:G:H5'	48:u:5:ARG:HB2	1.88	0.56
7:D:6:LYS:O	7:D:9:GLN:NE2	2.38	0.56
49:v:68:SER:HB3	49:v:71:LYS:HB3	1.88	0.56
1:1:1188:U:H2'	1:1:1189:A:H8	1.71	0.56
1:1:1528:A:N6	1:1:1543:G:O2'	2.39	0.56
2:2:1451:U:OP2	2:2:1452:C:N4	2.39	0.56
13:L:29:LYS:HG3	13:L:30:THR:HG23	1.87	0.56
2:2:668:G:P	47:t:50:HIS:HB2	2.46	0.56
17:P:30:VAL:HG12	17:P:81:VAL:HG12	1.86	0.56
25:X:5:CYS:HB2	25:X:33:LEU:HD11	1.88	0.56
1:1:668:A:H2'	1:1:670:A:H62	1.71	0.56
1:1:717:C:H3'	1:1:718:A:H8	1.71	0.56
1:1:2029:G:N1	1:1:2033:A:OP2	2.30	0.56
23:V:58:SER:O	23:V:73:LYS:NZ	2.38	0.56
2:2:8:A:N6	36:i:202:GLU:O	2.39	0.56

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:U:46:GLN:NE2	22:U:54:GLN:OE1	2.39	0.56
39:l:118:LEU:O	39:l:122:ASN:ND2	2.39	0.56
1:1:861:A:N3	3:3:79:G:O2'	2.37	0.55
2:2:376:G:O2'	48:u:5:ARG:NH1	2.39	0.55
2:2:933:G:N7	39:l:3:ARG:NE	2.54	0.55
5:B:2:ALA:N	5:B:20:VAL:O	2.39	0.55
1:1:2126:A:N3	1:1:2127:G:O2'	2.36	0.55
2:2:405:U:OP2	36:i:3:ARG:NH1	2.40	0.55
6:C:150:GLN:O	6:C:151:THR:O	2.23	0.55
29:b:30:VAL:HG22	29:b:37:LYS:HG2	1.87	0.55
2:2:1425:U:H2'	2:2:1426:G:H8	1.72	0.55
3:3:66:A:O5'	3:3:108:A:N6	2.39	0.55
5:B:66:ASP:OD2	5:B:102:ARG:NH1	2.40	0.55
5:B:71:LYS:NZ	5:B:100:GLU:OE1	2.35	0.55
1:1:1652:A:N6	15:N:11:ASN:OD1	2.39	0.55
2:2:1376:U:O4	39:l:10:ARG:NH1	2.38	0.55
47:t:53:ARG:HB3	47:t:57:LEU:HD12	1.88	0.55
1:1:307:G:N1	1:1:310:A:OP2	2.39	0.55
1:1:574:A:N6	1:1:2034:U:OP1	2.39	0.55
1:1:714:U:OP2	47:t:88:ARG:NH1	2.40	0.55
1:1:2189:U:H4'	1:1:2189:U:OP1	2.07	0.55
2:2:653:U:O4'	40:m:56:LYS:NZ	2.39	0.55
2:2:668:G:OP1	47:t:50:HIS:CD2	2.59	0.55
2:2:795:C:H4'	43:p:128:ARG:HH21	1.71	0.55
16:O:89:ASP:HA	16:O:116:GLN:HB3	1.88	0.55
47:t:57:LEU:HD23	47:t:60:VAL:HG23	1.87	0.55
1:1:1789:A:OP2	5:B:221:ARG:NH1	2.39	0.55
1:1:2419:U:OP1	32:e:41:LYS:NZ	2.36	0.55
1:1:2846:G:OP1	17:P:53:ARG:NH1	2.34	0.55
5:B:108:LYS:HA	5:B:196:GLY:HA2	1.88	0.55
23:V:57:TYR:OH	23:V:79:ARG:NH2	2.40	0.55
2:2:389:A:H2'	2:2:390:U:H5'	1.89	0.55
2:2:1317:C:OP1	46:s:24:ARG:NH2	2.39	0.55
2:2:1328:C:HO2'	45:r:29:ARG:HH11	1.55	0.55
5:B:117:GLN:O	5:B:128:ASN:ND2	2.33	0.55
2:2:1086:U:H2'	2:2:1087:G:H8	1.71	0.55
8:E:131:GLY:HA2	8:E:153:ASP:HA	1.88	0.55
15:N:87:PHE:HD1	15:N:90:ARG:HD3	1.72	0.55
45:r:89:LEU:HA	45:r:92:ARG:HG2	1.89	0.55
47:t:59:MET:HA	47:t:62:GLN:HB3	1.87	0.55
2:2:1249:C:N4	2:2:1288:A:OP2	2.40	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1913:A:N7	2:2:1493:A:O2'	2.35	0.55
1:1:2119:A:N6	1:1:2167:U:O2'	2.39	0.55
1:1:2507:C:OP1	55:A:256:ARG:NH1	2.40	0.55
2:2:80:A:OP2	2:2:83:C:N4	2.37	0.55
2:2:373:A:O2'	2:2:451:A:N7	2.40	0.55
47:t:57:LEU:HA	47:t:60:VAL:CG2	2.36	0.55
1:1:220:G:H22	1:1:427:U:H2'	1.71	0.54
1:1:807:U:OP2	13:L:41:ARG:NH1	2.40	0.54
1:1:1779:U:OP2	1:1:1784:A:N6	2.39	0.54
1:1:1864:U:H3	1:1:1878:G:H1	1.53	0.54
1:1:2692:G:O2'	1:1:2847:U:O2	2.24	0.54
2:2:227:G:O2'	48:u:63:GLN:OE1	2.25	0.54
2:2:1236:A:HO2'	2:2:1304:G:HO2'	1.53	0.54
10:G:129:GLU:HA	10:G:143:ILE:HA	1.88	0.54
19:R:52:PRO:O	19:R:53:PHE:CD2	2.59	0.54
20:S:77:ASP:HB2	20:S:102:HIS:HB2	1.89	0.54
1:1:247:G:OP2	1:1:249:C:N4	2.34	0.54
1:1:910:A:H61	1:1:2277:G:HO2'	1.53	0.54
1:1:1901:A:OP2	5:B:253:LYS:NZ	2.39	0.54
1:1:2530:A:O2'	1:1:2534:A:N6	2.40	0.54
2:2:110:C:H2'	2:2:111:G:O4'	2.06	0.54
2:2:542:G:O3'	36:i:14:ARG:NH2	2.38	0.54
2:2:579:A:H5'	2:2:728:A:H1'	1.89	0.54
6:C:181:ASP:HB3	6:C:186:LEU:HB2	1.88	0.54
7:D:117:ARG:HH21	7:D:184:ASP:HA	1.72	0.54
47:t:52:SER:CB	47:t:56:LEU:HD23	2.37	0.54
1:1:2391:G:N1	1:1:2425:A:OP1	2.23	0.54
1:1:2756:U:O4'	1:1:2757:A:C8	2.61	0.54
2:2:222:C:H2'	2:2:223:A:H8	1.72	0.54
2:2:246:A:N1	2:2:278:G:O2'	2.35	0.54
2:2:338:A:H2	2:2:351:G:H22	1.56	0.54
6:C:46:ARG:NH1	6:C:85:ALA:O	2.38	0.54
8:E:122:PHE:HA	8:E:128:TYR:HA	1.88	0.54
2:2:429:U:H3'	36:i:9:LEU:HD12	1.89	0.54
1:1:1028:A:OP2	1:1:1126:A:N6	2.36	0.54
2:2:668:G:H4'	47:t:49:ASP:CG	2.32	0.54
2:2:1209:C:O2'	2:2:1214:C:N4	2.39	0.54
24:W:37:ILE:HG22	24:W:38:VAL:HG23	1.89	0.54
41:n:36:GLU:OE1	41:n:45:ARG:NH1	2.41	0.54
1:1:956:G:O6	14:M:14:LYS:NZ	2.41	0.54
1:1:1469:A:OP2	1:1:1522:A:N6	2.40	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:F:29:LYS:NZ	9:F:80:THR:O	2.40	0.54
15:N:44:LEU:O	15:N:48:VAL:N	2.36	0.54
50:w:11:CYS:SG	50:w:12:ARG:N	2.81	0.54
1:1:177:G:OP2	1:1:177:G:N2	2.39	0.54
1:1:1419:A:H5'	1:1:1579:A:H61	1.71	0.54
1:1:2359:C:H2'	1:1:2360:G:C8	2.43	0.54
1:1:2451:A:N3	54:5:76:A:O2'	2.41	0.54
1:1:2532:G:O2'	1:1:2657:A:N1	2.40	0.54
2:2:86:G:O2'	2:2:87:C:O5'	2.23	0.54
2:2:265:G:H5'	49:v:65:ARG:HH22	1.73	0.54
2:2:362:G:N2	2:2:365:U:OP2	2.39	0.54
8:E:115:ARG:HA	28:a:47:LYS:HD2	1.90	0.54
10:G:117:LEU:HD21	10:G:130:VAL:HG22	1.89	0.54
14:M:47:GLU:OE2	14:M:50:ARG:NH1	2.41	0.54
34:g:3:THR:N	34:g:51:ASN:OD1	2.40	0.54
1:1:910:A:N3	1:1:2264:C:O2'	2.36	0.54
2:2:841:C:H2'	2:2:843:U:H5''	1.89	0.54
35:h:131:ARG:NH1	35:h:166:GLU:OE2	2.41	0.54
2:2:1227:A:OP1	51:x:80:TYR:OH	2.26	0.54
17:P:91:ALA:HB2	17:P:113:ARG:HA	1.90	0.54
19:R:8:GLY:O	19:R:10:LYS:NZ	2.41	0.54
20:S:34:ASP:OD2	29:b:37:LYS:NZ	2.36	0.54
1:1:265:A:O2'	1:1:428:A:N6	2.41	0.53
1:1:2308:G:H2'	1:1:2310:C:H41	1.72	0.53
2:2:979:C:OP1	2:2:1223:C:N4	2.41	0.53
2:2:1033:G:O2'	2:2:1034:G:O5'	2.20	0.53
22:U:40:ASN:ND2	22:U:64:ALA:O	2.42	0.53
46:s:49:GLN:NE2	51:x:11:ILE:O	2.34	0.53
55:A:274:CYS:SG	55:A:276:ASN:ND2	2.81	0.53
1:1:139:U:C5'	1:1:140:C:O5'	2.53	0.53
1:1:1071:G:H1'	1:1:1089:A:H2'	1.90	0.53
1:1:1418:G:N1	1:1:1579:A:OP2	2.41	0.53
2:2:71:A:H61	2:2:99:C:H1'	1.73	0.53
38:k:9:MET:HB2	38:k:86:ARG:H	1.73	0.53
1:1:29:U:H2'	1:1:30:G:H8	1.74	0.53
1:1:1363:C:O2'	1:1:1809:A:N3	2.39	0.53
1:1:1365:A:OP2	25:X:2:SER:OG	2.27	0.53
2:2:1071:C:H2'	2:2:1072:G:H8	1.72	0.53
8:E:34:ILE:HG12	8:E:156:ILE:HG12	1.90	0.53
1:1:1998:A:HO2'	1:1:2724:U:HO2'	1.55	0.53
2:2:865:A:N3	2:2:918:A:O2'	2.40	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1255:G:O2'	2:2:1258:G:N3	2.38	0.53
12:K:102:PRO:HD2	17:P:68:GLU:HG3	1.90	0.53
15:N:44:LEU:HA	15:N:47:VAL:HB	1.90	0.53
36:i:91:LEU:HD23	36:i:94:LEU:HD12	1.90	0.53
39:l:47:LEU:HD23	39:l:58:GLU:HB3	1.90	0.53
43:p:94:GLU:OE2	43:p:98:ARG:NH2	2.41	0.53
55:A:195:GLU:OE2	55:A:324:ARG:NH2	2.42	0.53
2:2:216:U:O2'	2:2:468:A:N6	2.41	0.53
2:2:1259:C:O2'	2:2:1283:U:O2	2.22	0.53
3:3:80:U:O4	23:V:14:LYS:NZ	2.39	0.53
7:D:62:GLN:HG3	7:D:63:LYS:HG3	1.91	0.53
37:j:12:GLN:HG3	37:j:117:VAL:HG12	1.91	0.53
1:1:1068:G:O2'	1:1:1070:A:N6	2.40	0.53
1:1:1682:G:OP2	1:1:1699:G:N2	2.42	0.53
1:1:1688:U:O2'	1:1:1700:A:N7	2.37	0.53
1:1:2133:G:H1	1:1:2157:G:H2'	1.73	0.53
11:J:68:LYS:HA	11:J:71:ASP:HB2	1.90	0.53
36:i:139:PRO:HA	36:i:182:PHE:HD2	1.73	0.53
40:m:74:SER:HB3	40:m:130:ALA:HB3	1.91	0.53
1:1:2449:U:O2'	1:1:2501:C:N4	2.42	0.53
2:2:258:G:H1	2:2:268:U:H3	1.57	0.53
15:N:98:LEU:HB2	15:N:112:TYR:HB2	1.90	0.53
27:Z:17:LEU:HB2	27:Z:20:HIS:HD2	1.74	0.53
30:c:8:LYS:HA	30:c:24:THR:HA	1.91	0.53
1:1:279:A:OP2	1:1:361:G:N2	2.42	0.53
1:1:2061:G:OP1	1:1:2503:2MA:HM23	2.06	0.53
1:1:2467:C:O2	14:M:123:LYS:NZ	2.41	0.53
1:1:2689:U:OP2	1:1:2691:C:N4	2.42	0.53
2:2:137:U:H2'	2:2:138:G:H8	1.73	0.53
2:2:1015:G:N2	2:2:1218:C:O2	2.40	0.53
2:2:1406:U:H5''	2:2:1407:5MC:HM52	1.91	0.53
1:1:1870:C:OP1	1:1:1871:A:N6	2.42	0.53
1:1:1966:A:O2'	1:1:1967:C:OP2	2.24	0.53
1:1:2006:C:O2'	1:1:2823:A:N3	2.42	0.53
1:1:2112:G:OP1	1:1:2115:G:N2	2.42	0.53
2:2:668:G:H4'	47:t:49:ASP:OD1	2.07	0.53
2:2:675:A:O2'	43:p:116:ILE:O	2.24	0.53
2:2:1305:G:H21	2:2:1332:A:H2	1.57	0.53
1:1:684:G:O2'	1:1:788:A:N7	2.42	0.53
15:N:47:VAL:O	15:N:51:LEU:N	2.42	0.53
21:T:22:THR:O	21:T:26:LYS:NZ	2.42	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:i:100:ASN:OD1	36:i:111:ARG:NH1	2.37	0.53
48:u:21:VAL:HG12	48:u:33:ILE:HB	1.91	0.53
1:1:2692:G:H2'	1:1:2693:G:H8	1.74	0.52
2:2:202:G:H21	2:2:466:A:H61	1.57	0.52
2:2:309:A:O2'	2:2:607:A:N1	2.39	0.52
51:x:36:ARG:NH2	51:x:72:GLY:O	2.43	0.52
1:1:2552:OMU:H2'	1:1:2554:U:OP2	2.09	0.52
2:2:668:G:OP1	47:t:50:HIS:CG	2.61	0.52
36:i:73:ARG:HG3	36:i:77:LYS:HE2	1.91	0.52
39:l:139:GLU:O	39:l:143:ARG:N	2.42	0.52
55:A:164:GLU:HB3	55:A:182:LYS:HB3	1.92	0.52
1:1:460:A:OP2	31:d:41:ARG:NH1	2.38	0.52
1:1:1926:U:N3	1:1:1929:G:OP2	2.42	0.52
1:1:2237:G:O2'	1:1:2239:G:N7	2.39	0.52
2:2:1304:G:H21	2:2:1333:A:H62	1.56	0.52
12:K:88:ASN:HB3	12:K:92:GLU:H	1.74	0.52
45:r:68:ASP:OD1	45:r:71:ARG:NH1	2.38	0.52
1:1:2901:C:H6	1:1:2901:C:H5''	1.75	0.52
2:2:939:G:OP1	39:l:95:ARG:NH2	2.40	0.52
40:m:49:PHE:HB2	40:m:59:LEU:HD11	1.91	0.52
1:1:739:A:H1'	1:1:740:C:H5	1.74	0.52
19:R:21:ARG:HD2	19:R:93:PHE:HB2	1.91	0.52
42:o:7:ARG:HB2	42:o:101:SER:HB2	1.92	0.52
43:p:88:GLY:H	43:p:114:THR:HG22	1.74	0.52
1:1:1077:A:N1	1:1:1088:A:O2'	2.37	0.52
1:1:1667:G:O2'	1:1:1991:U:O4	2.28	0.52
1:1:1817:G:OP1	5:B:87:ARG:NH2	2.39	0.52
1:1:1995:U:H3'	1:1:1996:C:H2'	1.91	0.52
2:2:299:G:N2	2:2:565:U:O2	2.42	0.52
2:2:1268:G:N3	2:2:1326:U:O2'	2.43	0.52
18:Q:49:ASP:O	18:Q:53:ARG:N	2.42	0.52
1:1:138:U:O2'	1:1:139:U:O2	2.26	0.52
1:1:673:C:OP1	7:D:49:ARG:NH2	2.38	0.52
1:1:2688:G:N1	1:1:2720:U:OP2	2.34	0.52
2:2:62:U:O2'	2:2:379:C:O2	2.27	0.52
2:2:1305:G:N2	2:2:1332:A:OP2	2.43	0.52
55:A:87:ALA:HA	55:A:92:ASP:HB3	1.92	0.52
1:1:1941:C:H2'	1:1:1942:C:O4'	2.10	0.52
1:1:2753:A:O2'	33:f:15:LYS:NZ	2.42	0.52
2:2:718:A:N6	50:w:70:TYR:O	2.41	0.52
2:2:859:G:OP2	2:2:869:G:N1	2.38	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S:4:ILE:HG12	20:S:106:VAL:HG22	1.91	0.52
23:V:72:VAL:HA	23:V:94:ALA:H	1.75	0.52
55:A:117:ARG:O	55:A:193:ARG:NH2	2.43	0.52
1:1:780:G:H5''	5:B:217:ARG:HH22	1.75	0.52
1:1:2590:A:O3'	5:B:238:ARG:NH1	2.43	0.52
18:Q:83:LEU:HA	18:Q:86:ALA:HB3	1.92	0.52
47:t:70:LEU:HA	47:t:73:LYS:HB2	1.90	0.52
55:A:117:ARG:NH1	55:A:358:GLU:O	2.42	0.52
55:A:203:ARG:HD3	55:A:328:LEU:HD12	1.92	0.52
12:K:43:ILE:HD12	12:K:56:ASP:HB2	1.92	0.52
35:h:70:THR:O	35:h:106:VAL:N	2.41	0.52
37:j:15:LEU:HA	37:j:37:THR:HG22	1.92	0.52
39:l:111:ARG:NH1	39:l:126:ASP:OD2	2.43	0.52
1:1:482:A:N6	1:1:506:G:O2'	2.43	0.51
1:1:1170:C:H5''	1:1:1170:C:C6	2.45	0.51
2:2:1441:A:H62	2:2:1461:G:H21	1.57	0.51
17:P:60:THR:HA	17:P:73:VAL:HG13	1.92	0.51
55:A:168:GLU:HA	55:A:179:VAL:HG12	1.92	0.51
1:1:182:A:N3	1:1:433:C:O2'	2.41	0.51
2:2:844:G:N3	2:2:844:G:C5'	2.73	0.51
3:3:66:A:O4'	3:3:108:A:N6	2.44	0.51
10:G:128:HIS:O	10:G:144:VAL:N	2.41	0.51
18:Q:12:ALA:HA	18:Q:15:LYS:HB2	1.92	0.51
37:j:45:ARG:NH2	37:j:73:ASN:OD1	2.42	0.51
1:1:287:G:O6	1:1:352:A:N6	2.43	0.51
1:1:781:A:OP1	5:B:217:ARG:NH2	2.43	0.51
1:1:2584:U:H2'	1:1:2585:U:H2'	1.92	0.51
2:2:219:U:H2'	2:2:220:G:H8	1.75	0.51
2:2:368:U:H2'	2:2:368:U:O2	2.09	0.51
2:2:764:C:C4'	47:t:53:ARG:HD2	2.30	0.51
10:G:51:ARG:HG3	10:G:54:LEU:HD23	1.92	0.51
34:g:94:HIS:ND1	34:g:146:ASN:O	2.43	0.51
1:1:1807:G:N2	1:1:1810:A:OP2	2.35	0.51
1:1:2684:U:O4'	12:K:70:ARG:NH1	2.42	0.51
1:1:2708:G:H2'	1:1:2709:G:H8	1.76	0.51
2:2:108:G:H5'	2:2:109:A:H5''	1.93	0.51
2:2:411:A:H4'	2:2:412:A:H5'	1.90	0.51
2:2:816:A:OP1	2:2:1526:G:O2'	2.27	0.51
2:2:1060:U:OP1	46:s:85:ARG:NH1	2.41	0.51
3:3:77:U:OP1	23:V:21:ARG:NH1	2.43	0.51
5:B:142:HIS:ND1	5:B:193:GLY:O	2.34	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:111:GLY:N	6:C:170:VAL:O	2.42	0.51
25:X:5:CYS:O	25:X:9:GLY:N	2.37	0.51
29:b:54:VAL:HG23	29:b:55:ILE:HG22	1.93	0.51
35:h:140:ASN:OD1	35:h:143:ARG:NH2	2.43	0.51
1:1:1586:A:H3'	1:1:1587:G:H8	1.76	0.51
1:1:2576:G:O2'	1:1:2579:C:OP2	2.24	0.51
2:2:373:A:N1	2:2:391:G:O2'	2.37	0.51
15:N:58:ASP:HB2	15:N:80:PHE:HB3	1.92	0.51
19:R:38:VAL:HG13	19:R:54:VAL:HB	1.92	0.51
38:k:42:TRP:HB2	38:k:59:TYR:HB2	1.93	0.51
51:x:3:ARG:NH1	51:x:9:PRO:O	2.43	0.51
55:A:78:GLU:O	55:A:82:GLY:N	2.43	0.51
1:1:336:C:H6	1:1:336:C:H5''	1.75	0.51
2:2:197:A:N1	2:2:220:G:O2'	2.36	0.51
2:2:826:C:O2	40:m:16:ASN:ND2	2.43	0.51
2:2:868:C:H2'	2:2:869:G:O4'	2.11	0.51
10:G:78:VAL:HG21	10:G:103:VAL:HG22	1.91	0.51
15:N:37:THR:HA	15:N:110:MET:HA	1.92	0.51
25:X:43:GLU:OE1	25:X:45:ARG:NH1	2.42	0.51
55:A:30:LYS:HZ2	55:A:63:LEU:HD23	1.75	0.51
55:A:150:ARG:HA	55:A:153:LEU:HB2	1.93	0.51
3:3:111:U:H2'	3:3:112:G:H8	1.75	0.51
5:B:37:ASN:HB2	5:B:62:TYR:HB2	1.93	0.51
49:v:17:MET:HG3	49:v:20:SER:HB2	1.93	0.51
49:v:59:VAL:HG23	49:v:78:VAL:HG22	1.92	0.51
1:1:458:G:O2'	1:1:469:G:O6	2.29	0.51
1:1:818:G:N1	1:1:1188:U:OP2	2.35	0.51
1:1:1028:A:N6	1:1:1126:A:OP1	2.43	0.51
1:1:1490:A:O2'	5:B:98:ASP:OD2	2.28	0.51
2:2:427:U:OP1	36:i:13:ARG:NH1	2.44	0.51
2:2:1130:A:N6	2:2:1144:G:N3	2.56	0.51
14:M:66:ARG:NH1	14:M:104:GLU:OE2	2.41	0.51
35:h:40:ARG:NH1	35:h:55:ILE:O	2.43	0.51
37:j:12:GLN:HE21	37:j:117:VAL:HA	1.73	0.51
52:y:4:ILE:HG22	52:y:6:SER:H	1.75	0.51
54:5:7:U:O2'	54:5:21:A:N1	2.35	0.51
1:1:335:C:O2	22:U:68:SER:OG	2.28	0.51
1:1:2134:A:OP1	1:1:2159:G:N2	2.43	0.51
1:1:2655:G:N2	1:1:2656:U:O4	2.40	0.51
3:3:39:A:H2	3:3:44:G:H5'	1.75	0.51
28:a:56:ARG:HH11	51:x:68:GLY:HA3	1.76	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:m:94:LYS:HG3	40:m:117:ARG:HH22	1.75	0.51
54:5:19:G:OP1	54:5:60:U:N3	2.44	0.51
1:1:447:A:OP1	18:Q:5:LYS:NZ	2.40	0.51
1:1:2680:U:H5'	6:C:194:PRO:HA	1.91	0.51
2:2:727:G:HO2'	47:t:51:HIS:CE1	2.23	0.51
6:C:4:LEU:HG	6:C:32:ASN:HD21	1.76	0.51
8:E:4:LEU:HA	8:E:7:TYR:HB3	1.92	0.51
10:G:76:GLU:HA	10:G:142:VAL:HG13	1.92	0.51
21:T:22:THR:HG22	21:T:26:LYS:HZ1	1.75	0.51
1:1:336:C:H5''	1:1:336:C:C6	2.46	0.50
1:1:2825:G:OP2	1:1:2825:G:N2	2.41	0.50
2:2:668:G:OP1	47:t:50:HIS:CB	2.58	0.50
7:D:46:GLN:HB3	7:D:83:VAL:HG21	1.92	0.50
8:E:129:SER:HA	8:E:155:THR:HA	1.94	0.50
55:A:242:ASP:HB2	55:A:262:ARG:HB3	1.92	0.50
1:1:1340:U:OP1	21:T:19:LYS:NZ	2.44	0.50
2:2:3:A:HO2'	2:2:612:C:HO2'	1.53	0.50
2:2:178:C:H2'	2:2:179:A:H8	1.76	0.50
3:3:5:U:OP1	3:3:61:G:O2'	2.29	0.50
24:W:68:LYS:NZ	24:W:69:PHE:O	2.40	0.50
1:1:1020:A:N1	1:1:1141:U:O2'	2.44	0.50
1:1:2045:C:O2	29:b:19:HIS:NE2	2.42	0.50
2:2:217:C:H4'	2:2:217:C:OP1	2.10	0.50
2:2:562:U:H1'	44:q:12:ARG:HD2	1.92	0.50
2:2:811:C:O2'	2:2:901:A:N1	2.40	0.50
5:B:69:ARG:NH2	5:B:127:GLY:O	2.39	0.50
1:1:301:G:OP2	22:U:82:ARG:NH1	2.41	0.50
1:1:442:G:N2	7:D:43:THR:O	2.43	0.50
1:1:781:A:H2'	1:1:1777:U:H1'	1.94	0.50
1:1:1419:A:O2'	1:1:1421:G:N7	2.44	0.50
1:1:2164:C:H5''	1:1:2171:A:H62	1.77	0.50
9:F:95:ARG:HB2	9:F:128:GLN:HB3	1.92	0.50
22:U:29:LEU:HD12	22:U:33:LYS:HB2	1.94	0.50
54:5:53:G:H3'	54:5:54:5MU:H73	1.94	0.50
1:1:48:G:N1	1:1:177:G:OP2	2.44	0.50
1:1:572:A:OP2	19:R:79:ARG:NH1	2.45	0.50
1:1:1135:C:N4	1:1:1138:G:OP2	2.37	0.50
1:1:1857:G:O2'	1:1:1884:G:N2	2.38	0.50
1:1:1954:G:O2'	1:1:1956:U:O4	2.27	0.50
1:1:2515:C:H2'	1:1:2516:A:H8	1.77	0.50
2:2:34:C:H2'	2:2:35:G:H8	1.75	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:668:G:O2'	47:t:46:HIS:ND1	2.40	0.50
2:2:1349:A:OP2	41:n:120:LYS:NZ	2.37	0.50
6:C:4:LEU:O	6:C:203:VAL:N	2.43	0.50
7:D:117:ARG:NH2	7:D:183:PHE:O	2.45	0.50
16:O:110:ALA:HB1	16:O:115:LEU:HD12	1.93	0.50
21:T:35:ALA:HB3	21:T:38:ALA:HB2	1.94	0.50
37:j:97:GLN:HB3	37:j:124:LEU:HB2	1.93	0.50
1:1:459:U:H2'	1:1:460:A:H8	1.77	0.50
1:1:545:U:O2'	1:1:547:A:OP1	2.27	0.50
1:1:1418:G:H1'	1:1:1581:G:H22	1.76	0.50
2:2:792:A:O2'	2:2:794:A:N7	2.41	0.50
3:3:28:C:H5''	16:O:31:THR:HG21	1.92	0.50
36:i:75:TYR:OH	36:i:97:ARG:NH1	2.44	0.50
37:j:55:GLU:HG3	37:j:57:PRO:HD2	1.94	0.50
1:1:138:U:H4'	1:1:139:U:C2	2.46	0.50
1:1:158:U:H2'	1:1:159:G:O4'	2.12	0.50
1:1:1009:A:OP1	11:J:39:LYS:NZ	2.44	0.50
1:1:2519:U:O4'	1:1:2542:A:N6	2.45	0.50
5:B:106:ALA:O	5:B:196:GLY:N	2.41	0.50
5:B:140:THR:HG22	5:B:163:GLN:HG2	1.92	0.50
10:G:48:GLU:HA	10:G:52:ALA:HB2	1.93	0.50
19:R:50:GLY:O	19:R:51:VAL:C	2.55	0.50
35:h:60:PRO:HB3	42:o:94:ALA:HB2	1.93	0.50
1:1:160:A:N3	1:1:2208:C:O2'	2.44	0.50
1:1:2060:A:N7	7:D:69:ARG:NH2	2.60	0.50
1:1:2595:G:N2	1:1:2598:A:OP2	2.32	0.50
3:3:43:C:OP1	28:a:6:HIS:NE2	2.37	0.50
3:3:43:C:H5''	28:a:1:MET:HG2	1.93	0.50
1:1:2668:G:H1'	9:F:110:SER:HB2	1.94	0.50
1:1:2790:U:OP2	1:1:2893:A:N6	2.45	0.50
1:1:2881:U:O2'	15:N:95:THR:O	2.27	0.50
2:2:14:U:N3	2:2:17:U:OP2	2.43	0.50
2:2:50:A:O2'	2:2:360:G:N2	2.45	0.50
2:2:490:C:H2'	2:2:491:G:H8	1.77	0.50
2:2:510:A:HO2'	2:2:542:G:HO2'	1.54	0.50
2:2:666:G:H5'	2:2:726:C:H1'	1.94	0.50
2:2:718:A:O2'	53:z:35:ARG:NH2	2.43	0.50
12:K:71:ARG:NE	12:K:106:GLU:OE2	2.42	0.50
36:i:202:GLU:OE1	37:j:112:ARG:NH1	2.45	0.50
40:m:5:ASP:OD2	40:m:77:ARG:NH1	2.38	0.50
1:1:61:C:OP1	26:Y:47:ARG:NH1	2.45	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:371:A:H61	1:1:401:A:H3'	1.77	0.49
1:1:1667:G:N1	1:1:1992:G:OP2	2.38	0.49
1:1:2013:A:H4'	20:S:96:ILE:HG22	1.93	0.49
1:1:2353:G:N2	24:W:34:GLY:O	2.40	0.49
1:1:2521:C:H42	1:1:2544:G:H1	1.59	0.49
1:1:2756:U:O4'	1:1:2757:A:H8	1.95	0.49
2:2:671:G:O2'	38:k:79:ARG:NH1	2.44	0.49
22:U:72:ILE:HD12	22:U:83:VAL:HG21	1.93	0.49
54:5:13:A:C3'	54:5:14:G:H5'	2.41	0.49
1:1:748:G:P	20:S:88:ARG:HE	2.34	0.49
1:1:973:A:OP2	19:R:81:LYS:NZ	2.35	0.49
1:1:1227:G:OP2	18:Q:16:LYS:NZ	2.38	0.49
1:1:1231:U:H2'	1:1:1232:G:H8	1.77	0.49
1:1:2117:A:N1	1:1:2170:A:N6	2.60	0.49
1:1:2131:U:H5'	1:1:2132:U:H5''	1.93	0.49
8:E:134:GLU:HG2	8:E:136:ILE:H	1.76	0.49
40:m:64:LYS:HG2	40:m:71:VAL:HG21	1.94	0.49
1:1:581:C:OP2	18:Q:33:ARG:NH2	2.45	0.49
2:2:753:A:H4'	2:2:754:C:O4'	2.11	0.49
2:2:1152:A:OP1	42:o:70:HIS:ND1	2.45	0.49
2:2:1218:C:H2'	2:2:1219:A:C8	2.47	0.49
5:B:244:PRO:O	5:B:251:GLN:NE2	2.45	0.49
10:G:47:PHE:O	10:G:52:ALA:N	2.45	0.49
48:u:77:GLU:HA	48:u:80:LYS:HB2	1.94	0.49
55:A:27:TYR:HE1	55:A:67:VAL:HA	1.78	0.49
1:1:411:G:OP2	1:1:2406:A:O2'	2.26	0.49
1:1:1250:G:N7	13:L:18:ARG:NH2	2.49	0.49
1:1:1416:G:O6	1:1:1583:A:N6	2.45	0.49
9:F:83:PHE:N	9:F:135:GLY:O	2.46	0.49
19:R:75:VAL:HG22	19:R:86:GLN:HE22	1.75	0.49
55:A:241:ILE:HG12	55:A:263:ILE:HG12	1.94	0.49
1:1:116:C:O2'	1:1:126:A:N3	2.40	0.49
1:1:514:A:N3	1:1:581:C:O2'	2.43	0.49
1:1:672:C:OP2	13:L:42:SER:OG	2.29	0.49
1:1:894:U:C6	1:1:895:U:H5	2.30	0.49
1:1:1170:C:H3'	1:1:1171:G:H8	1.76	0.49
1:1:1344:U:OP1	1:1:1345:C:N4	2.42	0.49
1:1:1798:U:OP2	5:B:271:ARG:NH2	2.41	0.49
1:1:2291:U:OP1	1:1:2380:C:O2'	2.28	0.49
2:2:66:A:H4'	2:2:173:U:C4	2.48	0.49
2:2:494:G:H2'	2:2:496:A:H8	1.77	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1060:U:O2'	42:o:58:ASN:OD1	2.28	0.49
8:E:47:LYS:HG2	8:E:51:ASP:HB2	1.93	0.49
17:P:46:VAL:N	17:P:62:ARG:O	2.41	0.49
23:V:1:MET:N	23:V:59:GLU:OE1	2.45	0.49
36:i:152:GLN:O	36:i:156:LYS:NZ	2.46	0.49
36:i:188:ARG:HH12	36:i:193:ALA:HA	1.78	0.49
1:1:662:G:H2'	1:1:663:G:H8	1.77	0.49
1:1:1089:A:H2	1:1:1090:A:H62	1.58	0.49
1:1:1936:A:N6	1:1:1963:U:O2	2.45	0.49
1:1:2061:G:H5'	1:1:2061:G:H8	1.76	0.49
1:1:2096:C:H2'	1:1:2097:A:C8	2.48	0.49
7:D:1:MET:HB3	7:D:14:VAL:HG23	1.94	0.49
22:U:36:VAL:HG11	22:U:39:ILE:HD12	1.94	0.49
23:V:75:GLN:HB2	23:V:92:VAL:HG23	1.95	0.49
35:h:36:ASP:OD1	35:h:59:ARG:NH2	2.45	0.49
1:1:2193:G:O2'	1:1:2194:U:OP1	2.31	0.49
2:2:880:C:H2'	2:2:881:G:H8	1.77	0.49
6:C:122:VAL:HB	6:C:141:ARG:HH21	1.77	0.49
14:M:47:GLU:OE2	14:M:51:ARG:NE	2.45	0.49
21:T:65:GLY:N	21:T:79:ASP:OD1	2.33	0.49
29:b:31:ASP:OD2	29:b:34:SER:N	2.39	0.49
34:g:20:THR:HA	34:g:39:HIS:HE1	1.75	0.49
35:h:180:ALA:HA	35:h:206:GLU:HA	1.93	0.49
1:1:958:U:N3	3:3:89:U:O2'	2.43	0.49
1:1:1006:C:O2'	11:J:108:MET:O	2.27	0.49
1:1:2131:U:O5'	1:1:2158:A:N6	2.44	0.49
2:2:411:A:OP1	36:i:26:ARG:NH1	2.46	0.49
21:T:11:LEU:HD11	21:T:47:VAL:HG22	1.94	0.49
34:g:97:LEU:H	34:g:100:MET:HE3	1.77	0.49
1:1:107:G:H2'	1:1:108:G:H8	1.77	0.49
1:1:183:C:O2'	1:1:432:A:N3	2.40	0.49
1:1:1056:G:O2'	1:1:1103:A:N6	2.46	0.49
1:1:1324:G:O2'	1:1:1326:U:OP2	2.31	0.49
1:1:1482:G:O2'	1:1:1509:A:N1	2.42	0.49
2:2:1136:C:H5'	2:2:1137:C:C5	2.47	0.49
24:W:46:HIS:CD2	24:W:77:ARG:HB3	2.47	0.49
46:s:86:GLU:HB3	46:s:90:ARG:HH12	1.77	0.49
1:1:395:U:O2'	1:1:396:G:N7	2.41	0.49
1:1:1808:A:O2'	1:1:1809:A:O4'	2.30	0.49
1:1:1822:C:H2'	1:1:1823:G:H8	1.77	0.49
1:1:2286:G:C8	1:1:2286:G:H5'	2.47	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2684:U:OP1	17:P:51:ARG:NH1	2.46	0.49
2:2:652:U:O4	2:2:752:G:O2'	2.27	0.49
3:3:5:U:H2'	3:3:6:G:H8	1.77	0.49
10:G:84:ALA:HA	10:G:91:PHE:H	1.77	0.49
19:R:51:VAL:CB	19:R:52:PRO:CD	2.83	0.49
40:m:78:VAL:HG12	40:m:85:ILE:HG13	1.95	0.49
41:n:130:ARG:HH12	54:5:32:4OC:H3'	1.78	0.49
47:t:39:LEU:HD23	47:t:43:PHE:HE2	1.77	0.49
55:A:14:LEU:HB2	55:A:77:LEU:HD21	1.94	0.49
1:1:220:G:O2'	1:1:233:A:N3	2.36	0.48
1:1:370:G:O2'	1:1:424:G:OP1	2.26	0.48
1:1:495:G:H21	20:S:61:ASN:HD21	1.60	0.48
1:1:729:G:N3	1:1:729:G:C2'	2.74	0.48
1:1:1712:U:H3'	1:1:1713:A:H2'	1.94	0.48
1:1:2508:G:O2'	1:1:2554:U:O2'	2.25	0.48
2:2:1027:C:H2'	2:2:1034:G:H22	1.78	0.48
8:E:68:THR:N	8:E:86:GLY:O	2.46	0.48
8:E:123:ASP:C	8:E:125:ARG:H	2.21	0.48
23:V:64:VAL:HG22	23:V:69:GLU:HG3	1.94	0.48
39:l:75:VAL:HA	39:l:88:PRO:HA	1.94	0.48
1:1:968:C:H2'	1:1:969:G:H8	1.78	0.48
1:1:994:C:O2'	1:1:996:A:OP1	2.28	0.48
1:1:1332:G:N7	1:1:1609:A:O2'	2.39	0.48
1:1:1919:A:O2'	2:2:1517:G:N3	2.42	0.48
1:1:2681:C:O2	1:1:2683:C:N4	2.46	0.48
2:2:252:U:O4	2:2:253:A:N6	2.47	0.48
2:2:404:G:H4'	2:2:439:U:H5	1.77	0.48
2:2:1422:G:O2'	12:K:49:ARG:NH2	2.46	0.48
36:i:62:ARG:NH1	36:i:69:GLU:OE1	2.47	0.48
1:1:865:C:O2	1:1:867:C:N4	2.37	0.48
1:1:1536:C:O2	1:1:1537:G:N2	2.47	0.48
2:2:429:U:H3	2:2:431:A:H62	1.61	0.48
2:2:1003:G:N2	2:2:1005:A:O5'	2.43	0.48
3:3:7:G:O2'	16:O:38:GLN:NE2	2.46	0.48
5:B:63:ARG:H	5:B:86:ASN:HD21	1.61	0.48
48:u:68:SER:OG	48:u:69:ASP:N	2.46	0.48
1:1:1310:G:O2'	1:1:1611:C:OP1	2.29	0.48
1:1:2039:U:H2'	1:1:2040:G:C8	2.48	0.48
1:1:2130:U:H5''	1:1:2133:G:H4'	1.95	0.48
1:1:2704:C:H3'	1:1:2705:A:C8	2.48	0.48
19:R:78:ARG:HB2	19:R:83:TYR:HB3	1.95	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:n:26:GLY:N	41:n:62:ASP:OD1	2.40	0.48
45:r:34:LEU:HA	45:r:37:ALA:HB3	1.95	0.48
55:A:19:ASP:HA	55:A:22:ARG:HH11	1.79	0.48
1:1:79:C:O2'	1:1:346:A:N3	2.42	0.48
1:1:1297:C:O2'	1:1:1302:A:N1	2.41	0.48
2:2:256:U:OP1	49:v:19:LYS:NZ	2.39	0.48
19:R:43:ASN:HB3	19:R:46:GLU:HB3	1.94	0.48
19:R:60:LYS:N	19:R:100:GLY:O	2.47	0.48
21:T:4:GLU:HA	21:T:7:LEU:HD12	1.95	0.48
36:i:58:LYS:NZ	36:i:69:GLU:OE1	2.46	0.48
55:A:41:LEU:HD23	55:A:46:VAL:HG21	1.96	0.48
1:1:1133:A:N6	1:1:2025:C:O2'	2.46	0.48
1:1:1306:C:N4	1:1:1607:C:OP2	2.46	0.48
1:1:2582:G:H2'	1:1:2583:G:H8	1.79	0.48
2:2:714:G:N2	2:2:777:A:N3	2.49	0.48
2:2:721:G:H4'	2:2:722:G:O4'	2.12	0.48
16:O:52:SER:OG	16:O:53:THR:N	2.44	0.48
17:P:24:ASP:O	17:P:47:VAL:N	2.45	0.48
17:P:104:THR:HA	17:P:108:ALA:HB2	1.95	0.48
38:k:46:GLN:HE22	38:k:55:HIS:HB3	1.77	0.48
45:r:54:ASP:OD1	45:r:57:ARG:NH1	2.47	0.48
50:w:42:SER:OG	50:w:47:THR:O	2.25	0.48
1:1:1438:U:H2'	1:1:1439:A:H8	1.78	0.48
1:1:2659:G:N2	1:1:2662:A:OP2	2.46	0.48
2:2:222:C:H2'	2:2:223:A:C8	2.48	0.48
2:2:1236:A:H4'	2:2:1304:G:H4'	1.95	0.48
8:E:158:THR:HG23	8:E:160:ALA:H	1.78	0.48
13:L:135:ILE:HG22	13:L:140:GLY:HA3	1.94	0.48
17:P:52:ASN:O	17:P:53:ARG:NH1	2.38	0.48
17:P:88:ARG:NH2	17:P:110:ILE:O	2.47	0.48
20:S:10:ALA:HB3	20:S:101:SER:HB2	1.95	0.48
53:z:31:GLU:OE2	53:z:34:ARG:NH2	2.38	0.48
1:1:824:U:O2'	1:1:2358:A:N7	2.42	0.48
1:1:2266:A:N6	1:1:2273:A:OP2	2.44	0.48
2:2:521:G:H4'	44:q:70:GLU:HG2	1.96	0.48
22:U:14:LEU:HD11	22:U:71:ALA:HB2	1.96	0.48
46:s:45:VAL:HG21	51:x:3:ARG:HH22	1.77	0.48
55:A:80:VAL:HG13	55:A:99:ALA:HB1	1.94	0.48
55:A:117:ARG:HH11	55:A:361:LEU:HB2	1.78	0.48
2:2:322:C:O2	2:2:332:G:N2	2.46	0.48
2:2:531:U:H2'	55:A:332:ARG:HH22	1.79	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:Q:72:ASN:HD22	18:Q:110:VAL:HG21	1.77	0.48
27:Z:49:ASN:HA	27:Z:52:SER:HB3	1.96	0.48
34:g:54:LEU:HD23	34:g:57:LEU:HD12	1.96	0.48
34:g:167:ASP:O	34:g:170:HIS:ND1	2.42	0.48
38:k:59:TYR:HE2	50:w:67:LEU:HD21	1.78	0.48
43:p:24:HIS:HB3	43:p:31:ILE:HB	1.95	0.48
55:A:128:CYS:HB3	55:A:189:TYR:HB2	1.96	0.48
1:1:894:U:H1'	1:1:895:U:H5'	1.95	0.48
1:1:958:U:C2	3:3:89:U:H1'	2.49	0.48
1:1:2692:G:H2'	1:1:2693:G:C8	2.49	0.48
2:2:127:G:O2'	49:v:6:ARG:NH1	2.47	0.48
2:2:269:C:H2'	2:2:270:A:C8	2.49	0.48
2:2:1241:G:H2'	2:2:1242:G:H8	1.79	0.48
12:K:61:VAL:HB	12:K:87:LEU:HD11	1.95	0.48
44:q:4:VAL:HA	44:q:7:LEU:HB2	1.95	0.48
1:1:1028:A:N3	1:1:2486:C:O2'	2.44	0.47
1:1:1252:G:OP2	1:1:1252:G:H4'	2.13	0.47
2:2:677:U:H3	2:2:713:G:H1	1.60	0.47
2:2:1256:A:O2'	2:2:1278:G:O6	2.30	0.47
5:B:84:ASP:OD1	5:B:86:ASN:ND2	2.46	0.47
8:E:4:LEU:O	8:E:8:TYR:N	2.39	0.47
14:M:33:LEU:HD13	14:M:117:PHE:HB3	1.96	0.47
31:d:9:VAL:O	31:d:13:ASN:ND2	2.46	0.47
55:A:242:ASP:N	55:A:262:ARG:O	2.37	0.47
1:1:1189:A:OP1	19:R:82:HIS:CD2	2.67	0.47
1:1:1849:G:H2'	1:1:1850:G:H8	1.80	0.47
1:1:2264:C:N4	24:W:15:ASP:OD2	2.47	0.47
1:1:2286:G:H21	1:1:2287:A:H62	1.61	0.47
2:2:59:A:H2	2:2:330:C:H42	1.62	0.47
2:2:217:C:H6	2:2:217:C:H5''	1.78	0.47
2:2:1328:C:H5''	45:r:28:THR:HG21	1.96	0.47
10:G:132:PHE:HB2	10:G:140:ALA:HB3	1.95	0.47
17:P:62:ARG:HD2	17:P:71:GLU:HG2	1.96	0.47
27:Z:37:GLU:O	27:Z:38:ARG:NH1	2.45	0.47
30:c:14:SER:OG	30:c:48:ILE:O	2.29	0.47
1:1:776:G:N7	1:1:793:A:O2'	2.43	0.47
1:1:2540:C:O2'	1:1:2740:A:N3	2.43	0.47
2:2:217:C:H5''	2:2:217:C:C6	2.49	0.47
2:2:695:A:H61	2:2:797:C:H1'	1.79	0.47
2:2:780:A:N6	2:2:801:U:OP2	2.42	0.47
6:C:43:ASP:HB3	6:C:45:TYR:CE1	2.49	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:C:125:TRP:CG	6:C:160:LYS:HB3	2.49	0.47
25:X:68:LEU:HD23	25:X:71:LEU:HD12	1.96	0.47
29:b:39:LEU:HB2	29:b:42:HIS:HB2	1.95	0.47
34:g:51:ASN:HA	34:g:54:LEU:HD12	1.96	0.47
35:h:131:ARG:NH2	35:h:168:TYR:OH	2.47	0.47
1:1:783:A:N3	1:1:783:A:C2'	2.75	0.47
1:1:974:G:N2	1:1:989:G:O2'	2.47	0.47
1:1:2351:G:H2'	1:1:2365:G:H22	1.80	0.47
2:2:17:U:O2'	2:2:1079:G:N3	2.47	0.47
2:2:452:A:O2'	48:u:70:ARG:NH2	2.44	0.47
7:D:98:LYS:HB3	7:D:102:ARG:HH22	1.79	0.47
35:h:79:LYS:HB2	35:h:82:GLU:HB2	1.97	0.47
40:m:29:SER:HB3	40:m:57:PRO:HB2	1.97	0.47
1:1:281:C:H2'	1:1:282:A:C8	2.50	0.47
2:2:111:G:HO2'	2:2:389:A:HO2'	1.60	0.47
10:G:124:THR:O	10:G:128:HIS:NE2	2.45	0.47
30:c:10:LYS:HA	30:c:22:THR:HA	1.97	0.47
32:e:32:ILE:O	32:e:32:ILE:HG22	2.12	0.47
55:A:170:GLU:HA	55:A:176:ILE:HA	1.95	0.47
1:1:282:A:H2'	1:1:283:G:H8	1.78	0.47
1:1:298:G:O2'	1:1:322:A:N1	2.43	0.47
1:1:2241:A:H2'	1:1:2242:G:C8	2.50	0.47
2:2:370:C:H2'	2:2:371:A:H8	1.80	0.47
2:2:618:C:H5'	2:2:619:U:H5''	1.96	0.47
2:2:1269:A:N1	2:2:1312:G:O2'	2.45	0.47
33:f:2:LYS:HB2	33:f:35:GLN:HG2	1.96	0.47
54:5:74:C:OP2	55:A:278:ARG:NH2	2.47	0.47
1:1:143:C:H6	1:1:143:C:H5''	1.80	0.47
1:1:894:U:C5	1:1:895:U:H5	2.32	0.47
1:1:1721:G:H22	1:1:1738:G:H2'	1.79	0.47
1:1:2138:G:N7	1:1:2139:U:O2'	2.43	0.47
1:1:2748:A:H5'	9:F:4:VAL:HG21	1.95	0.47
2:2:413:G:O3'	2:2:428:G:N2	2.46	0.47
2:2:1339:A:HO2'	54:5:40:C:HO2'	1.62	0.47
5:B:107:PRO:HD2	5:B:110:LEU:HD22	1.97	0.47
6:C:150:GLN:O	6:C:151:THR:C	2.58	0.47
7:D:161:ALA:HA	7:D:164:LEU:HD12	1.97	0.47
27:Z:42:PRO:HA	27:Z:45:ARG:HB2	1.97	0.47
37:j:87:GLY:O	37:j:94:VAL:N	2.40	0.47
39:l:141:VAL:O	39:l:145:ALA:N	2.43	0.47
41:n:21:ILE:HG23	41:n:61:LEU:HD13	1.96	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1026:G:OP1	1:1:1134:A:O2'	2.30	0.47
1:1:2756:U:H4'	1:1:2757:A:O5'	2.13	0.47
5:B:147:LYS:HD2	5:B:150:LYS:HD2	1.97	0.47
30:c:35:GLU:HG2	30:c:50:LYS:HA	1.97	0.47
1:1:12:U:O4	1:1:13:A:N6	2.48	0.47
1:1:568:U:H1'	1:1:2030:6MZ:H9C1	1.97	0.47
1:1:2371:G:O2'	30:c:46:HIS:ND1	2.47	0.47
35:h:151:VAL:HG12	35:h:200:VAL:HG23	1.96	0.47
38:k:11:HIS:HB3	38:k:14:GLN:HG2	1.97	0.47
40:m:92:LEU:O	40:m:117:ARG:NH2	2.41	0.47
1:1:35:G:O6	1:1:446:G:N1	2.48	0.47
1:1:154:U:H2'	1:1:155:A:C8	2.50	0.47
1:1:1463:C:H2'	1:1:1464:G:C8	2.50	0.47
1:1:1926:U:O2'	1:1:1928:A:N7	2.44	0.47
2:2:22:G:O2'	2:2:913:A:N1	2.42	0.47
2:2:1147:C:O2	41:n:18:ARG:NH2	2.47	0.47
2:2:1492:A:O2'	55:A:319:TRP:NE1	2.44	0.47
5:B:63:ARG:H	5:B:86:ASN:ND2	2.13	0.47
5:B:245:VAL:HG12	5:B:251:GLN:HA	1.96	0.47
37:j:84:PRO:HG3	37:j:97:GLN:HG3	1.97	0.47
37:j:111:MET:HA	37:j:114:VAL:HG12	1.97	0.47
39:l:12:ILE:HD13	39:l:28:ASN:HD21	1.79	0.47
47:t:54:ARG:NH2	47:t:58:ARG:HB2	2.29	0.47
55:A:234:ILE:HD11	55:A:292:LYS:HB2	1.96	0.47
1:1:1005:C:O2'	11:J:30:THR:OG1	2.27	0.46
1:1:1023:U:OP2	1:1:1025:G:O2'	2.33	0.46
1:1:1155:A:O3'	18:Q:55:ARG:NH2	2.41	0.46
1:1:1274:A:OP1	1:1:1646:C:N4	2.47	0.46
1:1:2645:G:OP2	1:1:2645:G:N2	2.35	0.46
1:1:2861:U:H2'	1:1:2862:G:H8	1.80	0.46
2:2:974:A:H5'	46:s:71:HIS:HB3	1.97	0.46
2:2:1418:A:N6	2:2:1482:G:O2'	2.48	0.46
10:G:40:THR:HG22	10:G:42:LYS:H	1.79	0.46
17:P:62:ARG:HB3	17:P:71:GLU:HA	1.96	0.46
36:i:147:GLU:O	36:i:151:LYS:NZ	2.43	0.46
39:l:69:VAL:HG23	39:l:100:ALA:HB1	1.97	0.46
39:l:93:PRO:HA	39:l:96:ARG:HD3	1.95	0.46
1:1:981:A:N1	1:1:2027:G:O2'	2.48	0.46
1:1:1386:C:H2'	1:1:1387:A:H8	1.80	0.46
1:1:2559:C:H2'	1:1:2560:A:H8	1.79	0.46
1:1:2704:C:H3'	1:1:2705:A:H8	1.79	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:509:A:H5'	36:i:51:TYR:HD2	1.80	0.46
2:2:1123:U:H4'	42:o:39:PRO:HD2	1.97	0.46
6:C:110:THR:HA	6:C:171:THR:HA	1.97	0.46
9:F:7:ALA:O	9:F:69:ARG:NE	2.47	0.46
40:m:112:THR:HG23	40:m:115:ALA:H	1.80	0.46
51:x:52:HIS:ND1	51:x:56:GLN:O	2.48	0.46
1:1:956:G:N2	1:1:960:A:OP2	2.37	0.46
1:1:1062:G:O6	1:1:1075:C:N4	2.48	0.46
1:1:1438:U:H2'	1:1:1439:A:C8	2.50	0.46
1:1:1954:G:N2	1:1:1956:U:O2	2.48	0.46
1:1:2529:G:H5'	9:F:175:LYS:HD3	1.98	0.46
2:2:397:A:O2'	2:2:399:G:OP2	2.28	0.46
2:2:844:G:N3	2:2:844:G:C3'	2.78	0.46
9:F:18:LYS:HE2	9:F:20:ASN:HB2	1.97	0.46
34:g:15:HIS:HB3	34:g:43:LEU:HD11	1.97	0.46
34:g:65:GLY:O	34:g:225:ARG:NH1	2.48	0.46
41:n:97:GLU:O	41:n:101:ALA:N	2.46	0.46
48:u:78:VAL:O	48:u:82:ALA:N	2.44	0.46
55:A:187:TYR:HD1	55:A:190:GLY:HA3	1.79	0.46
1:1:372:G:O2'	1:1:400:G:O6	2.32	0.46
1:1:532:A:N1	1:1:2035:G:N2	2.62	0.46
1:1:1022:G:H4'	1:1:1023:U:H5'	1.96	0.46
1:1:1398:C:H2'	1:1:1399:C:H6	1.79	0.46
2:2:77:A:H2'	2:2:78:A:C8	2.50	0.46
2:2:83:C:O2'	2:2:86:G:O6	2.30	0.46
2:2:1183:U:O2'	2:2:1185:G:OP2	2.33	0.46
19:R:66:HIS:ND1	19:R:94:THR:OG1	2.38	0.46
41:n:84:THR:HG21	41:n:103:PHE:HB3	1.98	0.46
42:o:64:GLN:O	46:s:99:ALA:N	2.44	0.46
55:A:270:ILE:HB	55:A:291:MET:HE1	1.97	0.46
1:1:282:A:H2'	1:1:283:G:C8	2.50	0.46
1:1:1030:C:OP2	14:M:127:LYS:NZ	2.48	0.46
1:1:1530:G:N3	1:1:1530:G:H2'	2.31	0.46
1:1:2642:G:H5'	11:J:80:HIS:CE1	2.51	0.46
2:2:54:C:H2'	2:2:352:C:H41	1.80	0.46
2:2:308:C:H2'	2:2:309:A:H8	1.80	0.46
2:2:1309:G:OP2	45:r:98:ARG:NE	2.38	0.46
5:B:6:CYS:SG	5:B:13:ARG:NH2	2.88	0.46
26:Y:44:LYS:HG3	26:Y:47:ARG:HH11	1.80	0.46
34:g:32:PHE:N	34:g:40:ILE:O	2.48	0.46
55:A:141:ALA:O	55:A:145:ALA:N	2.43	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:373:U:H2'	1:1:374:A:H8	1.80	0.46
1:1:671:C:OP2	13:L:33:ARG:NH1	2.48	0.46
1:1:1722:A:N6	1:1:1738:G:O2'	2.48	0.46
1:1:1987:A:H2'	1:1:1988:G:H8	1.81	0.46
1:1:2024:G:O3'	6:C:154:LYS:NZ	2.44	0.46
1:1:2838:G:O2'	15:N:49:GLU:OE1	2.23	0.46
2:2:1238:A:H5'	2:2:1336:C:H41	1.80	0.46
3:3:51:G:OP1	16:O:63:LYS:NZ	2.45	0.46
3:3:98:G:H1	23:V:14:LYS:HB2	1.81	0.46
5:B:141:VAL:HG12	5:B:192:LEU:HA	1.97	0.46
10:G:78:VAL:HB	10:G:144:VAL:HG22	1.97	0.46
16:O:60:GLU:HG3	16:O:61:GLN:HE21	1.79	0.46
16:O:66:GLY:O	16:O:102:ARG:NH2	2.49	0.46
18:Q:69:ALA:HB1	18:Q:74:ILE:HG23	1.98	0.46
28:a:30:HIS:ND1	28:a:31:ASP:O	2.45	0.46
35:h:156:ARG:H	35:h:163:ALA:HA	1.80	0.46
36:i:188:ARG:NH1	36:i:192:SER:O	2.49	0.46
47:t:32:LEU:HA	47:t:35:GLN:HB3	1.97	0.46
48:u:40:ASN:HB3	48:u:43:ALA:HB2	1.98	0.46
55:A:165:ILE:HA	55:A:181:ILE:HG13	1.97	0.46
1:1:154:U:H2'	1:1:155:A:H8	1.81	0.46
1:1:612:G:O2'	1:1:613:A:H5'	2.15	0.46
1:1:2096:C:H2'	1:1:2097:A:H8	1.80	0.46
1:1:2296:U:OP2	16:O:9:ARG:NH2	2.47	0.46
2:2:522:C:OP2	44:q:66:TYR:OH	2.25	0.46
2:2:937:A:N6	2:2:1345:U:O4	2.40	0.46
38:k:100:SER:HB2	38:k:103:VAL:HG23	1.97	0.46
47:t:10:LYS:O	47:t:14:GLU:N	2.49	0.46
47:t:82:ILE:HG22	47:t:87:LEU:HD12	1.97	0.46
1:1:191:A:OP2	1:1:204:A:N6	2.42	0.46
1:1:403:U:H5''	1:1:404:A:OP1	2.15	0.46
1:1:581:C:H2'	1:1:582:A:H8	1.81	0.46
1:1:1464:G:H2'	1:1:1465:G:C8	2.51	0.46
1:1:2039:U:H2'	1:1:2040:G:H8	1.79	0.46
2:2:401:C:N4	2:2:402:G:O6	2.48	0.46
2:2:1095:U:OP1	2:2:1108:G:N1	2.46	0.46
2:2:1303:C:H2'	2:2:1304:G:O4'	2.15	0.46
3:3:22:U:H2'	3:3:23:G:C8	2.51	0.46
5:B:155:ALA:HB2	5:B:162:VAL:HG23	1.97	0.46
9:F:65:ALA:O	9:F:69:ARG:N	2.46	0.46
19:R:48:LYS:HE2	19:R:103:ALA:HB1	1.97	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:S:73:LYS:HB2	20:S:106:VAL:HB	1.98	0.46
26:Y:21:LEU:HD12	26:Y:46:VAL:HG13	1.97	0.46
26:Y:28:LEU:O	26:Y:32:ALA:N	2.39	0.46
40:m:39:VAL:O	40:m:43:GLU:N	2.46	0.46
45:r:20:THR:HA	45:r:25:VAL:HG23	1.97	0.46
46:s:38:ASP:O	46:s:42:TRP:N	2.43	0.46
55:A:26:ASP:O	55:A:30:LYS:N	2.43	0.46
1:1:320:A:O2'	1:1:322:A:OP2	2.24	0.46
1:1:799:G:OP2	1:1:800:A:O2'	2.33	0.46
1:1:1278:C:H2'	1:1:1279:G:H8	1.81	0.46
1:1:1341:G:OP1	1:1:1397:U:N3	2.46	0.46
1:1:1753:G:N1	1:1:1756:G:OP2	2.40	0.46
1:1:2717:C:H2'	1:1:2718:G:O4'	2.15	0.46
2:2:438:U:O2'	2:2:494:G:O6	2.24	0.46
2:2:673:A:H4'	38:k:86:ARG:HH12	1.81	0.46
10:G:3:VAL:HA	10:G:38:PRO:HA	1.97	0.46
1:1:1967:C:H2'	1:1:1968:G:O4'	2.16	0.46
1:1:2832:U:H4'	1:1:2833:U:H2'	1.98	0.46
2:2:217:C:H2'	2:2:218:U:O4'	2.16	0.46
2:2:254:G:O2'	49:v:18:GLU:O	2.30	0.46
5:B:262:ARG:O	5:B:265:LYS:NZ	2.41	0.46
44:q:54:ARG:HD2	44:q:62:GLU:HG3	1.97	0.46
1:1:1475:G:O2'	1:1:1514:G:O6	2.27	0.45
1:1:1788:C:H2'	1:1:1789:A:C8	2.50	0.45
2:2:120:A:O2'	2:2:122:G:N7	2.37	0.45
5:B:132:MET:HE2	5:B:188:CYS:HB2	1.98	0.45
12:K:121:GLU:OE1	17:P:65:SER:OG	2.32	0.45
23:V:32:GLY:O	23:V:93:ARG:NH1	2.45	0.45
36:i:27:ALA:O	36:i:30:THR:OG1	2.31	0.45
36:i:61:VAL:HA	36:i:64:ILE:HD12	1.97	0.45
54:5:18:G:N2	54:5:58:A:O5'	2.49	0.45
55:A:40:GLU:HG3	55:A:43:GLN:HE21	1.81	0.45
1:1:371:A:N6	1:1:402:A:OP2	2.44	0.45
1:1:598:U:H2'	1:1:599:A:H8	1.81	0.45
1:1:949:G:H2'	1:1:950:G:H8	1.81	0.45
1:1:1128:G:N3	1:1:2516:A:O2'	2.43	0.45
1:1:1859:U:H2'	1:1:1860:G:C8	2.51	0.45
2:2:257:G:H2'	2:2:258:G:H8	1.81	0.45
2:2:563:A:O2'	2:2:566:G:O3'	2.33	0.45
2:2:1391:U:H2'	2:2:1392:G:C8	2.51	0.45
5:B:157:SER:OG	5:B:158:ALA:N	2.46	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:E:123:ASP:O	8:E:125:ARG:N	2.49	0.45
22:U:51:ALA:O	22:U:52:LEU:HB3	2.16	0.45
25:X:33:LEU:HD12	25:X:52:SER:HB3	1.98	0.45
25:X:40:VAL:HG12	25:X:43:GLU:H	1.81	0.45
37:j:102:GLY:H	37:j:122:ASN:ND2	2.14	0.45
47:t:51:HIS:CE1	47:t:54:ARG:CG	2.89	0.45
47:t:53:ARG:HA	47:t:57:LEU:HB2	1.96	0.45
48:u:44:SER:OG	48:u:45:GLU:N	2.49	0.45
1:1:321:U:O3'	7:D:162:ARG:NH1	2.45	0.45
1:1:581:C:H2'	1:1:582:A:C8	2.51	0.45
1:1:1501:G:OP1	5:B:101:ARG:NH2	2.45	0.45
1:1:1614:A:N6	20:S:88:ARG:O	2.49	0.45
1:1:2119:A:N7	1:1:2169:A:N6	2.64	0.45
2:2:362:G:H5''	44:q:58:THR:HG21	1.97	0.45
2:2:741:G:O2'	47:t:54:ARG:O	2.34	0.45
2:2:996:A:N1	2:2:1045:C:O2'	2.44	0.45
6:C:116:LYS:HG3	15:N:1:MET:HE1	1.96	0.45
6:C:152:PRO:O	6:C:154:LYS:N	2.49	0.45
11:J:58:ASN:ND2	11:J:128:ASN:OD1	2.46	0.45
12:K:70:ARG:HA	12:K:76:VAL:HA	1.98	0.45
35:h:81:GLY:HA2	35:h:84:VAL:HB	1.98	0.45
38:k:35:LYS:N	38:k:65:GLU:O	2.47	0.45
44:q:57:LEU:HD12	44:q:61:PHE:HB2	1.99	0.45
51:x:11:ILE:HG13	51:x:38:SER:HB3	1.97	0.45
55:A:56:LEU:HA	55:A:59:GLU:HB3	1.97	0.45
1:1:26:G:H1'	1:1:515:A:H61	1.80	0.45
1:1:69:C:O2	1:1:73:A:O2'	2.31	0.45
1:1:598:U:H2'	1:1:599:A:C8	2.52	0.45
1:1:690:G:O2'	1:1:780:G:OP1	2.33	0.45
1:1:1039:A:H2	1:1:1116:G:H22	1.64	0.45
1:1:1992:G:N2	1:1:1996:C:O2'	2.49	0.45
1:1:2112:G:H5'	1:1:2115:G:H22	1.81	0.45
1:1:2674:G:O2'	12:K:28:SER:O	2.31	0.45
1:1:2787:C:H1'	6:C:63:PRO:HG3	1.98	0.45
1:1:2806:C:H2'	1:1:2807:U:O4'	2.16	0.45
2:2:454:G:H2'	2:2:455:G:H8	1.81	0.45
5:B:145:GLU:HB2	5:B:188:CYS:HB3	1.98	0.45
7:D:121:VAL:HG21	7:D:124:PHE:HB2	1.97	0.45
12:K:24:VAL:HA	12:K:39:ILE:HG22	1.98	0.45
20:S:59:GLU:HB2	20:S:66:ILE:HD11	1.98	0.45
36:i:62:ARG:O	36:i:66:GLY:N	2.50	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1854:A:N6	1:1:1888:G:O2'	2.50	0.45
2:2:769:G:H4'	2:2:1513:A:H4'	1.99	0.45
2:2:1222:G:H5''	51:x:78:ARG:HD2	1.97	0.45
2:2:1273:C:H2'	2:2:1274:A:O4'	2.17	0.45
5:B:176:LEU:HD12	5:B:180:GLU:HB3	1.99	0.45
10:G:14:SER:OG	10:G:15:LEU:N	2.48	0.45
16:O:7:ARG:HH22	16:O:29:HIS:HE1	1.63	0.45
21:T:24:MET:HE2	21:T:30:ILE:HA	1.98	0.45
34:g:162:PHE:HA	34:g:184:PHE:HB2	1.99	0.45
35:h:56:VAL:HB	35:h:67:THR:HB	1.98	0.45
36:i:116:GLN:HE21	36:i:120:HIS:CE1	2.35	0.45
46:s:22:ALA:O	46:s:26:GLU:N	2.46	0.45
53:z:30:ALA:O	53:z:34:ARG:N	2.50	0.45
55:A:129:TYR:HE1	55:A:182:LYS:HE2	1.82	0.45
1:1:563:A:H2'	18:Q:37:GLN:HE21	1.82	0.45
1:1:1306:C:H2'	1:1:1307:A:C8	2.51	0.45
1:1:1651:G:H4'	15:N:39:PRO:HG2	1.98	0.45
2:2:157:U:H2'	2:2:158:G:H8	1.82	0.45
2:2:160:A:H61	2:2:347:G:H1'	1.81	0.45
2:2:208:U:O2'	2:2:211:G:O6	2.29	0.45
2:2:477:C:H2'	2:2:478:A:O4'	2.16	0.45
2:2:790:A:OP1	54:5:38:A:O2'	2.32	0.45
3:3:116:G:H2'	3:3:117:G:C8	2.51	0.45
10:G:83:LYS:HA	10:G:149:GLU:HB3	1.98	0.45
36:i:26:ARG:HE	36:i:31:LYS:HG2	1.82	0.45
51:x:15:LEU:HD13	51:x:33:THR:HG21	1.98	0.45
55:A:87:ALA:O	55:A:92:ASP:N	2.40	0.45
1:1:500:G:N1	1:1:503:A:OP2	2.34	0.45
1:1:1341:G:H1'	21:T:59:ASN:HB3	1.99	0.45
1:1:2216:G:H2'	1:1:2217:G:C8	2.52	0.45
1:1:2226:C:H2'	1:1:2227:A:O4'	2.16	0.45
55:A:29:ALA:HA	55:A:32:GLU:HB3	1.99	0.45
1:1:1463:C:H2'	1:1:1464:G:H8	1.82	0.45
1:1:2162:G:O2'	1:1:2163:A:N7	2.47	0.45
1:1:2285:C:OP2	30:c:6:ARG:NH1	2.45	0.45
1:1:2880:C:HO2'	15:N:90:ARG:NH2	2.14	0.45
2:2:376:G:H4'	48:u:5:ARG:HH11	1.82	0.45
2:2:1159:U:O4'	2:2:1182:G:N2	2.50	0.45
7:D:41:GLN:HG2	7:D:43:THR:HG23	1.99	0.45
14:M:17:ASN:OD1	14:M:97:GLN:NE2	2.50	0.45
28:a:26:SER:OG	28:a:27:THR:N	2.49	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:m:48:ASP:O	40:m:62:THR:N	2.49	0.45
46:s:41:ARG:NH2	51:x:6:LYS:O	2.50	0.45
47:t:33:THR:HA	47:t:63:ARG:HH11	1.81	0.45
47:t:43:PHE:CE2	47:t:56:LEU:HD13	2.52	0.45
55:A:263:ILE:O	55:A:272:THR:N	2.49	0.45
1:1:563:A:N3	18:Q:37:GLN:NE2	2.64	0.45
1:1:1019:U:H2'	1:1:1020:A:H8	1.81	0.45
1:1:1084:A:N3	1:1:1105:U:O2'	2.39	0.45
1:1:1123:C:H2'	1:1:1124:G:C8	2.52	0.45
1:1:1844:C:H2'	1:1:1845:G:H8	1.82	0.45
1:1:2368:C:H2'	1:1:2369:A:H8	1.80	0.45
1:1:2818:U:OP2	15:N:45:ARG:NH2	2.50	0.45
2:2:1356:G:H2'	2:2:1357:A:C8	2.52	0.45
36:i:34:ILE:HG23	36:i:35:GLU:HG2	1.99	0.45
36:i:202:GLU:OE2	37:j:105:ILE:N	2.46	0.45
45:r:25:VAL:HG12	45:r:29:ARG:HD2	1.99	0.45
47:t:56:LEU:HD12	47:t:56:LEU:O	2.17	0.45
48:u:8:ARG:H	48:u:28:ARG:HD2	1.82	0.45
55:A:324:ARG:HG2	55:A:335:ASP:HA	1.98	0.45
1:1:729:G:C4	1:1:1775:U:C2	3.05	0.45
1:1:2286:G:H3'	30:c:30:LYS:HE3	1.97	0.45
47:t:2:SER:HA	47:t:35:GLN:HE22	1.82	0.45
47:t:47:LYS:HE2	47:t:47:LYS:HB2	1.39	0.45
55:A:41:LEU:HD11	55:A:56:LEU:HB3	1.99	0.45
1:1:201:C:OP1	25:X:18:ARG:NH1	2.48	0.44
1:1:467:G:OP2	31:d:34:ARG:NH1	2.43	0.44
1:1:857:G:N2	1:1:921:C:O2	2.48	0.44
1:1:894:U:C6	1:1:894:U:OP2	2.70	0.44
1:1:1791:A:N6	1:1:1828:G:O2'	2.48	0.44
1:1:2098:U:H2'	1:1:2099:U:O4'	2.17	0.44
1:1:2699:C:H2'	1:1:2700:A:C8	2.52	0.44
2:2:957:U:H4'	51:x:79:THR:HG23	1.98	0.44
6:C:97:SER:OG	6:C:98:VAL:N	2.44	0.44
8:E:111:ILE:HB	8:E:114:PHE:HB2	1.98	0.44
18:Q:89:GLU:O	19:R:11:GLN:NE2	2.45	0.44
42:o:9:ARG:HB2	42:o:99:GLN:HB3	1.98	0.44
51:x:50:ALA:HB1	51:x:57:HIS:HB3	1.99	0.44
1:1:151:C:H2'	1:1:152:A:C8	2.52	0.44
1:1:564:C:O4'	18:Q:37:GLN:NE2	2.51	0.44
1:1:748:G:OP1	20:S:88:ARG:NH1	2.50	0.44
1:1:887:A:H4'	1:1:889:C:H5	1.82	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2824:C:H3'	1:1:2825:G:H21	1.83	0.44
2:2:437:U:O2'	36:i:120:HIS:ND1	2.44	0.44
2:2:1311:A:OP1	28:a:59:ARG:NH2	2.49	0.44
2:2:1359:C:OP2	46:s:75:ARG:NE	2.49	0.44
6:C:38:LYS:HD3	6:C:45:TYR:OH	2.17	0.44
6:C:68:PHE:O	6:C:72:GLY:N	2.48	0.44
41:n:39:PHE:O	41:n:45:ARG:NH2	2.41	0.44
42:o:8:ILE:HG12	42:o:100:ILE:HG22	1.99	0.44
42:o:45:ARG:HB3	42:o:69:THR:HB	1.98	0.44
54:5:19:G:OP2	54:5:20:H2U:H51	2.16	0.44
1:1:2271:G:H5'	24:W:20:ARG:HG2	1.99	0.44
2:2:519:C:N4	2:2:529:G:O2'	2.50	0.44
2:2:1239:A:O2'	2:2:1298:U:O4	2.36	0.44
5:B:161:TYR:HB3	5:B:194:GLU:HG2	1.98	0.44
8:E:123:ASP:CG	8:E:127:ASN:HB2	2.42	0.44
22:U:8:ASP:HB2	22:U:24:LYS:HD3	1.99	0.44
41:n:12:ARG:HA	41:n:12:ARG:HD2	1.70	0.44
49:v:47:HIS:N	49:v:73:TRP:O	2.46	0.44
55:A:196:THR:HG22	55:A:222:VAL:H	1.82	0.44
1:1:75:G:N2	1:1:112:U:O2	2.43	0.44
1:1:376:G:H2'	1:1:377:G:H8	1.82	0.44
1:1:405:U:C6	1:1:405:U:OP1	2.70	0.44
1:1:2128:G:N2	1:1:2174:C:O5'	2.50	0.44
2:2:496:A:H2'	2:2:496:A:N3	2.33	0.44
6:C:45:TYR:HE2	6:C:81:GLU:OE2	2.00	0.44
8:E:23:ASN:N	8:E:27:GLN:OE1	2.49	0.44
8:E:58:ALA:HB2	8:E:65:PRO:HD3	1.99	0.44
34:g:76:ALA:HB1	34:g:210:VAL:HG11	2.00	0.44
42:o:6:ILE:HB	42:o:76:ILE:HB	1.99	0.44
1:1:296:U:H2'	1:1:297:G:C8	2.53	0.44
1:1:558:U:H2'	1:1:559:G:H8	1.81	0.44
1:1:728:G:H4'	5:B:13:ARG:HD3	2.00	0.44
1:1:1980:G:O2'	1:1:1982:U:OP2	2.32	0.44
1:1:2087:G:H2'	1:1:2088:A:H8	1.83	0.44
2:2:739:C:O2'	47:t:42:HIS:ND1	2.47	0.44
2:2:1071:C:H2'	2:2:1072:G:C8	2.52	0.44
30:c:8:LYS:HD2	32:e:34:THR:HG21	1.98	0.44
1:1:5:A:H2'	1:1:6:A:C8	2.53	0.44
1:1:205:G:H1'	1:1:206:U:H5	1.81	0.44
1:1:372:G:O4'	25:X:61:LYS:NZ	2.48	0.44
1:1:406:G:C8	1:1:406:G:O5'	2.70	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:414:C:H2'	1:1:415:A:C8	2.52	0.44
1:1:616:A:H3'	1:1:617:G:H8	1.83	0.44
1:1:1000:A:OP2	1:1:1154:G:N1	2.37	0.44
1:1:1358:G:N1	1:1:1372:U:OP2	2.32	0.44
2:2:197:A:N3	2:2:198:G:H1'	2.32	0.44
2:2:1162:C:H2'	2:2:1163:A:H8	1.82	0.44
4:4:21:A:N6	55:A:215:THR:OG1	2.50	0.44
8:E:41:GLY:HA2	8:E:85:ILE:HD11	1.99	0.44
21:T:15:HIS:HB3	21:T:31:VAL:HG12	1.99	0.44
1:1:106:C:H2'	1:1:107:G:C8	2.53	0.44
1:1:177:G:H3'	1:1:178:G:H8	1.82	0.44
1:1:910:A:N6	1:1:2277:G:O2'	2.36	0.44
1:1:1580:A:H3'	1:1:1581:G:H8	1.83	0.44
1:1:1825:U:H2'	1:1:1826:G:C8	2.53	0.44
1:1:2314:A:H1'	8:E:155:THR:HG21	1.99	0.44
1:1:2831:G:O2'	1:1:2884:U:OP1	2.30	0.44
2:2:67:C:H2'	2:2:68:G:C8	2.53	0.44
2:2:499:A:H4'	2:2:500:G:H5'	2.00	0.44
2:2:711:G:H2'	2:2:712:A:H8	1.82	0.44
2:2:1158:C:O2	2:2:1158:C:H2'	2.17	0.44
2:2:1279:G:O2'	2:2:1281:C:OP2	2.25	0.44
2:2:1314:C:N4	51:x:2:PRO:O	2.33	0.44
38:k:8:PHE:HA	38:k:87:SER:HA	2.00	0.44
46:s:69:ARG:HD3	46:s:71:HIS:H	1.82	0.44
50:w:51:TYR:O	50:w:55:LEU:N	2.50	0.44
55:A:164:GLU:O	55:A:182:LYS:N	2.50	0.44
1:1:828:U:H2'	1:1:829:A:C8	2.52	0.44
1:1:894:U:C4'	1:1:895:U:OP1	2.65	0.44
1:1:995:C:N3	11:J:3:THR:N	2.65	0.44
1:1:1078:U:O2'	1:1:1088:A:O5'	2.35	0.44
1:1:1267:U:H2'	1:1:1268:A:C8	2.52	0.44
1:1:1631:G:N2	1:1:1634:A:OP2	2.46	0.44
1:1:1864:U:O2	1:1:1878:G:N2	2.34	0.44
2:2:1297:G:N2	2:2:1298:U:O4	2.50	0.44
2:2:1402:4OC:HM22	2:2:1403:C:H5'	2.00	0.44
34:g:19:GLN:HB2	34:g:22:TYR:HD2	1.83	0.44
35:h:20:SER:HB3	35:h:22:TRP:HE1	1.83	0.44
35:h:59:ARG:HA	35:h:64:ILE:HA	2.00	0.44
47:t:36:ILE:HB	47:t:63:ARG:NH1	2.32	0.44
1:1:558:U:H2'	1:1:559:G:C8	2.53	0.44
1:1:593:U:H2'	1:1:594:U:C6	2.53	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:696:G:H2'	1:1:697:G:H8	1.83	0.44
1:1:1564:C:OP2	5:B:26:LYS:NZ	2.40	0.44
1:1:2002:G:H5''	15:N:9:GLN:HE21	1.82	0.44
1:1:2461:A:N6	1:1:2488:G:O6	2.51	0.44
1:1:2503:2MA:O2'	1:1:2505:G:OP2	2.35	0.44
2:2:257:G:H2'	2:2:258:G:C8	2.53	0.44
2:2:1134:G:H1	2:2:1140:C:H42	1.65	0.44
2:2:1412:C:H2'	2:2:1413:A:C8	2.53	0.44
3:3:3:C:O2	3:3:117:G:N1	2.47	0.44
6:C:5:VAL:HG22	6:C:202:ILE:HG12	2.00	0.44
16:O:43:ASN:HD21	16:O:46:GLU:HG2	1.83	0.44
35:h:32:ASN:OD1	35:h:59:ARG:NH1	2.51	0.44
51:x:52:HIS:CD2	51:x:54:GLY:H	2.36	0.44
55:A:265:HIS:CD2	55:A:267:PRO:HD2	2.53	0.44
1:1:1270:C:H5''	1:1:1271:G:H5''	1.99	0.43
1:1:1534:U:O2'	1:1:1537:G:O6	2.26	0.43
1:1:1837:C:O2'	1:1:1927:A:N3	2.46	0.43
1:1:1915:3TD:H3'	1:1:1916:A:C8	2.45	0.43
2:2:111:G:H22	2:2:330:C:H41	1.65	0.43
2:2:199:A:H61	2:2:218:U:H3	1.66	0.43
2:2:531:U:OP2	55:A:213:ARG:NH2	2.50	0.43
2:2:1222:G:OP2	2:2:1322:C:N4	2.42	0.43
2:2:1406:U:H3'	2:2:1407:5MC:H6	1.83	0.43
26:Y:18:LEU:HB2	26:Y:53:VAL:HG11	2.00	0.43
35:h:148:GLY:HA2	35:h:171:GLY:HA3	2.00	0.43
41:n:42:GLU:OE2	41:n:45:ARG:NH1	2.45	0.43
50:w:48:ARG:HD3	50:w:50:LYS:H	1.83	0.43
1:1:7:G:H5''	11:J:123:LYS:HE2	2.00	0.43
1:1:964:C:O2'	1:1:2273:A:N3	2.36	0.43
1:1:1443:U:H2'	1:1:1444:G:H8	1.83	0.43
1:1:2552:OMU:H1'	1:1:2552:OMU:HM23	1.66	0.43
2:2:1261:A:N6	2:2:1274:A:O2'	2.37	0.43
20:S:20:VAL:HG21	20:S:43:ALA:HB3	2.00	0.43
31:d:17:GLY:HA2	31:d:45:SER:HB2	2.00	0.43
37:j:38:VAL:HA	37:j:48:PHE:HA	2.00	0.43
46:s:47:LYS:O	46:s:50:THR:OG1	2.29	0.43
47:t:57:LEU:C	47:t:59:MET:N	2.73	0.43
54:5:55:PSU:N3	54:5:58:A:OP2	2.40	0.43
1:1:441:U:H2'	1:1:442:G:C8	2.53	0.43
1:1:750:A:OP1	1:1:1615:C:N4	2.50	0.43
1:1:1102:C:H2'	1:1:1103:A:C8	2.53	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1364:G:OP1	25:X:50:ARG:NH1	2.42	0.43
1:1:2549:G:H2'	1:1:2550:G:H8	1.82	0.43
3:3:40:U:N3	3:3:44:G:OP2	2.39	0.43
9:F:27:LYS:HG2	9:F:32:GLU:HB2	2.01	0.43
14:M:121:ALA:HA	14:M:124:LEU:HD12	2.01	0.43
36:i:69:GLU:OE2	36:i:204:TYR:OH	2.28	0.43
38:k:78:PHE:HD1	38:k:84:VAL:HG11	1.83	0.43
46:s:41:ARG:HH22	51:x:6:LYS:HB2	1.83	0.43
1:1:1464:G:H2'	1:1:1465:G:H8	1.84	0.43
1:1:1583:A:H1'	1:1:1584:U:C2	2.54	0.43
2:2:806:C:H2'	2:2:807:A:H8	1.82	0.43
2:2:1376:U:H2'	2:2:1377:A:C8	2.53	0.43
9:F:84:THR:OG1	9:F:134:LYS:NZ	2.42	0.43
44:q:4:VAL:O	44:q:8:VAL:N	2.49	0.43
55:A:203:ARG:HH12	55:A:206:PRO:HD3	1.83	0.43
1:1:729:G:H4'	1:1:763:G:O5'	2.18	0.43
1:1:1065:U:O2	1:1:1073:A:N6	2.51	0.43
1:1:1568:G:OP2	5:B:63:ARG:NH1	2.42	0.43
1:1:1796:U:H2'	1:1:1797:G:C8	2.53	0.43
5:B:71:LYS:O	5:B:118:SER:OG	2.36	0.43
7:D:181:ILE:HG23	13:L:1:MET:HG2	2.01	0.43
27:Z:45:ARG:HA	27:Z:48:ILE:HD12	1.99	0.43
32:e:31:HIS:CD2	32:e:32:ILE:HG12	2.52	0.43
37:j:97:GLN:N	37:j:124:LEU:O	2.51	0.43
38:k:4:TYR:N	38:k:64:VAL:O	2.38	0.43
39:l:26:PHE:HA	39:l:29:ILE:HD12	2.01	0.43
45:r:101:ARG:HG3	45:r:104:THR:H	1.84	0.43
54:5:6:G:O2'	54:5:49:G:O4'	2.36	0.43
55:A:276:ASN:N	55:A:283:ASN:OD1	2.52	0.43
1:1:717:C:H3'	1:1:718:A:C8	2.51	0.43
1:1:1013:C:H2'	1:1:1014:A:C8	2.53	0.43
1:1:1038:G:H2'	1:1:1039:A:C8	2.53	0.43
1:1:1263:U:O2'	29:b:4:GLN:NE2	2.45	0.43
1:1:2081:U:H2'	1:1:2082:A:H8	1.83	0.43
1:1:2193:G:HO2'	1:1:2194:U:P	2.41	0.43
1:1:2425:A:H5'	1:1:2427:C:O4'	2.19	0.43
2:2:406:G:H21	36:i:116:GLN:HE22	1.67	0.43
2:2:674:G:H2'	2:2:675:A:C8	2.53	0.43
2:2:744:C:H2'	2:2:745:G:C8	2.53	0.43
18:Q:92:ARG:HA	18:Q:95:LEU:HB2	2.01	0.43
20:S:73:LYS:HB3	20:S:75:PHE:HE2	1.83	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:W:56:ASP:OD1	24:W:58:THR:OG1	2.34	0.43
26:Y:29:ARG:O	26:Y:33:ALA:N	2.50	0.43
39:l:5:ARG:NH1	39:l:7:ILE:HA	2.34	0.43
44:q:18:LYS:NZ	44:q:19:SER:O	2.48	0.43
54:5:51:C:H2'	54:5:52:G:H8	1.82	0.43
1:1:175:G:H2'	1:1:176:A:C8	2.54	0.43
1:1:476:G:O2'	1:1:502:A:N6	2.45	0.43
1:1:658:U:O2'	7:D:97:ASN:OD1	2.29	0.43
1:1:1398:C:H2'	1:1:1399:C:C6	2.53	0.43
1:1:1496:A:H2'	1:1:1498:C:C4	2.54	0.43
1:1:2056:G:O2'	29:b:5:GLN:NE2	2.43	0.43
1:1:2368:C:H2'	1:1:2369:A:C8	2.54	0.43
1:1:2840:C:H5''	15:N:56:LYS:HZ1	1.83	0.43
2:2:77:A:H2'	2:2:78:A:H8	1.83	0.43
6:C:13:ARG:HH11	17:P:56:HIS:HA	1.84	0.43
10:G:128:HIS:N	10:G:144:VAL:O	2.49	0.43
11:J:45:THR:HB	11:J:48:VAL:HB	1.99	0.43
35:h:65:ARG:HA	35:h:100:GLN:HB3	1.99	0.43
36:i:152:GLN:HB2	36:i:155:VAL:HG23	1.99	0.43
37:j:84:PRO:HG3	37:j:98:PRO:HD2	2.01	0.43
41:n:34:SER:OG	41:n:35:LEU:N	2.52	0.43
45:r:2:ALA:O	45:r:9:ILE:N	2.45	0.43
46:s:63:ARG:HB3	46:s:68:GLY:HA2	2.01	0.43
54:5:63:G:H2'	54:5:64:G:C8	2.53	0.43
55:A:242:ASP:O	55:A:262:ARG:N	2.52	0.43
1:1:458:G:N2	1:1:459:U:O4	2.50	0.43
1:1:578:G:OP1	1:1:1255:U:O2'	2.29	0.43
1:1:1700:A:H3'	1:1:1701:A:H8	1.84	0.43
1:1:2252:G:H2'	1:1:2253:G:H8	1.83	0.43
1:1:2708:G:O2'	15:N:71:ARG:NH1	2.52	0.43
2:2:1423:G:OP1	12:K:49:ARG:NH1	2.41	0.43
3:3:5:U:H2'	3:3:6:G:C8	2.53	0.43
10:G:125:THR:HG21	10:G:148:ALA:HB2	2.00	0.43
20:S:37:THR:OG1	20:S:48:LYS:NZ	2.44	0.43
41:n:12:ARG:HG3	41:n:13:LYS:H	1.83	0.43
1:1:968:C:H2'	1:1:969:G:C8	2.54	0.43
1:1:1114:C:H2'	1:1:1115:G:C8	2.53	0.43
1:1:1153:C:OP1	18:Q:76:TYR:OH	2.35	0.43
1:1:1222:U:H2'	1:1:1223:G:H8	1.84	0.43
1:1:1589:U:O2'	1:1:1590:A:H5'	2.18	0.43
1:1:1602:U:OP2	21:T:64:LYS:NZ	2.52	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1859:U:H2'	1:1:1860:G:H8	1.83	0.43
1:1:2241:A:H2'	1:1:2242:G:H8	1.84	0.43
2:2:161:A:N6	2:2:347:G:O2'	2.45	0.43
2:2:950:U:H3'	45:r:101:ARG:HH22	1.84	0.43
2:2:1086:U:H3	2:2:1099:G:H22	1.66	0.43
2:2:1173:U:H2'	2:2:1174:G:H8	1.83	0.43
14:M:136:MET:HE3	23:V:57:TYR:HB3	2.00	0.43
34:g:120:GLN:HA	34:g:124:GLY:HA3	2.01	0.43
36:i:103:TYR:O	36:i:165:ARG:NH2	2.51	0.43
36:i:170:TRP:CD2	36:i:186:PRO:HB3	2.54	0.43
37:j:114:VAL:HG13	37:j:115:LEU:HD22	2.00	0.43
42:o:34:ALA:HB3	42:o:78:GLU:HB2	2.01	0.43
43:p:46:THR:OG1	43:p:49:GLY:N	2.51	0.43
47:t:43:PHE:CZ	47:t:56:LEU:HD13	2.54	0.43
1:1:1408:G:O6	1:1:1593:A:N6	2.52	0.43
1:1:1914:C:N3	1:1:1915:3TD:H1'	2.34	0.43
1:1:2108:A:N6	1:1:2181:U:H3	2.17	0.43
2:2:740:U:OP1	47:t:38:HIS:NE2	2.42	0.43
2:2:1297:G:H21	39:l:114:LYS:HB3	1.84	0.43
9:F:10:VAL:HA	9:F:49:THR:HA	2.00	0.43
39:l:51:ALA:O	39:l:55:GLY:N	2.43	0.43
39:l:69:VAL:HG21	39:l:104:ILE:HD11	2.01	0.43
41:n:49:ARG:O	41:n:53:GLU:N	2.50	0.43
55:A:40:GLU:OE1	55:A:52:ARG:NE	2.48	0.43
55:A:59:GLU:O	55:A:63:LEU:N	2.46	0.43
55:A:117:ARG:HH22	55:A:362:LYS:HE2	1.83	0.43
1:1:45:G:H5''	1:1:46:G:H5'	2.01	0.42
1:1:851:C:O2'	27:Z:43:ALA:O	2.34	0.42
1:1:890:C:H2'	1:1:891:G:H4'	2.00	0.42
1:1:935:C:H2'	1:1:936:A:C8	2.54	0.42
1:1:995:C:H42	11:J:3:THR:H	1.67	0.42
1:1:1477:A:N6	1:1:1514:G:O2'	2.52	0.42
1:1:1700:A:N6	2:2:1475:G:OP1	2.40	0.42
2:2:67:C:O2'	2:2:171:A:N3	2.46	0.42
2:2:154:U:H2'	2:2:155:A:H8	1.84	0.42
2:2:711:G:H2'	2:2:712:A:C8	2.54	0.42
2:2:940:C:H2'	2:2:941:G:C8	2.54	0.42
6:C:13:ARG:HG2	17:P:56:HIS:CE1	2.53	0.42
29:b:31:ASP:HB3	29:b:36:GLU:H	1.83	0.42
31:d:23:ALA:O	31:d:28:ARG:NH1	2.51	0.42
43:p:35:THR:OG1	43:p:36:ASP:N	2.51	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:675:A:OP1	7:D:58:LYS:NZ	2.48	0.42
1:1:745:1MG:O2'	1:1:750:A:N6	2.52	0.42
1:1:1306:C:H2'	1:1:1307:A:H8	1.84	0.42
1:1:2087:G:H2'	1:1:2088:A:C8	2.54	0.42
1:1:2118:U:O2'	1:1:2172:U:O4	2.31	0.42
1:1:2127:G:N1	1:1:2161:C:N3	2.65	0.42
1:1:2233:U:H2'	1:1:2234:G:C8	2.54	0.42
1:1:2447:G:N2	1:1:2450:A:OP2	2.52	0.42
2:2:809:G:OP2	47:t:48:LYS:CE	2.64	0.42
2:2:1086:U:H3	2:2:1099:G:H1	1.67	0.42
6:C:48:ILE:HG23	6:C:84:LEU:HD11	2.01	0.42
7:D:2:GLU:HB3	7:D:11:ALA:HB1	2.00	0.42
7:D:29:HIS:HD2	13:L:6:LEU:HB3	1.83	0.42
9:F:127:THR:HB	9:F:130:GLU:HB3	2.01	0.42
10:G:103:VAL:HB	10:G:110:VAL:HG11	2.00	0.42
23:V:18:ARG:O	23:V:22:ALA:N	2.48	0.42
24:W:46:HIS:N	24:W:78:LYS:O	2.44	0.42
47:t:47:LYS:HB3	47:t:48:LYS:H	1.61	0.42
53:z:7:ARG:HH22	53:z:18:ARG:HH12	1.65	0.42
1:1:1059:G:H3'	1:1:1060:U:H3'	2.00	0.42
1:1:1067:A:OP1	55:A:54:GLN:NE2	2.52	0.42
1:1:1691:C:H2'	1:1:1692:U:C6	2.55	0.42
2:2:231:U:H2'	2:2:232:G:H8	1.84	0.42
2:2:366:A:O2'	2:2:394:G:N2	2.50	0.42
2:2:503:C:O2'	2:2:510:A:N1	2.49	0.42
2:2:776:G:N1	2:2:802:A:OP1	2.45	0.42
2:2:1091:U:O2'	2:2:1093:A:N7	2.43	0.42
24:W:33:ALA:N	24:W:64:ASP:OD1	2.52	0.42
37:j:160:SER:H	37:j:163:GLU:HB2	1.84	0.42
48:u:18:GLN:HE22	48:u:35:ARG:HH21	1.66	0.42
55:A:208:ASP:OD2	55:A:211:GLY:N	2.53	0.42
55:A:276:ASN:HD22	55:A:286:GLN:HG2	1.84	0.42
1:1:347:A:H2'	1:1:348:A:C8	2.55	0.42
1:1:409:G:H2'	1:1:410:G:C8	2.54	0.42
1:1:2833:U:H3'	1:1:2834:G:C8	2.55	0.42
2:2:294:U:OP1	2:2:610:U:O2'	2.32	0.42
2:2:490:C:H2'	2:2:491:G:C8	2.54	0.42
2:2:1126:U:O4	42:o:9:ARG:NH1	2.51	0.42
2:2:1178:G:O2'	2:2:1180:A:N7	2.52	0.42
3:3:86:G:H3'	3:3:88:C:H41	1.85	0.42
13:L:88:GLY:O	13:L:121:THR:N	2.45	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:O:30:ARG:HD3	16:O:102:ARG:NH1	2.35	0.42
51:x:3:ARG:HH11	51:x:10:PHE:HB2	1.83	0.42
51:x:39:THR:HA	51:x:70:LYS:HA	2.00	0.42
1:1:894:U:H4'	1:1:895:U:OP1	2.19	0.42
1:1:1278:C:H2'	1:1:1279:G:C8	2.54	0.42
1:1:2329:U:H2'	1:1:2330:G:C8	2.55	0.42
1:1:2563:U:O2'	1:1:2565:A:N7	2.44	0.42
2:2:770:C:H2'	2:2:771:G:H8	1.84	0.42
2:2:1129:C:O2	2:2:1130:A:N6	2.41	0.42
10:G:66:ASN:CG	10:G:135:HIS:HB3	2.44	0.42
35:h:107:ARG:HG3	35:h:108:LYS:HG3	2.01	0.42
35:h:152:GLU:N	35:h:199:LYS:O	2.53	0.42
39:l:78:ARG:HG2	39:l:80:VAL:HG13	2.01	0.42
45:r:33:ILE:O	45:r:37:ALA:N	2.53	0.42
47:t:36:ILE:O	47:t:40:GLN:N	2.52	0.42
1:1:910:A:N6	14:M:11:LYS:O	2.53	0.42
1:1:1076:C:H2'	1:1:1077:A:H8	1.83	0.42
1:1:1269:A:H61	1:1:2011:U:H3	1.67	0.42
1:1:2167:U:O2'	1:1:2169:A:N7	2.42	0.42
2:2:335:C:H2'	2:2:336:A:H8	1.85	0.42
2:2:1116:U:H2'	2:2:1117:A:C8	2.55	0.42
13:L:79:LEU:HD11	13:L:112:LEU:HD12	2.02	0.42
22:U:102:THR:HB	22:U:104:LYS:HE2	2.01	0.42
27:Z:8:THR:HB	27:Z:56:LYS:HB3	2.01	0.42
31:d:18:PHE:HA	31:d:43:THR:HG21	2.02	0.42
47:t:70:LEU:HD21	47:t:81:LEU:HD23	2.02	0.42
54:5:51:C:H2'	54:5:52:G:C8	2.55	0.42
1:1:181:A:H2'	1:1:182:A:C8	2.54	0.42
1:1:992:C:H2'	1:1:993:G:C8	2.54	0.42
1:1:1195:G:O2'	1:1:1226:A:N1	2.50	0.42
1:1:1443:U:H2'	1:1:1444:G:C8	2.55	0.42
1:1:2392:A:OP1	32:e:31:HIS:NE2	2.52	0.42
1:1:2544:G:H2'	1:1:2545:G:H8	1.83	0.42
3:3:23:G:H2'	3:3:24:G:C5	2.54	0.42
12:K:23:LYS:HB3	12:K:40:LYS:HB3	2.02	0.42
15:N:44:LEU:HG	15:N:48:VAL:HB	2.01	0.42
17:P:89:ARG:NE	17:P:113:ARG:O	2.53	0.42
20:S:77:ASP:O	20:S:102:HIS:N	2.50	0.42
26:Y:39:GLN:HB3	26:Y:41:HIS:CE1	2.55	0.42
37:j:152:MET:O	37:j:156:LYS:N	2.45	0.42
42:o:42:LEU:HB2	42:o:71:LEU:HB3	2.02	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1426:G:H3'	1:1:1427:A:H2'	2.02	0.42
1:1:1934:C:H2'	1:1:1935:G:H8	1.84	0.42
1:1:2428:G:H4'	1:1:2429:G:C4	2.55	0.42
2:2:137:U:H2'	2:2:138:G:C8	2.53	0.42
2:2:559:A:H4'	2:2:560:A:H3'	2.01	0.42
2:2:886:G:H1	2:2:911:U:H3	1.67	0.42
2:2:1266:G:N2	2:2:1269:A:OP2	2.41	0.42
2:2:1368:A:OP2	41:n:114:LYS:NZ	2.47	0.42
9:F:123:ALA:HA	9:F:133:LEU:HA	2.02	0.42
34:g:12:ALA:HB1	34:g:209:ALA:HA	2.02	0.42
45:r:13:LYS:HD3	45:r:17:ILE:HG22	2.01	0.42
47:t:54:ARG:NH2	47:t:58:ARG:HD2	2.35	0.42
1:1:321:U:H5''	7:D:131:THR:HG23	2.02	0.42
1:1:596:U:H2'	1:1:597:G:C8	2.55	0.42
1:1:1388:G:O2'	1:1:1525:A:O2'	2.38	0.42
1:1:2821:A:H2'	1:1:2822:G:H8	1.84	0.42
2:2:504:C:H42	2:2:541:G:H1	1.67	0.42
3:3:7:G:H5''	16:O:29:HIS:CE1	2.55	0.42
6:C:46:ARG:NH2	6:C:88:GLU:O	2.36	0.42
26:Y:18:LEU:HD21	26:Y:50:VAL:HG13	2.02	0.42
37:j:86:LYS:HA	37:j:95:PHE:HA	2.02	0.42
41:n:65:ILE:HD13	41:n:79:ILE:HG23	2.01	0.42
47:t:72:ARG:O	47:t:72:ARG:HG2	2.20	0.42
55:A:310:MET:HA	55:A:313:ASN:HD22	1.85	0.42
1:1:69:C:H2'	1:1:70:G:H8	1.85	0.42
1:1:82:U:H2'	1:1:83:A:C8	2.55	0.42
1:1:243:U:N3	1:1:255:A:N7	2.67	0.42
1:1:711:G:H1	1:1:720:U:H3	1.66	0.42
1:1:720:U:H2'	1:1:721:A:C8	2.55	0.42
1:1:1378:A:O2'	1:1:1380:G:N7	2.52	0.42
1:1:2375:G:N2	1:1:2378:A:OP2	2.38	0.42
1:1:2452:C:H5'	55:A:252:GLN:HB3	2.02	0.42
2:2:375:U:O3'	48:u:6:LEU:HB2	2.20	0.42
2:2:537:G:H2'	2:2:538:G:H8	1.85	0.42
2:2:1241:G:H2'	2:2:1242:G:C8	2.55	0.42
2:2:1386:G:H2'	2:2:1387:G:H8	1.85	0.42
8:E:158:THR:OG1	8:E:159:THR:N	2.53	0.42
13:L:23:ILE:HG12	19:R:82:HIS:CE1	2.54	0.42
14:M:42:THR:HA	14:M:93:VAL:HG12	2.01	0.42
19:R:6:GLN:HG3	19:R:39:LEU:HD11	2.02	0.42
37:j:156:LYS:HG2	40:m:71:VAL:HG13	2.02	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:k:36:ILE:HD11	38:k:39:LEU:HB2	2.02	0.42
47:t:58:ARG:O	47:t:58:ARG:HG3	2.18	0.42
52:y:35:VAL:HG11	52:y:79:LEU:HD13	2.01	0.42
52:y:67:ILE:HB	52:y:71:LYS:HD3	2.01	0.42
1:1:1094:U:H2'	1:1:1095:A:H2'	2.01	0.41
1:1:2175:C:H3'	1:1:2176:A:C8	2.55	0.41
2:2:21:G:H2'	2:2:22:G:C8	2.55	0.41
2:2:1135:U:O2'	2:2:1136:C:H5''	2.21	0.41
2:2:1221:G:H5''	51:x:36:ARG:HH11	1.84	0.41
2:2:1425:U:H2'	2:2:1426:G:C8	2.54	0.41
9:F:42:GLU:HA	9:F:55:ARG:NH2	2.34	0.41
15:N:38:LEU:O	15:N:42:LYS:N	2.50	0.41
22:U:51:ALA:O	22:U:52:LEU:CB	2.67	0.41
38:k:19:PRO:HA	38:k:22:ILE:HD12	2.02	0.41
38:k:40:GLU:OE1	38:k:100:SER:OG	2.32	0.41
41:n:34:SER:H	41:n:37:GLN:HB2	1.85	0.41
55:A:310:MET:HA	55:A:313:ASN:HB2	2.01	0.41
55:A:325:SER:N	55:A:334:LYS:O	2.50	0.41
1:1:372:G:C8	25:X:61:LYS:HD2	2.56	0.41
1:1:463:G:N2	1:1:466:A:OP2	2.38	0.41
1:1:577:G:O2'	1:1:1254:A:OP1	2.37	0.41
1:1:741:U:H2'	1:1:742:A:H8	1.85	0.41
1:1:918:A:N3	3:3:80:U:O2'	2.50	0.41
1:1:1024:G:O2'	1:1:1144:A:O2'	2.38	0.41
1:1:1671:U:N3	1:1:1674:G:OP2	2.34	0.41
1:1:1796:U:H2'	1:1:1797:G:H8	1.85	0.41
1:1:2002:G:H5'	15:N:13:ASN:HA	2.02	0.41
1:1:2522:U:O2'	1:1:2647:U:OP1	2.29	0.41
2:2:452:A:H2'	2:2:453:G:O4'	2.21	0.41
2:2:680:C:H2'	2:2:681:A:C8	2.55	0.41
2:2:720:C:O3'	50:w:52:GLN:NE2	2.53	0.41
2:2:750:C:H2'	2:2:751:U:C6	2.55	0.41
3:3:76:G:OP1	23:V:9:ARG:NH2	2.35	0.41
7:D:106:LYS:HG3	7:D:200:LEU:HD23	2.01	0.41
34:g:24:ASN:HD21	34:g:26:LYS:HD2	1.85	0.41
35:h:156:ARG:NH1	35:h:160:ALA:O	2.54	0.41
1:1:1003:G:O2'	1:1:1010:A:N1	2.47	0.41
1:1:1880:U:H2'	1:1:1881:C:H6	1.85	0.41
1:1:1914:C:H2'	1:1:1915:3TD:O4'	2.20	0.41
1:1:2113:U:O4	1:1:2114:A:N6	2.54	0.41
1:1:2128:G:H1'	1:1:2174:C:H1'	2.00	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2667:C:N3	9:F:110:SER:OG	2.43	0.41
2:2:34:C:H2'	2:2:35:G:C8	2.53	0.41
2:2:343:U:O2'	2:2:346:G:O6	2.34	0.41
2:2:672:U:H2'	2:2:673:A:C8	2.56	0.41
2:2:1060:U:H2'	2:2:1061:G:H8	1.85	0.41
5:B:199:GLU:HA	5:B:202:LEU:HD23	2.02	0.41
18:Q:31:VAL:HG12	18:Q:34:VAL:H	1.85	0.41
28:a:42:PRO:HB2	28:a:46:GLY:HA3	2.01	0.41
34:g:163:VAL:N	34:g:184:PHE:O	2.50	0.41
50:w:34:THR:HG23	50:w:37:GLY:H	1.85	0.41
55:A:115:PHE:O	55:A:119:PHE:N	2.51	0.41
1:1:1223:G:OP1	19:R:68:ARG:NH2	2.53	0.41
1:1:1844:C:O3'	5:B:256:LYS:NZ	2.49	0.41
1:1:2489:U:O2'	1:1:2518:A:N6	2.53	0.41
1:1:2861:U:H2'	1:1:2862:G:C8	2.55	0.41
2:2:269:C:H2'	2:2:270:A:H8	1.84	0.41
2:2:368:U:O2	2:2:368:U:C2'	2.68	0.41
2:2:1304:G:N2	2:2:1333:A:H62	2.19	0.41
2:2:1385:G:H2'	2:2:1386:G:C8	2.55	0.41
15:N:52:ILE:HD13	15:N:94:TYR:HB2	2.00	0.41
28:a:20:ASN:HB2	28:a:39:LYS:HD3	2.01	0.41
47:t:29:VAL:HG22	47:t:67:LEU:HD22	2.02	0.41
55:A:271:VAL:O	55:A:294:LYS:NZ	2.50	0.41
55:A:307:LYS:O	55:A:311:GLU:N	2.53	0.41
1:1:6:A:H2'	1:1:7:G:C8	2.55	0.41
1:1:455:C:N3	1:1:473:G:H5'	2.36	0.41
1:1:2124:G:H1	1:1:2174:C:H42	1.69	0.41
2:2:32:A:H2	44:q:28:PRO:HB3	1.86	0.41
2:2:126:G:OP1	2:2:605:U:O2'	2.25	0.41
2:2:129:A:H2	2:2:232:G:H22	1.69	0.41
2:2:583:A:N6	2:2:758:C:O2'	2.53	0.41
2:2:1162:C:H2'	2:2:1163:A:C8	2.55	0.41
15:N:28:LEU:HD13	15:N:34:ILE:HG12	2.02	0.41
17:P:63:LYS:HE2	17:P:65:SER:HB2	2.03	0.41
18:Q:49:ASP:HA	18:Q:52:GLN:HB2	2.03	0.41
22:U:40:ASN:O	22:U:63:ALA:N	2.53	0.41
38:k:21:MET:HG2	38:k:24:ARG:HH21	1.84	0.41
43:p:64:GLN:HB2	43:p:99:ALA:HB2	2.02	0.41
45:r:89:LEU:HD23	45:r:92:ARG:HE	1.86	0.41
55:A:83:LEU:O	55:A:87:ALA:N	2.53	0.41
1:1:1047:G:HO2'	1:1:1110:G:H1	1.68	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1820:U:C4	5:B:159:GLY:HA3	2.56	0.41
1:1:2200:C:OP2	25:X:37:ARG:NH1	2.50	0.41
1:1:2216:G:H2'	1:1:2217:G:H8	1.85	0.41
1:1:2796:U:O2'	1:1:2798:U:OP2	2.29	0.41
2:2:1004:A:H5''	2:2:1025:U:C2	2.56	0.41
2:2:1464:U:H2'	2:2:1465:A:H8	1.84	0.41
23:V:30:ILE:HA	23:V:91:PHE:HB2	2.03	0.41
39:l:2:PRO:HB2	39:l:3:ARG:H	1.69	0.41
42:o:12:ALA:O	42:o:70:HIS:N	2.53	0.41
55:A:198:VAL:HG22	55:A:219:SER:HB3	2.02	0.41
1:1:466:A:N1	1:1:795:C:O2'	2.39	0.41
1:1:1170:C:N4	1:1:1171:G:O6	2.54	0.41
1:1:2126:A:N6	1:1:2163:A:OP1	2.45	0.41
1:1:2304:G:H22	1:1:2312:U:H3	1.69	0.41
1:1:2406:A:O4'	13:L:69:ARG:NH1	2.52	0.41
1:1:2696:U:H2'	1:1:2697:G:C8	2.56	0.41
2:2:1372:U:OP1	41:n:73:SER:N	2.52	0.41
9:F:124:GLU:N	9:F:132:VAL:O	2.54	0.41
22:U:18:ASP:HB3	22:U:21:LYS:HD2	2.02	0.41
24:W:25:ARG:HH12	24:W:35:SER:HB3	1.86	0.41
47:t:57:LEU:HA	47:t:60:VAL:CB	2.50	0.41
52:y:28:MET:HE1	52:y:67:ILE:HG21	2.02	0.41
1:1:329:G:H1	22:U:17:LYS:HD3	1.85	0.41
1:1:1295:C:H4'	15:N:22:ARG:HH21	1.85	0.41
1:1:1342:A:OP1	21:T:40:LYS:NZ	2.34	0.41
1:1:1653:G:C6	15:N:9:GLN:HB3	2.56	0.41
1:1:1721:G:N2	1:1:1738:G:H2'	2.36	0.41
1:1:2183:A:H2'	1:1:2184:A:C8	2.55	0.41
1:1:2417:C:H2'	1:1:2418:A:H8	1.85	0.41
1:1:2563:U:H4'	12:K:28:SER:HA	2.02	0.41
2:2:1338:G:H21	54:5:41:C:H1'	1.84	0.41
2:2:1347:G:N2	2:2:1348:U:O4	2.39	0.41
2:2:1438:G:H5''	52:y:33:LYS:HZ1	1.85	0.41
6:C:125:TRP:NE1	6:C:161:MET:O	2.41	0.41
7:D:181:ILE:HG12	13:L:1:MET:HE3	2.03	0.41
8:E:99:PHE:HA	8:E:102:ARG:HE	1.85	0.41
8:E:115:ARG:HG2	28:a:47:LYS:HD3	2.03	0.41
8:E:122:PHE:HE1	8:E:170:LEU:HD12	1.85	0.41
11:J:18:VAL:HB	11:J:56:VAL:HA	2.02	0.41
19:R:51:VAL:CG2	19:R:52:PRO:HD3	2.50	0.41
28:a:10:GLU:N	28:a:26:SER:O	2.46	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:g:46:THR:HG23	34:g:201:PRO:HD2	2.03	0.41
40:m:28:PRO:HA	40:m:58:GLU:HA	2.02	0.41
40:m:48:ASP:H	40:m:62:THR:HB	1.85	0.41
54:5:7:U:H2'	54:5:12:C:H41	1.86	0.41
55:A:213:ARG:HH12	55:A:329:ASP:HB2	1.86	0.41
1:1:80:G:O2'	1:1:294:A:N1	2.50	0.41
1:1:219:A:N3	1:1:234:U:O2'	2.47	0.41
1:1:603:A:O5'	1:1:655:A:N6	2.53	0.41
1:1:660:C:H2'	1:1:661:A:C8	2.56	0.41
1:1:848:C:H2'	1:1:849:A:C8	2.55	0.41
1:1:1270:C:O2'	1:1:1648:U:OP2	2.31	0.41
1:1:1528:A:OP2	1:1:1543:G:N2	2.40	0.41
1:1:1529:G:C4	1:1:1530:G:C8	3.09	0.41
1:1:2131:U:O2'	1:1:2133:G:N7	2.47	0.41
1:1:2638:G:N1	1:1:2776:A:OP2	2.37	0.41
1:1:2789:C:H2'	1:1:2893:A:N7	2.36	0.41
2:2:157:U:H2'	2:2:158:G:C8	2.56	0.41
2:2:166:U:H2'	2:2:167:A:C8	2.56	0.41
2:2:309:A:H2'	2:2:310:G:H8	1.86	0.41
2:2:309:A:H5'	48:u:29:ASN:HB3	2.01	0.41
2:2:404:G:O2'	2:2:498:A:N1	2.47	0.41
2:2:675:A:H1'	43:p:118:HIS:CD2	2.56	0.41
2:2:823:C:HO2'	40:m:2:SER:HG	1.62	0.41
7:D:111:GLU:O	7:D:115:GLN:N	2.53	0.41
13:L:57:LEU:HD13	13:L:60:ARG:HH11	1.86	0.41
15:N:77:ALA:O	15:N:81:ASN:ND2	2.47	0.41
22:U:8:ASP:O	22:U:24:LYS:NZ	2.40	0.41
27:Z:12:SER:OG	27:Z:13:ALA:N	2.54	0.41
30:c:9:ILE:O	30:c:22:THR:OG1	2.26	0.41
30:c:39:PHE:HA	30:c:46:HIS:HA	2.02	0.41
48:u:20:VAL:HA	48:u:36:VAL:HG22	2.03	0.41
49:v:25:ILE:N	49:v:42:THR:O	2.48	0.41
53:z:16:LEU:HD23	53:z:20:LYS:HE2	2.03	0.41
55:A:64:GLU:HA	55:A:67:VAL:HB	2.03	0.41
55:A:169:SER:N	55:A:178:SER:O	2.53	0.41
1:1:171:U:H6	1:1:171:U:H5''	1.86	0.41
1:1:544:C:H3'	1:1:545:U:O2	2.21	0.41
1:1:910:A:N6	1:1:2277:G:HO2'	2.18	0.41
1:1:1000:A:H62	1:1:1154:G:H2'	1.86	0.41
1:1:1252:G:H5''	18:Q:32:TYR:HE2	1.85	0.41
1:1:1726:C:H2'	1:1:1727:C:C6	2.56	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2093:G:O2'	1:1:2198:A:N1	2.43	0.41
1:1:2520:C:H2'	1:1:2521:C:H6	1.85	0.41
2:2:166:U:H2'	2:2:167:A:H8	1.86	0.41
2:2:413:G:H1'	2:2:428:G:H21	1.85	0.41
2:2:741:G:O2'	47:t:55:GLY:HA2	2.21	0.41
2:2:1152:A:H2'	2:2:1153:G:C8	2.56	0.41
2:2:1323:G:H2'	2:2:1324:A:C8	2.56	0.41
2:2:1414:U:H2'	2:2:1415:G:C8	2.53	0.41
5:B:251:GLN:HB3	5:B:255:LYS:HD2	2.03	0.41
12:K:123:LEU:HA	17:P:41:GLN:HE22	1.86	0.41
14:M:36:VAL:H	14:M:128:THR:HA	1.85	0.41
28:a:16:CYS:HA	28:a:34:LEU:HB2	2.03	0.41
41:n:42:GLU:O	41:n:46:MET:N	2.54	0.41
43:p:36:ASP:OD1	43:p:40:ASN:N	2.54	0.41
46:s:54:ASP:HA	46:s:59:ARG:HG2	2.03	0.41
55:A:115:PHE:HB2	55:A:119:PHE:CE2	2.56	0.41
1:1:859:G:O2'	1:1:916:G:O6	2.31	0.40
1:1:922:C:H2'	1:1:923:G:H8	1.85	0.40
1:1:1426:G:O2'	1:1:1572:A:N6	2.54	0.40
1:1:1730:C:H1'	1:1:1731:G:C6	2.56	0.40
1:1:2106:U:O5'	1:1:2178:C:N4	2.53	0.40
1:1:2148:G:H2'	1:1:2149:U:C6	2.56	0.40
1:1:2262:U:H2'	1:1:2263:C:H6	1.87	0.40
1:1:2333:A:H5'	1:1:2335:A:H1'	2.03	0.40
1:1:2591:C:H2'	1:1:2592:G:C8	2.56	0.40
1:1:2602:A:C5	55:A:254:VAL:HG22	2.56	0.40
2:2:86:G:HO2'	2:2:87:C:C5'	2.34	0.40
2:2:235:C:H2'	2:2:236:A:C8	2.56	0.40
2:2:458:U:H2'	2:2:459:A:C8	2.56	0.40
2:2:493:A:H2'	2:2:494:G:C8	2.56	0.40
2:2:689:C:H2'	2:2:690:G:O4'	2.21	0.40
2:2:946:A:H2'	2:2:947:G:C8	2.56	0.40
6:C:4:LEU:HG	6:C:32:ASN:ND2	2.37	0.40
6:C:136:ASN:HD21	6:C:139:SER:HB2	1.86	0.40
10:G:72:ILE:H	10:G:72:ILE:HG13	1.81	0.40
24:W:48:GLY:N	24:W:80:ILE:O	2.53	0.40
25:X:33:LEU:HA	25:X:52:SER:HA	2.02	0.40
34:g:119:THR:O	34:g:124:GLY:N	2.45	0.40
35:h:6:HIS:HA	35:h:7:PRO:HD3	1.93	0.40
36:i:62:ARG:HH21	36:i:68:LEU:HA	1.86	0.40
36:i:124:MET:HG3	36:i:146:ARG:HB3	2.02	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:s:53:ARG:HD3	46:s:59:ARG:HH12	1.86	0.40
47:t:57:LEU:HA	47:t:60:VAL:HB	2.02	0.40
1:1:948:C:H2'	1:1:949:G:C8	2.56	0.40
1:1:1174:U:H1'	1:1:1177:G:C2	2.56	0.40
1:1:2127:G:H2'	1:1:2128:G:N7	2.36	0.40
1:1:2559:C:H2'	1:1:2560:A:C8	2.57	0.40
2:2:95:C:H2'	2:2:96:U:H6	1.86	0.40
2:2:328:C:H4'	2:2:329:A:H5'	2.03	0.40
2:2:1438:G:H1	2:2:1463:U:H3	1.69	0.40
3:3:6:G:H2'	3:3:7:G:C8	2.57	0.40
6:C:101:PHE:HD1	6:C:104:VAL:HG21	1.85	0.40
8:E:117:LEU:N	8:E:177:PHE:O	2.39	0.40
12:K:16:ALA:HA	12:K:46:ALA:HA	2.02	0.40
26:Y:31:GLN:HG2	26:Y:37:LEU:HB2	2.04	0.40
30:c:9:ILE:HA	30:c:54:ILE:HB	2.02	0.40
35:h:83:ASP:O	35:h:87:LEU:N	2.47	0.40
37:j:99:ALA:HB2	37:j:124:LEU:HG	2.03	0.40
39:l:140:ASP:OD1	39:l:143:ARG:NH1	2.43	0.40
44:q:52:VAL:HG23	44:q:66:TYR:HA	2.04	0.40
44:q:56:ARG:NE	44:q:62:GLU:OE1	2.50	0.40
46:s:33:ASP:HB3	46:s:36:ALA:HB2	2.03	0.40
50:w:41:PRO:HD2	50:w:44:ILE:HD12	2.03	0.40
51:x:4:SER:H	51:x:7:LYS:HD2	1.87	0.40
52:y:48:GLN:HG3	52:y:52:ASN:HD21	1.86	0.40
54:5:50:U:H3	54:5:64:G:H1	1.68	0.40
55:A:27:TYR:CE1	55:A:67:VAL:HA	2.54	0.40
1:1:69:C:H2'	1:1:70:G:C8	2.56	0.40
1:1:242:G:C8	32:e:3:LYS:HE3	2.56	0.40
1:1:405:U:OP1	1:1:405:U:C5	2.75	0.40
1:1:1161:C:H2'	1:1:1162:G:C8	2.56	0.40
1:1:2315:G:H2'	1:1:2316:G:H8	1.86	0.40
1:1:2359:C:H2'	1:1:2360:G:H8	1.86	0.40
1:1:2374:C:N4	1:1:2375:G:O6	2.55	0.40
2:2:94:G:H4'	2:2:95:C:O5'	2.22	0.40
2:2:801:U:H2'	2:2:802:A:C8	2.56	0.40
2:2:1347:G:H1'	2:2:1348:U:H5	1.86	0.40
3:3:86:G:H1	3:3:90:C:H42	1.70	0.40
5:B:67:PHE:CE1	5:B:156:ARG:HD2	2.56	0.40
6:C:184:ARG:HG3	6:C:186:LEU:HG	2.03	0.40
7:D:19:PHE:HE1	7:D:109:LEU:HD23	1.87	0.40
8:E:47:LYS:O	8:E:51:ASP:N	2.42	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:J:117:ALA:HA	11:J:120:ARG:HH21	1.85	0.40
12:K:13:ASN:CG	12:K:98:ARG:H	2.30	0.40
16:O:26:LEU:HB3	16:O:92:PHE:HA	2.03	0.40
35:h:19:ASN:OD1	35:h:54:ARG:NH2	2.44	0.40
35:h:132:ARG:HG2	35:h:136:ARG:HE	1.86	0.40
55:A:141:ALA:HB2	55:A:216:SER:HB2	2.03	0.40
1:1:21:A:N6	1:1:518:G:O6	2.54	0.40
1:1:992:C:H2'	1:1:993:G:H8	1.85	0.40
1:1:1528:A:H3'	1:1:1529:G:H8	1.87	0.40
1:1:2143:C:O2	1:1:2149:U:N3	2.52	0.40
2:2:460:A:H2'	2:2:461:A:C8	2.56	0.40
2:2:497:G:H2'	2:2:498:A:C8	2.57	0.40
2:2:509:A:N3	2:2:543:U:O2'	2.52	0.40
2:2:1103:C:OP1	34:g:95:ARG:NH2	2.53	0.40
8:E:80:ARG:HB2	8:E:83:TYR:CZ	2.56	0.40
16:O:56:LYS:HE2	16:O:56:LYS:HB2	1.93	0.40
27:Z:6:LYS:O	27:Z:58:GLU:N	2.55	0.40
35:h:172:ARG:HE	35:h:174:PRO:HD3	1.86	0.40
39:l:138:ARG:NE	39:l:139:GLU:OE2	2.54	0.40
47:t:54:ARG:HA	47:t:54:ARG:NH1	2.36	0.40
1:1:300:A:H2'	1:1:334:C:H1'	2.04	0.40
1:1:660:C:H2'	1:1:661:A:H8	1.87	0.40
1:1:1273:U:O2	1:1:2002:G:O2'	2.32	0.40
1:1:2425:A:H4'	1:1:2426:A:O5'	2.21	0.40
1:1:2685:G:H2'	1:1:2686:G:H8	1.86	0.40
1:1:2729:G:H5'	6:C:190:LYS:HE2	2.02	0.40
1:1:2796:U:H3	1:1:2799:A:H61	1.69	0.40
2:2:47:C:H5''	2:2:365:U:H2'	2.04	0.40
2:2:56:U:H2'	2:2:57:G:C8	2.57	0.40
2:2:154:U:H2'	2:2:155:A:C8	2.57	0.40
2:2:261:U:OP2	52:y:74:ARG:NH2	2.48	0.40
2:2:1039:G:H2'	2:2:1040:U:C6	2.57	0.40
2:2:1078:U:O2	37:j:135:ASN:ND2	2.42	0.40
2:2:1342:C:H2'	2:2:1343:G:C8	2.57	0.40
5:B:243:HIS:HA	5:B:244:PRO:HD3	1.95	0.40
7:D:25:GLU:OE2	13:L:7:SER:N	2.55	0.40
34:g:56:GLU:HG2	34:g:198:PHE:HE2	1.86	0.40
41:n:25:ASN:H	41:n:62:ASP:CG	2.28	0.40
54:5:18:G:OP2	54:5:60:U:O2'	2.31	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	B	269/271 (99%)	254 (94%)	15 (6%)	0	100	100
6	C	207/209 (99%)	198 (96%)	7 (3%)	2 (1%)	12	43
7	D	199/201 (99%)	191 (96%)	8 (4%)	0	100	100
8	E	175/177 (99%)	160 (91%)	14 (8%)	1 (1%)	21	52
9	F	173/175 (99%)	164 (95%)	9 (5%)	0	100	100
10	G	147/149 (99%)	135 (92%)	12 (8%)	0	100	100
11	J	140/142 (99%)	134 (96%)	6 (4%)	0	100	100
12	K	121/123 (98%)	117 (97%)	4 (3%)	0	100	100
13	L	142/144 (99%)	139 (98%)	3 (2%)	0	100	100
14	M	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
15	N	117/119 (98%)	106 (91%)	11 (9%)	0	100	100
16	O	114/116 (98%)	110 (96%)	4 (4%)	0	100	100
17	P	112/114 (98%)	107 (96%)	5 (4%)	0	100	100
18	Q	115/117 (98%)	114 (99%)	1 (1%)	0	100	100
19	R	101/103 (98%)	90 (89%)	10 (10%)	1 (1%)	12	43
20	S	108/110 (98%)	105 (97%)	3 (3%)	0	100	100
21	T	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
22	U	101/103 (98%)	92 (91%)	9 (9%)	0	100	100
23	V	92/94 (98%)	88 (96%)	4 (4%)	0	100	100
24	W	74/76 (97%)	68 (92%)	6 (8%)	0	100	100
25	X	75/77 (97%)	74 (99%)	1 (1%)	0	100	100
26	Y	60/62 (97%)	59 (98%)	1 (2%)	0	100	100
27	Z	56/58 (97%)	53 (95%)	3 (5%)	0	100	100
28	a	64/66 (97%)	56 (88%)	8 (12%)	0	100	100
29	b	54/56 (96%)	51 (94%)	3 (6%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	c	50/52 (96%)	49 (98%)	1 (2%)	0	100	100
31	d	44/46 (96%)	44 (100%)	0	0	100	100
32	e	62/64 (97%)	57 (92%)	4 (6%)	1 (2%)	7	35
33	f	36/38 (95%)	36 (100%)	0	0	100	100
34	g	223/225 (99%)	214 (96%)	9 (4%)	0	100	100
35	h	206/208 (99%)	189 (92%)	17 (8%)	0	100	100
36	i	203/205 (99%)	197 (97%)	6 (3%)	0	100	100
37	j	154/156 (99%)	142 (92%)	12 (8%)	0	100	100
38	k	102/104 (98%)	99 (97%)	3 (3%)	0	100	100
39	l	149/151 (99%)	147 (99%)	2 (1%)	0	100	100
40	m	127/129 (98%)	124 (98%)	3 (2%)	0	100	100
41	n	125/127 (98%)	114 (91%)	11 (9%)	0	100	100
42	o	97/99 (98%)	90 (93%)	7 (7%)	0	100	100
43	p	115/117 (98%)	108 (94%)	7 (6%)	0	100	100
44	q	85/87 (98%)	80 (94%)	5 (6%)	0	100	100
45	r	114/116 (98%)	110 (96%)	4 (4%)	0	100	100
46	s	98/100 (98%)	97 (99%)	1 (1%)	0	100	100
47	t	86/88 (98%)	73 (85%)	11 (13%)	2 (2%)	5	30
48	u	80/82 (98%)	74 (92%)	6 (8%)	0	100	100
49	v	78/80 (98%)	73 (94%)	5 (6%)	0	100	100
50	w	64/66 (97%)	63 (98%)	1 (2%)	0	100	100
51	x	81/83 (98%)	77 (95%)	4 (5%)	0	100	100
52	y	84/86 (98%)	84 (100%)	0	0	100	100
53	z	68/70 (97%)	66 (97%)	2 (3%)	0	100	100
55	A	355/357 (99%)	331 (93%)	24 (7%)	0	100	100
All	All	5928/6028 (98%)	5619 (95%)	302 (5%)	7 (0%)	49	78

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	C	151	THR
47	t	48	LYS
19	R	52	PRO

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
47	t	50	HIS
32	e	32	ILE
8	E	124	GLY
6	C	153	GLY

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	
5	B	216/216 (100%)	216 (100%)	0	100	100
6	C	164/164 (100%)	163 (99%)	1 (1%)	78	79
7	D	165/165 (100%)	165 (100%)	0	100	100
8	E	148/148 (100%)	147 (99%)	1 (1%)	76	77
9	F	136/136 (100%)	136 (100%)	0	100	100
10	G	114/114 (100%)	114 (100%)	0	100	100
11	J	116/116 (100%)	116 (100%)	0	100	100
12	K	104/104 (100%)	104 (100%)	0	100	100
13	L	103/103 (100%)	103 (100%)	0	100	100
14	M	109/109 (100%)	109 (100%)	0	100	100
15	N	99/99 (100%)	97 (98%)	2 (2%)	48	64
16	O	86/86 (100%)	86 (100%)	0	100	100
17	P	99/99 (100%)	99 (100%)	0	100	100
18	Q	89/89 (100%)	89 (100%)	0	100	100
19	R	84/84 (100%)	83 (99%)	1 (1%)	63	72
20	S	93/93 (100%)	93 (100%)	0	100	100
21	T	81/81 (100%)	81 (100%)	0	100	100
22	U	84/84 (100%)	84 (100%)	0	100	100
23	V	78/78 (100%)	77 (99%)	1 (1%)	61	71
24	W	58/58 (100%)	58 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	X	67/67 (100%)	67 (100%)	0	100	100
26	Y	54/54 (100%)	54 (100%)	0	100	100
27	Z	48/48 (100%)	48 (100%)	0	100	100
28	a	59/59 (100%)	59 (100%)	0	100	100
29	b	47/47 (100%)	47 (100%)	0	100	100
30	c	47/47 (100%)	47 (100%)	0	100	100
31	d	38/38 (100%)	38 (100%)	0	100	100
32	e	51/51 (100%)	51 (100%)	0	100	100
33	f	34/34 (100%)	34 (100%)	0	100	100
34	g	187/187 (100%)	186 (100%)	1 (0%)	81	80
35	h	171/171 (100%)	169 (99%)	2 (1%)	63	72
36	i	172/172 (100%)	172 (100%)	0	100	100
37	j	119/119 (100%)	119 (100%)	0	100	100
38	k	91/91 (100%)	91 (100%)	0	100	100
39	l	124/124 (100%)	124 (100%)	0	100	100
40	m	104/104 (100%)	104 (100%)	0	100	100
41	n	105/105 (100%)	105 (100%)	0	100	100
42	o	86/86 (100%)	86 (100%)	0	100	100
43	p	90/90 (100%)	90 (100%)	0	100	100
44	q	74/74 (100%)	74 (100%)	0	100	100
45	r	94/94 (100%)	94 (100%)	0	100	100
46	s	83/83 (100%)	83 (100%)	0	100	100
47	t	76/76 (100%)	67 (88%)	9 (12%)	5	23
48	u	65/65 (100%)	65 (100%)	0	100	100
49	v	74/74 (100%)	74 (100%)	0	100	100
50	w	57/57 (100%)	57 (100%)	0	100	100
51	x	72/72 (100%)	72 (100%)	0	100	100
52	y	65/65 (100%)	65 (100%)	0	100	100
53	z	60/60 (100%)	60 (100%)	0	100	100
55	A	304/305 (100%)	304 (100%)	0	100	100
All	All	4944/4945 (100%)	4926 (100%)	18 (0%)	81	81

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
6	C	151	THR
8	E	40	VAL
15	N	2	ARG
15	N	48	VAL
19	R	51	VAL
23	V	65	VAL
34	g	129	LEU
35	h	72	ARG
35	h	179	ARG
47	t	47	LYS
47	t	48	LYS
47	t	50	HIS
47	t	51	HIS
47	t	52	SER
47	t	53	ARG
47	t	54	ARG
47	t	58	ARG
47	t	72	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (79) such sidechains are listed below:

Mol	Chain	Res	Type
5	B	53	HIS
5	B	86	ASN
5	B	197	ASN
5	B	260	ASN
6	C	32	ASN
6	C	136	ASN
6	C	173	GLN
7	D	29	HIS
7	D	92	HIS
7	D	115	GLN
7	D	136	GLN
7	D	163	ASN
7	D	195	GLN
9	F	73	ASN
9	F	116	GLN
10	G	66	ASN
11	J	80	HIS
11	J	131	ASN
13	L	54	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
14	M	22	GLN
16	O	29	HIS
16	O	38	GLN
16	O	61	GLN
16	O	100	HIS
17	P	12	GLN
17	P	15	GLN
18	Q	44	GLN
18	Q	72	ASN
19	R	82	HIS
20	S	7	HIS
20	S	40	ASN
20	S	61	ASN
21	T	70	HIS
23	V	24	ASN
25	X	34	HIS
26	Y	15	ASN
26	Y	20	ASN
26	Y	39	GLN
26	Y	45	GLN
27	Z	20	HIS
28	a	20	ASN
29	b	6	ASN
29	b	42	HIS
30	c	26	ASN
31	d	16	HIS
33	f	37	GLN
34	g	39	HIS
34	g	51	ASN
34	g	177	ASN
35	h	8	ASN
35	h	41	GLN
36	i	59	GLN
36	i	116	GLN
36	i	198	HIS
37	j	12	GLN
37	j	97	GLN
37	j	121	HIS
38	k	46	GLN
38	k	63	ASN
38	k	68	GLN
39	l	28	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
39	l	130	ASN
42	o	20	GLN
43	p	40	ASN
43	p	119	ASN
44	q	5	ASN
47	t	20	ASN
47	t	40	GLN
47	t	50	HIS
47	t	51	HIS
48	u	26	ASN
50	w	52	GLN
51	x	57	HIS
55	A	43	GLN
55	A	199	HIS
55	A	255	ASN
55	A	276	ASN
55	A	281	HIS
55	A	313	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2902/2903 (99%)	758 (26%)	15 (0%)
2	2	1531/1534 (99%)	415 (27%)	4 (0%)
3	3	119/120 (99%)	23 (19%)	0
4	4	8/9 (88%)	2 (25%)	0
54	5	75/76 (98%)	22 (29%)	1 (1%)
All	All	4635/4642 (99%)	1220 (26%)	20 (0%)

All (1220) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	10	A
1	1	34	U
1	1	35	G
1	1	40	U
1	1	46	G
1	1	48	G
1	1	51	G
1	1	58	G
1	1	60	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	71	A
1	1	74	A
1	1	75	G
1	1	80	G
1	1	84	A
1	1	85	G
1	1	88	G
1	1	100	U
1	1	101	A
1	1	102	U
1	1	103	A
1	1	118	A
1	1	119	A
1	1	120	U
1	1	126	A
1	1	132	G
1	1	136	G
1	1	137	U
1	1	139	U
1	1	140	C
1	1	141	G
1	1	142	A
1	1	146	A
1	1	158	U
1	1	163	C
1	1	171	U
1	1	184	C
1	1	196	A
1	1	199	A
1	1	206	U
1	1	215	G
1	1	216	A
1	1	222	A
1	1	225	C
1	1	226	A
1	1	228	C
1	1	230	G
1	1	233	A
1	1	248	G
1	1	255	A
1	1	266	G
1	1	267	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	270	A
1	1	271	G
1	1	273	G
1	1	275	C
1	1	276	U
1	1	277	G
1	1	278	A
1	1	284	U
1	1	285	G
1	1	295	G
1	1	311	A
1	1	317	G
1	1	318	C
1	1	322	A
1	1	329	G
1	1	330	A
1	1	346	A
1	1	353	C
1	1	361	G
1	1	367	G
1	1	371	A
1	1	372	G
1	1	386	G
1	1	396	G
1	1	405	U
1	1	411	G
1	1	412	A
1	1	424	G
1	1	438	G
1	1	445	C
1	1	449	A
1	1	451	U
1	1	454	A
1	1	455	C
1	1	457	A
1	1	479	A
1	1	481	G
1	1	483	A
1	1	484	C
1	1	488	G
1	1	496	G
1	1	505	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	508	A
1	1	509	C
1	1	510	C
1	1	513	A
1	1	518	G
1	1	519	U
1	1	527	C
1	1	529	A
1	1	531	C
1	1	532	A
1	1	533	G
1	1	543	G
1	1	544	C
1	1	546	U
1	1	547	A
1	1	548	G
1	1	549	G
1	1	551	G
1	1	552	U
1	1	563	A
1	1	565	C
1	1	568	U
1	1	573	U
1	1	575	A
1	1	581	C
1	1	582	A
1	1	586	A
1	1	603	A
1	1	609	A
1	1	613	A
1	1	614	A
1	1	615	U
1	1	627	A
1	1	637	A
1	1	645	C
1	1	646	U
1	1	651	G
1	1	654	A
1	1	655	A
1	1	656	G
1	1	664	G
1	1	670	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	681	G
1	1	686	U
1	1	714	U
1	1	717	C
1	1	726	G
1	1	727	A
1	1	730	A
1	1	740	C
1	1	744	U
1	1	747	5MU
1	1	748	G
1	1	752	A
1	1	757	G
1	1	762	U
1	1	763	G
1	1	764	A
1	1	765	C
1	1	770	G
1	1	775	G
1	1	776	G
1	1	781	A
1	1	782	A
1	1	783	A
1	1	784	G
1	1	785	G
1	1	789	A
1	1	792	A
1	1	793	A
1	1	794	A
1	1	795	C
1	1	803	U
1	1	805	G
1	1	809	G
1	1	810	U
1	1	812	C
1	1	819	A
1	1	827	U
1	1	828	U
1	1	829	A
1	1	831	G
1	1	846	U
1	1	856	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	858	G
1	1	859	G
1	1	869	G
1	1	877	A
1	1	878	A
1	1	880	G
1	1	882	G
1	1	883	G
1	1	884	U
1	1	885	C
1	1	887	A
1	1	888	C
1	1	891	G
1	1	893	C
1	1	894	U
1	1	895	U
1	1	896	A
1	1	910	A
1	1	914	G
1	1	915	C
1	1	932	U
1	1	941	A
1	1	945	A
1	1	946	C
1	1	947	A
1	1	948	C
1	1	958	U
1	1	959	A
1	1	961	C
1	1	965	C
1	1	973	A
1	1	974	G
1	1	980	A
1	1	981	A
1	1	983	A
1	1	989	G
1	1	990	A
1	1	995	C
1	1	996	A
1	1	999	U
1	1	1005	C
1	1	1012	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	1013	C
1	1	1014	A
1	1	1017	G
1	1	1020	A
1	1	1022	G
1	1	1023	U
1	1	1024	G
1	1	1026	G
1	1	1033	U
1	1	1041	G
1	1	1042	G
1	1	1044	C
1	1	1045	C
1	1	1046	A
1	1	1047	G
1	1	1057	A
1	1	1058	U
1	1	1060	U
1	1	1061	U
1	1	1063	G
1	1	1064	C
1	1	1066	U
1	1	1067	A
1	1	1070	A
1	1	1071	G
1	1	1073	A
1	1	1074	G
1	1	1075	C
1	1	1077	A
1	1	1078	U
1	1	1079	C
1	1	1082	U
1	1	1083	U
1	1	1084	A
1	1	1085	A
1	1	1087	G
1	1	1088	A
1	1	1089	A
1	1	1095	A
1	1	1096	A
1	1	1097	U
1	1	1101	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	1110	G
1	1	1111	A
1	1	1112	G
1	1	1115	G
1	1	1119	U
1	1	1128	G
1	1	1129	A
1	1	1130	U
1	1	1131	G
1	1	1132	U
1	1	1134	A
1	1	1135	C
1	1	1136	G
1	1	1139	G
1	1	1141	U
1	1	1142	A
1	1	1151	A
1	1	1158	C
1	1	1161	C
1	1	1168	G
1	1	1169	A
1	1	1170	C
1	1	1171	G
1	1	1173	U
1	1	1174	U
1	1	1175	A
1	1	1176	U
1	1	1177	G
1	1	1178	C
1	1	1179	G
1	1	1182	G
1	1	1186	G
1	1	1190	G
1	1	1206	G
1	1	1211	C
1	1	1212	G
1	1	1217	U
1	1	1218	G
1	1	1227	G
1	1	1236	G
1	1	1238	G
1	1	1247	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	1248	G
1	1	1249	U
1	1	1251	C
1	1	1252	G
1	1	1253	A
1	1	1256	G
1	1	1266	G
1	1	1271	G
1	1	1272	A
1	1	1275	A
1	1	1287	A
1	1	1294	U
1	1	1300	G
1	1	1301	A
1	1	1306	C
1	1	1312	U
1	1	1324	G
1	1	1329	U
1	1	1332	G
1	1	1338	G
1	1	1341	G
1	1	1345	C
1	1	1351	C
1	1	1355	G
1	1	1360	G
1	1	1361	G
1	1	1365	A
1	1	1368	G
1	1	1378	A
1	1	1379	U
1	1	1380	G
1	1	1383	A
1	1	1385	A
1	1	1388	G
1	1	1394	U
1	1	1395	A
1	1	1396	U
1	1	1398	C
1	1	1403	A
1	1	1409	U
1	1	1410	G
1	1	1411	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	1412	U
1	1	1415	U
1	1	1416	G
1	1	1417	C
1	1	1419	A
1	1	1425	G
1	1	1428	C
1	1	1437	C
1	1	1449	G
1	1	1455	G
1	1	1458	U
1	1	1461	C
1	1	1467	U
1	1	1476	U
1	1	1478	G
1	1	1479	G
1	1	1482	G
1	1	1484	U
1	1	1489	C
1	1	1490	A
1	1	1491	G
1	1	1493	C
1	1	1494	A
1	1	1502	A
1	1	1503	A
1	1	1504	A
1	1	1508	A
1	1	1509	A
1	1	1515	A
1	1	1516	G
1	1	1523	U
1	1	1524	G
1	1	1529	G
1	1	1530	G
1	1	1531	C
1	1	1532	A
1	1	1534	U
1	1	1535	A
1	1	1536	C
1	1	1550	C
1	1	1559	U
1	1	1560	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	1566	A
1	1	1569	A
1	1	1578	U
1	1	1580	A
1	1	1581	G
1	1	1582	C
1	1	1583	A
1	1	1584	U
1	1	1586	A
1	1	1587	G
1	1	1589	U
1	1	1590	A
1	1	1607	C
1	1	1613	G
1	1	1616	A
1	1	1618	6MZ
1	1	1619	G
1	1	1626	A
1	1	1634	A
1	1	1639	C
1	1	1646	C
1	1	1647	U
1	1	1648	U
1	1	1649	G
1	1	1651	G
1	1	1657	U
1	1	1659	G
1	1	1660	G
1	1	1668	A
1	1	1669	A
1	1	1674	G
1	1	1693	U
1	1	1694	C
1	1	1695	G
1	1	1713	A
1	1	1715	G
1	1	1716	U
1	1	1722	A
1	1	1723	G
1	1	1724	G
1	1	1725	U
1	1	1729	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	1730	C
1	1	1732	C
1	1	1733	G
1	1	1738	G
1	1	1744	A
1	1	1751	U
1	1	1754	A
1	1	1756	G
1	1	1758	U
1	1	1759	A
1	1	1760	C
1	1	1764	C
1	1	1765	U
1	1	1773	A
1	1	1781	U
1	1	1784	A
1	1	1786	A
1	1	1800	C
1	1	1801	A
1	1	1802	A
1	1	1808	A
1	1	1816	C
1	1	1820	U
1	1	1829	A
1	1	1830	C
1	1	1833	C
1	1	1835	2MG
1	1	1847	A
1	1	1858	A
1	1	1859	U
1	1	1862	G
1	1	1865	U
1	1	1869	G
1	1	1870	C
1	1	1871	A
1	1	1872	A
1	1	1873	G
1	1	1884	G
1	1	1889	A
1	1	1899	A
1	1	1900	A
1	1	1903	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	1906	G
1	1	1913	A
1	1	1914	C
1	1	1915	3TD
1	1	1916	A
1	1	1923	U
1	1	1924	C
1	1	1929	G
1	1	1930	G
1	1	1936	A
1	1	1937	A
1	1	1941	C
1	1	1943	U
1	1	1955	U
1	1	1960	A
1	1	1962	5MC
1	1	1963	U
1	1	1967	C
1	1	1970	A
1	1	1971	U
1	1	1972	G
1	1	1982	U
1	1	1991	U
1	1	1992	G
1	1	1993	U
1	1	1997	C
1	1	2002	G
1	1	2010	G
1	1	2022	U
1	1	2023	C
1	1	2030	6MZ
1	1	2031	A
1	1	2032	G
1	1	2033	A
1	1	2034	U
1	1	2043	C
1	1	2047	C
1	1	2048	G
1	1	2049	G
1	1	2051	A
1	1	2052	A
1	1	2053	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	2055	C
1	1	2056	G
1	1	2057	G
1	1	2060	A
1	1	2061	G
1	1	2062	A
1	1	2069	G7M
1	1	2093	G
1	1	2094	A
1	1	2095	A
1	1	2102	G
1	1	2103	C
1	1	2105	U
1	1	2106	U
1	1	2108	A
1	1	2109	U
1	1	2111	U
1	1	2113	U
1	1	2115	G
1	1	2116	G
1	1	2117	A
1	1	2118	U
1	1	2119	A
1	1	2120	G
1	1	2121	G
1	1	2122	U
1	1	2123	G
1	1	2124	G
1	1	2125	G
1	1	2126	A
1	1	2127	G
1	1	2128	G
1	1	2130	U
1	1	2131	U
1	1	2132	U
1	1	2133	G
1	1	2134	A
1	1	2135	A
1	1	2136	G
1	1	2137	U
1	1	2138	G
1	1	2139	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	2140	G
1	1	2142	A
1	1	2145	C
1	1	2146	C
1	1	2147	A
1	1	2153	C
1	1	2156	G
1	1	2158	A
1	1	2160	C
1	1	2162	G
1	1	2163	A
1	1	2164	C
1	1	2165	C
1	1	2166	U
1	1	2167	U
1	1	2169	A
1	1	2170	A
1	1	2171	A
1	1	2172	U
1	1	2173	A
1	1	2174	C
1	1	2175	C
1	1	2178	C
1	1	2182	U
1	1	2183	A
1	1	2189	U
1	1	2190	G
1	1	2193	G
1	1	2194	U
1	1	2198	A
1	1	2204	G
1	1	2210	U
1	1	2211	A
1	1	2212	A
1	1	2213	U
1	1	2214	C
1	1	2225	A
1	1	2226	C
1	1	2229	U
1	1	2238	G
1	1	2239	G
1	1	2243	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	2250	G
1	1	2266	A
1	1	2269	G
1	1	2278	A
1	1	2279	G
1	1	2283	C
1	1	2287	A
1	1	2305	U
1	1	2309	A
1	1	2315	G
1	1	2319	G
1	1	2320	U
1	1	2321	U
1	1	2325	G
1	1	2327	A
1	1	2333	A
1	1	2335	A
1	1	2336	A
1	1	2344	U
1	1	2347	C
1	1	2350	C
1	1	2357	G
1	1	2361	G
1	1	2379	G
1	1	2383	G
1	1	2385	C
1	1	2388	A
1	1	2402	U
1	1	2403	C
1	1	2406	A
1	1	2410	G
1	1	2419	U
1	1	2422	C
1	1	2423	U
1	1	2425	A
1	1	2426	A
1	1	2428	G
1	1	2429	G
1	1	2430	A
1	1	2431	U
1	1	2435	A
1	1	2436	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	2439	A
1	1	2441	U
1	1	2445	2MG
1	1	2447	G
1	1	2448	A
1	1	2470	G
1	1	2476	A
1	1	2478	A
1	1	2480	C
1	1	2484	G
1	1	2490	G
1	1	2491	U
1	1	2492	U
1	1	2494	G
1	1	2501	C
1	1	2502	G
1	1	2503	2MA
1	1	2504	PSU
1	1	2505	G
1	1	2507	C
1	1	2513	A
1	1	2517	C
1	1	2518	A
1	1	2520	C
1	1	2529	G
1	1	2530	A
1	1	2531	A
1	1	2535	G
1	1	2547	A
1	1	2553	G
1	1	2554	U
1	1	2562	U
1	1	2564	A
1	1	2566	A
1	1	2567	G
1	1	2571	U
1	1	2572	A
1	1	2573	C
1	1	2574	G
1	1	2583	G
1	1	2585	U
1	1	2602	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	2604	U
1	1	2608	G
1	1	2609	U
1	1	2610	C
1	1	2613	U
1	1	2629	U
1	1	2630	G
1	1	2634	A
1	1	2636	C
1	1	2646	C
1	1	2654	A
1	1	2656	U
1	1	2673	G
1	1	2684	U
1	1	2689	U
1	1	2690	U
1	1	2707	U
1	1	2713	U
1	1	2716	C
1	1	2718	G
1	1	2719	G
1	1	2725	A
1	1	2726	A
1	1	2729	G
1	1	2731	G
1	1	2732	G
1	1	2733	A
1	1	2739	U
1	1	2744	G
1	1	2748	A
1	1	2750	A
1	1	2751	G
1	1	2756	U
1	1	2757	A
1	1	2765	A
1	1	2766	A
1	1	2773	C
1	1	2778	A
1	1	2787	C
1	1	2789	C
1	1	2794	C
1	1	2796	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	2798	U
1	1	2802	G
1	1	2804	U
1	1	2805	C
1	1	2806	C
1	1	2810	A
1	1	2811	G
1	1	2818	U
1	1	2820	A
1	1	2821	A
1	1	2832	U
1	1	2833	U
1	1	2834	G
1	1	2835	A
1	1	2837	A
1	1	2840	C
1	1	2841	C
1	1	2848	G
1	1	2849	U
1	1	2854	G
1	1	2861	U
1	1	2865	U
1	1	2866	U
1	1	2867	G
1	1	2873	A
1	1	2875	C
1	1	2879	A
1	1	2880	C
1	1	2883	A
1	1	2884	U
1	1	2886	A
1	1	2891	U
1	1	2893	A
1	1	2898	U
1	1	2901	C
2	2	4	U
2	2	5	U
2	2	6	G
2	2	7	A
2	2	8	A
2	2	9	G
2	2	22	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	2	29	U
2	2	32	A
2	2	39	G
2	2	41	G
2	2	42	G
2	2	43	C
2	2	44	A
2	2	47	C
2	2	48	C
2	2	49	U
2	2	50	A
2	2	51	A
2	2	54	C
2	2	61	G
2	2	64	G
2	2	65	A
2	2	66	A
2	2	68	G
2	2	70	U
2	2	71	A
2	2	72	A
2	2	74	A
2	2	77	A
2	2	78	A
2	2	79	G
2	2	81	A
2	2	82	G
2	2	83	C
2	2	84	U
2	2	85	U
2	2	86	G
2	2	87	C
2	2	88	U
2	2	89	U
2	2	91	U
2	2	92	U
2	2	93	U
2	2	95	C
2	2	104	G
2	2	106	C
2	2	108	G
2	2	110	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	2	116	A
2	2	119	A
2	2	120	A
2	2	121	U
2	2	123	U
2	2	130	A
2	2	131	A
2	2	138	G
2	2	141	G
2	2	144	G
2	2	149	A
2	2	154	U
2	2	156	C
2	2	161	A
2	2	164	G
2	2	165	G
2	2	168	G
2	2	173	U
2	2	177	G
2	2	178	C
2	2	181	A
2	2	182	A
2	2	183	C
2	2	184	G
2	2	188	C
2	2	191	G
2	2	195	A
2	2	197	A
2	2	201	G
2	2	202	G
2	2	204	G
2	2	209	U
2	2	210	C
2	2	211	G
2	2	212	G
2	2	214	C
2	2	215	C
2	2	217	C
2	2	222	C
2	2	225	C
2	2	234	C
2	2	240	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	2	243	A
2	2	245	U
2	2	247	G
2	2	251	G
2	2	253	A
2	2	266	G
2	2	267	C
2	2	279	A
2	2	281	G
2	2	289	G
2	2	293	G
2	2	306	A
2	2	308	C
2	2	310	G
2	2	319	G
2	2	321	A
2	2	328	C
2	2	330	C
2	2	332	G
2	2	345	C
2	2	347	G
2	2	348	G
2	2	351	G
2	2	352	C
2	2	353	A
2	2	354	G
2	2	355	C
2	2	363	A
2	2	367	U
2	2	368	U
2	2	369	G
2	2	372	C
2	2	376	G
2	2	381	C
2	2	384	G
2	2	388	G
2	2	390	U
2	2	391	G
2	2	398	U
2	2	401	C
2	2	402	G
2	2	404	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	2	406	G
2	2	411	A
2	2	412	A
2	2	413	G
2	2	414	A
2	2	421	U
2	2	422	C
2	2	424	G
2	2	428	G
2	2	429	U
2	2	438	U
2	2	439	U
2	2	444	G
2	2	451	A
2	2	452	A
2	2	456	A
2	2	457	G
2	2	459	A
2	2	463	U
2	2	464	U
2	2	466	A
2	2	467	U
2	2	468	A
2	2	476	U
2	2	478	A
2	2	479	U
2	2	480	U
2	2	481	G
2	2	482	A
2	2	486	U
2	2	488	C
2	2	490	C
2	2	495	A
2	2	496	A
2	2	497	G
2	2	505	G
2	2	511	C
2	2	515	G
2	2	517	G
2	2	518	C
2	2	521	G
2	2	524	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	2	527	G7M
2	2	531	U
2	2	532	A
2	2	533	A
2	2	545	C
2	2	547	A
2	2	554	A
2	2	562	U
2	2	568	G
2	2	572	A
2	2	573	A
2	2	576	C
2	2	577	G
2	2	578	C
2	2	581	G
2	2	587	G
2	2	588	G
2	2	596	A
2	2	603	U
2	2	615	G
2	2	618	C
2	2	632	U
2	2	633	G
2	2	640	A
2	2	641	U
2	2	648	A
2	2	649	A
2	2	650	G
2	2	653	U
2	2	665	A
2	2	668	G
2	2	673	A
2	2	686	U
2	2	687	A
2	2	695	A
2	2	700	G
2	2	703	G
2	2	717	U
2	2	718	A
2	2	721	G
2	2	723	U
2	2	724	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	2	731	G
2	2	734	G
2	2	744	C
2	2	747	A
2	2	748	G
2	2	752	G
2	2	753	A
2	2	755	G
2	2	761	G
2	2	772	U
2	2	773	G
2	2	774	G
2	2	777	A
2	2	793	U
2	2	794	A
2	2	798	U
2	2	799	G
2	2	814	A
2	2	815	A
2	2	817	C
2	2	820	U
2	2	821	G
2	2	823	C
2	2	828	U
2	2	829	G
2	2	832	G
2	2	841	C
2	2	843	U
2	2	844	G
2	2	845	A
2	2	846	G
2	2	849	G
2	2	851	G
2	2	864	A
2	2	876	C
2	2	877	G
2	2	878	A
2	2	884	U
2	2	885	G
2	2	893	C
2	2	902	G
2	2	913	A

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	2	914	A
2	2	926	G
2	2	930	C
2	2	934	C
2	2	935	A
2	2	942	G
2	2	958	A
2	2	960	U
2	2	966	2MG
2	2	969	A
2	2	971	G
2	2	975	A
2	2	976	G
2	2	977	A
2	2	987	G
2	2	989	U
2	2	992	U
2	2	993	G
2	2	994	A
2	2	996	A
2	2	1003	G
2	2	1004	A
2	2	1008	U
2	2	1009	U
2	2	1011	C
2	2	1017	U
2	2	1018	G
2	2	1019	A
2	2	1020	G
2	2	1023	U
2	2	1026	G
2	2	1028	C
2	2	1029	U
2	2	1030	U
2	2	1031	C
2	2	1033	G
2	2	1035	A
2	2	1036	A
2	2	1037	C
2	2	1038	C
2	2	1043	G
2	2	1050	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	2	1053	G
2	2	1054	C
2	2	1056	U
2	2	1065	U
2	2	1067	A
2	2	1085	U
2	2	1086	U
2	2	1089	G
2	2	1092	A
2	2	1094	G
2	2	1095	U
2	2	1101	A
2	2	1102	A
2	2	1104	G
2	2	1108	G
2	2	1124	G
2	2	1125	U
2	2	1126	U
2	2	1132	C
2	2	1133	G
2	2	1135	U
2	2	1136	C
2	2	1139	G
2	2	1140	C
2	2	1141	C
2	2	1145	A
2	2	1151	A
2	2	1152	A
2	2	1160	G
2	2	1167	A
2	2	1169	A
2	2	1171	A
2	2	1176	A
2	2	1177	G
2	2	1184	G
2	2	1193	G
2	2	1196	A
2	2	1197	A
2	2	1200	C
2	2	1201	A
2	2	1206	G
2	2	1207	2MG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	2	1212	U
2	2	1213	A
2	2	1214	C
2	2	1227	A
2	2	1228	C
2	2	1231	G
2	2	1238	A
2	2	1240	U
2	2	1241	G
2	2	1254	A
2	2	1256	A
2	2	1257	A
2	2	1258	G
2	2	1260	G
2	2	1261	A
2	2	1275	A
2	2	1279	G
2	2	1280	A
2	2	1286	U
2	2	1287	A
2	2	1297	G
2	2	1299	A
2	2	1301	U
2	2	1302	C
2	2	1305	G
2	2	1317	C
2	2	1320	C
2	2	1331	G
2	2	1336	C
2	2	1338	G
2	2	1340	A
2	2	1363	A
2	2	1368	A
2	2	1370	G
2	2	1379	G
2	2	1380	U
2	2	1384	C
2	2	1397	C
2	2	1398	A
2	2	1401	G
2	2	1402	4OC
2	2	1404	C

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	2	1419	G
2	2	1422	G
2	2	1429	A
2	2	1432	G
2	2	1441	A
2	2	1446	A
2	2	1451	U
2	2	1452	C
2	2	1453	G
2	2	1458	G
2	2	1475	G
2	2	1487	G
2	2	1489	G
2	2	1491	G
2	2	1492	A
2	2	1497	G
2	2	1499	A
2	2	1503	A
2	2	1507	A
2	2	1510	C
2	2	1511	G
2	2	1512	U
2	2	1517	G
2	2	1519	MA6
2	2	1520	C
2	2	1529	G
2	2	1530	G
2	2	1531	A
2	2	1533	C
2	2	1534	A
3	3	9	G
3	3	13	G
3	3	15	A
3	3	24	G
3	3	31	C
3	3	32	U
3	3	35	C
3	3	36	C
3	3	40	U
3	3	41	G
3	3	42	C
3	3	44	G

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
3	3	45	A
3	3	56	G
3	3	58	A
3	3	66	A
3	3	68	C
3	3	88	C
3	3	89	U
3	3	90	C
3	3	99	A
3	3	109	A
3	3	119	A
4	4	20	A
4	4	21	A
54	5	8	4SU
54	5	12	C
54	5	13	A
54	5	14	G
54	5	15	C
54	5	16	C
54	5	17	U
54	5	19	G
54	5	20	H2U
54	5	43	A
54	5	46	A
54	5	47	U
54	5	48	C
54	5	49	G
54	5	53	G
54	5	55	PSU
54	5	61	C
54	5	68	C
54	5	72	A
54	5	73	A
54	5	74	C
54	5	76	A

All (20) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	613	A
1	1	784	G
1	1	894	U

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	1	947	A
1	1	1170	C
1	1	1175	A
1	1	1252	G
1	1	1379	U
1	1	1530	G
1	1	2146	C
1	1	2189	U
1	1	2193	G
1	1	2286	G
1	1	2425	A
1	1	2756	U
2	2	83	C
2	2	210	C
2	2	496	A
2	2	516	PSU
54	5	15	C

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

38 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	OMC	1	2498	1	19,22,23	2.90	7 (36%)	25,31,34	0.91	1 (4%)
1	PSU	1	2580	1	18,21,22	1.10	2 (11%)	21,30,33	2.08	6 (28%)
54	4SU	5	8	54	18,21,22	3.70	7 (38%)	25,30,33	2.22	5 (20%)
1	6MZ	1	1618	1	22,25,26	2.85	6 (27%)	29,36,39	4.44	14 (48%)
1	5MU	1	747	1	19,22,23	4.81	7 (36%)	27,32,35	3.93	9 (33%)
1	PSU	1	2605	1	18,21,22	1.13	2 (11%)	21,30,33	2.08	5 (23%)
1	2MG	1	1835	1	23,26,27	2.89	7 (30%)	33,38,41	2.20	10 (30%)
1	5MU	1	1939	1	19,22,23	4.77	7 (36%)	27,32,35	3.83	10 (37%)
54	4OC	5	32	54	20,23,24	3.00	8 (40%)	25,32,35	1.02	2 (8%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	OMG	1	2251	1,54	23,26,27	2.40	8 (34%)	32,38,41	1.96	8 (25%)
2	UR3	2	1498	2	19,22,23	2.53	7 (36%)	26,32,35	1.56	3 (11%)
1	PSU	1	1911	1	18,21,22	1.13	2 (11%)	21,30,33	2.16	5 (23%)
54	H2U	5	20	54	18,21,22	3.37	5 (27%)	19,30,33	1.54	4 (21%)
1	G7M	1	2069	1	23,26,27	2.58	8 (34%)	34,39,42	2.51	11 (32%)
1	2MA	1	2503	1	22,25,26	3.71	8 (36%)	32,37,40	2.44	7 (21%)
2	5MC	2	967	2	19,22,23	3.84	8 (42%)	26,32,35	0.99	1 (3%)
1	1MG	1	745	1	23,26,27	2.83	7 (30%)	33,39,42	2.07	9 (27%)
1	PSU	1	746	1	18,21,22	1.09	2 (11%)	21,30,33	1.80	3 (14%)
1	3TD	1	1915	1	19,22,23	4.26	5 (26%)	23,32,35	2.01	4 (17%)
2	MA6	2	1518	2	23,26,27	1.56	5 (21%)	33,38,41	2.71	12 (36%)
54	5MU	5	54	54	19,22,23	4.81	7 (36%)	27,32,35	3.53	8 (29%)
1	PSU	1	955	1	18,21,22	1.04	1 (5%)	21,30,33	1.80	3 (14%)
1	2MG	1	2445	1	23,26,27	2.94	6 (26%)	33,38,41	2.27	7 (21%)
2	2MG	2	1207	2	23,26,27	2.89	7 (30%)	33,38,41	2.33	9 (27%)
1	PSU	1	2504	1	18,21,22	1.21	2 (11%)	21,30,33	1.93	4 (19%)
2	2MG	2	966	2	23,26,27	3.00	7 (30%)	33,38,41	2.30	7 (21%)
1	6MZ	1	2030	1	22,25,26	2.90	6 (27%)	29,36,39	4.48	13 (44%)
2	4OC	2	1402	2	20,23,24	3.00	8 (40%)	25,32,35	1.26	4 (16%)
2	5MC	2	1407	2	19,22,23	3.81	8 (42%)	26,32,35	1.12	2 (7%)
1	PSU	1	1917	1	18,21,22	1.11	1 (5%)	21,30,33	1.88	4 (19%)
1	5MC	1	1962	1	19,22,23	3.79	8 (42%)	26,32,35	1.02	2 (7%)
1	OMU	1	2552	1	19,22,23	2.88	8 (42%)	25,31,34	1.92	5 (20%)
2	G7M	2	527	2	23,26,27	3.59	12 (52%)	34,39,42	1.58	7 (20%)
2	PSU	2	516	2	18,21,22	1.02	1 (5%)	21,30,33	1.94	5 (23%)
54	PSU	5	55	54	18,21,22	1.11	1 (5%)	21,30,33	1.88	4 (19%)
2	2MG	2	1516	2	23,26,27	2.95	8 (34%)	33,38,41	2.14	10 (30%)
1	PSU	1	2457	1	18,21,22	1.17	3 (16%)	21,30,33	2.03	6 (28%)
2	MA6	2	1519	2	23,26,27	1.53	4 (17%)	33,38,41	2.76	13 (39%)

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	OMC	1	2498	1	-	0/9/27/28	0/2/2/2
1	PSU	1	2580	1	-	0/7/25/26	0/2/2/2
54	4SU	5	8	54	-	3/7/25/26	0/2/2/2
1	6MZ	1	1618	1	-	4/9/27/28	0/3/3/3
1	5MU	1	747	1	-	1/7/25/26	0/2/2/2
1	PSU	1	2605	1	-	0/7/25/26	0/2/2/2
1	2MG	1	1835	1	-	2/9/27/28	0/3/3/3
1	5MU	1	1939	1	-	0/7/25/26	0/2/2/2
54	4OC	5	32	54	-	0/9/29/30	0/2/2/2
1	OMG	1	2251	1,54	-	0/9/27/28	0/3/3/3
2	UR3	2	1498	2	-	0/7/25/26	0/2/2/2
1	PSU	1	1911	1	-	0/7/25/26	0/2/2/2
54	H2U	5	20	54	-	4/7/38/39	0/2/2/2
1	G7M	1	2069	1	-	1/7/25/26	0/3/3/3
1	2MA	1	2503	1	-	5/7/25/26	0/3/3/3
2	5MC	2	967	2	-	0/7/25/26	0/2/2/2
1	1MG	1	745	1	-	0/7/25/26	0/3/3/3
1	PSU	1	746	1	-	2/7/25/26	0/2/2/2
1	3TD	1	1915	1	-	4/7/25/26	0/2/2/2
2	MA6	2	1518	2	-	0/11/29/30	0/3/3/3
54	5MU	5	54	54	-	0/7/25/26	0/2/2/2
1	PSU	1	955	1	-	0/7/25/26	0/2/2/2
1	2MG	1	2445	1	-	2/9/27/28	0/3/3/3
2	2MG	2	1207	2	-	2/9/27/28	0/3/3/3
1	PSU	1	2504	1	-	2/7/25/26	0/2/2/2
2	2MG	2	966	2	-	0/9/27/28	0/3/3/3
1	6MZ	1	2030	1	-	3/9/27/28	0/3/3/3
2	4OC	2	1402	2	-	2/9/29/30	0/2/2/2
2	5MC	2	1407	2	-	0/7/25/26	0/2/2/2
1	PSU	1	1917	1	-	0/7/25/26	0/2/2/2
1	5MC	1	1962	1	-	2/7/25/26	0/2/2/2
1	OMU	1	2552	1	-	1/9/27/28	0/2/2/2
2	G7M	2	527	2	-	2/7/25/26	0/3/3/3
2	PSU	2	516	2	-	2/7/25/26	0/2/2/2
54	PSU	5	55	54	-	1/7/25/26	0/2/2/2
2	2MG	2	1516	2	-	0/9/27/28	0/3/3/3
1	PSU	1	2457	1	-	0/7/25/26	0/2/2/2
2	MA6	2	1519	2	-	3/11/29/30	0/3/3/3

All (216) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	1915	3TD	C6-C5	13.15	1.49	1.35
1	1	2503	2MA	C4-N3	11.40	1.49	1.34
1	1	2030	6MZ	C6-N6	11.37	1.47	1.34
1	1	747	5MU	C2-N1	11.29	1.56	1.38
54	5	20	H2U	C2-N1	11.12	1.51	1.35
1	1	1618	6MZ	C6-N6	11.00	1.46	1.34
54	5	54	5MU	C2-N1	10.95	1.55	1.38
1	1	1939	5MU	C2-N1	10.80	1.55	1.38
2	2	527	G7M	C8-N7	10.80	1.51	1.33
54	5	54	5MU	C6-N1	10.54	1.55	1.38
1	1	1939	5MU	C6-N1	10.19	1.55	1.38
1	1	747	5MU	C6-N1	10.02	1.55	1.38
1	1	1915	3TD	C2-N1	9.81	1.49	1.37
1	1	747	5MU	C4-C5	9.76	1.60	1.44
1	1	1939	5MU	C4-C5	9.75	1.60	1.44
54	5	54	5MU	C4-C5	9.73	1.60	1.44
1	1	1962	5MC	C6-C5	9.07	1.49	1.34
2	2	967	5MC	C6-C5	9.04	1.49	1.34
2	2	1407	5MC	C6-C5	8.98	1.49	1.34
54	5	8	4SU	C4-N3	8.13	1.46	1.37
1	1	747	5MU	C4-N3	-8.11	1.23	1.38
54	5	54	5MU	C4-N3	-8.10	1.23	1.38
1	1	1939	5MU	C4-N3	-8.02	1.23	1.38
54	5	8	4SU	C2-N1	7.68	1.50	1.38
1	1	2445	2MG	C2-N3	7.55	1.46	1.32
2	2	966	2MG	C2-N3	7.53	1.46	1.32
1	1	745	1MG	C2-N2	7.49	1.47	1.34
1	1	1835	2MG	C2-N3	7.21	1.45	1.32
2	2	1207	2MG	C2-N3	7.20	1.45	1.32
2	2	1516	2MG	C2-N3	7.20	1.45	1.32
2	2	967	5MC	C4-N3	7.07	1.45	1.34
1	1	2503	2MA	C2-N3	7.02	1.46	1.34
54	5	32	4OC	C4-N3	6.94	1.44	1.32
2	2	1402	4OC	C4-N3	6.94	1.44	1.32
1	1	1962	5MC	C4-N3	6.89	1.45	1.34
2	2	966	2MG	C4-N3	6.82	1.49	1.34
1	1	2445	2MG	C4-N3	6.68	1.49	1.34
2	2	966	2MG	C2-N2	6.67	1.47	1.33
2	2	1516	2MG	C2-N2	6.64	1.47	1.33
2	2	1407	5MC	C4-N3	6.64	1.44	1.34
1	1	745	1MG	C2-N3	6.62	1.44	1.33
54	5	20	H2U	C2-N3	6.61	1.49	1.38
1	1	2552	OMU	C2-N3	6.57	1.49	1.38

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	2069	G7M	C4-N3	6.57	1.49	1.34
1	1	745	1MG	C4-N3	6.54	1.49	1.34
2	2	1207	2MG	C4-N3	6.54	1.49	1.34
2	2	1516	2MG	C4-N3	6.52	1.49	1.34
1	1	2445	2MG	C2-N2	6.43	1.46	1.33
1	1	1835	2MG	C4-N3	6.40	1.48	1.34
1	1	2552	OMU	C2-N1	6.38	1.48	1.38
1	1	1835	2MG	C2-N2	6.30	1.46	1.33
2	2	1207	2MG	C2-N2	6.29	1.46	1.33
1	1	2498	OMC	C6-C5	6.29	1.49	1.35
2	2	1498	UR3	C2-N1	6.27	1.47	1.38
1	1	2251	OMG	C4-N3	6.25	1.48	1.34
2	2	967	5MC	C2-N3	6.23	1.48	1.36
1	1	1962	5MC	C5-C4	6.10	1.48	1.44
1	1	2498	OMC	C2-N3	6.10	1.48	1.36
1	1	1962	5MC	C2-N3	6.09	1.48	1.36
2	2	1407	5MC	C2-N3	6.07	1.48	1.36
2	2	1407	5MC	C5-C4	6.07	1.48	1.44
2	2	967	5MC	C5-C4	6.05	1.48	1.44
54	5	32	4OC	C6-C5	5.95	1.48	1.35
1	1	1939	5MU	C6-C5	5.94	1.44	1.34
54	5	8	4SU	C6-C5	5.87	1.48	1.35
2	2	1498	UR3	C6-C5	5.81	1.48	1.35
2	2	1402	4OC	C2-N3	5.81	1.47	1.36
54	5	8	4SU	C4-S4	-5.78	1.58	1.68
1	1	1915	3TD	C6-N1	5.76	1.45	1.36
54	5	32	4OC	C2-N3	5.75	1.47	1.36
2	2	1402	4OC	C6-C5	5.74	1.48	1.35
1	1	747	5MU	C6-C5	5.69	1.43	1.34
1	1	2503	2MA	C2-N1	5.65	1.43	1.34
54	5	54	5MU	C6-C5	5.65	1.43	1.34
54	5	8	4SU	C2-N3	5.63	1.47	1.38
2	2	527	G7M	C2-N3	5.62	1.46	1.33
1	1	2503	2MA	C6-N1	5.62	1.42	1.35
1	1	2498	OMC	C4-N3	5.61	1.45	1.34
2	2	527	G7M	C8-N9	5.48	1.50	1.35
2	2	527	G7M	C4-N3	5.44	1.46	1.34
1	1	2552	OMU	C6-C5	5.42	1.47	1.35
1	1	2069	G7M	C2-N3	5.27	1.46	1.33
1	1	2251	OMG	C2-N3	5.23	1.45	1.33
1	1	2069	G7M	C5-N7	-4.96	1.33	1.39
2	2	1407	5MC	C4-N4	4.82	1.46	1.34

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	967	5MC	C4-N4	4.81	1.46	1.34
1	1	1962	5MC	C4-N4	4.80	1.46	1.34
54	5	20	H2U	C4-N3	4.77	1.45	1.37
1	1	1915	3TD	C2-N3	4.76	1.48	1.38
2	2	527	G7M	C2-N2	4.76	1.45	1.34
1	1	2251	OMG	C2-N2	4.72	1.45	1.34
2	2	1402	4OC	C2-N1	4.56	1.49	1.40
2	2	1407	5MC	C6-N1	4.52	1.45	1.38
2	2	1498	UR3	C2-N3	4.47	1.47	1.39
2	2	1407	5MC	C2-N1	4.46	1.49	1.40
2	2	967	5MC	C6-N1	4.44	1.45	1.38
2	2	527	G7M	C5-N7	4.37	1.44	1.39
1	1	2069	G7M	C2-N2	4.26	1.44	1.34
2	2	1516	2MG	C2-N1	4.24	1.43	1.36
1	1	1962	5MC	C6-N1	4.21	1.45	1.38
1	1	2503	2MA	C5-C6	4.18	1.52	1.41
2	2	966	2MG	C2-N1	4.16	1.43	1.36
1	1	2504	PSU	C6-C5	4.11	1.39	1.35
2	2	967	5MC	C2-N1	4.06	1.48	1.40
1	1	1835	2MG	C2-N1	4.05	1.43	1.36
2	2	1207	2MG	C2-N1	4.00	1.43	1.36
54	5	32	4OC	C4-N4	3.97	1.44	1.36
2	2	1402	4OC	C4-N4	3.95	1.44	1.36
54	5	32	4OC	C2-N1	3.95	1.48	1.40
1	1	2069	G7M	C5-C6	3.93	1.54	1.43
1	1	2552	OMU	C4-N3	3.86	1.45	1.38
1	1	2445	2MG	C2-N1	3.78	1.42	1.36
1	1	1962	5MC	C2-N1	3.78	1.48	1.40
2	2	1519	MA6	C6-N6	3.74	1.47	1.36
1	1	2498	OMC	C2-N1	3.70	1.47	1.40
1	1	2498	OMC	C4-N4	3.68	1.42	1.33
1	1	2030	6MZ	C5-C4	-3.68	1.32	1.39
1	1	2503	2MA	C6-N6	-3.66	1.24	1.34
54	5	55	PSU	C6-C5	3.66	1.39	1.35
1	1	2445	2MG	C5-N7	-3.63	1.31	1.39
1	1	1618	6MZ	C5-C4	-3.62	1.32	1.39
1	1	2445	2MG	O6-C6	-3.62	1.16	1.23
54	5	32	4OC	C5-C4	3.60	1.48	1.41
1	1	2498	OMC	C6-N1	3.58	1.46	1.38
2	2	966	2MG	C5-N7	-3.57	1.31	1.39
2	2	1518	MA6	C6-N6	3.56	1.46	1.36
1	1	2030	6MZ	C8-N9	-3.55	1.31	1.37

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	1835	2MG	O6-C6	-3.50	1.16	1.23
2	2	966	2MG	O6-C6	-3.49	1.16	1.23
1	1	1835	2MG	C5-N7	-3.49	1.32	1.39
2	2	1207	2MG	C5-N7	-3.49	1.32	1.39
2	2	1516	2MG	C5-N7	-3.48	1.32	1.39
2	2	1516	2MG	O6-C6	-3.47	1.17	1.23
1	1	2457	PSU	C6-C5	3.45	1.39	1.35
1	1	2605	PSU	C6-C5	3.45	1.39	1.35
1	1	2503	2MA	C5-N7	-3.41	1.32	1.39
2	2	1207	2MG	O6-C6	-3.40	1.17	1.23
2	2	1518	MA6	C8-N9	-3.38	1.31	1.37
1	1	745	1MG	C2-N1	3.37	1.43	1.37
1	1	1962	5MC	O2-C2	-3.37	1.17	1.23
1	1	1917	PSU	C6-C5	3.36	1.39	1.35
2	2	527	G7M	C2-N1	3.35	1.45	1.37
1	1	1618	6MZ	C8-N9	-3.34	1.31	1.37
1	1	1618	6MZ	C4-N9	-3.30	1.30	1.37
1	1	1911	PSU	C6-C5	3.30	1.38	1.35
2	2	1402	4OC	C5-C4	3.30	1.48	1.41
54	5	8	4SU	C5-C4	3.28	1.46	1.42
2	2	527	G7M	C5-C6	3.27	1.52	1.43
2	2	1407	5MC	O2-C2	-3.27	1.17	1.23
1	1	745	1MG	C5-N7	-3.24	1.32	1.39
2	2	967	5MC	O2-C2	-3.23	1.17	1.23
1	1	746	PSU	C6-C5	3.22	1.38	1.35
1	1	2251	OMG	C5-N7	-3.20	1.32	1.39
1	1	2552	OMU	O4-C4	-3.13	1.18	1.24
2	2	1518	MA6	C5-N7	-3.13	1.33	1.39
1	1	955	PSU	C6-C5	3.12	1.38	1.35
2	2	1519	MA6	C5-N7	-3.12	1.33	1.39
2	2	516	PSU	C6-C5	3.10	1.38	1.35
2	2	1518	MA6	C5-C4	-3.01	1.33	1.39
2	2	1519	MA6	C8-N9	-3.01	1.32	1.37
1	1	747	5MU	O4-C4	-2.95	1.18	1.23
1	1	1915	3TD	C4-N3	2.94	1.46	1.40
1	1	2580	PSU	C6-C5	2.92	1.38	1.35
54	5	32	4OC	O2-C2	-2.91	1.18	1.23
54	5	32	4OC	C6-N1	2.89	1.45	1.38
1	1	1939	5MU	O4-C4	-2.88	1.18	1.23
54	5	54	5MU	O4-C4	-2.86	1.18	1.23
1	1	2498	OMC	O2-C2	-2.85	1.18	1.23
2	2	1402	4OC	C6-N1	2.83	1.44	1.38

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	2251	OMG	O6-C6	-2.82	1.18	1.23
1	1	747	5MU	O2-C2	-2.82	1.18	1.23
2	2	1519	MA6	C5-C4	-2.80	1.34	1.39
2	2	1402	4OC	O2-C2	-2.78	1.18	1.23
1	1	2069	G7M	O6-C6	-2.77	1.18	1.23
1	1	2030	6MZ	C4-N9	-2.76	1.31	1.37
2	2	527	G7M	O6-C6	-2.72	1.18	1.23
2	2	527	G7M	C6-N1	2.71	1.43	1.38
54	5	8	4SU	O2-C2	-2.70	1.18	1.23
1	1	2552	OMU	O2-C2	-2.69	1.18	1.23
1	1	1939	5MU	O2-C2	-2.61	1.18	1.23
1	1	2251	OMG	C2-N1	2.54	1.43	1.37
2	2	1498	UR3	C6-N1	2.46	1.44	1.38
1	1	2069	G7M	C2-N1	2.42	1.43	1.37
1	1	2552	OMU	C6-N1	2.42	1.43	1.38
54	5	54	5MU	O2-C2	-2.42	1.18	1.23
1	1	2580	PSU	O4'-C1'	-2.40	1.40	1.43
1	1	2030	6MZ	C6-N1	-2.39	1.31	1.35
1	1	1618	6MZ	C6-N1	-2.38	1.31	1.35
54	5	20	H2U	O4-C4	-2.37	1.18	1.23
2	2	1498	UR3	O4-C4	-2.37	1.18	1.23
2	2	1498	UR3	O2-C2	-2.37	1.18	1.22
1	1	1618	6MZ	C5-C6	-2.37	1.36	1.41
2	2	1207	2MG	C5-C6	2.34	1.53	1.44
54	5	20	H2U	O2-C2	-2.33	1.18	1.23
1	1	745	1MG	C5-C6	2.26	1.51	1.45
1	1	2069	G7M	C6-N1	2.25	1.43	1.38
1	1	2251	OMG	C4-N9	-2.24	1.32	1.38
1	1	2251	OMG	C5-C6	2.22	1.52	1.44
1	1	2503	2MA	C4-N9	-2.22	1.33	1.37
2	2	966	2MG	C5-C6	2.21	1.52	1.44
1	1	1835	2MG	C5-C6	2.18	1.52	1.44
1	1	2457	PSU	C4-C5	-2.17	1.38	1.44
1	1	2552	OMU	C5-C4	2.16	1.48	1.43
2	2	1516	2MG	C5-C6	2.14	1.52	1.44
1	1	746	PSU	C4-C5	-2.13	1.38	1.44
1	1	745	1MG	C4-N9	-2.11	1.32	1.38
1	1	1911	PSU	C4-C5	-2.11	1.38	1.44
1	1	2030	6MZ	C5-C6	-2.06	1.36	1.41
2	2	1516	2MG	C4-N9	-2.06	1.32	1.38
2	2	1498	UR3	C5-C4	2.05	1.49	1.43
2	2	527	G7M	C4-N9	2.04	1.43	1.38

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	2605	PSU	C4-C5	-2.02	1.38	1.44
2	2	527	G7M	C5-C4	2.02	1.43	1.38
1	1	2504	PSU	C4-C5	-2.02	1.38	1.44
2	2	1518	MA6	C5-C6	-2.01	1.36	1.41
1	1	2457	PSU	O4'-C1'	-2.00	1.41	1.43

All (242) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	1618	6MZ	C4-N9-C8	14.18	120.63	105.74
1	1	2030	6MZ	C4-N9-C8	13.95	120.39	105.74
1	1	747	5MU	C5-C4-N3	12.91	126.55	115.32
1	1	1939	5MU	C5-C4-N3	12.57	126.25	115.32
54	5	54	5MU	C5-C4-N3	12.04	125.79	115.32
1	1	747	5MU	C5-C6-N1	-10.70	111.69	123.31
1	1	2030	6MZ	N9-C8-N7	-10.51	99.03	113.94
1	1	1939	5MU	C5-C6-N1	-10.43	111.99	123.31
1	1	1618	6MZ	N9-C8-N7	-10.42	99.16	113.94
54	5	54	5MU	C5-C6-N1	-9.20	113.32	123.31
1	1	2030	6MZ	C5-C6-N1	8.74	127.53	118.15
2	2	1519	MA6	N1-C6-N6	-8.60	106.38	116.86
1	1	1618	6MZ	C5-C6-N1	8.33	127.10	118.15
2	2	1518	MA6	N1-C6-N6	-8.23	106.83	116.86
1	1	2503	2MA	C5-C4-N3	-7.74	119.03	127.18
54	5	8	4SU	C4-N3-C2	-7.04	120.57	127.31
2	2	966	2MG	C2-N3-C4	6.82	120.53	112.00
2	2	1207	2MG	C2-N3-C4	6.76	120.46	112.00
1	1	2030	6MZ	N3-C4-N9	6.47	138.17	127.17
1	1	2445	2MG	C2-N3-C4	6.39	120.00	112.00
2	2	966	2MG	C5-C4-N3	-6.20	118.53	128.39
2	2	1207	2MG	C5-C4-N3	-6.18	118.55	128.39
2	2	1519	MA6	N1-C2-N3	-6.18	119.23	128.58
1	1	1835	2MG	C2-N3-C4	6.17	119.71	112.00
1	1	2503	2MA	N3-C4-N9	6.12	134.76	126.99
2	2	1516	2MG	C2-N3-C4	6.10	119.64	112.00
2	2	1518	MA6	N1-C2-N3	-6.10	119.36	128.58
1	1	2445	2MG	C5-C4-N3	-6.09	118.70	128.39
1	1	2552	OMU	C4-N3-C2	-6.05	119.10	126.61
1	1	2069	G7M	CN7-N7-C5	5.99	134.26	126.80
1	1	1618	6MZ	N3-C4-N9	5.77	136.97	127.17
1	1	1915	3TD	C1'-C5-C4	5.76	126.35	117.61
2	2	1519	MA6	C5-C6-N6	5.73	134.40	125.33

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	1939	5MU	O4-C4-C5	-5.71	118.39	124.92
1	1	747	5MU	C4-N3-C2	-5.61	119.99	127.34
1	1	747	5MU	O4-C4-C5	-5.58	118.53	124.92
1	1	2030	6MZ	N1-C2-N3	-5.57	120.15	128.58
1	1	1618	6MZ	C9-N6-C6	-5.56	117.69	122.85
1	1	1618	6MZ	N1-C2-N3	-5.56	120.16	128.58
1	1	2069	G7M	C2-N3-C4	5.52	121.81	112.30
1	1	1911	PSU	N1-C2-N3	5.52	120.99	115.17
1	1	1835	2MG	C5-C4-N3	-5.49	119.66	128.39
1	1	745	1MG	C1'-N9-C4	-5.42	110.49	126.49
1	1	1939	5MU	C4-N3-C2	-5.40	120.26	127.34
1	1	1911	PSU	C4-N3-C2	-5.37	118.98	126.37
1	1	2251	OMG	C5-C4-N3	-5.36	119.86	128.39
1	1	2605	PSU	C4-N3-C2	-5.34	119.01	126.37
2	2	1498	UR3	C4-N3-C2	-5.34	120.28	124.58
1	1	2605	PSU	N1-C2-N3	5.27	120.72	115.17
2	2	1516	2MG	C5-C4-N3	-5.25	120.03	128.39
1	1	1618	6MZ	C5-C4-N9	-5.24	100.10	105.81
1	1	2503	2MA	N9-C8-N7	-5.20	106.56	113.94
1	1	2580	PSU	N1-C2-N3	5.20	120.65	115.17
1	1	1915	3TD	N1-C2-N3	5.19	119.90	116.13
2	2	1518	MA6	C5-C6-N6	5.19	133.55	125.33
1	1	2030	6MZ	C5-C4-N9	-5.19	100.16	105.81
1	1	2069	G7M	CN7-N7-C8	-5.11	117.05	124.79
1	1	2457	PSU	N1-C2-N3	5.09	120.54	115.17
54	5	8	4SU	C5-C4-N3	5.08	119.47	114.75
1	1	2069	G7M	C5-C4-N3	-5.07	118.57	128.15
54	5	54	5MU	O4-C4-C5	-5.00	119.20	124.92
1	1	955	PSU	C4-N3-C2	-4.96	119.54	126.37
1	1	2457	PSU	C4-N3-C2	-4.93	119.58	126.37
54	5	55	PSU	N1-C2-N3	4.92	120.36	115.17
1	1	2504	PSU	N1-C2-N3	4.88	120.31	115.17
1	1	1917	PSU	C4-N3-C2	-4.86	119.68	126.37
2	2	1207	2MG	C2-N1-C6	-4.85	118.69	124.55
2	2	516	PSU	N1-C2-N3	4.82	120.25	115.17
1	1	1917	PSU	N1-C2-N3	4.82	120.25	115.17
2	2	966	2MG	C2-N1-C6	-4.82	118.73	124.55
1	1	746	PSU	C4-N3-C2	-4.81	119.74	126.37
1	1	2504	PSU	C4-N3-C2	-4.81	119.75	126.37
1	1	2445	2MG	C2-N1-C6	-4.73	118.83	124.55
1	1	2580	PSU	C4-N3-C2	-4.72	119.87	126.37
1	1	745	1MG	C5-C4-N3	-4.66	120.97	128.39

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	1939	5MU	N3-C2-N1	4.66	120.96	114.89
54	5	55	PSU	C4-N3-C2	-4.66	119.95	126.37
2	2	516	PSU	C4-N3-C2	-4.64	119.97	126.37
1	1	1835	2MG	C2-N1-C6	-4.64	118.94	124.55
1	1	2251	OMG	C2-N3-C4	4.61	120.24	112.30
1	1	747	5MU	N3-C2-N1	4.60	120.88	114.89
2	2	1518	MA6	N9-C8-N7	-4.50	107.56	113.94
1	1	745	1MG	C1'-N9-C8	4.50	139.51	126.73
1	1	2445	2MG	N9-C4-N3	4.50	134.94	125.95
1	1	2069	G7M	C5-C6-N1	4.48	121.10	111.84
1	1	955	PSU	N1-C2-N3	4.46	119.87	115.17
1	1	2030	6MZ	C9-N6-C6	-4.40	118.77	122.85
1	1	2030	6MZ	C5-N7-C8	4.37	110.33	103.45
2	2	527	G7M	C2-N3-C4	4.32	119.74	112.30
1	1	746	PSU	N1-C2-N3	4.32	119.72	115.17
1	1	2030	6MZ	C1'-N9-C8	-4.31	117.52	127.09
54	5	54	5MU	C4-N3-C2	-4.31	121.69	127.34
2	2	1516	2MG	C2-N1-C6	-4.29	119.36	124.55
2	2	966	2MG	N9-C4-N3	4.28	134.52	125.95
2	2	1519	MA6	C5-C4-N3	-4.22	120.90	126.72
2	2	1518	MA6	C5-C4-N3	-4.21	120.92	126.72
2	2	1519	MA6	N9-C8-N7	-4.19	107.99	113.94
1	1	2503	2MA	C4-N9-C8	4.16	110.11	105.74
54	5	54	5MU	N3-C2-N1	4.12	120.25	114.89
2	2	1207	2MG	N9-C4-N3	4.09	134.13	125.95
1	1	2552	OMU	N3-C2-N1	3.94	120.02	114.89
54	5	54	5MU	C5M-C5-C4	3.94	122.99	118.78
1	1	1618	6MZ	C5-N7-C8	3.91	109.60	103.45
1	1	2069	G7M	N9-C4-N3	3.89	133.74	125.95
2	2	527	G7M	C5-C4-N3	-3.87	120.83	128.15
2	2	1519	MA6	C2-N1-C6	3.86	121.27	111.83
1	1	2552	OMU	C5-C4-N3	3.86	120.21	114.80
2	2	527	G7M	C5-C6-N1	3.79	119.68	111.84
1	1	747	5MU	C5M-C5-C6	-3.76	117.76	122.85
1	1	745	1MG	N9-C8-N7	-3.75	106.45	113.40
1	1	1915	3TD	C4-N3-C2	-3.74	120.65	124.61
2	2	1518	MA6	C2-N1-C6	3.74	120.97	111.83
2	2	1498	UR3	C5-C4-N3	3.74	119.96	115.04
54	5	8	4SU	C5-C4-S4	-3.69	120.09	124.31
1	1	2030	6MZ	C5-C4-N3	-3.67	121.66	126.72
1	1	1835	2MG	N9-C4-N3	3.64	133.24	125.95
1	1	2580	PSU	O2-C2-N1	-3.64	119.03	122.79

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	2069	G7M	C2-N1-C6	-3.61	118.57	125.11
1	1	2069	G7M	C1'-N9-C4	-3.60	115.86	126.49
54	5	20	H2U	C5-C6-N1	3.57	122.31	111.52
54	5	54	5MU	C5M-C5-C6	-3.56	118.03	122.85
1	1	1939	5MU	C5M-C5-C6	-3.47	118.15	122.85
1	1	1618	6MZ	C1'-N9-C8	-3.47	119.40	127.09
1	1	2030	6MZ	C2-N3-C4	3.46	120.29	111.83
2	2	1516	2MG	N9-C4-N3	3.45	132.85	125.95
1	1	2251	OMG	C2-N1-C6	-3.44	118.87	125.11
1	1	1962	5MC	C5-C6-N1	-3.41	119.61	123.31
54	5	8	4SU	N3-C2-N1	3.38	119.30	114.89
1	1	2069	G7M	O6-C6-C5	-3.38	120.47	128.01
2	2	1519	MA6	C4-C5-C6	3.37	119.39	115.91
1	1	2251	OMG	N9-C4-N3	3.37	132.68	125.95
2	2	1519	MA6	C2-N3-C4	3.34	119.98	111.83
1	1	745	1MG	C2-N3-C4	3.33	119.47	111.98
54	5	8	4SU	C1'-N1-C2	3.33	123.57	117.59
54	5	20	H2U	O2-C2-N3	-3.32	115.36	121.49
54	5	20	H2U	N3-C2-N1	3.32	119.98	116.65
1	1	747	5MU	C5M-C5-C4	3.30	122.30	118.78
2	2	1518	MA6	C4-C5-C6	3.30	119.32	115.91
1	1	745	1MG	N9-C4-N3	3.27	132.50	125.95
2	2	1518	MA6	C2-N3-C4	3.27	119.81	111.83
1	1	1911	PSU	O2-C2-N1	-3.26	119.43	122.79
2	2	1402	4OC	O2-C2-N3	-3.24	117.22	122.33
1	1	2251	OMG	N9-C8-N7	-3.23	107.41	113.40
1	1	2503	2MA	C5-N7-C8	3.19	108.47	103.45
2	2	967	5MC	C5-C6-N1	-3.18	119.86	123.31
1	1	1618	6MZ	C2-N3-C4	3.13	119.47	111.83
1	1	2580	PSU	C6-N1-C2	-3.11	119.81	122.69
1	1	1939	5MU	C5M-C5-C4	3.08	122.07	118.78
2	2	1518	MA6	C5-N7-C8	3.06	108.26	103.45
1	1	1835	2MG	N9-C8-N7	-3.04	107.77	113.40
1	1	2504	PSU	O2-C2-N1	-3.04	119.66	122.79
1	1	2552	OMU	O4-C4-C5	-2.99	120.00	125.16
2	2	1519	MA6	C5-N7-C8	2.99	108.15	103.45
1	1	2445	2MG	N9-C8-N7	-2.98	107.87	113.40
2	2	1207	2MG	N1-C2-N2	2.97	119.59	116.56
2	2	1516	2MG	N9-C8-N7	-2.93	107.98	113.40
2	2	966	2MG	C5-C6-N1	2.92	120.69	113.25
1	1	2251	OMG	C5-C6-N1	2.89	120.60	113.25
1	1	2503	2MA	N3-C2-N1	-2.89	120.68	125.77

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	1618	6MZ	C4-N9-C1'	-2.87	119.92	126.63
2	2	1518	MA6	C4-N9-C8	2.87	108.75	105.74
1	1	2445	2MG	C5-C6-N1	2.86	120.53	113.25
1	1	2504	PSU	C6-N1-C2	-2.86	120.04	122.69
1	1	1618	6MZ	C4-C5-C6	-2.86	114.40	116.78
1	1	1939	5MU	O2-C2-N1	-2.81	119.14	122.80
54	5	55	PSU	O2-C2-N1	-2.80	119.90	122.79
1	1	746	PSU	O2-C2-N1	-2.79	119.91	122.79
2	2	516	PSU	C6-N1-C2	-2.78	120.11	122.69
1	1	747	5MU	O4-C4-N3	-2.76	114.92	120.11
1	1	1618	6MZ	C5-C4-N3	-2.76	122.91	126.72
2	2	1207	2MG	C5-C6-N1	2.75	120.25	113.25
1	1	2251	OMG	O6-C6-C5	-2.75	119.28	126.53
1	1	1917	PSU	O2-C2-N1	-2.74	119.96	122.79
1	1	2445	2MG	O6-C6-C5	-2.74	119.31	126.53
1	1	1835	2MG	C5-C6-N1	2.73	120.19	113.25
54	5	54	5MU	O4-C4-N3	-2.72	115.01	120.11
2	2	966	2MG	O6-C6-C5	-2.71	119.38	126.53
2	2	1516	2MG	C1'-N9-C4	-2.71	118.49	126.49
2	2	1407	5MC	C5-C6-N1	-2.70	120.38	123.31
54	5	55	PSU	C6-N1-C2	-2.70	120.19	122.69
1	1	2069	G7M	C1'-N9-C8	2.70	135.85	126.74
1	1	1911	PSU	C6-N1-C2	-2.68	120.20	122.69
1	1	2457	PSU	C6-C5-C4	2.67	119.97	118.17
2	2	1516	2MG	O6-C6-C5	-2.66	119.50	126.53
2	2	1519	MA6	C4-C5-N7	-2.65	107.55	110.58
2	2	527	G7M	C2-N1-C6	-2.65	120.31	125.11
2	2	1516	2MG	C5-C6-N1	2.64	119.98	113.25
2	2	966	2MG	N9-C8-N7	-2.64	108.50	113.40
2	2	1407	5MC	O2-C2-N3	-2.64	118.17	122.33
1	1	2503	2MA	C6-C5-C4	2.60	120.73	117.18
54	5	32	4OC	C6-C5-C4	2.58	120.10	117.00
1	1	1917	PSU	C6-N1-C2	-2.57	120.31	122.69
1	1	745	1MG	C5-C6-N1	2.57	119.77	115.02
2	2	1207	2MG	CM2-N2-C2	-2.57	118.13	123.65
2	2	1207	2MG	N9-C8-N7	-2.56	108.65	113.40
2	2	527	G7M	N9-C8-N7	-2.56	106.27	112.48
1	1	2457	PSU	C6-N1-C2	-2.55	120.33	122.69
2	2	1518	MA6	N3-C4-N9	2.53	131.47	127.17
1	1	2552	OMU	O2-C2-N1	-2.53	119.50	122.80
1	1	1939	5MU	O4-C4-N3	-2.53	115.36	120.11
1	1	2605	PSU	O2-C2-N1	-2.48	120.23	122.79

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	1835	2MG	O6-C6-C5	-2.48	120.00	126.53
1	1	1618	6MZ	C6-C5-N7	2.45	135.10	132.43
1	1	1835	2MG	N1-C2-N2	2.44	119.06	116.56
2	2	527	G7M	C5-C4-N9	2.44	111.09	105.88
2	2	516	PSU	O2-C2-N1	-2.44	120.27	122.79
2	2	1518	MA6	C4-C5-N7	-2.42	107.81	110.58
2	2	1207	2MG	O6-C6-C5	-2.40	120.20	126.53
1	1	2580	PSU	O4'-C1'-C2'	2.37	108.43	105.15
1	1	1835	2MG	CM2-N2-C2	-2.36	118.57	123.65
1	1	2030	6MZ	C6-C5-N7	2.36	135.00	132.43
2	2	527	G7M	O6-C6-C5	-2.36	122.75	128.01
2	2	516	PSU	O3'-C3'-C4'	2.33	117.78	111.08
1	1	747	5MU	C6-C5-C4	2.33	119.94	118.02
1	1	1835	2MG	C1'-N9-C4	-2.33	119.61	126.49
1	1	745	1MG	C8-N7-C5	2.31	108.38	104.26
1	1	2457	PSU	O2-C2-N1	-2.31	120.41	122.79
1	1	1911	PSU	C6-C5-C4	2.30	119.72	118.17
1	1	2605	PSU	C6-N1-C2	-2.29	120.57	122.69
54	5	20	H2U	C5-C4-N3	2.28	119.11	116.69
2	2	1519	MA6	C5-C4-N9	2.28	108.30	105.81
2	2	1402	4OC	C1'-N1-C2	2.27	123.45	118.44
1	1	2498	OMC	O2-C2-N3	-2.25	118.78	122.33
1	1	2030	6MZ	C4-C5-C6	-2.25	114.91	116.78
1	1	1915	3TD	O4-C4-N3	-2.21	116.33	120.36
1	1	2605	PSU	C6-C5-C4	2.19	119.65	118.17
2	2	1498	UR3	C1'-N1-C2	2.19	120.62	117.04
2	2	1402	4OC	C6-C5-C4	2.18	119.62	117.00
2	2	1516	2MG	C1'-N9-C8	2.17	132.91	126.73
2	2	1519	MA6	C4-N9-C8	2.17	108.02	105.74
2	2	1516	2MG	N1-C2-N2	2.14	118.75	116.56
2	2	1519	MA6	N3-C4-N9	2.14	130.80	127.17
1	1	1939	5MU	C6-C5-C4	2.13	119.78	118.02
1	1	2251	OMG	C8-N7-C5	2.13	108.06	104.26
1	1	745	1MG	C8-N9-C4	2.11	109.98	106.03
1	1	2069	G7M	N2-C2-N1	2.10	121.19	116.76
1	1	955	PSU	O2-C2-N1	-2.09	120.63	122.79
1	1	2457	PSU	O4'-C1'-C2'	2.04	107.98	105.15
2	2	1402	4OC	O2-C2-N1	2.04	122.89	118.90
54	5	32	4OC	O2-C2-N3	-2.01	119.16	122.33
1	1	1962	5MC	CM5-C5-C6	-2.01	120.13	122.85
1	1	2580	PSU	C6-C5-C4	2.00	119.53	118.17

There are no chirality outliers.

All (48) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	1	1618	6MZ	C5-C6-N6-C9
1	1	1618	6MZ	N1-C6-N6-C9
1	1	1915	3TD	O4'-C1'-C5-C4
1	1	1915	3TD	O4'-C1'-C5-C6
1	1	2504	PSU	O4'-C4'-C5'-O5'
1	1	2552	OMU	C1'-C2'-O2'-CM2
2	2	516	PSU	O4'-C1'-C5-C4
2	2	516	PSU	O4'-C1'-C5-C6
2	2	1207	2MG	O4'-C4'-C5'-O5'
2	2	1402	4OC	O4'-C4'-C5'-O5'
2	2	1519	MA6	O4'-C4'-C5'-O5'
2	2	1519	MA6	C3'-C4'-C5'-O5'
54	5	20	H2U	O4'-C1'-N1-C2
54	5	20	H2U	O4'-C1'-N1-C6
1	1	1915	3TD	O4'-C4'-C5'-O5'
1	1	2030	6MZ	C3'-C4'-C5'-O5'
1	1	2445	2MG	C3'-C4'-C5'-O5'
2	2	527	G7M	C3'-C4'-C5'-O5'
2	2	1207	2MG	C3'-C4'-C5'-O5'
1	1	1618	6MZ	O4'-C4'-C5'-O5'
1	1	1618	6MZ	C3'-C4'-C5'-O5'
1	1	1835	2MG	O4'-C4'-C5'-O5'
1	1	1835	2MG	C3'-C4'-C5'-O5'
1	1	2504	PSU	C3'-C4'-C5'-O5'
2	2	527	G7M	O4'-C4'-C5'-O5'
2	2	1402	4OC	C3'-C4'-C5'-O5'
1	1	1915	3TD	C3'-C4'-C5'-O5'
1	1	2030	6MZ	O4'-C4'-C5'-O5'
54	5	20	H2U	O4'-C4'-C5'-O5'
1	1	2445	2MG	O4'-C4'-C5'-O5'
1	1	2503	2MA	O4'-C4'-C5'-O5'
54	5	20	H2U	C3'-C4'-C5'-O5'
1	1	2503	2MA	O4'-C1'-N9-C4
54	5	8	4SU	O4'-C1'-N1-C6
54	5	8	4SU	O4'-C1'-N1-C2
1	1	2503	2MA	C3'-C4'-C5'-O5'
1	1	2503	2MA	O4'-C1'-N9-C8
1	1	2030	6MZ	C4'-C5'-O5'-P
1	1	2503	2MA	C4'-C5'-O5'-P
2	2	1519	MA6	C4'-C5'-O5'-P
1	1	747	5MU	C4'-C5'-O5'-P
54	5	8	4SU	C4'-C5'-O5'-P

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
1	1	746	PSU	O4'-C1'-C5-C6
1	1	1962	5MC	C2'-C1'-N1-C6
1	1	746	PSU	C2'-C1'-C5-C6
1	1	1962	5MC	O4'-C1'-N1-C6
1	1	2069	G7M	O4'-C4'-C5'-O5'
54	5	55	PSU	C4'-C5'-O5'-P

There are no ring outliers.

15 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
54	5	8	4SU	1	0
54	5	32	4OC	1	0
54	5	20	H2U	1	0
1	1	2503	2MA	4	0
1	1	745	1MG	1	0
1	1	1915	3TD	4	0
54	5	54	5MU	1	0
1	1	2030	6MZ	1	0
2	2	1402	4OC	1	0
2	2	1407	5MC	2	0
1	1	1962	5MC	1	0
1	1	2552	OMU	2	0
54	5	55	PSU	1	0
2	2	1516	2MG	1	0
2	2	1519	MA6	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 14 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

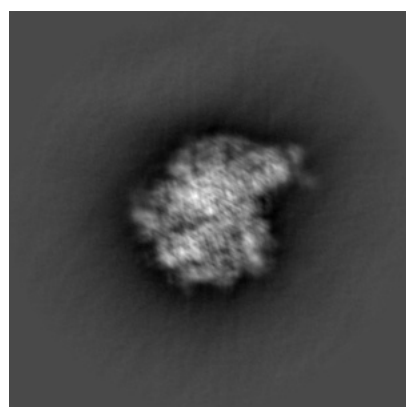
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20204. These allow visual inspection of the internal detail of the map and identification of artifacts.

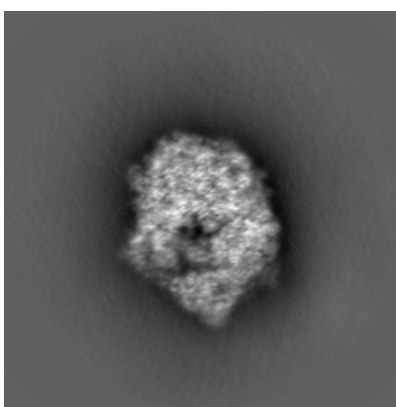
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

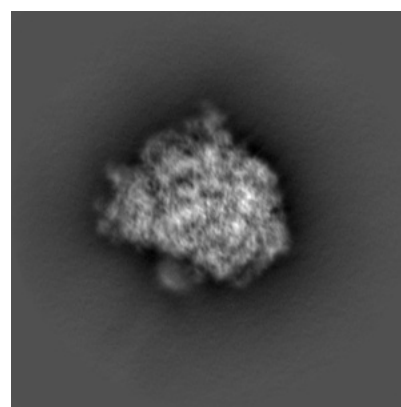
6.1.1 Primary map



X



Y

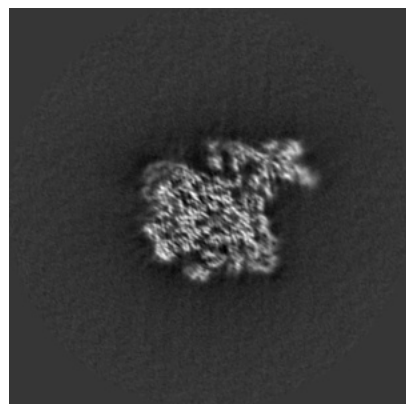


Z

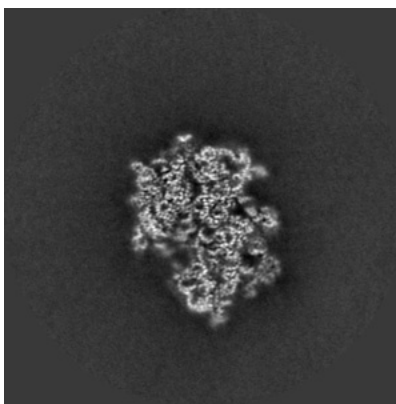
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

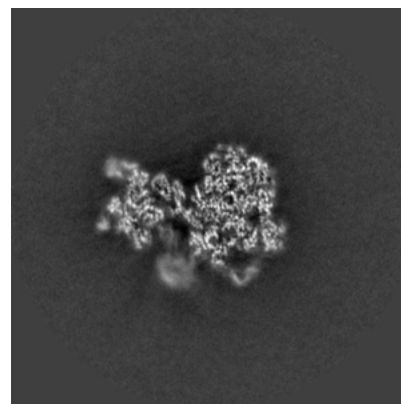
6.2.1 Primary map



X Index: 160



Y Index: 160

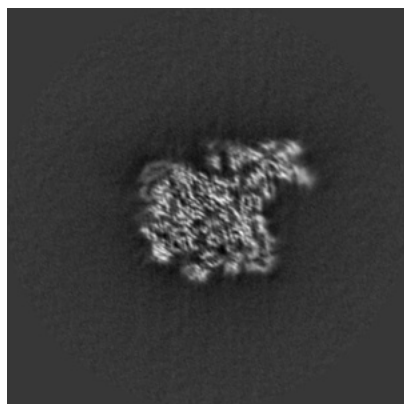


Z Index: 160

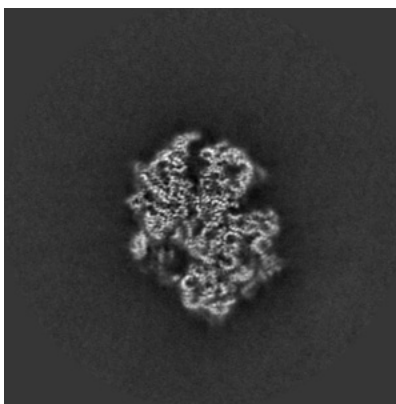
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

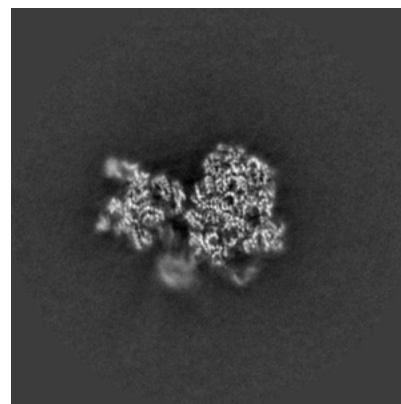
6.3.1 Primary map



X Index: 161



Y Index: 156

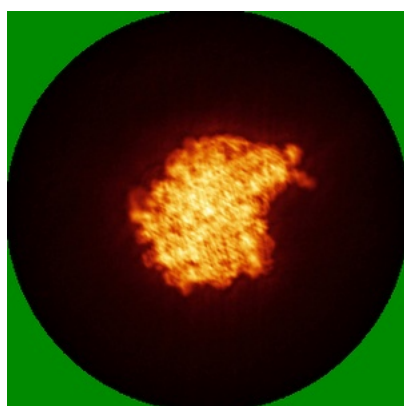


Z Index: 161

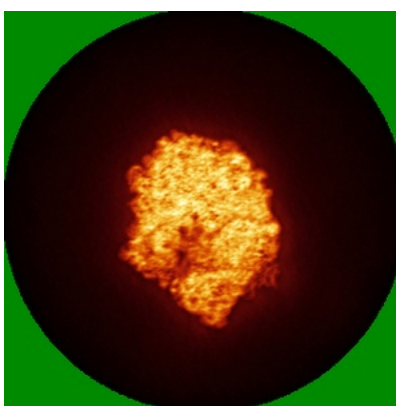
The images above show the largest variance slices of the map in three orthogonal directions.

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

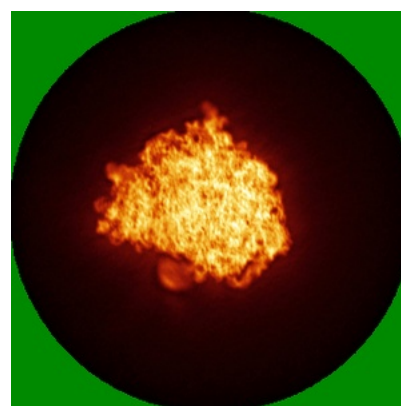
6.4.1 Primary map



X



Y

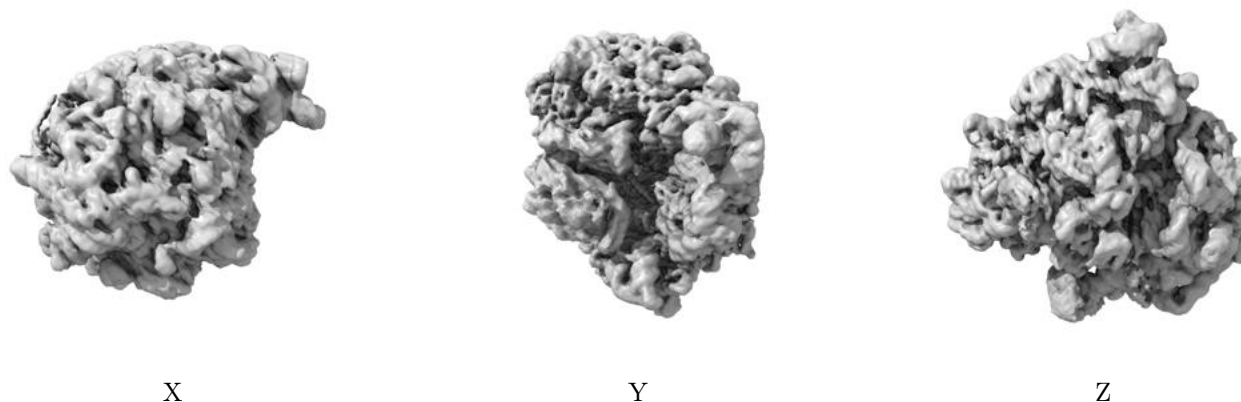


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

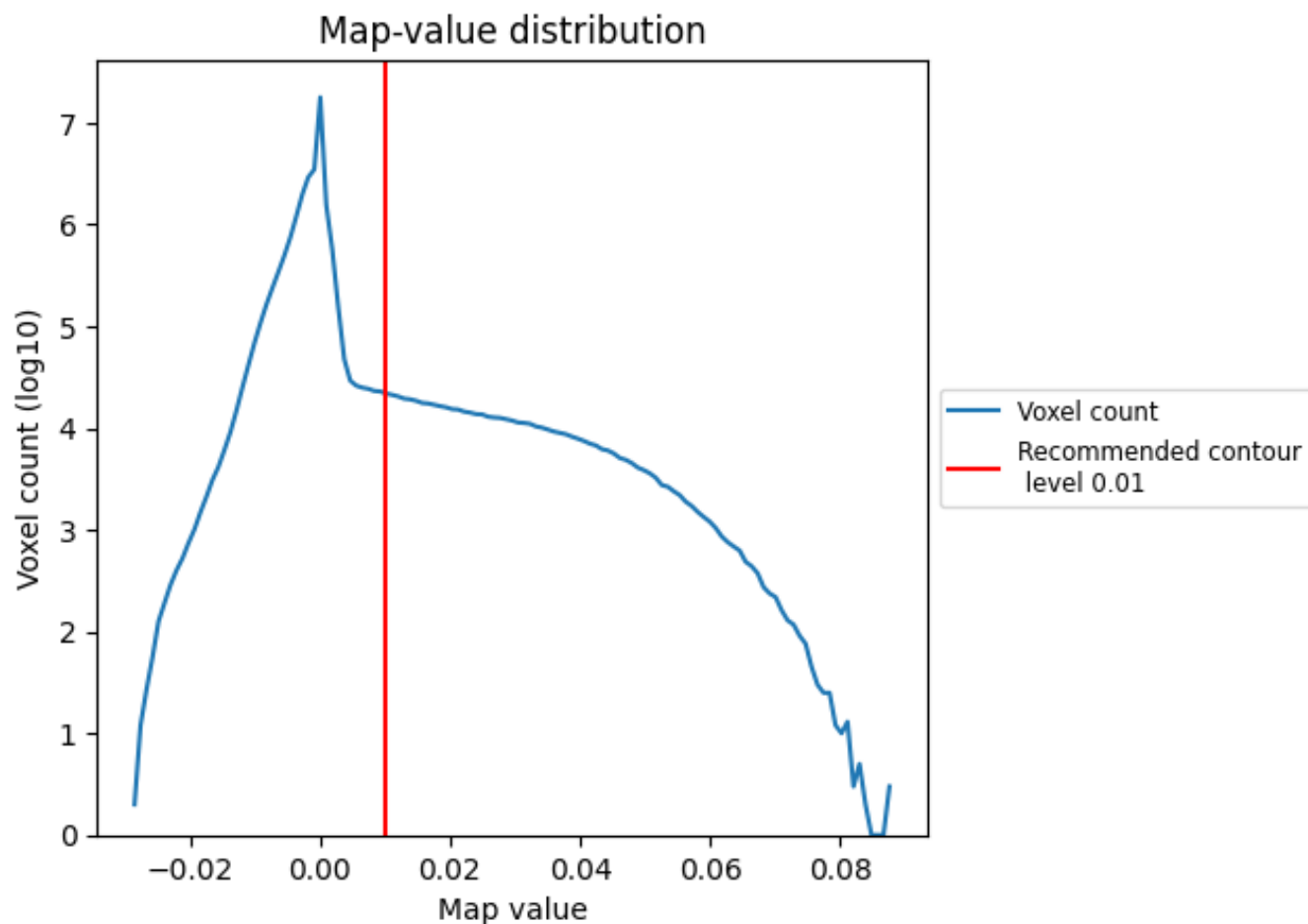
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

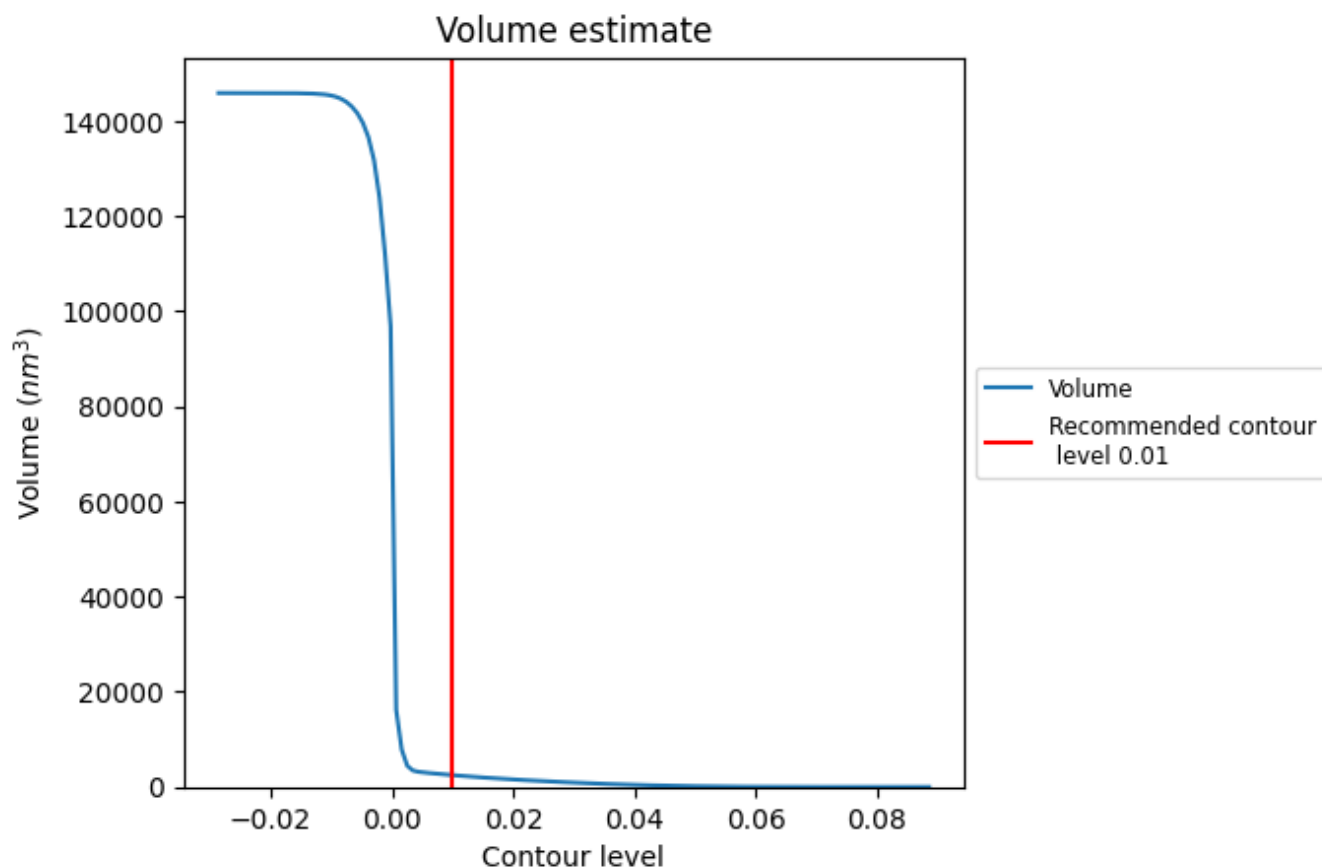
This section contains the results of statistical analysis of the map.

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.

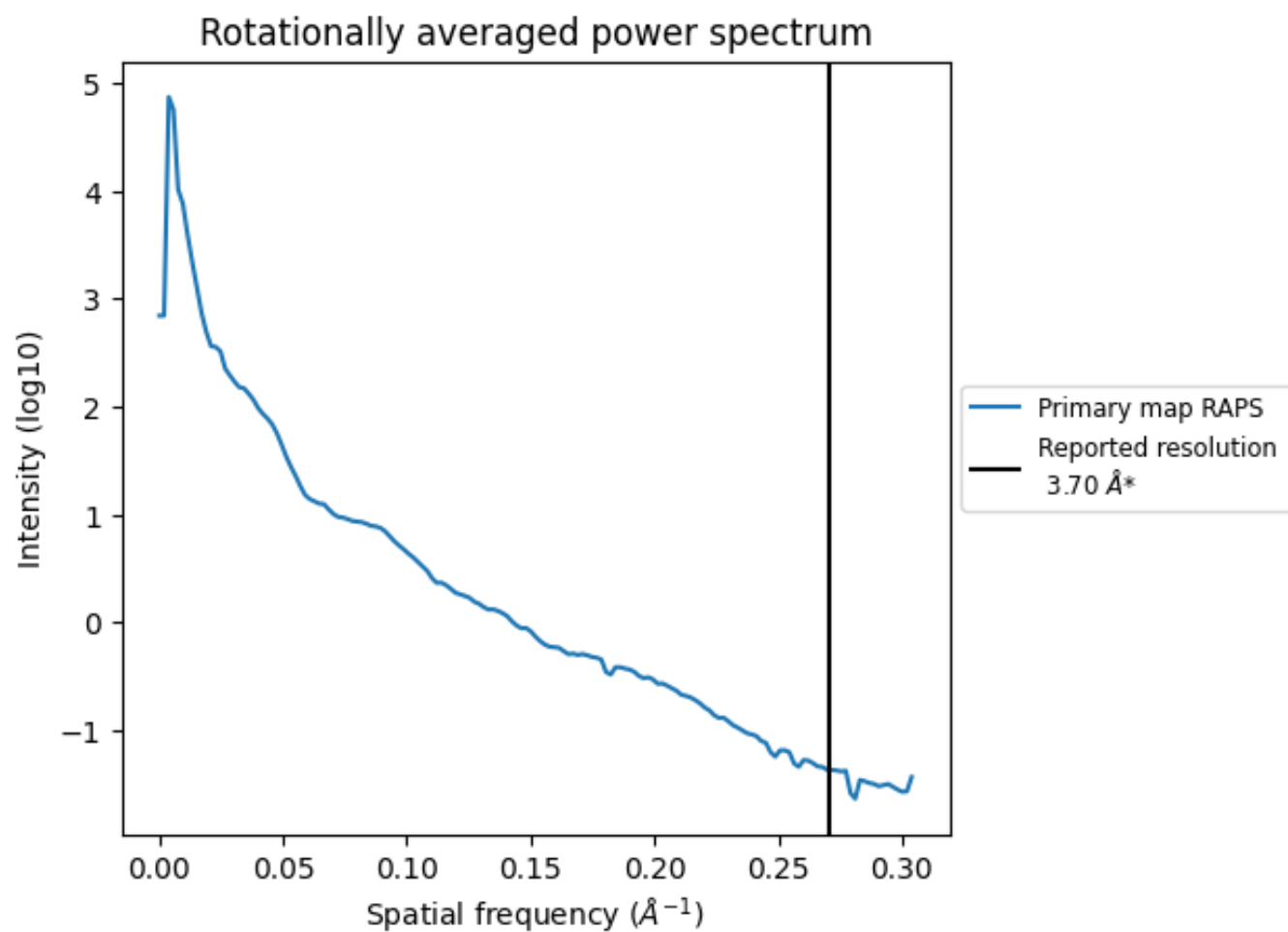
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2485 nm^3 ; this corresponds to an approximate mass of 2245 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 0.270 Å⁻¹

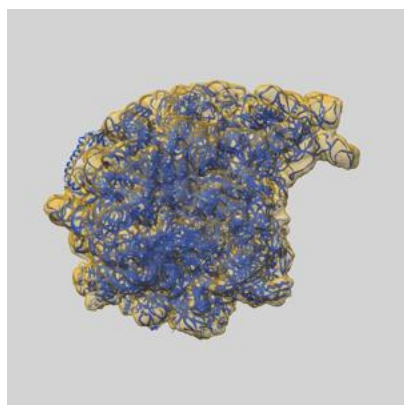
8 Fourier-Shell correlation ⓘ

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

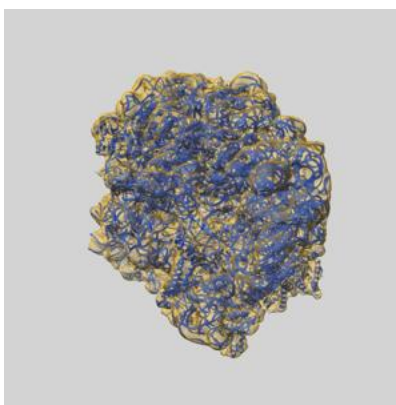
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-20204 and PDB model 6OUO. Per-residue inclusion information can be found in section [3](#) on page [15](#).

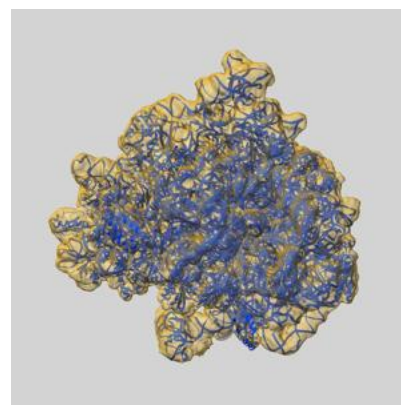
9.1 Map-model overlay [i](#)



X



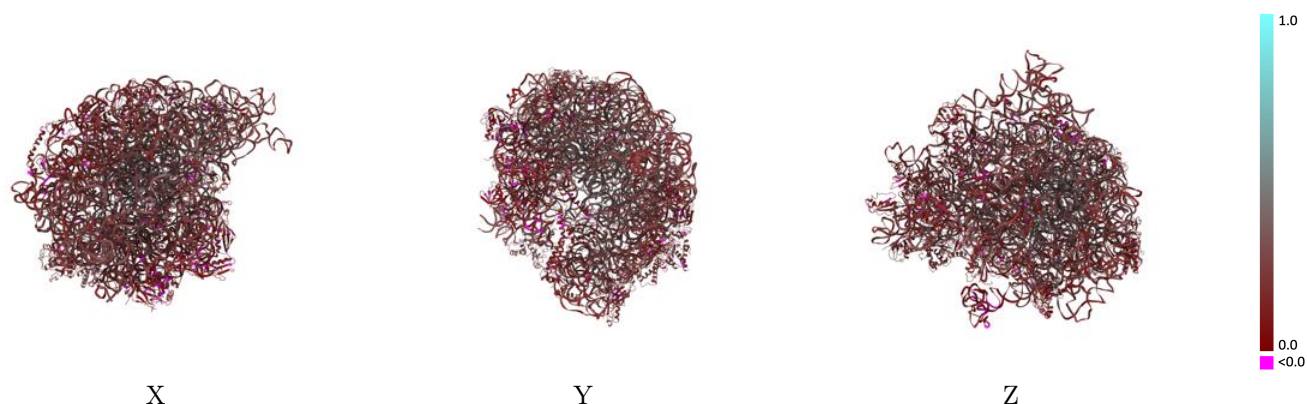
Y



Z

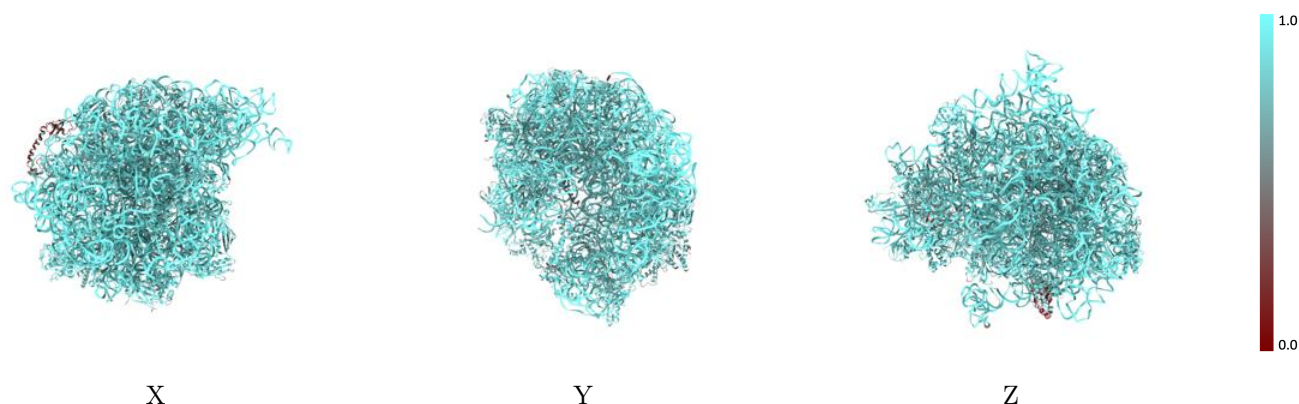
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



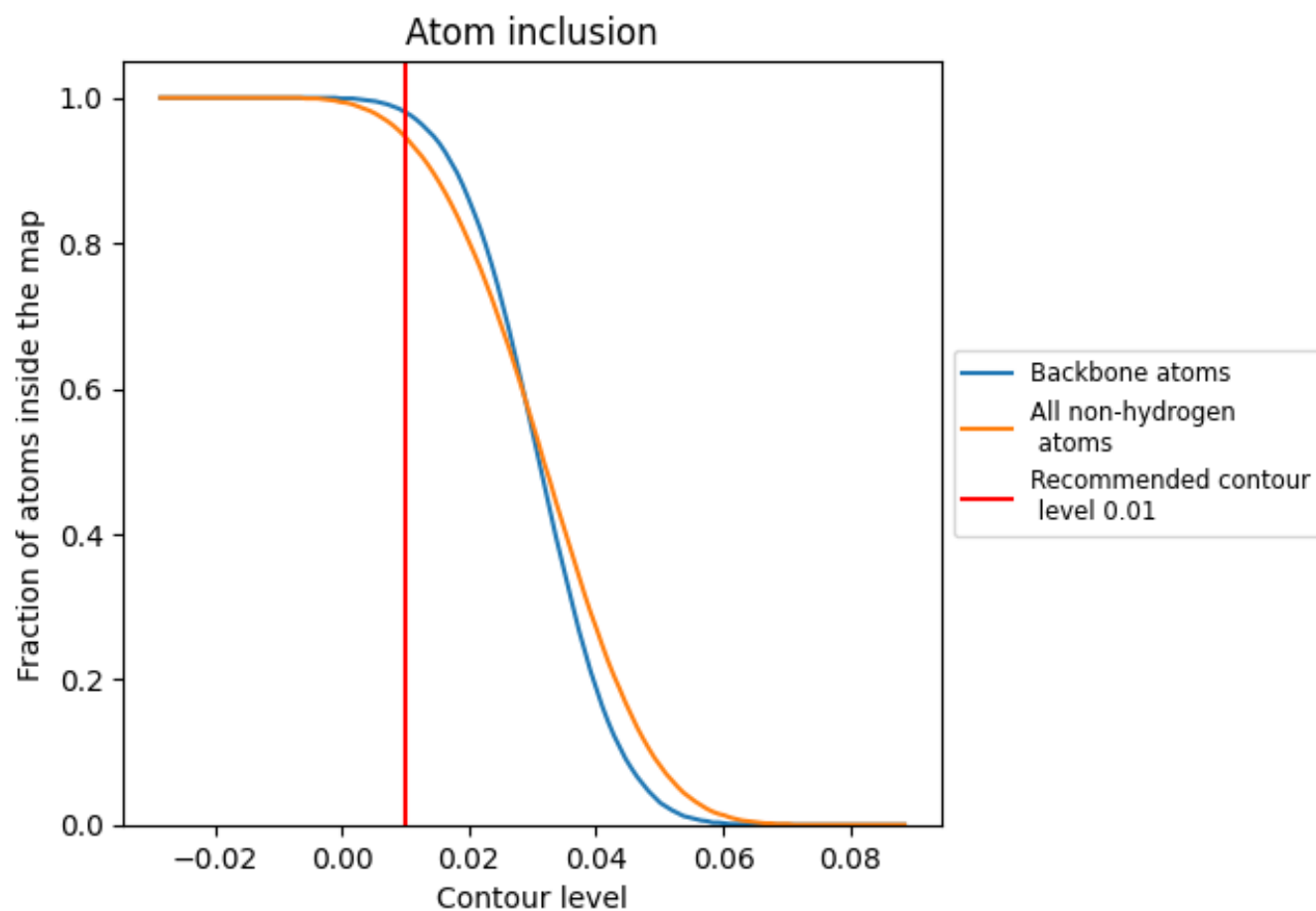
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 95% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9460	 0.2470
1	 0.9870	 0.2690
2	 0.9910	 0.2690
3	 0.9860	 0.1870
4	 0.9840	 0.3390
5	 0.9670	 0.2880
A	 0.7720	 0.1830
B	 0.8420	 0.2390
C	 0.8790	 0.2320
D	 0.8940	 0.2430
E	 0.9020	 0.1880
F	 0.8590	 0.1350
G	 0.3830	 0.1430
J	 0.8440	 0.1710
K	 0.8400	 0.2770
L	 0.9050	 0.2800
M	 0.8610	 0.1910
N	 0.9100	 0.2220
O	 0.9370	 0.1770
P	 0.8720	 0.2470
Q	 0.8700	 0.1650
R	 0.8880	 0.1620
S	 0.8760	 0.2750
T	 0.8810	 0.1940
U	 0.9140	 0.1960
V	 0.8580	 0.1450
W	 0.8710	 0.2180
X	 0.8340	 0.2310
Y	 0.8670	 0.1680
Z	 0.8370	 0.1800
a	 0.8610	 0.2030
b	 0.8850	 0.2450
c	 0.9380	 0.2860
d	 0.9130	 0.2800
e	 0.8820	 0.2890



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
f	 0.8500	 0.1160
g	 0.7430	 0.1740
h	 0.8810	 0.2050
i	 0.8940	 0.2100
j	 0.8750	 0.2260
k	 0.8590	 0.1670
l	 0.9160	 0.2370
m	 0.8720	 0.1770
n	 0.9240	 0.1990
o	 0.8780	 0.1870
p	 0.8890	 0.2240
q	 0.8650	 0.2650
r	 0.9050	 0.1950
s	 0.9070	 0.1920
t	 0.8570	 0.1270
u	 0.8840	 0.2020
v	 0.8830	 0.2110
w	 0.8390	 0.1670
x	 0.8900	 0.1540
y	 0.9170	 0.2160
z	 0.7530	 0.1820