



Full wwPDB EM Validation Report ⓘ

Jun 25, 2026 – 04:46 PM EDT

PDB ID : 6OT3 / pdb_00006ot3
EMDB ID : EMD-20193
Title : RF2 accommodated state bound Release complex 70S at 24 ms
Authors : Fu, Z.; Indrisiunaite, G.; Kaledhonkar, S.; Shah, B.; Sun, M.; Chen, B.; Grassucci, R.A.; Ehrenberg, M.; Frank, J.
Deposited on : 2019-05-02
Resolution : 3.90 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:

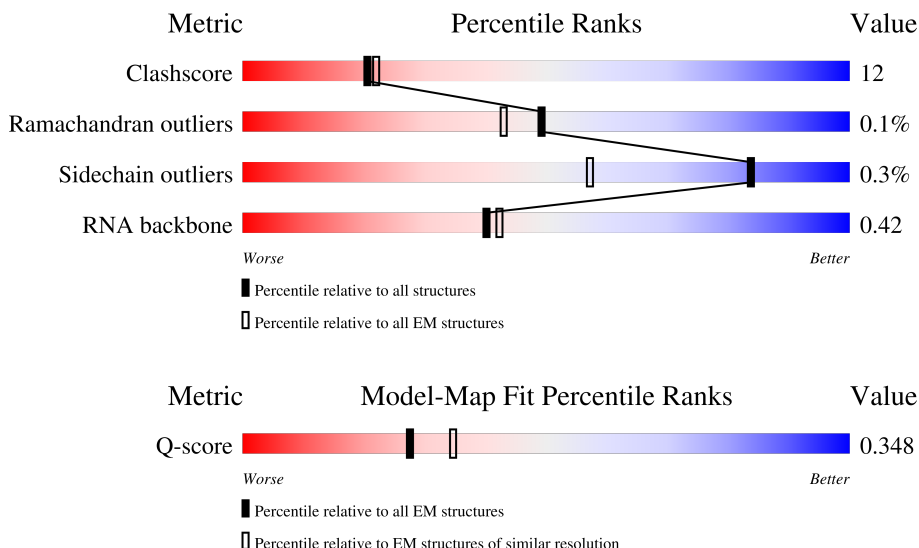
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
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 3.90 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.



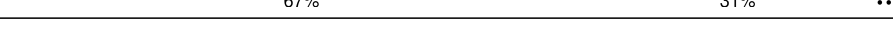
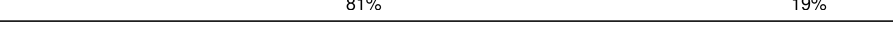
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	8855 (3.40 - 4.40)

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	

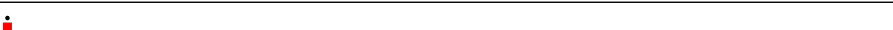
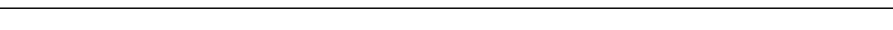
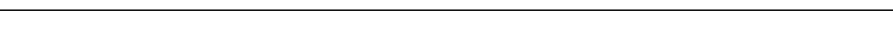
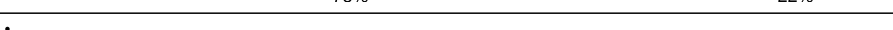
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Mol	Chain	Length	Quality of chain
4	4	9	 78%11%11%
5	B	271	 75%25%
6	C	209	 75%24%
7	D	201	 78%22%
8	E	177	 74%26%
9	F	175	 79%21%
10	G	149	 70%30%
11	J	142	 89%11%
12	K	123	 78%22%
13	L	144	 83%17%
14	M	136	 82%18%
15	N	119	 65%34%
16	O	116	 77%23%
17	P	114	 76%24%
18	Q	117	 76%24%
19	R	103	 67%31%..
20	S	110	 81%19%
21	T	94	 78%22%
22	U	103	 75%25%
23	V	94	 73%27%
24	W	76	 74%26%
25	X	77	 71%29%
26	Y	62	 77%23%
27	Z	58	 72%28%
28	a	66	 73%27%

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Mol	Chain	Length	Quality of chain
29	b	56	 70%30%
30	c	52	 73%27%
31	d	46	 74%26%
32	e	64	 88%9%
33	f	38	 82%18%
34	g	225	 79%20%
35	h	208	 74%26%
36	i	205	 76%24%
37	j	156	 76%24%
38	k	104	 66%34%
39	l	151	 74%26%
40	m	129	 81%19%
41	n	127	 76%24%
42	o	99	 78%22%
43	p	117	 82%18%
44	q	87	 82%18%
45	r	116	 80%20%
46	s	100	 78%22%
47	t	88	 57%33%8%
48	u	82	 68%32%
49	v	80	 79%21%
50	w	66	 77%23%
51	x	83	 70%30%
52	y	86	 91%9%
53	z	70	 91%9%

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Mol	Chain	Length	Quality of chain
54	5	76	49% 38% 9%
55	A	357	69% 31%
56	6	3	67% 33%

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 146899 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 a protein called FME-PHE-PHE.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	6	3	Total	C	N	O	S	0	0
			32	24	3	4	1		

- Molecule 57 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
57	1	2	Total	Mg	0
			2	2	
57	2	1	Total	Mg	0
			1	1	
57	3	8	Total	Mg	0
			8	8	
57	i	1	Total	Mg	0
			1	1	

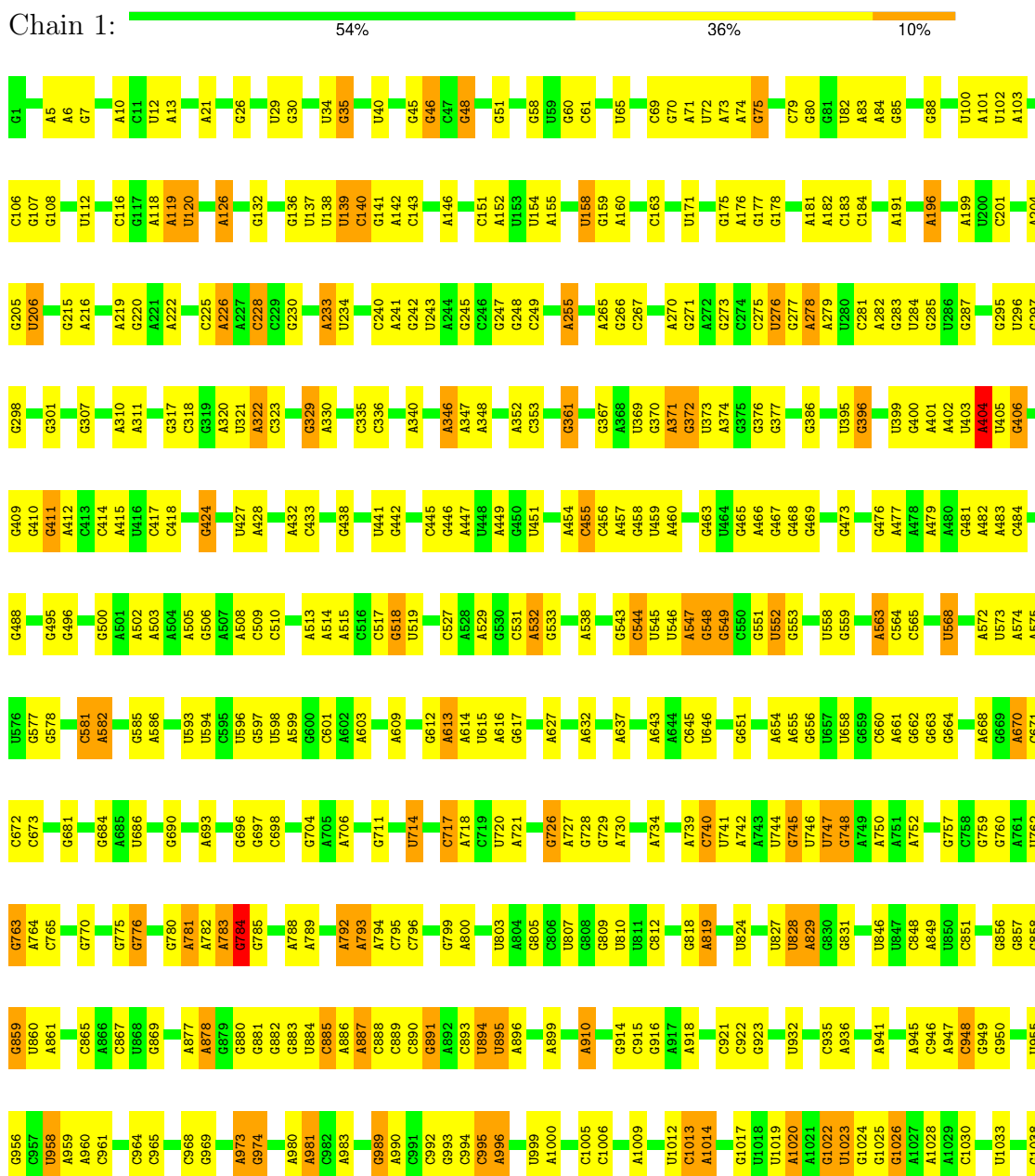
- Molecule 58 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

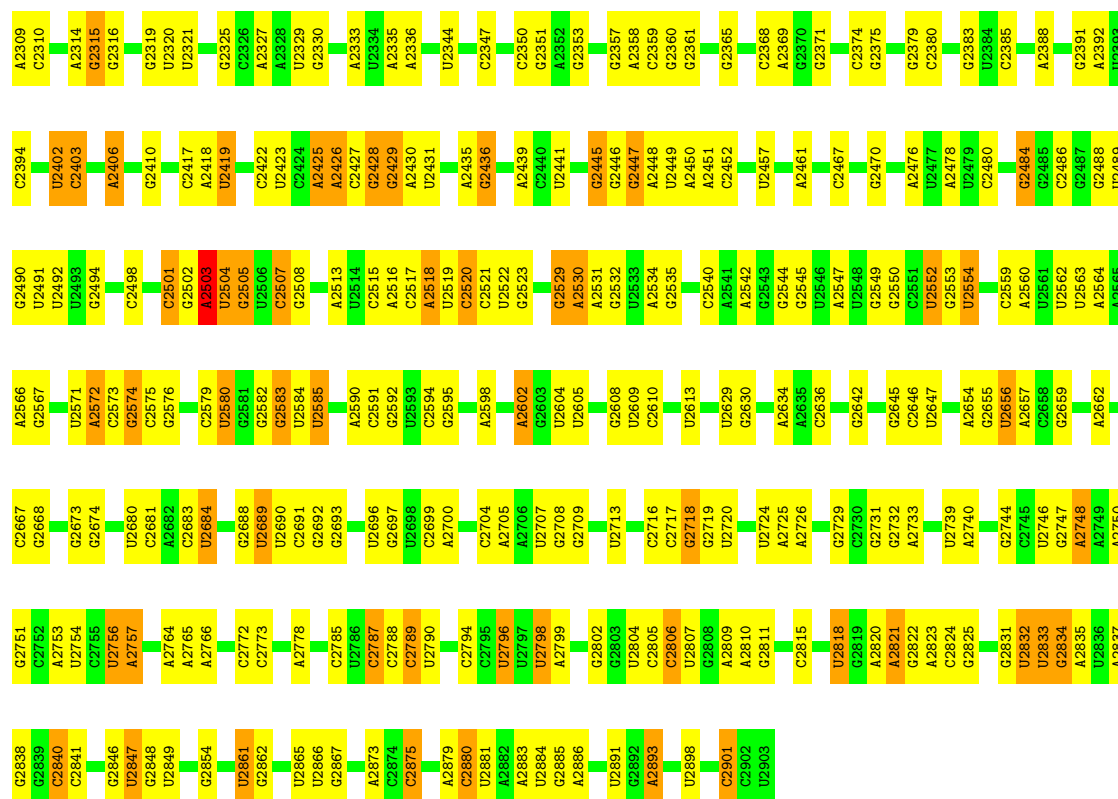
3 Residue-property plots

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.

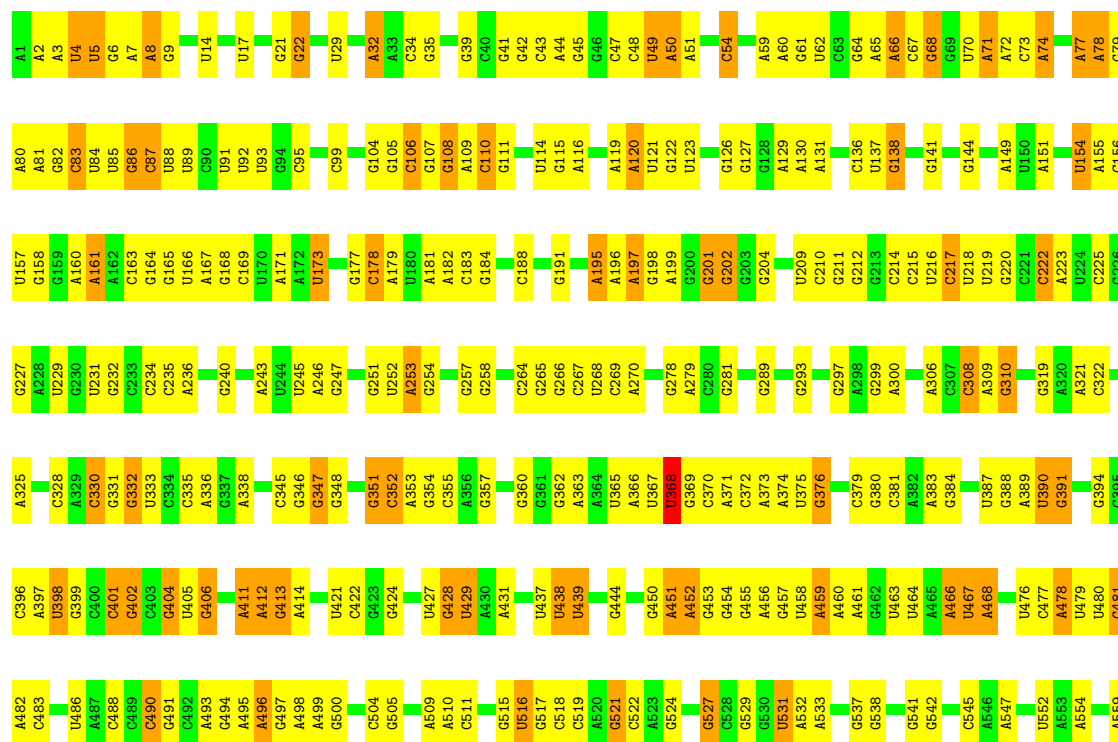
• Molecule 1: 23S ribosomal RNA

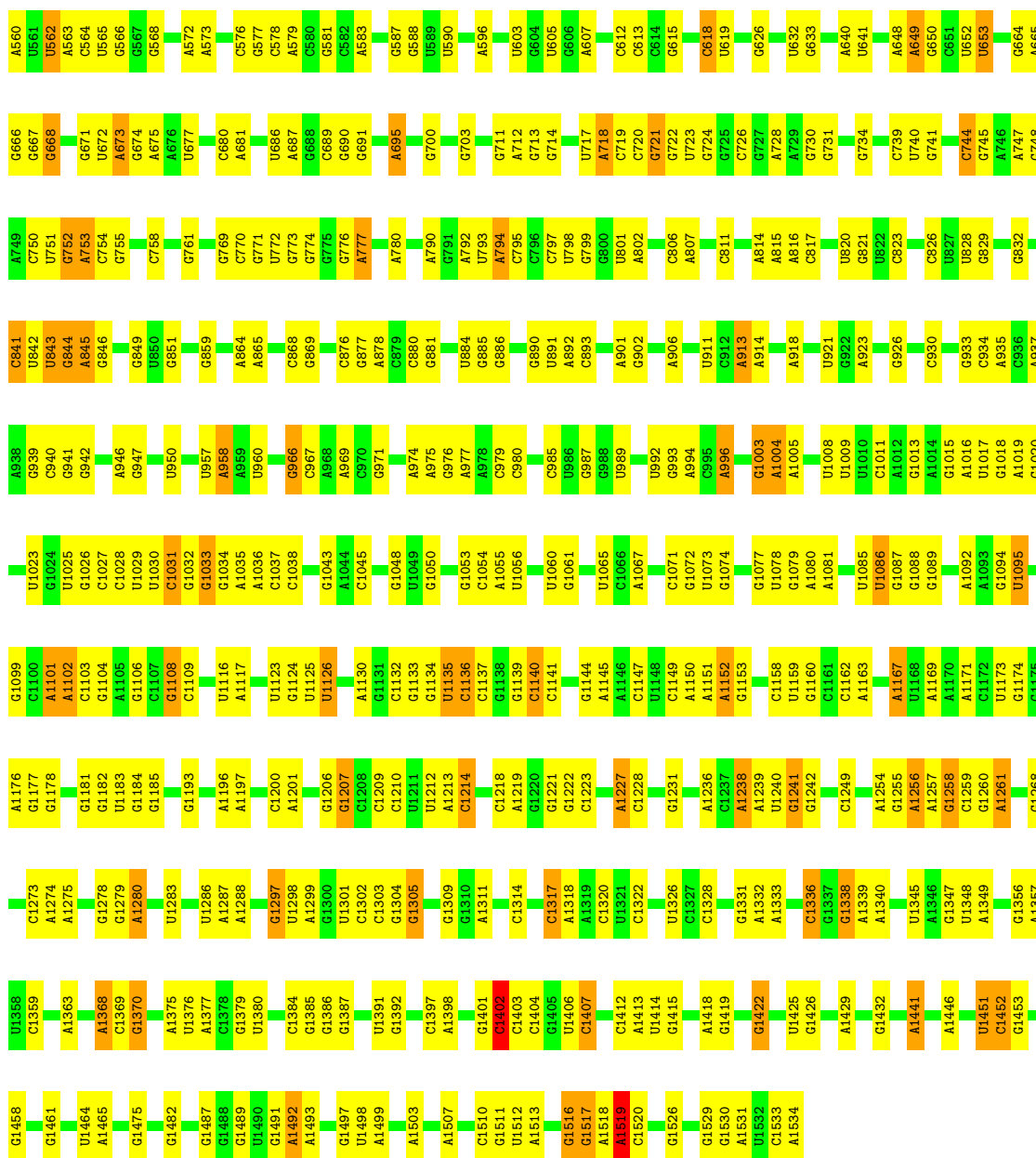


A2212	G2136	G2056	G1972	G1884	G1799	A1700	A1593	A1496	G1408	G1311	G1212	G1116	A1039
U2213	U2137	G2057	G1980	G1888	C1800	A1701	A1593	U1497	U1409	U1312	G1217	G1119	A1040
C2214	U2138	A2060	G1981	A1889	A1801	U1712	U1602	C1498	U1410	G1324	G1218	U1119	G1041
G2215	U2139	G2061	U1982	A1888	A1802	U1713	U1602	G1501	U1412	U1325	G1219	G1123	G1043
G2216	G2140	A2062	A1987	A1899	G1807	U1714	C1607	A1502	A1413	U1326	U1222	G1124	C1044
G2217	G2141	C2063	G1988	A1900	A1808	G1715	A1608	A1503	C1414	U1329	G1223	G1125	C1045
G2223	A2142	C2064	A1987	A1901	A1809	U1716	A1609	A1504	U1415	U1329	G1227	A1127	A1046
G2224	C2145	G2069	U1991	G1903	C1816	G1721	A1610	U1416	U1416	G1332	G1227	G1128	G1047
A2225	A2146	U2081	G1992	G1906	G1817	A1722	C1612	A1508	C1417	G1332	U1231	G1129	G1056
C2226	A2147	A2082	U1993	U1911	G1817	G1723	G1613	A1509	A1418	G1338	G1232	U1130	U1057
G2228	C2153	G2095	U1995	U1912	U1818	G1724	A1614	G1514	A1419	G1339	G1236	G1131	U1058
U2229	G2166	G2086	C1996	A1913	U1819	U1725	C1615	A1515	G1421	U1340	G1237	U1132	G1059
U2233	G2167	G2087	C1997	A1914	U1820	U1729	C1617	A1522	G1425	G1339	U1231	U1133	U1060
G2234	A2158	A2088	A1998	C1914	U1821	G1730	A1618	A1523	A1426	U1342	G1238	A1134	U1061
G2237	G2159	G2093	G2002	A1916	G1822	G1731	G1619	G1524	A1427	G1345	U1247	G1136	G1063
G2238	C2160	A2094	U2002	U1917	U1824	G1732	A1626	A1525	C1428	C1345	G1248	G1137	C1064
G2239	C2161	A2095	C2006	U1919	U1826	G1733	A1631	A1528	C1437	C1351	U1249	G1138	U1065
A2240	A2163	C2096	G2010	A1919	U1827	G1738	G1631	A1529	U1438	U1352	G1250	G1139	U1066
A2241	C2164	A2097	U2011	U1923	U1828	A1744	A1634	A1530	A1439	G1353	G1251	U1140	A1067
G2242	C2165	U2098	G2012	C1924	A1829	U1751	C1639	G1531	U1443	A1354	A1253	U1141	G1068
U2243	U2166	U2099	A2013	G1925	C1830	U1751	C1639	A1532	G1444	G1355	U1255	A1142	A1070
G2250	U2167	G2102	A2013	U1926	C1833	U1751	C1639	A1532	G1444	G1355	U1255	A1142	A1070
G2251	G2168	C2103	U2022	U1927	U1834	A1754	C1646	U1534	G1449	G1358	G1256	A1151	G1071
A2252	A2169	G2104	C2023	A1928	G1835	U1755	U1647	A1535	G1455	U1359	U1263	G1152	C1072
G2253	A2170	U2105	G2024	G1929	C1836	G1756	U1648	C1536	G1455	G1360	U1263	G1153	G1073
G2264	U2172	U2106	C2025	G1930	C1837	U1757	G1649	G1537	U1458	G1361	G1266	A1155	C1075
U2265	A2173	C2107	U2026	C1934	C1844	U1758	A1650	U1559	U1468	C1362	U1267	G1158	C1076
A2266	C2174	A2108	G2027	U1936	G1845	A1759	G1651	A1566	U1468	G1363	A1268	U1077	A1077
A2267	C2175	G2110	U2028	A1936	G1846	C1760	A1652	C1550	C1461	A1365	A1269	G1161	C1078
A2268	A2176	U2111	A2030	A1937	A1847	G1764	C1653	C1550	C1462	A1366	C1270	G1162	C1079
G2269	C2177	G2112	A2031	A1938	A1848	U1765	U1657	U1559	G1464	A1367	G1271	G1168	U1082
A2270	C2178	U2113	G2032	U1939	G1849	U1765	C1658	G1560	G1465	G1368	U1272	A1169	A1084
G2271	U2181	A2114	A2033	U1940	G1850	U1773	G1659	A1566	U1466	U1372	A1275	C1170	A1085
U2272	U2182	G2115	U2034	C1941	A1854	U1775	G1667	G1567	U1468	A1378	G1278	G1171	A1086
A2273	A2183	G2116	G2035	U1942	G1854	U1776	G1667	G1568	A1469	U1379	C1278	G1172	G1087
G2277	A2184	A2118	C2036	U1943	G1857	U1777	A1668	A1569	G1475	G1380	G1279	U1174	A1089
A2278	U2188	A2119	G2037	G1948	A1858	U1778	A1669	A1570	U1476	A1383	A1287	U1175	A1090
G2279	U2189	G2120	U2039	G1954	U1859	U1779	C1670	A1571	U1477	A1384	U1294	G1177	U1094
C2283	G2190	U2122	G2040	U1955	G1860	U1780	U1671	A1572	G1478	C1385	U1294	G1178	A1095
G2286	G2193	G2123	C2043	U1956	G1862	U1781	U1671	A1572	G1479	C1386	G1296	G1179	A1096
A2287	U2194	G2124	C2044	A1960	G1863	A1784	G1674	A1579	G1482	A1387	G1296	G1182	U1097
G2291	A2198	A2126	C2045	C1961	U1864	A1785	G1682	A1580	G1483	G1388	C1297	U1101	U1101
U2292	A2199	G2127	G2046	C1962	U1865	A1786	G1682	A1581	U1484	G1388	G1300	G1186	C1102
G2293	C2200	G2128	U2047	U1963	G1869	U1787	U1688	A1582	U1484	A1394	G1300	G1187	A1103
U2296	G2204	C2129	G2049	U1963	G1870	A1788	C1691	A1583	C1489	A1395	A1302	U1188	G1110
U2305	G2208	U2130	C2050	A1966	A1871	G1790	U1692	C1586	U1490	U1397	C1305	A1189	G1112
G2308	U2305	U2132	A2052	G1967	A1872	A1791	U1693	A1586	G1491	U1398	G1306	G1190	A1111
	G2209	G2133	G2053	A1969	G1873	U1796	G1694	G1587	G1492	C1399	A1307	G1206	U1113
	U2210	A2134	A2054	A1970	G1878	U1797	G1695	U1588	C1493	A1403	G1310	G1211	C1114
	A2211	A2135	C2055	U1971	G1878	U1798	G1699	A1590	A1495				G1115

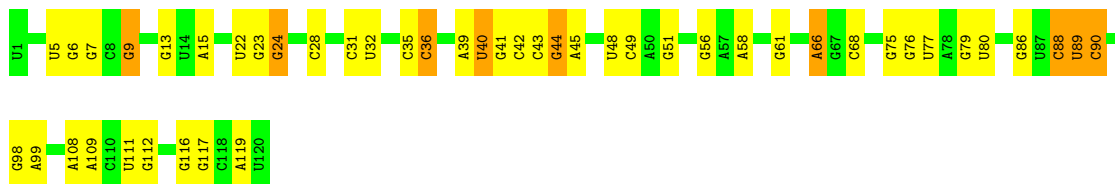


• Molecule 2: 16S ribosomal RNA





• Molecule 3: 5S ribosomal RNA



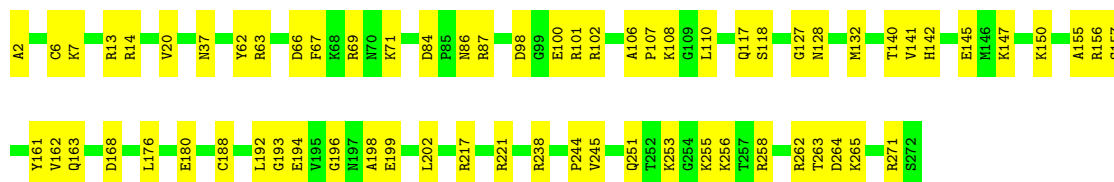
• Molecule 4: mRNA





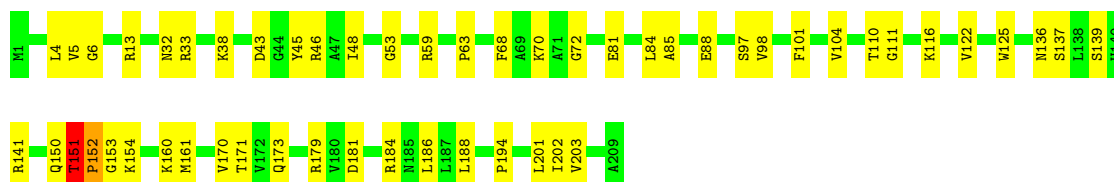
- Molecule 5: 50S ribosomal protein L2

Chain B: 75% 25%



- Molecule 6: 50S ribosomal protein L3

Chain C: 75% 24%



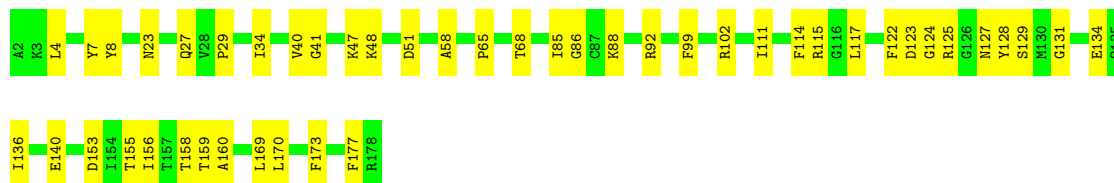
- Molecule 7: 50S ribosomal protein L4

Chain D: 78% 22%



- Molecule 8: 50S ribosomal protein L5

Chain E: 74% 26%



- Molecule 9: 50S ribosomal protein L6

Chain F: 79% 21%

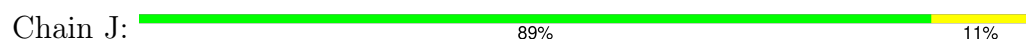




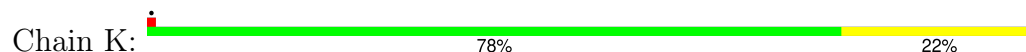
- Molecule 10: 50S ribosomal protein L9



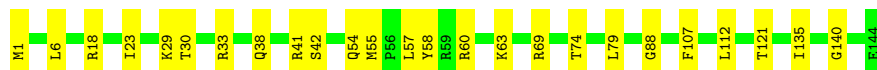
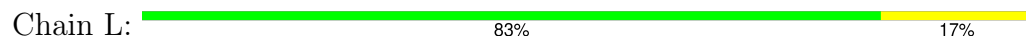
- Molecule 11: 50S ribosomal protein L13



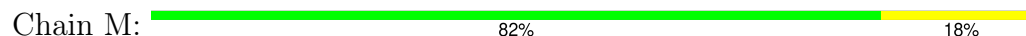
- Molecule 12: 50S ribosomal protein L14



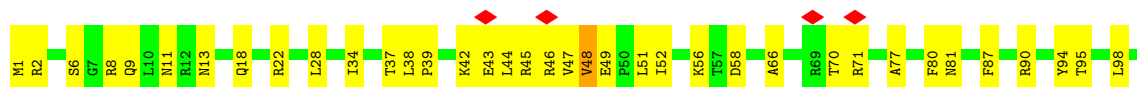
- Molecule 13: 50S ribosomal protein L15



- Molecule 14: 50S ribosomal protein L16



- Molecule 15: 50S ribosomal protein L17





- Molecule 16: 50S ribosomal protein L18

Chain O: 77% 23%



- Molecule 17: 50S ribosomal protein L19

Chain P: 76% 24%



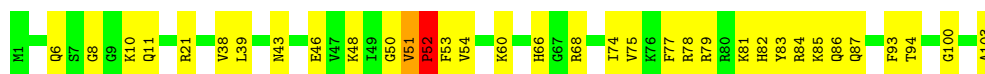
- Molecule 18: 50S ribosomal protein L20

Chain Q: 76% 24%



- Molecule 19: 50S ribosomal protein L21

Chain R: 67% 31%



- Molecule 20: 50S ribosomal protein L22

Chain S: 81% 19%



- Molecule 21: 50S ribosomal protein L23

Chain T: 78% 22%

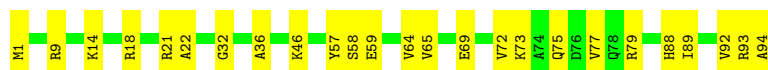


- Molecule 22: 50S ribosomal protein L24

Chain U: 75% 25%



- Molecule 23: 50S ribosomal protein L25



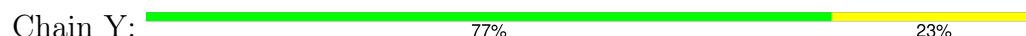
- Molecule 24: 50S ribosomal protein L27



- Molecule 25: 50S ribosomal protein L28



- Molecule 26: 50S ribosomal protein L29



- Molecule 27: 50S ribosomal protein L30



- Molecule 28: 50S ribosomal protein L31



- Molecule 29: 50S ribosomal protein L32





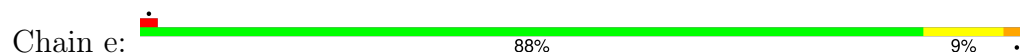
- Molecule 30: 50S ribosomal protein L33



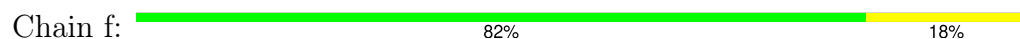
- Molecule 31: 50S ribosomal protein L34



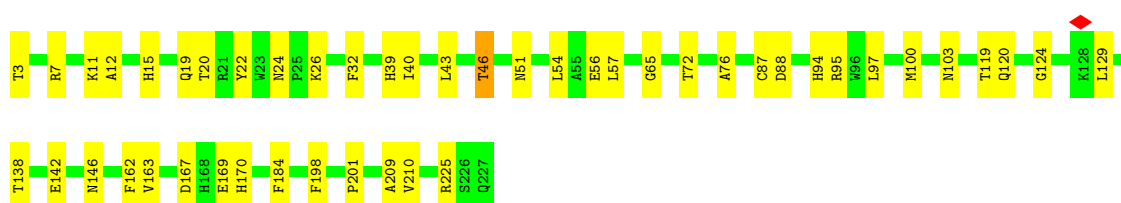
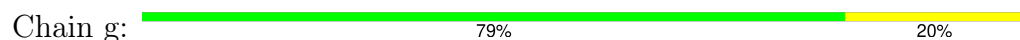
- Molecule 32: 50S ribosomal protein L35



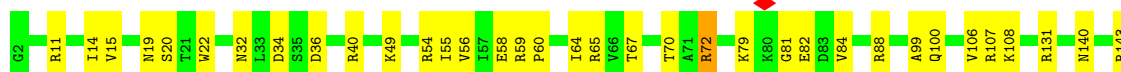
- Molecule 33: 50S ribosomal protein L36



- Molecule 34: 30S ribosomal protein S2



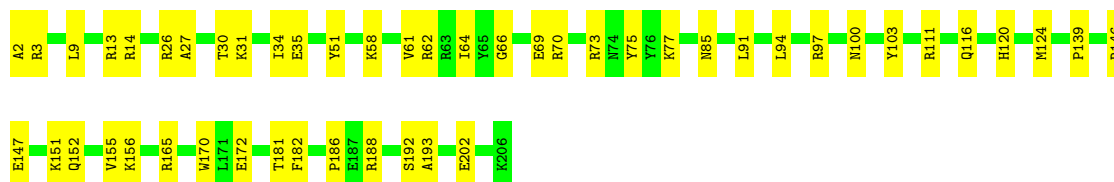
- Molecule 35: 30S ribosomal protein S3





- Molecule 36: 30S ribosomal protein S4

Chain i: 76% 24%



- Molecule 37: 30S ribosomal protein S5

Chain j: 76% 24%



- Molecule 38: 30S ribosomal protein S6

Chain k: 66% 34%



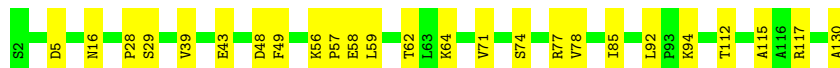
- Molecule 39: 30S ribosomal protein S7

Chain l: 74% 26%



- Molecule 40: 30S ribosomal protein S8

Chain m: 81% 19%



- Molecule 41: 30S ribosomal protein S9

Chain n:  76% 24%



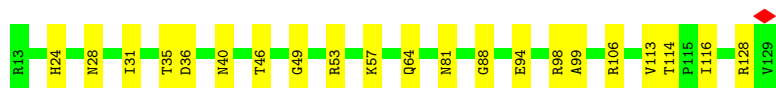
- Molecule 42: 30S ribosomal protein S10

Chain o:  78% 22%



- Molecule 43: 30S ribosomal protein S11

Chain p:  82% 18%



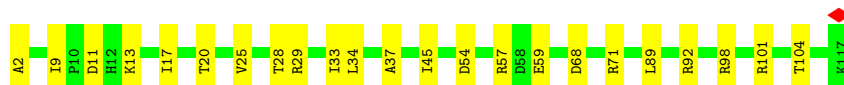
- Molecule 44: 30S ribosomal protein S12

Chain q:  82% 18%



- Molecule 45: 30S ribosomal protein S13

Chain r:  80% 20%



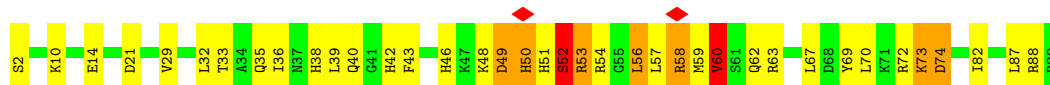
- Molecule 46: 30S ribosomal protein S14

Chain s:  78% 22%



- Molecule 47: 30S ribosomal protein S15

Chain t:  57% 33% 8%



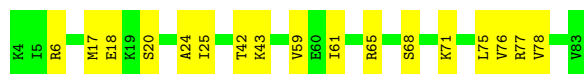
- Molecule 48: 30S ribosomal protein S16

Chain u:  68% 32%



- Molecule 49: 30S ribosomal protein S17

Chain v:  79% 21%



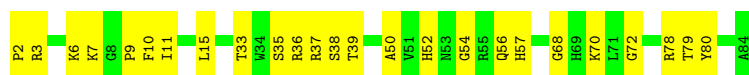
- Molecule 50: 30S ribosomal protein S18

Chain w:  77% 23%



- Molecule 51: 30S ribosomal protein S19

Chain x:  70% 30%



- Molecule 52: 30S ribosomal protein S20

Chain y:  91% 9%



- Molecule 53: 30S ribosomal protein S21

Chain z:  91% 9%

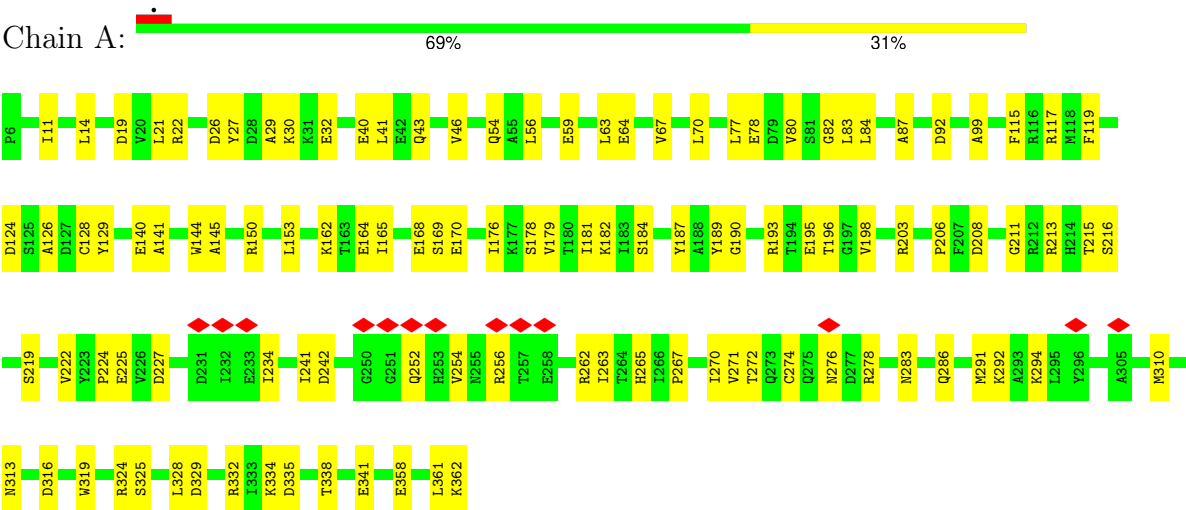


- Molecule 54: P-tRNA

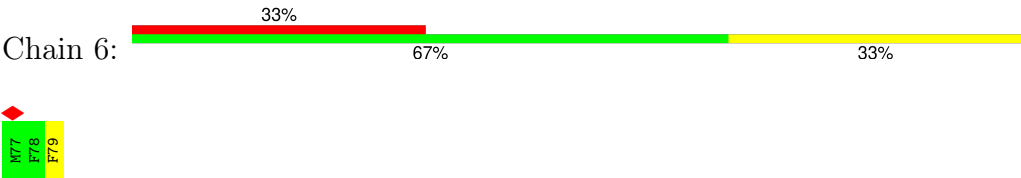
Chain 5:  49% 38% 9%



- Molecule 55: Peptide chain release factor 2



● Molecule 56: FME-PHE-PHE



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	193636	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	0.066	Depositor
Minimum map value	-0.024	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.005	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	424.96, 424.96, 424.96	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.66, 1.66, 1.66	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0.36	0/69286	0.37	4/108087 (0.0%)
2	2	0.35	0/36590	0.37	1/57074 (0.0%)
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	0.34	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	0.34	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	0.58	0/709
29	b	0.34	0/450	0.57	0/599
30	c	0.30	0/433	0.56	0/576
31	d	0.37	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	0.32	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	0.29	0/1034	0.61	0/1375
42	o	0.29	0/800	0.59	0/1082
43	p	0.31	0/893	0.53	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	0.38	0/722	0.95	4/964 (0.4%)
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	0.29	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	0.32	0/1704	0.35	0/2654
55	A	0.32	0/2873	0.65	4/3870 (0.1%)
56	6	0.43	0/23	0.44	0/29
All	All	0.35	1/158543 (0.0%)	0.45	19/236784 (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	-6.09	1.39	1.47

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
47	t	52	SER	N-CA-C	-8.02	101.31	112.45
47	t	60	VAL	N-CA-C	-7.78	103.27	110.82
47	t	58	ARG	N-CA-C	-7.00	103.64	111.28
32	e	31	HIS	O-C-N	6.44	130.59	123.25
1	1	784	G	C4'-C3'-O3'	5.80	121.70	113.00
1	1	404	A	C4'-C3'-O3'	5.79	118.09	109.40
34	g	46	THR	CA-C-N	5.79	125.99	120.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	g	46	THR	C-N-CA	5.79	125.99	120.43
1	1	784	G	C2'-C3'-O3'	-5.56	105.37	113.70
55	A	338	THR	CA-C-N	5.54	131.67	121.70
55	A	338	THR	C-N-CA	5.54	131.67	121.70
1	1	2847	U	C4'-C3'-O3'	-5.47	104.80	113.00
6	C	152	PRO	N-CA-C	-5.32	101.40	112.36
10	G	13	GLY	N-CA-C	5.27	117.55	110.43
19	R	52	PRO	N-CA-C	-5.25	101.66	112.47
47	t	56	LEU	N-CA-C	-5.04	105.87	111.36
55	A	227	ASP	CA-C-N	5.03	131.16	121.54
55	A	227	ASP	C-N-CA	5.03	131.16	121.54
2	2	368	U	C2'-C3'-O3'	-5.00	106.20	113.70

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	692	0
2	2	32929	0	16587	369	0
3	3	2569	0	1301	34	0
4	4	184	0	95	1	0
5	B	2082	0	2154	51	0
6	C	1565	0	1616	50	0
7	D	1552	0	1619	32	0
8	E	1410	0	1444	34	0
9	F	1313	0	1358	23	0
10	G	1111	0	1148	28	0
11	J	1129	0	1162	12	0
12	K	946	0	1023	20	0
13	L	1053	0	1129	21	0
14	M	1074	0	1157	17	0
15	N	951	0	994	36	0
16	O	892	0	923	21	0
17	P	917	0	962	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
18	Q	947	0	1019	22	0
19	R	816	0	839	36	0
20	S	857	0	922	18	0
21	T	746	0	811	14	0
22	U	788	0	844	19	0
23	V	753	0	780	18	0
24	W	582	0	599	13	0
25	X	625	0	652	18	0
26	Y	501	0	531	9	0
27	Z	448	0	488	9	0
28	a	522	0	520	14	0
29	b	444	0	458	14	0
30	c	426	0	464	10	0
31	d	377	0	418	8	0
32	e	504	0	572	10	0
33	f	302	0	340	6	0
34	g	1760	0	1787	27	0
35	h	1636	0	1710	34	0
36	i	1643	0	1707	37	0
37	j	1152	0	1196	27	0
38	k	848	0	846	25	0
39	l	1181	0	1238	27	0
40	m	979	0	1031	15	0
41	n	1022	0	1070	21	0
42	o	790	0	831	17	0
43	p	877	0	887	13	0
44	q	673	0	720	13	0
45	r	900	0	965	18	0
46	s	805	0	844	19	0
47	t	714	0	734	53	0
48	u	649	0	666	22	0
49	v	648	0	691	13	0
50	w	544	0	560	10	0
51	x	663	0	688	23	0
52	y	669	0	719	5	0
53	z	589	0	629	4	0
54	5	1627	0	832	22	0
55	A	2833	0	2729	76	0
56	6	32	0	28	1	0
57	1	2	0	0	0	0
57	2	1	0	0	0	0
57	3	8	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
57	i	1	0	0	0	0
58	a	1	0	0	0	0
58	f	1	0	0	0	0
All	All	146899	0	99407	1880	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 (1880) 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	1.40
19:R:51:VAL:CG1	19:R:52:PRO:HD3	1.55	1.36
1:1:402:A:C8	1:1:403:U:C6	2.18	1.30
6:C:151:THR:OG1	6:C:152:PRO:HD3	1.34	1.27
6:C:151:THR:HG23	6:C:152:PRO:CD	1.76	1.15
6:C:151:THR:CG2	6:C:152:PRO:HD2	1.81	1.10
19:R:52:PRO:HD2	19:R:53:PHE:H	1.13	1.07
1:1:402:A:N7	1:1:403:U:C6	2.25	1.02
1:1:403:U:H4'	1:1:406:G:O2'	1.61	1.00
6:C:151:THR:CG2	6:C:152:PRO:CD	2.40	0.99
1:1:402:A:C8	1:1:403:U:C5	2.51	0.98
19:R:52:PRO:CD	19:R:53:PHE:H	1.76	0.95
6:C:151:THR:OG1	6:C:152:PRO:CD	2.14	0.95
2:2:4:U:H3'	2:2:5:U:H5''	1.49	0.94
6:C:151:THR:HG23	6:C:152:PRO:HD2	0.93	0.93
47:t:57:LEU:HA	47:t:60:VAL:HB	1.49	0.93
6:C:151:THR:CB	6:C:152:PRO:CD	2.48	0.91
1:1:2875:C:HO2'	17:P:2:SER:N	1.70	0.88
1:1:139:U:H5'	1:1:140:C:O5'	1.73	0.88
1:1:2061:G:OP1	1:1:2503:2MA:CM2	2.21	0.88
2:2:357:G:H4'	2:2:368:U:H5''	1.55	0.87
1:1:402:A:H2'	1:1:403:U:O4'	1.74	0.87
1:1:402:A:N7	1:1:403:U:C5	2.44	0.84
6:C:151:THR:CB	6:C:152:PRO:HD3	2.06	0.84
1:1:402:A:C2	1:1:403:U:H1'	2.13	0.84
1:1:1065:U:O2'	1:1:1066:U:O4'	1.94	0.83
1:1:578:G:H21	1:1:1252:G:H22	1.25	0.83
47:t:56:LEU:O	47:t:60:VAL:HG23	1.79	0.83
1:1:402:A:C5	1:1:403:U:N1	2.47	0.82
19:R:52:PRO:HD2	19:R:53:PHE:N	1.94	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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
1:1:402:A:C4	1:1:403:U:C1'	2.65	0.80
8:E:122:PHE:O	8:E:123:ASP:OD1	2.00	0.79
8:E:123:ASP:OD2	8:E:127:ASN:HB2	1.83	0.79
47:t:70:LEU:HA	47:t:73:LYS:HB2	1.64	0.78
19:R:52:PRO:CD	19:R:53:PHE:N	2.41	0.78
2:2:467:U:H3'	2:2:467:U:OP2	1.84	0.78
1:1:403:U:C4'	1:1:406:G:O2'	2.32	0.78
1:1:402:A:C5	1:1:403:U:C6	2.72	0.78
15:N:48:VAL:HA	15:N:51:LEU:HB2	1.67	0.77
2:2:136:C:H42	2:2:227:G:H1	1.31	0.77
19:R:51:VAL:HG13	19:R:52:PRO:HD3	0.78	0.77
1:1:402:A:C4	1:1:403:U:H1'	2.21	0.76
1:1:729:G:N3	1:1:729:G:H2'	1.99	0.76
2:2:667:G:H4'	47:t:51:HIS:HB2	1.68	0.75
47:t:53:ARG:O	47:t:57:LEU:HG	1.86	0.75
1:1:881:G:H1	1:1:895:U:H3	1.33	0.75
47:t:73:LYS:O	47:t:74:ASP:HB2	1.86	0.74
22:U:46:GLN:HB3	22:U:57:GLY:H	1.52	0.74
2:2:158:G:H1	2:2:163:C:H42	1.34	0.74
2:2:590:U:H3	2:2:649:A:H61	1.33	0.74
1:1:2402:U:O2'	1:1:2403:C:H5''	1.87	0.74
47:t:56:LEU:O	47:t:60:VAL:N	2.22	0.72
15:N:8:ARG:HD2	15:N:43:GLU:HB2	1.72	0.72
38:k:35:LYS:HB2	38:k:65:GLU:HB3	1.72	0.72
2:2:958:A:N3	2:2:985:C:O2'	2.22	0.71
34:g:87:CYS:O	34:g:88:ASP:OD1	2.07	0.71
47:t:57:LEU:CA	47:t:60:VAL:HB	2.21	0.71
1:1:228:C:N3	1:1:417:C:O2'	2.22	0.71
27:Z:31:ARG:HD2	27:Z:34:HIS:HB2	1.72	0.71
1:1:402:A:C6	1:1:403:U:H1'	2.26	0.71
1:1:2171:A:H5'	1:1:2174:C:H41	1.55	0.70
1:1:748:G:OP1	20:S:88:ARG:NE	2.25	0.70
1:1:2756:U:OP2	33:f:19:ARG:HG2	1.92	0.70
2:2:376:G:H1	2:2:387:U:H3	1.38	0.70
1:1:402:A:C8	1:1:403:U:H6	2.02	0.70
47:t:58:ARG:O	47:t:62:GLN:HB2	1.91	0.70
1:1:245:G:N7	32:e:8:ARG:NH2	2.40	0.69
1:1:369:U:O2'	1:1:404:A:N6	2.25	0.69
1:1:2709:G:OP1	15:N:18:GLN:NE2	2.25	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:667:G:O2'	47:t:52:SER:N	2.26	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
55:A:26:ASP:HB3	55:A:29:ALA:HB3	1.75	0.69
1:1:2358:A:H61	13:L:54:GLN:HE22	1.40	0.68
2:2:450:G:H1	2:2:483:C:H42	1.41	0.68
1:1:465:G:H5''	31:d:44:VAL:HG21	1.76	0.68
7:D:150:THR:HG22	7:D:152:GLU:H	1.57	0.68
2:2:452:A:N3	48:u:70:ARG:NH1	2.42	0.68
54:5:8:4SU:HN3	54:5:23:C:H41	1.40	0.68
35:h:58:GLU:HG2	35:h:60:PRO:HD3	1.75	0.68
24:W:50:ASN:HB2	24:W:82:ILE:HB	1.74	0.68
48:u:12:LYS:HG2	48:u:13:LYS:HG2	1.76	0.68
47:t:57:LEU:HA	47:t:60:VAL:CB	2.24	0.68
19:R:51:VAL:HG13	19:R:52:PRO:HD2	1.66	0.68
1:1:1915:3TD:H3'	1:1:1916:A:H8	1.58	0.67
9:F:155:GLU:HG2	9:F:157:TYR:H	1.60	0.67
1:1:402:A:C5	1:1:403:U:H1'	2.29	0.67
47:t:58:ARG:O	47:t:62:GLN:CB	2.42	0.67
1:1:402:A:C5	1:1:403:U:C1'	2.77	0.67
1:1:538:A:H5''	11:J:7:LYS:HE2	1.76	0.67
1:1:729:G:H2'	1:1:1775:U:H1'	1.75	0.67
2:2:668:G:OP1	47:t:50:HIS:CD2	2.49	0.66
1:1:1124:G:N3	33:f:37:GLN:NE2	2.44	0.66
1:1:468:G:N7	31:d:39:ARG:NH2	2.43	0.65
2:2:668:G:H1'	47:t:49:ASP:OD1	1.95	0.65
38:k:29:ILE:HG22	38:k:34:GLY:HA3	1.78	0.65
1:1:2880:C:O2'	15:N:90:ARG:NH2	2.30	0.65
2:2:201:G:H1	2:2:216:U:H3	1.44	0.65
2:2:451:A:H61	2:2:481:G:H5'	1.60	0.65
2:2:891:U:H2'	2:2:892:A:H8	1.60	0.65
12:K:78:ARG:HB2	17:P:71:GLU:HB2	1.77	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
1:1:2692:G:H1'	1:1:2847:U:H1'	1.79	0.65
2:2:107:G:OP1	2:2:325:A:N6	2.30	0.65
1:1:783:A:H2'	1:1:783:A:N3	2.11	0.65
35:h:156:ARG:HD3	35:h:193:TYR:HB3	1.78	0.65
25:X:33:LEU:HD23	25:X:50:ARG:HG2	1.79	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2881:U:H5'	15:N:90:ARG:HH22	1.63	0.64
3:3:43:C:O2	8:E:92:ARG:NH2	2.30	0.64
2:2:668:G:OP1	47:t:50:HIS:HD2	1.81	0.64
2:2:1328:C:O2'	45:r:29:ARG:NH1	2.30	0.64
39:l:115:SER:H	39:l:118:LEU:HD12	1.61	0.64
2:2:4:U:C3'	2:2:5:U:H5''	2.26	0.63
19:R:74:ILE:HB	19:R:87:GLN:HB3	1.80	0.63
2:2:49:U:H3	2:2:362:G:H1'	1.62	0.63
36:i:172:GLU:HB3	36:i:181:THR:HB	1.80	0.63
2:2:376:G:H4'	48:u:5:ARG:HD3	1.80	0.63
2:2:1081:A:N7	37:j:52:LYS:NZ	2.46	0.63
1:1:1817:G:H3'	5:B:156:ARG:HH21	1.62	0.63
5:B:258:ARG:NH2	5:B:263:THR:OG1	2.32	0.63
47:t:58:ARG:O	47:t:62:GLN:N	2.30	0.63
16:O:29:HIS:HB3	16:O:36:TYR:HB2	1.79	0.63
33:f:16:ILE:HG12	33:f:25:VAL:HG22	1.81	0.63
2:2:1106:G:H5''	35:h:172:ARG:HB3	1.81	0.63
10:G:76:GLU:HG3	10:G:142:VAL:HA	1.81	0.63
41:n:6:TYR:HB2	41:n:21:ILE:HB	1.80	0.63
2:2:380:G:N2	2:2:383:A:OP2	2.32	0.62
29:b:9:THR:HG22	29:b:11:SER:H	1.64	0.62
47:t:36:ILE:HA	47:t:39:LEU:HB2	1.80	0.62
1:1:2029:G:N1	1:1:2033:A:OP2	2.30	0.62
2:2:979:C:O2	46:s:59:ARG:NH1	2.32	0.62
27:Z:9:GLN:HB2	27:Z:29:LEU:HD13	1.81	0.62
55:A:141:ALA:HA	55:A:144:TRP:HB3	1.80	0.62
1:1:1652:A:OP1	15:N:8:ARG:NH2	2.31	0.62
1:1:2425:A:H5''	1:1:2427:C:O4'	2.00	0.62
1:1:2200:C:H42	1:1:2223:G:H1	1.48	0.62
1:1:2788:C:O2'	1:1:2809:A:N3	2.33	0.62
13:L:74:THR:HG22	13:L:107:PHE:HB2	1.81	0.62
1:1:860:U:H2'	1:1:861:A:H8	1.65	0.62
20:S:7:HIS:HB3	20:S:103:ILE:HB	1.81	0.62
55:A:21:LEU:HD23	55:A:70:LEU:HD21	1.82	0.62
1:1:1754:A:O2'	17:P:103:ARG:NH2	2.32	0.62
1:1:698:C:O2'	1:1:734:A:N6	2.33	0.62
2:2:563:A:OP1	44:q:14:ARG:NH1	2.33	0.62
35:h:14:ILE:HG22	35:h:15:VAL:HG13	1.80	0.62
1:1:2134:A:N6	1:1:2157:G:O2'	2.32	0.62
6:C:151:THR:CG2	6:C:152:PRO:HD3	2.23	0.61
12:K:1:MET:SD	12:K:67:LYS:NZ	2.73	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:R:52:PRO:O	19:R:53:PHE:CG	2.52	0.61
22:U:86:ARG:NH2	22:U:102:THR:OG1	2.33	0.61
35:h:49:LYS:O	35:h:72:ARG:NH1	2.33	0.61
41:n:106:ARG:NH1	41:n:107:ASP:O	2.33	0.61
15:N:103:ARG:NH2	15:N:106:ASP:OD2	2.33	0.61
18:Q:44:GLN:HE21	19:R:77:PHE:HB3	1.65	0.61
19:R:51:VAL:CG1	19:R:52:PRO:CD	2.38	0.61
28:a:11:GLU:HA	28:a:25:ARG:HA	1.82	0.61
28:a:16:CYS:SG	28:a:17:SER:N	2.74	0.61
38:k:99:ALA:HB1	38:k:103:VAL:HG21	1.81	0.61
1:1:2117:A:N1	1:1:2165:C:N4	2.47	0.61
2:2:890:G:O2'	2:2:906:A:N6	2.34	0.61
16:O:32:PRO:HA	16:O:102:ARG:HH22	1.64	0.61
1:1:2579:C:O2'	6:C:136:ASN:ND2	2.32	0.61
2:2:1013:G:N2	2:2:1016:A:OP2	2.32	0.61
10:G:47:PHE:HA	10:G:51:ARG:HB2	1.82	0.61
43:p:113:VAL:HG12	50:w:73:ARG:HD2	1.81	0.61
2:2:59:A:H3'	2:2:331:G:H22	1.65	0.61
3:3:90:C:H5'	14:M:18:ARG:HB3	1.81	0.61
8:E:48:LYS:HA	8:E:51:ASP:HB3	1.83	0.61
1:1:65:U:O2'	1:1:456:C:N3	2.32	0.61
1:1:1263:U:OP1	29:b:13:ARG:NH1	2.34	0.61
38:k:1:MET:N	38:k:1:MET:SD	2.73	0.61
1:1:2010:G:H5''	20:S:42:LYS:HB2	1.81	0.61
9:F:98:VAL:HG22	9:F:103:ILE:HG12	1.82	0.61
22:U:52:LEU:HD23	22:U:52:LEU:O	2.01	0.61
2:2:4:U:H3'	2:2:5:U:C5'	2.27	0.60
6:C:111:GLY:HA2	6:C:201:LEU:HD22	1.83	0.60
38:k:2:ARG:HB3	38:k:91:ARG:HH12	1.66	0.60
1:1:885:C:H2'	1:1:886:A:H8	1.66	0.60
1:1:1305:C:N4	1:1:1607:C:OP1	2.34	0.60
2:2:2:A:N3	2:2:613:C:O2'	2.34	0.60
2:2:1031:C:O5'	2:2:1032:G:N2	2.34	0.60
18:Q:58:ARG:HE	18:Q:62:ILE:HD11	1.66	0.60
1:1:119:A:H4'	1:1:120:U:H5'	1.84	0.60
2:2:1033:G:H2'	2:2:1034:G:H8	1.66	0.60
35:h:11:ARG:NH2	35:h:177:THR:O	2.32	0.60
1:1:2188:U:H3'	1:1:2189:U:H5''	1.82	0.60
18:Q:76:TYR:OH	18:Q:92:ARG:NH1	2.34	0.60
25:X:17:ASN:OD1	25:X:27:ARG:NH1	2.35	0.60
1:1:402:A:N9	1:1:403:U:C6	2.67	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2279:G:N7	24:W:14:ARG:NH2	2.50	0.60
23:V:77:VAL:HG23	23:V:89:ILE:HG12	1.83	0.60
38:k:38:ARG:NH1	38:k:98:GLU:O	2.33	0.60
2:2:346:G:OP1	17:P:39:ARG:NH2	2.32	0.60
30:c:37:LYS:HA	30:c:48:ILE:HA	1.83	0.60
33:f:25:VAL:HB	33:f:35:GLN:HB2	1.83	0.60
1:1:819:A:OP2	1:1:1187:G:N2	2.34	0.60
1:1:1428:C:N4	1:1:1570:A:OP2	2.33	0.60
1:1:2061:G:N7	1:1:2501:C:O2'	2.35	0.60
6:C:179:ARG:HB3	6:C:188:LEU:HD12	1.84	0.60
1:1:2772:C:H5'	6:C:173:GLN:HE21	1.67	0.60
3:3:9:G:OP2	16:O:15:ARG:NH1	2.35	0.60
10:G:86:ASP:OD2	38:k:24:ARG:NH1	2.35	0.60
13:L:55:MET:O	13:L:60:ARG:NH2	2.35	0.60
1:1:340:A:O2'	7:D:162:ARG:NH1	2.35	0.59
3:3:36:C:N4	3:3:49:C:O2	2.35	0.59
23:V:36:ALA:O	23:V:93:ARG:NH2	2.35	0.59
2:2:933:G:O6	39:l:3:ARG:NH2	2.33	0.59
13:L:58:TYR:O	32:e:13:ARG:NH2	2.35	0.59
1:1:796:C:OP1	7:D:57:LYS:NZ	2.34	0.59
2:2:1071:C:OP1	37:j:54:ARG:NH2	2.35	0.59
38:k:6:ILE:HG12	38:k:89:VAL:HG22	1.84	0.59
55:A:140:GLU:OE2	55:A:203:ARG:NH2	2.36	0.59
1:1:226:A:N1	1:1:418:C:O2'	2.35	0.59
30:c:17:THR:HG22	30:c:19:HIS:H	1.67	0.59
1:1:1715:G:N2	1:1:1744:A:OP2	2.34	0.59
2:2:1368:A:OP1	42:o:64:GLN:NE2	2.35	0.59
2:2:1377:A:OP1	39:l:92:ARG:NH1	2.36	0.59
49:v:24:ALA:HA	49:v:43:LYS:HA	1.83	0.59
1:1:1693:U:O2	5:B:14:ARG:NH1	2.35	0.59
2:2:626:G:O3'	48:u:51:ARG:NH1	2.36	0.59
2:2:246:A:N1	2:2:278:G:O2'	2.35	0.59
2:2:1073:U:O2	34:g:103:ASN:ND2	2.35	0.59
9:F:35:ARG:NH1	9:F:75:MET:SD	2.75	0.59
1:1:1079:C:H41	1:1:1088:A:H5'	1.67	0.59
2:2:664:G:H22	2:2:741:G:H1	1.50	0.59
2:2:1318:A:N3	51:x:37:ARG:NH1	2.51	0.59
1:1:1266:G:OP1	29:b:16:ARG:NE	2.27	0.59
1:1:1417:C:N4	1:1:1581:G:O6	2.36	0.59
2:2:1033:G:O2'	2:2:1034:G:O5'	2.20	0.59
37:j:13:GLU:HG2	37:j:39:VAL:HG12	1.85	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1365:A:O2'	25:X:11:ARG:NH1	2.35	0.58
1:1:2293:G:H5''	16:O:94:ARG:HH22	1.68	0.58
1:1:2305:U:H5''	8:E:131:GLY:HA3	1.85	0.58
1:1:2885:G:N1	29:b:30:VAL:O	2.36	0.58
2:2:3:A:HO2'	2:2:612:C:HO2'	1.51	0.58
2:2:373:A:H61	2:2:391:G:H1'	1.68	0.58
2:2:811:C:H4'	2:2:901:A:H61	1.67	0.58
21:T:54:GLU:HB3	21:T:88:LYS:HD2	1.84	0.58
32:e:31:HIS:HD2	32:e:32:ILE:HG12	1.67	0.58
10:G:51:ARG:HA	10:G:54:LEU:HB3	1.85	0.58
49:v:76:VAL:HG23	49:v:77:ARG:HG2	1.85	0.58
55:A:124:ASP:OD1	55:A:193:ARG:NH1	2.36	0.58
1:1:2126:A:N3	1:1:2127:G:O2'	2.36	0.58
3:3:75:G:HO2'	23:V:88:HIS:HE2	1.51	0.58
20:S:83:LYS:HB3	20:S:97:LEU:HD13	1.85	0.58
35:h:34:ASP:HB2	46:s:65:ARG:HH21	1.69	0.58
1:1:517:C:OP2	29:b:10:ARG:NH2	2.36	0.58
2:2:45:G:H1	2:2:396:C:H42	1.49	0.58
2:2:229:U:O2'	48:u:25:ARG:NH2	2.37	0.58
2:2:1055:A:O2'	35:h:156:ARG:NH2	2.36	0.58
1:1:276:U:O2	1:1:278:A:N6	2.37	0.58
1:1:323:C:H5'	7:D:163:ASN:HD21	1.69	0.58
1:1:1287:A:H5'	15:N:103:ARG:HD2	1.85	0.58
1:1:2107:G:N1	1:1:2183:A:N1	2.51	0.58
1:1:2425:A:C5'	1:1:2427:C:O4'	2.51	0.58
1:1:2747:G:H1	1:1:2754:U:H2'	1.68	0.58
2:2:333:U:OP1	52:y:2:ALA:N	2.36	0.58
2:2:1136:C:H5'	2:2:1137:C:C6	2.39	0.58
55:A:11:ILE:HD11	55:A:84:LEU:HD12	1.86	0.58
12:K:21:CYS:HA	12:K:41:ILE:HG22	1.85	0.58
2:2:73:C:N3	2:2:74:A:N6	2.52	0.58
37:j:87:GLY:N	37:j:94:VAL:O	2.37	0.58
1:1:1266:G:O2'	1:1:2012:G:O6	2.21	0.58
1:1:2831:G:OP2	6:C:59:ARG:NH1	2.37	0.58
2:2:667:G:O3'	47:t:50:HIS:HB2	2.04	0.58
2:2:1101:A:OP2	34:g:95:ARG:NH1	2.37	0.58
2:2:1150:A:H4'	42:o:43:PRO:HG3	1.84	0.58
5:B:117:GLN:O	5:B:128:ASN:ND2	2.33	0.58
2:2:1048:G:N1	2:2:1210:C:N3	2.52	0.58
2:2:1414:U:H2'	2:2:1415:G:H8	1.68	0.58
54:5:7:U:O2'	54:5:21:A:N1	2.35	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:402:A:N1	1:1:403:U:H1'	2.19	0.57
1:1:784:G:N7	1:1:792:A:C5	2.72	0.57
1:1:878:A:N6	1:1:899:A:O2'	2.35	0.57
1:1:2134:A:H1'	1:1:2159:G:H1'	1.85	0.57
1:1:2846:G:OP1	17:P:53:ARG:NH1	2.34	0.57
2:2:264:C:O3'	49:v:65:ARG:NH2	2.37	0.57
6:C:181:ASP:OD2	6:C:184:ARG:NH2	2.37	0.57
14:M:34:LYS:HA	14:M:101:VAL:HA	1.86	0.57
39:l:27:VAL:HG12	39:l:43:VAL:HG21	1.85	0.57
49:v:61:ILE:HA	49:v:75:LEU:HA	1.86	0.57
55:A:334:LYS:HG2	55:A:341:GLU:HG2	1.85	0.57
1:1:643:A:N1	1:1:2369:A:O2'	2.35	0.57
1:1:1935:G:H3'	1:1:1962:5MC:HN41	1.69	0.57
1:1:2061:G:N2	56:6:79:PHE:HB3	2.19	0.57
2:2:923:A:N6	2:2:1392:G:O6	2.37	0.57
5:B:71:LYS:NZ	5:B:100:GLU:OE1	2.35	0.57
1:1:601:C:O2'	7:D:99:LYS:NZ	2.37	0.57
15:N:44:LEU:O	15:N:48:VAL:N	2.36	0.57
17:P:30:VAL:HG12	17:P:81:VAL:HG12	1.86	0.57
37:j:133:PRO:HA	37:j:136:VAL:HG12	1.85	0.57
2:2:467:U:O2	2:2:467:U:H2'	2.04	0.57
51:x:3:ARG:HE	51:x:7:LYS:HB3	1.68	0.57
2:2:1297:G:O2'	39:l:114:LYS:NZ	2.35	0.57
2:2:1516:2MG:N2	2:2:1519:MA6:OP2	2.37	0.57
1:1:1077:A:N1	1:1:1088:A:O2'	2.37	0.57
1:1:1871:A:N7	1:1:1872:A:N6	2.52	0.57
1:1:2114:A:N6	1:1:2167:U:O2'	2.38	0.57
1:1:2204:G:OP2	5:B:147:LYS:NZ	2.37	0.57
1:1:2419:U:OP1	32:e:41:LYS:NZ	2.36	0.57
2:2:626:G:OP1	48:u:35:ARG:NH2	2.38	0.57
6:C:6:GLY:N	6:C:201:LEU:O	2.31	0.57
45:r:11:ASP:HA	45:r:45:ILE:HB	1.86	0.57
1:1:799:G:H3'	1:1:800:A:H2'	1.86	0.57
36:i:85:ASN:HA	37:j:102:GLY:HA3	1.86	0.57
1:1:2163:A:H3'	1:1:2164:C:H4'	1.86	0.57
2:2:1033:G:H2'	2:2:1034:G:C8	2.39	0.57
13:L:23:ILE:HB	19:R:84:ARG:HH22	1.70	0.57
55:A:162:LYS:HB3	55:A:184:SER:HB3	1.87	0.57
1:1:477:A:N6	1:1:500:G:O3'	2.37	0.57
2:2:980:C:O2'	46:s:13:ARG:NH1	2.38	0.57
9:F:16:ASP:HB3	9:F:27:LYS:HB2	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:G:6:LEU:HD11	10:G:37:VAL:HG23	1.87	0.57
1:1:243:U:OP2	32:e:8:ARG:NH1	2.38	0.56
1:1:1170:C:H6	1:1:1170:C:H5''	1.70	0.56
2:2:1178:G:N2	2:2:1181:G:OP2	2.38	0.56
15:N:6:SER:OG	15:N:46:ARG:NE	2.34	0.56
17:P:60:THR:HG23	17:P:73:VAL:HG22	1.85	0.56
1:1:910:A:N3	1:1:2264:C:O2'	2.36	0.56
1:1:1901:A:OP2	5:B:253:LYS:NZ	2.39	0.56
2:2:86:G:O2'	2:2:87:C:O5'	2.23	0.56
2:2:405:U:O4	36:i:2:ALA:N	2.38	0.56
2:2:674:G:OP1	38:k:86:ARG:NH2	2.39	0.56
2:2:1072:G:O6	2:2:1102:A:N6	2.38	0.56
6:C:150:GLN:O	6:C:151:THR:O	2.23	0.56
1:1:918:A:OP2	1:1:2268:A:N6	2.38	0.56
1:1:2351:G:O6	32:e:42:ARG:NH1	2.39	0.56
5:B:142:HIS:ND1	5:B:193:GLY:O	2.34	0.56
5:B:258:ARG:NH1	5:B:264:ASP:OD1	2.38	0.56
7:D:6:LYS:O	7:D:9:GLN:NE2	2.38	0.56
10:G:72:ILE:HD11	10:G:108:VAL:HG23	1.86	0.56
10:G:127:GLU:HA	10:G:145:ASN:HA	1.86	0.56
22:U:46:GLN:NE2	22:U:54:GLN:OE1	2.39	0.56
39:l:72:THR:HA	39:l:96:ARG:HH12	1.71	0.56
55:A:126:ALA:HB1	55:A:225:GLU:HB3	1.86	0.56
1:1:563:A:OP2	19:R:79:ARG:NH2	2.37	0.56
2:2:151:A:OP2	2:2:169:C:N4	2.38	0.56
2:2:1451:U:OP2	2:2:1452:C:N4	2.39	0.56
3:3:66:A:O5'	3:3:108:A:N6	2.38	0.56
29:b:30:VAL:HG22	29:b:37:LYS:HG2	1.87	0.56
2:2:254:G:N2	49:v:18:GLU:OE2	2.32	0.56
2:2:728:A:H62	47:t:54:ARG:HD3	1.71	0.56
49:v:68:SER:HB3	49:v:71:LYS:HB3	1.88	0.56
1:1:574:A:N6	1:1:2034:U:OP1	2.39	0.56
1:1:1864:U:H3	1:1:1878:G:H1	1.53	0.56
8:E:122:PHE:HA	8:E:128:TYR:HA	1.88	0.56
1:1:668:A:H2'	1:1:670:A:H62	1.71	0.56
1:1:1779:U:OP2	1:1:1784:A:N6	2.39	0.56
1:1:1188:U:H2'	1:1:1189:A:H8	1.71	0.56
2:2:1086:U:H2'	2:2:1087:G:H8	1.71	0.56
10:G:129:GLU:HA	10:G:143:ILE:HA	1.88	0.56
23:V:58:SER:O	23:V:73:LYS:NZ	2.39	0.56
1:1:329:G:OP2	22:U:69:ASN:ND2	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:390:U:H2'	2:2:391:G:H8	1.68	0.56
1:1:2692:G:O2'	1:1:2847:U:O2	2.24	0.56
2:2:1376:U:O4	39:l:10:ARG:NH1	2.38	0.56
1:1:2119:A:N6	1:1:2167:U:O2'	2.39	0.55
5:B:2:ALA:N	5:B:20:VAL:O	2.39	0.55
8:E:29:PRO:HB2	8:E:169:LEU:HD22	1.88	0.55
13:L:29:LYS:HG3	13:L:30:THR:HG23	1.87	0.55
16:O:89:ASP:HA	16:O:116:GLN:HB3	1.88	0.55
2:2:1317:C:OP1	46:s:24:ARG:NH2	2.39	0.55
49:v:20:SER:OG	49:v:71:LYS:NZ	2.35	0.55
1:1:717:C:H3'	1:1:718:A:H8	1.71	0.55
1:1:1913:A:N7	2:2:1493:A:O2'	2.35	0.55
1:1:2530:A:O2'	1:1:2534:A:N6	2.40	0.55
2:2:376:G:O2'	48:u:5:ARG:NH1	2.39	0.55
2:2:1149:C:O2'	2:2:1280:A:N1	2.37	0.55
6:C:181:ASP:HB3	6:C:186:LEU:HB2	1.88	0.55
1:1:177:G:OP2	1:1:177:G:N2	2.38	0.55
1:1:2061:G:OP1	1:1:2503:2MA:HM23	2.06	0.55
2:2:795:C:H4'	43:p:128:ARG:HH21	1.71	0.55
3:3:48:U:OP1	16:O:30:ARG:NH2	2.38	0.55
39:l:118:LEU:O	39:l:122:ASN:ND2	2.39	0.55
1:1:1414:C:O2	1:1:1588:G:N2	2.39	0.55
1:1:2746:U:H5'	9:F:138:LYS:HG2	1.87	0.55
2:2:373:A:N1	2:2:391:G:O2'	2.38	0.55
8:E:131:GLY:HA2	8:E:153:ASP:HA	1.89	0.55
23:V:57:TYR:OH	23:V:79:ARG:NH2	2.40	0.55
29:b:31:ASP:OD2	29:b:34:SER:N	2.39	0.55
1:1:1040:A:OP1	23:V:46:LYS:NZ	2.39	0.55
1:1:1652:A:N6	15:N:11:ASN:OD1	2.39	0.55
2:2:110:C:H2'	2:2:111:G:O4'	2.06	0.55
2:2:374:A:N1	2:2:390:U:O2'	2.38	0.55
2:2:1425:U:H2'	2:2:1426:G:H8	1.71	0.55
19:R:6:GLN:HG2	19:R:11:GLN:HG2	1.88	0.55
47:t:59:MET:HA	47:t:62:GLN:HB3	1.87	0.55
1:1:673:C:OP1	7:D:49:ARG:NH2	2.38	0.55
1:1:1227:G:OP2	18:Q:16:LYS:NZ	2.38	0.55
1:1:1419:A:H5'	1:1:1579:A:H61	1.71	0.55
1:1:2507:C:OP1	55:A:256:ARG:NH1	2.40	0.55
19:R:52:PRO:O	19:R:53:PHE:CD2	2.59	0.55
34:g:3:THR:N	34:g:51:ASN:OD1	2.40	0.55
54:5:33:U:N3	54:5:36:A:OP2	2.33	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:247:G:OP2	1:1:249:C:N4	2.34	0.55
1:1:1998:A:HO2'	1:1:2724:U:HO2'	1.53	0.55
2:2:222:C:H2'	2:2:223:A:H8	1.72	0.55
2:2:297:G:N2	2:2:300:A:OP2	2.36	0.55
2:2:362:G:N2	2:2:365:U:OP2	2.39	0.55
1:1:714:U:OP2	47:t:88:ARG:NH1	2.40	0.55
2:2:8:A:N6	36:i:202:GLU:O	2.39	0.55
2:2:405:U:OP2	36:i:3:ARG:NH1	2.40	0.55
2:2:429:U:H3'	36:i:9:LEU:HD12	1.89	0.55
2:2:1249:C:N4	2:2:1288:A:OP2	2.40	0.55
7:D:117:ARG:HH21	7:D:184:ASP:HA	1.72	0.55
25:X:5:CYS:HB2	25:X:33:LEU:HD11	1.88	0.55
25:X:36:HIS:ND1	25:X:37:ARG:O	2.38	0.55
1:1:2036:C:H2'	1:1:2037:A:H8	1.70	0.55
1:1:2308:G:H2'	1:1:2310:C:H41	1.72	0.55
2:2:373:A:O2'	2:2:451:A:N7	2.40	0.55
24:W:68:LYS:NZ	24:W:69:PHE:O	2.40	0.55
1:1:220:G:H22	1:1:427:U:H2'	1.72	0.54
1:1:861:A:N3	3:3:79:G:O2'	2.37	0.54
1:1:1363:C:O2'	1:1:1809:A:N3	2.39	0.54
2:2:216:U:O2'	2:2:468:A:N6	2.41	0.54
2:2:389:A:H2'	2:2:390:U:H5'	1.89	0.54
2:2:1304:G:H21	2:2:1333:A:H62	1.55	0.54
5:B:66:ASP:OD2	5:B:102:ARG:NH1	2.40	0.54
1:1:1789:A:OP2	5:B:221:ARG:NH1	2.39	0.54
2:2:309:A:O2'	2:2:607:A:N1	2.39	0.54
17:P:52:ASN:O	17:P:53:ARG:NH1	2.38	0.54
24:W:37:ILE:HG22	24:W:38:VAL:HG23	1.89	0.54
1:1:460:A:OP2	31:d:41:ARG:NH1	2.38	0.54
1:1:1528:A:N6	1:1:1543:G:O2'	2.39	0.54
14:M:47:GLU:OE2	14:M:50:ARG:NH1	2.41	0.54
1:1:402:A:H2'	1:1:403:U:H5'	1.90	0.54
2:2:542:G:O3'	36:i:14:ARG:NH2	2.38	0.54
12:K:102:PRO:HD2	17:P:68:GLU:HG3	1.90	0.54
15:N:87:PHE:HD1	15:N:90:ARG:HD3	1.71	0.54
47:t:57:LEU:O	47:t:60:VAL:HB	2.07	0.54
1:1:402:A:H2'	1:1:403:U:C5'	2.38	0.54
1:1:956:G:O6	14:M:14:LYS:NZ	2.41	0.54
1:1:2189:U:H4'	1:1:2189:U:OP1	2.07	0.54
2:2:120:A:O2'	2:2:122:G:N7	2.37	0.54
2:2:691:G:O6	43:p:53:ARG:NH2	2.36	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1259:C:O2'	2:2:1283:U:O2	2.22	0.54
17:P:91:ALA:HB2	17:P:113:ARG:HA	1.90	0.54
50:w:11:CYS:SG	50:w:12:ARG:N	2.81	0.54
1:1:1250:G:N7	13:L:18:ARG:NH2	2.49	0.54
1:1:2532:G:O2'	1:1:2657:A:N1	2.40	0.54
2:2:376:G:H5'	48:u:5:ARG:HB2	1.88	0.54
2:2:841:C:H2'	2:2:843:U:H5''	1.89	0.54
2:2:865:A:N3	2:2:918:A:O2'	2.40	0.54
5:B:108:LYS:HA	5:B:196:GLY:HA2	1.88	0.54
36:i:139:PRO:HA	36:i:182:PHE:HD2	1.73	0.54
1:1:1807:G:N2	1:1:1810:A:OP2	2.35	0.54
2:2:71:A:H61	2:2:99:C:H1'	1.73	0.54
2:2:1015:G:N2	2:2:1218:C:O2	2.39	0.54
37:j:12:GLN:HE21	37:j:117:VAL:HA	1.73	0.54
45:r:68:ASP:OD1	45:r:71:ARG:NH1	2.38	0.54
2:2:197:A:N1	2:2:220:G:O2'	2.37	0.54
2:2:653:U:O4'	40:m:56:LYS:NZ	2.39	0.54
39:l:47:LEU:HD23	39:l:58:GLU:HB3	1.90	0.54
45:r:89:LEU:HA	45:r:92:ARG:HG2	1.89	0.54
1:1:2467:C:O2	14:M:123:LYS:NZ	2.41	0.54
2:2:510:A:HO2'	2:2:542:G:HO2'	1.55	0.54
35:h:131:ARG:NH1	35:h:166:GLU:OE2	2.41	0.54
1:1:2576:G:O2'	1:1:2579:C:OP2	2.24	0.54
1:1:2756:U:O4'	1:1:2757:A:C8	2.61	0.54
2:2:1071:C:H2'	2:2:1072:G:H8	1.72	0.54
1:1:2688:G:N1	1:1:2720:U:OP2	2.34	0.53
8:E:115:ARG:HA	28:a:47:LYS:HD2	1.90	0.53
20:S:77:ASP:HB2	20:S:102:HIS:HB2	1.89	0.53
1:1:2825:G:OP2	1:1:2825:G:N2	2.41	0.53
2:2:933:G:N7	39:l:3:ARG:NE	2.54	0.53
19:R:21:ARG:HD2	19:R:93:PHE:HB2	1.91	0.53
1:1:1068:G:O2'	1:1:1070:A:N6	2.40	0.53
1:1:2359:C:H2'	1:1:2360:G:C8	2.43	0.53
1:1:2451:A:N3	54:5:76:A:O2'	2.41	0.53
2:2:137:U:H2'	2:2:138:G:H8	1.73	0.53
8:E:34:ILE:HG12	8:E:156:ILE:HG12	1.90	0.53
10:G:117:LEU:HD21	10:G:130:VAL:HG22	1.89	0.53
30:c:8:LYS:HA	30:c:24:THR:HA	1.91	0.53
1:1:1418:G:N1	1:1:1579:A:OP2	2.41	0.53
1:1:2133:G:H1	1:1:2157:G:H2'	1.73	0.53
1:1:2484:G:OP1	14:M:44:ARG:NH1	2.35	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:258:G:H1	2:2:268:U:H3	1.57	0.53
2:2:411:A:H4'	2:2:412:A:H5'	1.90	0.53
2:2:1060:U:OP1	46:s:85:ARG:NH1	2.41	0.53
14:M:66:ARG:NH1	14:M:104:GLU:OE2	2.41	0.53
43:p:28:ASN:O	43:p:57:LYS:NZ	2.34	0.53
55:A:274:CYS:SG	55:A:276:ASN:ND2	2.81	0.53
1:1:739:A:H1'	1:1:740:C:H5	1.74	0.53
1:1:1071:G:H1'	1:1:1089:A:H2'	1.90	0.53
1:1:2006:C:O2'	1:1:2823:A:N3	2.42	0.53
1:1:2449:U:O2'	1:1:2501:C:N4	2.42	0.53
2:2:1406:U:H5''	2:2:1407:5MC:HM52	1.90	0.53
43:p:88:GLY:H	43:p:114:THR:HG22	1.74	0.53
1:1:1365:A:OP2	25:X:2:SER:OG	2.27	0.53
22:U:40:ASN:ND2	22:U:64:ALA:O	2.42	0.53
36:i:73:ARG:HG3	36:i:77:LYS:HE2	1.91	0.53
41:n:36:GLU:OE1	41:n:45:ARG:NH1	2.41	0.53
6:C:46:ARG:NH1	6:C:85:ALA:O	2.38	0.53
55:A:117:ARG:NH1	55:A:358:GLU:O	2.42	0.53
1:1:265:A:O2'	1:1:428:A:N6	2.41	0.53
2:2:227:G:O2'	48:u:63:GLN:OE1	2.25	0.53
38:k:9:MET:HB2	38:k:86:ARG:H	1.73	0.53
1:1:807:U:OP2	13:L:41:ARG:NH1	2.40	0.53
1:1:973:A:OP2	19:R:81:LYS:NZ	2.35	0.53
1:1:2508:G:HO2'	1:1:2554:U:HO2'	1.54	0.53
21:T:22:THR:O	21:T:26:LYS:NZ	2.42	0.53
1:1:402:A:H2'	1:1:403:U:C4'	2.39	0.53
1:1:865:C:O2	1:1:867:C:N4	2.37	0.53
2:2:979:C:OP1	2:2:1223:C:N4	2.41	0.53
8:E:4:LEU:O	8:E:8:TYR:N	2.39	0.53
17:P:46:VAL:N	17:P:62:ARG:O	2.41	0.53
25:X:43:GLU:OE1	25:X:45:ARG:NH1	2.42	0.53
48:u:21:VAL:HG12	48:u:33:ILE:HB	1.91	0.53
1:1:2680:U:H5'	6:C:194:PRO:HA	1.91	0.52
2:2:338:A:H2	2:2:351:G:H22	1.56	0.52
12:K:43:ILE:HD12	12:K:56:ASP:HB2	1.91	0.52
51:x:36:ARG:NH2	51:x:72:GLY:O	2.43	0.52
52:y:4:ILE:HG22	52:y:6:SER:H	1.75	0.52
1:1:1364:G:N2	1:1:1367:A:OP2	2.34	0.52
1:1:2692:G:H2'	1:1:2693:G:H8	1.74	0.52
1:1:2901:C:H6	1:1:2901:C:H5''	1.74	0.52
2:2:299:G:N2	2:2:565:U:O2	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:t:50:HIS:HA	47:t:53:ARG:HH11	1.73	0.52
1:1:402:A:C4	1:1:403:U:C6	2.97	0.52
1:1:1344:U:OP1	1:1:1345:C:N4	2.42	0.52
2:2:300:A:O2'	2:2:564:C:N3	2.35	0.52
2:2:579:A:H5'	2:2:728:A:H1'	1.89	0.52
2:2:728:A:N6	47:t:54:ARG:HD3	2.24	0.52
5:B:262:ARG:O	5:B:265:LYS:NZ	2.41	0.52
12:K:71:ARG:NE	12:K:106:GLU:OE2	2.42	0.52
15:N:47:VAL:O	15:N:51:LEU:N	2.42	0.52
40:m:49:PHE:HB2	40:m:59:LEU:HD11	1.91	0.52
40:m:74:SER:HB3	40:m:130:ALA:HB3	1.91	0.52
1:1:1682:G:OP2	1:1:1699:G:N2	2.42	0.52
1:1:1995:U:H3'	1:1:1996:C:H2'	1.91	0.52
2:2:265:G:H5'	49:v:65:ARG:HH22	1.73	0.52
2:2:1268:G:N3	2:2:1326:U:O2'	2.43	0.52
3:3:80:U:O4	23:V:14:LYS:NZ	2.39	0.52
11:J:68:LYS:HA	11:J:71:ASP:HB2	1.90	0.52
37:j:45:ARG:NH2	37:j:73:ASN:OD1	2.42	0.52
47:t:69:TYR:O	47:t:72:ARG:C	2.52	0.52
55:A:242:ASP:HB2	55:A:262:ARG:HB3	1.92	0.52
1:1:29:U:H2'	1:1:30:G:H8	1.74	0.52
1:1:279:A:OP2	1:1:361:G:N2	2.42	0.52
1:1:500:G:N1	1:1:503:A:OP2	2.34	0.52
1:1:2552:OMU:H2'	1:1:2554:U:OP2	2.09	0.52
2:2:202:G:H21	2:2:466:A:H61	1.56	0.52
6:C:111:GLY:N	6:C:170:VAL:O	2.42	0.52
1:1:307:G:N1	1:1:310:A:OP2	2.39	0.52
1:1:2584:U:H2'	1:1:2585:U:H2'	1.92	0.52
2:2:718:A:N6	50:w:70:TYR:O	2.41	0.52
2:2:1305:G:N2	2:2:1332:A:OP2	2.43	0.52
2:2:1441:A:H62	2:2:1461:G:H21	1.57	0.52
10:G:78:VAL:HG21	10:G:103:VAL:HG22	1.91	0.52
36:i:91:LEU:HD23	36:i:94:LEU:HD12	1.90	0.52
55:A:117:ARG:O	55:A:193:ARG:NH2	2.43	0.52
55:A:195:GLU:OE2	55:A:324:ARG:NH2	2.42	0.52
1:1:2689:U:OP2	1:1:2691:C:N4	2.42	0.52
2:2:826:C:O2	40:m:16:ASN:ND2	2.43	0.52
2:2:1227:A:OP1	51:x:80:TYR:OH	2.26	0.52
3:3:75:G:O2'	23:V:88:HIS:NE2	2.42	0.52
3:3:111:U:H2'	3:3:112:G:H8	1.75	0.52
20:S:4:ILE:HG12	20:S:106:VAL:HG22	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:t:50:HIS:HA	47:t:53:ARG:HD2	1.92	0.52
55:A:168:GLU:HA	55:A:179:VAL:HG12	1.92	0.52
1:1:287:G:O6	1:1:352:A:N6	2.43	0.52
1:1:781:A:OP1	5:B:217:ARG:NH2	2.43	0.52
2:2:1261:A:N6	2:2:1274:A:O2'	2.37	0.52
7:D:62:GLN:HG3	7:D:63:LYS:HG3	1.91	0.52
1:1:1817:G:OP1	5:B:87:ARG:NH2	2.39	0.52
1:1:1870:C:OP1	1:1:1871:A:N6	2.42	0.52
1:1:2753:A:O2'	33:f:15:LYS:NZ	2.42	0.52
2:2:1305:G:H21	2:2:1332:A:H2	1.57	0.52
3:3:39:A:H2	3:3:44:G:H5'	1.75	0.52
15:N:44:LEU:HA	15:N:47:VAL:HB	1.90	0.52
19:R:75:VAL:HG22	19:R:86:GLN:HE22	1.75	0.52
51:x:3:ARG:NH1	51:x:9:PRO:O	2.43	0.52
1:1:2112:G:OP1	1:1:2115:G:N2	2.42	0.52
2:2:1003:G:N2	2:2:1005:A:O5'	2.43	0.52
9:F:29:LYS:NZ	9:F:80:THR:O	2.40	0.52
9:F:95:ARG:HB2	9:F:128:GLN:HB3	1.92	0.52
15:N:98:LEU:HB2	15:N:112:TYR:HB2	1.90	0.52
19:R:8:GLY:O	19:R:10:LYS:NZ	2.41	0.52
27:Z:17:LEU:HB2	27:Z:20:HIS:HD2	1.74	0.52
37:j:12:GLN:HG3	37:j:117:VAL:HG12	1.91	0.52
1:1:402:A:C2'	1:1:403:U:H5'	2.40	0.51
1:1:442:G:N2	7:D:43:THR:O	2.43	0.51
1:1:2391:G:N1	1:1:2425:A:OP1	2.23	0.51
2:2:62:U:O2'	2:2:379:C:O2	2.27	0.51
7:D:46:GLN:HB3	7:D:83:VAL:HG21	1.92	0.51
12:K:88:ASN:HB3	12:K:92:GLU:H	1.74	0.51
1:1:335:C:O2	22:U:68:SER:OG	2.28	0.51
1:1:336:C:H6	1:1:336:C:H5''	1.75	0.51
1:1:482:A:N6	1:1:506:G:O2'	2.43	0.51
1:1:2045:C:O2	29:b:19:HIS:NE2	2.42	0.51
1:1:2590:A:O3'	5:B:238:ARG:NH1	2.43	0.51
2:2:34:C:H2'	2:2:35:G:H8	1.75	0.51
2:2:368:U:H2'	2:2:368:U:O2	2.09	0.51
10:G:76:GLU:HA	10:G:142:VAL:HG13	1.92	0.51
55:A:203:ARG:HD3	55:A:328:LEU:HD12	1.92	0.51
1:1:1941:C:H2'	1:1:1942:C:O4'	2.10	0.51
1:1:2134:A:OP1	1:1:2159:G:N2	2.43	0.51
1:1:2645:G:OP2	1:1:2645:G:N2	2.35	0.51
3:3:77:U:OP1	23:V:21:ARG:NH1	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:E:4:LEU:HA	8:E:7:TYR:HB3	1.92	0.51
10:G:51:ARG:HG3	10:G:54:LEU:HD23	1.92	0.51
39:l:139:GLU:O	39:l:143:ARG:N	2.42	0.51
54:5:18:G:OP2	54:5:60:U:O2'	2.28	0.51
1:1:1028:A:N6	1:1:1126:A:OP1	2.43	0.51
1:1:2131:U:H5'	1:1:2132:U:H5''	1.93	0.51
2:2:438:U:O2'	2:2:494:G:O6	2.24	0.51
3:3:28:C:H5''	16:O:31:THR:HG21	1.93	0.51
5:B:140:THR:HG22	5:B:163:GLN:HG2	1.92	0.51
36:i:75:TYR:OH	36:i:97:ARG:NH1	2.44	0.51
43:p:94:GLU:OE2	43:p:98:ARG:NH2	2.41	0.51
1:1:265:A:N1	1:1:427:U:O2'	2.42	0.51
1:1:298:G:O2'	1:1:322:A:N1	2.43	0.51
1:1:1020:A:N1	1:1:1141:U:O2'	2.44	0.51
2:2:217:C:H4'	2:2:217:C:OP1	2.10	0.51
19:R:38:VAL:HG13	19:R:54:VAL:HB	1.92	0.51
34:g:20:THR:HA	34:g:39:HIS:HE1	1.75	0.51
35:h:140:ASN:OD1	35:h:143:ARG:NH2	2.43	0.51
1:1:780:G:H5''	5:B:217:ARG:HH22	1.75	0.51
1:1:1326:U:O2'	1:1:2010:G:O2'	2.26	0.51
1:1:1798:U:OP2	5:B:271:ARG:NH2	2.41	0.51
1:1:2131:U:O5'	1:1:2158:A:N6	2.44	0.51
2:2:1209:C:O2'	2:2:1214:C:N4	2.39	0.51
22:U:72:ILE:HD12	22:U:83:VAL:HG21	1.93	0.51
1:1:1586:A:H3'	1:1:1587:G:H8	1.76	0.51
1:1:2684:U:O4'	12:K:70:ARG:NH1	2.42	0.51
2:2:1255:G:O2'	2:2:1258:G:N3	2.38	0.51
5:B:106:ALA:O	5:B:196:GLY:N	2.41	0.51
18:Q:47:TYR:OH	18:Q:51:ARG:NH2	2.34	0.51
23:V:72:VAL:HA	23:V:94:ALA:H	1.75	0.51
34:g:94:HIS:ND1	34:g:146:ASN:O	2.43	0.51
38:k:42:TRP:HB2	38:k:59:TYR:HB2	1.93	0.51
49:v:17:MET:HG3	49:v:20:SER:HB2	1.92	0.51
54:5:15:C:H5''	54:5:15:C:O2	2.10	0.51
1:1:994:C:O2'	1:1:996:A:OP1	2.28	0.51
1:1:1170:C:H5''	1:1:1170:C:C6	2.45	0.51
1:1:2061:G:H5'	1:1:2061:G:H8	1.76	0.51
1:1:2266:A:N6	1:1:2273:A:OP2	2.44	0.51
1:1:2521:C:H42	1:1:2544:G:H1	1.59	0.51
2:2:219:U:H2'	2:2:220:G:H8	1.75	0.51
2:2:868:C:H2'	2:2:869:G:O4'	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3:66:A:O4'	3:3:108:A:N6	2.44	0.51
18:Q:12:ALA:HA	18:Q:15:LYS:HB2	1.92	0.51
1:1:1089:A:H2	1:1:1090:A:H62	1.58	0.51
1:1:1667:G:O2'	1:1:1991:U:O4	2.28	0.51
2:2:14:U:N3	2:2:17:U:OP2	2.43	0.51
2:2:80:A:OP2	2:2:83:C:N4	2.37	0.51
8:E:134:GLU:HG2	8:E:136:ILE:H	1.76	0.51
29:b:54:VAL:HG23	29:b:55:ILE:HG22	1.93	0.51
36:i:100:ASN:OD1	36:i:111:ARG:NH1	2.37	0.51
40:m:94:LYS:HG3	40:m:117:ARG:HH22	1.75	0.51
42:o:7:ARG:HB2	42:o:101:SER:HB2	1.92	0.51
3:3:76:G:OP1	23:V:9:ARG:NH2	2.35	0.51
6:C:97:SER:OG	6:C:98:VAL:N	2.44	0.51
8:E:47:LYS:HG2	8:E:51:ASP:HB2	1.93	0.51
15:N:37:THR:HA	15:N:110:MET:HA	1.92	0.51
39:l:111:ARG:NH1	39:l:126:ASP:OD2	2.43	0.51
1:1:514:A:N3	1:1:581:C:O2'	2.43	0.50
1:1:1340:U:OP1	21:T:19:LYS:NZ	2.44	0.50
2:2:427:U:OP1	36:i:13:ARG:NH1	2.44	0.50
1:1:447:A:OP1	18:Q:5:LYS:NZ	2.40	0.50
15:N:58:ASP:HB2	15:N:80:PHE:HB3	1.92	0.50
16:O:110:ALA:HB1	16:O:115:LEU:HD12	1.94	0.50
1:1:220:G:O2'	1:1:233:A:N3	2.36	0.50
1:1:336:C:H5''	1:1:336:C:C6	2.46	0.50
1:1:1490:A:O2'	5:B:98:ASP:OD2	2.28	0.50
7:D:117:ARG:NH2	7:D:183:PHE:O	2.45	0.50
10:G:47:PHE:O	10:G:52:ALA:N	2.45	0.50
21:T:22:THR:HG22	21:T:26:LYS:HZ1	1.76	0.50
35:h:36:ASP:OD1	35:h:59:ARG:NH2	2.45	0.50
35:h:60:PRO:HB3	42:o:94:ALA:HB2	1.93	0.50
47:t:48:LYS:C	47:t:50:HIS:H	2.19	0.50
1:1:61:C:OP1	26:Y:47:ARG:NH1	2.45	0.50
1:1:403:U:O2	1:1:403:U:H2'	2.10	0.50
1:1:572:A:OP2	19:R:79:ARG:NH1	2.45	0.50
1:1:1170:C:H3'	1:1:1171:G:H8	1.76	0.50
1:1:2164:C:H5''	1:1:2171:A:H62	1.76	0.50
2:2:562:U:H1'	44:q:12:ARG:HD2	1.92	0.50
6:C:4:LEU:HG	6:C:32:ASN:HD21	1.76	0.50
28:a:56:ARG:HH11	51:x:68:GLY:HA3	1.76	0.50
35:h:40:ARG:NH1	35:h:55:ILE:O	2.43	0.50
46:s:86:GLU:HB3	46:s:90:ARG:HH12	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:A:80:VAL:HG13	55:A:99:ALA:HB1	1.94	0.50
1:1:458:G:O2'	1:1:469:G:O6	2.29	0.50
1:1:684:G:O2'	1:1:788:A:N7	2.42	0.50
1:1:1006:C:O2'	11:J:108:MET:O	2.27	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
5:B:244:PRO:O	5:B:251:GLN:NE2	2.45	0.50
34:g:167:ASP:O	34:g:170:HIS:ND1	2.42	0.50
54:5:53:G:H3'	54:5:54:5MU:H73	1.94	0.50
55:A:150:ARG:HA	55:A:153:LEU:HB2	1.93	0.50
55:A:164:GLU:HB3	55:A:182:LYS:HB3	1.92	0.50
55:A:241:ILE:HG12	55:A:263:ILE:HG12	1.94	0.50
1:1:818:G:N1	1:1:1188:U:OP2	2.35	0.50
1:1:1712:U:H3'	1:1:1713:A:H2'	1.94	0.50
1:1:1822:C:H2'	1:1:1823:G:H8	1.77	0.50
1:1:2708:G:H2'	1:1:2709:G:H8	1.76	0.50
2:2:1136:C:H5'	2:2:1137:C:C5	2.47	0.50
17:P:60:THR:HA	17:P:73:VAL:HG13	1.92	0.50
18:Q:49:ASP:O	18:Q:53:ARG:N	2.42	0.50
25:X:5:CYS:O	25:X:9:GLY:N	2.37	0.50
46:s:49:GLN:NE2	51:x:11:ILE:O	2.34	0.50
1:1:404:A:H5'	1:1:406:G:H1'	1.93	0.50
1:1:545:U:O2'	1:1:547:A:OP1	2.27	0.50
1:1:672:C:OP2	13:L:42:SER:OG	2.29	0.50
1:1:824:U:O2'	1:1:2358:A:N7	2.42	0.50
1:1:1469:A:OP2	1:1:1522:A:N6	2.40	0.50
1:1:2756:U:O4'	1:1:2757:A:H8	1.95	0.50
2:2:816:A:OP1	2:2:1526:G:O2'	2.27	0.50
40:m:5:ASP:OD2	40:m:77:ARG:NH1	2.38	0.50
1:1:107:G:H2'	1:1:108:G:H8	1.77	0.50
1:1:2013:A:H4'	20:S:96:ILE:HG22	1.93	0.50
1:1:2138:G:N7	1:1:2139:U:O2'	2.43	0.50
1:1:2286:G:C8	1:1:2286:G:H5'	2.47	0.50
1:1:2790:U:OP2	1:1:2893:A:N6	2.45	0.50
2:2:404:G:H4'	2:2:439:U:H5	1.77	0.50
2:2:753:A:H4'	2:2:754:C:O4'	2.11	0.50
13:L:135:ILE:HG22	13:L:140:GLY:HA3	1.94	0.50
1:1:395:U:O2'	1:1:396:G:N7	2.41	0.50
1:1:581:C:OP2	18:Q:33:ARG:NH2	2.45	0.50
1:1:748:G:P	20:S:88:ARG:HE	2.34	0.50
2:2:126:G:OP1	2:2:605:U:O2'	2.25	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:490:C:H2'	2:2:491:G:H8	1.77	0.50
2:2:718:A:O2'	53:z:35:ARG:NH2	2.43	0.50
2:2:1218:C:H2'	2:2:1219:A:C8	2.47	0.50
10:G:124:THR:O	10:G:128:HIS:NE2	2.45	0.50
19:R:43:ASN:HB3	19:R:46:GLU:HB3	1.94	0.50
19:R:50:GLY:O	19:R:51:VAL:C	2.55	0.50
37:j:15:LEU:HA	37:j:37:THR:HG22	1.92	0.50
46:s:45:VAL:HG21	51:x:3:ARG:HH22	1.77	0.50
49:v:59:VAL:HG23	49:v:78:VAL:HG22	1.93	0.50
55:A:14:LEU:HB2	55:A:77:LEU:HD21	1.94	0.50
1:1:158:U:H2'	1:1:159:G:O4'	2.12	0.49
1:1:1416:G:O6	1:1:1583:A:N6	2.45	0.49
2:2:50:A:O2'	2:2:360:G:N2	2.45	0.49
2:2:721:G:H4'	2:2:722:G:O4'	2.12	0.49
6:C:122:VAL:HB	6:C:141:ARG:HH21	1.77	0.49
18:Q:83:LEU:HA	18:Q:86:ALA:HB3	1.92	0.49
21:T:11:LEU:HD11	21:T:47:VAL:HG22	1.94	0.49
22:U:36:VAL:HG11	22:U:39:ILE:HD12	1.94	0.49
1:1:138:U:H4'	1:1:139:U:C2	2.47	0.49
1:1:776:G:N7	1:1:793:A:O2'	2.43	0.49
1:1:1009:A:OP1	11:J:39:LYS:NZ	2.44	0.49
1:1:1324:G:O2'	1:1:1326:U:OP2	2.31	0.49
1:1:1936:A:N6	1:1:1963:U:O2	2.45	0.49
1:1:2519:U:O4'	1:1:2542:A:N6	2.45	0.49
2:2:254:G:O2'	49:v:18:GLU:O	2.30	0.49
5:B:37:ASN:HB2	5:B:62:TYR:HB2	1.93	0.49
18:Q:72:ASN:HD22	18:Q:110:VAL:HG21	1.77	0.49
36:i:202:GLU:OE1	37:j:112:ARG:NH1	2.45	0.49
55:A:87:ALA:O	55:A:92:ASP:N	2.40	0.49
1:1:138:U:O2'	1:1:139:U:O2	2.26	0.49
1:1:320:A:O2'	1:1:322:A:OP2	2.24	0.49
1:1:403:U:C5'	1:1:406:G:O2'	2.59	0.49
2:2:677:U:H3	2:2:713:G:H1	1.60	0.49
2:2:880:C:H2'	2:2:881:G:H8	1.77	0.49
2:2:1236:A:H4'	2:2:1304:G:H4'	1.95	0.49
3:3:43:C:H5''	28:a:1:MET:HG2	1.93	0.49
24:W:46:HIS:CD2	24:W:77:ARG:HB3	2.47	0.49
32:e:32:ILE:O	32:e:32:ILE:HG22	2.12	0.49
37:j:97:GLN:HB3	37:j:124:LEU:HB2	1.93	0.49
38:k:46:GLN:HE22	38:k:55:HIS:HB3	1.77	0.49
39:l:75:VAL:HA	39:l:88:PRO:HA	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:A:87:ALA:HA	55:A:92:ASP:HB3	1.92	0.49
1:1:48:G:N1	1:1:177:G:OP2	2.44	0.49
1:1:1418:G:H1'	1:1:1581:G:H22	1.76	0.49
1:1:1889:A:N3	1:1:2086:U:O2'	2.41	0.49
1:1:2704:C:H3'	1:1:2705:A:C8	2.48	0.49
2:2:108:G:H5'	2:2:109:A:H5''	1.93	0.49
2:2:792:A:O2'	2:2:794:A:N7	2.41	0.49
2:2:1060:U:O2'	42:o:58:ASN:OD1	2.28	0.49
2:2:1328:C:HO2'	45:r:29:ARG:HH11	1.56	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
2:2:668:G:P	47:t:50:HIS:HB2	2.53	0.49
2:2:1422:G:O2'	12:K:49:ARG:NH2	2.46	0.49
6:C:4:LEU:O	6:C:203:VAL:N	2.43	0.49
16:O:52:SER:OG	16:O:53:THR:N	2.44	0.49
22:U:29:LEU:HD12	22:U:33:LYS:HB2	1.94	0.49
31:d:9:VAL:O	31:d:13:ASN:ND2	2.46	0.49
40:m:92:LEU:O	40:m:117:ARG:NH2	2.42	0.49
1:1:79:C:O2'	1:1:346:A:N3	2.42	0.49
1:1:495:G:H21	20:S:61:ASN:HD21	1.60	0.49
1:1:1231:U:H2'	1:1:1232:G:H8	1.77	0.49
1:1:2667:C:N3	9:F:110:SER:OG	2.43	0.49
23:V:64:VAL:HG22	23:V:69:GLU:HG3	1.94	0.49
55:A:27:TYR:HE1	55:A:67:VAL:HA	1.78	0.49
1:1:459:U:H2'	1:1:460:A:H8	1.77	0.49
1:1:662:G:H2'	1:1:663:G:H8	1.77	0.49
1:1:1028:A:OP2	1:1:1126:A:N6	2.36	0.49
1:1:1808:A:O2'	1:1:1809:A:O4'	2.30	0.49
1:1:2684:U:OP1	17:P:51:ARG:NH1	2.46	0.49
1:1:2815:C:O2'	29:b:41:HIS:ND1	2.42	0.49
2:2:1152:A:OP1	42:o:70:HIS:ND1	2.45	0.49
8:E:68:THR:N	8:E:86:GLY:O	2.46	0.49
8:E:129:SER:HA	8:E:155:THR:HA	1.93	0.49
22:U:8:ASP:O	22:U:24:LYS:NZ	2.40	0.49
1:1:371:A:H61	1:1:401:A:H3'	1.77	0.49
1:1:1133:A:N6	1:1:2025:C:O2'	2.46	0.49
2:2:411:A:OP1	36:i:26:ARG:NH1	2.46	0.49
10:G:48:GLU:HA	10:G:52:ALA:HB2	1.93	0.49
14:M:47:GLU:OE2	14:M:51:ARG:NE	2.45	0.49
19:R:78:ARG:HB2	19:R:83:TYR:HB3	1.95	0.49
21:T:65:GLY:N	21:T:79:ASP:OD1	2.33	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:h:180:ALA:HA	35:h:206:GLU:HA	1.93	0.49
47:t:39:LEU:HD23	47:t:43:PHE:HE2	1.77	0.49
1:1:402:A:N3	1:1:403:U:H1'	2.25	0.49
1:1:781:A:H2'	1:1:1777:U:H1'	1.94	0.49
2:2:494:G:H2'	2:2:496:A:H8	1.77	0.49
3:3:5:U:H2'	3:3:6:G:H8	1.77	0.49
7:D:1:MET:HB3	7:D:14:VAL:HG23	1.94	0.49
9:F:83:PHE:N	9:F:135:GLY:O	2.46	0.49
21:T:35:ALA:HB3	21:T:38:ALA:HB2	1.94	0.49
34:g:97:LEU:H	34:g:100:MET:HE3	1.77	0.49
37:j:55:GLU:HG3	37:j:57:PRO:HD2	1.94	0.49
40:m:64:LYS:HG2	40:m:71:VAL:HG21	1.94	0.49
48:u:77:GLU:HA	48:u:80:LYS:HB2	1.94	0.49
1:1:894:U:C6	1:1:895:U:H5	2.31	0.49
1:1:2668:G:H1'	9:F:110:SER:HB2	1.94	0.49
2:2:222:C:H2'	2:2:223:A:C8	2.48	0.49
2:2:1130:A:N6	2:2:1144:G:N3	2.56	0.49
40:m:78:VAL:HG12	40:m:85:ILE:HG13	1.95	0.49
1:1:1926:U:N3	1:1:1929:G:OP2	2.42	0.48
1:1:2756:U:H4'	1:1:2757:A:O5'	2.13	0.48
2:2:217:C:H6	2:2:217:C:H5''	1.78	0.48
3:3:43:C:OP1	28:a:6:HIS:NE2	2.37	0.48
29:b:39:LEU:HB2	29:b:42:HIS:HB2	1.95	0.48
47:t:57:LEU:HA	47:t:60:VAL:CG2	2.43	0.48
1:1:467:G:OP2	31:d:34:ARG:NH1	2.43	0.48
1:1:894:U:H1'	1:1:895:U:H5'	1.95	0.48
1:1:1297:C:O2'	1:1:1302:A:N1	2.41	0.48
1:1:1306:C:N4	1:1:1607:C:OP2	2.46	0.48
1:1:1310:G:O2'	1:1:1611:C:OP1	2.29	0.48
1:1:1919:A:O2'	2:2:1517:G:N3	2.42	0.48
1:1:2595:G:N2	1:1:2598:A:OP2	2.32	0.48
16:O:60:GLU:HG3	16:O:61:GLN:HE21	1.79	0.48
39:l:93:PRO:HA	39:l:96:ARG:HD3	1.95	0.48
41:n:21:ILE:HG23	41:n:61:LEU:HD13	1.96	0.48
1:1:139:U:C5'	1:1:140:C:O5'	2.53	0.48
1:1:1252:G:OP2	1:1:1252:G:H4'	2.13	0.48
1:1:2117:A:N1	1:1:2170:A:N6	2.60	0.48
2:2:780:A:N6	2:2:801:U:OP2	2.42	0.48
8:E:123:ASP:C	8:E:125:ARG:H	2.21	0.48
17:P:104:THR:HA	17:P:108:ALA:HB2	1.95	0.48
22:U:14:LEU:HD11	22:U:71:ALA:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:i:188:ARG:HH12	36:i:193:ALA:HA	1.78	0.48
45:r:2:ALA:O	45:r:9:ILE:N	2.45	0.48
47:t:57:LEU:C	47:t:60:VAL:HB	2.39	0.48
1:1:1688:U:O2'	1:1:1700:A:N7	2.37	0.48
1:1:2039:U:H2'	1:1:2040:G:H8	1.78	0.48
1:1:2039:U:H2'	1:1:2040:G:C8	2.48	0.48
1:1:2515:C:H2'	1:1:2516:A:H8	1.77	0.48
1:1:2582:G:H2'	1:1:2583:G:H8	1.79	0.48
2:2:22:G:O2'	2:2:913:A:N1	2.42	0.48
2:2:675:A:O2'	43:p:116:ILE:O	2.24	0.48
12:K:61:VAL:HB	12:K:87:LEU:HD11	1.95	0.48
36:i:202:GLU:OE2	37:j:105:ILE:N	2.46	0.48
55:A:19:ASP:HA	55:A:22:ARG:HH11	1.79	0.48
55:A:78:GLU:O	55:A:82:GLY:N	2.43	0.48
1:1:968:C:H2'	1:1:969:G:H8	1.78	0.48
1:1:1056:G:O2'	1:1:1103:A:N6	2.46	0.48
1:1:1482:G:O2'	1:1:1509:A:N1	2.41	0.48
1:1:2096:C:H2'	1:1:2097:A:C8	2.48	0.48
2:2:695:A:H61	2:2:797:C:H1'	1.79	0.48
2:2:1147:C:O2	41:n:18:ARG:NH2	2.47	0.48
3:3:7:G:O2'	16:O:38:GLN:NE2	2.46	0.48
5:B:69:ARG:NH2	5:B:127:GLY:O	2.39	0.48
9:F:84:THR:OG1	9:F:134:LYS:NZ	2.42	0.48
10:G:84:ALA:HA	10:G:91:PHE:H	1.77	0.48
10:G:132:PHE:HB2	10:G:140:ALA:HB3	1.96	0.48
17:P:88:ARG:NH2	17:P:110:ILE:O	2.46	0.48
21:T:4:GLU:HA	21:T:7:LEU:HD12	1.95	0.48
23:V:75:GLN:HB2	23:V:92:VAL:HG23	1.95	0.48
44:q:4:VAL:HA	44:q:7:LEU:HB2	1.96	0.48
47:t:73:LYS:HD2	47:t:73:LYS:HA	1.68	0.48
55:A:41:LEU:HD23	55:A:46:VAL:HG21	1.96	0.48
1:1:116:C:O2'	1:1:126:A:N3	2.40	0.48
5:B:84:ASP:OD1	5:B:86:ASN:ND2	2.46	0.48
20:S:34:ASP:OD2	29:b:37:LYS:NZ	2.36	0.48
38:k:59:TYR:HE2	50:w:67:LEU:HD21	1.78	0.48
40:m:39:VAL:O	40:m:43:GLU:N	2.46	0.48
55:A:141:ALA:O	55:A:145:ALA:N	2.43	0.48
1:1:282:A:H2'	1:1:283:G:H8	1.78	0.48
1:1:2130:U:H5''	1:1:2133:G:H4'	1.94	0.48
2:2:127:G:O2'	49:v:6:ARG:NH1	2.47	0.48
2:2:1256:A:O2'	2:2:1278:G:O6	2.30	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:g:51:ASN:HA	34:g:54:LEU:HD12	1.96	0.48
41:n:26:GLY:N	41:n:62:ASP:OD1	2.40	0.48
43:p:24:HIS:HB3	43:p:31:ILE:HB	1.95	0.48
47:t:69:TYR:CE2	47:t:73:LYS:HD3	2.49	0.48
55:A:26:ASP:O	55:A:30:LYS:N	2.43	0.48
1:1:532:A:N1	1:1:2035:G:N2	2.62	0.48
1:1:1189:A:OP1	19:R:82:HIS:CD2	2.67	0.48
6:C:125:TRP:NE1	6:C:161:MET:O	2.41	0.48
46:s:38:ASP:O	46:s:42:TRP:N	2.43	0.48
48:u:78:VAL:O	48:u:82:ALA:N	2.44	0.48
54:5:74:C:OP2	55:A:278:ARG:NH2	2.47	0.48
55:A:128:CYS:HB3	55:A:189:TYR:HB2	1.96	0.48
55:A:170:GLU:HA	55:A:176:ILE:HA	1.95	0.48
1:1:2559:C:H2'	1:1:2560:A:H8	1.79	0.48
2:2:66:A:H4'	2:2:173:U:C4	2.48	0.48
2:2:269:C:H2'	2:2:270:A:C8	2.49	0.48
2:2:666:G:H5'	2:2:726:C:H1'	1.94	0.48
2:2:1241:G:H2'	2:2:1242:G:H8	1.79	0.48
6:C:125:TRP:CG	6:C:160:LYS:HB3	2.49	0.48
36:i:62:ARG:NH1	36:i:69:GLU:OE1	2.46	0.48
1:1:1438:U:H2'	1:1:1439:A:H8	1.78	0.48
1:1:1568:G:OP2	5:B:63:ARG:NH1	2.42	0.48
1:1:1667:G:N1	1:1:1992:G:OP2	2.38	0.48
1:1:1721:G:H22	1:1:1738:G:H2'	1.79	0.48
2:2:413:G:O3'	2:2:428:G:N2	2.46	0.48
10:G:40:THR:HG22	10:G:42:LYS:H	1.79	0.48
36:i:27:ALA:O	36:i:30:THR:OG1	2.31	0.48
45:r:54:ASP:OD1	45:r:57:ARG:NH1	2.47	0.48
46:s:47:LYS:O	46:s:50:THR:OG1	2.29	0.48
1:1:182:A:N3	1:1:433:C:O2'	2.41	0.47
1:1:301:G:OP2	22:U:82:ARG:NH1	2.41	0.47
1:1:578:G:OP1	1:1:1255:U:O2'	2.29	0.47
1:1:894:U:C5	1:1:895:U:H5	2.32	0.47
1:1:1022:G:H4'	1:1:1023:U:H5'	1.96	0.47
1:1:1274:A:OP1	1:1:1646:C:N4	2.48	0.47
1:1:2796:U:O2'	1:1:2798:U:OP2	2.29	0.47
1:1:2881:U:O2'	15:N:95:THR:O	2.27	0.47
6:C:43:ASP:HB3	6:C:45:TYR:CE1	2.49	0.47
27:Z:37:GLU:O	27:Z:38:ARG:NH1	2.45	0.47
38:k:35:LYS:N	38:k:65:GLU:O	2.47	0.47
55:A:187:TYR:HD1	55:A:190:GLY:HA3	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:859:G:O2'	1:1:916:G:O6	2.31	0.47
1:1:974:G:N2	1:1:989:G:O2'	2.47	0.47
1:1:2118:U:O2'	1:1:2172:U:O4	2.31	0.47
1:1:2692:G:H2'	1:1:2693:G:C8	2.49	0.47
2:2:217:C:H5''	2:2:217:C:C6	2.49	0.47
2:2:252:U:O4	2:2:253:A:N6	2.47	0.47
2:2:531:U:H2'	55:A:332:ARG:HH22	1.79	0.47
9:F:18:LYS:HE2	9:F:20:ASN:HB2	1.96	0.47
17:P:62:ARG:HD2	17:P:71:GLU:HG2	1.96	0.47
36:i:58:LYS:NZ	36:i:69:GLU:OE1	2.46	0.47
55:A:234:ILE:HD11	55:A:292:LYS:HB2	1.96	0.47
1:1:1849:G:H2'	1:1:1850:G:H8	1.80	0.47
1:1:1954:G:O2'	1:1:1956:U:O4	2.27	0.47
2:2:322:C:O2	2:2:332:G:N2	2.46	0.47
2:2:1314:C:N4	51:x:2:PRO:O	2.33	0.47
11:J:58:ASN:ND2	11:J:128:ASN:OD1	2.46	0.47
48:u:68:SER:OG	48:u:69:ASP:N	2.46	0.47
55:A:117:ARG:HH11	55:A:361:LEU:HB2	1.78	0.47
1:1:281:C:H2'	1:1:282:A:C8	2.50	0.47
1:1:1023:U:OP2	1:1:1025:G:O2'	2.33	0.47
1:1:2748:A:H5'	9:F:4:VAL:HG21	1.95	0.47
2:2:67:C:O2'	2:2:171:A:N3	2.46	0.47
2:2:362:G:H5''	44:q:58:THR:HG21	1.97	0.47
2:2:1238:A:H5'	2:2:1336:C:H41	1.80	0.47
10:G:78:VAL:HB	10:G:144:VAL:HG22	1.97	0.47
19:R:48:LYS:HE2	19:R:103:ALA:HB1	1.97	0.47
26:Y:21:LEU:HD12	26:Y:46:VAL:HG13	1.97	0.47
1:1:160:A:N3	1:1:2208:C:O2'	2.44	0.47
1:1:1386:C:H2'	1:1:1387:A:H8	1.80	0.47
1:1:1966:A:O2'	1:1:1967:C:OP2	2.24	0.47
1:1:2237:G:O2'	1:1:2239:G:N7	2.39	0.47
1:1:2681:C:O2	1:1:2683:C:N4	2.46	0.47
14:M:33:LEU:HD13	14:M:117:PHE:HB3	1.96	0.47
55:A:30:LYS:HZ2	55:A:63:LEU:HD23	1.79	0.47
1:1:75:G:N2	1:1:112:U:O2	2.43	0.47
1:1:1536:C:O2	1:1:1537:G:N2	2.47	0.47
1:1:1926:U:O2'	1:1:1928:A:N7	2.44	0.47
1:1:2060:A:N7	7:D:69:ARG:NH2	2.60	0.47
1:1:2704:C:H3'	1:1:2705:A:H8	1.79	0.47
25:X:68:LEU:HD23	25:X:71:LEU:HD12	1.96	0.47
1:1:373:U:H2'	1:1:374:A:H8	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:690:G:O2'	1:1:780:G:OP1	2.33	0.47
1:1:729:G:N3	1:1:729:G:C2'	2.74	0.47
1:1:958:U:C2	3:3:89:U:H1'	2.49	0.47
1:1:1438:U:H2'	1:1:1439:A:C8	2.50	0.47
1:1:2241:A:H2'	1:1:2242:G:C8	2.50	0.47
1:1:2264:C:N4	24:W:15:ASP:OD2	2.47	0.47
1:1:2540:C:O2'	1:1:2740:A:N3	2.44	0.47
1:1:2572:A:O2'	1:1:2575:C:OP1	2.29	0.47
2:2:54:C:H2'	2:2:352:C:H41	1.80	0.47
2:2:429:U:H3	2:2:431:A:H62	1.61	0.47
2:2:618:C:H5'	2:2:619:U:H5''	1.96	0.47
2:2:671:G:O2'	38:k:79:ARG:NH1	2.44	0.47
5:B:63:ARG:H	5:B:86:ASN:HD21	1.61	0.47
8:E:140:GLU:OE2	28:a:26:SER:OG	2.31	0.47
8:E:158:THR:HG23	8:E:160:ALA:H	1.78	0.47
16:O:7:ARG:HH22	16:O:29:HIS:HE1	1.63	0.47
17:P:62:ARG:HB3	17:P:71:GLU:HA	1.96	0.47
20:S:10:ALA:HB3	20:S:101:SER:HB2	1.95	0.47
27:Z:49:ASN:HA	27:Z:52:SER:HB3	1.96	0.47
33:f:2:LYS:HB2	33:f:35:GLN:HG2	1.96	0.47
34:g:54:LEU:HD23	34:g:57:LEU:HD12	1.96	0.47
35:h:156:ARG:H	35:h:163:ALA:HA	1.80	0.47
36:i:147:GLU:O	36:i:151:LYS:NZ	2.43	0.47
45:r:34:LEU:HA	45:r:37:ALA:HB3	1.95	0.47
1:1:12:U:O4	1:1:13:A:N6	2.48	0.47
2:2:161:A:N6	2:2:347:G:O2'	2.45	0.47
2:2:1027:C:H2'	2:2:1034:G:H22	1.78	0.47
2:2:1222:G:H5''	51:x:78:ARG:HD2	1.97	0.47
2:2:1418:A:N6	2:2:1482:G:O2'	2.48	0.47
35:h:151:VAL:HG12	35:h:200:VAL:HG23	1.96	0.47
39:l:69:VAL:HG23	39:l:100:ALA:HB1	1.97	0.47
40:m:29:SER:HB3	40:m:57:PRO:HB2	1.97	0.47
40:m:112:THR:HG23	40:m:115:ALA:H	1.80	0.47
42:o:64:GLN:O	46:s:99:ALA:N	2.44	0.47
45:r:20:THR:HA	45:r:25:VAL:HG23	1.97	0.47
55:A:165:ILE:HA	55:A:181:ILE:HG13	1.97	0.47
1:1:2659:G:N2	1:1:2662:A:OP2	2.46	0.47
1:1:2861:U:H2'	1:1:2862:G:H8	1.80	0.47
2:2:1349:A:OP2	41:n:120:LYS:NZ	2.37	0.47
5:B:6:CYS:SG	5:B:13:ARG:NH2	2.88	0.47
6:C:110:THR:HA	6:C:171:THR:HA	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:98:LYS:HB3	7:D:102:ARG:HH22	1.79	0.47
10:G:128:HIS:O	10:G:144:VAL:N	2.41	0.47
1:1:370:G:O2'	1:1:424:G:OP1	2.26	0.47
1:1:658:U:O2'	7:D:97:ASN:OD1	2.29	0.47
1:1:958:U:N3	3:3:89:U:O2'	2.43	0.47
1:1:2193:G:O2'	1:1:2194:U:OP1	2.31	0.47
1:1:2296:U:OP2	16:O:9:ARG:NH2	2.47	0.47
2:2:401:C:N4	2:2:402:G:O6	2.48	0.47
2:2:974:A:H5'	46:s:71:HIS:HB3	1.97	0.47
2:2:1077:G:N2	2:2:1080:A:OP2	2.38	0.47
5:B:147:LYS:HD2	5:B:150:LYS:HD2	1.97	0.47
7:D:161:ALA:HA	7:D:164:LEU:HD12	1.97	0.47
26:Y:44:LYS:HG3	26:Y:47:ARG:HH11	1.80	0.47
30:c:35:GLU:HG2	30:c:50:LYS:HA	1.97	0.47
35:h:131:ARG:NH2	35:h:168:TYR:OH	2.47	0.47
39:l:12:ILE:HD13	39:l:28:ASN:HD21	1.79	0.47
1:1:910:A:N6	1:1:2277:G:O2'	2.36	0.46
1:1:1398:C:H2'	1:1:1399:C:H6	1.79	0.46
1:1:2278:A:OP2	24:W:12:ASN:ND2	2.39	0.46
2:2:521:G:H4'	44:q:70:GLU:HG2	1.96	0.46
2:2:921:U:O2'	37:j:24:THR:O	2.29	0.46
2:2:1183:U:O2'	2:2:1185:G:OP2	2.33	0.46
5:B:155:ALA:HB2	5:B:162:VAL:HG23	1.97	0.46
5:B:245:VAL:HG12	5:B:251:GLN:HA	1.96	0.46
6:C:116:LYS:HG3	15:N:1:MET:HE1	1.96	0.46
9:F:7:ALA:O	9:F:69:ARG:NE	2.47	0.46
10:G:3:VAL:HA	10:G:38:PRO:HA	1.97	0.46
37:j:84:PRO:HG3	37:j:97:GLN:HG3	1.97	0.46
41:n:130:ARG:HH12	54:5:32:4OC:H3'	1.79	0.46
1:1:26:G:H1'	1:1:515:A:H61	1.80	0.46
1:1:154:U:H2'	1:1:155:A:C8	2.50	0.46
1:1:183:C:O2'	1:1:432:A:N3	2.40	0.46
1:1:402:A:C5	1:1:403:U:C2	3.02	0.46
1:1:1062:G:O6	1:1:1075:C:N4	2.48	0.46
1:1:1463:C:H2'	1:1:1464:G:C8	2.50	0.46
2:2:510:A:O2'	2:2:542:G:O2'	2.30	0.46
2:2:776:G:N1	2:2:802:A:OP1	2.45	0.46
2:2:843:U:OP1	2:2:844:G:N2	2.47	0.46
2:2:1328:C:H5''	45:r:28:THR:HG21	1.96	0.46
37:j:111:MET:HA	37:j:114:VAL:HG12	1.97	0.46
38:k:100:SER:HB2	38:k:103:VAL:HG23	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:t:32:LEU:HA	47:t:35:GLN:HB3	1.97	0.46
55:A:40:GLU:HG3	55:A:43:GLN:HE21	1.81	0.46
1:1:411:G:OP2	1:1:2406:A:O2'	2.26	0.46
1:1:568:U:H1'	1:1:2030:6MZ:H9C1	1.97	0.46
1:1:2286:G:H21	1:1:2287:A:H62	1.62	0.46
2:2:17:U:O2'	2:2:1079:G:N3	2.47	0.46
2:2:77:A:H2'	2:2:78:A:C8	2.50	0.46
2:2:563:A:O2'	2:2:566:G:O3'	2.33	0.46
2:2:1303:C:H2'	2:2:1304:G:O4'	2.15	0.46
25:X:33:LEU:HD12	25:X:52:SER:HB3	1.98	0.46
41:n:84:THR:HG21	41:n:103:PHE:HB3	1.97	0.46
44:q:54:ARG:HD2	44:q:62:GLU:HG3	1.97	0.46
47:t:50:HIS:CA	47:t:53:ARG:HD2	2.45	0.46
51:x:11:ILE:HG13	51:x:38:SER:HB3	1.97	0.46
1:1:143:C:H6	1:1:143:C:H5''	1.80	0.46
1:1:1155:A:O3'	18:Q:55:ARG:NH2	2.41	0.46
1:1:1530:G:N3	1:1:1530:G:H2'	2.31	0.46
1:1:1671:U:N3	1:1:1674:G:OP2	2.34	0.46
1:1:2096:C:H2'	1:1:2097:A:H8	1.80	0.46
1:1:2286:G:H3'	30:c:30:LYS:HE3	1.97	0.46
1:1:2717:C:H2'	1:1:2718:G:O4'	2.15	0.46
2:2:477:C:H2'	2:2:478:A:O4'	2.16	0.46
2:2:859:G:OP2	2:2:869:G:N1	2.38	0.46
6:C:68:PHE:O	6:C:72:GLY:N	2.48	0.46
27:Z:42:PRO:HA	27:Z:45:ARG:HB2	1.97	0.46
1:1:1019:U:H2'	1:1:1020:A:H8	1.81	0.46
1:1:1987:A:H2'	1:1:1988:G:H8	1.81	0.46
1:1:2226:C:H2'	1:1:2227:A:O4'	2.16	0.46
2:2:652:U:O4	2:2:752:G:O2'	2.27	0.46
2:2:739:C:O2'	47:t:42:HIS:ND1	2.47	0.46
2:2:790:A:OP1	54:5:38:A:O2'	2.32	0.46
5:B:63:ARG:H	5:B:86:ASN:ND2	2.13	0.46
7:D:121:VAL:HG21	7:D:124:PHE:HB2	1.97	0.46
23:V:18:ARG:O	23:V:22:ALA:N	2.48	0.46
36:i:61:VAL:HA	36:i:64:ILE:HD12	1.97	0.46
54:5:55:PSU:N3	54:5:58:A:OP2	2.40	0.46
55:A:242:ASP:N	55:A:262:ARG:O	2.37	0.46
1:1:1501:G:OP1	5:B:101:ARG:NH2	2.45	0.46
1:1:1722:A:N6	1:1:1738:G:O2'	2.48	0.46
1:1:1859:U:H2'	1:1:1860:G:C8	2.51	0.46
1:1:2832:U:H4'	1:1:2833:U:H2'	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:740:U:OP1	47:t:38:HIS:NE2	2.42	0.46
2:2:937:A:N6	2:2:1345:U:O4	2.40	0.46
8:E:123:ASP:O	8:E:125:ARG:N	2.49	0.46
10:G:14:SER:OG	10:G:15:LEU:N	2.48	0.46
39:l:51:ALA:O	39:l:55:GLY:N	2.43	0.46
54:5:15:C:O2'	54:5:60:U:O2	2.32	0.46
1:1:1039:A:H2	1:1:1116:G:H22	1.64	0.46
1:1:1306:C:H2'	1:1:1307:A:C8	2.51	0.46
1:1:1788:C:H2'	1:1:1789:A:C8	2.50	0.46
1:1:1857:G:O2'	1:1:1884:G:N2	2.38	0.46
1:1:1967:C:H2'	1:1:1968:G:O4'	2.16	0.46
2:2:939:G:OP1	39:l:95:ARG:NH2	2.40	0.46
5:B:161:TYR:HB3	5:B:194:GLU:HG2	1.98	0.46
19:R:60:LYS:N	19:R:100:GLY:O	2.47	0.46
30:c:10:LYS:HA	30:c:22:THR:HA	1.97	0.46
40:m:48:ASP:O	40:m:62:THR:N	2.49	0.46
51:x:52:HIS:ND1	51:x:56:GLN:O	2.48	0.46
1:1:135:G:O6	1:1:446:G:N1	2.48	0.46
1:1:612:G:O2'	1:1:613:A:H5'	2.15	0.46
1:1:964:C:O2'	1:1:2273:A:N3	2.36	0.46
1:1:2655:G:N2	1:1:2656:U:O4	2.40	0.46
1:1:2806:C:H2'	1:1:2807:U:O4'	2.16	0.46
2:2:308:C:H2'	2:2:309:A:H8	1.80	0.46
2:2:1359:C:OP2	46:s:75:ARG:NE	2.49	0.46
12:K:70:ARG:HA	12:K:76:VAL:HA	1.97	0.46
34:g:65:GLY:O	34:g:225:ARG:NH1	2.48	0.46
35:h:56:VAL:HB	35:h:67:THR:HB	1.98	0.46
36:i:188:ARG:NH1	36:i:192:SER:O	2.49	0.46
47:t:33:THR:HA	47:t:63:ARG:HH11	1.81	0.46
1:1:581:C:H2'	1:1:582:A:H8	1.81	0.46
2:2:370:C:H2'	2:2:371:A:H8	1.80	0.46
2:2:509:A:H5'	36:i:51:TYR:HD2	1.80	0.46
18:Q:89:GLU:O	19:R:11:GLN:NE2	2.45	0.46
20:S:59:GLU:HB2	20:S:66:ILE:HD11	1.98	0.46
35:h:79:LYS:HB2	35:h:82:GLU:HB2	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
55:A:270:ILE:HB	55:A:291:MET:HE1	1.97	0.46
1:1:191:A:OP2	1:1:204:A:N6	2.42	0.46
1:1:282:A:H2'	1:1:283:G:C8	2.50	0.46
1:1:321:U:O3'	7:D:162:ARG:NH1	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:671:C:OP2	13:L:33:ARG:NH1	2.48	0.46
1:1:857:G:N2	1:1:921:C:O2	2.48	0.46
1:1:981:A:N1	1:1:2027:G:O2'	2.48	0.46
1:1:1364:G:OP1	25:X:50:ARG:NH1	2.42	0.46
1:1:1980:G:O2'	1:1:1982:U:OP2	2.32	0.46
1:1:2351:G:H2'	1:1:2365:G:H22	1.80	0.46
1:1:2642:G:H5'	11:J:80:HIS:CE1	2.51	0.46
2:2:1368:A:OP2	41:n:114:LYS:NZ	2.47	0.46
3:3:22:U:H2'	3:3:23:G:C8	2.51	0.46
3:3:116:G:H2'	3:3:117:G:C8	2.51	0.46
5:B:107:PRO:HD2	5:B:110:LEU:HD22	1.97	0.46
5:B:141:VAL:HG12	5:B:192:LEU:HA	1.97	0.46
6:C:150:GLN:O	6:C:151:THR:C	2.58	0.46
35:h:70:THR:O	35:h:106:VAL:N	2.41	0.46
1:1:205:G:H1'	1:1:206:U:H5	1.81	0.45
1:1:402:A:C6	1:1:403:U:C2	3.04	0.45
1:1:598:U:H2'	1:1:599:A:C8	2.52	0.45
1:1:1341:G:OP1	1:1:1397:U:N3	2.46	0.45
1:1:2529:G:H5'	9:F:175:LYS:HD3	1.98	0.45
2:2:437:U:O2'	36:i:120:HIS:ND1	2.44	0.45
2:2:1311:A:OP1	28:a:59:ARG:NH2	2.49	0.45
20:S:73:LYS:HB2	20:S:106:VAL:HB	1.98	0.45
36:i:26:ARG:HE	36:i:31:LYS:HG2	1.82	0.45
42:o:9:ARG:HB2	42:o:99:GLN:HB3	1.98	0.45
50:w:42:SER:OG	50:w:47:THR:O	2.25	0.45
55:A:56:LEU:HA	55:A:59:GLU:HB3	1.97	0.45
55:A:263:ILE:O	55:A:272:THR:N	2.49	0.45
1:1:581:C:H2'	1:1:582:A:C8	2.51	0.45
1:1:1528:A:OP2	1:1:1543:G:N2	2.40	0.45
1:1:1818:U:OP2	5:B:156:ARG:NE	2.37	0.45
1:1:1844:C:O3'	5:B:256:LYS:NZ	2.49	0.45
1:1:2056:G:O2'	29:b:5:GLN:NE2	2.43	0.45
1:1:2112:G:H5'	1:1:2115:G:H22	1.81	0.45
3:3:98:G:H1	23:V:14:LYS:HB2	1.81	0.45
8:E:111:ILE:HB	8:E:114:PHE:HB2	1.98	0.45
28:a:26:SER:OG	28:a:27:THR:N	2.49	0.45
51:x:15:LEU:HD13	51:x:33:THR:HG21	1.98	0.45
55:A:324:ARG:HG2	55:A:335:ASP:HA	1.99	0.45
1:1:154:U:H2'	1:1:155:A:H8	1.81	0.45
1:1:476:G:O2'	1:1:502:A:N6	2.45	0.45
1:1:2522:U:O2'	1:1:2647:U:OP1	2.29	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:160:A:H61	2:2:347:G:H1'	1.81	0.45
21:T:24:MET:HE2	21:T:30:ILE:HA	1.98	0.45
26:Y:28:LEU:O	26:Y:32:ALA:N	2.39	0.45
38:k:11:HIS:HB3	38:k:14:GLN:HG2	1.97	0.45
42:o:45:ARG:HB3	42:o:69:THR:HB	1.98	0.45
45:r:25:VAL:HG12	45:r:29:ARG:HD2	1.99	0.45
47:t:56:LEU:C	47:t:60:VAL:HG23	2.41	0.45
1:1:201:C:OP1	25:X:18:ARG:NH1	2.48	0.45
1:1:1464:G:H2'	1:1:1465:G:C8	2.51	0.45
2:2:217:C:H2'	2:2:218:U:O4'	2.16	0.45
2:2:519:C:N4	2:2:529:G:O2'	2.50	0.45
2:2:673:A:H4'	38:k:86:ARG:HH12	1.81	0.45
2:2:1123:U:H4'	42:o:39:PRO:HD2	1.97	0.45
2:2:1222:G:OP2	2:2:1322:C:N4	2.42	0.45
8:E:41:GLY:HA2	8:E:85:ILE:HD11	1.99	0.45
12:K:24:VAL:HA	12:K:39:ILE:HG22	1.98	0.45
19:R:66:HIS:ND1	19:R:94:THR:OG1	2.38	0.45
35:h:81:GLY:HA2	35:h:84:VAL:HB	1.98	0.45
37:j:102:GLY:H	37:j:122:ASN:ND2	2.14	0.45
1:1:376:G:H2'	1:1:377:G:H8	1.82	0.45
1:1:1135:C:N4	1:1:1138:G:OP2	2.37	0.45
2:2:83:C:O2'	2:2:86:G:O6	2.30	0.45
2:2:1391:U:H2'	2:2:1392:G:C8	2.51	0.45
8:E:23:ASN:N	8:E:27:GLN:OE1	2.49	0.45
1:1:1078:U:O2'	1:1:1088:A:O5'	2.35	0.45
1:1:2353:G:N2	24:W:34:GLY:O	2.40	0.45
2:2:1309:G:OP2	45:r:98:ARG:NE	2.38	0.45
9:F:65:ALA:O	9:F:69:ARG:N	2.46	0.45
25:X:40:VAL:HG12	25:X:43:GLU:H	1.81	0.45
34:g:15:HIS:HB3	34:g:43:LEU:HD11	1.98	0.45
35:h:19:ASN:OD1	35:h:54:ARG:NH2	2.44	0.45
48:u:8:ARG:H	48:u:28:ARG:HD2	1.82	0.45
55:A:129:TYR:HE1	55:A:182:LYS:HE2	1.82	0.45
1:1:887:A:H4'	1:1:889:C:H5	1.82	0.45
1:1:1614:A:N6	20:S:88:ARG:O	2.49	0.45
1:1:2699:C:H2'	1:1:2700:A:C8	2.52	0.45
1:1:2785:C:O3'	6:C:70:LYS:NZ	2.46	0.45
2:2:1159:U:O4'	2:2:1182:G:N2	2.50	0.45
2:2:1356:G:H2'	2:2:1357:A:C8	2.52	0.45
5:B:132:MET:HE2	5:B:188:CYS:HB2	1.98	0.45
6:C:38:LYS:HD3	6:C:45:TYR:OH	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:M:17:ASN:OD1	14:M:97:GLN:NE2	2.50	0.45
16:O:66:GLY:O	16:O:102:ARG:NH2	2.49	0.45
18:Q:69:ALA:HB1	18:Q:74:ILE:HG23	1.98	0.45
34:g:119:THR:O	34:g:124:GLY:N	2.45	0.45
38:k:40:GLU:OE1	38:k:100:SER:OG	2.32	0.45
1:1:414:C:H2'	1:1:415:A:C8	2.52	0.45
1:1:598:U:H2'	1:1:599:A:H8	1.81	0.45
1:1:828:U:H2'	1:1:829:A:C8	2.52	0.45
1:1:1992:G:N2	1:1:1996:C:O2'	2.49	0.45
1:1:2314:A:OP1	8:E:88:LYS:NZ	2.40	0.45
5:B:176:LEU:HD12	5:B:180:GLU:HB3	1.99	0.45
6:C:152:PRO:O	6:C:154:LYS:N	2.49	0.45
17:P:24:ASP:O	17:P:47:VAL:N	2.45	0.45
54:5:19:G:OP2	54:5:20:H2U:H51	2.16	0.45
54:5:51:C:H2'	54:5:52:G:H8	1.82	0.45
1:1:748:G:OP1	20:S:88:ARG:NH1	2.50	0.45
1:1:995:C:N3	11:J:3:THR:N	2.65	0.45
1:1:2368:C:H2'	1:1:2369:A:H8	1.80	0.45
1:1:2787:C:H1'	6:C:63:PRO:HG3	1.98	0.45
2:2:59:A:H2	2:2:330:C:H42	1.62	0.45
2:2:454:G:H2'	2:2:455:G:H8	1.81	0.45
2:2:1492:A:O2'	55:A:319:TRP:NE1	2.44	0.45
41:n:12:ARG:HA	41:n:12:ARG:HD2	1.70	0.45
46:s:41:ARG:NH2	51:x:6:LYS:O	2.50	0.45
1:1:151:C:H2'	1:1:152:A:C8	2.52	0.45
1:1:1267:U:H2'	1:1:1268:A:C8	2.52	0.45
1:1:1915:3TD:H3'	1:1:1916:A:C8	2.45	0.45
1:1:2128:G:N2	1:1:2174:C:O5'	2.50	0.45
2:2:452:A:O2'	48:u:70:ARG:NH2	2.44	0.45
2:2:531:U:OP2	55:A:213:ARG:NH2	2.50	0.45
2:2:957:U:H4'	51:x:79:THR:HG23	1.98	0.45
4:4:21:A:N6	55:A:215:THR:OG1	2.50	0.45
8:E:140:GLU:OE1	28:a:27:THR:OG1	2.28	0.45
10:G:83:LYS:HA	10:G:149:GLU:HB3	1.98	0.45
36:i:116:GLN:HE21	36:i:120:HIS:CE1	2.35	0.45
41:n:39:PHE:O	41:n:45:ARG:NH2	2.41	0.45
44:q:57:LEU:HD12	44:q:61:PHE:HB2	1.99	0.45
48:u:40:ASN:HB3	48:u:43:ALA:HB2	1.98	0.45
53:z:30:ALA:O	53:z:34:ARG:N	2.50	0.45
1:1:404:A:O5'	1:1:404:A:C8	2.70	0.44
1:1:711:G:H1	1:1:720:U:H3	1.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1047:G:HO2'	1:1:1110:G:H1	1.63	0.44
1:1:1123:C:H2'	1:1:1124:G:C8	2.52	0.44
1:1:2271:G:H5'	24:W:20:ARG:HG2	1.99	0.44
1:1:2503:2MA:O2'	1:1:2505:G:OP2	2.35	0.44
2:2:157:U:H2'	2:2:158:G:H8	1.82	0.44
2:2:257:G:H2'	2:2:258:G:H8	1.81	0.44
3:3:112:G:N2	16:O:45:SER:O	2.42	0.44
6:C:45:TYR:HE2	6:C:81:GLU:OE2	2.00	0.44
47:t:36:ILE:HB	47:t:63:ARG:NH1	2.32	0.44
55:A:196:THR:HG22	55:A:222:VAL:H	1.82	0.44
1:1:894:U:C6	1:1:894:U:OP2	2.70	0.44
2:2:197:A:N3	2:2:198:G:H1'	2.32	0.44
5:B:145:GLU:HB2	5:B:188:CYS:HB3	1.98	0.44
8:E:58:ALA:HB2	8:E:65:PRO:HD3	1.99	0.44
11:J:45:THR:HB	11:J:48:VAL:HB	1.99	0.44
22:U:51:ALA:O	22:U:52:LEU:HB3	2.16	0.44
42:o:6:ILE:HB	42:o:76:ILE:HB	1.99	0.44
46:s:69:ARG:HD3	46:s:71:HIS:H	1.82	0.44
53:z:31:GLU:OE2	53:z:34:ARG:NH2	2.38	0.44
54:5:60:U:OP2	54:5:60:U:C6	2.71	0.44
1:1:558:U:H2'	1:1:559:G:H8	1.81	0.44
1:1:717:C:H3'	1:1:718:A:C8	2.51	0.44
1:1:1114:C:H2'	1:1:1115:G:C8	2.53	0.44
1:1:1419:A:O2'	1:1:1421:G:N7	2.43	0.44
1:1:2119:A:N7	1:1:2169:A:N6	2.64	0.44
1:1:2127:G:N1	1:1:2161:C:N3	2.65	0.44
1:1:296:U:H2'	1:1:297:G:C8	2.53	0.44
1:1:404:A:H5'	1:1:406:G:C1'	2.48	0.44
1:1:463:G:N2	1:1:466:A:OP2	2.38	0.44
1:1:1026:G:OP1	1:1:1134:A:O2'	2.30	0.44
1:1:1270:C:H5''	1:1:1271:G:H5''	1.99	0.44
1:1:1651:G:H4'	15:N:39:PRO:HG2	1.98	0.44
1:1:2216:G:H2'	1:1:2217:G:C8	2.52	0.44
1:1:2371:G:O2'	30:c:46:HIS:ND1	2.47	0.44
2:2:806:C:H2'	2:2:807:A:H8	1.83	0.44
26:Y:29:ARG:O	26:Y:33:ALA:N	2.50	0.44
35:h:65:ARG:HA	35:h:100:GLN:HB3	1.99	0.44
47:t:73:LYS:O	47:t:73:LYS:HD2	2.17	0.44
1:1:632:A:N3	1:1:2403:C:O2'	2.44	0.44
2:2:711:G:H2'	2:2:712:A:H8	1.82	0.44
10:G:125:THR:HG21	10:G:148:ALA:HB2	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:M:136:MET:HE3	23:V:57:TYR:HB3	2.00	0.44
20:S:20:VAL:HG21	20:S:43:ALA:HB3	2.00	0.44
53:z:7:ARG:HH22	53:z:18:ARG:HH12	1.65	0.44
54:5:18:G:N2	54:5:58:A:O5'	2.49	0.44
1:1:616:A:H3'	1:1:617:G:H8	1.83	0.44
1:1:1463:C:H2'	1:1:1464:G:H8	1.82	0.44
1:1:2314:A:H1'	8:E:155:THR:HG21	1.99	0.44
2:2:32:A:OP2	2:2:398:U:O2'	2.29	0.44
2:2:257:G:H2'	2:2:258:G:C8	2.53	0.44
2:2:769:G:H4'	2:2:1513:A:H4'	1.99	0.44
2:2:1158:C:O2	2:2:1158:C:H2'	2.17	0.44
2:2:1402:4OC:HM22	2:2:1403:C:H5'	2.00	0.44
39:l:141:VAL:O	39:l:145:ALA:N	2.43	0.44
47:t:2:SER:HA	47:t:35:GLN:HE22	1.82	0.44
48:u:44:SER:OG	48:u:45:GLU:N	2.49	0.44
1:1:402:A:H3'	1:1:403:U:H6	1.82	0.44
1:1:728:G:H4'	5:B:13:ARG:HD3	2.00	0.44
1:1:750:A:OP1	1:1:1615:C:N4	2.50	0.44
1:1:894:U:C4'	1:1:895:U:OP1	2.65	0.44
1:1:1076:C:H2'	1:1:1077:A:H8	1.83	0.44
1:1:1153:C:OP1	18:Q:76:TYR:OH	2.35	0.44
1:1:2098:U:H2'	1:1:2099:U:O4'	2.17	0.44
2:2:397:A:O2'	2:2:399:G:OP2	2.28	0.44
2:2:674:G:H2'	2:2:675:A:C8	2.53	0.44
35:h:148:GLY:HA2	35:h:171:GLY:HA3	2.00	0.44
36:i:152:GLN:HB2	36:i:155:VAL:HG23	1.99	0.44
41:n:49:ARG:O	41:n:53:GLU:N	2.50	0.44
44:q:4:VAL:O	44:q:8:VAL:N	2.49	0.44
47:t:57:LEU:C	47:t:60:VAL:H	2.25	0.44
55:A:41:LEU:HD11	55:A:56:LEU:HB3	1.99	0.44
1:1:1825:U:H2'	1:1:1826:G:C8	2.53	0.44
1:1:2200:C:OP2	25:X:37:ARG:NH1	2.50	0.44
1:1:2824:C:H3'	1:1:2825:G:H21	1.83	0.44
2:2:499:A:H4'	2:2:500:G:H5'	2.00	0.44
2:2:730:G:H1	47:t:51:HIS:HE1	1.64	0.44
2:2:1086:U:H3	2:2:1099:G:H22	1.66	0.44
2:2:1239:A:O2'	2:2:1298:U:O4	2.36	0.44
2:2:1297:G:N2	2:2:1298:U:O4	2.50	0.44
6:C:13:ARG:HG2	17:P:56:HIS:CE1	2.53	0.44
7:D:41:GLN:HG2	7:D:43:THR:HG23	1.99	0.44
21:T:15:HIS:HB3	21:T:31:VAL:HG12	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:T:38:ALA:O	21:T:81:LYS:NZ	2.38	0.44
34:g:76:ALA:HB1	34:g:210:VAL:HG11	1.99	0.44
51:x:50:ALA:HB1	51:x:57:HIS:HB3	1.99	0.44
55:A:325:SER:N	55:A:334:LYS:O	2.50	0.44
1:1:106:C:H2'	1:1:107:G:C8	2.53	0.44
1:1:729:G:C4	1:1:1775:U:C2	3.05	0.44
1:1:1589:U:O2'	1:1:1590:A:H5'	2.18	0.44
1:1:1854:A:N6	1:1:1888:G:O2'	2.50	0.44
1:1:2544:G:H2'	1:1:2545:G:H8	1.83	0.44
2:2:1078:U:O2	37:j:135:ASN:ND2	2.42	0.44
2:2:1162:C:H2'	2:2:1163:A:H8	1.82	0.44
3:3:5:U:H2'	3:3:6:G:C8	2.53	0.44
6:C:151:THR:HG1	6:C:152:PRO:HD3	1.66	0.44
54:5:63:G:H2'	54:5:64:G:C8	2.53	0.44
1:1:177:G:H3'	1:1:178:G:H8	1.82	0.43
1:1:558:U:H2'	1:1:559:G:C8	2.53	0.43
1:1:1044:C:O2'	1:1:1111:A:N1	2.47	0.43
1:1:1332:G:N7	1:1:1609:A:O2'	2.39	0.43
1:1:1443:U:H2'	1:1:1444:G:H8	1.83	0.43
1:1:1796:U:H2'	1:1:1797:G:C8	2.53	0.43
1:1:2002:G:H5''	15:N:9:GLN:HE21	1.82	0.43
2:2:1273:C:H2'	2:2:1274:A:O4'	2.17	0.43
2:2:1406:U:H3'	2:2:1407:5MC:H6	1.83	0.43
5:B:71:LYS:O	5:B:118:SER:OG	2.36	0.43
7:D:29:HIS:HD2	13:L:6:LEU:HB3	1.83	0.43
15:N:52:ILE:HD13	15:N:94:TYR:HB2	2.00	0.43
27:Z:45:ARG:HA	27:Z:48:ILE:HD12	1.99	0.43
31:d:17:GLY:HA2	31:d:45:SER:HB2	2.00	0.43
34:g:7:ARG:O	34:g:11:LYS:N	2.47	0.43
36:i:62:ARG:O	36:i:66:GLY:N	2.50	0.43
54:5:6:G:O2'	54:5:49:G:O4'	2.36	0.43
55:A:117:ARG:HH22	55:A:362:LYS:HE2	1.83	0.43
1:1:1273:U:O2	1:1:2002:G:O2'	2.32	0.43
1:1:1475:G:O2'	1:1:1514:G:O6	2.27	0.43
1:1:2461:A:N6	1:1:2488:G:O6	2.51	0.43
2:2:67:C:H2'	2:2:68:G:C8	2.53	0.43
2:2:199:A:H61	2:2:218:U:H3	1.66	0.43
2:2:366:A:O2'	2:2:394:G:N2	2.50	0.43
2:2:552:U:O2'	44:q:83:ARG:O	2.30	0.43
6:C:5:VAL:HG22	6:C:202:ILE:HG12	2.00	0.43
9:F:10:VAL:HA	9:F:49:THR:HA	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:c:9:ILE:O	30:c:22:THR:OG1	2.26	0.43
35:h:20:SER:HB3	35:h:22:TRP:HE1	1.83	0.43
43:p:46:THR:OG1	43:p:49:GLY:N	2.51	0.43
1:1:564:C:O4'	18:Q:37:GLN:NE2	2.51	0.43
1:1:593:U:H2'	1:1:594:U:C6	2.53	0.43
1:1:949:G:H2'	1:1:950:G:H8	1.81	0.43
1:1:1038:G:H2'	1:1:1039:A:C8	2.53	0.43
1:1:1358:G:N1	1:1:1372:U:OP2	2.32	0.43
1:1:1631:G:N2	1:1:1634:A:OP2	2.46	0.43
1:1:2291:U:OP1	1:1:2380:C:O2'	2.28	0.43
1:1:2549:G:H2'	1:1:2550:G:H8	1.82	0.43
2:2:1173:U:H2'	2:2:1174:G:H8	1.83	0.43
2:2:1297:G:H21	39:l:114:LYS:HB3	1.84	0.43
30:c:8:LYS:HD2	32:e:34:THR:HG21	1.98	0.43
35:h:59:ARG:HA	35:h:64:ILE:HA	2.00	0.43
36:i:103:TYR:O	36:i:165:ARG:NH2	2.51	0.43
42:o:8:ILE:HG12	42:o:100:ILE:HG22	1.99	0.43
51:x:52:HIS:CD2	51:x:54:GLY:H	2.36	0.43
55:A:242:ASP:O	55:A:262:ARG:N	2.52	0.43
55:A:271:VAL:O	55:A:294:LYS:NZ	2.50	0.43
1:1:402:A:C4	1:1:403:U:O4'	2.70	0.43
1:1:729:G:H4'	1:1:763:G:O5'	2.18	0.43
1:1:890:C:H2'	1:1:891:G:H4'	2.00	0.43
1:1:1030:C:OP2	14:M:127:LYS:NZ	2.49	0.43
1:1:1342:A:OP1	21:T:40:LYS:NZ	2.34	0.43
1:1:1791:A:N6	1:1:1828:G:O2'	2.48	0.43
1:1:1844:C:H2'	1:1:1845:G:H8	1.82	0.43
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
2:2:77:A:H2'	2:2:78:A:H8	1.83	0.43
2:2:376:G:H4'	48:u:5:ARG:HH11	1.82	0.43
2:2:1376:U:H2'	2:2:1377:A:C8	2.53	0.43
8:E:123:ASP:CG	8:E:127:ASN:HB2	2.42	0.43
22:U:8:ASP:HB2	22:U:24:LYS:HD3	1.99	0.43
31:d:23:ALA:O	31:d:28:ARG:NH1	2.51	0.43
34:g:32:PHE:N	34:g:40:ILE:O	2.48	0.43
36:i:34:ILE:HG23	36:i:35:GLU:HG2	1.99	0.43
45:r:101:ARG:HG3	45:r:104:THR:H	1.84	0.43
50:w:48:ARG:HD3	50:w:50:LYS:H	1.83	0.43
55:A:265:HIS:CD2	55:A:267:PRO:HD2	2.53	0.43
1:1:242:G:N2	1:1:255:A:OP2	2.37	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1278:C:H2'	1:1:1279:G:H8	1.81	0.43
1:1:1464:G:H2'	1:1:1465:G:H8	1.84	0.43
2:2:111:G:H22	2:2:330:C:H41	1.65	0.43
2:2:137:U:H2'	2:2:138:G:C8	2.53	0.43
2:2:406:G:H21	36:i:116:GLN:HE22	1.67	0.43
2:2:1464:U:H2'	2:2:1465:A:H8	1.84	0.43
7:D:2:GLU:HB3	7:D:11:ALA:HB1	2.00	0.43
20:S:77:ASP:O	20:S:102:HIS:N	2.50	0.43
28:a:20:ASN:HB2	28:a:39:LYS:HD3	2.01	0.43
34:g:162:PHE:HA	34:g:184:PHE:HB2	1.99	0.43
37:j:97:GLN:N	37:j:124:LEU:O	2.51	0.43
1:1:7:G:H5''	11:J:123:LYS:HE2	2.01	0.43
1:1:784:G:C8	1:1:792:A:N7	2.87	0.43
1:1:968:C:H2'	1:1:969:G:C8	2.54	0.43
1:1:2128:G:H1'	1:1:2174:C:H1'	2.00	0.43
2:2:490:C:H2'	2:2:491:G:C8	2.54	0.43
2:2:496:A:H2'	2:2:496:A:N3	2.33	0.43
2:2:886:G:H1	2:2:911:U:H3	1.67	0.43
2:2:1412:C:H2'	2:2:1413:A:C8	2.53	0.43
7:D:181:ILE:HG23	13:L:1:MET:HG2	2.01	0.43
9:F:27:LYS:HG2	9:F:32:GLU:HB2	2.01	0.43
10:G:66:ASN:CG	10:G:135:HIS:HB3	2.44	0.43
29:b:31:ASP:HB3	29:b:36:GLU:H	1.83	0.43
34:g:19:GLN:HB2	34:g:22:TYR:HD2	1.83	0.43
37:j:114:VAL:HG13	37:j:115:LEU:HD22	2.00	0.43
39:l:26:PHE:HA	39:l:29:ILE:HD12	2.01	0.43
55:A:169:SER:HG	55:A:178:SER:HG	1.64	0.43
1:1:5:A:H2'	1:1:6:A:C8	2.53	0.43
1:1:458:G:N2	1:1:459:U:O4	2.50	0.43
1:1:1583:A:N3	1:1:1584:U:N3	2.66	0.43
1:1:2425:A:H5'	1:1:2427:C:O4'	2.19	0.43
1:1:2447:G:N2	1:1:2450:A:OP2	2.52	0.43
15:N:66:ALA:O	15:N:70:THR:OG1	2.27	0.43
25:X:69:ALA:O	25:X:73:ALA:N	2.43	0.43
26:Y:18:LEU:HB2	26:Y:53:VAL:HG11	2.00	0.43
37:j:84:PRO:HG3	37:j:98:PRO:HD2	2.01	0.43
38:k:78:PHE:HD1	38:k:84:VAL:HG11	1.83	0.43
52:y:35:VAL:HG11	52:y:79:LEU:HD13	2.01	0.43
52:y:67:ILE:HB	52:y:71:LYS:HD3	2.01	0.43
1:1:563:A:H2'	18:Q:37:GLN:HE21	1.82	0.43
1:1:974:G:O2'	1:1:989:G:N2	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1065:U:O2	1:1:1073:A:N6	2.51	0.43
1:1:1820:U:N3	5:B:198:ALA:O	2.46	0.43
1:1:2087:G:H2'	1:1:2088:A:H8	1.83	0.43
1:1:2251:OMG:OP1	14:M:81:ARG:NH1	2.50	0.43
1:1:2392:A:OP1	32:e:31:HIS:NE2	2.52	0.43
1:1:2674:G:O2'	12:K:28:SER:O	2.31	0.43
2:2:1375:A:OP1	39:l:25:LYS:NZ	2.45	0.43
16:O:43:ASN:HD21	16:O:46:GLU:HG2	1.83	0.43
28:a:30:HIS:ND1	28:a:31:ASP:O	2.45	0.43
55:A:203:ARG:HH12	55:A:206:PRO:HD3	1.83	0.43
1:1:441:U:H2'	1:1:442:G:C8	2.53	0.43
1:1:1306:C:H2'	1:1:1307:A:H8	1.84	0.43
1:1:1820:U:O2'	5:B:157:SER:OG	2.34	0.43
1:1:1914:C:N3	1:1:1915:3TD:H1'	2.34	0.43
1:1:2572:A:OP1	1:1:2574:G:O2'	2.33	0.43
2:2:60:A:N1	2:2:107:G:O2'	2.49	0.43
2:2:750:C:O2'	47:t:21:ASP:O	2.27	0.43
2:2:940:C:H2'	2:2:941:G:C8	2.54	0.43
7:D:106:LYS:HG3	7:D:200:LEU:HD23	2.01	0.43
9:F:42:GLU:HA	9:F:55:ARG:NH2	2.34	0.43
10:G:103:VAL:HB	10:G:110:VAL:HG11	2.01	0.43
13:L:88:GLY:O	13:L:121:THR:N	2.45	0.43
41:n:97:GLU:O	41:n:101:ALA:N	2.46	0.43
51:x:39:THR:HA	51:x:70:LYS:HA	2.00	0.43
55:A:29:ALA:HA	55:A:32:GLU:HB3	1.99	0.43
1:1:1013:C:H2'	1:1:1014:A:C8	2.53	0.43
1:1:1128:G:N3	1:1:2516:A:O2'	2.43	0.43
1:1:1341:G:H1'	21:T:59:ASN:HB3	1.99	0.43
2:2:522:C:OP2	44:q:66:TYR:OH	2.25	0.43
2:2:1086:U:H3	2:2:1099:G:H1	1.67	0.43
2:2:1338:G:H21	54:5:41:C:H1'	1.84	0.43
3:3:23:G:H2'	3:3:24:G:C5	2.54	0.43
3:3:51:G:OP1	16:O:63:LYS:NZ	2.45	0.43
23:V:32:GLY:O	23:V:93:ARG:NH1	2.45	0.43
27:Z:8:THR:HB	27:Z:56:LYS:HB3	2.01	0.43
36:i:170:TRP:CD2	36:i:186:PRO:HB3	2.54	0.43
41:n:12:ARG:HG3	41:n:13:LYS:H	1.83	0.43
1:1:745:1MG:O2'	1:1:750:A:N6	2.52	0.42
1:1:1102:C:H2'	1:1:1103:A:C8	2.53	0.42
1:1:1602:U:OP2	21:T:64:LYS:NZ	2.52	0.42
1:1:2406:A:O4'	13:L:69:ARG:NH1	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:996:A:N1	2:2:1045:C:O2'	2.44	0.42
6:C:13:ARG:HH11	17:P:56:HIS:HA	1.84	0.42
35:h:107:ARG:HG3	35:h:108:LYS:HG3	2.01	0.42
37:j:38:VAL:HA	37:j:48:PHE:HA	2.00	0.42
41:n:34:SER:OG	41:n:35:LEU:N	2.52	0.42
50:w:51:TYR:O	50:w:55:LEU:N	2.50	0.42
1:1:45:G:H5''	1:1:46:G:H5'	2.01	0.42
1:1:935:C:H2'	1:1:936:A:C8	2.54	0.42
1:1:956:G:N2	1:1:960:A:OP2	2.37	0.42
1:1:1000:A:OP2	1:1:1154:G:N1	2.37	0.42
1:1:1222:U:H2'	1:1:1223:G:H8	1.84	0.42
1:1:2087:G:H2'	1:1:2088:A:C8	2.54	0.42
1:1:2368:C:H2'	1:1:2369:A:C8	2.54	0.42
2:2:269:C:H2'	2:2:270:A:H8	1.84	0.42
2:2:309:A:H5'	48:u:29:ASN:HB3	2.02	0.42
2:2:1095:U:OP1	2:2:1108:G:N1	2.46	0.42
6:C:48:ILE:HG23	6:C:84:LEU:HD11	2.01	0.42
20:S:73:LYS:HB3	20:S:75:PHE:HE2	1.83	0.42
34:g:120:GLN:HA	34:g:124:GLY:HA3	2.01	0.42
43:p:35:THR:OG1	43:p:36:ASP:N	2.51	0.42
46:s:63:ARG:HB3	46:s:68:GLY:HA2	2.01	0.42
1:1:577:G:O2'	1:1:1254:A:OP1	2.37	0.42
1:1:894:U:H4'	1:1:895:U:OP1	2.19	0.42
1:1:910:A:N6	14:M:11:LYS:O	2.52	0.42
1:1:1278:C:H2'	1:1:1279:G:C8	2.54	0.42
1:1:1700:A:H3'	1:1:1701:A:H8	1.84	0.42
1:1:1914:C:H2'	1:1:1915:3TD:O4'	2.20	0.42
1:1:2108:A:N6	1:1:2181:U:H3	2.17	0.42
2:2:504:C:H42	2:2:541:G:H1	1.67	0.42
2:2:711:G:H2'	2:2:712:A:C8	2.54	0.42
2:2:744:C:H2'	2:2:745:G:C8	2.53	0.42
5:B:199:GLU:HA	5:B:202:LEU:HD23	2.02	0.42
15:N:44:LEU:HG	15:N:48:VAL:HB	2.01	0.42
22:U:102:THR:HB	22:U:104:LYS:HE2	2.01	0.42
28:a:42:PRO:HB2	28:a:46:GLY:HA3	2.01	0.42
35:h:152:GLU:N	35:h:199:LYS:O	2.53	0.42
55:A:276:ASN:N	55:A:283:ASN:OD1	2.52	0.42
1:1:1287:A:N6	15:N:105:GLY:O	2.49	0.42
1:1:1948:G:O2'	2:2:1418:A:N1	2.48	0.42
1:1:2252:G:H2'	1:1:2253:G:H8	1.83	0.42
1:1:2880:C:HO2'	15:N:90:ARG:NH2	2.15	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:357:G:C4'	2:2:368:U:H5''	2.38	0.42
2:2:1134:G:H1	2:2:1140:C:H42	1.65	0.42
15:N:38:LEU:O	15:N:42:LYS:N	2.50	0.42
43:p:64:GLN:HB2	43:p:99:ALA:HB2	2.02	0.42
46:s:41:ARG:HH22	51:x:6:LYS:HB2	1.83	0.42
47:t:36:ILE:O	47:t:40:GLN:N	2.52	0.42
55:A:164:GLU:O	55:A:182:LYS:N	2.50	0.42
55:A:276:ASN:HD22	55:A:286:GLN:HG2	1.84	0.42
1:1:706:A:OP1	5:B:7:LYS:NZ	2.37	0.42
1:1:918:A:N3	3:3:80:U:O2'	2.50	0.42
1:1:1398:C:H2'	1:1:1399:C:C6	2.53	0.42
1:1:1954:G:N2	1:1:1956:U:O2	2.48	0.42
1:1:2233:U:H2'	1:1:2234:G:C8	2.54	0.42
2:2:335:C:H2'	2:2:336:A:H8	1.85	0.42
2:2:368:U:O2	2:2:368:U:C2'	2.68	0.42
2:2:404:G:O2'	2:2:498:A:N1	2.47	0.42
2:2:750:C:H2'	2:2:751:U:C6	2.55	0.42
2:2:950:U:H3'	45:r:101:ARG:HH22	1.84	0.42
2:2:1221:G:H5''	51:x:36:ARG:HH11	1.84	0.42
13:L:23:ILE:HG12	19:R:82:HIS:CE1	2.54	0.42
34:g:163:VAL:N	34:g:184:PHE:O	2.50	0.42
38:k:36:ILE:HD11	38:k:39:LEU:HB2	2.02	0.42
39:l:87:VAL:HA	39:l:88:PRO:HD3	1.94	0.42
1:1:69:C:O2	1:1:73:A:O2'	2.31	0.42
1:1:181:A:H2'	1:1:182:A:C8	2.54	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
1:1:851:C:O2'	27:Z:43:ALA:O	2.34	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
1:1:1496:A:H2'	1:1:1498:C:C4	2.54	0.42
1:1:1580:A:H3'	1:1:1581:G:H8	1.83	0.42
1:1:2833:U:H3'	1:1:2834:G:C8	2.55	0.42
1:1:2861:U:H2'	1:1:2862:G:C8	2.55	0.42
6:C:101:PHE:HD1	6:C:104:VAL:HG21	1.85	0.42
12:K:16:ALA:HA	12:K:46:ALA:HA	2.02	0.42
22:U:51:ALA:O	22:U:52:LEU:CB	2.67	0.42
24:W:33:ALA:N	24:W:64:ASP:OD1	2.52	0.42
45:r:13:LYS:HD3	45:r:17:ILE:HG22	2.01	0.42
48:u:18:GLN:HE22	48:u:35:ARG:HH21	1.66	0.42
1:1:585:G:O6	1:1:1251:C:O2'	2.25	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:696:G:H2'	1:1:697:G:H8	1.83	0.42
1:1:1477:A:N6	1:1:1514:G:O2'	2.52	0.42
1:1:1583:A:H1'	1:1:1584:U:C2	2.54	0.42
1:1:2523:G:O2'	1:1:2764:A:O2'	2.34	0.42
1:1:2708:G:O2'	15:N:71:ARG:NH1	2.52	0.42
2:2:714:G:N2	2:2:777:A:N3	2.49	0.42
14:M:121:ALA:HA	14:M:124:LEU:HD12	2.01	0.42
35:h:32:ASN:OD1	35:h:59:ARG:NH1	2.51	0.42
39:l:78:ARG:HG2	39:l:80:VAL:HG13	2.01	0.42
51:x:3:ARG:HH11	51:x:10:PHE:HB2	1.83	0.42
1:1:219:A:N3	1:1:234:U:O2'	2.47	0.42
1:1:596:U:H2'	1:1:597:G:C8	2.55	0.42
1:1:1426:G:H3'	1:1:1427:A:H2'	2.02	0.42
1:1:1443:U:H2'	1:1:1444:G:C8	2.55	0.42
1:1:1934:C:H2'	1:1:1935:G:H8	1.84	0.42
1:1:2081:U:H2'	1:1:2082:A:H8	1.83	0.42
1:1:2251:OMG:HM23	1:1:2251:OMG:H1'	1.87	0.42
1:1:2821:A:H2'	1:1:2822:G:H8	1.84	0.42
2:2:21:G:H2'	2:2:22:G:C8	2.55	0.42
2:2:1060:U:H2'	2:2:1061:G:H8	1.85	0.42
7:D:58:LYS:HA	7:D:59:PRO:HD3	1.94	0.42
34:g:12:ALA:HB1	34:g:209:ALA:HA	2.02	0.42
38:k:8:PHE:HA	38:k:87:SER:HA	2.00	0.42
38:k:21:MET:HG2	38:k:24:ARG:HH21	1.84	0.42
40:m:28:PRO:HA	40:m:58:GLU:HA	2.02	0.42
52:y:28:MET:HE1	52:y:67:ILE:HG21	2.02	0.42
1:1:175:G:H2'	1:1:176:A:C8	2.54	0.42
1:1:1028:A:N3	1:1:2486:C:O2'	2.44	0.42
1:1:1295:C:H4'	15:N:22:ARG:HH21	1.85	0.42
1:1:2520:C:H2'	1:1:2521:C:H6	1.85	0.42
2:2:559:A:H4'	2:2:560:A:H3'	2.01	0.42
2:2:1386:G:H2'	2:2:1387:G:H8	1.85	0.42
3:3:86:G:H3'	3:3:88:C:H41	1.84	0.42
8:E:99:PHE:HA	8:E:102:ARG:HE	1.85	0.42
8:E:122:PHE:HE1	8:E:170:LEU:HD12	1.85	0.42
11:J:117:ALA:HA	11:J:120:ARG:HH21	1.85	0.42
12:K:23:LYS:HB3	12:K:40:LYS:HB3	2.02	0.42
16:O:30:ARG:HD3	16:O:102:ARG:NH1	2.35	0.42
26:Y:39:GLN:HB3	26:Y:41:HIS:CE1	2.55	0.42
47:t:49:ASP:O	47:t:52:SER:N	2.49	0.42
1:1:371:A:N6	1:1:402:A:OP2	2.44	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:783:A:N3	1:1:783:A:C2'	2.81	0.42
1:1:1408:G:O6	1:1:1593:A:N6	2.52	0.42
1:1:2162:G:O2'	1:1:2163:A:N7	2.47	0.42
1:1:2193:G:HO2'	1:1:2194:U:P	2.43	0.42
1:1:2580:PSU:OP1	6:C:137:SER:OG	2.31	0.42
2:2:154:U:H2'	2:2:155:A:H8	1.84	0.42
2:2:375:U:O3'	48:u:6:LEU:HB2	2.20	0.42
9:F:127:THR:HB	9:F:130:GLU:HB3	2.01	0.42
42:o:42:LEU:HB2	42:o:71:LEU:HB3	2.01	0.42
55:A:208:ASP:OD2	55:A:211:GLY:N	2.53	0.42
1:1:82:U:H2'	1:1:83:A:C8	2.55	0.41
1:1:720:U:H2'	1:1:721:A:C8	2.55	0.41
1:1:741:U:H2'	1:1:742:A:H8	1.85	0.41
1:1:992:C:H2'	1:1:993:G:C8	2.54	0.41
1:1:1252:G:H5''	18:Q:32:TYR:HE2	1.85	0.41
1:1:2183:A:H2'	1:1:2184:A:C8	2.55	0.41
2:2:195:A:H2'	2:2:196:A:C8	2.55	0.41
2:2:231:U:H2'	2:2:232:G:H8	1.84	0.41
2:2:583:A:N6	2:2:758:C:O2'	2.53	0.41
2:2:770:C:H2'	2:2:771:G:H8	1.84	0.41
8:E:117:LEU:N	8:E:177:PHE:O	2.39	0.41
18:Q:31:VAL:HG12	18:Q:34:VAL:H	1.85	0.41
1:1:848:C:H2'	1:1:849:A:C8	2.55	0.41
1:1:2124:G:H1	1:1:2174:C:H42	1.68	0.41
1:1:2508:G:O2'	1:1:2554:U:O2'	2.25	0.41
2:2:34:C:H2'	2:2:35:G:C8	2.53	0.41
2:2:1241:G:H2'	2:2:1242:G:C8	2.55	0.41
6:C:46:ARG:NH2	6:C:88:GLU:O	2.36	0.41
14:M:36:VAL:H	14:M:128:THR:HA	1.85	0.41
19:R:51:VAL:CG2	19:R:52:PRO:HD3	2.50	0.41
25:X:33:LEU:HA	25:X:52:SER:HA	2.02	0.41
30:c:9:ILE:HA	30:c:54:ILE:HB	2.02	0.41
36:i:124:MET:HG3	36:i:146:ARG:HB3	2.02	0.41
41:n:65:ILE:HD13	41:n:79:ILE:HG23	2.01	0.41
55:A:198:VAL:HG22	55:A:219:SER:HB3	2.02	0.41
1:1:1653:G:C6	15:N:9:GLN:HB3	2.56	0.41
1:1:2175:C:H3'	1:1:2176:A:C8	2.55	0.41
2:2:1126:U:O4	42:o:9:ARG:NH1	2.51	0.41
2:2:1369:C:H2'	2:2:1370:G:C8	2.56	0.41
3:3:7:G:H5''	16:O:29:HIS:CE1	2.55	0.41
5:B:251:GLN:HB3	5:B:255:LYS:HD2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:D:83:VAL:HB	7:D:86:ALA:HB2	2.02	0.41
9:F:123:ALA:HA	9:F:133:LEU:HA	2.02	0.41
15:N:28:LEU:HD13	15:N:34:ILE:HG12	2.02	0.41
17:P:89:ARG:NE	17:P:113:ARG:O	2.53	0.41
37:j:86:LYS:HA	37:j:95:PHE:HA	2.02	0.41
37:j:156:LYS:HG2	40:m:71:VAL:HG13	2.02	0.41
41:n:128:SER:OG	41:n:130:ARG:OXT	2.34	0.41
42:o:28:THR:O	42:o:32:THR:OG1	2.32	0.41
42:o:34:ALA:HB3	42:o:78:GLU:HB2	2.01	0.41
44:q:18:LYS:NZ	44:q:19:SER:O	2.48	0.41
47:t:51:HIS:HA	47:t:54:ARG:HB3	2.02	0.41
1:1:992:C:H2'	1:1:993:G:H8	1.85	0.41
1:1:1187:G:OP1	19:R:85:LYS:NZ	2.42	0.41
1:1:1269:A:H61	1:1:2011:U:H3	1.67	0.41
1:1:1864:U:O2	1:1:1878:G:N2	2.34	0.41
1:1:1870:C:O2'	1:1:1871:A:O4'	2.38	0.41
1:1:2002:G:H5'	15:N:13:ASN:HA	2.02	0.41
1:1:2216:G:H2'	1:1:2217:G:H8	1.85	0.41
1:1:2452:C:H5'	55:A:252:GLN:HB3	2.02	0.41
1:1:2838:G:O2'	15:N:49:GLU:OE1	2.23	0.41
2:2:452:A:H2'	2:2:453:G:O4'	2.21	0.41
2:2:493:A:H2'	2:2:494:G:C8	2.56	0.41
3:3:40:U:N3	3:3:44:G:OP2	2.39	0.41
15:N:77:ALA:O	15:N:81:ASN:ND2	2.47	0.41
18:Q:92:ARG:HA	18:Q:95:LEU:HB2	2.01	0.41
39:l:5:ARG:NH1	39:l:7:ILE:HA	2.34	0.41
41:n:25:ASN:H	41:n:62:ASP:CG	2.28	0.41
46:s:53:ARG:HD3	46:s:59:ARG:HH12	1.85	0.41
55:A:115:PHE:O	55:A:119:PHE:N	2.50	0.41
1:1:69:C:H2'	1:1:70:G:H8	1.85	0.41
1:1:1094:U:H2'	1:1:1095:A:H2'	2.01	0.41
1:1:1127:A:N7	1:1:2488:G:O2'	2.54	0.41
1:1:1691:C:H2'	1:1:1692:U:C6	2.55	0.41
1:1:2329:U:H2'	1:1:2330:G:C8	2.55	0.41
1:1:2428:G:H4'	1:1:2429:G:C4	2.55	0.41
2:2:672:U:H2'	2:2:673:A:C8	2.56	0.41
2:2:1071:C:H2'	2:2:1072:G:C8	2.52	0.41
13:L:57:LEU:HD13	13:L:60:ARG:HH11	1.86	0.41
17:P:63:LYS:HE2	17:P:65:SER:HB2	2.03	0.41
22:U:18:ASP:HB3	22:U:21:LYS:HD2	2.02	0.41
35:h:156:ARG:NH1	35:h:160:ALA:O	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:i:170:TRP:CE3	36:i:186:PRO:HB3	2.56	0.41
41:n:34:SER:H	41:n:37:GLN:HB2	1.85	0.41
49:v:25:ILE:N	49:v:42:THR:O	2.48	0.41
54:5:51:C:H2'	54:5:52:G:C8	2.55	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
1:1:544:C:H3'	1:1:545:U:O2	2.21	0.41
1:1:552:U:H2'	1:1:553:G:C8	2.56	0.41
1:1:1161:C:H2'	1:1:1162:G:C8	2.56	0.41
1:1:1837:C:O2'	1:1:1927:A:N3	2.46	0.41
1:1:2106:U:O5'	1:1:2178:C:N4	2.53	0.41
2:2:1162:C:H2'	2:2:1163:A:C8	2.55	0.41
8:E:158:THR:OG1	8:E:159:THR:N	2.53	0.41
14:M:42:THR:HA	14:M:93:VAL:HG12	2.01	0.41
34:g:138:THR:O	34:g:142:GLU:N	2.44	0.41
39:l:140:ASP:OD1	39:l:143:ARG:NH1	2.43	0.41
45:r:33:ILE:O	45:r:37:ALA:N	2.53	0.41
50:w:34:THR:HG23	50:w:37:GLY:H	1.85	0.41
1:1:321:U:H5''	7:D:131:THR:HG23	2.02	0.41
1:1:372:G:C8	25:X:61:LYS:HD2	2.56	0.41
1:1:948:C:H2'	1:1:949:G:C8	2.56	0.41
1:1:995:C:H42	11:J:3:THR:H	1.67	0.41
1:1:1388:G:O2'	1:1:1525:A:O2'	2.38	0.41
1:1:2064:C:H42	1:1:2446:G:H1	1.68	0.41
1:1:2291:U:H2'	1:1:2292:U:C6	2.56	0.41
1:1:2563:U:H4'	12:K:28:SER:HA	2.02	0.41
1:1:2796:U:H3	1:1:2799:A:H61	1.69	0.41
1:1:2840:C:H5''	15:N:56:LYS:HZ1	1.85	0.41
2:2:1116:U:H2'	2:2:1117:A:C8	2.55	0.41
6:C:33:ARG:NH1	6:C:53:GLY:O	2.38	0.41
7:D:181:ILE:HG12	13:L:1:MET:HE3	2.03	0.41
24:W:56:ASP:OD1	24:W:58:THR:OG1	2.34	0.41
31:d:18:PHE:HA	31:d:43:THR:HG21	2.02	0.41
34:g:46:THR:HG23	34:g:201:PRO:HD2	2.03	0.41
39:l:69:VAL:HG21	39:l:104:ILE:HD11	2.01	0.41
45:r:33:ILE:HD12	45:r:59:GLU:HB3	2.03	0.41
55:A:213:ARG:HH12	55:A:329:ASP:HB2	1.86	0.41
1:1:548:G:H3'	1:1:549:G:O4'	2.21	0.41
1:1:563:A:N3	18:Q:37:GLN:NE2	2.65	0.41
1:1:1223:G:OP1	19:R:68:ARG:NH2	2.53	0.41
1:1:1267:U:H2'	1:1:1268:A:H8	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1529:G:C4	1:1:1530:G:C8	3.09	0.41
1:1:2818:U:OP2	15:N:45:ARG:NH2	2.50	0.41
2:2:309:A:H2'	2:2:310:G:H8	1.86	0.41
2:2:680:C:H2'	2:2:681:A:C8	2.55	0.41
2:2:1280:A:OP2	42:o:9:ARG:NH2	2.46	0.41
6:C:136:ASN:HD21	6:C:139:SER:HB2	1.86	0.41
47:t:43:PHE:CD1	47:t:56:LEU:HD22	2.56	0.41
55:A:310:MET:HA	55:A:313:ASN:HB2	2.01	0.41
55:A:310:MET:HA	55:A:313:ASN:HD22	1.85	0.41
1:1:693:A:O2'	1:1:1353:A:N3	2.48	0.41
1:1:922:C:H2'	1:1:923:G:H8	1.85	0.41
1:1:1170:C:N4	1:1:1171:G:O6	2.54	0.41
1:1:1426:G:O2'	1:1:1572:A:N6	2.54	0.41
1:1:2024:G:O3'	6:C:154:LYS:NZ	2.44	0.41
1:1:2489:U:O2'	1:1:2518:A:N6	2.53	0.41
2:2:105:G:H2'	2:2:106:C:C6	2.56	0.41
2:2:460:A:H2'	2:2:461:A:C8	2.56	0.41
2:2:719:C:O2'	50:w:39:ILE:O	2.37	0.41
2:2:720:C:O3'	50:w:52:GLN:NE2	2.53	0.41
2:2:842:U:O2'	2:2:845:A:OP2	2.32	0.41
2:2:1088:G:H21	2:2:1167:A:H61	1.69	0.41
2:2:1103:C:OP1	34:g:95:ARG:NH2	2.53	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
6:C:184:ARG:HG3	6:C:186:LEU:HG	2.03	0.41
7:D:149:ILE:HG12	7:D:188:MET:HA	2.02	0.41
7:D:157:LEU:HG	7:D:169:VAL:HG21	2.03	0.41
7:D:176:ASP:N	7:D:176:ASP:OD1	2.53	0.41
8:E:8:TYR:HB2	8:E:173:PHE:HZ	1.86	0.41
9:F:124:GLU:N	9:F:132:VAL:O	2.54	0.41
10:G:126:GLY:O	10:G:146:VAL:N	2.52	0.41
11:J:18:VAL:HB	11:J:56:VAL:HA	2.02	0.41
12:K:78:ARG:N	17:P:71:GLU:O	2.38	0.41
19:R:6:GLN:HG3	19:R:39:LEU:HD11	2.02	0.41
24:W:46:HIS:N	24:W:78:LYS:O	2.44	0.41
34:g:72:THR:OG1	34:g:169:GLU:OE2	2.31	0.41
41:n:42:GLU:O	41:n:46:MET:N	2.54	0.41
47:t:29:VAL:HG22	47:t:67:LEU:HD22	2.02	0.41
48:u:76:LYS:O	48:u:80:LYS:N	2.51	0.41
55:A:83:LEU:O	55:A:87:ALA:N	2.53	0.41
55:A:141:ALA:HB2	55:A:216:SER:HB2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:A:189:TYR:CG	55:A:224:PRO:HB3	2.56	0.41
55:A:316:ASP:OD1	55:A:316:ASP:N	2.53	0.41
1:1:242:G:C8	32:e:3:LYS:HE3	2.56	0.41
1:1:243:U:N3	1:1:255:A:N7	2.67	0.41
1:1:784:G:C5	1:1:792:A:C5	3.08	0.41
1:1:1857:G:N2	1:1:1884:G:O2'	2.42	0.41
1:1:1987:A:H2'	1:1:1988:G:C8	2.56	0.41
1:1:2167:U:O2'	1:1:2169:A:N7	2.42	0.41
1:1:2315:G:H2'	1:1:2316:G:H8	1.86	0.41
1:1:2594:C:H2'	1:1:2595:G:C8	2.56	0.41
1:1:2696:U:H2'	1:1:2697:G:C8	2.56	0.41
2:2:157:U:H2'	2:2:158:G:C8	2.56	0.41
5:B:67:PHE:CE1	5:B:156:ARG:HD2	2.56	0.41
10:G:15:LEU:HD22	10:G:56:ALA:HB2	2.03	0.41
13:L:79:LEU:HD11	13:L:112:LEU:HD12	2.02	0.41
24:W:25:ARG:HH12	24:W:35:SER:HB3	1.86	0.41
35:h:172:ARG:HE	35:h:174:PRO:HD3	1.86	0.41
38:k:19:PRO:HA	38:k:22:ILE:HD12	2.02	0.41
1:1:21:A:N6	1:1:518:G:O6	2.54	0.40
1:1:69:C:H2'	1:1:70:G:C8	2.56	0.40
1:1:1000:A:H62	1:1:1154:G:H2'	1.86	0.40
1:1:2394:C:H5''	13:L:63:LYS:HE2	2.03	0.40
1:1:2436:G:O2'	1:1:2598:A:N1	2.52	0.40
1:1:2602:A:C5	55:A:254:VAL:HG22	2.57	0.40
2:2:235:C:H2'	2:2:236:A:C8	2.56	0.40
2:2:537:G:H2'	2:2:538:G:H8	1.85	0.40
2:2:689:C:H2'	2:2:690:G:O4'	2.21	0.40
2:2:1135:U:O2'	2:2:1136:C:H5''	2.21	0.40
2:2:1152:A:H2'	2:2:1153:G:C8	2.56	0.40
12:K:53:LYS:N	12:K:56:ASP:OD2	2.54	0.40
16:O:67:ASN:OD1	16:O:70:ALA:N	2.52	0.40
26:Y:18:LEU:HD21	26:Y:50:VAL:HG13	2.02	0.40
34:g:56:GLU:HG2	34:g:198:PHE:HE2	1.86	0.40
35:h:157:LEU:HB2	35:h:164:ARG:CZ	2.51	0.40
44:q:56:ARG:NE	44:q:62:GLU:OE1	2.50	0.40
46:s:54:ASP:HA	46:s:59:ARG:HG2	2.03	0.40
51:x:52:HIS:HB2	51:x:57:HIS:CE1	2.57	0.40
1:1:329:G:H1	22:U:17:LYS:HD3	1.85	0.40
1:1:660:C:H2'	1:1:661:A:C8	2.56	0.40
1:1:704:G:N2	1:1:726:G:O2'	2.54	0.40
1:1:2552:OMU:HM22	1:1:2554:U:H5	1.87	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:E:47:LYS:O	8:E:51:ASP:N	2.42	0.40
12:K:121:GLU:OE1	17:P:65:SER:OG	2.32	0.40
43:p:81:ASN:OD1	43:p:106:ARG:NH1	2.54	0.40
45:r:89:LEU:HD23	45:r:92:ARG:HE	1.86	0.40
54:5:50:U:H3	54:5:64:G:H1	1.68	0.40
1:1:240:C:OP2	1:1:241:A:O2'	2.37	0.40
1:1:759:G:H2'	1:1:760:G:H8	1.87	0.40
1:1:2425:A:H4'	1:1:2426:A:O5'	2.21	0.40
2:2:114:U:H2'	2:2:115:G:C8	2.57	0.40
2:2:1339:A:O2'	54:5:40:C:O2'	2.35	0.40
2:2:1347:G:H1'	2:2:1348:U:H5	1.86	0.40
2:2:1425:U:H2'	2:2:1426:G:C8	2.54	0.40
6:C:4:LEU:HG	6:C:32:ASN:ND2	2.37	0.40
34:g:24:ASN:HD21	34:g:26:LYS:HD2	1.85	0.40
37:j:16:ILE:HD12	37:j:36:LEU:HG	2.03	0.40
1:1:196:A:N7	13:L:38:GLN:NE2	2.56	0.40
1:1:1094:U:H1'	1:1:1097:U:H5	1.87	0.40
1:1:1796:U:H2'	1:1:1797:G:H8	1.85	0.40
1:1:2113:U:O4	1:1:2114:A:N6	2.54	0.40
1:1:2374:C:N4	1:1:2375:G:O6	2.55	0.40
1:1:2591:C:H2'	1:1:2592:G:C8	2.57	0.40
2:2:166:U:H2'	2:2:167:A:C8	2.56	0.40
2:2:166:U:H2'	2:2:167:A:H8	1.85	0.40
2:2:458:U:H2'	2:2:459:A:C8	2.56	0.40
2:2:668:G:O2'	47:t:46:HIS:ND1	2.40	0.40
2:2:946:A:H2'	2:2:947:G:C8	2.56	0.40
2:2:1074:G:O2'	2:2:1101:A:N1	2.52	0.40
5:B:168:ASP:N	5:B:168:ASP:OD1	2.54	0.40
12:K:123:LEU:HA	17:P:41:GLN:HE22	1.86	0.40
16:O:56:LYS:HE2	16:O:56:LYS:HB2	1.93	0.40
18:Q:49:ASP:HA	18:Q:52:GLN:HB2	2.02	0.40
28:a:16:CYS:HA	28:a:34:LEU:HB2	2.03	0.40
37:j:99:ALA:HB2	37:j:124:LEU:HG	2.03	0.40
43:p:36:ASP:OD1	43:p:40:ASN:N	2.54	0.40
1:1:399:U:H2'	1:1:400:G:O4'	2.22	0.40
1:1:552:U:H2'	1:1:553:G:H8	1.86	0.40
1:1:2417:C:H2'	1:1:2418:A:H8	1.85	0.40
1:1:2789:C:H2'	1:1:2893:A:N7	2.36	0.40
2:2:129:A:H2	2:2:232:G:H22	1.69	0.40
2:2:1004:A:H5''	2:2:1025:U:C2	2.56	0.40
7:D:111:GLU:O	7:D:115:GLN:N	2.53	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:F:72:LEU:HA	9:F:75:MET:HB2	2.03	0.40
25:X:70:GLU:O	25:X:74:ARG:N	2.52	0.40
35:h:20:SER:HB3	35:h:22:TRP:NE1	2.37	0.40
38:k:18:VAL:HA	38:k:21:MET:HE3	2.04	0.40
55:A:64:GLU:HA	55:A:67:VAL:HB	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	B	269/271 (99%)	254 (94%)	15 (6%)	0	100	100
6	C	207/209 (99%)	198 (96%)	7 (3%)	2 (1%)	12	45
7	D	199/201 (99%)	191 (96%)	8 (4%)	0	100	100
8	E	175/177 (99%)	160 (91%)	14 (8%)	1 (1%)	21	55
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	45
20	S	108/110 (98%)	105 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
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	36
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%)	115 (92%)	10 (8%)	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%)	79 (92%)	5 (6%)	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

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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
56	6	1/3 (33%)	1 (100%)	0	0	100	100
All	All	5929/6031 (98%)	5627 (95%)	295 (5%)	7 (0%)	49	80

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
6	C	151	THR
47	t	50	HIS
47	t	74	ASP
19	R	52	PRO
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	80
7	D	165/165 (100%)	165 (100%)	0	100	100
8	E	148/148 (100%)	147 (99%)	1 (1%)	76	78
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
15	N	99/99 (100%)	97 (98%)	2 (2%)	48	65
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
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	82
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

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
46	s	83/83 (100%)	83 (100%)	0	100	100
47	t	76/76 (100%)	71 (93%)	5 (7%)	15	41
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
56	6	2/2 (100%)	2 (100%)	0	100	100
All	All	4946/4947 (100%)	4932 (100%)	14 (0%)	84	85

All (14) 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	49	ASP
47	t	52	SER
47	t	53	ARG
47	t	60	VAL
47	t	73	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (83) 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

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Mol	Chain	Res	Type
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
13	L	54	GLN
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	37	GLN
18	Q	44	GLN
18	Q	72	ASN
19	R	12	HIS
20	S	7	HIS
20	S	40	ASN
20	S	61	ASN
21	T	70	HIS
22	U	46	GLN
22	U	54	GLN
23	V	75	GLN
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	13	ASN
31	d	16	HIS

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Mol	Chain	Res	Type
32	e	26	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	121	HIS
38	k	46	GLN
38	k	63	ASN
38	k	68	GLN
39	l	28	ASN
39	l	130	ASN
43	p	40	ASN
43	p	119	ASN
44	q	5	ASN
45	r	8	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	52	HIS
51	x	57	HIS
52	y	48	GLN
52	y	52	ASN
55	A	43	GLN
55	A	199	HIS
55	A	255	ASN
55	A	276	ASN
55	A	281	HIS
55	A	313	ASN

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2902/2903 (99%)	759 (26%)	16 (0%)
2	2	1532/1534 (99%)	415 (27%)	5 (0%)
3	3	119/120 (99%)	23 (19%)	0
4	4	8/9 (88%)	2 (25%)	0
54	5	75/76 (98%)	19 (25%)	0
All	All	4636/4642 (99%)	1218 (26%)	21 (0%)

All (1218) 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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
1	1	386	G
1	1	396	G
1	1	405	U
1	1	406	G
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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
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	16	C
54	5	17	U
54	5	19	G
54	5	20	H2U
54	5	43	A

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Mol	Chain	Res	Type
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	68	C
54	5	72	A
54	5	73	A
54	5	74	C
54	5	76	A

All (21) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	404	A
1	1	613	A
1	1	784	G
1	1	894	U
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
2	2	1109	C

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

39 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	2MG	1	2445	1	23,26,27	2.94	6 (26%)	33,38,41	2.27	7 (21%)
54	PSU	5	55	54	18,21,22	1.10	1 (5%)	21,30,33	1.88	4 (19%)
1	2MA	1	2503	1	22,25,26	3.71	8 (36%)	32,37,40	2.44	7 (21%)
2	5MC	2	1407	2	19,22,23	3.81	8 (42%)	26,32,35	1.12	3 (11%)
1	PSU	1	1911	1	18,21,22	1.13	2 (11%)	21,30,33	2.16	5 (23%)
1	PSU	1	2504	1	18,21,22	1.22	2 (11%)	21,30,33	1.93	4 (19%)
2	2MG	2	1516	2	23,26,27	2.95	8 (34%)	33,38,41	2.14	10 (30%)
2	4OC	2	1402	2	20,23,24	3.00	8 (40%)	25,32,35	1.25	4 (16%)
1	PSU	1	2457	1	18,21,22	1.17	3 (16%)	21,30,33	2.02	6 (28%)
1	PSU	1	2605	1	18,21,22	1.12	2 (11%)	21,30,33	2.10	5 (23%)
1	PSU	1	746	1	18,21,22	1.08	2 (11%)	21,30,33	1.81	4 (19%)
1	OMG	1	2251	54,1	23,26,27	2.40	8 (34%)	32,38,41	1.95	8 (25%)
2	5MC	2	967	2	19,22,23	3.83	8 (42%)	26,32,35	0.99	1 (3%)
2	PSU	2	516	2	18,21,22	1.02	1 (5%)	21,30,33	1.95	5 (23%)
1	G7M	1	2069	1	23,26,27	2.58	8 (34%)	34,39,42	2.51	11 (32%)
2	2MG	2	1207	2	23,26,27	2.88	7 (30%)	33,38,41	2.34	9 (27%)
54	5MU	5	54	54	19,22,23	4.81	7 (36%)	27,32,35	3.52	8 (29%)
1	5MC	1	1962	1	19,22,23	3.79	8 (42%)	26,32,35	1.02	2 (7%)
2	2MG	2	966	2	23,26,27	2.99	7 (30%)	33,38,41	2.30	7 (21%)
1	2MG	1	1835	1	23,26,27	2.89	7 (30%)	33,38,41	2.20	10 (30%)
1	6MZ	1	1618	1	22,25,26	2.85	6 (27%)	29,36,39	4.45	14 (48%)
1	PSU	1	1917	1	18,21,22	1.10	1 (5%)	21,30,33	1.88	4 (19%)
2	G7M	2	527	2	23,26,27	3.59	12 (52%)	34,39,42	1.57	7 (20%)
54	4OC	5	32	54	20,23,24	3.00	8 (40%)	25,32,35	1.02	1 (4%)
1	PSU	1	2580	1	18,21,22	1.10	2 (11%)	21,30,33	2.07	5 (23%)
1	1MG	1	745	1	23,26,27	2.83	7 (30%)	33,39,42	2.07	9 (27%)
1	6MZ	1	2030	1	22,25,26	2.89	6 (27%)	29,36,39	4.47	13 (44%)
2	MA6	2	1518	2	23,26,27	1.56	5 (21%)	33,38,41	2.71	12 (36%)
2	UR3	2	1498	2	19,22,23	2.53	7 (36%)	26,32,35	1.56	3 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
54	4SU	5	8	54	18,21,22	3.69	7 (38%)	25,30,33	2.22	5 (20%)
54	H2U	5	20	54	18,21,22	3.38	5 (27%)	19,30,33	1.55	4 (21%)
56	FME	6	77	56	8,9,10	0.92	0	8,9,11	0.73	0
1	PSU	1	955	1	18,21,22	1.04	1 (5%)	21,30,33	1.80	3 (14%)
1	5MU	1	1939	1	19,22,23	4.77	7 (36%)	27,32,35	3.82	10 (37%)
1	3TD	1	1915	1	19,22,23	4.25	5 (26%)	23,32,35	2.02	4 (17%)
2	MA6	2	1519	2	23,26,27	1.53	4 (17%)	33,38,41	2.77	13 (39%)
1	5MU	1	747	1	19,22,23	4.82	7 (36%)	27,32,35	3.92	9 (33%)
1	OMU	1	2552	1	19,22,23	2.88	8 (42%)	25,31,34	1.92	5 (20%)
1	OMC	1	2498	1	19,22,23	2.91	7 (36%)	25,31,34	0.91	1 (4%)

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	2MG	1	2445	1	-	2/9/27/28	0/3/3/3
54	PSU	5	55	54	-	1/7/25/26	0/2/2/2
1	2MA	1	2503	1	-	5/7/25/26	0/3/3/3
2	5MC	2	1407	2	-	0/7/25/26	0/2/2/2
1	PSU	1	1911	1	-	0/7/25/26	0/2/2/2
1	PSU	1	2504	1	-	2/7/25/26	0/2/2/2
2	2MG	2	1516	2	-	0/9/27/28	0/3/3/3
2	4OC	2	1402	2	-	2/9/29/30	0/2/2/2
1	PSU	1	2457	1	-	0/7/25/26	0/2/2/2
1	PSU	1	2605	1	-	0/7/25/26	0/2/2/2
1	PSU	1	746	1	-	2/7/25/26	0/2/2/2
1	OMG	1	2251	54,1	-	0/9/27/28	0/3/3/3
2	5MC	2	967	2	-	0/7/25/26	0/2/2/2
2	PSU	2	516	2	-	2/7/25/26	0/2/2/2
1	G7M	1	2069	1	-	1/7/25/26	0/3/3/3
2	2MG	2	1207	2	-	2/9/27/28	0/3/3/3
54	5MU	5	54	54	-	0/7/25/26	0/2/2/2
1	5MC	1	1962	1	-	2/7/25/26	0/2/2/2
2	2MG	2	966	2	-	0/9/27/28	0/3/3/3
1	2MG	1	1835	1	-	2/9/27/28	0/3/3/3
1	6MZ	1	1618	1	-	4/9/27/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	PSU	1	1917	1	-	0/7/25/26	0/2/2/2
2	G7M	2	527	2	-	2/7/25/26	0/3/3/3
54	4OC	5	32	54	-	0/9/29/30	0/2/2/2
1	PSU	1	2580	1	-	0/7/25/26	0/2/2/2
1	1MG	1	745	1	-	0/7/25/26	0/3/3/3
1	6MZ	1	2030	1	-	3/9/27/28	0/3/3/3
2	MA6	2	1518	2	-	0/11/29/30	0/3/3/3
2	UR3	2	1498	2	-	0/7/25/26	0/2/2/2
54	4SU	5	8	54	-	3/7/25/26	0/2/2/2
54	H2U	5	20	54	-	4/7/38/39	0/2/2/2
56	FME	6	77	56	-	3/7/9/11	-
1	PSU	1	955	1	-	0/7/25/26	0/2/2/2
1	5MU	1	1939	1	-	0/7/25/26	0/2/2/2
1	3TD	1	1915	1	-	4/7/25/26	0/2/2/2
2	MA6	2	1519	2	-	3/11/29/30	0/3/3/3
1	5MU	1	747	1	-	1/7/25/26	0/2/2/2
1	OMU	1	2552	1	-	1/9/27/28	0/2/2/2
1	OMC	1	2498	1	-	0/9/27/28	0/2/2/2

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	11.48	1.49	1.34
1	1	2030	6MZ	C6-N6	11.32	1.47	1.34
1	1	747	5MU	C2-N1	11.29	1.56	1.38
54	5	20	H2U	C2-N1	11.13	1.51	1.35
1	1	1618	6MZ	C6-N6	11.01	1.46	1.34
54	5	54	5MU	C2-N1	10.95	1.55	1.38
1	1	1939	5MU	C2-N1	10.83	1.55	1.38
2	2	527	G7M	C8-N7	10.78	1.51	1.33
54	5	54	5MU	C6-N1	10.57	1.56	1.38
1	1	1939	5MU	C6-N1	10.20	1.55	1.38
1	1	747	5MU	C6-N1	10.03	1.55	1.38
1	1	747	5MU	C4-C5	9.79	1.60	1.44
1	1	1915	3TD	C2-N1	9.77	1.49	1.37
1	1	1939	5MU	C4-C5	9.76	1.60	1.44
54	5	54	5MU	C4-C5	9.74	1.60	1.44
1	1	1962	5MC	C6-C5	9.03	1.49	1.34
2	2	967	5MC	C6-C5	9.03	1.49	1.34
2	2	1407	5MC	C6-C5	8.97	1.49	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	747	5MU	C4-N3	-8.09	1.23	1.38
54	5	54	5MU	C4-N3	-8.06	1.23	1.38
54	5	8	4SU	C4-N3	8.02	1.45	1.37
1	1	1939	5MU	C4-N3	-7.98	1.23	1.38
54	5	8	4SU	C2-N1	7.71	1.50	1.38
2	2	966	2MG	C2-N3	7.56	1.46	1.32
1	1	2445	2MG	C2-N3	7.54	1.46	1.32
1	1	745	1MG	C2-N2	7.48	1.47	1.34
1	1	1835	2MG	C2-N3	7.24	1.45	1.32
2	2	1516	2MG	C2-N3	7.21	1.45	1.32
2	2	1207	2MG	C2-N3	7.18	1.45	1.32
2	2	967	5MC	C4-N3	7.10	1.45	1.34
1	1	2503	2MA	C2-N3	7.00	1.46	1.34
2	2	1402	4OC	C4-N3	6.94	1.44	1.32
1	1	1962	5MC	C4-N3	6.92	1.45	1.34
54	5	32	4OC	C4-N3	6.88	1.44	1.32
2	2	966	2MG	C4-N3	6.80	1.49	1.34
2	2	1407	5MC	C4-N3	6.65	1.44	1.34
1	1	2445	2MG	C4-N3	6.64	1.49	1.34
2	2	966	2MG	C2-N2	6.64	1.47	1.33
1	1	745	1MG	C2-N3	6.62	1.44	1.33
2	2	1516	2MG	C2-N2	6.62	1.47	1.33
54	5	20	H2U	C2-N3	6.60	1.49	1.38
1	1	2552	OMU	C2-N3	6.59	1.49	1.38
1	1	2069	G7M	C4-N3	6.56	1.49	1.34
1	1	745	1MG	C4-N3	6.56	1.49	1.34
2	2	1207	2MG	C4-N3	6.54	1.49	1.34
2	2	1516	2MG	C4-N3	6.49	1.49	1.34
1	1	2445	2MG	C2-N2	6.41	1.46	1.33
1	1	1835	2MG	C4-N3	6.41	1.48	1.34
1	1	2552	OMU	C2-N1	6.37	1.48	1.38
1	1	1835	2MG	C2-N2	6.31	1.46	1.33
2	2	1207	2MG	C2-N2	6.29	1.46	1.33
1	1	2498	OMC	C6-C5	6.28	1.49	1.35
2	2	1498	UR3	C2-N1	6.26	1.47	1.38
1	1	2251	OMG	C4-N3	6.23	1.48	1.34
2	2	967	5MC	C2-N3	6.20	1.48	1.36
1	1	1962	5MC	C5-C4	6.19	1.48	1.44
1	1	1962	5MC	C2-N3	6.09	1.48	1.36
1	1	2498	OMC	C2-N3	6.08	1.48	1.36
2	2	1407	5MC	C2-N3	6.08	1.48	1.36
2	2	1407	5MC	C5-C4	6.05	1.48	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	967	5MC	C5-C4	5.98	1.48	1.44
54	5	32	4OC	C6-C5	5.94	1.48	1.35
1	1	1939	5MU	C6-C5	5.90	1.44	1.34
54	5	8	4SU	C6-C5	5.86	1.48	1.35
2	2	1498	UR3	C6-C5	5.84	1.48	1.35
2	2	1402	4OC	C2-N3	5.82	1.47	1.36
54	5	32	4OC	C2-N3	5.77	1.47	1.36
54	5	8	4SU	C4-S4	-5.73	1.58	1.68
1	1	1915	3TD	C6-N1	5.73	1.45	1.36
2	2	1402	4OC	C6-C5	5.72	1.48	1.35
1	1	747	5MU	C6-C5	5.65	1.43	1.34
2	2	527	G7M	C2-N3	5.64	1.46	1.33
1	1	2503	2MA	C2-N1	5.64	1.43	1.34
54	5	54	5MU	C6-C5	5.63	1.43	1.34
1	1	2498	OMC	C4-N3	5.63	1.45	1.34
54	5	8	4SU	C2-N3	5.62	1.47	1.38
1	1	2503	2MA	C6-N1	5.58	1.42	1.35
2	2	527	G7M	C8-N9	5.49	1.50	1.35
2	2	527	G7M	C4-N3	5.43	1.46	1.34
1	1	2552	OMU	C6-C5	5.40	1.47	1.35
1	1	2069	G7M	C2-N3	5.26	1.45	1.33
1	1	2251	OMG	C2-N3	5.22	1.45	1.33
1	1	2069	G7M	C5-N7	-4.95	1.33	1.39
2	2	967	5MC	C4-N4	4.82	1.46	1.34
1	1	1962	5MC	C4-N4	4.80	1.46	1.34
2	2	1407	5MC	C4-N4	4.79	1.46	1.34
54	5	20	H2U	C4-N3	4.79	1.45	1.37
1	1	1915	3TD	C2-N3	4.76	1.48	1.38
2	2	527	G7M	C2-N2	4.75	1.45	1.34
1	1	2251	OMG	C2-N2	4.70	1.45	1.34
2	2	1402	4OC	C2-N1	4.54	1.49	1.40
2	2	1407	5MC	C6-N1	4.53	1.45	1.38
2	2	1498	UR3	C2-N3	4.49	1.47	1.39
2	2	1407	5MC	C2-N1	4.46	1.49	1.40
2	2	967	5MC	C6-N1	4.43	1.45	1.38
2	2	527	G7M	C5-N7	4.40	1.44	1.39
2	2	1516	2MG	C2-N1	4.26	1.43	1.36
1	1	2069	G7M	C2-N2	4.26	1.44	1.34
1	1	1962	5MC	C6-N1	4.22	1.45	1.38
1	1	2503	2MA	C5-C6	4.19	1.52	1.41
2	2	966	2MG	C2-N1	4.17	1.43	1.36
1	1	2504	PSU	C6-C5	4.13	1.39	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	967	5MC	C2-N1	4.08	1.48	1.40
1	1	1835	2MG	C2-N1	4.03	1.43	1.36
54	5	32	4OC	C4-N4	3.99	1.44	1.36
2	2	1207	2MG	C2-N1	3.98	1.43	1.36
54	5	32	4OC	C2-N1	3.96	1.48	1.40
1	1	2069	G7M	C5-C6	3.93	1.54	1.43
2	2	1402	4OC	C4-N4	3.93	1.44	1.36
1	1	2552	OMU	C4-N3	3.85	1.45	1.38
1	1	1962	5MC	C2-N1	3.79	1.48	1.40
1	1	2445	2MG	C2-N1	3.79	1.42	1.36
2	2	1519	MA6	C6-N6	3.74	1.47	1.36
1	1	2498	OMC	C2-N1	3.71	1.47	1.40
1	1	2498	OMC	C4-N4	3.69	1.42	1.33
1	1	2030	6MZ	C5-C4	-3.67	1.32	1.39
1	1	2445	2MG	C5-N7	-3.66	1.31	1.39
1	1	2503	2MA	C6-N6	-3.65	1.24	1.34
1	1	1618	6MZ	C5-C4	-3.62	1.32	1.39
54	5	55	PSU	C6-C5	3.61	1.39	1.35
1	1	2445	2MG	O6-C6	-3.61	1.16	1.23
1	1	2498	OMC	C6-N1	3.60	1.46	1.38
54	5	32	4OC	C5-C4	3.59	1.48	1.41
2	2	1518	MA6	C6-N6	3.56	1.46	1.36
2	2	966	2MG	C5-N7	-3.54	1.32	1.39
1	1	2030	6MZ	C8-N9	-3.53	1.31	1.37
1	1	1835	2MG	O6-C6	-3.52	1.16	1.23
2	2	966	2MG	O6-C6	-3.51	1.16	1.23
1	1	1835	2MG	C5-N7	-3.50	1.32	1.39
2	2	1516	2MG	C5-N7	-3.48	1.32	1.39
2	2	1207	2MG	C5-N7	-3.47	1.32	1.39
2	2	1516	2MG	O6-C6	-3.44	1.17	1.23
1	1	2457	PSU	C6-C5	3.43	1.39	1.35
1	1	2503	2MA	C5-N7	-3.42	1.32	1.39
1	1	2605	PSU	C6-C5	3.41	1.39	1.35
2	2	1207	2MG	O6-C6	-3.41	1.17	1.23
2	2	1518	MA6	C8-N9	-3.38	1.31	1.37
1	1	1618	6MZ	C8-N9	-3.37	1.31	1.37
2	2	527	G7M	C2-N1	3.37	1.45	1.37
1	1	745	1MG	C2-N1	3.37	1.43	1.37
1	1	1962	5MC	O2-C2	-3.35	1.17	1.23
1	1	1911	PSU	C6-C5	3.34	1.39	1.35
2	2	1402	4OC	C5-C4	3.34	1.48	1.41
2	2	1407	5MC	O2-C2	-3.32	1.17	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	1917	PSU	C6-C5	3.32	1.39	1.35
54	5	8	4SU	C5-C4	3.31	1.46	1.42
1	1	1618	6MZ	C4-N9	-3.31	1.30	1.37
2	2	527	G7M	C5-C6	3.28	1.52	1.43
1	1	745	1MG	C5-N7	-3.21	1.32	1.39
2	2	967	5MC	O2-C2	-3.20	1.17	1.23
1	1	2251	OMG	C5-N7	-3.17	1.32	1.39
1	1	746	PSU	C6-C5	3.17	1.38	1.35
2	2	1518	MA6	C5-N7	-3.11	1.33	1.39
1	1	2552	OMU	O4-C4	-3.11	1.18	1.24
1	1	955	PSU	C6-C5	3.10	1.38	1.35
2	2	516	PSU	C6-C5	3.10	1.38	1.35
2	2	1519	MA6	C5-N7	-3.09	1.33	1.39
2	2	1518	MA6	C5-C4	-3.05	1.33	1.39
2	2	1519	MA6	C8-N9	-2.99	1.32	1.37
1	1	747	5MU	O4-C4	-2.98	1.17	1.23
1	1	1915	3TD	C4-N3	2.96	1.46	1.40
54	5	32	4OC	O2-C2	-2.94	1.18	1.23
1	1	1939	5MU	O4-C4	-2.93	1.18	1.23
1	1	2580	PSU	C6-C5	2.92	1.38	1.35
54	5	32	4OC	C6-N1	2.90	1.45	1.38
1	1	2498	OMC	O2-C2	-2.88	1.18	1.23
54	5	54	5MU	O4-C4	-2.88	1.18	1.23
1	1	747	5MU	O2-C2	-2.86	1.18	1.23
2	2	1402	4OC	C6-N1	2.85	1.44	1.38
1	1	2251	OMG	O6-C6	-2.83	1.18	1.23
2	2	1519	MA6	C5-C4	-2.81	1.34	1.39
1	1	2069	G7M	O6-C6	-2.80	1.18	1.23
1	1	2030	6MZ	C4-N9	-2.78	1.31	1.37
2	2	1402	4OC	O2-C2	-2.74	1.18	1.23
2	2	527	G7M	O6-C6	-2.72	1.18	1.23
1	1	2552	OMU	O2-C2	-2.71	1.18	1.23
54	5	8	4SU	O2-C2	-2.70	1.18	1.23
2	2	527	G7M	C6-N1	2.68	1.43	1.38
1	1	1939	5MU	O2-C2	-2.58	1.18	1.23
1	1	2251	OMG	C2-N1	2.54	1.43	1.37
2	2	1498	UR3	C6-N1	2.47	1.44	1.38
54	5	54	5MU	O2-C2	-2.46	1.18	1.23
1	1	2552	OMU	C6-N1	2.42	1.43	1.38
1	1	2069	G7M	C2-N1	2.41	1.43	1.37
1	1	1618	6MZ	C6-N1	-2.41	1.31	1.35
2	2	1498	UR3	O4-C4	-2.39	1.18	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	2580	PSU	O4'-C1'	-2.39	1.40	1.43
2	2	1498	UR3	O2-C2	-2.38	1.18	1.22
1	1	2030	6MZ	C6-N1	-2.37	1.31	1.35
1	1	1618	6MZ	C5-C6	-2.36	1.36	1.41
54	5	20	H2U	O4-C4	-2.34	1.18	1.23
54	5	20	H2U	O2-C2	-2.33	1.18	1.23
2	2	1207	2MG	C5-C6	2.32	1.53	1.44
1	1	745	1MG	C5-C6	2.25	1.51	1.45
1	1	2069	G7M	C6-N1	2.25	1.43	1.38
1	1	2251	OMG	C4-N9	-2.23	1.32	1.38
1	1	2503	2MA	C4-N9	-2.22	1.33	1.37
1	1	2251	OMG	C5-C6	2.21	1.52	1.44
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	745	1MG	C4-N9	-2.11	1.32	1.38
1	1	746	PSU	C4-C5	-2.10	1.38	1.44
1	1	1911	PSU	C4-C5	-2.10	1.38	1.44
2	2	1498	UR3	C5-C4	2.08	1.49	1.43
1	1	2030	6MZ	C5-C6	-2.07	1.36	1.41
2	2	1516	2MG	C4-N9	-2.06	1.32	1.38
2	2	527	G7M	C4-N9	2.05	1.43	1.38
2	2	527	G7M	C5-C4	2.03	1.43	1.38
1	1	2605	PSU	C4-C5	-2.03	1.38	1.44
1	1	2457	PSU	O4'-C1'	-2.02	1.41	1.43
1	1	2504	PSU	C4-C5	-2.02	1.38	1.44
2	2	1518	MA6	C5-C6	-2.00	1.36	1.41

All (242) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	1618	6MZ	C4-N9-C8	14.23	120.68	105.74
1	1	2030	6MZ	C4-N9-C8	13.98	120.42	105.74
1	1	747	5MU	C5-C4-N3	12.88	126.52	115.32
1	1	1939	5MU	C5-C4-N3	12.51	126.19	115.32
54	5	54	5MU	C5-C4-N3	11.98	125.74	115.32
1	1	747	5MU	C5-C6-N1	-10.67	111.72	123.31
1	1	2030	6MZ	N9-C8-N7	-10.51	99.03	113.94
1	1	1618	6MZ	N9-C8-N7	-10.43	99.14	113.94
1	1	1939	5MU	C5-C6-N1	-10.42	112.00	123.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	5	54	5MU	C5-C6-N1	-9.21	113.31	123.31
1	1	2030	6MZ	C5-C6-N1	8.70	127.49	118.15
2	2	1519	MA6	N1-C6-N6	-8.58	106.41	116.86
1	1	1618	6MZ	C5-C6-N1	8.37	127.13	118.15
2	2	1518	MA6	N1-C6-N6	-8.24	106.81	116.86
1	1	2503	2MA	C5-C4-N3	-7.75	119.01	127.18
54	5	8	4SU	C4-N3-C2	-6.99	120.61	127.31
2	2	966	2MG	C2-N3-C4	6.83	120.54	112.00
2	2	1207	2MG	C2-N3-C4	6.76	120.46	112.00
1	1	2030	6MZ	N3-C4-N9	6.48	138.18	127.17
1	1	2445	2MG	C2-N3-C4	6.41	120.02	112.00
2	2	966	2MG	C5-C4-N3	-6.19	118.53	128.39
2	2	1519	MA6	N1-C2-N3	-6.19	119.21	128.58
2	2	1207	2MG	C5-C4-N3	-6.18	118.55	128.39
1	1	1835	2MG	C2-N3-C4	6.16	119.71	112.00
1	1	2503	2MA	N3-C4-N9	6.14	134.78	126.99
2	2	1516	2MG	C2-N3-C4	6.11	119.64	112.00
2	2	1518	MA6	N1-C2-N3	-6.09	119.37	128.58
1	1	2552	OMU	C4-N3-C2	-6.07	119.08	126.61
1	1	2445	2MG	C5-C4-N3	-6.06	118.74	128.39
1	1	2069	G7M	CN7-N7-C5	6.03	134.31	126.80
1	1	1618	6MZ	N3-C4-N9	5.77	136.98	127.17
1	1	1915	3TD	C1'-C5-C4	5.75	126.34	117.61
2	2	1519	MA6	C5-C6-N6	5.71	134.37	125.33
1	1	1939	5MU	O4-C4-C5	-5.68	118.42	124.92
1	1	747	5MU	C4-N3-C2	-5.60	120.00	127.34
1	1	2030	6MZ	N1-C2-N3	-5.57	120.15	128.58
1	1	1618	6MZ	C9-N6-C6	-5.55	117.70	122.85
1	1	747	5MU	O4-C4-C5	-5.55	118.57	124.92
1	1	1618	6MZ	N1-C2-N3	-5.54	120.20	128.58
1	1	1911	PSU	N1-C2-N3	5.53	121.00	115.17
1	1	2069	G7M	C2-N3-C4	5.51	121.79	112.30
1	1	1835	2MG	C5-C4-N3	-5.50	119.64	128.39
1	1	745	1MG	C1'-N9-C4	-5.41	110.49	126.49
1	1	1939	5MU	C4-N3-C2	-5.41	120.25	127.34
1	1	1911	PSU	C4-N3-C2	-5.40	118.94	126.37
1	1	2605	PSU	C4-N3-C2	-5.36	118.99	126.37
1	1	2251	OMG	C5-C4-N3	-5.34	119.89	128.39
1	1	2605	PSU	N1-C2-N3	5.32	120.78	115.17
2	2	1498	UR3	C4-N3-C2	-5.31	120.30	124.58
1	1	1618	6MZ	C5-C4-N9	-5.26	100.07	105.81
2	2	1516	2MG	C5-C4-N3	-5.24	120.05	128.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	1915	3TD	N1-C2-N3	5.22	119.93	116.13
1	1	2503	2MA	N9-C8-N7	-5.19	106.57	113.94
2	2	1518	MA6	C5-C6-N6	5.19	133.54	125.33
1	1	2030	6MZ	C5-C4-N9	-5.18	100.16	105.81
1	1	2580	PSU	N1-C2-N3	5.16	120.61	115.17
1	1	2069	G7M	CN7-N7-C8	-5.11	117.05	124.79
54	5	8	4SU	C5-C4-N3	5.09	119.49	114.75
1	1	2457	PSU	N1-C2-N3	5.07	120.52	115.17
1	1	2069	G7M	C5-C4-N3	-5.06	118.58	128.15
54	5	54	5MU	O4-C4-C5	-4.97	119.23	124.92
1	1	955	PSU	C4-N3-C2	-4.94	119.56	126.37
54	5	55	PSU	N1-C2-N3	4.94	120.38	115.17
1	1	2457	PSU	C4-N3-C2	-4.92	119.60	126.37
1	1	2504	PSU	N1-C2-N3	4.86	120.30	115.17
2	2	516	PSU	N1-C2-N3	4.86	120.29	115.17
1	1	1917	PSU	C4-N3-C2	-4.85	119.69	126.37
2	2	1207	2MG	C2-N1-C6	-4.84	118.70	124.55
1	1	746	PSU	C4-N3-C2	-4.83	119.71	126.37
1	1	1917	PSU	N1-C2-N3	4.82	120.25	115.17
2	2	966	2MG	C2-N1-C6	-4.81	118.74	124.55
1	1	2504	PSU	C4-N3-C2	-4.79	119.78	126.37
1	1	2445	2MG	C2-N1-C6	-4.75	118.81	124.55
1	1	2580	PSU	C4-N3-C2	-4.74	119.85	126.37
1	1	1939	5MU	N3-C2-N1	4.69	121.00	114.89
1	1	745	1MG	C5-C4-N3	-4.68	120.94	128.39
2	2	516	PSU	C4-N3-C2	-4.68	119.93	126.37
54	5	55	PSU	C4-N3-C2	-4.64	119.97	126.37
1	1	1835	2MG	C2-N1-C6	-4.62	118.97	124.55
1	1	2251	OMG	C2-N3-C4	4.61	120.24	112.30
1	1	747	5MU	N3-C2-N1	4.59	120.87	114.89
1	1	2445	2MG	N9-C4-N3	4.50	134.95	125.95
1	1	745	1MG	C1'-N9-C8	4.49	139.48	126.73
2	2	1518	MA6	N9-C8-N7	-4.48	107.58	113.94
1	1	2069	G7M	C5-C6-N1	4.48	121.09	111.84
1	1	955	PSU	N1-C2-N3	4.47	119.88	115.17
1	1	2030	6MZ	C9-N6-C6	-4.39	118.78	122.85
1	1	746	PSU	N1-C2-N3	4.36	119.76	115.17
1	1	2030	6MZ	C5-N7-C8	4.34	110.27	103.45
1	1	2030	6MZ	C1'-N9-C8	-4.33	117.48	127.09
2	2	527	G7M	C2-N3-C4	4.32	119.73	112.30
2	2	1516	2MG	C2-N1-C6	-4.29	119.36	124.55
54	5	54	5MU	C4-N3-C2	-4.29	121.71	127.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	966	2MG	N9-C4-N3	4.27	134.49	125.95
2	2	1519	MA6	C5-C4-N3	-4.24	120.88	126.72
2	2	1519	MA6	N9-C8-N7	-4.21	107.97	113.94
2	2	1518	MA6	C5-C4-N3	-4.20	120.94	126.72
1	1	2503	2MA	C4-N9-C8	4.14	110.08	105.74
54	5	54	5MU	N3-C2-N1	4.11	120.25	114.89
2	2	1207	2MG	N9-C4-N3	4.10	134.15	125.95
1	1	2552	OMU	N3-C2-N1	3.94	120.02	114.89
54	5	54	5MU	C5M-C5-C4	3.91	122.95	118.78
1	1	1618	6MZ	C5-N7-C8	3.90	109.58	103.45
1	1	2069	G7M	N9-C4-N3	3.89	133.73	125.95
2	2	1519	MA6	C2-N1-C6	3.87	121.29	111.83
2	2	527	G7M	C5-C4-N3	-3.87	120.84	128.15
1	1	2552	OMU	C5-C4-N3	3.86	120.20	114.80
2	2	527	G7M	C5-C6-N1	3.79	119.68	111.84
1	1	1915	3TD	C4-N3-C2	-3.76	120.63	124.61
1	1	745	1MG	N9-C8-N7	-3.76	106.43	113.40
2	2	1498	UR3	C5-C4-N3	3.74	119.97	115.04
54	5	8	4SU	C5-C4-S4	-3.74	120.03	124.31
1	1	747	5MU	C5M-C5-C6	-3.74	117.79	122.85
2	2	1518	MA6	C2-N1-C6	3.73	120.95	111.83
1	1	2030	6MZ	C5-C4-N3	-3.68	121.64	126.72
1	1	1835	2MG	N9-C4-N3	3.67	133.29	125.95
1	1	2069	G7M	C2-N1-C6	-3.61	118.56	125.11
1	1	2069	G7M	C1'-N9-C4	-3.59	115.89	126.49
1	1	2580	PSU	O2-C2-N1	-3.58	119.09	122.79
54	5	20	H2U	C5-C6-N1	3.57	122.33	111.52
54	5	54	5MU	C5M-C5-C6	-3.57	118.03	122.85
1	1	1939	5MU	C5M-C5-C6	-3.48	118.15	122.85
1	1	1618	6MZ	C1'-N9-C8	-3.47	119.39	127.09
1	1	2030	6MZ	C2-N3-C4	3.46	120.28	111.83
1	1	2251	OMG	C2-N1-C6	-3.45	118.85	125.11
2	2	1516	2MG	N9-C4-N3	3.45	132.84	125.95
2	2	1519	MA6	C4-C5-C6	3.38	119.41	115.91
1	1	1962	5MC	C5-C6-N1	-3.38	119.64	123.31
1	1	2069	G7M	O6-C6-C5	-3.38	120.47	128.01
54	5	20	H2U	N3-C2-N1	3.37	120.04	116.65
1	1	2251	OMG	N9-C4-N3	3.36	132.68	125.95
54	5	8	4SU	N3-C2-N1	3.35	119.26	114.89
2	2	1519	MA6	C2-N3-C4	3.34	120.00	111.83
54	5	20	H2U	O2-C2-N3	-3.34	115.33	121.49
54	5	8	4SU	C1'-N1-C2	3.33	123.57	117.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	745	1MG	C2-N3-C4	3.33	119.46	111.98
2	2	1518	MA6	C4-C5-C6	3.28	119.31	115.91
1	1	745	1MG	N9-C4-N3	3.28	132.51	125.95
2	2	1518	MA6	C2-N3-C4	3.26	119.80	111.83
1	1	747	5MU	C5M-C5-C4	3.26	122.26	118.78
1	1	1911	PSU	O2-C2-N1	-3.24	119.44	122.79
2	2	1402	4OC	O2-C2-N3	-3.24	117.22	122.33
1	1	2251	OMG	N9-C8-N7	-3.21	107.45	113.40
1	1	2503	2MA	C5-N7-C8	3.20	108.48	103.45
2	2	967	5MC	C5-C6-N1	-3.19	119.84	123.31
1	1	1618	6MZ	C2-N3-C4	3.11	119.43	111.83
1	1	2580	PSU	C6-N1-C2	-3.10	119.82	122.69
1	1	1835	2MG	N9-C8-N7	-3.04	107.76	113.40
1	1	1939	5MU	C5M-C5-C4	3.04	122.03	118.78
1	1	2504	PSU	O2-C2-N1	-3.04	119.66	122.79
2	2	1518	MA6	C5-N7-C8	3.04	108.22	103.45
2	2	1519	MA6	C5-N7-C8	2.99	108.15	103.45
2	2	1207	2MG	N1-C2-N2	2.99	119.61	116.56
1	1	2552	OMU	O4-C4-C5	-2.99	120.01	125.16
1	1	2445	2MG	N9-C8-N7	-2.97	107.89	113.40
2	2	1516	2MG	N9-C8-N7	-2.91	108.00	113.40
2	2	966	2MG	C5-C6-N1	2.91	120.66	113.25
1	1	1618	6MZ	C4-N9-C1'	-2.89	119.88	126.63
1	1	1618	6MZ	C4-C5-C6	-2.88	114.38	116.78
1	1	2251	OMG	C5-C6-N1	2.87	120.56	113.25
1	1	2445	2MG	C5-C6-N1	2.87	120.56	113.25
1	1	2504	PSU	C6-N1-C2	-2.87	120.03	122.69
1	1	2503	2MA	N3-C2-N1	-2.86	120.72	125.77
2	2	1518	MA6	C4-N9-C8	2.85	108.73	105.74
54	5	55	PSU	O2-C2-N1	-2.83	119.87	122.79
2	2	516	PSU	C6-N1-C2	-2.82	120.07	122.69
1	1	1939	5MU	O2-C2-N1	-2.81	119.14	122.80
1	1	746	PSU	O2-C2-N1	-2.79	119.91	122.79
1	1	747	5MU	O4-C4-N3	-2.77	114.91	120.11
54	5	55	PSU	C6-N1-C2	-2.76	120.13	122.69
1	1	1917	PSU	O2-C2-N1	-2.75	119.95	122.79
1	1	1618	6MZ	C5-C4-N3	-2.75	122.94	126.72
1	1	2445	2MG	O6-C6-C5	-2.75	119.28	126.53
2	2	1207	2MG	C5-C6-N1	2.74	120.23	113.25
2	2	1407	5MC	C5-C6-N1	-2.74	120.34	123.31
1	1	1835	2MG	C5-C6-N1	2.73	120.19	113.25
1	1	2251	OMG	O6-C6-C5	-2.72	119.35	126.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	1516	2MG	C1'-N9-C4	-2.71	118.49	126.49
54	5	54	5MU	O4-C4-N3	-2.71	115.03	120.11
1	1	2069	G7M	C1'-N9-C8	2.70	135.84	126.74
2	2	966	2MG	O6-C6-C5	-2.69	119.43	126.53
2	2	1519	MA6	C4-C5-N7	-2.67	107.53	110.58
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	1516	2MG	C5-C6-N1	2.65	119.99	113.25
1	1	1911	PSU	C6-N1-C2	-2.65	120.23	122.69
2	2	527	G7M	C2-N1-C6	-2.64	120.32	125.11
2	2	1407	5MC	O2-C2-N3	-2.63	118.18	122.33
2	2	966	2MG	N9-C8-N7	-2.62	108.54	113.40
1	1	1917	PSU	C6-N1-C2	-2.60	120.28	122.69
2	2	1207	2MG	N9-C8-N7	-2.58	108.61	113.40
1	1	2503	2MA	C6-C5-C4	2.58	120.70	117.18
54	5	32	4OC	C6-C5-C4	2.57	120.10	117.00
2	2	1207	2MG	CM2-N2-C2	-2.56	118.14	123.65
2	2	527	G7M	N9-C8-N7	-2.56	106.27	112.48
1	1	2457	PSU	C6-N1-C2	-2.53	120.34	122.69
1	1	745	1MG	C5-C6-N1	2.52	119.68	115.02
1	1	2605	PSU	O2-C2-N1	-2.52	120.18	122.79
2	2	1518	MA6	N3-C4-N9	2.52	131.45	127.17
1	1	2552	OMU	O2-C2-N1	-2.52	119.52	122.80
1	1	1939	5MU	O4-C4-N3	-2.51	115.39	120.11
1	1	1835	2MG	N1-C2-N2	2.49	119.10	116.56
1	1	1835	2MG	O6-C6-C5	-2.47	120.02	126.53
1	1	1618	6MZ	C6-C5-N7	2.46	135.11	132.43
2	2	516	PSU	O2-C2-N1	-2.45	120.27	122.79
2	2	527	G7M	C5-C4-N9	2.44	111.09	105.88
2	2	1207	2MG	O6-C6-C5	-2.39	120.23	126.53
2	2	1518	MA6	C4-C5-N7	-2.39	107.86	110.58
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
2	2	527	G7M	O6-C6-C5	-2.36	122.75	128.01
1	1	1835	2MG	C1'-N9-C4	-2.34	119.56	126.49
1	1	2605	PSU	C6-N1-C2	-2.34	120.52	122.69
1	1	747	5MU	C6-C5-C4	2.34	119.95	118.02
2	2	516	PSU	O3'-C3'-C4'	2.33	117.78	111.08
1	1	745	1MG	C8-N7-C5	2.31	108.38	104.26
2	2	1519	MA6	C5-C4-N9	2.31	108.33	105.81
1	1	2457	PSU	O2-C2-N1	-2.30	120.42	122.79
1	1	2030	6MZ	C6-C5-N7	2.30	134.94	132.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
54	5	20	H2U	C5-C4-N3	2.30	119.13	116.69
2	2	1402	4OC	C1'-N1-C2	2.28	123.47	118.44
1	1	2605	PSU	C6-C5-C4	2.24	119.69	118.17
1	1	2498	OMC	O2-C2-N3	-2.24	118.80	122.33
1	1	1911	PSU	C6-C5-C4	2.23	119.68	118.17
1	1	1915	3TD	O4-C4-N3	-2.20	116.33	120.36
2	2	1498	UR3	C1'-N1-C2	2.20	120.64	117.04
1	1	2030	6MZ	C4-C5-C6	-2.19	114.95	116.78
1	1	1939	5MU	C6-C5-C4	2.19	119.83	118.02
2	2	1519	MA6	C4-N9-C8	2.18	108.03	105.74
2	2	1516	2MG	C1'-N9-C8	2.18	132.91	126.73
2	2	1402	4OC	C6-C5-C4	2.16	119.60	117.00
2	2	1516	2MG	N1-C2-N2	2.14	118.74	116.56
2	2	1519	MA6	N3-C4-N9	2.13	130.79	127.17
1	1	745	1MG	C8-N9-C4	2.12	110.00	106.03
1	1	2251	OMG	C8-N7-C5	2.11	108.01	104.26
1	1	955	PSU	O2-C2-N1	-2.10	120.62	122.79
1	1	2069	G7M	N2-C2-N1	2.09	121.17	116.76
1	1	2457	PSU	O4'-C1'-C2'	2.05	107.98	105.15
1	1	746	PSU	C6-N1-C2	-2.02	120.82	122.69
2	2	1402	4OC	O2-C2-N1	2.02	122.85	118.90
1	1	1962	5MC	CM5-C5-C6	-2.01	120.13	122.85
2	2	1407	5MC	C5-C4-N3	-2.01	119.70	121.75

There are no chirality outliers.

All (51) 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

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Mol	Chain	Res	Type	Atoms
56	6	77	FME	O1-CN-N-CA
56	6	77	FME	N-CA-CB-CG
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
56	6	77	FME	C-CA-CB-CG
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
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.

17 monomers are involved in 25 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
54	5	55	PSU	1	0
1	1	2503	2MA	4	0
2	2	1407	5MC	2	0
2	2	1516	2MG	1	0
2	2	1402	4OC	1	0
1	1	2251	OMG	2	0
54	5	54	5MU	1	0
1	1	1962	5MC	1	0
54	5	32	4OC	1	0
1	1	2580	PSU	1	0
1	1	745	1MG	1	0
1	1	2030	6MZ	1	0
54	5	8	4SU	1	0
54	5	20	H2U	1	0
1	1	1915	3TD	4	0
2	2	1519	MA6	1	0
1	1	2552	OMU	2	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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

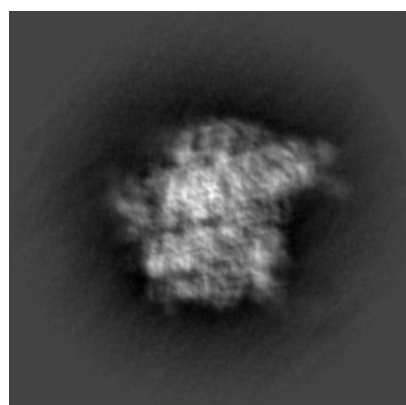
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20193. These allow visual inspection of the internal detail of the map and identification of artifacts.

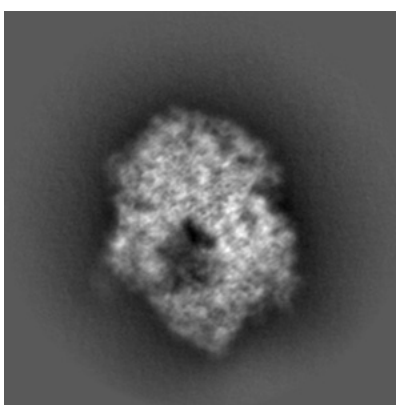
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

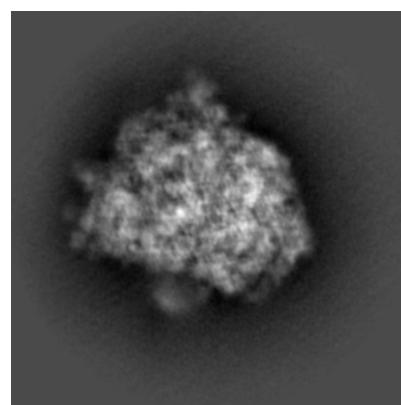
6.1.1 Primary map



X



Y

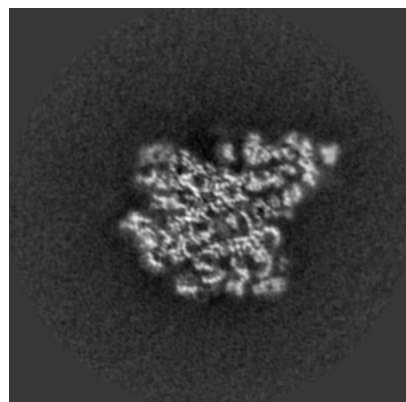


Z

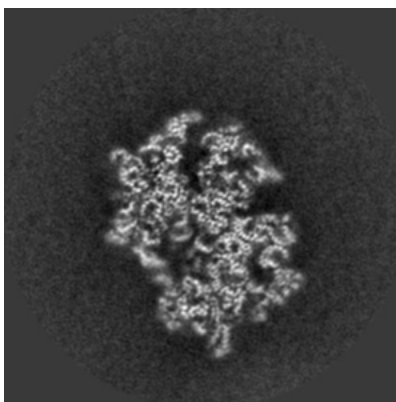
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

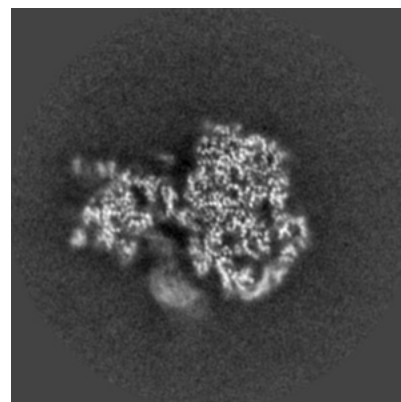
6.2.1 Primary map



X Index: 128



Y Index: 128

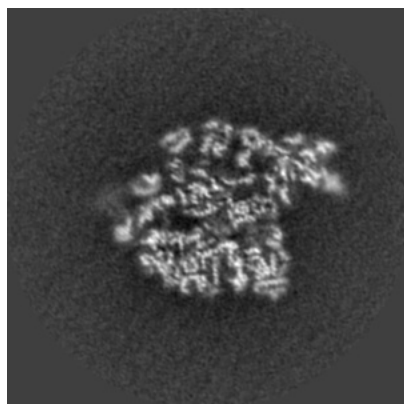


Z Index: 128

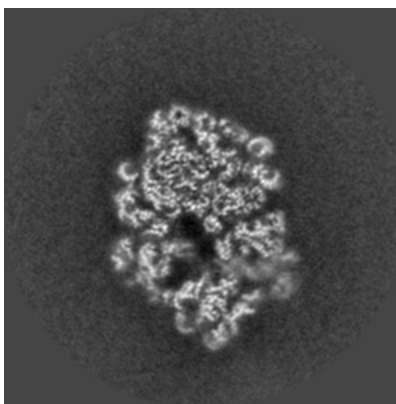
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

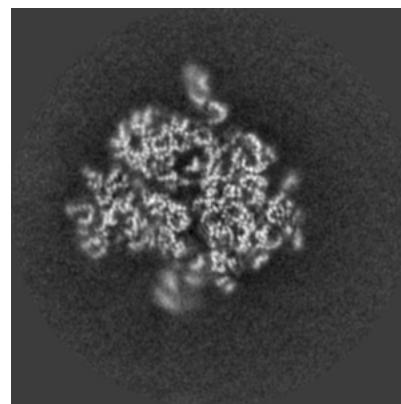
6.3.1 Primary map



X Index: 122



Y Index: 114

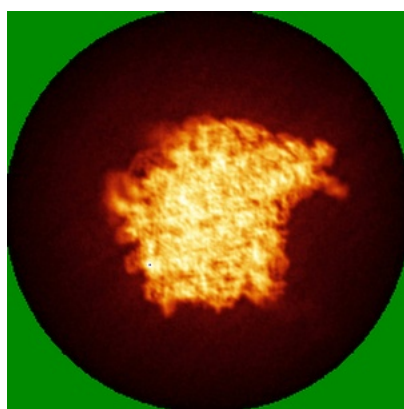


Z Index: 143

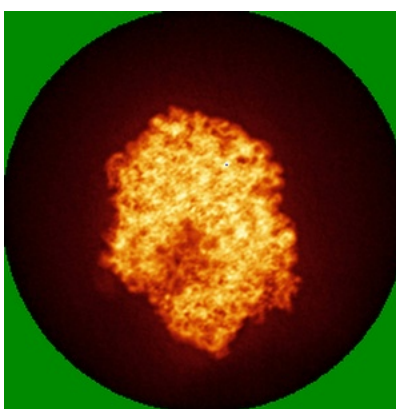
The images above show the largest variance slices of the map in three orthogonal directions.

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

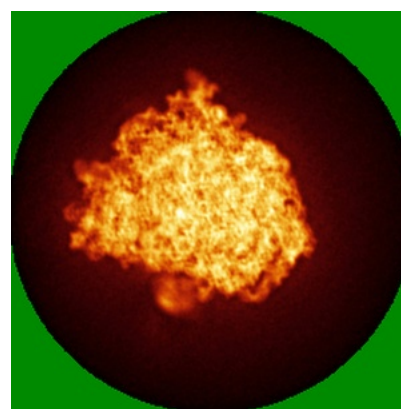
6.4.1 Primary map



X



Y

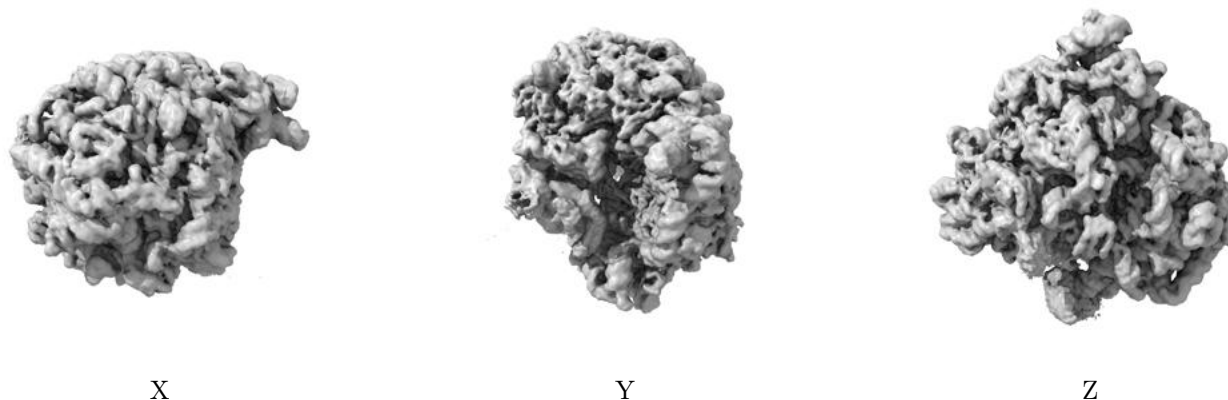


Z

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.

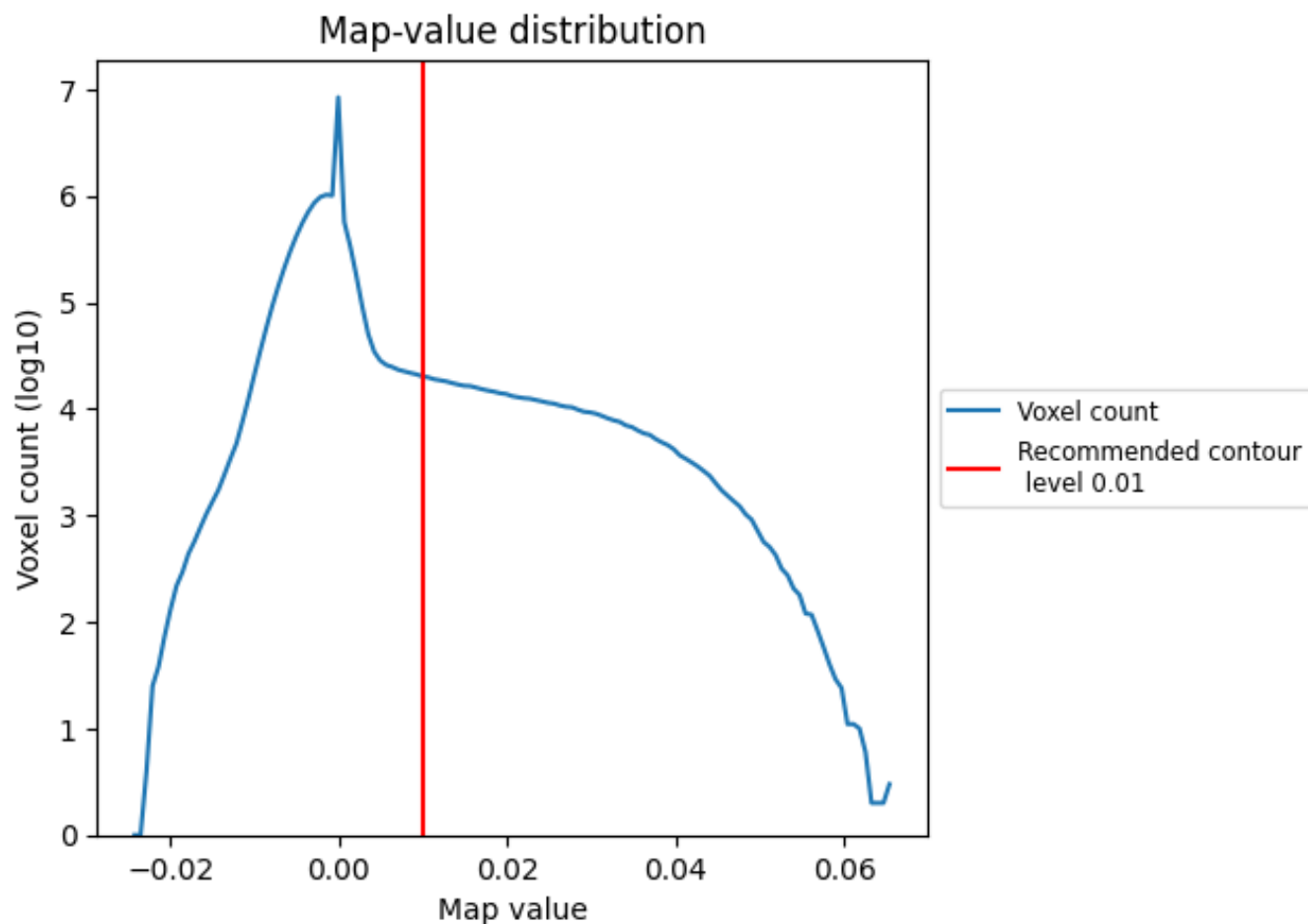
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

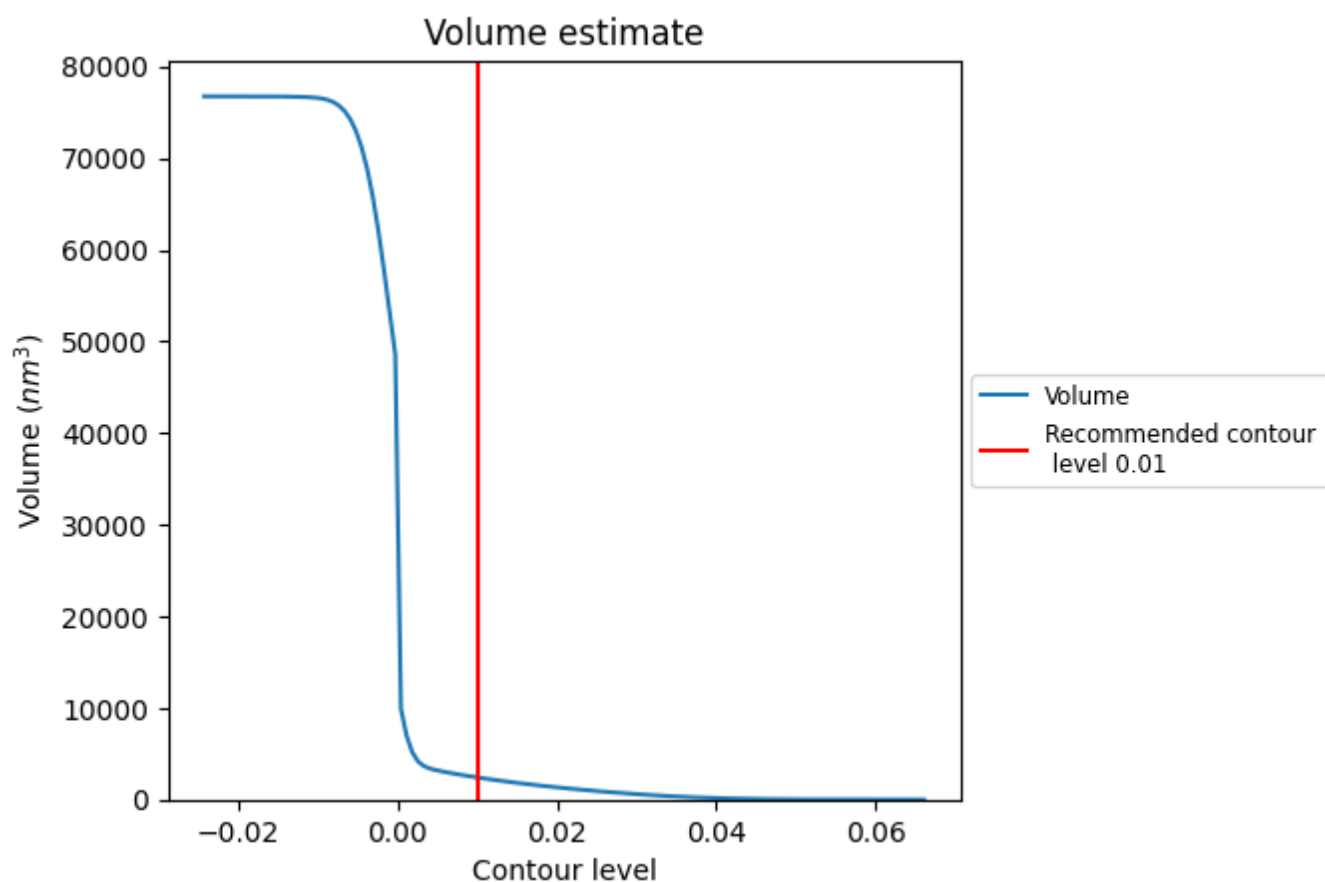
This section contains the results of statistical analysis of the map.

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.

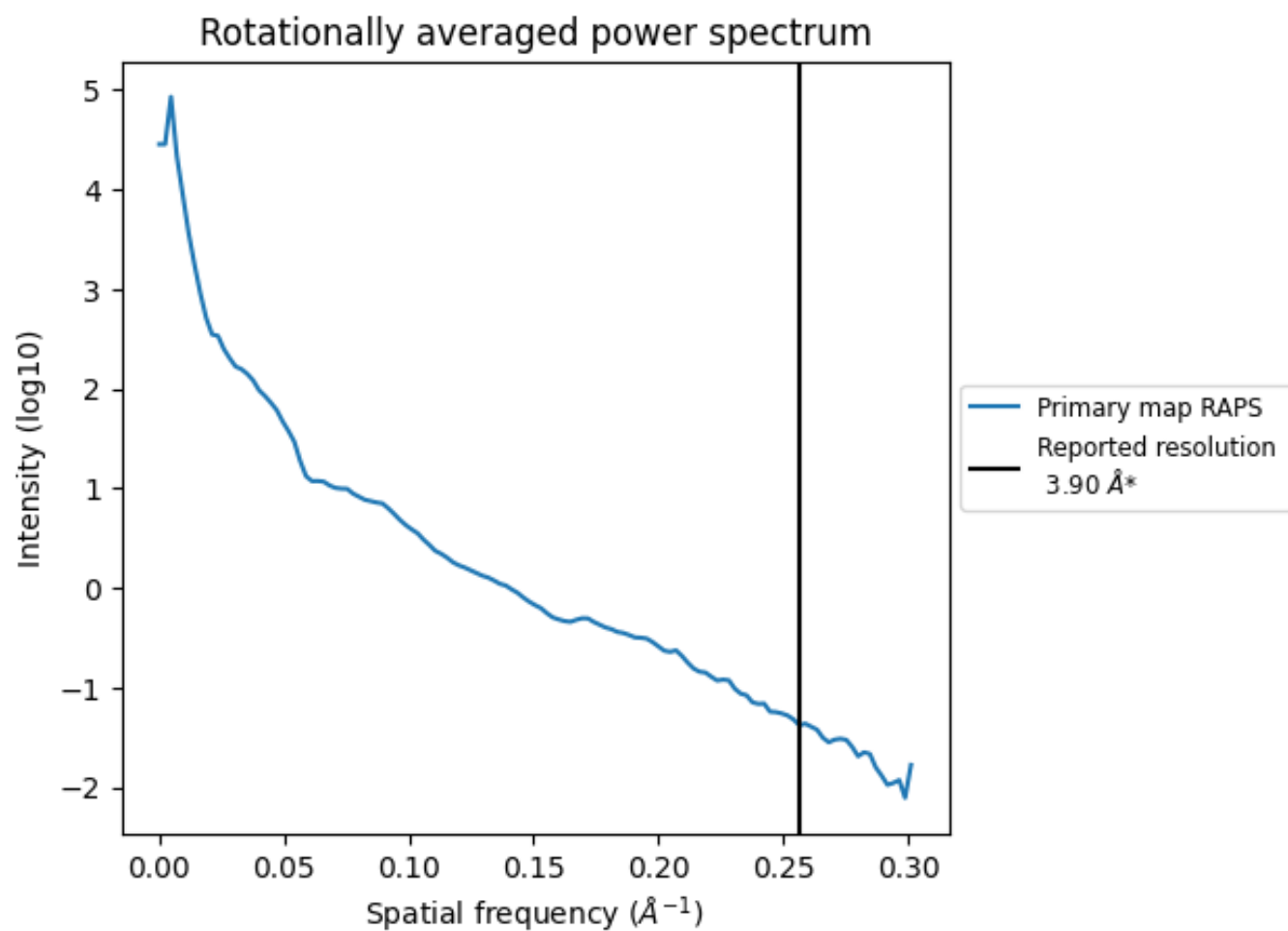
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2414 nm³; this corresponds to an approximate mass of 2180 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 0.256 Å⁻¹

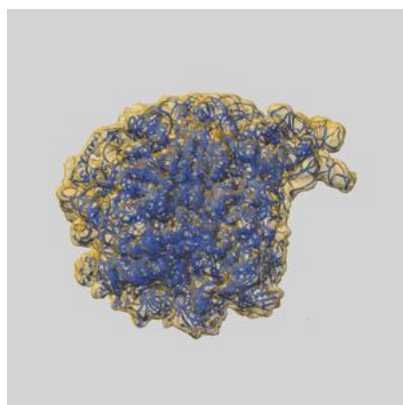
8 Fourier-Shell correlation

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

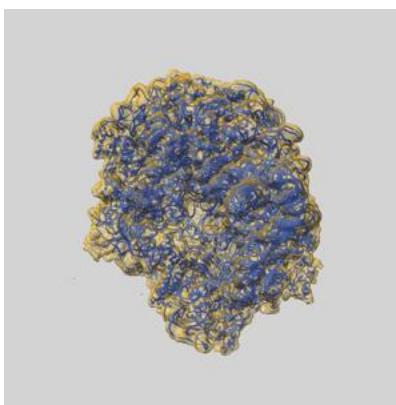
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-20193 and PDB model 6OT3. Per-residue inclusion information can be found in [section 3](#) on [page 15](#).

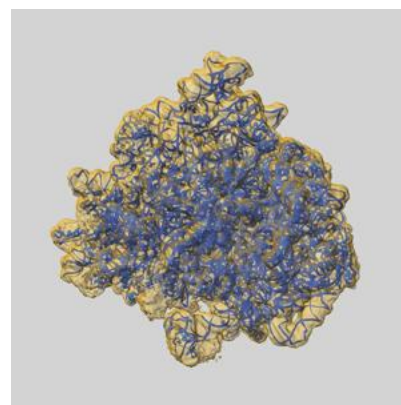
9.1 Map-model overlay [i](#)



X



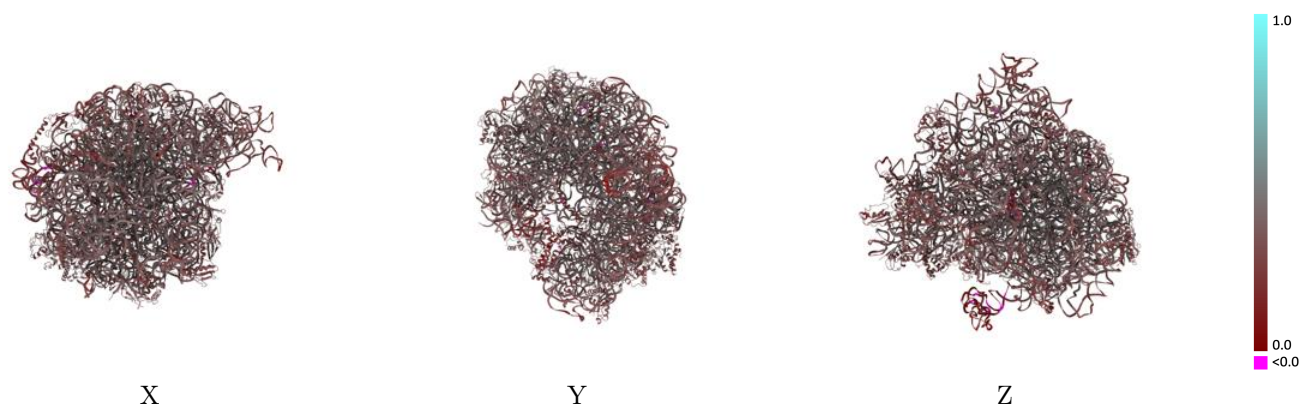
Y



Z

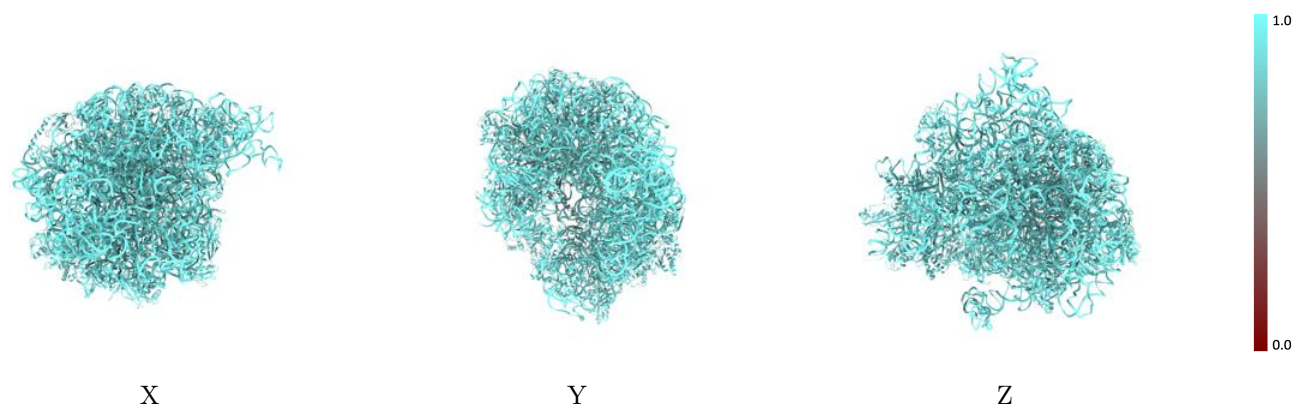
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



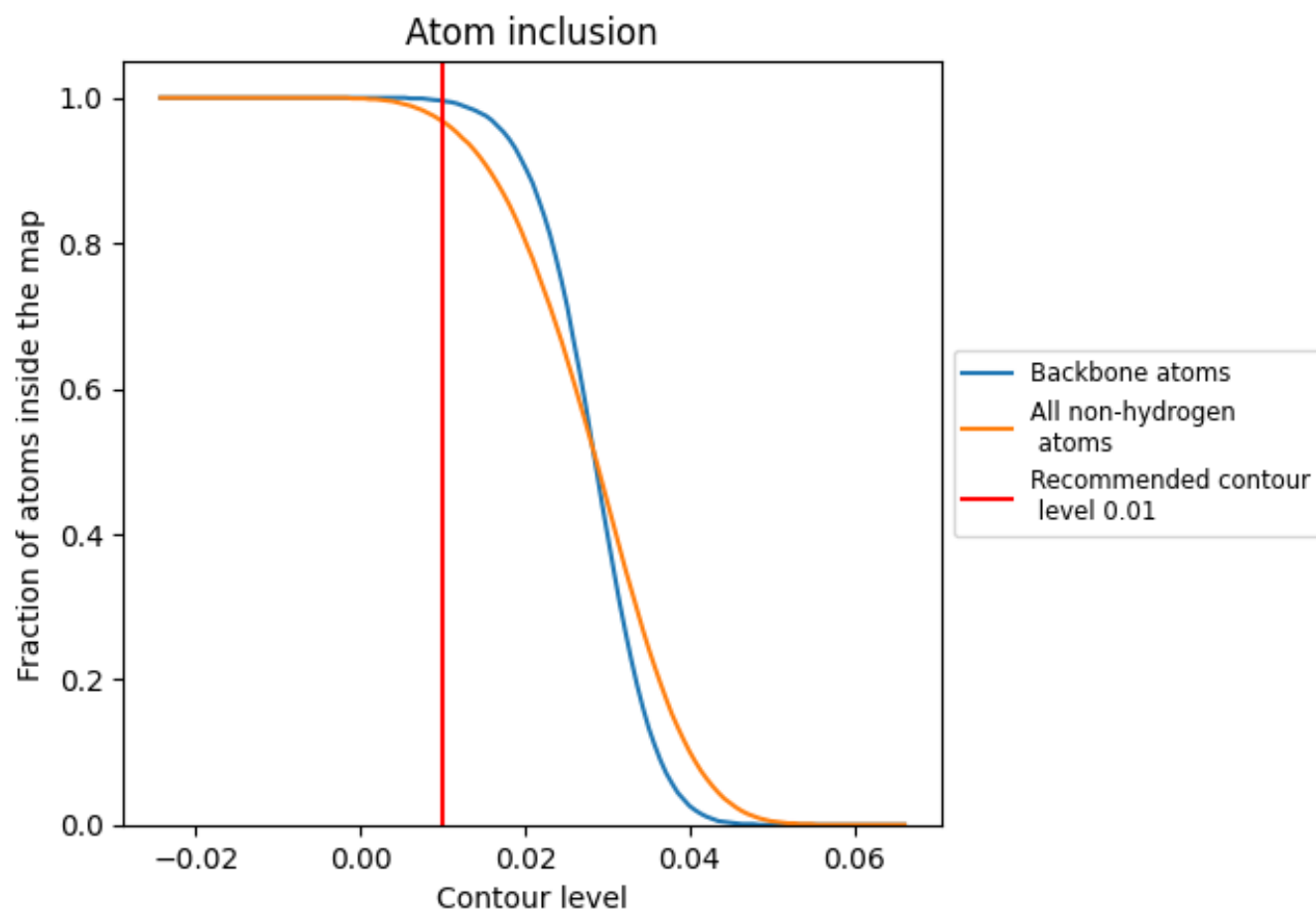
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.01).

9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 97% 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	 0.9670	 0.3480
1	 0.9960	 0.3640
2	 0.9980	 0.3560
3	 0.9990	 0.3490
4	 0.9950	 0.3690
5	 0.9740	 0.3360
6	 0.7190	 0.2220
A	 0.8140	 0.2480
B	 0.8930	 0.3790
C	 0.9180	 0.3550
D	 0.9160	 0.3480
E	 0.9160	 0.2980
F	 0.9440	 0.3200
G	 0.8460	 0.2660
J	 0.9140	 0.3540
K	 0.8350	 0.3410
L	 0.9240	 0.3660
M	 0.8970	 0.3630
N	 0.9070	 0.2820
O	 0.9590	 0.3270
P	 0.8960	 0.3220
Q	 0.9220	 0.3150
R	 0.9280	 0.3610
S	 0.8740	 0.3610
T	 0.8990	 0.3340
U	 0.9500	 0.3290
V	 0.9550	 0.3380
W	 0.9130	 0.3650
X	 0.9000	 0.3440
Y	 0.9490	 0.2730
Z	 0.9130	 0.3570
a	 0.8980	 0.2840
b	 0.9250	 0.3540
c	 0.9280	 0.3520
d	 0.8930	 0.3530



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Chain	Atom inclusion	Q-score
e	 0.8840	 0.3580
f	 0.9250	 0.3470
g	 0.9020	 0.2960
h	 0.8910	 0.3320
i	 0.9350	 0.3090
j	 0.9200	 0.3470
k	 0.8980	 0.3010
l	 0.9080	 0.2950
m	 0.9270	 0.3470
n	 0.9350	 0.3150
o	 0.9050	 0.3120
p	 0.9070	 0.3450
q	 0.8620	 0.3460
r	 0.9170	 0.2960
s	 0.9330	 0.3170
t	 0.8970	 0.2190
u	 0.9520	 0.3230
v	 0.9290	 0.3360
w	 0.8720	 0.3110
x	 0.9300	 0.3120
y	 0.9250	 0.2880
z	 0.8300	 0.2790