



Full wwPDB EM Validation Report ⓘ

Mar 27, 2026 – 06:04 PM UTC

PDB ID : 7ST6 / pdb_00007st6
EMDB ID : EMD-25420
Title : Pre translocation, non-rotated 70S ribosome (Structure I)
Authors : Carbone, C.E.; Korostelev, A.A.
Deposited on : 2021-11-12
Resolution : 3.00 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

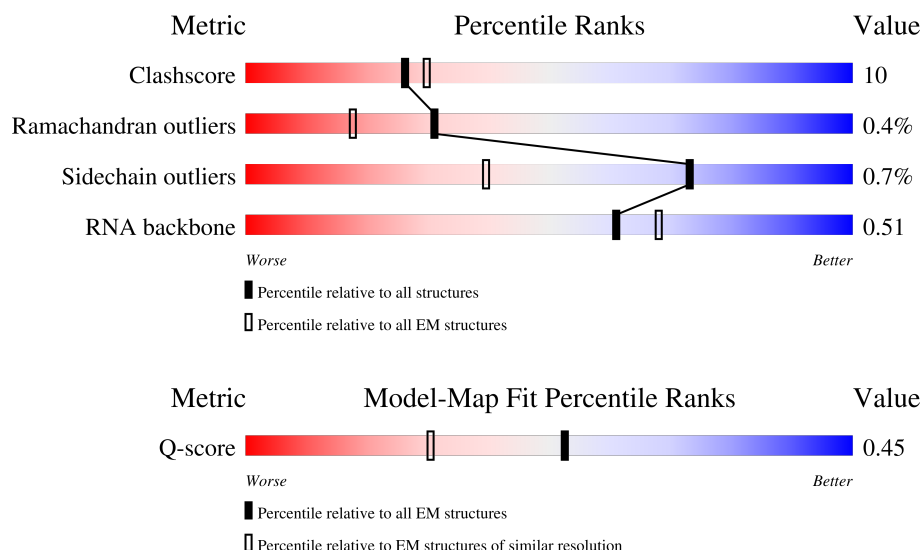
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.00 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	14081 (2.50 - 3.50)

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	3	1539	
2	1	2903	
3	2	120	

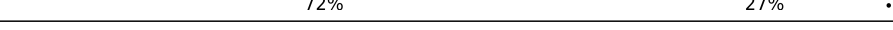
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Mol	Chain	Length	Quality of chain
4	5	77	
5	6	77	
5	7	77	
6	b	271	
7	c	209	
8	d	201	
9	e	177	
10	f	176	
11	g	149	
12	i	142	
13	j	142	
14	k	122	
15	l	143	
16	m	136	
17	n	120	
18	o	116	
19	p	114	
20	q	117	
21	r	103	
22	s	110	
23	t	93	
24	u	102	
25	v	94	
26	w	75	
27	x	77	

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Mol	Chain	Length	Quality of chain
28	y	63	
29	z	58	
30	A	66	
31	B	56	
32	C	50	
33	D	46	
34	E	64	
35	F	38	
36	4	35	
37	G	225	
38	H	206	
39	I	205	
40	J	157	
41	K	100	
42	L	151	
43	M	129	
44	N	127	
45	O	98	
46	P	116	
47	Q	123	
48	R	114	
49	S	100	
50	T	88	
51	U	82	
52	V	80	

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Mol	Chain	Length	Quality of chain
53	W	65	78% 22%
54	X	79	85% 15%
55	Y	85	78% 22%
56	Z	65	69% 28%

2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 147982 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 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	3	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

- Molecule 2 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	2903	Total	C	N	O	P	0	0
			62317	27801	11468	20146	2902		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 802133627

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	120	Total	C	N	O	P	0	0
			2568	1145	471	833	119		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	120	A	-	insertion	GB 1266961702

- Molecule 4 is a RNA chain called tRNA Pro.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	5	77	Total	C	N	O	P	0	0
			1647	733	295	542	77		

- Molecule 5 is a RNA chain called tRNA fMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	7	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		
5	6	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	b	271	Total	C	N	O	S	0	0
			2083	1288	423	365	7		

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

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

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

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

- Molecule 9 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	e	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

- Molecule 10 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	f	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 11 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	g	52	Total	C	N	O	S	0	0
			400	256	73	70	1		

- Molecule 12 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	i	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 13 is a protein called 50S ribosomal protein L13.

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

- Molecule 14 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	k	122	Total	C	N	O	S	0	0
			939	587	180	166	6		

- Molecule 15 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	l	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 16 is a protein called 50S ribosomal protein L16.

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

- Molecule 17 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	n	120	Total	C	N	O	S	0	0
			961	593	196	167	5		

- Molecule 18 is a protein called 50S ribosomal protein L18.

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

- Molecule 19 is a protein called 50S ribosomal protein L19.

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

- Molecule 20 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	q	117	Total	C	N	O	S	0	0
			947	604	192	151			

- Molecule 21 is a protein called 50S ribosomal protein L21.

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

- Molecule 22 is a protein called 50S ribosomal protein L22.

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

- Molecule 23 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	t	93	Total	C	N	O	S	0	0
			739	466	139	132	2		

- Molecule 24 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	u	102	Total	C	N	O	S	0	0
			780	492	146	142			

- Molecule 25 is a protein called 50S ribosomal protein L25.

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

- Molecule 26 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	w	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 27 is a protein called 50S ribosomal protein L28.

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

- Molecule 28 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	y	63	Total	C	N	O	S	0	0
			509	313	99	95	2		

- Molecule 29 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	z	58	Total	C	N	O	S	0	0
			449	281	87	79	2		

- Molecule 30 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	A	66	Total	C	N	O	S	0	0
			523	323	99	95	6		

- Molecule 31 is a protein called 50S ribosomal protein L32.

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

- Molecule 32 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	C	50	Total	C	N	O	0	0
			410	263	75	72		

- Molecule 33 is a protein called 50S ribosomal protein L34.

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

- Molecule 34 is a protein called 50S ribosomal protein L35.

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

- Molecule 35 is a protein called 50S ribosomal protein L36.

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

- Molecule 36 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	4	18	Total	C	N	O	P	0	0
			390	176	80	117	17		

- Molecule 37 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	G	218	Total	C	N	O	S	0	0
			1705	1081	305	312	7		

- Molecule 38 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	H	206	Total	C	N	O	S	0	0
			1625	1028	305	289	3		

- Molecule 39 is a protein called 30S ribosomal protein S4.

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

- Molecule 40 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	J	157	Total	C	N	O	S	0	0
			1157	719	218	214	6		

- Molecule 41 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	K	100	Total	C	N	O	S	0	0
			818	515	148	149	6		

- Molecule 42 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	L	151	Total	C	N	O	S	0	0
			1182	735	227	216	4		

- Molecule 43 is a protein called 30S ribosomal protein S8.

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

- Molecule 44 is a protein called 30S ribosomal protein S9.

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

- Molecule 45 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	O	98	Total	C	N	O	S	0	0
			787	493	150	143	1		

- Molecule 46 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	P	116	Total	C	N	O	S	0	0
			870	535	173	159	3		

- Molecule 47 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Q	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 48 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	R	114	Total	C	N	O	S	0	0
			884	546	178	157	3		

- Molecule 49 is a protein called 30S ribosomal protein S14.

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

- Molecule 50 is a protein called 30S ribosomal protein S15.

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

- Molecule 51 is a protein called 30S ribosomal protein S16.

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

- Molecule 52 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	V	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 53 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	W	65	Total	C	N	O	S	0	0
			536	339	100	96	1		

- Molecule 54 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	X	79	Total	C	N	O	S	0	0
			638	408	120	108	2		

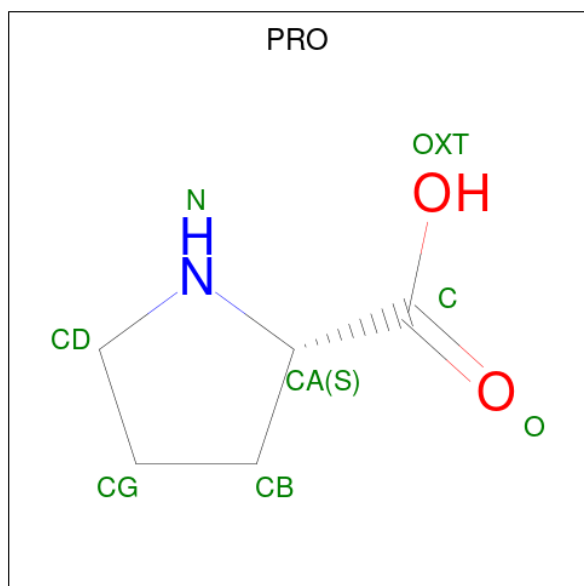
- Molecule 55 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Y	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 56 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	Z	65	Total	C	N	O	S	0	0
			545	335	117	92	1		

- Molecule 57 is PROLINE (CCD ID: PRO) (formula: $C_5H_9NO_2$).

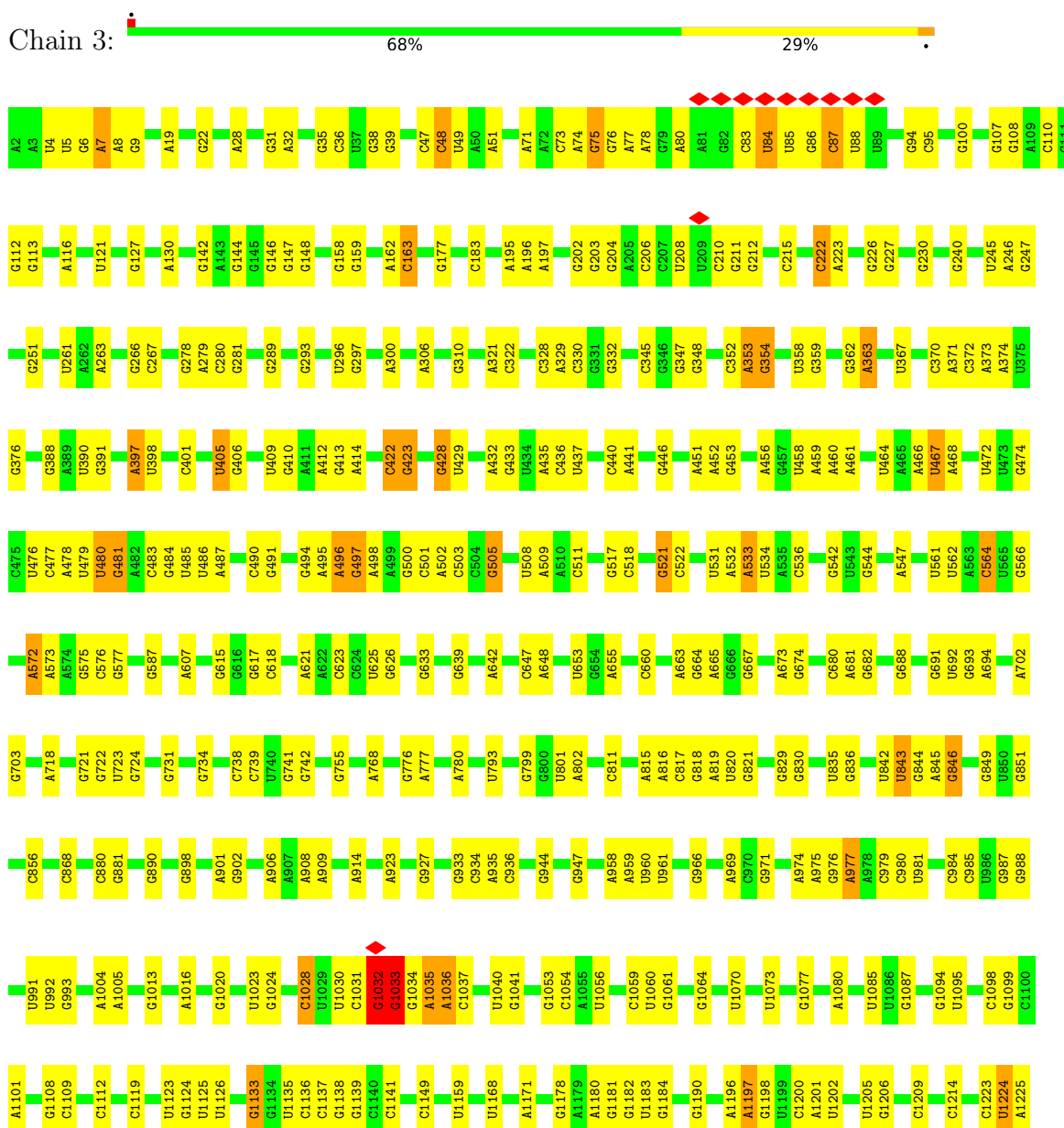


Mol	Chain	Residues	Atoms				AltConf
57	5	1	Total	C	N	O	0
			7	5	1	1	

3 Residue-property plots

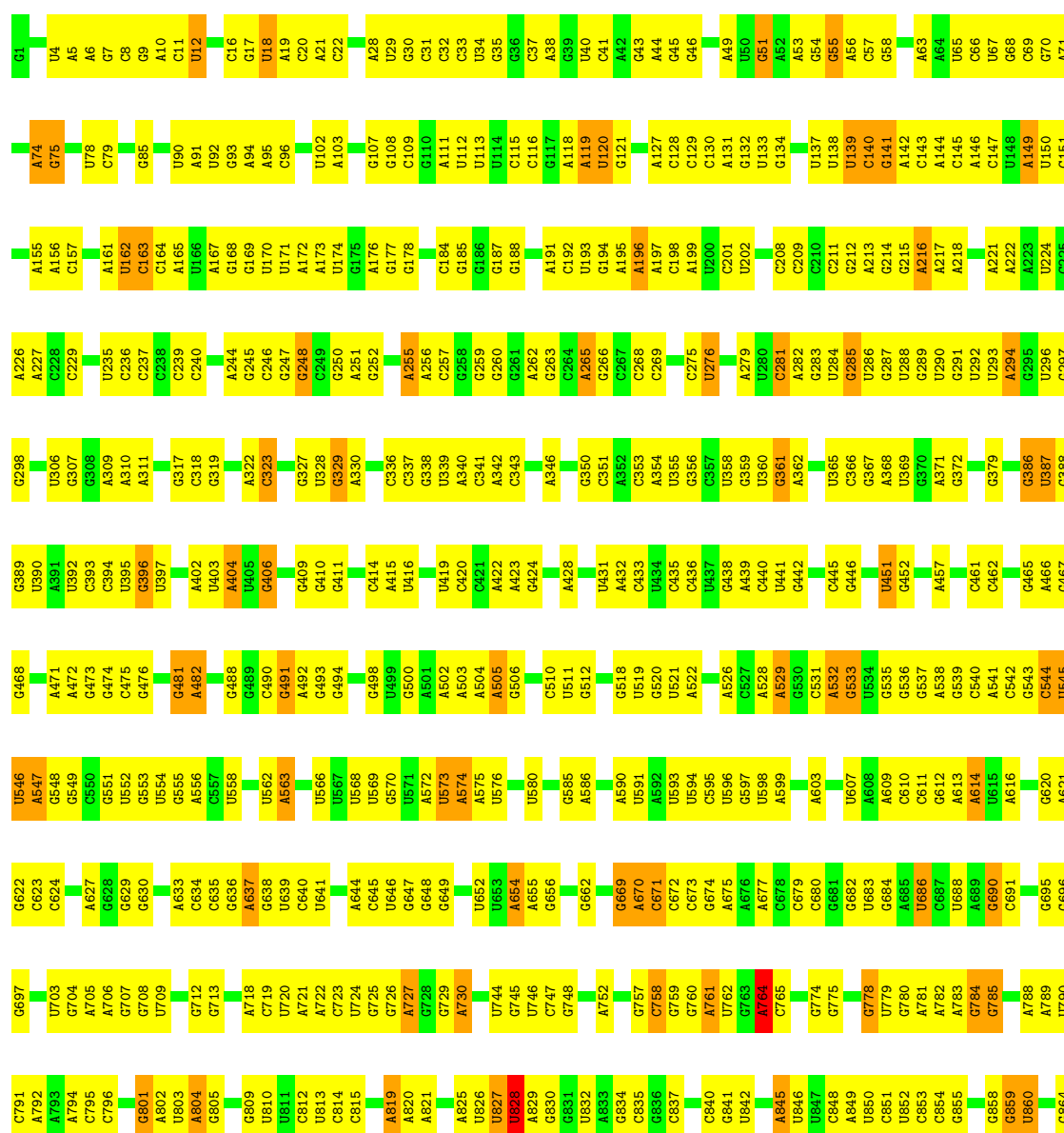
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 16S rRNA

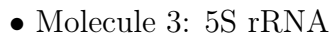




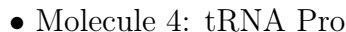
• Molecule 2: 23S rRNA



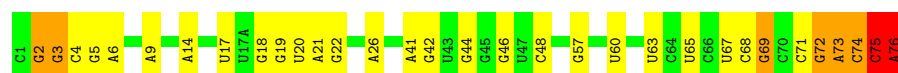
G1879	C1880	G1733	U1554	U1486	U1316	G1239	C1161	G1091	G0938	C0865
U1955	A1801	G1734	G1585	U1487	G1317	U1240	G1162	C1092	G939	C866
U1956	A1802	A1735	C1588	C1488	C1318	A1246	G1163	C1093	G940	U870
U1963	G1807	U1736	C1589	C1489	C1319	A1247	U1094	A1246	U871	U872
G1964	A1808	G1737	U1559	A1490	C1320	A1247	A1095	A1096	U872	C873
C1965	A1809	U1738	U1560	U1411	A1321	G1260	G1166	U1097	C946	
A1966	A1809	U1739	C1561	U1412	A1322	U1260	C1170	A1098	A947	C876
G1967	A1810	G1740	U1562	A1413	C1323	C1261	G1171	A1099	U955	A877
G1968	G1811	U1741	C1563	C1414	G1324	G1262	C1172	C1100	U878	A878
A1969	U1812	G1742	C1564	U1415	U1326	A1263	U1173	U1101	G956	G879
A1890	G1813	G1743	U1565	U1416	U1326	A1264	U1174	C1102	C957	
C1893	C1816	A1744	G1566	G1417	A1328	U1265	A1175	A1103	U958	C885
C1894	G1817	A1745	G1567	G1418	U1329	C1266	U1176	C1104	A959	A886
A1901	U1818	A1746	A1568	A1419	C1330	U1267	C1177	U1105	A960	U887
C1902	A1819	U1747	A1569	A1420	G1333	G1266	U1179	G1107	C968	C888
C1903	A1820	C1748	A1570	G1426	U1334	U1267	G1180	U1108	C969	C889
C1904	U1821	U1749	A1571	G1427	C1335	U1267	U1181	C1109	C970	C890
C1905	A1822	G1750	G1572	G1428	A1336	C1270	G1182	G1110	U970	G891
G1906	C1823	C1752	C1575	A1429	U1337	A1271	U1183	A1111	G971	A892
G1983	G1824	G1753	U1578	G1430	G1338	G1272	U1184	G1112	A972	C893
G1984	U1825	A1754	A1579	A1431	U1339	A1273	G1185	U1113	U894	U895
C1985	G1826	G1755	A1580	G1432	G1343	U1274	G1186	C1114	A974	A896
C1986	U1827	A1756	G1581	A1433	U1344	A1275	G1187	G1115	A975	C887
A1912	G1828	U1758	C1582	A1434	C1345	A1275	U1188	G1116	C966	C888
A1913	A1913	C1761	A1583	G1436	C1346	C1278	G1193	C1117	A1057	A899
A1914	C1832	A1762	A1584	U1437	C1348	G1279	A1194	C1118	U1058	A900
U1915	C1833	G1763	U1589	A1438	C1349	G1280	G1195	U1119	G1059	C901
A1916	U1834	C1764	U1590	U1439	U1352	G1281	C1196	G1120	U1060	C902
U1917	U1765	U1765	A1591	U1440	U1352	U1282	C1197	U1061	U1061	C903
A1918	G1845	G1766	A1592	G1441	A1353	U1283	G1198	G1062	G1062	C904
A1919	G1846	G1767	C1592	G1442	A1354	A1284	U1199	G1063	G1063	C905
C1920	A1847	C1768	U1593	U1443	A1365	A1285	C1200	G1064	G1064	U906
G1921	A1848	C1769	U1594	G1444	A1366	A1286	C1201	U1065	G907	C908
G1922	G1849	U1769	C1595	G1445	A1367	A1287	A1204	U1066	U1066	C909
U1923	U1851	A1772	A1596	G1446	G1368	G1288	A1205	U1067	U1067	A909
C1924	A1852	C1774	A1597	G1447	U1377	C1289	C1209	G1068	G1068	A910
A1927	A1853	U1775	A1598	C1451	G1378	G1292	G1210	A1069	A1069	A911
G1928	U1854	G1776	U1599	A1452	U1379	C1293	G1211	G1070	G1070	
U1929	U1855	U1777	C1600	A1453	G1380	U1294	G1212	G1071	G1071	C914
G1930	G1857	A1780	G1601	A1454	G1381	C1295	A1213	G1072	G1072	C915
U1931	A1858	U1781	A1602	C1455	G1382	G1296	C1219	A1073	A1073	
G1935	U1863	U1782	C1603	C1461	A1383	G1297	G1220	G1074	G1074	A918
A1936	U1864	A1783	C1604	C1462	A1384	C1298	G1221	C1075	C1075	U919
A1937	U1865	G1784	C1605	C1463	C1386	C1299	G1222	G1076	G1076	G923
A1938	U1866	A1785	C1606	G1464	U1387	G1299	G1223	U1077	U1077	G924
U1939	G1867	U1786	A1607	G1465	A1388	G1300	G1224	U1078	U1078	A925
	C1868	A1787	A1608	U1466	G1389	A1301	A1225	C1079	C1079	G926
	C1869	C1788	A1614	U1467	U1390	A1302	G1226	A1147	A1147	A927
C1942	U1869	U1789	C1615	U1468	U1391	C1306	G1227	U1148	U1148	U928
U1943	C1870	C1790	A1616	A1469	U1394	C1307	G1228	G1149	U1081	A928
U1944	A1871	C1726	A1617	A1470	U1400	G1310	C1229	C1150	U1082	U929
G1945	A1872	C1727	C1625	A1471	G1401	G1311	A1230	A1151	A1083	U932
	C1874	C1728	A1626	U1472	U1402	G1312	G1231	C1152	U1084	U933
G1948	G1875	U1729	A1634	U1473	U1403	G1313	G1232	C1153	A1085	A934
	G1876	C1730	A1635	U1474	U1404	C1314	G1233	G1154	A1086	U935
A1952	G1877	G1731	A1636	U1475	U1405	C1315	A1237	A1155	G1087	A936
A1953	G1878	C1732	G1642	U1485	C1404			G1160	A1088	C937



78% 19% .

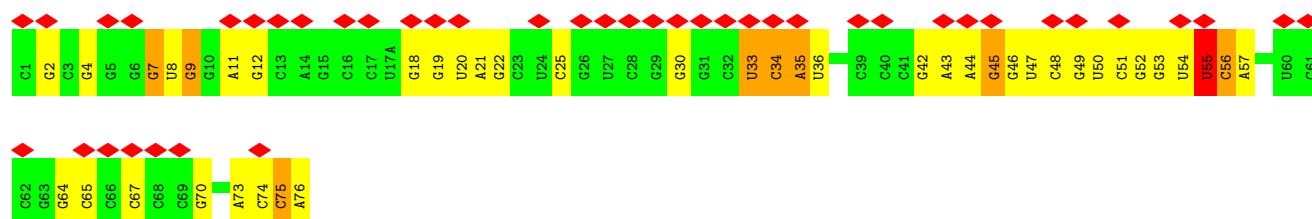


Chain 5:  58% 31% 8% .



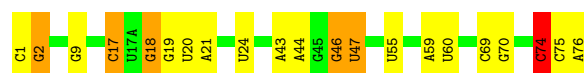
• Molecule 5: tRNA fMet

Chain 7:  45% 56% 43% 10% .



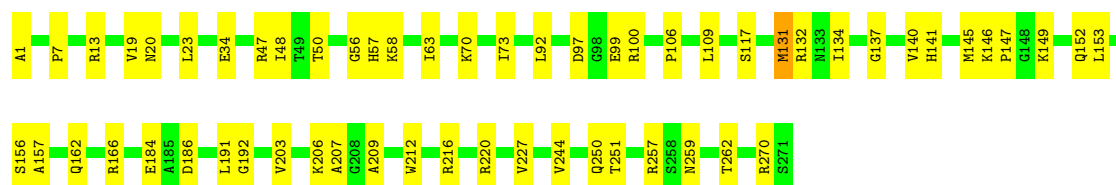
• Molecule 5: tRNA fMet

Chain 6:  73% 19% 6% .



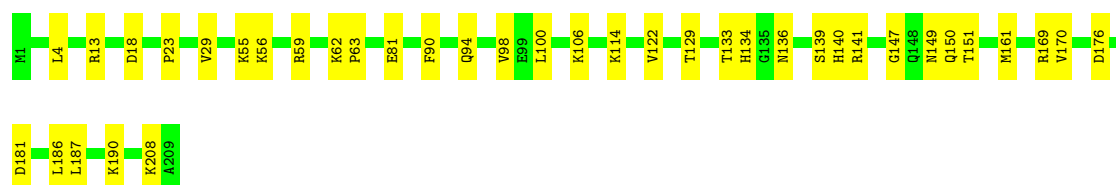
• Molecule 6: 50S ribosomal protein L2

Chain b:  79% 21%



• Molecule 7: 50S ribosomal protein L3

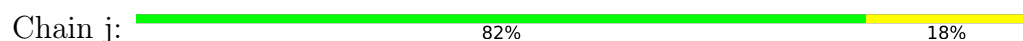
Chain c:  82% 18%

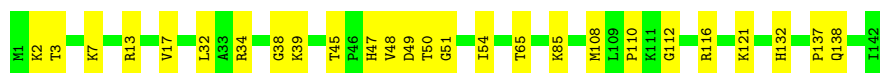


• Molecule 8: 50S ribosomal protein L4

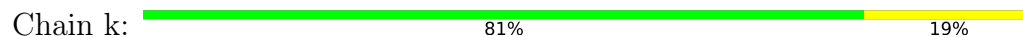
Chain d:  80% 20%



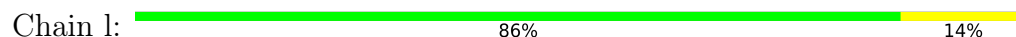




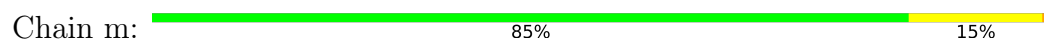
- Molecule 14: 50S ribosomal protein L14



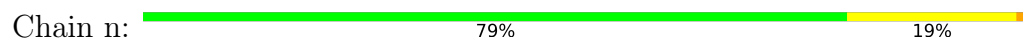
- Molecule 15: 50S ribosomal protein L15



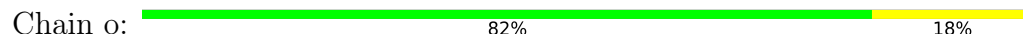
- Molecule 16: 50S ribosomal protein L16



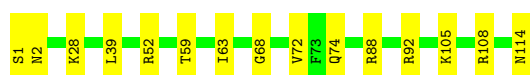
- Molecule 17: 50S ribosomal protein L17



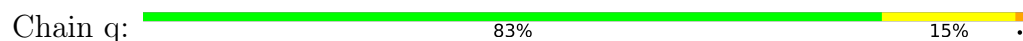
- Molecule 18: 50S ribosomal protein L18



- Molecule 19: 50S ribosomal protein L19



- Molecule 20: 50S ribosomal protein L20





- Molecule 21: 50S ribosomal protein L21

Chain r: 75% 25%



- Molecule 22: 50S ribosomal protein L22

Chain s: 84% 16%



- Molecule 23: 50S ribosomal protein L23

Chain t: 80% 20%



- Molecule 24: 50S ribosomal protein L24

Chain u: 73% 27%



- Molecule 25: 50S ribosomal protein L25

Chain v: 85% 14%



- Molecule 26: 50S ribosomal protein L27

Chain w: 83% 17%

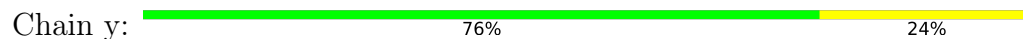


- Molecule 27: 50S ribosomal protein L28

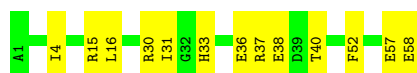
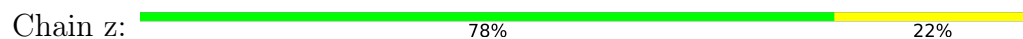
Chain x: 77% 22%



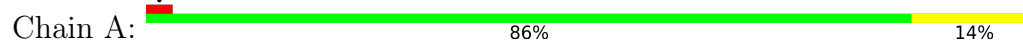
- Molecule 28: 50S ribosomal protein L29



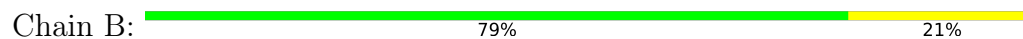
- Molecule 29: 50S ribosomal protein L30



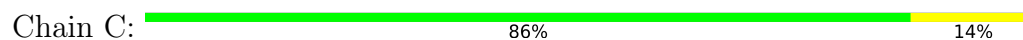
- Molecule 30: 50S ribosomal protein L31



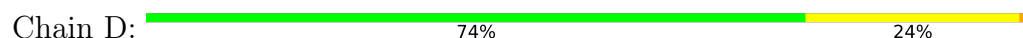
- Molecule 31: 50S ribosomal protein L32



- Molecule 32: 50S ribosomal protein L33



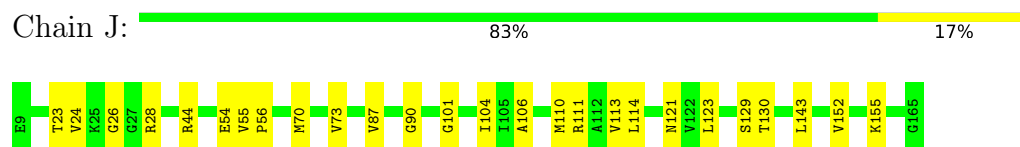
- Molecule 33: 50S ribosomal protein L34



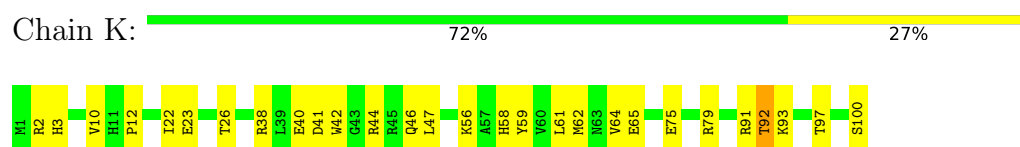
- Molecule 34: 50S ribosomal protein L35



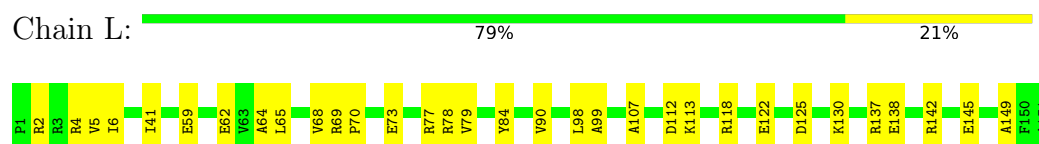
- Molecule 40: 30S ribosomal protein S5



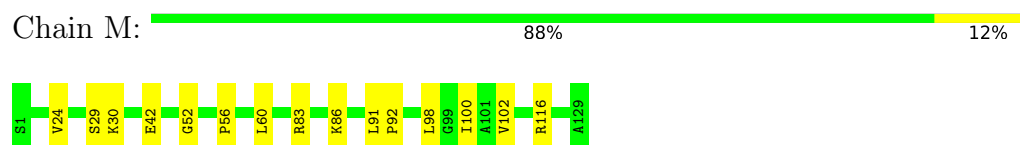
- Molecule 41: 30S ribosomal protein S6



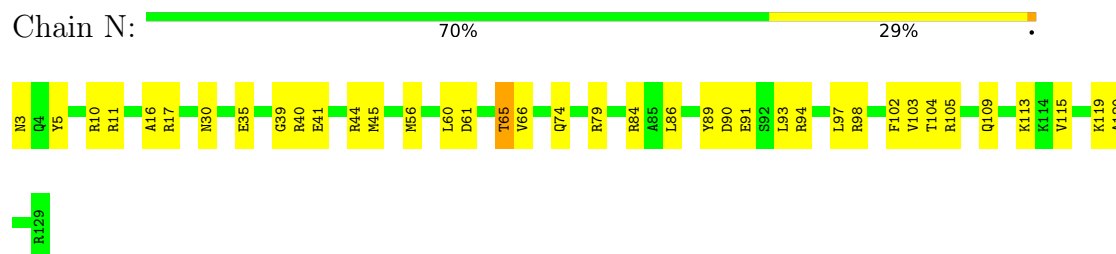
- Molecule 42: 30S ribosomal protein S7



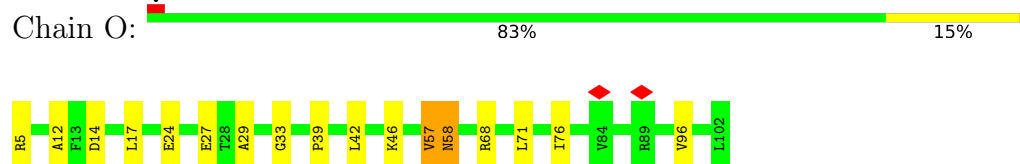
- Molecule 43: 30S ribosomal protein S8



- Molecule 44: 30S ribosomal protein S9



- Molecule 45: 30S ribosomal protein S10



- Molecule 46: 30S ribosomal protein S11

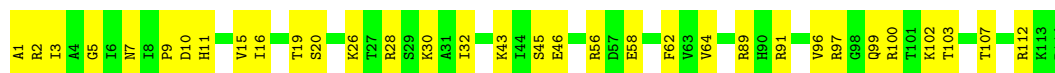




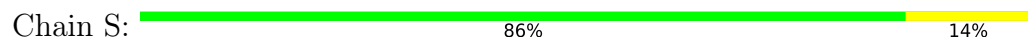
- Molecule 47: 30S ribosomal protein S12



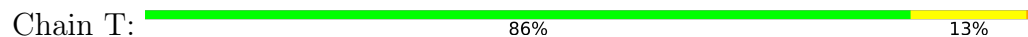
- Molecule 48: 30S ribosomal protein S13



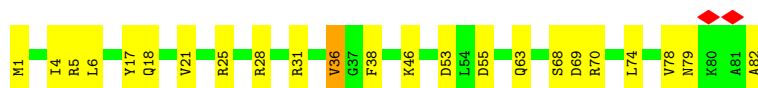
- Molecule 49: 30S ribosomal protein S14



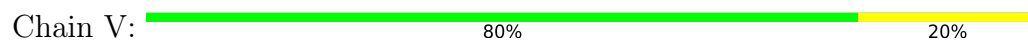
- Molecule 50: 30S ribosomal protein S15



- Molecule 51: 30S ribosomal protein S16



- Molecule 52: 30S ribosomal protein S17



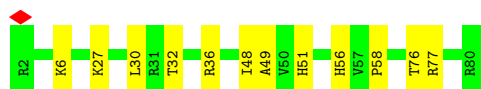
- Molecule 53: 30S ribosomal protein S18

Chain W:  78% 22%



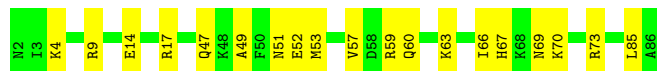
- Molecule 54: 30S ribosomal protein S19

Chain X:  85% 15%



- Molecule 55: 30S ribosomal protein S20

Chain Y:  78% 22%



- Molecule 56: 30S ribosomal protein S21

Chain Z:  69% 28%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	37252	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40.2	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	14.154	Depositor
Minimum map value	-4.209	Depositor
Average map value	0.009	Depositor
Map value standard deviation	0.866	Depositor
Recommended contour level	1.35	Depositor
Map size (Å)	381.8, 381.8, 381.8	wwPDB
Map dimensions	460, 460, 460	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83, 0.83, 0.83	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	3	0.40	0/36963	0.40	4/57662 (0.0%)
2	1	0.50	2/69796 (0.0%)	0.62	34/108888 (0.0%)
3	2	0.38	0/2872	0.41	0/4479
4	5	0.38	0/1840	0.60	5/2868 (0.2%)
5	6	0.37	0/1832	0.82	4/2855 (0.1%)
5	7	0.40	0/1832	0.60	3/2855 (0.1%)
6	b	0.47	0/2122	0.64	0/2852
7	c	0.42	0/1586	0.59	2/2134 (0.1%)
8	d	0.37	0/1571	0.62	0/2113
9	e	0.35	0/1435	0.64	4/1926 (0.2%)
10	f	0.28	0/1343	0.54	0/1816
11	g	0.32	0/405	0.75	0/544
12	i	0.31	0/1046	0.77	3/1410 (0.2%)
13	j	0.41	0/1152	0.55	1/1551 (0.1%)
14	k	0.44	0/948	0.66	0/1268
15	l	0.40	0/1054	0.63	0/1403
16	m	0.45	0/1093	0.72	4/1460 (0.3%)
17	n	0.40	0/974	0.70	1/1301 (0.1%)
18	o	0.31	0/902	0.51	0/1209
19	p	0.41	0/929	0.61	0/1242
20	q	0.45	0/960	0.71	3/1278 (0.2%)
21	r	0.38	0/829	0.63	0/1107
22	s	0.39	0/864	0.55	0/1156
23	t	0.33	0/745	0.52	0/994
24	u	0.31	0/788	0.75	0/1051
25	v	0.34	0/766	0.51	0/1025
26	w	0.40	0/582	0.52	0/769
27	x	0.43	0/635	0.63	1/848 (0.1%)
28	y	0.29	0/510	0.64	0/677
29	z	0.41	0/453	0.53	0/605
30	A	0.26	0/532	0.54	0/709
31	B	0.40	0/450	0.60	0/599
32	C	0.27	0/417	0.52	0/554
33	D	0.47	0/380	0.76	2/498 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
34	E	0.44	0/513	0.58	0/676
35	F	0.42	0/303	0.71	0/397
36	4	0.54	0/439	0.62	0/684
37	G	0.29	0/1736	0.63	2/2338 (0.1%)
38	H	0.34	0/1652	0.55	0/2225
39	I	0.29	0/1665	0.69	0/2227
40	J	0.38	0/1170	0.68	2/1573 (0.1%)
41	K	0.33	0/836	0.75	0/1128
42	L	0.30	0/1196	0.67	3/1602 (0.2%)
43	M	0.34	0/989	0.52	0/1326
44	N	0.31	0/1034	0.72	0/1375
45	O	0.29	0/797	0.69	2/1077 (0.2%)
46	P	0.37	0/886	0.71	1/1195 (0.1%)
47	Q	0.37	0/969	0.87	4/1300 (0.3%)
48	R	0.33	0/893	0.73	2/1193 (0.2%)
49	S	0.32	0/817	0.61	0/1088
50	T	0.36	0/722	0.55	0/964
51	U	0.29	0/659	0.71	2/884 (0.2%)
52	V	0.33	0/658	0.68	0/881
53	W	0.37	0/545	0.68	0/731
54	X	0.27	0/653	0.55	0/877
55	Y	0.28	0/671	0.52	0/888
56	Z	0.34	0/551	0.99	2/728 (0.3%)
All	All	0.44	2/160960 (0.0%)	0.58	91/241063 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	3	1	0
2	1	0	40
4	5	2	0
5	7	1	0
6	b	0	1
8	d	0	1
9	e	0	1
16	m	0	1
17	n	0	1
20	q	0	2
21	r	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
24	u	0	1
34	E	0	1
35	F	0	1
37	G	0	1
39	I	0	1
41	K	0	1
44	N	0	1
46	P	0	1
47	Q	0	2
50	T	0	1
52	V	0	1
53	W	0	2
56	Z	0	2
All	All	4	65

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	1	2587	A	O3'-P	8.26	1.73	1.61
2	1	2059	A	O3'-P	-5.30	1.53	1.61

All (91) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	6	74	C	OP2-P-O3'	20.86	170.57	108.00
5	6	74	C	P-O3'-C3'	-19.93	90.30	120.20
5	6	74	C	O3'-P-O5'	-18.56	76.16	104.00
5	6	74	C	OP1-P-O3'	-14.65	64.06	108.00
5	7	55	U	C2'-C3'-O3'	11.04	130.25	113.70
4	5	76	A	C4'-C3'-O3'	9.17	126.76	113.00
46	P	73	VAL	N-CA-C	-9.02	104.54	113.20
1	3	1032	G	C2'-C3'-O3'	8.94	127.11	113.70
2	1	2587	A	P-O3'-C3'	-8.88	106.88	120.20
20	q	33	VAL	N-CA-C	-8.75	104.77	112.12
2	1	2059	A	O3'-P-O5'	-7.76	92.36	104.00
42	L	64	ALA	N-CA-C	-7.68	105.08	114.75
2	1	1130	U	C2'-C3'-O3'	7.63	120.94	109.50
5	7	55	U	C4'-C3'-O3'	7.37	124.05	113.00
2	1	2326	C	C2'-C3'-O3'	7.21	120.32	109.50
16	m	69	PRO	CA-C-N	7.20	135.29	121.54
16	m	69	PRO	C-N-CA	7.20	135.29	121.54
4	5	76	A	C2'-C3'-O3'	6.99	124.18	113.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	5	75	C	C2'-C3'-O3'	6.78	123.87	113.70
2	1	2324	U	N1-C1'-C2'	6.71	122.06	112.00
20	q	3	VAL	CA-C-N	6.41	133.79	121.54
20	q	3	VAL	C-N-CA	6.41	133.79	121.54
9	e	175	PRO	CA-C-N	6.35	133.67	121.54
9	e	175	PRO	C-N-CA	6.35	133.67	121.54
1	3	1032	G	C4'-C3'-O3'	6.34	122.51	113.00
2	1	746	U	N1-C1'-C2'	6.32	121.47	112.00
7	c	147	GLY	CA-C-N	-6.03	115.26	122.44
7	c	147	GLY	C-N-CA	-6.03	115.26	122.44
2	1	1952	A	N9-C1'-C2'	5.96	120.93	112.00
2	1	727	A	N9-C1'-C2'	5.95	120.92	112.00
4	5	72	G	C4'-C3'-O3'	-5.84	100.64	109.40
4	5	75	C	C4'-C3'-O3'	5.82	121.73	113.00
2	1	669	G	N9-C1'-C2'	5.75	120.62	112.00
2	1	2820	A	N9-C1'-C2'	5.73	120.59	112.00
2	1	790	U	N1-C1'-C2'	5.71	120.56	112.00
16	m	57	VAL	CA-C-N	5.69	132.41	121.54
16	m	57	VAL	C-N-CA	5.69	132.41	121.54
2	1	828	U	N1-C1'-C2'	5.62	120.43	112.00
56	Z	35	GLU	CA-C-N	5.62	132.28	121.54
56	Z	35	GLU	C-N-CA	5.62	132.28	121.54
2	1	827	U	N1-C1'-C2'	5.62	120.43	112.00
2	1	1790	C	N1-C1'-C2'	5.62	120.42	112.00
45	O	57	VAL	CA-C-N	5.59	132.22	121.54
45	O	57	VAL	C-N-CA	5.59	132.22	121.54
17	n	47	VAL	N-CA-C	-5.57	107.44	112.12
40	J	155	LYS	N-CA-C	-5.51	107.81	114.75
2	1	1451	C	N1-C1'-C2'	5.49	120.23	112.00
2	1	960	A	N9-C1'-C2'	5.47	120.21	112.00
2	1	2587	A	OP2-P-O3'	5.47	124.42	108.00
2	1	1696	G	N9-C1'-C2'	5.40	120.10	112.00
2	1	1020	A	C2'-C3'-O3'	5.40	117.60	109.50
33	D	3	ARG	CA-C-N	5.37	127.74	120.38
33	D	3	ARG	C-N-CA	5.37	127.74	120.38
2	1	802	A	N9-C1'-C2'	5.37	120.05	112.00
47	Q	32	VAL	CA-C-N	5.35	131.75	121.54
47	Q	32	VAL	C-N-CA	5.35	131.75	121.54
1	3	1033	G	N9-C1'-C2'	5.34	120.02	112.00
37	G	17	HIS	CA-C-N	5.32	131.70	121.54
37	G	17	HIS	C-N-CA	5.32	131.70	121.54
2	1	2547	A	N9-C1'-C2'	5.32	119.97	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	1	1782	U	N1-C1'-C2'	5.31	119.97	112.00
12	i	24	GLY	N-CA-C	5.30	123.14	112.34
2	1	2428	G	N9-C1'-C2'	5.29	119.93	112.00
42	L	5	VAL	CA-C-N	5.28	127.78	120.49
42	L	5	VAL	C-N-CA	5.28	127.78	120.49
2	1	2055	C	N1-C1'-C2'	5.27	119.91	112.00
9	e	141	ASP	CA-C-N	5.24	131.55	121.54
9	e	141	ASP	C-N-CA	5.24	131.55	121.54
2	1	980	A	N9-C1'-C2'	5.21	119.82	112.00
13	j	110	PRO	N-CA-C	5.20	120.68	113.98
51	U	78	VAL	CA-C-N	5.19	129.66	121.56
51	U	78	VAL	C-N-CA	5.19	129.66	121.56
2	1	2576	G	N9-C1'-C2'	5.19	119.78	112.00
2	1	2430	A	N9-C1'-C2'	5.18	119.77	112.00
2	1	1225	G	N9-C1'-C2'	5.15	119.72	112.00
2	1	1565	C	N1-C1'-C2'	5.14	119.71	112.00
1	3	1032	G	N9-C1'-C2'	5.13	119.70	112.00
40	J	87	VAL	N-CA-C	5.12	116.01	109.30
2	1	1328	A	N9-C1'-C2'	5.11	119.66	112.00
2	1	2777	G	N9-C1'-C2'	5.10	119.64	112.00
48	R	3	ILE	CA-C-N	5.09	131.26	121.54
48	R	3	ILE	C-N-CA	5.09	131.26	121.54
12	i	71	LYS	CA-C-N	5.08	134.18	121.80
12	i	71	LYS	C-N-CA	5.08	134.18	121.80
27	x	25	LYS	N-CA-C	5.06	121.57	110.80
2	1	1087	G	N9-C1'-C2'	5.05	119.57	112.00
47	Q	42	LYS	CA-C-N	5.04	129.54	121.62
47	Q	42	LYS	C-N-CA	5.04	129.54	121.62
2	1	1672	A	N9-C1'-C2'	5.03	119.55	112.00
5	7	33	U	C2'-C3'-O3'	5.03	121.24	113.70
2	1	972	A	N9-C1'-C2'	5.02	119.53	112.00

All (4) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	3	1032	G	C3'
4	5	75	C	C3'
4	5	76	A	C3'
5	7	55	U	C3'

All (65) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	1	1133	A	Sidechain
2	1	1188	U	Sidechain
2	1	1225	G	Sidechain
2	1	1652	A	Sidechain
2	1	1673	G	Sidechain
2	1	1701	A	Sidechain
2	1	1779	U	Sidechain
2	1	1798	U	Sidechain
2	1	18	U	Sidechain
2	1	1809	A	Sidechain
2	1	1826	G	Sidechain
2	1	1834	U	Sidechain
2	1	1905	C	Sidechain
2	1	1927	A	Sidechain
2	1	1978	A	Sidechain
2	1	1989	G	Sidechain
2	1	2019	A	Sidechain
2	1	2022	U	Sidechain
2	1	2024	G	Sidechain
2	1	2034	U	Sidechain
2	1	2069	G	Sidechain
2	1	2081	U	Sidechain
2	1	2274	A	Sidechain
2	1	2275	C	Sidechain
2	1	2391	G	Sidechain
2	1	2498	C	Sidechain
2	1	2547	A	Sidechain
2	1	2605	U	Sidechain
2	1	2732	G	Sidechain
2	1	562	U	Sidechain
2	1	576	U	Sidechain
2	1	683	U	Sidechain
2	1	690	G	Sidechain
2	1	761	A	Sidechain
2	1	764	A	Sidechain
2	1	778	G	Sidechain
2	1	801	G	Sidechain
2	1	804	A	Sidechain
2	1	828	U	Sidechain
2	1	971	G	Sidechain
34	E	30	HIS	Peptide
35	F	36	ARG	Peptide
37	G	14	HIS	Peptide

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Mol	Chain	Res	Type	Group
39	I	46	ARG	Peptide
41	K	91	ARG	Peptide
44	N	56	MET	Peptide
46	P	125	LYS	Peptide
47	Q	18	SER	Peptide
47	Q	32	VAL	Peptide
50	T	87	ARG	Peptide
52	V	49	ASN	Peptide
53	W	16	GLY	Peptide
53	W	19	GLU	Peptide
56	Z	23	GLU	Peptide
56	Z	7	GLU	Peptide
6	b	131	MET	Peptide
8	d	82	GLY	Peptide
9	e	174	PHE	Peptide
16	m	58	LYS	Peptide
17	n	10	LEU	Peptide
20	q	24	TYR	Peptide
20	q	3	VAL	Peptide
21	r	53	PHE	Peptide
21	r	54	VAL	Peptide
24	u	99	SER	Peptide

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	3	33012	0	16618	204	0
2	1	62317	0	31346	1551	0
3	2	2568	0	1303	12	0
4	5	1647	0	831	34	0
5	6	1640	0	837	12	0
5	7	1640	0	837	33	0
6	b	2083	0	2157	49	0
7	c	1565	0	1616	32	0
8	d	1552	0	1619	28	0
9	e	1411	0	1447	23	0
10	f	1323	0	1374	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	g	400	0	423	7	0
12	i	1032	0	1088	42	0
13	j	1129	0	1162	22	0
14	k	939	0	1012	18	0
15	l	1045	0	1117	16	0
16	m	1074	0	1157	13	0
17	n	961	0	1000	19	0
18	o	892	0	923	15	0
19	p	917	0	965	16	0
20	q	947	0	1022	15	0
21	r	816	0	839	17	0
22	s	857	0	922	12	0
23	t	739	0	807	11	0
24	u	780	0	834	16	0
25	v	753	0	780	9	0
26	w	575	0	592	9	0
27	x	625	0	655	11	0
28	y	509	0	543	12	0
29	z	449	0	491	8	0
30	A	523	0	524	7	0
31	B	444	0	461	9	0
32	C	410	0	440	5	0
33	D	377	0	418	12	0
34	E	504	0	574	4	0
35	F	302	0	343	5	0
36	4	390	0	198	5	0
37	G	1705	0	1732	31	0
38	H	1625	0	1699	25	0
39	I	1643	0	1710	37	0
40	J	1157	0	1199	15	0
41	K	818	0	808	17	0
42	L	1182	0	1240	19	0
43	M	979	0	1034	10	0
44	N	1022	0	1070	25	0
45	O	787	0	828	11	0
46	P	870	0	878	20	0
47	Q	955	0	1019	32	0
48	R	884	0	944	19	0
49	S	805	0	847	11	0
50	T	714	0	737	10	0
51	U	649	0	666	18	0
52	V	649	0	691	9	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
53	W	536	0	552	8	0
54	X	638	0	665	9	0
55	Y	665	0	714	13	0
56	Z	545	0	579	14	0
57	5	7	0	7	0	0
All	All	147982	0	98894	2415	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 10.

All (2415) 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)
2:1:2720:U:H5''	19:p:52:ARG:HH21	0.95	1.10
2:1:275:C:H2'	2:1:276:U:H4'	1.37	1.04
2:1:1082:U:H3'	2:1:1083:U:H5''	1.41	1.02
2:1:2713:U:H3'	2:1:2714:G:H5'	1.41	1.01
2:1:1672:A:C2	2:1:2582:G:H5'	1.95	1.01
2:1:1666:G:H2'	2:1:1667:G:H5'	1.41	1.01
2:1:1847:A:HO2'	2:1:1848:A:H8	1.06	1.00
2:1:2720:U:H5''	19:p:52:ARG:NH2	1.79	0.98
2:1:1807:G:H2'	2:1:1808:A:H5'	1.44	0.96
2:1:2156:G:H2'	2:1:2157:G:H5'	1.47	0.94
1:3:1032:G:N3	1:3:1033:G:OP1	2.00	0.94
2:1:1019:U:H3	2:1:1142:A:H62	1.17	0.93
2:1:655:A:H4'	2:1:656:G:H5'	1.50	0.93
2:1:2713:U:H3'	2:1:2714:G:C5'	1.98	0.92
2:1:1702:G:H2'	2:1:1703:G:H5''	1.51	0.92
2:1:2312:U:H5'	9:e:84:ILE:HD13	1.51	0.92
2:1:2305:U:H5''	9:e:130:GLY:HA3	1.51	0.92
2:1:644:A:H2'	2:1:645:C:H5''	1.50	0.91
2:1:1102:C:H2'	2:1:1103:A:H8	1.34	0.91
2:1:1668:A:H4'	2:1:1669:A:H5'	1.54	0.90
44:N:3:ASN:N	44:N:5:TYR:HH	1.68	0.90
2:1:890:C:H2'	2:1:891:G:H5'	1.53	0.90
2:1:2097:A:H2'	2:1:2098:U:C6	2.08	0.89
2:1:11:C:H2'	2:1:12:U:H5''	1.55	0.88
2:1:2529:G:H4'	10:f:174:LYS:HG3	1.56	0.88
2:1:1060:U:H4'	2:1:1061:U:H5''	1.55	0.88
4:5:68:C:H2'	4:5:69:G:H5''	1.57	0.87
2:1:2584:U:H2'	2:1:2585:U:H5'	1.58	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:1387:A:H5'	2:1:1469:A:H1'	1.58	0.86
5:7:18:G:O6	5:7:55:U:C5	2.29	0.86
2:1:803:U:O2'	2:1:804:A:H5'	1.75	0.85
2:1:2333:A:H5'	2:1:2334:U:H2'	1.57	0.85
2:1:1869:G:H3'	2:1:1870:C:H5'	1.57	0.85
2:1:1666:G:C2'	2:1:1667:G:H5'	2.07	0.84
2:1:1796:U:H2'	2:1:1797:G:H8	1.43	0.84
2:1:2720:U:C5'	19:p:52:ARG:HH21	1.86	0.84
2:1:2792:A:H2'	2:1:2793:C:H5''	1.59	0.83
2:1:849:A:H2'	2:1:850:U:C6	2.14	0.83
5:7:55:U:N3	5:7:57:A:N7	2.26	0.83
2:1:475:C:H4'	2:1:510:C:H5'	1.59	0.82
2:1:757:G:H2'	2:1:758:C:H5'	1.61	0.82
2:1:1175:A:H3'	2:1:1176:U:H5'	1.59	0.82
2:1:2348:U:H4'	32:C:40:PRO:HG3	1.63	0.81
4:5:2:G:N1	4:5:72:G:O6	2.13	0.81
2:1:2360:G:H2'	2:1:2361:G:H5'	1.62	0.81
2:1:784:G:H5'	2:1:785:G:OP1	1.81	0.81
2:1:1278:C:OP1	17:n:36:THR:HG22	1.80	0.81
2:1:670:A:H4'	2:1:671:C:H5'	1.61	0.81
2:1:1141:U:H4'	2:1:1142:A:O4'	1.80	0.80
2:1:1082:U:H5'	12:i:119:ALA:HB2	1.60	0.80
2:1:2112:G:H2'	2:1:2113:U:H5'	1.63	0.80
2:1:2224:G:H4'	2:1:2226:C:C2	2.16	0.80
2:1:279:A:H61	2:1:361:G:H1'	1.46	0.80
2:1:545:U:C2	2:1:546:U:H1'	2.16	0.80
2:1:1071:G:O2'	2:1:1089:A:H2'	1.82	0.80
2:1:1064:C:H41	2:1:1069:A:H5''	1.47	0.80
2:1:1087:G:N2	2:1:1103:A:H1'	1.97	0.80
2:1:1197:G:O2'	2:1:1198:U:H5'	1.81	0.79
2:1:1060:U:OP2	12:i:55:PRO:HG3	1.83	0.79
5:7:46:G:H2'	5:7:47:U:H5'	1.64	0.79
2:1:1666:G:O2'	14:k:6:THR:HG22	1.83	0.78
2:1:2286:G:H4'	2:1:2287:A:O4'	1.82	0.78
2:1:1775:U:H2'	2:1:1776:G:H5'	1.64	0.78
2:1:1297:C:OP1	2:1:2710:C:H4'	1.82	0.78
2:1:1536:C:H4'	2:1:1537:G:C2	2.18	0.78
2:1:1394:U:H4'	2:1:1603:A:H4'	1.66	0.78
2:1:1310:G:C2'	2:1:1311:G:H5'	2.14	0.78
2:1:2799:A:H2'	2:1:2800:A:H5'	1.63	0.78
2:1:368:A:H2'	2:1:369:U:H5'	1.66	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:1702:G:C2'	2:1:1703:G:H5''	2.13	0.78
2:1:275:C:H2'	2:1:276:U:C4'	2.14	0.78
2:1:2130:U:H2'	2:1:2131:U:H5''	1.65	0.78
2:1:2215:C:H2'	2:1:2216:G:C8	2.18	0.78
2:1:275:C:H3'	2:1:276:U:H5''	1.66	0.78
2:1:310:A:O2'	2:1:311:A:H2'	1.84	0.77
4:5:2:G:C6	4:5:72:G:O6	2.37	0.77
2:1:2680:U:OP1	7:c:114:LYS:HB2	1.84	0.77
2:1:2792:A:C3'	2:1:2793:C:H5''	2.14	0.77
2:1:548:G:H2'	2:1:549:G:O4'	1.84	0.77
2:1:1275:A:N6	2:1:1296:G:H4'	2.00	0.77
2:1:1736:U:H2'	2:1:1737:G:O4'	1.85	0.77
2:1:2156:G:C2'	2:1:2157:G:H5'	2.14	0.76
2:1:1063:G:H1	2:1:1075:C:N4	1.83	0.76
2:1:2097:A:H2'	2:1:2098:U:H6	1.50	0.76
2:1:2322:A:H2'	2:1:2323:G:C8	2.21	0.76
2:1:1773:A:H2'	2:1:1774:C:H5'	1.68	0.76
2:1:1083:U:H2'	2:1:1085:A:OP2	1.86	0.75
2:1:2432:A:H1'	5:7:75:C:O4'	1.86	0.75
4:5:74:C:H2'	4:5:75:C:O4'	1.85	0.75
2:1:543:G:H2'	2:1:544:C:H5''	1.68	0.74
2:1:958:U:H2'	3:2:89:U:O2	1.87	0.74
2:1:1020:A:H5'	2:1:1021:A:C8	2.22	0.74
2:1:2792:A:C2'	2:1:2793:C:H5''	2.16	0.74
2:1:2611:C:O2	2:1:2611:C:H2'	1.86	0.74
2:1:1310:G:H2'	2:1:1311:G:H5'	1.69	0.74
2:1:545:U:H2'	2:1:546:U:O4'	1.87	0.74
2:1:404:A:H1'	2:1:406:G:C4	2.23	0.73
2:1:481:G:H1'	2:1:506:G:N2	2.04	0.73
2:1:1670:C:H2'	2:1:1671:U:H5'	1.70	0.73
2:1:2036:C:H2'	2:1:2037:A:C8	2.23	0.73
2:1:1425:G:H2'	2:1:1426:G:C8	2.23	0.73
2:1:2834:G:H2'	2:1:2879:A:H61	1.54	0.73
2:1:322:A:H5'	2:1:340:A:C1'	2.19	0.73
2:1:1061:U:H3'	2:1:1062:G:C5'	2.18	0.73
2:1:1555:G:H5'	2:1:1555:G:H8	1.51	0.73
2:1:1872:A:H2'	2:1:1873:G:O4'	1.89	0.73
2:1:1433:A:H2'	2:1:1434:A:O4'	1.89	0.72
2:1:250:G:H4'	15:l:59:ARG:HD2	1.71	0.72
2:1:1779:U:H5	2:1:1784:A:N7	1.88	0.72
1:3:456:A:H61	1:3:476:U:H3	1.36	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:f:15:ASP:HB3	10:f:26:LYS:H	1.54	0.72
2:1:394:C:H2'	2:1:395:U:O4'	1.90	0.72
2:1:368:A:C2'	2:1:369:U:H5'	2.20	0.72
2:1:2671:G:H2'	2:1:2672:U:C6	2.25	0.72
2:1:2713:U:C3'	2:1:2714:G:C5'	2.67	0.71
2:1:538:A:H4'	13:j:7:LYS:HG2	1.73	0.71
2:1:864:G:O2'	2:1:865:C:H5'	1.89	0.71
5:7:50:U:H2'	5:7:51:C:C4	2.24	0.71
2:1:1441:G:H2'	2:1:1442:U:C6	2.25	0.71
1:3:452:A:H61	1:3:480:U:H3	1.37	0.71
2:1:612:G:H2'	2:1:614:A:C8	2.26	0.71
2:1:1102:C:H2'	2:1:1103:A:C8	2.22	0.71
2:1:1795:C:H2'	2:1:1796:U:O4'	1.90	0.71
2:1:633:A:H2'	2:1:634:C:H5'	1.72	0.71
2:1:1386:C:H2'	2:1:1387:A:H8	1.56	0.70
2:1:774:G:H5''	6:b:47:ARG:NH2	2.07	0.70
2:1:1858:A:H1'	2:1:1885:A:C2	2.26	0.70
2:1:890:C:C2'	2:1:891:G:H5'	2.21	0.70
2:1:1670:C:C2'	2:1:1671:U:H5'	2.21	0.70
2:1:1983:G:O2'	2:1:1984:G:H5'	1.91	0.70
2:1:322:A:H5'	2:1:340:A:H1'	1.73	0.70
2:1:940:G:H2'	2:1:941:A:H5''	1.73	0.70
2:1:572:A:OP2	21:r:79:ARG:NH1	2.25	0.70
2:1:1137:G:O2'	2:1:1138:G:H5'	1.92	0.70
2:1:1827:U:H2'	2:1:1828:G:H5'	1.73	0.70
2:1:2297:A:N1	2:1:2321:U:H5	1.89	0.70
2:1:2151:U:H2'	2:1:2152:G:C8	2.27	0.69
2:1:723:C:H2'	2:1:724:U:C6	2.27	0.69
2:1:419:U:H2'	2:1:420:C:C6	2.27	0.69
2:1:1337:G:H2'	2:1:1338:G:H8	1.58	0.69
1:3:663:A:H61	1:3:742:G:H1	1.39	0.69
2:1:528:A:C8	2:1:528:A:H3'	2.27	0.69
2:1:1292:G:H2'	2:1:1293:C:C6	2.27	0.69
2:1:402:A:H2'	2:1:403:U:H5'	1.74	0.69
2:1:744:U:H2'	2:1:745:G:H5'	1.75	0.69
2:1:1555:G:H5'	2:1:1555:G:C8	2.27	0.69
2:1:2151:U:H2'	2:1:2152:G:H8	1.56	0.69
2:1:2267:A:H5''	2:1:2268:A:H5''	1.74	0.69
2:1:2403:C:O2'	2:1:2404:U:H5'	1.92	0.69
2:1:644:A:H2'	2:1:645:C:C5'	2.21	0.69
2:1:810:U:O4	15:l:30:THR:HG22	1.93	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:928:A:H5'	29:z:38:GLU:OE2	1.94	0.68
2:1:2325:G:H3'	2:1:2325:G:OP1	1.92	0.68
2:1:2800:A:H3'	2:1:2801:G:C5'	2.23	0.68
2:1:1078:U:H2'	2:1:1088:A:OP1	1.94	0.68
2:1:2595:G:N2	2:1:2598:A:OP2	2.23	0.68
2:1:2626:C:O2'	2:1:2627:G:H5'	1.91	0.68
38:H:117:ASP:HA	38:H:120:THR:HG22	1.75	0.68
2:1:282:A:H2'	2:1:283:G:H8	1.57	0.68
2:1:392:U:H2'	2:1:393:C:H6	1.58	0.68
2:1:419:U:H2'	2:1:420:C:H6	1.58	0.68
2:1:956:G:N7	16:m:14:LYS:NZ	2.35	0.68
2:1:849:A:H2'	2:1:850:U:H6	1.58	0.68
2:1:905:A:C2'	2:1:906:U:H5'	2.23	0.68
2:1:1702:G:C3'	2:1:1703:G:H5''	2.24	0.68
2:1:1827:U:C2'	2:1:1828:G:H5'	2.24	0.68
2:1:2869:G:H2'	2:1:2870:C:C6	2.28	0.68
2:1:894:U:H2'	2:1:895:U:O4'	1.93	0.68
2:1:1063:G:H1	2:1:1075:C:H41	1.42	0.68
2:1:2092:U:H4'	2:1:2093:G:H5''	1.75	0.68
2:1:2233:U:H2'	2:1:2234:G:H8	1.59	0.68
2:1:2758:A:H2'	2:1:2759:G:H5'	1.75	0.68
2:1:1889:A:H2'	2:1:1890:A:H8	1.58	0.68
24:u:25:LYS:HD3	24:u:36:GLU:HB3	1.75	0.68
2:1:226:A:H2'	2:1:227:A:O4'	1.93	0.68
2:1:1653:G:O6	17:n:11:ASN:ND2	2.27	0.68
2:1:1082:U:H3'	2:1:1083:U:C5'	2.22	0.68
2:1:2114:A:H2	2:1:2167:U:H1'	1.58	0.67
2:1:2013:A:H5''	2:1:2013:A:H8	1.59	0.67
2:1:2157:G:H2'	2:1:2158:A:H2	1.59	0.67
2:1:1270:C:H5''	2:1:1271:G:H5'	1.77	0.67
27:x:16:ASN:ND2	27:x:26:ARG:HB3	2.09	0.67
2:1:2898:U:H2'	2:1:2899:A:C8	2.29	0.67
2:1:246:C:H2'	2:1:247:G:H5'	1.76	0.67
2:1:533:G:H5'	20:q:23:TYR:CD1	2.30	0.67
2:1:1176:U:H2'	2:1:1177:G:C8	2.29	0.67
2:1:2747:G:O6	2:1:2755:C:H5''	1.93	0.67
2:1:1454:C:H5'	17:n:63:ARG:NE	2.10	0.67
2:1:2510:C:N4	2:1:2511:U:O4	2.27	0.67
2:1:319:G:H1	2:1:323:C:H5	1.41	0.67
2:1:466:A:H2'	2:1:467:G:H5'	1.76	0.67
2:1:1270:C:H5''	2:1:1271:G:C5'	2.25	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:Q:47:ALA:HB3	47:Q:49:ARG:HE	1.60	0.67
2:1:1438:U:O2'	2:1:1439:A:H5'	1.94	0.67
2:1:2800:A:H3'	2:1:2801:G:H5'	1.77	0.67
2:1:703:U:C2'	2:1:704:G:H5'	2.25	0.67
2:1:1020:A:H1'	2:1:1021:A:OP2	1.95	0.67
2:1:1061:U:H3'	2:1:1062:G:H5'	1.76	0.67
2:1:1717:A:H2'	2:1:1718:G:H5'	1.77	0.67
39:I:73:ASN:HA	39:I:76:LYS:HB2	1.77	0.67
47:Q:109:ARG:HH21	47:Q:112:ALA:HB3	1.60	0.67
2:1:1019:U:H3	2:1:1142:A:N6	1.89	0.67
2:1:2221:G:O2'	2:1:2222:C:H5'	1.95	0.67
2:1:521:U:H2'	2:1:522:A:C8	2.30	0.66
2:1:1889:A:H2'	2:1:1890:A:C8	2.29	0.66
2:1:1999:C:H5''	2:1:2723:C:O2'	1.94	0.66
2:1:2516:A:O2'	2:1:2517:C:H5'	1.95	0.66
2:1:1030:C:O2'	2:1:1031:G:H5'	1.95	0.66
2:1:1098:A:H2'	2:1:1099:G:H5'	1.77	0.66
2:1:2278:A:C3'	2:1:2279:G:H5''	2.25	0.66
2:1:2625:G:H2'	2:1:2626:C:C6	2.30	0.66
2:1:1064:C:N4	2:1:1069:A:H5''	2.10	0.66
2:1:1484:U:H2'	2:1:1485:U:C6	2.30	0.66
2:1:673:C:H2'	2:1:674:G:H5'	1.77	0.66
2:1:1796:U:H2'	2:1:1797:G:C8	2.27	0.66
2:1:1942:C:H4'	4:5:72:G:OP2	1.95	0.66
2:1:803:U:C2'	2:1:804:A:H5'	2.25	0.66
2:1:1432:G:O2'	2:1:1433:A:H5'	1.94	0.66
2:1:707:G:O2'	2:1:708:G:H5'	1.94	0.66
7:c:4:LEU:HD23	7:c:29:VAL:HG11	1.77	0.66
37:G:67:LEU:HD12	37:G:153:MET:HE1	1.78	0.66
2:1:635:C:H2'	2:1:636:G:C8	2.31	0.66
2:1:1161:C:H2'	2:1:1162:G:H8	1.61	0.66
2:1:414:C:H2'	2:1:415:A:C8	2.31	0.66
2:1:703:U:H2'	2:1:704:G:H5'	1.77	0.66
2:1:2052:A:O2'	2:1:2053:G:H5'	1.96	0.66
10:f:154:GLU:HG3	10:f:156:TYR:H	1.61	0.66
2:1:644:A:C2'	2:1:645:C:H5''	2.22	0.65
2:1:905:A:H2'	2:1:906:U:H5'	1.78	0.65
2:1:2290:G:H2'	2:1:2291:U:C6	2.32	0.65
33:D:37:LYS:HD3	33:D:39:ARG:HD3	1.77	0.65
2:1:488:G:N2	2:1:491:G:H5''	2.11	0.65
2:1:2278:A:H3'	2:1:2279:G:H5''	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:2844:G:H2'	2:1:2845:U:C6	2.31	0.65
2:1:528:A:H3'	2:1:528:A:H8	1.59	0.65
2:1:1572:A:O2'	2:1:1573:G:H5'	1.97	0.65
2:1:1733:G:O2'	2:1:1734:G:H5'	1.95	0.65
12:i:27:LEU:HD22	12:i:32:VAL:HG21	1.78	0.65
2:1:65:U:H2'	2:1:66:C:H6	1.59	0.65
2:1:870:U:C2'	2:1:871:U:H5'	2.26	0.65
2:1:1746:A:H2'	2:1:1747:U:C6	2.31	0.65
4:5:68:C:C2'	4:5:69:G:H5''	2.26	0.65
2:1:536:G:H2'	2:1:537:G:H5'	1.79	0.65
2:1:613:A:H5''	2:1:614:A:C8	2.32	0.65
2:1:2760:C:O2'	2:1:2761:A:H5'	1.96	0.65
2:1:112:U:H2'	2:1:113:U:H5'	1.76	0.65
2:1:2193:G:H2'	2:1:2194:U:C6	2.32	0.65
2:1:2799:A:C2'	2:1:2800:A:H5'	2.27	0.65
2:1:2448:A:OP2	2:1:2498:C:OP2	2.15	0.65
2:1:2733:A:O2'	2:1:2734:A:H5'	1.96	0.65
2:1:2555:U:H2'	2:1:2556:C:H5'	1.78	0.65
2:1:2572:A:OP2	7:c:149:ASN:HB3	1.97	0.65
1:3:437:U:H3	1:3:495:A:H62	1.42	0.65
2:1:201:C:O2'	2:1:202:U:H5'	1.97	0.65
2:1:543:G:H2'	2:1:544:C:C5'	2.26	0.65
2:1:942:G:OP2	15:l:39:LYS:NZ	2.28	0.65
2:1:1038:G:H2'	2:1:1039:A:C8	2.32	0.65
2:1:1788:C:O2'	2:1:1789:A:H5'	1.96	0.65
2:1:2114:A:N7	2:1:2115:G:H1'	2.12	0.65
2:1:2233:U:H2'	2:1:2234:G:C8	2.30	0.65
41:K:38:ARG:HE	41:K:97:THR:HA	1.62	0.65
2:1:1098:A:C2'	2:1:1099:G:H5'	2.27	0.64
2:1:2834:G:O2'	2:1:2835:A:H5'	1.97	0.64
1:3:85:U:H5''	1:3:86:G:H5'	1.78	0.64
2:1:494:G:H4'	22:s:6:LYS:HB2	1.78	0.64
2:1:2073:C:O2'	2:1:2074:U:H5'	1.98	0.64
56:Z:22:CYS:SG	56:Z:23:GLU:N	2.71	0.64
2:1:784:G:C2	6:b:227:VAL:HG11	2.31	0.64
33:D:24:THR:HG23	33:D:27:GLY:H	1.61	0.64
2:1:870:U:H2'	2:1:871:U:H5'	1.80	0.64
2:1:2170:A:H2'	2:1:2171:A:O4'	1.97	0.64
2:1:2404:U:O2'	2:1:2405:G:H5'	1.97	0.64
46:P:19:VAL:HG22	46:P:82:GLU:HB2	1.79	0.64
49:S:38:GLU:HA	49:S:41:TRP:HB3	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:1181:U:H2'	2:1:1182:G:C8	2.33	0.64
2:1:2314:A:H2'	2:1:2315:G:C8	2.33	0.64
2:1:2469:A:H2'	2:1:2470:G:O4'	1.98	0.64
2:1:1766:G:O2'	2:1:1767:G:H5'	1.98	0.64
2:1:445:C:H2'	2:1:446:G:O4'	1.98	0.64
2:1:359:G:O2'	2:1:360:U:H5'	1.97	0.64
2:1:905:A:O2'	2:1:906:U:H5'	1.97	0.64
2:1:940:G:C3'	2:1:941:A:H5''	2.28	0.63
2:1:1857:G:H22	2:1:1884:G:H2'	1.62	0.63
2:1:256:A:O2'	2:1:257:C:H5'	1.98	0.63
2:1:414:C:H2'	2:1:415:A:H8	1.63	0.63
39:I:152:SER:H	39:I:155:LYS:HD3	1.63	0.63
2:1:161:A:N7	2:1:162:U:H5	1.96	0.63
2:1:306:U:H2'	2:1:307:G:O4'	1.98	0.63
2:1:2112:G:C2'	2:1:2113:U:H5'	2.27	0.63
42:L:59:GLU:HA	42:L:62:GLU:HB3	1.80	0.63
2:1:212:G:O2'	2:1:213:A:H5'	1.99	0.63
2:1:622:G:O2'	2:1:623:C:H5'	1.98	0.63
2:1:2811:G:O2'	2:1:2812:G:H5'	1.97	0.63
2:1:161:A:H3'	2:1:162:U:H5''	1.81	0.63
2:1:889:C:H2'	2:1:890:C:O4'	1.99	0.63
2:1:1280:G:O2'	2:1:1281:G:H5'	1.99	0.63
2:1:1666:G:H2'	2:1:1667:G:C5'	2.24	0.63
46:P:87:GLY:H	46:P:113:THR:HG22	1.62	0.63
1:3:959:A:HO2'	1:3:984:C:HO2'	1.46	0.63
2:1:65:U:H2'	2:1:66:C:C6	2.33	0.63
2:1:317:G:H2'	2:1:318:C:H6	1.64	0.63
2:1:1853:A:H2'	2:1:1854:A:C8	2.32	0.63
2:1:1164:C:O2'	2:1:1165:A:H5'	1.99	0.63
2:1:1921:G:O2'	2:1:1922:G:H5'	1.98	0.63
15:l:62:PRO:HB2	34:E:29:ARG:HH11	1.64	0.63
1:3:373:A:H61	1:3:391:G:H1'	1.64	0.63
1:3:521:G:H4'	47:Q:69:GLU:HG3	1.79	0.63
2:1:1909:C:H2'	2:1:1910:G:H8	1.64	0.63
2:1:1149:G:H2'	2:1:1150:C:C6	2.34	0.62
2:1:1524:G:H2'	2:1:1525:A:H8	1.63	0.62
6:b:106:PRO:HD2	6:b:109:LEU:HD22	1.80	0.62
37:G:173:LYS:O	37:G:177:ASN:ND2	2.32	0.62
1:3:1087:G:N3	56:Z:65:ARG:NH2	2.47	0.62
2:1:197:A:H4'	2:1:2069:G:OP2	1.99	0.62
2:1:815:C:C2	2:1:1193:G:N2	2.66	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:37:C:O2'	2:1:38:A:H5'	1.99	0.62
2:1:940:G:C2'	2:1:941:A:H5''	2.30	0.62
4:5:18:G:O2'	4:5:57:G:N2	2.28	0.62
56:Z:32:ARG:HG2	56:Z:33:ARG:HG3	1.80	0.62
2:1:590:A:O2'	2:1:591:U:H5'	2.00	0.62
2:1:723:C:H2'	2:1:724:U:H6	1.64	0.62
1:3:811:C:O2'	1:3:901:A:N1	2.32	0.62
2:1:872:U:O2'	2:1:873:C:H5'	1.99	0.62
2:1:973:A:H5'	2:1:1188:U:H1'	1.80	0.62
46:P:58:THR:HG22	46:P:60:PHE:H	1.65	0.62
2:1:1086:A:H5'	2:1:1103:A:H2	1.65	0.62
2:1:554:U:H2'	2:1:555:G:O4'	1.99	0.62
2:1:1383:A:H2	2:1:1406:U:H1'	1.64	0.62
2:1:1553:A:HO2'	2:1:1554:U:H5	1.48	0.62
2:1:1935:G:H1'	2:1:1964:G:N2	2.15	0.62
2:1:2298:A:H2'	2:1:2299:U:O4'	1.99	0.62
2:1:2529:G:C4'	10:f:174:LYS:HG3	2.29	0.62
2:1:2637:U:H2'	2:1:2638:G:H5'	1.82	0.62
2:1:1680:U:H2'	2:1:1681:G:O4'	2.00	0.61
46:P:108:ASN:HD22	56:Z:4:LYS:HE2	1.64	0.61
2:1:941:A:H2'	2:1:942:G:O4'	2.00	0.61
2:1:1508:A:H2'	2:1:1509:A:O4'	2.01	0.61
2:1:2092:U:H5	2:1:2199:A:H2	1.48	0.61
2:1:2734:A:H2'	2:1:2735:G:H5'	1.82	0.61
2:1:529:A:OP2	13:j:116:ARG:NH2	2.32	0.61
2:1:2091:C:H5	2:1:2092:U:HO2'	1.47	0.61
2:1:2792:A:H3'	2:1:2793:C:H5''	1.80	0.61
2:1:236:C:H2'	2:1:237:C:H6	1.64	0.61
2:1:2188:U:H2'	2:1:2189:U:O4'	2.01	0.61
2:1:2404:U:H2'	2:1:2405:G:O4'	2.01	0.61
5:7:35:A:H62	36:4:14:A:H61	1.48	0.61
2:1:1352:U:O2'	2:1:1353:A:H5'	2.00	0.61
2:1:2802:G:H2'	2:1:2803:G:C8	2.35	0.61
22:s:3:THR:OG1	22:s:107:VAL:O	2.19	0.61
48:R:102:LYS:HG2	48:R:103:THR:HG23	1.83	0.61
2:1:435:C:H2'	2:1:436:C:H5'	1.82	0.61
2:1:1717:A:C2'	2:1:1718:G:H5'	2.31	0.61
2:1:1775:U:H2'	2:1:1776:G:C5'	2.29	0.61
2:1:1775:U:C2'	2:1:1776:G:H5'	2.30	0.61
3:2:43:C:H5''	30:A:1:MET:HG2	1.82	0.61
1:3:451:A:H5'	51:U:70:ARG:HH22	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:7:G:H5'	13:j:132:HIS:CD2	2.36	0.61
2:1:11:C:C2'	2:1:12:U:H5''	2.29	0.61
2:1:283:G:H2'	2:1:284:U:H5'	1.83	0.61
2:1:995:C:N3	13:j:3:THR:N	2.48	0.61
2:1:1448:G:H2'	2:1:1449:G:H8	1.64	0.61
2:1:2636:C:H2'	2:1:2637:U:H6	1.64	0.61
2:1:2804:U:H2'	2:1:2805:C:C6	2.36	0.61
2:1:2898:U:H2'	2:1:2899:A:H8	1.64	0.61
13:j:45:THR:HB	13:j:48:VAL:HG22	1.81	0.61
16:m:17:ASN:O	16:m:38:ARG:NH1	2.34	0.61
18:o:4:LYS:HD3	18:o:7:ARG:HH21	1.65	0.61
33:D:3:ARG:O	33:D:6:GLN:NE2	2.34	0.61
2:1:558:U:H6	2:1:558:U:O5'	1.84	0.61
2:1:1954:G:H1'	2:1:1956:U:O4	2.01	0.61
2:1:2097:A:H2'	2:1:2098:U:O4'	2.00	0.61
2:1:2386:A:O2'	2:1:2387:U:H5'	2.01	0.61
2:1:936:A:H2'	2:1:937:C:C6	2.36	0.60
2:1:1503:A:H3'	2:1:1504:A:H5''	1.81	0.60
2:1:322:A:H5'	2:1:340:A:O4'	2.00	0.60
5:7:55:U:H5''	5:7:56:C:P	2.41	0.60
52:V:30:HIS:HD2	52:V:33:TYR:H	1.48	0.60
2:1:198:C:H42	2:1:248:G:H1	1.49	0.60
2:1:893:C:H2'	2:1:894:U:C6	2.37	0.60
2:1:2327:A:H2'	2:1:2328:A:C8	2.35	0.60
23:t:53:VAL:HG12	23:t:92:ASN:HD22	1.65	0.60
2:1:1256:G:H21	8:d:77:ILE:CG2	2.14	0.60
2:1:1437:C:H2'	2:1:1438:U:C6	2.36	0.60
2:1:2852:G:O2'	2:1:2853:C:H5'	2.01	0.60
2:1:547:A:H3'	2:1:547:A:N3	2.16	0.60
2:1:1009:A:OP1	13:j:39:LYS:HE3	2.01	0.60
2:1:2345:G:N3	2:1:2381:A:H2'	2.15	0.60
9:e:51:ASN:OD1	9:e:149:ARG:NH1	2.34	0.60
44:N:40:ARG:NH2	44:N:41:GLU:OE2	2.34	0.60
1:3:1040:U:H2'	1:3:1041:G:H8	1.67	0.60
5:7:46:G:C2'	5:7:47:U:H5'	2.29	0.60
7:c:181:ASP:HB3	7:c:186:LEU:HB2	1.82	0.60
52:V:11:VAL:HA	52:V:22:VAL:HA	1.83	0.60
2:1:1040:A:H2	2:1:1115:G:H22	1.48	0.60
2:1:1062:G:H21	12:i:135:MET:HE2	1.65	0.60
50:T:13:GLU:O	50:T:83:ARG:NH2	2.35	0.60
2:1:49:A:H5''	2:1:51:G:O4'	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:794:A:H2'	2:1:795:C:O4'	2.02	0.60
2:1:854:C:O2'	2:1:855:G:H5'	2.02	0.60
2:1:1287:A:C5	2:1:1288:G:C6	2.89	0.60
2:1:2093:G:O2'	2:1:2094:A:H5'	2.01	0.60
5:7:34:C:OP1	42:L:78:ARG:NH2	2.34	0.60
46:P:125:LYS:O	56:Z:33:ARG:NH1	2.35	0.60
35:F:14:CYS:SG	35:F:33:HIS:ND1	2.75	0.60
2:1:1538:G:H2'	2:1:1539:U:C6	2.37	0.59
2:1:1799:G:C2	6:b:153:LEU:HD23	2.37	0.59
2:1:2330:G:H21	26:w:38:GLY:HA2	1.66	0.59
2:1:2643:G:H2'	2:1:2644:G:H5'	1.84	0.59
2:1:2834:G:H2'	2:1:2879:A:N6	2.17	0.59
8:d:149:ILE:HG23	8:d:188:MET:HB3	1.83	0.59
1:3:1534:A:H61	36:4:11:U:H3	1.49	0.59
2:1:937:C:H2'	2:1:938:G:C8	2.37	0.59
2:1:1042:G:H2'	2:1:1043:C:C6	2.37	0.59
2:1:1198:U:H2'	2:1:1199:U:C6	2.37	0.59
2:1:1773:A:C2'	2:1:1774:C:H5'	2.31	0.59
21:r:4:VAL:HG22	21:r:40:MET:HG2	1.85	0.59
2:1:1068:G:H21	12:i:25:PRO:HG2	1.68	0.59
2:1:1077:A:C8	2:1:1078:U:H1'	2.38	0.59
11:g:50:ARG:HH22	11:g:51:ARG:HH21	1.48	0.59
44:N:79:ARG:HH21	44:N:102:PHE:HA	1.67	0.59
2:1:1256:G:H21	8:d:77:ILE:HG23	1.68	0.59
2:1:1826:G:O2'	2:1:1971:U:OP2	2.20	0.59
2:1:2743:U:H3'	2:1:2744:G:H5''	1.84	0.59
6:b:34:GLU:HG3	6:b:63:ILE:HD11	1.84	0.59
7:c:55:LYS:NZ	7:c:59:ARG:O	2.36	0.59
1:3:1418:A:H2	2:1:1948:G:H21	1.49	0.59
2:1:841:G:O2'	2:1:842:U:H5'	2.02	0.59
2:1:851:C:H2'	2:1:852:U:C6	2.36	0.59
2:1:1071:G:H1'	2:1:1089:A:C8	2.37	0.59
2:1:1670:C:H2'	2:1:1671:U:C5'	2.31	0.59
2:1:2165:C:H2'	2:1:2166:U:C6	2.38	0.59
44:N:17:ARG:HB2	44:N:65:THR:HG23	1.84	0.59
1:3:409:U:H3	1:3:433:G:H1	1.51	0.59
2:1:215:G:H4'	2:1:216:A:H4'	1.84	0.59
2:1:2322:A:H2'	2:1:2323:G:H8	1.68	0.59
2:1:2812:G:H2'	2:1:2813:A:C8	2.36	0.59
2:1:2812:G:H2'	2:1:2813:A:H8	1.68	0.59
46:P:45:THR:HG23	46:P:48:GLY:H	1.65	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:X:30:LEU:HB2	54:X:48:ILE:HG22	1.85	0.59
56:Z:6:ARG:HG2	56:Z:8:ASN:HA	1.84	0.59
2:1:1333:G:O2'	2:1:1334:G:H5'	2.03	0.59
2:1:2717:C:C4	2:1:2718:G:N7	2.70	0.59
2:1:2749:A:OP2	2:1:2751:G:H5''	2.02	0.59
1:3:422:C:O2'	1:3:423:G:N2	2.36	0.59
2:1:2020:A:O2'	2:1:2021:C:H5'	2.03	0.59
2:1:2533:U:H2'	2:1:2534:A:H5'	1.85	0.59
2:1:1857:G:N2	2:1:1884:G:H2'	2.17	0.59
16:m:66:ARG:NH1	16:m:104:GLU:OE2	2.36	0.59
2:1:172:A:H2'	2:1:173:A:H8	1.66	0.59
2:1:528:A:C8	2:1:528:A:C3'	2.86	0.59
2:1:1098:A:H2'	2:1:1099:G:C5'	2.33	0.59
2:1:1171:G:H2'	2:1:1172:C:O4'	2.02	0.59
2:1:1845:G:O2'	2:1:1846:G:H5'	2.02	0.59
2:1:2137:U:H2'	2:1:2138:G:H8	1.67	0.59
2:1:2183:A:H2'	2:1:2184:A:C4	2.38	0.59
2:1:2787:C:H1'	7:c:63:PRO:HG3	1.85	0.59
1:3:1133:G:H1	1:3:1141:C:H42	1.48	0.58
2:1:1337:G:H2'	2:1:1338:G:C8	2.38	0.58
2:1:1463:C:H2'	2:1:1464:G:H8	1.68	0.58
2:1:2570:G:H2'	2:1:2571:U:H5'	1.85	0.58
45:O:46:LYS:HG2	45:O:68:ARG:HG2	1.84	0.58
1:3:1125:U:H2'	1:3:1126:U:H2'	1.86	0.58
2:1:1561:C:H2'	2:1:1562:U:C6	2.39	0.58
2:1:2330:G:O2'	26:w:40:LYS:HE3	2.03	0.58
2:1:2789:C:H2'	2:1:2893:A:N7	2.17	0.58
1:3:401:C:OP2	39:I:69:ARG:NH1	2.36	0.58
2:1:1183:U:H2'	2:1:1184:U:C6	2.37	0.58
2:1:1579:A:H2'	2:1:1580:A:C8	2.38	0.58
2:1:2187:U:O2'	2:1:2188:U:H5'	2.02	0.58
2:1:2506:U:O2'	4:5:76:A:H3'	2.03	0.58
6:b:141:HIS:ND1	6:b:192:GLY:O	2.35	0.58
24:u:40:LEU:HD12	24:u:59:GLU:HG2	1.84	0.58
2:1:246:C:C2'	2:1:247:G:H5'	2.33	0.58
2:1:1469:A:H2'	2:1:1470:A:C8	2.38	0.58
2:1:1725:U:H2'	2:1:1726:C:C6	2.38	0.58
2:1:2636:C:H2'	2:1:2637:U:C6	2.39	0.58
18:o:69:ASP:N	18:o:69:ASP:OD1	2.36	0.58
29:z:4:ILE:HD11	29:z:58:GLU:HG2	1.86	0.58
37:G:114:LYS:HE3	37:G:151:LYS:HB2	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:G:86:CYS:SG	37:G:87:ASP:N	2.74	0.58
3:2:65:U:H3'	3:2:108:A:H61	1.68	0.58
7:c:129:THR:OG1	7:c:140:HIS:O	2.22	0.58
1:3:261:U:OP2	55:Y:73:ARG:NH2	2.36	0.58
2:1:327:G:O2'	2:1:328:U:H5'	2.04	0.58
2:1:1255:U:C5	8:d:68:ALA:HA	2.37	0.58
2:1:1526:C:H2'	2:1:1527:G:O4'	2.04	0.58
2:1:1820:U:C2	6:b:157:ALA:O	2.56	0.58
2:1:2360:G:C2'	2:1:2361:G:H5'	2.31	0.58
2:1:2897:U:H2'	2:1:2898:U:C6	2.39	0.58
9:e:116:LEU:O	9:e:177:ARG:N	2.37	0.58
24:u:36:GLU:HA	24:u:61:GLU:HG2	1.86	0.58
2:1:640:C:O2'	2:1:641:U:H5'	2.04	0.58
2:1:1026:G:H2'	2:1:1027:A:H8	1.67	0.58
40:J:54:GLU:HG2	40:J:56:PRO:HD2	1.86	0.58
10:f:151:ARG:HB3	10:f:161:VAL:HG23	1.86	0.58
17:n:54:LEU:HD23	17:n:66:ALA:HB2	1.86	0.58
20:q:90:ASP:OD1	20:q:90:ASP:N	2.37	0.58
2:1:1067:A:O2'	12:i:22:PRO:HA	2.04	0.58
2:1:1565:C:O2'	2:1:1566:A:H8	1.87	0.58
2:1:2762:C:H2'	2:1:2763:G:H5'	1.86	0.58
5:7:52:G:H2'	5:7:53:G:H8	1.69	0.58
5:6:74:C:C2'	5:6:75:C:H5'	2.33	0.58
37:G:45:THR:O	37:G:49:PHE:N	2.35	0.58
44:N:35:GLU:HA	44:N:39:GLY:HA3	1.85	0.58
2:1:580:U:O3'	20:q:30:VAL:HG13	2.04	0.57
2:1:1227:G:O2'	2:1:1228:G:H5'	2.04	0.57
2:1:1524:G:H2'	2:1:1525:A:C8	2.38	0.57
2:1:2092:U:H4'	2:1:2093:G:C5'	2.34	0.57
2:1:2215:C:H2'	2:1:2216:G:H8	1.65	0.57
9:e:47:LYS:O	9:e:51:ASN:ND2	2.37	0.57
28:y:19:LEU:O	28:y:23:ARG:N	2.35	0.57
53:W:49:LYS:HA	53:W:52:ARG:HH21	1.68	0.57
2:1:621:A:H2'	2:1:622:G:H5'	1.86	0.57
2:1:1400:U:O2'	2:1:1401:G:H5'	2.04	0.57
2:1:1454:C:H5'	17:n:63:ARG:CZ	2.34	0.57
2:1:2186:G:O2'	2:1:2187:U:H5'	2.04	0.57
2:1:2457:U:O2'	2:1:2458:G:H5'	2.04	0.57
2:1:2529:G:H4'	10:f:174:LYS:HE2	1.86	0.57
8:d:1:MET:HG2	8:d:16:GLU:HG2	1.86	0.57
1:3:202:G:H21	1:3:466:A:H61	1.53	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:235:U:H2'	2:1:236:C:C6	2.39	0.57
2:1:673:C:C2'	2:1:674:G:H5'	2.34	0.57
2:1:1678:A:H2'	2:1:1679:A:H5'	1.86	0.57
2:1:2153:C:H2'	2:1:2154:A:H5'	1.85	0.57
2:1:2899:A:O2'	2:1:2900:A:H5'	2.05	0.57
3:2:117:G:OP1	18:o:56:LYS:NZ	2.36	0.57
30:A:26:SER:OG	30:A:27:THR:N	2.37	0.57
2:1:1511:G:H2'	2:1:1512:C:C6	2.38	0.57
2:1:1597:A:H5''	2:1:1598:A:H5'	1.87	0.57
8:d:110:SER:HB3	8:d:114:ARG:HH22	1.70	0.57
1:3:981:U:H5''	49:S:5:MET:HE1	1.86	0.57
2:1:2662:A:H2'	2:1:2663:G:O4'	2.05	0.57
29:z:15:ARG:HE	29:z:52:PHE:HE2	1.53	0.57
40:J:44:ARG:NH2	40:J:70:MET:SD	2.78	0.57
2:1:69:C:H2'	2:1:70:G:H8	1.70	0.57
2:1:287:G:H2'	2:1:288:U:C6	2.40	0.57
2:1:366:C:O2'	2:1:367:G:H5'	2.04	0.57
2:1:1789:A:OP2	6:b:220:ARG:NH1	2.38	0.57
3:2:8:C:O3'	18:o:25:ARG:NH1	2.37	0.57
4:5:74:C:H2'	4:5:75:C:C4'	2.35	0.57
1:3:8:A:N6	39:I:201:GLU:O	2.36	0.57
2:1:1893:C:H2'	2:1:1894:C:H5'	1.85	0.57
25:v:57:TYR:OH	25:v:79:ARG:NH2	2.38	0.57
2:1:184:C:H2'	2:1:185:G:H8	1.70	0.57
2:1:593:U:H2'	2:1:594:U:C6	2.40	0.57
2:1:1404:C:O2'	2:1:1405:U:H5'	2.05	0.57
2:1:2498:C:O2	2:1:2498:C:H2'	2.05	0.57
5:7:49:G:H1	5:7:65:C:H42	1.53	0.57
37:G:58:LYS:O	37:G:62:ARG:NH1	2.38	0.57
39:I:10:LEU:HD23	39:I:62:ARG:HB3	1.86	0.57
1:3:263:A:OP1	55:Y:73:ARG:NH1	2.38	0.57
2:1:32:C:H2'	2:1:33:C:C6	2.40	0.57
2:1:543:G:H2'	2:1:544:C:O4'	2.05	0.57
2:1:834:G:H2'	2:1:835:C:O4'	2.04	0.57
2:1:1173:U:C5	2:1:1174:U:H1'	2.40	0.57
2:1:1319:C:O2'	2:1:1320:C:H5'	2.05	0.57
2:1:78:U:H2'	2:1:79:C:C6	2.40	0.57
2:1:503:A:H4'	2:1:505:A:H5''	1.87	0.57
4:5:72:G:H1'	4:5:73:A:H5'	1.87	0.57
6:b:250:GLN:NE2	6:b:251:THR:O	2.38	0.57
9:e:9:ASP:N	9:e:9:ASP:OD1	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:k:65:THR:HG23	14:k:68:GLY:H	1.69	0.57
2:1:877:A:N1	2:1:899:A:H2'	2.20	0.56
2:1:1110:G:HO2'	2:1:1111:A:H8	1.53	0.56
1:3:522:C:H41	47:Q:49:ARG:HH22	1.53	0.56
2:1:74:A:H4'	2:1:75:G:O5'	2.05	0.56
2:1:146:A:H2'	2:1:147:C:C6	2.39	0.56
2:1:1130:U:O2'	2:1:1131:G:OP1	2.20	0.56
2:1:1917:U:O2'	2:1:1918:A:H5'	2.05	0.56
2:1:2510:C:C4	2:1:2511:U:C4	2.93	0.56
24:u:85:ARG:NH2	24:u:100:GLU:O	2.38	0.56
1:3:49:U:H3	1:3:362:G:H1'	1.71	0.56
1:3:722:G:OP2	56:Z:44:ARG:NH1	2.39	0.56
2:1:128:C:H2'	2:1:129:C:H6	1.71	0.56
2:1:780:G:H21	2:1:783:A:H62	1.54	0.56
2:1:1275:A:C6	2:1:1296:G:H4'	2.40	0.56
2:1:1520:U:O2'	2:1:1521:G:H5'	2.05	0.56
2:1:2845:U:H2'	2:1:2846:G:H8	1.69	0.56
5:7:55:U:O2	5:7:55:U:H2'	2.05	0.56
6:b:259:ASN:ND2	6:b:262:THR:OG1	2.38	0.56
10:f:40:VAL:O	10:f:54:ARG:NH2	2.38	0.56
39:I:98:ASP:OD1	39:I:98:ASP:N	2.36	0.56
41:K:12:PRO:HB2	41:K:44:ARG:HH21	1.70	0.56
46:P:92:ARG:NH2	46:P:111:ASP:OD1	2.38	0.56
48:R:100:ARG:NH1	48:R:103:THR:OG1	2.38	0.56
2:1:323:C:H3'	2:1:323:C:OP2	2.05	0.56
2:1:358:U:H2'	2:1:359:G:C8	2.41	0.56
1:3:738:C:OP1	41:K:2:ARG:NH1	2.39	0.56
2:1:613:A:H2'	2:1:613:A:N3	2.21	0.56
2:1:1120:G:O2'	2:1:1121:C:H5'	2.05	0.56
2:1:1410:G:H2'	2:1:1411:U:C6	2.41	0.56
17:n:22:ARG:HG3	17:n:70:THR:HA	1.86	0.56
47:Q:33:CYS:HA	47:Q:54:VAL:HG12	1.87	0.56
51:U:69:ASP:OD1	51:U:69:ASP:N	2.39	0.56
2:1:96:C:OP1	28:y:39:GLN:HG2	2.05	0.56
2:1:1772:A:H5'	2:1:1773:A:OP2	2.06	0.56
10:f:44:HIS:HA	10:f:49:LEU:HG	1.87	0.56
1:3:177:G:OP1	55:Y:59:ARG:NH1	2.37	0.56
2:1:163:C:H2'	2:1:164:C:O4'	2.05	0.56
2:1:296:U:H2'	2:1:297:G:C8	2.41	0.56
2:1:1108:U:H2'	2:1:1109:C:C2	2.40	0.56
2:1:1675:C:C4	7:c:134:HIS:CE1	2.94	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:n:2:ARG:HA	17:n:5:LYS:HD3	1.88	0.56
2:1:1309:G:OP1	33:D:9:VAL:HG22	2.06	0.56
2:1:2395:C:H42	2:1:2421:G:H1	1.54	0.56
2:1:2626:C:H2'	2:1:2627:G:O4'	2.06	0.56
2:1:2637:U:C2'	2:1:2638:G:H5'	2.36	0.56
28:y:49:ASP:OD1	28:y:52:ARG:NH2	2.39	0.56
40:J:23:THR:HA	40:J:28:ARG:HA	1.88	0.56
1:3:158:G:N2	1:3:163:C:O2	2.36	0.56
2:1:288:U:H2'	2:1:289:G:H8	1.71	0.56
2:1:825:A:O2'	2:1:826:U:H5'	2.06	0.56
2:1:1097:U:H2'	2:1:1098:A:O4'	2.06	0.56
2:1:1528:A:H2'	2:1:1529:G:H5'	1.87	0.56
2:1:2533:U:C2'	2:1:2534:A:H5'	2.36	0.56
7:c:18:ASP:OD1	7:c:18:ASP:N	2.36	0.56
16:m:27:SER:H	16:m:66:ARG:HH12	1.54	0.56
1:3:159:G:N2	1:3:162:A:OP2	2.34	0.55
2:1:720:U:H2'	2:1:721:A:C8	2.41	0.55
2:1:1310:G:O2'	2:1:1311:G:H5'	2.06	0.55
2:1:2236:U:H2'	2:1:2237:G:H5'	1.88	0.55
14:k:70:ARG:HG2	14:k:76:VAL:HG12	1.89	0.55
1:3:1036:A:H2'	1:3:1037:C:H5'	1.88	0.55
2:1:481:G:H1'	2:1:506:G:H21	1.71	0.55
2:1:764:A:O2'	2:1:765:C:H5'	2.06	0.55
2:1:885:C:N4	2:1:886:A:H62	2.03	0.55
2:1:2850:A:N1	2:1:2869:G:H4'	2.21	0.55
12:i:5:GLN:O	12:i:30:GLN:NE2	2.40	0.55
18:o:52:SER:OG	18:o:53:THR:N	2.39	0.55
42:L:73:GLU:HG2	42:L:90:VAL:HG22	1.89	0.55
1:3:505:G:H5''	1:3:534:U:H2'	1.89	0.55
2:1:184:C:H2'	2:1:185:G:C8	2.41	0.55
2:1:359:G:C2'	2:1:360:U:H5'	2.36	0.55
2:1:781:A:OP1	6:b:216:ARG:NH2	2.38	0.55
2:1:1086:A:H5'	2:1:1103:A:C2	2.41	0.55
2:1:1506:U:H2'	2:1:1507:C:C6	2.41	0.55
2:1:118:A:OP2	2:1:119:A:H5''	2.06	0.55
2:1:172:A:H2'	2:1:173:A:C8	2.40	0.55
2:1:955:U:OP1	16:m:86:LYS:NZ	2.33	0.55
2:1:1048:A:H2'	2:1:1049:C:H5'	1.88	0.55
2:1:2827:C:O2'	2:1:2828:G:H5'	2.07	0.55
4:5:72:G:N3	4:5:73:A:O4'	2.39	0.55
16:m:64:TRP:HB2	16:m:104:GLU:HB2	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:H:39:ARG:NH1	38:H:54:ILE:O	2.39	0.55
1:3:1059:C:O3'	49:S:84:ARG:NH2	2.40	0.55
1:3:1239:A:O2'	42:L:113:LYS:O	2.23	0.55
2:1:296:U:H2'	2:1:297:G:H8	1.71	0.55
2:1:392:U:H2'	2:1:393:C:C6	2.42	0.55
2:1:635:C:H2'	2:1:636:G:H8	1.70	0.55
2:1:1545:A:H2'	2:1:1546:G:O4'	2.06	0.55
2:1:2012:G:OP1	22:s:98:LYS:HD3	2.06	0.55
9:e:23:SER:HB3	9:e:26:GLN:HB2	1.88	0.55
37:G:19:THR:HA	37:G:37:VAL:HA	1.88	0.55
55:Y:60:GLN:HA	55:Y:63:LYS:HB3	1.89	0.55
2:1:112:U:C2'	2:1:113:U:H5'	2.37	0.55
2:1:439:A:H2'	2:1:440:C:C6	2.42	0.55
2:1:1485:U:H2'	2:1:1486:U:C6	2.41	0.55
2:1:1541:C:O2'	2:1:1542:U:H5'	2.06	0.55
2:1:1909:C:H2'	2:1:1910:G:C8	2.41	0.55
2:1:2590:A:C2	2:1:2605:U:O2	2.60	0.55
28:y:28:LEU:HA	28:y:31:GLN:HB2	1.88	0.55
49:S:26:LEU:HA	49:S:30:ILE:HD12	1.87	0.55
1:3:414:A:OP2	1:3:428:G:N2	2.34	0.55
1:3:1073:U:O2	37:G:102:ASN:ND2	2.39	0.55
2:1:585:G:N7	20:q:5:ARG:NH1	2.55	0.55
2:1:923:G:O2'	2:1:924:G:H5'	2.07	0.55
2:1:1182:G:H2'	2:1:1183:U:O4'	2.06	0.55
2:1:1565:C:HO2'	2:1:1566:A:H8	1.54	0.55
2:1:2114:A:C8	2:1:2115:G:H1'	2.42	0.55
10:f:7:PRO:O	10:f:68:ARG:NH2	2.38	0.55
46:P:63:GLN:HG3	46:P:98:ALA:HB2	1.88	0.55
46:P:86:LYS:HG3	46:P:114:PRO:HD3	1.89	0.55
2:1:340:A:H2'	2:1:341:C:O4'	2.06	0.55
2:1:673:C:H5''	8:d:76:PRO:HD2	1.89	0.55
2:1:1590:A:O2'	2:1:1591:A:H5'	2.05	0.55
2:1:1601:G:C2'	2:1:1602:U:H5'	2.37	0.55
2:1:2217:G:O2'	2:1:2218:G:H5'	2.07	0.55
5:7:9:G:C2	5:7:45:G:O6	2.60	0.55
37:G:91:VAL:HG22	37:G:150:ILE:HD11	1.88	0.55
1:3:880:C:OP1	47:Q:8:ARG:NH2	2.36	0.55
1:3:1350:A:N7	44:N:119:LYS:NZ	2.53	0.55
2:1:133:U:O2'	2:1:134:G:H5'	2.06	0.55
2:1:317:G:H2'	2:1:318:C:C6	2.42	0.55
2:1:877:A:C2'	2:1:878:A:H5''	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:1061:U:C2	12:i:10:LEU:HA	2.42	0.55
2:1:2195:U:O2'	2:1:2196:C:H5'	2.06	0.55
2:1:2845:U:H2'	2:1:2846:G:C8	2.42	0.55
1:3:1494:G:H4'	2:1:1913:A:N7	2.22	0.55
2:1:633:A:C2'	2:1:634:C:H5'	2.35	0.55
2:1:1979:U:C2'	2:1:1980:G:H5'	2.37	0.55
2:1:2488:G:O2'	2:1:2489:U:H5'	2.07	0.55
49:S:52:ARG:O	49:S:58:ARG:NH1	2.39	0.55
2:1:155:A:H2'	2:1:156:A:C8	2.41	0.54
2:1:461:C:H2'	2:1:462:C:C6	2.41	0.54
2:1:1091:G:H2'	2:1:1092:C:C6	2.42	0.54
2:1:1745:A:O2'	2:1:1746:A:H5'	2.07	0.54
2:1:2529:G:H4'	10:f:174:LYS:CG	2.34	0.54
1:3:1040:U:H2'	1:3:1041:G:C8	2.42	0.54
2:1:543:G:H2'	2:1:544:C:C4'	2.37	0.54
2:1:2345:G:H5'	2:1:2347:C:H5'	1.89	0.54
2:1:2584:U:C2'	2:1:2585:U:H5'	2.34	0.54
3:2:40:U:N3	3:2:44:G:OP2	2.40	0.54
5:7:18:G:O6	5:7:55:U:C6	2.61	0.54
28:y:15:ASN:O	28:y:19:LEU:N	2.41	0.54
37:G:53:LEU:HD21	37:G:215:ALA:HB1	1.88	0.54
42:L:4:ARG:HB3	42:L:6:ILE:HG23	1.88	0.54
2:1:744:U:C2'	2:1:745:G:H5'	2.37	0.54
2:1:1807:G:C2'	2:1:1808:A:H5'	2.29	0.54
2:1:2742:G:O2'	2:1:2743:U:H5'	2.08	0.54
5:7:11:A:H2'	5:7:12:G:H8	1.72	0.54
47:Q:64:SER:OG	47:Q:65:TYR:N	2.41	0.54
1:3:923:A:N6	1:3:1392:G:O6	2.40	0.54
2:1:141:G:H3'	2:1:142:A:O4'	2.07	0.54
2:1:143:C:H2'	2:1:144:A:H8	1.72	0.54
2:1:358:U:H2'	2:1:359:G:H8	1.72	0.54
2:1:757:G:H2'	2:1:758:C:C5'	2.35	0.54
2:1:784:G:C5'	2:1:785:G:OP1	2.54	0.54
2:1:1485:U:H2'	2:1:1486:U:H6	1.70	0.54
2:1:2545:G:O2'	2:1:2546:U:H5'	2.07	0.54
2:1:2802:G:H2'	2:1:2803:G:H8	1.72	0.54
15:l:80:SER:HB3	15:l:114:GLY:HA3	1.89	0.54
1:3:1381:U:O2	42:L:77:ARG:NH2	2.41	0.54
2:1:563:A:H1'	2:1:2018:G:N2	2.23	0.54
2:1:876:C:H2'	2:1:877:A:O4'	2.08	0.54
2:1:1528:A:C2'	2:1:1529:G:H5'	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:2092:U:C4'	2:1:2093:G:H5''	2.37	0.54
2:1:2092:U:C5	2:1:2199:A:H2	2.26	0.54
23:t:54:GLU:HB3	23:t:88:LYS:HE3	1.90	0.54
1:3:927:G:O2'	1:3:1503:A:N7	2.38	0.54
2:1:1297:C:H2'	2:1:1298:C:C6	2.43	0.54
3:2:31:C:H2'	3:2:53:A:H61	1.73	0.54
5:7:55:U:H2'	5:7:56:C:H5	1.73	0.54
14:k:76:VAL:H	19:p:72:VAL:HG22	1.71	0.54
26:w:55:LEU:HD12	26:w:76:ILE:HD12	1.89	0.54
55:Y:47:GLN:NE2	55:Y:51:ASN:OD1	2.40	0.54
2:1:21:A:O2'	2:1:22:C:H5'	2.08	0.54
2:1:176:A:O2'	2:1:177:G:H5'	2.08	0.54
2:1:359:G:H2'	2:1:360:U:O4'	2.07	0.54
2:1:670:A:H4'	2:1:671:C:C5'	2.35	0.54
2:1:1005:C:H6	2:1:1005:C:O5'	1.90	0.54
2:1:2743:U:C3'	2:1:2744:G:H5''	2.37	0.54
4:5:71:C:H2'	4:5:72:G:H5'	1.90	0.54
12:i:27:LEU:HD13	12:i:32:VAL:HG11	1.90	0.54
2:1:282:A:H2'	2:1:283:G:C8	2.42	0.54
2:1:1063:G:N1	2:1:1075:C:N4	2.52	0.54
2:1:1530:G:H22	2:1:1542:U:H1'	1.73	0.54
2:1:1670:C:O5'	2:1:1670:C:H6	1.90	0.54
2:1:2190:G:O2'	2:1:2191:A:H5'	2.08	0.54
13:j:38:GLY:HA3	13:j:50:THR:HG23	1.90	0.54
38:H:71:ARG:HB3	38:H:74:ILE:HD13	1.89	0.54
2:1:8:C:H2'	2:1:9:G:H8	1.73	0.54
2:1:1068:G:N2	2:1:1096:A:H1'	2.23	0.54
2:1:1448:G:H2'	2:1:1449:G:C8	2.42	0.54
2:1:1601:G:O2'	2:1:1602:U:H5'	2.08	0.54
2:1:1748:C:H2'	2:1:1749:A:H8	1.73	0.54
2:1:1856:U:H2'	2:1:1857:G:O4'	2.08	0.54
17:n:35:LYS:NZ	17:n:100:CYS:SG	2.81	0.54
1:3:1032:G:H21	1:3:1033:G:H4'	1.73	0.54
2:1:820:A:O2'	2:1:821:A:H5'	2.08	0.54
2:1:1389:G:O2'	2:1:1390:U:H5'	2.07	0.54
2:1:2480:C:H2'	2:1:2481:G:H5'	1.89	0.54
15:l:20:GLY:HA2	15:l:28:GLY:HA2	1.90	0.54
19:p:1:SER:OG	19:p:2:ASN:N	2.37	0.54
37:G:138:ARG:NH1	37:G:141:GLU:OE2	2.40	0.54
1:3:830:G:H1	1:3:856:C:H42	1.53	0.53
2:1:44:A:O2'	2:1:45:G:H5'	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:613:A:H5''	2:1:614:A:N7	2.22	0.53
2:1:995:C:N3	13:j:2:LYS:HA	2.23	0.53
2:1:1599:U:H2'	2:1:1600:C:C6	2.43	0.53
9:e:21:TYR:OH	9:e:164:GLU:OE1	2.26	0.53
15:l:89:VAL:HG23	15:l:121:THR:HG23	1.88	0.53
25:v:83:LYS:HD3	25:v:85:LYS:HZ1	1.71	0.53
2:1:279:A:N6	2:1:361:G:H1'	2.20	0.53
2:1:752:A:H62	2:1:2609:U:H3	1.56	0.53
2:1:1171:G:H2'	2:1:1172:C:C4'	2.38	0.53
2:1:2123:G:H2'	2:1:2124:G:H8	1.73	0.53
2:1:2504:U:H2'	2:1:2505:G:H5'	1.89	0.53
2:1:2631:G:O2'	2:1:2632:A:H5'	2.09	0.53
18:o:31:THR:HG23	18:o:34:HIS:H	1.73	0.53
21:r:75:VAL:HG23	21:r:86:GLN:HG2	1.90	0.53
40:J:104:ILE:O	40:J:111:ARG:NH1	2.41	0.53
1:3:1266:G:N2	1:3:1269:A:OP2	2.29	0.53
2:1:2328:A:H8	2:1:2328:A:O5'	1.91	0.53
37:G:126:ASP:OD1	37:G:126:ASP:N	2.41	0.53
39:I:55:ARG:O	39:I:59:LYS:N	2.41	0.53
1:3:458:U:H3	1:3:474:G:H1	1.56	0.53
2:1:57:C:H2'	2:1:58:G:O4'	2.08	0.53
2:1:472:A:H2'	2:1:473:G:H5'	1.90	0.53
2:1:611:C:H2'	2:1:612:G:O4'	2.09	0.53
2:1:1083:U:H2'	2:1:1084:A:H3'	1.89	0.53
2:1:1288:G:C6	2:1:1327:A:C2	2.96	0.53
2:1:1441:G:H2'	2:1:1442:U:H6	1.71	0.53
2:1:1662:U:H2'	2:1:1663:G:O4'	2.09	0.53
2:1:2348:U:H5'	32:C:20:TYR:OH	2.08	0.53
6:b:132:ARG:O	6:b:166:ARG:NH1	2.41	0.53
9:e:162:ASP:OD1	9:e:162:ASP:N	2.37	0.53
39:I:154:VAL:HA	39:I:157:ALA:HB3	1.91	0.53
2:1:53:A:H2'	2:1:54:G:H5'	1.89	0.53
2:1:268:C:H2'	2:1:269:C:H6	1.73	0.53
2:1:784:G:N1	6:b:227:VAL:HG11	2.23	0.53
2:1:925:A:O2'	2:1:926:G:H5'	2.08	0.53
10:f:103:ASN:ND2	10:f:113:ASP:OD1	2.41	0.53
2:1:268:C:H2'	2:1:269:C:C6	2.44	0.53
2:1:1560:G:H2'	2:1:1560:G:N3	2.24	0.53
2:1:2747:G:O6	2:1:2754:U:H2'	2.09	0.53
6:b:132:ARG:NE	6:b:186:ASP:OD1	2.41	0.53
40:J:152:VAL:HG21	43:M:98:LEU:HD13	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3:1023:U:H2'	1:3:1024:G:C8	2.43	0.53
2:1:213:A:O2'	2:1:214:G:H5'	2.09	0.53
2:1:1530:G:N2	2:1:1542:U:H1'	2.23	0.53
2:1:1782:U:H2'	2:1:1783:A:H5''	1.90	0.53
2:1:2644:G:O2'	2:1:2645:G:H5'	2.09	0.53
2:1:2734:A:C2'	2:1:2735:G:H5'	2.38	0.53
5:7:43:A:H2'	5:7:44:A:C8	2.44	0.53
6:b:257:ARG:NH2	6:b:262:THR:OG1	2.42	0.53
9:e:101:ARG:NH2	30:A:9:TYR:OH	2.41	0.53
1:3:835:U:OP1	53:W:52:ARG:NH2	2.42	0.53
2:1:894:U:O2'	2:1:895:U:H5'	2.09	0.53
2:1:1111:A:H2'	2:1:1112:G:H4'	1.90	0.53
2:1:1278:C:O2'	2:1:1279:G:H5'	2.09	0.53
2:1:1338:G:H2'	2:1:1339:G:H8	1.74	0.53
2:1:1678:A:H2'	2:1:1679:A:C5'	2.38	0.53
31:B:43:THR:HG1	31:B:46:GLY:H	1.53	0.53
37:G:61:SER:OG	37:G:62:ARG:NH1	2.42	0.53
2:1:441:U:O2'	2:1:442:G:H5'	2.08	0.53
2:1:2102:G:H2'	2:1:2103:C:O4'	2.09	0.53
29:z:36:GLU:O	29:z:37:ARG:NH1	2.42	0.53
46:P:15:VAL:HG12	46:P:76:TYR:HB3	1.90	0.53
2:1:682:G:N2	2:1:796:C:O2	2.41	0.53
2:1:1071:G:HO2'	2:1:1089:A:H2'	1.71	0.53
2:1:1161:C:H2'	2:1:1162:G:C8	2.44	0.53
2:1:1574:C:H2'	2:1:1575:C:H6	1.74	0.53
2:1:1789:A:H2'	2:1:1790:C:O4'	2.09	0.53
2:1:1917:U:C2'	2:1:1918:A:H5'	2.39	0.53
2:1:2389:G:H5''	2:1:2390:U:O4'	2.09	0.53
2:1:2707:U:H2'	2:1:2708:G:C8	2.44	0.53
2:1:2758:A:H2'	2:1:2759:G:C5'	2.39	0.53
2:1:2762:C:C2'	2:1:2763:G:H5'	2.39	0.53
4:5:2:G:N1	4:5:72:G:C6	2.77	0.53
43:M:92:PRO:O	43:M:116:ARG:NH2	2.42	0.53
2:1:368:A:H2'	2:1:369:U:C5'	2.39	0.52
2:1:492:A:H2'	2:1:493:G:O4'	2.09	0.52
2:1:1014:A:H2'	2:1:1015:U:C6	2.43	0.52
2:1:1542:U:O2'	2:1:1543:G:H5'	2.09	0.52
2:1:2092:U:C5	2:1:2199:A:C2	2.97	0.52
6:b:257:ARG:HH22	6:b:262:THR:HG1	1.57	0.52
9:e:177:ARG:O	30:A:47:LYS:NZ	2.41	0.52
18:o:40:ILE:HG22	18:o:47:VAL:HG12	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
30:A:35:ASP:OD1	30:A:35:ASP:N	2.42	0.52
2:1:40:U:H2'	2:1:41:C:C6	2.43	0.52
2:1:53:A:C2'	2:1:54:G:H5'	2.39	0.52
2:1:341:C:O2'	2:1:342:A:H5'	2.08	0.52
2:1:878:A:H2'	2:1:879:G:O4'	2.09	0.52
2:1:2290:G:H2'	2:1:2291:U:H6	1.74	0.52
2:1:2470:G:O2'	2:1:2471:A:H5'	2.10	0.52
2:1:2625:G:O2'	2:1:2626:C:H5'	2.09	0.52
2:1:2850:A:C2	2:1:2869:G:H4'	2.44	0.52
47:Q:18:SER:OG	47:Q:19:ASN:N	2.42	0.52
47:Q:36:VAL:HG21	47:Q:73:LEU:HB3	1.91	0.52
47:Q:49:ARG:NH1	47:Q:88:ASP:OD2	2.42	0.52
55:Y:66:ILE:HG21	55:Y:70:LYS:HB3	1.91	0.52
1:3:203:G:N2	1:3:204:G:O6	2.43	0.52
2:1:138:U:C5	2:1:139:U:H5	2.28	0.52
2:1:723:C:O2'	2:1:724:U:H5'	2.09	0.52
2:1:1511:G:H2'	2:1:1512:C:H6	1.73	0.52
2:1:1722:A:H62	2:1:1738:G:H1'	1.75	0.52
24:u:87:GLU:HG2	24:u:92:VAL:HG21	1.91	0.52
1:3:460:A:H2'	1:3:461:A:H8	1.75	0.52
1:3:1023:U:H2'	1:3:1024:G:H8	1.74	0.52
2:1:521:U:H2'	2:1:522:A:H8	1.73	0.52
2:1:1310:G:H2'	2:1:1311:G:C5'	2.38	0.52
5:7:25:C:H42	5:7:45:G:H22	1.56	0.52
30:A:35:ASP:OD1	48:R:2:ARG:NH1	2.42	0.52
38:H:133:MET:HE3	38:H:167:TYR:HB2	1.91	0.52
51:U:6:LEU:HD22	51:U:17:TYR:HB3	1.91	0.52
1:3:1077:G:N2	1:3:1080:A:OP2	2.40	0.52
2:1:2194:U:H2'	2:1:2195:U:C6	2.45	0.52
2:1:2236:U:C2'	2:1:2237:G:H5'	2.39	0.52
2:1:2297:A:N1	2:1:2321:U:C5	2.75	0.52
2:1:2481:G:HO2'	2:1:2482:A:H8	1.58	0.52
5:7:9:G:O4'	5:7:46:G:N3	2.42	0.52
5:7:55:U:C2	5:7:57:A:N7	2.78	0.52
19:p:28:LYS:HB3	19:p:39:LEU:HD21	1.91	0.52
22:s:109:ASP:OD1	22:s:109:ASP:N	2.42	0.52
1:3:113:G:N3	1:3:353:A:O2'	2.42	0.52
1:3:1244:G:H1	1:3:1293:C:H42	1.57	0.52
2:1:729:G:H5''	2:1:730:A:H5''	1.91	0.52
2:1:1798:U:H5	6:b:270:ARG:NH2	2.08	0.52
2:1:2682:A:N3	7:c:23:PRO:HB3	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:1794:A:O2'	2:1:1795:C:H5'	2.10	0.52
2:1:2204:G:H2'	2:1:2205:A:C8	2.44	0.52
2:1:2570:G:C2'	2:1:2571:U:H5'	2.40	0.52
2:1:2617:U:H2'	2:1:2618:G:H5'	1.91	0.52
2:1:2758:A:C2'	2:1:2759:G:H5'	2.40	0.52
2:1:2776:A:C6	2:1:2782:G:H1'	2.45	0.52
6:b:92:LEU:HD11	6:b:100:ARG:HB3	1.91	0.52
16:m:38:ARG:HB3	16:m:98:PRO:HD3	1.92	0.52
18:o:40:ILE:HD12	18:o:44:GLY:HA2	1.90	0.52
40:J:23:THR:HG22	40:J:28:ARG:HB3	1.91	0.52
41:K:92:THR:OG1	41:K:93:LYS:N	2.43	0.52
56:Z:28:LEU:HA	56:Z:31:VAL:HG12	1.90	0.52
2:1:140:C:H2'	2:1:141:G:H5'	1.90	0.52
2:1:215:G:C4'	2:1:216:A:H4'	2.39	0.52
2:1:586:A:H5'	8:d:84:THR:HG21	1.92	0.52
2:1:1409:U:H2'	2:1:1410:G:C8	2.44	0.52
2:1:1807:G:H2'	2:1:1808:A:C5'	2.30	0.52
2:1:1930:G:HO2'	2:1:1931:U:P	2.33	0.52
14:k:42:THR:HG22	14:k:57:VAL:HG12	1.91	0.52
5:6:43:A:H2'	5:6:44:A:C8	2.45	0.52
39:I:150:LYS:O	39:I:155:LYS:NZ	2.43	0.52
41:K:23:GLU:HA	41:K:26:THR:HG22	1.90	0.52
1:3:1367:C:H5''	44:N:115:VAL:HG23	1.91	0.52
2:1:543:G:C2'	2:1:544:C:H5''	2.37	0.52
2:1:597:G:H2'	2:1:598:U:C6	2.45	0.52
2:1:995:C:H6	2:1:995:C:H5'	1.74	0.52
2:1:1558:C:O4'	2:1:1560:G:C8	2.62	0.52
2:1:1697:G:H4'	2:1:1978:A:H5''	1.91	0.52
2:1:2463:C:O2'	2:1:2464:G:H5'	2.10	0.52
19:p:105:LYS:O	19:p:108:ARG:NH2	2.42	0.52
38:H:30:ASP:N	38:H:30:ASP:OD1	2.41	0.52
44:N:89:TYR:HB3	44:N:93:LEU:HD21	1.92	0.52
44:N:90:ASP:OD1	44:N:90:ASP:N	2.43	0.52
2:1:870:U:O2'	2:1:871:U:H5'	2.10	0.52
2:1:1175:A:H3'	2:1:1176:U:C5'	2.37	0.52
2:1:2529:G:H5''	2:1:2530:A:H5''	1.91	0.52
5:6:1:C:H2'	5:6:2:G:H8	1.75	0.52
5:6:74:C:C2'	5:6:75:C:C5'	2.88	0.52
1:3:1123:U:H4'	45:O:39:PRO:HD2	1.92	0.51
2:1:355:U:H2'	2:1:356:G:C8	2.45	0.51
2:1:1878:G:O2'	2:1:1879:C:H5'	2.09	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:1923:U:H2'	2:1:1924:C:C6	2.45	0.51
2:1:2230:G:H5''	27:x:29:LEU:HD12	1.91	0.51
2:1:2587:A:H5''	2:1:2588:G:OP2	2.10	0.51
23:t:65:GLY:N	23:t:79:ASP:OD1	2.43	0.51
25:v:51:GLN:OE1	25:v:79:ARG:NH2	2.40	0.51
45:O:5:ARG:N	45:O:76:ILE:O	2.43	0.51
1:3:202:G:H1	1:3:215:C:H42	1.57	0.51
2:1:1754:A:C6	2:1:1755:A:C6	2.98	0.51
2:1:2105:U:N3	2:1:2184:A:C2	2.78	0.51
2:1:2216:G:H2'	2:1:2217:G:H8	1.74	0.51
2:1:2651:C:O2'	2:1:2652:C:H5'	2.10	0.51
2:1:2670:A:H2'	2:1:2671:G:C8	2.45	0.51
35:F:19:ARG:HB2	35:F:24:ARG:HD2	1.92	0.51
38:H:130:ARG:NH2	38:H:165:GLU:OE1	2.43	0.51
40:J:106:ALA:O	40:J:111:ARG:NH2	2.43	0.51
2:1:8:C:H2'	2:1:9:G:C8	2.45	0.51
2:1:519:U:H2'	2:1:520:G:H8	1.75	0.51
2:1:655:A:H4'	2:1:656:G:C5'	2.30	0.51
2:1:1112:G:H2'	2:1:1113:U:O4'	2.10	0.51
9:e:69:ALA:O	9:e:80:GLN:NE2	2.44	0.51
2:1:251:A:H2'	2:1:252:G:O4'	2.10	0.51
2:1:291:G:O2'	2:1:292:U:H5'	2.11	0.51
2:1:1910:G:H1	2:1:1920:C:H42	1.58	0.51
2:1:2425:A:H4'	2:1:2426:A:H5''	1.91	0.51
5:7:54:U:H6	5:7:54:U:H5''	1.74	0.51
1:3:544:G:OP1	39:I:55:ARG:NH1	2.43	0.51
1:3:544:G:OP1	39:I:58:GLN:NE2	2.44	0.51
2:1:1403:A:H2'	2:1:1404:C:C6	2.45	0.51
2:1:1503:A:C3'	2:1:1504:A:H5''	2.40	0.51
2:1:2114:A:C2	2:1:2167:U:H1'	2.41	0.51
12:i:49:GLU:OE1	12:i:81:LYS:NZ	2.41	0.51
21:r:4:VAL:HG12	21:r:13:ARG:HA	1.91	0.51
2:1:672:C:H5	15:l:42:SER:HB2	1.76	0.51
2:1:752:A:OP1	33:D:3:ARG:NH1	2.43	0.51
2:1:1047:G:N2	2:1:1110:G:H2'	2.25	0.51
2:1:1678:A:C2'	2:1:1679:A:H5'	2.41	0.51
2:1:1722:A:O2'	2:1:1723:G:H5'	2.10	0.51
2:1:1979:U:H2'	2:1:1980:G:H5'	1.93	0.51
2:1:2593:U:O2'	2:1:2594:C:H5'	2.11	0.51
14:k:75:SER:OG	19:p:72:VAL:O	2.26	0.51
24:u:73:ASN:ND2	24:u:80:ASP:OD2	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:L:65:LEU:O	42:L:69:ARG:N	2.43	0.51
43:M:29:SER:OG	43:M:30:LYS:N	2.44	0.51
2:1:49:A:O5'	2:1:51:G:H5'	2.09	0.51
2:1:707:G:H2'	2:1:708:G:O4'	2.11	0.51
2:1:891:G:H2'	2:1:892:A:C8	2.46	0.51
2:1:1717:A:H2'	2:1:1718:G:C5'	2.40	0.51
2:1:2052:A:C2'	2:1:2053:G:H5'	2.41	0.51
2:1:2285:C:O2'	2:1:2286:G:H5'	2.11	0.51
2:1:2670:A:H2'	2:1:2671:G:H8	1.75	0.51
12:i:53:PRO:HD2	12:i:77:VAL:HG11	1.91	0.51
1:3:376:G:H5''	51:U:5:ARG:HB3	1.93	0.51
2:1:208:C:O5'	2:1:208:C:H6	1.93	0.51
2:1:2286:G:H21	2:1:2287:A:N6	2.09	0.51
2:1:2525:G:N2	2:1:2539:C:C2	2.79	0.51
2:1:2618:G:H2'	2:1:2619:C:O4'	2.11	0.51
2:1:2732:G:OP1	7:c:208:LYS:HD3	2.11	0.51
45:O:29:ALA:O	45:O:33:GLY:N	2.42	0.51
47:Q:17:LYS:HG3	47:Q:18:SER:H	1.75	0.51
2:1:1068:G:N2	12:i:25:PRO:HG2	2.24	0.51
2:1:1416:G:H2'	2:1:1417:C:C6	2.46	0.51
2:1:1507:C:H2'	2:1:1508:A:C4'	2.40	0.51
50:T:2:LEU:HD22	50:T:34:GLN:HB2	1.92	0.51
2:1:155:A:H2'	2:1:156:A:H8	1.76	0.51
2:1:402:A:C2'	2:1:403:U:H5'	2.38	0.51
2:1:905:A:H2'	2:1:906:U:C5'	2.41	0.51
2:1:2283:C:H2'	2:1:2284:A:O4'	2.11	0.51
2:1:69:C:H2'	2:1:70:G:C8	2.46	0.50
2:1:580:U:O5'	2:1:580:U:H6	1.94	0.50
2:1:1095:A:C2	12:i:25:PRO:HG3	2.46	0.50
2:1:1270:C:H5''	2:1:1271:G:H5''	1.93	0.50
2:1:2015:A:C6	31:B:2:VAL:HG23	2.46	0.50
2:1:2050:C:O2	7:c:161:MET:HE1	2.11	0.50
2:1:2420:C:H5''	32:C:7:LYS:HD3	1.93	0.50
2:1:2815:C:O2'	2:1:2816:G:H5'	2.11	0.50
6:b:147:PRO:HG3	6:b:184:GLU:HG2	1.92	0.50
6:b:156:SER:OG	6:b:157:ALA:N	2.44	0.50
12:i:110:GLN:HG2	12:i:121:ILE:HD13	1.93	0.50
1:3:1540:U:H3	36:4:5:A:H61	1.59	0.50
2:1:386:G:H3'	2:1:387:U:C5'	2.41	0.50
2:1:760:G:H2'	2:1:761:A:H5'	1.94	0.50
2:1:1415:U:H1'	2:1:1588:G:N2	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:1468:U:H2'	2:1:1522:A:N6	2.26	0.50
2:1:1930:G:C2'	2:1:1931:U:OP2	2.58	0.50
5:7:55:U:O2	5:7:55:U:C2'	2.59	0.50
6:b:1:ALA:N	6:b:19:VAL:O	2.41	0.50
8:d:191:ASP:O	8:d:195:GLN:NE2	2.44	0.50
5:6:74:C:O2'	5:6:75:C:H5'	2.11	0.50
38:H:107:LYS:HB3	38:H:110:LEU:HD23	1.92	0.50
52:V:60:ILE:HA	52:V:74:LEU:HA	1.93	0.50
53:W:71:ASP:N	53:W:71:ASP:OD1	2.44	0.50
1:3:1109:C:OP2	38:H:175:HIS:ND1	2.44	0.50
1:3:1178:G:N2	1:3:1181:G:OP2	2.43	0.50
2:1:19:A:O2'	2:1:20:C:H5'	2.11	0.50
2:1:1465:G:HO2'	2:1:1466:U:H5'	1.76	0.50
2:1:2625:G:H2'	2:1:2626:C:H6	1.76	0.50
2:1:2676:C:OP2	14:k:31:ARG:NH2	2.43	0.50
9:e:135:ILE:HG23	9:e:140:ILE:HD11	1.93	0.50
12:i:56:VAL:HB	12:i:68:PHE:HB2	1.92	0.50
24:u:88:ASP:OD1	24:u:88:ASP:N	2.43	0.50
41:K:42:TRP:HB2	41:K:59:TYR:HB2	1.93	0.50
1:3:1538:C:O2'	1:3:1539:C:H5'	2.11	0.50
2:1:704:G:H2'	2:1:726:G:H22	1.77	0.50
2:1:729:G:C8	6:b:206:LYS:HD2	2.46	0.50
2:1:1293:C:H2'	2:1:1294:U:C6	2.46	0.50
2:1:2734:A:H2'	2:1:2735:G:C5'	2.42	0.50
1:3:110:C:O2'	51:U:25:ARG:O	2.28	0.50
2:1:67:U:H2'	2:1:68:G:H8	1.77	0.50
2:1:1062:G:N2	12:i:134:SER:OG	2.45	0.50
2:1:1377:G:O3'	33:D:14:ARG:NH1	2.44	0.50
2:1:1528:A:H2'	2:1:1529:G:O4'	2.11	0.50
47:Q:110:LYS:HG3	47:Q:121:PRO:HG3	1.94	0.50
2:1:386:G:H3'	2:1:387:U:H5''	1.93	0.50
2:1:488:G:H22	2:1:491:G:H5''	1.77	0.50
2:1:539:G:O2'	2:1:540:C:H5'	2.12	0.50
2:1:1095:A:N1	12:i:25:PRO:HB3	2.27	0.50
2:1:1534:U:H2'	2:1:1536:C:O4'	2.10	0.50
1:3:664:G:H22	1:3:741:G:H1	1.60	0.50
2:1:131:A:H2'	2:1:132:G:H8	1.77	0.50
2:1:275:C:C3'	2:1:276:U:H5''	2.40	0.50
2:1:724:U:O2'	2:1:725:G:H5'	2.11	0.50
2:1:928:A:O2'	2:1:929:U:H5'	2.10	0.50
2:1:1593:A:H2'	2:1:1594:U:C6	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:1676:A:H8	2:1:1676:A:O5'	1.95	0.50
2:1:1916:A:H2'	2:1:1917:U:O4'	2.12	0.50
5:7:9:G:O4'	5:7:46:G:C2	2.65	0.50
38:H:4:VAL:HG21	38:H:9:ILE:HD13	1.93	0.50
45:O:24:GLU:HA	45:O:27:GLU:HB2	1.93	0.50
2:1:262:A:H2'	2:1:263:G:O4'	2.12	0.50
2:1:1779:U:C5	2:1:1784:A:N7	2.74	0.50
2:1:2836:U:H2'	2:1:2837:A:C8	2.47	0.50
6:b:137:GLY:O	6:b:162:GLN:NE2	2.45	0.50
20:q:103:VAL:HA	20:q:106:THR:HG22	1.94	0.50
1:3:7:A:H2'	40:J:123:LEU:HD12	1.92	0.50
2:1:54:G:H2'	2:1:55:G:O4'	2.12	0.50
2:1:197:A:H2	2:1:2434:A:N6	2.10	0.50
2:1:609:A:H2'	2:1:610:C:O4'	2.11	0.50
2:1:886:A:C5	2:1:887:U:H1'	2.47	0.50
2:1:1324:G:O2'	2:1:1326:U:OP2	2.29	0.50
2:1:2013:A:H5''	2:1:2013:A:C8	2.44	0.50
2:1:2302:U:O2'	2:1:2303:G:H5'	2.12	0.50
23:t:7:LEU:HD13	23:t:46:ALA:HA	1.94	0.50
37:G:103:TRP:HA	37:G:106:VAL:HG12	1.93	0.50
2:1:246:C:H2'	2:1:247:G:C5'	2.40	0.49
2:1:438:G:H2'	2:1:439:A:H8	1.76	0.49
2:1:482:A:H1'	2:1:498:G:N2	2.27	0.49
2:1:563:A:OP2	21:r:79:ARG:NH2	2.45	0.49
2:1:673:C:H2'	2:1:674:G:C5'	2.41	0.49
2:1:1077:A:H8	2:1:1078:U:H1'	1.77	0.49
2:1:1256:G:N2	8:d:77:ILE:HG23	2.26	0.49
2:1:1388:G:O2'	2:1:1389:G:H5'	2.12	0.49
2:1:1790:C:O2'	6:b:207:ALA:HB2	2.11	0.49
2:1:1813:G:H21	6:b:50:THR:HG23	1.76	0.49
2:1:1827:U:H2'	2:1:1828:G:C5'	2.41	0.49
2:1:2257:U:O2'	2:1:2258:C:H5'	2.12	0.49
10:f:136:ASP:HB3	10:f:139:VAL:HG12	1.92	0.49
25:v:77:VAL:HG23	25:v:89:ILE:HG12	1.92	0.49
27:x:64:ASP:N	27:x:64:ASP:OD1	2.43	0.49
1:3:780:A:N6	1:3:801:U:OP2	2.42	0.49
1:3:933:G:O6	42:L:2:ARG:NH2	2.46	0.49
2:1:30:G:H2'	2:1:31:C:C6	2.47	0.49
2:1:286:U:H2'	2:1:287:G:C8	2.47	0.49
2:1:355:U:H2'	2:1:356:G:H8	1.77	0.49
2:1:898:C:H2'	2:1:899:A:O4'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:940:G:H2'	2:1:941:A:C5'	2.41	0.49
2:1:1061:U:H4'	2:1:1070:A:H1'	1.93	0.49
2:1:1539:U:H2'	2:1:1540:G:H8	1.76	0.49
2:1:1668:A:C4'	2:1:1669:A:H5'	2.36	0.49
2:1:2241:A:O2'	2:1:2242:G:H5'	2.12	0.49
2:1:2687:U:H2'	2:1:2688:G:O4'	2.11	0.49
2:1:2830:C:H5''	7:c:56:LYS:NZ	2.28	0.49
2:1:2888:C:H2'	2:1:2889:C:H6	1.77	0.49
5:7:9:G:C2	5:7:45:G:C6	3.00	0.49
16:m:74:THR:HG21	16:m:86:LYS:HG2	1.94	0.49
5:6:18:G:H1	5:6:55:U:H6	1.58	0.49
44:N:91:GLU:HA	44:N:94:ARG:HB2	1.94	0.49
1:3:494:G:H2'	1:3:496:A:H8	1.76	0.49
2:1:145:C:H2'	2:1:146:A:C8	2.46	0.49
2:1:286:U:H2'	2:1:287:G:H8	1.75	0.49
2:1:553:G:H2'	2:1:554:U:O4'	2.13	0.49
2:1:841:G:C2	2:1:938:G:C2	3.01	0.49
2:1:1144:A:H2'	2:1:1145:C:C6	2.48	0.49
2:1:1614:A:H2'	2:1:1615:C:H5'	1.94	0.49
2:1:1645:G:H5''	2:1:1646:C:H5'	1.94	0.49
2:1:2393:U:H2'	2:1:2394:C:H5'	1.94	0.49
2:1:2803:G:O2'	2:1:2804:U:H5'	2.12	0.49
10:f:87:GLN:NE2	10:f:129:GLU:OE2	2.45	0.49
45:O:42:LEU:HB3	45:O:71:LEU:HB2	1.94	0.49
1:3:481:G:O2'	1:3:483:C:N4	2.46	0.49
2:1:1534:U:H4'	2:1:1535:A:N1	2.28	0.49
2:1:2298:A:O2'	2:1:2299:U:H5'	2.12	0.49
8:d:143:LEU:HD13	8:d:146:VAL:HG11	1.94	0.49
41:K:46:GLN:HA	41:K:56:LYS:HB3	1.94	0.49
1:3:1228:C:H2'	1:3:1229:A:H8	1.77	0.49
2:1:187:G:C6	2:1:188:G:N7	2.80	0.49
2:1:439:A:H2'	2:1:440:C:H6	1.75	0.49
2:1:1251:C:OP2	20:q:5:ARG:NH2	2.42	0.49
2:1:1465:G:H2'	2:1:1466:U:O4'	2.13	0.49
2:1:2636:C:O5'	7:c:81:GLU:HG3	2.13	0.49
5:7:54:U:H6	5:7:54:U:C5'	2.26	0.49
25:v:79:ARG:HA	25:v:86:LEU:HA	1.95	0.49
1:3:1061:G:O2'	45:O:58:ASN:ND2	2.45	0.49
1:3:1064:G:O2'	1:3:1190:G:N2	2.46	0.49
2:1:288:U:H2'	2:1:289:G:C8	2.47	0.49
2:1:630:G:H4'	2:1:640:C:H4'	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:900:A:H2'	2:1:901:C:H5'	1.94	0.49
2:1:1084:A:O2'	2:1:1105:U:H4'	2.12	0.49
2:1:1348:C:C5	2:1:1349:C:C5	3.00	0.49
2:1:1386:C:H2'	2:1:1387:A:C8	2.41	0.49
2:1:1813:G:N2	6:b:50:THR:HG23	2.27	0.49
2:1:2250:G:H8	2:1:2250:G:O5'	1.95	0.49
6:b:146:LYS:HB2	6:b:149:LYS:HB2	1.93	0.49
37:G:15:PHE:HB2	37:G:39:ILE:HG23	1.94	0.49
37:G:221:ARG:HG2	37:G:224:ARG:HH11	1.77	0.49
47:Q:70:GLY:O	47:Q:107:LYS:NZ	2.44	0.49
1:3:142:G:O2'	1:3:196:A:N1	2.45	0.49
1:3:974:A:OP1	49:S:68:ARG:NH2	2.45	0.49
2:1:78:U:H2'	2:1:79:C:H6	1.77	0.49
2:1:554:U:O2'	2:1:555:G:H5'	2.13	0.49
2:1:995:C:N4	13:j:2:LYS:HG2	2.27	0.49
2:1:1345:C:H6	2:1:1345:C:H5'	1.77	0.49
2:1:2634:A:O2'	2:1:2635:A:H5'	2.12	0.49
39:I:12:ARG:NH1	39:I:32:LYS:O	2.42	0.49
44:N:44:ARG:HG2	44:N:45:MET:HE2	1.95	0.49
1:3:500:G:H5'	47:Q:120:ARG:HH12	1.77	0.49
2:1:40:U:H2'	2:1:41:C:H6	1.78	0.49
2:1:118:A:H2'	2:1:120:U:O4	2.13	0.49
2:1:718:A:H2'	2:1:719:C:O4'	2.12	0.49
2:1:1020:A:C1'	2:1:1021:A:OP2	2.61	0.49
2:1:1409:U:H2'	2:1:1410:G:H8	1.76	0.49
2:1:2730:C:O2'	2:1:2731:G:H5'	2.13	0.49
6:b:92:LEU:HD21	6:b:100:ARG:HD3	1.93	0.49
9:e:57:ALA:HB2	9:e:64:PRO:HD3	1.95	0.49
17:n:10:LEU:O	17:n:12:ARG:N	2.45	0.49
21:r:71:LYS:HA	21:r:90:ARG:HG2	1.95	0.49
2:1:173:A:H2'	2:1:174:U:C6	2.47	0.49
2:1:644:A:H2'	2:1:645:C:C4'	2.42	0.49
2:1:1080:A:H4'	12:i:126:ARG:HD2	1.93	0.49
2:1:1111:A:H2'	2:1:1111:A:N3	2.28	0.49
2:1:1748:C:H2'	2:1:1749:A:C8	2.47	0.49
2:1:2311:A:H1'	9:e:84:ILE:HD11	1.94	0.49
2:1:2367:G:O2'	2:1:2368:C:H5'	2.13	0.49
2:1:2649:C:O2'	2:1:2650:U:H5'	2.13	0.49
2:1:2670:A:O2'	2:1:2671:G:H5'	2.12	0.49
4:5:75:C:OP2	4:5:75:C:C6	2.65	0.49
5:7:55:U:C4	5:7:57:A:N7	2.81	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:r:68:ARG:O	21:r:90:ARG:NH2	2.46	0.49
42:L:107:ALA:HA	42:L:122:GLU:HG3	1.95	0.49
1:3:880:C:H2'	1:3:881:G:H8	1.78	0.49
1:3:1229:A:OP2	48:R:112:ARG:NH1	2.46	0.49
2:1:1026:G:OP2	2:1:1134:A:H1'	2.13	0.49
2:1:1537:G:H3'	2:1:1537:G:N3	2.28	0.49
2:1:1668:A:N3	2:1:1670:C:N4	2.60	0.49
2:1:2281:A:O2'	2:1:2282:G:H5'	2.13	0.49
2:1:2843:G:O2'	2:1:2844:G:H5'	2.13	0.49
6:b:70:LYS:O	6:b:117:SER:OG	2.30	0.49
19:p:59:THR:HG22	19:p:72:VAL:HG12	1.95	0.49
27:x:1:SER:O	27:x:49:ARG:NH1	2.46	0.49
47:Q:97:VAL:HG12	47:Q:99:GLY:H	1.78	0.49
55:Y:59:ARG:O	55:Y:63:LYS:N	2.46	0.49
2:1:69:C:O2'	2:1:70:G:H5'	2.13	0.48
2:1:217:A:H2'	2:1:218:A:O4'	2.13	0.48
2:1:236:C:H2'	2:1:237:C:C6	2.46	0.48
2:1:898:C:C2'	2:1:899:A:H5'	2.43	0.48
2:1:898:C:O2'	2:1:899:A:H5'	2.13	0.48
10:f:163:TYR:HB2	10:f:166:GLU:HB2	1.95	0.48
30:A:37:CYS:O	30:A:41:HIS:N	2.45	0.48
46:P:96:ILE:HD13	46:P:109:ILE:HD13	1.94	0.48
1:3:1119:C:OP2	44:N:10:ARG:NH2	2.47	0.48
1:3:1531:A:O2'	1:3:1532:U:H5'	2.13	0.48
2:1:415:A:H2'	2:1:416:U:C6	2.49	0.48
2:1:473:G:O2'	2:1:474:G:H5'	2.14	0.48
2:1:476:G:H4'	2:1:502:A:N1	2.28	0.48
2:1:555:G:O2'	2:1:556:A:H8	1.96	0.48
2:1:840:C:O2'	2:1:841:G:H5'	2.12	0.48
2:1:1087:G:H2'	2:1:1089:A:H5'	1.94	0.48
2:1:1250:G:H5''	20:q:5:ARG:CD	2.43	0.48
2:1:2180:U:O2'	2:1:2181:U:H5'	2.13	0.48
2:1:2348:U:O2'	2:1:2349:G:H5'	2.12	0.48
2:1:2828:G:O2'	2:1:2829:A:H5'	2.13	0.48
12:i:85:ILE:HD12	12:i:97:VAL:HG12	1.95	0.48
24:u:100:GLU:HG2	24:u:101:THR:H	1.78	0.48
1:3:768:A:N3	1:3:1512:U:O2'	2.46	0.48
2:1:481:G:C2'	2:1:482:A:OP2	2.61	0.48
2:1:572:A:H8	2:1:572:A:O5'	1.97	0.48
2:1:686:U:H5''	33:D:11:LYS:HZ3	1.78	0.48
2:1:1910:G:N2	2:1:1911:U:C2	2.81	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:2:8:C:OP1	18:o:15:ARG:NH2	2.47	0.48
7:c:13:ARG:NH2	19:p:74:GLN:OE1	2.43	0.48
10:f:16:VAL:HA	10:f:25:ILE:HG12	1.96	0.48
51:U:36:VAL:HG12	51:U:53:ASP:HB3	1.95	0.48
1:3:38:G:H22	1:3:397:A:H5'	1.78	0.48
1:3:890:G:O2'	1:3:906:A:N6	2.46	0.48
2:1:214:G:H2'	2:1:215:G:C8	2.48	0.48
2:1:2050:C:N4	2:1:2051:A:C6	2.81	0.48
2:1:2527:C:O2'	2:1:2528:U:H5'	2.13	0.48
2:1:2533:U:H2'	2:1:2534:A:C5'	2.42	0.48
2:1:2555:U:O2	2:1:2555:U:O4'	2.29	0.48
9:e:27:VAL:O	9:e:29:ARG:NH1	2.41	0.48
10:f:122:ALA:HB2	10:f:132:LEU:HD23	1.94	0.48
11:g:8:LYS:HD3	11:g:14:SER:HA	1.95	0.48
39:I:94:GLU:HG3	39:I:190:LEU:HD21	1.95	0.48
2:1:149:A:H2'	2:1:150:U:C6	2.49	0.48
2:1:1267:U:O2	2:1:1267:U:H2'	2.14	0.48
2:1:2149:U:H2'	2:1:2150:C:C6	2.49	0.48
2:1:2208:C:H2'	2:1:2209:G:C8	2.48	0.48
2:1:2248:C:H2'	2:1:2249:U:H5'	1.93	0.48
2:1:2510:C:N4	2:1:2511:U:C4	2.81	0.48
4:5:26:A:H61	4:5:44:G:H1	1.62	0.48
12:i:79:LEU:HD13	12:i:132:ALA:HB2	1.94	0.48
39:I:49:ASP:OD2	39:I:49:ASP:N	2.43	0.48
50:T:23:SER:OG	50:T:25:GLU:OE1	2.30	0.48
2:1:1464:G:H2'	2:1:1465:G:H8	1.78	0.48
2:1:1742:U:O2'	2:1:1743:G:H5'	2.14	0.48
2:1:2156:G:C3'	2:1:2157:G:H5'	2.44	0.48
6:b:56:GLY:HA2	6:b:212:TRP:HA	1.94	0.48
37:G:101:THR:HG23	37:G:174:GLU:HG3	1.95	0.48
44:N:61:ASP:OD1	44:N:61:ASP:N	2.42	0.48
50:T:38:LEU:HD22	50:T:55:LEU:HD13	1.96	0.48
55:Y:53:MET:HE2	55:Y:57:VAL:HG21	1.94	0.48
56:Z:55:HIS:HA	56:Z:58:LYS:HD2	1.95	0.48
1:3:410:G:H21	1:3:432:A:H62	1.62	0.48
1:3:1240:U:H5'	42:L:41:ILE:HD11	1.94	0.48
2:1:691:C:OP1	6:b:216:ARG:NH1	2.46	0.48
2:1:1437:C:H2'	2:1:1438:U:H6	1.77	0.48
4:5:17:U:OP1	4:5:60:U:O2'	2.32	0.48
10:f:41:GLU:HG2	10:f:54:ARG:HH21	1.78	0.48
51:U:18:GLN:HA	51:U:38:PHE:HA	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3:435:A:N3	39:I:153:ARG:NH2	2.61	0.48
1:3:776:G:N2	1:3:802:A:OP2	2.39	0.48
2:1:129:C:H2'	2:1:130:C:H6	1.79	0.48
2:1:367:G:H2'	2:1:368:A:O4'	2.13	0.48
2:1:1785:A:O2'	2:1:1786:A:H8	1.96	0.48
2:1:2126:A:H5'	2:1:2127:G:O5'	2.12	0.48
2:1:2214:C:H2'	2:1:2215:C:O4'	2.14	0.48
2:1:2481:G:O2'	2:1:2482:A:H8	1.96	0.48
2:1:2507:C:H6	2:1:2507:C:O5'	1.96	0.48
2:1:2729:G:H4'	7:c:190:LYS:HE2	1.95	0.48
7:c:176:ASP:OD2	7:c:176:ASP:N	2.44	0.48
8:d:48:THR:OG1	8:d:49:ARG:N	2.47	0.48
41:K:75:GLU:O	41:K:79:ARG:N	2.47	0.48
44:N:94:ARG:HG2	44:N:97:LEU:HD12	1.95	0.48
2:1:360:U:H2'	2:1:361:G:C1'	2.44	0.48
2:1:636:G:OP1	15:l:129:LYS:HG2	2.14	0.48
2:1:706:A:H2'	2:1:707:G:H5'	1.95	0.48
2:1:852:U:H2'	2:1:853:C:C6	2.49	0.48
2:1:877:A:O2'	2:1:878:A:H5''	2.14	0.48
2:1:1257:C:O5'	2:1:1257:C:H6	1.97	0.48
2:1:1297:C:H2'	2:1:1298:C:H6	1.79	0.48
2:1:1389:G:C2	2:1:1390:U:C2	3.02	0.48
2:1:1400:U:H2'	2:1:1401:G:H8	1.78	0.48
2:1:1486:U:O2'	2:1:1487:U:H5'	2.14	0.48
2:1:2079:U:C4	2:1:2080:A:N7	2.82	0.48
2:1:2506:U:HO2'	4:5:76:A:H3'	1.76	0.48
5:7:50:U:H2'	5:7:51:C:C5	2.49	0.48
11:g:47:PHE:HA	11:g:51:ARG:HB2	1.96	0.48
17:n:100:CYS:H	17:n:111:ALA:HA	1.79	0.48
35:F:27:CYS:HG	35:F:33:HIS:HD1	1.60	0.48
5:6:17:C:OP1	5:6:60:U:O2'	2.28	0.48
38:H:171:ARG:HG2	38:H:173:PRO:HD3	1.96	0.48
46:P:34:THR:OG1	46:P:35:ASP:N	2.47	0.48
1:3:898:G:N2	1:3:901:A:OP2	2.46	0.48
2:1:435:C:C2'	2:1:436:C:H5'	2.44	0.48
2:1:471:A:OP1	8:d:79:ARG:NH2	2.35	0.48
2:1:519:U:H2'	2:1:520:G:C8	2.48	0.48
2:1:762:U:N3	2:1:1431:A:OP1	2.47	0.48
2:1:1871:A:H2'	2:1:1872:A:O4'	2.13	0.48
2:1:2286:G:H21	2:1:2287:A:H61	1.62	0.48
12:i:20:SER:HA	12:i:24:GLY:HA3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:u:39:ASN:HB3	24:u:62:ALA:HB3	1.95	0.48
2:1:1067:A:H2'	2:1:1068:G:C8	2.49	0.47
2:1:2642:G:O5'	2:1:2642:G:H8	1.98	0.47
1:3:358:U:H2'	1:3:359:G:H8	1.78	0.47
1:3:979:C:OP1	1:3:1223:C:N4	2.46	0.47
2:1:1087:G:O6	2:1:1089:A:C2	2.67	0.47
2:1:1117:C:H2'	2:1:1118:C:H6	1.78	0.47
2:1:1119:U:O2'	2:1:1120:G:H5'	2.13	0.47
2:1:1464:G:H2'	2:1:1465:G:C8	2.49	0.47
2:1:1668:A:H5''	14:k:5:GLN:HE21	1.78	0.47
2:1:1729:U:H5	2:1:1731:G:N2	2.12	0.47
2:1:2455:G:C6	2:1:2456:C:N4	2.83	0.47
2:1:2899:A:H2'	2:1:2900:A:O4'	2.15	0.47
28:y:16:THR:O	28:y:20:ASN:ND2	2.46	0.47
44:N:86:LEU:HD12	44:N:97:LEU:HD11	1.95	0.47
47:Q:82:ARG:O	47:Q:95:HIS:N	2.47	0.47
1:3:816:A:OP1	1:3:1526:G:O2'	2.28	0.47
2:1:708:G:H2'	2:1:709:U:C6	2.50	0.47
2:1:1266:G:O2'	2:1:2012:G:O6	2.25	0.47
2:1:1480:C:H2'	2:1:1481:U:C6	2.49	0.47
2:1:1536:C:H5''	2:1:1537:G:C4	2.48	0.47
2:1:1680:U:O2'	2:1:1681:G:H5'	2.13	0.47
2:1:2314:A:H2'	2:1:2315:G:H8	1.78	0.47
21:r:7:SER:OG	21:r:8:GLY:N	2.47	0.47
1:3:673:A:H2'	1:3:674:G:C8	2.49	0.47
2:1:92:U:H2'	2:1:93:G:H5'	1.95	0.47
2:1:107:G:O2'	2:1:108:G:H5'	2.14	0.47
2:1:538:A:O2'	2:1:539:G:H5'	2.14	0.47
2:1:788:A:OP1	2:1:791:C:N4	2.47	0.47
2:1:1105:U:H2'	2:1:1106:G:H8	1.80	0.47
2:1:2180:U:H2'	2:1:2181:U:O4'	2.14	0.47
2:1:2298:A:C2'	2:1:2299:U:H5'	2.45	0.47
2:1:2445:G:C6	2:1:2446:G:C6	3.02	0.47
2:1:2554:U:H2'	2:1:2555:U:O2	2.15	0.47
12:i:79:LEU:HD21	12:i:105:LEU:HD21	1.96	0.47
17:n:49:GLU:O	17:n:53:THR:OG1	2.29	0.47
33:D:29:GLN:O	33:D:29:GLN:NE2	2.47	0.47
1:3:1494:G:H4'	2:1:1913:A:C8	2.49	0.47
2:1:85:G:P	24:u:6:ARG:HB2	2.55	0.47
2:1:596:U:C2	2:1:662:G:N2	2.82	0.47
2:1:820:A:H2'	2:1:821:A:O4'	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:1098:A:O2'	2:1:1099:G:H5'	2.15	0.47
2:1:1285:A:H2'	2:1:1286:A:H5'	1.96	0.47
2:1:2155:U:H2'	2:1:2156:G:O4'	2.15	0.47
12:i:54:ILE:HD12	12:i:73:PRO:HD3	1.95	0.47
37:G:129:THR:HB	37:G:132:GLU:HB2	1.96	0.47
1:3:1200:C:H5''	1:3:1201:A:H3'	1.97	0.47
2:1:214:G:O2'	2:1:215:G:H5'	2.14	0.47
2:1:859:G:C2'	2:1:860:U:OP2	2.62	0.47
2:1:1141:U:H4'	2:1:1142:A:C1'	2.45	0.47
2:1:1491:G:H2'	2:1:1492:G:H8	1.80	0.47
2:1:1768:C:H42	2:1:1984:G:H1	1.62	0.47
2:1:1825:U:O5'	2:1:1825:U:H6	1.97	0.47
2:1:2362:C:O5'	2:1:2362:C:H6	1.97	0.47
2:1:2579:C:O2'	7:c:136:ASN:OD1	2.32	0.47
23:t:70:HIS:N	23:t:73:ARG:O	2.44	0.47
1:3:691:G:O6	46:P:56:LYS:NZ	2.38	0.47
1:3:692:U:O2'	1:3:694:A:N7	2.39	0.47
2:1:30:G:C5	2:1:31:C:C4	3.03	0.47
2:1:121:G:H4'	2:1:149:A:H5'	1.95	0.47
2:1:338:G:O2'	2:1:339:U:H5'	2.14	0.47
2:1:551:G:O2'	2:1:552:U:H5'	2.15	0.47
2:1:686:U:C5'	33:D:11:LYS:HZ3	2.27	0.47
2:1:712:G:H2'	2:1:713:G:H5'	1.96	0.47
2:1:854:C:H2'	2:1:855:G:H8	1.79	0.47
2:1:940:G:H3'	2:1:941:A:H5''	1.97	0.47
2:1:1726:C:H2'	2:1:1727:C:C6	2.50	0.47
2:1:2194:U:O2'	2:1:2195:U:H5'	2.15	0.47
2:1:2259:U:H2'	2:1:2260:C:O4'	2.15	0.47
2:1:2329:U:H2'	2:1:2330:G:H8	1.78	0.47
2:1:2895:G:H2'	2:1:2896:C:C6	2.49	0.47
3:2:43:C:O2	9:e:91:ARG:NH2	2.36	0.47
8:d:119:ILE:HB	8:d:187:VAL:HG12	1.96	0.47
10:f:87:GLN:HB3	10:f:162:ARG:HG3	1.97	0.47
10:f:100:ASN:OD1	10:f:100:ASN:N	2.47	0.47
26:w:19:VAL:HA	26:w:34:VAL:HG22	1.97	0.47
26:w:29:ALA:N	26:w:60:ASP:OD2	2.48	0.47
2:1:143:C:H2'	2:1:144:A:C8	2.49	0.47
2:1:283:G:C2'	2:1:284:U:H5'	2.45	0.47
2:1:297:G:H2'	2:1:298:G:O4'	2.14	0.47
2:1:1117:C:H2'	2:1:1118:C:C6	2.50	0.47
2:1:1344:U:H3'	2:1:1345:C:H5'	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:1922:G:H2'	2:1:1923:U:C6	2.50	0.47
2:1:2360:G:H2'	2:1:2361:G:C5'	2.40	0.47
12:i:8:VAL:HG21	12:i:26:ALA:HB1	1.96	0.47
20:q:24:TYR:O	20:q:26:ALA:N	2.48	0.47
34:E:5:THR:HG22	34:E:62:PRO:HD2	1.97	0.47
47:Q:70:GLY:O	47:Q:98:ARG:NH2	2.47	0.47
1:3:517:G:N2	1:3:533:A:OP2	2.34	0.47
1:3:1397:C:OP2	40:J:28:ARG:NH2	2.38	0.47
2:1:1059:G:H4'	12:i:115:ASP:OD2	2.14	0.47
2:1:1219:U:O2'	2:1:1220:G:H5'	2.15	0.47
2:1:1400:U:H2'	2:1:1401:G:C8	2.50	0.47
2:1:1528:A:H2'	2:1:1529:G:C5'	2.44	0.47
2:1:1818:U:N3	6:b:152:GLN:HB3	2.29	0.47
2:1:2876:G:H4'	19:p:2:ASN:HD21	1.79	0.47
4:5:74:C:C2'	4:5:75:C:H5'	2.44	0.47
4:5:76:A:H5''	4:5:76:A:C8	2.50	0.47
39:I:171:GLU:HB3	39:I:180:THR:HG22	1.97	0.47
42:L:70:PRO:HG3	42:L:98:LEU:HD23	1.97	0.47
50:T:37:HIS:HD2	50:T:38:LEU:HD12	1.80	0.47
1:3:1522:U:H2'	1:3:1523:G:H8	1.80	0.47
2:1:828:U:H2'	2:1:829:A:C8	2.50	0.47
2:1:832:U:OP1	15:l:39:LYS:HG2	2.15	0.47
2:1:1019:U:N3	2:1:1142:A:N6	2.57	0.47
2:1:1090:A:C2	2:1:1102:C:H1'	2.50	0.47
2:1:1183:U:H2'	2:1:1184:U:H6	1.80	0.47
2:1:1766:G:C2'	2:1:1767:G:H5'	2.45	0.47
2:1:2141:G:H1	2:1:2151:U:H3	1.63	0.47
2:1:2563:U:H2'	2:1:2565:A:OP2	2.15	0.47
2:1:2679:A:H5'	7:c:170:VAL:HG21	1.97	0.47
2:1:2813:A:O2'	2:1:2814:A:H5'	2.15	0.47
11:g:1:MET:N	11:g:20:ASN:OD1	2.40	0.47
26:w:37:ARG:HA	26:w:37:ARG:HD3	1.70	0.47
42:L:112:ASP:HB2	42:L:118:ARG:HG2	1.97	0.47
48:R:16:ILE:O	48:R:19:THR:OG1	2.26	0.47
1:3:230:G:O2'	51:U:25:ARG:NH1	2.48	0.46
2:1:5:A:H2'	2:1:6:A:C8	2.49	0.46
2:1:519:U:C2	2:1:520:G:C8	3.03	0.46
2:1:813:U:C2	2:1:1195:G:N2	2.82	0.46
2:1:995:C:C4	13:j:2:LYS:HA	2.50	0.46
2:1:1141:U:OP2	13:j:65:THR:HG22	2.15	0.46
2:1:1146:C:O2'	2:1:1147:A:H5'	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:1338:G:H2'	2:1:1339:G:C8	2.51	0.46
2:1:1509:A:H2'	2:1:1510:G:C8	2.49	0.46
2:1:2098:U:H2'	2:1:2099:U:O4'	2.14	0.46
8:d:149:ILE:HD11	8:d:172:ALA:HA	1.96	0.46
10:f:29:ASN:ND2	10:f:80:GLU:O	2.48	0.46
28:y:30:MET:HE3	28:y:30:MET:HB3	1.83	0.46
41:K:3:HIS:HA	41:K:65:GLU:HA	1.97	0.46
1:3:401:C:O2'	1:3:621:A:N3	2.45	0.46
2:1:554:U:C2'	2:1:555:G:H5'	2.45	0.46
2:1:848:C:H2'	2:1:849:A:H8	1.80	0.46
2:1:1140:C:H2'	2:1:1141:U:H5'	1.97	0.46
2:1:1287:A:O2'	2:1:1288:G:H5'	2.16	0.46
2:1:1435:G:O2'	2:1:1436:G:H5'	2.15	0.46
39:I:93:LEU:O	39:I:99:ASN:ND2	2.39	0.46
47:Q:29:LYS:HD3	47:Q:29:LYS:HA	1.68	0.46
48:R:7:ASN:HD22	48:R:20:SER:HB2	1.80	0.46
49:S:32:ASP:O	49:S:34:ASN:ND2	2.48	0.46
2:1:156:A:H2'	2:1:157:C:C6	2.50	0.46
2:1:409:G:H2'	2:1:410:G:C8	2.50	0.46
2:1:563:A:OP1	20:q:40:LYS:NZ	2.46	0.46
2:1:900:A:C2'	2:1:901:C:H5'	2.44	0.46
2:1:1210:G:P	2:1:1212:G:H5'	2.56	0.46
2:1:1874:C:H2'	2:1:1875:G:O4'	2.15	0.46
2:1:2290:G:O2'	2:1:2291:U:H5'	2.16	0.46
2:1:2295:C:O2'	2:1:2296:U:H5'	2.15	0.46
2:1:2749:A:OP1	10:f:1:SER:HA	2.16	0.46
7:c:4:LEU:HD11	7:c:100:LEU:HD21	1.98	0.46
22:s:72:THR:OG1	22:s:73:LYS:N	2.48	0.46
28:y:15:ASN:OD1	28:y:16:THR:N	2.48	0.46
5:6:21:A:H62	5:6:47:U:H1'	1.81	0.46
2:1:570:G:H5'	2:1:983:A:C2	2.50	0.46
2:1:1034:G:C5	2:1:1035:U:C4	3.04	0.46
2:1:1387:A:C5'	2:1:1469:A:H1'	2.38	0.46
2:1:1672:A:N3	2:1:2582:G:H5'	2.27	0.46
2:1:1869:G:H3'	2:1:1870:C:C5'	2.38	0.46
2:1:2241:A:H2'	2:1:2242:G:C8	2.50	0.46
37:G:17:HIS:ND1	37:G:18:GLN:OE1	2.45	0.46
56:Z:29:ALA:O	56:Z:32:ARG:NH1	2.49	0.46
1:3:459:A:H2'	1:3:460:A:C8	2.50	0.46
1:3:1035:A:H1'	1:3:1036:A:O5'	2.16	0.46
1:3:1291:U:O3'	44:N:40:ARG:NH2	2.38	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3:1347:G:O6	44:N:11:ARG:NH2	2.49	0.46
2:1:1367:A:H3'	2:1:1368:G:O4'	2.15	0.46
2:1:1922:G:O2'	2:1:1923:U:H5'	2.15	0.46
2:1:2016:U:O5'	2:1:2016:U:H6	1.97	0.46
2:1:2047:C:O5'	2:1:2047:C:H6	1.98	0.46
2:1:2350:C:H2'	2:1:2351:G:O4'	2.16	0.46
2:1:2636:C:O2'	2:1:2637:U:H5'	2.16	0.46
46:P:125:LYS:HB2	56:Z:33:ARG:HG2	1.97	0.46
1:3:617:G:H1	1:3:623:C:H42	1.62	0.46
1:3:647:C:H2'	1:3:648:A:H8	1.81	0.46
2:1:389:G:O2'	2:1:390:U:H5'	2.15	0.46
2:1:654:A:N3	2:1:654:A:H5''	2.31	0.46
2:1:1488:C:H2'	2:1:1489:C:C6	2.51	0.46
12:i:109:ALA:HA	12:i:112:LYS:HB2	1.98	0.46
5:6:74:C:C2'	5:6:75:C:O5'	2.59	0.46
39:I:159:GLU:HA	39:I:162:GLU:HB2	1.97	0.46
2:1:44:A:H2'	2:1:45:G:O4'	2.15	0.46
2:1:342:A:H2'	2:1:343:C:O4'	2.16	0.46
2:1:540:C:O2'	2:1:541:A:H5'	2.16	0.46
2:1:569:U:H1'	2:1:947:A:O4'	2.16	0.46
2:1:1288:G:C5	2:1:1327:A:C2	3.04	0.46
2:1:1381:G:H2'	2:1:1382:G:H5'	1.98	0.46
2:1:1516:G:O2'	2:1:1517:G:H5'	2.15	0.46
2:1:1517:G:O2'	2:1:1518:C:H5'	2.15	0.46
2:1:1851:U:OP1	5:7:4:G:H4'	2.15	0.46
2:1:2085:U:O2'	2:1:2086:U:H5'	2.16	0.46
2:1:2101:A:H2'	2:1:2102:G:H8	1.81	0.46
12:i:106:GLN:OE1	12:i:125:THR:OG1	2.31	0.46
12:i:112:LYS:HD2	12:i:128:ILE:HD12	1.97	0.46
26:w:7:ARG:HA	26:w:7:ARG:HD3	1.77	0.46
27:x:30:PRO:HG2	27:x:32:LEU:HD11	1.98	0.46
1:3:112:G:N2	1:3:354:G:O5'	2.49	0.46
2:1:198:C:N4	2:1:248:G:H1	2.14	0.46
2:1:1173:U:C6	2:1:1174:U:H1'	2.51	0.46
2:1:2294:G:O2'	2:1:2295:C:H5'	2.15	0.46
2:1:2406:A:C2	15:l:69:ARG:NH1	2.84	0.46
2:1:2528:U:O2'	2:1:2529:G:H3'	2.16	0.46
2:1:2626:C:H2'	2:1:2627:G:H8	1.80	0.46
5:7:7:G:H3'	5:7:49:G:OP2	2.16	0.46
5:7:55:U:H5''	5:7:56:C:OP2	2.15	0.46
8:d:147:LEU:HD11	8:d:170:ARG:HG2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:f:90:GLY:HA2	10:f:159:LYS:HG2	1.98	0.46
38:H:5:HIS:CE1	38:H:7:ASN:HB3	2.51	0.46
38:H:152:VAL:HG12	38:H:197:VAL:HG22	1.98	0.46
2:1:290:U:O2'	2:1:291:G:H5'	2.16	0.46
2:1:438:G:O2'	2:1:439:A:H5'	2.16	0.46
2:1:466:A:H2'	2:1:467:G:C5'	2.44	0.46
2:1:536:G:H2'	2:1:537:G:C5'	2.43	0.46
2:1:1574:C:H2'	2:1:1575:C:C6	2.50	0.46
2:1:1863:G:H2'	2:1:1864:U:C6	2.51	0.46
2:1:1866:A:H2'	2:1:1867:G:O4'	2.16	0.46
2:1:1979:U:O2'	2:1:1980:G:H5'	2.16	0.46
2:1:2247:A:H2'	2:1:2248:C:H6	1.81	0.46
2:1:2507:C:C5'	2:1:2573:C:N4	2.79	0.46
2:1:2679:A:O2'	2:1:2680:U:H5'	2.15	0.46
2:1:2743:U:H2'	2:1:2744:G:O4'	2.16	0.46
5:7:48:C:H5''	5:7:50:U:OP1	2.15	0.46
28:y:6:LEU:HD13	28:y:56:LEU:HD22	1.98	0.46
31:B:8:THR:OG1	31:B:9:ARG:N	2.49	0.46
41:K:62:MET:HB3	41:K:64:VAL:HG13	1.98	0.46
41:K:100:SER:O	41:K:100:SER:OG	2.34	0.46
42:L:142:ARG:HA	42:L:145:GLU:HG3	1.97	0.46
52:V:10:ARG:NE	52:V:55:GLY:O	2.48	0.46
2:1:6:A:H2'	2:1:7:G:C8	2.51	0.46
2:1:595:C:C2	2:1:596:U:C5	3.04	0.46
2:1:1036:G:O2'	2:1:1037:G:H5'	2.15	0.46
2:1:1068:G:H2'	2:1:1069:A:H4'	1.96	0.46
2:1:1536:C:H5''	2:1:1537:G:C5	2.50	0.46
2:1:1873:G:O2'	2:1:1874:C:H5'	2.15	0.46
2:1:1882:U:O2'	2:1:1883:U:H5'	2.17	0.46
2:1:2315:G:H2'	2:1:2316:G:H8	1.80	0.46
2:1:2329:U:H2'	2:1:2330:G:C8	2.51	0.46
2:1:2626:C:H2'	2:1:2627:G:C8	2.51	0.46
2:1:2658:C:H2'	2:1:2659:G:O4'	2.16	0.46
2:1:2836:U:H2'	2:1:2837:A:H8	1.81	0.46
2:1:2844:G:H2'	2:1:2845:U:O4'	2.16	0.46
4:5:3:G:N1	4:5:71:C:O2	2.48	0.46
6:b:184:GLU:HG3	6:b:186:ASP:H	1.80	0.46
14:k:47:ILE:HG22	14:k:49:ARG:H	1.80	0.46
39:I:173:ASP:HB3	39:I:178:GLU:HB3	1.98	0.46
41:K:10:VAL:HG23	41:K:58:HIS:HB3	1.97	0.46
41:K:41:ASP:OD2	41:K:58:HIS:NE2	2.39	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:L:79:VAL:HB	42:L:84:TYR:HD2	1.80	0.46
2:1:93:G:O2'	2:1:94:A:H5'	2.16	0.45
2:1:465:G:OP1	33:D:12:ARG:NH1	2.49	0.45
2:1:1138:G:H21	13:j:108:MET:CE	2.29	0.45
2:1:1170:C:H2'	2:1:1171:G:C8	2.51	0.45
2:1:1322:A:H5''	22:s:82:MET:HE1	1.98	0.45
2:1:1572:A:H2'	2:1:1573:G:O4'	2.16	0.45
2:1:2032:G:H1'	7:c:150:GLN:HE22	1.81	0.45
2:1:2339:C:H2'	2:1:2340:A:H8	1.81	0.45
2:1:2395:C:H2'	2:1:2396:G:O4'	2.15	0.45
5:7:11:A:H2'	5:7:12:G:C8	2.52	0.45
7:c:106:LYS:HA	7:c:176:ASP:HA	1.99	0.45
9:e:122:ASP:OD2	9:e:126:ASN:ND2	2.42	0.45
48:R:97:ARG:HB2	48:R:99:GLN:HE22	1.81	0.45
1:3:1253:G:H2'	1:3:1254:A:C8	2.52	0.45
2:1:688:U:H5'	2:1:1780:A:C2	2.51	0.45
2:1:1090:A:H61	2:1:1101:U:H3	1.62	0.45
2:1:1130:U:C4	7:c:151:THR:O	2.70	0.45
2:1:1463:C:H2'	2:1:1464:G:C8	2.49	0.45
2:1:1550:C:O2'	2:1:1551:A:H5'	2.17	0.45
2:1:1710:G:H2'	2:1:1711:A:C8	2.51	0.45
2:1:1710:G:O2'	2:1:1711:A:H5'	2.17	0.45
2:1:2047:C:O2'	2:1:2048:G:H5'	2.16	0.45
2:1:2768:U:OP1	13:j:85:LYS:NZ	2.49	0.45
2:1:2849:U:H4'	2:1:2868:A:C2	2.51	0.45
2:1:2858:C:H2'	2:1:2859:G:O4'	2.15	0.45
10:f:88:LEU:HD21	10:f:104:LEU:HD23	1.97	0.45
40:J:101:GLY:H	40:J:121:ASN:HB3	1.81	0.45
46:P:17:ASP:OD1	46:P:17:ASP:N	2.44	0.45
51:U:55:ASP:OD1	51:U:55:ASP:N	2.38	0.45
1:3:980:C:H4'	49:S:58:ARG:HH21	1.81	0.45
2:1:167:A:H2'	2:1:168:G:O4'	2.16	0.45
2:1:637:A:C6	2:1:652:U:H4'	2.51	0.45
2:1:1500:G:O2'	2:1:1501:G:H5'	2.17	0.45
2:1:1605:C:H2'	2:1:1606:C:H5'	1.98	0.45
2:1:2581:G:H2'	2:1:2581:G:N3	2.30	0.45
2:1:2684:U:O4'	14:k:70:ARG:NH1	2.49	0.45
3:2:49:C:H5''	18:o:68:LYS:HE3	1.97	0.45
14:k:121:GLU:HG2	14:k:122:VAL:HG23	1.97	0.45
25:v:26:PHE:HE2	25:v:89:ILE:HG13	1.80	0.45
27:x:14:GLY:HA3	27:x:28:PHE:HE2	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:Q:72:ASN:HD21	47:Q:103:CYS:HA	1.81	0.45
1:3:542:G:O3'	39:I:13:ARG:NH1	2.50	0.45
2:1:195:A:H3'	2:1:196:A:H4'	1.98	0.45
2:1:289:G:H2'	2:1:290:U:C6	2.50	0.45
2:1:355:U:H6	2:1:355:U:O5'	1.99	0.45
2:1:607:U:O4	2:1:620:G:H5'	2.17	0.45
2:1:845:A:N3	2:1:845:A:H3'	2.31	0.45
2:1:970:U:H2'	2:1:971:G:H8	1.82	0.45
2:1:1412:U:H2'	2:1:1413:A:H8	1.81	0.45
2:1:1800:C:H2'	6:b:145:MET:HE1	1.97	0.45
2:1:1923:U:O2'	2:1:1924:C:H5'	2.16	0.45
2:1:2661:G:O2'	2:1:2662:A:H5'	2.16	0.45
8:d:132:LYS:HG2	8:d:136:GLN:HE22	1.81	0.45
44:N:105:ARG:NH1	44:N:109:GLN:OE1	2.49	0.45
51:U:79:ASN:HB2	51:U:82:ALA:HB3	1.99	0.45
1:3:693:G:O4'	36:4:13:A:H5'	2.16	0.45
1:3:1297:G:H21	42:L:113:LYS:HB3	1.82	0.45
2:1:28:A:O2'	2:1:29:U:H5'	2.16	0.45
2:1:360:U:H2'	2:1:361:G:H1'	1.99	0.45
2:1:438:G:H2'	2:1:439:A:C8	2.51	0.45
2:1:1209:U:O3'	2:1:1212:G:H5'	2.15	0.45
2:1:1868:C:H2'	2:1:1869:G:C8	2.52	0.45
2:1:1936:A:H2	2:1:1943:U:H3	1.65	0.45
2:1:2605:U:H2'	2:1:2606:C:C6	2.51	0.45
2:1:2648:G:C2	2:1:2649:C:C2	3.04	0.45
2:1:2651:C:H2'	2:1:2652:C:H6	1.81	0.45
2:1:2783:U:H2'	2:1:2784:U:C6	2.51	0.45
12:i:91:LYS:HB2	12:i:91:LYS:HE3	1.72	0.45
20:q:83:LYS:HE2	20:q:83:LYS:HB3	1.72	0.45
37:G:65:LYS:HG2	37:G:153:MET:HG3	1.98	0.45
37:G:166:ASP:HB3	37:G:190:SER:HB2	1.98	0.45
37:G:172:ILE:O	37:G:176:ASN:ND2	2.50	0.45
1:3:1376:U:H2'	1:3:1377:A:C8	2.52	0.45
2:1:1020:A:C2	2:1:1141:U:C2	3.05	0.45
2:1:1416:G:H2'	2:1:1417:C:H6	1.82	0.45
2:1:1800:C:O2	2:1:1802:A:C8	2.70	0.45
2:1:2480:C:C2'	2:1:2481:G:H5'	2.46	0.45
18:o:29:HIS:HB3	18:o:36:TYR:HB2	1.98	0.45
21:r:19:THR:OG1	21:r:95:ASP:OD2	2.35	0.45
31:B:8:THR:HG23	31:B:11:LYS:H	1.82	0.45
42:L:149:ALA:HB1	46:P:58:THR:HG21	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3:947:G:O3'	48:R:107:THR:OG1	2.35	0.45
2:1:163:C:O2'	2:1:164:C:H5'	2.17	0.45
2:1:848:C:H2'	2:1:849:A:C8	2.51	0.45
2:1:1049:C:C2'	2:1:1050:A:H5'	2.47	0.45
2:1:1255:U:C6	8:d:68:ALA:HA	2.52	0.45
2:1:1491:G:O2'	6:b:99:GLU:OE2	2.33	0.45
2:1:1670:C:O2'	2:1:1671:U:H5'	2.16	0.45
2:1:2700:A:O2'	2:1:2701:U:H5'	2.16	0.45
40:J:73:VAL:HG11	40:J:143:LEU:HB3	1.98	0.45
1:3:587:G:OP1	43:M:83:ARG:NH2	2.43	0.45
2:1:239:C:H2'	2:1:240:C:O4'	2.16	0.45
2:1:1832:C:O5'	2:1:1832:C:H6	2.00	0.45
2:1:2885:G:N2	31:B:31:LYS:HG2	2.31	0.45
8:d:188:MET:HB2	8:d:192:ALA:HB3	1.99	0.45
20:q:82:LEU:HD22	20:q:87:VAL:HB	1.98	0.45
23:t:34:VAL:HG21	23:t:43:ILE:HD11	1.99	0.45
37:G:162:VAL:N	37:G:183:PHE:O	2.38	0.45
40:J:24:VAL:HG23	40:J:26:GLY:H	1.82	0.45
2:1:367:G:O2'	2:1:368:A:H5'	2.17	0.45
2:1:979:A:H2'	2:1:982:C:H42	1.80	0.45
2:1:1365:A:OP2	27:x:1:SER:OG	2.35	0.45
2:1:1668:A:H5''	14:k:5:GLN:NE2	2.31	0.45
2:1:1680:U:C2'	2:1:1681:G:H5'	2.47	0.45
2:1:1923:U:H5''	5:6:24:U:O2'	2.17	0.45
2:1:1952:A:C8	14:k:42:THR:HG21	2.52	0.45
2:1:2054:A:C2	31:B:4:GLN:HG3	2.52	0.45
2:1:2236:U:H2'	2:1:2237:G:C5'	2.46	0.45
2:1:2467:C:OP1	35:F:8:LYS:NZ	2.37	0.45
8:d:32:VAL:HG21	15:l:6:LEU:HD13	1.99	0.45
19:p:92:ARG:H	19:p:92:ARG:HG2	1.60	0.45
21:r:1:MET:HE3	21:r:101:ILE:HB	1.99	0.45
43:M:86:LYS:HA	43:M:86:LYS:HD3	1.81	0.45
48:R:15:VAL:HG11	48:R:30:LYS:HG2	1.97	0.45
2:1:30:G:H2'	2:1:31:C:O4'	2.17	0.45
2:1:639:U:H2'	2:1:640:C:C6	2.52	0.45
2:1:707:G:C2'	2:1:708:G:H5'	2.47	0.45
2:1:853:C:O2'	2:1:854:C:H5'	2.16	0.45
2:1:893:C:H2'	2:1:894:U:O4'	2.17	0.45
2:1:1140:C:C2'	2:1:1141:U:H5'	2.47	0.45
2:1:1520:U:H2'	2:1:1521:G:O4'	2.16	0.45
2:1:2889:C:O2'	2:1:2890:G:H5'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:G:107:ARG:HE	37:G:107:ARG:HB3	1.63	0.45
1:3:222:C:H2'	1:3:223:A:C8	2.51	0.44
1:3:618:C:N4	1:3:621:A:OP2	2.49	0.44
1:3:1030:U:C5	1:3:1033:G:O2'	2.70	0.44
2:1:395:U:H2'	2:1:396:G:C8	2.52	0.44
2:1:854:C:H2'	2:1:855:G:C8	2.52	0.44
2:1:2496:C:H2'	2:1:2497:A:O4'	2.16	0.44
2:1:2741:A:H2'	2:1:2742:G:H5'	1.98	0.44
10:f:106:LEU:O	10:f:151:ARG:NH2	2.37	0.44
28:y:20:ASN:HA	28:y:23:ARG:HB2	1.99	0.44
5:6:46:G:H5''	5:6:47:U:OP2	2.17	0.44
37:G:33:ALA:HB3	37:G:37:VAL:HG12	1.99	0.44
40:J:104:ILE:HD11	40:J:114:LEU:HD13	1.99	0.44
46:P:35:ASP:OD1	46:P:39:ASN:N	2.50	0.44
1:3:162:A:C5	1:3:163:C:H1'	2.53	0.44
2:1:161:A:C5	2:1:162:U:H5	2.36	0.44
2:1:696:G:H2'	2:1:697:G:O4'	2.18	0.44
2:1:1250:G:H5''	20:q:5:ARG:HD3	1.98	0.44
2:1:1779:U:H5	2:1:1784:A:C8	2.34	0.44
2:1:1927:A:H8	2:1:1927:A:O5'	2.00	0.44
2:1:2241:A:H2'	2:1:2242:G:H8	1.82	0.44
2:1:2402:U:O2'	2:1:2403:C:H3'	2.17	0.44
17:n:86:ARG:NH2	17:n:117:ASP:OD2	2.47	0.44
24:u:76:THR:HB	24:u:78:LYS:HE3	1.99	0.44
41:K:38:ARG:HH11	41:K:61:LEU:HD21	1.83	0.44
51:U:1:MET:HE2	51:U:1:MET:HB3	1.87	0.44
52:V:11:VAL:HG13	52:V:58:VAL:HG21	1.98	0.44
1:3:908:A:H2'	1:3:909:A:H8	1.83	0.44
1:3:1180:A:H5'	44:N:104:THR:HG23	1.99	0.44
2:1:107:G:H2'	2:1:108:G:H8	1.82	0.44
2:1:208:C:O2'	2:1:209:C:H5'	2.18	0.44
2:1:545:U:O2	2:1:546:U:H1'	2.17	0.44
2:1:721:A:H2'	2:1:722:A:C8	2.53	0.44
2:1:1239:G:O2'	2:1:1240:U:H5'	2.17	0.44
2:1:1287:A:H3'	2:1:1288:G:N2	2.33	0.44
2:1:1452:G:H2'	2:1:1453:A:OP2	2.17	0.44
2:1:2122:U:H2'	2:1:2123:G:O4'	2.17	0.44
2:1:2204:G:H2'	2:1:2205:A:H8	1.81	0.44
2:1:2312:U:O2'	2:1:2313:C:H5'	2.17	0.44
2:1:2844:G:H2'	2:1:2845:U:H6	1.80	0.44
20:q:47:ARG:NH2	20:q:51:GLN:OE1	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:s:67:ASP:OD1	22:s:67:ASP:N	2.39	0.44
23:t:68:LYS:HA	23:t:68:LYS:HD3	1.83	0.44
24:u:12:VAL:HA	24:u:69:VAL:HG12	1.99	0.44
48:R:1:ALA:HB3	48:R:56:ARG:HH22	1.82	0.44
1:3:390:U:O2'	51:U:28:ARG:NH1	2.46	0.44
1:3:1200:C:O2'	1:3:1205:U:O4	2.35	0.44
1:3:1249:C:O2'	44:N:74:GLN:OE1	2.35	0.44
2:1:43:G:H2'	2:1:44:A:C8	2.53	0.44
2:1:623:C:O2'	2:1:624:C:H5'	2.18	0.44
2:1:1280:G:C2'	2:1:1281:G:H5'	2.46	0.44
2:1:1465:G:O2'	2:1:1466:U:H5'	2.17	0.44
2:1:1625:C:H2'	2:1:1626:A:O4'	2.18	0.44
2:1:2201:G:H2'	2:1:2202:U:O4'	2.17	0.44
2:1:2482:A:HO2'	4:5:63:U:HO2'	1.62	0.44
2:1:2869:G:H2'	2:1:2870:C:O4'	2.17	0.44
3:2:39:A:O2'	3:2:46:A:N1	2.47	0.44
4:5:75:C:OP2	4:5:75:C:C5	2.71	0.44
6:b:7:PRO:HB3	6:b:13:ARG:HG3	2.00	0.44
38:H:134:LYS:HG2	38:H:138:GLN:HE21	1.82	0.44
48:R:43:LYS:HB2	48:R:46:GLU:HG2	1.99	0.44
50:T:87:ARG:HD2	50:T:87:ARG:HA	1.71	0.44
1:3:1383:C:H4'	5:7:35:A:H2	1.81	0.44
2:1:432:A:O2'	2:1:433:C:H5'	2.17	0.44
2:1:648:G:H5''	2:1:2352:A:H5''	2.00	0.44
2:1:1061:U:OP1	12:i:9:LYS:HD2	2.17	0.44
2:1:1062:G:H21	12:i:135:MET:CE	2.30	0.44
2:1:2805:C:O2'	2:1:2806:C:H5'	2.18	0.44
4:5:68:C:C3'	4:5:69:G:H5''	2.47	0.44
8:d:136:GLN:HA	8:d:139:LYS:HE2	1.99	0.44
18:o:40:ILE:HA	18:o:47:VAL:HA	2.00	0.44
24:u:32:LYS:HG2	24:u:65:GLN:HA	1.99	0.44
39:I:114:ARG:HA	39:I:117:VAL:HG22	1.98	0.44
1:3:19:A:O2'	1:3:572:A:N1	2.46	0.44
1:3:667:G:O2'	50:T:48:ASP:OD1	2.25	0.44
2:1:29:U:O5'	2:1:29:U:H6	2.01	0.44
2:1:156:A:O2'	2:1:157:C:H5'	2.18	0.44
2:1:293:U:H2'	2:1:294:A:H5''	1.99	0.44
2:1:354:A:H2'	2:1:355:U:O4'	2.18	0.44
2:1:974:G:H1'	2:1:975:A:C8	2.52	0.44
2:1:1915:U:O2	2:1:1915:U:O4'	2.34	0.44
2:1:1998:A:O2'	2:1:1999:C:H5'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:2285:C:C2'	2:1:2286:G:H5'	2.48	0.44
2:1:2717:C:N3	2:1:2718:G:N7	2.65	0.44
2:1:2720:U:OP1	19:p:52:ARG:NH2	2.50	0.44
8:d:6:LYS:HB2	8:d:6:LYS:HE3	1.84	0.44
27:x:71:ARG:NH2	27:x:77:TYR:OH	2.42	0.44
29:z:30:ARG:HG2	29:z:33:HIS:HB2	1.99	0.44
51:U:70:ARG:O	51:U:74:LEU:N	2.47	0.44
53:W:47:ARG:HD3	53:W:47:ARG:HA	1.80	0.44
1:3:1197:A:H2'	1:3:1198:G:H8	1.83	0.44
2:1:30:G:O2'	2:1:31:C:H5'	2.17	0.44
2:1:1095:A:H3'	2:1:1096:A:H8	1.83	0.44
2:1:1536:C:H4'	2:1:1537:G:N1	2.32	0.44
2:1:1702:G:H2'	2:1:1703:G:C5'	2.35	0.44
2:1:1749:A:H2'	2:1:1750:G:H8	1.82	0.44
22:s:74:ILE:HB	22:s:105:VAL:HG23	1.99	0.44
24:u:17:ASP:HA	24:u:20:LYS:HE2	2.00	0.44
38:H:5:HIS:HE1	38:H:7:ASN:HB3	1.82	0.44
50:T:2:LEU:HD12	50:T:2:LEU:HA	1.83	0.44
53:W:33:THR:OG1	53:W:34:GLU:N	2.49	0.44
54:X:32:THR:OG1	54:X:49:ALA:O	2.31	0.44
1:3:75:G:H2'	1:3:76:G:C8	2.53	0.44
1:3:490:C:H2'	1:3:491:G:C8	2.53	0.44
2:1:327:G:H2'	2:1:328:U:O4'	2.17	0.44
2:1:566:U:O4	21:r:80:ARG:HD3	2.17	0.44
2:1:757:G:C2'	2:1:758:C:H5'	2.38	0.44
2:1:1989:G:O2'	2:1:1990:C:H5'	2.18	0.44
2:1:2106:U:H2'	2:1:2107:G:O4'	2.18	0.44
5:6:69:C:H2'	5:6:70:G:H8	1.83	0.44
40:J:90:GLY:O	40:J:129:SER:OG	2.36	0.44
51:U:4:ILE:HG12	51:U:21:VAL:HG22	2.00	0.44
1:3:36:C:O2'	47:Q:113:ARG:NH1	2.51	0.44
1:3:1418:A:H2	2:1:1948:G:N2	2.16	0.44
1:3:1442:G:H1	1:3:1460:C:H42	1.66	0.44
2:1:111:A:O2'	2:1:112:U:H5'	2.17	0.44
2:1:169:G:O2'	2:1:170:U:H5'	2.18	0.44
2:1:192:C:H2'	2:1:193:U:H5'	1.99	0.44
2:1:465:G:P	33:D:12:ARG:HH12	2.41	0.44
2:1:473:G:C2'	2:1:474:G:H5'	2.48	0.44
2:1:888:C:OP1	48:R:91:ARG:HD2	2.18	0.44
2:1:1199:U:H2'	2:1:1200:C:C6	2.52	0.44
2:1:1507:C:H2'	2:1:1508:A:O4'	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:2364:C:O2'	2:1:2365:G:H5'	2.17	0.44
4:5:74:C:H3'	4:5:75:C:C6	2.53	0.44
10:f:132:LEU:HB3	10:f:140:ILE:HD11	1.99	0.44
13:j:13:ARG:NH1	13:j:49:ASP:O	2.41	0.44
32:C:13:SER:OG	32:C:47:ILE:O	2.27	0.44
39:I:85:THR:HA	39:I:88:ASN:HB2	2.00	0.44
47:Q:45:ASN:ND2	47:Q:88:ASP:OD2	2.39	0.44
49:S:44:VAL:O	49:S:48:GLN:NE2	2.50	0.44
1:3:477:C:H2'	1:3:478:A:C8	2.52	0.43
1:3:501:C:H2'	1:3:502:A:C8	2.53	0.43
1:3:521:G:O2'	47:Q:69:GLU:OE2	2.27	0.43
1:3:1513:A:H2'	1:3:1514:G:H8	1.83	0.43
2:1:12:U:O2	2:1:12:U:H2'	2.18	0.43
2:1:150:U:H2'	2:1:151:C:C6	2.52	0.43
2:1:150:U:O2'	2:1:151:C:H5'	2.18	0.43
2:1:466:A:C2'	2:1:467:G:H5'	2.46	0.43
2:1:779:U:OP2	6:b:48:ILE:HG12	2.18	0.43
2:1:1087:G:H5''	2:1:1088:A:OP2	2.18	0.43
2:1:1287:A:H5'	17:n:103:ARG:HH11	1.82	0.43
2:1:1507:C:H2'	2:1:1508:A:H4'	1.99	0.43
2:1:1717:A:C2	2:1:1718:G:H1'	2.53	0.43
2:1:1761:C:H2'	2:1:1762:A:O4'	2.18	0.43
2:1:1922:G:H2'	2:1:1923:U:O4'	2.18	0.43
2:1:2226:C:C5	2:1:2227:A:N7	2.86	0.43
12:i:129:GLU:HG3	12:i:139:VAL:HG21	2.00	0.43
38:H:51:VAL:HA	38:H:69:THR:HG22	2.00	0.43
39:I:120:LYS:HG2	39:I:130:ASN:HB3	1.99	0.43
1:3:28:A:O2'	1:3:296:U:OP1	2.33	0.43
1:3:436:C:H4'	39:I:152:SER:HB3	2.00	0.43
1:3:1119:C:OP1	44:N:84:ARG:NH2	2.48	0.43
2:1:28:A:H2'	2:1:29:U:C6	2.53	0.43
2:1:131:A:H2'	2:1:132:G:C8	2.53	0.43
2:1:336:C:O2'	2:1:337:C:H5'	2.18	0.43
2:1:1539:U:H2'	2:1:1540:G:C8	2.53	0.43
2:1:2137:U:H2'	2:1:2138:G:C8	2.50	0.43
2:1:2144:G:H1'	2:1:2147:A:N6	2.33	0.43
28:y:11:VAL:HA	28:y:14:LEU:HB2	2.00	0.43
36:4:13:A:H2'	36:4:14:A:C8	2.53	0.43
47:Q:72:ASN:OD1	47:Q:72:ASN:N	2.50	0.43
1:3:1253:G:H2'	1:3:1254:A:H8	1.83	0.43
2:1:365:U:H2'	2:1:366:C:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:451:U:H4'	8:d:47:LYS:HE2	2.00	0.43
2:1:1031:G:C2	2:1:1032:A:C4	3.05	0.43
2:1:1232:G:H2'	2:1:1233:C:C6	2.53	0.43
2:1:2411:A:H2'	2:1:2412:A:C8	2.53	0.43
15:l:95:LEU:HD22	15:l:100:ILE:HD11	2.00	0.43
37:G:122:ASP:OD2	37:G:122:ASP:N	2.51	0.43
46:P:115:ILE:HD12	46:P:116:PRO:HD2	1.99	0.43
55:Y:14:GLU:OE1	55:Y:17:ARG:NH2	2.51	0.43
2:1:388:G:N7	2:1:390:U:H2'	2.33	0.43
2:1:500:G:N2	2:1:502:A:H3'	2.32	0.43
2:1:536:G:H21	13:j:47:HIS:CG	2.37	0.43
2:1:684:G:C2	2:1:794:A:C2	3.06	0.43
2:1:928:A:H5'	29:z:38:GLU:CD	2.43	0.43
2:1:935:C:O2'	2:1:936:A:H5'	2.19	0.43
2:1:1081:U:H4'	12:i:123:ALA:HB1	2.00	0.43
2:1:1487:U:H2'	2:1:1488:C:C6	2.54	0.43
2:1:2462:C:H2'	2:1:2463:C:C6	2.53	0.43
2:1:2810:A:H5''	7:c:62:LYS:NZ	2.34	0.43
4:5:72:G:HO2'	4:5:73:A:C5'	2.30	0.43
16:m:34:LYS:N	16:m:129:THR:O	2.47	0.43
2:1:108:G:O2'	2:1:109:C:H5'	2.18	0.43
2:1:402:A:H2'	2:1:403:U:C5'	2.44	0.43
2:1:648:G:H2'	2:1:649:G:H8	1.83	0.43
2:1:819:A:H5'	2:1:973:A:N1	2.33	0.43
2:1:1060:U:O4	12:i:131:THR:HB	2.18	0.43
2:1:1426:G:C6	2:1:1427:A:C6	3.06	0.43
2:1:1747:U:H2'	2:1:1748:C:C6	2.53	0.43
2:1:1893:C:C2'	2:1:1894:C:H5'	2.47	0.43
12:i:10:LEU:HD21	12:i:27:LEU:HD21	1.99	0.43
13:j:34:ARG:NH2	13:j:39:LYS:O	2.51	0.43
26:w:12:SER:OG	26:w:13:GLU:N	2.51	0.43
37:G:26:MET:HE1	37:G:186:VAL:HB	1.99	0.43
44:N:113:LYS:HA	44:N:120:ALA:HB2	2.01	0.43
48:R:11:HIS:HA	48:R:43:LYS:HD2	2.01	0.43
48:R:89:ARG:HB2	48:R:96:VAL:HG22	2.01	0.43
52:V:44:HIS:HB3	52:V:70:LYS:HG2	1.99	0.43
2:1:68:G:H2'	2:1:69:C:O4'	2.18	0.43
2:1:350:G:H2'	2:1:351:C:O4'	2.18	0.43
2:1:481:G:H2'	2:1:482:A:OP2	2.19	0.43
2:1:541:A:H2'	2:1:542:C:O4'	2.19	0.43
2:1:690:G:O2'	2:1:691:C:H5'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:870:U:H2'	2:1:871:U:C5'	2.48	0.43
2:1:936:A:H2'	2:1:937:C:H6	1.84	0.43
2:1:1059:G:N2	12:i:127:SER:OG	2.51	0.43
2:1:1751:U:H2'	2:1:1752:C:C6	2.54	0.43
2:1:2305:U:O2'	2:1:2306:C:H5'	2.19	0.43
4:5:74:C:H2'	4:5:75:C:H5'	2.00	0.43
10:f:133:LYS:NZ	10:f:134:GLY:O	2.44	0.43
13:j:51:GLY:HA3	13:j:121:LYS:HE2	2.00	0.43
14:k:38:ILE:HG22	14:k:61:VAL:HB	2.00	0.43
44:N:30:ASN:HD21	44:N:66:VAL:H	1.66	0.43
54:X:76:THR:OG1	54:X:77:ARG:N	2.51	0.43
55:Y:67:HIS:O	55:Y:69:ASN:ND2	2.51	0.43
1:3:1098:C:OP1	37:G:142:LYS:NZ	2.49	0.43
1:3:1306:A:H61	1:3:1331:G:H1'	1.82	0.43
2:1:536:G:N2	13:j:47:HIS:CG	2.87	0.43
2:1:1010:A:H1'	2:1:1153:C:H1'	1.99	0.43
2:1:1258:U:H2'	2:1:1259:G:C8	2.54	0.43
2:1:1741:C:O2'	2:1:1742:U:H5'	2.19	0.43
2:1:2482:A:O2'	4:5:63:U:O2'	2.33	0.43
2:1:2839:G:O2'	2:1:2840:C:H5'	2.18	0.43
2:1:2880:C:H2'	2:1:2880:C:O2	2.17	0.43
23:t:40:LYS:HE3	23:t:60:THR:HG22	2.01	0.43
28:y:19:LEU:HD23	28:y:19:LEU:HA	1.86	0.43
39:I:125:ASN:HB2	39:I:127:ARG:HD3	2.01	0.43
47:Q:67:GLY:O	47:Q:98:ARG:NH1	2.52	0.43
1:3:146:G:N2	1:3:177:G:N7	2.66	0.43
1:3:958:A:N3	1:3:985:C:O2'	2.48	0.43
1:3:977:A:N6	1:3:1224:U:OP1	2.52	0.43
2:1:255:A:H2'	2:1:256:A:O4'	2.18	0.43
2:1:572:A:O5'	2:1:572:A:C8	2.72	0.43
2:1:1049:C:H2'	2:1:1050:A:H5'	2.00	0.43
2:1:1383:A:C2	2:1:1406:U:H1'	2.48	0.43
2:1:1500:G:H2'	2:1:1501:G:H8	1.83	0.43
2:1:1565:C:C5	2:1:1567:G:C6	3.06	0.43
2:1:1571:A:H2'	2:1:1572:A:C8	2.54	0.43
2:1:1864:U:O5'	2:1:1864:U:H6	2.02	0.43
2:1:2660:A:H2'	2:1:2661:G:O4'	2.18	0.43
16:m:17:ASN:OD1	16:m:97:GLN:NE2	2.51	0.43
1:3:739:C:O2'	50:T:41:HIS:ND1	2.45	0.43
1:3:1060:U:C5	38:H:1:GLY:HA2	2.54	0.43
2:1:8:C:C2	2:1:9:G:C8	3.07	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:16:C:H2'	2:1:17:G:H8	1.84	0.43
2:1:94:A:H2'	2:1:95:A:C8	2.54	0.43
2:1:778:G:H5'	6:b:47:ARG:NH1	2.33	0.43
2:1:814:C:H1'	2:1:1225:G:N2	2.34	0.43
2:1:841:G:C2'	2:1:842:U:H5'	2.49	0.43
2:1:1172:C:H2'	2:1:1173:U:O4'	2.19	0.43
2:1:1383:A:H2	2:1:1406:U:C1'	2.29	0.43
2:1:1615:C:C6	22:s:87:PRO:HG3	2.54	0.43
2:1:1779:U:O2	2:1:1783:A:C6	2.72	0.43
2:1:1964:G:H4'	2:1:1965:C:OP2	2.19	0.43
2:1:2221:G:HO2'	2:1:2222:C:H5'	1.80	0.43
2:1:2736:A:O2'	2:1:2737:G:H5'	2.19	0.43
2:1:2870:C:H5''	17:n:65:LEU:HD11	2.00	0.43
8:d:127:GLU:O	8:d:156:ASN:ND2	2.51	0.43
21:r:62:GLU:HG3	21:r:97:LYS:HB3	2.01	0.43
38:H:76:ILE:HB	38:H:80:GLY:HA2	2.00	0.43
44:N:98:ARG:HG2	44:N:103:VAL:HG21	2.01	0.43
47:Q:18:SER:OG	47:Q:20:VAL:N	2.52	0.43
53:W:33:THR:HG22	53:W:37:LYS:H	1.83	0.43
1:3:297:G:N2	1:3:300:A:OP2	2.39	0.43
1:3:1028:C:N3	1:3:1033:G:O6	2.51	0.43
2:1:467:G:O2'	2:1:468:G:H5'	2.19	0.43
2:1:532:A:H2'	2:1:532:A:N3	2.34	0.43
2:1:629:G:H2'	2:1:630:G:O4'	2.19	0.43
2:1:673:C:O2'	2:1:674:G:H5'	2.19	0.43
2:1:760:G:C2'	2:1:761:A:H5'	2.49	0.43
2:1:1155:A:H5''	20:q:54:ARG:HD3	2.01	0.43
2:1:1187:G:OP1	21:r:85:LYS:NZ	2.50	0.43
2:1:1230:A:H2'	2:1:1231:U:O4'	2.19	0.43
2:1:1381:G:C2'	2:1:1382:G:H5'	2.49	0.43
2:1:1433:A:H2'	2:1:1434:A:C1'	2.49	0.43
2:1:1993:U:O2	2:1:1993:U:H2'	2.18	0.43
2:1:2152:G:N3	2:1:2152:G:H2'	2.33	0.43
2:1:2371:G:O2'	2:1:2372:U:H5'	2.19	0.43
6:b:140:VAL:HG12	6:b:191:LEU:HD23	2.01	0.43
11:g:1:MET:HE3	11:g:1:MET:HB3	1.77	0.43
19:p:88:ARG:HH11	19:p:114:ASN:HD21	1.66	0.43
43:M:52:GLY:HA3	43:M:56:PRO:HA	2.01	0.43
56:Z:23:GLU:HG3	56:Z:27:VAL:HG11	2.01	0.43
1:3:490:C:H2'	1:3:491:G:H8	1.84	0.42
2:1:712:G:C2'	2:1:713:G:H5'	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:871:U:H2'	2:1:872:U:C6	2.54	0.42
2:1:993:G:O2'	2:1:994:C:H5'	2.19	0.42
2:1:1024:G:H21	2:1:1144:A:C4'	2.32	0.42
2:1:1092:C:H2'	2:1:1093:G:O4'	2.18	0.42
2:1:1505:A:O2'	2:1:1506:U:H5'	2.19	0.42
2:1:2701:U:H3'	2:1:2702:G:H5''	2.01	0.42
7:c:90:PHE:HD1	7:c:94:GLN:HG2	1.83	0.42
14:k:17:ARG:HD3	14:k:47:ILE:HD11	2.01	0.42
47:Q:50:LYS:HE2	47:Q:70:GLY:HA2	2.01	0.42
2:1:281:C:H2'	2:1:282:A:C8	2.54	0.42
2:1:518:G:O2'	2:1:519:U:H5'	2.18	0.42
2:1:892:A:O2'	2:1:893:C:H5'	2.20	0.42
2:1:1054:A:H2'	2:1:1055:G:C8	2.54	0.42
2:1:1306:C:N4	2:1:1606:C:H2'	2.34	0.42
2:1:1520:U:C2'	2:1:1521:G:H5'	2.49	0.42
2:1:1936:A:N6	2:1:1963:U:H3	2.17	0.42
2:1:2095:A:OP1	11:g:11:ASN:ND2	2.53	0.42
2:1:2584:U:O5'	2:1:2584:U:H6	2.02	0.42
2:1:2834:G:C2'	2:1:2835:A:H5'	2.49	0.42
3:2:98:G:H1	25:v:14:LYS:HB2	1.84	0.42
21:r:51:VAL:HG22	21:r:52:PRO:HD2	2.01	0.42
1:3:322:C:O2	1:3:332:G:N2	2.52	0.42
2:1:439:A:H2'	2:1:440:C:O4'	2.19	0.42
2:1:528:A:C2	2:1:2043:C:H4'	2.53	0.42
2:1:745:G:O2'	2:1:748:G:H1'	2.19	0.42
2:1:759:G:H1'	2:1:1981:A:C2	2.55	0.42
2:1:809:G:C6	2:1:810:U:C4	3.08	0.42
2:1:864:G:C2'	2:1:865:C:H5'	2.48	0.42
2:1:1246:A:H2'	2:1:1247:A:O4'	2.19	0.42
2:1:1901:A:C2	2:1:1902:C:C5	3.08	0.42
2:1:1907:G:C5	2:1:1908:C:C4	3.07	0.42
2:1:2073:C:C2'	2:1:2074:U:H5'	2.49	0.42
2:1:2200:C:OP2	27:x:36:ARG:NH2	2.52	0.42
2:1:2671:G:C2	2:1:2672:U:C2	3.06	0.42
6:b:58:LYS:HB2	6:b:58:LYS:HE3	1.87	0.42
9:e:137:PHE:HA	9:e:138:PRO:HD3	1.91	0.42
24:u:8:ASP:OD2	24:u:93:ARG:NH1	2.52	0.42
38:H:37:LYS:HA	38:H:37:LYS:HD3	1.81	0.42
38:H:61:LYS:HE2	38:H:96:VAL:HG12	2.01	0.42
39:I:119:HIS:O	39:I:145:ARG:NH2	2.52	0.42
42:L:137:ARG:NH1	42:L:138:GLU:OE2	2.48	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:535:G:O2'	2:1:536:G:H5'	2.20	0.42
2:1:563:A:H1'	2:1:2018:G:H22	1.83	0.42
2:1:1173:U:H5	2:1:1174:U:H1'	1.81	0.42
2:1:1327:A:H2'	2:1:1328:A:H5'	2.01	0.42
2:1:2056:G:O2'	31:B:4:GLN:NE2	2.52	0.42
2:1:2102:G:H1	2:1:2187:U:H3	1.66	0.42
2:1:2406:A:N3	15:l:69:ARG:CZ	2.82	0.42
10:f:175:LYS:HD3	10:f:175:LYS:HA	1.70	0.42
15:l:108:ALA:HB3	15:l:125:LEU:HG	2.01	0.42
34:E:30:HIS:HD2	34:E:31:ILE:HG12	1.83	0.42
43:M:24:VAL:HG23	43:M:60:LEU:HB2	2.00	0.42
1:3:503:C:OP1	47:Q:115:LYS:NZ	2.40	0.42
1:3:1209:C:O2'	1:3:1214:C:N4	2.52	0.42
2:1:90:U:H2'	2:1:91:A:C8	2.55	0.42
2:1:837:C:O5'	2:1:837:C:H6	2.02	0.42
2:1:908:C:O2'	2:1:909:A:H5'	2.19	0.42
2:1:918:A:H2'	2:1:919:U:O4'	2.19	0.42
2:1:1154:G:OP2	20:q:57:ARG:NH1	2.52	0.42
2:1:1306:C:H41	2:1:1606:C:H2'	1.84	0.42
2:1:1316:U:O2'	2:1:1317:G:H5'	2.20	0.42
2:1:1746:A:H2'	2:1:1747:U:H6	1.82	0.42
2:1:1799:G:N2	6:b:153:LEU:HD23	2.33	0.42
2:1:1917:U:H2'	2:1:1918:A:H5'	2.01	0.42
2:1:2098:U:C2'	2:1:2099:U:H5'	2.49	0.42
2:1:2287:A:C4	2:1:2289:G:N7	2.88	0.42
2:1:2466:C:C2	2:1:2485:G:C2	3.07	0.42
37:G:67:LEU:HD21	37:G:91:VAL:HG23	2.00	0.42
39:I:101:VAL:HG22	39:I:106:PHE:HB2	2.01	0.42
1:3:35:G:O2'	47:Q:114:SER:O	2.30	0.42
1:3:310:G:H5''	51:U:31:ARG:HB2	2.01	0.42
1:3:422:C:H4'	1:3:423:G:C2	2.54	0.42
1:3:842:U:H3'	1:3:843:U:H4'	2.01	0.42
1:3:1348:U:H2'	1:3:1349:A:H8	1.84	0.42
1:3:1513:A:H2'	1:3:1514:G:C8	2.55	0.42
2:1:452:G:H8	8:d:53:THR:HB	1.85	0.42
2:1:598:U:H2'	2:1:599:A:C8	2.54	0.42
2:1:644:A:C3'	2:1:645:C:H5''	2.49	0.42
2:1:704:G:O2'	2:1:726:G:N2	2.52	0.42
2:1:729:G:C5	6:b:206:LYS:HB2	2.54	0.42
2:1:783:A:C8	2:1:783:A:H3'	2.54	0.42
2:1:1095:A:N1	12:i:25:PRO:HG3	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:1336:A:H2'	2:1:1337:G:H8	1.85	0.42
2:1:2562:U:C2'	2:1:2563:U:H5'	2.49	0.42
6:b:244:VAL:HG12	6:b:250:GLN:HA	2.01	0.42
27:x:51:SER:OG	27:x:54:GLY:N	2.48	0.42
39:I:97:LEU:O	39:I:101:VAL:N	2.38	0.42
39:I:98:ASP:HA	39:I:101:VAL:HG12	2.01	0.42
48:R:28:ARG:HH21	48:R:62:PHE:HB2	1.84	0.42
50:T:13:GLU:HG2	50:T:83:ARG:HH21	1.85	0.42
52:V:11:VAL:HG23	52:V:55:GLY:H	1.85	0.42
2:1:636:G:N7	15:l:109:LYS:HE2	2.34	0.42
2:1:937:C:H2'	2:1:938:G:H8	1.83	0.42
2:1:1042:G:H2'	2:1:1043:C:H6	1.85	0.42
2:1:1275:A:C2	17:n:16:HIS:CD2	3.07	0.42
2:1:1739:A:H2'	2:1:1740:G:O4'	2.18	0.42
2:1:1810:A:H2'	2:1:1811:G:O4'	2.19	0.42
2:1:2628:C:H3'	2:1:2629:U:H5'	2.01	0.42
2:1:2658:C:H5''	10:f:157:LYS:HD3	2.02	0.42
2:1:2741:A:H2'	2:1:2742:G:C5'	2.50	0.42
2:1:2870:C:H2'	2:1:2871:U:H5'	2.01	0.42
4:5:71:C:C2'	4:5:72:G:H5'	2.48	0.42
9:e:77:LYS:HE2	9:e:77:LYS:HB2	1.90	0.42
19:p:88:ARG:H	19:p:88:ARG:HG2	1.62	0.42
31:B:27:LEU:HD23	31:B:27:LEU:HA	1.84	0.42
32:C:52:LYS:HE2	32:C:52:LYS:HB2	1.89	0.42
47:Q:3:VAL:HA	47:Q:6:LEU:HD12	2.00	0.42
54:X:51:HIS:HB2	54:X:56:HIS:CE1	2.55	0.42
1:3:1314:C:OP1	54:X:6:LYS:NZ	2.52	0.42
2:1:518:G:H2'	2:1:519:U:C6	2.55	0.42
2:1:1048:A:C2'	2:1:1049:C:H5'	2.49	0.42
2:1:1452:G:C2'	2:1:1453:A:OP2	2.68	0.42
2:1:2060:A:O2'	2:1:2061:G:OP2	2.35	0.42
2:1:2070:A:C2	2:1:2442:C:C2	3.07	0.42
2:1:2248:C:C2'	2:1:2249:U:H5'	2.49	0.42
14:k:7:MET:HE2	14:k:18:ARG:HD3	2.01	0.42
23:t:66:LYS:HB3	23:t:66:LYS:HE2	1.70	0.42
38:H:110:LEU:HD21	38:H:143:LEU:HB3	2.02	0.42
39:I:30:LYS:HD3	39:I:30:LYS:HA	1.81	0.42
40:J:110:MET:HA	40:J:113:VAL:HG12	2.01	0.42
49:S:5:MET:HE3	49:S:5:MET:HB3	1.85	0.42
1:3:246:A:N1	1:3:278:G:O2'	2.50	0.42
1:3:1243:C:H2'	1:3:1244:G:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:3:1320:C:N4	54:X:36:ARG:HB3	2.34	0.42
2:1:191:A:C2	2:1:192:C:C4	3.08	0.42
2:1:191:A:C6	2:1:192:C:N4	2.88	0.42
2:1:309:A:N3	2:1:329:G:O2'	2.53	0.42
2:1:595:C:H2'	2:1:596:U:C6	2.54	0.42
2:1:849:A:H2'	2:1:850:U:C5	2.54	0.42
2:1:1181:U:H2'	2:1:1182:G:H8	1.81	0.42
2:1:1314:C:H42	2:1:1338:G:H1	1.68	0.42
2:1:2643:G:C2'	2:1:2644:G:H5'	2.49	0.42
2:1:2812:G:O2'	2:1:2813:A:H5'	2.19	0.42
6:b:131:MET:HG2	6:b:134:ILE:HD12	2.01	0.42
18:o:16:ARG:HD3	18:o:16:ARG:HA	1.84	0.42
22:s:70:LYS:N	22:s:108:SER:O	2.45	0.42
43:M:42:GLU:HG2	43:M:100:ILE:HG21	2.02	0.42
45:O:57:VAL:HG22	45:O:58:ASN:H	1.85	0.42
46:P:30:ILE:HG23	46:P:45:THR:HB	2.02	0.42
55:Y:49:ALA:HA	55:Y:52:GLU:HG3	2.00	0.42
1:3:202:G:H2'	1:3:203:G:C8	2.55	0.42
1:3:409:U:H4'	39:I:24:VAL:HG22	2.02	0.42
1:3:842:U:H5''	1:3:846:G:C6	2.55	0.42
1:3:1382:C:H2'	1:3:1383:C:H6	1.84	0.42
2:1:510:C:H2'	2:1:511:U:H6	1.85	0.42
2:1:675:A:C5	2:1:804:A:C2	3.08	0.42
2:1:688:U:O5'	2:1:688:U:H6	2.03	0.42
2:1:1034:G:C6	2:1:1035:U:N3	2.88	0.42
2:1:1213:A:C1'	2:1:1237:A:C2	3.03	0.42
2:1:1335:C:H2'	2:1:1336:A:H8	1.84	0.42
2:1:2160:C:H2'	2:1:2161:C:O4'	2.20	0.42
2:1:2194:U:H2'	2:1:2195:U:H6	1.84	0.42
2:1:2437:G:O4'	2:1:2598:A:C2	2.73	0.42
2:1:2852:G:H2'	2:1:2853:C:O4'	2.20	0.42
4:5:74:C:H2'	4:5:75:C:C5'	2.50	0.42
6:b:20:ASN:HB3	6:b:23:LEU:HD13	2.01	0.42
10:f:84:LYS:HA	10:f:84:LYS:HD2	1.87	0.42
17:n:10:LEU:HA	17:n:10:LEU:HD23	1.83	0.42
22:s:9:HIS:H	22:s:102:HIS:CE1	2.38	0.42
48:R:32:ILE:HG23	48:R:58:GLU:HB3	2.02	0.42
1:3:73:C:H2'	1:3:74:A:C8	2.55	0.41
1:3:1305:G:N2	1:3:1331:G:H2'	2.34	0.41
1:3:1531:A:C2'	1:3:1532:U:H5'	2.49	0.41
2:1:115:C:O2'	2:1:116:C:H5'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:518:G:C2	2:1:519:U:C2	3.08	0.41
2:1:552:U:O2'	2:1:553:G:H5'	2.20	0.41
2:1:955:U:H2'	2:1:956:G:H5'	2.02	0.41
2:1:1467:U:C4	2:1:1468:U:C4	3.08	0.41
2:1:1488:C:H2'	2:1:1489:C:H6	1.84	0.41
2:1:1567:G:H5'	6:b:57:HIS:ND1	2.35	0.41
2:1:1721:G:H1'	2:1:1739:A:N6	2.35	0.41
2:1:1812:U:H6	2:1:1812:U:H5''	1.85	0.41
2:1:1930:G:O2'	2:1:1931:U:OP2	2.33	0.41
2:1:2092:U:OP2	11:g:28:ASN:ND2	2.36	0.41
2:1:2612:C:O5'	2:1:2612:C:H6	2.03	0.41
2:1:2741:A:N6	2:1:2742:G:C2	2.88	0.41
12:i:109:ALA:O	12:i:113:ALA:N	2.52	0.41
51:U:68:SER:OG	51:U:69:ASP:N	2.53	0.41
56:Z:23:GLU:HB2	56:Z:27:VAL:HB	2.02	0.41
1:3:84:U:O2	1:3:87:C:O2'	2.34	0.41
1:3:405:U:O4	39:I:1:ALA:N	2.45	0.41
1:3:497:G:H2'	1:3:498:A:C8	2.55	0.41
1:3:987:G:H2'	1:3:988:G:H8	1.84	0.41
1:3:1032:G:C2	1:3:1033:G:OP1	2.70	0.41
2:1:170:U:H2'	2:1:171:U:C6	2.55	0.41
2:1:431:U:O5'	2:1:431:U:H6	2.03	0.41
2:1:623:C:H2'	2:1:624:C:H6	1.85	0.41
2:1:638:G:H2'	2:1:639:U:C6	2.55	0.41
2:1:1176:U:H2'	2:1:1177:G:N9	2.35	0.41
2:1:1719:G:O2'	2:1:1720:U:H5'	2.20	0.41
2:1:1914:C:O2	2:1:1914:C:O4'	2.37	0.41
2:1:1931:U:C5	2:1:1968:G:N2	2.88	0.41
2:1:2600:A:H8	2:1:2600:A:O5'	2.03	0.41
6:b:70:LYS:HD2	6:b:73:ILE:HD12	2.02	0.41
41:K:40:GLU:HB3	41:K:61:LEU:HB3	2.02	0.41
42:L:125:ASP:HB2	42:L:130:LYS:HG3	2.03	0.41
1:3:227:G:O2'	51:U:63:GLN:OE1	2.36	0.41
1:3:460:A:H2'	1:3:461:A:C8	2.54	0.41
1:3:680:C:H2'	1:3:681:A:H8	1.84	0.41
1:3:1124:G:H1	1:3:1149:C:H42	1.68	0.41
2:1:112:U:H2'	2:1:113:U:C5'	2.48	0.41
2:1:284:U:H2'	2:1:285:G:C8	2.55	0.41
2:1:1601:G:H2'	2:1:1602:U:H5'	2.01	0.41
2:1:1710:G:H2'	2:1:1711:A:H8	1.85	0.41
2:1:1750:G:H2'	2:1:1751:U:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:2411:A:O2'	2:1:2412:A:H5'	2.20	0.41
2:1:2467:C:O2	16:m:123:LYS:HE2	2.20	0.41
2:1:2697:G:C2	2:1:2711:A:C2	3.08	0.41
2:1:2743:U:H2'	2:1:2744:G:C4'	2.50	0.41
13:j:112:GLY:O	13:j:116:ARG:N	2.47	0.41
52:V:24:ILE:HG23	52:V:41:THR:HB	2.03	0.41
1:3:1028:C:N3	1:3:1033:G:C6	2.88	0.41
2:1:259:G:O2'	2:1:260:G:H5'	2.20	0.41
2:1:568:U:O4	21:r:81:LYS:NZ	2.54	0.41
2:1:630:G:N2	2:1:634:C:C4	2.88	0.41
2:1:722:A:H2'	2:1:723:C:C6	2.56	0.41
2:1:1063:G:N2	2:1:1075:C:H41	2.18	0.41
2:1:1107:G:H2'	2:1:1108:U:O4'	2.20	0.41
2:1:1614:A:C8	2:1:1614:A:O5'	2.73	0.41
2:1:1642:G:H2'	2:1:1643:G:O4'	2.20	0.41
2:1:1868:C:H2'	2:1:1869:G:H8	1.86	0.41
2:1:2123:G:H2'	2:1:2124:G:C8	2.55	0.41
2:1:2583:G:H8	2:1:2583:G:O5'	2.03	0.41
6:b:97:ASP:OD1	6:b:97:ASP:N	2.44	0.41
7:c:136:ASN:ND2	7:c:139:SER:O	2.52	0.41
12:i:2:LYS:HD3	12:i:2:LYS:HA	1.89	0.41
18:o:24:THR:HB	18:o:42:PRO:HG3	2.02	0.41
39:I:53:GLN:HA	39:I:198:LEU:HD12	2.01	0.41
42:L:68:VAL:HG23	42:L:99:ALA:HB1	2.02	0.41
51:U:46:LYS:HE3	51:U:46:LYS:HB2	1.85	0.41
1:3:148:G:H1'	1:3:1447:A:H1'	2.02	0.41
2:1:127:A:H5''	2:1:128:C:O4'	2.21	0.41
2:1:196:A:H2'	2:1:196:A:N3	2.35	0.41
2:1:244:A:H2'	2:1:245:G:O4'	2.20	0.41
2:1:555:G:HO2'	2:1:556:A:H8	1.68	0.41
2:1:573:U:O2'	2:1:574:A:H3'	2.20	0.41
2:1:706:A:H2'	2:1:707:G:C5'	2.51	0.41
2:1:1070:A:H5'	2:1:1072:C:OP1	2.20	0.41
2:1:1077:A:H3'	2:1:1078:U:H4'	2.02	0.41
2:1:1197:G:C2'	2:1:1198:U:H5'	2.50	0.41
2:1:1204:A:H4'	2:1:1205:A:H5''	2.02	0.41
2:1:1482:G:H2'	2:1:1483:G:H8	1.85	0.41
2:1:1589:U:H2'	2:1:1590:A:C8	2.55	0.41
2:1:1808:A:H3'	2:1:1809:A:C8	2.55	0.41
2:1:1886:U:O2'	2:1:1887:C:H5'	2.20	0.41
2:1:2335:A:N7	2:1:2337:G:C5	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:5:2:G:O2'	4:5:3:G:O5'	2.38	0.41
4:5:67:U:H2'	4:5:68:C:C6	2.55	0.41
19:p:63:ILE:HA	19:p:68:GLY:HA2	2.01	0.41
38:H:106:ARG:HG2	38:H:107:LYS:HG3	2.01	0.41
1:3:146:G:H2'	1:3:147:G:C8	2.56	0.41
1:3:944:G:N1	1:3:1338:G:OP2	2.34	0.41
1:3:1013:G:N2	1:3:1016:A:OP2	2.35	0.41
2:1:49:A:P	2:1:51:G:H5'	2.60	0.41
2:1:79:C:O2	2:1:346:A:H2	2.03	0.41
2:1:686:U:H4'	33:D:11:LYS:NZ	2.36	0.41
2:1:724:U:C4	2:1:725:G:C6	3.08	0.41
2:1:724:U:H2'	2:1:725:G:O4'	2.21	0.41
2:1:1020:A:H5'	2:1:1021:A:N7	2.35	0.41
2:1:1020:A:O5'	2:1:1020:A:H8	2.02	0.41
2:1:1045:C:H1'	2:1:1047:G:C2	2.56	0.41
2:1:1317:G:H2'	2:1:1318:U:C6	2.56	0.41
2:1:1727:C:O2'	2:1:1728:C:H5'	2.20	0.41
2:1:1822:C:H2'	2:1:1823:G:H8	1.85	0.41
2:1:1991:U:H2'	2:1:1992:G:H5'	2.02	0.41
2:1:2271:G:OP1	26:w:14:ALA:HB1	2.19	0.41
2:1:2469:A:H4'	16:m:55:ARG:HE	1.85	0.41
2:1:2751:G:H4'	10:f:3:VAL:HG13	2.02	0.41
16:m:96:ILE:HD13	16:m:96:ILE:HA	1.82	0.41
41:K:47:LEU:HG	41:K:56:LYS:HA	2.01	0.41
52:V:7:LEU:N	52:V:59:GLU:OE2	2.53	0.41
2:1:256:A:C2'	2:1:257:C:H5'	2.50	0.41
2:1:422:A:H2'	2:1:423:A:O4'	2.20	0.41
2:1:1418:G:H1'	2:1:1581:G:N2	2.36	0.41
2:1:1591:A:H2'	2:1:1592:C:C6	2.56	0.41
2:1:2049:G:O2'	2:1:2050:C:H5'	2.21	0.41
2:1:2326:C:H42	2:1:2389:G:H1	1.69	0.41
2:1:2392:A:OP2	34:E:30:HIS:CE1	2.74	0.41
2:1:2848:G:C2	2:1:2867:G:C4	3.08	0.41
29:z:57:GLU:OE1	29:z:57:GLU:N	2.53	0.41
2:1:4:U:O2'	2:1:5:A:H5'	2.20	0.41
2:1:137:U:H3	2:1:142:A:H61	1.69	0.41
2:1:359:G:H2'	2:1:360:U:C5'	2.51	0.41
2:1:397:U:O5'	2:1:397:U:H6	2.03	0.41
2:1:510:C:OP1	2:1:510:C:H3'	2.20	0.41
2:1:597:G:H2'	2:1:598:U:H6	1.85	0.41
2:1:724:U:H2'	2:1:725:G:C8	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:989:G:P	29:z:31:ILE:HD11	2.61	0.41
2:1:1048:A:N6	2:1:1111:A:C8	2.89	0.41
2:1:1063:G:O2'	12:i:89:SER:HB3	2.20	0.41
2:1:1782:U:C2'	2:1:1783:A:H5''	2.51	0.41
2:1:2379:G:H2'	2:1:2380:C:C6	2.56	0.41
2:1:2467:C:N4	2:1:2468:A:C6	2.89	0.41
2:1:2469:A:C2	2:1:2482:A:H1'	2.55	0.41
2:1:2830:C:H5''	7:c:56:LYS:HZ1	1.86	0.41
8:d:106:LYS:HG3	8:d:200:LEU:HD13	2.01	0.41
21:r:24:LYS:HE2	21:r:24:LYS:HB3	1.89	0.41
25:v:58:SER:OG	25:v:59:GLU:OE1	2.36	0.41
27:x:38:TRP:NE1	27:x:40:GLU:OE1	2.41	0.41
38:H:156:LEU:H	38:H:156:LEU:HG	1.65	0.41
39:I:101:VAL:HG13	39:I:113:ALA:HB1	2.03	0.41
43:M:60:LEU:HD23	43:M:60:LEU:HA	1.94	0.41
47:Q:98:ARG:HA	47:Q:103:CYS:HB2	2.02	0.41
48:R:7:ASN:CG	48:R:9:PRO:HD2	2.46	0.41
53:W:24:ASP:OD1	53:W:24:ASP:N	2.53	0.41
56:Z:39:LYS:HA	56:Z:42:THR:HB	2.02	0.41
1:3:107:G:O6	55:Y:9:ARG:NH1	2.53	0.41
1:3:146:G:H2'	1:3:147:G:H8	1.86	0.41
1:3:440:C:H2'	1:3:441:A:H8	1.85	0.41
1:3:464:U:N3	1:3:467:U:OP2	2.42	0.41
2:1:56:A:H1'	2:1:127:A:C2	2.55	0.41
2:1:679:C:H2'	2:1:680:C:C6	2.56	0.41
2:1:720:U:H2'	2:1:721:A:H8	1.82	0.41
2:1:723:C:H2'	2:1:724:U:O4'	2.21	0.41
2:1:924:G:O2'	2:1:925:A:H5'	2.21	0.41
2:1:970:U:H2'	2:1:971:G:C8	2.56	0.41
2:1:1092:C:O2'	2:1:1093:G:H5'	2.21	0.41
2:1:1160:G:C6	2:1:1161:C:C4	3.09	0.41
2:1:1165:A:O2'	2:1:1166:G:H5'	2.21	0.41
2:1:1283:G:N2	2:1:1285:A:H3'	2.35	0.41
2:1:1343:G:N3	2:1:1343:G:H2'	2.35	0.41
2:1:1412:U:H2'	2:1:1413:A:C8	2.56	0.41
2:1:1430:G:H2'	2:1:1431:A:O4'	2.21	0.41
2:1:1594:U:O2'	2:1:1595:C:H5'	2.20	0.41
2:1:1930:G:O2'	2:1:1931:U:P	2.79	0.41
2:1:2061:G:H2'	2:1:2501:C:O2'	2.21	0.41
2:1:2098:U:H2'	2:1:2099:U:C5'	2.51	0.41
2:1:2193:G:H2'	2:1:2194:U:H6	1.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:2502:G:H5''	2:1:2503:A:H5''	2.03	0.41
2:1:2507:C:C2	2:1:2583:G:N2	2.89	0.41
2:1:2649:C:N3	2:1:2650:U:C4	2.89	0.41
6:b:209:ALA:HA	6:b:212:TRP:CE2	2.55	0.41
7:c:4:LEU:HD21	7:c:98:VAL:HA	2.02	0.41
13:j:17:VAL:HG13	13:j:137:PRO:HB2	2.03	0.41
13:j:138:GLN:H	13:j:138:GLN:HG2	1.63	0.41
21:r:4:VAL:HG23	21:r:39:LEU:HB2	2.03	0.41
37:G:190:SER:OG	37:G:191:ASP:N	2.53	0.41
38:H:19:SER:HB2	38:H:39:ARG:HH21	1.85	0.41
44:N:16:ALA:HA	44:N:66:VAL:HA	2.03	0.41
45:O:14:ASP:HB2	45:O:17:LEU:HB3	2.02	0.41
48:R:26:LYS:O	48:R:30:LYS:NZ	2.54	0.41
49:S:73:LEU:HD23	49:S:73:LEU:HA	1.96	0.41
53:W:25:ILE:HA	53:W:28:LEU:HB2	2.03	0.41
1:3:987:G:H2'	1:3:988:G:C8	2.56	0.41
2:1:18:U:O2'	2:1:19:A:H5'	2.21	0.41
2:1:1333:G:C2'	2:1:1334:G:H5'	2.51	0.41
2:1:1430:G:O2'	2:1:1431:A:H5'	2.21	0.41
2:1:1553:A:O2'	2:1:1554:U:H5	2.02	0.41
2:1:1600:C:H2'	2:1:1601:G:C8	2.55	0.41
2:1:1827:U:O2'	2:1:1828:G:H5'	2.21	0.41
2:1:2575:C:H2'	2:1:2578:G:O6	2.21	0.41
2:1:2648:G:O2'	2:1:2649:C:H5'	2.21	0.41
2:1:2660:A:H2'	2:1:2661:G:C8	2.56	0.41
2:1:2773:C:H4'	7:c:169:ARG:O	2.21	0.41
4:5:2:G:O6	4:5:72:G:O6	2.39	0.41
14:k:110:GLU:H	14:k:113:MET:HE3	1.86	0.41
23:t:8:LEU:H	23:t:8:LEU:HG	1.67	0.41
37:G:161:PHE:HA	37:G:183:PHE:HB2	2.02	0.41
39:I:87:GLU:N	39:I:87:GLU:OE2	2.53	0.41
43:M:91:LEU:HD23	43:M:91:LEU:HA	1.90	0.41
1:3:31:G:N2	1:3:48:C:OP1	2.41	0.40
2:1:211:C:O2'	2:1:212:G:H5'	2.21	0.40
2:1:224:U:O4	2:1:420:C:H5'	2.21	0.40
2:1:674:G:H3'	2:1:674:G:C8	2.56	0.40
2:1:890:C:H2'	2:1:891:G:C5'	2.39	0.40
2:1:903:C:H2'	2:1:904:G:H8	1.86	0.40
2:1:1420:A:C2	2:1:2211:A:N1	2.90	0.40
2:1:1715:G:O2'	2:1:1716:U:C6	2.75	0.40
2:1:1722:A:H2'	2:1:1723:G:O4'	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:1767:G:N2	2:1:1986:C:C2	2.89	0.40
2:1:1944:U:H3'	2:1:1945:G:H5'	2.03	0.40
2:1:2105:U:C2	2:1:2184:A:H2	2.39	0.40
2:1:2292:U:H2'	2:1:2293:G:C8	2.55	0.40
2:1:2403:C:HO2'	2:1:2404:U:H5'	1.86	0.40
2:1:2709:G:H5'	17:n:22:ARG:HH22	1.86	0.40
2:1:2788:C:H2'	2:1:2789:C:C6	2.56	0.40
9:e:64:PRO:HA	9:e:88:VAL:HG22	2.03	0.40
23:t:28:ASN:HD21	23:t:91:GLN:HB3	1.85	0.40
39:I:146:GLU:HA	39:I:149:LYS:HZ3	1.86	0.40
55:Y:4:LYS:HA	55:Y:4:LYS:HD3	1.86	0.40
1:3:370:C:H2'	1:3:371:A:H8	1.86	0.40
1:3:1005:A:OP2	1:3:1024:G:N2	2.48	0.40
2:1:128:C:H2'	2:1:129:C:C6	2.53	0.40
2:1:265:A:C8	2:1:428:A:C2	3.09	0.40
2:1:1152:C:H2'	2:1:1153:C:C6	2.55	0.40
2:1:1239:G:H2'	2:1:1240:U:O4'	2.21	0.40
2:1:1410:G:H2'	2:1:1411:U:H6	1.85	0.40
2:1:1469:A:H2'	2:1:1470:A:H8	1.83	0.40
2:1:2020:A:H62	31:B:5:ASN:ND2	2.19	0.40
2:1:2221:G:H2'	2:1:2222:C:C6	2.56	0.40
2:1:2224:G:H4'	2:1:2226:C:N3	2.35	0.40
2:1:2646:C:H2'	2:1:2647:U:O4'	2.21	0.40
2:1:2828:G:N1	2:1:2829:A:C5	2.90	0.40
8:d:145:ASP:HA	8:d:166:LYS:HB3	2.02	0.40
17:n:114:GLU:OE1	17:n:118:ARG:NH1	2.50	0.40
18:o:8:ILE:O	18:o:12:THR:OG1	2.33	0.40
45:O:12:ALA:HB2	45:O:96:VAL:HG13	2.03	0.40
1:3:363:A:H5'	47:Q:30:ARG:HG3	2.02	0.40
1:3:1405:G:H21	1:3:1518:A:H8	1.68	0.40
2:1:85:G:OP1	24:u:6:ARG:N	2.52	0.40
2:1:543:G:C3'	2:1:544:C:H5''	2.51	0.40
2:1:914:G:H5'	2:1:915:C:OP2	2.21	0.40
2:1:1080:A:H4'	12:i:126:ARG:CD	2.52	0.40
2:1:1087:G:H22	2:1:1103:A:H1'	1.76	0.40
2:1:1302:A:H5'	2:1:1608:A:OP1	2.21	0.40
2:1:1328:A:H2'	2:1:1330:C:C4	2.56	0.40
2:1:1776:G:H8	2:1:1776:G:O5'	2.05	0.40
2:1:1788:C:C2'	2:1:1789:A:H5'	2.52	0.40
2:1:2293:G:O2'	2:1:2294:G:H5'	2.21	0.40
2:1:2527:C:H5''	35:F:31:PRO:HB2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:2568:U:H6	2:1:2568:U:O5'	2.04	0.40
2:1:2713:U:C3'	2:1:2714:G:H5'	2.27	0.40
4:5:75:C:H6	4:5:75:C:P	2.45	0.40
7:c:133:THR:OG1	7:c:134:HIS:N	2.54	0.40
7:c:187:LEU:HD12	7:c:187:LEU:HA	1.94	0.40
8:d:138:LEU:HG	8:d:143:LEU:HD12	2.03	0.40
9:e:39:VAL:HG12	9:e:85:GLY:HA2	2.03	0.40
9:e:49:LEU:HD22	9:e:83:PRO:HB2	2.04	0.40
10:f:151:ARG:HD3	10:f:151:ARG:HA	1.88	0.40
17:n:82:GLU:O	17:n:86:ARG:N	2.47	0.40
22:s:29:VAL:HG21	22:s:55:ILE:HG21	2.03	0.40
25:v:70:ILE:HG22	25:v:72:VAL:HG22	2.03	0.40
41:K:22:ILE:H	41:K:22:ILE:HG13	1.70	0.40
45:O:46:LYS:HB2	45:O:46:LYS:HE3	1.88	0.40
54:X:27:LYS:HE2	54:X:27:LYS:HB3	1.77	0.40
1:3:195:A:H2'	1:3:196:A:C8	2.57	0.40
1:3:564:C:P	47:Q:11:ARG:HH21	2.45	0.40
2:1:164:C:H2'	2:1:165:A:O4'	2.21	0.40
2:1:367:G:H2'	2:1:368:A:C8	2.57	0.40
2:1:622:G:HO2'	2:1:623:C:H5'	1.84	0.40
2:1:934:U:H2'	2:1:935:C:C6	2.56	0.40
2:1:1083:U:C2'	2:1:1084:A:H3'	2.51	0.40
2:1:1160:G:C2	2:1:1161:C:C2	3.10	0.40
2:1:1910:G:H1	2:1:1920:C:N4	2.20	0.40
2:1:2038:G:H2'	2:1:2039:U:O4'	2.21	0.40
2:1:2106:U:H3'	2:1:2107:G:H8	1.86	0.40
2:1:2529:G:H8	2:1:2529:G:O5'	2.05	0.40
7:c:122:VAL:HG11	7:c:141:ARG:HH21	1.86	0.40
13:j:32:LEU:HD22	13:j:54:ILE:HG21	2.04	0.40
38:H:134:LYS:HB3	38:H:134:LYS:HE2	1.84	0.40
39:I:123:MET:HB2	39:I:143:SER:HB3	2.04	0.40
46:P:99:LEU:HA	46:P:102:ALA:HB3	2.03	0.40
48:R:10:ASP:HB3	48:R:45:SER:HB3	2.03	0.40
1:3:625:U:H2'	1:3:626:G:H8	1.87	0.40
1:3:1112:C:O2'	38:H:178:ARG:NH1	2.54	0.40
2:1:194:G:O6	2:1:195:A:C6	2.75	0.40
2:1:379:G:N1	2:1:396:G:C6	2.89	0.40
2:1:511:U:H2'	2:1:512:G:H5'	2.02	0.40
2:1:705:A:C2	2:1:727:A:H1'	2.57	0.40
2:1:1101:U:H2'	2:1:1102:C:H6	1.87	0.40
2:1:1150:C:C2	2:1:1151:A:C8	3.09	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:1:1283:G:H22	2:1:1286:A:P	2.44	0.40
2:1:1749:A:H2'	2:1:1750:G:C8	2.57	0.40
2:1:2216:G:H2'	2:1:2217:G:C8	2.54	0.40
2:1:2516:A:C2'	2:1:2517:C:H5'	2.51	0.40
4:5:76:A:H5''	4:5:76:A:H8	1.87	0.40
12:i:78:LEU:HA	12:i:81:LYS:HB3	2.02	0.40
14:k:13:ASN:HB3	14:k:100:PHE:CZ	2.57	0.40
54:X:49:ALA:HA	54:X:58:PRO:HA	2.03	0.40
54:X:77:ARG:H	54:X:77:ARG:HG2	1.66	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	
6	b	269/271 (99%)	244 (91%)	25 (9%)	0	100	100
7	c	207/209 (99%)	190 (92%)	17 (8%)	0	100	100
8	d	199/201 (99%)	184 (92%)	15 (8%)	0	100	100
9	e	175/177 (99%)	158 (90%)	15 (9%)	2 (1%)	11	43
10	f	174/176 (99%)	158 (91%)	16 (9%)	0	100	100
11	g	50/149 (34%)	44 (88%)	5 (10%)	1 (2%)	6	28
12	i	139/142 (98%)	116 (84%)	23 (16%)	0	100	100
13	j	140/142 (99%)	128 (91%)	12 (9%)	0	100	100
14	k	120/122 (98%)	106 (88%)	14 (12%)	0	100	100
15	l	141/143 (99%)	129 (92%)	12 (8%)	0	100	100
16	m	134/136 (98%)	126 (94%)	5 (4%)	3 (2%)	5	26
17	n	118/120 (98%)	101 (86%)	16 (14%)	1 (1%)	16	50
18	o	114/116 (98%)	109 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
19	p	112/114 (98%)	103 (92%)	9 (8%)	0	100	100
20	q	115/117 (98%)	104 (90%)	8 (7%)	3 (3%)	4	23
21	r	101/103 (98%)	87 (86%)	14 (14%)	0	100	100
22	s	108/110 (98%)	100 (93%)	8 (7%)	0	100	100
23	t	91/93 (98%)	82 (90%)	9 (10%)	0	100	100
24	u	100/102 (98%)	83 (83%)	17 (17%)	0	100	100
25	v	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
26	w	73/75 (97%)	67 (92%)	6 (8%)	0	100	100
27	x	75/77 (97%)	72 (96%)	2 (3%)	1 (1%)	9	38
28	y	61/63 (97%)	55 (90%)	6 (10%)	0	100	100
29	z	56/58 (97%)	52 (93%)	4 (7%)	0	100	100
30	A	64/66 (97%)	59 (92%)	5 (8%)	0	100	100
31	B	54/56 (96%)	48 (89%)	4 (7%)	2 (4%)	2	15
32	C	48/50 (96%)	41 (85%)	7 (15%)	0	100	100
33	D	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
34	E	62/64 (97%)	58 (94%)	3 (5%)	1 (2%)	7	34
35	F	36/38 (95%)	32 (89%)	4 (11%)	0	100	100
37	G	216/225 (96%)	189 (88%)	27 (12%)	0	100	100
38	H	204/206 (99%)	194 (95%)	10 (5%)	0	100	100
39	I	203/205 (99%)	172 (85%)	31 (15%)	0	100	100
40	J	155/157 (99%)	138 (89%)	17 (11%)	0	100	100
41	K	98/100 (98%)	83 (85%)	14 (14%)	1 (1%)	12	45
42	L	149/151 (99%)	130 (87%)	19 (13%)	0	100	100
43	M	127/129 (98%)	118 (93%)	9 (7%)	0	100	100
44	N	125/127 (98%)	102 (82%)	23 (18%)	0	100	100
45	O	96/98 (98%)	84 (88%)	11 (12%)	1 (1%)	12	45
46	P	114/116 (98%)	98 (86%)	14 (12%)	2 (2%)	6	31
47	Q	121/123 (98%)	90 (74%)	30 (25%)	1 (1%)	16	50
48	R	112/114 (98%)	99 (88%)	12 (11%)	1 (1%)	14	48
49	S	98/100 (98%)	83 (85%)	15 (15%)	0	100	100
50	T	86/88 (98%)	76 (88%)	10 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
51	U	80/82 (98%)	69 (86%)	11 (14%)	0	100	100
52	V	78/80 (98%)	67 (86%)	11 (14%)	0	100	100
53	W	63/65 (97%)	53 (84%)	9 (14%)	1 (2%)	7	34
54	X	77/79 (98%)	71 (92%)	6 (8%)	0	100	100
55	Y	83/85 (98%)	78 (94%)	5 (6%)	0	100	100
56	Z	63/65 (97%)	43 (68%)	18 (29%)	2 (3%)	3	18
All	All	5620/5825 (96%)	5002 (89%)	595 (11%)	23 (0%)	31	65

All (23) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	e	175	PRO
17	n	11	ASN
27	x	25	LYS
9	e	176	PHE
16	m	70	ASP
20	q	4	LYS
53	W	13	THR
16	m	69	PRO
41	K	92	THR
11	g	12	LEU
16	m	59	ARG
31	B	23	ALA
34	E	31	ILE
48	R	5	GLY
56	Z	8	ASN
45	O	58	ASN
46	P	126	ARG
47	Q	33	CYS
20	q	3	VAL
20	q	25	GLY
56	Z	10	PRO
31	B	24	VAL
46	P	88	PRO

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	
6	b	216/216 (100%)	215 (100%)	1 (0%)	81	89
7	c	164/164 (100%)	164 (100%)	0	100	100
8	d	165/165 (100%)	163 (99%)	2 (1%)	63	82
9	e	148/148 (100%)	147 (99%)	1 (1%)	76	86
10	f	137/137 (100%)	135 (98%)	2 (2%)	57	80
11	g	41/114 (36%)	38 (93%)	3 (7%)	13	42
12	i	109/110 (99%)	108 (99%)	1 (1%)	70	85
13	j	116/116 (100%)	116 (100%)	0	100	100
14	k	103/103 (100%)	103 (100%)	0	100	100
15	l	102/102 (100%)	101 (99%)	1 (1%)	68	84
16	m	109/109 (100%)	109 (100%)	0	100	100
17	n	100/100 (100%)	100 (100%)	0	100	100
18	o	86/86 (100%)	86 (100%)	0	100	100
19	p	99/99 (100%)	99 (100%)	0	100	100
20	q	89/89 (100%)	89 (100%)	0	100	100
21	r	84/84 (100%)	84 (100%)	0	100	100
22	s	93/93 (100%)	93 (100%)	0	100	100
23	t	80/80 (100%)	80 (100%)	0	100	100
24	u	83/83 (100%)	82 (99%)	1 (1%)	63	82
25	v	78/78 (100%)	77 (99%)	1 (1%)	61	81
26	w	57/57 (100%)	57 (100%)	0	100	100
27	x	67/67 (100%)	67 (100%)	0	100	100
28	y	55/55 (100%)	55 (100%)	0	100	100
29	z	48/48 (100%)	46 (96%)	2 (4%)	26	61
30	A	59/59 (100%)	58 (98%)	1 (2%)	53	78
31	B	47/47 (100%)	47 (100%)	0	100	100
32	C	45/45 (100%)	44 (98%)	1 (2%)	45	74
33	D	38/38 (100%)	37 (97%)	1 (3%)	40	72
34	E	51/51 (100%)	51 (100%)	0	100	100
35	F	34/34 (100%)	34 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	G	180/186 (97%)	179 (99%)	1 (1%)	78	88
38	H	170/170 (100%)	167 (98%)	3 (2%)	51	77
39	I	172/172 (100%)	171 (99%)	1 (1%)	78	88
40	J	119/119 (100%)	117 (98%)	2 (2%)	53	78
41	K	87/87 (100%)	87 (100%)	0	100	100
42	L	124/124 (100%)	124 (100%)	0	100	100
43	M	104/104 (100%)	103 (99%)	1 (1%)	68	84
44	N	105/105 (100%)	103 (98%)	2 (2%)	50	76
45	O	86/86 (100%)	86 (100%)	0	100	100
46	P	89/89 (100%)	89 (100%)	0	100	100
47	Q	103/103 (100%)	102 (99%)	1 (1%)	68	84
48	R	92/92 (100%)	91 (99%)	1 (1%)	65	83
49	S	83/83 (100%)	83 (100%)	0	100	100
50	T	76/76 (100%)	76 (100%)	0	100	100
51	U	65/65 (100%)	64 (98%)	1 (2%)	57	80
52	V	74/74 (100%)	74 (100%)	0	100	100
53	W	56/56 (100%)	55 (98%)	1 (2%)	51	77
54	X	70/70 (100%)	70 (100%)	0	100	100
55	Y	65/65 (100%)	64 (98%)	1 (2%)	57	80
56	Z	55/55 (100%)	55 (100%)	0	100	100
All	All	4678/4758 (98%)	4645 (99%)	33 (1%)	73	86

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

Mol	Chain	Res	Type
6	b	203	VAL
8	d	14	VAL
8	d	198	GLU
9	e	39	VAL
10	f	9	VAL
10	f	131	VAL
11	g	4	ILE
11	g	5	LEU
11	g	9	VAL
12	i	22	PRO

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Mol	Chain	Res	Type
15	l	85	VAL
24	u	35	VAL
25	v	72	VAL
29	z	16	LEU
29	z	40	THR
30	A	21	VAL
32	C	22	THR
33	D	44	VAL
37	G	29	PHE
38	H	74	ILE
38	H	156	LEU
38	H	164	THR
39	I	47	LEU
40	J	55	VAL
40	J	130	THR
43	M	102	VAL
44	N	60	LEU
44	N	65	THR
47	Q	15	VAL
48	R	64	VAL
51	U	36	VAL
53	W	70	THR
55	Y	85	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (99) such sidechains are listed below:

Mol	Chain	Res	Type
6	b	24	HIS
6	b	69	ASN
6	b	89	ASN
6	b	142	ASN
6	b	162	GLN
6	b	259	ASN
7	c	49	GLN
7	c	134	HIS
7	c	150	GLN
7	c	164	GLN
7	c	173	GLN
8	d	41	GLN
8	d	62	GLN
8	d	90	GLN
8	d	94	GLN

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Mol	Chain	Res	Type
8	d	165	HIS
9	e	4	HIS
9	e	80	GLN
10	f	47	ASN
10	f	87	GLN
11	g	2	GLN
12	i	29	GLN
12	i	30	GLN
13	j	58	ASN
13	j	135	GLN
14	k	3	GLN
14	k	5	GLN
14	k	93	GLN
15	l	4	ASN
15	l	104	GLN
16	m	13	HIS
17	n	11	ASN
19	p	2	ASN
19	p	114	ASN
20	q	55	GLN
20	q	58	GLN
21	r	18	GLN
21	r	82	HIS
22	s	7	HIS
23	t	28	ASN
23	t	59	ASN
23	t	92	ASN
24	u	52	ASN
24	u	68	ASN
25	v	87	GLN
26	w	53	HIS
27	x	16	ASN
27	x	33	HIS
28	y	31	GLN
28	y	41	HIS
29	z	8	GLN
30	A	20	ASN
30	A	33	ASN
30	A	61	ASN
31	B	4	GLN
31	B	5	ASN
32	C	25	ASN

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Mol	Chain	Res	Type
34	E	30	HIS
35	F	37	GLN
37	G	108	GLN
37	G	119	GLN
37	G	121	GLN
37	G	167	HIS
38	H	7	ASN
38	H	68	HIS
38	H	99	GLN
38	H	122	GLN
38	H	138	GLN
38	H	139	ASN
39	I	135	GLN
39	I	197	HIS
40	J	121	ASN
42	L	85	GLN
42	L	121	ASN
42	L	147	ASN
43	M	3	GLN
43	M	37	ASN
43	M	66	GLN
44	N	4	GLN
44	N	30	ASN
45	O	20	GLN
45	O	35	GLN
45	O	58	ASN
46	P	80	ASN
47	Q	71	HIS
48	R	7	ASN
48	R	99	GLN
49	S	59	GLN
50	T	19	ASN
50	T	39	GLN
50	T	79	GLN
52	V	30	HIS
52	V	50	ASN
53	W	18	GLN
53	W	53	GLN
54	X	56	HIS
54	X	68	HIS
55	Y	2	ASN
55	Y	77	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3	1538/1539 (99%)	248 (16%)	3 (0%)
2	1	2902/2903 (99%)	377 (12%)	12 (0%)
3	2	119/120 (99%)	16 (13%)	2 (1%)
36	4	17/35 (48%)	3 (17%)	1 (5%)
4	5	76/77 (98%)	20 (26%)	3 (3%)
5	6	76/77 (98%)	11 (14%)	0
5	7	76/77 (98%)	23 (30%)	2 (2%)
All	All	4804/4828 (99%)	698 (14%)	23 (0%)

All (698) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3	4	U
1	3	5	U
1	3	6	G
1	3	7	A
1	3	9	G
1	3	22	G
1	3	32	A
1	3	39	G
1	3	47	C
1	3	48	C
1	3	51	A
1	3	71	A
1	3	75	G
1	3	77	A
1	3	78	A
1	3	80	A
1	3	83	C
1	3	84	U
1	3	87	C
1	3	88	U
1	3	94	G
1	3	95	C
1	3	100	G
1	3	108	G
1	3	116	A
1	3	121	U
1	3	127	G
1	3	130	A
1	3	144	G

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Mol	Chain	Res	Type
1	3	163	C
1	3	183	C
1	3	197	A
1	3	206	C
1	3	208	U
1	3	210	C
1	3	211	G
1	3	212	G
1	3	222	C
1	3	226	G
1	3	240	G
1	3	245	U
1	3	247	G
1	3	251	G
1	3	266	G
1	3	267	C
1	3	279	A
1	3	280	C
1	3	281	G
1	3	289	G
1	3	293	G
1	3	306	A
1	3	321	A
1	3	328	C
1	3	329	A
1	3	330	C
1	3	345	C
1	3	347	G
1	3	348	G
1	3	352	C
1	3	353	A
1	3	354	G
1	3	363	A
1	3	367	U
1	3	372	C
1	3	374	A
1	3	388	G
1	3	397	A
1	3	398	U
1	3	405	U
1	3	406	G
1	3	412	A

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Mol	Chain	Res	Type
1	3	413	G
1	3	422	C
1	3	423	G
1	3	428	G
1	3	429	U
1	3	446	G
1	3	453	G
1	3	467	U
1	3	468	A
1	3	472	U
1	3	479	U
1	3	480	U
1	3	481	G
1	3	484	G
1	3	485	U
1	3	486	U
1	3	487	A
1	3	496	A
1	3	497	G
1	3	505	G
1	3	508	U
1	3	509	A
1	3	511	C
1	3	518	C
1	3	521	G
1	3	531	U
1	3	532	A
1	3	533	A
1	3	536	C
1	3	547	A
1	3	561	U
1	3	562	U
1	3	564	C
1	3	566	G
1	3	572	A
1	3	573	A
1	3	575	G
1	3	576	C
1	3	577	G
1	3	607	A
1	3	615	G
1	3	633	G

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Mol	Chain	Res	Type
1	3	639	G
1	3	642	A
1	3	653	U
1	3	655	A
1	3	660	C
1	3	665	A
1	3	682	G
1	3	688	G
1	3	702	A
1	3	703	G
1	3	718	A
1	3	721	G
1	3	723	U
1	3	724	G
1	3	731	G
1	3	734	G
1	3	755	G
1	3	777	A
1	3	793	U
1	3	799	G
1	3	815	A
1	3	817	C
1	3	818	G
1	3	819	A
1	3	820	U
1	3	821	G
1	3	829	G
1	3	836	G
1	3	843	U
1	3	844	G
1	3	845	A
1	3	846	G
1	3	849	G
1	3	851	G
1	3	868	C
1	3	902	G
1	3	914	A
1	3	934	C
1	3	935	A
1	3	936	C
1	3	960	U
1	3	961	U

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Mol	Chain	Res	Type
1	3	966	G
1	3	969	A
1	3	971	G
1	3	975	A
1	3	976	G
1	3	977	A
1	3	991	U
1	3	992	U
1	3	993	G
1	3	1004	A
1	3	1020	G
1	3	1028	C
1	3	1031	C
1	3	1032	G
1	3	1033	G
1	3	1034	G
1	3	1036	A
1	3	1053	G
1	3	1054	C
1	3	1056	U
1	3	1070	U
1	3	1085	U
1	3	1094	G
1	3	1095	U
1	3	1099	G
1	3	1101	A
1	3	1108	G
1	3	1133	G
1	3	1135	U
1	3	1136	C
1	3	1137	C
1	3	1138	G
1	3	1139	G
1	3	1159	U
1	3	1168	U
1	3	1171	A
1	3	1182	G
1	3	1183	U
1	3	1184	G
1	3	1196	A
1	3	1197	A
1	3	1202	U

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Mol	Chain	Res	Type
1	3	1206	G
1	3	1224	U
1	3	1225	A
1	3	1226	C
1	3	1237	C
1	3	1238	A
1	3	1240	U
1	3	1241	G
1	3	1250	A
1	3	1256	A
1	3	1260	G
1	3	1261	A
1	3	1275	A
1	3	1278	G
1	3	1280	A
1	3	1281	C
1	3	1282	C
1	3	1286	U
1	3	1287	A
1	3	1290	G
1	3	1300	G
1	3	1302	C
1	3	1305	G
1	3	1312	G
1	3	1317	C
1	3	1322	C
1	3	1335	U
1	3	1336	C
1	3	1340	A
1	3	1363	A
1	3	1370	G
1	3	1379	G
1	3	1394	A
1	3	1400	C
1	3	1404	C
1	3	1419	G
1	3	1429	A
1	3	1446	A
1	3	1448	C
1	3	1452	C
1	3	1453	G
1	3	1487	G

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Mol	Chain	Res	Type
1	3	1492	A
1	3	1497	G
1	3	1503	A
1	3	1506	U
1	3	1507	A
1	3	1517	G
1	3	1519	A
1	3	1529	G
1	3	1530	G
2	1	10	A
2	1	12	U
2	1	34	U
2	1	35	G
2	1	46	G
2	1	51	G
2	1	55	G
2	1	63	A
2	1	71	A
2	1	74	A
2	1	75	G
2	1	102	U
2	1	103	A
2	1	119	A
2	1	120	U
2	1	139	U
2	1	140	C
2	1	141	G
2	1	149	A
2	1	162	U
2	1	163	C
2	1	178	G
2	1	196	A
2	1	199	A
2	1	216	A
2	1	221	A
2	1	222	A
2	1	229	C
2	1	248	G
2	1	255	A
2	1	265	A
2	1	266	G
2	1	276	U

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Mol	Chain	Res	Type
2	1	281	C
2	1	285	G
2	1	294	A
2	1	323	C
2	1	329	G
2	1	330	A
2	1	353	C
2	1	361	G
2	1	362	A
2	1	371	A
2	1	372	G
2	1	386	G
2	1	387	U
2	1	396	G
2	1	404	A
2	1	406	G
2	1	411	G
2	1	424	G
2	1	451	U
2	1	457	A
2	1	481	G
2	1	482	A
2	1	491	G
2	1	504	A
2	1	505	A
2	1	526	A
2	1	529	A
2	1	531	C
2	1	532	A
2	1	533	G
2	1	544	C
2	1	545	U
2	1	546	U
2	1	547	A
2	1	563	A
2	1	573	U
2	1	574	A
2	1	575	A
2	1	603	A
2	1	614	A
2	1	616	A
2	1	627	A

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Mol	Chain	Res	Type
2	1	637	A
2	1	646	U
2	1	647	G
2	1	654	A
2	1	669	G
2	1	670	A
2	1	671	C
2	1	677	A
2	1	686	U
2	1	695	G
2	1	730	A
2	1	747	C
2	1	758	C
2	1	764	A
2	1	775	G
2	1	782	A
2	1	784	G
2	1	785	G
2	1	789	A
2	1	792	A
2	1	801	G
2	1	805	G
2	1	812	C
2	1	819	A
2	1	827	U
2	1	828	U
2	1	830	G
2	1	845	A
2	1	846	U
2	1	858	G
2	1	860	U
2	1	878	A
2	1	887	U
2	1	896	A
2	1	910	A
2	1	911	A
2	1	932	U
2	1	941	A
2	1	946	C
2	1	961	C
2	1	968	C
2	1	974	G

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Mol	Chain	Res	Type
2	1	981	A
2	1	983	A
2	1	985	C
2	1	995	C
2	1	996	A
2	1	1005	C
2	1	1012	U
2	1	1013	C
2	1	1021	A
2	1	1022	G
2	1	1033	U
2	1	1045	C
2	1	1046	A
2	1	1047	G
2	1	1057	A
2	1	1058	U
2	1	1060	U
2	1	1061	U
2	1	1063	G
2	1	1065	U
2	1	1066	U
2	1	1068	G
2	1	1069	A
2	1	1070	A
2	1	1071	G
2	1	1073	A
2	1	1075	C
2	1	1078	U
2	1	1083	U
2	1	1084	A
2	1	1086	A
2	1	1088	A
2	1	1104	C
2	1	1111	A
2	1	1131	G
2	1	1135	C
2	1	1139	G
2	1	1142	A
2	1	1143	A
2	1	1175	A
2	1	1177	G
2	1	1178	C

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Mol	Chain	Res	Type
2	1	1180	U
2	1	1186	G
2	1	1212	G
2	1	1225	G
2	1	1253	A
2	1	1256	G
2	1	1271	G
2	1	1272	A
2	1	1273	U
2	1	1289	C
2	1	1294	U
2	1	1300	G
2	1	1301	A
2	1	1345	C
2	1	1352	U
2	1	1365	A
2	1	1378	A
2	1	1379	U
2	1	1383	A
2	1	1416	G
2	1	1419	A
2	1	1420	A
2	1	1427	A
2	1	1429	G
2	1	1452	G
2	1	1453	A
2	1	1461	C
2	1	1482	G
2	1	1490	A
2	1	1491	G
2	1	1497	U
2	1	1504	A
2	1	1515	A
2	1	1524	G
2	1	1533	C
2	1	1535	A
2	1	1536	C
2	1	1537	G
2	1	1555	G
2	1	1560	G
2	1	1565	C
2	1	1569	A

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Mol	Chain	Res	Type
2	1	1578	U
2	1	1583	A
2	1	1608	A
2	1	1616	A
2	1	1634	A
2	1	1647	U
2	1	1648	U
2	1	1674	G
2	1	1698	A
2	1	1699	G
2	1	1703	G
2	1	1715	G
2	1	1716	U
2	1	1729	U
2	1	1730	C
2	1	1732	C
2	1	1738	G
2	1	1758	U
2	1	1764	C
2	1	1773	A
2	1	1783	A
2	1	1784	A
2	1	1786	A
2	1	1800	C
2	1	1801	A
2	1	1802	A
2	1	1808	A
2	1	1809	A
2	1	1816	C
2	1	1829	A
2	1	1833	C
2	1	1870	C
2	1	1871	A
2	1	1901	A
2	1	1906	G
2	1	1913	A
2	1	1914	C
2	1	1929	G
2	1	1931	U
2	1	1936	A
2	1	1937	A
2	1	1938	A

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Mol	Chain	Res	Type
2	1	1939	U
2	1	1955	U
2	1	1967	C
2	1	1970	A
2	1	1971	U
2	1	1972	G
2	1	1993	U
2	1	1997	C
2	1	2022	U
2	1	2023	C
2	1	2027	G
2	1	2030	A
2	1	2031	A
2	1	2033	A
2	1	2043	C
2	1	2052	A
2	1	2055	C
2	1	2056	G
2	1	2060	A
2	1	2061	G
2	1	2069	G
2	1	2093	G
2	1	2096	C
2	1	2100	G
2	1	2110	G
2	1	2111	U
2	1	2118	U
2	1	2119	A
2	1	2123	G
2	1	2128	G
2	1	2131	U
2	1	2132	U
2	1	2133	G
2	1	2134	A
2	1	2137	U
2	1	2141	G
2	1	2145	C
2	1	2149	U
2	1	2162	G
2	1	2164	C
2	1	2166	U
2	1	2172	U

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Mol	Chain	Res	Type
2	1	2173	A
2	1	2174	C
2	1	2189	U
2	1	2192	U
2	1	2198	A
2	1	2204	G
2	1	2211	A
2	1	2213	U
2	1	2225	A
2	1	2238	G
2	1	2239	G
2	1	2243	U
2	1	2268	A
2	1	2279	G
2	1	2283	C
2	1	2287	A
2	1	2288	A
2	1	2305	U
2	1	2309	A
2	1	2325	G
2	1	2326	C
2	1	2327	A
2	1	2333	A
2	1	2334	U
2	1	2345	G
2	1	2350	C
2	1	2382	G
2	1	2383	G
2	1	2385	C
2	1	2402	U
2	1	2406	A
2	1	2407	A
2	1	2423	U
2	1	2426	A
2	1	2427	C
2	1	2429	G
2	1	2430	A
2	1	2435	A
2	1	2436	G
2	1	2440	C
2	1	2441	U
2	1	2445	G

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Mol	Chain	Res	Type
2	1	2447	G
2	1	2448	A
2	1	2476	A
2	1	2482	A
2	1	2491	U
2	1	2492	U
2	1	2498	C
2	1	2502	G
2	1	2505	G
2	1	2518	A
2	1	2547	A
2	1	2554	U
2	1	2566	A
2	1	2567	G
2	1	2572	A
2	1	2573	C
2	1	2582	G
2	1	2602	A
2	1	2609	U
2	1	2613	U
2	1	2629	U
2	1	2630	G
2	1	2642	G
2	1	2646	C
2	1	2689	U
2	1	2690	U
2	1	2714	G
2	1	2726	A
2	1	2744	G
2	1	2748	A
2	1	2751	G
2	1	2758	A
2	1	2764	A
2	1	2765	A
2	1	2778	A
2	1	2779	U
2	1	2793	C
2	1	2798	U
2	1	2799	A
2	1	2800	A
2	1	2801	G
2	1	2820	A

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Mol	Chain	Res	Type
2	1	2861	U
2	1	2867	G
2	1	2868	A
2	1	2872	A
2	1	2879	A
2	1	2880	C
2	1	2884	U
2	1	2901	C
3	2	9	G
3	2	30	C
3	2	35	C
3	2	36	C
3	2	44	G
3	2	45	A
3	2	53	A
3	2	66	A
3	2	67	G
3	2	87	U
3	2	88	C
3	2	89	U
3	2	90	C
3	2	108	A
3	2	109	A
3	2	120	A
4	5	2	G
4	5	4	C
4	5	5	G
4	5	6	A
4	5	9	A
4	5	14	A
4	5	19	G
4	5	20	U
4	5	21	A
4	5	22	G
4	5	41	A
4	5	42	G
4	5	46	G
4	5	48	C
4	5	65	U
4	5	69	G
4	5	73	A
4	5	74	C

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Mol	Chain	Res	Type
4	5	75	C
4	5	76	A
5	7	2	G
5	7	7	G
5	7	8	U
5	7	9	G
5	7	19	G
5	7	20	U
5	7	21	A
5	7	22	G
5	7	30	G
5	7	34	C
5	7	35	A
5	7	36	U
5	7	42	G
5	7	45	G
5	7	55	U
5	7	56	C
5	7	64	G
5	7	67	C
5	7	70	G
5	7	73	A
5	7	74	C
5	7	75	C
5	7	76	A
36	4	12	A
36	4	13	A
36	4	19	C
5	6	2	G
5	6	9	G
5	6	17	C
5	6	18	G
5	6	19	G
5	6	20	U
5	6	46	G
5	6	47	U
5	6	59	A
5	6	74	C
5	6	76	A

All (23) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	3	4	U
1	3	1032	G
1	3	1035	A
2	1	481	G
2	1	490	C
2	1	784	G
2	1	859	G
2	1	1020	A
2	1	1130	U
2	1	1715	G
2	1	1783	A
2	1	1801	A
2	1	1930	G
2	1	2326	C
2	1	2481	G
3	2	52	A
3	2	66	A
4	5	3	G
4	5	41	A
4	5	75	C
5	7	33	U
5	7	55	U
36	4	18	G

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	$\# Z > 2$
57	PRO	5	101	4	6,7,8	4.57	4 (66%)	7,8,10	1.50	1 (14%)

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
57	PRO	5	101	4	-	0/0/9/11	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	5	101	PRO	CA-N	7.75	1.62	1.48
57	5	101	PRO	CD-N	-5.57	1.29	1.49
57	5	101	PRO	O-C	5.00	1.39	1.20
57	5	101	PRO	CB-CA	-2.59	1.32	1.51

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
57	5	101	PRO	O-C-CA	-2.97	117.13	124.77

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 [i](#)

There are no chain breaks in this entry.

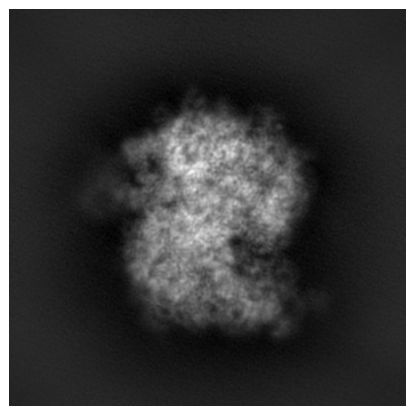
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25420. These allow visual inspection of the internal detail of the map and identification of artifacts.

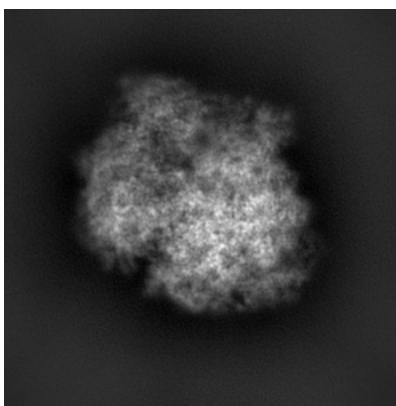
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

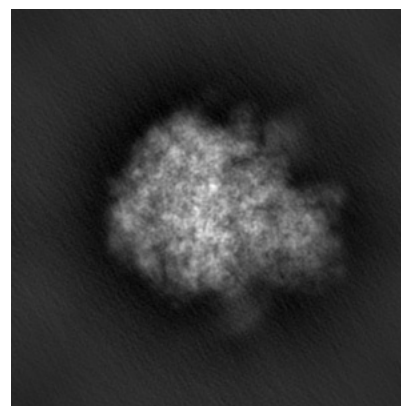
6.1.1 Primary map



X

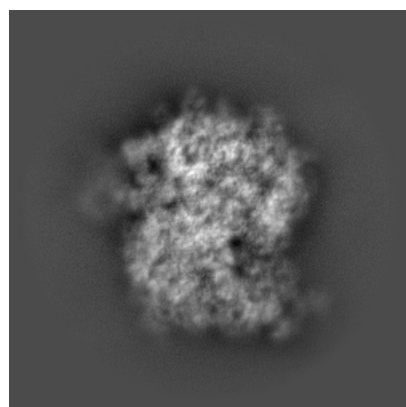


Y

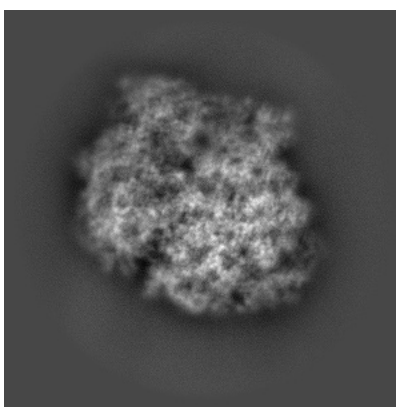


Z

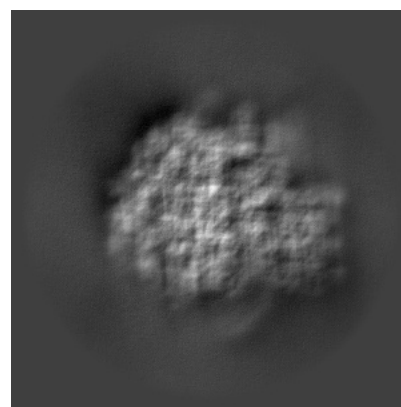
6.1.2 Raw map



X



Y

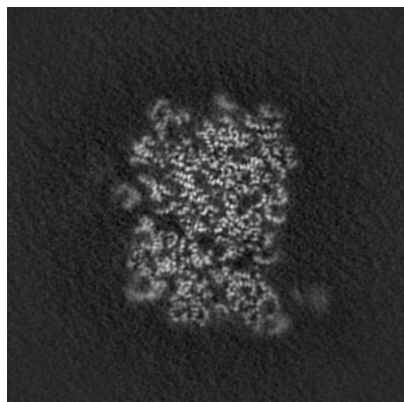


Z

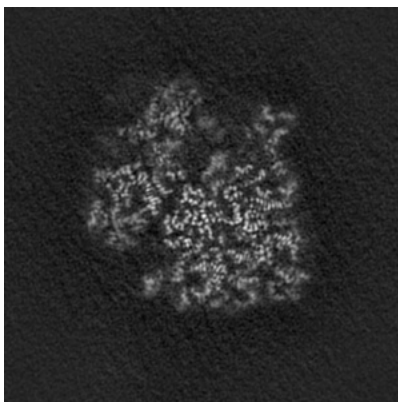
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

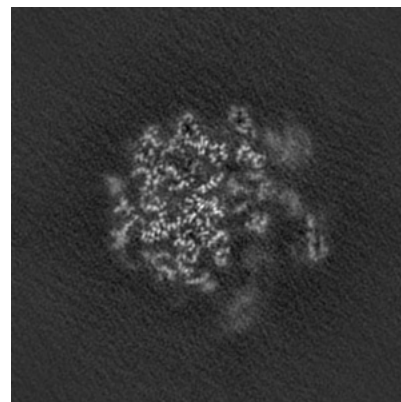
6.2.1 Primary map



X Index: 230

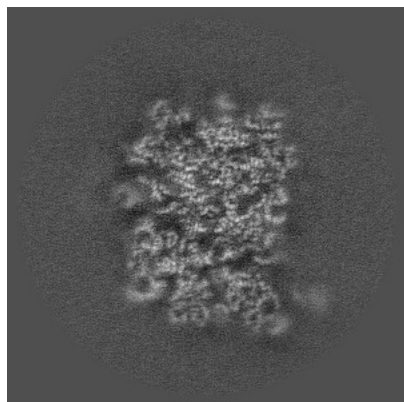


Y Index: 230

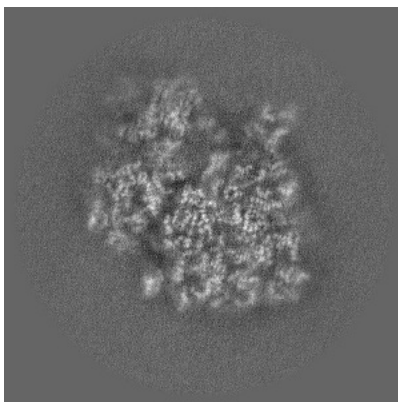


Z Index: 230

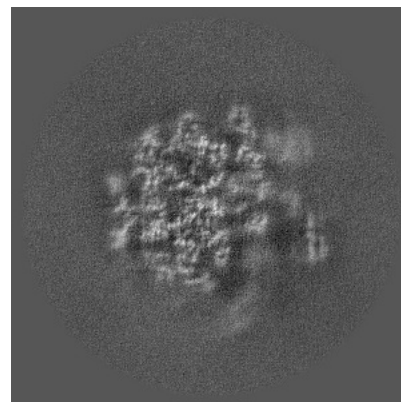
6.2.2 Raw map



X Index: 230



Y Index: 230

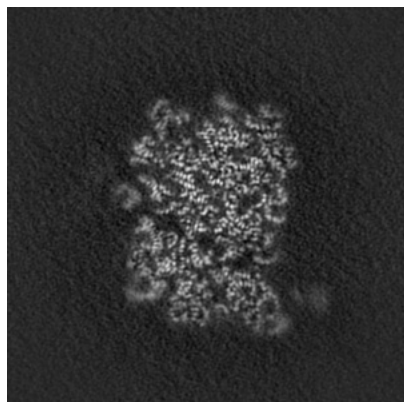


Z Index: 230

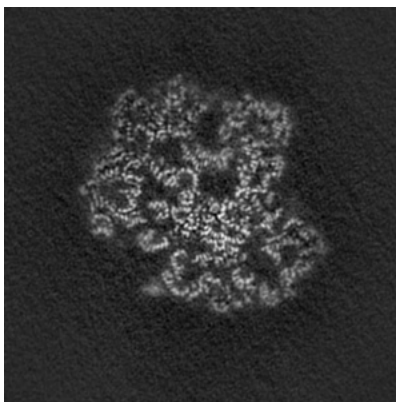
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

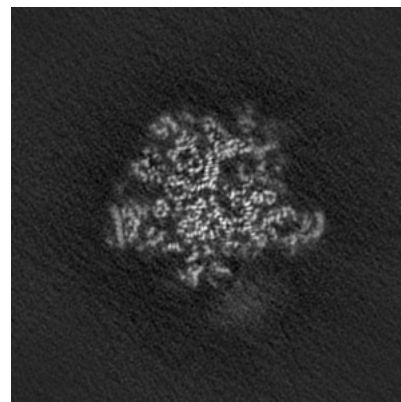
6.3.1 Primary map



X Index: 230

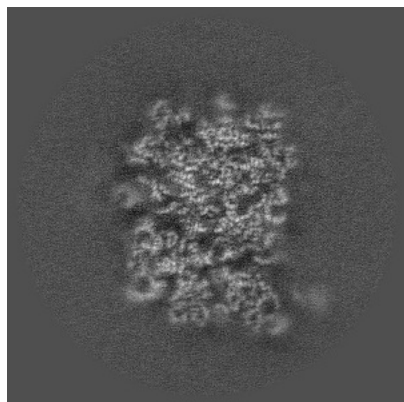


Y Index: 213

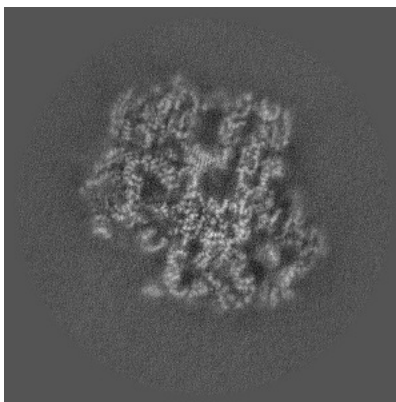


Z Index: 279

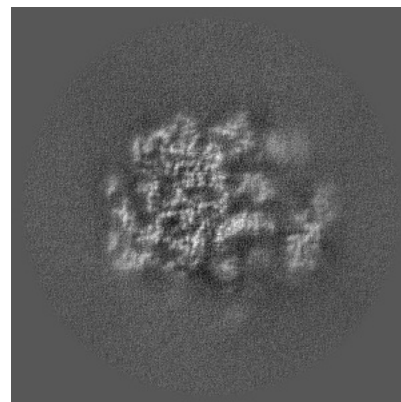
6.3.2 Raw map



X Index: 230



Y Index: 210

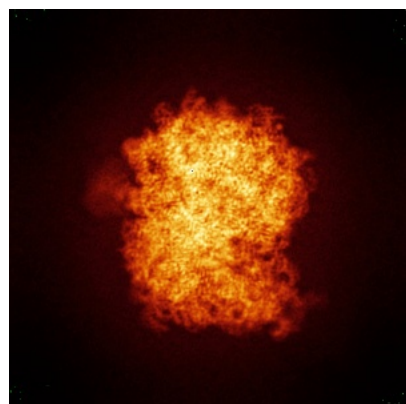


Z Index: 220

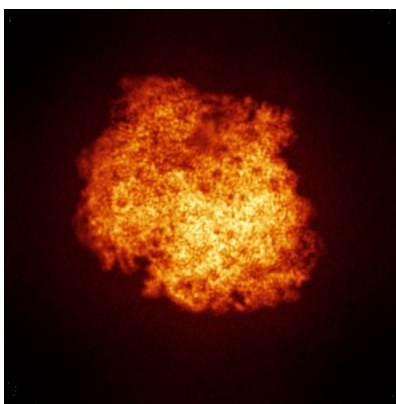
The images above show the largest variance slices of the map in three orthogonal directions.

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

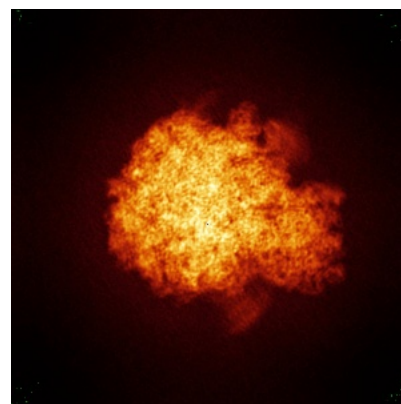
6.4.1 Primary map



X

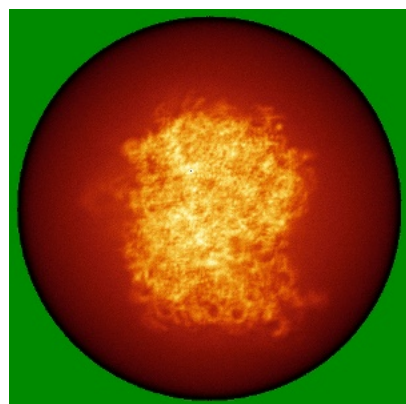


Y

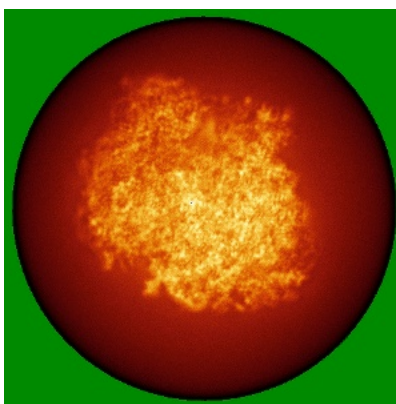


Z

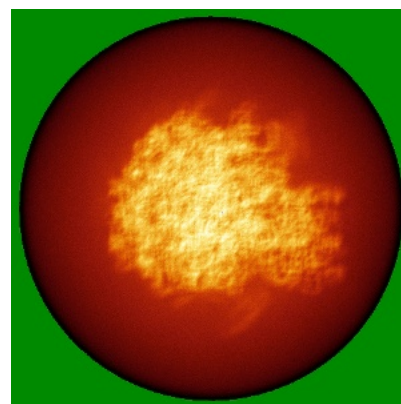
6.4.2 Raw map



X



Y

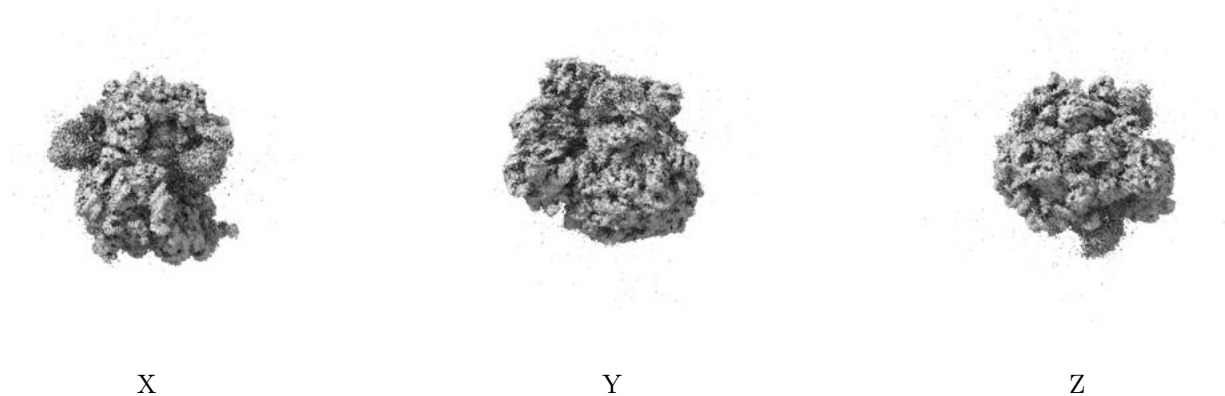


Z

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.

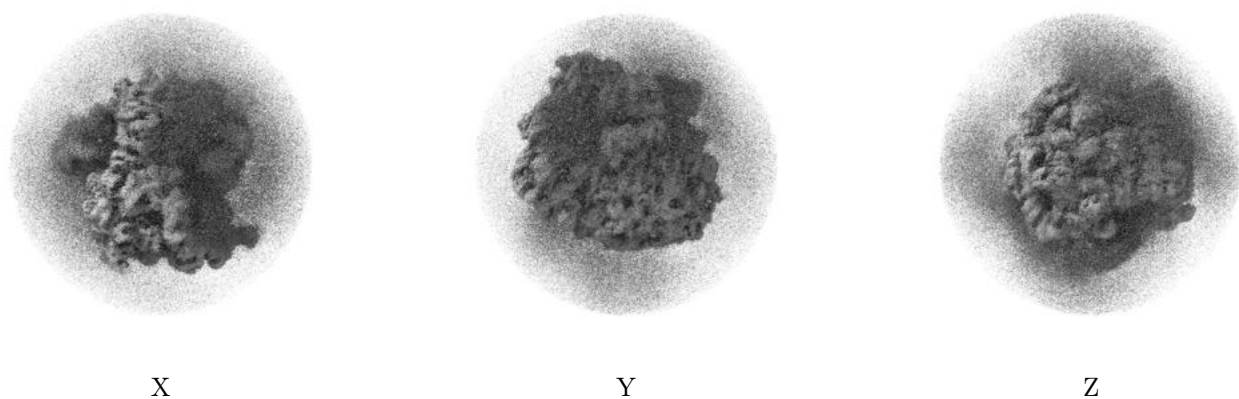
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.35. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

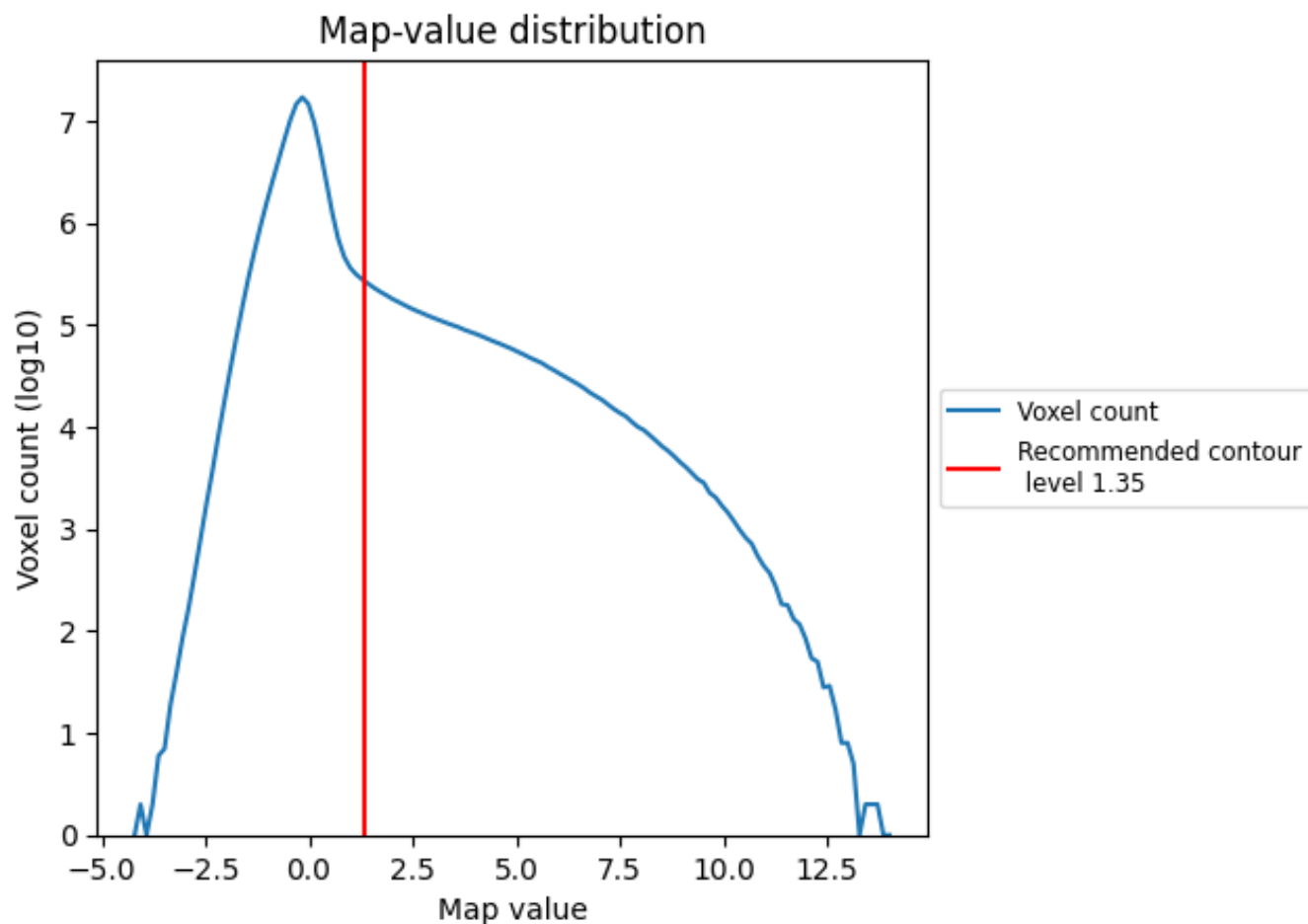
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

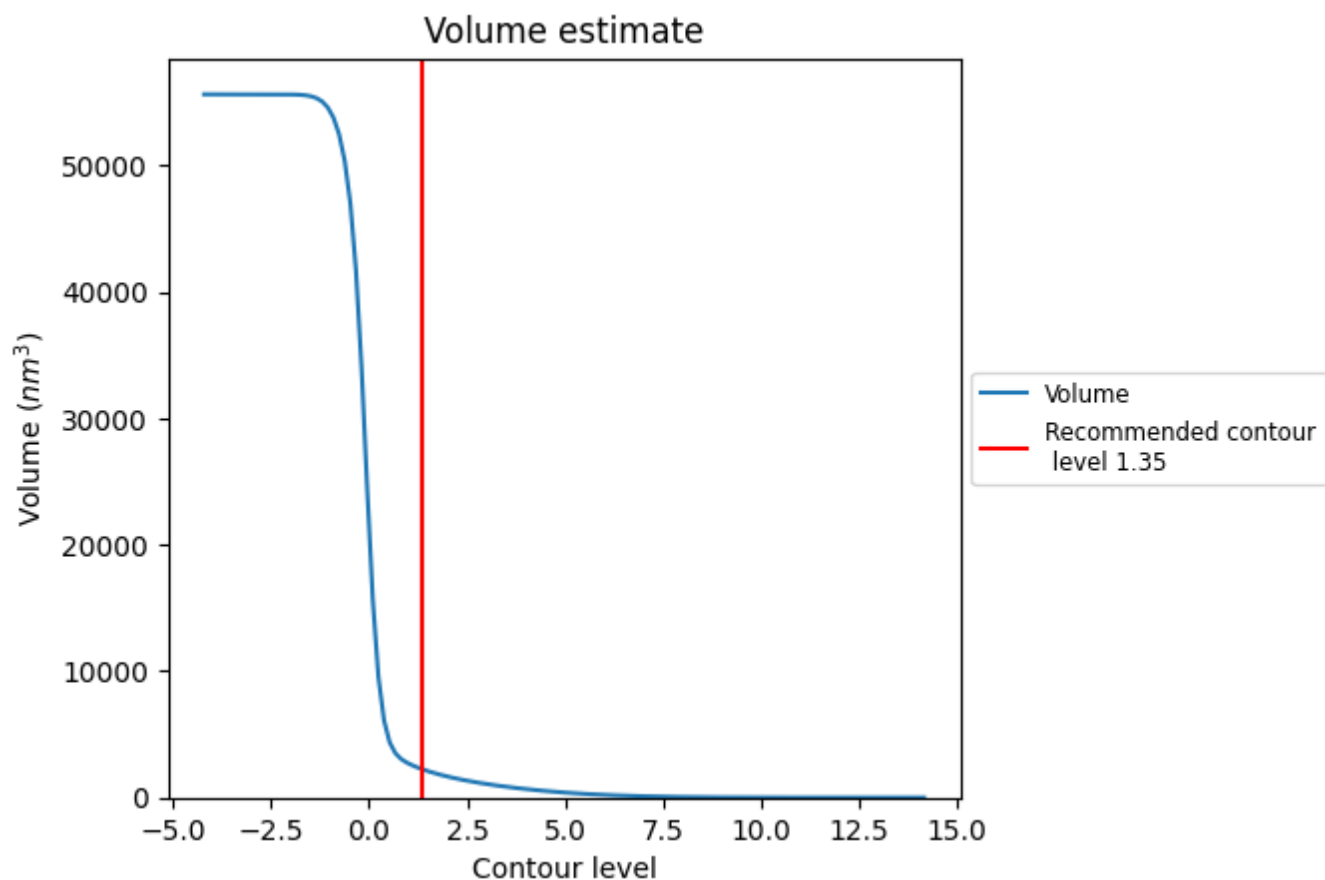
This section contains the results of statistical analysis of the map.

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.

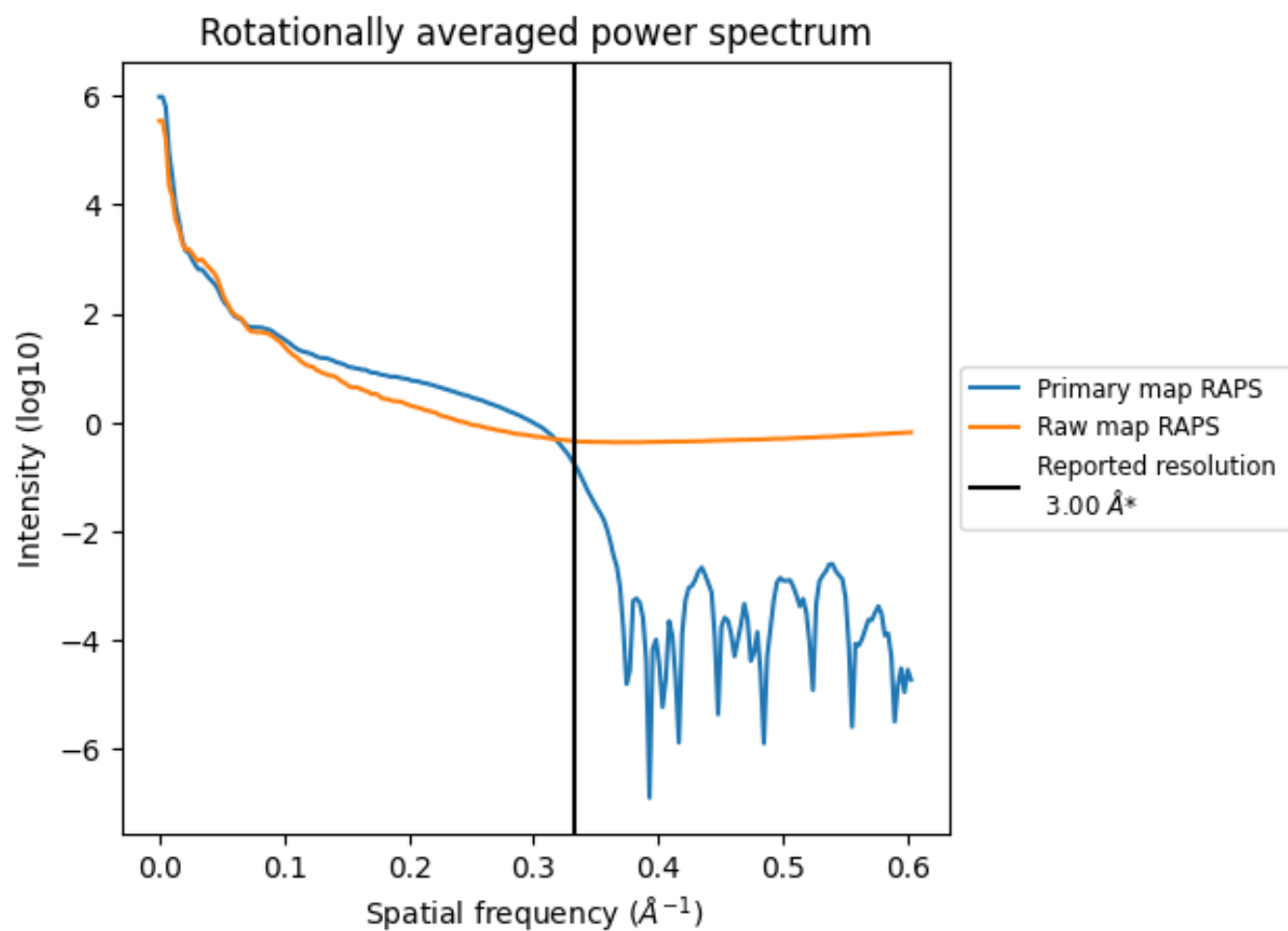
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2252 nm³; this corresponds to an approximate mass of 2034 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 ⓘ

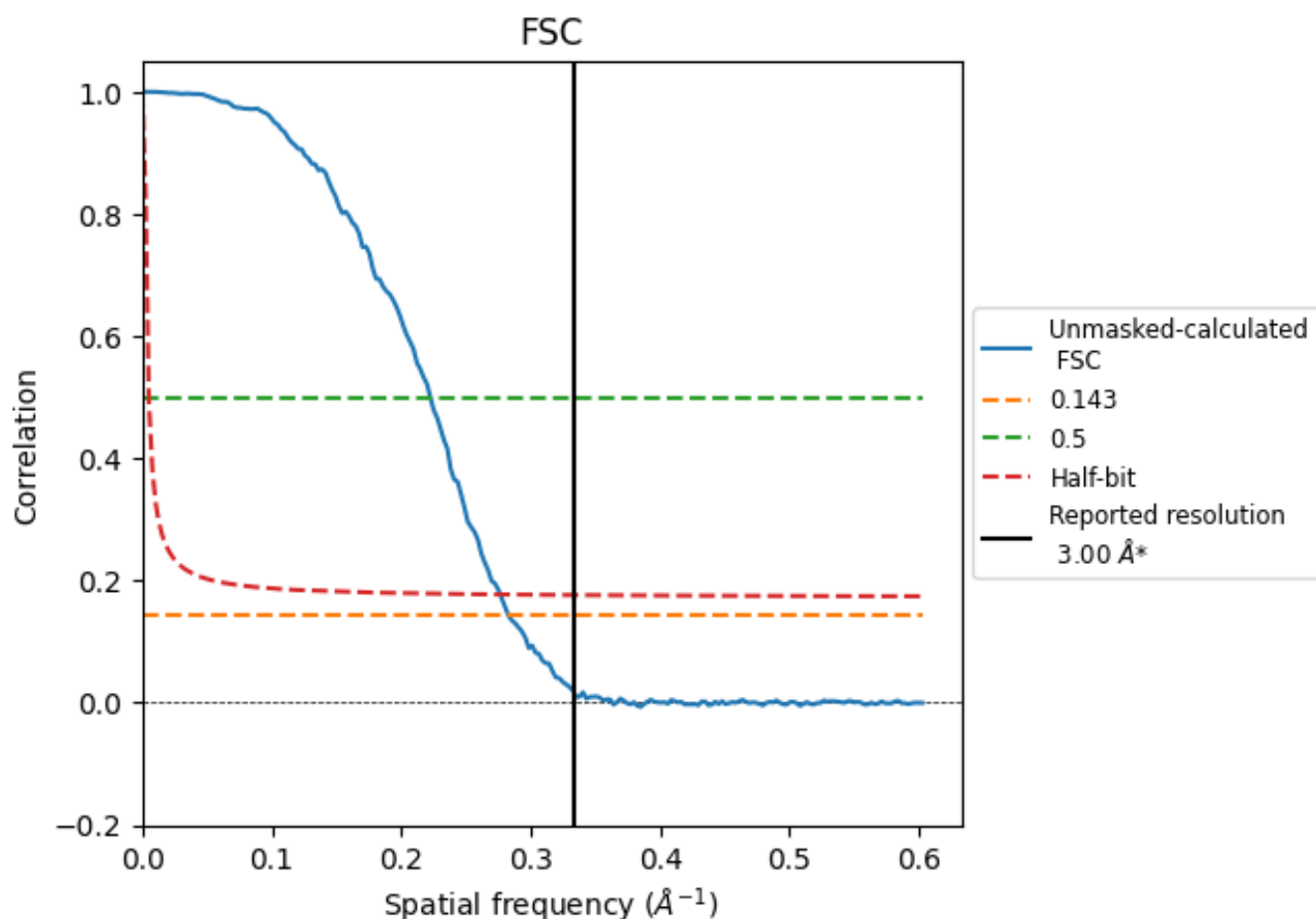


*Reported resolution corresponds to spatial frequency of 0.333 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.333 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

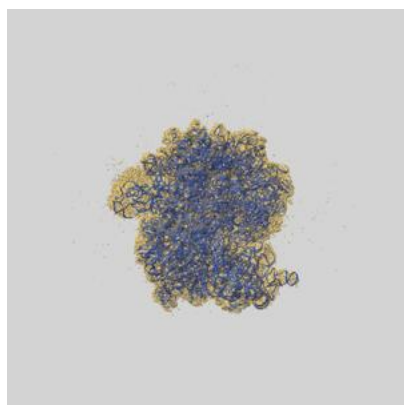
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.00	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.54	4.49	3.62

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.54 differs from the reported value 3.0 by more than 10 %

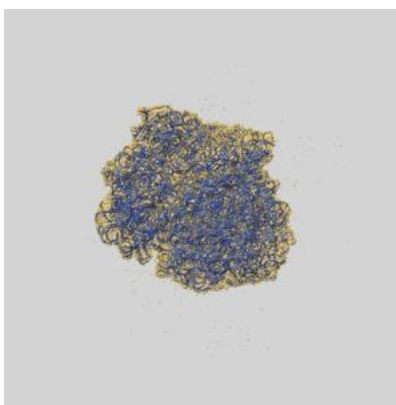
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-25420 and PDB model 7ST6. Per-residue inclusion information can be found in section [3](#) on page [15](#).

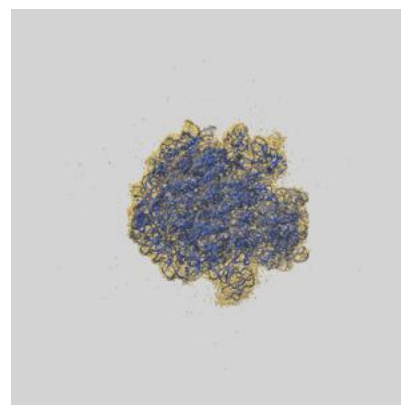
9.1 Map-model overlay [i](#)



X



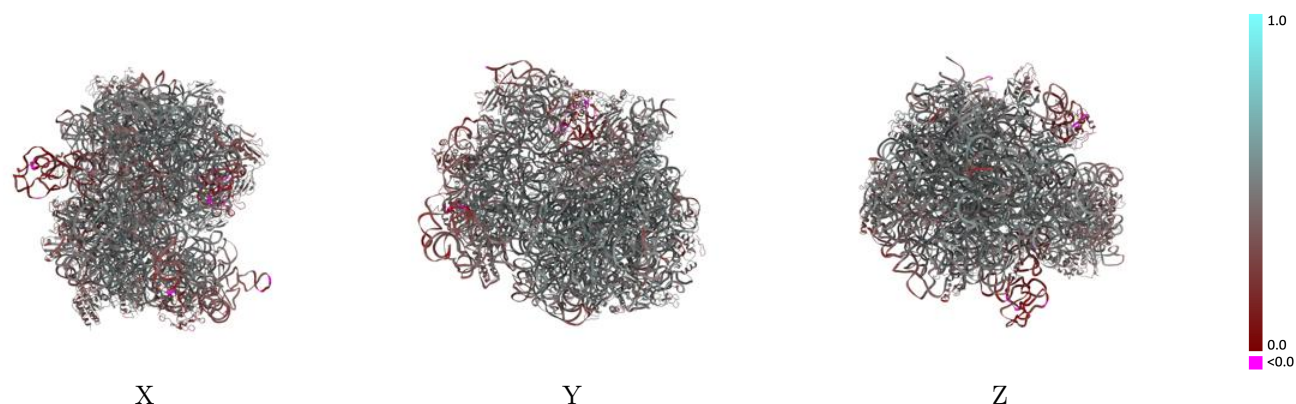
Y



Z

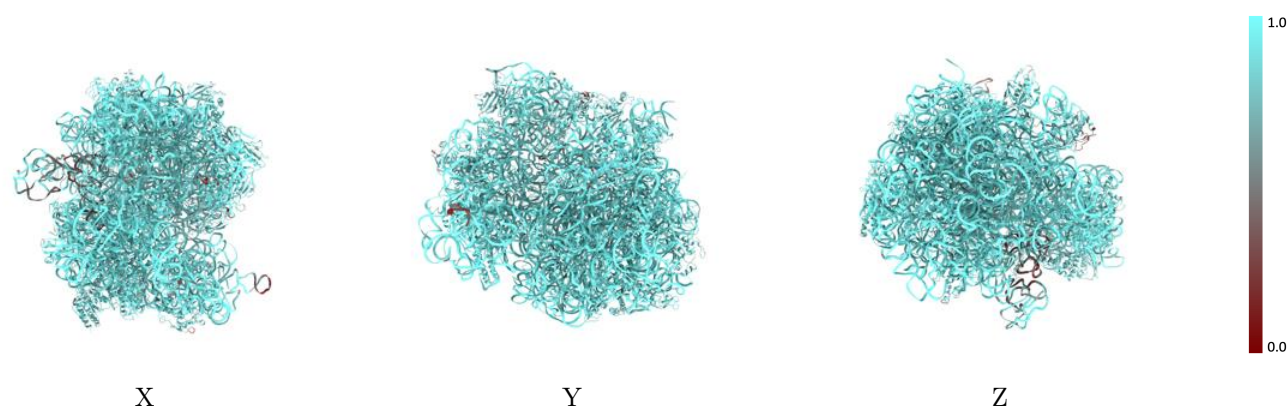
The images above show the 3D surface view of the map at the recommended contour level 1.35 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



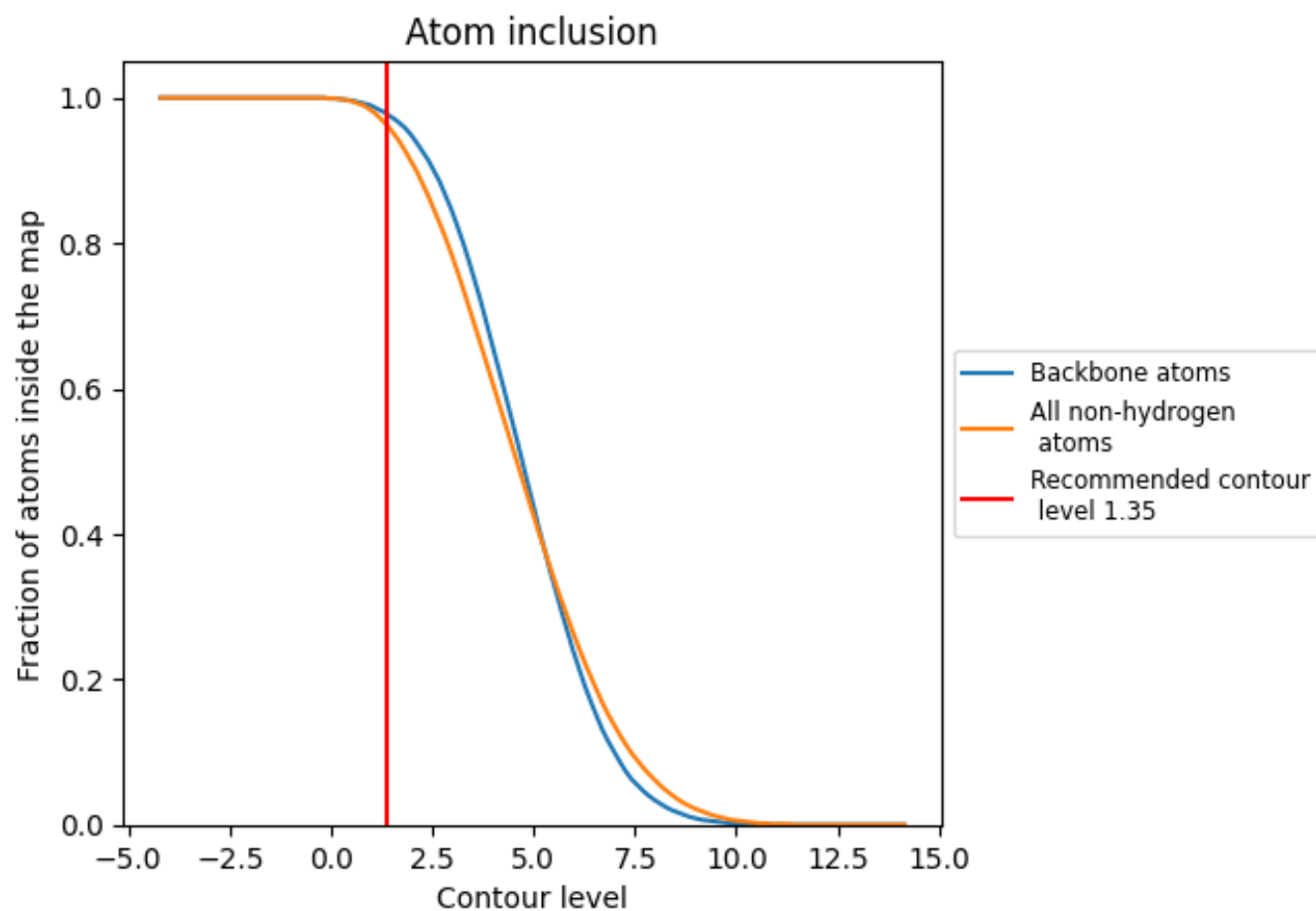
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (1.35).

9.4 Atom inclusion ⓘ



At the recommended contour level, 98% of all backbone atoms, 96% 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 (1.35) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9640	 0.4500
1	 0.9870	 0.4610
2	 0.9950	 0.4690
3	 0.9860	 0.4510
4	 0.9510	 0.3680
5	 0.9900	 0.4360
6	 0.9970	 0.4620
7	 0.3890	 0.2140
A	 0.9040	 0.3850
B	 0.9790	 0.4930
C	 0.9500	 0.4560
D	 0.9780	 0.4940
E	 0.9780	 0.5100
F	 0.9490	 0.4910
G	 0.8810	 0.3980
H	 0.8840	 0.4570
I	 0.8650	 0.3460
J	 0.9490	 0.4680
K	 0.9550	 0.4000
L	 0.9130	 0.3990
M	 0.9500	 0.4620
N	 0.9110	 0.4140
O	 0.8160	 0.4130
P	 0.9630	 0.4590
Q	 0.9260	 0.4210
R	 0.9390	 0.4240
S	 0.9300	 0.4350
T	 0.9830	 0.4460
U	 0.9030	 0.4020
V	 0.9750	 0.4120
W	 0.9710	 0.4410
X	 0.9240	 0.4300
Y	 0.9180	 0.3950
Z	 0.8710	 0.3280
b	 0.9790	 0.5090



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Chain	Atom inclusion	Q-score
c	 0.9750	 0.4970
d	 0.9340	 0.4470
e	 0.9510	 0.4240
f	 0.9180	 0.4110
g	 0.8320	 0.3760
i	 0.7020	 0.1810
j	 0.9710	 0.4920
k	 0.9650	 0.5000
l	 0.9690	 0.4910
m	 0.9760	 0.5060
n	 0.9720	 0.4800
o	 0.9640	 0.4540
p	 0.9540	 0.4980
q	 0.9650	 0.4870
r	 0.9330	 0.4780
s	 0.9680	 0.4690
t	 0.9590	 0.4510
u	 0.9350	 0.4380
v	 0.9430	 0.4720
w	 0.9930	 0.5200
x	 0.9750	 0.4840
y	 0.9030	 0.3840
z	 0.9540	 0.4810