



Full wwPDB EM Validation Report ⓘ

Mar 8, 2026 – 11:58 AM UTC

PDB ID : 9P4I / pdb_00009p4i
EMDB ID : EMD-71268
Title : YsxC-GTP treated 44.5SYsxC particles. Class 5.
Authors : Ortega, J.; Seffouh, A.
Deposited on : 2025-06-16
Resolution : 2.80 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:

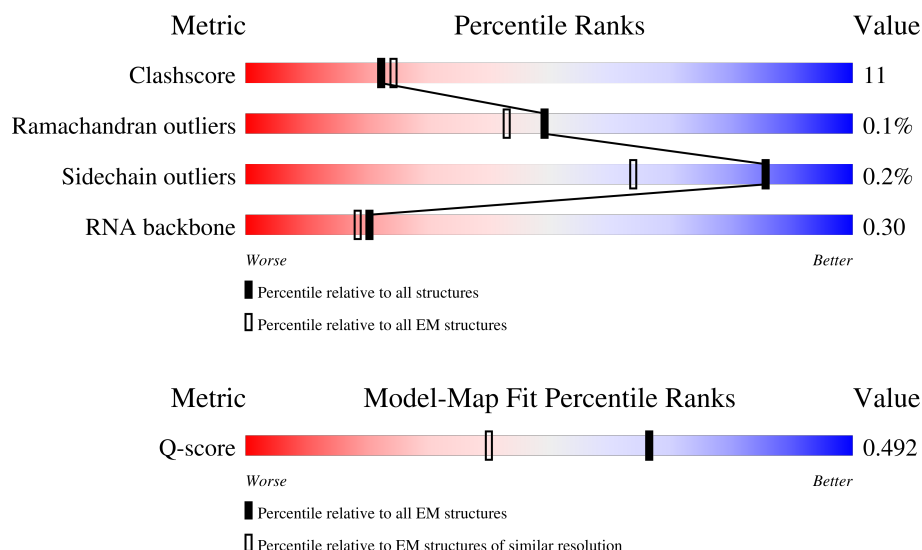
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 2.80 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.



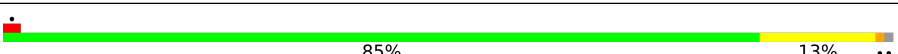
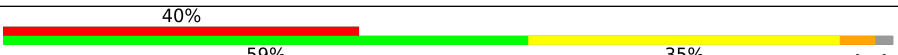
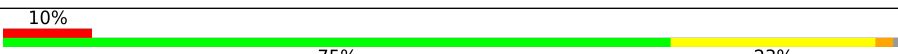
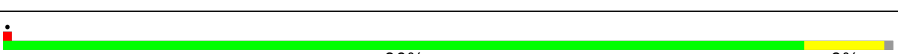
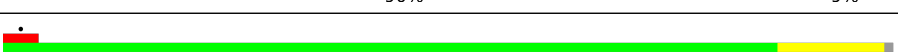
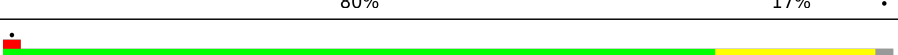
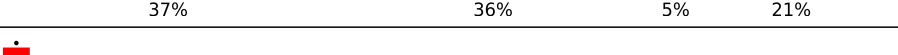
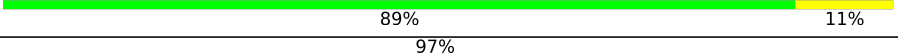
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11806 (2.30 - 3.30)

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

Mol	Chain	Length	Quality of chain
1	A	2927	
2	B	119	
3	C	277	

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Mol	Chain	Length	Quality of chain
4	D	209	 82% 17% .
5	E	207	 7% 82% 16% .
6	G	179	 50% 63% 34% ..
7	J	145	 81% 17% .
8	K	122	 77% 23% .
9	L	146	 24% 75% 25%
10	N	120	 85% 13% ..
11	O	120	 40% 59% 35% . .
12	P	115	 10% 75% 23% ..
13	Q	118	 90% 9% .
14	R	102	 87% 12% .
15	S	113	 80% 17% .
16	T	95	 80% 18% .
17	U	103	 9% 81% 17% .
18	V	94	 29% 37% 36% 5% 21%
19	Y	66	 68% 30% .
20	Z	59	 76% 22% .
21	b	59	 12% 69% 22% 8%
22	d	44	 89% 11%
23	f	37	 97% 76% 22% .

2 Entry composition

There are 23 unique types of molecules in this entry. The entry contains 82115 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2818	Total	C	N	O	P	0	0
			60508	26994	11168	19528	2818		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	267	C	U	conflict	GB 2210155072
A	1558	C	G	conflict	GB 2210155072

- Molecule 2 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	112	Total	C	N	O	P	0	0
			2395	1068	435	780	112		

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	275	Total	C	N	O	S	0	0
			2111	1312	416	377	6		

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	207	Total	C	N	O	S	0	0
			1575	988	290	292	5		

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	205	Total	C	N	O	S	0	0
			1561	980	289	290	2		

- Molecule 6 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	175	Total	C	N	O	S	0	0
			1342	835	248	257	2		

- Molecule 7 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	J	142	Total	C	N	O	S	0	0
			1123	710	206	202	5		

- Molecule 8 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	K	122	Total	C	N	O	S	0	0
			920	571	173	172	4		

- Molecule 9 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L	146	Total	C	N	O	S	0	0
			1081	671	207	201	2		

- Molecule 10 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	N	119	Total	C	N	O	S	0	0
			953	583	186	180	4		

- Molecule 11 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	O	118	Total	C	N	O	S	0	0
			892	549	173	169	1		

- Molecule 12 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
12	P	114	Total	C	N	O	0	0
			936	595	184	157		

- Molecule 13 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Q	117	Total	C	N	O	S	0	0
			940	591	189	156	4		

- Molecule 14 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	R	101	Total	C	N	O		0	0
			786	501	139	146			

- Molecule 15 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	S	109	Total	C	N	O	S	0	0
			842	525	164	150	3		

- Molecule 16 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	T	93	Total	C	N	O	S	0	0
			752	472	137	139	4		

- Molecule 17 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	U	100	Total	C	N	O	S	0	0
			754	473	141	137	3		

- Molecule 18 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	V	74	Total	C	N	O		0	0
			578	359	113	106			

- Molecule 19 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	Y	65	Total	C	N	O	S	0	0
			530	328	102	98	2		

- Molecule 20 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Z	58	Total	C	N	O	S	0	0
			455	281	89	84	1		

- Molecule 21 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	b	54	Total	C	N	O	S	0	0
			426	262	86	71	7		

- Molecule 22 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	d	44	Total	C	N	O	S	0	0
			367	222	89	54	2		

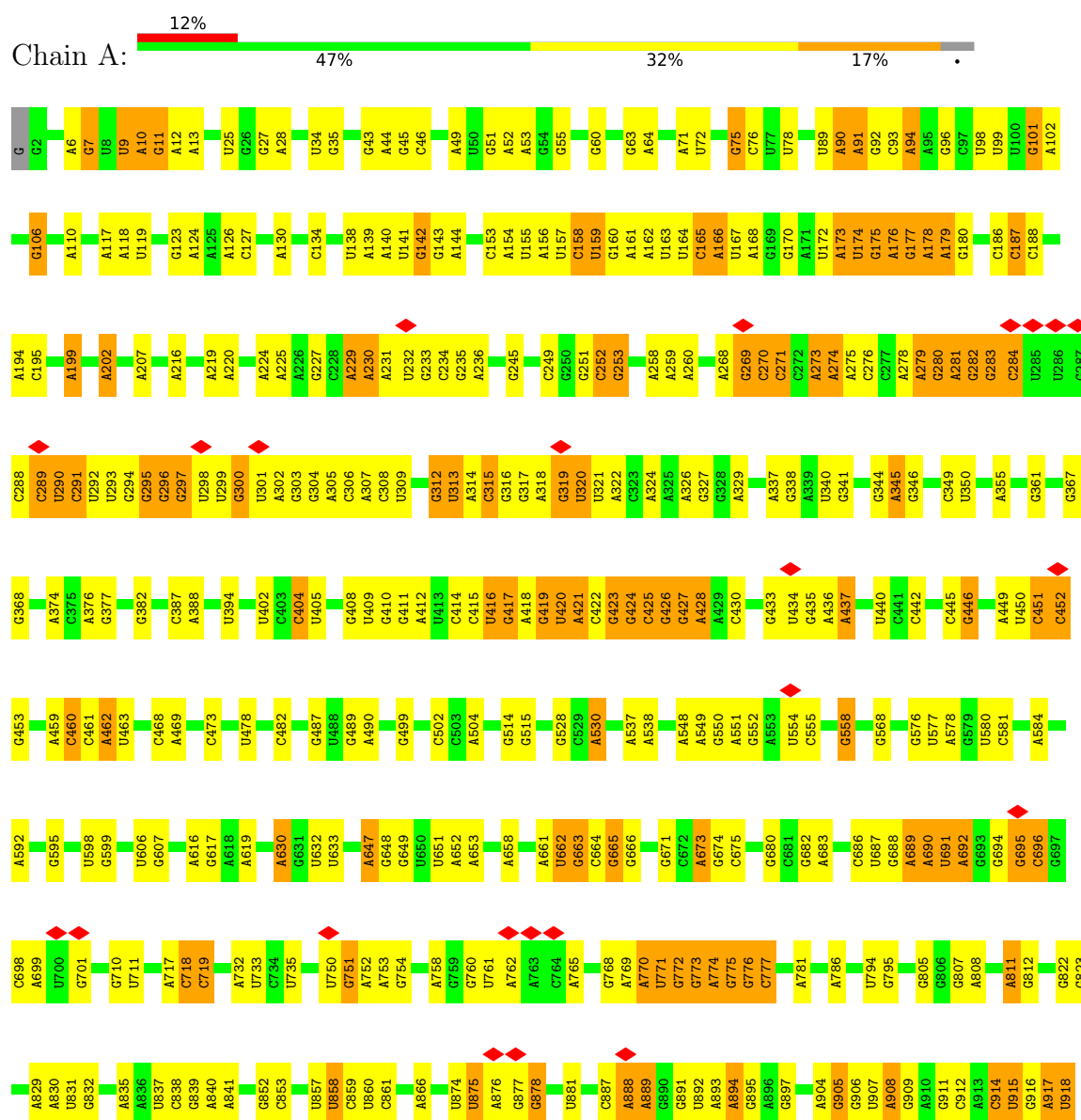
- Molecule 23 is a protein called Large ribosomal subunit protein bL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	f	36	Total	C	N	O	S	0	0
			288	181	59	44	4		

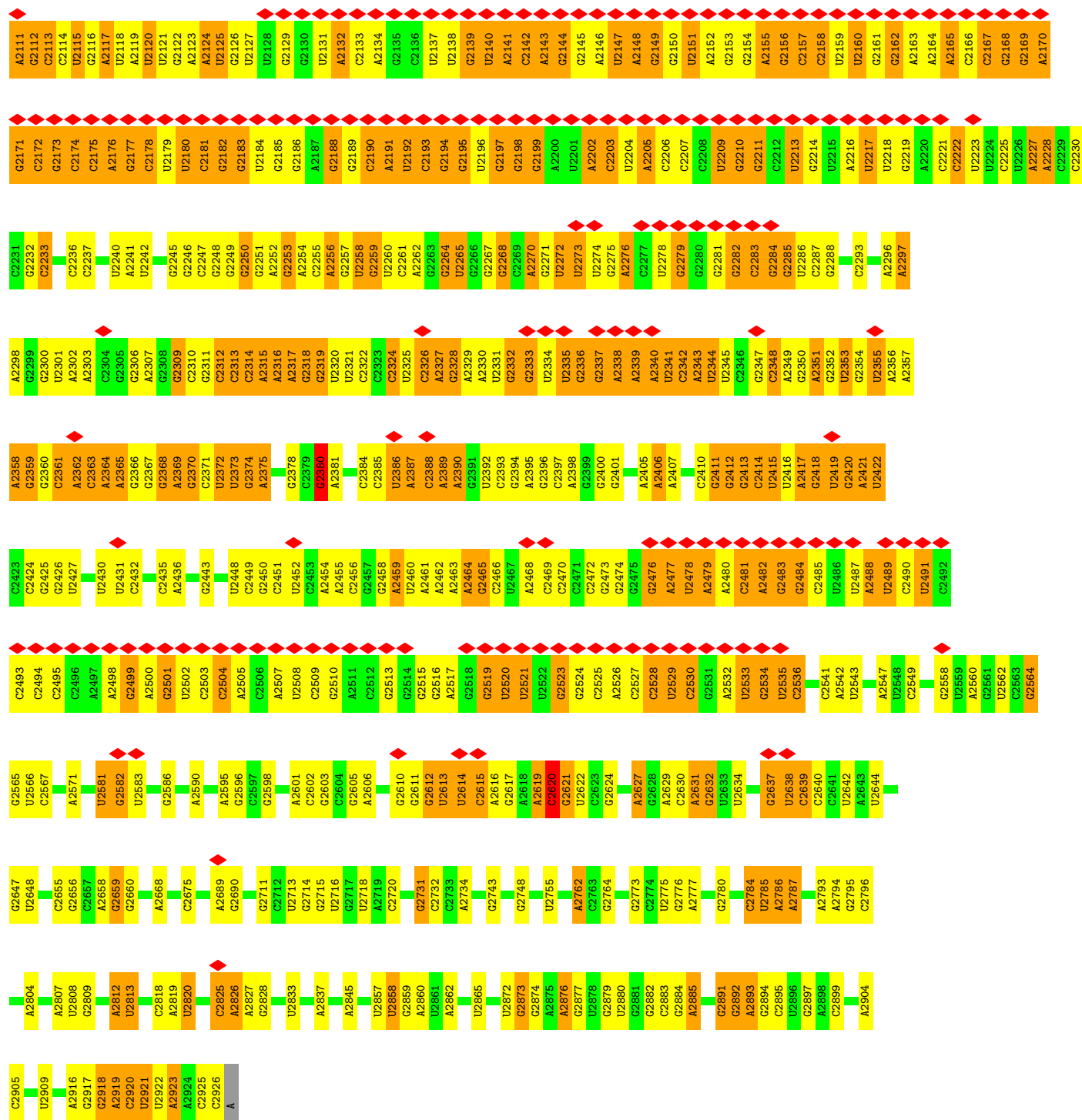
3 Residue-property plots

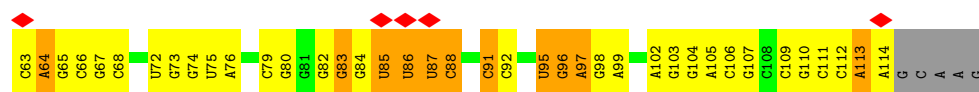
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 23S rRNA

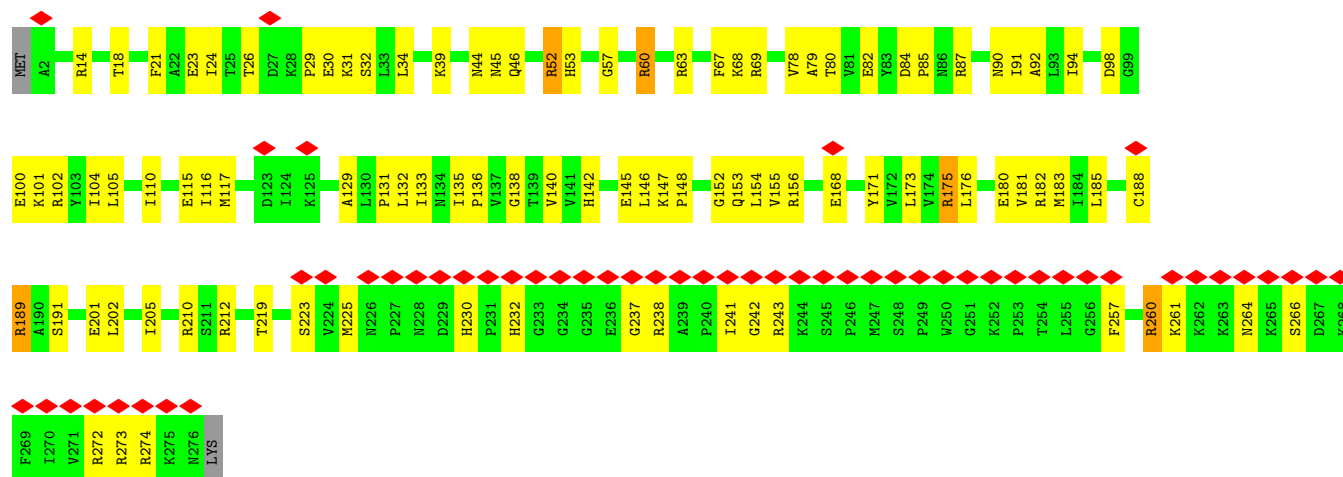


A1999	G	A1813	A1727	A1614	A1534	A1485	U1249	G1156	A1096	U919
A2000	U	A1814	C1726	A1615	U1535	U1486	G1250	A1357	A1097	G920
G2001	A	A1815	G1736	G1616	G1457	G1457	G1251	U1159	C1098	G921
G2002	A	A1816	A1734	A1617	A1537	G1468	G1252	G1160	C1099	A922
C2003	C	C1817	A1735	A1618	G1538	G1469	G1260	G1161	A1006	A923
G2004	U	A1818	G1744	A1619	G1539	G1470	C1261	U1162	G1007	C923
C2005	A	G1821	A1745	A1620	A1540	G1471	G1264	A1008	U1009	U924
A2006	U	G1822	A1746	G1621	G1546	G1472	G1265	A1103	G1015	A925
G2007	A	U1823	G1752	C1622	C1551	C1473	A1266	U1104	G1016	G926
C2008	A	C1824	C1753	C1623	C1552	C1474	G1267	U1105	G1017	G927
A2009	G	U1825	U1754	A1624	A1553	C1476	G1268	U1106	G1018	G928
G2010	C	C1826	G1757	A1627	U1554	G1477	A1277	U1107	G1019	G929
U2011	U	U1827	U1758	G1628	A1555	G1478	G1278	G1108	A1020	C930
U2020	C	C1828	U1759	G1629	A1556	A1480	C1279	G1109	A1026	C931
G2021	U	G1830	A1760	A1631	G1557	A1485	G1280	C1110	A1027	C932
C2022	A	A1831	G1761	G1632	G1561	G1488	U1289	U1111	C1028	C933
G2023	C	C1832	G1762	G1633	A1562	U1489	G1290	U1112	A1029	U934
U2024	G	A1838	U1763	G1637	G1563	A1490	A1291	A1113	G1030	A935
C2025	U	A1839	U1764	A1638	A1564	A1491	G1292	G1114	C1031	C936
A2026	A	G1840	G1765	G1639	U1565	G1492	A1293	A1115	A1036	C937
G2027	C	C1841	C1766	G1640	G1566	C1493	G1296	A1116	C1041	G938
A2052	C	A1844	A1767	U1641	U1567	G1494	A1308	A1117	A1042	G939
A2060	G	A1845	A1768	G1642	G1568	C1495	G1311	A1118	A1046	G940
G2061	A	G1846	C1770	G1651	A1569	G1496	A1312	A1119	A1047	U941
A2062	A	A1847	G1771	C1652	U1570	G1497	G1313	G1120	A1055	A942
G2068	G	U1848	C1772	A1653	G1571	U1498	A1314	C1121	A1056	A943
C2072	U	U1849	U1773	A1654	C1572	A1499	G1315	C1122	G1057	C944
U2073	C	G1850	A1774	A1655	C1573	U1500	A1194	A1123	U1058	C945
G2080	C	A1851	G1775	A1656	U1574	U1501	G1316	C1124	A1059	G946
A2080	C	G1852	A1776	G1664	G1575	G1502	G1317	C1125	U1065	A947
C2084	U	G1853	G1777	A1667	G1576	A1504	A1323	A1126	A1066	A948
A2087	A	C1854	A1778	G1673	G1577	U1505	G1324	U1127	A1067	U949
G2088	U	U1855	C1779	A1677	G1578	A1506	A1325	U1128	G1068	U950
A2089	U	G1856	G1780	G1674	A1579	A1507	U1214	U1129	A1072	A951
G2090	G	A1857	C1781	G1675	A1580	C1508	U1215	A1130	A1073	A952
A2091	A	C1858	G1782	G1676	U1581	U1509	U1216	A1131	A1074	G953
C2092	C	G1859	C1783	A1679	U1582	C1509	C1217	A1132	A1075	U954
G2093	G	U1860	A1784	A1680	A1583	G1512	U1217	G1133	G1076	A955
C2094	C	G1861	G1785	U1681	A1584	C1513	U1218	A1134	G1077	A956
G2095	C	C1862	U1786	C1682	A1585	G1514	G1219	G1135	U1078	A957
C2096	C	U1863	G1787	G1689	G1586	A1515	A1221	U1136	U1079	A958
U2097	A	G1864	A1791	U1689	U1587	A1516	A1222	C1137	U1080	C959
G2098	U	C1865	G1792	A1691	A1588	A1517	C1223	C1138	U1081	A964
C2099	G	U1866	G1793	U1692	A1593	A1518	G1227	U1139	G1082	G973
A2100	A	G	G1801	C1693	G1594	A1519	G1234	U1140	C1089	A974
G2101	A	A	A1802	U1694	U1595	C1526	U1240	A1141	A1092	G975
C2102	C	C	U1803	G1695	U1596	G1527	A1244	A1142	G1093	U976
U2103	G	U	G1804	A1697	C1597	U1528	G1245	U1143	U1094	U977
G2104	C	C	U1805	U1698	U1598	G1529	G1247	A1144	A1095	A978
A2105	C	U	G1806	G1712	U1599	G1530	U1352	G1145	C1146	U979
U2106	G	G	U1807	G1719	G1600	A1531	U1351	U1147	C1147	C980
C2107	G	A	U1808	G1720	A1606	A1532	A1461	A1149	C1148	G981
U2108	C	C	A	A	C1607	A1533	A1464	U1151	U1150	G985
G2109	C	A	A	A	A1608	A1533	A1464	G1152	G1151	G986
C2110	C	C	A	A	A1608	A1533	A1464	U1152	U1151	A987
A1998	U	A	A1812	A	A1608	A1533	A1464	C1155	C1155	C992

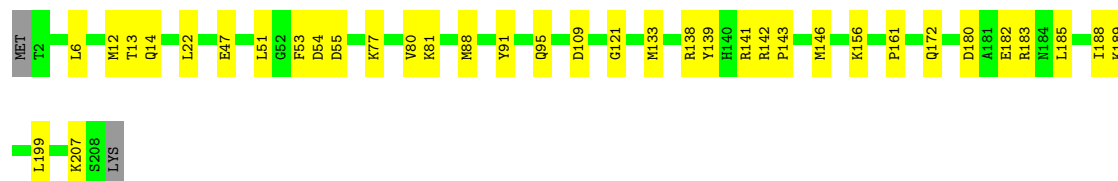
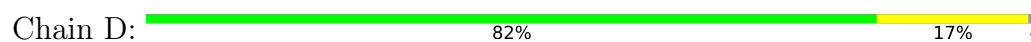




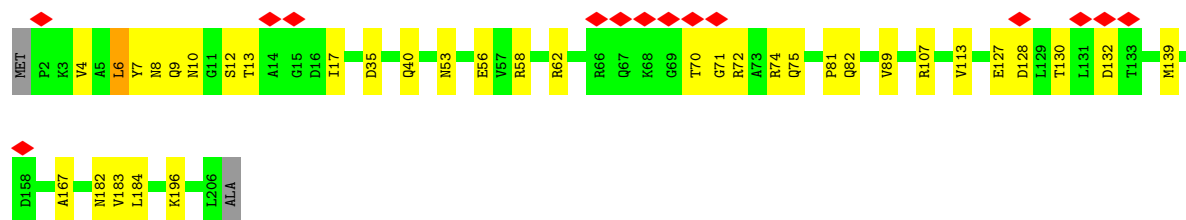
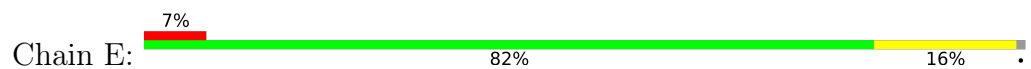
• Molecule 3: 50S ribosomal protein L2



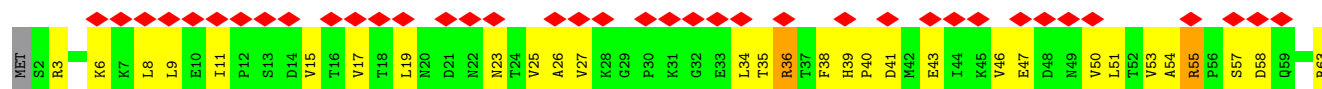
• Molecule 4: 50S ribosomal protein L3

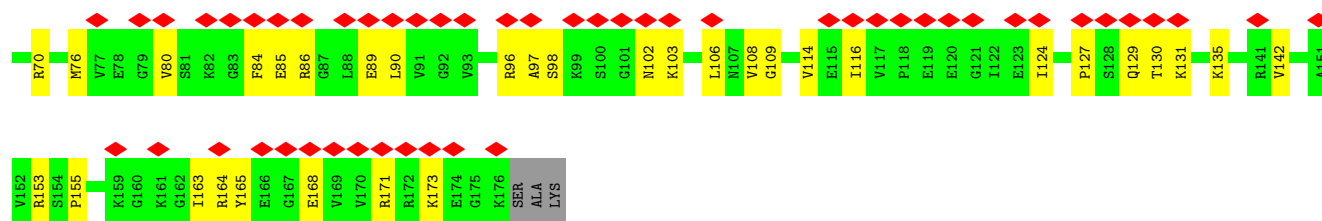


• Molecule 5: 50S ribosomal protein L4

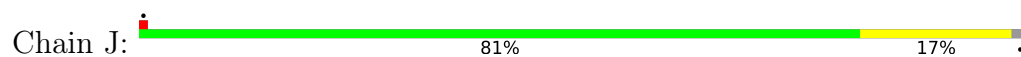


• Molecule 6: 50S ribosomal protein L6

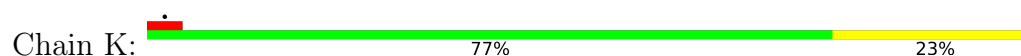




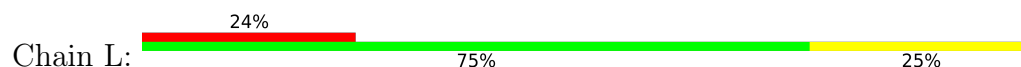
• Molecule 7: 50S ribosomal protein L13



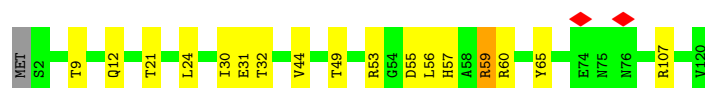
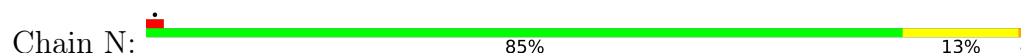
• Molecule 8: 50S ribosomal protein L14



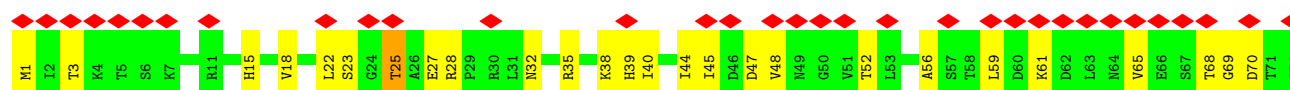
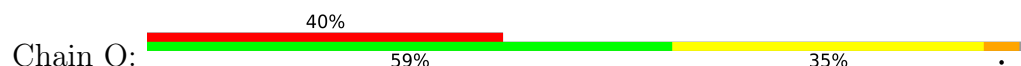
• Molecule 9: 50S ribosomal protein L15

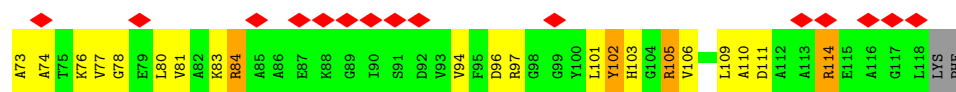


• Molecule 10: 50S ribosomal protein L17

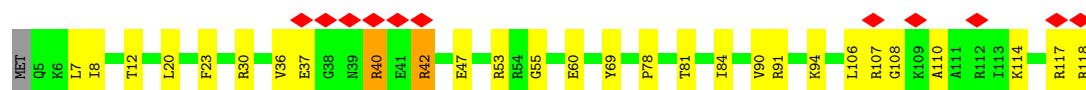
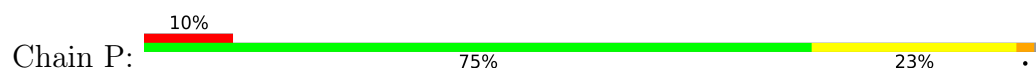


• Molecule 11: 50S ribosomal protein L18

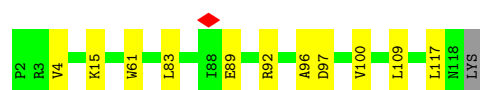




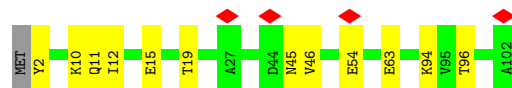
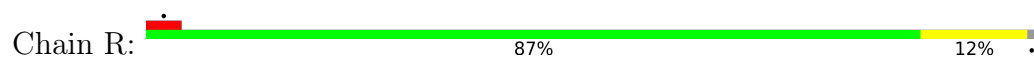
- Molecule 12: 50S ribosomal protein L19



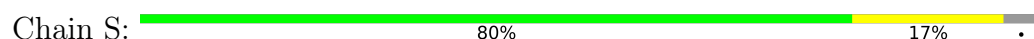
- Molecule 13: 50S ribosomal protein L20



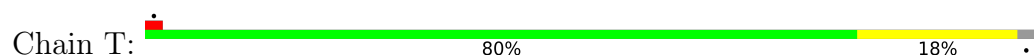
- Molecule 14: 50S ribosomal protein L21



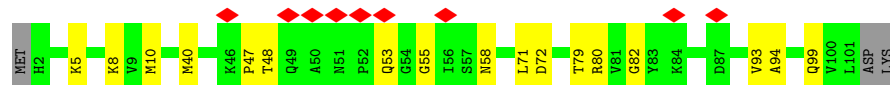
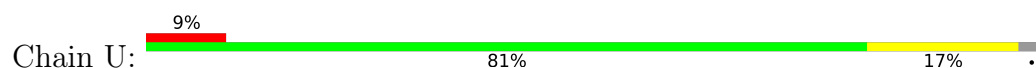
- Molecule 15: 50S ribosomal protein L22



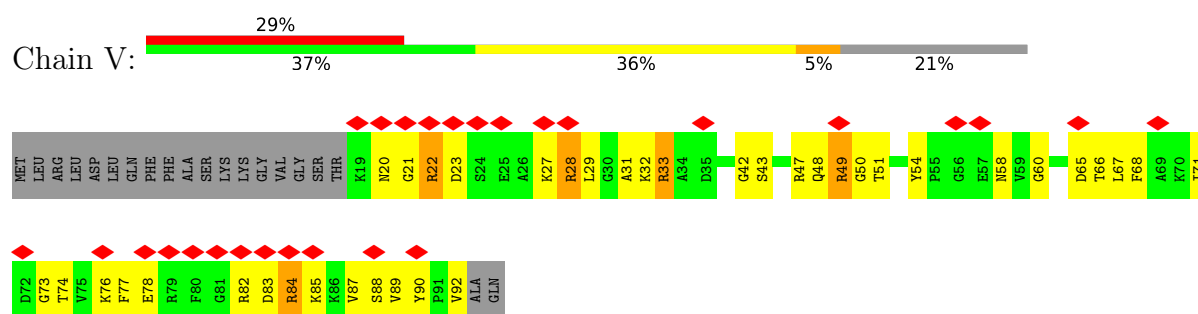
- Molecule 16: 50S ribosomal protein L23



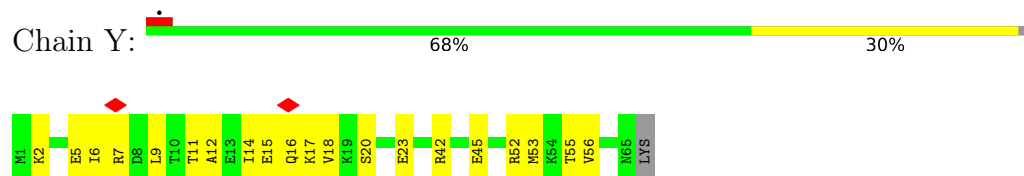
- Molecule 17: 50S ribosomal protein L24



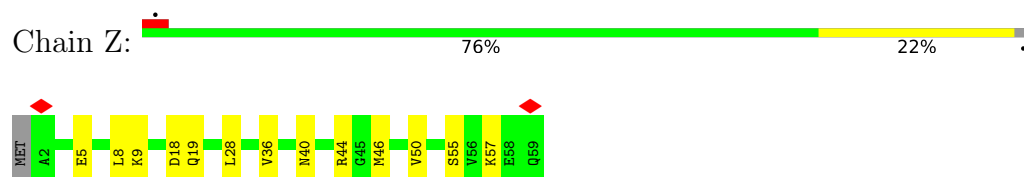
- Molecule 18: 50S ribosomal protein L27



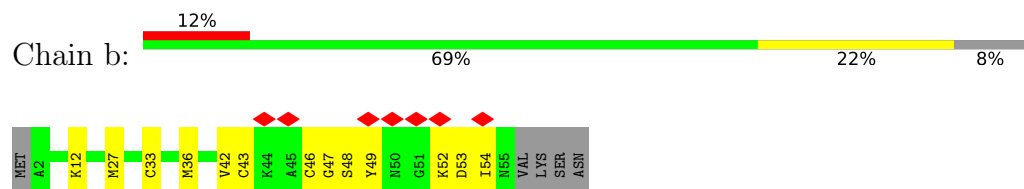
- Molecule 19: 50S ribosomal protein L29



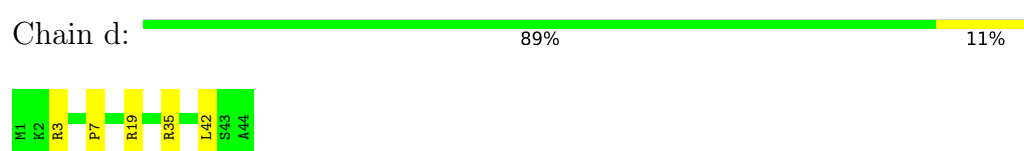
- Molecule 20: 50S ribosomal protein L30



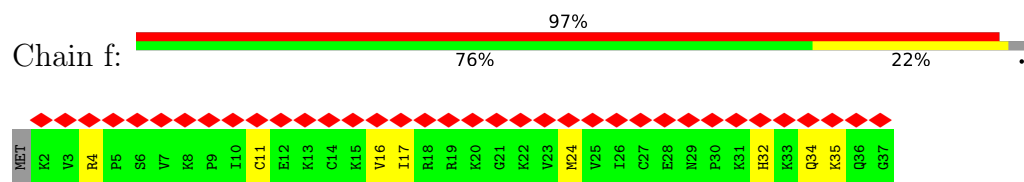
- Molecule 21: 50S ribosomal protein L32



- Molecule 22: 50S ribosomal protein L34



- Molecule 23: Large ribosomal subunit protein bL36



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	113285	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.314	Depositor
Minimum map value	-0.104	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.066	Depositor
Map size (Å)	383.04, 383.04, 383.04	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.855, 0.855, 0.855	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	A	0.42	0/67774	0.57	6/105732 (0.0%)
2	B	0.72	0/2678	0.93	0/4174
3	C	0.96	0/2148	1.12	0/2881
4	D	0.40	0/1597	0.54	0/2140
5	E	0.52	0/1580	0.65	0/2132
6	G	0.48	0/1360	0.64	0/1832
7	J	0.30	0/1146	0.37	0/1542
8	K	0.39	0/927	0.56	0/1245
9	L	0.32	0/1093	0.60	0/1457
10	N	0.45	0/960	0.61	0/1284
11	O	0.64	0/900	0.91	1/1209 (0.1%)
12	P	0.38	0/949	0.54	0/1269
13	Q	0.34	0/952	0.47	0/1266
14	R	0.42	0/797	0.59	0/1070
15	S	0.35	0/851	0.51	0/1146
16	T	0.44	0/759	0.69	0/1011
17	U	0.31	0/764	0.57	0/1022
18	V	0.70	0/586	0.96	0/779
19	Y	0.39	0/531	0.71	0/707
20	Z	0.23	0/457	0.38	0/613
21	b	0.27	0/433	0.44	0/574
22	d	0.29	0/370	0.32	0/483
23	f	0.15	0/291	0.39	0/383
All	All	0.45	0/89903	0.61	7/135951 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
3	C	0	13
4	D	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
5	E	0	2
6	G	0	2
7	J	0	1
10	N	0	3
11	O	0	3
12	P	0	2
15	S	0	1
18	V	0	7
All	All	0	37

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	2380	G	C3'-C2'-C1'	-6.61	94.89	101.50
1	A	2620	C	O3'-P-O5'	6.09	113.14	104.00
1	A	1863	U	C1'-O4'-C4'	-5.85	103.85	109.70
1	A	2348	C	C2'-C3'-O3'	5.36	117.53	109.50
1	A	2621	G	C3'-C2'-C1'	-5.27	96.23	101.50
11	O	25	THR	N-CA-CB	-5.19	102.48	110.42
1	A	1464	A	C3'-C2'-C1'	-5.14	96.36	101.50

There are no chirality outliers.

All (37) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	102	ARG	Sidechain
3	C	14	ARG	Sidechain
3	C	175	ARG	Sidechain
3	C	182	ARG	Sidechain
3	C	189	ARG	Sidechain
3	C	212	ARG	Sidechain
3	C	260	ARG	Sidechain
3	C	273	ARG	Sidechain
3	C	274	ARG	Sidechain
3	C	52	ARG	Sidechain
3	C	60	ARG	Sidechain
3	C	63	ARG	Sidechain
3	C	87	ARG	Sidechain
4	D	138	ARG	Sidechain
4	D	141	ARG	Sidechain

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Mol	Chain	Res	Type	Group
4	D	142	ARG	Sidechain
5	E	107	ARG	Sidechain
5	E	74	ARG	Sidechain
6	G	36	ARG	Sidechain
6	G	55	ARG	Sidechain
7	J	38	ARG	Sidechain
10	N	53	ARG	Sidechain
10	N	59	ARG	Sidechain
10	N	60	ARG	Sidechain
11	O	105	ARG	Sidechain
11	O	114	ARG	Sidechain
11	O	84	ARG	Sidechain
12	P	40	ARG	Sidechain
12	P	42	ARG	Sidechain
15	S	41	ARG	Sidechain
18	V	22	ARG	Sidechain
18	V	28	ARG	Sidechain
18	V	33	ARG	Sidechain
18	V	47	ARG	Sidechain
18	V	49	ARG	Sidechain
18	V	82	ARG	Sidechain
18	V	84	ARG	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	60508	0	30450	854	0
2	B	2395	0	1212	61	0
3	C	2111	0	2200	122	0
4	D	1575	0	1642	31	0
5	E	1561	0	1647	42	0
6	G	1342	0	1388	72	0
7	J	1123	0	1162	17	0
8	K	920	0	977	38	0
9	L	1081	0	1132	35	0
10	N	953	0	983	14	0
11	O	892	0	925	93	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	P	936	0	1008	32	0
13	Q	940	0	1005	13	0
14	R	786	0	826	9	0
15	S	842	0	899	16	0
16	T	752	0	802	17	0
17	U	754	0	809	19	0
18	V	578	0	586	42	0
19	Y	530	0	568	29	0
20	Z	455	0	491	13	0
21	b	426	0	445	12	0
22	d	367	0	410	5	0
23	f	288	0	327	4	0
All	All	82115	0	51894	1496	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 11.

All (1496) 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)
6:G:46:VAL:CA	6:G:51:LEU:HD22	1.08	1.55
6:G:46:VAL:C	6:G:51:LEU:CD2	1.90	1.43
6:G:46:VAL:C	6:G:51:LEU:HD22	1.42	1.40
6:G:46:VAL:CA	6:G:51:LEU:CD2	2.00	1.36
6:G:47:GLU:N	6:G:51:LEU:CD2	1.89	1.35
11:O:18:VAL:O	11:O:22:LEU:HD13	1.25	1.27
1:A:2250:G:O2'	3:C:147:LYS:CE	1.85	1.23
1:A:2250:G:O2'	3:C:147:LYS:HE2	1.06	1.22
6:G:46:VAL:HA	6:G:51:LEU:CD2	1.62	1.22
19:Y:17:LYS:CG	19:Y:53:MET:HE1	1.72	1.20
1:A:2359:G:H21	18:V:49:ARG:HG2	1.02	1.19
11:O:28:ARG:CZ	11:O:94:VAL:HG22	1.74	1.17
6:G:47:GLU:N	6:G:51:LEU:HD23	1.54	1.16
3:C:52:ARG:NH2	3:C:53:HIS:NE2	1.92	1.15
19:Y:17:LYS:HG3	19:Y:53:MET:CE	1.76	1.14
1:A:753:A:H62	1:A:772:G:N2	1.46	1.13
19:Y:11:THR:O	19:Y:15:GLU:HG2	1.49	1.13
11:O:40:ILE:CD1	11:O:109:LEU:HD11	1.78	1.13
11:O:40:ILE:HG21	11:O:105:ARG:CD	1.77	1.12
1:A:753:A:N6	1:A:772:G:H21	1.49	1.11
16:T:36:LYS:HG2	16:T:56:ILE:HD12	1.35	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:128:ASP:OD1	5:E:130:THR:HG23	1.53	1.06
11:O:22:LEU:HD23	11:O:96:ASP:OD1	1.56	1.06
9:L:89:THR:OG1	9:L:121:LEU:HD23	1.54	1.05
12:P:106:LEU:HD11	12:P:110:ALA:CB	1.87	1.04
11:O:40:ILE:HD13	11:O:109:LEU:HD11	1.38	1.04
12:P:106:LEU:HD11	12:P:110:ALA:HB1	1.35	1.03
8:K:8:LEU:HD13	8:K:82:ASN:HB3	1.41	1.03
1:A:499:G:C8	5:E:58:ARG:HD3	1.94	1.03
3:C:135:ILE:HG23	3:C:136:PRO:HD2	1.37	1.03
1:A:2359:G:N2	18:V:49:ARG:HG2	1.74	1.02
1:A:1847:U:H2'	3:C:156:ARG:HD3	1.40	1.02
1:A:1847:U:H2'	3:C:156:ARG:CD	1.89	1.01
11:O:40:ILE:HG21	11:O:105:ARG:HD2	1.37	1.01
1:A:1847:U:C2'	3:C:156:ARG:HG2	1.90	1.01
17:U:82:GLY:O	17:U:93:VAL:HG12	1.60	1.00
11:O:28:ARG:NH1	11:O:94:VAL:HG22	1.77	0.99
6:G:46:VAL:C	6:G:51:LEU:HD21	1.88	0.98
8:K:8:LEU:CD1	8:K:82:ASN:HB3	1.93	0.98
1:A:9:U:H3'	1:A:10:A:H4'	1.46	0.98
11:O:40:ILE:HD13	11:O:109:LEU:CD1	1.92	0.97
19:Y:17:LYS:HG3	19:Y:53:MET:HE1	0.99	0.97
1:A:1474:C:HO2'	1:A:1617:A:H8	1.01	0.97
1:A:162:A:H62	1:A:165:C:H42	1.10	0.97
3:C:44:ASN:HD22	3:C:46:GLN:HG3	1.25	0.96
4:D:14:GLN:HB3	4:D:22:LEU:HD11	1.47	0.96
1:A:2359:G:N2	18:V:49:ARG:CG	2.28	0.96
5:E:70:THR:HG21	5:E:72:ARG:NH2	1.80	0.96
2:B:10:G:N3	18:V:83:ASP:OD1	1.99	0.96
1:A:153:C:H42	1:A:174:U:H3	1.12	0.95
11:O:78:GLY:HA2	11:O:109:LEU:HD22	1.46	0.95
18:V:58:ASN:ND2	18:V:71:ILE:HD12	1.82	0.95
8:K:120:GLU:CG	12:P:69:TYR:HE2	1.79	0.95
20:Z:9:LYS:HD2	20:Z:55:SER:HB2	1.46	0.94
11:O:110:ALA:HB1	11:O:114:ARG:NH1	1.84	0.93
1:A:2359:G:H21	18:V:49:ARG:CG	1.81	0.92
1:A:1500:U:H5'	10:N:59:ARG:HH11	1.34	0.92
12:P:37:GLU:OE2	12:P:42:ARG:HD2	1.68	0.92
4:D:6:LEU:HD13	4:D:199:LEU:HD11	1.50	0.91
6:G:47:GLU:H	6:G:51:LEU:HD23	1.21	0.91
1:A:772:G:H1'	1:A:773:G:H5'	1.49	0.91
7:J:24:LYS:HB2	7:J:29:LEU:HD23	1.53	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:U:93:VAL:HG23	17:U:99:GLN:O	1.72	0.89
1:A:2318:G:H1	1:A:2372:U:H3	1.21	0.89
1:A:2309:G:H4'	1:A:2356:A:H5'	1.54	0.88
19:Y:17:LYS:CG	19:Y:53:MET:CE	2.44	0.88
11:O:28:ARG:CZ	11:O:94:VAL:CG2	2.52	0.87
3:C:181:VAL:CG2	3:C:272:ARG:HD3	2.05	0.87
9:L:127:LYS:HD3	9:L:128:PHE:H	1.40	0.87
5:E:9:GLN:HE21	5:E:130:THR:H	1.19	0.87
11:O:40:ILE:HD11	11:O:109:LEU:HD11	1.54	0.87
4:D:47:GLU:HB3	4:D:88:MET:SD	2.14	0.87
11:O:78:GLY:CA	11:O:109:LEU:CD2	2.53	0.86
11:O:40:ILE:CD1	11:O:109:LEU:CD1	2.51	0.86
3:C:52:ARG:NH2	3:C:53:HIS:CE1	2.43	0.86
2:B:10:G:C2	18:V:83:ASP:OD1	2.28	0.86
1:A:1521:G:H22	1:A:1563:G:H1	1.16	0.86
8:K:120:GLU:HG2	12:P:69:TYR:CE2	2.11	0.85
3:C:181:VAL:HG23	3:C:272:ARG:HD3	1.58	0.85
11:O:40:ILE:HG21	11:O:105:ARG:HD3	1.56	0.85
6:G:46:VAL:HA	6:G:51:LEU:HD22	0.86	0.84
3:C:94:ILE:HD12	3:C:104:ILE:HG13	1.57	0.84
20:Z:9:LYS:HD2	20:Z:55:SER:CB	2.08	0.84
17:U:40:MET:HE2	17:U:58:ASN:ND2	1.92	0.84
1:A:2312:C:H2'	1:A:2313:C:H5'	1.60	0.83
3:C:135:ILE:CG2	3:C:136:PRO:HD2	2.07	0.83
1:A:2424:C:O2	1:A:2450:G:N2	2.10	0.83
1:A:2306:G:C8	18:V:20:ASN:ND2	2.47	0.83
1:A:2155:A:H4'	1:A:2156:G:H4'	1.61	0.82
8:K:120:GLU:CG	12:P:69:TYR:CE2	2.61	0.82
11:O:74:ALA:HB1	11:O:105:ARG:HG3	1.61	0.82
1:A:805:G:H21	1:A:2010:A:H62	1.27	0.82
3:C:67:PHE:CE2	3:C:156:ARG:NH2	2.47	0.82
1:A:1082:G:H22	1:A:1165:U:H3	1.26	0.82
1:A:695:G:H3'	1:A:696:C:H5''	1.60	0.82
8:K:120:GLU:HG3	12:P:69:TYR:HE2	1.43	0.81
16:T:62:LYS:H	16:T:73:THR:HG22	1.45	0.81
1:A:1847:U:C3'	3:C:156:ARG:HG2	2.11	0.80
9:L:89:THR:HG1	9:L:121:LEU:HD23	1.44	0.80
6:G:171:ARG:HH22	6:G:173:LYS:HB2	1.45	0.80
5:E:128:ASP:OD1	5:E:130:THR:CG2	2.27	0.80
1:A:302:A:H1'	1:A:303:G:C8	2.17	0.80
1:A:2352:G:H1	1:A:2361:C:H42	1.28	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:O:78:GLY:CA	11:O:109:LEU:HD22	2.12	0.80
1:A:515:G:O2'	5:E:62:ARG:NH2	2.14	0.80
1:A:2614:U:H4'	1:A:2615:C:H4'	1.64	0.80
1:A:2389:A:H3'	1:A:2390:A:H8	1.46	0.79
3:C:145:GLU:OE2	3:C:154:LEU:HD21	1.82	0.79
1:A:934:U:H5'	1:A:936:C:H2'	1.64	0.79
1:A:1108:G:N2	1:A:1122:C:O2	2.13	0.79
16:T:54:VAL:HG22	16:T:81:VAL:HG12	1.64	0.79
1:A:274:A:N6	1:A:295:G:N3	2.31	0.79
1:A:422:C:H42	1:A:445:C:H42	1.29	0.79
1:A:928:G:H3'	1:A:929:G:H8	1.47	0.78
1:A:1847:U:C2'	3:C:156:ARG:CG	2.61	0.78
1:A:1847:U:H3'	3:C:156:ARG:CG	2.12	0.78
11:O:18:VAL:O	11:O:22:LEU:CD1	2.21	0.78
11:O:110:ALA:CB	11:O:114:ARG:HH12	1.96	0.78
1:A:153:C:N4	1:A:174:U:H3	1.80	0.78
8:K:19:VAL:HG13	8:K:42:THR:O	1.83	0.78
11:O:110:ALA:CB	11:O:114:ARG:NH1	2.46	0.78
6:G:46:VAL:HA	6:G:51:LEU:CG	2.09	0.78
5:E:139:MET:HG2	5:E:167:ALA:HB2	1.64	0.78
18:V:73:GLY:HA3	18:V:92:VAL:HG23	1.65	0.78
1:A:499:G:N7	5:E:58:ARG:HD3	1.98	0.78
1:A:2358:A:H2'	1:A:2359:G:C8	2.19	0.78
1:A:2535:U:H3	1:A:2612:G:H22	1.31	0.78
6:G:55:ARG:NH2	6:G:58:ASP:O	2.15	0.77
1:A:1847:U:H2'	3:C:156:ARG:CG	2.13	0.77
5:E:9:GLN:NE2	5:E:130:THR:H	1.81	0.77
18:V:48:GLN:NE2	18:V:51:THR:HA	1.99	0.77
6:G:34:LEU:HB2	6:G:80:VAL:CG2	2.15	0.77
1:A:1864:G:H1'	1:A:1998:A:C8	2.20	0.76
2:B:13:A:H3'	2:B:14:G:H8	1.51	0.76
2:B:36:C:H1'	2:B:46:A:H1'	1.68	0.76
11:O:18:VAL:HG22	11:O:97:ARG:NH2	1.99	0.76
12:P:40:ARG:CD	12:P:42:ARG:HE	1.99	0.76
3:C:44:ASN:ND2	3:C:46:GLN:HG3	1.99	0.76
1:A:274:A:N7	1:A:295:G:C2	2.54	0.76
20:Z:18:ASP:OD1	20:Z:19:GLN:N	2.17	0.76
1:A:2317:A:H3'	1:A:2318:G:H8	1.50	0.75
1:A:751:G:H22	1:A:775:G:H1	1.32	0.75
11:O:74:ALA:CB	11:O:105:ARG:HG3	2.16	0.75
1:A:1847:U:H3'	3:C:156:ARG:HG3	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:732:A:H8	1:A:735:U:H3	1.34	0.75
17:U:40:MET:HE2	17:U:58:ASN:HD22	1.51	0.75
1:A:687:U:H3	1:A:692:A:H61	1.35	0.75
1:A:1078:A:H2	1:A:1168:G:H22	1.35	0.75
1:A:2373:U:H3'	1:A:2374:G:H3'	1.69	0.75
2:B:56:A:H3'	2:B:57:G:H8	1.51	0.74
1:A:1359:G:H22	1:A:1370:C:N4	1.86	0.74
11:O:18:VAL:HG22	11:O:97:ARG:HH21	1.51	0.74
11:O:28:ARG:NH1	11:O:94:VAL:CG2	2.49	0.74
3:C:115:GLU:O	3:C:115:GLU:HG2	1.87	0.74
3:C:131:PRO:HB3	3:C:189:ARG:HG2	1.70	0.74
1:A:1587:U:H2'	1:A:1588:A:H8	1.52	0.74
11:O:101:LEU:HD12	11:O:101:LEU:O	1.87	0.74
17:U:40:MET:CE	17:U:58:ASN:ND2	2.49	0.74
1:A:1752:G:H1	1:A:1780:C:H5	1.33	0.74
1:A:2250:G:HO2'	3:C:147:LYS:HE2	0.91	0.73
11:O:105:ARG:HH11	11:O:105:ARG:HB2	1.53	0.73
1:A:2250:G:O2'	3:C:147:LYS:CD	2.36	0.73
1:A:1616:G:O3'	1:A:1617:A:H4'	1.86	0.73
1:A:2120:U:H3	1:A:2257:G:H1	1.33	0.73
11:O:40:ILE:HG12	11:O:105:ARG:HD3	1.70	0.73
1:A:177:G:H2'	1:A:178:A:C8	2.23	0.73
1:A:1472:G:C8	1:A:1473:A:C8	2.76	0.73
1:A:202:A:H61	1:A:2462:A:H2'	1.54	0.73
1:A:1444:C:H2'	1:A:1445:A:H8	1.54	0.73
11:O:101:LEU:CD1	11:O:103:HIS:O	2.37	0.73
1:A:1863:U:H4'	1:A:1997:G:N2	2.04	0.72
1:A:2501:G:H2'	1:A:2504:C:H41	1.53	0.72
18:V:29:LEU:O	18:V:33:ARG:NH2	2.22	0.72
1:A:933:C:H2'	1:A:934:U:H2'	1.71	0.72
3:C:23:GLU:HG3	3:C:90:ASN:HD22	1.53	0.72
1:A:2158:C:H4'	1:A:2203:C:H4'	1.70	0.72
18:V:60:GLY:H	18:V:68:PHE:HB2	1.55	0.72
3:C:44:ASN:CG	3:C:45:ASN:H	1.98	0.72
5:E:128:ASP:CG	5:E:130:THR:HG23	2.14	0.72
1:A:1471:G:H2'	1:A:1472:G:C8	2.25	0.71
18:V:78:GLU:H	18:V:88:SER:HA	1.55	0.71
1:A:1864:G:H1'	1:A:1998:A:H8	1.52	0.71
1:A:2194:G:H8	1:A:2195:G:H21	1.38	0.71
1:A:2203:C:H2'	1:A:2204:U:C6	2.26	0.71
12:P:106:LEU:HD11	12:P:110:ALA:HB3	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:V:58:ASN:ND2	18:V:71:ILE:CD1	2.53	0.71
1:A:1460:G:H4'	1:A:1631:A:H62	1.54	0.71
1:A:1491:A:H62	1:A:1512:G:H22	1.37	0.71
11:O:102:TYR:CD1	11:O:106:VAL:HG12	2.26	0.71
11:O:78:GLY:CA	11:O:109:LEU:HD23	2.20	0.71
12:P:36:VAL:HG22	12:P:36:VAL:O	1.89	0.71
7:J:24:LYS:CB	7:J:29:LEU:HD23	2.20	0.71
11:O:80:LEU:HD12	11:O:83:LYS:HE2	1.72	0.71
1:A:158:C:HO2'	1:A:159:U:H6	1.39	0.70
10:N:55:ASP:O	10:N:59:ARG:HG3	1.91	0.70
5:E:13:THR:HG23	5:E:13:THR:O	1.91	0.70
1:A:49:A:H61	1:A:179:A:N6	1.89	0.70
1:A:2332:G:H1	1:A:2341:U:H3	1.39	0.70
1:A:2359:G:N2	18:V:49:ARG:HG3	2.06	0.70
2:B:112:C:H4'	11:O:52:THR:HB	1.74	0.70
5:E:4:VAL:HG22	5:E:4:VAL:O	1.90	0.70
1:A:1817:C:H5'	1:A:2619:A:H4'	1.73	0.70
11:O:102:TYR:HD1	11:O:106:VAL:HG12	1.56	0.70
1:A:1516:A:H62	1:A:1568:G:H8	1.38	0.70
1:A:2615:C:H3'	1:A:2616:A:H8	1.57	0.70
6:G:55:ARG:HE	6:G:63:ARG:CG	2.05	0.70
8:K:120:GLU:HG3	12:P:69:TYR:CE2	2.24	0.70
4:D:14:GLN:HB3	4:D:22:LEU:CD1	2.20	0.70
1:A:2118:U:H3	1:A:2259:G:H1	1.40	0.69
1:A:2279:G:H1'	1:A:2281:G:H5''	1.74	0.69
1:A:907:U:HO2'	1:A:908:A:H8	1.39	0.69
1:A:928:G:H3'	1:A:929:G:C8	2.26	0.69
1:A:1847:U:C3'	3:C:156:ARG:CG	2.70	0.69
3:C:53:HIS:CG	3:C:219:THR:HG22	2.27	0.69
1:A:2189:G:H3'	1:A:2190:C:H4'	1.72	0.69
3:C:133:ILE:HG22	3:C:133:ILE:O	1.92	0.69
11:O:111:ASP:HA	11:O:114:ARG:HD2	1.74	0.69
1:A:1696:G:HO2'	1:A:1697:A:H8	1.38	0.68
1:A:630:A:H62	1:A:1291:A:H2	1.42	0.68
1:A:772:G:H4'	1:A:773:G:OP1	1.94	0.68
1:A:1101:G:C4	1:A:1102:G:H1'	2.29	0.68
6:G:34:LEU:HB2	6:G:80:VAL:HG22	1.74	0.68
1:A:162:A:H62	1:A:165:C:N4	1.88	0.68
1:A:1081:U:H3	1:A:1166:G:H22	1.42	0.68
1:A:958:A:H8	1:A:2293:C:H1'	1.60	0.67
6:G:11:ILE:HB	6:G:50:VAL:HA	1.75	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:K:120:GLU:HG2	12:P:69:TYR:HE2	1.48	0.67
12:P:40:ARG:HD2	12:P:42:ARG:HE	1.60	0.67
1:A:1444:C:H2'	1:A:1445:A:C8	2.30	0.67
11:O:78:GLY:HA3	11:O:109:LEU:HD23	1.75	0.67
1:A:2250:G:HO2'	3:C:147:LYS:CE	1.84	0.67
3:C:132:LEU:O	3:C:133:ILE:HD13	1.95	0.67
15:S:24:ILE:HD11	15:S:32:ALA:HB1	1.76	0.67
1:A:306:C:H42	1:A:410:G:H22	1.41	0.66
1:A:942:U:H2'	1:A:944:C:C4	2.30	0.66
3:C:23:GLU:OE2	3:C:90:ASN:ND2	2.28	0.66
1:A:2330:A:H2'	1:A:2344:U:H3	1.59	0.66
3:C:171:TYR:CE1	3:C:185:LEU:HD12	2.29	0.66
11:O:1:MET:HG2	11:O:3:THR:HG22	1.76	0.66
1:A:2112:G:H3'	1:A:2113:C:H6	1.61	0.66
1:A:176:A:OP1	1:A:177:G:H4'	1.96	0.66
1:A:661:A:H1'	5:E:182:ASN:HD22	1.61	0.66
1:A:2279:G:H21	1:A:2283:C:H41	1.44	0.66
1:A:2250:G:C2'	3:C:147:LYS:HE2	2.23	0.66
4:D:188:ILE:HG22	4:D:189:LYS:N	2.10	0.65
5:E:9:GLN:O	5:E:10:ASN:OD1	2.13	0.65
12:P:117:ARG:HG2	12:P:118:ARG:HG2	1.78	0.65
1:A:1136:U:H3'	1:A:1137:G:H5''	1.77	0.65
1:A:1817:C:H2'	1:A:1818:A:C8	2.31	0.65
2:B:84:G:H3'	2:B:86:U:H3	1.60	0.65
16:T:91:GLU:HG3	16:T:91:GLU:O	1.96	0.65
1:A:2363:C:H4'	1:A:2364:A:H5'	1.77	0.65
5:E:70:THR:HG21	5:E:72:ARG:HH22	1.58	0.65
11:O:38:LYS:HB3	11:O:39:HIS:HD2	1.61	0.65
1:A:2620:C:H5	3:C:237:GLY:HA2	1.62	0.65
1:A:300:G:N7	1:A:468:C:H2'	2.12	0.65
1:A:2233:C:C1'	3:C:146:LEU:HD21	2.27	0.65
1:A:2639:C:H4'	1:A:2640:C:H5'	1.78	0.65
1:A:1491:A:N6	1:A:1512:G:H1	1.95	0.65
1:A:1470:G:H21	1:A:1622:C:H41	1.44	0.65
1:A:1586:G:H2'	1:A:1587:U:C6	2.32	0.65
1:A:1806:U:H3'	1:A:1807:U:H4'	1.77	0.65
1:A:1074:A:H2'	1:A:1075:A:C8	2.32	0.64
3:C:53:HIS:ND1	3:C:219:THR:HG22	2.12	0.64
6:G:23:ASN:HB3	6:G:40:PRO:HB3	1.79	0.64
11:O:74:ALA:O	11:O:109:LEU:CD2	2.44	0.64
1:A:1520:A:H61	1:A:1564:C:H42	1.45	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:O:77:VAL:HG13	11:O:109:LEU:HD21	1.78	0.64
1:A:2389:A:H3'	1:A:2390:A:C8	2.31	0.64
6:G:47:GLU:N	6:G:51:LEU:HD22	1.81	0.64
1:A:1863:U:H4'	1:A:1997:G:H22	1.61	0.64
1:A:2111:A:H5'	1:A:2112:G:H8	1.62	0.64
1:A:423:G:H2'	1:A:424:G:C8	2.33	0.64
3:C:84:ASP:HB2	3:C:91:ILE:HD12	1.78	0.64
17:U:82:GLY:O	17:U:93:VAL:CG1	2.41	0.64
21:b:27:MET:HG3	21:b:36:MET:HE2	1.78	0.64
3:C:171:TYR:HE1	3:C:185:LEU:HD12	1.61	0.64
3:C:201:GLU:HG3	3:C:202:LEU:HG	1.78	0.64
1:A:752:A:C6	1:A:774:A:C5	2.86	0.64
6:G:43:GLU:HB2	6:G:54:ALA:HB3	1.80	0.64
1:A:1347:A:H62	1:A:1651:G:H8	1.46	0.63
1:A:2154:G:H22	1:A:2192:U:H4'	1.62	0.63
15:S:29:VAL:HG21	15:S:69:LEU:HB2	1.80	0.63
4:D:80:VAL:O	4:D:81:LYS:HG3	1.97	0.63
11:O:110:ALA:HB3	11:O:114:ARG:HH12	1.62	0.63
1:A:751:G:N2	1:A:775:G:H1	1.94	0.63
1:A:2637:G:H5'	1:A:2638:U:H5'	1.80	0.63
3:C:131:PRO:HA	3:C:189:ARG:HA	1.79	0.63
8:K:18:GLU:OE1	8:K:44:LYS:HB2	1.99	0.63
1:A:1468:G:H1	1:A:1624:U:H3	1.45	0.63
6:G:106:LEU:HB2	6:G:114:VAL:HB	1.79	0.63
8:K:106:LEU:HD21	8:K:114:ILE:HD13	1.81	0.63
1:A:2318:G:N2	1:A:2372:U:O2	2.28	0.63
11:O:74:ALA:O	11:O:109:LEU:HD21	1.99	0.63
1:A:1447:C:H42	1:A:1638:A:H61	1.45	0.62
1:A:1521:G:N2	1:A:1563:G:H1	1.94	0.62
1:A:2362:A:H4'	1:A:2364:A:H5''	1.80	0.62
3:C:94:ILE:HD12	3:C:104:ILE:CG1	2.27	0.62
3:C:185:LEU:CD1	3:C:185:LEU:H	2.12	0.62
1:A:1076:G:H2'	1:A:1077:G:O4'	1.99	0.62
1:A:2615:C:H3'	1:A:2616:A:C8	2.33	0.62
1:A:1807:U:H2'	1:A:1808:U:C5	2.35	0.62
1:A:2177:G:H2'	1:A:2178:C:C5	2.34	0.62
1:A:296:G:O2'	1:A:297:G:H5'	1.99	0.62
3:C:44:ASN:ND2	3:C:45:ASN:OD1	2.32	0.62
1:A:949:U:H2'	1:A:950:U:C6	2.34	0.62
3:C:241:ILE:H	3:C:243:ARG:HH21	1.46	0.62
4:D:14:GLN:CB	4:D:22:LEU:HD11	2.26	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:P:106:LEU:CD1	12:P:110:ALA:CB	2.72	0.62
1:A:1517:A:H61	1:A:1567:U:H3	1.47	0.62
1:A:1847:U:O2'	3:C:156:ARG:HG2	2.00	0.62
1:A:11:G:H2'	1:A:12:A:H8	1.65	0.62
3:C:154:LEU:N	3:C:154:LEU:HD12	2.14	0.62
7:J:78:HIS:HB2	7:J:85:LEU:HD12	1.81	0.62
11:O:101:LEU:HD13	11:O:103:HIS:HB3	1.82	0.62
1:A:1652:C:H4'	1:A:1653:A:O5'	1.97	0.62
1:A:2133:C:H2'	1:A:2134:A:C8	2.34	0.62
5:E:17:ILE:HD11	5:E:196:LYS:HD3	1.82	0.62
11:O:40:ILE:CG2	11:O:105:ARG:HD3	2.30	0.62
1:A:776:G:H22	1:A:1802:A:H2	1.48	0.62
1:A:752:A:C4	1:A:774:A:C6	2.88	0.61
1:A:2358:A:H2'	1:A:2359:G:H8	1.65	0.61
6:G:86:ARG:CD	6:G:142:VAL:HG12	2.30	0.61
12:P:40:ARG:HD3	12:P:42:ARG:HE	1.64	0.61
1:A:2336:G:C8	1:A:2338:A:H5'	2.34	0.61
3:C:116:ILE:HG22	3:C:117:MET:N	2.14	0.61
3:C:148:PRO:HD3	3:C:188:CYS:HA	1.81	0.61
8:K:22:ILE:HG22	8:K:23:LYS:HG2	1.81	0.61
1:A:2169:G:H1	1:A:2180:U:H3	1.47	0.61
1:A:2312:C:H2'	1:A:2313:C:C5'	2.29	0.61
1:A:2209:U:H2'	1:A:2210:G:C8	2.36	0.61
2:B:24:C:H3'	2:B:25:A:H8	1.64	0.61
6:G:97:ALA:H	6:G:129:GLN:HB3	1.65	0.61
11:O:65:VAL:HG13	11:O:68:THR:H	1.65	0.61
1:A:530:A:H1'	17:U:55:GLY:HA3	1.82	0.61
8:K:4:GLN:HG2	8:K:5:GLU:HG2	1.83	0.61
1:A:2356:A:H1'	1:A:2357:A:C8	2.35	0.61
1:A:2419:U:H4'	1:A:2420:G:H5''	1.82	0.61
8:K:107:ARG:HD3	8:K:112:MET:HE1	1.83	0.61
11:O:25:THR:HG23	11:O:47:ASP:HB2	1.82	0.61
1:A:2873:G:H21	1:A:2891:G:H21	1.48	0.61
4:D:180:ASP:HB3	4:D:185:LEU:HB2	1.82	0.61
15:S:21:MET:HE1	15:S:103:ILE:HG23	1.82	0.61
1:A:1974:G:C6	1:A:1990:C:H1'	2.35	0.61
1:A:2227:A:H3'	1:A:2228:A:H8	1.66	0.61
1:A:2422:U:H5'	9:L:60:ARG:HH12	1.67	0.60
6:G:53:VAL:HG12	6:G:54:ALA:N	2.16	0.60
1:A:1387:G:H2'	1:A:1388:A:H5''	1.82	0.60
2:B:56:A:H3'	2:B:57:G:C8	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:86:ARG:HD2	6:G:142:VAL:HG12	1.81	0.60
11:O:40:ILE:CG2	11:O:105:ARG:CD	2.68	0.60
6:G:55:ARG:NE	6:G:63:ARG:HG2	2.15	0.60
7:J:24:LYS:HB2	7:J:29:LEU:CD2	2.31	0.60
11:O:35:ARG:HA	11:O:40:ILE:HG22	1.82	0.60
1:A:1581:A:H8	1:A:1582:U:HO2'	1.47	0.60
1:A:1857:G:H3'	1:A:1858:A:H8	1.66	0.60
9:L:16:ARG:HG2	9:L:17:ASN:N	2.17	0.60
12:P:40:ARG:HD2	12:P:42:ARG:NE	2.16	0.60
8:K:22:ILE:O	8:K:23:LYS:HD2	2.01	0.60
1:A:2204:U:H2'	1:A:2205:A:C8	2.37	0.60
6:G:26:ALA:HA	6:G:35:THR:HG22	1.82	0.60
8:K:8:LEU:CD1	8:K:82:ASN:CB	2.76	0.60
15:S:29:VAL:HG23	15:S:69:LEU:O	2.01	0.60
1:A:153:C:H2'	1:A:154:A:H8	1.67	0.60
1:A:291:C:H2'	1:A:292:U:C6	2.37	0.60
1:A:2316:A:H61	1:A:2353:U:H1'	1.66	0.60
3:C:44:ASN:CG	3:C:45:ASN:N	2.60	0.60
1:A:1696:G:O2'	1:A:1697:A:H8	1.85	0.60
1:A:1825:U:H3	1:A:1852:G:H1	1.47	0.60
1:A:2412:G:H2'	1:A:2413:G:C8	2.37	0.60
1:A:774:A:C5	1:A:775:G:C5	2.90	0.60
1:A:2233:C:O4'	3:C:146:LEU:HD21	2.00	0.60
2:B:24:C:H3'	2:B:25:A:C8	2.35	0.59
8:K:111:PHE:HB3	8:K:114:ILE:HG21	1.83	0.59
2:B:3:U:H4'	2:B:25:A:H1'	1.83	0.59
3:C:67:PHE:HE2	3:C:156:ARG:NH2	1.97	0.59
3:C:205:ILE:CG2	3:C:210:ARG:HB3	2.31	0.59
4:D:109:ASP:OD1	4:D:172:GLN:HA	2.02	0.59
5:E:17:ILE:HD13	5:E:196:LYS:CD	2.32	0.59
9:L:36:LYS:HA	9:L:40:ALA:HB3	1.82	0.59
9:L:135:ALA:HA	9:L:138:ALA:HB3	1.83	0.59
11:O:101:LEU:HD12	11:O:103:HIS:O	2.02	0.59
18:V:48:GLN:HE22	18:V:51:THR:HA	1.66	0.59
1:A:420:U:H3'	1:A:421:A:C8	2.37	0.59
1:A:2111:A:H5'	1:A:2112:G:C8	2.37	0.59
1:A:2786:A:H2'	1:A:2787:A:H5''	1.84	0.59
2:B:113:A:H3'	2:B:114:A:H8	1.66	0.59
18:V:54:TYR:HB2	18:V:87:VAL:HG12	1.85	0.59
21:b:42:VAL:HG11	21:b:54:ILE:HB	1.85	0.59
1:A:162:A:N6	1:A:165:C:H42	1.92	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1003:A:H62	1:A:2523:G:H22	1.51	0.59
1:A:2148:A:H5'	1:A:2177:G:H21	1.67	0.59
1:A:2629:A:H62	3:C:238:ARG:HG2	1.67	0.59
1:A:155:U:H2'	1:A:156:A:C8	2.38	0.59
11:O:101:LEU:HD11	11:O:103:HIS:O	2.02	0.59
1:A:1989:A:H2'	1:A:1990:C:C6	2.37	0.59
2:B:95:U:H3'	2:B:96:G:H8	1.67	0.59
6:G:55:ARG:HE	6:G:63:ARG:HG2	1.64	0.59
8:K:17:ARG:HB2	8:K:45:GLN:HG2	1.84	0.59
12:P:90:VAL:HG12	12:P:91:ARG:HG3	1.84	0.59
1:A:274:A:N6	1:A:295:G:C4	2.70	0.59
1:A:919:U:H2'	1:A:920:G:H8	1.68	0.59
1:A:2141:A:H61	1:A:2149:G:H4'	1.68	0.59
12:P:106:LEU:CD1	12:P:110:ALA:HB3	2.32	0.59
21:b:33:CYS:HB2	21:b:46:CYS:HB3	1.84	0.59
1:A:1491:A:H62	1:A:1512:G:H1	1.51	0.58
3:C:175:ARG:HH21	3:C:272:ARG:HH22	1.49	0.58
1:A:973:G:H2'	1:A:974:A:C8	2.38	0.58
1:A:2338:A:H5''	1:A:2339:A:N7	2.18	0.58
19:Y:14:ILE:HG23	19:Y:15:GLU:N	2.17	0.58
1:A:2386:U:H4'	1:A:2387:A:H3'	1.84	0.58
8:K:111:PHE:O	8:K:114:ILE:HG22	2.03	0.58
23:f:11:CYS:HB3	23:f:32:HIS:CE1	2.38	0.58
1:A:1079:U:O2'	1:A:1080:G:H4'	2.03	0.58
1:A:2358:A:C6	1:A:2359:G:C6	2.91	0.58
15:S:35:ILE:HG12	21:b:27:MET:HE1	1.85	0.58
19:Y:7:ARG:CZ	19:Y:7:ARG:HA	2.33	0.58
1:A:1518:G:H22	1:A:1566:G:H1	1.52	0.58
1:A:2417:A:H5'	1:A:2418:G:H2'	1.85	0.58
11:O:73:ALA:HA	11:O:76:LYS:HB3	1.84	0.58
11:O:69:GLY:H	11:O:73:ALA:HB3	1.67	0.58
20:Z:9:LYS:CD	20:Z:55:SER:HB2	2.29	0.58
1:A:753:A:H61	1:A:773:G:H5''	1.68	0.58
1:A:1496:G:H1	1:A:1507:U:H3	0.74	0.58
1:A:2124:A:H2'	1:A:2125:U:H5'	1.85	0.58
1:A:2276:A:H2	1:A:2286:U:H3	1.50	0.58
10:N:9:THR:OG1	10:N:12:GLN:HG3	2.04	0.58
19:Y:17:LYS:HG2	19:Y:53:MET:CE	2.32	0.58
1:A:1975:U:H3	1:A:1988:G:H1	1.51	0.58
8:K:114:ILE:HG23	8:K:115:VAL:N	2.17	0.58
9:L:16:ARG:HG2	9:L:17:ASN:H	1.69	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:O:39:HIS:CD2	11:O:59:LEU:HD13	2.38	0.58
11:O:70:ASP:O	11:O:105:ARG:NH1	2.37	0.58
1:A:9:U:C5	1:A:10:A:H1'	2.39	0.58
1:A:274:A:N7	1:A:295:G:N2	2.51	0.58
1:A:1496:G:O6	1:A:1507:U:O4	2.21	0.58
1:A:1821:G:H22	1:A:1857:G:H8	1.52	0.58
1:A:2357:A:C4	1:A:2358:A:H1'	2.39	0.58
5:E:6:LEU:HD21	5:E:127:GLU:OE2	2.04	0.58
6:G:25:VAL:HB	6:G:38:PHE:HE2	1.66	0.57
13:Q:92:ARG:HH22	14:R:10:LYS:HA	1.69	0.57
1:A:919:U:H2'	1:A:920:G:C8	2.38	0.57
6:G:8:LEU:C	6:G:8:LEU:HD12	2.29	0.57
1:A:270:C:H42	1:A:473:C:H42	1.50	0.57
1:A:2535:U:H3	1:A:2612:G:N2	2.01	0.57
6:G:55:ARG:HE	6:G:63:ARG:HG3	1.69	0.57
19:Y:5:GLU:CG	19:Y:56:VAL:HG11	2.34	0.57
1:A:918:U:H2'	1:A:919:U:C6	2.40	0.57
1:A:2143:A:H3'	1:A:2144:G:C8	2.38	0.57
1:A:2149:G:H2'	1:A:2150:G:C8	2.39	0.57
1:A:1618:A:H3'	1:A:1619:A:C8	2.39	0.57
1:A:2318:G:H2'	1:A:2319:G:H5''	1.87	0.57
2:B:27:A:H1'	2:B:57:G:H21	1.69	0.57
12:P:37:GLU:OE2	12:P:42:ARG:CD	2.46	0.57
19:Y:18:VAL:HG23	19:Y:53:MET:HE2	1.86	0.57
1:A:1082:G:N2	1:A:1165:U:H3	1.99	0.57
1:A:2264:G:H3'	1:A:2265:U:C6	2.40	0.57
2:B:27:A:N3	2:B:57:G:N2	2.52	0.57
1:A:751:G:O2'	1:A:752:A:H5'	2.05	0.57
1:A:752:A:H2'	1:A:753:A:O4'	2.05	0.57
1:A:1767:A:H3'	1:A:1768:A:C8	2.40	0.57
1:A:2258:U:H3'	1:A:2259:G:H8	1.70	0.57
3:C:171:TYR:HE1	3:C:185:LEU:CD1	2.18	0.57
1:A:1992:C:H2'	1:A:1993:G:O4'	2.04	0.57
6:G:46:VAL:HA	6:G:51:LEU:CB	2.34	0.57
11:O:28:ARG:CD	11:O:94:VAL:HG23	2.35	0.57
1:A:2180:U:H2'	1:A:2181:C:C6	2.39	0.57
1:A:2516:G:H2'	1:A:2517:A:C8	2.40	0.57
3:C:185:LEU:HD12	3:C:185:LEU:N	2.19	0.57
6:G:19:LEU:HD22	6:G:46:VAL:HB	1.86	0.57
9:L:127:LYS:HD2	9:L:131:SER:H	1.70	0.57
12:P:78:PRO:HG2	12:P:81:THR:HB	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:52:ARG:HH21	3:C:53:HIS:CE1	2.23	0.56
12:P:81:THR:HG23	12:P:84:ILE:HG12	1.87	0.56
20:Z:5:GLU:HG3	20:Z:36:VAL:HG12	1.87	0.56
1:A:153:C:H2'	1:A:154:A:C8	2.40	0.56
1:A:499:G:N7	5:E:58:ARG:CD	2.68	0.56
1:A:175:G:C4	1:A:177:G:H1'	2.39	0.56
1:A:753:A:H62	1:A:772:G:H21	0.72	0.56
1:A:2332:G:H3'	1:A:2333:G:C8	2.39	0.56
6:G:165:TYR:HB2	6:G:168:GLU:HB2	1.86	0.56
5:E:17:ILE:CD1	5:E:196:LYS:HD3	2.35	0.56
16:T:26:TYR:HD2	16:T:92:ILE:HD12	1.70	0.56
1:A:153:C:N4	1:A:174:U:N3	2.46	0.56
3:C:145:GLU:OE2	3:C:154:LEU:HD11	2.06	0.56
7:J:25:THR:HB	7:J:28:ARG:HB2	1.88	0.56
19:Y:11:THR:C	19:Y:15:GLU:HG2	2.29	0.56
1:A:63:G:H2'	1:A:64:A:H8	1.70	0.56
1:A:178:A:H1'	1:A:179:A:C8	2.41	0.56
1:A:229:A:H2'	1:A:230:A:C8	2.40	0.56
1:A:1187:U:H4'	1:A:1188:A:O4'	2.06	0.56
2:B:10:G:C4	18:V:83:ASP:OD1	2.59	0.56
1:A:907:U:O2'	1:A:908:A:H8	1.89	0.56
1:A:2160:U:H1'	1:A:2162:G:H21	1.69	0.56
1:A:2258:U:H3'	1:A:2259:G:C8	2.41	0.56
11:O:102:TYR:HD1	11:O:106:VAL:CG1	2.19	0.56
12:P:94:LYS:HD3	12:P:114:LYS:HD3	1.86	0.56
1:A:774:A:O2'	1:A:775:G:H8	1.89	0.56
2:B:38:U:H5'	2:B:44:A:N1	2.21	0.56
11:O:78:GLY:N	11:O:109:LEU:CD2	2.69	0.56
1:A:141:U:H2'	1:A:142:G:C8	2.41	0.56
1:A:924:U:H2'	1:A:942:U:O4	2.06	0.56
1:A:1568:G:H5''	1:A:1569:A:H2'	1.87	0.56
1:A:2112:G:H3'	1:A:2113:C:C6	2.41	0.56
11:O:78:GLY:HA2	11:O:109:LEU:CD2	2.17	0.56
1:A:1100:A:H2'	1:A:1101:G:C8	2.41	0.55
3:C:30:GLU:HG3	3:C:32:SER:H	1.72	0.55
6:G:46:VAL:HA	6:G:51:LEU:HB3	1.88	0.55
10:N:21:THR:HG21	10:N:65:TYR:HE2	1.71	0.55
1:A:2329:A:H3'	1:A:2330:A:H8	1.70	0.55
1:A:948:A:H3'	1:A:949:U:H6	1.70	0.55
1:A:2100:A:H2'	1:A:2101:G:C8	2.42	0.55
3:C:154:LEU:N	3:C:154:LEU:CD1	2.69	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:L:112:LEU:HD12	9:L:112:LEU:O	2.05	0.55
21:b:27:MET:HG3	21:b:36:MET:CE	2.36	0.55
1:A:421:A:H2	1:A:446:G:H22	1.54	0.55
3:C:116:ILE:CG2	3:C:117:MET:N	2.69	0.55
19:Y:7:ARG:HA	19:Y:7:ARG:NH1	2.22	0.55
1:A:1359:G:H22	1:A:1370:C:H41	1.55	0.55
1:A:1478:G:H2'	1:A:1479:G:C8	2.41	0.55
5:E:17:ILE:HD13	5:E:196:LYS:HD2	1.86	0.55
6:G:96:ARG:HH12	6:G:98:SER:HB3	1.71	0.55
1:A:157:U:H3	1:A:170:G:H1	1.53	0.55
1:A:1617:A:H2'	1:A:1618:A:O4'	2.07	0.55
1:A:1695:A:H2'	1:A:1696:G:H5'	1.89	0.55
1:A:2204:U:H2'	1:A:2205:A:H8	1.72	0.55
1:A:284:C:H1'	1:A:288:C:H42	1.71	0.55
1:A:805:G:HO2'	1:A:2010:A:H8	1.54	0.55
1:A:1491:A:H62	1:A:1512:G:N2	2.05	0.55
1:A:1525:G:H2'	1:A:1526:G:C8	2.42	0.55
1:A:1765:G:N2	1:A:1767:A:H5''	2.21	0.55
1:A:2478:U:C4	1:A:2479:A:H1'	2.42	0.55
7:J:89:THR:HG22	7:J:92:GLU:HG2	1.89	0.55
1:A:1806:U:H2'	1:A:1807:U:O2'	2.06	0.55
1:A:2612:G:H2'	1:A:2613:U:H5''	1.89	0.55
3:C:21:PHE:HB3	3:C:24:ILE:HD12	1.89	0.55
1:A:1546:G:N2	3:C:98:ASP:O	2.37	0.55
1:A:2140:U:H5	1:A:2172:C:H2'	1.71	0.55
3:C:53:HIS:CE1	3:C:219:THR:HG22	2.42	0.55
9:L:111:ILE:O	9:L:131:SER:HA	2.07	0.55
1:A:1727:A:H2'	1:A:1728:C:H6	1.70	0.55
1:A:1807:U:H2'	1:A:1808:U:C6	2.42	0.55
1:A:2001:G:H3'	1:A:2002:G:C8	2.42	0.55
1:A:2119:A:H2	1:A:2258:U:H3	1.55	0.54
1:A:2146:A:N7	1:A:2178:C:H5'	2.22	0.54
2:B:36:C:H2'	2:B:37:A:H4'	1.89	0.54
6:G:11:ILE:HD12	6:G:51:LEU:H	1.72	0.54
8:K:21:THR:HA	8:K:41:CYS:HB3	1.89	0.54
1:A:1801:G:H22	1:A:2007:A:H2	1.54	0.54
1:A:12:A:H2	1:A:2655:C:H4'	1.72	0.54
1:A:811:A:H62	1:A:1803:C:H42	1.53	0.54
1:A:1003:A:H62	1:A:2523:G:N2	2.06	0.54
1:A:2356:A:H1'	1:A:2357:A:N7	2.22	0.54
1:A:2826:A:H2'	1:A:2827:A:C4	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:17:ILE:CD1	5:E:196:LYS:CD	2.85	0.54
16:T:26:TYR:CD2	16:T:92:ILE:HD12	2.42	0.54
1:A:1823:U:H3	1:A:1854:G:H22	1.55	0.54
6:G:34:LEU:HD23	6:G:80:VAL:HG22	1.90	0.54
1:A:940:G:H2'	1:A:941:U:C6	2.43	0.54
3:C:135:ILE:CG2	3:C:136:PRO:CD	2.81	0.54
13:Q:61:TRP:HA	13:Q:97:ASP:OD2	2.07	0.54
1:A:174:U:O2'	1:A:175:G:H5'	2.07	0.54
1:A:1500:U:C5'	10:N:59:ARG:HH11	2.14	0.54
8:K:7:ARG:HD2	8:K:18:GLU:OE2	2.08	0.54
14:R:11:GLN:C	14:R:12:ILE:HD13	2.32	0.54
1:A:1081:U:H3	1:A:1166:G:H1	1.55	0.54
1:A:2329:A:H3'	1:A:2330:A:C8	2.43	0.54
1:A:2534:G:H2'	1:A:2535:U:H5	1.72	0.54
11:O:111:ASP:HA	11:O:114:ARG:CD	2.38	0.54
1:A:306:C:H42	1:A:410:G:N2	2.05	0.54
4:D:55:ASP:HA	4:D:77:LYS:HA	1.90	0.54
1:A:300:G:C2	1:A:302:A:C4	2.96	0.53
1:A:2264:G:H3'	1:A:2265:U:H6	1.73	0.53
1:A:2501:G:H2'	1:A:2504:C:N4	2.23	0.53
2:B:58:C:H2'	2:B:59:U:C6	2.43	0.53
5:E:6:LEU:HD12	5:E:7:TYR:H	1.71	0.53
1:A:159:U:H3	1:A:168:A:H61	1.56	0.53
1:A:1113:A:H3'	1:A:1114:G:C8	2.43	0.53
1:A:1840:G:N2	3:C:44:ASN:HD21	2.06	0.53
1:A:2089:A:H1'	1:A:2090:G:H5'	1.90	0.53
1:A:2153:G:H3'	1:A:2154:G:H8	1.73	0.53
1:A:2529:U:H1'	1:A:2530:C:C5	2.42	0.53
2:B:3:U:H2'	2:B:4:G:C8	2.44	0.53
11:O:28:ARG:NE	11:O:94:VAL:HG23	2.23	0.53
1:A:2315:A:O2'	1:A:2316:A:H5''	2.08	0.53
1:A:2317:A:C8	1:A:2318:G:C8	2.97	0.53
1:A:2363:C:H2'	1:A:2365:A:N3	2.23	0.53
4:D:188:ILE:CG2	4:D:189:LYS:N	2.72	0.53
6:G:11:ILE:H	6:G:50:VAL:HG22	1.73	0.53
19:Y:14:ILE:HG23	19:Y:15:GLU:H	1.71	0.53
1:A:93:C:H2'	1:A:94:A:C8	2.44	0.53
1:A:904:A:H3'	1:A:905:G:H5''	1.90	0.53
1:A:1461:A:H61	1:A:1630:G:H1'	1.73	0.53
1:A:2227:A:H3'	1:A:2228:A:C8	2.43	0.53
1:A:312:G:H1'	1:A:313:U:O4'	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:35:C:H1'	2:B:47:C:H4'	1.90	0.53
4:D:91:TYR:HA	4:D:95:GLN:OE1	2.09	0.53
9:L:89:THR:OG1	9:L:121:LEU:CD2	2.44	0.53
11:O:28:ARG:NE	11:O:94:VAL:CG2	2.71	0.53
14:R:54:GLU:CD	14:R:54:GLU:H	2.16	0.53
1:A:1445:A:H2	1:A:1640:G:H22	1.57	0.53
1:A:1864:G:H21	1:A:1999:A:H8	1.55	0.53
1:A:2918:G:H5'	1:A:2919:A:OP1	2.08	0.53
3:C:181:VAL:HG21	3:C:272:ARG:HD3	1.89	0.53
1:A:279:A:H5'	1:A:280:G:OP2	2.09	0.53
1:A:302:A:N7	1:A:451:C:C2	2.77	0.53
1:A:1821:G:H1	1:A:1857:G:H2'	1.73	0.53
1:A:929:G:H2'	1:A:930:C:C6	2.44	0.53
1:A:1105:G:H2'	1:A:1106:U:C5	2.44	0.53
1:A:1115:A:H1'	1:A:1142:A:H4'	1.90	0.53
1:A:1994:C:H2'	1:A:1995:A:C4	2.44	0.53
5:E:40:GLN:NE2	5:E:184:LEU:HB2	2.23	0.53
8:K:111:PHE:HB3	8:K:114:ILE:CG2	2.39	0.53
1:A:157:U:O2'	1:A:158:C:H5'	2.09	0.53
1:A:1077:G:H2'	1:A:1078:A:C8	2.44	0.53
1:A:290:U:HO2'	1:A:291:C:H6	1.57	0.53
1:A:2131:U:H2'	1:A:2132:A:C8	2.44	0.53
1:A:2296:A:H5''	1:A:2297:A:H5''	1.91	0.53
1:A:2620:C:C5	3:C:237:GLY:HA2	2.42	0.53
20:Z:8:LEU:HB2	20:Z:28:LEU:HD13	1.90	0.53
1:A:1042:A:H4'	13:Q:92:ARG:CZ	2.39	0.52
1:A:1618:A:H3'	1:A:1619:A:H8	1.74	0.52
1:A:1807:U:O4	1:A:1812:A:H3'	2.09	0.52
2:B:48:G:H5''	11:O:70:ASP:HB3	1.91	0.52
2:B:83:G:H2'	2:B:84:G:C8	2.45	0.52
4:D:47:GLU:OE1	4:D:88:MET:HE2	2.08	0.52
7:J:115:LEU:HG	7:J:119:MET:HE3	1.90	0.52
17:U:47:PRO:HA	17:U:53:GLN:HE22	1.74	0.52
1:A:752:A:C5	1:A:774:A:C6	2.98	0.52
1:A:2121:U:H2'	1:A:2122:G:C8	2.45	0.52
1:A:345:A:N6	17:U:10:MET:SD	2.82	0.52
1:A:418:A:H4'	1:A:419:G:O4'	2.09	0.52
1:A:2154:G:H3'	1:A:2155:A:H8	1.74	0.52
2:B:38:U:H4'	2:B:39:A:C6	2.45	0.52
8:K:40:VAL:CG2	8:K:59:LYS:NZ	2.72	0.52
9:L:88:GLY:O	9:L:89:THR:OG1	2.25	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:f:4:ARG:HH11	23:f:34:GLN:HG2	1.74	0.52
1:A:1074:A:H2'	1:A:1075:A:H8	1.74	0.52
1:A:1113:A:H3'	1:A:1114:G:H8	1.73	0.52
2:B:104:G:H3'	2:B:105:A:C8	2.45	0.52
7:J:18:VAL:HG22	7:J:56:ILE:HD11	1.91	0.52
1:A:2519:G:H1'	1:A:2520:U:H5	1.74	0.52
3:C:185:LEU:HD12	3:C:185:LEU:H	1.73	0.52
6:G:36:ARG:HB3	6:G:76:MET:HE1	1.91	0.52
1:A:425:C:H2'	1:A:426:G:C8	2.45	0.52
1:A:1248:C:H2'	1:A:1249:U:C6	2.44	0.52
1:A:2099:G:H2'	1:A:2100:A:C8	2.45	0.52
2:B:11:A:C4	2:B:14:G:H1'	2.44	0.52
11:O:56:ALA:HB2	11:O:84:ARG:HG2	1.91	0.52
14:R:2:TYR:HB3	14:R:15:GLU:HG2	1.92	0.52
1:A:1515:C:H2'	1:A:1516:A:C8	2.44	0.52
1:A:2138:U:H5''	1:A:2171:G:H4'	1.92	0.52
11:O:101:LEU:HD12	11:O:101:LEU:C	2.34	0.52
22:d:35:ARG:HG3	22:d:42:LEU:HD21	1.92	0.52
1:A:946:G:N2	1:A:947:A:H62	2.08	0.52
1:A:2302:A:H2'	1:A:2303:A:C8	2.45	0.52
3:C:94:ILE:CD1	3:C:104:ILE:HG13	2.34	0.52
1:A:1155:C:H2'	1:A:1156:G:O4'	2.09	0.52
1:A:1587:U:H2'	1:A:1588:A:C8	2.38	0.52
1:A:2338:A:H5''	1:A:2339:A:C8	2.45	0.52
1:A:930:C:N4	1:A:938:G:N7	2.57	0.51
1:A:1574:G:H21	1:A:1593:A:H62	1.58	0.51
1:A:2149:G:H2'	1:A:2150:G:H8	1.74	0.51
2:B:13:A:H3'	2:B:14:G:C8	2.39	0.51
3:C:185:LEU:CD1	3:C:185:LEU:N	2.74	0.51
4:D:139:TYR:OH	4:D:143:PRO:O	2.28	0.51
5:E:6:LEU:HD12	5:E:7:TYR:N	2.24	0.51
6:G:55:ARG:NH1	6:G:63:ARG:HE	2.07	0.51
1:A:106:G:H4'	1:A:337:A:H5''	1.91	0.51
1:A:123:G:N7	22:d:19:ARG:NH2	2.59	0.51
1:A:1485:A:H61	1:A:1600:G:H8	1.58	0.51
1:A:2233:C:H1'	3:C:146:LEU:HD21	1.90	0.51
1:A:2317:A:N6	1:A:2373:U:H3	2.08	0.51
1:A:2357:A:C6	1:A:2358:A:C5	2.98	0.51
1:A:2884:G:H2'	1:A:2885:A:C8	2.45	0.51
11:O:39:HIS:CE1	11:O:59:LEU:H	2.29	0.51
18:V:28:ARG:O	18:V:29:LEU:C	2.53	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1472:G:C5	1:A:1473:A:N7	2.78	0.51
1:A:1553:A:O2'	1:A:1554:U:H5'	2.11	0.51
1:A:1801:G:N3	1:A:1801:G:H2'	2.25	0.51
1:A:1859:C:H42	1:A:2003:C:H42	1.58	0.51
3:C:29:PRO:HG2	3:C:34:LEU:HD11	1.92	0.51
6:G:55:ARG:CZ	6:G:58:ASP:O	2.58	0.51
1:A:927:G:H2'	1:A:928:G:H8	1.75	0.51
1:A:1065:U:H3	1:A:1188:A:H62	1.57	0.51
1:A:1220:G:H2'	1:A:1221:A:C8	2.45	0.51
1:A:1692:U:H5'	1:A:1693:C:OP1	2.10	0.51
1:A:2142:C:H3'	1:A:2143:A:H8	1.75	0.51
1:A:2184:U:H3'	1:A:2185:G:C8	2.46	0.51
1:A:2228:A:H61	1:A:2253:G:H1'	1.75	0.51
20:Z:9:LYS:CD	20:Z:55:SER:CB	2.87	0.51
1:A:774:A:C6	1:A:775:G:C2	2.99	0.51
11:O:70:ASP:H	11:O:105:ARG:NH2	2.09	0.51
13:Q:92:ARG:NH2	14:R:10:LYS:HA	2.25	0.51
19:Y:17:LYS:HG2	19:Y:53:MET:HE3	1.93	0.51
1:A:2148:A:N6	1:A:2197:G:H22	2.08	0.51
8:K:8:LEU:HD12	8:K:82:ASN:C	2.35	0.51
1:A:270:C:H2'	1:A:271:C:O4'	2.11	0.51
1:A:1003:A:N1	1:A:2487:U:H4'	2.26	0.51
1:A:1094:A:H1'	1:A:1158:G:H21	1.75	0.51
1:A:1998:A:H1'	1:A:1999:A:H5'	1.92	0.51
1:A:1110:C:H2'	1:A:1111:U:H5''	1.93	0.51
1:A:2336:G:H8	1:A:2338:A:H5'	1.76	0.51
1:A:2490:C:H1'	1:A:2521:U:H3	1.76	0.51
3:C:52:ARG:HH22	3:C:53:HIS:CE1	2.08	0.51
1:A:652:A:H2'	1:A:653:A:C8	2.46	0.50
1:A:888:A:H3'	1:A:889:A:C5'	2.41	0.50
1:A:1762:G:C2	1:A:1763:G:C5	2.99	0.50
1:A:1774:A:H3'	1:A:1775:G:H8	1.76	0.50
1:A:2099:G:H2'	1:A:2100:A:H8	1.76	0.50
1:A:2893:A:N3	1:A:2894:G:N7	2.59	0.50
2:B:22:G:H4'	2:B:23:U:H5'	1.93	0.50
8:K:111:PHE:C	8:K:114:ILE:HG22	2.36	0.50
19:Y:20:SER:HA	19:Y:23:GLU:HG2	1.93	0.50
1:A:1392:A:H2'	1:A:1393:A:C8	2.47	0.50
6:G:90:LEU:HB2	6:G:130:THR:HA	1.93	0.50
10:N:55:ASP:OD1	10:N:56:LEU:N	2.40	0.50
1:A:911:G:H2'	1:A:912:C:C6	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1116:A:H62	1:A:1141:A:H61	1.60	0.50
1:A:1821:G:N2	1:A:1857:G:H8	2.09	0.50
1:A:2278:U:H3'	1:A:2283:C:H42	1.75	0.50
1:A:2372:U:H2'	1:A:2373:U:O4'	2.12	0.50
1:A:2478:U:H5	1:A:2533:U:O4	1.94	0.50
2:B:6:U:H5''	11:O:15:HIS:HE1	1.76	0.50
1:A:75:G:H22	1:A:110:A:H2	1.58	0.50
1:A:1681:U:H2'	1:A:1682:C:C6	2.47	0.50
1:A:2100:A:H2'	1:A:2101:G:H8	1.75	0.50
1:A:2314:C:H1'	1:A:2315:A:H5''	1.94	0.50
3:C:23:GLU:HG3	3:C:90:ASN:ND2	2.25	0.50
18:V:84:ARG:O	18:V:85:LYS:HG3	2.11	0.50
20:Z:40:ASN:O	20:Z:44:ARG:HG2	2.12	0.50
1:A:1827:U:H4'	3:C:257:PHE:O	2.12	0.50
1:A:2213:U:H2'	1:A:2214:G:C8	2.47	0.50
1:A:2359:G:H22	18:V:49:ARG:CG	2.21	0.50
1:A:2566:U:H2'	1:A:2567:C:H6	1.75	0.50
6:G:55:ARG:HH11	6:G:63:ARG:HE	1.60	0.50
1:A:165:C:H2'	1:A:166:A:C8	2.46	0.50
1:A:1220:G:H2'	1:A:1221:A:H8	1.77	0.50
1:A:1362:G:H2'	1:A:1363:G:H5''	1.94	0.50
1:A:1496:G:N2	1:A:1507:U:O2	2.26	0.50
1:A:1579:A:C8	1:A:1588:A:C6	2.99	0.50
2:B:83:G:H2'	2:B:84:G:H8	1.77	0.50
3:C:223:SER:HB2	3:C:243:ARG:HD3	1.94	0.50
21:b:48:SER:HA	21:b:53:ASP:HA	1.93	0.50
1:A:1221:A:H2'	1:A:1222:A:C8	2.47	0.50
1:A:2359:G:H22	18:V:49:ARG:HG3	1.77	0.50
1:A:2535:U:HO2'	1:A:2536:C:H6	1.58	0.50
5:E:71:GLY:O	5:E:72:ARG:CG	2.60	0.50
1:A:1046:A:H2'	1:A:1047:A:C8	2.47	0.50
15:S:29:VAL:HG23	15:S:69:LEU:C	2.37	0.50
15:S:64:MET:HE3	15:S:109:GLU:HG2	1.94	0.50
18:V:78:GLU:N	18:V:88:SER:HA	2.26	0.50
20:Z:9:LYS:HD2	20:Z:55:SER:OG	2.11	0.50
20:Z:50:VAL:HG23	20:Z:50:VAL:O	2.12	0.50
1:A:948:A:H3'	1:A:949:U:C6	2.46	0.49
3:C:176:LEU:HD12	3:C:180:GLU:HG3	1.94	0.49
1:A:155:U:H2'	1:A:156:A:H8	1.76	0.49
1:A:698:C:H2'	1:A:699:A:O4'	2.12	0.49
1:A:770:A:H2'	1:A:771:U:H5'	1.95	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1134:A:C5'	1:A:1135:G:H8	2.24	0.49
1:A:2114:C:H2'	1:A:2115:U:C6	2.46	0.49
1:A:2631:A:H2'	1:A:2632:G:C8	2.47	0.49
2:B:104:G:H3'	2:B:105:A:H8	1.77	0.49
8:K:40:VAL:HG22	8:K:59:LYS:HZ3	1.77	0.49
1:A:2363:C:H1'	1:A:2366:G:N1	2.26	0.49
1:A:752:A:C6	1:A:753:A:C5	3.01	0.49
1:A:1474:C:H6	1:A:1617:A:H5'	1.77	0.49
1:A:2164:A:C8	1:A:2188:G:H1'	2.47	0.49
1:A:2322:C:OP1	11:O:97:ARG:NH2	2.46	0.49
10:N:24:LEU:HD23	10:N:44:VAL:HG21	1.95	0.49
1:A:303:G:C2	1:A:304:G:C5	3.00	0.49
1:A:888:A:H1'	1:A:1234:G:H5'	1.95	0.49
1:A:1099:C:H2'	1:A:1100:A:C8	2.48	0.49
1:A:1984:U:O2'	1:A:1985:U:O2	2.29	0.49
1:A:2324:C:H42	1:A:2369:A:H61	1.58	0.49
3:C:145:GLU:CD	3:C:154:LEU:HD11	2.37	0.49
8:K:40:VAL:CG2	8:K:59:LYS:HZ3	2.25	0.49
11:O:105:ARG:HB2	11:O:105:ARG:NH1	2.24	0.49
18:V:48:GLN:CD	18:V:51:THR:HA	2.37	0.49
20:Z:9:LYS:CD	20:Z:55:SER:OG	2.60	0.49
2:B:91:C:H2'	2:B:92:C:C6	2.48	0.49
3:C:225:MET:HE2	3:C:230:HIS:HB2	1.95	0.49
1:A:927:G:H2'	1:A:928:G:C8	2.48	0.49
1:A:1137:G:H2'	1:A:1138:C:C6	2.47	0.49
1:A:1154:U:H2'	1:A:1155:C:C6	2.47	0.49
1:A:1495:C:N4	1:A:1508:C:H42	2.11	0.49
1:A:2316:A:C2	1:A:2317:A:H4'	2.48	0.49
1:A:2387:A:H4'	1:A:2388:C:H5	1.76	0.49
1:A:2876:A:H2'	1:A:2877:G:C8	2.48	0.49
17:U:48:THR:H	17:U:53:GLN:CD	2.20	0.49
1:A:199:A:H62	1:A:878:G:H21	1.60	0.49
1:A:2193:C:H2'	1:A:2194:G:H5'	1.93	0.49
1:A:2281:G:H2'	1:A:2282:G:C8	2.47	0.49
5:E:70:THR:OG1	5:E:72:ARG:NH1	2.46	0.49
1:A:154:A:H61	1:A:173:A:H61	1.60	0.49
1:A:2175:C:H5'	1:A:2176:A:C4	2.48	0.49
2:B:113:A:H3'	2:B:114:A:C8	2.45	0.49
3:C:60:ARG:HD3	3:C:85:PRO:HB2	1.93	0.49
11:O:74:ALA:O	11:O:109:LEU:HD23	2.12	0.49
2:B:25:A:H2	2:B:58:C:H1'	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:131:PRO:CB	3:C:189:ARG:HG2	2.41	0.49
3:C:238:ARG:HB2	3:C:241:ILE:HD11	1.95	0.49
11:O:25:THR:CG2	11:O:48:VAL:HG23	2.43	0.49
1:A:2285:G:H2'	1:A:2286:U:O4'	2.13	0.48
1:A:2353:U:H5'	1:A:2354:G:OP2	2.13	0.48
1:A:2356:A:H1'	1:A:2357:A:C5	2.48	0.48
1:A:2406:A:H61	11:O:97:ARG:HD3	1.77	0.48
1:A:2865:U:H5''	10:N:49:THR:HG21	1.95	0.48
2:B:98:G:H3'	2:B:99:A:H8	1.78	0.48
5:E:81:PRO:HB3	5:E:89:VAL:HG23	1.95	0.48
9:L:127:LYS:HB3	9:L:130:ALA:H	1.78	0.48
12:P:23:PHE:CE2	12:P:53:ARG:NH1	2.81	0.48
19:Y:9:LEU:HD12	19:Y:12:ALA:H	1.78	0.48
1:A:753:A:H2'	1:A:754:G:C8	2.48	0.48
1:A:760:G:H2'	1:A:761:U:C6	2.47	0.48
1:A:786:A:H5''	1:A:1813:A:N6	2.27	0.48
1:A:934:U:H5''	1:A:935:A:H3'	1.95	0.48
1:A:1727:A:H2'	1:A:1728:C:C6	2.48	0.48
1:A:1861:C:H3'	1:A:1862:C:C6	2.48	0.48
1:A:2332:G:H3'	1:A:2333:G:H8	1.77	0.48
11:O:28:ARG:HD3	11:O:94:VAL:HG23	1.93	0.48
1:A:186:C:H2'	1:A:187:C:H5'	1.95	0.48
1:A:306:C:N4	1:A:410:G:H1	2.11	0.48
1:A:892:U:H2'	1:A:894:A:H2	1.78	0.48
2:B:38:U:H4'	2:B:39:A:C5	2.48	0.48
4:D:207:LYS:HE2	4:D:207:LYS:H	1.76	0.48
1:A:2337:G:N7	1:A:2340:A:H3'	2.28	0.48
1:A:2484:G:H2'	1:A:2485:C:C6	2.49	0.48
11:O:22:LEU:CD2	11:O:96:ASP:OD1	2.44	0.48
11:O:38:LYS:HE2	11:O:59:LEU:HD22	1.94	0.48
1:A:911:G:H2'	1:A:912:C:H6	1.78	0.48
1:A:1460:G:H4'	1:A:1631:A:N6	2.27	0.48
1:A:1464:A:H1'	1:A:1465:A:O4'	2.13	0.48
1:A:2417:A:H2'	1:A:2418:G:C5	2.48	0.48
1:A:939:G:H2'	1:A:940:G:C8	2.48	0.48
1:A:275:A:N6	1:A:296:G:H1'	2.29	0.48
1:A:1500:U:H5'	10:N:59:ARG:NH1	2.16	0.48
1:A:1517:A:H3'	1:A:1518:G:C8	2.48	0.48
12:P:8:ILE:O	12:P:12:THR:HG23	2.13	0.48
1:A:887:C:H2'	1:A:889:A:C8	2.49	0.48
1:A:1474:C:C5	1:A:1617:A:H3'	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:12:SER:O	5:E:13:THR:C	2.56	0.48
1:A:920:G:C5	1:A:921:G:H1'	2.49	0.48
1:A:2103:U:H2'	1:A:2104:U:C6	2.48	0.48
1:A:2316:A:N6	1:A:2353:U:H1'	2.29	0.48
2:B:75:U:H2'	2:B:76:A:H8	1.79	0.48
3:C:26:THR:CG2	3:C:80:THR:HB	2.43	0.48
9:L:127:LYS:HD2	9:L:131:SER:N	2.29	0.48
18:V:22:ARG:O	18:V:23:ASP:C	2.56	0.48
18:V:84:ARG:O	18:V:85:LYS:CG	2.62	0.48
1:A:153:C:N4	1:A:174:U:C4	2.82	0.48
1:A:302:A:H1'	1:A:303:G:N9	2.29	0.48
1:A:750:U:N3	1:A:751:G:H1'	2.29	0.48
1:A:772:G:C1'	1:A:773:G:H5'	2.34	0.48
1:A:875:U:H4'	1:A:878:G:C6	2.49	0.48
1:A:1555:A:C4	1:A:1556:A:C8	3.02	0.48
1:A:2148:A:H62	1:A:2197:G:H22	1.62	0.48
19:Y:5:GLU:HG2	19:Y:56:VAL:HG11	1.95	0.48
21:b:43:CYS:HB3	21:b:47:GLY:HA3	1.94	0.48
1:A:752:A:H8	1:A:773:G:H21	1.55	0.47
1:A:2320:U:H2'	1:A:2321:U:C6	2.49	0.47
1:A:2327:A:O4'	1:A:2350:G:H1'	2.14	0.47
3:C:78:VAL:HG21	3:C:110:ILE:HD11	1.95	0.47
23:f:16:VAL:O	23:f:17:ILE:HD13	2.14	0.47
1:A:2121:U:H5	1:A:2256:A:H61	1.62	0.47
7:J:119:MET:O	7:J:122:LYS:HG2	2.14	0.47
9:L:95:LEU:HA	9:L:98:GLU:OE2	2.14	0.47
15:S:6:VAL:HG12	15:S:7:ALA:N	2.29	0.47
19:Y:18:VAL:CG2	19:Y:53:MET:HE2	2.44	0.47
1:A:2375:A:H5'	1:A:2411:G:OP2	2.15	0.47
1:A:2529:U:H1'	1:A:2530:C:C4	2.49	0.47
2:B:23:U:H2'	2:B:24:C:C6	2.49	0.47
12:P:47:GLU:OE2	12:P:47:GLU:N	2.47	0.47
1:A:319:G:OP1	1:A:320:U:H4'	2.14	0.47
1:A:1531:G:H2'	1:A:1532:A:H8	1.80	0.47
1:A:2422:U:H5'	9:L:60:ARG:NH1	2.28	0.47
1:A:2891:G:OP2	1:A:2891:G:H3'	2.14	0.47
2:B:42:G:N2	2:B:45:C:N3	2.53	0.47
2:B:64:A:H1'	2:B:66:C:H41	1.80	0.47
6:G:108:VAL:HG21	6:G:153:ARG:HG2	1.96	0.47
1:A:1219:C:H3'	1:A:1220:G:O4'	2.14	0.47
1:A:1998:A:H4'	1:A:1999:A:OP1	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:39:A:H2'	2:B:40:C:H2'	1.96	0.47
3:C:153:GLN:C	3:C:154:LEU:HD12	2.39	0.47
1:A:580:U:H2'	1:A:581:C:C6	2.49	0.47
1:A:1673:G:H2'	1:A:1674:G:H8	1.79	0.47
1:A:2222:C:H2'	1:A:2223:U:C6	2.49	0.47
1:A:2459:A:N3	1:A:2459:A:H2'	2.29	0.47
6:G:47:GLU:H	6:G:51:LEU:CD2	1.83	0.47
13:Q:89:GLU:CD	13:Q:109:LEU:HD22	2.39	0.47
1:A:63:G:H2'	1:A:64:A:C8	2.49	0.47
1:A:259:A:H2'	1:A:260:A:H8	1.78	0.47
1:A:269:G:H4'	1:A:270:C:OP1	2.12	0.47
1:A:273:A:H2	1:A:417:G:H22	1.63	0.47
1:A:283:G:H3'	1:A:284:C:C6	2.49	0.47
1:A:300:G:N3	1:A:302:A:O4'	2.48	0.47
1:A:750:U:C2	1:A:751:G:H1'	2.50	0.47
1:A:897:G:H21	20:Z:46:MET:HE1	1.79	0.47
1:A:1264:G:H2'	1:A:1265:A:C8	2.50	0.47
1:A:1457:U:H3'	1:A:1459:U:C4	2.48	0.47
1:A:1529:G:H2'	1:A:1530:G:C8	2.49	0.47
1:A:1812:A:N6	1:A:2617:G:H2'	2.30	0.47
1:A:1823:U:H3	1:A:1854:G:H1	1.60	0.47
1:A:1847:U:H2'	3:C:156:ARG:HG2	1.74	0.47
1:A:2156:G:N2	1:A:2190:C:O2'	2.48	0.47
1:A:2182:G:H2'	1:A:2183:G:O4'	2.14	0.47
1:A:2326:C:H1'	1:A:2350:G:N2	2.30	0.47
1:A:2590:A:O2'	8:K:23:LYS:HG3	2.14	0.47
9:L:112:LEU:HD12	9:L:112:LEU:C	2.39	0.47
13:Q:96:ALA:O	13:Q:100:VAL:HG23	2.14	0.47
15:S:21:MET:HA	15:S:24:ILE:HG22	1.97	0.47
19:Y:42:ARG:HD2	19:Y:45:GLU:OE2	2.14	0.47
1:A:2328:G:H2'	1:A:2329:A:O4'	2.15	0.47
7:J:70:LEU:HD23	7:J:70:LEU:HA	1.76	0.47
9:L:127:LYS:HD3	9:L:129:SER:H	1.80	0.47
1:A:282:G:C4	1:A:283:G:C8	3.02	0.47
1:A:689:A:H2'	1:A:690:A:O4'	2.15	0.47
1:A:194:A:H2'	1:A:195:C:C6	2.50	0.47
1:A:274:A:C5	1:A:295:G:C2	3.03	0.47
1:A:695:G:H3'	1:A:696:C:C5'	2.39	0.47
1:A:752:A:C6	1:A:774:A:N7	2.83	0.47
1:A:772:G:HO2'	1:A:773:G:H8	1.56	0.47
1:A:979:U:HO2'	1:A:980:C:H6	1.61	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1981:A:H2'	1:A:1982:A:C8	2.50	0.47
1:A:2397:C:H2'	1:A:2398:A:C8	2.49	0.47
9:L:132:ALA:O	9:L:133:LYS:HG2	2.14	0.47
1:A:160:G:H21	1:A:167:U:H5	1.63	0.46
1:A:946:G:H21	1:A:947:A:H62	1.62	0.46
1:A:1065:U:O2'	1:A:1067:A:H2	1.98	0.46
1:A:1081:U:H3	1:A:1166:G:N2	2.09	0.46
1:A:1131:A:H2'	1:A:1132:A:C8	2.50	0.46
1:A:1571:G:C2'	1:A:1572:G:H5'	2.45	0.46
1:A:1827:U:H3'	1:A:1828:G:H21	1.80	0.46
1:A:2093:C:H1'	1:A:2477:A:H2	1.80	0.46
1:A:2198:G:H21	1:A:2199:G:H5''	1.79	0.46
1:A:2762:A:C2	4:D:207:LYS:HB3	2.50	0.46
1:A:2825:C:H5''	1:A:2826:A:N7	2.29	0.46
2:B:75:U:H2'	2:B:76:A:C8	2.50	0.46
6:G:53:VAL:HG12	6:G:54:ALA:H	1.77	0.46
1:A:158:C:O2'	1:A:159:U:H6	1.97	0.46
2:B:11:A:H1'	2:B:13:A:H2'	1.96	0.46
17:U:72:ASP:HB2	17:U:79:THR:OG1	2.15	0.46
1:A:274:A:C5	1:A:295:G:N2	2.84	0.46
1:A:1055:A:C8	1:A:1199:C:O2'	2.69	0.46
1:A:2384:C:H3'	1:A:2385:C:H6	1.81	0.46
2:B:97:A:H3'	2:B:98:G:H8	1.79	0.46
3:C:205:ILE:HG23	3:C:210:ARG:HB3	1.96	0.46
18:V:42:GLY:O	18:V:43:SER:C	2.59	0.46
1:A:2318:G:N2	1:A:2373:U:H1'	2.30	0.46
2:B:20:A:H2'	2:B:21:G:C8	2.50	0.46
3:C:23:GLU:CG	3:C:90:ASN:ND2	2.79	0.46
3:C:39:LYS:NZ	3:C:57:GLY:C	2.74	0.46
4:D:13:THR:OG1	4:D:14:GLN:N	2.46	0.46
19:Y:11:THR:HB	19:Y:15:GLU:OE2	2.16	0.46
1:A:89:U:H5''	1:A:90:A:H2'	1.97	0.46
1:A:774:A:O2'	1:A:775:G:C8	2.69	0.46
1:A:1041:C:N3	7:J:5:PRO:HD2	2.30	0.46
1:A:1141:A:C2	1:A:1142:A:H1'	2.51	0.46
1:A:1169:C:H2'	1:A:1170:C:C5	2.50	0.46
3:C:79:ALA:C	3:C:80:THR:HG23	2.40	0.46
17:U:40:MET:HE3	17:U:58:ASN:ND2	2.29	0.46
17:U:93:VAL:CG2	17:U:99:GLN:O	2.55	0.46
1:A:288:C:O2'	1:A:289:C:H5'	2.16	0.46
1:A:303:G:H2'	1:A:304:G:H8	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:682:G:O5'	9:L:132:ALA:HB1	2.16	0.46
1:A:1339:A:H4'	1:A:1340:A:O5'	2.14	0.46
1:A:2117:A:N1	1:A:2260:U:H5	2.14	0.46
1:A:2309:G:H4'	1:A:2356:A:C5'	2.37	0.46
1:A:2357:A:C6	1:A:2358:A:C4	3.03	0.46
1:A:2393:C:H2'	1:A:2394:G:C8	2.51	0.46
3:C:173:LEU:HD12	3:C:173:LEU:HA	1.72	0.46
16:T:36:LYS:HG2	16:T:56:ILE:CD1	2.26	0.46
16:T:50:LYS:HB2	16:T:87:SER:HB3	1.98	0.46
1:A:887:C:O2'	1:A:888:A:N7	2.45	0.46
1:A:2356:A:C4	1:A:2357:A:C6	3.03	0.46
1:A:2660:G:H4'	1:A:2916:A:H5'	1.97	0.46
6:G:127:PRO:HG2	6:G:131:LYS:HB2	1.98	0.46
1:A:90:A:H4'	1:A:91:A:O5'	2.16	0.46
1:A:1055:A:H8	1:A:1199:C:O2'	1.99	0.46
1:A:1167:C:H6	1:A:1167:C:O5'	1.99	0.46
1:A:2121:U:H3'	1:A:2122:G:H2'	1.97	0.46
3:C:39:LYS:HZ3	3:C:57:GLY:C	2.24	0.46
3:C:142:HIS:CD2	3:C:152:GLY:HA3	2.51	0.46
16:T:56:ILE:HG22	16:T:57:MET:N	2.31	0.46
1:A:274:A:N7	1:A:296:G:N1	2.64	0.46
1:A:1096:A:C4	1:A:1097:A:C8	3.03	0.46
1:A:1996:C:H41	1:A:2000:A:H1'	1.81	0.46
7:J:29:LEU:C	7:J:29:LEU:HD12	2.40	0.46
1:A:664:C:HO2'	1:A:665:G:H8	1.62	0.46
1:A:1762:G:H2'	1:A:1763:G:C8	2.50	0.46
1:A:1863:U:H5'	1:A:1999:A:H61	1.81	0.46
1:A:2284:G:H2'	1:A:2285:G:C8	2.51	0.46
5:E:6:LEU:HD11	5:E:127:GLU:HG3	1.98	0.46
1:A:49:A:C5	1:A:178:A:N6	2.84	0.45
1:A:1470:G:N2	1:A:1622:C:H41	2.11	0.45
1:A:1494:G:H3'	1:A:1495:C:H5''	1.98	0.45
1:A:2353:U:H5	1:A:2355:U:C5	2.34	0.45
1:A:2498:A:H3'	1:A:2499:G:H8	1.81	0.45
6:G:36:ARG:CB	6:G:76:MET:HE1	2.46	0.45
6:G:53:VAL:CG1	6:G:54:ALA:N	2.78	0.45
11:O:45:ILE:N	11:O:45:ILE:HD12	2.31	0.45
19:Y:17:LYS:CB	19:Y:53:MET:HE1	2.43	0.45
1:A:1518:G:H1	1:A:1566:G:H1	1.64	0.45
3:C:261:LYS:O	3:C:264:ASN:ND2	2.49	0.45
5:E:53:ASN:HB3	5:E:56:GLU:HG3	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:25:VAL:HB	6:G:38:PHE:CE2	2.49	0.45
6:G:80:VAL:HG12	6:G:80:VAL:O	2.16	0.45
1:A:420:U:H3'	1:A:421:A:H8	1.80	0.45
1:A:2192:U:H2'	1:A:2193:C:O4'	2.16	0.45
1:A:2476:G:O2'	1:A:2529:U:H2'	2.16	0.45
1:A:2581:U:H4'	1:A:2582:G:OP1	2.16	0.45
15:S:36:LEU:HD23	15:S:36:LEU:HA	1.78	0.45
18:V:87:VAL:O	18:V:89:VAL:HG23	2.17	0.45
1:A:1585:A:H3'	1:A:1586:G:O4'	2.17	0.45
1:A:2195:G:H2'	1:A:2197:G:N7	2.32	0.45
2:B:72:U:H3'	2:B:73:G:H8	1.81	0.45
4:D:156:LYS:HB2	4:D:156:LYS:HE2	1.74	0.45
8:K:42:THR:HG22	8:K:57:VAL:HG12	1.97	0.45
1:A:774:A:N6	1:A:775:G:N1	2.64	0.45
1:A:1358:G:H2'	1:A:1359:G:C8	2.51	0.45
1:A:2316:A:H5'	1:A:2317:A:O4'	2.17	0.45
1:A:2519:G:H1'	1:A:2520:U:C5	2.52	0.45
3:C:26:THR:HG23	3:C:80:THR:HB	1.99	0.45
7:J:29:LEU:HD12	7:J:30:SER:N	2.31	0.45
11:O:69:GLY:O	11:O:73:ALA:HB3	2.16	0.45
1:A:409:U:H2'	1:A:410:G:C8	2.52	0.45
1:A:1074:A:N6	1:A:1171:G:H1'	2.32	0.45
1:A:2279:G:H1'	1:A:2281:G:OP2	2.16	0.45
1:A:2324:C:C2	1:A:2368:G:C2	3.05	0.45
1:A:2374:G:P	1:A:2410:C:H4'	2.57	0.45
3:C:67:PHE:HE1	3:C:105:LEU:HD22	1.81	0.45
6:G:55:ARG:NE	6:G:63:ARG:CG	2.76	0.45
12:P:30:ARG:HG3	12:P:47:GLU:HB3	1.97	0.45
1:A:1005:A:H2'	1:A:1006:A:C8	2.51	0.45
1:A:2250:G:O2'	3:C:147:LYS:HD3	2.16	0.45
1:A:2359:G:C6	1:A:2360:G:C6	3.05	0.45
8:K:111:PHE:O	8:K:114:ILE:CG2	2.65	0.45
9:L:127:LYS:CD	9:L:128:PHE:H	2.21	0.45
19:Y:52:ARG:O	19:Y:55:THR:HG22	2.16	0.45
1:A:1554:U:H5''	1:A:1555:A:C8	2.52	0.45
1:A:1998:A:H1'	1:A:1999:A:C5'	2.46	0.45
11:O:44:ILE:O	11:O:52:THR:HA	2.17	0.45
1:A:427:G:N3	1:A:427:G:H2'	2.32	0.45
1:A:688:G:C2	1:A:690:A:H5''	2.51	0.45
1:A:860:U:H1'	1:A:1266:A:H1'	1.99	0.45
1:A:1216:C:N3	1:A:1217:U:H1'	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2188:G:H2'	1:A:2189:G:C8	2.52	0.45
1:A:2335:U:H6	1:A:2335:U:H2'	1.62	0.45
1:A:2566:U:H2'	1:A:2567:C:C6	2.51	0.45
3:C:116:ILE:CG2	3:C:117:MET:H	2.30	0.45
4:D:188:ILE:HG22	4:D:189:LYS:H	1.80	0.45
18:V:48:GLN:NE2	18:V:50:GLY:O	2.50	0.45
18:V:48:GLN:HE21	18:V:65:ASP:HB3	1.82	0.45
21:b:42:VAL:HG13	21:b:49:TYR:HB2	1.99	0.45
1:A:1493:C:H2'	1:A:1494:G:H8	1.82	0.45
1:A:1761:G:C6	1:A:1762:G:C6	3.05	0.45
1:A:2487:U:H6	1:A:2488:A:H62	1.64	0.45
1:A:2917:G:H8	1:A:2917:G:OP2	2.00	0.45
2:B:87:U:H3'	2:B:88:C:O4'	2.17	0.45
7:J:113:GLY:O	7:J:117:ARG:HG3	2.17	0.45
1:A:2191:A:H2'	1:A:2192:U:C6	2.52	0.44
1:A:2421:A:H3'	1:A:2422:U:H6	1.82	0.44
1:A:2488:A:C4	1:A:2489:U:H1'	2.52	0.44
2:B:23:U:H2'	2:B:24:C:H6	1.82	0.44
3:C:171:TYR:CE1	3:C:185:LEU:CD1	2.95	0.44
18:V:32:LYS:HE2	18:V:32:LYS:HB3	1.60	0.44
21:b:12:LYS:HA	21:b:12:LYS:HD2	1.76	0.44
1:A:305:A:H2'	1:A:306:C:H6	1.81	0.44
1:A:1073:A:H3'	1:A:1074:A:H8	1.80	0.44
1:A:1480:A:H62	1:A:1606:A:H61	1.65	0.44
1:A:1817:C:H2'	1:A:1818:A:H8	1.79	0.44
1:A:1853:G:H2'	1:A:1854:G:C8	2.52	0.44
1:A:2916:A:H2'	1:A:2917:G:C8	2.52	0.44
3:C:168:GLU:OE1	3:C:183:MET:SD	2.76	0.44
5:E:13:THR:O	5:E:13:THR:CG2	2.61	0.44
5:E:71:GLY:O	5:E:72:ARG:HG3	2.16	0.44
8:K:40:VAL:HG22	8:K:59:LYS:NZ	2.32	0.44
8:K:114:ILE:HG23	8:K:115:VAL:H	1.83	0.44
11:O:27:GLU:O	11:O:28:ARG:C	2.60	0.44
14:R:19:THR:HG22	14:R:96:THR:HG22	1.98	0.44
16:T:50:LYS:HE3	16:T:50:LYS:HB3	1.89	0.44
1:A:663:G:O2'	1:A:664:C:H5'	2.18	0.44
1:A:1984:U:C4'	1:A:2581:U:H5''	2.47	0.44
1:A:2306:G:H8	18:V:20:ASN:HD21	1.65	0.44
1:A:682:G:O6	9:L:110:LYS:HE2	2.16	0.44
1:A:1076:G:N2	1:A:2494:C:O2'	2.51	0.44
1:A:2324:C:H42	1:A:2369:A:N6	2.15	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:273:A:H2	1:A:417:G:H1	1.58	0.44
1:A:927:G:OP1	1:A:938:G:H5'	2.17	0.44
1:A:1072:A:O2'	1:A:1073:A:H5''	2.17	0.44
1:A:1518:G:N2	1:A:1566:G:H1	2.15	0.44
3:C:115:GLU:O	3:C:115:GLU:CG	2.63	0.44
6:G:9:LEU:HB2	6:G:70:ARG:NH2	2.33	0.44
8:K:104:ARG:C	8:K:106:LEU:H	2.25	0.44
1:A:124:A:OP2	22:d:19:ARG:NE	2.50	0.44
1:A:2146:A:H4'	1:A:2147:U:C4	2.52	0.44
1:A:2516:G:H2'	1:A:2517:A:H8	1.81	0.44
3:C:67:PHE:HE2	3:C:156:ARG:HH22	1.66	0.44
4:D:182:GLU:HG2	4:D:183:ARG:HG3	1.99	0.44
1:A:167:U:H3'	1:A:168:A:H8	1.83	0.44
1:A:283:G:H3'	1:A:284:C:H6	1.83	0.44
1:A:300:G:N2	1:A:302:A:C8	2.86	0.44
1:A:1140:U:C2	1:A:1142:A:H5''	2.53	0.44
1:A:2272:U:H5'	1:A:2273:U:OP2	2.18	0.44
5:E:75:GLN:OE1	5:E:82:GLN:NE2	2.51	0.44
1:A:281:A:H1'	1:A:282:G:H5'	2.00	0.44
1:A:349:C:H2'	1:A:350:U:C6	2.53	0.44
1:A:929:G:H2'	1:A:930:C:H6	1.81	0.44
1:A:1092:A:H3'	1:A:1092:A:N3	2.33	0.44
1:A:2564:G:H2'	1:A:2565:G:H8	1.82	0.44
4:D:12:MET:HB3	4:D:12:MET:HE2	1.82	0.44
6:G:85:GLU:HB3	6:G:135:LYS:HD3	1.98	0.44
9:L:47:ARG:HB3	9:L:50:PHE:HB2	2.00	0.44
10:N:21:THR:HG21	10:N:65:TYR:CE2	2.52	0.44
10:N:30:ILE:HG22	10:N:31:GLU:N	2.33	0.44
16:T:52:ASP:OD1	16:T:52:ASP:C	2.60	0.44
1:A:1570:U:H5''	1:A:1571:G:H8	1.83	0.44
1:A:2090:G:H1'	1:A:2091:A:H2'	2.00	0.44
1:A:2177:G:H2'	1:A:2178:C:C6	2.53	0.44
1:A:2647:G:N2	4:D:146:MET:HE1	2.33	0.44
2:B:41:C:O2'	2:B:43:A:N6	2.51	0.44
5:E:35:ASP:OD1	5:E:35:ASP:N	2.49	0.44
15:S:29:VAL:HG21	15:S:69:LEU:CB	2.48	0.44
1:A:259:A:H2'	1:A:260:A:C8	2.53	0.43
1:A:954:U:H2'	1:A:955:C:O4'	2.18	0.43
1:A:1829:C:H4'	1:A:1830:G:H5''	2.00	0.43
1:A:2312:C:H4'	1:A:2312:C:OP1	2.17	0.43
1:A:2361:C:H2'	1:A:2364:A:H1'	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:6:U:H4'	11:O:32:ASN:ND2	2.32	0.43
4:D:188:ILE:CG2	4:D:189:LYS:H	2.30	0.43
1:A:917:A:H2'	1:A:918:U:H1'	1.99	0.43
1:A:1551:C:H2'	1:A:1552:C:C6	2.52	0.43
11:O:110:ALA:O	11:O:114:ARG:N	2.51	0.43
16:T:26:TYR:CG	16:T:90:ILE:HD11	2.53	0.43
16:T:36:LYS:CG	16:T:56:ILE:HD12	2.26	0.43
19:Y:14:ILE:CG2	19:Y:15:GLU:N	2.81	0.43
1:A:6:A:H2'	1:A:7:G:C8	2.53	0.43
1:A:451:C:H4'	1:A:452:C:H5''	2.00	0.43
1:A:1520:A:N6	1:A:1564:C:H42	2.13	0.43
1:A:1976:C:H1'	1:A:1977:G:H5'	2.00	0.43
6:G:38:PHE:O	6:G:39:HIS:C	2.61	0.43
11:O:77:VAL:CG1	11:O:109:LEU:HD21	2.48	0.43
1:A:1471:G:O2'	1:A:1472:G:H5'	2.18	0.43
1:A:1472:G:C4	1:A:1473:A:N7	2.86	0.43
1:A:1814:A:C4	1:A:1816:A:C8	3.05	0.43
1:A:1821:G:H1	1:A:1857:G:C2'	2.30	0.43
1:A:1831:A:H2'	1:A:1832:A:C8	2.54	0.43
1:A:2150:G:H2'	1:A:2151:U:C6	2.53	0.43
1:A:2321:U:H2'	1:A:2322:C:C6	2.54	0.43
1:A:2464:A:H2'	1:A:2465:G:O4'	2.19	0.43
1:A:2479:A:C8	1:A:2533:U:H2'	2.54	0.43
1:A:2784:C:H4'	1:A:2785:U:OP1	2.17	0.43
8:K:8:LEU:CD1	8:K:82:ASN:C	2.91	0.43
10:N:31:GLU:HG3	10:N:31:GLU:O	2.18	0.43
15:S:69:LEU:HB3	15:S:107:VAL:CG1	2.49	0.43
1:A:11:G:C4	1:A:12:A:C8	3.06	0.43
1:A:99:U:H5''	1:A:101:G:H1'	2.01	0.43
1:A:428:A:H2	1:A:440:U:H3	1.67	0.43
1:A:805:G:N2	1:A:2010:A:H62	2.06	0.43
1:A:914:C:H2'	1:A:915:U:C6	2.53	0.43
1:A:1015:G:H2'	1:A:1016:U:C6	2.53	0.43
1:A:2314:C:N4	1:A:2412:G:H1	2.15	0.43
1:A:2384:C:H3'	1:A:2385:C:C6	2.53	0.43
3:C:260:ARG:HD2	3:C:264:ASN:OD1	2.19	0.43
18:V:76:LYS:HB2	18:V:90:TYR:HB3	2.01	0.43
1:A:303:G:N3	1:A:304:G:C8	2.86	0.43
1:A:1581:A:N7	1:A:1584:U:H1'	2.33	0.43
1:A:2354:G:H4'	1:A:2355:U:H5'	2.01	0.43
1:A:2374:G:H5''	1:A:2412:G:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2715:G:H2'	1:A:2716:U:C6	2.54	0.43
9:L:81:LYS:HB3	9:L:81:LYS:HE3	1.80	0.43
12:P:107:ARG:HG3	12:P:108:GLY:H	1.83	0.43
1:A:647:A:N1	1:A:671:G:O2'	2.51	0.43
1:A:1172:A:H5''	1:A:1173:A:H5'	2.01	0.43
1:A:1806:U:C3'	1:A:1807:U:H4'	2.45	0.43
1:A:2153:G:H3'	1:A:2154:G:C8	2.51	0.43
1:A:2167:C:N4	1:A:2168:G:O6	2.52	0.43
1:A:2414:C:O2	18:V:49:ARG:HD2	2.19	0.43
1:A:2534:G:H2'	1:A:2535:U:C5	2.52	0.43
1:A:2872:U:H2'	1:A:2873:G:O4'	2.18	0.43
3:C:78:VAL:CG2	3:C:110:ILE:HD11	2.49	0.43
11:O:40:ILE:CG1	11:O:105:ARG:HD3	2.45	0.43
19:Y:2:LYS:HE3	19:Y:6:ILE:HD11	1.99	0.43
20:Z:57:LYS:HB3	20:Z:57:LYS:HE2	1.80	0.43
1:A:1471:G:N7	3:C:31:LYS:NZ	2.67	0.43
1:A:1771:C:N3	1:A:1772:C:N4	2.67	0.43
1:A:2025:C:H4'	1:A:2026:A:OP1	2.19	0.43
1:A:2320:U:H2'	1:A:2321:U:C5	2.53	0.43
1:A:2387:A:H4'	1:A:2388:C:C5	2.54	0.43
1:A:2417:A:H2'	1:A:2418:G:C6	2.53	0.43
2:B:66:C:H2'	2:B:67:G:O4'	2.19	0.43
4:D:121:GLY:HA2	4:D:161:PRO:HB3	2.01	0.43
11:O:77:VAL:O	11:O:81:VAL:HG13	2.19	0.43
17:U:5:LYS:HB2	17:U:5:LYS:HE3	1.75	0.43
1:A:1326:A:H5'	10:N:107:ARG:HD2	2.00	0.43
1:A:1470:G:H3'	1:A:1471:G:H8	1.83	0.43
1:A:1480:A:N6	1:A:1606:A:H61	2.16	0.43
1:A:1801:G:N2	1:A:2007:A:H2	2.17	0.43
1:A:2316:A:H5'	1:A:2317:A:N3	2.33	0.43
1:A:2582:G:N2	1:A:2583:U:H5''	2.34	0.43
2:B:14:G:H3'	2:B:15:C:H6	1.84	0.43
2:B:79:C:H2'	2:B:80:G:C8	2.53	0.43
4:D:53:PHE:CZ	4:D:54:ASP:HB2	2.54	0.43
6:G:17:VAL:HG22	6:G:27:VAL:HG13	2.01	0.43
6:G:96:ARG:NH1	6:G:98:SER:HB3	2.34	0.43
9:L:38:GLN:HA	9:L:41:ARG:HB3	2.01	0.43
11:O:23:SER:C	11:O:25:THR:N	2.75	0.43
11:O:70:ASP:N	11:O:105:ARG:NH2	2.67	0.43
13:Q:83:LEU:HD22	13:Q:89:GLU:OE1	2.19	0.43
22:d:3:ARG:HA	22:d:3:ARG:HD3	1.59	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1124:C:H1'	1:A:1134:A:C2	2.54	0.43
1:A:2418:G:H1'	1:A:2419:U:O4'	2.19	0.43
1:A:2484:G:H2'	1:A:2485:C:H6	1.82	0.43
1:A:2891:G:O3'	1:A:2892:G:H4'	2.19	0.43
6:G:124:ILE:HD12	6:G:124:ILE:N	2.34	0.43
7:J:69:LYS:HA	7:J:72:ASP:HB3	2.00	0.43
16:T:35:ASN:OD1	16:T:38:GLU:HG3	2.19	0.43
17:U:8:LYS:HE2	17:U:8:LYS:HB3	1.94	0.43
1:A:27:G:H22	1:A:558:G:H2'	1.84	0.42
1:A:1170:C:C5	1:A:1171:G:N7	2.87	0.42
1:A:1317:G:OP1	10:N:32:THR:HG22	2.18	0.42
1:A:1517:A:H3'	1:A:1518:G:H8	1.83	0.42
1:A:1689:U:H2'	1:A:1690:G:H5'	2.01	0.42
1:A:2111:A:H3'	1:A:2112:G:O4'	2.18	0.42
1:A:2124:A:C2'	1:A:2125:U:H5'	2.47	0.42
1:A:2206:C:H2'	1:A:2207:C:C6	2.54	0.42
1:A:2221:C:H2'	1:A:2222:C:C6	2.54	0.42
3:C:264:ASN:C	3:C:266:SER:H	2.27	0.42
15:S:95:GLN:HG3	15:S:96:ILE:N	2.33	0.42
19:Y:5:GLU:HG3	19:Y:56:VAL:HG11	1.99	0.42
1:A:318:A:H3'	1:A:319:G:O4'	2.19	0.42
1:A:775:G:N2	1:A:777:C:H1'	2.34	0.42
1:A:786:A:H5''	1:A:1813:A:C6	2.54	0.42
1:A:1158:G:H2'	1:A:1159:U:C6	2.54	0.42
1:A:1222:A:H2'	1:A:1223:C:C6	2.54	0.42
1:A:1817:C:C5'	1:A:2619:A:H4'	2.44	0.42
1:A:2125:U:H2'	1:A:2126:G:O4'	2.19	0.42
1:A:2151:U:H3	1:A:2205:A:H61	1.67	0.42
1:A:2217:U:H2'	1:A:2218:U:C6	2.54	0.42
1:A:2344:U:H2'	1:A:2345:U:C6	2.54	0.42
1:A:2481:C:C6	1:A:2483:G:H5''	2.54	0.42
1:A:2659:G:O4'	1:A:2918:G:H1'	2.19	0.42
1:A:2819:A:H4'	1:A:2820:U:H5''	2.01	0.42
6:G:47:GLU:O	6:G:51:LEU:HD23	2.19	0.42
1:A:49:A:N6	1:A:179:A:N6	2.63	0.42
1:A:1473:A:C8	1:A:1474:C:C4	3.08	0.42
1:A:1534:A:H2'	1:A:1535:U:C6	2.55	0.42
1:A:1595:U:H2'	1:A:1596:U:C6	2.54	0.42
1:A:2318:G:C5	1:A:2319:G:N2	2.88	0.42
1:A:2581:U:H6	1:A:2581:U:H2'	1.62	0.42
2:B:66:C:H3'	2:B:67:G:H8	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:718:C:HO2'	1:A:719:C:H6	1.63	0.42
1:A:2210:G:H2'	1:A:2211:G:C8	2.55	0.42
1:A:2627:A:OP1	3:C:241:ILE:HA	2.18	0.42
5:E:184:LEU:HD23	5:E:184:LEU:HA	1.78	0.42
11:O:61:LYS:HB2	11:O:61:LYS:HE2	1.89	0.42
16:T:21:MET:HE3	16:T:21:MET:HB2	1.75	0.42
1:A:178:A:HO2'	1:A:179:A:H8	1.59	0.42
1:A:770:A:H2'	1:A:770:A:N3	2.34	0.42
1:A:1097:A:C6	1:A:1098:C:C4	3.07	0.42
1:A:1108:G:N3	1:A:1108:G:H2'	2.34	0.42
1:A:1124:C:H5''	1:A:1125:C:O5'	2.19	0.42
1:A:1472:G:H2'	1:A:1473:A:H8	1.85	0.42
1:A:2001:G:H3'	1:A:2002:G:H8	1.84	0.42
1:A:2342:C:H2'	1:A:2343:A:C8	2.54	0.42
1:A:2387:A:H1'	1:A:2389:A:C8	2.55	0.42
3:C:129:ALA:HA	3:C:191:SER:HA	2.02	0.42
6:G:53:VAL:CG1	6:G:54:ALA:H	2.32	0.42
7:J:61:GLU:H	7:J:61:GLU:HG2	1.67	0.42
13:Q:117:LEU:HD23	13:Q:117:LEU:HA	1.81	0.42
18:V:74:THR:H	18:V:92:VAL:H	1.68	0.42
1:A:1018:G:H3'	1:A:1019:A:H2'	2.02	0.42
1:A:1348:G:H4'	22:d:7:PRO:HB2	2.01	0.42
1:A:1570:U:H5''	1:A:1571:G:C8	2.54	0.42
1:A:2153:G:H2'	1:A:2154:G:O4'	2.20	0.42
1:A:2311:G:H1'	1:A:2418:G:OP2	2.20	0.42
1:A:2482:A:C8	1:A:2533:U:H1'	2.55	0.42
5:E:113:VAL:HG21	5:E:183:VAL:HG13	2.00	0.42
12:P:37:GLU:O	12:P:37:GLU:HG3	2.20	0.42
16:T:56:ILE:CG2	16:T:57:MET:N	2.82	0.42
1:A:11:G:H22	1:A:2656:G:H5''	1.85	0.42
1:A:292:U:H2'	1:A:293:U:C6	2.54	0.42
1:A:416:U:H3'	1:A:417:G:C8	2.54	0.42
1:A:2169:G:H2'	1:A:2170:A:O4'	2.19	0.42
5:E:8:ASN:O	5:E:9:GLN:C	2.61	0.42
12:P:20:LEU:HD22	12:P:20:LEU:H	1.84	0.42
12:P:55:GLY:HA2	12:P:60:GLU:HA	2.00	0.42
21:b:43:CYS:HB3	21:b:47:GLY:CA	2.50	0.42
1:A:753:A:N6	1:A:772:G:N2	2.30	0.42
1:A:1240:U:H1'	13:Q:4:VAL:HG22	2.01	0.42
1:A:1581:A:C5	1:A:1584:U:H1'	2.55	0.42
1:A:2363:C:H1'	1:A:2366:G:C2	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2493:C:H2'	1:A:2494:C:C6	2.54	0.42
2:B:53:U:H3'	2:B:54:U:H5''	2.02	0.42
5:E:132:ASP:OD1	5:E:132:ASP:N	2.51	0.42
6:G:89:GLU:HB2	6:G:164:ARG:HB2	2.01	0.42
6:G:171:ARG:NH2	6:G:173:LYS:HB2	2.24	0.42
11:O:102:TYR:O	11:O:103:HIS:C	2.62	0.42
1:A:662:U:H2'	1:A:663:G:H8	1.85	0.42
1:A:908:A:H2'	1:A:909:G:O4'	2.20	0.42
1:A:1640:G:H2'	1:A:1642:G:OP1	2.20	0.42
1:A:1997:G:N2	1:A:1998:A:N7	2.66	0.42
1:A:2197:G:N3	1:A:2198:G:N1	2.67	0.42
1:A:2380:G:N3	1:A:2380:G:O2'	2.47	0.42
1:A:2582:G:H3'	1:A:2582:G:N3	2.35	0.42
8:K:114:ILE:CG2	8:K:115:VAL:N	2.82	0.42
9:L:79:LEU:HA	9:L:79:LEU:HD23	1.80	0.42
11:O:80:LEU:HD12	11:O:83:LYS:CE	2.44	0.42
1:A:27:G:N2	1:A:558:G:H2'	2.35	0.42
1:A:140:A:H2'	1:A:141:U:O4'	2.19	0.42
1:A:161:A:N3	1:A:2237:C:O2'	2.47	0.42
1:A:461:C:H2'	1:A:462:A:C8	2.55	0.42
1:A:598:U:H2'	1:A:599:G:O4'	2.19	0.42
1:A:752:A:C2	1:A:753:A:C4	3.08	0.42
1:A:957:A:H5'	1:A:958:A:OP1	2.20	0.42
1:A:1042:A:H4'	13:Q:92:ARG:NE	2.35	0.42
1:A:1134:A:H5'	1:A:1135:G:H8	1.83	0.42
1:A:1556:A:H2'	1:A:1557:G:O4'	2.20	0.42
1:A:2270:A:H2'	1:A:2271:G:O4'	2.19	0.42
1:A:2278:U:H5''	1:A:2279:G:OP2	2.20	0.42
1:A:2306:G:H5''	18:V:20:ASN:HD21	1.85	0.42
1:A:2472:C:H2'	1:A:2473:G:C8	2.55	0.42
2:B:40:C:H1'	2:B:41:C:C5	2.55	0.42
3:C:24:ILE:HG23	3:C:82:GLU:HA	2.02	0.42
5:E:4:VAL:O	5:E:4:VAL:CG2	2.60	0.42
13:Q:89:GLU:OE2	13:Q:109:LEU:HD22	2.20	0.42
19:Y:17:LYS:CG	19:Y:53:MET:HE3	2.40	0.42
1:A:274:A:C6	1:A:295:G:N3	2.88	0.41
1:A:807:G:H2'	1:A:808:A:O4'	2.20	0.41
1:A:1244:A:C2'	1:A:1245:G:H5'	2.50	0.41
1:A:1314:A:H4'	1:A:1315:G:OP1	2.19	0.41
1:A:1580:A:H3'	1:A:1581:A:N3	2.34	0.41
1:A:2193:C:OP2	1:A:2195:G:N2	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:2565:G:H2'	1:A:2566:U:C6	2.55	0.41
11:O:32:ASN:ND2	11:O:45:ILE:HD11	2.35	0.41
13:Q:92:ARG:HH22	14:R:10:LYS:HG3	1.84	0.41
19:Y:14:ILE:CG2	19:Y:15:GLU:H	2.31	0.41
1:A:52:A:H2'	1:A:53:A:C8	2.55	0.41
1:A:2268:G:N3	1:A:2268:G:H2'	2.35	0.41
1:A:2332:G:H2'	1:A:2332:G:N3	2.35	0.41
1:A:2605:G:N3	1:A:2605:G:H2'	2.35	0.41
1:A:2812:A:H2'	1:A:2813:U:C6	2.55	0.41
3:C:67:PHE:CE1	3:C:105:LEU:HD22	2.55	0.41
3:C:205:ILE:HG22	3:C:210:ARG:HB3	2.01	0.41
5:E:70:THR:CG2	5:E:72:ARG:NH2	2.66	0.41
6:G:155:PRO:HD3	6:G:163:ILE:O	2.18	0.41
16:T:36:LYS:HA	16:T:56:ILE:HD11	2.01	0.41
1:A:419:G:H1'	1:A:420:U:P	2.60	0.41
1:A:1169:C:H2'	1:A:1170:C:C6	2.55	0.41
1:A:1518:G:N2	1:A:1566:G:H22	2.18	0.41
1:A:2080:A:H4'	4:D:146:MET:HG3	2.01	0.41
1:A:2358:A:C4	1:A:2359:G:N7	2.88	0.41
3:C:91:ILE:HG22	3:C:92:ALA:N	2.35	0.41
3:C:138:GLY:O	3:C:140:VAL:HG23	2.21	0.41
6:G:108:VAL:HG22	6:G:109:GLY:H	1.84	0.41
9:L:19:VAL:HG13	9:L:27:ASN:HB3	2.01	0.41
14:R:45:ASN:O	14:R:46:VAL:C	2.63	0.41
14:R:63:GLU:OE2	14:R:94:LYS:HG2	2.20	0.41
17:U:48:THR:H	17:U:53:GLN:NE2	2.19	0.41
18:V:58:ASN:HD22	18:V:71:ILE:CD1	2.32	0.41
1:A:1111:U:C4	1:A:1120:G:C4	3.08	0.41
1:A:1148:C:H2'	1:A:1149:A:C8	2.55	0.41
1:A:1215:U:H2'	1:A:1216:C:C6	2.56	0.41
1:A:1493:C:C2	1:A:1494:G:C8	3.08	0.41
1:A:1553:A:H2'	1:A:1554:U:C2	2.56	0.41
1:A:2370:G:H2'	1:A:2370:G:N3	2.34	0.41
1:A:2920:C:H2'	1:A:2921:U:C6	2.54	0.41
3:C:100:GLU:O	3:C:101:LYS:HB2	2.20	0.41
3:C:131:PRO:HA	3:C:189:ARG:HG2	2.03	0.41
6:G:3:ARG:NH1	6:G:6:LYS:HG3	2.35	0.41
17:U:79:THR:HG22	17:U:80:ARG:O	2.20	0.41
19:Y:15:GLU:O	19:Y:16:GLN:C	2.63	0.41
1:A:78:U:OP1	19:Y:2:LYS:HG2	2.20	0.41
1:A:436:A:H3'	1:A:437:A:H8	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1148:C:C2	1:A:1149:A:C8	3.08	0.41
1:A:1332:U:H2'	1:A:1333:C:C6	2.56	0.41
1:A:2137:U:H3'	1:A:2138:U:C6	2.54	0.41
1:A:2351:A:H2'	1:A:2352:G:O4'	2.20	0.41
1:A:2414:C:H2'	1:A:2415:U:C6	2.56	0.41
4:D:51:LEU:O	4:D:80:VAL:HA	2.21	0.41
13:Q:15:LYS:HE2	13:Q:15:LYS:HB3	1.84	0.41
1:A:1067:A:H62	1:A:1187:U:H3	1.67	0.41
1:A:1466:U:H6	1:A:1540:A:N6	2.18	0.41
1:A:2354:G:H22	1:A:2417:A:H61	1.68	0.41
2:B:31:G:H2'	2:B:31:G:N3	2.35	0.41
3:C:225:MET:CE	3:C:230:HIS:HB2	2.50	0.41
6:G:102:ASN:OD1	6:G:103:LYS:HG3	2.21	0.41
9:L:16:ARG:CG	9:L:17:ASN:N	2.83	0.41
1:A:154:A:N1	1:A:173:A:N1	2.68	0.41
1:A:235:G:OP2	1:A:235:G:H8	2.04	0.41
1:A:252:C:H4'	1:A:253:G:O5'	2.19	0.41
1:A:290:U:O2'	1:A:291:C:H5'	2.21	0.41
1:A:937:C:H2'	1:A:938:G:O4'	2.20	0.41
1:A:1485:A:N1	1:A:1600:G:C8	2.88	0.41
1:A:1577:C:C4	1:A:1578:G:H1'	2.56	0.41
1:A:1772:C:OP2	1:A:1773:G:H5''	2.20	0.41
1:A:2104:U:O2'	1:A:2105:U:H2'	2.21	0.41
1:A:2131:U:H2'	1:A:2132:A:H8	1.82	0.41
1:A:2322:C:OP1	11:O:97:ARG:CZ	2.68	0.41
1:A:2857:U:H4'	1:A:2858:U:H5'	2.03	0.41
3:C:68:LYS:O	3:C:69:ARG:C	2.63	0.41
4:D:6:LEU:C	4:D:6:LEU:HD12	2.46	0.41
6:G:39:HIS:CD2	6:G:41:ASP:HB3	2.55	0.41
6:G:116:ILE:HD12	6:G:116:ILE:N	2.36	0.41
23:f:24:MET:SD	23:f:35:LYS:HG2	2.61	0.41
1:A:340:U:H2'	1:A:341:G:O4'	2.20	0.41
1:A:752:A:C5	1:A:774:A:N6	2.88	0.41
1:A:1005:A:H8	1:A:1005:A:OP1	2.04	0.41
1:A:1075:A:H3'	1:A:1076:G:C8	2.55	0.41
1:A:1154:U:H2'	1:A:1155:C:H6	1.85	0.41
1:A:2106:A:C6	1:A:2107:C:C4	3.08	0.41
1:A:2165:A:O5'	1:A:2165:A:H8	2.03	0.41
1:A:2306:G:H5''	18:V:20:ASN:ND2	2.36	0.41
1:A:2872:U:H3	1:A:2893:A:H61	1.69	0.41
1:A:2891:G:C4	1:A:2893:A:H1'	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:133:MET:HB3	4:D:133:MET:HE3	1.79	0.41
11:O:39:HIS:HB3	11:O:68:THR:HG22	2.01	0.41
18:V:20:ASN:O	18:V:21:GLY:C	2.63	0.41
1:A:313:U:H2'	1:A:404:C:N3	2.36	0.41
1:A:858:U:H2'	9:L:21:ARG:HA	2.02	0.41
1:A:1095:C:C2	1:A:1096:A:C8	3.09	0.41
1:A:1521:G:N2	1:A:1563:G:H22	2.19	0.41
1:A:1571:G:O2'	1:A:1572:G:H5'	2.20	0.41
1:A:1581:A:H8	1:A:1582:U:O2'	2.02	0.41
1:A:1780:C:H5'	1:A:2885:A:N1	2.36	0.41
1:A:2138:U:H2'	1:A:2139:G:N1	2.35	0.41
1:A:2157:C:H4'	1:A:2202:A:C2	2.56	0.41
1:A:2173:G:O3'	1:A:2174:C:H3'	2.21	0.41
1:A:2313:C:N4	1:A:2413:G:O6	2.54	0.41
2:B:26:C:H2'	2:B:27:A:O4'	2.20	0.41
2:B:35:C:H2'	2:B:36:C:C6	2.56	0.41
4:D:80:VAL:O	4:D:81:LYS:CG	2.66	0.41
6:G:25:VAL:HG23	6:G:38:PHE:HD2	1.86	0.41
11:O:111:ASP:HA	11:O:114:ARG:CG	2.51	0.41
15:S:21:MET:HE2	15:S:76:VAL:HG23	2.03	0.41
17:U:10:MET:HB2	17:U:71:LEU:HD11	2.02	0.41
18:V:66:THR:HG22	18:V:67:LEU:H	1.86	0.41
1:A:302:A:C2	1:A:303:G:C2	3.09	0.41
1:A:673:A:N6	9:L:112:LEU:CD1	2.84	0.41
1:A:1115:A:O2'	1:A:1142:A:H4'	2.21	0.41
1:A:1152:G:C2	1:A:1153:G:C8	3.09	0.41
1:A:2061:G:H2'	1:A:2528:C:H42	1.85	0.41
1:A:2301:U:OP2	18:V:27:LYS:HG3	2.21	0.41
1:A:2615:C:H5'	1:A:2637:G:H22	1.86	0.41
1:A:2922:U:H2'	1:A:2923:A:C8	2.56	0.41
3:C:264:ASN:C	3:C:266:SER:N	2.78	0.41
8:K:9:LYS:HE2	8:K:9:LYS:HB2	1.86	0.41
8:K:119:PRO:O	8:K:120:GLU:C	2.65	0.41
12:P:7:LEU:HD12	12:P:7:LEU:H	1.85	0.41
15:S:88:ARG:HB2	15:S:92:ARG:HB2	2.03	0.41
21:b:52:LYS:HG3	21:b:54:ILE:HD12	2.03	0.41
1:A:11:G:H22	1:A:2656:G:C5'	2.33	0.40
1:A:1471:G:C6	1:A:1472:G:C6	3.09	0.40
1:A:1474:C:H5	1:A:1618:A:OP2	2.04	0.40
1:A:2373:U:H6	1:A:2373:U:OP2	2.04	0.40
1:A:2487:U:H1'	1:A:2488:A:N7	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:84:G:H21	2:B:85:U:H5	1.69	0.40
4:D:109:ASP:OD1	4:D:172:GLN:HB3	2.21	0.40
1:A:154:A:N6	1:A:173:A:H61	2.19	0.40
1:A:632:U:H2'	1:A:633:U:C6	2.56	0.40
1:A:1120:G:C2	1:A:1121:C:C4	3.08	0.40
1:A:1331:C:H2'	1:A:1332:U:C6	2.57	0.40
1:A:1475:G:H2'	1:A:1476:C:C6	2.57	0.40
1:A:1816:A:H3'	1:A:1817:C:H6	1.85	0.40
1:A:1994:C:H2'	1:A:1995:A:N3	2.37	0.40
1:A:2119:A:H2'	1:A:2120:U:C6	2.56	0.40
1:A:2490:C:H2'	1:A:2491:U:C6	2.56	0.40
1:A:2731:G:C2	1:A:2732:C:C6	3.10	0.40
1:A:2893:A:O2'	1:A:2894:G:H8	2.05	0.40
2:B:27:A:H2	2:B:54:U:H3	1.68	0.40
9:L:39:ASN:OD1	9:L:45:GLY:HA3	2.21	0.40
15:S:6:VAL:CG1	15:S:7:ALA:N	2.84	0.40
1:A:460:C:H6	1:A:460:C:H2'	1.75	0.40
1:A:1128:U:H2'	1:A:1129:U:O4'	2.20	0.40
1:A:1457:U:H3'	1:A:1459:U:C5	2.57	0.40
1:A:1460:G:HO2'	1:A:1461:A:H8	1.67	0.40
1:A:2318:G:C4	1:A:2319:G:N2	2.90	0.40
1:A:2417:A:H5''	1:A:2418:G:C8	2.57	0.40
3:C:232:HIS:HB3	3:C:242:GLY:O	2.20	0.40
5:E:8:ASN:CG	5:E:9:GLN:H	2.30	0.40
7:J:45:TYR:HA	7:J:51:THR:HG21	2.03	0.40
9:L:16:ARG:CG	9:L:17:ASN:H	2.34	0.40
9:L:93:PRO:HD3	9:L:124:LYS:O	2.20	0.40
17:U:93:VAL:HG22	17:U:94:ALA:N	2.35	0.40
21:b:36:MET:HE3	21:b:36:MET:HA	2.03	0.40
1:A:315:C:O2'	1:A:316:G:C8	2.73	0.40
1:A:674:G:H2'	1:A:675:C:C6	2.56	0.40
1:A:691:U:O2'	1:A:692:A:C8	2.74	0.40
1:A:1689:U:C2'	1:A:1690:G:H5'	2.51	0.40
1:A:1838:A:H2'	1:A:1839:A:C8	2.56	0.40
1:A:2925:C:H2'	1:A:2926:C:O4'	2.20	0.40
6:G:57:SER:OG	6:G:58:ASP:N	2.54	0.40
9:L:137:GLU:HG2	9:L:138:ALA:N	2.35	0.40
1:A:157:U:H2'	1:A:158:C:C6	2.55	0.40
6:G:15:VAL:CG2	6:G:17:VAL:HG23	2.51	0.40
18:V:77:PHE:CD2	18:V:88:SER:HB2	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	273/277 (99%)	227 (83%)	45 (16%)	1 (0%)	30	60
4	D	205/209 (98%)	191 (93%)	14 (7%)	0	100	100
5	E	203/207 (98%)	179 (88%)	24 (12%)	0	100	100
6	G	173/179 (97%)	155 (90%)	18 (10%)	0	100	100
7	J	140/145 (97%)	128 (91%)	12 (9%)	0	100	100
8	K	120/122 (98%)	105 (88%)	15 (12%)	0	100	100
9	L	144/146 (99%)	119 (83%)	25 (17%)	0	100	100
10	N	117/120 (98%)	107 (92%)	10 (8%)	0	100	100
11	O	116/120 (97%)	92 (79%)	24 (21%)	0	100	100
12	P	112/115 (97%)	101 (90%)	11 (10%)	0	100	100
13	Q	115/118 (98%)	107 (93%)	8 (7%)	0	100	100
14	R	99/102 (97%)	86 (87%)	13 (13%)	0	100	100
15	S	107/113 (95%)	97 (91%)	10 (9%)	0	100	100
16	T	91/95 (96%)	87 (96%)	4 (4%)	0	100	100
17	U	98/103 (95%)	83 (85%)	15 (15%)	0	100	100
18	V	72/94 (77%)	54 (75%)	17 (24%)	1 (1%)	9	30
19	Y	63/66 (96%)	59 (94%)	4 (6%)	0	100	100
20	Z	56/59 (95%)	56 (100%)	0	0	100	100
21	b	52/59 (88%)	47 (90%)	5 (10%)	0	100	100
22	d	42/44 (96%)	39 (93%)	3 (7%)	0	100	100
23	f	34/37 (92%)	27 (79%)	7 (21%)	0	100	100
All	All	2432/2530 (96%)	2146 (88%)	284 (12%)	2 (0%)	49	77

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
18	V	31	ALA
3	C	155	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	223/225 (99%)	222 (100%)	1 (0%)	84	94
4	D	168/170 (99%)	168 (100%)	0	100	100
5	E	169/170 (99%)	168 (99%)	1 (1%)	78	92
6	G	148/151 (98%)	147 (99%)	1 (1%)	76	91
7	J	120/123 (98%)	120 (100%)	0	100	100
8	K	101/101 (100%)	101 (100%)	0	100	100
9	L	110/110 (100%)	110 (100%)	0	100	100
10	N	99/100 (99%)	98 (99%)	1 (1%)	68	88
11	O	91/93 (98%)	90 (99%)	1 (1%)	65	87
12	P	99/100 (99%)	99 (100%)	0	100	100
13	Q	96/97 (99%)	96 (100%)	0	100	100
14	R	83/84 (99%)	83 (100%)	0	100	100
15	S	90/93 (97%)	90 (100%)	0	100	100
16	T	84/85 (99%)	84 (100%)	0	100	100
17	U	84/87 (97%)	84 (100%)	0	100	100
18	V	58/74 (78%)	58 (100%)	0	100	100
19	Y	56/57 (98%)	56 (100%)	0	100	100
20	Z	52/53 (98%)	52 (100%)	0	100	100
21	b	48/53 (91%)	48 (100%)	0	100	100
22	d	39/39 (100%)	39 (100%)	0	100	100
23	f	34/35 (97%)	34 (100%)	0	100	100
All	All	2052/2100 (98%)	2047 (100%)	5 (0%)	85	96

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	18	THR
5	E	6	LEU
6	G	84	PHE
10	N	57	HIS
11	O	102	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	44	ASN
3	C	61	GLN
3	C	90	ASN
3	C	111	GLN
3	C	226	ASN
4	D	14	GLN
4	D	140	HIS
5	E	9	GLN
5	E	189	HIS
6	G	39	HIS
6	G	59	GLN
6	G	66	HIS
9	L	83	ASN
11	O	15	HIS
11	O	32	ASN
11	O	39	HIS
11	O	43	GLN
12	P	15	GLN
15	S	95	GLN
17	U	58	ASN
18	V	48	GLN
19	Y	65	ASN
20	Z	48	ASN
23	f	32	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2816/2927 (96%)	1077 (38%)	82 (2%)
2	B	111/119 (93%)	64 (57%)	8 (7%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	2927/3046 (96%)	1141 (38%)	90 (3%)

All (1141) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	7	G
1	A	9	U
1	A	10	A
1	A	11	G
1	A	13	A
1	A	25	U
1	A	28	A
1	A	34	U
1	A	35	G
1	A	44	A
1	A	45	G
1	A	46	C
1	A	51	G
1	A	55	G
1	A	60	G
1	A	71	A
1	A	72	U
1	A	75	G
1	A	76	C
1	A	91	A
1	A	92	G
1	A	94	A
1	A	96	G
1	A	98	U
1	A	101	G
1	A	102	A
1	A	106	G
1	A	117	A
1	A	118	A
1	A	119	U
1	A	126	A
1	A	127	C
1	A	130	A
1	A	134	C
1	A	138	U
1	A	139	A
1	A	142	G

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Mol	Chain	Res	Type
1	A	143	G
1	A	144	A
1	A	158	C
1	A	159	U
1	A	163	U
1	A	164	U
1	A	165	C
1	A	166	A
1	A	172	U
1	A	173	A
1	A	174	U
1	A	175	G
1	A	176	A
1	A	177	G
1	A	178	A
1	A	179	A
1	A	180	G
1	A	187	C
1	A	188	C
1	A	199	A
1	A	202	A
1	A	207	A
1	A	216	A
1	A	219	A
1	A	220	A
1	A	224	A
1	A	225	A
1	A	227	G
1	A	230	A
1	A	231	A
1	A	232	U
1	A	233	G
1	A	234	C
1	A	236	A
1	A	245	G
1	A	249	C
1	A	251	G
1	A	252	C
1	A	253	G
1	A	258	A
1	A	268	A
1	A	269	G

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Mol	Chain	Res	Type
1	A	270	C
1	A	271	C
1	A	273	A
1	A	274	A
1	A	276	C
1	A	278	A
1	A	279	A
1	A	280	G
1	A	281	A
1	A	282	G
1	A	283	G
1	A	284	C
1	A	289	C
1	A	290	U
1	A	291	C
1	A	294	G
1	A	295	G
1	A	296	G
1	A	297	G
1	A	298	U
1	A	299	U
1	A	300	G
1	A	301	U
1	A	307	A
1	A	308	C
1	A	309	U
1	A	312	G
1	A	313	U
1	A	314	A
1	A	315	C
1	A	317	G
1	A	319	G
1	A	320	U
1	A	321	U
1	A	322	A
1	A	324	A
1	A	326	A
1	A	327	G
1	A	329	A
1	A	338	G
1	A	344	G
1	A	345	A

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Mol	Chain	Res	Type
1	A	346	G
1	A	355	A
1	A	361	G
1	A	367	G
1	A	368	G
1	A	374	A
1	A	376	A
1	A	377	G
1	A	382	G
1	A	387	C
1	A	388	A
1	A	394	U
1	A	402	U
1	A	404	C
1	A	405	U
1	A	408	G
1	A	411	G
1	A	412	A
1	A	414	C
1	A	415	C
1	A	416	U
1	A	417	G
1	A	419	G
1	A	420	U
1	A	421	A
1	A	423	G
1	A	424	G
1	A	425	C
1	A	426	G
1	A	427	G
1	A	428	A
1	A	430	C
1	A	433	G
1	A	434	U
1	A	435	G
1	A	437	A
1	A	442	C
1	A	446	G
1	A	449	A
1	A	450	U
1	A	451	C
1	A	452	C

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Mol	Chain	Res	Type
1	A	453	G
1	A	459	A
1	A	460	C
1	A	462	A
1	A	463	U
1	A	469	A
1	A	478	U
1	A	482	C
1	A	487	G
1	A	489	G
1	A	490	A
1	A	502	C
1	A	504	A
1	A	514	G
1	A	528	G
1	A	530	A
1	A	537	A
1	A	538	A
1	A	548	A
1	A	550	G
1	A	551	A
1	A	552	G
1	A	554	U
1	A	555	C
1	A	558	G
1	A	568	G
1	A	576	G
1	A	577	U
1	A	578	A
1	A	584	A
1	A	592	A
1	A	595	G
1	A	606	U
1	A	607	G
1	A	616	A
1	A	617	G
1	A	619	A
1	A	630	A
1	A	647	A
1	A	648	G
1	A	649	G
1	A	651	U

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Mol	Chain	Res	Type
1	A	658	A
1	A	663	G
1	A	665	G
1	A	666	G
1	A	673	A
1	A	680	G
1	A	683	A
1	A	686	C
1	A	689	A
1	A	690	A
1	A	691	U
1	A	692	A
1	A	694	G
1	A	695	G
1	A	696	C
1	A	701	G
1	A	710	G
1	A	711	U
1	A	717	A
1	A	718	C
1	A	719	C
1	A	733	U
1	A	751	G
1	A	758	A
1	A	762	A
1	A	765	A
1	A	768	G
1	A	769	A
1	A	770	A
1	A	771	U
1	A	772	G
1	A	773	G
1	A	774	A
1	A	775	G
1	A	776	G
1	A	777	C
1	A	781	A
1	A	794	U
1	A	795	G
1	A	811	A
1	A	812	G
1	A	822	G

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Mol	Chain	Res	Type
1	A	823	G
1	A	829	A
1	A	830	A
1	A	831	U
1	A	832	G
1	A	835	A
1	A	837	U
1	A	838	C
1	A	839	G
1	A	840	A
1	A	841	A
1	A	852	G
1	A	853	C
1	A	857	U
1	A	858	U
1	A	859	C
1	A	861	C
1	A	866	A
1	A	874	U
1	A	875	U
1	A	876	A
1	A	877	G
1	A	878	G
1	A	881	U
1	A	888	A
1	A	889	A
1	A	891	G
1	A	893	A
1	A	894	A
1	A	895	G
1	A	905	G
1	A	906	G
1	A	908	A
1	A	914	C
1	A	915	U
1	A	916	G
1	A	917	A
1	A	918	U
1	A	919	U
1	A	921	G
1	A	922	A
1	A	923	C

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Mol	Chain	Res	Type
1	A	924	U
1	A	925	A
1	A	926	G
1	A	931	C
1	A	933	C
1	A	934	U
1	A	935	A
1	A	936	C
1	A	937	C
1	A	939	G
1	A	940	G
1	A	942	U
1	A	943	A
1	A	944	C
1	A	945	C
1	A	948	A
1	A	951	C
1	A	953	G
1	A	954	U
1	A	955	C
1	A	956	A
1	A	957	A
1	A	959	C
1	A	964	A
1	A	973	G
1	A	975	C
1	A	978	A
1	A	979	U
1	A	980	C
1	A	981	C
1	A	985	G
1	A	986	G
1	A	987	A
1	A	991	A
1	A	992	G
1	A	1004	U
1	A	1005	A
1	A	1007	G
1	A	1009	U
1	A	1020	A
1	A	1026	A
1	A	1027	A

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Mol	Chain	Res	Type
1	A	1029	A
1	A	1030	G
1	A	1031	C
1	A	1036	A
1	A	1042	A
1	A	1057	G
1	A	1058	U
1	A	1059	A
1	A	1068	G
1	A	1072	A
1	A	1073	A
1	A	1074	A
1	A	1075	A
1	A	1076	G
1	A	1079	U
1	A	1080	G
1	A	1089	C
1	A	1092	A
1	A	1093	G
1	A	1094	A
1	A	1097	A
1	A	1102	G
1	A	1103	A
1	A	1104	U
1	A	1106	U
1	A	1107	U
1	A	1108	G
1	A	1109	G
1	A	1110	C
1	A	1111	U
1	A	1113	A
1	A	1114	G
1	A	1116	A
1	A	1117	G
1	A	1118	C
1	A	1119	A
1	A	1121	C
1	A	1122	C
1	A	1123	A
1	A	1124	C
1	A	1125	C
1	A	1126	A

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Mol	Chain	Res	Type
1	A	1127	U
1	A	1128	U
1	A	1130	A
1	A	1131	A
1	A	1132	A
1	A	1134	A
1	A	1135	G
1	A	1136	U
1	A	1137	G
1	A	1138	C
1	A	1139	G
1	A	1141	A
1	A	1142	A
1	A	1143	U
1	A	1145	G
1	A	1147	U
1	A	1150	C
1	A	1152	G
1	A	1153	G
1	A	1158	G
1	A	1159	U
1	A	1160	G
1	A	1161	A
1	A	1162	C
1	A	1163	U
1	A	1169	C
1	A	1170	C
1	A	1171	G
1	A	1172	A
1	A	1173	A
1	A	1174	A
1	A	1176	U
1	A	1179	A
1	A	1180	C
1	A	1181	C
1	A	1182	G
1	A	1185	G
1	A	1188	A
1	A	1194	A
1	A	1201	A
1	A	1214	U
1	A	1217	U

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Mol	Chain	Res	Type
1	A	1218	U
1	A	1219	C
1	A	1220	G
1	A	1221	A
1	A	1222	A
1	A	1223	C
1	A	1227	G
1	A	1245	G
1	A	1246	G
1	A	1247	G
1	A	1248	C
1	A	1249	U
1	A	1251	U
1	A	1252	G
1	A	1260	A
1	A	1261	C
1	A	1276	G
1	A	1278	G
1	A	1280	G
1	A	1289	U
1	A	1293	A
1	A	1296	G
1	A	1308	A
1	A	1311	G
1	A	1312	A
1	A	1315	G
1	A	1323	A
1	A	1327	U
1	A	1328	C
1	A	1339	A
1	A	1340	A
1	A	1341	U
1	A	1344	C
1	A	1345	U
1	A	1346	A
1	A	1351	U
1	A	1352	U
1	A	1359	G
1	A	1360	A
1	A	1363	G
1	A	1364	C
1	A	1377	G

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Mol	Chain	Res	Type
1	A	1380	U
1	A	1384	C
1	A	1385	G
1	A	1388	A
1	A	1391	U
1	A	1404	A
1	A	1414	G
1	A	1418	U
1	A	1423	A
1	A	1424	A
1	A	1425	C
1	A	1426	A
1	A	1432	A
1	A	1435	U
1	A	1441	U
1	A	1442	A
1	A	1449	C
1	A	1450	C
1	A	1451	U
1	A	1452	C
1	A	1456	A
1	A	1457	U
1	A	1458	U
1	A	1460	G
1	A	1461	A
1	A	1464	A
1	A	1465	A
1	A	1466	U
1	A	1470	G
1	A	1471	G
1	A	1472	G
1	A	1473	A
1	A	1474	C
1	A	1475	G
1	A	1488	G
1	A	1490	A
1	A	1495	C
1	A	1498	U
1	A	1499	A
1	A	1501	U
1	A	1503	G
1	A	1504	A

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Mol	Chain	Res	Type
1	A	1506	A
1	A	1507	U
1	A	1519	C
1	A	1521	G
1	A	1528	U
1	A	1529	G
1	A	1530	G
1	A	1533	A
1	A	1534	A
1	A	1537	G
1	A	1539	C
1	A	1540	A
1	A	1551	C
1	A	1554	U
1	A	1555	A
1	A	1556	A
1	A	1557	G
1	A	1561	G
1	A	1566	G
1	A	1572	G
1	A	1573	C
1	A	1576	G
1	A	1578	G
1	A	1579	A
1	A	1582	U
1	A	1583	A
1	A	1584	U
1	A	1585	A
1	A	1586	G
1	A	1596	U
1	A	1598	C
1	A	1600	G
1	A	1607	C
1	A	1608	A
1	A	1614	A
1	A	1616	G
1	A	1617	A
1	A	1618	A
1	A	1619	A
1	A	1620	A
1	A	1621	G
1	A	1624	U

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Mol	Chain	Res	Type
1	A	1627	A
1	A	1628	G
1	A	1630	G
1	A	1631	A
1	A	1632	G
1	A	1633	G
1	A	1637	G
1	A	1639	G
1	A	1640	G
1	A	1641	U
1	A	1642	G
1	A	1652	C
1	A	1653	A
1	A	1655	A
1	A	1664	G
1	A	1667	A
1	A	1679	A
1	A	1689	U
1	A	1690	G
1	A	1693	C
1	A	1695	A
1	A	1697	A
1	A	1712	G
1	A	1719	G
1	A	1720	C
1	A	1727	A
1	A	1734	A
1	A	1735	A
1	A	1744	G
1	A	1745	A
1	A	1746	A
1	A	1752	G
1	A	1754	U
1	A	1757	G
1	A	1758	U
1	A	1759	U
1	A	1760	A
1	A	1761	G
1	A	1762	G
1	A	1763	G
1	A	1765	G
1	A	1766	C

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Mol	Chain	Res	Type
1	A	1768	A
1	A	1769	G
1	A	1771	C
1	A	1772	C
1	A	1773	G
1	A	1774	A
1	A	1775	G
1	A	1776	A
1	A	1777	G
1	A	1778	A
1	A	1779	G
1	A	1780	C
1	A	1781	C
1	A	1782	G
1	A	1783	C
1	A	1784	A
1	A	1785	G
1	A	1786	U
1	A	1787	G
1	A	1791	A
1	A	1792	G
1	A	1793	G
1	A	1801	G
1	A	1802	A
1	A	1803	C
1	A	1804	U
1	A	1807	U
1	A	1808	U
1	A	1814	A
1	A	1815	A
1	A	1816	A
1	A	1817	C
1	A	1822	G
1	A	1828	G
1	A	1829	C
1	A	1830	G
1	A	1831	A
1	A	1832	A
1	A	1838	A
1	A	1841	G
1	A	1844	A
1	A	1845	A

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Mol	Chain	Res	Type
1	A	1846	G
1	A	1847	U
1	A	1848	A
1	A	1849	U
1	A	1851	G
1	A	1856	U
1	A	1857	G
1	A	1858	A
1	A	1861	C
1	A	1862	C
1	A	1864	G
1	A	1865	C
1	A	1974	G
1	A	1975	U
1	A	1976	C
1	A	1977	G
1	A	1978	G
1	A	1980	U
1	A	1983	G
1	A	1984	U
1	A	1985	U
1	A	1986	C
1	A	1987	C
1	A	1988	G
1	A	1989	A
1	A	1991	C
1	A	1992	C
1	A	1993	G
1	A	1994	C
1	A	1996	C
1	A	1997	G
1	A	1998	A
1	A	1999	A
1	A	2000	A
1	A	2001	G
1	A	2002	G
1	A	2003	C
1	A	2005	C
1	A	2007	A
1	A	2008	C
1	A	2009	G
1	A	2010	A

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Mol	Chain	Res	Type
1	A	2011	U
1	A	2020	U
1	A	2022	U
1	A	2024	U
1	A	2026	A
1	A	2052	A
1	A	2060	A
1	A	2062	A
1	A	2068	G
1	A	2072	C
1	A	2080	A
1	A	2084	C
1	A	2087	A
1	A	2088	A
1	A	2089	A
1	A	2090	G
1	A	2091	A
1	A	2092	C
1	A	2093	C
1	A	2094	C
1	A	2096	G
1	A	2098	G
1	A	2106	A
1	A	2107	C
1	A	2108	U
1	A	2109	G
1	A	2110	C
1	A	2111	A
1	A	2112	G
1	A	2113	C
1	A	2115	U
1	A	2116	G
1	A	2117	A
1	A	2120	U
1	A	2123	A
1	A	2124	A
1	A	2125	U
1	A	2127	U
1	A	2129	G
1	A	2132	A
1	A	2139	G
1	A	2140	U

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Mol	Chain	Res	Type
1	A	2141	A
1	A	2142	C
1	A	2143	A
1	A	2144	G
1	A	2145	G
1	A	2147	U
1	A	2148	A
1	A	2149	G
1	A	2151	U
1	A	2152	A
1	A	2155	A
1	A	2156	G
1	A	2157	C
1	A	2158	C
1	A	2159	U
1	A	2160	U
1	A	2161	G
1	A	2162	G
1	A	2163	A
1	A	2165	A
1	A	2166	C
1	A	2167	C
1	A	2168	G
1	A	2169	G
1	A	2170	A
1	A	2171	G
1	A	2172	C
1	A	2173	G
1	A	2174	C
1	A	2175	C
1	A	2176	A
1	A	2177	G
1	A	2178	C
1	A	2179	U
1	A	2180	U
1	A	2181	C
1	A	2182	G
1	A	2183	G
1	A	2186	G
1	A	2188	G
1	A	2190	C
1	A	2191	A

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Mol	Chain	Res	Type
1	A	2192	U
1	A	2193	C
1	A	2194	G
1	A	2195	G
1	A	2196	U
1	A	2197	G
1	A	2198	G
1	A	2199	G
1	A	2202	A
1	A	2203	C
1	A	2205	A
1	A	2209	U
1	A	2210	G
1	A	2211	G
1	A	2213	U
1	A	2216	A
1	A	2217	U
1	A	2219	G
1	A	2222	C
1	A	2225	C
1	A	2227	A
1	A	2228	A
1	A	2230	C
1	A	2232	G
1	A	2233	C
1	A	2236	C
1	A	2240	U
1	A	2241	A
1	A	2242	U
1	A	2245	G
1	A	2246	G
1	A	2247	C
1	A	2248	G
1	A	2249	G
1	A	2250	G
1	A	2251	G
1	A	2252	A
1	A	2253	G
1	A	2254	A
1	A	2255	C
1	A	2256	A
1	A	2258	U

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Mol	Chain	Res	Type
1	A	2259	G
1	A	2261	C
1	A	2262	A
1	A	2264	G
1	A	2265	U
1	A	2267	G
1	A	2268	G
1	A	2270	A
1	A	2272	U
1	A	2273	U
1	A	2274	U
1	A	2275	G
1	A	2276	A
1	A	2279	G
1	A	2282	G
1	A	2283	C
1	A	2284	G
1	A	2285	G
1	A	2287	C
1	A	2288	G
1	A	2297	A
1	A	2298	A
1	A	2300	G
1	A	2307	A
1	A	2309	G
1	A	2310	C
1	A	2312	C
1	A	2313	C
1	A	2314	C
1	A	2315	A
1	A	2316	A
1	A	2317	A
1	A	2318	G
1	A	2319	G
1	A	2324	C
1	A	2325	U
1	A	2326	C
1	A	2327	A
1	A	2328	G
1	A	2331	U
1	A	2332	G
1	A	2333	G

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Mol	Chain	Res	Type
1	A	2334	U
1	A	2335	U
1	A	2336	G
1	A	2337	G
1	A	2338	A
1	A	2339	A
1	A	2340	A
1	A	2341	U
1	A	2342	C
1	A	2343	A
1	A	2344	U
1	A	2347	G
1	A	2348	C
1	A	2349	A
1	A	2351	A
1	A	2353	U
1	A	2355	U
1	A	2358	A
1	A	2359	G
1	A	2361	C
1	A	2362	A
1	A	2363	C
1	A	2364	A
1	A	2365	A
1	A	2367	G
1	A	2368	G
1	A	2369	A
1	A	2370	G
1	A	2371	C
1	A	2372	U
1	A	2373	U
1	A	2374	G
1	A	2375	A
1	A	2378	G
1	A	2380	G
1	A	2381	A
1	A	2386	U
1	A	2387	A
1	A	2388	C
1	A	2389	A
1	A	2390	A
1	A	2392	U

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Mol	Chain	Res	Type
1	A	2395	A
1	A	2396	G
1	A	2400	G
1	A	2401	G
1	A	2405	A
1	A	2406	A
1	A	2407	A
1	A	2411	G
1	A	2412	G
1	A	2413	G
1	A	2414	C
1	A	2415	U
1	A	2416	U
1	A	2417	A
1	A	2418	G
1	A	2419	U
1	A	2420	G
1	A	2421	A
1	A	2422	U
1	A	2425	G
1	A	2426	G
1	A	2427	U
1	A	2430	U
1	A	2431	U
1	A	2432	C
1	A	2435	C
1	A	2436	A
1	A	2443	G
1	A	2448	U
1	A	2449	C
1	A	2451	C
1	A	2452	U
1	A	2454	A
1	A	2455	A
1	A	2456	C
1	A	2458	G
1	A	2459	A
1	A	2460	U
1	A	2461	A
1	A	2463	A
1	A	2464	A
1	A	2465	G

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Mol	Chain	Res	Type
1	A	2466	C
1	A	2468	A
1	A	2469	C
1	A	2470	C
1	A	2474	G
1	A	2476	G
1	A	2477	A
1	A	2478	U
1	A	2479	A
1	A	2480	A
1	A	2481	C
1	A	2482	A
1	A	2483	G
1	A	2484	G
1	A	2488	A
1	A	2489	U
1	A	2491	U
1	A	2495	C
1	A	2499	G
1	A	2500	A
1	A	2501	G
1	A	2502	U
1	A	2503	C
1	A	2504	C
1	A	2505	A
1	A	2507	A
1	A	2508	U
1	A	2509	C
1	A	2510	G
1	A	2513	G
1	A	2515	G
1	A	2519	G
1	A	2520	U
1	A	2521	U
1	A	2523	G
1	A	2524	G
1	A	2525	C
1	A	2526	A
1	A	2527	C
1	A	2528	C
1	A	2529	U
1	A	2530	C

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Mol	Chain	Res	Type
1	A	2532	A
1	A	2533	U
1	A	2534	G
1	A	2535	U
1	A	2536	C
1	A	2541	C
1	A	2542	A
1	A	2543	U
1	A	2547	A
1	A	2549	C
1	A	2558	G
1	A	2560	A
1	A	2562	U
1	A	2564	G
1	A	2571	A
1	A	2582	G
1	A	2586	G
1	A	2595	A
1	A	2596	G
1	A	2598	G
1	A	2601	A
1	A	2602	C
1	A	2603	G
1	A	2606	A
1	A	2610	G
1	A	2611	G
1	A	2612	G
1	A	2613	U
1	A	2614	U
1	A	2615	C
1	A	2619	A
1	A	2620	C
1	A	2621	G
1	A	2622	U
1	A	2624	G
1	A	2627	A
1	A	2630	C
1	A	2631	A
1	A	2632	G
1	A	2634	U
1	A	2637	G
1	A	2638	U

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Mol	Chain	Res	Type
1	A	2639	C
1	A	2642	U
1	A	2644	U
1	A	2648	U
1	A	2658	A
1	A	2659	G
1	A	2668	A
1	A	2675	C
1	A	2689	A
1	A	2690	G
1	A	2711	G
1	A	2713	U
1	A	2714	G
1	A	2718	U
1	A	2720	C
1	A	2731	G
1	A	2734	A
1	A	2743	G
1	A	2748	G
1	A	2755	U
1	A	2762	A
1	A	2764	G
1	A	2773	G
1	A	2775	U
1	A	2776	G
1	A	2777	A
1	A	2780	G
1	A	2784	C
1	A	2785	U
1	A	2786	A
1	A	2787	A
1	A	2793	A
1	A	2794	A
1	A	2795	G
1	A	2796	C
1	A	2804	A
1	A	2807	A
1	A	2808	U
1	A	2809	G
1	A	2813	U
1	A	2818	C
1	A	2820	U

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Mol	Chain	Res	Type
1	A	2825	C
1	A	2826	A
1	A	2828	G
1	A	2833	U
1	A	2837	A
1	A	2845	A
1	A	2858	U
1	A	2859	G
1	A	2860	A
1	A	2862	A
1	A	2873	G
1	A	2874	G
1	A	2876	A
1	A	2879	G
1	A	2880	U
1	A	2882	G
1	A	2883	C
1	A	2885	A
1	A	2891	G
1	A	2892	G
1	A	2893	A
1	A	2895	C
1	A	2897	G
1	A	2899	C
1	A	2904	A
1	A	2905	C
1	A	2909	U
1	A	2918	G
1	A	2919	A
1	A	2920	C
1	A	2921	U
1	A	2923	A
2	B	4	G
2	B	7	G
2	B	10	G
2	B	11	A
2	B	12	U
2	B	13	A
2	B	14	G
2	B	15	C
2	B	16	G
2	B	17	A

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Mol	Chain	Res	Type
2	B	19	G
2	B	20	A
2	B	23	U
2	B	26	C
2	B	28	C
2	B	31	G
2	B	32	U
2	B	33	U
2	B	34	C
2	B	35	C
2	B	37	A
2	B	38	U
2	B	39	A
2	B	40	C
2	B	41	C
2	B	42	G
2	B	43	A
2	B	45	C
2	B	46	A
2	B	47	C
2	B	48	G
2	B	51	A
2	B	52	G
2	B	53	U
2	B	54	U
2	B	55	A
2	B	56	A
2	B	57	G
2	B	58	C
2	B	61	U
2	B	62	U
2	B	63	C
2	B	64	A
2	B	65	G
2	B	68	C
2	B	74	G
2	B	82	G
2	B	83	G
2	B	85	U
2	B	86	U
2	B	87	U
2	B	88	C

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Mol	Chain	Res	Type
2	B	91	C
2	B	95	U
2	B	96	G
2	B	97	A
2	B	102	A
2	B	103	G
2	B	106	C
2	B	107	G
2	B	109	C
2	B	110	G
2	B	111	C
2	B	113	A

All (90) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	43	G
1	A	90	A
1	A	101	G
1	A	172	U
1	A	175	G
1	A	177	G
1	A	229	A
1	A	252	C
1	A	269	G
1	A	319	G
1	A	416	U
1	A	419	G
1	A	489	G
1	A	537	A
1	A	549	A
1	A	662	U
1	A	690	A
1	A	691	U
1	A	772	G
1	A	837	U
1	A	934	U
1	A	935	A
1	A	936	C
1	A	939	G
1	A	943	A
1	A	977	U

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Mol	Chain	Res	Type
1	A	1004	U
1	A	1030	G
1	A	1107	U
1	A	1246	G
1	A	1247	G
1	A	1325	A
1	A	1327	U
1	A	1339	A
1	A	1351	U
1	A	1449	C
1	A	1457	U
1	A	1464	A
1	A	1473	A
1	A	1528	U
1	A	1581	A
1	A	1595	U
1	A	1641	U
1	A	1652	C
1	A	1780	C
1	A	1785	G
1	A	1813	A
1	A	1830	G
1	A	1847	U
1	A	1848	A
1	A	1856	U
1	A	1863	U
1	A	1987	C
1	A	1998	A
1	A	2096	G
1	A	2110	C
1	A	2115	U
1	A	2116	G
1	A	2139	G
1	A	2143	A
1	A	2161	G
1	A	2170	A
1	A	2313	C
1	A	2314	C
1	A	2335	U
1	A	2348	C
1	A	2374	G
1	A	2380	G

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Mol	Chain	Res	Type
1	A	2405	A
1	A	2406	A
1	A	2411	G
1	A	2435	C
1	A	2479	A
1	A	2481	C
1	A	2504	C
1	A	2581	U
1	A	2631	A
1	A	2784	C
1	A	2785	U
1	A	2812	A
1	A	2858	U
1	A	2918	G
2	B	12	U
2	B	13	A
2	B	32	U
2	B	37	A
2	B	40	C
2	B	47	C
2	B	64	A
2	B	106	C

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

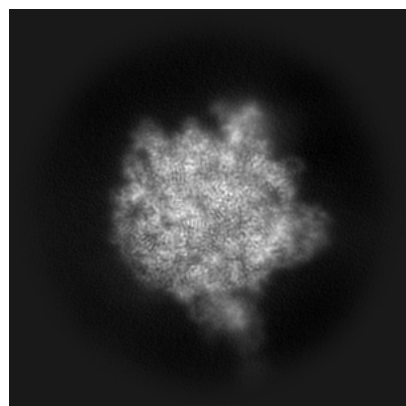
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-71268. These allow visual inspection of the internal detail of the map and identification of artifacts.

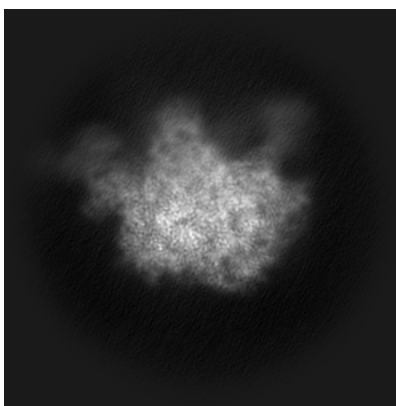
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

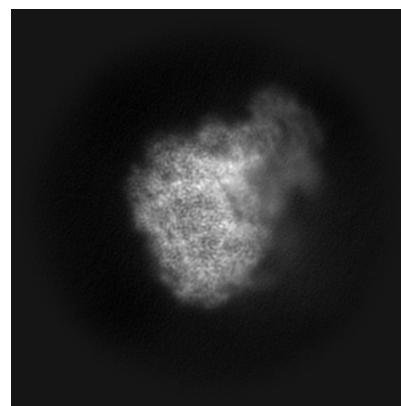
6.1.1 Primary map



X

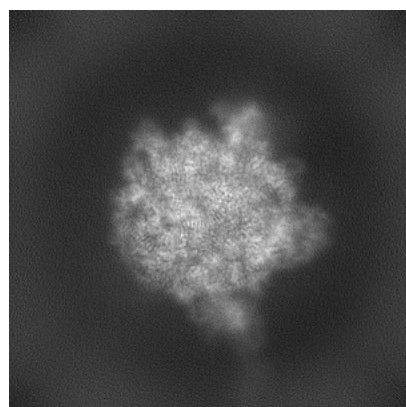


Y

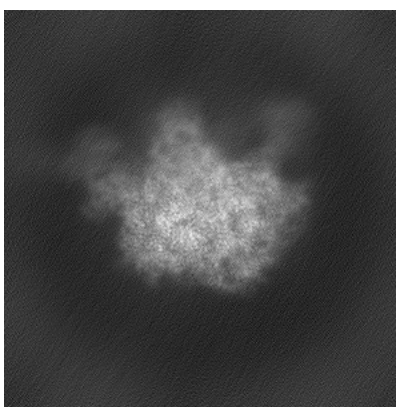


Z

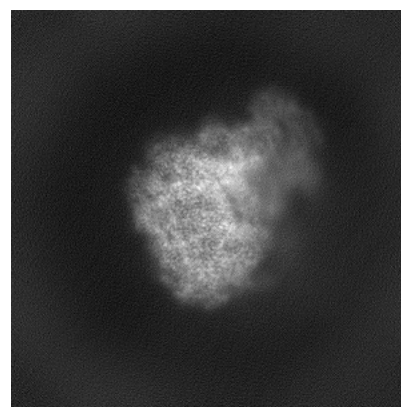
6.1.2 Raw map



X



Y

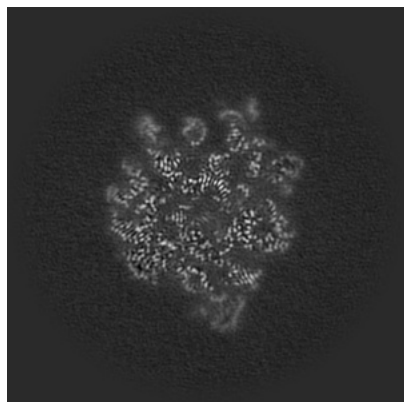


Z

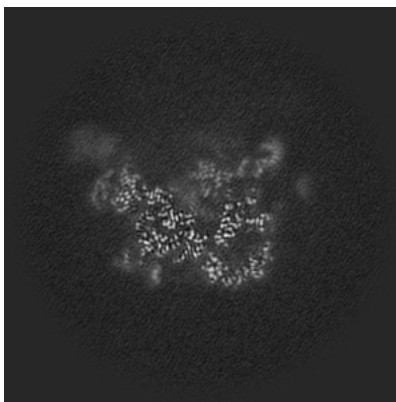
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

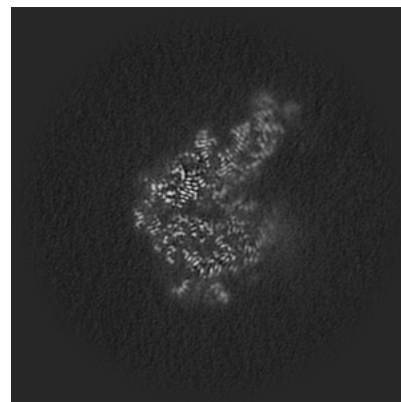
6.2.1 Primary map



X Index: 224

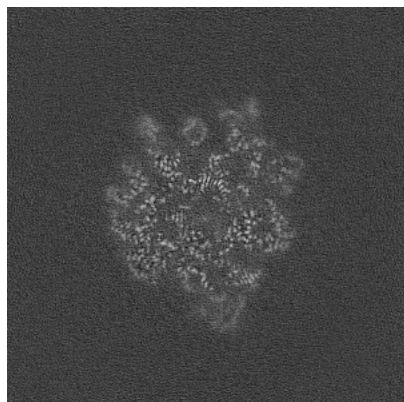


Y Index: 224

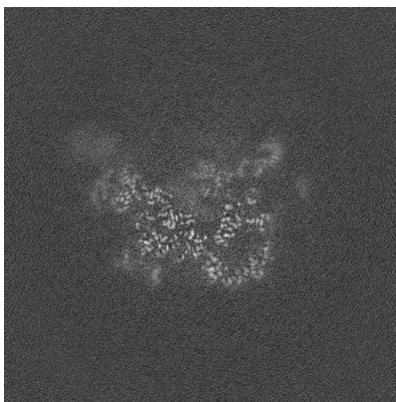


Z Index: 224

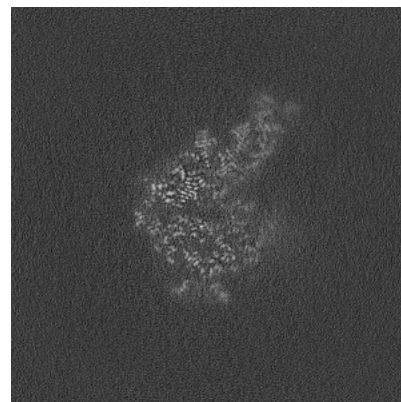
6.2.2 Raw map



X Index: 224



Y Index: 224

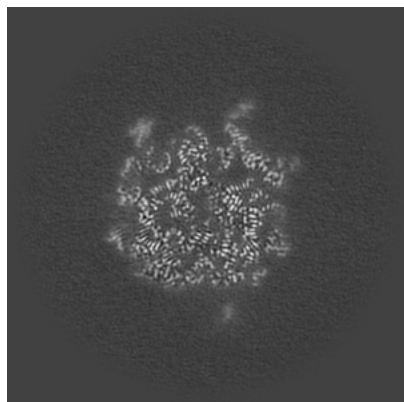


Z Index: 224

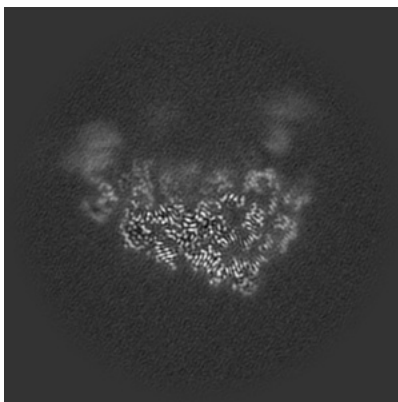
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

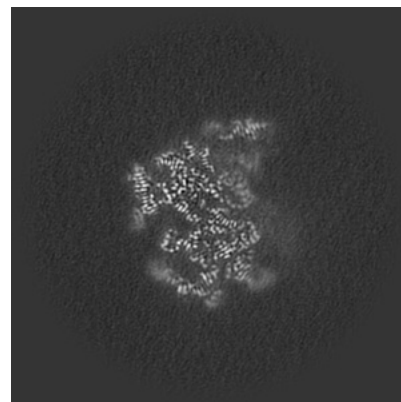
6.3.1 Primary map



X Index: 212

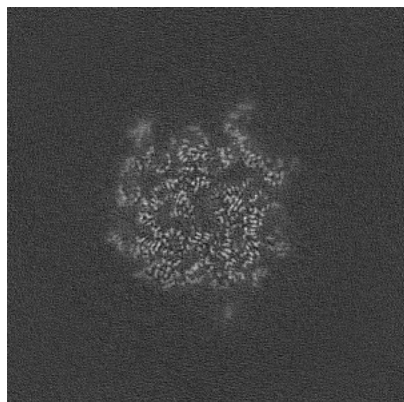


Y Index: 248

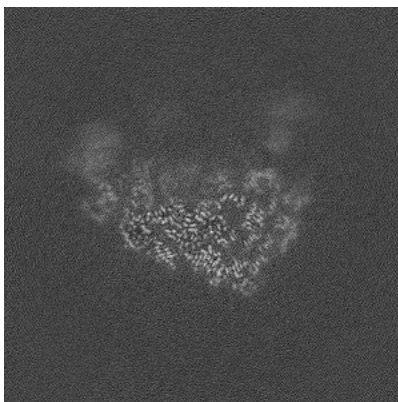


Z Index: 241

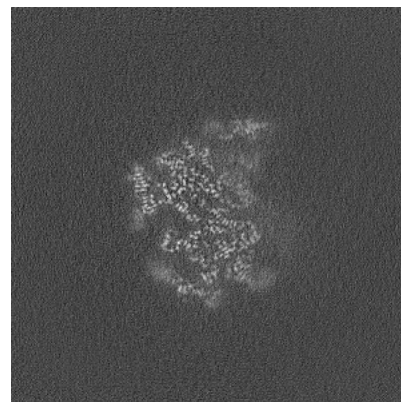
6.3.2 Raw map



X Index: 211



Y Index: 248

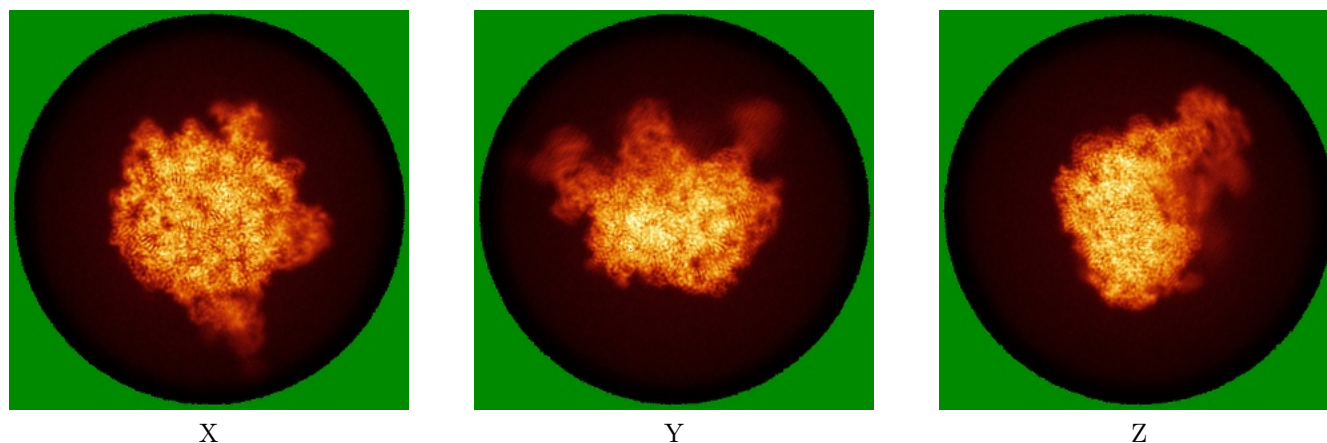


Z Index: 241

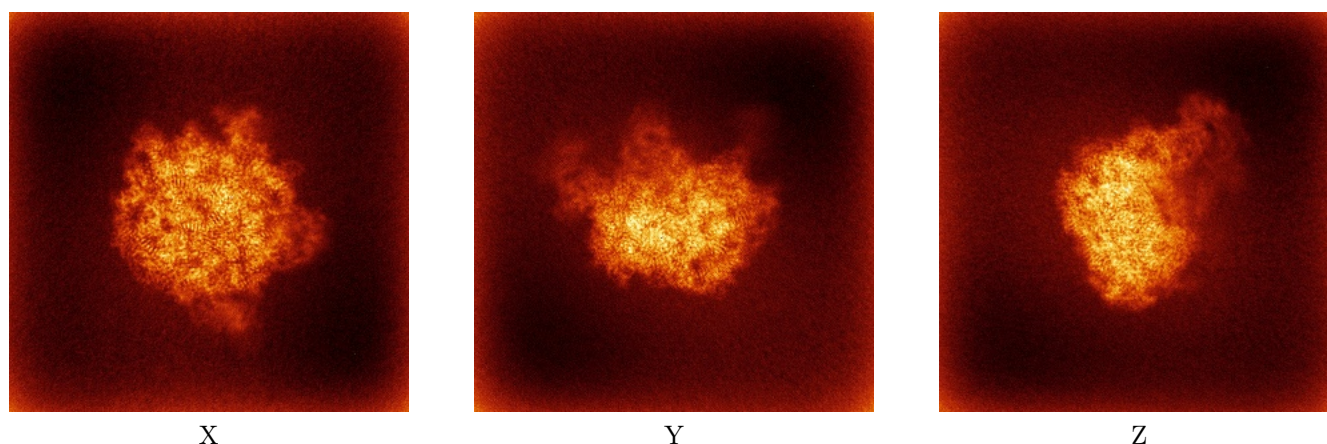
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



6.4.2 Raw map



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](#)

This section was not generated.

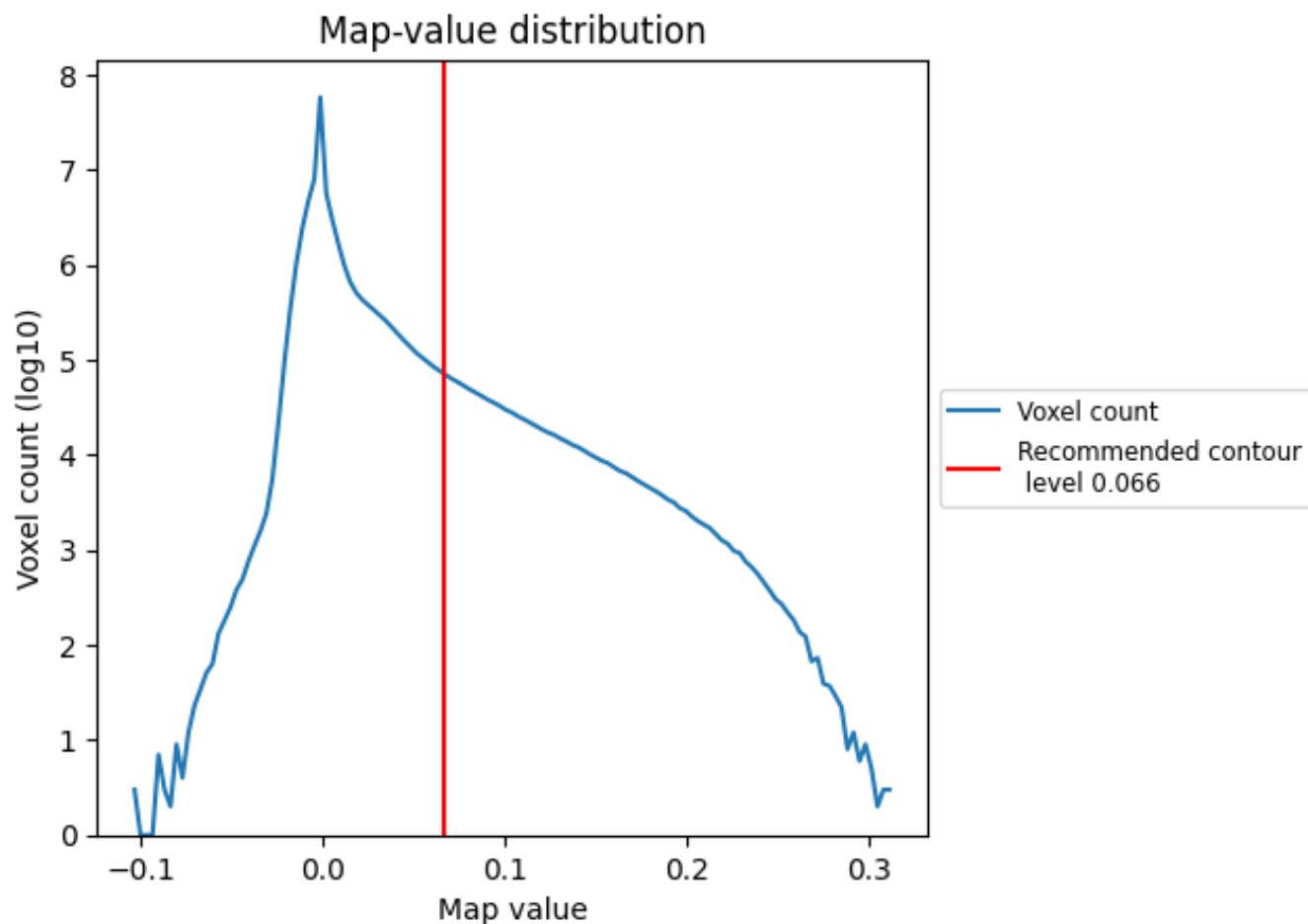
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

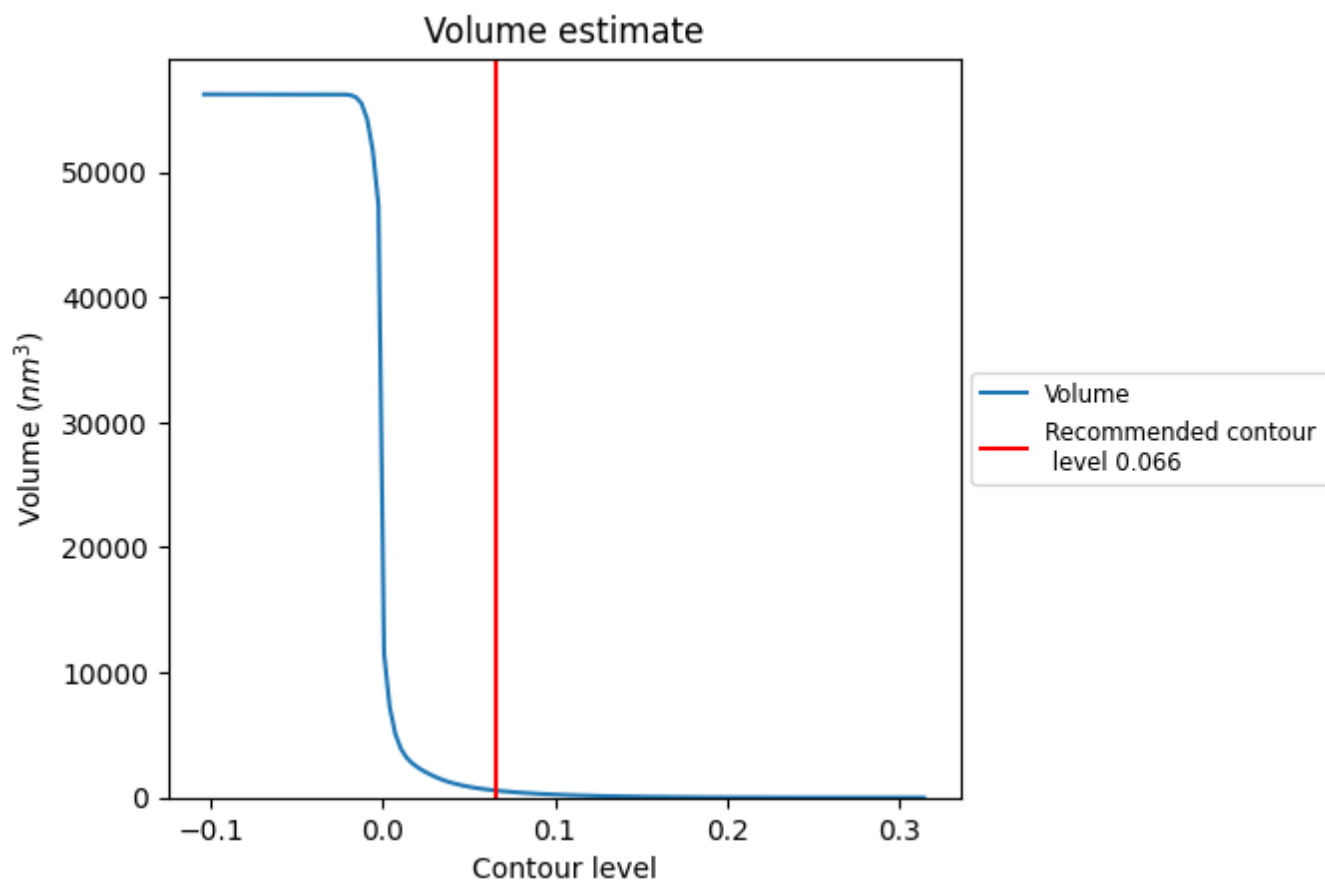
This section contains the results of statistical analysis of the map.

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.

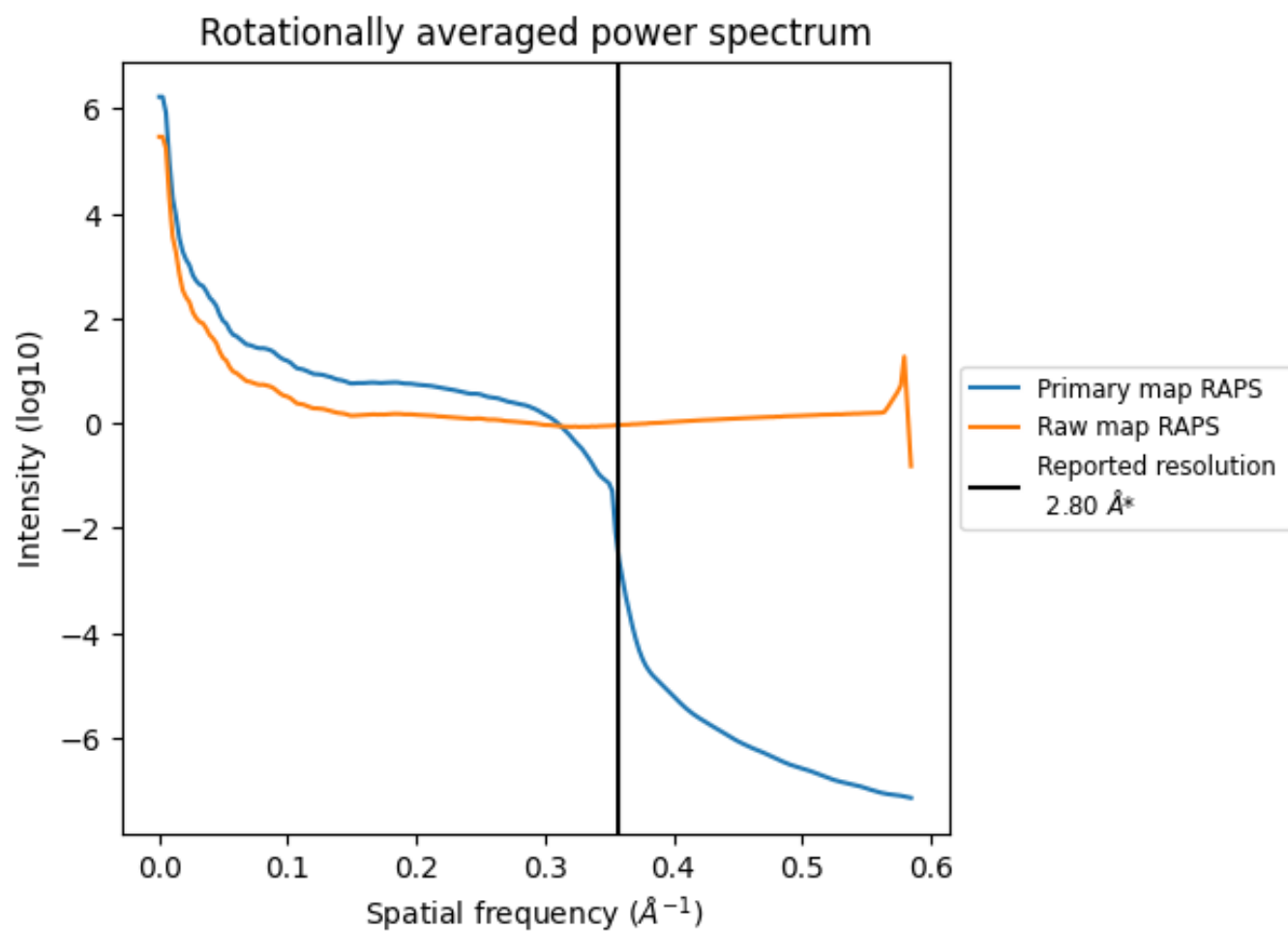
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 558 nm³; this corresponds to an approximate mass of 504 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 ⓘ

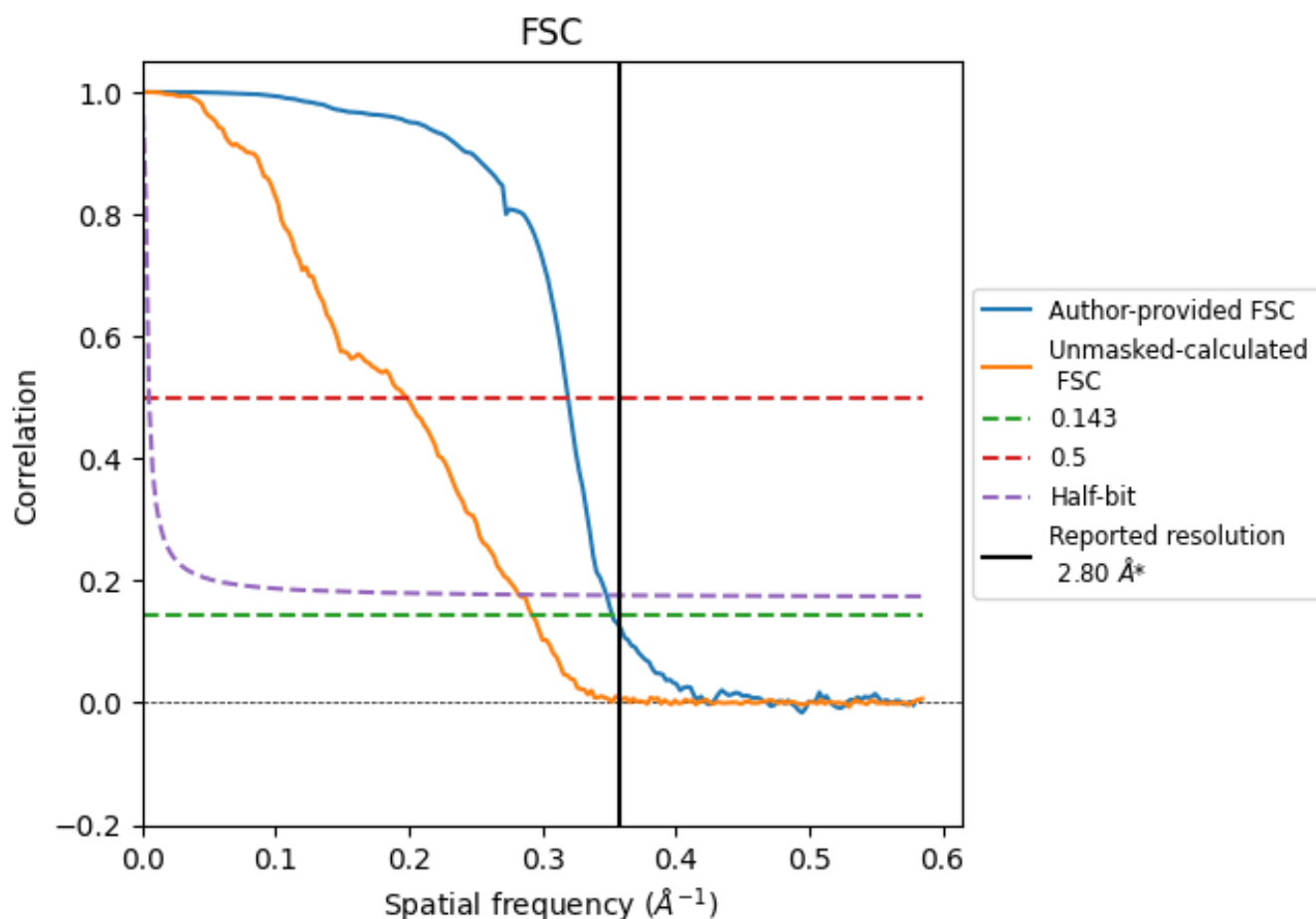


*Reported resolution corresponds to spatial frequency of 0.357 Å⁻¹

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 0.357 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

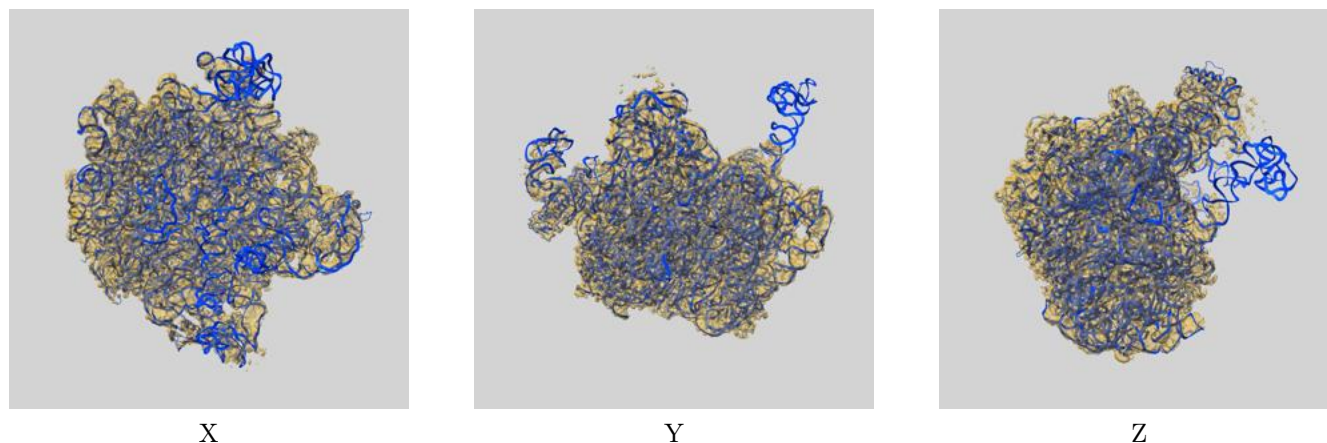
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.80	-	-
Author-provided FSC curve	2.84	3.13	2.87
Unmasked-calculated*	3.42	5.04	3.54

*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 3.42 differs from the reported value 2.8 by more than 10 %

9 Map-model fit [i](#)

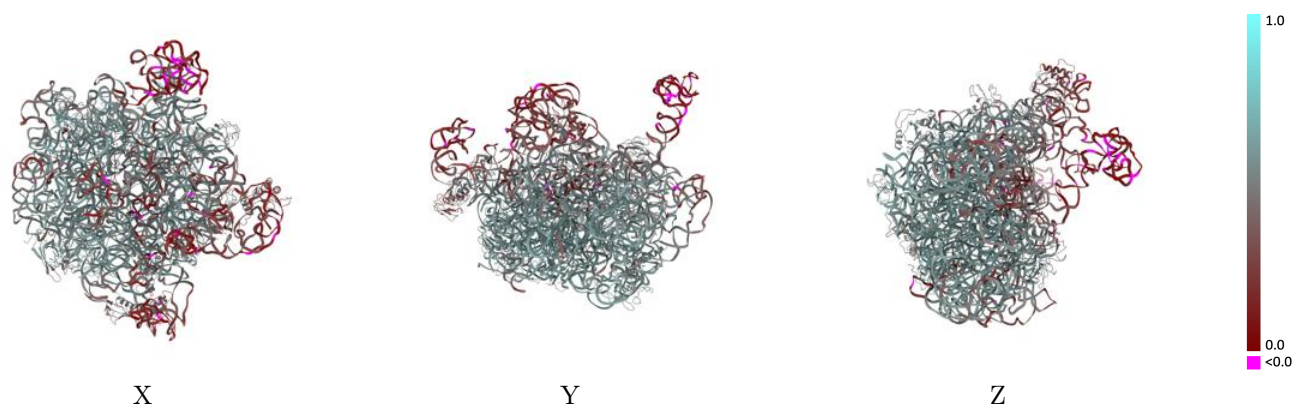
This section contains information regarding the fit between EMDB map EMD-71268 and PDB model 9P4I. Per-residue inclusion information can be found in section 3 on page 8.

9.1 Map-model overlay [i](#)



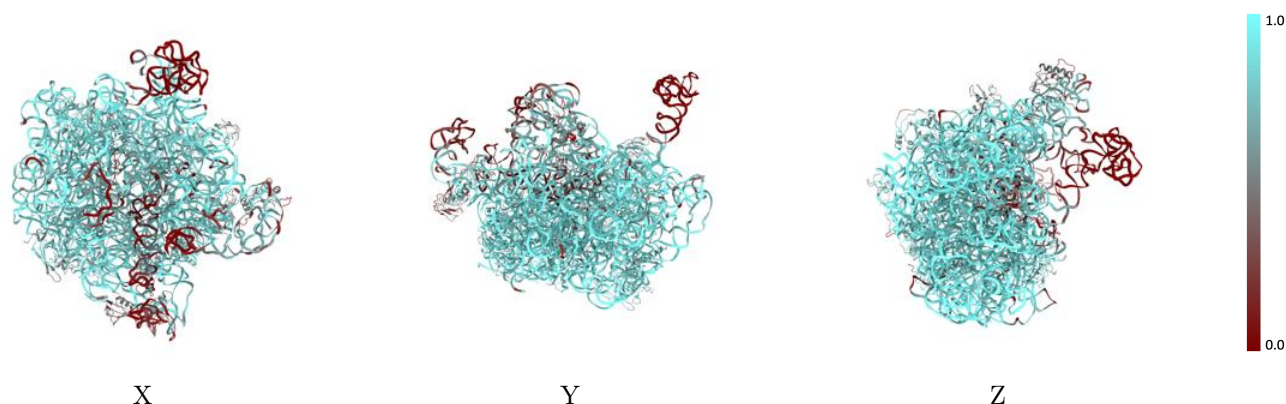
The images above show the 3D surface view of the map at the recommended contour level 0.066 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



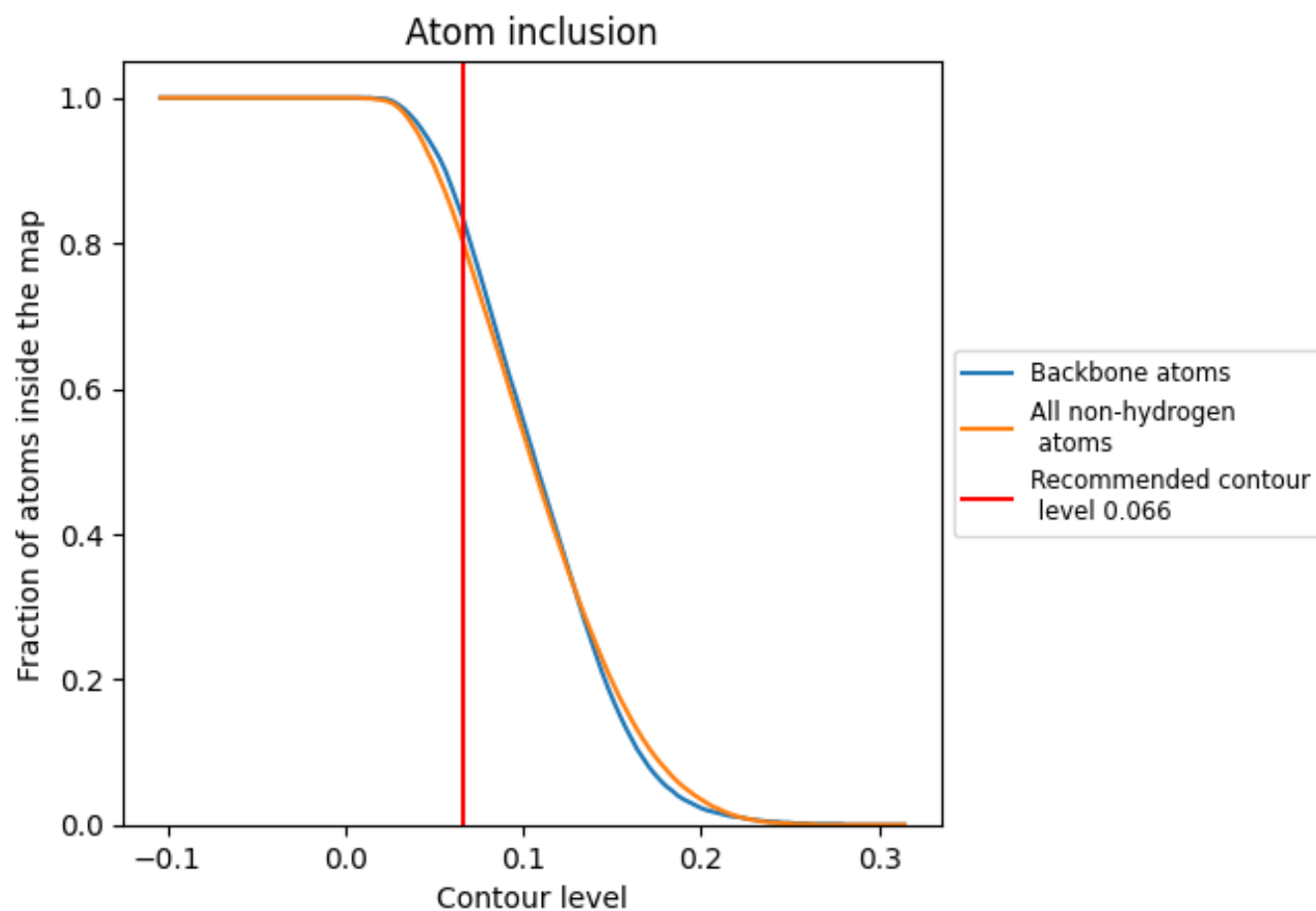
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.066).

9.4 Atom inclusion [i](#)



At the recommended contour level, 84% of all backbone atoms, 80% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.066) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8030	 0.4920
A	 0.8320	 0.4920
B	 0.6550	 0.2850
C	 0.6520	 0.4910
D	 0.8600	 0.5710
E	 0.7890	 0.5330
G	 0.3900	 0.3820
J	 0.8990	 0.5770
K	 0.7450	 0.5270
L	 0.6200	 0.4730
N	 0.8750	 0.5670
O	 0.4290	 0.3540
P	 0.7460	 0.5300
Q	 0.8970	 0.5720
R	 0.8470	 0.5710
S	 0.9020	 0.5880
T	 0.8450	 0.5640
U	 0.7540	 0.5310
V	 0.4540	 0.4620
Y	 0.7840	 0.5110
Z	 0.8290	 0.5570
b	 0.7940	 0.5180
d	 0.9330	 0.6170
f	 0.0960	 0.4660

