



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 05:19 PM UTC

PDB ID : 8RWG / pdb_00008rwg
EMDB ID : EMD-19547
Title : PAO1 wild-type ribosome, R, reference map
Authors : Mesa, P.; Montoya, G.
Deposited on : 2024-02-04
Resolution : 2.46 Å (reported)
Based on initial model : 4YBB

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:

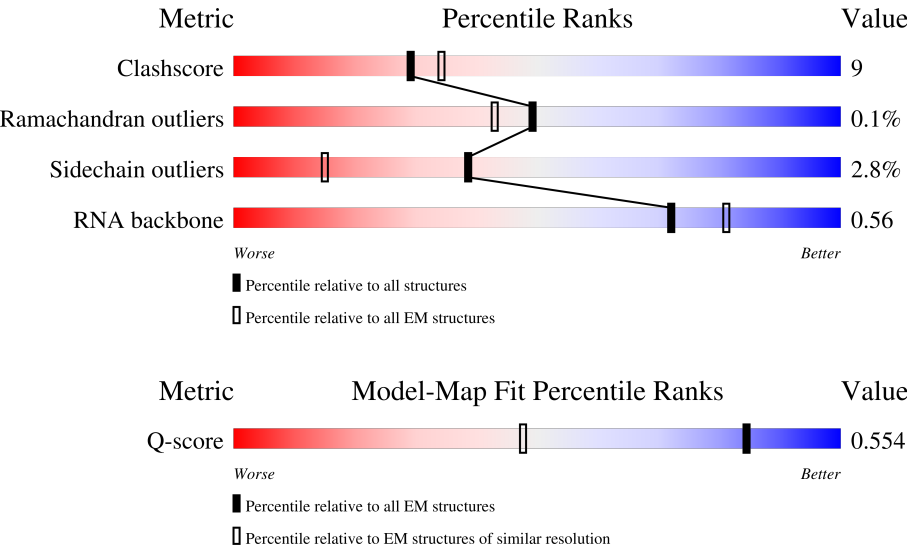
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 2.46 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.



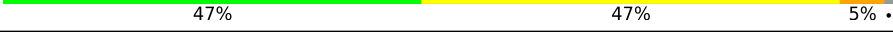
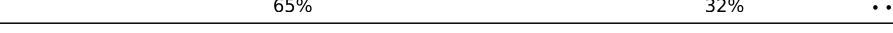
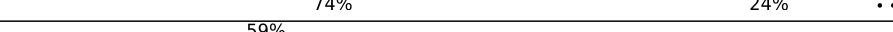
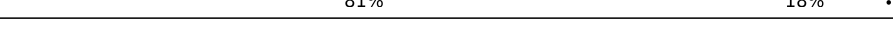
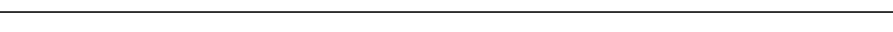
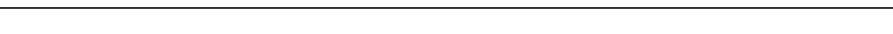
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	6014 (1.96 - 2.96)

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

Mol	Chain	Length	Quality of chain
1	1	85	
2	2	78	
3	3	63	

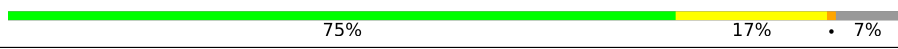
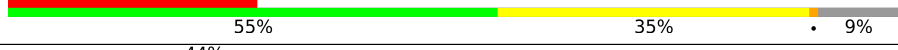
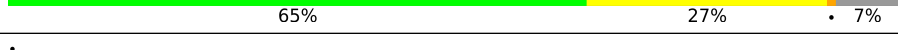
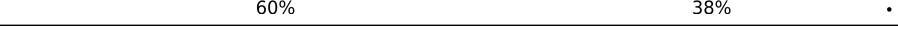
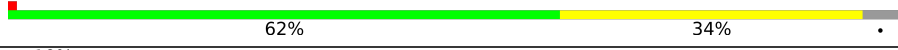
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Mol	Chain	Length	Quality of chain
4	4	58	 93% . . .
5	5	60	 73% 17% 8%
6	6	51	 75% 22% . .
7	7	44	 82% 18%
8	8	64	 78% 20% .
9	9	38	 79% 21%
10	A	2891	 61% 33% . .
11	B	1536	 47% 47% 5% .
12	C	121	 72% 26% . .
13	D	273	 75% 24%
14	E	211	 83% 14% .
15	F	200	 85% 15%
16	G	179	 65% 32% . .
17	H	177	 74% 24% . .
18	I	148	 59% 65% 27% 8%
19	J	142	 81% 18% . .
20	K	122	 75% 24% .
21	L	144	 78% 20% .
22	M	137	 79% 20% .
23	N	129	 71% 19% . 8%
24	O	116	 74% 23% . .
25	P	116	 75% 22% . .
26	Q	118	 80% 19% .
27	R	103	 83% 17%
28	S	110	 80% 19% .

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Mol	Chain	Length	Quality of chain
29	T	99	
30	U	104	
31	V	204	
32	a	246	
33	b	228	
34	c	206	
35	d	166	
36	e	139	
37	f	156	
38	g	130	
39	h	130	
40	i	103	
41	j	129	
42	k	123	
43	l	118	
44	m	101	
45	n	89	
46	o	83	
47	p	88	
48	q	76	
49	r	91	
50	s	91	
51	t	71	

2 Entry composition

There are 54 unique types of molecules in this entry. The entry contains 140256 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 protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	1	75	Total	C	N	O	0	0
			569	361	110	98		

- Molecule 2 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	77	Total	C	N	O	S	0	0
			630	391	134	103	2		

- Molecule 3 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	62	Total	C	N	O	S	0	0
			494	303	97	92	2		

- Molecule 4 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	56	Total	C	N	O	S	0	0
			440	275	86	77	2		

- Molecule 5 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	55	Total	C	N	O	S	0	0
			433	261	93	78	1		

- Molecule 6 is a protein called Large ribosomal subunit protein bL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	50	Total	C	N	O	S	0	0
			416	266	76	73	1		

- Molecule 7 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	7	44	Total	C	N	O	S	0	0
			365	222	87	54	2		

- Molecule 8 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	8	63	Total	C	N	O	S	0	0
			506	314	108	81	3		

- Molecule 9 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	9	38	Total	C	N	O	S	0	0
			306	186	69	47	4		

- Molecule 10 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	A	2805	Total	C	N	O	P	0	0
			60189	26855	11041	19488	2805		

- Molecule 11 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	B	1527	Total	C	N	O	P	0	0
			32768	14616	6016	10610	1526		

- Molecule 12 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	C	120	Total	C	N	O	P	0	0
			2555	1141	455	839	120		

- Molecule 13 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	D	272	Total	C	N	O	S	0	0
			2071	1276	426	363	6		

- Molecule 14 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	E	206	Total	C	N	O	S	0	0
			1552	961	296	290	5		

- Molecule 15 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	F	200	Total	C	N	O	S	0	0
			1524	956	283	282	3		

- Molecule 16 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	G	177	Total	C	N	O	S	0	0
			1393	892	249	248	4		

- Molecule 17 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	H	174	Total	C	N	O	S	0	0
			1316	829	242	243	2		

- Molecule 18 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	I	136	Total	C	N	O	S	0	0
			945	598	175	171	1		

- Molecule 19 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	J	141	Total	C	N	O	S	0	0
			1122	713	205	201	3		

- Molecule 20 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	K	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 21 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	L	144	Total	C	N	O	S	0	0
			1066	654	215	194	3		

- Molecule 22 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	M	137	Total	C	N	O	S	0	0
			1085	689	211	181	4		

- Molecule 23 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	N	119	Total	C	N	O	S	0	0
			952	595	191	161	5		

- Molecule 24 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	O	114	Total	C	N	O	S	0	0
			875	541	173	159	2		

- Molecule 25 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	P	113	Total	C	N	O	S	0	0
			894	563	170	160	1		

- Molecule 26 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Q	117	Total	C	N	O	S	0	0
			935	592	196	147			

- Molecule 27 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	R	103	Total	C	N	O	S	0	0
			822	521	156	143	2		

- Molecule 28 is a protein called Large ribosomal subunit protein uL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	S	110	Total	C	N	O	S	0	0
			833	515	161	153	4		

- Molecule 29 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	T	92	Total	C	N	O	S	0	0
			720	459	132	128	1		

- Molecule 30 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	U	103	Total	C	N	O	S	0	0
			791	497	152	141	1		

- Molecule 31 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	V	190	Total	C	N	O	S	0	0
			1434	908	260	263	3		

- Molecule 32 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	a	224	Total	C	N	O	S	0	0
			1725	1092	309	314	10		

- Molecule 33 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	b	208	Total	C	N	O	S	0	0
			1660	1050	314	290	6		

- Molecule 34 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	c	205	Total	C	N	O	S	0	0
			1627	1003	316	303	5		

- Molecule 35 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	d	155	Total	C	N	O	S	0	0
			1142	717	211	208	6		

- Molecule 36 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	e	103	Total	C	N	O	S	0	0
			845	525	155	159	6		

- Molecule 37 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	f	153	Total	C	N	O	S	0	0
			1199	752	232	210	5		

- Molecule 38 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	g	128	Total	C	N	O	S	0	0
			976	615	172	183	6		

- Molecule 39 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	h	126	Total	C	N	O	S	0	0
			994	616	198	179	1		

- Molecule 40 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	i	101	Total	C	N	O	S	0	0
			810	505	154	150	1		

- Molecule 41 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	j	118	Total	C	N	O	S	0	0
			873	540	170	161	2		

- Molecule 42 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	k	121	Total	C	N	O	S	0	0
			949	582	196	167	4		

- Molecule 43 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	l	116	Total	C	N	O	S	0	0
			904	553	184	163	4		

- Molecule 44 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	m	100	Total	C	N	O	S	0	0
			804	496	167	138	3		

- Molecule 45 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	n	89	Total	C	N	O	S	0	0
			711	439	140	130	2		

- Molecule 46 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	o	80	Total	C	N	O	S	0	0
			631	394	124	112	1		

- Molecule 47 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	p	80	Total	C	N	O	S	0	0
			645	404	124	115	2		

- Molecule 48 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	q	59	Total	C	N	O	0	0
			466	297	83	86		

- Molecule 49 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	r	82	Total	C	N	O	S	0	0
			658	419	128	108	3		

- Molecule 50 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	s	87	Total	C	N	O	S	0	0
			671	414	138	117	2		

- Molecule 51 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	t	55	Total	C	N	O	S	0	0
			447	280	90	76	1		

- Molecule 52 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
52	9	1	Total	Zn	0
			1	1	

- Molecule 53 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
53	A	175	Total	Mg	0
			175	175	
53	C	5	Total	Mg	0
			5	5	
53	E	1	Total	Mg	0
			1	1	
53	N	2	Total	Mg	0
			2	2	
53	T	1	Total	Mg	0
			1	1	

- Molecule 54 is water.

Mol	Chain	Residues	Atoms		AltConf
54	A	383	Total	O	0
			383	383	
54	D	4	Total	O	0
			4	4	

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Mol	Chain	Residues	Atoms		AltConf
54	E	3	Total	O	0
			3	3	
54	L	5	Total	O	0
			5	5	

3 Residue-property plots [i](#)

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: 50S ribosomal protein L27

Chain 1: 



- Molecule 2: 50S ribosomal protein L28

Chain 2: 

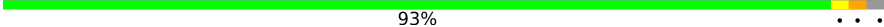


- Molecule 3: 50S ribosomal protein L29

Chain 3: 



- Molecule 4: 50S ribosomal protein L30

Chain 4: 



- Molecule 5: 50S ribosomal protein L32

Chain 5: 



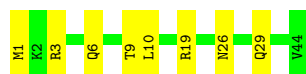
- Molecule 6: Large ribosomal subunit protein bL33

Chain 6:  75% 22% . .



- Molecule 7: 50S ribosomal protein L34

Chain 7:  82% 18%



- Molecule 8: 50S ribosomal protein L35

Chain 8:  78% 20% .



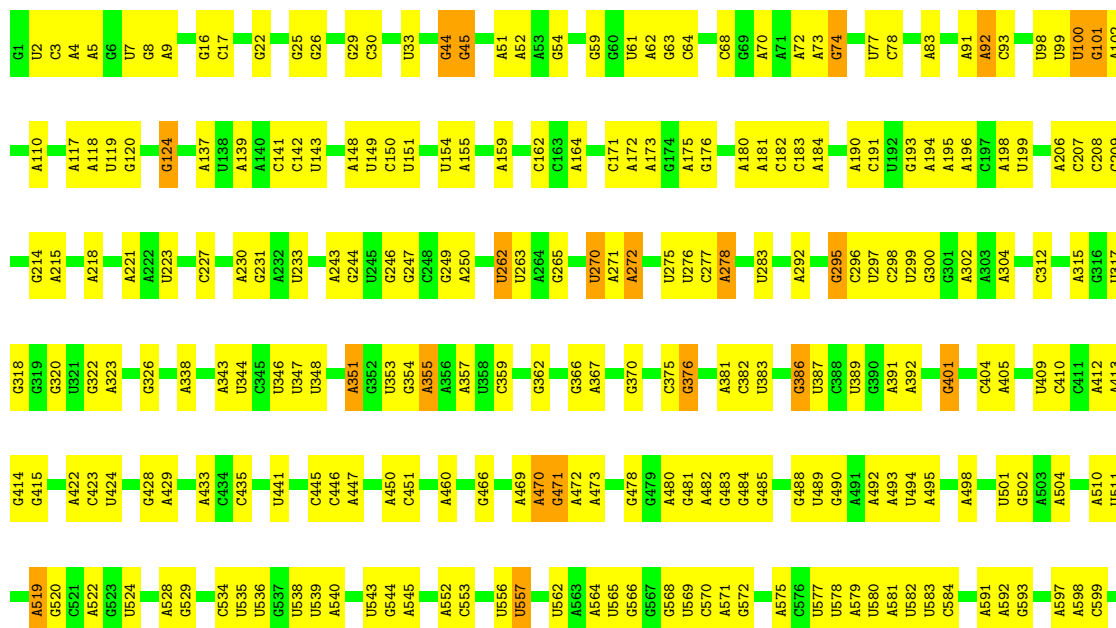
- Molecule 9: 50S ribosomal protein L36

Chain 9:  79% 21%

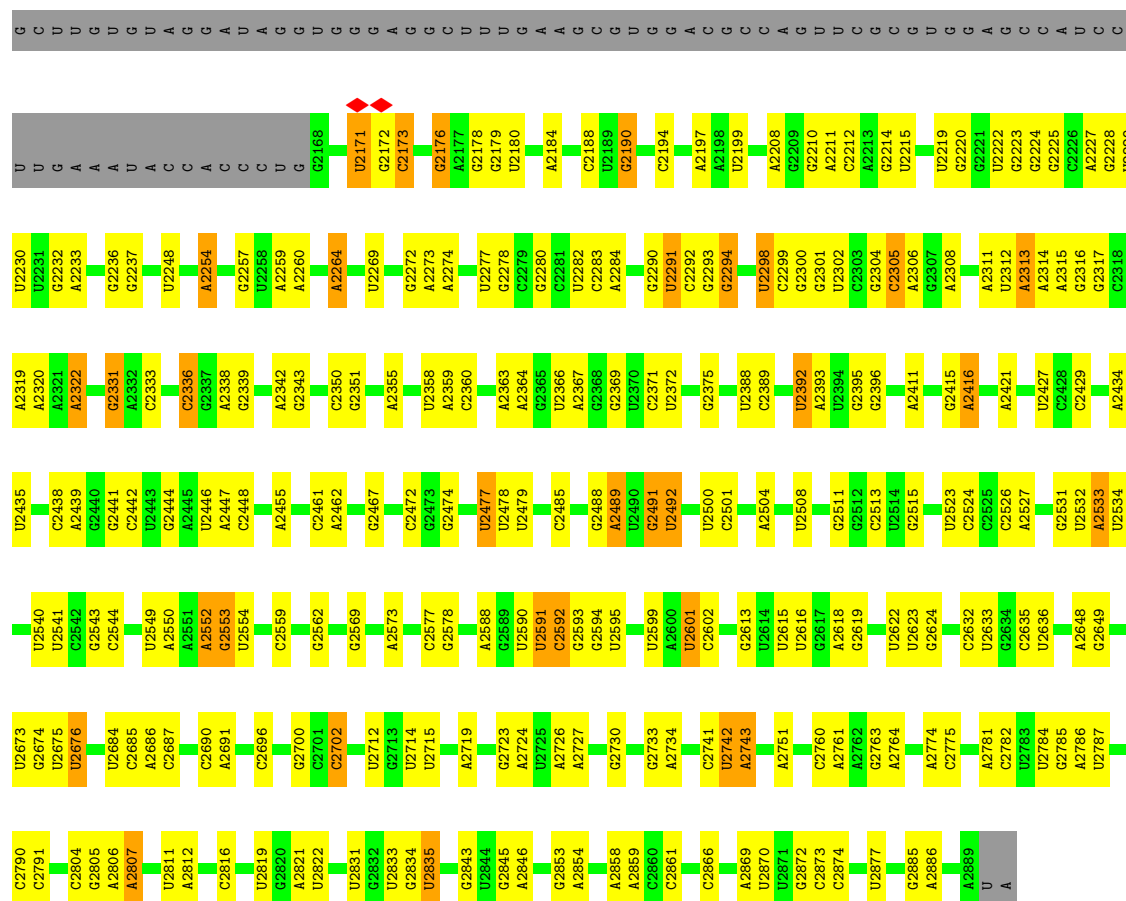


- Molecule 10: 23S ribosomal RNA

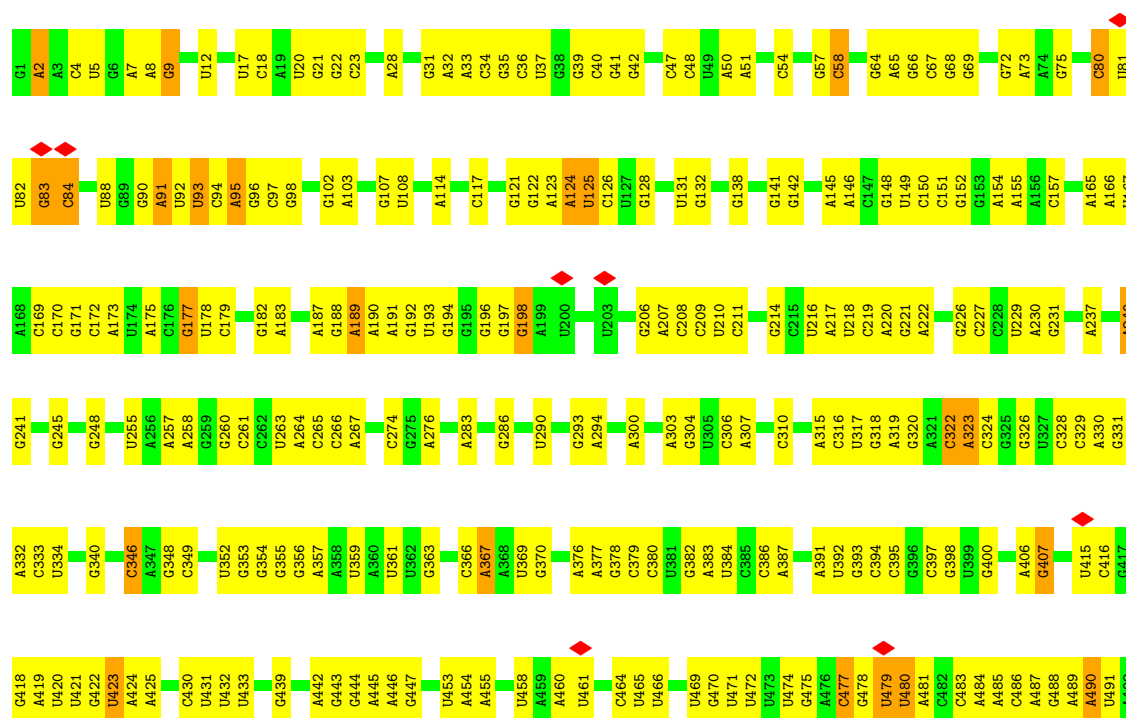
Chain A:  61% 33% . .

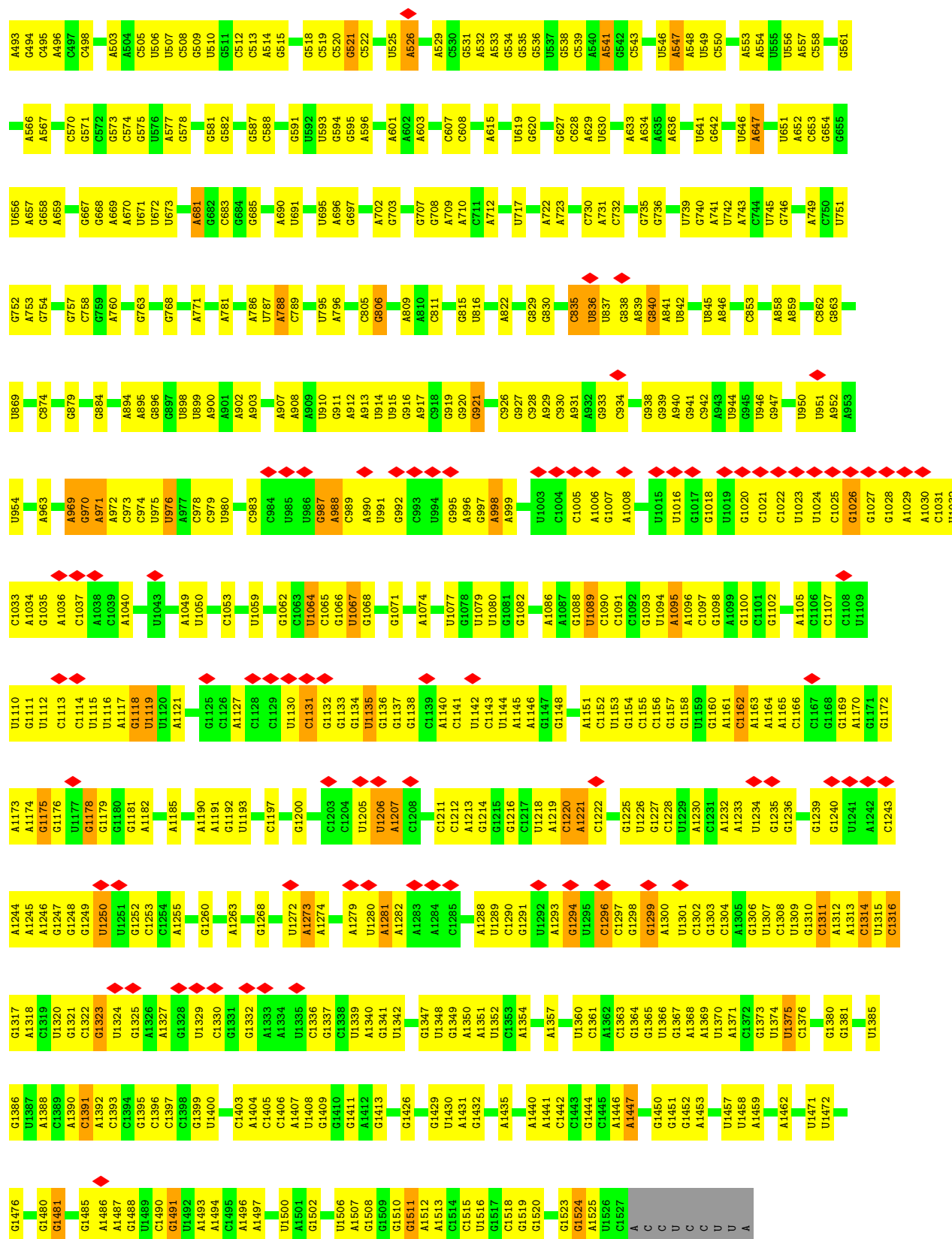


G1996	G1859	G1771	G1663	A1533	U1424	C1316	U1185	A1084	U1002	U882	G797	A695	U602
U1997	C1860	A1772	C1664	U1539	A1425	U1326	C1186	A1085	U1008	U883	G798	U699	A603
A1999	G1861	C1776	A1665	U1540	A1430	U1338	G1192	U1086	A1009	U884	U799	U700	A616
A2000	U1869	A1777	A1666	G1541	G1431	U1339	G1221	A1087	U1015	C885	U800	C801	
A2001	G1870				C1432	A1340		G1088	A1016	C886	U802	A707	A621
	A1875	A1780	U1669	C1545	U1433	A1341	U1224	A1092	A1017	C895	C803		A622
	A1876	C1781	G1670		U1434	G1342		G1093	A1018	C896	U816	G710	G623
		U1782	G1671	U1552	G1438	C1343	A1233	U1094		A897	U817	G711	G624
	G1882	U1784	A1673	C1553		G1344	A1234	A1095	U1022	A898	A818	C712	G625
	G1785	G1785	A1555	C1554	U1446	A1345	U1235	A1099	G1023	A899	U819	U713	A626
	C1786	U1677		A1556		G1346	U1236	A1100	U1024	C900	G820		G627
	A1887	A1787	U1682	G1557	A1449	G1347	C1287	A1101		U901	U821	C629	U628
	C1888	A1788	U1683	A1558	A1450	C1348	A1238	G1101	A1036	C902	A822	U630	C629
A2016	G1889	A1789			A1455		G1239	A1104	G1036	A912	G823	U718	U631
A2017	A1789		A1689	U1567	A1456	A1351	A1241	G1105	A1037	G913	U632	U719	A632
G2018	C1790	A1791	G1699	U1572	A1456	C1356	U1241	G1114	A1038	C919	U828	A723	A633
A2019	G1792			U1573		G1357	G1242	G1115	A1039	C921	A830	C725	U634
		G1793		C1574	U1459	A1357		A1116	A1043	A922	U831	C726	A635
G2024	A1905	A1794	G1704	U1578	G1460	U1364	G1252	G1117	G1044		A834	A727	G636
U2025	A1795	A1795	G1705	U1579		U1365	A1255	A1118	G1045	C936	U835	A728	G640
G2026	A1796		U1706	A1468		U1365	C1256	U1119	A1046	A936	C836	C729	A644
U2029	A1914	G1800	U1707	A1469	G1468	A1369	G1257	U1120	G1047	C937	A837	C731	G645
C2030	G1915	A1801	G1708	A1470	A1479	A1370	A1258	U1121	G1048		C838	U730	U646
C2031	G1916	C1802	A1709	A1471	A1479	A1371	C1259	U1122	U1049		C839	C732	U647
G2035	U1917	G1803	A1710	C1472		A1372		A1123	U1050	A948	C840	U736	G648
A1918	G1803	U1804	G1711	C1473	C1473	A1373	U1288	A1124	G1051	A949		C737	C649
G1919	U1804			C1473	A1476	A1374	G1269	G1125	G1052	C950	G844	A738	
A1905	A1805	U1714	U1715	A1587		G1375	U1275		C1053		G845	A739	A655
U1923	U1806	U1716	C1593	C1594	U1479	U1376	A1276	U1130	C1054	U956	G846	A740	U656
A1924	U1810	A1717	C1595	C1596	A1480	U1382	C1277	C1131	U1055	C957	G847		A657
U1925	U1811	C1718	A1597	A1481	A1482	U1382		A1132	A1056		G852	G743	C661
C1928	G1812		A1598	A1483		U1391	C1283	C1140	A1057	C971	A853	U744	C662
U1929	A1815	C1721	A1599	A1484		U1392	A1286		G1058	A972	A854	A749	G663
U1932		U1722	A1607		G1496	U1394	A1287		A1059	A973	U858	A750	A666
C1933	C1819	U1723	G1615	A1501		G1395	A1288	C1143	G1060	C976	U859	A753	C667
G1940	G1828	A1724	G1615	A1501	G1510	U1398	G1295	A1146	C1061	A977	U860	G759	C668
U1941	C1829		G1620			A1399	G1296	U1157	A1062	G978	U865		G670
U1942	A1834	A1740	G1624	U1516	U1516	C1400	U1297	C1156	G1063		A866	G764	G671
C1943		A1748	C1628	C1517	C1517	U1401	G1298	U1157	C1064	G982	A867	G765	U675
C1944	A1839	G1749	C1628	U1518	U1518	C1402	U1299	C1158	C1065	C983	G868		U676
C1953	A1840	G1750	C1628	U1519	U1519	C1403	C1300	A1159	C1066	C984	G869	A771	C677
	U1841	G1750	U1636	C1520	C1520	G1407	C1301	C1160	A1067	A985	G870	U772	U677
U1942	U1842		U1637	U1521	U1521		G1303	U1162	C1067	A989	G871	G773	A678
G1843	G1843	U1755	U1638	U1522	U1522	A1413	C1304	A1163	C1068	A990	U872	G774	U679
		A1759	G1638	U1523	U1523	C1414	C1305	A1164	C1069	C991	C873		
U1850	U1851		C1645	A1524	A1524	G1415	C1306	U1165	U1070	G992	A	G783	A682
G1975	A1852	G1762	U1646	A1525	A1525	C1416	A1307	U1166	U1071	U993	U	C784	U683
U2084	C1853	U1763	G1647	G1526	G1526	A1417		G1167	U1072	C994	C	U785	
G2085	G1978	U1764	G1648	U1527	U1527	C1418	U1311	C1168	U1072		C	C786	C687
A2087	C1978	U1764	G1648	U1527	U1527	A1419	U1312	C1169		A996			
G2088	G1978	U1764	G1648	U1527	U1527	A1419	U1312	C1169		A996			
C2089	C1983	U1768	A1653	U1528	U1528	A1420	A1313	G1170	A1075	A999	G	G794	U692
		A1769	G1529	G1529	G1529	G1421	A1314	G1183	G1076	G1000	A880	C795	G693
U		A1770	A1656	A1530	A1530		U1315	U1184	G1076	U1001	C881	U796	A694



• Molecule 11: 16S ribosomal RNA



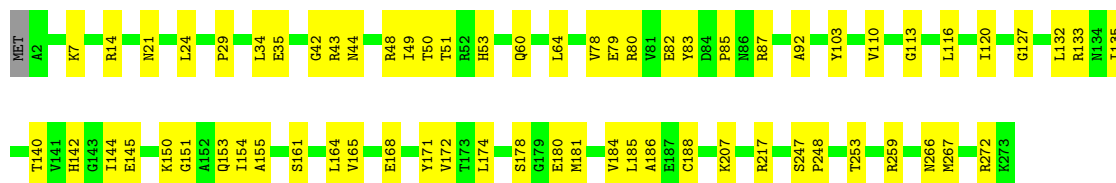


Chain C:  72% 26% ..



- Molecule 13: 50S ribosomal protein L2

Chain D:  75% 24%



- Molecule 14: 50S ribosomal protein L3

Chain E:  83% 14% .



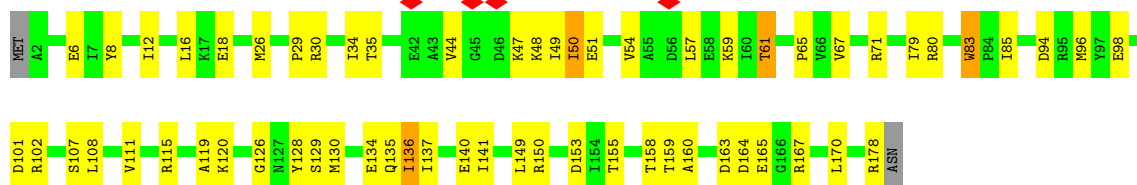
- Molecule 15: 50S ribosomal protein L4

Chain F:  85% 15%



- Molecule 16: 50S ribosomal protein L5

Chain G:  65% 32% ..



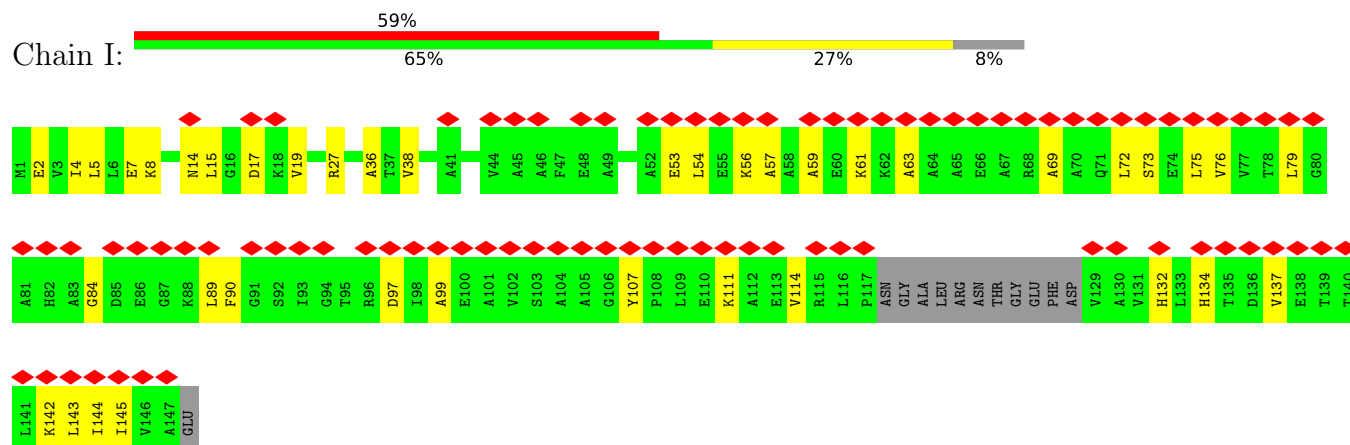
- Molecule 17: 50S ribosomal protein L6

Chain H:  74% 24% ..

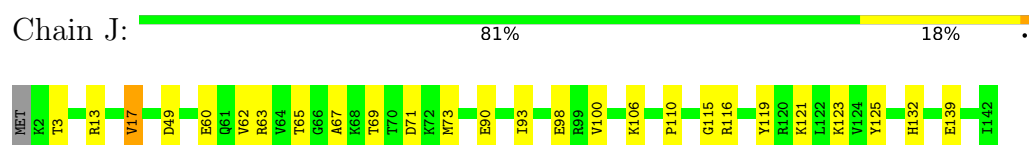




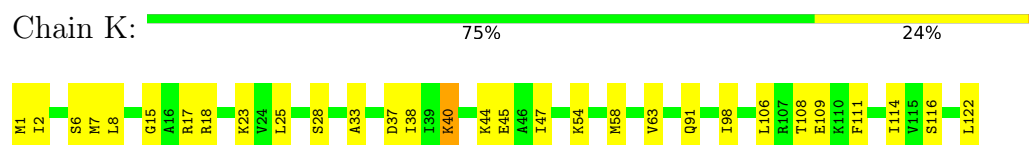
• Molecule 18: 50S ribosomal protein L9



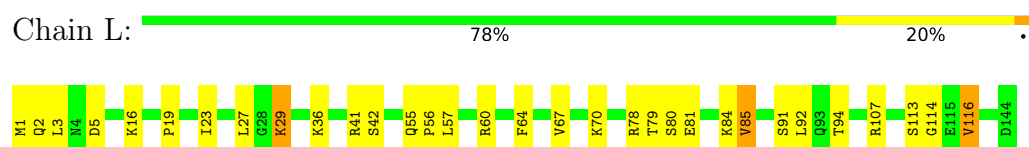
• Molecule 19: 50S ribosomal protein L13



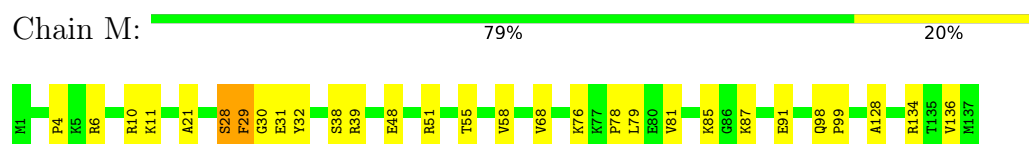
• Molecule 20: 50S ribosomal protein L14



• Molecule 21: 50S ribosomal protein L15

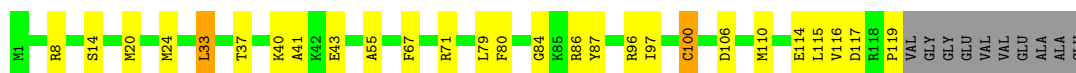


• Molecule 22: 50S ribosomal protein L16



• Molecule 23: 50S ribosomal protein L17





- Molecule 24: 50S ribosomal protein L18

Chain O: 74% 23% ..



- Molecule 25: 50S ribosomal protein L19

Chain P: 75% 22% ..



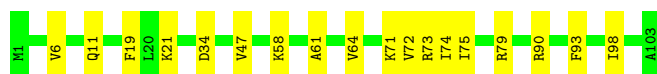
- Molecule 26: 50S ribosomal protein L20

Chain Q: 80% 19% .



- Molecule 27: 50S ribosomal protein L21

Chain R: 83% 17%



- Molecule 28: Large ribosomal subunit protein uL22

Chain S: 80% 19% .



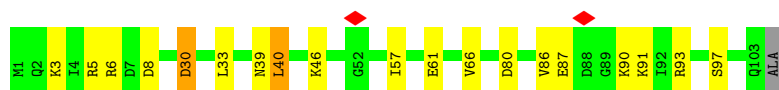
- Molecule 29: 50S ribosomal protein L23

Chain T: 72% 21% 7%



- Molecule 30: 50S ribosomal protein L24

Chain U: 81% 16% ..



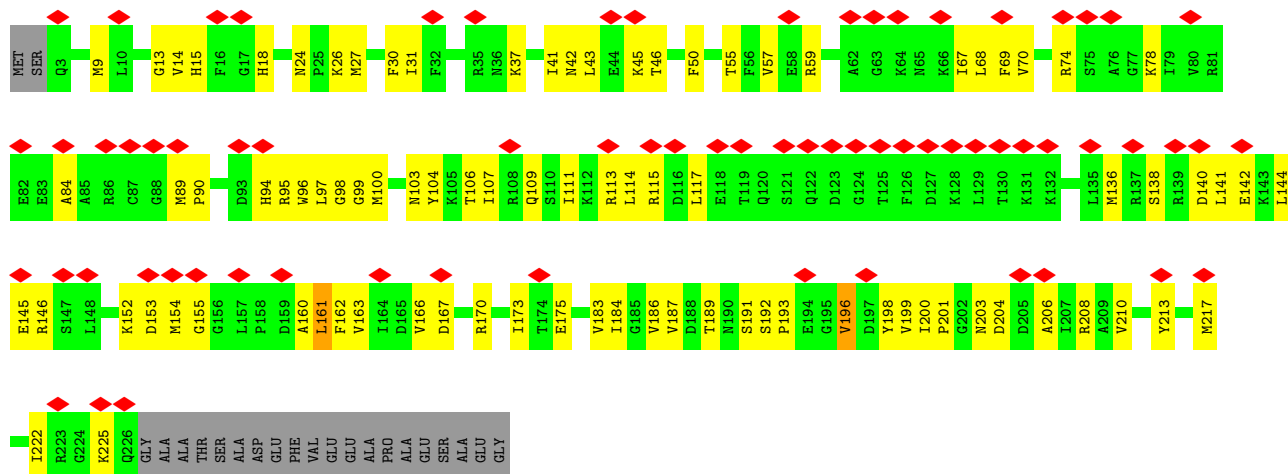
• Molecule 31: 50S ribosomal protein L25

Chain V: 75% 17% 7%



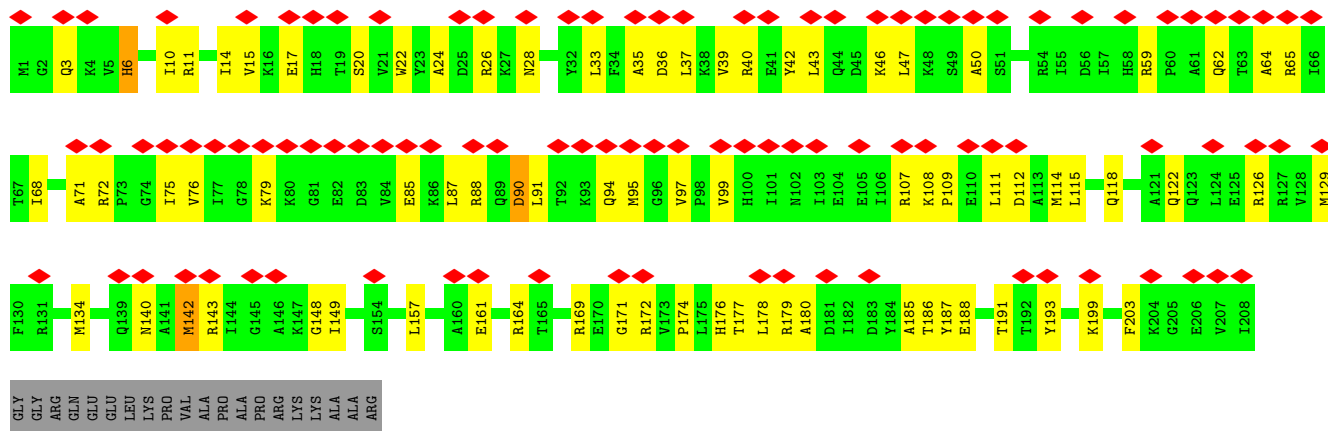
• Molecule 32: 30S ribosomal protein S2

Chain a: 28% 55% 35% 9%



• Molecule 33: 30S ribosomal protein S3

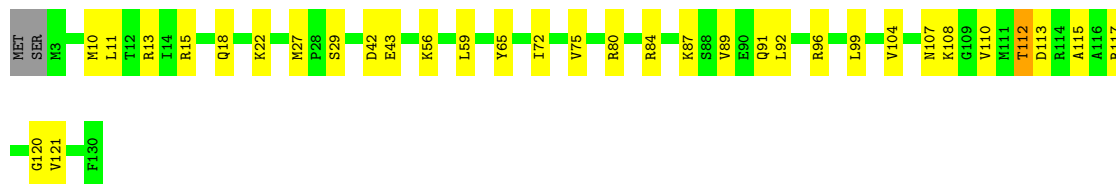
Chain b: 44% 57% 33% 9%



• Molecule 34: 30S ribosomal protein S4

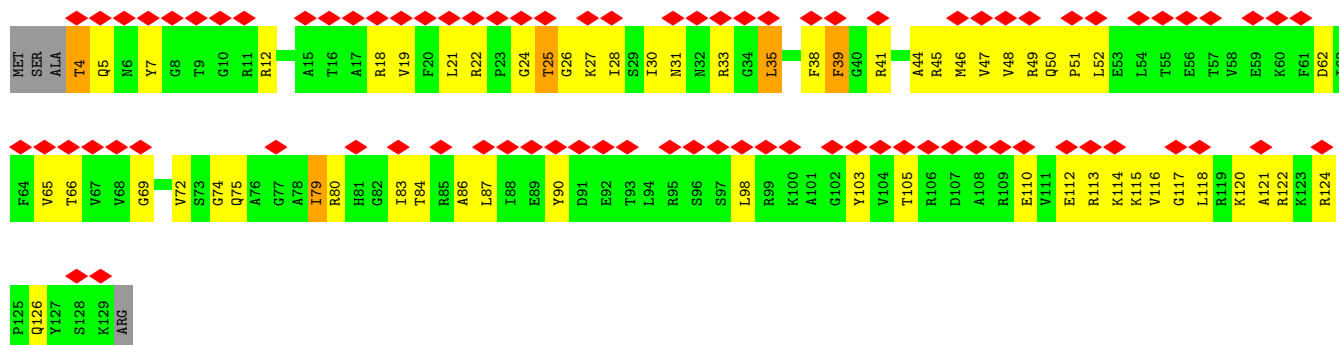


Chain g:  73% 25% ..



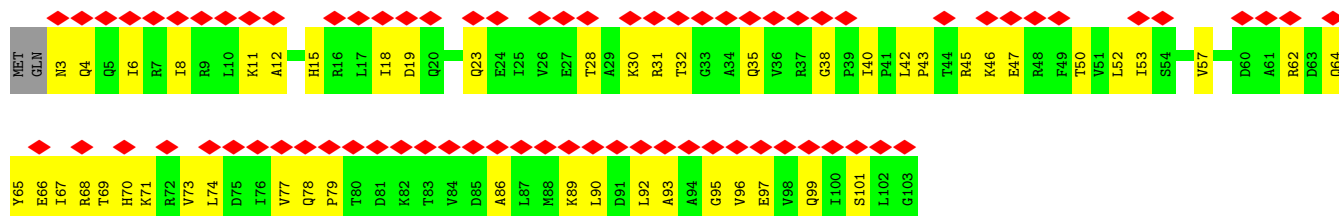
- Molecule 39: 30S ribosomal protein S9

Chain h:  64% 52% 42% . .



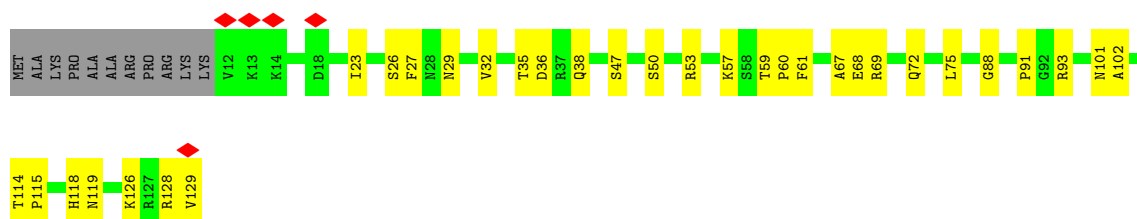
- Molecule 40: 30S ribosomal protein S10

Chain i:  73% 50% 49% .



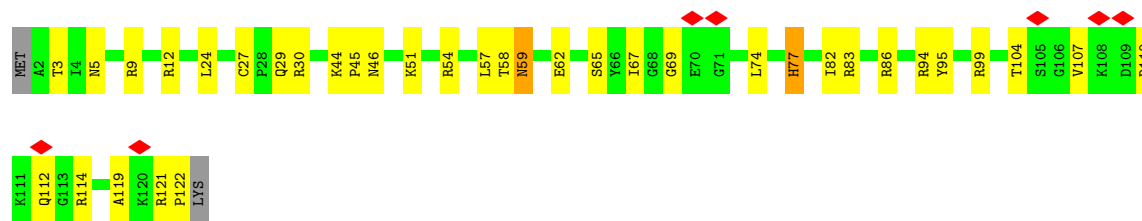
- Molecule 41: 30S ribosomal protein S11

Chain j:  67% 25% 9%

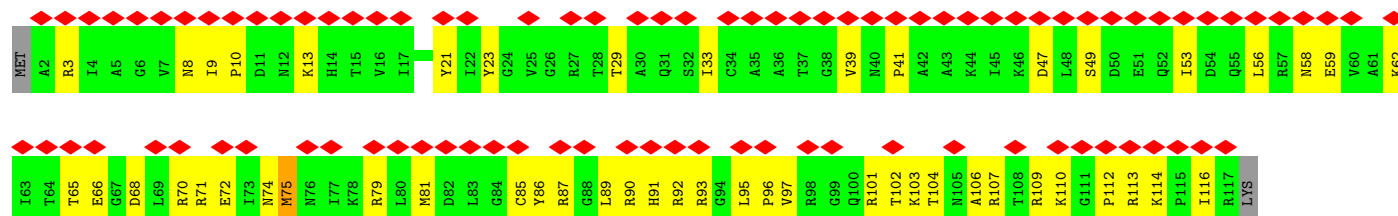
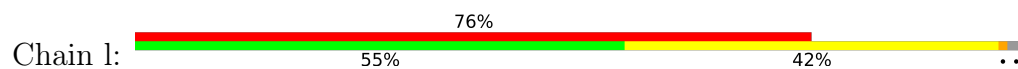


- Molecule 42: 30S ribosomal protein S12

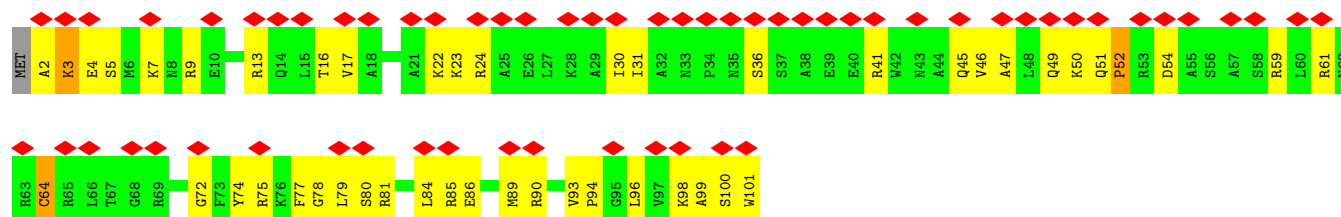
Chain k:  6% 69% 28% . .



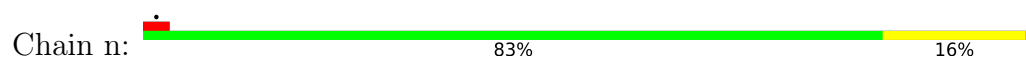
• Molecule 43: 30S ribosomal protein S13



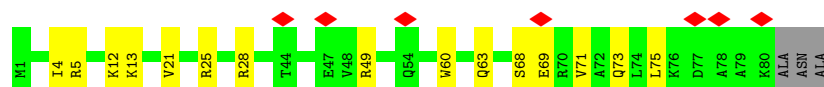
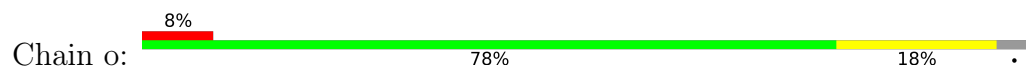
• Molecule 44: 30S ribosomal protein S14



• Molecule 45: 30S ribosomal protein S15



• Molecule 46: 30S ribosomal protein S16



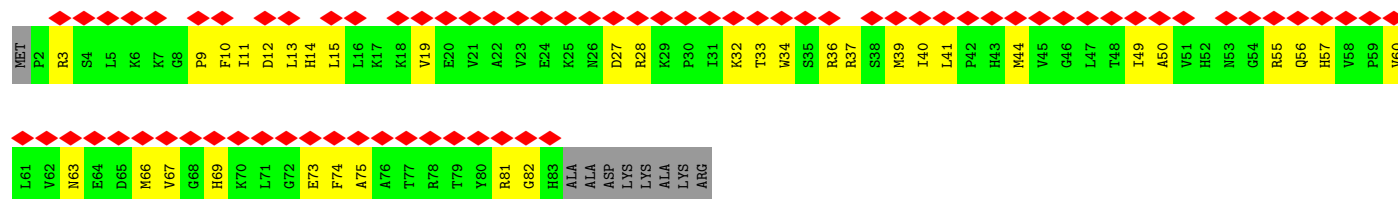
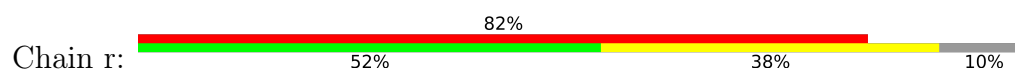
• Molecule 47: 30S ribosomal protein S17



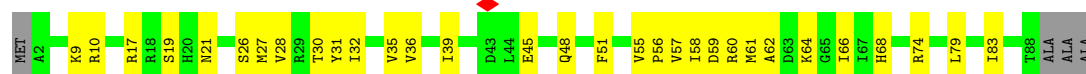
- Molecule 48: 30S ribosomal protein S18



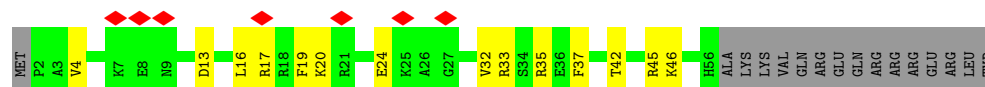
- Molecule 49: 30S ribosomal protein S19



- Molecule 50: 30S ribosomal protein S20



- Molecule 51: 30S ribosomal protein S21



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	166770	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	96000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.870	Depositor
Minimum map value	-0.435	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.028	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	282.88, 282.88, 282.88	wwPDB
Map dimensions	340, 340, 340	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.832, 0.832, 0.832	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, MG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	1	0.27	0/577	0.32	0/767
2	2	0.27	0/641	0.32	0/854
3	3	0.19	0/495	0.26	0/659
4	4	0.22	0/444	0.28	0/597
5	5	0.25	0/439	0.36	0/585
6	6	0.20	0/423	0.30	0/565
7	7	0.31	0/368	0.39	0/482
8	8	0.29	0/511	0.44	0/668
9	9	0.28	0/307	0.37	0/404
10	A	0.35	0/67406	0.34	1/105146 (0.0%)
11	B	0.15	0/36694	0.26	0/57245
12	C	0.22	0/2855	0.24	0/4447
13	D	0.28	0/2107	0.40	0/2831
14	E	0.28	0/1575	0.35	0/2121
15	F	0.25	0/1544	0.34	0/2079
16	G	0.17	0/1414	0.43	0/1901
17	H	0.90	4/1334 (0.3%)	0.78	5/1797 (0.3%)
18	I	0.15	0/953	0.41	0/1291
19	J	0.27	0/1148	0.35	0/1549
20	K	0.25	0/947	0.32	0/1268
21	L	0.25	0/1078	0.39	0/1436
22	M	0.28	0/1105	0.39	0/1476
23	N	0.28	0/968	0.33	0/1294
24	O	0.18	0/882	0.31	0/1175
25	P	0.25	0/903	0.31	0/1208
26	Q	0.27	0/945	0.33	0/1257
27	R	0.27	0/835	0.31	0/1117
28	S	0.27	0/837	0.37	0/1114
29	T	0.24	0/729	0.40	0/975
30	U	0.22	0/799	0.32	0/1068
31	V	0.19	0/1457	0.33	0/1975
32	a	0.20	0/1753	0.52	0/2362

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	b	0.15	0/1689	0.46	0/2275
34	c	0.13	0/1646	0.38	0/2201
35	d	0.17	0/1156	0.43	0/1555
36	e	0.19	0/859	0.53	0/1156
37	f	0.17	0/1217	0.48	0/1627
38	g	0.17	0/987	0.41	0/1324
39	h	0.15	0/1006	0.47	0/1347
40	i	0.20	0/820	0.56	0/1106
41	j	0.16	0/889	0.40	0/1202
42	k	0.20	0/963	0.53	1/1292 (0.1%)
43	l	0.60	2/913 (0.2%)	0.91	5/1227 (0.4%)
44	m	0.21	0/816	0.59	1/1087 (0.1%)
45	n	0.14	0/718	0.32	0/957
46	o	0.20	0/642	0.41	0/863
47	p	0.20	0/653	0.54	0/881
48	q	0.13	0/473	0.32	0/637
49	r	0.13	0/673	0.45	0/905
50	s	0.14	0/678	0.35	0/904
51	t	0.14	0/454	0.39	0/603
All	All	0.29	6/151725 (0.0%)	0.35	13/226862 (0.0%)

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	H	112	PRO	CG-CD	-26.36	0.61	1.50
17	H	112	PRO	CB-CG	14.38	2.21	1.49
43	l	112	PRO	CG-CD	-13.53	1.04	1.50
17	H	112	PRO	N-CD	9.28	1.60	1.47
43	l	112	PRO	N-CD	7.68	1.58	1.47
17	H	112	PRO	N-CA	-5.80	1.39	1.47

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	H	112	PRO	CB-CG-CD	-16.04	54.78	106.10
17	H	112	PRO	N-CD-CG	-15.08	80.58	103.20
43	l	112	PRO	N-CD-CG	-14.70	81.15	103.20
17	H	112	PRO	CA-N-CD	-12.61	94.34	112.00
43	l	41	PRO	CA-N-CD	-12.33	94.74	112.00
42	k	122	PRO	CA-N-CD	-11.74	95.56	112.00
17	H	112	PRO	CA-CB-CG	-11.33	82.97	104.50
43	l	112	PRO	CA-N-CD	-11.19	96.33	112.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
43	l	112	PRO	CA-CB-CG	-9.15	87.12	104.50
17	H	112	PRO	N-CA-CB	-9.03	93.77	103.25
44	m	52	PRO	CA-N-CD	-8.96	99.45	112.00
43	l	41	PRO	N-CD-CG	-5.85	94.42	103.20
10	A	502	G	O4'-C1'-N9	5.55	116.53	108.20

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	569	0	593	8	0
2	2	630	0	653	9	0
3	3	494	0	523	7	0
4	4	440	0	469	1	0
5	5	433	0	431	9	0
6	6	416	0	444	8	0
7	7	365	0	409	8	0
8	8	506	0	569	11	0
9	9	306	0	342	8	0
10	A	60189	0	30263	560	0
11	B	32768	0	16488	619	0
12	C	2555	0	1294	19	0
13	D	2071	0	2152	47	0
14	E	1552	0	1563	18	0
15	F	1524	0	1583	20	0
16	G	1393	0	1447	50	0
17	H	1316	0	1372	27	0
18	I	945	0	957	25	0
19	J	1122	0	1148	17	0
20	K	938	0	1012	20	0
21	L	1066	0	1112	23	0
22	M	1085	0	1157	20	0
23	N	952	0	996	15	0
24	O	875	0	915	17	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
25	P	894	0	951	17	0
26	Q	935	0	1025	21	0
27	R	822	0	858	12	0
28	S	833	0	897	16	0
29	T	720	0	775	20	0
30	U	791	0	846	13	0
31	V	1434	0	1462	26	0
32	a	1725	0	1736	76	0
33	b	1660	0	1717	67	0
34	c	1627	0	1663	52	0
35	d	1142	0	1192	35	0
36	e	845	0	822	27	0
37	f	1199	0	1253	55	0
38	g	976	0	1031	26	0
39	h	994	0	1028	60	0
40	i	810	0	847	46	0
41	j	873	0	887	28	0
42	k	949	0	996	27	0
43	l	904	0	949	51	0
44	m	804	0	841	44	0
45	n	711	0	739	12	0
46	o	631	0	641	13	0
47	p	645	0	689	28	0
48	q	466	0	490	8	0
49	r	658	0	692	32	0
50	s	671	0	722	25	0
51	t	447	0	470	15	0
52	9	1	0	0	0	0
53	A	175	0	0	0	0
53	C	5	0	0	0	0
53	E	1	0	0	0	0
53	N	2	0	0	0	0
53	T	1	0	0	0	0
54	A	383	0	0	8	0
54	D	4	0	0	0	0
54	E	3	0	0	0	0
54	L	5	0	0	1	0
All	All	140256	0	94111	2126	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 9.

All (2126) 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)
11:B:1221:A:H2'	43:l:114:LYS:HE2	1.37	1.01
11:B:75:G:H1	11:B:88:U:H3	1.14	0.92
25:P:89:ARG:NH2	25:P:111:ILE:O	2.08	0.86
10:A:271:A:H62	10:A:355:A:H2	1.21	0.86
11:B:68:G:H1	11:B:95:A:H61	1.22	0.85
16:G:48:LYS:H	16:G:48:LYS:HE2	1.43	0.82
41:j:68:GLU:OE1	41:j:72:GLN:NE2	2.12	0.82
16:G:134:GLU:HB2	16:G:149:LEU:HD11	1.60	0.81
36:e:90:MET:SD	48:q:61:ARG:NH1	2.54	0.81
43:l:23:TYR:HE1	43:l:70:ARG:HB2	1.47	0.79
11:B:667:G:H2'	11:B:668:G:C8	2.18	0.79
37:f:27:MET:HE2	37:f:27:MET:HA	1.64	0.79
11:B:439:G:N2	11:B:483:C:O2	2.14	0.78
33:b:46:LYS:HG3	33:b:47:LEU:HD22	1.63	0.78
31:V:165:LEU:HD11	31:V:184:VAL:HG21	1.65	0.78
39:h:27:LYS:HE3	39:h:62:ASP:HB2	1.65	0.78
11:B:340:G:OP1	25:P:40:ARG:NH2	2.15	0.78
32:a:90:PRO:HG2	32:a:154:MET:HG3	1.66	0.78
10:A:1094:U:H2'	10:A:1095:A:H8	1.48	0.77
50:s:55:VAL:HG23	50:s:56:PRO:HD3	1.65	0.77
42:k:114:ARG:HB3	42:k:119:ALA:HB3	1.66	0.77
11:B:124:A:N6	11:B:227:C:O2	2.17	0.77
10:A:271:A:N6	10:A:355:A:H2	1.84	0.76
11:B:998:A:H5'	11:B:1018:G:H22	1.51	0.76
11:B:80:C:O2	11:B:83:G:N2	2.18	0.76
32:a:78:LYS:H	32:a:78:LYS:HE2	1.50	0.75
11:B:668:G:H2'	11:B:669:A:H8	1.51	0.75
11:B:712:A:H5'	41:j:119:ASN:HB2	1.68	0.75
10:A:355:A:OP1	10:A:415:G:O2'	2.05	0.75
49:r:41:LEU:H	49:r:44:MET:HE1	1.52	0.75
29:T:1:MET:HE3	29:T:6:VAL:HG22	1.67	0.75
10:A:800:U:OP1	54:A:3101:HOH:O	2.05	0.74
11:B:1233:A:H3'	37:f:116:MET:HE1	1.70	0.74
5:5:49:ARG:NH1	10:A:2869:A:OP2	2.19	0.74
25:P:8:GLN:NE2	25:P:12:GLU:OE2	2.20	0.74
36:e:29:ILE:HD11	36:e:66:CYS:HB3	1.69	0.74
11:B:607:C:OP1	34:c:81:ARG:NH1	2.19	0.74
47:p:14:ARG:HH21	47:p:61:LEU:HD13	1.53	0.73
11:B:541:A:OP2	34:c:70:ARG:NH2	2.22	0.72
11:B:1146:A:OP1	40:i:70:HIS:ND1	2.22	0.72
35:d:83:GLN:HB3	35:d:148:MET:HE1	1.71	0.72
11:B:34:C:H2'	11:B:35:G:H8	1.54	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:G:18:GLU:OE1	16:G:18:GLU:N	2.23	0.72
11:B:730:C:H2'	11:B:731:A:H8	1.54	0.71
40:i:66:GLU:HG2	44:m:99:ALA:HB2	1.70	0.71
11:B:874:C:OP1	42:k:9:ARG:NH2	2.22	0.71
11:B:1339:U:OP1	39:h:122:ARG:NH1	2.23	0.71
16:G:34:ILE:HD12	16:G:96:MET:HG2	1.72	0.71
40:i:8:ILE:HD11	40:i:74:LEU:HB3	1.73	0.71
39:h:4:THR:OG1	39:h:5:GLN:N	2.24	0.70
47:p:72:LYS:HG3	47:p:73:THR:HG23	1.73	0.70
30:U:5:ARG:HG2	30:U:5:ARG:HH11	1.56	0.70
32:a:67:ILE:HG22	32:a:160:ALA:HB3	1.72	0.70
33:b:79:LYS:H	33:b:79:LYS:HD3	1.55	0.70
43:l:93:ARG:HD2	43:l:95:LEU:HD12	1.72	0.70
10:A:1996:G:N7	54:A:3116:HOH:O	2.24	0.70
11:B:1260:G:N2	11:B:1263:A:OP2	2.19	0.70
32:a:136:MET:HA	32:a:140:ASP:HB3	1.72	0.70
35:d:78:ASN:O	35:d:78:ASN:ND2	2.21	0.70
33:b:126:ARG:NH1	33:b:126:ARG:HA	2.06	0.70
33:b:114:MET:HE2	33:b:185:ALA:HB1	1.74	0.69
11:B:495:C:OP1	42:k:114:ARG:NH2	2.25	0.69
10:A:271:A:N6	10:A:355:A:C2	2.56	0.69
11:B:1067:U:O2	32:a:103:ASN:ND2	2.25	0.69
11:B:263:U:H2'	11:B:264:A:H8	1.56	0.69
11:B:1071:G:N2	11:B:1074:A:OP2	2.22	0.69
21:L:85:VAL:HG22	21:L:94:THR:HG22	1.75	0.69
32:a:114:LEU:HG	32:a:152:LYS:HE2	1.73	0.69
10:A:2277:U:H2'	10:A:2278:G:C8	2.28	0.69
11:B:1350:A:H2'	11:B:1351:A:C8	2.28	0.69
18:I:14:ASN:HB2	18:I:17:ASP:HB2	1.74	0.69
11:B:742:U:H2'	11:B:743:A:H8	1.58	0.69
11:B:1100:G:H5''	33:b:172:ARG:HG2	1.73	0.69
16:G:135:GLN:O	16:G:136:ILE:HG12	1.93	0.69
40:i:11:LYS:HG3	40:i:71:LYS:HG2	1.75	0.69
43:l:102:THR:HA	43:l:106:ALA:HB2	1.74	0.68
11:B:1291:G:O2'	37:f:114:LYS:NZ	2.26	0.68
11:B:1020:G:H1	11:B:1029:A:N6	1.92	0.68
11:B:486:C:H2'	11:B:487:A:C8	2.28	0.68
42:k:74:LEU:HD11	42:k:104:THR:HB	1.76	0.68
10:A:1785:G:OP1	13:D:259:ARG:NH1	2.23	0.68
12:C:41:C:N4	16:G:67:VAL:O	2.26	0.68
32:a:55:THR:HG22	32:a:59:ARG:HH22	1.59	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:190:A:H2'	10:A:191:C:C6	2.29	0.67
11:B:123:A:H2	11:B:226:G:H1	1.42	0.67
44:m:49:GLN:HG2	49:r:13:LEU:HD13	1.76	0.67
15:F:144:ASP:HB3	15:F:183:ASP:HB2	1.75	0.67
32:a:24:ASN:OD1	32:a:26:LYS:NZ	2.27	0.67
41:j:38:GLN:OE1	41:j:38:GLN:N	2.27	0.67
11:B:683:C:OP2	41:j:53:ARG:NH2	2.27	0.67
10:A:582:U:H2'	10:A:583:U:C6	2.30	0.67
10:A:2314:A:H2'	10:A:2315:A:C8	2.29	0.67
10:A:1586:A:H5''	10:A:1587:A:H5'	1.74	0.67
10:A:1770:A:OP1	54:A:3103:HOH:O	2.13	0.67
11:B:707:G:H2'	11:B:708:G:C8	2.30	0.67
23:N:37:THR:HG22	23:N:110:MET:HE1	1.76	0.67
11:B:671:U:H3	11:B:707:G:H22	1.41	0.67
32:a:170:ARG:NH2	32:a:192:SER:OG	2.28	0.67
18:I:99:ALA:HB2	18:I:111:LYS:HD2	1.76	0.67
49:r:81:ARG:NH1	49:r:81:ARG:O	2.28	0.67
8:8:35:MET:HE2	8:8:40:LYS:HG2	1.77	0.67
37:f:25:LYS:HA	37:f:28:ASN:HB3	1.75	0.67
2:2:6:GLN:O	2:2:74:ARG:NH2	2.28	0.66
11:B:68:G:H1	11:B:95:A:N6	1.91	0.66
22:M:11:LYS:HD3	22:M:87:LYS:HD3	1.77	0.66
11:B:395:C:O2'	11:B:615:A:N3	2.27	0.66
36:e:38:ARG:HB3	36:e:63:ASN:HB3	1.77	0.66
47:p:28:ILE:HB	47:p:45:THR:HB	1.76	0.66
32:a:115:ARG:NH2	32:a:152:LYS:O	2.28	0.66
33:b:72:ARG:HD2	33:b:75:ILE:HG12	1.76	0.66
10:A:1810:G:O2'	13:D:253:THR:HG21	1.96	0.66
11:B:1033:C:H2'	11:B:1034:A:H8	1.58	0.66
10:A:1812:G:O2'	10:A:1957:U:OP2	2.14	0.66
10:A:2290:G:H22	10:A:2298:U:H3	1.42	0.66
16:G:51:GLU:OE2	16:G:51:GLU:N	2.24	0.66
23:N:114:GLU:HB2	23:N:119:PRO:HB3	1.78	0.66
38:g:22:LYS:O	38:g:65:TYR:OH	2.13	0.66
10:A:1047:G:H2'	10:A:1048:G:C8	2.30	0.66
10:A:1236:G:H5''	26:Q:6:ARG:HD2	1.78	0.66
11:B:124:A:N3	11:B:257:A:O2'	2.27	0.66
11:B:1097:C:H4'	32:a:97:LEU:HD21	1.76	0.65
35:d:65:MET:HA	35:d:65:MET:HE3	1.78	0.65
32:a:103:ASN:OD1	32:a:106:THR:OG1	2.14	0.65
11:B:397:C:H5''	34:c:133:PRO:HD2	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:G:80:ARG:HG2	16:G:80:ARG:HH11	1.62	0.65
9:9:7:VAL:HG22	9:9:38:GLY:HA3	1.77	0.65
30:U:3:LYS:O	30:U:93:ARG:NH1	2.29	0.65
33:b:129:MET:HA	33:b:129:MET:HE3	1.79	0.65
34:c:171:VAL:HG12	34:c:182:PHE:HA	1.79	0.65
35:d:104:THR:O	35:d:123:ASN:ND2	2.28	0.65
39:h:49:ARG:HG2	39:h:52:LEU:HD11	1.79	0.65
11:B:177:G:O6	11:B:188:G:N1	2.20	0.65
11:B:1212:C:H2'	11:B:1213:A:C8	2.32	0.65
10:A:983:C:OP1	26:Q:53:ARG:NH2	2.30	0.65
10:A:2086:G:H1'	10:A:2176:G:H22	1.61	0.65
11:B:189:A:N3	11:B:216:U:O2'	2.29	0.65
24:O:56:ASP:OD1	24:O:80:ARG:NH2	2.29	0.65
11:B:546:U:H2'	11:B:547:A:H8	1.62	0.65
10:A:271:A:N7	10:A:355:A:N1	2.45	0.65
50:s:32:ILE:HG23	50:s:79:LEU:HD11	1.77	0.65
11:B:1311:C:H5	49:r:37:ARG:HH12	1.45	0.65
21:L:80:SER:HB3	21:L:114:GLY:HA3	1.79	0.65
25:P:28:ILE:HG12	25:P:45:GLU:HG3	1.78	0.65
32:a:184:ILE:HG12	32:a:198:TYR:HB2	1.79	0.65
36:e:18:VAL:HA	36:e:21:MET:HE2	1.79	0.65
39:h:33:ARG:HB2	39:h:38:PHE:HD1	1.62	0.65
10:A:278:A:N6	10:A:348:U:O4	2.19	0.64
11:B:1212:C:H2'	11:B:1213:A:H8	1.62	0.64
34:c:97:ARG:HE	34:c:134:SER:HA	1.62	0.64
10:A:2236:G:OP1	22:M:85:LYS:NZ	2.27	0.64
11:B:98:G:N7	50:s:9:LYS:NZ	2.41	0.64
10:A:524:U:O2'	26:Q:49:ASP:OD2	2.14	0.64
11:B:1218:U:O2'	11:B:1316:C:OP1	2.11	0.64
11:B:1366:U:OP1	39:h:74:GLY:N	2.30	0.64
34:c:142:VAL:HG23	34:c:181:THR:HG22	1.78	0.64
38:g:29:SER:HB3	38:g:59:LEU:HB2	1.78	0.64
10:A:1804:U:O2'	13:D:154:ILE:O	2.14	0.64
11:B:422:G:OP2	34:c:10:LYS:NZ	2.30	0.64
11:B:940:A:H2'	11:B:941:G:C8	2.33	0.64
11:B:8:A:N6	34:c:202:GLU:O	2.31	0.64
25:P:63:ARG:NH1	25:P:72:GLU:OE2	2.30	0.64
44:m:89:MET:HA	44:m:89:MET:HE3	1.79	0.64
10:A:1480:A:H2'	10:A:1481:A:C8	2.32	0.64
11:B:668:G:H2'	11:B:669:A:C8	2.33	0.64
11:B:1339:U:O2'	37:f:5:ARG:NH1	2.32	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:B:1337:G:H5''	39:h:124:ARG:HE	1.62	0.63
22:M:39:ARG:HB2	22:M:99:PRO:HD3	1.80	0.63
11:B:1169:G:H2'	11:B:1170:A:H8	1.63	0.63
11:B:1249:G:H3'	11:B:1273:A:H61	1.63	0.63
17:H:115:TYR:OH	17:H:147:GLU:OE1	2.14	0.63
14:E:27:VAL:HG22	14:E:188:LEU:HD22	1.79	0.63
31:V:173:LEU:HD12	31:V:176:LEU:HD12	1.81	0.63
11:B:730:C:H2'	11:B:731:A:C8	2.33	0.63
33:b:47:LEU:HB3	33:b:50:ALA:HB3	1.81	0.63
10:A:1455:A:H2'	10:A:1456:A:C8	2.33	0.63
16:G:134:GLU:N	16:G:134:GLU:OE2	2.31	0.63
11:B:329:C:H2'	11:B:330:A:H8	1.63	0.63
16:G:54:VAL:HG13	16:G:65:PRO:HG2	1.80	0.63
37:f:69:ILE:HD11	37:f:127:ALA:HB1	1.81	0.63
11:B:668:G:H21	41:j:118:HIS:HB2	1.63	0.62
11:B:1290:C:O3'	43:l:13:LYS:NZ	2.32	0.62
11:B:1314:C:H42	49:r:36:ARG:HB2	1.63	0.62
11:B:1141:C:O2'	39:h:7:TYR:OH	2.15	0.62
11:B:1375:U:H1'	37:f:78:ARG:HH22	1.62	0.62
11:B:258:A:O2'	47:p:69:PRO:O	2.15	0.62
11:B:1197:C:OP1	44:m:2:ALA:N	2.32	0.62
16:G:119:ALA:O	16:G:167:ARG:NH2	2.32	0.62
10:A:822:A:H2'	10:A:823:G:C8	2.34	0.62
11:B:869:U:O2'	38:g:15:ARG:NH1	2.27	0.62
11:B:1314:C:H1'	49:r:73:GLU:HG2	1.81	0.62
10:A:1008:U:OP1	10:A:1024:U:O2'	2.16	0.62
11:B:495:C:H2'	11:B:496:A:H8	1.65	0.62
7:7:29:GLN:NE2	10:A:209:C:OP1	2.32	0.62
10:A:1287:A:H2	10:A:1615:G:H21	1.48	0.62
11:B:263:U:H2'	11:B:264:A:C8	2.34	0.62
10:A:597:A:H2'	10:A:598:A:C8	2.34	0.62
16:G:30:ARG:H	16:G:159:THR:HG22	1.63	0.62
11:B:708:G:H2'	11:B:709:A:C8	2.35	0.62
11:B:1520:G:OP1	51:t:45:ARG:NH2	2.32	0.62
15:F:175:ASP:N	15:F:175:ASP:OD1	2.31	0.62
20:K:38:ILE:HD13	20:K:91:GLN:HE22	1.65	0.62
11:B:658:G:H22	11:B:735:G:H1	1.48	0.62
43:l:71:ARG:HA	43:l:74:ASN:HD21	1.65	0.62
10:A:699:U:H2'	10:A:700:A:C8	2.35	0.61
11:B:453:U:H2'	11:B:454:A:H8	1.65	0.61
32:a:161:LEU:HB3	32:a:183:VAL:HG22	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:858:U:H2'	10:A:859:U:H5''	1.82	0.61
33:b:191:THR:HG23	33:b:193:TYR:H	1.65	0.61
10:A:566:G:O2'	10:A:1240:A:OP1	2.18	0.61
10:A:2048:A:N7	10:A:2489:A:N6	2.48	0.61
11:B:1235:G:H2'	11:B:1236:G:H8	1.65	0.61
10:A:2088:G:H22	10:A:2173:C:H1'	1.65	0.61
11:B:591:G:HO2'	47:p:40:TYR:HE1	1.46	0.61
11:B:656:U:H2'	11:B:657:A:C8	2.35	0.61
14:E:181:ASP:HB3	14:E:186:LEU:HB2	1.80	0.61
10:A:2229:U:H2'	10:A:2230:U:C6	2.35	0.61
42:k:110:ARG:NH1	42:k:112:GLN:O	2.34	0.61
11:B:533:A:H2'	11:B:534:G:C8	2.36	0.61
11:B:975:U:OP1	44:m:9:ARG:NH1	2.34	0.61
16:G:136:ILE:HA	16:G:141:ILE:HD11	1.82	0.61
34:c:109:SER:OG	34:c:113:GLU:OE1	2.17	0.61
10:A:785:U:H2'	10:A:786:C:C6	2.35	0.61
11:B:1049:A:O2'	33:b:161:GLU:O	2.15	0.61
20:K:111:PHE:HB3	20:K:114:ILE:HD12	1.82	0.61
40:i:28:THR:HA	40:i:31:ARG:HH21	1.64	0.61
10:A:1782:U:H2'	10:A:1783:C:C6	2.36	0.61
22:M:78:PRO:HG2	22:M:81:VAL:HG21	1.82	0.61
24:O:59:LEU:HD21	24:O:72:LYS:HB3	1.83	0.61
33:b:14:ILE:HG22	33:b:15:VAL:HG13	1.82	0.61
34:c:4:TYR:OH	34:c:7:PRO:O	2.17	0.61
35:d:158:ARG:NH2	38:g:43:GLU:OE1	2.25	0.61
10:A:866:A:H3'	10:A:867:G:H8	1.64	0.60
11:B:521:G:O2'	11:B:529:A:N1	2.31	0.60
11:B:646:U:O4	11:B:746:G:O2'	2.16	0.60
13:D:21:ASN:HB3	13:D:24:LEU:HG	1.83	0.60
10:A:2282:U:OP2	24:O:10:ARG:NH2	2.34	0.60
11:B:1380:G:H2'	11:B:1381:G:H8	1.65	0.60
10:A:2060:U:H2'	10:A:2061:U:C6	2.36	0.60
11:B:21:G:H2'	11:B:22:G:C8	2.37	0.60
16:G:48:LYS:HE2	16:G:48:LYS:N	2.15	0.60
34:c:29:ASP:N	34:c:29:ASP:OD1	2.34	0.60
11:B:187:A:H2'	11:B:188:G:C8	2.36	0.60
30:U:30:ASP:OD1	30:U:30:ASP:N	2.32	0.60
33:b:169:ARG:NH1	33:b:171:GLY:O	2.35	0.60
11:B:739:U:OP1	11:B:845:U:O2'	2.19	0.60
11:B:1301:U:H5''	43:l:109:ARG:HH21	1.66	0.60
29:T:1:MET:HG3	29:T:41:GLU:HG2	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:m:24:ARG:NH1	44:m:51:GLN:OE1	2.34	0.60
10:A:2774:A:H2'	10:A:2775:C:C6	2.37	0.60
11:B:141:G:H2'	11:B:142:G:C8	2.36	0.60
11:B:987:G:O2'	11:B:988:A:N7	2.34	0.60
29:T:17:GLU:CD	29:T:17:GLU:H	2.09	0.60
33:b:115:LEU:HA	33:b:118:GLN:HB2	1.83	0.60
10:A:1419:A:H2'	10:A:1420:A:C8	2.36	0.60
11:B:546:U:H5'	42:k:83:ARG:HH12	1.67	0.60
11:B:667:G:H2'	11:B:668:G:H8	1.66	0.60
32:a:89:MET:HA	32:a:89:MET:HE2	1.83	0.60
37:f:37:ALA:HB1	39:h:41:ARG:HE	1.66	0.60
2:2:10:LYS:NZ	10:A:386:G:OP2	2.31	0.60
10:A:1420:A:O2'	10:A:1421:G:O5'	2.19	0.60
11:B:37:U:O2'	11:B:541:A:N1	2.35	0.60
33:b:118:GLN:NE2	33:b:122:GLN:OE1	2.35	0.60
34:c:102:VAL:HG13	34:c:107:PHE:HB2	1.84	0.60
11:B:64:G:H4'	11:B:65:A:H3'	1.84	0.60
11:B:944:U:H3	11:B:1225:G:H1	1.48	0.60
38:g:92:LEU:HD22	38:g:104:VAL:HG21	1.83	0.60
7:7:3:ARG:O	7:7:6:GLN:NE2	2.34	0.60
10:A:1855:G:N2	10:A:1858:A:OP2	2.30	0.60
10:A:1094:U:H2'	10:A:1095:A:C8	2.34	0.59
10:A:1682:U:O2'	13:D:14:ARG:NH2	2.34	0.59
11:B:94:C:H2'	11:B:95:A:C8	2.38	0.59
11:B:1349:G:H2'	11:B:1350:A:H8	1.66	0.59
14:E:183:GLU:OE2	14:E:183:GLU:N	2.27	0.59
33:b:46:LYS:HD2	33:b:87:LEU:HD12	1.83	0.59
11:B:1341:G:O6	39:h:12:ARG:NH2	2.35	0.59
11:B:1507:A:H2'	11:B:1508:G:C8	2.37	0.59
24:O:110:ARG:NH1	24:O:116:PHE:O	2.35	0.59
31:V:186:ASN:C	31:V:186:ASN:HD22	2.10	0.59
10:A:485:G:H21	28:S:61:ASN:HD21	1.50	0.59
10:A:1481:A:H2'	10:A:1482:A:C8	2.38	0.59
10:A:2078:U:OP2	18:I:27:ARG:NH1	2.35	0.59
11:B:477:C:H2'	11:B:478:G:C8	2.37	0.59
11:B:763:G:H4'	11:B:1507:A:H4'	1.84	0.59
11:B:1312:A:H4'	49:r:10:PHE:CD2	2.36	0.59
25:P:34:LYS:NZ	25:P:36:GLY:O	2.35	0.59
1:1:25:LEU:HD13	1:1:31:VAL:HG12	1.84	0.59
11:B:740:G:H2'	11:B:741:A:C8	2.37	0.59
17:H:69:ARG:HH12	17:H:73:ASN:HD22	1.51	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:B:128:G:H1'	11:B:319:A:C5	2.37	0.59
11:B:495:C:H2'	11:B:496:A:C8	2.36	0.59
11:B:940:A:H2'	11:B:941:G:H8	1.65	0.59
13:D:78:VAL:O	13:D:79:GLU:HG3	2.02	0.59
11:B:884:G:O2'	11:B:900:A:N6	2.36	0.59
10:A:844:G:H2'	10:A:845:G:C8	2.37	0.59
10:A:2320:A:OP2	24:O:13:ARG:NH1	2.36	0.59
11:B:221:G:O2'	46:o:63:GLN:OE1	2.20	0.59
42:k:57:LEU:HD21	42:k:82:ILE:HG12	1.85	0.59
10:A:2304:G:N7	10:A:2305:C:N4	2.50	0.58
11:B:532:A:H2'	11:B:533:A:H8	1.67	0.58
10:A:982:G:OP2	26:Q:51:ARG:NH2	2.35	0.58
11:B:171:G:OP1	50:s:60:ARG:NH2	2.37	0.58
18:I:84:GLY:H	18:I:89:LEU:HA	1.69	0.58
38:g:108:LYS:HD2	38:g:121:VAL:HG21	1.84	0.58
33:b:24:ALA:HB1	33:b:28:ASN:OD1	2.03	0.58
42:k:86:ARG:HB3	42:k:94:ARG:HA	1.85	0.58
10:A:1313:A:OP2	54:A:3105:HOH:O	2.16	0.58
10:A:2050:C:H2'	10:A:2051:C:C6	2.38	0.58
10:A:2533:A:H2'	10:A:2534:U:C6	2.38	0.58
43:l:62:LYS:HE2	43:l:62:LYS:N	2.17	0.58
11:B:151:C:H2'	11:B:152:G:H8	1.69	0.58
11:B:216:U:H2'	11:B:217:A:H8	1.68	0.58
11:B:709:A:H2'	11:B:710:A:C8	2.39	0.58
11:B:1205:U:H4'	11:B:1206:U:O5'	2.02	0.58
11:B:1354:A:OP2	44:m:75:ARG:NH2	2.31	0.58
34:c:69:GLU:O	34:c:73:ARG:N	2.21	0.58
35:d:82:LEU:HG	35:d:148:MET:HE2	1.85	0.58
17:H:22:GLN:OE1	17:H:55:ARG:NH2	2.36	0.58
17:H:56:ASN:O	17:H:61:THR:OG1	2.21	0.58
21:L:70:LYS:O	21:L:107:ARG:NH2	2.31	0.58
36:e:45:ARG:NH1	36:e:45:ARG:HB2	2.19	0.58
39:h:114:LYS:NZ	39:h:115:LYS:O	2.37	0.58
41:j:32:VAL:HG21	41:j:67:ALA:HA	1.85	0.58
10:A:632:A:N1	10:A:2355:A:O2'	2.30	0.58
11:B:478:G:H4'	11:B:479:U:H2'	1.85	0.58
16:G:101:ASP:OD1	16:G:102:ARG:N	2.36	0.58
16:G:163:ASP:OD1	16:G:163:ASP:N	2.36	0.58
33:b:36:ASP:OD1	33:b:59:ARG:NH2	2.22	0.58
37:f:9:LYS:HA	37:f:9:LYS:HE3	1.85	0.58
37:f:139:GLU:O	37:f:143:ARG:N	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:i:97:GLU:N	40:i:97:GLU:OE1	2.37	0.58
47:p:23:THR:OG1	47:p:49:ALA:O	2.20	0.58
10:A:2492:U:H3	10:A:2569:G:H1	1.49	0.58
11:B:1441:A:OP1	11:B:1442:C:N4	2.21	0.58
31:V:127:ILE:HD13	31:V:187:ILE:HD11	1.84	0.58
42:k:59:ASN:OD1	42:k:59:ASN:N	2.30	0.58
11:B:934:C:OP1	37:f:102:ARG:NH1	2.37	0.58
11:B:1336:C:H2'	11:B:1337:G:C8	2.38	0.58
44:m:64:CYS:HB2	44:m:80:SER:HB3	1.86	0.58
11:B:786:A:O2'	11:B:788:A:N7	2.36	0.58
11:B:1216:G:OP1	11:B:1315:U:O2'	2.14	0.58
11:B:1406:C:H2'	11:B:1407:A:C8	2.39	0.58
23:N:24:MET:HE1	23:N:40:LYS:HD3	1.86	0.58
35:d:48:GLY:HA2	35:d:142:PHE:HZ	1.69	0.58
37:f:116:MET:N	37:f:116:MET:SD	2.77	0.58
44:m:30:ILE:O	44:m:36:SER:OG	2.20	0.58
49:r:63:ASN:N	49:r:66:MET:SD	2.71	0.58
11:B:453:U:H2'	11:B:454:A:C8	2.39	0.57
18:I:97:ASP:OD1	18:I:97:ASP:N	2.36	0.57
40:i:93:ALA:HB1	40:i:96:VAL:HB	1.85	0.57
22:M:21:ALA:HB2	22:M:98:GLN:HB2	1.86	0.57
11:B:123:A:H1'	11:B:124:A:C8	2.39	0.57
11:B:331:G:H2'	11:B:332:A:C8	2.39	0.57
11:B:357:A:N6	42:k:27:CYS:SG	2.76	0.57
11:B:1181:G:N3	44:m:100:SER:OG	2.33	0.57
39:h:87:LEU:HA	39:h:90:TYR:HB3	1.87	0.57
44:m:3:LYS:HZ2	44:m:5:SER:H	1.52	0.57
1:1:18:SER:HB3	10:A:2257:G:OP1	2.05	0.57
11:B:683:C:OP1	41:j:29:ASN:ND2	2.34	0.57
29:T:53:LYS:H	29:T:90:GLN:HE21	1.53	0.57
41:j:23:ILE:HG23	41:j:32:VAL:HG12	1.87	0.57
44:m:49:GLN:NE2	44:m:50:LYS:HG3	2.18	0.57
9:9:31:PRO:HB2	10:A:2513:C:H5''	1.87	0.57
11:B:34:C:H2'	11:B:35:G:C8	2.37	0.57
12:C:2:G:H2'	12:C:3:C:H6	1.69	0.57
13:D:133:ARG:HB3	13:D:186:ALA:HB1	1.86	0.57
39:h:46:MET:O	39:h:50:GLN:N	2.33	0.57
10:A:1525:A:H1'	10:A:1526:G:H21	1.70	0.57
11:B:430:C:H2'	11:B:431:U:C6	2.39	0.57
7:7:9:THR:OG1	10:A:124:G:N2	2.37	0.57
10:A:935:C:OP2	54:A:3106:HOH:O	2.18	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:2208:A:H4'	13:D:185:LEU:HD11	1.86	0.57
49:r:9:PRO:HB2	49:r:39:MET:HG2	1.86	0.57
10:A:646:U:H2'	10:A:647:C:C6	2.40	0.57
10:A:692:U:H2'	10:A:693:G:O4'	2.04	0.57
36:e:17:GLN:OE1	36:e:17:GLN:N	2.37	0.57
11:B:987:G:N7	11:B:1207:A:N6	2.52	0.57
16:G:8:TYR:HA	16:G:12:ILE:HB	1.86	0.57
19:J:60:GLU:H	19:J:60:GLU:CD	2.13	0.57
34:c:59:GLN:HB3	34:c:63:ARG:HE	1.70	0.57
43:l:85:CYS:HB3	49:r:74:PHE:CE1	2.39	0.57
10:A:1782:U:H2'	10:A:1783:C:H6	1.68	0.56
11:B:370:G:H4'	46:o:5:ARG:HD2	1.86	0.56
11:B:934:C:P	37:f:102:ARG:HH12	2.27	0.56
41:j:50:SER:OG	41:j:69:ARG:NH2	2.37	0.56
10:A:534:C:O2'	10:A:535:U:H2'	2.04	0.56
42:k:51:LYS:HD3	42:k:51:LYS:N	2.21	0.56
10:A:243:A:H5''	21:L:67:VAL:HG11	1.87	0.56
10:A:2313:A:H2'	10:A:2314:A:C8	2.39	0.56
11:B:171:G:H5'	50:s:60:ARG:HH12	1.70	0.56
11:B:1323:G:OP1	43:l:29:THR:N	2.33	0.56
19:J:63:ARG:HH21	19:J:65:THR:HG22	1.69	0.56
22:M:28:SER:O	22:M:30:GLY:N	2.39	0.56
36:e:1:MET:N	36:e:66:CYS:O	2.30	0.56
10:A:1418:G:H2'	10:A:1419:A:C8	2.40	0.56
11:B:230:A:H5''	47:p:47:LEU:HD11	1.87	0.56
11:B:741:A:H2'	11:B:742:U:C6	2.41	0.56
11:B:1349:G:H2'	11:B:1350:A:C8	2.40	0.56
12:C:15:A:OP2	12:C:69:G:N2	2.37	0.56
32:a:26:LYS:HZ3	32:a:26:LYS:HB2	1.70	0.56
43:l:103:LYS:HG3	43:l:104:THR:HG23	1.86	0.56
10:A:44:G:H5'	10:A:45:G:H5'	1.86	0.56
10:A:99:U:O4	30:U:5:ARG:NH2	2.36	0.56
10:A:898:A:H2'	10:A:899:A:C8	2.40	0.56
10:A:1794:A:H3'	10:A:1795:A:C8	2.41	0.56
10:A:2088:G:N1	10:A:2173:C:O2	2.38	0.56
37:f:150:ALA:HB1	41:j:59:THR:HG21	1.88	0.56
10:A:196:A:N6	10:A:2416:A:O2'	2.39	0.56
10:A:802:U:H2'	10:A:803:C:C6	2.41	0.56
11:B:1232:A:H5'	11:B:1330:C:H41	1.69	0.56
11:B:1336:C:H2'	11:B:1337:G:H8	1.71	0.56
17:H:16:GLU:N	17:H:16:GLU:OE1	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:570:C:H2'	10:A:571:A:C8	2.41	0.56
10:A:1017:A:H2'	10:A:1018:A:C8	2.41	0.56
10:A:1185:U:H2'	10:A:1186:C:C6	2.40	0.56
10:A:2277:U:OP1	10:A:2366:U:O2'	2.24	0.56
11:B:17:U:H2'	11:B:18:C:C6	2.40	0.56
11:B:187:A:H2'	11:B:188:G:H8	1.71	0.56
11:B:1082:G:H21	11:B:1161:A:H62	1.52	0.56
11:B:1350:A:H2'	11:B:1351:A:H8	1.71	0.56
18:I:53:GLU:HA	18:I:56:LYS:HE3	1.88	0.56
10:A:246:G:H4'	10:A:376:G:C5	2.41	0.56
11:B:124:A:O2'	11:B:125:U:O4'	2.23	0.56
11:B:423:U:H5'	34:c:32:CYS:SG	2.45	0.56
11:B:480:U:H2'	11:B:481:A:H8	1.71	0.56
43:l:101:ARG:HG3	43:l:103:LYS:H	1.71	0.56
11:B:1181:G:H5''	39:h:115:LYS:NZ	2.21	0.56
32:a:70:VAL:HG21	32:a:96:TRP:HE3	1.70	0.56
10:A:543:U:H2'	10:A:544:G:O4'	2.06	0.56
11:B:1090:C:H2'	11:B:1091:C:H6	1.71	0.56
11:B:1524:G:H2'	11:B:1525:A:H8	1.71	0.56
10:A:2684:U:H2'	10:A:2685:C:C6	2.40	0.55
16:G:47:LYS:HZ1	16:G:83:TRP:CD1	2.23	0.55
18:I:69:ALA:O	18:I:73:SER:OG	2.22	0.55
33:b:20:SER:OG	33:b:40:ARG:NH2	2.30	0.55
10:A:1419:A:O2'	10:A:1420:A:H5'	2.06	0.55
11:B:370:G:OP1	46:o:68:SER:OG	2.24	0.55
11:B:1185:A:P	33:b:3:GLN:HE21	2.30	0.55
36:e:10:VAL:HG11	36:e:18:VAL:HG12	1.87	0.55
10:A:1839:A:H2'	10:A:1840:A:C8	2.41	0.55
11:B:835:C:H6	11:B:837:U:H5'	1.70	0.55
9:9:16:ILE:HD13	9:9:25:VAL:HG22	1.87	0.55
10:A:412:A:H2'	10:A:413:A:C8	2.41	0.55
10:A:695:A:OP1	13:D:7:LYS:NZ	2.30	0.55
11:B:1320:U:H2'	11:B:1321:G:C8	2.42	0.55
16:G:59:LYS:HG3	16:G:140:GLU:HB3	1.89	0.55
16:G:135:GLN:HB2	16:G:150:ARG:O	2.07	0.55
22:M:58:VAL:O	31:V:191:ARG:NH2	2.30	0.55
32:a:117:LEU:HD21	32:a:140:ASP:OD1	2.06	0.55
35:d:78:ASN:HD22	35:d:78:ASN:C	2.07	0.55
37:f:78:ARG:NH2	37:f:79:ARG:O	2.33	0.55
10:A:4:A:H2'	10:A:5:A:C8	2.40	0.55
11:B:1444:G:H21	11:B:1447:A:H2	1.54	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:142:MET:HE2	33:b:149:ILE:HG22	1.88	0.55
51:t:20:LYS:O	51:t:24:GLU:HG2	2.07	0.55
6:6:21:LYS:NZ	6:6:47:GLU:OE1	2.36	0.55
10:A:553:C:OP2	27:R:79:ARG:NH1	2.39	0.55
20:K:2:ILE:HG13	20:K:8:LEU:HD21	1.89	0.55
10:A:404:C:H2'	10:A:405:A:C8	2.42	0.55
10:A:1740:A:C8	25:P:95:LYS:HE2	2.42	0.55
11:B:41:G:H2'	11:B:42:G:H8	1.72	0.55
33:b:90:ASP:OD2	33:b:90:ASP:N	2.37	0.55
39:h:21:LEU:HD11	39:h:83:ILE:HG23	1.88	0.55
2:2:32:ASN:HB2	10:A:387:U:H5''	1.89	0.55
11:B:915:U:O2	35:d:25:THR:OG1	2.25	0.55
29:T:56:ARG:HH11	29:T:58:THR:HG23	1.70	0.55
32:a:68:LEU:HB3	32:a:161:LEU:HD22	1.89	0.55
37:f:25:LYS:HG3	37:f:101:MET:HE1	1.89	0.55
44:m:36:SER:O	44:m:41:ARG:NH2	2.39	0.55
10:A:2057:A:H2'	10:A:2058:C:C6	2.41	0.55
11:B:1299:G:N2	11:B:1325:G:O2'	2.39	0.55
33:b:35:ALA:HB3	33:b:59:ARG:HH22	1.72	0.55
33:b:39:VAL:O	33:b:43:LEU:N	2.34	0.55
11:B:539:C:O2'	11:B:543:C:H5''	2.07	0.54
11:B:916:G:H2'	11:B:917:A:C8	2.42	0.54
11:B:1369:A:OP1	37:f:28:ASN:ND2	2.39	0.54
11:B:1426:G:H1'	11:B:1462:A:H62	1.72	0.54
33:b:107:ARG:HE	33:b:107:ARG:H	1.52	0.54
35:d:149:GLN:HE22	35:d:157:LYS:HD3	1.72	0.54
11:B:1370:U:H2'	11:B:1371:A:C8	2.43	0.54
11:B:532:A:H2'	11:B:533:A:C8	2.43	0.54
11:B:575:G:N1	11:B:753:A:OP2	2.31	0.54
11:B:581:G:OP1	38:g:84:ARG:NH2	2.40	0.54
31:V:123:ALA:HB1	31:V:156:LEU:HD22	1.88	0.54
32:a:200:ILE:O	32:a:200:ILE:HD12	2.07	0.54
10:A:77:U:H2'	10:A:78:C:C6	2.43	0.54
11:B:229:U:H2'	11:B:230:A:H8	1.72	0.54
11:B:971:A:O2'	11:B:973:C:OP2	2.20	0.54
11:B:1033:C:H2'	11:B:1034:A:C8	2.40	0.54
41:j:126:LYS:NZ	51:t:37:PHE:HB2	2.23	0.54
50:s:57:VAL:O	50:s:61:MET:HG2	2.07	0.54
11:B:274:C:N3	47:p:44:SER:OG	2.37	0.54
23:N:86:ARG:HD3	23:N:117:ASP:HB3	1.89	0.54
33:b:108:LYS:HB2	33:b:111:LEU:HB2	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:l:96:PRO:HA	43:l:109:ARG:NH1	2.21	0.54
11:B:538:G:OP1	34:c:59:GLN:NE2	2.40	0.54
11:B:1244:A:H2'	11:B:1245:A:C8	2.43	0.54
23:N:41:ALA:HB1	23:N:97:ILE:HD12	1.90	0.54
36:e:88:LEU:HD13	48:q:64:TYR:CD1	2.42	0.54
11:B:1065:C:H2'	11:B:1066:G:H8	1.72	0.54
11:B:1156:C:H2'	11:B:1157:G:H8	1.73	0.54
14:E:106:MET:HE1	14:E:176:GLU:HG3	1.89	0.54
10:A:1185:U:H2'	10:A:1186:C:H6	1.73	0.54
10:A:1788:A:H2'	10:A:1789:A:C8	2.42	0.54
11:B:1361:C:OP1	39:h:117:GLY:N	2.37	0.54
33:b:140:ASN:OD1	33:b:143:ARG:NH2	2.40	0.54
39:h:47:VAL:HG13	39:h:80:ARG:HD3	1.88	0.54
42:k:114:ARG:HH22	42:k:121:ARG:HB2	1.73	0.54
10:A:738:A:H4'	10:A:1257:G:N3	2.23	0.54
10:A:897:A:H2'	10:A:900:C:C5	2.43	0.54
10:A:1672:C:H2'	10:A:1673:A:C8	2.43	0.54
11:B:1375:U:H1'	37:f:78:ARG:NH2	2.23	0.54
29:T:53:LYS:HB2	29:T:90:GLN:HE22	1.72	0.54
32:a:114:LEU:HD13	32:a:144:LEU:HB3	1.90	0.54
49:r:66:MET:HE2	49:r:66:MET:O	2.08	0.54
10:A:989:A:H2'	10:A:990:A:C8	2.43	0.54
10:A:1067:C:O2'	10:A:1077:A:OP1	2.26	0.54
10:A:1785:G:O2'	13:D:180:GLU:OE2	2.17	0.54
10:A:2016:A:C2	10:A:2485:C:H5''	2.43	0.54
11:B:1247:G:OP1	40:i:46:LYS:NZ	2.35	0.54
11:B:1310:G:N1	11:B:1313:A:OP2	2.40	0.54
37:f:53:ARG:HH22	37:f:125:LEU:HD13	1.72	0.54
43:l:101:ARG:O	43:l:102:THR:HG22	2.08	0.54
10:A:1407:G:O2'	10:A:1480:A:N6	2.41	0.53
20:K:63:VAL:HG12	20:K:106:LEU:HD11	1.90	0.53
1:l:66:VAL:HG23	1:l:83:VAL:HG23	1.90	0.53
10:A:143:U:H5'	29:T:3:GLN:NE2	2.23	0.53
10:A:569:U:H2'	10:A:570:C:C6	2.43	0.53
10:A:1017:A:N3	10:A:2472:C:O2'	2.37	0.53
11:B:331:G:H2'	11:B:332:A:H8	1.73	0.53
11:B:1308:C:H2'	11:B:1309:U:C6	2.44	0.53
11:B:1314:C:N4	49:r:36:ARG:HB2	2.23	0.53
11:B:1340:A:N1	11:B:1368:A:H5''	2.24	0.53
38:g:107:ASN:O	38:g:107:ASN:ND2	2.40	0.53
10:A:631:U:O2'	10:A:633:A:N7	2.32	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:852:G:H2'	10:A:853:C:C6	2.44	0.53
10:A:1468:G:H2'	10:A:1469:A:H8	1.72	0.53
10:A:1925:U:OP1	10:A:2590:U:O2'	2.25	0.53
10:A:2816:C:P	14:E:56:ARG:HH12	2.31	0.53
11:B:471:U:H2'	11:B:472:U:C6	2.44	0.53
11:B:1135:U:H2'	11:B:1136:G:H8	1.73	0.53
10:A:271:A:H2'	10:A:272:A:C8	2.43	0.53
10:A:1252:G:O2'	10:A:1998:G:O6	2.22	0.53
11:B:82:U:H5''	11:B:83:G:H5''	1.91	0.53
11:B:997:G:H21	11:B:999:A:H5'	1.73	0.53
11:B:1308:C:H2'	11:B:1309:U:H6	1.72	0.53
10:A:628:U:H2'	10:A:629:C:C6	2.43	0.53
10:A:718:G:C5	13:D:207:LYS:HB2	2.44	0.53
10:A:1455:A:H2'	10:A:1456:A:H8	1.73	0.53
10:A:2416:A:H2'	10:A:2416:A:N3	2.22	0.53
11:B:230:A:H2'	11:B:231:G:H8	1.73	0.53
11:B:1303:G:P	43:l:91:HIS:HE2	2.32	0.53
17:H:143:GLN:O	17:H:147:GLU:HG3	2.09	0.53
32:a:26:LYS:HE2	32:a:193:PRO:HD2	1.91	0.53
48:q:37:GLY:O	48:q:63:ARG:NH2	2.38	0.53
10:A:1780:A:H2'	10:A:1781:C:C6	2.43	0.53
11:B:722:A:H2'	11:B:723:A:C8	2.44	0.53
11:B:1163:A:H2'	11:B:1164:A:C8	2.44	0.53
15:F:2:GLN:NE2	15:F:12:GLU:OE1	2.41	0.53
16:G:135:GLN:NE2	16:G:141:ILE:HG12	2.23	0.53
39:h:50:GLN:NE2	39:h:103:TYR:OH	2.35	0.53
41:j:101:ASN:OD1	41:j:102:ALA:N	2.42	0.53
10:A:1286:A:H4'	10:A:1287:A:H5''	1.91	0.53
10:A:2232:G:H2'	10:A:2233:A:C8	2.44	0.53
10:A:2577:C:H2'	10:A:2578:G:C8	2.43	0.53
11:B:1321:G:H2'	11:B:1322:C:C6	2.44	0.53
19:J:13:ARG:NH2	19:J:49:ASP:O	2.41	0.53
10:A:149:U:H2'	10:A:150:C:C6	2.44	0.53
10:A:2317:G:O2'	10:A:2322:A:N1	2.41	0.53
11:B:1111:G:H21	11:B:1174:A:H1'	1.73	0.53
11:B:1304:C:P	43:l:87:ARG:HH22	2.31	0.53
11:B:1507:A:H2'	11:B:1508:G:H8	1.74	0.53
18:I:79:LEU:HB2	18:I:145:ILE:HD13	1.91	0.53
10:A:1302:U:H2'	10:A:1303:G:H8	1.73	0.53
10:A:1459:U:H2'	10:A:1460:G:O4'	2.09	0.53
10:A:1526:G:H2'	10:A:1527:A:O4'	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:B:989:C:N3	11:B:1040:A:O2'	2.36	0.53
11:B:1144:U:H4'	40:i:43:PRO:HG3	1.91	0.53
11:B:1216:G:OP2	11:B:1316:C:N4	2.40	0.53
11:B:1281:A:H2'	11:B:1282:A:C8	2.44	0.53
15:F:133:LEU:HD23	15:F:163:LEU:HD12	1.91	0.53
24:O:35:HIS:O	24:O:101:ARG:NH2	2.42	0.53
43:l:39:VAL:HG11	43:l:56:LEU:HD11	1.91	0.53
10:A:936:A:H2'	10:A:937:C:C6	2.43	0.53
27:R:74:ILE:C	27:R:75:ILE:HG13	2.34	0.53
28:S:82:LEU:HD23	28:S:84:ARG:NH2	2.23	0.53
10:A:649:C:H5''	15:F:93:GLN:HB3	1.91	0.52
10:A:1468:G:H2'	10:A:1469:A:C8	2.44	0.52
11:B:124:A:C4	47:p:68:ARG:NH2	2.76	0.52
11:B:165:A:H2'	11:B:166:A:C8	2.43	0.52
11:B:1404:A:H2'	11:B:1405:C:C6	2.44	0.52
11:B:1458:U:H2'	11:B:1459:A:H8	1.73	0.52
32:a:113:ARG:O	32:a:117:LEU:HB2	2.09	0.52
35:d:16:LEU:HD12	35:d:38:THR:HG22	1.91	0.52
49:r:11:ILE:HG22	49:r:39:MET:HE3	1.91	0.52
10:A:299:U:H2'	10:A:300:G:O4'	2.08	0.52
10:A:2429:C:OP1	15:F:62:LYS:HD3	2.09	0.52
11:B:34:C:O4'	42:k:29:GLN:NE2	2.41	0.52
11:B:1250:U:H5''	33:b:26:ARG:HH12	1.74	0.52
11:B:1390:A:H4'	11:B:1391:C:H5''	1.90	0.52
29:T:70:ALA:O	29:T:71:ARG:HG2	2.08	0.52
30:U:80:ASP:OD2	30:U:97:SER:OG	2.22	0.52
40:i:40:ILE:HB	40:i:73:VAL:HB	1.90	0.52
10:A:469:A:N3	10:A:471:G:H5''	2.24	0.52
21:L:91:SER:OG	21:L:92:LEU:N	2.42	0.52
10:A:519:A:OP2	19:J:116:ARG:NH2	2.29	0.52
10:A:1060:G:O2'	10:A:1078:A:OP2	2.26	0.52
35:d:88:SER:OG	35:d:140:ALA:O	2.23	0.52
37:f:111:ARG:NH1	37:f:113:GLU:OE2	2.43	0.52
39:h:5:GLN:OE1	39:h:22:ARG:NH1	2.42	0.52
11:B:619:U:H2'	11:B:620:G:H8	1.75	0.52
11:B:829:G:OP1	48:q:53:ARG:NH2	2.43	0.52
17:H:125:THR:O	17:H:125:THR:OG1	2.28	0.52
30:U:40:LEU:HD13	30:U:61:GLU:HG3	1.92	0.52
39:h:28:ILE:HG21	39:h:35:LEU:HB2	1.90	0.52
5:5:41:HIS:ND1	23:N:100:CYS:O	2.40	0.52
11:B:407:G:H22	11:B:423:U:P	2.32	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:b:87:LEU:O	33:b:91:LEU:HD22	2.09	0.52
11:B:912:A:H2'	11:B:913:A:C8	2.45	0.52
11:B:1089:U:OP1	11:B:1102:G:N2	2.28	0.52
11:B:1244:A:H2	11:B:1364:G:H1'	1.75	0.52
11:B:1320:U:H2'	11:B:1321:G:H8	1.73	0.52
17:H:133:ILE:HG22	17:H:141:VAL:HG13	1.92	0.52
20:K:2:ILE:HG23	20:K:6:SER:HB3	1.92	0.52
44:m:77:PHE:CD1	44:m:84:LEU:HD11	2.44	0.52
6:6:26:LYS:HE3	10:A:2272:G:OP1	2.10	0.52
10:A:1523:U:H5''	10:A:1525:A:N1	2.25	0.52
11:B:1020:G:N1	11:B:1029:A:N6	2.57	0.52
11:B:1220:C:O2'	43:l:102:THR:O	2.15	0.52
47:p:55:GLN:OE1	47:p:55:GLN:N	2.42	0.52
8:8:49:LEU:HD11	21:L:57:LEU:HD21	1.92	0.52
10:A:871:G:H3'	10:A:872:U:H5''	1.92	0.52
11:B:192:G:H2'	11:B:193:U:C6	2.45	0.52
11:B:990:A:H2'	11:B:991:U:C6	2.45	0.52
33:b:64:ALA:C	33:b:65:ARG:HE	2.17	0.52
39:h:83:ILE:O	39:h:87:LEU:HD12	2.09	0.52
44:m:16:THR:HG21	44:m:54:ASP:HB2	1.91	0.52
44:m:46:VAL:HG22	49:r:13:LEU:HD21	1.92	0.52
10:A:1415:G:H2'	10:A:1416:G:H8	1.75	0.52
11:B:229:U:H2'	11:B:230:A:C8	2.45	0.52
26:Q:72:ASN:O	26:Q:114:LYS:NZ	2.41	0.52
33:b:187:TYR:HD2	33:b:188:GLU:H	1.57	0.52
42:k:24:LEU:HD12	42:k:30:ARG:HG2	1.90	0.52
43:l:75:MET:O	43:l:79:ARG:N	2.24	0.52
44:m:47:ALA:HA	44:m:50:LYS:HZ1	1.75	0.52
10:A:2833:U:H2'	10:A:2834:G:O4'	2.09	0.51
11:B:2:A:H1'	11:B:607:C:O2'	2.11	0.51
11:B:1110:U:O2'	39:h:110:GLU:OE2	2.28	0.51
11:B:1118:G:H1'	11:B:1119:U:H5	1.75	0.51
11:B:1232:A:H2	11:B:1235:G:N3	2.08	0.51
30:U:33:LEU:HD23	30:U:66:VAL:HG23	1.92	0.51
36:e:5:GLU:OE2	48:q:23:TYR:OH	2.24	0.51
36:e:82:ASP:N	36:e:82:ASP:OD1	2.37	0.51
36:e:88:LEU:HD23	36:e:90:MET:HE1	1.92	0.51
43:l:47:ASP:OD2	43:l:47:ASP:N	2.42	0.51
1:1:70:GLU:HG2	1:1:79:TYR:HB2	1.91	0.51
10:A:1297:G:OP2	10:A:1297:G:N2	2.28	0.51
10:A:1372:C:H2'	10:A:1373:A:C8	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:1755:U:O2'	10:A:1944:C:OP1	2.27	0.51
11:B:969:A:H62	40:i:50:THR:HB	1.75	0.51
11:B:1510:G:N2	11:B:1513:A:OP2	2.42	0.51
16:G:153:ASP:OD1	16:G:153:ASP:N	2.41	0.51
32:a:173:ILE:HD12	32:a:196:VAL:HG12	1.92	0.51
37:f:116:MET:SD	37:f:119:ARG:NH2	2.83	0.51
43:l:96:PRO:HG2	43:l:102:THR:HB	1.92	0.51
10:A:1238:G:C2	26:Q:33:ARG:HB2	2.45	0.51
10:A:1780:A:H2'	10:A:1781:C:H6	1.76	0.51
11:B:124:A:O4'	47:p:68:ARG:NH1	2.40	0.51
11:B:549:U:H2'	11:B:550:C:C6	2.44	0.51
40:i:3:ASN:OD1	40:i:4:GLN:HG3	2.10	0.51
10:A:578:U:H2'	10:A:579:A:C8	2.44	0.51
10:A:1184:U:H2'	10:A:1185:U:C6	2.45	0.51
10:A:2190:G:H4'	13:D:150:LYS:HD3	1.93	0.51
10:A:2214:G:H2'	10:A:2215:U:C6	2.45	0.51
17:H:7:ASN:OD1	17:H:69:ARG:NH2	2.33	0.51
32:a:217:MET:HA	32:a:217:MET:HE2	1.91	0.51
34:c:146:ARG:HH21	34:c:148:LYS:HE2	1.74	0.51
46:o:69:GLU:OE2	46:o:69:GLU:N	2.34	0.51
2:2:18:ILE:HD12	10:A:370:G:H5'	1.92	0.51
10:A:1391:U:H2'	10:A:1392:U:C6	2.46	0.51
10:A:1579:A:H2'	10:A:1580:A:H8	1.74	0.51
10:A:1656:G:O2'	10:A:1977:U:O4	2.22	0.51
11:B:671:U:O2	11:B:771:A:O2'	2.27	0.51
11:B:1026:G:H2'	11:B:1027:G:O4'	2.10	0.51
32:a:42:ASN:O	32:a:46:THR:OG1	2.25	0.51
33:b:50:ALA:HA	33:b:72:ARG:HH12	1.76	0.51
36:e:10:VAL:HB	36:e:58:HIS:HB3	1.91	0.51
10:A:2219:U:H2'	10:A:2220:G:C8	2.46	0.51
11:B:121:G:O3'	47:p:9:ARG:NH2	2.44	0.51
11:B:1114:C:H2'	11:B:1115:U:H6	1.75	0.51
11:B:1281:A:N3	11:B:1347:G:O2'	2.38	0.51
32:a:161:LEU:HD12	32:a:163:VAL:HG22	1.92	0.51
35:d:47:VAL:HG23	35:d:118:VAL:HG12	1.92	0.51
37:f:93:PRO:HA	37:f:96:ARG:HG2	1.91	0.51
43:l:10:PRO:HD3	43:l:21:TYR:HD1	1.76	0.51
10:A:1009:A:N1	10:A:1130:U:H2'	2.25	0.51
10:A:1045:G:H21	10:A:1092:A:H62	1.59	0.51
11:B:672:U:H2'	11:B:673:U:C6	2.45	0.51
11:B:1141:C:H2'	11:B:1142:U:H6	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
41:j:72:GLN:HA	41:j:75:LEU:HD12	1.93	0.51
43:l:23:TYR:HB3	43:l:66:GLU:HA	1.93	0.51
48:q:32:TYR:CG	48:q:55:LEU:HD11	2.46	0.51
49:r:50:ALA:HB1	49:r:57:HIS:HB3	1.93	0.51
10:A:1552:U:H2'	10:A:1553:C:C6	2.45	0.51
10:A:2723:G:H2'	10:A:2724:A:C8	2.46	0.51
11:B:40:C:H2'	11:B:41:G:H8	1.75	0.51
11:B:702:A:H2'	11:B:703:G:H8	1.75	0.51
11:B:916:G:H4'	35:d:26:VAL:HA	1.93	0.51
11:B:1090:C:H2'	11:B:1091:C:C6	2.46	0.51
12:C:2:G:H2'	12:C:3:C:C6	2.44	0.51
18:I:15:LEU:HD21	18:I:54:LEU:HD11	1.93	0.51
34:c:88:GLU:O	34:c:92:GLN:HG3	2.11	0.51
34:c:99:ASP:OD1	34:c:100:ASN:N	2.42	0.51
50:s:35:VAL:O	50:s:39:ILE:HD12	2.11	0.51
10:A:743:G:H2'	10:A:744:U:C6	2.45	0.51
10:A:2613:G:N2	10:A:2763:G:OP2	2.39	0.51
11:B:28:A:O2'	11:B:290:U:OP1	2.24	0.51
11:B:940:A:O2'	11:B:1327:A:N3	2.40	0.51
11:B:1117:A:H4'	40:i:38:GLY:HA3	1.92	0.51
51:t:16:LEU:C	51:t:20:LYS:HZ2	2.19	0.51
10:A:1433:U:O2'	10:A:1533:A:N3	2.41	0.51
11:B:1363:C:H2'	11:B:1364:G:C8	2.46	0.51
13:D:132:LEU:HA	13:D:135:ILE:HD12	1.92	0.51
15:F:96:ASN:HB2	15:F:99:MET:HB2	1.93	0.51
17:H:30:LYS:NZ	17:H:81:GLN:O	2.41	0.51
10:A:68:C:O2	10:A:72:A:O2'	2.29	0.50
11:B:470:G:H2'	11:B:471:U:C6	2.46	0.50
11:B:1112:U:H2'	11:B:1113:C:C6	2.46	0.50
11:B:1431:A:H2'	11:B:1432:G:H8	1.76	0.50
16:G:80:ARG:HG2	16:G:80:ARG:NH1	2.25	0.50
20:K:122:LEU:HD13	25:P:71:VAL:HG11	1.93	0.50
36:e:22:VAL:O	36:e:26:THR:HG22	2.11	0.50
42:k:44:LYS:HB3	42:k:45:PRO:HD3	1.92	0.50
5:5:54:VAL:HG22	5:5:56:LYS:H	1.76	0.50
10:A:802:U:H2'	10:A:803:C:H6	1.76	0.50
10:A:1449:A:H2'	10:A:1450:A:C8	2.46	0.50
11:B:82:U:H5'	11:B:83:G:H21	1.76	0.50
11:B:653:C:H2'	11:B:654:G:H8	1.75	0.50
11:B:938:G:N1	11:B:1332:G:OP2	2.33	0.50
15:F:167:ASP:HB2	15:F:182:TYR:CZ	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:s:48:GLN:HA	50:s:51:PHE:HB3	1.93	0.50
10:A:796:U:O2'	10:A:2046:A:N1	2.44	0.50
11:B:102:G:N1	50:s:10:ARG:HG2	2.26	0.50
11:B:210:U:H2'	11:B:211:C:C6	2.46	0.50
11:B:1494:A:H5''	11:B:1502:G:H5''	1.93	0.50
33:b:157:LEU:H	33:b:157:LEU:HD12	1.77	0.50
39:h:86:ALA:O	39:h:90:TYR:N	2.40	0.50
8:8:44:ARG:NH1	10:A:2336:C:OP2	2.44	0.50
10:A:699:U:H2'	10:A:700:A:H8	1.77	0.50
10:A:1433:U:H2'	10:A:1434:U:C6	2.47	0.50
11:B:329:C:H2'	11:B:330:A:C8	2.45	0.50
11:B:595:G:H2'	11:B:596:A:H8	1.75	0.50
11:B:672:U:H2'	11:B:673:U:H6	1.76	0.50
18:I:7:GLU:HG2	18:I:8:LYS:N	2.25	0.50
28:S:109:ASP:OD1	28:S:109:ASP:N	2.41	0.50
36:e:45:ARG:HB3	36:e:59:TYR:CE2	2.47	0.50
38:g:87:LYS:HG3	38:g:91:GLN:HB3	1.93	0.50
10:A:159:A:N3	10:A:2194:C:O2'	2.44	0.50
10:A:821:U:H2'	10:A:822:A:C8	2.47	0.50
11:B:939:G:C2	11:B:940:A:C8	2.99	0.50
16:G:135:GLN:CD	16:G:136:ILE:H	2.20	0.50
30:U:5:ARG:HG2	30:U:5:ARG:NH1	2.23	0.50
46:o:49:ARG:HG2	46:o:49:ARG:HH11	1.75	0.50
3:3:26:PHE:CZ	29:T:49:LEU:HD13	2.47	0.50
10:A:271:A:H2'	10:A:272:A:H8	1.76	0.50
11:B:421:U:H5''	34:c:10:LYS:HE2	1.92	0.50
11:B:508:C:H2'	11:B:509:G:H8	1.76	0.50
11:B:695:U:OP1	11:B:696:A:O2'	2.20	0.50
11:B:751:U:H2'	11:B:752:G:O4'	2.12	0.50
11:B:1135:U:H2'	11:B:1136:G:C8	2.47	0.50
16:G:128:TYR:CE1	16:G:130:MET:HB3	2.47	0.50
32:a:26:LYS:NZ	32:a:26:LYS:HB2	2.27	0.50
32:a:111:ILE:HD12	32:a:152:LYS:HA	1.93	0.50
33:b:42:TYR:O	33:b:46:LYS:HG2	2.12	0.50
44:m:46:VAL:O	44:m:49:GLN:HG3	2.12	0.50
47:p:33:LYS:HB3	47:p:40:TYR:HE2	1.77	0.50
10:A:773:G:H5'	10:A:774:G:OP1	2.11	0.50
11:B:82:U:O2'	11:B:84:C:N4	2.41	0.50
11:B:1112:U:H2'	11:B:1113:C:H6	1.77	0.50
22:M:58:VAL:HG23	31:V:191:ARG:HH12	1.75	0.50
32:a:136:MET:O	32:a:141:LEU:HD22	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:h:83:ILE:H	39:h:83:ILE:HD12	1.76	0.50
50:s:17:ARG:HG2	50:s:21:ASN:HD21	1.77	0.50
10:A:2578:G:N7	54:A:3149:HOH:O	2.35	0.50
11:B:995:G:O6	11:B:1034:A:N6	2.45	0.50
11:B:1138:G:N2	11:B:1140:A:H62	2.10	0.50
31:V:138:CYS:HB3	31:V:171:VAL:HA	1.93	0.50
8:8:35:MET:HE2	8:8:40:LYS:CG	2.41	0.50
10:A:270:U:H2'	10:A:355:A:N6	2.26	0.50
10:A:583:U:H2'	10:A:584:C:C6	2.47	0.50
10:A:1347:G:H2'	10:A:1348:C:C6	2.46	0.50
11:B:91:A:H2'	11:B:92:U:O4'	2.12	0.50
11:B:840:G:H2'	11:B:841:A:H8	1.77	0.50
11:B:1303:G:OP1	43:l:91:HIS:NE2	2.36	0.50
21:L:19:PRO:HA	21:L:27:LEU:HB3	1.93	0.50
29:T:46:VAL:HG21	29:T:84:ILE:HD13	1.93	0.50
33:b:39:VAL:HG11	33:b:95:MET:SD	2.51	0.50
44:m:47:ALA:HA	44:m:50:LYS:NZ	2.27	0.50
44:m:72:GLY:HA3	44:m:81:ARG:HG2	1.94	0.50
10:A:154:U:H2'	10:A:155:A:C8	2.47	0.49
10:A:539:U:H2'	10:A:540:A:H8	1.77	0.49
10:A:1371:A:O2'	10:A:1382:U:O2	2.29	0.49
10:A:1671:G:H2'	10:A:1672:C:C6	2.47	0.49
11:B:41:G:H2'	11:B:42:G:C8	2.47	0.49
14:E:30:VAL:O	14:E:185:ASN:HB3	2.12	0.49
10:A:1539:U:OP1	10:A:1707:U:O2'	2.24	0.49
10:A:2264:A:OP1	22:M:10:ARG:NH2	2.46	0.49
10:A:2284:A:OP1	16:G:71:ARG:NH1	2.37	0.49
10:A:2301:G:H2'	10:A:2302:U:C6	2.46	0.49
10:A:2591:U:H2'	10:A:2592:C:C6	2.47	0.49
10:A:2686:A:H2'	10:A:2687:C:C6	2.46	0.49
11:B:384:U:O3'	46:o:28:ARG:NH2	2.34	0.49
11:B:731:A:H2'	11:B:732:C:H6	1.76	0.49
11:B:910:U:H2'	11:B:911:G:H8	1.77	0.49
11:B:941:G:C8	43:l:107:ARG:NH2	2.79	0.49
11:B:946:U:H2'	11:B:947:G:H8	1.75	0.49
11:B:1062:G:OP1	11:B:1381:G:O2'	2.31	0.49
11:B:1211:C:OP1	44:m:9:ARG:NE	2.40	0.49
35:d:55:ARG:HH11	35:d:55:ARG:HG3	1.77	0.49
49:r:40:ILE:HD12	49:r:69:HIS:HB2	1.94	0.49
7:7:10:LEU:HD12	10:A:759:G:H5''	1.93	0.49
7:7:19:ARG:NH1	10:A:124:G:OP2	2.41	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:731:C:H2'	10:A:732:C:C6	2.47	0.49
10:A:1035:A:H3'	10:A:1036:G:H5'	1.93	0.49
10:A:1424:U:H2'	10:A:1425:A:C8	2.48	0.49
10:A:1709:A:C5	10:A:1710:A:H1'	2.48	0.49
11:B:418:G:H2'	11:B:419:A:H8	1.76	0.49
11:B:898:U:H2'	11:B:899:U:C6	2.47	0.49
11:B:1131:C:O2	11:B:1132:G:N1	2.45	0.49
39:h:18:ARG:HB2	39:h:66:THR:HG22	1.93	0.49
43:l:3:ARG:HH21	43:l:8:ASN:HB2	1.76	0.49
10:A:839:U:H2'	10:A:840:C:C6	2.48	0.49
10:A:1255:A:H2'	10:A:1256:C:C6	2.47	0.49
10:A:1472:U:H2'	10:A:1473:C:C6	2.47	0.49
10:A:2277:U:H2'	10:A:2278:G:H8	1.78	0.49
10:A:2363:A:H2'	10:A:2364:A:C8	2.48	0.49
10:A:2573:A:OP1	54:A:3107:HOH:O	2.20	0.49
11:B:1165:A:H2'	11:B:1166:C:C6	2.48	0.49
32:a:142:GLU:O	32:a:146:ARG:HG3	2.13	0.49
10:A:626:A:N1	10:A:640:G:O2'	2.43	0.49
10:A:633:A:H2'	10:A:635:A:N7	2.27	0.49
10:A:1424:U:H2'	10:A:1425:A:H8	1.78	0.49
10:A:2299:C:H2'	10:A:2300:G:H8	1.77	0.49
11:B:431:U:H2'	11:B:432:U:O4'	2.12	0.49
11:B:546:U:H5'	42:k:83:ARG:NH1	2.27	0.49
11:B:1192:G:H2'	11:B:1193:U:C6	2.48	0.49
36:e:29:ILE:HD11	36:e:66:CYS:CB	2.41	0.49
38:g:112:THR:HG23	38:g:115:ALA:H	1.77	0.49
10:A:154:U:H2'	10:A:155:A:H8	1.78	0.49
10:A:401:G:OP2	10:A:2392:U:O2'	2.29	0.49
11:B:206:G:C2	11:B:207:A:C8	3.01	0.49
11:B:971:A:N6	11:B:1218:U:O4'	2.46	0.49
29:T:68:ARG:HA	29:T:73:LEU:HA	1.93	0.49
32:a:222:ILE:HA	32:a:225:LYS:HD2	1.94	0.49
37:f:20:SER:HB3	37:f:59:LEU:HD21	1.94	0.49
41:j:119:ASN:H	51:t:35:ARG:HH12	1.60	0.49
10:A:1017:A:N6	10:A:1114:G:H2'	2.26	0.49
10:A:2845:G:H2'	10:A:2846:A:C8	2.48	0.49
11:B:1097:C:C4'	32:a:97:LEU:HD21	2.42	0.49
11:B:1244:A:OP1	39:h:69:GLY:N	2.39	0.49
43:l:68:ASP:HA	43:l:71:ARG:HB3	1.93	0.49
10:A:1579:A:H2'	10:A:1580:A:C8	2.48	0.49
10:A:1677:U:O2'	10:A:1689:A:N7	2.39	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:B:317:U:H2'	11:B:318:G:O4'	2.13	0.49
19:J:106:LYS:HE2	19:J:119:TYR:CZ	2.48	0.49
35:d:79:GLY:O	35:d:80:THR:HG22	2.13	0.49
35:d:89:ALA:HB2	35:d:94:LYS:HG3	1.94	0.49
10:A:728:A:H1'	10:A:729:C:H5	1.78	0.49
10:A:1305:G:O2'	10:A:1306:C:H5'	2.13	0.49
11:B:690:A:H2'	11:B:691:U:H6	1.78	0.49
11:B:914:U:H2'	11:B:915:U:C6	2.48	0.49
11:B:1524:G:H2'	11:B:1525:A:C8	2.48	0.49
16:G:44:VAL:HG12	16:G:79:ILE:HG22	1.95	0.49
28:S:81:SER:HB3	28:S:97:VAL:HG13	1.95	0.49
30:U:86:VAL:HG22	30:U:91:LYS:HG3	1.95	0.49
37:f:18:TYR:HB3	37:f:59:LEU:HD22	1.95	0.49
5:5:4:GLN:HA	10:A:2601:U:C2	2.48	0.49
10:A:631:U:N3	10:A:634:U:OP2	2.37	0.49
10:A:1058:A:N6	10:A:1085:A:OP1	2.46	0.49
10:A:1795:A:H2'	10:A:1796:A:C8	2.47	0.49
11:B:507:U:H2'	11:B:508:C:C6	2.47	0.49
11:B:998:A:H2'	11:B:999:A:O4'	2.12	0.49
16:G:51:GLU:HA	16:G:54:VAL:HG23	1.95	0.49
17:H:69:ARG:NH1	17:H:73:ASN:HD22	2.10	0.49
32:a:100:MET:HA	32:a:107:ILE:HG13	1.94	0.49
10:A:1704:G:H2'	10:A:1705:G:H5''	1.95	0.48
10:A:2523:U:H2'	10:A:2524:C:C6	2.48	0.48
10:A:2831:U:H5''	25:P:53:ASN:O	2.13	0.48
11:B:2:A:H4'	34:c:83:LYS:NZ	2.28	0.48
11:B:1022:C:H2'	11:B:1023:U:O4'	2.12	0.48
23:N:79:LEU:O	23:N:84:GLY:N	2.46	0.48
32:a:186:VAL:HA	32:a:200:ILE:HD12	1.95	0.48
45:n:64:ARG:NH1	45:n:68:ASP:OD2	2.46	0.48
10:A:565:U:H2'	10:A:566:G:C8	2.48	0.48
10:A:1996:G:H5''	28:S:42:LYS:HB2	1.95	0.48
11:B:67:C:H2'	11:B:68:G:C8	2.48	0.48
11:B:352:U:H2'	11:B:353:G:C8	2.48	0.48
11:B:745:U:H2'	11:B:746:G:O4'	2.12	0.48
11:B:853:C:OP2	11:B:863:G:N1	2.38	0.48
11:B:1116:U:O4	11:B:1117:A:N6	2.46	0.48
14:E:183:GLU:H	14:E:183:GLU:CD	2.18	0.48
39:h:18:ARG:HH11	39:h:66:THR:HG21	1.78	0.48
43:l:58:ASN:O	43:l:62:LYS:HE3	2.13	0.48
10:A:243:A:H2'	10:A:244:G:O4'	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:718:G:C6	13:D:207:LYS:HB2	2.48	0.48
10:A:1183:G:H2'	10:A:1184:U:H6	1.77	0.48
11:B:469:U:H2'	11:B:470:G:C8	2.47	0.48
11:B:557:A:H2'	11:B:561:G:C8	2.48	0.48
11:B:1313:A:C8	11:B:1317:G:C6	3.00	0.48
19:J:17:VAL:HG13	19:J:139:GLU:HA	1.94	0.48
19:J:98:GLU:CD	19:J:98:GLU:H	2.18	0.48
28:S:47:MET:HE2	28:S:47:MET:HB2	1.76	0.48
36:e:103:LEU:HD23	36:e:103:LEU:H	1.78	0.48
40:i:67:ILE:C	40:i:68:ARG:HD2	2.37	0.48
45:n:85:LEU:HB3	45:n:87:LEU:HD23	1.94	0.48
10:A:172:A:H2'	10:A:173:A:C8	2.49	0.48
10:A:276:U:H2'	10:A:277:C:C6	2.48	0.48
10:A:473:A:H5''	30:U:46:LYS:HG2	1.94	0.48
10:A:1275:C:H2'	10:A:1276:A:C8	2.48	0.48
10:A:1842:U:H2'	10:A:1843:G:O4'	2.13	0.48
10:A:2508:U:O2'	10:A:2633:U:OP1	2.21	0.48
11:B:926:C:H2'	11:B:927:G:C8	2.49	0.48
11:B:973:C:H41	11:B:1354:A:H62	1.61	0.48
13:D:79:GLU:H	13:D:113:GLY:H	1.59	0.48
30:U:87:GLU:N	30:U:90:LYS:O	2.42	0.48
32:a:203:ASN:O	32:a:213:TYR:OH	2.18	0.48
40:i:77:VAL:O	40:i:78:GLN:HG3	2.14	0.48
49:r:15:LEU:O	49:r:19:VAL:HG23	2.13	0.48
7:7:9:THR:HG23	10:A:1295:G:OP1	2.13	0.48
10:A:749:G:H2'	10:A:750:A:O4'	2.13	0.48
10:A:1394:U:H2'	10:A:1395:G:H8	1.77	0.48
11:B:255:U:OP2	50:s:74:ARG:NH1	2.42	0.48
11:B:1113:C:H2'	11:B:1114:C:H6	1.78	0.48
18:I:76:VAL:HG12	18:I:76:VAL:O	2.14	0.48
24:O:15:ALA:O	24:O:19:MET:HG2	2.12	0.48
39:h:84:THR:HG23	39:h:98:LEU:HD22	1.94	0.48
6:6:6:ARG:O	6:6:48:ALA:N	2.40	0.48
10:A:1520:C:H42	10:A:1527:A:N6	2.11	0.48
10:A:1776:C:H2'	10:A:1777:A:C5	2.49	0.48
10:A:2805:G:H2'	10:A:2807:A:N7	2.28	0.48
11:B:1137:G:H2'	11:B:1138:G:H8	1.76	0.48
11:B:1385:U:H2'	11:B:1386:G:C8	2.49	0.48
20:K:25:LEU:HD21	20:K:40:LYS:HG2	1.96	0.48
21:L:2:GLN:HB2	21:L:5:ASP:HB2	1.94	0.48
32:a:50:PHE:HA	32:a:200:ILE:HG21	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:f:130:GLY:HA2	37:f:135:VAL:HG21	1.94	0.48
51:t:17:ARG:N	51:t:20:LYS:HZ2	2.12	0.48
51:t:42:THR:HA	51:t:45:ARG:HE	1.79	0.48
10:A:1287:A:O2'	10:A:1288:A:H3'	2.14	0.48
10:A:2188:C:O2'	10:A:2190:G:OP1	2.26	0.48
10:A:2292:C:OP2	10:A:2293:G:O2'	2.25	0.48
10:A:2861:C:H4'	25:P:3:ASN:HB3	1.94	0.48
11:B:293:G:H2'	11:B:294:A:C8	2.49	0.48
11:B:376:A:H2'	11:B:377:A:C8	2.47	0.48
11:B:442:A:H3'	11:B:443:G:H8	1.79	0.48
11:B:443:G:H2'	11:B:444:G:C8	2.48	0.48
11:B:1367:G:H5'	37:f:36:LYS:HD2	1.95	0.48
11:B:1490:C:H2'	11:B:1491:G:O4'	2.14	0.48
17:H:86:LYS:HB3	17:H:165:ALA:HB2	1.95	0.48
19:J:69:THR:HG22	19:J:90:GLU:HB2	1.96	0.48
27:R:6:VAL:HG22	27:R:11:GLN:HG2	1.95	0.48
34:c:148:LYS:HD2	34:c:148:LYS:C	2.39	0.48
10:A:998:A:N3	10:A:1143:C:O2'	2.43	0.48
10:A:2790:C:H2'	10:A:2791:C:C6	2.48	0.48
11:B:485:A:H2'	11:B:486:C:C6	2.49	0.48
11:B:546:U:H2'	11:B:547:A:C8	2.47	0.48
11:B:731:A:H2'	11:B:732:C:C6	2.49	0.48
11:B:1244:A:C2	11:B:1364:G:H1'	2.49	0.48
11:B:1342:U:OP1	39:h:112:GLU:HG3	2.14	0.48
29:T:66:THR:HB	29:T:73:LEU:HD11	1.94	0.48
32:a:13:GLY:HA3	32:a:208:ARG:HH21	1.77	0.48
45:n:82:ILE:O	45:n:86:GLY:N	2.47	0.48
9:9:8:LYS:HB3	9:9:8:LYS:HE2	1.65	0.48
10:A:1276:A:H2'	10:A:1277:C:C6	2.49	0.48
10:A:1326:U:OP2	29:T:81:LYS:NZ	2.46	0.48
10:A:2632:C:H2'	10:A:2633:U:O4'	2.14	0.48
10:A:2790:C:H2'	10:A:2791:C:H6	1.79	0.48
11:B:393:G:H2'	11:B:394:C:C6	2.48	0.48
11:B:548:A:H2'	11:B:549:U:C6	2.48	0.48
11:B:845:U:H2'	11:B:846:A:C8	2.48	0.48
11:B:1301:U:H5''	43:l:109:ARG:NH2	2.28	0.48
14:E:13:THR:OG1	14:E:14:ARG:N	2.47	0.48
31:V:114:GLU:OE1	31:V:129:HIS:NE2	2.38	0.48
40:i:67:ILE:HD12	40:i:67:ILE:O	2.13	0.48
42:k:3:THR:HG22	42:k:5:ASN:H	1.78	0.48
43:l:71:ARG:HA	43:l:74:ASN:ND2	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:n:30:ALA:HA	45:n:85:LEU:HD11	1.96	0.48
49:r:55:ARG:HG2	49:r:56:GLN:HG2	1.96	0.48
10:A:206:A:H2'	10:A:207:C:O4'	2.13	0.48
10:A:1286:A:OP1	54:A:3108:HOH:O	2.20	0.48
10:A:1312:U:O2'	10:A:1996:G:O2'	2.31	0.48
10:A:1669:U:H2'	10:A:1670:G:O4'	2.14	0.48
11:B:1304:C:OP1	43:l:79:ARG:NH2	2.46	0.48
12:C:30:C:H2'	12:C:31:C:H5'	1.96	0.48
35:d:61:ILE:HD12	35:d:62:GLN:N	2.29	0.48
10:A:74:G:H22	10:A:110:A:H2	1.61	0.47
10:A:539:U:H2'	10:A:540:A:C8	2.49	0.47
10:A:912:A:H2'	10:A:913:G:C8	2.49	0.47
10:A:1472:U:H2'	10:A:1473:C:H6	1.78	0.47
10:A:1539:U:H2'	10:A:1540:U:C6	2.49	0.47
11:B:522:C:H41	42:k:46:ASN:HD21	1.62	0.47
11:B:1296:C:OP1	43:l:13:LYS:HE2	2.14	0.47
14:E:32:PRO:HB3	14:E:97:THR:HG22	1.96	0.47
40:i:6:ILE:HD13	40:i:79:PRO:HG3	1.96	0.47
43:l:89:LEU:O	43:l:92:ARG:HG3	2.13	0.47
44:m:86:GLU:OE2	44:m:90:ARG:NH1	2.47	0.47
50:s:32:ILE:O	50:s:36:VAL:HG23	2.13	0.47
10:A:623:G:H2'	10:A:624:C:C6	2.49	0.47
10:A:656:U:H2'	10:A:657:A:O4'	2.14	0.47
10:A:1302:U:H2'	10:A:1303:G:C8	2.48	0.47
10:A:1415:G:H2'	10:A:1416:G:C8	2.49	0.47
10:A:2733:G:O6	10:A:2741:C:H5''	2.14	0.47
11:B:151:C:H2'	11:B:152:G:C8	2.49	0.47
11:B:539:C:OP1	34:c:62:ARG:NH1	2.47	0.47
11:B:591:G:O2'	47:p:40:TYR:HE1	1.96	0.47
11:B:1118:G:N2	11:B:1119:U:O4	2.44	0.47
11:B:1348:U:H2'	11:B:1349:G:C8	2.50	0.47
13:D:78:VAL:HG13	13:D:92:ALA:HB1	1.97	0.47
16:G:57:LEU:O	16:G:61:THR:OG1	2.32	0.47
39:h:62:ASP:OD1	39:h:62:ASP:N	2.42	0.47
40:i:67:ILE:HG23	44:m:96:LEU:HD13	1.96	0.47
45:n:73:LYS:HD3	45:n:73:LYS:HA	1.69	0.47
47:p:32:VAL:HG12	47:p:43:ARG:HG3	1.95	0.47
50:s:45:GLU:CD	50:s:45:GLU:H	2.22	0.47
10:A:295:G:H2'	10:A:296:C:C6	2.49	0.47
11:B:346:C:O2	11:B:349:C:N4	2.47	0.47
11:B:670:A:H5''	41:j:115:PRO:HB3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:B:919:G:C2	11:B:921:G:C8	3.02	0.47
11:B:1035:G:H2'	11:B:1036:A:C8	2.49	0.47
11:B:1065:C:H2'	11:B:1066:G:C8	2.48	0.47
26:Q:68:GLY:O	26:Q:72:ASN:ND2	2.46	0.47
33:b:107:ARG:H	33:b:107:ARG:NE	2.12	0.47
37:f:67:ASP:O	37:f:138:ARG:NH1	2.48	0.47
39:h:4:THR:HG1	39:h:5:GLN:H	1.59	0.47
10:A:472:A:H1'	10:A:488:G:N2	2.30	0.47
10:A:1119:U:O2	10:A:2011:C:H5''	2.12	0.47
10:A:1932:U:H2'	10:A:1933:C:C6	2.49	0.47
10:A:2543:G:H2'	10:A:2544:C:C6	2.49	0.47
11:B:378:G:H2'	11:B:379:C:C6	2.49	0.47
11:B:556:U:H1'	42:k:12:ARG:HD2	1.96	0.47
11:B:1282:A:N1	11:B:1365:G:H1'	2.29	0.47
34:c:148:LYS:HE3	34:c:149:SER:HB2	1.95	0.47
42:k:65:SER:HB3	42:k:95:TYR:HB2	1.95	0.47
47:p:60:ASP:N	47:p:60:ASP:OD2	2.46	0.47
50:s:55:VAL:CG2	50:s:56:PRO:HD3	2.42	0.47
1:1:19:LYS:HD3	1:1:19:LYS:HA	1.69	0.47
6:6:22:ASN:OD1	6:6:24:ARG:NH2	2.47	0.47
8:8:4:MET:HB3	8:8:62:ARG:HG3	1.96	0.47
10:A:83:A:N1	10:A:98:U:O2'	2.39	0.47
10:A:628:U:H2'	10:A:629:C:H6	1.79	0.47
10:A:837:A:H2'	10:A:838:C:C6	2.49	0.47
11:B:641:U:H2'	11:B:642:G:H8	1.78	0.47
11:B:910:U:H2'	11:B:911:G:C8	2.50	0.47
11:B:1348:U:H2'	11:B:1349:G:H8	1.79	0.47
17:H:7:ASN:O	17:H:69:ARG:NE	2.42	0.47
35:d:55:ARG:HG3	35:d:55:ARG:NH1	2.30	0.47
10:A:207:C:H2'	10:A:208:C:C6	2.50	0.47
10:A:718:G:C8	13:D:207:LYS:HD2	2.50	0.47
10:A:1918:A:H2'	10:A:1919:G:O4'	2.15	0.47
11:B:1317:G:H2'	11:B:1318:A:C8	2.49	0.47
16:G:80:ARG:HB2	16:G:83:TRP:CZ3	2.50	0.47
31:V:154:VAL:HG13	31:V:158:GLN:HB3	1.97	0.47
32:a:167:ASP:OD1	32:a:191:SER:HA	2.14	0.47
33:b:10:ILE:HG23	33:b:11:ARG:HG3	1.97	0.47
35:d:57:VAL:O	35:d:61:ILE:HG13	2.14	0.47
41:j:88:GLY:O	41:j:93:ARG:NH2	2.48	0.47
9:9:37:GLN:HE21	10:A:1114:G:C5'	2.27	0.47
10:A:510:A:H2'	10:A:511:U:C6	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:544:G:HO2'	10:A:545:A:H8	1.62	0.47
10:A:828:U:H2'	10:A:829:C:C6	2.49	0.47
10:A:1167:G:H2'	10:A:1168:A:C8	2.49	0.47
10:A:2350:C:H2'	10:A:2351:G:O4'	2.15	0.47
10:A:2444:G:O2'	10:A:2446:U:O4	2.28	0.47
11:B:303:A:O2'	11:B:601:A:N1	2.45	0.47
11:B:991:U:H2'	11:B:992:G:H8	1.79	0.47
13:D:145:GLU:HG2	13:D:151:GLY:C	2.40	0.47
21:L:55:GLN:O	21:L:60:ARG:NH1	2.43	0.47
29:T:53:LYS:HE2	29:T:90:GLN:HE22	1.79	0.47
33:b:187:TYR:HD2	33:b:188:GLU:N	2.13	0.47
38:g:27:MET:HB3	38:g:27:MET:HE2	1.78	0.47
40:i:45:ARG:HH12	40:i:47:GLU:HB2	1.79	0.47
46:o:4:ILE:HG22	46:o:71:VAL:HG11	1.97	0.47
10:A:1672:C:H2'	10:A:1673:A:H8	1.80	0.47
10:A:1721:C:H2'	10:A:1722:G:O4'	2.14	0.47
10:A:1764:U:H2'	10:A:1770:A:N6	2.30	0.47
11:B:209:C:H2'	11:B:210:U:C6	2.50	0.47
11:B:354:G:H2'	11:B:355:G:C8	2.49	0.47
11:B:974:C:H2'	11:B:975:U:O4'	2.15	0.47
11:B:1185:A:OP2	33:b:3:GLN:NE2	2.47	0.47
26:Q:50:ARG:NH2	27:R:73:ARG:O	2.47	0.47
32:a:141:LEU:O	32:a:145:GLU:HG2	2.15	0.47
37:f:5:ARG:HD2	37:f:7:ALA:HA	1.96	0.47
49:r:12:ASP:HB3	49:r:14:HIS:CE1	2.50	0.47
10:A:466:G:H4'	10:A:492:A:N1	2.29	0.47
10:A:678:A:H2'	10:A:679:U:C6	2.50	0.47
10:A:687:C:O2'	10:A:723:A:N6	2.48	0.47
10:A:2500:U:H2'	10:A:2501:C:C6	2.50	0.47
10:A:2781:A:H2'	10:A:2782:C:C6	2.49	0.47
11:B:328:C:H2'	11:B:329:C:H6	1.80	0.47
11:B:1173:A:H4'	39:h:105:THR:HA	1.97	0.47
13:D:29:PRO:HG2	13:D:34:LEU:HD11	1.97	0.47
35:d:76:ASP:OD1	35:d:76:ASP:O	2.33	0.47
44:m:4:GLU:HA	44:m:7:LYS:HD2	1.97	0.47
10:A:1501:A:O2'	10:A:1545:C:O2'	2.32	0.47
10:A:1523:U:OP2	10:A:1525:A:N6	2.45	0.47
11:B:125:U:H2'	11:B:126:C:C6	2.49	0.47
11:B:379:C:H2'	11:B:380:C:C6	2.50	0.47
11:B:1255:A:N6	11:B:1268:G:H1'	2.30	0.47
11:B:1395:G:H2'	11:B:1396:C:O4'	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
31:V:57:GLU:OE1	31:V:57:GLU:HA	2.15	0.47
33:b:6:HIS:ND1	44:m:89:MET:HB3	2.29	0.47
34:c:72:PHE:HA	34:c:75:TYR:HB2	1.97	0.47
34:c:72:PHE:CE2	34:c:90:LEU:HD11	2.49	0.47
9:9:37:GLN:HE21	10:A:1114:G:H4'	1.80	0.46
10:A:51:A:H2'	10:A:52:A:C8	2.49	0.46
10:A:737:G:C8	28:S:89:ALA:HB1	2.50	0.46
10:A:1015:U:OP1	10:A:1123:A:O2'	2.21	0.46
10:A:1791:A:O2'	13:D:50:THR:HA	2.15	0.46
11:B:317:U:O3'	50:s:17:ARG:HD2	2.14	0.46
11:B:333:C:H2'	11:B:334:U:C6	2.50	0.46
12:C:30:C:OP1	24:O:4:LYS:NZ	2.39	0.46
13:D:142:HIS:HA	13:D:155:ALA:HB3	1.97	0.46
18:I:72:LEU:HD11	18:I:107:TYR:H	1.80	0.46
20:K:17:ARG:HH11	20:K:17:ARG:HG3	1.79	0.46
20:K:23:LYS:HB3	20:K:40:LYS:HB2	1.97	0.46
32:a:70:VAL:HG21	32:a:96:TRP:CE3	2.50	0.46
35:d:66:GLU:H	35:d:66:GLU:CD	2.22	0.46
39:h:31:ASN:HB2	39:h:38:PHE:CE1	2.49	0.46
43:l:114:LYS:O	43:l:114:LYS:HD2	2.14	0.46
50:s:51:PHE:CD2	50:s:83:ILE:HD12	2.50	0.46
10:A:77:U:H2'	10:A:78:C:H6	1.79	0.46
10:A:193:G:H2'	10:A:194:A:O4'	2.15	0.46
10:A:570:C:OP1	26:Q:33:ARG:HG2	2.15	0.46
11:B:17:U:H2'	11:B:18:C:H6	1.81	0.46
11:B:148:G:H2'	11:B:149:U:C6	2.50	0.46
11:B:1142:U:H2'	11:B:1143:C:O4'	2.15	0.46
11:B:1294:G:H1'	11:B:1297:C:N4	2.31	0.46
17:H:11:LEU:HD21	17:H:17:ILE:HD11	1.97	0.46
19:J:106:LYS:HE3	19:J:106:LYS:HB2	1.62	0.46
24:O:35:HIS:ND1	24:O:54:THR:OG1	2.48	0.46
31:V:151:MET:O	31:V:153:LYS:N	2.48	0.46
32:a:41:ILE:HG21	32:a:201:PRO:HB2	1.98	0.46
35:d:66:GLU:HA	35:d:69:ARG:HG2	1.96	0.46
5:5:4:GLN:HB3	10:A:2601:U:H1'	1.96	0.46
10:A:4:A:H2'	10:A:5:A:H8	1.79	0.46
10:A:569:U:O3'	26:Q:31:VAL:HG13	2.15	0.46
10:A:1314:A:H2'	10:A:1316:C:C4	2.50	0.46
11:B:469:U:H2'	11:B:470:G:H8	1.79	0.46
11:B:1336:C:H1'	39:h:126:GLN:HE22	1.81	0.46
16:G:140:GLU:OE2	16:G:140:GLU:N	2.44	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
19:J:67:ALA:O	19:J:71:ASP:HB2	2.15	0.46
19:J:123:LYS:HB3	19:J:125:TYR:CE2	2.50	0.46
31:V:131:ILE:HD13	31:V:182:LEU:HB3	1.97	0.46
40:i:12:ALA:HB3	40:i:18:ILE:HB	1.97	0.46
43:l:81:MET:C	43:l:81:MET:HE2	2.40	0.46
10:A:1069:C:H2'	10:A:1070:U:C6	2.51	0.46
10:A:1480:A:O2'	10:A:1481:A:OP1	2.32	0.46
10:A:2447:A:H2'	10:A:2448:C:C6	2.50	0.46
11:B:149:U:H2'	11:B:150:C:H6	1.80	0.46
11:B:494:G:H2'	11:B:495:C:C6	2.50	0.46
11:B:1404:A:H2'	11:B:1405:C:H6	1.79	0.46
11:B:1457:U:H2'	11:B:1458:U:C6	2.50	0.46
32:a:94:HIS:CD2	32:a:146:ARG:HB3	2.50	0.46
34:c:170:TRP:CD1	34:c:171:VAL:HG13	2.50	0.46
39:h:44:ALA:HA	39:h:47:VAL:HB	1.98	0.46
44:m:22:LYS:HD3	44:m:23:LYS:N	2.31	0.46
10:A:1914:A:H2'	10:A:1915:G:O4'	2.15	0.46
11:B:378:G:H2'	11:B:379:C:H6	1.81	0.46
11:B:842:U:OP1	32:a:37:LYS:NZ	2.41	0.46
11:B:930:C:C4	11:B:931:A:N7	2.84	0.46
19:J:49:ASP:OD2	19:J:121:LYS:NZ	2.41	0.46
23:N:55:ALA:HA	23:N:80:PHE:CE1	2.51	0.46
23:N:96:ARG:NH1	23:N:114:GLU:OE1	2.40	0.46
33:b:180:ALA:HB1	33:b:203:PHE:CE1	2.51	0.46
39:h:19:VAL:HG12	39:h:65:VAL:HG13	1.97	0.46
40:i:69:THR:HG22	40:i:71:LYS:HZ2	1.80	0.46
10:A:61:U:H5	10:A:92:A:N1	2.14	0.46
10:A:1236:G:C5'	26:Q:6:ARG:HD2	2.45	0.46
10:A:1394:U:H2'	10:A:1395:G:C8	2.51	0.46
10:A:1414:C:C5	10:A:1558:A:H5''	2.51	0.46
10:A:1483:U:H5''	10:A:1484:C:H5	1.81	0.46
10:A:2553:G:H2'	10:A:2554:U:C6	2.50	0.46
11:B:20:U:H2'	11:B:21:G:O4'	2.15	0.46
11:B:218:U:H2'	11:B:219:C:H6	1.81	0.46
11:B:480:U:H2'	11:B:481:A:C8	2.50	0.46
11:B:1006:A:H2'	11:B:1007:G:C8	2.50	0.46
11:B:1243:C:O3'	39:h:75:GLN:NE2	2.49	0.46
16:G:94:ASP:O	16:G:98:GLU:HG3	2.16	0.46
26:Q:9:ILE:HD12	26:Q:12:ARG:NH2	2.31	0.46
32:a:113:ARG:HD3	32:a:144:LEU:HD11	1.98	0.46
38:g:13:ARG:HD2	38:g:27:MET:HE2	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:i:53:ILE:HG22	44:m:85:ARG:HE	1.80	0.46
44:m:89:MET:HE1	44:m:98:LYS:HZ2	1.81	0.46
2:2:22:HIS:HB3	10:A:199:U:H4'	1.97	0.46
10:A:489:U:H2'	10:A:490:G:O4'	2.15	0.46
10:A:570:C:H2'	10:A:571:A:H8	1.81	0.46
10:A:712:C:H2'	10:A:713:U:O4'	2.15	0.46
10:A:897:A:H2'	10:A:900:C:H5	1.80	0.46
10:A:1165:G:H2'	10:A:1166:U:C6	2.51	0.46
11:B:367:A:O2'	11:B:445:A:N7	2.49	0.46
11:B:595:G:H2'	11:B:596:A:C8	2.49	0.46
11:B:751:U:OP1	11:B:816:U:O2'	2.31	0.46
11:B:894:A:H2'	11:B:895:A:C8	2.51	0.46
11:B:972:A:H61	11:B:1310:G:H1'	1.81	0.46
15:F:175:ASP:OD1	15:F:178:SER:OG	2.28	0.46
22:M:136:VAL:HB	31:V:60:PHE:CE2	2.50	0.46
25:P:89:ARG:HD2	25:P:113:GLU:HG3	1.97	0.46
32:a:15:HIS:HB3	32:a:43:LEU:HD21	1.97	0.46
33:b:134:MET:HE2	33:b:134:MET:HB2	1.70	0.46
37:f:114:LYS:HA	37:f:114:LYS:HD3	1.62	0.46
38:g:89:VAL:HG11	38:g:120:GLY:HA2	1.98	0.46
3:3:7:ARG:HH11	3:3:59:GLN:HE22	1.64	0.46
10:A:171:C:H2'	10:A:172:A:C8	2.51	0.46
10:A:450:A:H2'	10:A:451:C:O4'	2.15	0.46
10:A:1157:U:H2'	10:A:1158:C:C6	2.51	0.46
11:B:230:A:H2'	11:B:231:G:C8	2.50	0.46
11:B:508:C:H2'	11:B:509:G:C8	2.51	0.46
11:B:934:C:O5'	11:B:934:C:H6	1.98	0.46
11:B:975:U:H2'	11:B:976:U:C5	2.51	0.46
11:B:1172:G:N2	11:B:1175:G:OP2	2.47	0.46
11:B:1173:A:H2'	11:B:1174:A:O4'	2.16	0.46
11:B:1301:U:H2'	11:B:1302:C:C6	2.50	0.46
14:E:20:GLY:HA2	25:P:80:PRO:HD2	1.98	0.46
32:a:99:GLY:HA2	32:a:175:GLU:OE1	2.16	0.46
34:c:81:ARG:HB3	34:c:81:ARG:CZ	2.45	0.46
34:c:146:ARG:NH2	34:c:148:LYS:HE2	2.31	0.46
35:d:62:GLN:OE1	35:d:62:GLN:HA	2.16	0.46
37:f:91:VAL:O	37:f:96:ARG:NH1	2.48	0.46
40:i:46:LYS:HB3	40:i:68:ARG:HE	1.80	0.46
44:m:49:GLN:HE22	44:m:50:LYS:HG3	1.80	0.46
10:A:315:A:OP2	15:F:162:ASN:HB2	2.16	0.46
10:A:661:C:OP2	21:L:42:SER:OG	2.32	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:1540:U:H2'	10:A:1541:G:O4'	2.16	0.46
11:B:433:U:O2'	34:c:131:ASN:ND2	2.45	0.46
11:B:483:C:H2'	11:B:484:A:H8	1.81	0.46
11:B:647:A:O4'	38:g:56:LYS:NZ	2.46	0.46
26:Q:74:LEU:HG	26:Q:114:LYS:HD2	1.98	0.46
33:b:43:LEU:HD21	33:b:68:ILE:HG12	1.98	0.46
37:f:150:ALA:HA	41:j:61:PHE:HB3	1.96	0.46
1:1:31:VAL:HG21	1:1:82:ILE:HG12	1.97	0.46
10:A:1653:A:H2	20:K:1:MET:HE1	1.81	0.46
11:B:33:A:H2'	11:B:34:C:C6	2.51	0.46
11:B:248:G:OP1	47:p:73:THR:OG1	2.26	0.46
11:B:789:C:O2'	41:j:128:ARG:O	2.29	0.46
11:B:862:C:H2'	11:B:863:G:O4'	2.16	0.46
31:V:109:LEU:HD22	31:V:132:SER:HA	1.98	0.46
37:f:49:LYS:HE2	37:f:49:LYS:HB2	1.69	0.46
40:i:68:ARG:HD2	40:i:68:ARG:N	2.31	0.46
10:A:1156:G:H2'	10:A:1157:U:C6	2.51	0.45
10:A:2298:U:H5'	16:G:85:ILE:HD11	1.98	0.45
11:B:154:A:H2'	11:B:155:A:O4'	2.15	0.45
11:B:628:C:H2'	11:B:629:A:H8	1.80	0.45
11:B:681:A:N7	11:B:695:U:N3	2.63	0.45
10:A:227:C:N4	10:A:2393:A:N3	2.63	0.45
10:A:297:U:H2'	10:A:298:C:C6	2.51	0.45
10:A:577:U:OP1	21:L:16:LYS:NZ	2.49	0.45
10:A:799:U:C4	21:L:29:LYS:O	2.69	0.45
10:A:846:G:N3	10:A:2254:A:H2'	2.31	0.45
10:A:976:C:H2'	10:A:977:A:O4'	2.16	0.45
10:A:2227:A:H2'	10:A:2228:G:C8	2.51	0.45
10:A:2232:G:H2'	10:A:2233:A:H8	1.80	0.45
10:A:2280:G:P	24:O:93:ARG:HH22	2.38	0.45
10:A:2673:U:H2'	10:A:2674:G:O4'	2.16	0.45
10:A:2726:A:H2'	10:A:2727:A:C8	2.52	0.45
11:B:93:U:O2'	11:B:94:C:H5''	2.15	0.45
11:B:333:C:H2'	11:B:334:U:H6	1.81	0.45
11:B:619:U:H2'	11:B:620:G:C8	2.51	0.45
11:B:1155:C:H2'	11:B:1156:C:C6	2.51	0.45
13:D:120:ILE:HG21	18:I:90:PHE:HA	1.97	0.45
14:E:5:VAL:HG22	14:E:101:PHE:HE2	1.82	0.45
18:I:142:LYS:HD3	18:I:143:LEU:N	2.31	0.45
22:M:4:PRO:C	22:M:6:ARG:H	2.24	0.45
23:N:106:ASP:OD1	23:N:106:ASP:N	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:e:102:MET:HA	36:e:102:MET:HE3	1.99	0.45
37:f:103:TRP:HH2	37:f:141:VAL:HG21	1.82	0.45
10:A:409:U:H2'	10:A:410:C:C6	2.51	0.45
10:A:836:C:H2'	10:A:837:A:H8	1.82	0.45
10:A:1857:A:H8	10:A:1858:A:C8	2.34	0.45
10:A:2259:A:H2'	10:A:2260:A:C8	2.52	0.45
10:A:2342:A:H2'	10:A:2343:G:O4'	2.16	0.45
10:A:2601:U:H2'	10:A:2602:C:H6	1.81	0.45
10:A:2676:U:O2'	10:A:2858:A:H1'	2.16	0.45
11:B:319:A:N1	46:o:25:ARG:NH2	2.60	0.45
35:d:145:LEU:O	35:d:148:MET:HB2	2.15	0.45
37:f:72:LEU:HA	37:f:96:ARG:HH21	1.81	0.45
39:h:25:THR:HG23	39:h:26:GLY:H	1.80	0.45
40:i:30:LYS:N	40:i:30:LYS:HD2	2.32	0.45
10:A:937:C:H1'	10:A:973:A:C8	2.52	0.45
10:A:1104:G:HO2'	10:A:1105:G:H5''	1.81	0.45
10:A:2024:G:H2'	10:A:2025:U:O4'	2.17	0.45
10:A:2299:C:H2'	10:A:2300:G:C8	2.51	0.45
10:A:2885:G:H2'	10:A:2886:A:C8	2.52	0.45
11:B:946:U:H2'	11:B:947:G:C8	2.51	0.45
11:B:1066:G:H21	32:a:106:THR:HG21	1.81	0.45
11:B:1157:G:H2'	11:B:1158:G:H8	1.81	0.45
13:D:266:ASN:ND2	13:D:267:MET:HE2	2.31	0.45
14:E:186:LEU:HD11	25:P:5:ILE:HG23	1.98	0.45
23:N:87:TYR:OH	23:N:115:LEU:HB3	2.17	0.45
31:V:119:GLY:HA2	31:V:123:ALA:HB3	1.98	0.45
33:b:62:GLN:OE1	33:b:97:VAL:HG23	2.15	0.45
39:h:33:ARG:HH21	39:h:38:PHE:HA	1.81	0.45
39:h:46:MET:N	39:h:46:MET:SD	2.89	0.45
40:i:65:TYR:HB3	44:m:96:LEU:HD11	1.98	0.45
2:2:3:ARG:NH1	10:A:1351:A:OP1	2.38	0.45
10:A:428:G:H2'	10:A:429:A:C8	2.51	0.45
10:A:2072:U:H2'	10:A:2073:U:C6	2.51	0.45
10:A:2816:C:OP1	14:E:56:ARG:NH1	2.49	0.45
11:B:972:A:C2	11:B:1313:A:C4	3.05	0.45
11:B:1288:A:H2'	11:B:1289:U:C6	2.51	0.45
17:H:87:LEU:HB2	17:H:131:ILE:HB	1.99	0.45
31:V:149:VAL:C	31:V:150:ASP:OD1	2.59	0.45
34:c:91:LEU:HD12	34:c:91:LEU:H	1.81	0.45
39:h:50:GLN:HE21	39:h:103:TYR:HH	1.60	0.45
39:h:87:LEU:HD12	39:h:87:LEU:H	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:m:13:ARG:O	44:m:17:VAL:HG22	2.17	0.45
47:p:15:VAL:HA	47:p:26:VAL:HA	1.97	0.45
10:A:1520:C:H42	10:A:1527:A:H61	1.64	0.45
10:A:2438:C:H2'	10:A:2439:A:C8	2.51	0.45
11:B:40:C:H2'	11:B:41:G:C8	2.52	0.45
11:B:379:C:H2'	11:B:380:C:H6	1.82	0.45
11:B:607:C:H2'	11:B:608:C:C6	2.52	0.45
11:B:1145:A:O2'	11:B:1146:A:H8	1.99	0.45
14:E:47:ARG:HE	14:E:47:ARG:HB2	1.63	0.45
17:H:42:GLU:HG2	17:H:55:ARG:HG2	1.99	0.45
17:H:132:LEU:HD12	17:H:132:LEU:HA	1.82	0.45
18:I:2:GLU:OE1	18:I:2:GLU:HA	2.14	0.45
31:V:72:LYS:HB2	31:V:72:LYS:HE2	1.74	0.45
36:e:26:THR:HA	36:e:29:ILE:HG22	1.98	0.45
37:f:70:ALA:HB1	37:f:96:ARG:HB2	1.99	0.45
10:A:381:A:H1'	10:A:401:G:O4'	2.17	0.45
10:A:1139:A:H2'	10:A:1140:C:C6	2.51	0.45
10:A:1430:A:H2'	10:A:1431:G:C8	2.52	0.45
10:A:1850:U:OP1	10:A:2396:G:O2'	2.29	0.45
10:A:2314:A:H2'	10:A:2315:A:H8	1.80	0.45
11:B:189:A:H2'	11:B:190:A:C8	2.51	0.45
28:S:23:GLN:O	28:S:27:LYS:HD2	2.16	0.45
37:f:49:LYS:HG3	37:f:53:ARG:HH11	1.82	0.45
39:h:41:ARG:HD3	39:h:41:ARG:HA	1.81	0.45
41:j:27:PHE:HE1	51:t:33:ARG:HH21	1.63	0.45
43:l:97:VAL:H	43:l:109:ARG:HH12	1.64	0.45
10:A:577:U:H2'	10:A:578:U:C6	2.52	0.45
10:A:621:A:H2'	10:A:622:A:C8	2.52	0.45
10:A:1038:C:C2	10:A:1039:A:C8	3.05	0.45
10:A:2623:U:H2'	10:A:2624:G:O4'	2.16	0.45
11:B:970:G:OP2	11:B:1352:U:O2'	2.34	0.45
11:B:979:C:H2'	11:B:980:U:C6	2.51	0.45
11:B:1137:G:H2'	11:B:1138:G:C8	2.52	0.45
11:B:1506:U:H2'	11:B:1507:A:C8	2.52	0.45
22:M:76:LYS:HB2	22:M:91:GLU:HG3	1.97	0.45
32:a:9:MET:HE2	32:a:9:MET:HA	1.98	0.45
33:b:126:ARG:HA	33:b:126:ARG:HH11	1.80	0.45
33:b:161:GLU:N	33:b:161:GLU:OE2	2.50	0.45
34:c:107:PHE:HA	34:c:155:ILE:HG13	1.99	0.45
40:i:35:GLN:CD	40:i:78:GLN:HE21	2.24	0.45
10:A:1620:G:H1'	10:A:1624:A:H61	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:2618:A:H2'	10:A:2619:G:C8	2.52	0.45
11:B:1068:G:O2'	11:B:1095:A:N1	2.41	0.45
11:B:1110:U:H2'	11:B:1111:G:C8	2.52	0.45
11:B:1213:A:H2'	11:B:1214:G:C8	2.52	0.45
11:B:1340:A:H5'	39:h:122:ARG:NH2	2.32	0.45
15:F:107:ILE:HG12	21:L:1:MET:HE1	1.99	0.45
27:R:61:ALA:HB2	27:R:98:ILE:HD13	1.99	0.45
31:V:9:GLN:HB2	31:V:44:THR:HG22	1.99	0.45
38:g:112:THR:OG1	38:g:113:ASP:N	2.50	0.45
43:l:86:TYR:O	43:l:90:ARG:HG2	2.17	0.45
10:A:207:C:H2'	10:A:208:C:H6	1.82	0.45
10:A:730:U:H2'	10:A:731:C:C6	2.52	0.45
10:A:1343:C:H2'	10:A:1344:G:O4'	2.16	0.45
11:B:407:G:H21	11:B:422:G:H1'	1.81	0.45
13:D:80:ARG:NH1	13:D:82:GLU:OE2	2.37	0.45
34:c:72:PHE:O	34:c:76:TYR:N	2.37	0.45
47:p:7:THR:OG1	47:p:8:VAL:N	2.50	0.45
50:s:17:ARG:O	50:s:21:ASN:ND2	2.33	0.45
50:s:61:MET:HA	50:s:64:LYS:HB2	1.99	0.45
10:A:783:G:H2'	10:A:784:C:C6	2.52	0.44
11:B:219:C:C2	11:B:220:A:C8	3.05	0.44
11:B:240:A:C2	11:B:276:A:C5	3.05	0.44
11:B:507:U:H2'	11:B:508:C:H6	1.82	0.44
11:B:1113:C:H2'	11:B:1114:C:C6	2.52	0.44
11:B:1403:C:H2'	11:B:1404:A:H8	1.82	0.44
12:C:48:U:P	24:O:31:ARG:HH22	2.40	0.44
13:D:42:GLY:O	13:D:49:ILE:O	2.35	0.44
25:P:6:ILE:O	25:P:10:GLU:HG3	2.17	0.44
27:R:21:LYS:HG2	27:R:93:PHE:CD1	2.51	0.44
34:c:60:LYS:HZ1	34:c:195:ILE:HA	1.81	0.44
43:l:33:ILE:HG23	43:l:59:GLU:HB3	2.00	0.44
51:t:13:ASP:OD1	51:t:17:ARG:NE	2.50	0.44
10:A:2:U:H2'	10:A:3:C:C6	2.51	0.44
10:A:230:A:H2'	10:A:231:G:O4'	2.17	0.44
10:A:598:A:H2'	10:A:599:C:O4'	2.17	0.44
10:A:2000:A:H2'	10:A:2001:A:C8	2.52	0.44
11:B:2:A:H8	11:B:2:A:OP2	2.00	0.44
11:B:131:U:H2'	11:B:132:G:H8	1.82	0.44
11:B:1213:A:H2'	11:B:1214:G:H8	1.82	0.44
12:C:3:C:H2'	12:C:4:U:H6	1.82	0.44
13:D:78:VAL:O	13:D:80:ARG:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:E:102:GLN:NE2	14:E:105:GLN:OE1	2.50	0.44
14:E:152:PRO:HG3	14:E:156:PHE:CZ	2.52	0.44
16:G:29:PRO:HB3	16:G:160:ALA:HB2	1.99	0.44
18:I:132:HIS:NE2	18:I:134:HIS:O	2.50	0.44
24:O:10:ARG:HA	24:O:13:ARG:HG3	1.98	0.44
33:b:11:ARG:NH2	33:b:177:THR:O	2.40	0.44
33:b:174:PRO:C	33:b:176:HIS:H	2.26	0.44
8:8:4:MET:HE3	8:8:62:ARG:HB3	1.99	0.44
10:A:1043:A:H2'	10:A:1044:G:C8	2.51	0.44
10:A:1527:A:OP2	10:A:1527:A:H8	2.01	0.44
10:A:1890:G:O2'	10:A:1914:A:N1	2.48	0.44
10:A:2300:G:H5'	16:G:35:THR:HG21	2.00	0.44
10:A:2577:C:H2'	10:A:2578:G:H8	1.79	0.44
11:B:398:G:H4'	11:B:433:U:C2	2.52	0.44
11:B:421:U:O2'	11:B:535:G:OP1	2.34	0.44
11:B:651:U:H2'	11:B:652:A:H8	1.81	0.44
11:B:1141:C:H2'	11:B:1142:U:C6	2.51	0.44
16:G:6:GLU:OE2	16:G:6:GLU:N	2.51	0.44
17:H:37:VAL:HG13	17:H:68:THR:HG21	1.99	0.44
31:V:173:LEU:HB2	31:V:176:LEU:HB2	1.99	0.44
33:b:10:ILE:HG13	33:b:178:LEU:HD11	1.99	0.44
40:i:12:ALA:HB2	40:i:96:VAL:HG22	1.98	0.44
40:i:65:TYR:HA	44:m:98:LYS:HA	1.99	0.44
10:A:171:C:H2'	10:A:172:A:H8	1.83	0.44
10:A:830:A:H2'	10:A:831:U:C6	2.53	0.44
10:A:1183:G:H2'	10:A:1184:U:C6	2.51	0.44
10:A:1593:C:O2'	10:A:1599:A:N1	2.43	0.44
10:A:1722:G:H2'	10:A:1723:U:C6	2.53	0.44
10:A:1828:G:H2'	10:A:1829:C:C6	2.53	0.44
10:A:1875:A:H2'	10:A:1876:A:C8	2.53	0.44
10:A:2835:U:H4'	10:A:2854:A:C2	2.53	0.44
11:B:175:A:O2'	11:B:177:G:N1	2.40	0.44
11:B:518:G:H2'	11:B:519:C:C6	2.53	0.44
11:B:995:G:C6	11:B:1034:A:C6	3.06	0.44
11:B:1524:G:N7	51:t:46:LYS:NZ	2.63	0.44
40:i:86:ALA:HA	40:i:89:LYS:HE3	2.00	0.44
51:t:4:VAL:HG11	51:t:19:PHE:HA	1.99	0.44
8:8:15:LYS:HG2	21:L:64:PHE:CZ	2.51	0.44
8:8:24:LYS:HG2	21:L:64:PHE:CG	2.53	0.44
10:A:150:C:H2'	10:A:151:U:C6	2.53	0.44
10:A:1887:A:H2'	10:A:1888:C:C6	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:2441:G:H2'	10:A:2442:C:C6	2.52	0.44
11:B:685:G:O6	41:j:57:LYS:NZ	2.39	0.44
11:B:902:A:H2'	11:B:903:A:H8	1.81	0.44
11:B:1032:U:H2'	11:B:1033:C:C6	2.53	0.44
11:B:1399:G:H2'	11:B:1400:U:H6	1.83	0.44
17:H:17:ILE:HG22	17:H:19:LEU:H	1.83	0.44
24:O:29:VAL:HG11	24:O:102:VAL:HG13	1.98	0.44
32:a:170:ARG:NH2	32:a:192:SER:HG	2.15	0.44
33:b:180:ALA:HB1	33:b:203:PHE:HE1	1.83	0.44
41:j:126:LYS:HZ2	51:t:37:PHE:HB2	1.81	0.44
47:p:65:ARG:HB2	47:p:67:THR:HG23	2.00	0.44
10:A:2179:G:H2'	10:A:2180:U:C6	2.52	0.44
11:B:442:A:H3'	11:B:443:G:C8	2.52	0.44
11:B:1089:U:P	11:B:1102:G:H1	2.41	0.44
14:E:121:THR:HB	14:E:127:PHE:CD2	2.52	0.44
20:K:40:LYS:HA	20:K:40:LYS:HD2	1.69	0.44
27:R:34:ASP:HB3	27:R:58:LYS:HD3	1.99	0.44
32:a:78:LYS:H	32:a:78:LYS:CE	2.24	0.44
34:c:71:GLN:O	34:c:75:TYR:N	2.42	0.44
50:s:27:MET:HE2	50:s:27:MET:HB2	1.83	0.44
50:s:31:TYR:O	50:s:35:VAL:HG23	2.17	0.44
10:A:142:C:O2'	29:T:3:GLN:NE2	2.51	0.44
10:A:568:G:O2'	10:A:2005:A:OP1	2.36	0.44
10:A:1471:A:H2'	10:A:1472:U:C6	2.52	0.44
11:B:1407:A:H2	11:B:1481:G:H22	1.64	0.44
13:D:44:ASN:N	13:D:48:ARG:O	2.49	0.44
19:J:93:ILE:HG12	19:J:100:VAL:HG21	1.99	0.44
20:K:18:ARG:HB2	20:K:45:GLU:HB2	1.99	0.44
33:b:112:ASP:HB3	33:b:115:LEU:HD23	2.00	0.44
40:i:3:ASN:HB3	40:i:6:ILE:HD11	1.99	0.44
41:j:101:ASN:OD1	41:j:101:ASN:C	2.61	0.44
47:p:45:THR:HG22	47:p:47:LEU:HD13	2.00	0.44
49:r:66:MET:HB2	49:r:74:PHE:CZ	2.52	0.44
10:A:725:C:H2'	10:A:726:C:C6	2.53	0.44
10:A:836:C:H2'	10:A:837:A:C8	2.53	0.44
10:A:1556:A:OP2	13:D:83:TYR:OH	2.22	0.44
10:A:2338:A:H2'	10:A:2339:G:O4'	2.18	0.44
10:A:2686:A:H2'	10:A:2687:C:H6	1.83	0.44
11:B:594:G:H2'	11:B:595:G:H8	1.81	0.44
11:B:815:G:H2'	11:B:816:U:C6	2.53	0.44
11:B:972:A:N6	11:B:1310:G:H1'	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
16:G:126:GLY:O	16:G:158:THR:OG1	2.28	0.44
21:L:81:GLU:HA	21:L:84:LYS:HE2	1.99	0.44
22:M:51:ARG:O	22:M:55:THR:OG1	2.31	0.44
34:c:59:GLN:HB3	34:c:63:ARG:NE	2.31	0.44
34:c:65:TYR:CG	34:c:94:LEU:HD12	2.53	0.44
35:d:40:VAL:O	35:d:48:GLY:N	2.49	0.44
35:d:138:VAL:O	35:d:142:PHE:HB2	2.18	0.44
35:d:143:LYS:HB2	35:d:143:LYS:HE2	1.68	0.44
37:f:126:ASP:OD2	37:f:131:LYS:HE2	2.17	0.44
40:i:66:GLU:HA	40:i:66:GLU:OE2	2.18	0.44
6:6:21:LYS:HE2	6:6:26:LYS:O	2.18	0.44
10:A:182:C:O2'	10:A:422:A:N3	2.41	0.44
10:A:469:A:H1'	10:A:470:A:H5''	1.99	0.44
10:A:732:C:O2'	10:A:1648:G:OP1	2.33	0.44
10:A:1398:U:H2'	10:A:1399:A:C8	2.53	0.44
10:A:1804:U:O2'	13:D:153:GLN:O	2.35	0.44
11:B:593:U:H2'	11:B:594:G:H8	1.83	0.44
11:B:1089:U:H2'	11:B:1090:C:C6	2.53	0.44
11:B:1111:G:H5'	39:h:110:GLU:OE1	2.18	0.44
11:B:1155:C:H2'	11:B:1156:C:H6	1.83	0.44
11:B:1324:U:C4	11:B:1325:G:C6	3.06	0.44
11:B:1374:U:O2	11:B:1376:C:N4	2.42	0.44
13:D:272:ARG:NE	13:D:272:ARG:HA	2.33	0.44
17:H:149:ARG:HA	17:H:162:VAL:HB	2.00	0.44
32:a:104:TYR:OH	32:a:155:GLY:O	2.29	0.44
37:f:137:LYS:HA	37:f:140:ASP:OD2	2.18	0.44
39:h:24:GLY:HA3	39:h:62:ASP:CG	2.42	0.44
39:h:48:VAL:HG12	39:h:79:ILE:HG13	2.00	0.44
42:k:77:HIS:ND1	42:k:77:HIS:N	2.66	0.44
43:l:49:SER:O	43:l:53:ILE:HG13	2.17	0.44
3:3:22:LEU:HD13	29:T:4:GLU:HB2	2.00	0.43
10:A:298:C:H2'	10:A:299:U:C6	2.53	0.43
10:A:478:G:O2'	28:S:49:LYS:HE3	2.19	0.43
10:A:866:A:H3'	10:A:867:G:C8	2.50	0.43
10:A:1928:C:OP2	10:A:1929:U:O2'	2.31	0.43
10:A:2291:U:H2'	10:A:2292:C:C6	2.53	0.43
11:B:553:A:H4'	11:B:554:A:H3'	2.00	0.43
11:B:916:G:H2'	11:B:917:A:H8	1.83	0.43
11:B:1226:U:H5''	39:h:126:GLN:O	2.18	0.43
11:B:1230:A:H4'	11:B:1298:G:H4'	2.00	0.43
33:b:95:MET:HE3	33:b:95:MET:HB3	1.74	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
39:h:28:ILE:HD12	39:h:28:ILE:HA	1.88	0.43
40:i:47:GLU:H	40:i:67:ILE:HD12	1.82	0.43
43:l:114:LYS:HD2	43:l:114:LYS:C	2.43	0.43
45:n:88:ARG:HA	45:n:88:ARG:HE	1.82	0.43
47:p:84:ARG:HG2	47:p:86:VAL:HG13	2.00	0.43
49:r:36:ARG:NH2	49:r:75:ALA:O	2.51	0.43
10:A:1399:A:H2'	10:A:1400:C:C6	2.53	0.43
10:A:1800:G:H4'	13:D:51:THR:HG21	2.00	0.43
11:B:149:U:H2'	11:B:150:C:C6	2.53	0.43
11:B:454:A:H2'	11:B:455:A:H8	1.82	0.43
11:B:513:C:H2'	11:B:514:A:O4'	2.18	0.43
11:B:531:G:H5''	42:k:110:ARG:HH21	1.83	0.43
11:B:548:A:H2'	11:B:549:U:H6	1.83	0.43
11:B:670:A:H2'	11:B:671:U:H6	1.83	0.43
11:B:712:A:H4'	51:t:35:ARG:HH22	1.83	0.43
11:B:1119:U:C2	11:B:1121:A:C8	3.07	0.43
11:B:1157:G:H2'	11:B:1158:G:C8	2.53	0.43
11:B:1408:U:H2'	11:B:1409:G:H8	1.82	0.43
32:a:74:ARG:O	32:a:78:LYS:NZ	2.50	0.43
37:f:99:LEU:O	37:f:102:ARG:HB3	2.18	0.43
10:A:1339:A:H2'	10:A:1340:A:C8	2.53	0.43
11:B:50:A:O2'	11:B:354:G:N2	2.51	0.43
11:B:124:A:C5	47:p:68:ARG:NH2	2.87	0.43
11:B:757:G:H2'	11:B:758:C:C6	2.52	0.43
11:B:1178:G:C2	11:B:1179:G:C8	3.06	0.43
22:M:79:LEU:HD23	22:M:79:LEU:HA	1.83	0.43
28:S:36:LEU:HD13	28:S:48:LYS:HA	1.99	0.43
33:b:22:TRP:HB3	33:b:59:ARG:HB2	1.99	0.43
33:b:94:GLN:OE1	33:b:94:GLN:HA	2.19	0.43
43:l:106:ALA:O	43:l:110:LYS:HG2	2.18	0.43
10:A:16:G:H2'	10:A:17:C:C6	2.53	0.43
10:A:343:A:H2'	10:A:344:U:C6	2.53	0.43
10:A:591:A:O2'	10:A:593:G:O2'	2.28	0.43
11:B:197:G:HO2'	11:B:198:G:H8	1.62	0.43
11:B:997:G:N2	11:B:999:A:H5'	2.32	0.43
16:G:50:ILE:HD12	16:G:50:ILE:HA	1.75	0.43
18:I:14:ASN:OD1	18:I:14:ASN:N	2.51	0.43
20:K:44:LYS:O	20:K:54:LYS:HD2	2.18	0.43
37:f:27:MET:HA	37:f:27:MET:CE	2.44	0.43
49:r:40:ILE:HD13	49:r:66:MET:CE	2.48	0.43
10:A:528:A:H2'	10:A:529:G:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:839:U:H2'	10:A:840:C:H6	1.84	0.43
10:A:990:A:H2'	10:A:991:G:O4'	2.18	0.43
10:A:1724:A:H2'	10:A:1725:A:O4'	2.19	0.43
10:A:1905:A:O2'	11:B:1511:G:N3	2.48	0.43
11:B:123:A:N1	11:B:226:G:O6	2.51	0.43
11:B:221:G:H2'	11:B:222:A:C8	2.53	0.43
11:B:1245:A:H2'	11:B:1246:A:C8	2.54	0.43
11:B:1313:A:C8	11:B:1317:G:C5	3.07	0.43
12:C:34:A:O2'	12:C:35:U:H5''	2.19	0.43
13:D:78:VAL:HG21	13:D:110:VAL:HG13	2.00	0.43
16:G:108:LEU:HD23	16:G:108:LEU:HA	1.84	0.43
16:G:160:ALA:HB1	16:G:165:GLU:HB2	2.01	0.43
21:L:36:LYS:HB2	54:L:204:HOH:O	2.18	0.43
22:M:30:GLY:O	22:M:134:ARG:HD2	2.19	0.43
32:a:70:VAL:HG12	32:a:162:PHE:O	2.18	0.43
35:d:74:GLN:OE1	35:d:74:GLN:HA	2.18	0.43
37:f:27:MET:HE3	37:f:43:VAL:CG1	2.48	0.43
10:A:249:G:H2'	10:A:250:A:C8	2.53	0.43
10:A:275:U:H3	10:A:351:A:H61	1.65	0.43
10:A:382:C:H2'	10:A:383:U:H6	1.83	0.43
10:A:1275:C:H2'	10:A:1276:A:H8	1.82	0.43
10:A:1578:U:H2'	10:A:1579:A:C8	2.54	0.43
11:B:208:C:C2	11:B:209:C:C5	3.07	0.43
11:B:418:G:H2'	11:B:419:A:C8	2.52	0.43
11:B:574:C:H2'	11:B:575:G:O4'	2.18	0.43
11:B:1077:U:O2'	11:B:1096:A:OP2	2.36	0.43
17:H:11:LEU:HD11	17:H:50:LEU:HD12	2.00	0.43
18:I:72:LEU:HB3	18:I:75:LEU:HD23	2.01	0.43
26:Q:15:LYS:HB3	26:Q:15:LYS:HE2	1.88	0.43
31:V:117:ALA:HA	31:V:152:ALA:O	2.19	0.43
37:f:108:ALA:HB2	37:f:123:GLU:HG3	1.99	0.43
42:k:114:ARG:HH22	42:k:121:ARG:CB	2.32	0.43
45:n:26:GLU:OE2	45:n:77:ARG:HG2	2.19	0.43
3:3:1:MET:HE3	3:3:5:GLU:HG3	2.00	0.43
9:9:37:GLN:HE21	10:A:1114:G:H5'	1.84	0.43
10:A:149:U:H2'	10:A:150:C:H6	1.83	0.43
10:A:504:A:N3	10:A:570:C:O2'	2.50	0.43
10:A:603:A:OP1	10:A:603:A:H2'	2.18	0.43
10:A:1869:U:H2'	10:A:1870:G:O4'	2.18	0.43
10:A:2025:U:H2'	10:A:2026:G:C8	2.54	0.43
10:A:2540:U:H2'	10:A:2541:U:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:B:35:G:H2'	11:B:36:C:C6	2.53	0.43
11:B:172:C:C2	11:B:173:A:C8	3.06	0.43
11:B:386:C:H5'	46:o:12:LYS:NZ	2.34	0.43
11:B:1064:U:H2'	11:B:1065:C:C6	2.54	0.43
11:B:1151:A:H4'	11:B:1152:C:O4'	2.18	0.43
11:B:1281:A:H2	11:B:1347:G:H1'	1.83	0.43
11:B:1393:C:O2	11:B:1496:A:N6	2.52	0.43
16:G:111:VAL:HG12	16:G:137:ILE:HG12	2.00	0.43
16:G:164:ASP:OD1	16:G:165:GLU:N	2.51	0.43
20:K:98:ILE:HD12	20:K:114:ILE:HG23	2.01	0.43
21:L:79:THR:HB	21:L:116:VAL:HG22	2.00	0.43
23:N:33:LEU:HD12	23:N:114:GLU:HB3	2.00	0.43
35:d:18:GLN:HE21	35:d:20:ASN:HB2	1.84	0.43
10:A:579:A:H2'	10:A:580:U:C6	2.54	0.43
10:A:668:C:H2'	10:A:669:G:H8	1.84	0.43
10:A:676:C:H2'	10:A:677:U:O4'	2.19	0.43
10:A:1645:C:H2'	10:A:1646:U:H6	1.84	0.43
10:A:2742:U:H1'	10:A:2743:A:H5''	2.00	0.43
11:B:57:G:H2'	11:B:58:C:C6	2.54	0.43
11:B:465:U:H2'	11:B:466:U:H6	1.84	0.43
11:B:509:G:H2'	11:B:510:U:H6	1.82	0.43
11:B:941:G:H2'	11:B:942:C:C6	2.54	0.43
11:B:995:G:H2'	11:B:996:A:H8	1.84	0.43
11:B:1175:G:H1'	11:B:1176:G:C4	2.54	0.43
25:P:90:ARG:NH2	25:P:114:LYS:HD2	2.34	0.43
29:T:49:LEU:C	29:T:51:SER:H	2.26	0.43
32:a:69:PHE:CZ	32:a:217:MET:HG3	2.53	0.43
33:b:88:ARG:NH2	33:b:99:VAL:O	2.44	0.43
34:c:95:GLU:O	34:c:100:ASN:ND2	2.52	0.43
35:d:46:ARG:NH2	35:d:72:MET:HE2	2.34	0.43
37:f:65:ALA:O	37:f:69:ILE:HG12	2.19	0.43
40:i:66:GLU:O	44:m:96:LEU:HD12	2.19	0.43
1:1:16:SER:OG	10:A:2248:U:OP2	2.31	0.43
4:4:11:SER:HB3	10:A:977:A:P	2.59	0.43
7:7:26:ASN:CG	10:A:671:G:H5'	2.44	0.43
10:A:100:U:H3'	10:A:101:G:H5'	1.99	0.43
10:A:575:A:N1	10:A:798:G:O2'	2.48	0.43
10:A:796:U:OP2	21:L:41:ARG:NH2	2.51	0.43
10:A:1430:A:H2'	10:A:1431:G:H8	1.83	0.43
10:A:1852:A:H2'	10:A:1853:G:O4'	2.19	0.43
10:A:2051:C:H1'	10:A:2435:U:C5	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:2359:A:H2'	10:A:2360:C:C6	2.54	0.43
11:B:376:A:H2'	11:B:377:A:H8	1.84	0.43
11:B:506:U:H2'	11:B:507:U:C6	2.53	0.43
11:B:577:A:H2'	11:B:578:G:O4'	2.19	0.43
11:B:668:G:N2	41:j:118:HIS:HB2	2.32	0.43
11:B:979:C:H2'	11:B:980:U:H6	1.82	0.43
11:B:1306:G:H2'	11:B:1307:U:C6	2.53	0.43
12:C:114:C:H2'	12:C:115:A:C8	2.54	0.43
13:D:140:THR:HG23	13:D:161:SER:HB2	2.00	0.43
28:S:3:VAL:HG21	28:S:58:ALA:HA	2.01	0.43
31:V:132:SER:OG	31:V:133:GLU:N	2.52	0.43
38:g:10:MET:HE2	38:g:10:MET:HB3	1.84	0.43
40:i:42:LEU:HB3	40:i:71:LYS:HB2	2.01	0.43
50:s:26:SER:O	50:s:30:THR:HG22	2.19	0.43
5:5:52:LYS:HG2	5:5:55:ASP:OD1	2.19	0.43
10:A:435:C:OP1	26:Q:2:ALA:HB3	2.19	0.43
10:A:483:G:O2'	28:S:7:LEU:HA	2.19	0.43
11:B:322:C:H4'	11:B:323:A:H5''	1.99	0.43
11:B:424:A:C2	11:B:425:A:H1'	2.54	0.43
11:B:742:U:H2'	11:B:743:A:C8	2.46	0.43
11:B:978:C:H2'	11:B:979:C:H6	1.83	0.43
11:B:1021:C:H2'	11:B:1022:C:C6	2.54	0.43
11:B:1114:C:H2'	11:B:1115:U:C6	2.53	0.43
11:B:1227:G:H2'	11:B:1228:C:C6	2.54	0.43
12:C:13:A:N1	12:C:69:G:O2'	2.49	0.43
25:P:52:ARG:O	25:P:58:SER:HA	2.19	0.43
32:a:27:MET:HE2	32:a:191:SER:O	2.19	0.43
32:a:31:ILE:HD13	32:a:31:ILE:HA	1.85	0.43
34:c:202:GLU:HG3	35:d:105:GLY:HA3	2.01	0.43
36:e:15:SER:HB3	36:e:44:ARG:HH21	1.84	0.43
39:h:30:ILE:HD13	39:h:65:VAL:HG12	2.01	0.43
39:h:50:GLN:N	39:h:51:PRO:HD2	2.34	0.43
39:h:113:ARG:HD2	44:m:101:TRP:CE2	2.54	0.43
44:m:54:ASP:CG	44:m:59:ARG:HH21	2.27	0.43
10:A:29:G:H2'	10:A:30:C:C6	2.54	0.42
10:A:292:A:N3	10:A:312:C:O2'	2.45	0.42
10:A:482:A:H2'	10:A:483:G:O4'	2.18	0.42
11:B:196:G:H21	11:B:460:A:H61	1.66	0.42
11:B:940:A:C2	11:B:941:G:C5	3.06	0.42
11:B:950:U:H2'	11:B:951:U:C6	2.54	0.42
16:G:135:GLN:OE1	16:G:135:GLN:HA	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:L:78:ARG:HG2	21:L:113:SER:HB3	2.01	0.42
24:O:27:LEU:HD23	24:O:91:PHE:HD1	1.84	0.42
49:r:63:ASN:O	49:r:67:VAL:HG23	2.19	0.42
1:l:56:ASP:HA	10:A:2372:U:H4'	2.01	0.42
6:6:13:THR:HG21	6:6:38:VAL:HB	2.00	0.42
10:A:737:G:O5'	28:S:89:ALA:HB2	2.20	0.42
11:B:356:G:N2	11:B:359:U:OP2	2.52	0.42
11:B:383:A:H3'	11:B:384:U:H6	1.83	0.42
11:B:1152:C:C4	11:B:1154:G:C8	3.07	0.42
11:B:1160:G:C6	11:B:1162:C:H5''	2.54	0.42
12:C:28:C:H2'	12:C:29:A:C8	2.54	0.42
12:C:49:C:H2'	12:C:50:A:C8	2.53	0.42
13:D:145:GLU:HB2	13:D:188:CYS:HB3	2.01	0.42
13:D:247:SER:HB2	13:D:248:PRO:HD2	2.01	0.42
23:N:8:ARG:HH11	23:N:43:GLU:HG2	1.84	0.42
33:b:95:MET:HG3	33:b:99:VAL:HG21	2.00	0.42
37:f:25:LYS:H	37:f:25:LYS:HG2	1.60	0.42
43:l:9:ILE:HG22	43:l:21:TYR:HB3	2.01	0.42
46:o:21:VAL:HG21	46:o:60:TRP:CD1	2.53	0.42
46:o:75:LEU:HD23	46:o:75:LEU:HA	1.82	0.42
50:s:61:MET:HB3	50:s:66:ILE:HG13	2.00	0.42
2:2:6:GLN:HG3	2:2:50:ARG:O	2.19	0.42
10:A:710:G:H2'	10:A:711:A:C8	2.55	0.42
11:B:464:C:H2'	11:B:465:U:H6	1.83	0.42
11:B:531:G:H5''	42:k:110:ARG:NH2	2.35	0.42
22:M:31:GLU:HG3	22:M:32:TYR:CE2	2.54	0.42
31:V:73:GLU:HG2	31:V:75:VAL:HG13	2.01	0.42
34:c:28:LEU:HD23	34:c:34:ALA:HB2	2.01	0.42
34:c:102:VAL:HG12	34:c:114:SER:HB2	2.01	0.42
37:f:62:PHE:CE2	37:f:66:LEU:HD23	2.54	0.42
37:f:70:ALA:HB2	37:f:100:ALA:HB2	2.01	0.42
39:h:83:ILE:O	39:h:86:ALA:N	2.51	0.42
40:i:30:LYS:C	40:i:32:THR:H	2.27	0.42
10:A:633:A:H2'	10:A:635:A:C8	2.54	0.42
10:A:1516:U:H2'	10:A:1517:C:C6	2.55	0.42
10:A:2050:C:H2'	10:A:2051:C:H6	1.82	0.42
10:A:2171:U:H3'	10:A:2172:G:H8	1.84	0.42
11:B:122:G:H5'	47:p:9:ARG:HH12	1.85	0.42
11:B:533:A:H2'	11:B:534:G:H8	1.81	0.42
11:B:1008:A:N3	11:B:1213:A:H1'	2.34	0.42
11:B:1116:U:H2'	11:B:1117:A:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:B:1309:U:H2'	11:B:1310:G:C8	2.54	0.42
11:B:1312:A:H5''	49:r:3:ARG:NH1	2.35	0.42
11:B:1369:A:P	37:f:28:ASN:HD21	2.43	0.42
12:C:3:C:H2'	12:C:4:U:C6	2.53	0.42
29:T:53:LYS:H	29:T:90:GLN:NE2	2.17	0.42
32:a:96:TRP:NE1	32:a:175:GLU:OE2	2.28	0.42
33:b:157:LEU:HD13	33:b:164:ARG:HG3	2.00	0.42
34:c:68:LEU:HD13	34:c:70:ARG:HH21	1.83	0.42
34:c:162:CYS:O	34:c:165:ARG:HG2	2.20	0.42
46:o:49:ARG:HG2	46:o:49:ARG:NH1	2.33	0.42
10:A:629:C:H2'	10:A:630:U:C6	2.55	0.42
10:A:743:G:H2'	10:A:744:U:H6	1.85	0.42
10:A:2455:A:N6	10:A:2467:G:O2'	2.44	0.42
11:B:218:U:H2'	11:B:219:C:C6	2.54	0.42
11:B:446:A:O2'	46:o:73:GLN:OE1	2.28	0.42
11:B:493:A:O3'	11:B:494:G:H8	2.02	0.42
11:B:702:A:H2'	11:B:703:G:C8	2.54	0.42
11:B:1105:A:C2	33:b:177:THR:HG23	2.54	0.42
11:B:1248:G:N2	11:B:1253:C:O2'	2.53	0.42
11:B:1323:G:C6	11:B:1324:U:C5	3.08	0.42
15:F:47:THR:O	15:F:51:VAL:HG23	2.19	0.42
34:c:11:LEU:HG	34:c:63:ARG:NH1	2.35	0.42
37:f:25:LYS:O	37:f:29:HIS:ND1	2.49	0.42
38:g:11:LEU:HD12	38:g:75:VAL:HG21	2.01	0.42
39:h:84:THR:HG21	39:h:103:TYR:HB3	2.01	0.42
41:j:60:PRO:HD3	41:j:91:PRO:HB2	2.02	0.42
44:m:79:LEU:HD23	44:m:79:LEU:HA	1.81	0.42
2:2:10:LYS:HE2	2:2:54:LYS:HD3	2.01	0.42
10:A:150:C:H2'	10:A:151:U:H6	1.84	0.42
10:A:183:C:H2'	10:A:184:A:C8	2.55	0.42
10:A:262:U:H2'	10:A:263:U:O4'	2.19	0.42
10:A:300:G:N2	10:A:302:A:H3'	2.34	0.42
10:A:556:U:H2'	10:A:557:U:O4'	2.19	0.42
10:A:859:U:H2'	10:A:860:U:C6	2.54	0.42
10:A:1185:U:H1'	26:Q:4:VAL:HG22	2.02	0.42
10:A:1234:G:OP1	15:F:43:LYS:NZ	2.52	0.42
10:A:1356:C:H2'	10:A:1357:G:O4'	2.19	0.42
10:A:2477:U:HO2'	10:A:2478:U:H5	1.67	0.42
11:B:328:C:H2'	11:B:329:C:C6	2.54	0.42
11:B:594:G:C6	11:B:633:A:C6	3.07	0.42
11:B:869:U:O2'	38:g:15:ARG:HD2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:B:995:G:H2'	11:B:996:A:C8	2.54	0.42
11:B:1080:U:H3	11:B:1093:G:H22	1.68	0.42
11:B:1086:A:H5''	37:f:4:ARG:CZ	2.50	0.42
11:B:1324:U:H2'	11:B:1325:G:O4'	2.20	0.42
16:G:107:SER:OG	16:G:137:ILE:HG22	2.19	0.42
18:I:5:LEU:HA	18:I:36:ALA:HA	2.02	0.42
27:R:71:LYS:HE3	27:R:71:LYS:HB2	1.80	0.42
28:S:108:ALA:HB1	28:S:110:LYS:HG2	2.00	0.42
34:c:85:SER:HB2	35:d:103:GLY:HA3	2.02	0.42
40:i:19:ASP:O	40:i:23:GLN:HG2	2.20	0.42
40:i:52:LEU:HD23	40:i:52:LEU:H	1.85	0.42
44:m:22:LYS:HD3	44:m:23:LYS:H	1.84	0.42
49:r:49:ILE:O	49:r:60:VAL:N	2.49	0.42
5:5:22:LEU:HG	28:S:19:LEU:HB3	2.00	0.42
6:6:3:GLU:HB2	6:6:23:LYS:HZ3	1.84	0.42
10:A:1043:A:H2'	10:A:1044:G:H8	1.84	0.42
10:A:2714:U:H2'	10:A:2715:U:C6	2.55	0.42
10:A:2873:C:H2'	10:A:2874:C:C6	2.55	0.42
11:B:1034:A:C2	11:B:1035:G:C5	3.08	0.42
11:B:1064:U:H2'	11:B:1065:C:H6	1.84	0.42
11:B:1107:C:O2'	33:b:14:ILE:HD11	2.20	0.42
11:B:1250:U:H5''	33:b:26:ARG:NH1	2.34	0.42
11:B:1480:G:H2'	11:B:1481:G:O4'	2.19	0.42
11:B:1515:C:H2'	11:B:1516:U:C6	2.54	0.42
17:H:3:ARG:HG2	17:H:6:LYS:HE3	2.02	0.42
19:J:110:PRO:O	19:J:115:GLY:HA3	2.19	0.42
22:M:28:SER:HB2	22:M:29:PHE:CD2	2.55	0.42
22:M:38:SER:HB3	22:M:128:ALA:HB3	2.01	0.42
30:U:5:ARG:HG2	30:U:6:ARG:N	2.34	0.42
33:b:108:LYS:HE3	33:b:108:LYS:HA	2.00	0.42
36:e:42:TRP:CZ2	36:e:61:LEU:HD12	2.55	0.42
37:f:136:LYS:HB3	37:f:136:LYS:HE3	1.69	0.42
38:g:96:ARG:O	38:g:99:LEU:HG	2.20	0.42
50:s:28:VAL:HG13	50:s:58:ILE:HG22	2.01	0.42
51:t:17:ARG:H	51:t:17:ARG:HG2	1.64	0.42
10:A:1016:A:C2	10:A:2474:G:H5'	2.55	0.42
10:A:1120:G:O2'	10:A:2012:U:H5'	2.20	0.42
10:A:1803:G:OP1	13:D:87:ARG:NH2	2.51	0.42
10:A:1975:G:H2'	10:A:1976:C:O4'	2.19	0.42
11:B:22:G:H4'	11:B:879:G:C8	2.54	0.42
11:B:653:C:H2'	11:B:654:G:C8	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:B:902:A:H2'	11:B:903:A:C8	2.55	0.42
13:D:168:GLU:HG2	13:D:171:TYR:O	2.20	0.42
16:G:59:LYS:HD2	16:G:59:LYS:HA	1.69	0.42
31:V:119:GLY:O	31:V:124:GLY:N	2.53	0.42
37:f:123:GLU:HA	37:f:126:ASP:HB3	2.01	0.42
10:A:391:A:H2'	10:A:392:A:C8	2.54	0.42
10:A:956:U:H2'	10:A:957:C:C6	2.55	0.42
10:A:1785:G:O6	13:D:178:SER:HB3	2.19	0.42
10:A:1940:G:O2'	10:A:1942:U:O4	2.28	0.42
10:A:2222:U:H2'	10:A:2223:G:O4'	2.20	0.42
10:A:2294:G:H2'	10:A:2294:G:N3	2.35	0.42
10:A:2300:G:H1'	16:G:155:THR:HG21	2.01	0.42
11:B:1429:G:H2'	11:B:1430:U:C6	2.55	0.42
12:C:114:C:H2'	12:C:115:A:H8	1.84	0.42
13:D:60:GLN:HG2	13:D:85:PRO:HB2	2.02	0.42
16:G:115:ARG:O	16:G:178:ARG:NE	2.43	0.42
18:I:4:ILE:HD12	18:I:4:ILE:O	2.19	0.42
32:a:42:ASN:OD1	32:a:42:ASN:C	2.63	0.42
33:b:85:GLU:HA	33:b:88:ARG:HG2	2.01	0.42
35:d:158:ARG:NH1	38:g:99:LEU:O	2.30	0.42
39:h:116:VAL:HG21	40:i:62:ARG:HG3	2.01	0.42
50:s:59:ASP:HA	50:s:62:ALA:HB3	2.01	0.42
6:6:6:ARG:NH1	6:6:49:LYS:O	2.52	0.42
8:8:50:ASN:O	8:8:54:VAL:HG23	2.20	0.42
10:A:63:G:H2'	10:A:64:C:C6	2.55	0.42
10:A:1340:A:H2'	10:A:1341:G:O4'	2.20	0.42
11:B:316:C:H2'	11:B:317:U:C6	2.55	0.42
15:F:22:PHE:CE1	21:L:1:MET:HE3	2.55	0.42
24:O:3:VAL:HG13	24:O:6:GLU:H	1.85	0.42
37:f:116:MET:CE	37:f:116:MET:H	2.32	0.42
41:j:72:GLN:H	41:j:72:GLN:HG2	1.56	0.42
43:l:71:ARG:HD3	43:l:75:MET:SD	2.60	0.42
43:l:75:MET:HE2	43:l:75:MET:HB2	1.78	0.42
3:3:26:PHE:CE1	3:3:30:MET:HE3	2.54	0.41
10:A:172:A:H2'	10:A:173:A:H8	1.85	0.41
10:A:1104:G:O2'	10:A:1105:G:H5''	2.20	0.41
10:A:1268:U:H2'	10:A:1269:G:O4'	2.20	0.41
10:A:2331:G:N3	10:A:2367:A:H2'	2.35	0.41
10:A:2690:C:H2'	10:A:2691:A:O4'	2.20	0.41
10:A:2843:G:N2	10:A:2846:A:OP2	2.40	0.41
11:B:131:U:H2'	11:B:132:G:C8	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:B:941:G:OP2	43:l:113:ARG:NH2	2.53	0.41
41:j:26:SER:OG	41:j:27:PHE:N	2.53	0.41
47:p:50:HIS:NE2	47:p:52:GLU:HG3	2.35	0.41
10:A:404:C:H2'	10:A:405:A:H8	1.81	0.41
10:A:992:G:O2'	10:A:999:A:N1	2.50	0.41
10:A:2219:U:H2'	10:A:2220:G:H8	1.84	0.41
10:A:2648:A:H2'	10:A:2649:G:O4'	2.20	0.41
11:B:895:A:C5	11:B:896:G:H1'	2.55	0.41
12:C:49:C:H2'	12:C:50:A:H8	1.84	0.41
14:E:125:TRP:CD2	14:E:160:LYS:HG2	2.55	0.41
16:G:16:LEU:HD23	16:G:29:PRO:HG2	2.03	0.41
18:I:57:ALA:O	18:I:61:LYS:HD3	2.20	0.41
26:Q:105:ALA:HA	27:R:47:VAL:HG21	2.01	0.41
36:e:18:VAL:HG21	36:e:58:HIS:NE2	2.35	0.41
36:e:19:GLY:HA2	36:e:22:VAL:HG12	2.01	0.41
36:e:52:ASN:OD1	36:e:53:ASN:N	2.49	0.41
37:f:49:LYS:HE3	37:f:118:LEU:HB3	2.02	0.41
39:h:79:ILE:O	39:h:83:ILE:HD12	2.19	0.41
43:l:72:GLU:HA	43:l:75:MET:HE1	2.02	0.41
47:p:71:ALA:HB3	47:p:74:LYS:HB2	2.03	0.41
49:r:28:ARG:HD3	49:r:28:ARG:HA	1.80	0.41
10:A:275:U:H2'	10:A:276:U:C6	2.54	0.41
10:A:571:A:H2'	10:A:572:G:C8	2.56	0.41
10:A:1146:A:C8	26:Q:51:ARG:HG2	2.56	0.41
10:A:1418:G:H2'	10:A:1419:A:H8	1.85	0.41
10:A:1665:A:H2'	10:A:1666:A:O4'	2.20	0.41
10:A:2056:A:H2'	10:A:2057:A:C8	2.56	0.41
10:A:2478:U:H2'	10:A:2479:U:C6	2.55	0.41
10:A:2526:C:H2'	10:A:2527:A:O4'	2.20	0.41
11:B:9:G:H5'	35:d:109:GLY:HA3	2.02	0.41
11:B:587:G:H2'	11:B:588:C:H6	1.85	0.41
11:B:629:A:H2'	11:B:630:U:C6	2.55	0.41
11:B:739:U:H5'	11:B:829:G:N2	2.36	0.41
11:B:1452:G:H2'	11:B:1453:A:H8	1.85	0.41
11:B:1471:U:H2'	11:B:1472:U:C6	2.54	0.41
17:H:36:LYS:HD3	17:H:36:LYS:HA	1.87	0.41
17:H:61:THR:HA	17:H:64:MET:HB2	2.02	0.41
30:U:5:ARG:O	30:U:8:ASP:HB2	2.20	0.41
32:a:97:LEU:HD23	32:a:98:GLY:N	2.35	0.41
32:a:138:SER:O	32:a:142:GLU:HB3	2.21	0.41
42:k:69:GLY:HA3	42:k:107:VAL:HG11	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:3:18:LEU:HD11	3:3:50:ILE:HG23	2.03	0.41
10:A:1470:A:H2'	10:A:1471:A:C8	2.56	0.41
10:A:2011:C:H2'	10:A:2012:U:C6	2.55	0.41
10:A:2872:G:H2'	10:A:2873:C:C6	2.55	0.41
11:B:526:A:N6	11:B:1200:G:O2'	2.51	0.41
11:B:594:G:H2'	11:B:595:G:C8	2.56	0.41
11:B:1396:C:H2'	11:B:1397:C:O4'	2.21	0.41
23:N:67:PHE:O	23:N:71:ARG:HD2	2.21	0.41
26:Q:86:ALA:O	26:Q:88:ILE:N	2.53	0.41
29:T:68:ARG:HB2	29:T:73:LEU:HD13	2.01	0.41
32:a:187:VAL:HB	32:a:191:SER:HB2	2.02	0.41
33:b:115:LEU:H	33:b:115:LEU:HD22	1.85	0.41
37:f:108:ALA:O	37:f:119:ARG:HG2	2.20	0.41
40:i:99:GLN:HE22	40:i:101:SER:HB2	1.84	0.41
5:5:28:SER:OG	5:5:39:ARG:HD2	2.20	0.41
10:A:181:A:H2'	10:A:182:C:H6	1.85	0.41
10:A:578:U:H2'	10:A:579:A:H8	1.85	0.41
10:A:668:C:H2'	10:A:669:G:C8	2.56	0.41
10:A:1283:C:OP1	10:A:2696:C:H4'	2.21	0.41
10:A:2593:G:H2'	10:A:2594:G:O4'	2.21	0.41
10:A:2601:U:H2'	10:A:2602:C:C6	2.56	0.41
11:B:22:G:H2'	11:B:23:C:H6	1.85	0.41
11:B:498:C:C2	11:B:536:G:N2	2.89	0.41
11:B:736:G:OP1	45:n:58:ARG:NH2	2.53	0.41
11:B:1053:C:OP2	33:b:199:LYS:NZ	2.53	0.41
11:B:1239:G:H2'	11:B:1240:G:H8	1.86	0.41
13:D:165:VAL:HG21	13:D:181:MET:SD	2.61	0.41
15:F:142:LEU:HD13	15:F:145:VAL:HG21	2.01	0.41
19:J:125:TYR:OH	19:J:132:HIS:NE2	2.34	0.41
20:K:33:ALA:HB1	20:K:37:ASP:HB2	2.02	0.41
20:K:108:THR:HG22	20:K:109:GLU:H	1.85	0.41
24:O:20:ARG:C	24:O:22:LEU:H	2.29	0.41
32:a:18:HIS:HB2	32:a:189:THR:HG22	2.02	0.41
32:a:30:PHE:HE1	32:a:45:LYS:HE3	1.85	0.41
33:b:33:LEU:O	33:b:37:LEU:HG	2.20	0.41
34:c:206:LYS:HZ3	34:c:206:LYS:HB2	1.85	0.41
38:g:42:ASP:OD2	38:g:42:ASP:N	2.52	0.41
39:h:35:LEU:HD21	39:h:45:ARG:HA	2.02	0.41
50:s:56:PRO:C	50:s:60:ARG:HD3	2.46	0.41
7:7:1:MET:HE3	7:7:1:MET:HB2	1.91	0.41
8:8:6:THR:HG23	8:8:61:LEU:HA	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:A:7:U:H2'	10:A:8:G:O4'	2.21	0.41
10:A:423:C:O2'	10:A:424:U:H5'	2.20	0.41
11:B:117:C:OP1	11:B:306:C:H5'	2.20	0.41
11:B:266:C:C2	11:B:267:A:C8	3.09	0.41
11:B:420:U:H4'	34:c:39:GLY:O	2.20	0.41
11:B:858:A:H2'	11:B:859:A:C8	2.55	0.41
11:B:898:U:H2'	11:B:899:U:H6	1.86	0.41
11:B:1307:U:H2'	11:B:1308:C:H6	1.85	0.41
11:B:1411:G:N2	11:B:1476:G:H2'	2.35	0.41
12:C:66:A:H61	12:C:107:U:H2'	1.85	0.41
32:a:153:ASP:OD2	32:a:153:ASP:N	2.53	0.41
32:a:166:VAL:HG11	32:a:196:VAL:HG11	2.02	0.41
32:a:204:ASP:C	32:a:204:ASP:OD1	2.63	0.41
41:j:114:THR:HG21	51:t:32:VAL:HG11	2.03	0.41
43:l:101:ARG:HG3	43:l:103:LYS:HB3	2.01	0.41
44:m:51:GLN:HA	44:m:52:PRO:HD2	1.92	0.41
45:n:70:LEU:HD12	45:n:70:LEU:HA	1.93	0.41
10:A:447:A:N1	10:A:460:A:H5''	2.36	0.41
10:A:881:C:H2'	10:A:882:U:C6	2.56	0.41
10:A:1580:A:H2'	10:A:1581:C:C6	2.56	0.41
10:A:2315:A:H2'	10:A:2316:G:C8	2.56	0.41
10:A:2549:U:H1'	10:A:2552:A:C6	2.56	0.41
11:B:95:A:H2'	11:B:96:G:H5'	2.02	0.41
11:B:178:U:H2'	11:B:179:C:H6	1.85	0.41
11:B:1181:G:H2'	11:B:1182:A:C8	2.55	0.41
11:B:1181:G:H2'	11:B:1182:A:H8	1.85	0.41
11:B:1307:U:H2'	11:B:1308:C:C6	2.56	0.41
11:B:1450:G:H2'	11:B:1451:G:O4'	2.19	0.41
15:F:146:LEU:HD11	15:F:169:ARG:HG3	2.03	0.41
16:G:120:LYS:H	16:G:120:LYS:HZ3	1.68	0.41
18:I:134:HIS:HB3	18:I:137:VAL:HG23	2.01	0.41
31:V:109:LEU:HD11	31:V:134:VAL:HG12	2.01	0.41
32:a:109:GLN:OE1	32:a:109:GLN:C	2.63	0.41
45:n:88:ARG:HA	45:n:88:ARG:NE	2.36	0.41
49:r:41:LEU:HB2	49:r:44:MET:SD	2.61	0.41
10:A:218:A:N3	10:A:233:U:O2'	2.50	0.41
10:A:544:G:O2'	10:A:545:A:H8	2.03	0.41
10:A:784:C:H2'	10:A:785:U:C6	2.55	0.41
10:A:1553:C:H2'	10:A:1554:C:C6	2.56	0.41
11:B:12:U:H4'	11:B:520:C:H4'	2.03	0.41
11:B:264:A:H2'	11:B:265:C:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:B:454:A:H2'	11:B:455:A:C8	2.55	0.41
11:B:549:U:H2'	11:B:550:C:H6	1.84	0.41
11:B:760:A:OP2	11:B:806:G:N2	2.53	0.41
11:B:1306:G:H2'	11:B:1307:U:H6	1.86	0.41
13:D:116:LEU:HD22	13:D:127:GLY:HA3	2.03	0.41
13:D:174:LEU:HD12	13:D:184:VAL:HG21	2.02	0.41
15:F:153:ASP:HB3	15:F:156:LEU:HB3	2.02	0.41
17:H:124:GLU:CD	17:H:124:GLU:N	2.79	0.41
18:I:27:ARG:O	18:I:27:ARG:HG3	2.21	0.41
18:I:142:LYS:HD3	18:I:142:LYS:C	2.45	0.41
20:K:58:MET:HE2	20:K:58:MET:HB3	1.95	0.41
33:b:22:TRP:HA	40:i:95:GLY:HA2	2.02	0.41
34:c:101:VAL:HG22	34:c:182:PHE:HE2	1.85	0.41
49:r:32:LYS:HE3	49:r:34:TRP:HH2	1.86	0.41
3:3:15:ASN:O	3:3:19:LEU:HD23	2.21	0.41
10:A:663:G:H5''	15:F:70:GLY:N	2.36	0.41
10:A:948:A:H2'	10:A:949:A:C8	2.56	0.41
10:A:984:C:O2	19:J:3:THR:OG1	2.35	0.41
10:A:1159:A:H2'	10:A:1160:C:C6	2.55	0.41
10:A:1257:G:N7	10:A:1311:U:H5	2.18	0.41
10:A:1375:G:H2'	10:A:1376:U:O4'	2.20	0.41
10:A:2491:G:H2'	10:A:2562:G:O6	2.21	0.41
10:A:2531:G:H2'	10:A:2532:U:O4'	2.21	0.41
11:B:94:C:H2'	11:B:95:A:H8	1.82	0.41
11:B:169:C:H2'	11:B:170:C:C6	2.56	0.41
11:B:193:U:H2'	11:B:194:G:C8	2.56	0.41
11:B:836:U:H3'	11:B:837:U:H5''	2.02	0.41
11:B:933:G:H2'	11:B:934:C:C6	2.55	0.41
11:B:1005:C:H2'	11:B:1006:A:H8	1.86	0.41
11:B:1066:G:H2'	11:B:1067:U:C6	2.56	0.41
13:D:132:LEU:HD11	13:D:144:ILE:HG23	2.03	0.41
18:I:59:ALA:O	18:I:63:ALA:N	2.46	0.41
22:M:136:VAL:HG13	31:V:133:GLU:OE1	2.21	0.41
25:P:92:ASP:HB3	25:P:112:LYS:HE3	2.03	0.41
28:S:110:LYS:HA	28:S:110:LYS:HD3	1.87	0.41
34:c:35:GLU:HG2	34:c:36:ASN:OD1	2.20	0.41
34:c:58:LYS:HE3	34:c:58:LYS:HB3	1.95	0.41
38:g:18:GLN:NE2	38:g:72:ILE:HB	2.35	0.41
39:h:39:PHE:HE2	39:h:72:VAL:HG13	1.85	0.41
39:h:120:LYS:O	39:h:121:ALA:C	2.64	0.41
40:i:15:HIS:HB3	40:i:70:HIS:CE1	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:l:21:TYR:HD2	43:l:21:TYR:O	2.04	0.41
44:m:74:TYR:O	44:m:78:GLY:N	2.53	0.41
45:n:84:ARG:NH1	45:n:84:ARG:HB2	2.35	0.41
47:p:68:ARG:HE	47:p:69:PRO:HD2	1.86	0.41
48:q:41:PRO:HD2	48:q:44:ILE:HG13	2.03	0.41
49:r:81:ARG:NH2	49:r:82:GLY:O	2.54	0.41
10:A:25:G:H2'	10:A:26:G:O4'	2.20	0.41
10:A:120:G:H4'	10:A:148:A:H5'	2.03	0.41
10:A:175:A:O2'	10:A:176:G:H5'	2.21	0.41
10:A:1740:A:N1	10:A:2702:C:O2'	2.40	0.41
10:A:1860:C:H2'	10:A:1861:G:O4'	2.21	0.41
11:B:145:A:H3'	11:B:146:A:H8	1.85	0.41
11:B:392:U:H2'	11:B:393:G:C8	2.56	0.41
11:B:1452:G:H2'	11:B:1453:A:C8	2.56	0.41
11:B:1512:A:H2'	11:B:1513:A:C8	2.56	0.41
11:B:1518:C:H2'	11:B:1519:G:C8	2.56	0.41
15:F:1:MET:HE3	15:F:1:MET:HB2	1.98	0.41
16:G:135:GLN:CG	16:G:136:ILE:H	2.34	0.41
26:Q:21:ALA:HB1	26:Q:28:ARG:O	2.21	0.41
27:R:71:LYS:HA	27:R:90:ARG:HG2	2.03	0.41
29:T:56:ARG:HG2	29:T:57:VAL:N	2.36	0.41
32:a:68:LEU:HD12	32:a:70:VAL:HB	2.02	0.41
32:a:117:LEU:HD21	32:a:140:ASP:CG	2.46	0.41
33:b:71:ALA:HB1	33:b:109:PRO:HG3	2.03	0.41
38:g:113:ASP:OD2	38:g:117:ARG:NH2	2.30	0.41
44:m:61:ARG:HD2	44:m:61:ARG:HA	1.76	0.41
49:r:27:ASP:OD1	49:r:27:ASP:N	2.54	0.41
2:2:31:PRO:HA	10:A:386:G:O3'	2.21	0.40
9:9:1:MET:HE2	9:9:1:MET:HB2	1.84	0.40
10:A:347:U:H2'	10:A:348:U:O4'	2.21	0.40
10:A:2635:C:H2'	10:A:2636:U:H6	1.85	0.40
11:B:303:A:H2'	11:B:304:G:H8	1.86	0.40
11:B:593:U:H2'	11:B:594:G:C8	2.55	0.40
11:B:795:U:H2'	11:B:796:A:C8	2.56	0.40
11:B:1324:U:H5''	43:l:23:TYR:HD2	1.86	0.40
17:H:26:ILE:HD13	17:H:76:VAL:HG23	2.03	0.40
22:M:48:GLU:OE2	22:M:48:GLU:HA	2.21	0.40
27:R:19:PHE:HE2	27:R:64:VAL:HG21	1.86	0.40
33:b:148:GLY:HA3	33:b:172:ARG:O	2.21	0.40
40:i:50:THR:HG23	40:i:64:GLN:OE1	2.21	0.40
42:k:54:ARG:HE	42:k:62:GLU:HG3	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
45:n:74:ASP:OD2	45:n:74:ASP:C	2.65	0.40
48:q:34:SER:OG	48:q:35:GLU:N	2.54	0.40
10:A:366:G:H2'	10:A:367:A:H8	1.86	0.40
10:A:682:A:H2'	10:A:683:U:C6	2.57	0.40
10:A:1114:G:OP2	10:A:1115:A:O2'	2.30	0.40
10:A:2210:G:H4'	10:A:2212:C:C2	2.56	0.40
10:A:2811:U:H3'	10:A:2812:A:H8	1.84	0.40
11:B:171:G:C5	11:B:172:C:C5	3.09	0.40
11:B:286:G:O2'	11:B:603:A:N6	2.54	0.40
11:B:306:C:H2'	11:B:307:A:C8	2.55	0.40
11:B:1211:C:P	44:m:9:ARG:HH21	2.44	0.40
11:B:1406:C:H2'	11:B:1407:A:H8	1.85	0.40
12:C:60:C:H2'	12:C:61:G:H8	1.86	0.40
20:K:15:GLY:O	20:K:47:ILE:HG12	2.21	0.40
21:L:3:LEU:HD23	21:L:3:LEU:HA	1.81	0.40
32:a:57:VAL:HG11	32:a:217:MET:HE1	2.03	0.40
34:c:11:LEU:HG	34:c:63:ARG:HG2	2.02	0.40
39:h:118:LEU:HD13	39:h:124:ARG:HA	2.03	0.40
40:i:30:LYS:HE3	40:i:35:GLN:HA	2.03	0.40
44:m:31:ILE:HD11	44:m:45:GLN:HA	2.03	0.40
47:p:33:LYS:HB3	47:p:40:TYR:CE2	2.55	0.40
5:5:15:MET:SD	10:A:2031:C:H5''	2.61	0.40
10:A:501:U:H4'	10:A:1221:G:H4'	2.02	0.40
10:A:535:U:N3	10:A:539:U:O2	2.36	0.40
10:A:1670:G:N3	10:A:1748:A:H2'	2.36	0.40
10:A:2552:A:N1	20:K:28:SER:OG	2.40	0.40
10:A:2760:C:H2'	10:A:2761:A:O4'	2.21	0.40
11:B:103:A:C6	11:B:320:G:C6	3.09	0.40
11:B:107:G:H2'	11:B:108:U:C6	2.57	0.40
11:B:1370:U:H2'	11:B:1371:A:H8	1.86	0.40
11:B:1506:U:H2'	11:B:1507:A:H8	1.87	0.40
12:C:75:G:H2'	12:C:76:G:O4'	2.21	0.40
13:D:82:GLU:OE1	13:D:103:TYR:OH	2.31	0.40
20:K:7:MET:HE1	20:K:18:ARG:HB3	2.03	0.40
24:O:68:ASP:OD1	24:O:68:ASP:N	2.55	0.40
26:Q:107:THR:O	26:Q:111:GLU:HG2	2.21	0.40
32:a:136:MET:HB3	32:a:136:MET:HE3	1.81	0.40
32:a:206:ALA:O	32:a:210:VAL:HG13	2.21	0.40
36:e:15:SER:CB	36:e:44:ARG:HH21	2.34	0.40
37:f:27:MET:HE3	37:f:43:VAL:HG11	2.04	0.40
38:g:56:LYS:HB3	38:g:56:LYS:HE3	1.66	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:i:90:LEU:HD21	40:i:92:LEU:HB3	2.04	0.40
49:r:9:PRO:HG2	49:r:39:MET:HE2	2.03	0.40
49:r:15:LEU:HD21	49:r:33:THR:HB	2.03	0.40
8:8:4:MET:HG2	10:A:655:A:H1'	2.03	0.40
10:A:490:G:N1	10:A:493:A:OP2	2.48	0.40
11:B:488:G:O2'	11:B:490:A:H1'	2.22	0.40
11:B:636:A:N7	38:g:107:ASN:ND2	2.70	0.40
11:B:1094:U:OP2	32:a:95:ARG:HD3	2.21	0.40
11:B:1222:C:H4'	43:l:114:LYS:HE3	2.02	0.40
13:D:35:GLU:OE2	13:D:64:LEU:HD11	2.22	0.40
13:D:164:LEU:HA	13:D:174:LEU:HD23	2.03	0.40
17:H:26:ILE:HG22	17:H:79:VAL:HG21	2.02	0.40
19:J:71:ASP:O	19:J:73:MET:HG2	2.22	0.40
23:N:20:MET:HE2	23:N:20:MET:HB3	1.97	0.40
32:a:84:ALA:HB1	32:a:89:MET:O	2.21	0.40
32:a:162:PHE:HA	32:a:184:ILE:O	2.22	0.40
36:e:76:ASP:OD1	36:e:76:ASP:C	2.64	0.40
41:j:35:THR:HG23	41:j:36:ASP:O	2.22	0.40
43:l:95:LEU:HD23	43:l:95:LEU:HA	1.96	0.40
44:m:3:LYS:HA	44:m:3:LYS:HD2	1.89	0.40
44:m:93:VAL:HA	44:m:94:PRO:HD3	1.91	0.40
11:B:216:U:H2'	11:B:217:A:C8	2.52	0.40
11:B:432:U:OP1	34:c:148:LYS:NZ	2.54	0.40
11:B:464:C:H2'	11:B:465:U:C6	2.56	0.40
11:B:465:U:H2'	11:B:466:U:C6	2.57	0.40
11:B:636:A:C8	38:g:107:ASN:HA	2.57	0.40
11:B:1232:A:OP1	11:B:1329:U:O2'	2.36	0.40
11:B:1360:U:O2'	40:i:62:ARG:NH2	2.52	0.40
13:D:53:HIS:HA	13:D:217:ARG:HB2	2.04	0.40
15:F:163:LEU:HA	15:F:163:LEU:HD23	1.88	0.40
21:L:56:PRO:O	21:L:60:ARG:HG3	2.22	0.40
27:R:19:PHE:CE2	27:R:64:VAL:HG21	2.56	0.40
36:e:38:ARG:NH1	36:e:61:LEU:HD11	2.37	0.40
42:k:67:ILE:HD11	42:k:74:LEU:HD12	2.03	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	
1	1	73/85 (86%)	69 (94%)	4 (6%)	0	100	100
2	2	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
3	3	60/63 (95%)	59 (98%)	1 (2%)	0	100	100
4	4	54/58 (93%)	54 (100%)	0	0	100	100
5	5	53/60 (88%)	52 (98%)	1 (2%)	0	100	100
6	6	48/51 (94%)	48 (100%)	0	0	100	100
7	7	42/44 (96%)	42 (100%)	0	0	100	100
8	8	61/64 (95%)	57 (93%)	4 (7%)	0	100	100
9	9	36/38 (95%)	35 (97%)	1 (3%)	0	100	100
13	D	270/273 (99%)	255 (94%)	15 (6%)	0	100	100
14	E	204/211 (97%)	193 (95%)	11 (5%)	0	100	100
15	F	198/200 (99%)	196 (99%)	2 (1%)	0	100	100
16	G	175/179 (98%)	165 (94%)	9 (5%)	1 (1%)	21	27
17	H	172/177 (97%)	163 (95%)	8 (5%)	1 (1%)	21	27
18	I	132/148 (89%)	122 (92%)	10 (8%)	0	100	100
19	J	139/142 (98%)	134 (96%)	5 (4%)	0	100	100
20	K	120/122 (98%)	118 (98%)	2 (2%)	0	100	100
21	L	142/144 (99%)	133 (94%)	9 (6%)	0	100	100
22	M	135/137 (98%)	124 (92%)	10 (7%)	1 (1%)	18	24
23	N	117/129 (91%)	112 (96%)	5 (4%)	0	100	100
24	O	112/116 (97%)	109 (97%)	3 (3%)	0	100	100
25	P	111/116 (96%)	108 (97%)	3 (3%)	0	100	100
26	Q	115/118 (98%)	113 (98%)	2 (2%)	0	100	100
27	R	101/103 (98%)	100 (99%)	1 (1%)	0	100	100
28	S	108/110 (98%)	103 (95%)	5 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	T	90/99 (91%)	77 (86%)	13 (14%)	0	100	100
30	U	101/104 (97%)	96 (95%)	5 (5%)	0	100	100
31	V	188/204 (92%)	175 (93%)	12 (6%)	1 (0%)	24	32
32	a	222/246 (90%)	205 (92%)	17 (8%)	0	100	100
33	b	206/228 (90%)	196 (95%)	10 (5%)	0	100	100
34	c	203/206 (98%)	196 (97%)	7 (3%)	0	100	100
35	d	153/166 (92%)	143 (94%)	10 (6%)	0	100	100
36	e	101/139 (73%)	93 (92%)	8 (8%)	0	100	100
37	f	151/156 (97%)	143 (95%)	8 (5%)	0	100	100
38	g	126/130 (97%)	125 (99%)	1 (1%)	0	100	100
39	h	124/130 (95%)	113 (91%)	11 (9%)	0	100	100
40	i	99/103 (96%)	90 (91%)	8 (8%)	1 (1%)	12	14
41	j	116/129 (90%)	112 (97%)	4 (3%)	0	100	100
42	k	119/123 (97%)	115 (97%)	4 (3%)	0	100	100
43	l	114/118 (97%)	105 (92%)	9 (8%)	0	100	100
44	m	98/101 (97%)	92 (94%)	6 (6%)	0	100	100
45	n	87/89 (98%)	85 (98%)	2 (2%)	0	100	100
46	o	78/83 (94%)	73 (94%)	5 (6%)	0	100	100
47	p	78/88 (89%)	74 (95%)	4 (5%)	0	100	100
48	q	57/76 (75%)	55 (96%)	2 (4%)	0	100	100
49	r	80/91 (88%)	78 (98%)	2 (2%)	0	100	100
50	s	85/91 (93%)	84 (99%)	0	1 (1%)	10	11
51	t	53/71 (75%)	53 (100%)	0	0	100	100
All	All	5582/5937 (94%)	5316 (95%)	260 (5%)	6 (0%)	49	61

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	G	136	ILE
17	H	59	GLN
22	M	29	PHE
31	V	152	ALA
40	i	57	VAL
50	s	68	HIS

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	
1	1	56/61 (92%)	54 (96%)	2 (4%)	31	45
2	2	66/67 (98%)	62 (94%)	4 (6%)	17	24
3	3	54/55 (98%)	53 (98%)	1 (2%)	50	64
4	4	48/49 (98%)	46 (96%)	2 (4%)	26	39
5	5	46/52 (88%)	45 (98%)	1 (2%)	45	60
6	6	46/47 (98%)	45 (98%)	1 (2%)	45	60
7	7	37/37 (100%)	37 (100%)	0	100	100
8	8	54/55 (98%)	53 (98%)	1 (2%)	50	64
9	9	34/34 (100%)	34 (100%)	0	100	100
13	D	212/213 (100%)	210 (99%)	2 (1%)	70	81
14	E	159/162 (98%)	154 (97%)	5 (3%)	35	50
15	F	158/158 (100%)	156 (99%)	2 (1%)	61	73
16	G	144/153 (94%)	137 (95%)	7 (5%)	22	33
17	H	137/141 (97%)	133 (97%)	4 (3%)	37	52
18	I	82/107 (77%)	78 (95%)	4 (5%)	22	33
19	J	118/119 (99%)	116 (98%)	2 (2%)	53	67
20	K	102/102 (100%)	100 (98%)	2 (2%)	48	63
21	L	106/106 (100%)	102 (96%)	4 (4%)	29	43
22	M	110/110 (100%)	108 (98%)	2 (2%)	51	65
23	N	98/104 (94%)	94 (96%)	4 (4%)	27	40
24	O	85/87 (98%)	81 (95%)	4 (5%)	23	35
25	P	95/98 (97%)	94 (99%)	1 (1%)	65	76
26	Q	87/88 (99%)	87 (100%)	0	100	100
27	R	86/86 (100%)	85 (99%)	1 (1%)	63	74
28	S	87/87 (100%)	84 (97%)	3 (3%)	32	47
29	T	77/82 (94%)	77 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	U	85/88 (97%)	81 (95%)	4 (5%)	23	35
31	V	151/164 (92%)	148 (98%)	3 (2%)	48	63
32	a	178/202 (88%)	174 (98%)	4 (2%)	45	60
33	b	171/187 (91%)	164 (96%)	7 (4%)	27	40
34	c	173/174 (99%)	165 (95%)	8 (5%)	24	36
35	d	114/124 (92%)	108 (95%)	6 (5%)	20	30
36	e	89/119 (75%)	85 (96%)	4 (4%)	24	37
37	f	119/122 (98%)	115 (97%)	4 (3%)	32	47
38	g	107/109 (98%)	104 (97%)	3 (3%)	38	54
39	h	102/106 (96%)	97 (95%)	5 (5%)	22	33
40	i	90/92 (98%)	90 (100%)	0	100	100
41	j	90/98 (92%)	88 (98%)	2 (2%)	45	60
42	k	105/107 (98%)	101 (96%)	4 (4%)	29	43
43	l	96/99 (97%)	93 (97%)	3 (3%)	35	50
44	m	81/82 (99%)	79 (98%)	2 (2%)	42	56
45	n	75/75 (100%)	74 (99%)	1 (1%)	61	73
46	o	64/65 (98%)	63 (98%)	1 (2%)	55	69
47	p	73/79 (92%)	67 (92%)	6 (8%)	10	13
48	q	49/64 (77%)	47 (96%)	2 (4%)	27	40
49	r	72/78 (92%)	72 (100%)	0	100	100
50	s	69/70 (99%)	68 (99%)	1 (1%)	59	72
51	t	45/60 (75%)	45 (100%)	0	100	100
All	All	4582/4824 (95%)	4453 (97%)	129 (3%)	38	54

All (129) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1	41	ARG
1	1	43	THR
2	2	2	SER
2	2	22	HIS
2	2	71	LEU
2	2	76	GLU
3	3	19	LEU

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Mol	Chain	Res	Type
4	4	11	SER
4	4	56	VAL
5	5	54	VAL
6	6	24	ARG
8	8	29	SER
13	D	43	ARG
13	D	172	VAL
14	E	23	ILE
14	E	138	VAL
14	E	149	CYS
14	E	168	GLU
14	E	188	LEU
15	F	104	LEU
15	F	106	SER
16	G	26	MET
16	G	49	ILE
16	G	50	ILE
16	G	61	THR
16	G	83	TRP
16	G	129	SER
16	G	170	LEU
17	H	9	VAL
17	H	76	VAL
17	H	113	VAL
17	H	167	GLU
18	I	19	VAL
18	I	38	VAL
18	I	114	VAL
18	I	144	ILE
19	J	17	VAL
19	J	62	VAL
20	K	40	LYS
20	K	116	SER
21	L	23	ILE
21	L	29	LYS
21	L	85	VAL
21	L	116	VAL
22	M	28	SER
22	M	68	VAL
23	N	14	SER
23	N	33	LEU
23	N	100	CYS

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Mol	Chain	Res	Type
23	N	116	VAL
24	O	29	VAL
24	O	53	SER
24	O	76	LEU
24	O	87	THR
25	P	53	ASN
27	R	72	VAL
28	S	3	VAL
28	S	73	THR
28	S	92	ARG
30	U	30	ASP
30	U	39	ASN
30	U	40	LEU
30	U	57	ILE
31	V	44	THR
31	V	74	THR
31	V	186	ASN
32	a	14	VAL
32	a	161	LEU
32	a	196	VAL
32	a	199	VAL
33	b	6	HIS
33	b	17	GLU
33	b	76	VAL
33	b	90	ASP
33	b	142	MET
33	b	179	ARG
33	b	186	THR
34	c	4	TYR
34	c	36	ASN
34	c	77	GLN
34	c	105	MET
34	c	125	VAL
34	c	136	GLN
34	c	137	VAL
34	c	175	LEU
35	d	12	TYR
35	d	22	VAL
35	d	37	LEU
35	d	72	MET
35	d	80	THR
35	d	122	GLN

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Mol	Chain	Res	Type
36	e	2	ARG
36	e	84	VAL
36	e	97	THR
36	e	103	LEU
37	f	31	MET
37	f	61	THR
37	f	97	ASN
37	f	124	LEU
38	g	80	ARG
38	g	110	VAL
38	g	112	THR
39	h	4	THR
39	h	25	THR
39	h	35	LEU
39	h	39	PHE
39	h	79	ILE
41	j	47	SER
41	j	129	VAL
42	k	58	THR
42	k	59	ASN
42	k	77	HIS
42	k	99	ARG
43	l	65	THR
43	l	75	MET
43	l	116	ILE
44	m	3	LYS
44	m	64	CYS
45	n	85	LEU
46	o	13	LYS
47	p	10	THR
47	p	15	VAL
47	p	24	VAL
47	p	41	VAL
47	p	56	CYS
47	p	58	ILE
48	q	36	THR
48	q	74	HIS
50	s	19	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (41) such sidechains are listed below:

Mol	Chain	Res	Type
2	2	17	ASN
2	2	36	HIS
3	3	13	GLN
3	3	17	GLN
4	4	18	ASN
4	4	38	GLN
9	9	37	GLN
13	D	46	ASN
13	D	53	HIS
13	D	90	HIS
13	D	134	ASN
13	D	261	ASN
14	E	102	GLN
14	E	173	GLN
17	H	73	ASN
20	K	3	GLN
20	K	91	GLN
21	L	2	GLN
22	M	22	HIS
22	M	98	GLN
28	S	61	ASN
29	T	90	GLN
30	U	39	ASN
30	U	65	HIS
30	U	73	ASN
31	V	178	HIS
32	a	18	HIS
33	b	69	HIS
33	b	118	GLN
34	c	41	HIS
35	d	133	ASN
38	g	85	GLN
38	g	107	ASN
41	j	72	GLN
43	l	52	GLN
44	m	43	ASN
44	m	49	GLN
45	n	46	ASN
49	r	56	GLN
50	s	70	ASN
50	s	82	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
10	A	2802/2891 (96%)	387 (13%)	7 (0%)
11	B	1526/1536 (99%)	213 (13%)	2 (0%)
12	C	119/121 (98%)	11 (9%)	0
All	All	4447/4548 (97%)	611 (13%)	9 (0%)

All (611) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
10	A	9	A
10	A	22	G
10	A	33	U
10	A	44	G
10	A	45	G
10	A	54	G
10	A	59	G
10	A	62	A
10	A	70	A
10	A	73	A
10	A	74	G
10	A	91	A
10	A	92	A
10	A	93	C
10	A	100	U
10	A	101	G
10	A	102	A
10	A	117	A
10	A	118	A
10	A	119	U
10	A	124	G
10	A	137	A
10	A	139	A
10	A	141	C
10	A	162	C
10	A	164	A
10	A	180	A
10	A	195	A
10	A	198	A
10	A	214	G
10	A	215	A
10	A	221	A
10	A	223	U
10	A	247	G
10	A	262	U

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Mol	Chain	Res	Type
10	A	265	G
10	A	270	U
10	A	272	A
10	A	278	A
10	A	283	U
10	A	295	G
10	A	304	A
10	A	317	U
10	A	318	G
10	A	320	G
10	A	322	G
10	A	323	A
10	A	326	G
10	A	338	A
10	A	346	U
10	A	351	A
10	A	354	G
10	A	355	A
10	A	357	A
10	A	359	C
10	A	362	G
10	A	375	C
10	A	376	G
10	A	386	G
10	A	389	U
10	A	401	G
10	A	414	G
10	A	433	A
10	A	441	U
10	A	445	C
10	A	446	C
10	A	470	A
10	A	471	G
10	A	480	A
10	A	481	G
10	A	484	G
10	A	494	U
10	A	495	A
10	A	498	A
10	A	519	A
10	A	520	G
10	A	522	A

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Mol	Chain	Res	Type
10	A	536	U
10	A	538	U
10	A	552	A
10	A	557	U
10	A	562	U
10	A	564	A
10	A	581	A
10	A	592	A
10	A	602	U
10	A	603	A
10	A	616	A
10	A	626	A
10	A	634	U
10	A	635	A
10	A	636	G
10	A	644	A
10	A	666	A
10	A	675	U
10	A	693	G
10	A	701	G
10	A	707	A
10	A	717	G
10	A	719	A
10	A	729	C
10	A	736	U
10	A	740	A
10	A	753	A
10	A	764	G
10	A	765	G
10	A	771	A
10	A	773	G
10	A	774	G
10	A	794	G
10	A	801	C
10	A	816	U
10	A	817	U
10	A	819	G
10	A	834	A
10	A	847	G
10	A	854	A
10	A	859	U
10	A	865	U

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Mol	Chain	Res	Type
10	A	869	G
10	A	872	U
10	A	884	A
10	A	886	C
10	A	895	G
10	A	898	A
10	A	902	C
10	A	919	C
10	A	920	C
10	A	921	G
10	A	922	A
10	A	935	C
10	A	950	C
10	A	963	A
10	A	971	C
10	A	972	A
10	A	973	A
10	A	978	G
10	A	985	A
10	A	992	G
10	A	994	C
10	A	1001	U
10	A	1002	U
10	A	1015	U
10	A	1022	U
10	A	1035	A
10	A	1036	G
10	A	1037	A
10	A	1046	A
10	A	1050	U
10	A	1059	A
10	A	1060	G
10	A	1062	A
10	A	1072	U
10	A	1077	A
10	A	1079	A
10	A	1082	G
10	A	1087	A
10	A	1099	G
10	A	1101	G
10	A	1117	G
10	A	1119	U

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Mol	Chain	Res	Type
10	A	1121	U
10	A	1122	A
10	A	1124	C
10	A	1125	G
10	A	1131	C
10	A	1132	A
10	A	1161	G
10	A	1162	U
10	A	1163	A
10	A	1166	U
10	A	1170	G
10	A	1192	G
10	A	1224	G
10	A	1233	A
10	A	1236	G
10	A	1239	A
10	A	1242	G
10	A	1257	G
10	A	1258	A
10	A	1259	C
10	A	1286	A
10	A	1287	A
10	A	1298	U
10	A	1300	C
10	A	1307	A
10	A	1315	U
10	A	1338	U
10	A	1345	A
10	A	1351	A
10	A	1364	A
10	A	1365	U
10	A	1369	A
10	A	1402	G
10	A	1403	C
10	A	1413	A
10	A	1414	C
10	A	1420	A
10	A	1421	G
10	A	1438	G
10	A	1446	U
10	A	1468	G
10	A	1476	A

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Mol	Chain	Res	Type
10	A	1479	U
10	A	1480	A
10	A	1481	A
10	A	1483	U
10	A	1496	G
10	A	1501	A
10	A	1510	G
10	A	1518	G
10	A	1519	U
10	A	1521	U
10	A	1522	U
10	A	1523	U
10	A	1525	A
10	A	1526	G
10	A	1529	G
10	A	1530	A
10	A	1555	A
10	A	1558	A
10	A	1567	U
10	A	1572	U
10	A	1573	U
10	A	1574	C
10	A	1595	C
10	A	1596	C
10	A	1597	A
10	A	1607	A
10	A	1628	C
10	A	1636	U
10	A	1637	U
10	A	1638	G
10	A	1663	G
10	A	1699	G
10	A	1704	G
10	A	1705	G
10	A	1710	A
10	A	1711	G
10	A	1714	U
10	A	1715	U
10	A	1716	U
10	A	1717	A
10	A	1718	C
10	A	1727	C

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Mol	Chain	Res	Type
10	A	1750	G
10	A	1759	A
10	A	1762	G
10	A	1768	U
10	A	1770	A
10	A	1772	A
10	A	1786	C
10	A	1787	A
10	A	1793	G
10	A	1794	A
10	A	1802	C
10	A	1806	U
10	A	1815	A
10	A	1819	C
10	A	1834	A
10	A	1856	C
10	A	1882	G
10	A	1892	G
10	A	1902	A
10	A	1915	G
10	A	1916	G
10	A	1923	A
10	A	1924	A
10	A	1941	U
10	A	1953	C
10	A	1956	A
10	A	1957	U
10	A	1958	G
10	A	1977	U
10	A	1979	U
10	A	1983	C
10	A	2009	C
10	A	2017	A
10	A	2019	A
10	A	2029	U
10	A	2035	G
10	A	2041	C
10	A	2042	G
10	A	2046	A
10	A	2047	G
10	A	2048	A
10	A	2049	C

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Mol	Chain	Res	Type
10	A	2055	G
10	A	2084	U
10	A	2086	G
10	A	2171	U
10	A	2173	C
10	A	2176	G
10	A	2178	G
10	A	2184	A
10	A	2190	G
10	A	2197	A
10	A	2199	U
10	A	2211	A
10	A	2224	G
10	A	2225	G
10	A	2237	G
10	A	2254	A
10	A	2264	A
10	A	2269	U
10	A	2273	A
10	A	2274	A
10	A	2283	C
10	A	2291	U
10	A	2294	G
10	A	2298	U
10	A	2305	C
10	A	2306	A
10	A	2308	A
10	A	2311	A
10	A	2312	U
10	A	2313	A
10	A	2319	A
10	A	2322	A
10	A	2331	G
10	A	2333	C
10	A	2336	C
10	A	2358	U
10	A	2369	G
10	A	2371	C
10	A	2375	G
10	A	2388	U
10	A	2389	C
10	A	2392	U

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Mol	Chain	Res	Type
10	A	2395	G
10	A	2411	A
10	A	2415	G
10	A	2416	A
10	A	2421	A
10	A	2427	U
10	A	2434	A
10	A	2461	C
10	A	2462	A
10	A	2477	U
10	A	2488	G
10	A	2489	A
10	A	2491	G
10	A	2492	U
10	A	2504	A
10	A	2511	G
10	A	2515	G
10	A	2533	A
10	A	2550	A
10	A	2552	A
10	A	2553	G
10	A	2559	C
10	A	2588	A
10	A	2591	U
10	A	2592	C
10	A	2595	U
10	A	2599	U
10	A	2601	U
10	A	2615	U
10	A	2616	U
10	A	2622	U
10	A	2675	U
10	A	2676	U
10	A	2700	G
10	A	2702	C
10	A	2712	U
10	A	2719	A
10	A	2730	G
10	A	2734	A
10	A	2743	A
10	A	2751	A
10	A	2764	A

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Mol	Chain	Res	Type
10	A	2784	U
10	A	2785	G
10	A	2786	A
10	A	2787	U
10	A	2804	C
10	A	2806	A
10	A	2807	A
10	A	2819	U
10	A	2821	A
10	A	2822	U
10	A	2835	U
10	A	2853	G
10	A	2859	A
10	A	2866	C
10	A	2870	U
10	A	2877	U
11	B	2	A
11	B	4	C
11	B	5	U
11	B	7	A
11	B	9	G
11	B	31	G
11	B	32	A
11	B	39	G
11	B	47	C
11	B	48	C
11	B	51	A
11	B	54	C
11	B	58	C
11	B	66	G
11	B	69	G
11	B	72	G
11	B	73	A
11	B	81	U
11	B	83	G
11	B	84	C
11	B	90	G
11	B	91	A
11	B	93	U
11	B	95	A
11	B	97	C
11	B	114	A

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Mol	Chain	Res	Type
11	B	124	A
11	B	125	U
11	B	138	G
11	B	157	C
11	B	167	U
11	B	177	G
11	B	182	G
11	B	183	A
11	B	189	A
11	B	191	A
11	B	198	G
11	B	214	G
11	B	237	A
11	B	240	A
11	B	241	G
11	B	245	G
11	B	260	G
11	B	261	C
11	B	283	A
11	B	300	A
11	B	310	C
11	B	315	A
11	B	322	C
11	B	323	A
11	B	324	C
11	B	326	G
11	B	346	C
11	B	348	G
11	B	361	U
11	B	363	G
11	B	366	C
11	B	367	A
11	B	369	U
11	B	382	G
11	B	387	A
11	B	391	A
11	B	400	G
11	B	406	A
11	B	407	G
11	B	415	U
11	B	416	C
11	B	423	U

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Mol	Chain	Res	Type
11	B	447	G
11	B	458	U
11	B	461	U
11	B	474	U
11	B	475	G
11	B	477	C
11	B	479	U
11	B	480	U
11	B	489	A
11	B	490	A
11	B	491	U
11	B	503	A
11	B	505	C
11	B	512	C
11	B	515	G
11	B	521	G
11	B	525	U
11	B	526	A
11	B	541	A
11	B	547	A
11	B	558	C
11	B	566	A
11	B	567	A
11	B	570	C
11	B	571	G
11	B	573	G
11	B	582	G
11	B	627	G
11	B	634	A
11	B	647	A
11	B	659	A
11	B	681	A
11	B	697	G
11	B	717	U
11	B	749	A
11	B	754	G
11	B	768	G
11	B	781	A
11	B	787	U
11	B	788	A
11	B	806	G
11	B	809	A

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Mol	Chain	Res	Type
11	B	811	C
11	B	822	A
11	B	830	G
11	B	835	C
11	B	836	U
11	B	838	G
11	B	839	A
11	B	840	G
11	B	907	A
11	B	908	A
11	B	920	G
11	B	921	G
11	B	928	C
11	B	929	A
11	B	952	A
11	B	954	U
11	B	963	A
11	B	969	A
11	B	970	G
11	B	971	A
11	B	976	U
11	B	983	C
11	B	987	G
11	B	988	A
11	B	998	A
11	B	1016	U
11	B	1024	U
11	B	1025	C
11	B	1026	G
11	B	1028	G
11	B	1030	A
11	B	1031	C
11	B	1037	C
11	B	1050	U
11	B	1059	U
11	B	1064	U
11	B	1067	U
11	B	1079	U
11	B	1088	G
11	B	1089	U
11	B	1095	A
11	B	1098	G

Continued on next page...

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Mol	Chain	Res	Type
11	B	1118	G
11	B	1119	U
11	B	1127	A
11	B	1130	U
11	B	1131	C
11	B	1133	G
11	B	1134	G
11	B	1135	U
11	B	1148	G
11	B	1153	U
11	B	1162	C
11	B	1175	G
11	B	1178	G
11	B	1190	A
11	B	1191	A
11	B	1206	U
11	B	1207	A
11	B	1219	A
11	B	1220	C
11	B	1221	A
11	B	1234	U
11	B	1250	U
11	B	1252	G
11	B	1272	U
11	B	1273	A
11	B	1274	A
11	B	1279	A
11	B	1280	U
11	B	1281	A
11	B	1293	A
11	B	1294	G
11	B	1296	C
11	B	1299	G
11	B	1300	A
11	B	1311	C
11	B	1314	C
11	B	1316	C
11	B	1323	G
11	B	1357	A
11	B	1373	G
11	B	1375	U
11	B	1388	A

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Mol	Chain	Res	Type
11	B	1391	C
11	B	1392	A
11	B	1413	G
11	B	1435	A
11	B	1440	A
11	B	1446	A
11	B	1447	A
11	B	1481	G
11	B	1485	G
11	B	1486	A
11	B	1487	A
11	B	1488	G
11	B	1491	G
11	B	1493	A
11	B	1497	A
11	B	1500	U
11	B	1511	G
11	B	1523	G
11	B	1524	G
12	C	13	A
12	C	24	G
12	C	35	U
12	C	44	G
12	C	56	G
12	C	67	U
12	C	88	C
12	C	89	U
12	C	91	C
12	C	105	G
12	C	109	A

All (9) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
10	A	353	U
10	A	602	U
10	A	773	G
10	A	1480	A
10	A	2416	A
10	A	2591	U
10	A	2742	U
11	B	80	C

Continued on next page...

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Mol	Chain	Res	Type
11	B	805	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](#)

Of 185 ligands modelled in this entry, 185 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

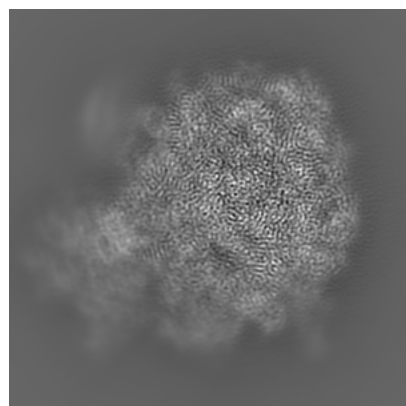
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-19547. These allow visual inspection of the internal detail of the map and identification of artifacts.

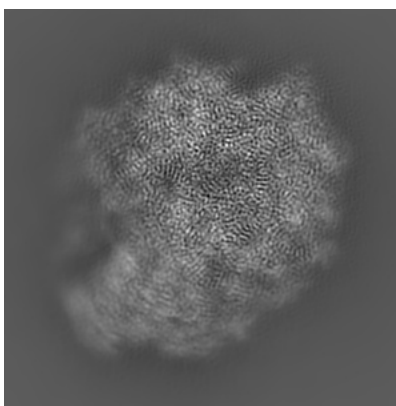
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

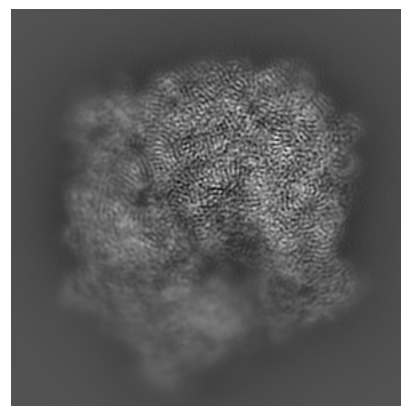
6.1.1 Primary map



X

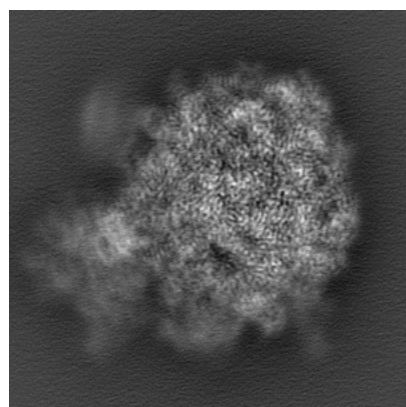


Y

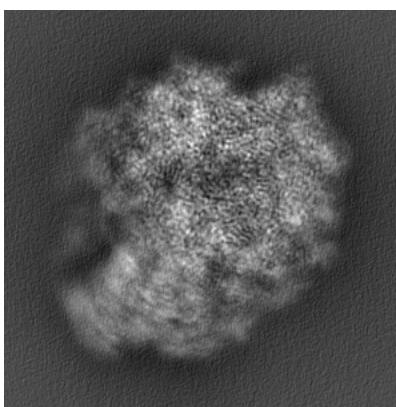


Z

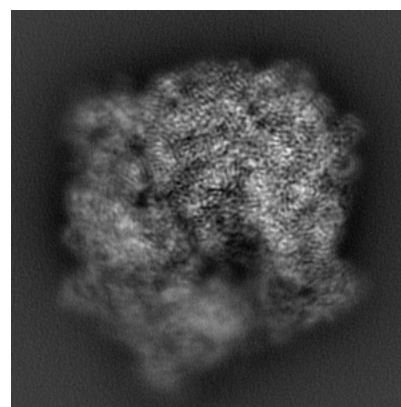
6.1.2 Raw map



X



Y

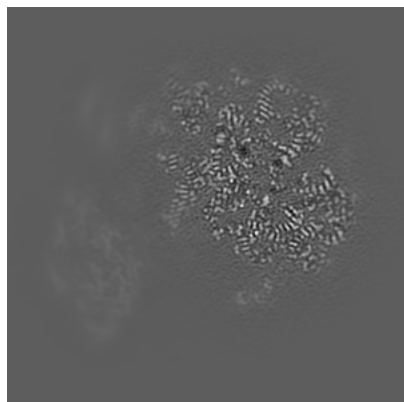


Z

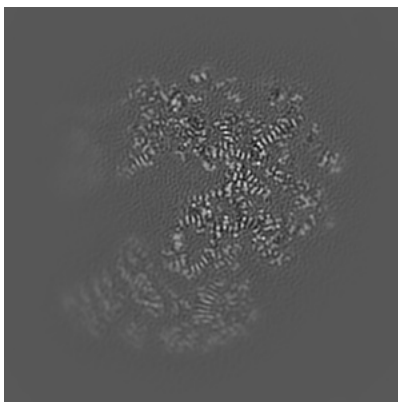
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

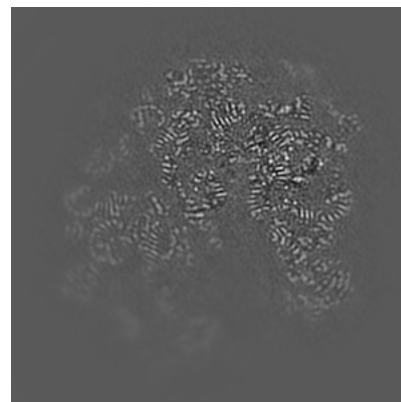
6.2.1 Primary map



X Index: 170

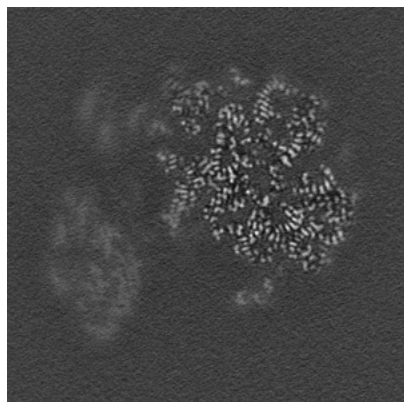


Y Index: 170

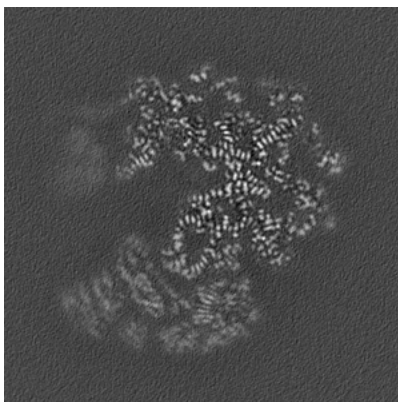


Z Index: 170

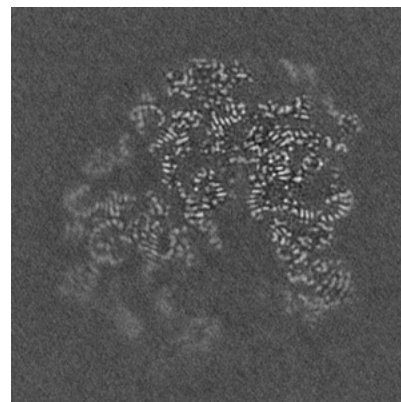
6.2.2 Raw map



X Index: 170



Y Index: 170

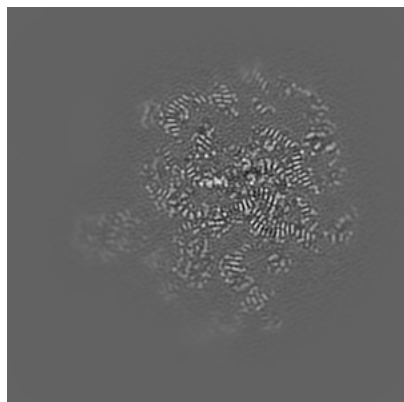


Z Index: 170

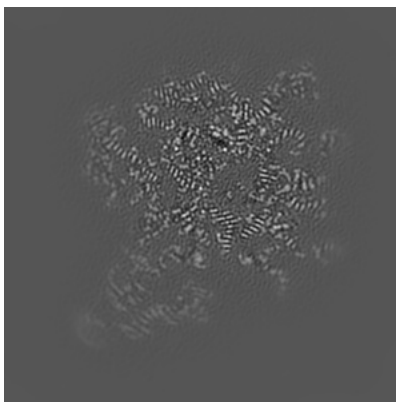
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

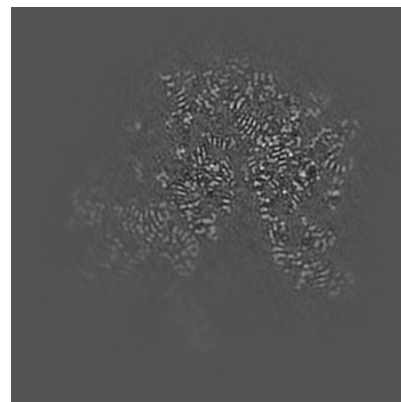
6.3.1 Primary map



X Index: 228

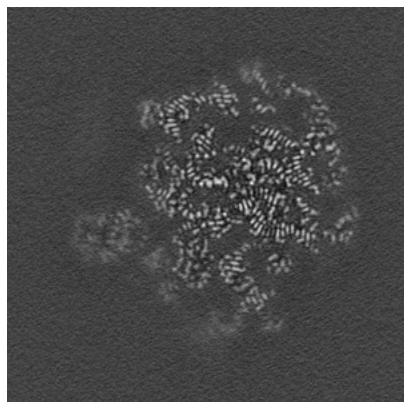


Y Index: 217

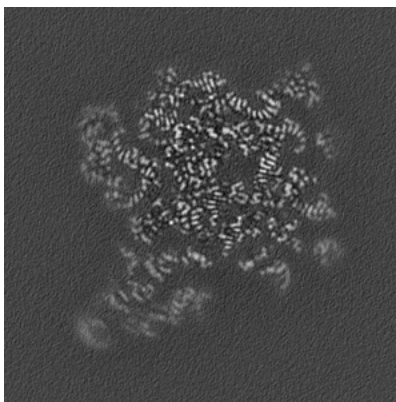


Z Index: 182

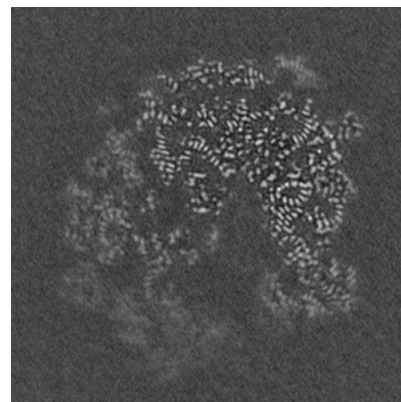
6.3.2 Raw map



X Index: 228



Y Index: 221

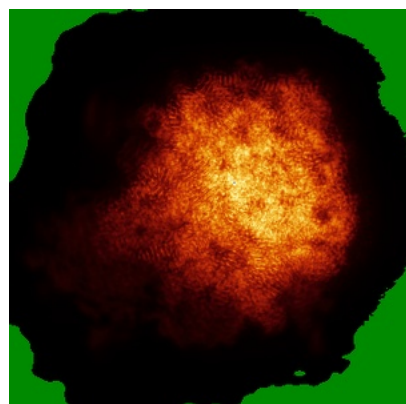


Z Index: 163

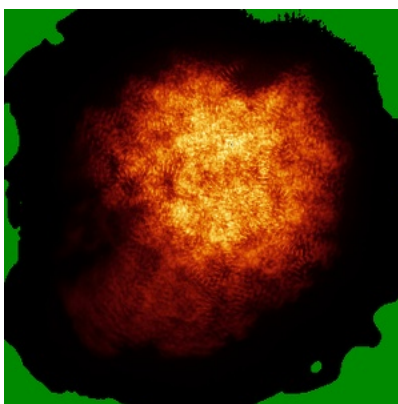
The images above show the largest variance slices of the map in three orthogonal directions.

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

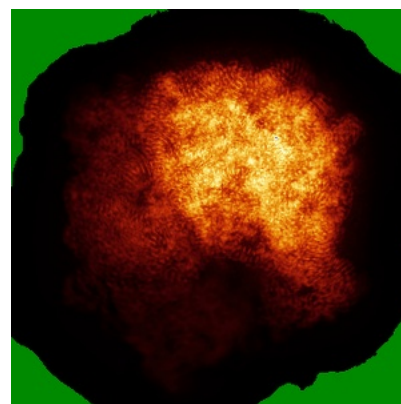
6.4.1 Primary map



X

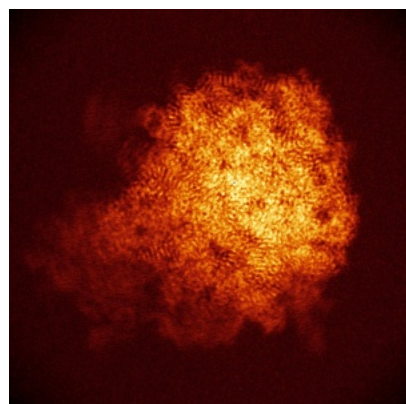


Y

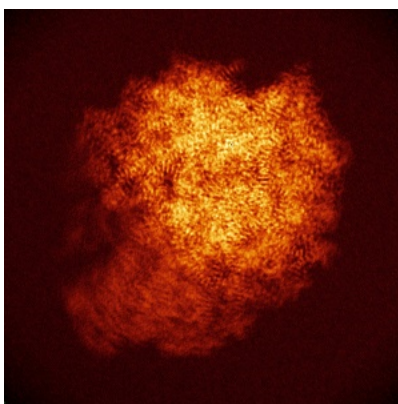


Z

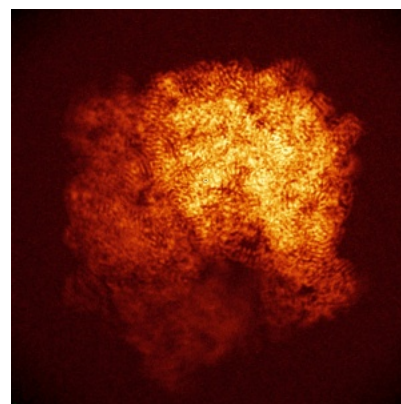
6.4.2 Raw map



X



Y

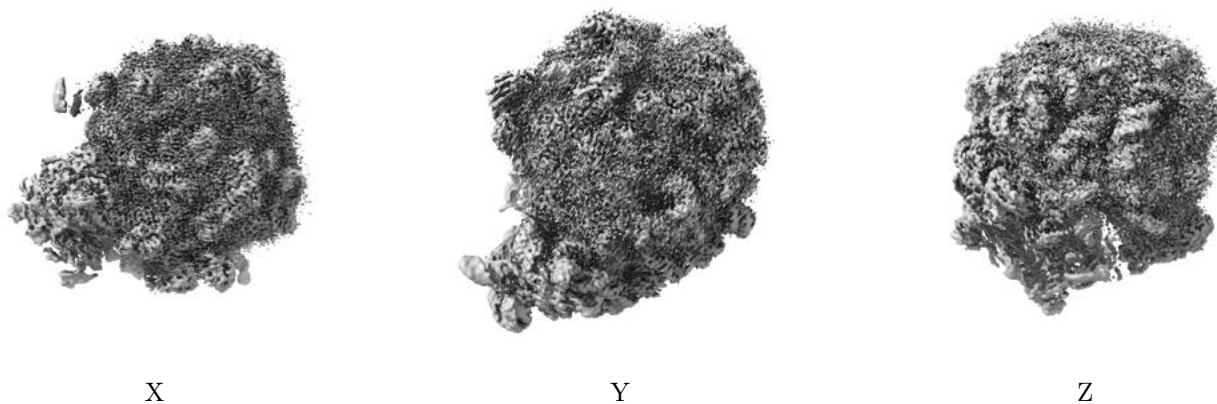


Z

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

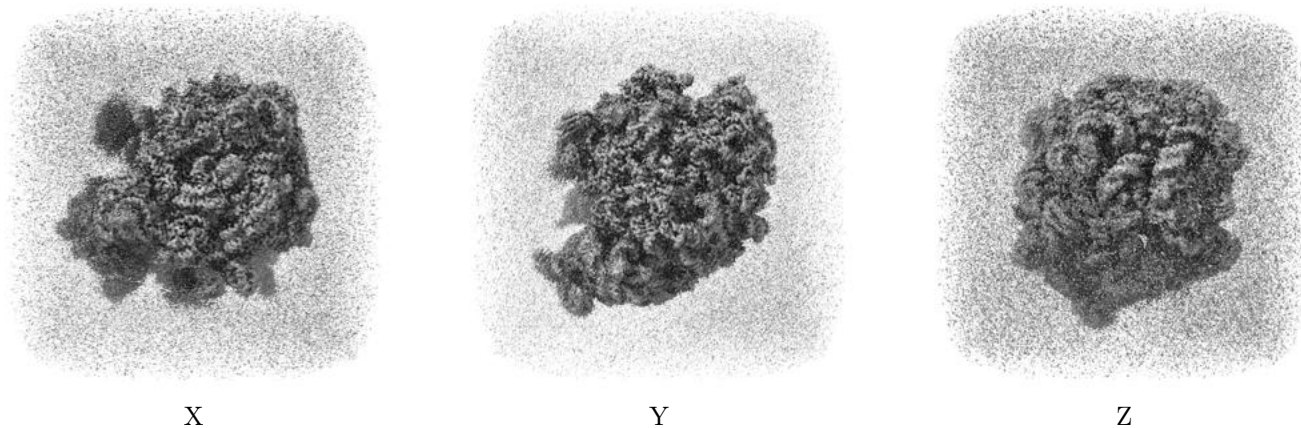
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

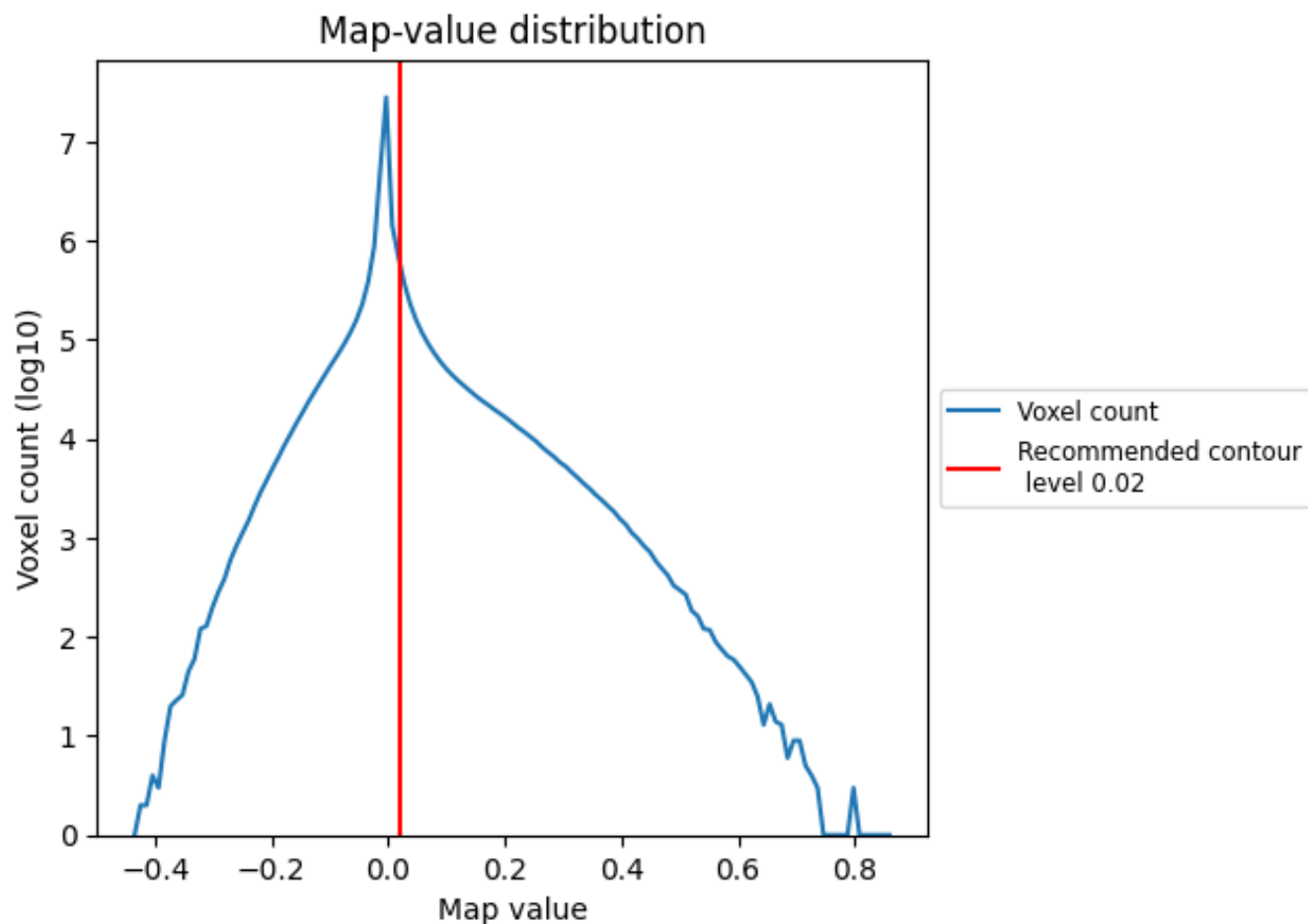
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

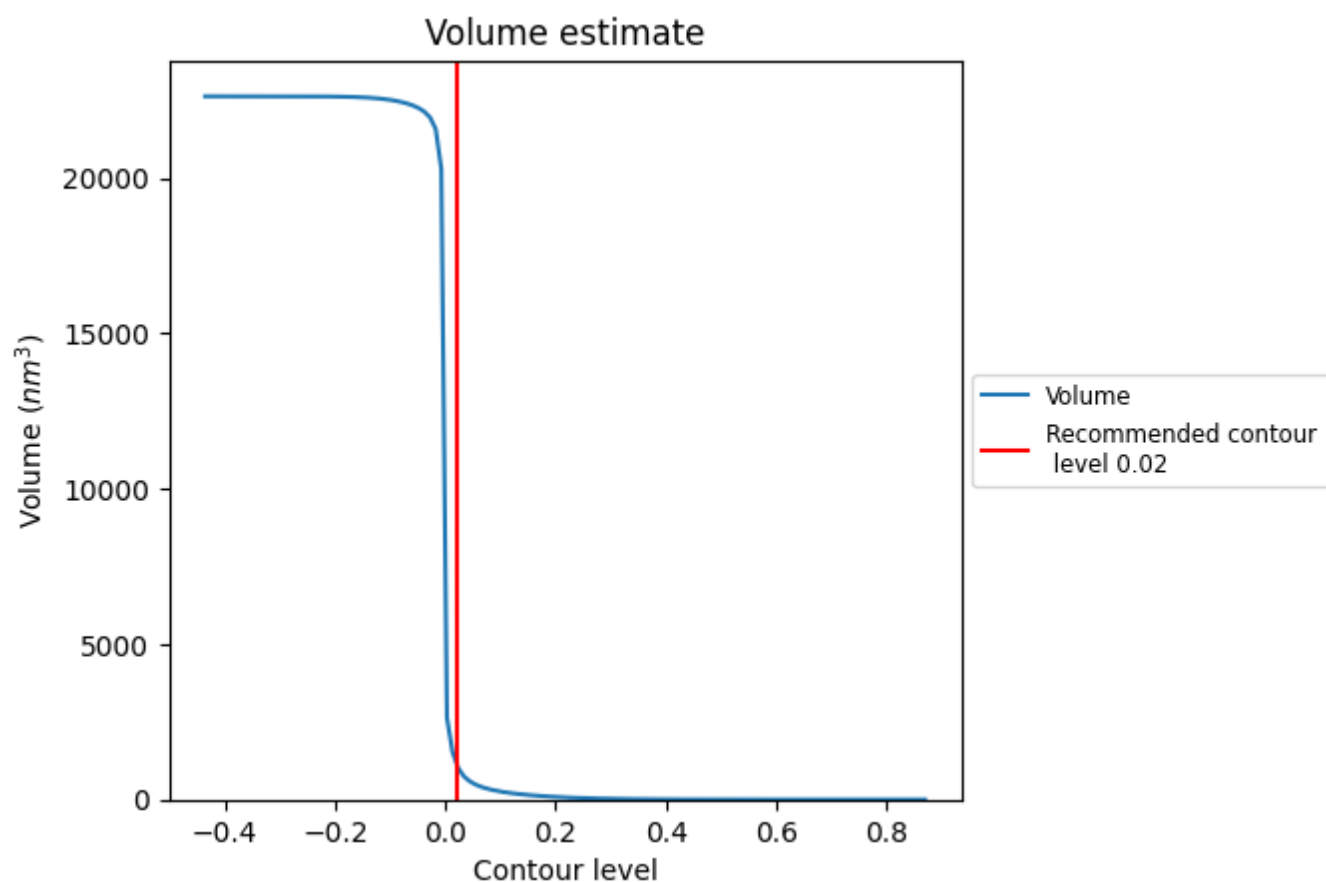
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

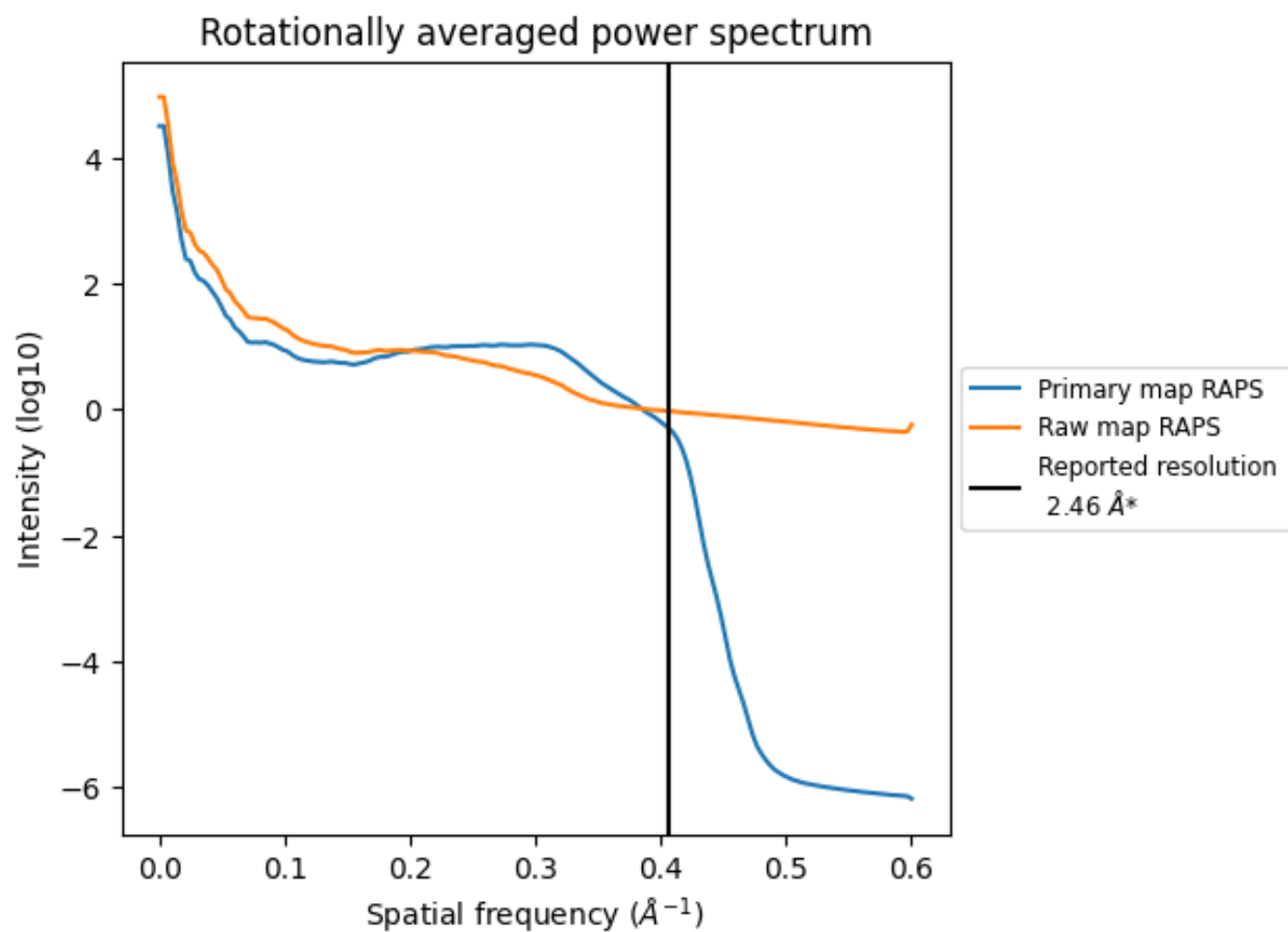
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1192 nm³; this corresponds to an approximate mass of 1077 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 ⓘ

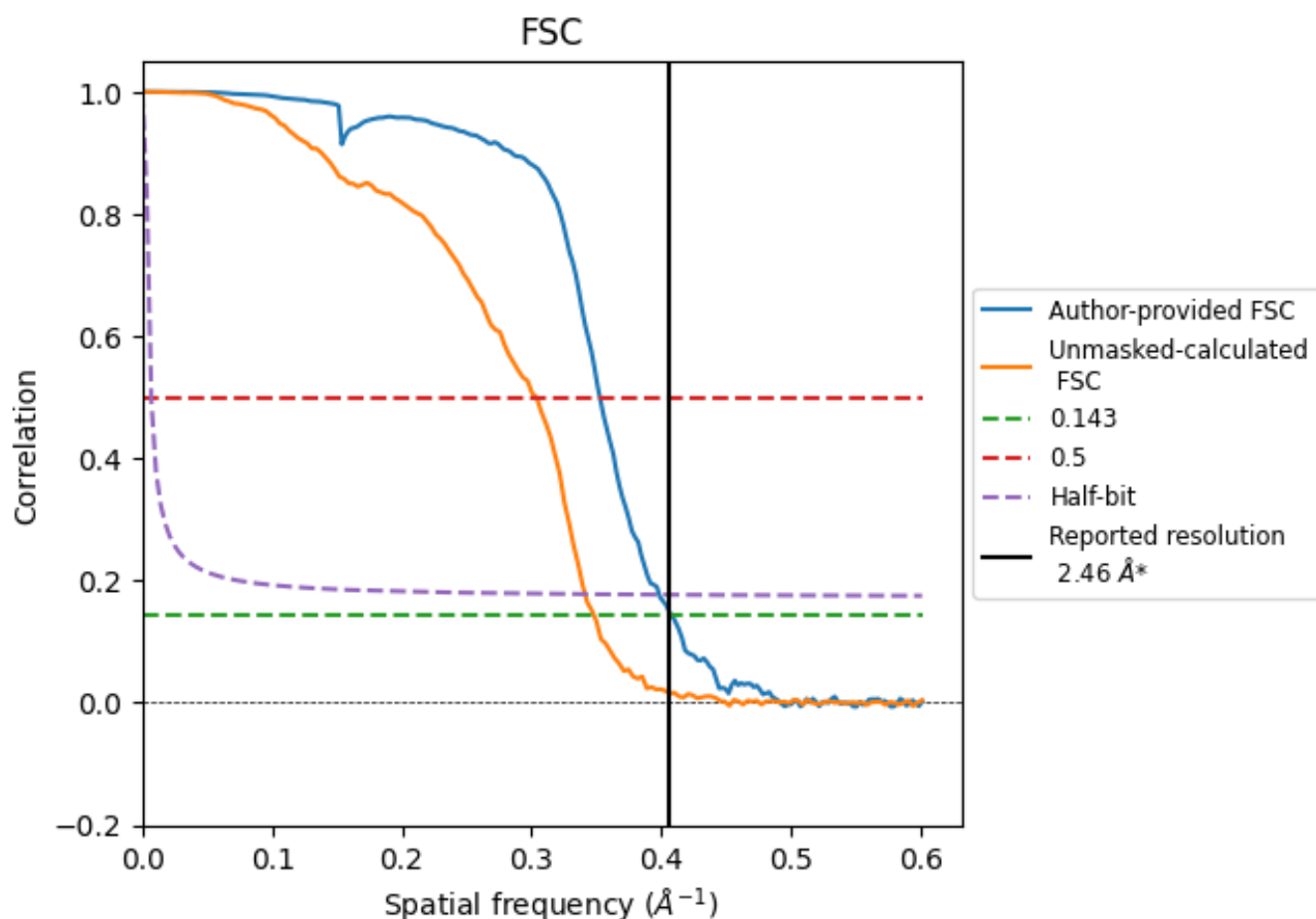


*Reported resolution corresponds to spatial frequency of 0.407 Å⁻¹

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 0.407 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.46	-	-
Author-provided FSC curve	2.45	2.84	2.51
Unmasked-calculated*	2.87	3.29	2.93

*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 2.87 differs from the reported value 2.46 by more than 10 %

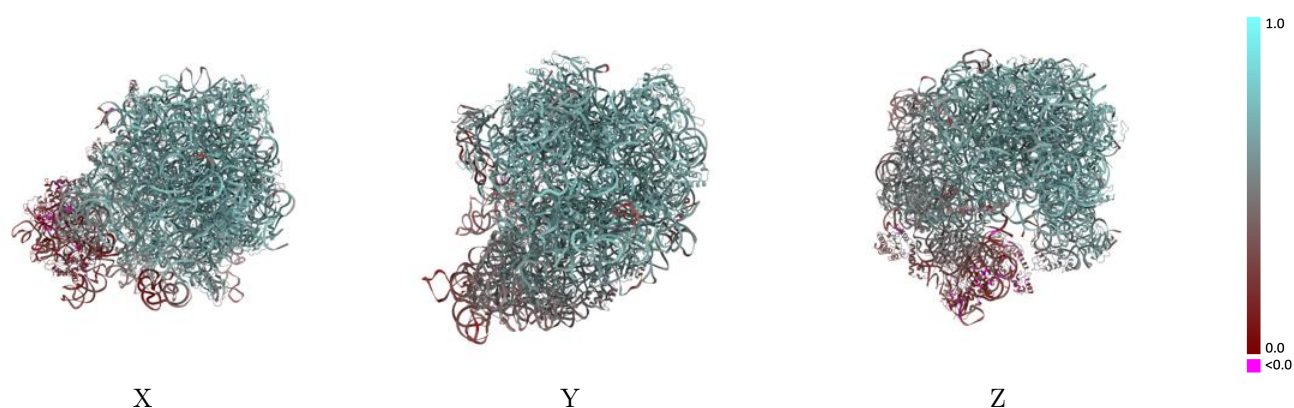
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-19547 and PDB model 8RWG. Per-residue inclusion information can be found in section 3 on page 14.

9.1 Map-model overlay [i](#)

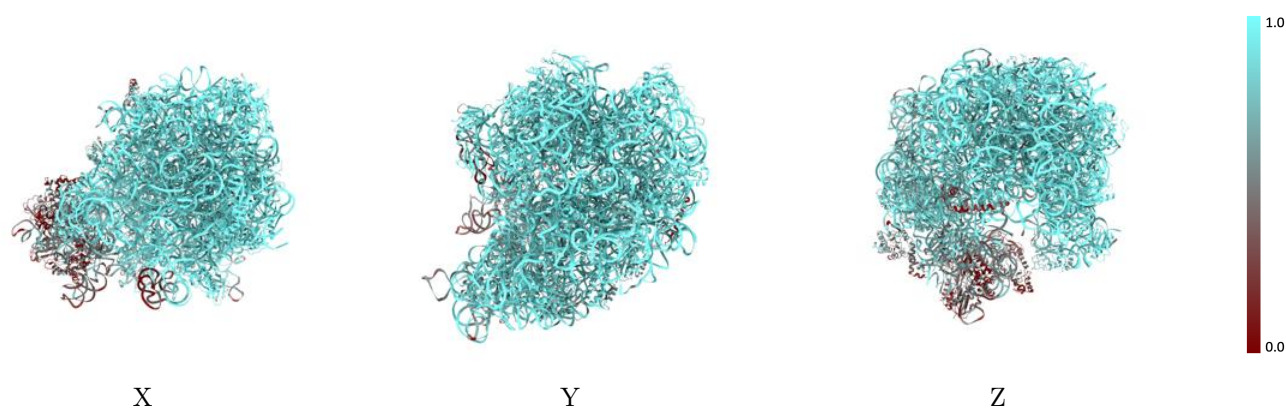
This section was not generated.

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



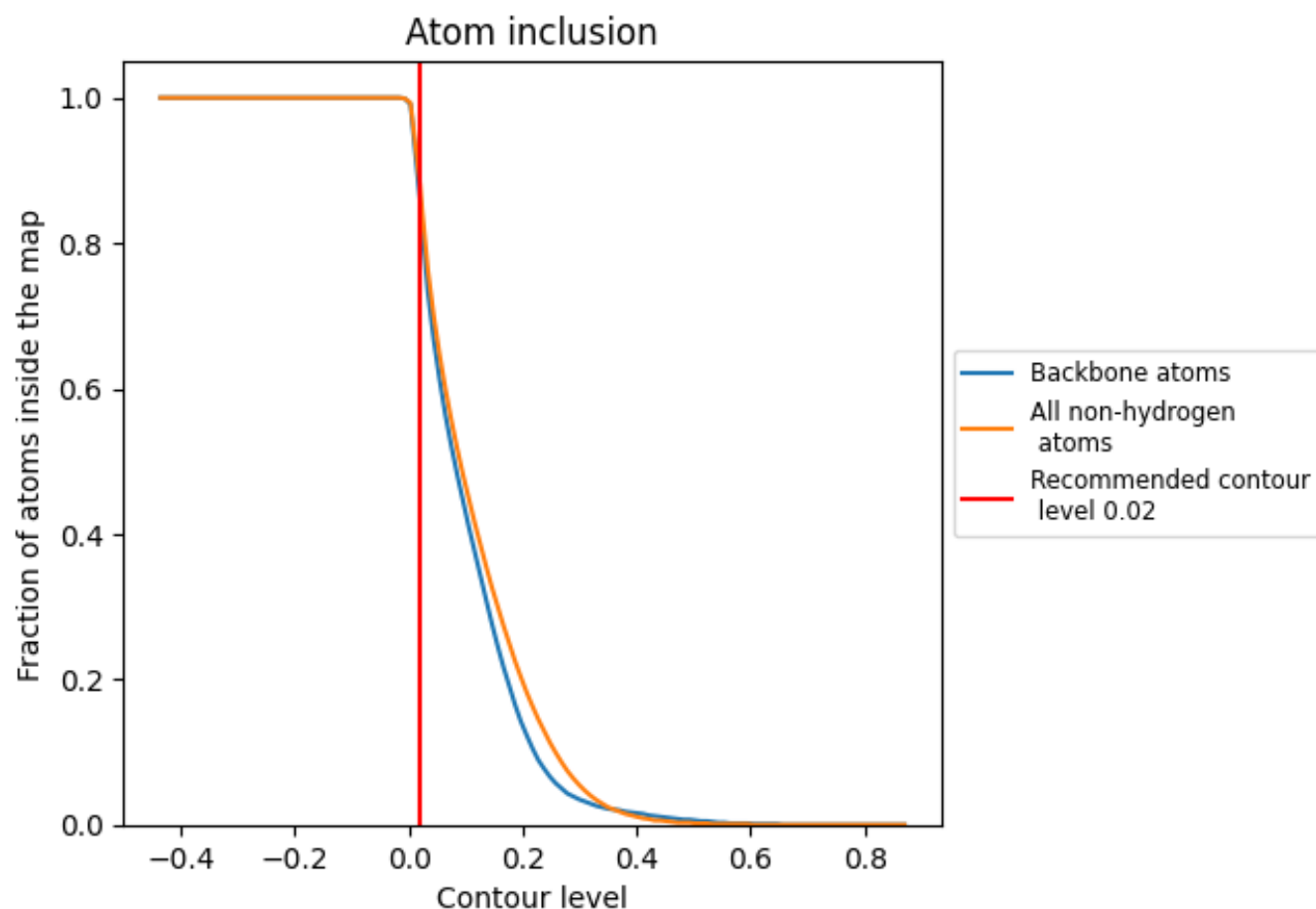
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 88% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8800	 0.5540
1	 0.9950	 0.6740
2	 0.9670	 0.6510
3	 0.9690	 0.6180
4	 0.9950	 0.6640
5	 0.9710	 0.6580
6	 0.9730	 0.6310
7	 0.9940	 0.7060
8	 0.9920	 0.6790
9	 0.9830	 0.6500
A	 0.9740	 0.6430
B	 0.8330	 0.4280
C	 0.9780	 0.5870
D	 0.9850	 0.6690
E	 0.9880	 0.6770
F	 0.9830	 0.6610
G	 0.8410	 0.4850
H	 0.9260	 0.5710
I	 0.3590	 0.4250
J	 0.9830	 0.6640
K	 0.9790	 0.6620
L	 0.9770	 0.6620
M	 0.9810	 0.6540
N	 0.9900	 0.6810
O	 0.9570	 0.5950
P	 0.9840	 0.6580
Q	 0.9910	 0.6880
R	 0.9730	 0.6490
S	 0.9870	 0.6720
T	 0.9650	 0.6270
U	 0.9590	 0.6050
V	 0.9080	 0.5920
a	 0.5170	 0.3480
b	 0.4150	 0.3520
c	 0.5660	 0.3760



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Chain	Atom inclusion	Q-score
d	 0.7760	 0.4890
e	 0.8030	 0.4980
f	 0.2030	 0.2060
g	 0.8200	 0.4980
h	 0.2920	 0.1840
i	 0.2410	 0.2340
j	 0.8230	 0.5110
k	 0.7520	 0.5030
l	 0.2110	 0.1460
m	 0.3770	 0.2920
n	 0.8680	 0.5260
o	 0.7570	 0.4570
p	 0.8110	 0.4840
q	 0.8030	 0.5120
r	 0.1110	 0.1560
s	 0.8810	 0.5030
t	 0.6930	 0.4970