



Full wwPDB EM Validation Report ⓘ

Mar 25, 2026 – 01:26 AM UTC

PDB ID : 5GAH / pdb_00005gah
EMDB ID : EMD-8004
Title : RNC in complex with SRP with detached NG domain
Authors : Jomaa, A.; Boehringer, D.; Leibundgut, M.; Ban, N.
Deposited on : 2015-11-26
Resolution : 3.80 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

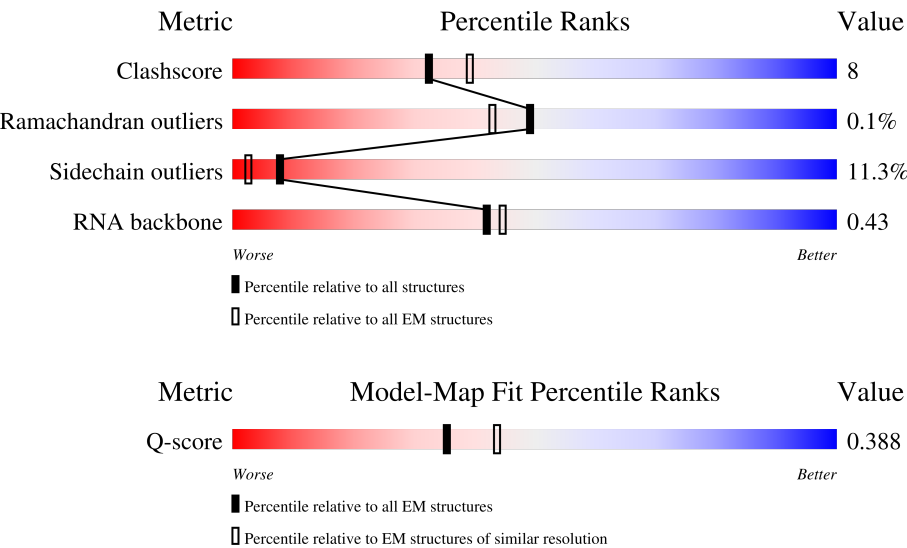
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



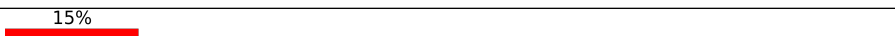
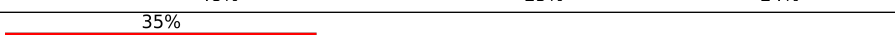
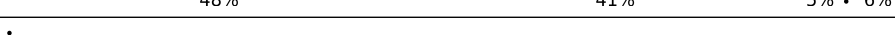
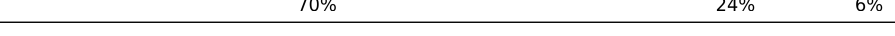
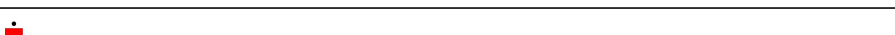
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	10198 (3.30 - 4.30)

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

Mol	Chain	Length	Quality of chain
1	1	113	15%21%62%
2	2	3	33%67%
3	A	2903	56%36%7%

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Mol	Chain	Length	Quality of chain
4	B	120	
5	C	273	
6	D	209	
7	E	201	
8	F	179	
9	G	177	
10	H	149	
11	I	165	
12	J	142	
13	K	142	
14	L	123	
15	M	144	
16	N	136	
17	O	127	
18	P	117	
19	Q	115	
20	R	118	
21	S	103	
22	T	110	
23	U	100	
24	V	104	
25	W	94	
26	X	85	
27	Y	78	
28	Z	63	

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Mol	Chain	Length	Quality of chain
29	a	59	69%27%
30	b	57	56%32%11%
31	c	55	71%20%7%
32	d	46	70%26%
33	e	65	57%40%
34	f	38	68%24%8%
35	i	453	9%17%10%72%
36	k	18	22%56%33%11%

2 Entry composition

There are 38 unique types of molecules in this entry. The entry contains 94027 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called SRP 4.5S RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	43	Total	C	N	O	P	0	0
			926	413	174	296	43		

- Molecule 2 is a RNA chain called tRNA CCAend.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	3	Total	C	N	O	P	0	0
			62	28	11	20	3		

- Molecule 3 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	2883	Total	C	N	O	P	0	0
			61902	27613	11397	20009	2883		

- Molecule 4 is a RNA chain called 5S rRNA.

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	H	149	Total	C	N	O	S	0	0
			1110	699	197	213	1		

- Molecule 11 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	I	125	Total	C	N	O	S	0	0
			946	599	169	175	3		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	85	VAL	SER	conflict	UNP P0A7J3
I	86	THR	MET	conflict	UNP P0A7J3

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	J	134	Total	C	N	O	S	0	0
			979	619	169	185	6		

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	O	125	Total	C	N	O	S	0	0
			993	613	202	173	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	P	117	Total	C	N	O	S	0	0
			900	557	179	163	1		

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	U	95	Total	C	N	O	S	0	0
			756	479	141	135	1		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
24	V	102	Total	C	N	O	0	0
			779	492	146	141		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	X	76	Total	C	N	O	S	0	0
			580	359	117	103	1		

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

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

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

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

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

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

- Molecule 30 is a protein called 50S ribosomal protein L32.

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

- Molecule 31 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	c	51	Total	C	N	O	0	0
			414	266	76	72		

- Molecule 32 is a protein called 50S ribosomal protein L34.

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

- Molecule 33 is a protein called 50S ribosomal protein L35.

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

- Molecule 34 is a protein called 50S ribosomal protein L36.

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

- Molecule 35 is a protein called Signal recognition particle protein Ffh.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	i	126	Total	C	N	O	S	0	0
			916	575	169	161	11		

- Molecule 36 is a protein called 1A9L SS.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	18	Total	C	N	O	S	0	0
			137	94	20	22	1		

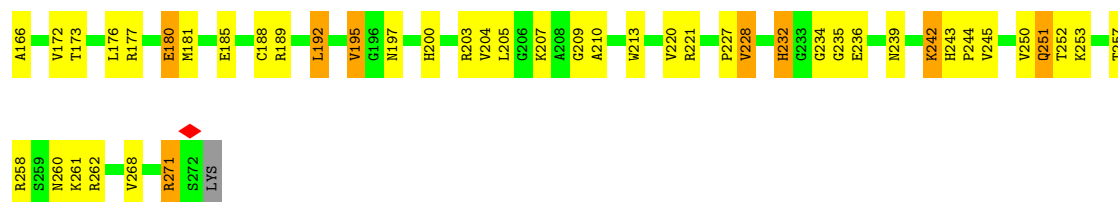
- Molecule 37 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
37	2	1	Total	Mg	0
			1	1	
37	A	412	Total	Mg	0
			412	412	
37	B	11	Total	Mg	0
			11	11	
37	C	2	Total	Mg	0
			2	2	
37	D	1	Total	Mg	0
			1	1	
37	E	1	Total	Mg	0
			1	1	
37	P	1	Total	Mg	0
			1	1	
37	R	1	Total	Mg	0
			1	1	
37	b	1	Total	Mg	0
			1	1	

- Molecule 38 is ZINC ION (CCD ID: ZN) (formula: Zn).

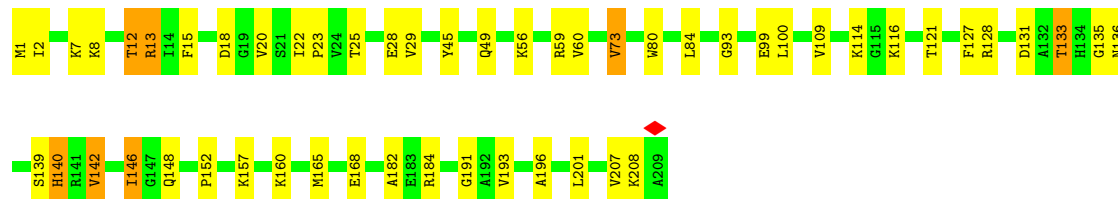
Mol	Chain	Residues	Atoms		AltConf
38	f	1	Total	Zn	0
			1	1	

A1853	G1763	U1648	A1545	A1453	U1379	G1259	C1140	A1067	A983	G879	G799	A706	U519
A1858	C1764	G1649	G1546	C1463	U1379	A1262	U1141	G1068	A984	G880	A800	G707	G520
U1859	G1770	G1653	U1554	G1464	A1383	A1262	A1142	A1069	A981	G881	A609	C610	U521
G1869	A1773	A1655	G1560	U1466	C1386	U1267	G1149	G1071	C987	G	A804	G713	A526
C1870	C1774	A1655	U1563	U1467	A1387	A1268	C1150	A1070	A980	U	G805	A613	G527
A1871	U1775	G1660	C1564	U1468	G1388	A1269	G1154	A1073	A992	C	U807	A614	A528
A1872	U1780	G1667	C1566	U1469	U1394	A1272	A1155	C1076	C994	C	G808	U615	A529
C1873	U1781	A1672	U1566	U1474	A1395	A1272	A1169	A1077	C994	C	U811	G620	C531
G1875	U1782	G1673	A1569	U1482	U1396	A1275	G1170	U1078	A996	C	U812	A621	A532
A1876	A1785	G1674	A1570	G1482	U1397	A1275	C1170	C1079	G997	A	C814	G622	G533
A1878	U1786	A1677	A1572	G1483	C1398	A1287	U1173	U1082	C998	C	A819	A627	G543
U1880	A1789	A1677	A1572	U1484	C1399	G1288	U	U1083	U999	U894	G628	A627	C544
C1881	C1790	G1681	U1576	U1485	G1401	C1289	U	A1084	A1001	U895	G629	U	U545
G1888	A1791	A1689	C1577	C1489	U1402	C1290	G1177	A1085	A1000	A	G630	A631	G548
A1794	U1794	A1689	U1578	A1490	C1404	U1294	G1178	A1086	G1002	A896	A632	A632	G549
C1795	C1795	A1700	G1581	A1491	U1405	G1300	U1179	A1087	C1005	C897	A633	A633	C550
U1796	U1796	G1706	C1582	C1492	U1406	A1301	U1180	A1088	C1006	C898	A634	A634	G551
G1797	U1797	G1707	U1583	A1493	U1406	A1302	U1181	A1089	C1007	A899	G637	A637	U552
U1798	U1798	G1707	U1584	A1494	G1410	A1302	G1182	A1090	A1008	C908	A637	A637	U558
G1799	C1799	A1689	C1585	A1495	C1414	A1308	G1187	G1093	A1009	A909	G638	A638	U558
C1800	U1709	A1689	U1585	A1496	U1415	A1308	G1187	U1094	U1012	A910	U639	U639	G561
A1801	G1710	A1689	A1590	C1497	U1416	U1313	G1187	A1095	C1013	A911	U640	U640	U562
A1802	A1711	A1689	A1591	C1498	U1416	U1313	G1187	A1096	U1013	U832	U641	U641	U562
G1906	G1906	A1711	C1592	G1500	U1418	U1313	U1199	A1097	A1021	C915	U642	U642	C564
C1807	G1807	G1715	A1597	G1501	A1419	G1324	U1199	A1098	G1022	A917	G647	G647	C565
A1808	A1808	A1721	A1598	A1502	A1420	A1327	A1205	A1099	U1023	G916	G648	G648	U566
C1809	U1709	A1722	U1598	A1503	G1421	A1328	G1206	U1101	G1024	U839	G649	G649	U567
U1810	C1810	A1722	A1603	C1507	G1422	U1329	U1206	C1102	G1025	C840	U650	U650	U568
G1811	U1811	A1725	A1603	U1507	G1423	G1332	G1210	C1103	A1026	G930	U651	U651	U569
C1816	U1917	U1725	A1603	A1508	G1424	G1332	G1211	U832	A1027	U931	U653	U653	G570
G1817	U1817	U1729	C1606	A1509	G1425	A1337	G1212	A933	A1028	U847	A654	A654	U571
U1818	C1818	C1730	C1607	G1510	U1426	U1338	G1218	C946	U1033	U848	A655	A655	A572
A1819	U1819	C1732	A1608	G1511	A1427	G1339	G1218	A947	U1033	U849	U657	U657	U573
U1820	C1820	C1732	A1610	A1515	C1428	U1340	A1230	C948	G1038	U850	U658	U658	A574
A1821	U1821	A1735	A1614	G1516	G1432	U1341	U1231	C949	A1039	U857	U658	U658	A575
C1822	C1822	U1736	C1615	G1517	A1434	A1342	U1231	G953	A1040	G857	A668	A668	G577
U1825	U1825	G1737	A1616	G1524	G1435	U1344	G1236	G953	C1044	G858	G669	G669	C581
G1738	U1738	G1737	A1616	A1525	U1436	C1345	A1237	C957	C1045	U860	A670	A670	G581
G1738	U1738	G1737	A1616	A1525	U1436	C1345	A1237	U958	A1046	U861	C671	C671	G585
U1826	U1826	G1738	G1627	G1526	G1437	G1346	G1238	A959	G1047	G862	C672	C672	A586
U1827	U1827	G1743	G1628	G1527	U1438	G1346	C1243	A960	A1048	A863	C673	C673	A586
G1829	A1829	A1744	G1631	A1528	A1439	G1351	A1247	C961	G1056	G864	A675	A675	U591
C1837	C1837	U1751	G1631	G1529	U1442	A1354	A1247	C961	G1056	G865	A676	A676	A592
U1838	U1838	C1752	A1634	C1533	U1443	G1355	G1248	C968	A1057	U790	U677	U677	U593
G1839	G1839	G1756	A1637	U1534	G1446	C1363	U1249	G969	U1060	U791	C678	C678	U594
G1846	U1757	A1757	C1638	A1536	C1447	C1363	G1251	U970	U1061	A792	C679	C679	C595
A1847	U1758	U1758	C1639	G1537	G1448	A1365	G1252	U971	U1062	A793	C680	C680	C595
A1848	U1759	A1759	G1645	A1366	G1449	A1366	A1253	A972	G1063	A794	G681	G681	C601
U1849	C1760	C1761	G1645	A1367	U1450	A1367	C1256	A973	G1064	C795	A685	A685	A602
G1850	U1850	A1762	U1647	A1544	G1452	G1374	C1257	A974	U1065	G796	U686	U686	A603
C1947	C1947	A1762	U1647	A1544	G1452	G1374	C1257	A974	U1065	G797	A686	A686	G605



• Molecule 6: 50S ribosomal protein L3

Chain D: 75% 22% .



• Molecule 7: 50S ribosomal protein L4

Chain E: 75% 23% .



• Molecule 8: 50S ribosomal protein L5

Chain F: 57% 36% 6% .



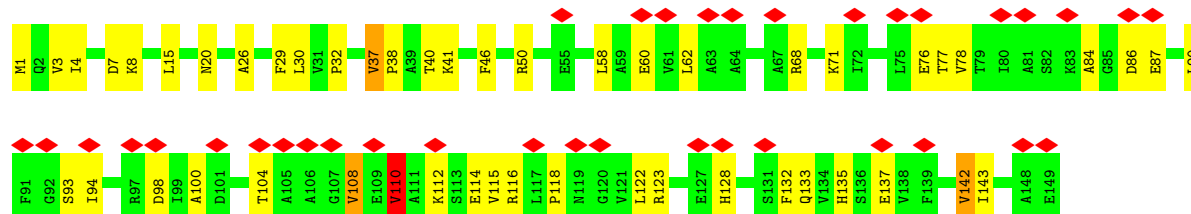
• Molecule 9: 50S ribosomal protein L6

Chain G: 67% 29% .

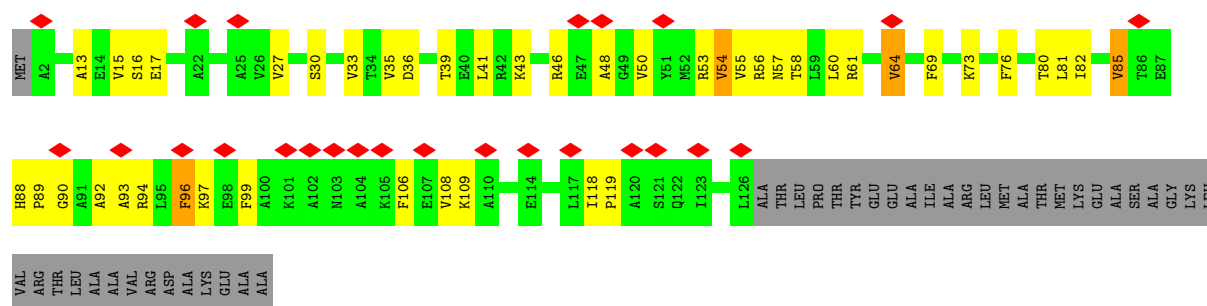




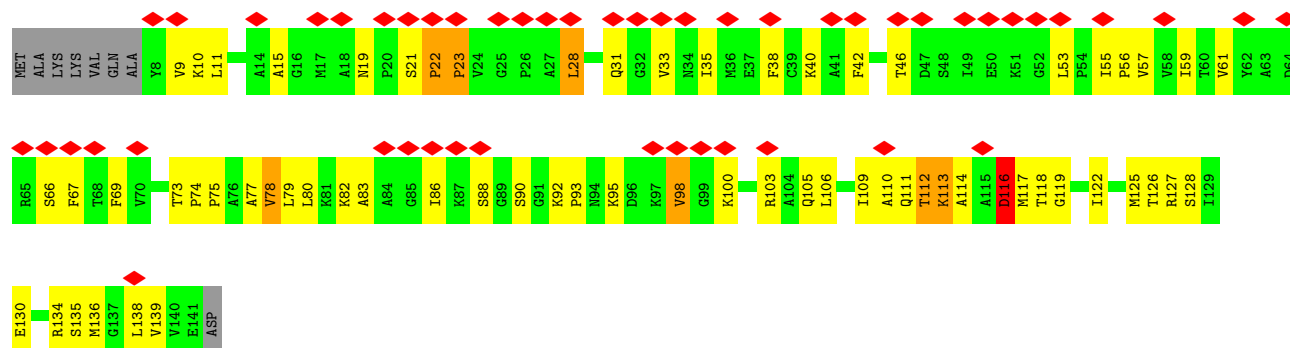
- Molecule 10: 50S ribosomal protein L9



- Molecule 11: 50S ribosomal protein L10

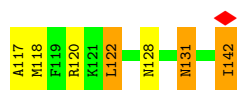


- Molecule 12: 50S ribosomal protein L11



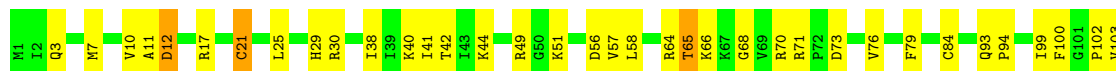
- Molecule 13: 50S ribosomal protein L13





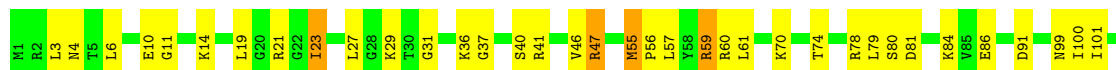
- Molecule 14: 50S ribosomal protein L14

Chain L: 67% 30%



- Molecule 15: 50S ribosomal protein L15

Chain M: 71% 26%



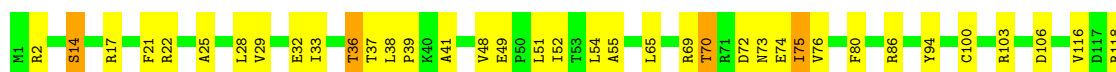
- Molecule 16: 50S ribosomal protein L16

Chain N: 68% 29%



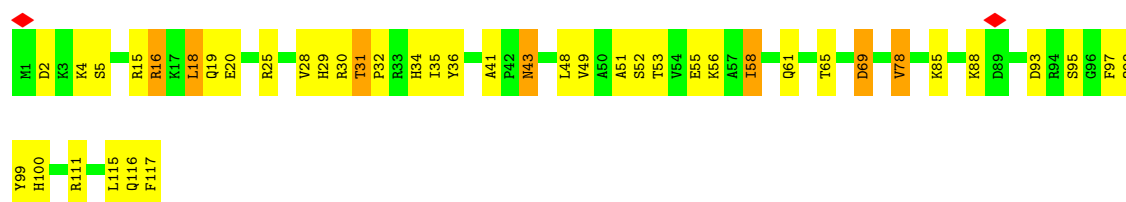
- Molecule 17: 50S ribosomal protein L17

Chain O: 69% 27%



- Molecule 18: 50S ribosomal protein L18

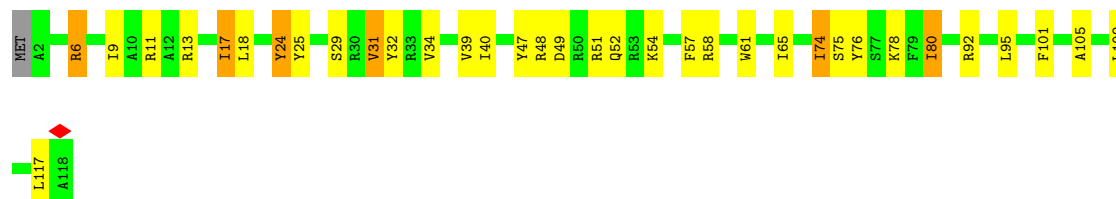
Chain P: 63% 31% 6%



- Molecule 19: 50S ribosomal protein L19



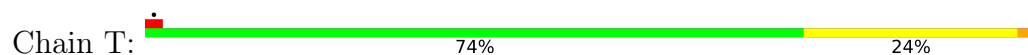
- Molecule 20: 50S ribosomal protein L20



- Molecule 21: 50S ribosomal protein L21



- Molecule 22: 50S ribosomal protein L22

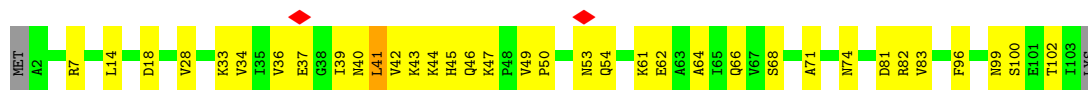


- Molecule 23: 50S ribosomal protein L23



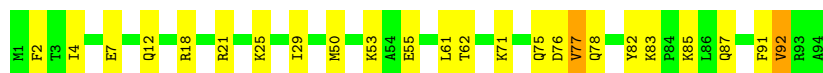
- Molecule 24: 50S ribosomal protein L24

Chain V:  64% 33% ..



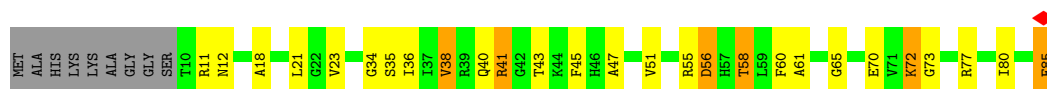
- Molecule 25: 50S ribosomal protein L25

Chain W:  74% 23% .



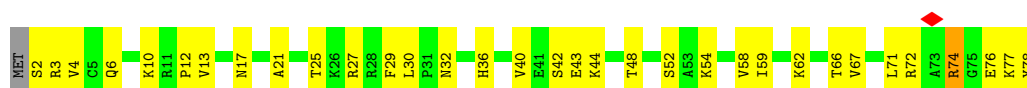
- Molecule 26: 50S ribosomal protein L27

Chain X:  58% 25% 7% 11%



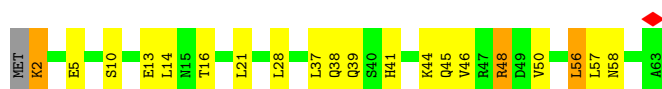
- Molecule 27: 50S ribosomal protein L28

Chain Y:  56% 41% ..



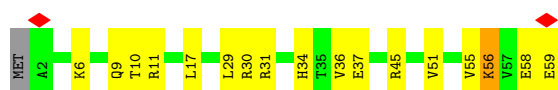
- Molecule 28: 50S ribosomal protein L29

Chain Z:  67% 27% 5% .



- Molecule 29: 50S ribosomal protein L30

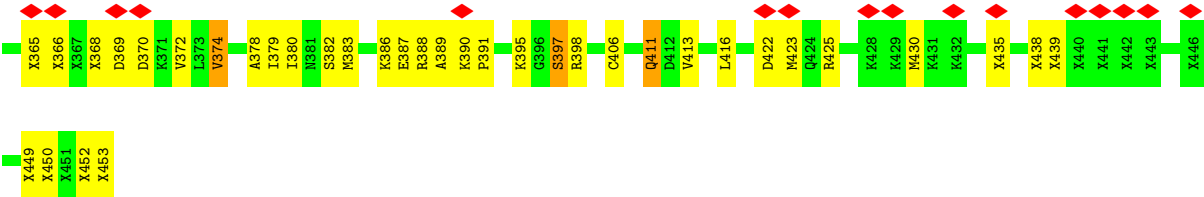
Chain a:  69% 27% ..



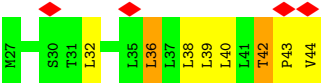
- Molecule 30: 50S ribosomal protein L32

Chain b:  56% 32% 11% .





● Molecule 36: 1A9L SS



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	46409	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 ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.390	Depositor
Minimum map value	-0.215	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	398.88, 398.88, 398.88	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.385, 1.385, 1.385	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	0.42	0/1037	0.52	0/1616
2	2	0.35	0/68	0.51	0/103
3	A	0.35	0/69329	0.48	1/108152 (0.0%)
4	B	0.27	0/2872	0.40	0/4478
5	C	0.60	0/2121	0.96	1/2852 (0.0%)
6	D	0.60	0/1586	0.95	5/2134 (0.2%)
7	E	0.57	0/1571	0.91	0/2113
8	F	0.51	1/1434 (0.1%)	0.93	5/1926 (0.3%)
9	G	0.51	0/1343	0.97	3/1816 (0.2%)
10	H	0.59	0/1121	0.89	1/1515 (0.1%)
11	I	0.72	0/958	0.95	0/1292
12	J	0.94	1/993 (0.1%)	1.13	8/1341 (0.6%)
13	K	0.58	0/1152	0.88	2/1551 (0.1%)
14	L	0.57	0/955	0.97	2/1279 (0.2%)
15	M	0.57	0/1062	0.98	3/1413 (0.2%)
16	N	0.58	0/1093	0.96	6/1460 (0.4%)
17	O	0.61	0/1006	0.95	1/1345 (0.1%)
18	P	0.50	0/910	0.93	0/1219
19	Q	0.54	0/929	0.94	2/1242 (0.2%)
20	R	0.73	0/960	0.91	1/1278 (0.1%)
21	S	0.57	0/829	0.95	0/1107
22	T	0.66	0/864	1.05	2/1156 (0.2%)
23	U	0.60	1/763 (0.1%)	0.95	0/1021
24	V	0.45	0/787	0.88	2/1051 (0.2%)
25	W	0.47	0/766	0.92	0/1025
26	X	0.59	0/587	0.98	2/776 (0.3%)
27	Y	0.61	0/635	0.92	0/848
28	Z	0.51	0/502	0.90	0/667
29	a	0.53	0/453	0.87	0/605
30	b	0.55	0/450	0.89	0/599
31	c	0.55	0/421	1.01	2/561 (0.4%)
32	d	0.66	0/380	0.95	0/498

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	e	0.62	0/513	0.97	0/676
34	f	0.60	0/303	0.99	0/397
35	i	0.61	0/672	0.90	2/883 (0.2%)
36	k	1.03	1/137 (0.7%)	1.04	1/186 (0.5%)
All	All	0.43	4/101562 (0.0%)	0.63	52/152181 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
5	C	0	1
9	G	0	1
12	J	0	1
All	All	0	3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	J	22	PRO	CA-C	5.63	1.57	1.52
8	F	108	VAL	CA-CB	5.52	1.57	1.53
36	k	42	THR	CA-C	5.24	1.58	1.52
23	U	94	ASP	N-CA	5.13	1.52	1.46

All (52) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	G	155	GLU	CA-C-N	9.38	129.01	119.82
9	G	155	GLU	C-N-CA	9.38	129.01	119.82
12	J	116	ASP	N-CA-C	8.00	123.25	113.17
12	J	98	VAL	N-CA-C	7.57	120.32	112.83
12	J	22	PRO	N-CA-C	6.55	118.69	110.70
16	N	71	LYS	CA-C-N	6.45	126.67	119.90
16	N	71	LYS	C-N-CA	6.45	126.67	119.90
6	D	140	HIS	N-CA-C	-6.29	103.69	112.12
6	D	142	VAL	CA-C-N	6.28	126.19	119.28
6	D	142	VAL	C-N-CA	6.28	126.19	119.28
14	L	12	ASP	N-CA-C	6.25	117.67	108.86
16	N	108	VAL	CA-C-N	6.22	126.16	119.76
16	N	108	VAL	C-N-CA	6.22	126.16	119.76
8	F	175	PHE	CA-C-N	6.16	126.52	119.93

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	F	175	PHE	C-N-CA	6.16	126.52	119.93
13	K	7	LYS	CA-C-N	6.12	126.56	119.47
13	K	7	LYS	C-N-CA	6.12	126.56	119.47
17	O	70	THR	N-CA-C	6.08	120.86	113.38
35	i	390	LYS	CA-C-N	6.06	125.76	119.82
35	i	390	LYS	C-N-CA	6.06	125.76	119.82
15	M	23	ILE	N-CA-C	5.90	117.35	110.62
14	L	51	LYS	N-CA-C	-5.79	105.97	113.16
6	D	146	ILE	N-CA-C	5.75	118.52	112.83
15	M	61	LEU	N-CA-C	5.71	117.27	110.07
9	G	47	ASP	CB-CA-C	-5.71	110.01	116.63
31	c	40	ASP	CA-C-N	5.51	125.03	119.19
31	c	40	ASP	C-N-CA	5.51	125.03	119.19
12	J	92	LYS	CA-C-N	5.47	125.74	119.83
12	J	92	LYS	C-N-CA	5.47	125.74	119.83
3	A	2423	U	N1-C1'-C2'	5.34	120.01	112.00
36	k	42	THR	N-CA-C	5.31	119.39	112.17
26	X	73	GLY	CA-C-N	5.26	124.93	119.56
26	X	73	GLY	C-N-CA	5.26	124.93	119.56
12	J	119	GLY	N-CA-C	5.26	117.98	111.93
10	H	110	VAL	N-CA-C	5.25	116.18	109.30
16	N	124	LEU	CA-C-N	5.25	124.86	119.56
16	N	124	LEU	C-N-CA	5.25	124.86	119.56
19	Q	21	ARG	CA-C-N	-5.22	114.86	120.03
19	Q	21	ARG	C-N-CA	-5.22	114.86	120.03
15	M	59	ARG	N-CA-C	-5.15	105.84	112.68
12	J	23	PRO	N-CA-C	5.14	120.28	113.40
20	R	101	PHE	N-CA-C	5.12	116.94	111.36
8	F	106	ILE	CB-CA-C	-5.10	107.38	111.71
24	V	49	VAL	CA-C-N	5.09	124.58	119.19
24	V	49	VAL	C-N-CA	5.09	124.58	119.19
12	J	100	LYS	N-CA-C	5.07	117.42	108.75
22	T	86	MET	CA-C-N	5.04	125.32	119.93
22	T	86	MET	C-N-CA	5.04	125.32	119.93
6	D	191	GLY	N-CA-C	5.03	118.14	111.70
5	C	154	LEU	N-CA-C	5.01	117.49	110.23
8	F	83	TYR	CA-C-N	-5.01	114.17	119.98
8	F	83	TYR	C-N-CA	-5.01	114.17	119.98

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	C	232	HIS	Peptide
9	G	47	ASP	Peptide
12	J	19	ASN	Peptide

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	926	0	467	17	0
2	2	62	0	34	1	0
3	A	61902	0	31133	716	0
4	B	2569	0	1301	20	0
5	C	2082	0	2154	50	0
6	D	1565	0	1616	33	0
7	E	1552	0	1619	29	0
8	F	1410	0	1444	43	0
9	G	1323	0	1371	36	0
10	H	1110	0	1148	23	0
11	I	946	0	978	31	0
12	J	979	0	1028	42	0
13	K	1129	0	1162	24	0
14	L	946	0	1023	22	0
15	M	1053	0	1129	28	0
16	N	1074	0	1157	25	0
17	O	993	0	1034	26	0
18	P	900	0	935	23	0
19	Q	917	0	962	20	0
20	R	947	0	1019	26	0
21	S	816	0	839	23	0
22	T	857	0	922	16	0
23	U	756	0	817	15	0
24	V	779	0	831	21	0
25	W	753	0	780	16	0
26	X	580	0	594	16	0
27	Y	625	0	652	17	0
28	Z	501	0	531	13	0
29	a	449	0	488	9	0
30	b	444	0	458	18	0
31	c	414	0	442	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
32	d	377	0	418	7	0
33	e	504	0	572	15	0
34	f	302	0	340	13	0
35	i	916	0	945	48	0
36	k	137	0	168	11	0
37	2	1	0	0	0	0
37	A	412	0	0	0	0
37	B	11	0	0	0	0
37	C	2	0	0	0	0
37	D	1	0	0	0	0
37	E	1	0	0	0	0
37	P	1	0	0	0	0
37	R	1	0	0	0	0
37	b	1	0	0	0	0
38	f	1	0	0	0	0
All	All	94027	0	62511	1312	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 8.

All (1312) 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)
3:A:1818:U:OP2	5:C:156:ARG:NH1	2.00	0.95
3:A:1168:G:H1	3:A:1181:U:H3	1.20	0.90
3:A:63:A:H5'	35:i:449:UNK:HG1	1.54	0.89
3:A:276:U:O2	3:A:278:A:N6	2.08	0.87
3:A:1827:U:OP2	5:C:221:ARG:NH1	2.08	0.86
10:H:3:VAL:HG12	10:H:38:PRO:HA	1.57	0.86
3:A:2135:A:N6	3:A:2156:G:O2'	2.10	0.84
3:A:287:G:O6	3:A:352:A:N6	2.10	0.84
3:A:2107:G:H1	3:A:2182:U:H3	1.22	0.83
5:C:107:PRO:HD2	5:C:110:LEU:HD22	1.59	0.82
3:A:2478:A:H5'	34:f:32:LYS:HD3	1.62	0.81
3:A:807:U:OP2	15:M:41:ARG:NH1	2.14	0.81
15:M:109:LYS:HG2	15:M:126:ARG:HB2	1.64	0.80
3:A:994:C:O2	21:S:10:LYS:NZ	2.16	0.79
3:A:2128:G:N3	3:A:2173:A:O2'	2.14	0.79
18:P:15:ARG:NH2	18:P:95:SER:OG	2.18	0.77
11:I:41:LEU:HD21	11:I:96:PHE:HE1	1.50	0.77
30:b:43:ILE:HG22	30:b:49:TYR:HB2	1.66	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
35:i:380:ILE:O	35:i:388:ARG:NH1	2.18	0.77
5:C:245:VAL:HG12	5:C:251:GLN:HA	1.67	0.76
3:A:614:A:O2'	3:A:616:A:N7	2.18	0.76
3:A:2135:A:HO2'	3:A:2159:G:HO2'	1.32	0.76
29:a:6:LYS:HG2	29:a:37:GLU:HG2	1.68	0.75
3:A:2599:G:N7	5:C:236:GLU:HB2	2.02	0.74
3:A:545:U:O2	3:A:548:G:N1	2.19	0.74
34:f:18:LYS:HE2	34:f:21:GLY:HA2	1.70	0.73
3:A:2848:G:O2'	3:A:2867:G:N2	2.19	0.73
5:C:181:MET:HB2	5:C:268:VAL:HB	1.69	0.73
3:A:92:U:H3	35:i:453:UNK:HB1	1.54	0.72
3:A:720:U:H2'	3:A:721:A:C8	2.24	0.72
13:K:131:ASN:OD1	13:K:131:ASN:N	2.22	0.72
3:A:2119:A:N6	3:A:2167:U:O2	2.22	0.72
3:A:331:C:H41	3:A:1210:G:H22	1.37	0.72
7:E:1:MET:HG3	7:E:14:VAL:HG23	1.71	0.71
13:K:70:THR:OG1	13:K:71:ASP:OD1	2.08	0.71
3:A:331:C:H41	3:A:1210:G:N2	1.89	0.71
3:A:2423:U:H2'	3:A:2424:C:O4'	1.89	0.71
14:L:70:ARG:HD3	14:L:76:VAL:HG22	1.72	0.70
3:A:1801:A:OP2	5:C:150:LYS:NZ	2.18	0.70
3:A:2310:C:H2'	8:F:77:PHE:HE2	1.54	0.70
3:A:2163:A:OP1	3:A:2170:A:O2'	2.08	0.70
11:I:50:VAL:HG22	11:I:85:VAL:HG13	1.74	0.70
3:A:62:U:H4'	35:i:449:UNK:HB2	1.73	0.70
3:A:1069:A:H4'	3:A:1070:A:H5''	1.71	0.70
3:A:971:G:H2'	3:A:972:A:O4'	1.92	0.70
3:A:258:G:H1'	15:M:104:GLN:HE22	1.56	0.69
21:S:40:MET:HE2	21:S:42:ALA:HB2	1.74	0.69
3:A:93:G:H22	35:i:450:UNK:HB2	1.56	0.69
3:A:513:A:O2'	20:R:11:ARG:NH1	2.26	0.69
3:A:1340:U:OP1	23:U:19:LYS:NZ	2.26	0.69
9:G:35:ARG:HD3	9:G:71:LEU:HD13	1.74	0.69
11:I:43:LYS:HG2	11:I:46:ARG:HH22	1.56	0.68
14:L:79:PHE:HD1	19:Q:70:VAL:HG22	1.58	0.68
3:A:1536:C:H4'	3:A:1537:G:H5''	1.75	0.68
24:V:53:ASN:HD21	35:i:365:UNK:HA	1.57	0.68
3:A:2830:C:H5''	6:D:56:LYS:HE3	1.75	0.68
3:A:362:A:H3'	3:A:363:G:H8	1.59	0.68
3:A:2135:A:O2'	3:A:2159:G:O2'	2.06	0.68
12:J:79:LEU:HB3	12:J:109:ILE:HG12	1.76	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:L:21:CYS:HA	14:L:41:ILE:HG22	1.76	0.68
3:A:249:C:O2	33:e:12:LYS:NZ	2.26	0.67
3:A:878:A:H3'	3:A:879:G:H8	1.60	0.67
3:A:358:U:H2'	3:A:359:G:H8	1.60	0.67
18:P:31:THR:HG22	18:P:34:HIS:H	1.59	0.67
4:B:54:G:H21	8:F:26:MET:HE3	1.58	0.67
3:A:286:U:H2'	3:A:287:G:H8	1.60	0.67
3:A:2103:C:O2	3:A:2186:G:N1	2.27	0.67
3:A:2122:U:OP1	3:A:2168:G:N2	2.26	0.67
3:A:196:A:OP2	15:M:47:ARG:NH1	2.28	0.66
3:A:1105:U:H2'	3:A:1106:G:C8	2.29	0.66
3:A:286:U:H2'	3:A:287:G:C8	2.31	0.66
27:Y:32:ASN:O	27:Y:52:SER:HA	1.95	0.66
3:A:2209:G:H1	3:A:2215:C:H42	1.44	0.66
3:A:2590:A:H2'	3:A:2591:C:H6	1.61	0.66
13:K:31:GLU:HG3	13:K:142:ILE:HG13	1.77	0.66
3:A:2305:U:C2	8:F:151:GLY:HA3	2.31	0.66
3:A:2713:U:H3'	3:A:2714:G:H5''	1.77	0.66
10:H:84:ALA:HA	10:H:90:LEU:HA	1.78	0.66
4:B:43:C:O2	8:F:92:ARG:NH2	2.28	0.66
3:A:2216:G:H2'	3:A:2217:G:H8	1.60	0.66
3:A:572:A:OP2	21:S:80:ARG:NH2	2.27	0.66
35:i:383:MET:O	35:i:388:ARG:NH2	2.29	0.66
3:A:2303:G:O2'	8:F:121:SER:O	2.13	0.65
28:Z:10:SER:N	28:Z:13:GLU:OE1	2.26	0.65
3:A:1344:U:O2'	3:A:1345:C:OP1	2.14	0.65
3:A:1597:A:H5''	3:A:1598:A:H5'	1.78	0.65
9:G:9:VAL:HG22	9:G:69:ARG:HE	1.61	0.65
3:A:860:U:H1'	3:A:2268:A:H5'	1.78	0.65
7:E:87:ALA:O	7:E:88:ARG:NH2	2.30	0.65
16:N:50:ARG:O	16:N:54:THR:OG1	2.13	0.65
1:1:49:G:H1	1:1:60:A:H61	1.43	0.65
8:F:158:THR:HG22	8:F:160:ALA:H	1.62	0.65
25:W:2:PHE:HB3	25:W:50:MET:HE3	1.77	0.65
3:A:370:G:O2'	3:A:424:G:OP1	2.11	0.65
3:A:1794:A:H2'	3:A:1795:C:H6	1.61	0.65
3:A:1869:G:N2	3:A:1871:A:O2'	2.30	0.64
3:A:1007:C:OP1	13:K:37:ARG:NH2	2.29	0.64
3:A:1342:A:O2'	3:A:1344:U:OP2	2.16	0.64
3:A:2674:G:H4'	14:L:30:ARG:HG3	1.78	0.64
3:A:1510:G:H2'	3:A:1511:G:C8	2.32	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:2788:C:O2'	3:A:2809:A:N3	2.28	0.64
26:X:65:GLY:HA2	26:X:85:GLU:HG2	1.78	0.64
3:A:2424:C:H5''	3:A:2425:A:H5'	1.79	0.64
30:b:28:LEU:HD13	30:b:37:LYS:HB3	1.78	0.64
3:A:968:C:H2'	3:A:969:G:H8	1.62	0.64
3:A:1105:U:H2'	3:A:1106:G:H8	1.63	0.64
35:i:368:UNK:HG2	35:i:372:VAL:HG23	1.79	0.64
3:A:322:A:H5'	3:A:340:A:H1'	1.78	0.63
3:A:2102:G:N2	3:A:2187:U:O2	2.31	0.63
20:R:74:ILE:HD11	20:R:78:LYS:HB3	1.80	0.63
3:A:1094:U:N3	3:A:1097:U:OP2	2.30	0.63
3:A:1614:A:N1	22:T:93:ALA:HB2	2.13	0.63
8:F:74:VAL:HG22	8:F:79:ILE:HD11	1.79	0.63
8:F:144:ASP:N	8:F:144:ASP:OD1	2.30	0.63
16:N:14:LYS:O	16:N:71:LYS:NZ	2.32	0.63
3:A:1980:G:O2'	3:A:1982:U:OP2	2.16	0.63
21:S:41:ILE:HB	21:S:48:LYS:HD2	1.79	0.63
22:T:82:MET:HB3	22:T:84:ARG:HH22	1.63	0.63
3:A:284:U:H3	3:A:356:G:H1	1.44	0.63
36:k:39:LEU:O	36:k:42:THR:N	2.29	0.63
3:A:2151:U:H2'	3:A:2152:G:C8	2.34	0.63
19:Q:91:ALA:HB2	19:Q:113:ARG:HA	1.80	0.63
3:A:2116:G:N7	3:A:2165:C:N4	2.44	0.62
9:G:170:ARG:NH1	34:f:29:ALA:O	2.24	0.62
25:W:21:ARG:NH2	25:W:87:GLN:O	2.28	0.62
3:A:1433:A:N1	3:A:1434:A:N6	2.47	0.62
3:A:2742:G:OP2	34:f:24:ARG:NH1	2.32	0.62
13:K:117:ALA:HA	13:K:120:ARG:HH21	1.64	0.62
3:A:514:A:N3	3:A:581:C:O2'	2.32	0.62
17:O:49:GLU:HA	17:O:52:ILE:HD12	1.79	0.62
20:R:58:ARG:HA	20:R:61:TRP:CE3	2.34	0.62
3:A:784:G:C6	5:C:228:VAL:HG11	2.35	0.62
19:Q:4:ILE:HD12	19:Q:4:ILE:H	1.65	0.62
3:A:825:A:H2'	3:A:826:U:O4'	1.98	0.62
3:A:2809:A:H2'	3:A:2810:A:C8	2.34	0.62
3:A:2590:A:H2'	3:A:2591:C:C6	2.35	0.62
35:i:350:UNK:HG1	36:k:38:LEU:HD13	1.82	0.62
10:H:68:ARG:HA	10:H:71:LYS:HD2	1.81	0.62
16:N:50:ARG:HA	16:N:53:MET:HE3	1.82	0.62
1:1:62:C:O2'	35:i:382:SER:O	2.15	0.61
3:A:2822:G:O6	17:O:2:ARG:NH1	2.32	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:J:53:LEU:HD11	12:J:82:LYS:HD2	1.83	0.61
11:I:57:ASN:ND2	11:I:76:PHE:O	2.33	0.61
3:A:1079:C:O2'	12:J:134:ARG:NH1	2.33	0.61
15:M:57:LEU:HD13	15:M:60:ARG:HH11	1.65	0.61
35:i:333:ASP:OD1	35:i:333:ASP:N	2.33	0.61
3:A:2310:C:H2'	8:F:77:PHE:CE2	2.35	0.61
3:A:2639:A:H2'	3:A:2640:G:O4'	2.01	0.61
17:O:54:LEU:HD21	17:O:65:LEU:HD23	1.82	0.61
3:A:1001:A:H2'	3:A:1002:G:O4'	2.01	0.61
3:A:2636:C:HO2'	6:D:45:TYR:HH	1.47	0.61
5:C:235:GLY:HA3	5:C:239:ASN:HB2	1.83	0.61
11:I:41:LEU:HD21	11:I:96:PHE:CE1	2.34	0.61
3:A:585:G:N7	20:R:6:ARG:NH1	2.48	0.60
3:A:503:A:H4'	3:A:504:A:H5'	1.83	0.60
22:T:6:LYS:HG2	22:T:104:THR:HG23	1.82	0.60
3:A:570:G:H2'	3:A:2030:A:N7	2.16	0.60
9:G:137:ASP:O	9:G:141:ILE:HG22	2.01	0.60
26:X:56:ASP:OD1	26:X:56:ASP:N	2.28	0.60
30:b:38:HIS:ND1	30:b:39:LEU:O	2.30	0.60
3:A:1076:C:H2'	3:A:1077:A:C8	2.37	0.60
3:A:1363:C:O2'	3:A:1809:A:N3	2.33	0.60
30:b:52:ARG:HB2	30:b:52:ARG:NH2	2.16	0.60
3:A:1794:A:H2'	3:A:1795:C:C6	2.37	0.60
6:D:2:ILE:HG13	6:D:100:LEU:HD21	1.83	0.60
30:b:52:ARG:HB2	30:b:52:ARG:HH21	1.66	0.60
11:I:27:VAL:HG22	11:I:82:ILE:HG22	1.83	0.60
7:E:97:ASN:N	7:E:97:ASN:OD1	2.34	0.60
15:M:81:ASP:HA	15:M:84:LYS:HD2	1.82	0.60
3:A:776:G:O2'	3:A:777:G:OP1	2.19	0.60
3:A:2831:G:OP1	6:D:56:LYS:NZ	2.35	0.60
3:A:355:U:H2'	3:A:356:G:C8	2.37	0.59
6:D:116:LYS:HG3	6:D:165:MET:HE2	1.83	0.59
8:F:44:ILE:HG21	8:F:79:ILE:HG22	1.83	0.59
3:A:2615:U:C2	30:b:4:GLN:HA	2.37	0.59
3:A:1796:U:H2'	3:A:1797:G:H8	1.67	0.59
3:A:1535:A:C8	35:i:435:UNK:HB1	2.37	0.59
3:A:2584:U:H3'	3:A:2585:U:H5''	1.84	0.59
3:A:2819:G:H2'	3:A:2821:A:N7	2.17	0.59
13:K:36:LEU:HD11	13:K:122:LEU:HB2	1.83	0.59
30:b:50:ARG:HB2	30:b:52:ARG:HH12	1.65	0.59
9:G:27:LYS:NZ	9:G:27:LYS:HB3	2.17	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:P:99:TYR:OH	18:P:111:ARG:NH1	2.36	0.59
25:W:4:ILE:HG12	25:W:50:MET:HE1	1.85	0.59
3:A:878:A:H3'	3:A:879:G:C8	2.38	0.59
3:A:2205:A:H61	3:A:2219:U:H3	1.50	0.59
6:D:12:THR:OG1	6:D:13:ARG:N	2.34	0.59
11:I:64:VAL:HG22	11:I:69:PHE:HB2	1.84	0.59
24:V:81:ASP:OD1	24:V:82:ARG:N	2.35	0.59
4:B:7:G:OP1	18:P:4:LYS:NZ	2.27	0.59
3:A:1170:C:O2	3:A:1179:G:N2	2.33	0.58
3:A:2021:C:OP1	20:R:25:TYR:OH	2.21	0.58
3:A:2127:G:O2'	3:A:2128:G:O5'	2.19	0.58
3:A:1808:A:H3'	3:A:1809:A:C8	2.38	0.58
35:i:350:UNK:HA	35:i:353:UNK:HG3	1.84	0.58
3:A:396:G:OP2	27:Y:10:LYS:NZ	2.36	0.58
3:A:833:A:H2'	3:A:834:G:C8	2.38	0.58
3:A:1130:U:O2'	3:A:1131:G:H8	1.87	0.58
3:A:2127:G:O2'	3:A:2128:G:O4'	2.20	0.58
17:O:73:ASN:HA	17:O:76:VAL:HG22	1.86	0.58
21:S:37:GLU:HB3	21:S:53:PHE:CE1	2.39	0.58
25:W:76:ASP:OD1	25:W:77:VAL:N	2.37	0.58
12:J:106:LEU:HB3	12:J:126:THR:HG23	1.85	0.58
33:e:15:LYS:HB2	33:e:23:LYS:HE3	1.84	0.58
18:P:41:ALA:HB2	18:P:48:LEU:HD21	1.86	0.58
6:D:148:GLN:HB2	6:D:152:PRO:HD2	1.85	0.58
3:A:1715:G:O2'	3:A:1743:G:O6	2.17	0.57
3:A:2412:A:H2'	3:A:2413:G:O4'	2.04	0.57
7:E:21:ARG:HD3	7:E:106:LYS:HB3	1.85	0.57
3:A:2291:U:H2'	3:A:2292:U:C6	2.38	0.57
3:A:2602:A:H4'	3:A:2603:G:O5'	2.04	0.57
5:C:227:PRO:HG3	5:C:234:GLY:H	1.69	0.57
17:O:118:ARG:NH2	30:b:54:VAL:O	2.37	0.57
12:J:59:ILE:HD13	12:J:69:PHE:HB3	1.86	0.57
3:A:849:A:H2'	3:A:850:U:C6	2.39	0.57
6:D:157:LYS:HD2	13:K:80:HIS:CE1	2.40	0.57
17:O:94:TYR:O	17:O:116:VAL:HG23	2.05	0.57
3:A:1645:G:H5''	3:A:1646:C:H5'	1.86	0.57
3:A:2447:G:N2	3:A:2450:A:OP2	2.37	0.57
10:H:37:VAL:HG22	10:H:38:PRO:HD2	1.85	0.57
25:W:55:GLU:H	25:W:55:GLU:CD	2.12	0.57
3:A:340:A:H2'	3:A:341:C:O4'	2.05	0.57
3:A:839:U:H2'	3:A:840:C:C6	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:D:13:ARG:HD2	6:D:15:PHE:CZ	2.38	0.57
7:E:112:LEU:HB3	7:E:118:LEU:HB2	1.87	0.57
3:A:876:C:H2'	3:A:877:A:O4'	2.05	0.57
6:D:1:MET:HG2	6:D:2:ILE:H	1.70	0.57
3:A:2216:G:H2'	3:A:2217:G:C8	2.40	0.56
8:F:33:LYS:HG2	8:F:157:THR:HB	1.87	0.56
24:V:18:ASP:OD2	24:V:40:ASN:N	2.38	0.56
3:A:299:A:N1	3:A:322:A:O2'	2.27	0.56
3:A:1905:C:H2'	3:A:1930:G:C8	2.40	0.56
3:A:26:G:C6	3:A:27:G:N1	2.73	0.56
3:A:721:A:H2'	3:A:722:A:C8	2.41	0.56
3:A:859:G:O2'	3:A:916:G:O6	2.22	0.56
3:A:1063:G:H5'	12:J:77:ALA:HB1	1.87	0.56
3:A:1796:U:H2'	3:A:1797:G:C8	2.40	0.56
11:I:60:LEU:O	11:I:64:VAL:HB	2.06	0.56
3:A:480:A:OP2	24:V:44:LYS:NZ	2.23	0.56
5:C:166:ALA:HB3	5:C:173:THR:HB	1.86	0.56
35:i:331:LEU:HD12	35:i:391:PRO:HB3	1.88	0.56
3:A:2162:G:H5''	3:A:2171:A:H2'	1.86	0.56
3:A:388:G:N7	3:A:390:U:H2'	2.21	0.56
3:A:1790:C:H3'	3:A:1828:G:N2	2.21	0.56
9:G:30:ASN:HB3	9:G:79:VAL:HA	1.88	0.56
3:A:1076:C:H2'	3:A:1077:A:H8	1.69	0.56
3:A:2491:U:H5''	3:A:2570:G:H5''	1.88	0.56
4:B:42:C:C5	8:F:66:LEU:HD22	2.41	0.56
3:A:490:C:H41	35:i:425:ARG:HG3	1.70	0.56
3:A:2133:G:H2'	3:A:2157:G:H1	1.70	0.56
3:A:2430:A:N3	3:A:2430:A:H2'	2.21	0.56
3:A:2584:U:H3'	3:A:2585:U:C5'	2.36	0.56
12:J:73:THR:HB	12:J:112:THR:HG22	1.87	0.56
3:A:812:C:H4'	20:R:13:ARG:NH1	2.21	0.56
3:A:1251:C:OP2	20:R:6:ARG:NH2	2.35	0.56
3:A:2298:A:H2'	3:A:2299:U:O4'	2.05	0.56
12:J:53:LEU:HD22	12:J:78:VAL:HG13	1.87	0.56
13:K:72:LYS:HE3	13:K:74:TYR:CE1	2.39	0.56
3:A:1442:U:H2'	3:A:1443:U:C6	2.41	0.55
17:O:2:ARG:NH1	17:O:2:ARG:HB3	2.21	0.55
25:W:62:THR:HG22	25:W:71:LYS:HG2	1.88	0.55
30:b:49:TYR:O	30:b:52:ARG:NH2	2.39	0.55
12:J:127:ARG:HA	12:J:130:GLU:HB2	1.89	0.55
18:P:16:ARG:HA	18:P:16:ARG:HH21	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:19:A:H2'	3:A:20:C:C6	2.41	0.55
3:A:93:G:N2	35:i:450:UNK:HB2	2.21	0.55
3:A:2576:G:O2'	3:A:2579:C:OP2	2.23	0.55
32:d:25:LYS:HG3	32:d:29:GLN:HE21	1.72	0.55
3:A:849:A:H2'	3:A:850:U:H6	1.70	0.55
3:A:1800:C:H5'	5:C:146:MET:HE1	1.88	0.55
3:A:2171:A:H3'	3:A:2173:A:C8	2.41	0.55
35:i:361:UNK:HG1	36:k:43:PRO:HB3	1.89	0.55
3:A:2783:U:H2'	3:A:2784:U:C6	2.42	0.55
10:H:7:ASP:OD1	10:H:8:LYS:N	2.40	0.55
24:V:33:LYS:HB3	24:V:64:ALA:HB1	1.87	0.55
3:A:184:C:H2'	3:A:185:G:C8	2.41	0.55
3:A:591:U:H2'	3:A:592:A:H8	1.72	0.55
3:A:882:G:H1	3:A:894:U:H3	1.54	0.55
5:C:160:THR:HG22	5:C:177:ARG:HG2	1.89	0.55
1:i:48:G:H22	35:i:406:CYS:HB3	1.71	0.55
3:A:639:U:H2'	3:A:640:C:C6	2.42	0.55
3:A:2591:C:H2'	3:A:2592:G:C8	2.41	0.55
17:O:48:VAL:O	17:O:51:LEU:HB2	2.05	0.55
33:e:29:LEU:HD22	33:e:44:LEU:HB3	1.89	0.55
3:A:2070:A:H2'	3:A:2071:A:C8	2.42	0.55
6:D:8:LYS:HB2	6:D:201:LEU:HD11	1.88	0.55
8:F:132:VAL:HG22	8:F:152:LEU:HB3	1.88	0.55
18:P:69:ASP:N	18:P:69:ASP:OD1	2.40	0.55
33:e:17:THR:HG21	33:e:49:MET:HE1	1.87	0.55
3:A:2262:U:H2'	3:A:2263:C:H6	1.72	0.54
8:F:134:GLU:HB3	8:F:136:ILE:HG12	1.89	0.54
3:A:833:A:H2'	3:A:834:G:H8	1.72	0.54
6:D:184:ARG:NH1	19:Q:7:GLN:OE1	2.40	0.54
7:E:88:ARG:HA	7:E:88:ARG:HH21	1.72	0.54
13:K:34:ARG:HH22	13:K:40:HIS:HB3	1.71	0.54
3:A:586:A:H5'	7:E:84:THR:HG21	1.90	0.54
3:A:609:A:H2'	3:A:610:C:O4'	2.08	0.54
3:A:1837:C:H2'	3:A:1899:A:H61	1.73	0.54
3:A:2619:C:H5''	6:D:157:LYS:HG3	1.89	0.54
3:A:996:A:OP2	21:S:10:LYS:HD3	2.07	0.54
3:A:2424:C:H5''	3:A:2425:A:C5'	2.37	0.54
12:J:79:LEU:HA	12:J:82:LYS:HG2	1.88	0.54
3:A:1923:U:H2'	3:A:1924:C:C6	2.43	0.54
3:A:2267:A:H5''	3:A:2268:A:H5''	1.89	0.54
12:J:56:PRO:HD3	12:J:75:PRO:HD3	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:K:37:ARG:HG3	13:K:118:MET:HE1	1.89	0.54
3:A:172:A:H2'	3:A:173:A:C8	2.43	0.54
21:S:48:LYS:HE3	21:S:103:ALA:HB1	1.90	0.54
23:U:68:LYS:HG3	23:U:77:ARG:NH2	2.23	0.54
33:e:54:ASP:O	33:e:58:VAL:HG23	2.08	0.54
23:U:56:GLU:HA	23:U:88:LYS:HE3	1.89	0.54
3:A:2579:C:O2'	6:D:136:ASN:ND2	2.41	0.54
3:A:2845:U:H5''	19:Q:52:ASN:O	2.08	0.54
9:G:104:ASN:ND2	9:G:114:ASP:OD1	2.41	0.54
35:i:365:UNK:O	36:k:42:THR:HG23	2.08	0.54
3:A:2390:U:OP2	33:e:35:LYS:NZ	2.22	0.54
3:A:2834:G:O6	3:A:2879:A:H2'	2.08	0.54
3:A:92:U:N3	35:i:453:UNK:HB1	2.22	0.53
21:S:20:VAL:HG13	21:S:96:VAL:HG23	1.89	0.53
3:A:2443:C:H2'	3:A:2444:G:C8	2.43	0.53
3:A:1048:A:N1	3:A:1112:G:O2'	2.36	0.53
3:A:2808:G:O2'	3:A:2890:G:O6	2.21	0.53
5:C:145:GLU:HB2	5:C:188:CYS:HB3	1.89	0.53
3:A:284:U:O2	3:A:356:G:N2	2.37	0.53
30:b:39:LEU:HB2	30:b:42:HIS:HB2	1.90	0.53
30:b:50:ARG:CB	30:b:52:ARG:HH12	2.21	0.53
3:A:608:A:H2'	3:A:609:A:C8	2.44	0.53
14:L:38:ILE:HD11	14:L:112:PHE:HZ	1.73	0.53
3:A:2547:A:H4'	14:L:29:HIS:CD2	2.44	0.53
14:L:40:LYS:HE3	14:L:57:VAL:HG12	1.91	0.53
33:e:27:ALA:O	33:e:28:ASN:HB2	2.07	0.53
3:A:9:G:O2'	3:A:2800:A:N6	2.42	0.53
3:A:720:U:H2'	3:A:721:A:H8	1.72	0.53
3:A:1056:G:H5''	3:A:1057:A:H5'	1.90	0.53
11:I:88:HIS:ND1	11:I:89:PRO:O	2.42	0.53
3:A:788:A:OP1	3:A:791:C:N4	2.41	0.53
3:A:1069:A:C2	3:A:1096:A:H5''	2.44	0.53
5:C:145:GLU:HG2	5:C:151:GLY:C	2.34	0.53
11:I:54:VAL:HG22	11:I:81:LEU:HD13	1.90	0.53
32:d:25:LYS:HB2	32:d:25:LYS:NZ	2.22	0.53
3:A:2171:A:H3'	3:A:2173:A:H8	1.74	0.53
3:A:1056:G:O2'	3:A:1103:A:N6	2.40	0.52
3:A:1873:G:H2'	3:A:1874:C:H6	1.74	0.52
10:H:116:ARG:HH21	10:H:133:GLN:HB3	1.74	0.52
17:O:36:THR:HG23	17:O:41:ALA:HB2	1.90	0.52
3:A:2086:U:H2'	3:A:2087:G:C8	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:2210:U:H4'	3:A:2211:A:H5'	1.91	0.52
3:A:2280:G:O2'	3:A:2388:A:N1	2.37	0.52
5:C:62:TYR:HA	5:C:86:ASN:HD21	1.73	0.52
35:i:336:GLU:HA	35:i:339:ARG:HG2	1.91	0.52
3:A:68:G:H2'	3:A:69:C:O4'	2.10	0.52
3:A:653:U:H1'	3:A:654:A:H5''	1.91	0.52
3:A:679:C:H2'	3:A:680:C:C6	2.44	0.52
3:A:1187:G:OP1	21:S:85:LYS:NZ	2.31	0.52
3:A:1425:G:H2'	3:A:1426:G:O4'	2.09	0.52
3:A:1428:C:C5	3:A:1569:A:H5''	2.45	0.52
3:A:1993:U:H4'	6:D:133:THR:OG1	2.10	0.52
1:1:60:A:H2'	1:1:61:G:O4'	2.09	0.52
3:A:671:C:H2'	3:A:672:C:H6	1.74	0.52
3:A:1410:G:H1	3:A:1592:C:H42	1.57	0.52
8:F:99:PHE:HD1	8:F:102:ARG:HH22	1.57	0.52
13:K:3:THR:HB	20:R:57:PHE:HE1	1.75	0.52
32:d:8:SER:HB3	32:d:11:LYS:HB2	1.92	0.52
3:A:1421:G:C2	3:A:1422:G:C8	2.98	0.52
1:1:47:A:OP2	1:1:61:G:N1	2.42	0.52
1:1:48:G:H3'	1:1:49:G:H8	1.75	0.52
3:A:845:A:H61	3:A:932:U:H3	1.58	0.52
3:A:1791:A:N6	3:A:1828:G:O2'	2.42	0.52
3:A:2127:G:H2'	3:A:2128:G:C8	2.45	0.52
6:D:114:LYS:HD3	6:D:196:ALA:HB2	1.92	0.52
14:L:7:MET:HE1	14:L:44:LYS:HG3	1.91	0.52
3:A:898:C:H2'	3:A:899:A:O4'	2.10	0.52
21:S:52:PRO:HG2	21:S:53:PHE:CD2	2.45	0.52
30:b:55:ILE:HG22	30:b:57:LYS:HB2	1.92	0.52
3:A:1289:C:H2'	3:A:1290:C:C6	2.45	0.52
3:A:1798:U:H5''	5:C:258:ARG:HB2	1.92	0.52
3:A:2637:U:C2'	3:A:2638:G:H5'	2.39	0.52
4:B:93:C:OP2	25:W:18:ARG:NH1	2.42	0.52
7:E:28:VAL:O	7:E:32:VAL:HG13	2.09	0.52
23:U:93:LEU:HD13	23:U:95:PHE:CZ	2.44	0.52
3:A:90:U:H3'	3:A:91:A:H8	1.74	0.52
3:A:1451:C:H1'	3:A:1452:G:C2	2.45	0.52
3:A:1681:G:H21	3:A:1762:A:H3'	1.75	0.52
3:A:120:U:H4'	3:A:121:G:H5''	1.89	0.52
3:A:2133:G:H21	3:A:2158:A:H62	1.58	0.52
24:V:74:ASN:HD21	24:V:99:ASN:HD21	1.58	0.52
3:A:1437:C:H2'	3:A:1438:U:C6	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1535:A:H8	35:i:435:UNK:HB1	1.73	0.51
12:J:73:THR:OG1	12:J:113:LYS:NZ	2.40	0.51
3:A:256:A:H2'	3:A:257:C:H6	1.74	0.51
3:A:2439:A:H4'	3:A:2440:C:H5''	1.91	0.51
3:A:2850:A:N7	3:A:2868:A:O2'	2.39	0.51
28:Z:2:LYS:HG3	28:Z:5:GLU:OE1	2.10	0.51
33:e:9:GLY:O	33:e:13:ARG:NH2	2.40	0.51
34:f:12:ARG:HB2	34:f:12:ARG:NH1	2.26	0.51
3:A:1790:C:H2'	3:A:1791:A:C5	2.45	0.51
8:F:128:TYR:HE2	8:F:130:MET:HG2	1.76	0.51
3:A:968:C:H2'	3:A:969:G:C8	2.42	0.51
3:A:1000:A:OP2	3:A:1154:G:N1	2.32	0.51
3:A:1115:G:O2'	3:A:1116:G:H5''	2.10	0.51
3:A:1414:C:H2'	3:A:1415:U:O4'	2.11	0.51
7:E:24:ASN:ND2	7:E:27:LEU:HB2	2.25	0.51
3:A:948:C:H2'	3:A:949:G:C8	2.45	0.51
3:A:2647:U:H2'	3:A:2648:G:H8	1.76	0.51
3:A:2720:U:OP1	19:Q:53:ARG:NH2	2.41	0.51
17:O:55:ALA:HA	17:O:80:PHE:CE2	2.45	0.51
1:1:48:G:N2	35:i:378:ALA:O	2.43	0.51
3:A:141:G:H2'	3:A:142:A:O4'	2.11	0.51
3:A:499:U:H2'	3:A:500:G:O4'	2.10	0.51
7:E:145:ASP:HA	7:E:166:LYS:HB3	1.92	0.51
20:R:24:TYR:N	20:R:24:TYR:CD1	2.78	0.51
35:i:435:UNK:HG2	36:k:32:LEU:CD1	2.41	0.51
1:1:39:A:N1	35:i:397:SER:HB3	2.25	0.51
3:A:364:C:H2'	3:A:365:U:C6	2.45	0.51
3:A:576:U:H2'	3:A:577:G:C8	2.46	0.51
7:E:41:GLN:HG2	7:E:43:THR:HG23	1.92	0.51
15:M:36:LYS:O	15:M:40:SER:HB3	2.11	0.51
1:1:63:A:HO2'	35:i:388:ARG:NH2	2.08	0.51
3:A:621:A:OP2	15:M:99:ASN:ND2	2.40	0.51
3:A:2045:C:H4'	30:b:15:MET:HG2	1.93	0.51
3:A:2755:C:C4	34:f:19:ARG:NH1	2.79	0.51
19:Q:16:ASP:OD1	19:Q:16:ASP:N	2.33	0.51
21:S:28:ALA:HB3	21:S:31:GLU:HG3	1.93	0.51
33:e:16:LYS:HE3	33:e:20:GLY:HA2	1.93	0.51
35:i:450:UNK:HG2	35:i:453:UNK:C	2.41	0.51
3:A:645:C:O2'	3:A:646:U:OP1	2.24	0.51
3:A:2271:G:H5''	26:X:18:ALA:HB1	1.93	0.51
3:A:2502:G:H5''	3:A:2503:A:H5''	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:O:36:THR:OG1	17:O:37:THR:N	2.42	0.51
24:V:53:ASN:ND2	35:i:365:UNK:HA	2.26	0.51
33:e:26:HIS:HB3	33:e:44:LEU:HD22	1.93	0.51
3:A:1405:U:H2'	3:A:1406:U:C6	2.46	0.51
3:A:2333:A:P	26:X:77:ARG:HH22	2.34	0.51
12:J:113:LYS:HE3	12:J:116:ASP:HB3	1.92	0.50
16:N:1:MET:HA	16:N:47:GLU:HG3	1.94	0.50
3:A:1394:U:H4'	3:A:1603:A:H4'	1.92	0.50
13:K:32:LEU:O	13:K:36:LEU:HB2	2.12	0.50
22:T:23:LEU:HD22	30:b:24:ALA:HB2	1.92	0.50
3:A:357:C:H2'	3:A:358:U:C6	2.47	0.50
3:A:1132:U:H2'	3:A:1133:A:C8	2.46	0.50
3:A:1927:A:H2'	3:A:1928:A:C8	2.46	0.50
8:F:40:VAL:HG11	8:F:43:ALA:HB2	1.92	0.50
16:N:30:SER:H	16:N:106:ASP:HB3	1.75	0.50
22:T:40:ASN:O	22:T:41:LYS:HG2	2.10	0.50
3:A:256:A:H2'	3:A:257:C:C6	2.46	0.50
3:A:2024:G:H2'	3:A:2025:C:H6	1.76	0.50
3:A:2282:G:C6	3:A:2425:A:C2	3.00	0.50
14:L:64:ARG:NH1	14:L:102:PRO:O	2.44	0.50
15:M:23:ILE:HG12	21:S:82:HIS:CD2	2.47	0.50
3:A:128:C:H2'	3:A:129:C:C6	2.46	0.50
6:D:184:ARG:HH11	19:Q:7:GLN:CD	2.20	0.50
23:U:7:LEU:HD13	23:U:46:ALA:HA	1.92	0.50
20:R:65:ILE:HD11	20:R:95:LEU:HB2	1.93	0.50
24:V:46:GLN:OE1	24:V:54:GLN:NE2	2.44	0.50
35:i:395:LYS:H	35:i:398:ARG:HG3	1.76	0.50
1:l:63:A:O2'	35:i:388:ARG:NH2	2.44	0.50
3:A:90:U:C2	3:A:91:A:N7	2.80	0.50
3:A:987:C:O2'	3:A:1000:A:N3	2.44	0.50
3:A:2183:A:H2'	3:A:2184:A:C8	2.46	0.50
10:H:94:ILE:HB	10:H:122:LEU:HB2	1.94	0.50
28:Z:39:GLN:HB3	28:Z:41:HIS:CE1	2.47	0.50
3:A:738:G:H1'	3:A:759:G:N2	2.27	0.50
3:A:2308:G:H3'	3:A:2310:C:OP2	2.11	0.50
4:B:2:G:H2'	4:B:3:C:C6	2.47	0.50
5:C:132:MET:HG2	5:C:135:ILE:HD12	1.94	0.50
9:G:127:THR:HG22	9:G:128:GLN:H	1.77	0.50
20:R:76:TYR:CZ	20:R:80:ILE:HG13	2.46	0.50
29:a:10:THR:HG22	29:a:11:ARG:HG3	1.92	0.50
8:F:17:MET:SD	8:F:22:TYR:HB2	2.52	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:G:83:PHE:O	9:G:134:LYS:HA	2.12	0.50
12:J:83:ALA:O	12:J:105:GLN:NE2	2.45	0.50
3:A:878:A:N6	3:A:899:A:O2'	2.45	0.49
3:A:1021:A:H3'	3:A:1021:A:N3	2.27	0.49
3:A:1327:A:N6	3:A:1647:U:O2	2.45	0.49
3:A:1638:C:H1'	3:A:2698:U:O2'	2.12	0.49
17:O:14:SER:HA	17:O:17:ARG:NH1	2.27	0.49
25:W:75:GLN:HB2	25:W:92:VAL:HG12	1.94	0.49
3:A:613:A:O2'	3:A:614:A:O5'	2.30	0.49
3:A:2171:A:H5'	3:A:2173:A:N7	2.26	0.49
9:G:8:PRO:HB3	9:G:51:THR:HG22	1.94	0.49
19:Q:23:GLY:O	19:Q:90:GLY:HA3	2.11	0.49
3:A:1506:U:H2'	3:A:1507:C:C6	2.48	0.49
3:A:2483:C:N3	16:N:123:LYS:NZ	2.60	0.49
3:A:2747:G:O2'	9:G:67:THR:HG23	2.12	0.49
3:A:2809:A:H2'	3:A:2810:A:H8	1.75	0.49
8:F:50:LEU:O	8:F:54:ALA:N	2.38	0.49
18:P:30:ARG:HG3	18:P:35:ILE:HD12	1.94	0.49
26:X:34:GLY:N	26:X:61:ALA:O	2.37	0.49
35:i:362:UNK:HG2	35:i:365:UNK:HB1	1.93	0.49
3:A:1088:A:N6	12:J:135:SER:HB3	2.26	0.49
3:A:1825:U:O2	5:C:253:LYS:NZ	2.31	0.49
3:A:2626:C:H2'	3:A:2627:G:O4'	2.12	0.49
35:i:387:GLU:CG	35:i:398:ARG:HH11	2.25	0.49
7:E:184:ASP:OD1	7:E:184:ASP:N	2.43	0.49
9:G:101:ASN:ND2	9:G:116:GLN:OE1	2.46	0.49
15:M:4:ASN:OD1	15:M:4:ASN:N	2.39	0.49
3:A:27:G:N2	3:A:512:G:H1'	2.28	0.49
3:A:671:C:H2'	3:A:672:C:C6	2.47	0.49
3:A:1939:U:OP1	3:A:2604:U:O2'	2.28	0.49
3:A:2073:C:H2'	3:A:2074:U:H6	1.77	0.49
3:A:563:A:C4	3:A:2018:G:C2	3.01	0.49
3:A:1243:C:H1'	15:M:4:ASN:O	2.13	0.49
11:I:33:VAL:HG21	11:I:106:PHE:CE2	2.47	0.49
15:M:19:LEU:HD23	15:M:27:LEU:HD13	1.95	0.49
3:A:1606:C:H5'	3:A:1607:C:OP1	2.13	0.49
21:S:65:ALA:HB3	21:S:95:ASP:HB2	1.94	0.49
3:A:1005:C:H2'	3:A:1006:C:C6	2.47	0.49
3:A:1903:G:C2	3:A:1904:G:C8	3.00	0.49
3:A:2564:A:OP1	3:A:2648:G:O2'	2.19	0.49
7:E:23:PHE:CD1	7:E:111:GLU:HG3	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:H:110:VAL:HG12	10:H:114:GLU:HB2	1.94	0.49
14:L:10:VAL:HG12	14:L:12:ASP:H	1.78	0.49
3:A:184:C:H2'	3:A:185:G:H8	1.77	0.48
3:A:1093:G:C2'	3:A:1098:A:H61	2.26	0.48
3:A:1819:A:H5''	5:C:160:THR:HG21	1.94	0.48
3:A:2151:U:H2'	3:A:2152:G:H8	1.77	0.48
3:A:784:G:H5'	3:A:785:G:OP1	2.13	0.48
12:J:113:LYS:O	12:J:117:MET:N	2.46	0.48
3:A:1654:A:H2'	3:A:1655:A:H8	1.78	0.48
3:A:1790:C:H3'	3:A:1828:G:H22	1.77	0.48
3:A:2290:G:H2'	3:A:2291:U:O4'	2.12	0.48
4:B:116:G:H2'	4:B:117:G:C8	2.49	0.48
27:Y:6:GLN:NE2	27:Y:76:GLU:OE2	2.39	0.48
27:Y:17:ASN:HB2	27:Y:25:THR:OG1	2.13	0.48
3:A:719:C:H2'	3:A:720:U:H6	1.78	0.48
35:i:354:UNK:HG1	36:k:39:LEU:CD1	2.43	0.48
35:i:435:UNK:HG2	36:k:32:LEU:HD11	1.96	0.48
35:i:452:UNK:O	35:i:453:UNK:HG2	2.13	0.48
3:A:140:C:H4'	3:A:141:G:OP1	2.13	0.48
3:A:813:U:H2'	3:A:814:C:C6	2.49	0.48
3:A:2116:G:C5	3:A:2165:C:N4	2.82	0.48
9:G:86:LYS:HG2	9:G:132:VAL:HG22	1.96	0.48
27:Y:17:ASN:OD1	27:Y:27:ARG:HD2	2.13	0.48
3:A:136:G:H2'	3:A:137:U:O4'	2.13	0.48
3:A:467:G:H2'	3:A:468:G:O4'	2.13	0.48
3:A:1179:G:H2'	3:A:1180:U:C6	2.48	0.48
3:A:1773:A:N7	3:A:1829:A:H1'	2.28	0.48
3:A:2158:A:H4'	3:A:2159:G:O5'	2.14	0.48
9:G:80:THR:OG1	9:G:81:GLU:N	2.46	0.48
18:P:51:ALA:HB3	18:P:78:VAL:HG13	1.95	0.48
23:U:68:LYS:HG3	23:U:77:ARG:HH21	1.79	0.48
26:X:40:GLN:NE2	26:X:43:THR:HA	2.29	0.48
1:1:49:G:H1	1:1:60:A:N6	2.10	0.48
3:A:2209:G:H1	3:A:2215:C:N4	2.11	0.48
17:O:38:LEU:HB3	17:O:39:PRO:HD3	1.95	0.48
3:A:175:G:N2	3:A:176:A:N3	2.62	0.48
3:A:428:A:H2'	3:A:429:A:C8	2.49	0.48
3:A:914:G:H5'	3:A:915:C:OP2	2.13	0.48
3:A:2428:G:H21	15:M:60:ARG:NH2	2.12	0.48
13:K:72:LYS:HE3	13:K:74:TYR:CZ	2.49	0.48
28:Z:14:LEU:HB3	28:Z:57:LEU:HD21	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:160:A:N3	3:A:2208:C:O2'	2.43	0.48
3:A:782:A:N7	5:C:220:VAL:HG21	2.29	0.48
3:A:1028:A:N3	3:A:2486:C:O2'	2.42	0.48
3:A:1132:U:H3'	3:A:1133:A:H5''	1.95	0.48
3:A:2433:A:H2	27:Y:21:ALA:HB1	1.79	0.48
6:D:25:THR:HG21	6:D:193:VAL:HG22	1.95	0.48
8:F:7:TYR:CD1	8:F:11:GLU:HG3	2.48	0.48
10:H:115:VAL:HG22	10:H:132:PHE:CE2	2.48	0.48
16:N:11:LYS:HD3	16:N:86:LYS:HD3	1.96	0.48
23:U:58:VAL:HG22	23:U:85:VAL:HG22	1.96	0.48
31:c:9:ILE:HD13	31:c:25:LYS:HB2	1.95	0.48
3:A:1268:A:H2'	3:A:1269:A:O4'	2.13	0.48
3:A:1386:C:H2'	3:A:1387:A:C8	2.49	0.48
3:A:1527:G:N1	3:A:1544:A:OP2	2.32	0.48
3:A:1846:G:H5''	3:A:1847:A:OP2	2.14	0.48
3:A:2305:U:H5''	8:F:131:GLY:HA3	1.96	0.48
3:A:2570:G:H2'	3:A:2571:U:O4'	2.14	0.48
3:A:2834:G:H2'	3:A:2879:A:N6	2.29	0.48
5:C:260:ASN:OD1	5:C:262:ARG:N	2.37	0.48
13:K:58:ASN:ND2	13:K:128:ASN:OD1	2.42	0.48
16:N:41:LEU:HG	16:N:96:ILE:HG13	1.95	0.48
3:A:156:A:H2'	3:A:157:C:O4'	2.13	0.47
3:A:483:A:O4'	24:V:45:HIS:HB3	2.14	0.47
3:A:2226:C:H2'	3:A:2227:A:O4'	2.13	0.47
9:G:155:GLU:OE1	9:G:157:TYR:N	2.45	0.47
10:H:142:VAL:HG12	10:H:143:ILE:H	1.79	0.47
3:A:208:C:H2'	3:A:209:C:H6	1.78	0.47
3:A:477:A:H2'	3:A:478:A:C8	2.49	0.47
3:A:910:A:H2'	3:A:911:A:C8	2.48	0.47
3:A:2060:A:H3'	7:E:63:LYS:NZ	2.29	0.47
3:A:2444:G:OP2	7:E:63:LYS:HD2	2.14	0.47
13:K:78:THR:HG23	13:K:83:GLY:O	2.13	0.47
36:k:32:LEU:O	36:k:36:LEU:HG	2.15	0.47
6:D:56:LYS:HB2	6:D:59:ARG:HB2	1.95	0.47
9:G:35:ARG:CD	9:G:71:LEU:HD13	2.44	0.47
10:H:93:SER:HB3	10:H:123:ARG:HG2	1.95	0.47
12:J:10:LYS:O	12:J:11:LEU:HD12	2.15	0.47
12:J:42:PHE:O	12:J:46:THR:OG1	2.32	0.47
22:T:96:ILE:HD13	22:T:96:ILE:HA	1.74	0.47
3:A:112:U:H5'	28:Z:58:ASN:HD21	1.80	0.47
3:A:795:C:H2'	3:A:796:C:C6	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:957:C:C5	3:A:959:A:C5	3.01	0.47
3:A:995:C:OP2	20:R:54:LYS:NZ	2.44	0.47
3:A:1027:A:C6	3:A:1126:A:C4	3.02	0.47
3:A:1438:U:H2'	3:A:1439:A:H8	1.79	0.47
3:A:2060:A:H3'	7:E:63:LYS:HZ3	1.79	0.47
5:C:200:HIS:C	5:C:200:HIS:CD2	2.92	0.47
13:K:114:LEU:O	13:K:118:MET:HG3	2.14	0.47
3:A:1446:C:H2'	3:A:1447:C:C6	2.49	0.47
3:A:1873:G:H2'	3:A:1874:C:C6	2.49	0.47
11:I:85:VAL:HG22	11:I:92:ALA:HB2	1.96	0.47
12:J:40:LYS:N	12:J:40:LYS:HD2	2.30	0.47
15:M:55:MET:SD	15:M:56:PRO:HD2	2.55	0.47
24:V:14:LEU:HD11	24:V:71:ALA:HB2	1.95	0.47
3:A:127:A:H5''	3:A:128:C:O4'	2.14	0.47
3:A:1007:C:H5''	13:K:37:ARG:NH2	2.28	0.47
3:A:2347:C:O2'	31:c:39:PHE:HB3	2.14	0.47
3:A:2592:G:C6	3:A:2593:U:N3	2.83	0.47
18:P:30:ARG:HB3	18:P:97:PHE:CE1	2.50	0.47
18:P:31:THR:HG23	18:P:32:PRO:HD2	1.96	0.47
18:P:43:ASN:ND2	18:P:43:ASN:H	2.13	0.47
1:I:45:U:H3	1:I:64:G:H1	1.63	0.47
3:A:911:A:H2'	16:N:9:PHE:HZ	1.78	0.47
3:A:911:A:H2'	16:N:9:PHE:CZ	2.50	0.47
3:A:1085:A:H61	11:I:35:VAL:HG22	1.78	0.47
3:A:1672:A:C6	3:A:1673:G:C6	3.03	0.47
3:A:2431:U:H5	3:A:2433:A:H5''	1.79	0.47
3:A:2557:G:H2'	3:A:2558:C:C6	2.49	0.47
6:D:121:THR:HB	6:D:127:PHE:CD2	2.50	0.47
7:E:125:SER:OG	7:E:126:VAL:N	2.46	0.47
7:E:149:ILE:HB	7:E:188:MET:HG2	1.96	0.47
9:G:102:VAL:HG22	9:G:116:GLN:HE22	1.78	0.47
10:H:29:PHE:O	10:H:32:PRO:HD2	2.15	0.47
27:Y:62:LYS:HE3	27:Y:66:THR:HG21	1.96	0.47
35:i:332:ASN:HD21	35:i:389:ALA:HB2	1.79	0.47
35:i:334:PHE:CE2	35:i:338:LEU:HD11	2.49	0.47
3:A:323:C:C4	3:A:333:G:C8	3.03	0.47
8:F:25:VAL:O	8:F:28:VAL:HG12	2.14	0.47
22:T:7:HIS:CE1	22:T:10:ALA:HB2	2.49	0.47
3:A:713:G:H2'	3:A:714:U:C6	2.50	0.47
3:A:825:A:C2	3:A:833:A:C2	3.03	0.47
3:A:975:A:H1'	3:A:990:A:C2	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:998:C:H2'	3:A:999:U:O4'	2.14	0.47
3:A:1799:G:C5	5:C:176:LEU:HD13	2.50	0.47
3:A:2419:U:O2'	3:A:2420:C:H5'	2.15	0.47
12:J:28:LEU:HD11	12:J:33:VAL:HG11	1.97	0.47
12:J:75:PRO:HD2	12:J:78:VAL:HB	1.96	0.47
17:O:25:ALA:O	17:O:29:VAL:HG23	2.15	0.47
19:Q:100:LEU:HA	19:Q:100:LEU:HD23	1.67	0.47
27:Y:40:VAL:HG12	27:Y:43:GLU:H	1.80	0.47
30:b:36:GLU:OE2	30:b:46:ASP:HB2	2.15	0.47
1:1:37:U:O4	1:1:68:A:N6	2.49	0.47
3:A:861:A:C6	3:A:917:A:C8	3.03	0.47
3:A:1060:U:C2	3:A:1062:G:H5'	2.50	0.47
3:A:1689:A:C6	3:A:1700:A:C2	3.03	0.47
3:A:2339:C:H2'	3:A:2340:A:H8	1.80	0.47
8:F:73:SER:OG	8:F:81:GLN:N	2.33	0.47
24:V:41:LEU:HD22	24:V:62:GLU:HG2	1.96	0.47
3:A:857:G:H2'	3:A:858:G:O4'	2.16	0.46
3:A:2039:U:H2'	3:A:2040:G:C8	2.51	0.46
5:C:252:THR:OG1	5:C:253:LYS:N	2.48	0.46
9:G:42:GLU:CG	9:G:55:ARG:HH21	2.29	0.46
11:I:39:THR:HG22	11:I:43:LYS:HE3	1.98	0.46
19:Q:88:ARG:NH2	19:Q:112:GLU:HB2	2.31	0.46
29:a:31:ARG:HG2	29:a:34:HIS:HB2	1.97	0.46
3:A:144:A:H1'	23:U:3:ARG:HH22	1.80	0.46
3:A:1038:G:H2'	3:A:1039:A:C8	2.50	0.46
3:A:1097:U:H2'	3:A:1098:A:O4'	2.15	0.46
3:A:1130:U:HO2'	3:A:1131:G:H8	1.63	0.46
3:A:1808:A:H3'	3:A:1809:A:H8	1.79	0.46
3:A:1946:U:H2'	3:A:1947:C:C6	2.51	0.46
10:H:40:THR:HG22	10:H:41:LYS:H	1.79	0.46
21:S:38:VAL:O	21:S:54:VAL:HG23	2.15	0.46
35:i:347:UNK:HB2	35:i:366:UNK:HB2	1.98	0.46
3:A:75:G:H4'	28:Z:48:ARG:CZ	2.45	0.46
3:A:789:A:C4	32:d:3:ARG:NH1	2.84	0.46
3:A:796:C:H2'	3:A:797:G:C8	2.51	0.46
3:A:861:A:H2'	3:A:862:G:O4'	2.15	0.46
3:A:871:U:H2'	3:A:872:U:C6	2.50	0.46
3:A:2230:G:H2'	3:A:2231:U:C6	2.51	0.46
9:G:121:ILE:HD13	9:G:135:GLY:HA3	1.98	0.46
11:I:27:VAL:HG13	11:I:80:THR:HG23	1.97	0.46
18:P:53:THR:HB	18:P:65:THR:HB	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:R:49:ASP:HA	20:R:52:GLN:HB2	1.96	0.46
33:e:28:ASN:O	33:e:36:LYS:NZ	2.38	0.46
1:1:59:A:H2'	1:1:60:A:C8	2.50	0.46
3:A:247:G:H4'	3:A:386:G:C5	2.50	0.46
3:A:1028:A:N6	3:A:1125:G:H2'	2.30	0.46
3:A:1420:A:N7	3:A:2211:A:N6	2.62	0.46
3:A:2047:C:O2'	3:A:2823:A:N1	2.42	0.46
4:B:116:G:H2'	4:B:117:G:H8	1.80	0.46
13:K:98:GLU:OE1	13:K:98:GLU:N	2.41	0.46
20:R:18:LEU:HD11	20:R:32:TYR:HA	1.97	0.46
31:c:17:THR:HG21	31:c:42:VAL:HB	1.97	0.46
3:A:483:A:H5''	24:V:47:LYS:HG2	1.97	0.46
3:A:1062:G:N2	12:J:93:PRO:HG2	2.30	0.46
3:A:1510:G:H2'	3:A:1511:G:H8	1.78	0.46
3:A:2392:A:H2	15:M:55:MET:HE3	1.81	0.46
3:A:2788:C:H2'	3:A:2789:C:C6	2.50	0.46
5:C:176:LEU:HD23	5:C:176:LEU:HA	1.80	0.46
5:C:232:HIS:NE2	5:C:244:PRO:HA	2.30	0.46
15:M:21:ARG:HD3	15:M:21:ARG:HA	1.66	0.46
25:W:2:PHE:HB3	25:W:50:MET:CE	2.45	0.46
3:A:2821:A:H2'	3:A:2822:G:C8	2.51	0.46
14:L:73:ASP:OD1	14:L:73:ASP:N	2.39	0.46
3:A:125:A:OP2	32:d:19:ARG:HD3	2.15	0.46
3:A:358:U:H2'	3:A:359:G:C8	2.44	0.46
3:A:2126:A:H61	3:A:2163:A:H5'	1.80	0.46
5:C:125:LYS:HE2	5:C:125:LYS:HB2	1.77	0.46
13:K:95:ARG:HG2	13:K:96:ARG:N	2.30	0.46
16:N:66:ARG:HB2	16:N:101:VAL:O	2.16	0.46
3:A:878:A:H5'	3:A:879:G:OP2	2.16	0.46
3:A:1342:A:C6	3:A:1397:U:C5	3.04	0.46
3:A:1709:U:H2'	3:A:1710:G:H8	1.80	0.46
3:A:2786:U:H2'	3:A:2787:C:H6	1.79	0.46
5:C:33:LEU:HD23	5:C:33:LEU:HA	1.58	0.46
14:L:25:LEU:HA	14:L:25:LEU:HD23	1.67	0.46
22:T:25:ARG:NH2	22:T:74:ILE:O	2.49	0.46
35:i:354:UNK:HG2	35:i:354:UNK:O	2.15	0.46
3:A:532:A:N3	3:A:532:A:H2'	2.31	0.46
3:A:880:G:N2	3:A:898:C:C2	2.84	0.46
3:A:1387:A:H5'	3:A:1469:A:H1'	1.97	0.46
3:A:2069:G:N2	3:A:2443:C:C2	2.83	0.46
3:A:2344:U:OP1	31:c:37:LYS:HD2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:95:U:H2'	4:B:96:G:H8	1.81	0.46
9:G:155:GLU:OE2	9:G:158:LYS:N	2.48	0.46
11:I:30:SER:HB3	11:I:81:LEU:HB2	1.98	0.46
19:Q:106:LYS:O	19:Q:109:ARG:NH2	2.45	0.46
3:A:1785:A:O2'	3:A:1786:A:H2'	2.16	0.46
3:A:1869:G:N2	3:A:1873:G:C5	2.83	0.46
3:A:2229:U:H2'	3:A:2230:G:C8	2.51	0.46
6:D:99:GLU:OE2	6:D:182:ALA:HB2	2.15	0.46
17:O:28:LEU:O	17:O:32:GLU:N	2.45	0.46
3:A:372:G:O2'	3:A:400:G:O6	2.31	0.45
3:A:1563:U:H2'	3:A:1564:C:C6	2.51	0.45
7:E:1:MET:HE3	7:E:1:MET:HB2	1.88	0.45
12:J:80:LEU:HB3	12:J:138:LEU:CD1	2.46	0.45
12:J:122:ILE:O	12:J:126:THR:OG1	2.22	0.45
20:R:105:ALA:HB1	21:S:40:MET:HE1	1.98	0.45
24:V:81:ASP:OD2	24:V:96:PHE:HB3	2.16	0.45
30:b:52:ARG:HB3	30:b:54:VAL:HG13	1.98	0.45
35:i:370:ASP:O	35:i:374:VAL:HB	2.15	0.45
3:A:208:C:H2'	3:A:209:C:C6	2.52	0.45
3:A:1570:A:H5'	5:C:36:LYS:HB2	1.98	0.45
22:T:13:SER:O	22:T:17:VAL:HG23	2.17	0.45
3:A:772:C:H2'	3:A:773:U:C6	2.52	0.45
3:A:1706:C:O2'	3:A:1757:A:H5'	2.17	0.45
3:A:1848:A:H3'	3:A:1849:G:H8	1.80	0.45
5:C:160:THR:O	5:C:195:VAL:HG23	2.17	0.45
14:L:17:ARG:HA	14:L:17:ARG:HD3	1.77	0.45
14:L:79:PHE:CD1	19:Q:70:VAL:HG22	2.46	0.45
15:M:27:LEU:O	15:M:31:GLY:HA2	2.16	0.45
35:i:430:MET:HA	35:i:438:UNK:HG1	1.98	0.45
3:A:1086:A:H4'	3:A:1103:A:C2	2.52	0.45
3:A:1149:G:H2'	3:A:1150:C:C6	2.50	0.45
8:F:20:PHE:CZ	8:F:165:GLU:HA	2.51	0.45
24:V:37:GLU:O	24:V:39:ILE:HG12	2.17	0.45
3:A:1466:U:H5''	3:A:1467:U:H5'	1.98	0.45
3:A:1653:G:H3'	17:O:2:ARG:HG3	1.98	0.45
3:A:2052:A:OP1	6:D:146:ILE:HG12	2.17	0.45
6:D:207:VAL:HG13	6:D:208:LYS:HG3	1.98	0.45
10:H:62:LEU:HD23	10:H:135:HIS:CD2	2.52	0.45
11:I:53:ARG:O	11:I:81:LEU:HD12	2.16	0.45
14:L:66:LYS:HB3	14:L:66:LYS:HE2	1.64	0.45
18:P:88:LYS:HG2	18:P:116:GLN:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:W:25:LYS:HB3	25:W:25:LYS:HE2	1.71	0.45
34:f:1:MET:HE2	34:f:1:MET:HB2	1.75	0.45
35:i:411:GLN:H	35:i:411:GLN:HG3	1.45	0.45
3:A:111:A:H2'	3:A:112:U:O4'	2.16	0.45
3:A:172:A:H2'	3:A:173:A:H8	1.81	0.45
3:A:257:C:H2'	3:A:258:G:O4'	2.15	0.45
3:A:831:G:H5''	15:M:37:GLY:HA2	1.97	0.45
3:A:908:C:O2'	16:N:70:ASP:OD2	2.30	0.45
3:A:1545:A:H2'	3:A:1546:G:O4'	2.17	0.45
3:A:1848:A:N3	3:A:1849:G:C8	2.85	0.45
3:A:2667:C:H1'	9:G:109:PHE:CD1	2.52	0.45
6:D:49:GLN:HA	6:D:80:TRP:O	2.16	0.45
23:U:34:VAL:HG21	23:U:43:ILE:HD11	1.99	0.45
25:W:83:LYS:HB3	25:W:85:LYS:HG3	1.98	0.45
26:X:23:VAL:HG22	26:X:38:VAL:HB	1.99	0.45
3:A:499:U:H5''	24:V:43:LYS:HE3	1.99	0.45
3:A:1313:U:H2'	3:A:1610:A:C2	2.51	0.45
3:A:1416:G:N2	3:A:1582:C:O2	2.33	0.45
3:A:1631:G:N2	3:A:1634:A:OP2	2.32	0.45
3:A:2165:C:H2'	3:A:2166:U:O4'	2.16	0.45
3:A:2433:A:H5'	3:A:2434:A:P	2.57	0.45
14:L:99:ILE:HG12	14:L:118:LEU:HB2	1.98	0.45
29:a:56:LYS:NZ	29:a:58:GLU:HG2	2.31	0.45
3:A:239:C:H2'	3:A:240:C:O4'	2.16	0.45
3:A:629:G:H5''	3:A:650:C:O2'	2.16	0.45
3:A:657:U:H2'	3:A:658:U:C6	2.52	0.45
3:A:706:A:C2	3:A:707:G:H1'	2.52	0.45
3:A:1022:G:O2'	3:A:1024:G:O6	2.27	0.45
3:A:1287:A:H3'	3:A:1288:G:N2	2.32	0.45
3:A:1972:G:H2'	3:A:1973:G:H8	1.81	0.45
3:A:2134:A:H1'	3:A:2159:G:H21	1.82	0.45
3:A:2396:G:N3	3:A:2421:G:N2	2.64	0.45
3:A:2667:C:H1'	9:G:109:PHE:HD1	1.82	0.45
10:H:100:ALA:O	10:H:104:THR:HG23	2.17	0.45
18:P:18:LEU:HA	18:P:18:LEU:HD23	1.71	0.45
33:e:24:HIS:ND1	33:e:25:LYS:O	2.43	0.45
3:A:593:U:H2'	3:A:594:U:C6	2.52	0.45
3:A:718:A:H2'	3:A:719:C:O4'	2.16	0.45
3:A:764:A:H5'	5:C:209:GLY:HA2	1.98	0.45
3:A:948:C:H1'	3:A:984:A:C8	2.52	0.45
3:A:2327:A:H2'	3:A:2328:A:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:2524:G:H2'	3:A:2525:G:O4'	2.16	0.45
12:J:117:MET:HB2	12:J:125:MET:HG2	1.99	0.45
17:O:2:ARG:HB3	17:O:2:ARG:CZ	2.47	0.45
17:O:17:ARG:HG2	17:O:21:PHE:HE2	1.82	0.45
33:e:29:LEU:HD12	33:e:29:LEU:HA	1.57	0.45
3:A:1177:G:H2'	3:A:1178:C:C6	2.51	0.45
3:A:1918:A:O2'	3:A:1920:C:N4	2.50	0.45
5:C:243:HIS:HA	5:C:244:PRO:HD3	1.79	0.45
8:F:136:ILE:HG22	8:F:141:ILE:HG21	1.98	0.45
9:G:148:LEU:HD23	9:G:148:LEU:HA	1.71	0.45
11:I:41:LEU:HB2	11:I:99:PHE:CE1	2.52	0.45
13:K:69:ARG:O	13:K:89:PHE:HB3	2.17	0.45
16:N:65:ILE:HG12	16:N:103:TYR:CD2	2.51	0.45
21:S:4:VAL:HA	21:S:12:HIS:O	2.16	0.45
21:S:40:MET:HE3	21:S:47:VAL:HG13	1.99	0.45
35:i:331:LEU:HA	35:i:334:PHE:HB3	1.99	0.45
3:A:154:U:H2'	3:A:155:A:C8	2.53	0.44
3:A:2273:A:H2'	3:A:2274:A:C8	2.52	0.44
3:A:2313:C:H5''	8:F:88:LYS:HD3	1.98	0.44
3:A:2683:C:H4'	6:D:13:ARG:HH12	1.81	0.44
6:D:7:LYS:HB3	6:D:7:LYS:HE2	1.78	0.44
12:J:86:ILE:CD1	12:J:138:LEU:HD21	2.46	0.44
12:J:130:GLU:HB3	12:J:134:ARG:NH2	2.32	0.44
19:Q:89:ARG:HB3	19:Q:113:ARG:NH1	2.32	0.44
3:A:594:U:H2'	3:A:595:C:C6	2.51	0.44
3:A:620:G:H4'	3:A:621:A:O5'	2.17	0.44
3:A:1450:G:C6	3:A:1451:C:N4	2.86	0.44
3:A:1667:G:N2	3:A:1992:G:OP2	2.44	0.44
3:A:2230:G:H1'	27:Y:32:ASN:HB2	1.99	0.44
3:A:2396:G:C2	3:A:2421:G:C2	3.05	0.44
7:E:121:VAL:O	7:E:189:THR:HA	2.18	0.44
13:K:65:THR:O	13:K:68:LYS:HB2	2.16	0.44
16:N:90:GLU:HB3	16:N:91:TYR:CD1	2.53	0.44
26:X:55:ARG:HE	26:X:55:ARG:HB2	1.45	0.44
3:A:198:C:O2'	3:A:199:A:H5'	2.17	0.44
3:A:2489:U:C4	3:A:2490:G:C6	3.06	0.44
3:A:2569:G:C2	3:A:2570:G:C8	3.05	0.44
3:A:2776:A:C8	3:A:2782:G:C5	3.05	0.44
9:G:117:LEU:HD13	9:G:121:ILE:HG22	1.99	0.44
15:M:10:GLU:OE2	15:M:11:GLY:N	2.50	0.44
21:S:27:ILE:HG22	21:S:28:ALA:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:77:G:H2'	3:A:78:U:O4'	2.16	0.44
3:A:1198:U:H2'	3:A:1199:U:C6	2.52	0.44
3:A:2387:U:H1'	26:X:41:ARG:NH1	2.32	0.44
3:A:2704:C:H2'	3:A:2705:A:O4'	2.17	0.44
3:A:2742:G:P	34:f:24:ARG:HH12	2.40	0.44
19:Q:62:ARG:NH2	19:Q:101:ARG:HG2	2.32	0.44
24:V:50:PRO:HG2	36:k:44:VAL:O	2.18	0.44
25:W:21:ARG:HE	25:W:87:GLN:HA	1.83	0.44
26:X:36:ILE:HG23	26:X:58:THR:HG23	2.00	0.44
28:Z:56:LEU:HD22	28:Z:56:LEU:HA	1.82	0.44
3:A:141:G:C8	3:A:141:G:H3'	2.51	0.44
3:A:1420:A:N7	3:A:2211:A:C6	2.85	0.44
3:A:1508:A:O2'	3:A:1509:A:O4'	2.19	0.44
3:A:2318:G:C6	3:A:2319:G:N1	2.86	0.44
14:L:3:GLN:HE21	14:L:3:GLN:HB3	1.66	0.44
3:A:57:C:H2'	3:A:58:G:O4'	2.18	0.44
3:A:149:A:C2	3:A:150:U:C2	3.06	0.44
3:A:356:G:H2'	3:A:357:C:O4'	2.18	0.44
3:A:870:U:OP1	16:N:6:ARG:NH1	2.51	0.44
3:A:1591:A:H2'	3:A:1592:C:C6	2.53	0.44
3:A:2377:A:H2'	3:A:2378:A:C8	2.53	0.44
8:F:67:ILE:HD12	8:F:84:PRO:HB3	2.00	0.44
8:F:147:ASP:OD1	8:F:150:ARG:NH2	2.51	0.44
3:A:181:A:H1'	3:A:435:C:O4'	2.17	0.44
3:A:630:G:N2	3:A:633:A:OP2	2.43	0.44
3:A:997:G:H5''	20:R:92:ARG:NH1	2.33	0.44
3:A:1082:U:O2'	11:I:39:THR:HG23	2.18	0.44
3:A:1301:A:H2'	3:A:1301:A:N3	2.33	0.44
3:A:2683:C:H4'	6:D:13:ARG:NH1	2.33	0.44
16:N:97:GLN:CD	16:N:97:GLN:N	2.76	0.44
34:f:2:LYS:HE2	34:f:2:LYS:HB3	1.77	0.44
3:A:1056:G:H1'	3:A:1103:A:N6	2.33	0.44
3:A:1082:U:H4'	11:I:46:ARG:NH1	2.32	0.44
3:A:1093:G:H1'	3:A:1099:G:N1	2.32	0.44
3:A:2024:G:H2'	3:A:2025:C:C6	2.53	0.44
3:A:2678:C:H2'	3:A:2679:A:O4'	2.18	0.44
10:H:26:ALA:HA	10:H:30:LEU:HB2	1.99	0.44
18:P:52:SER:O	18:P:58:ILE:HD12	2.18	0.44
19:Q:53:ARG:HB2	19:Q:56:HIS:HB2	1.99	0.44
27:Y:59:ILE:HG12	27:Y:67:VAL:HG21	1.99	0.44
29:a:9:GLN:HB2	29:a:29:LEU:HD13	2.00	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:33:C:N4	3:A:446:G:O2'	2.45	0.44
3:A:277:G:H4'	3:A:278:A:N7	2.33	0.44
3:A:1205:A:H2'	7:E:165:HIS:HE1	1.83	0.44
3:A:1230:A:H2'	3:A:1231:U:O4'	2.18	0.44
3:A:1614:A:C2	22:T:93:ALA:HB2	2.52	0.44
3:A:2443:C:H2'	3:A:2444:G:H8	1.82	0.44
5:C:141:VAL:HG12	5:C:192:LEU:HA	1.98	0.44
8:F:128:TYR:CE2	8:F:130:MET:HG2	2.53	0.44
9:G:42:GLU:HG3	9:G:55:ARG:HH21	1.83	0.44
18:P:85:LYS:HE2	18:P:85:LYS:HB3	1.79	0.44
19:Q:25:THR:HB	19:Q:88:ARG:HG2	1.99	0.44
3:A:1266:G:N2	3:A:2012:G:H2'	2.33	0.43
3:A:1287:A:H5'	17:O:103:ARG:HD2	1.98	0.43
3:A:1710:G:H2'	3:A:1711:A:C8	2.53	0.43
3:A:1853:A:N6	3:A:1888:G:O2'	2.51	0.43
3:A:2292:U:H2'	3:A:2293:G:C8	2.52	0.43
4:B:114:C:H2'	4:B:115:A:H8	1.83	0.43
12:J:110:ALA:O	12:J:114:ALA:HB2	2.18	0.43
15:M:70:LYS:O	15:M:74:THR:OG1	2.31	0.43
22:T:7:HIS:C	22:T:7:HIS:CD2	2.96	0.43
23:U:31:VAL:O	23:U:32:LEU:HD23	2.18	0.43
29:a:17:LEU:HD23	29:a:17:LEU:HA	1.76	0.43
3:A:475:C:N4	3:A:476:G:C6	2.86	0.43
3:A:677:A:O2'	3:A:2071:A:H5'	2.17	0.43
3:A:1962:C:H4'	3:A:1963:U:C5	2.52	0.43
3:A:2654:A:OP1	3:A:2654:A:H8	2.01	0.43
12:J:90:SER:HB2	12:J:136:MET:O	2.18	0.43
3:A:380:G:H2'	3:A:381:G:O4'	2.18	0.43
3:A:969:G:H2'	3:A:970:U:C6	2.53	0.43
3:A:1062:G:O2'	12:J:135:SER:OG	2.32	0.43
3:A:1344:U:HO2'	3:A:1345:C:P	2.41	0.43
3:A:1351:C:H4'	3:A:1572:A:O4'	2.18	0.43
3:A:2172:U:H4'	3:A:2173:A:H5'	2.00	0.43
8:F:145:LYS:HA	8:F:145:LYS:HD3	1.89	0.43
15:M:80:SER:O	15:M:84:LYS:HE3	2.19	0.43
21:S:91:GLN:NE2	21:S:92:TRP:H	2.16	0.43
31:c:33:LYS:HD3	31:c:33:LYS:HA	1.74	0.43
34:f:22:VAL:HG12	34:f:24:ARG:HG3	2.00	0.43
3:A:776:G:HO2'	3:A:777:G:P	2.39	0.43
3:A:973:A:OP2	21:S:81:LYS:HE3	2.18	0.43
3:A:1735:A:H2'	3:A:1736:U:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:2647:U:H2'	3:A:2648:G:C8	2.54	0.43
22:T:47:VAL:HG22	22:T:103:ILE:HD13	2.00	0.43
3:A:93:G:H2'	3:A:94:A:H8	1.84	0.43
3:A:1044:C:O2'	3:A:1111:A:N1	2.45	0.43
3:A:1354:A:H2'	3:A:1355:G:O4'	2.19	0.43
3:A:1515:A:H3'	3:A:1516:G:H8	1.84	0.43
3:A:1627:G:C2	3:A:1628:G:C8	3.07	0.43
3:A:2292:U:H2'	3:A:2293:G:H8	1.84	0.43
4:B:49:C:H2'	4:B:50:A:C8	2.54	0.43
10:H:46:PHE:HD1	10:H:50:ARG:NH2	2.16	0.43
11:I:93:ALA:O	11:I:97:LYS:NZ	2.41	0.43
17:O:86:ARG:HD3	17:O:121:LYS:HG3	1.98	0.43
20:R:24:TYR:O	20:R:29:SER:HB3	2.19	0.43
34:f:2:LYS:HD3	34:f:4:ARG:NH2	2.33	0.43
3:A:11:C:H2'	3:A:12:U:H5'	2.00	0.43
3:A:112:U:H5'	28:Z:58:ASN:ND2	2.34	0.43
3:A:463:G:N1	3:A:467:G:C6	2.86	0.43
3:A:834:G:C2	3:A:835:C:C2	3.06	0.43
3:A:976:G:HO2'	3:A:1155:A:HO2'	1.60	0.43
3:A:1434:A:C2	3:A:1435:G:C5	3.07	0.43
3:A:2786:U:H2'	3:A:2787:C:C6	2.53	0.43
5:C:153:GLN:O	5:C:156:ARG:HG3	2.18	0.43
6:D:131:ASP:O	6:D:140:HIS:HD2	2.01	0.43
7:E:108:ILE:O	7:E:112:LEU:HG	2.18	0.43
8:F:138:PHE:HA	8:F:139:PRO:HD3	1.90	0.43
1:1:55:A:H2'	1:1:56:A:C8	2.53	0.43
3:A:14:A:C6	3:A:526:A:C2	3.07	0.43
3:A:76:C:H6	3:A:76:C:O5'	2.02	0.43
3:A:2138:G:C6	3:A:2154:A:C2	3.06	0.43
3:A:2847:U:H2'	3:A:2848:G:O4'	2.18	0.43
5:C:90:ASN:ND2	5:C:197:ASN:HB2	2.34	0.43
10:H:62:LEU:HD22	10:H:137:GLU:OE1	2.19	0.43
15:M:6:LEU:HD23	15:M:6:LEU:HA	1.82	0.43
20:R:74:ILE:HG12	20:R:75:SER:N	2.34	0.43
22:T:46:LEU:HA	22:T:46:LEU:HD23	1.82	0.43
36:k:39:LEU:HD23	36:k:39:LEU:HA	1.86	0.43
3:A:239:C:HO2'	3:A:622:G:HO2'	1.62	0.43
3:A:566:U:H5''	15:M:29:LYS:HE3	1.99	0.43
3:A:591:U:H2'	3:A:592:A:C8	2.54	0.43
3:A:783:A:C5	3:A:785:G:H1'	2.53	0.43
3:A:1542:U:H2'	3:A:1543:G:O4'	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1597:A:C5'	3:A:1598:A:H5'	2.47	0.43
3:A:1858:A:H2'	3:A:1859:U:O4'	2.17	0.43
3:A:2114:A:C2	3:A:2166:U:H2'	2.53	0.43
3:A:2130:U:O2'	3:A:2133:G:O2'	2.32	0.43
3:A:2512:C:H5''	3:A:2513:A:OP2	2.17	0.43
3:A:2588:G:O6	3:A:2607:G:C6	2.72	0.43
7:E:128:ALA:O	7:E:130:LYS:N	2.51	0.43
11:I:118:ILE:HA	11:I:119:PRO:HD2	1.84	0.43
16:N:26:VAL:HB	16:N:133:LYS:HB2	2.00	0.43
20:R:9:ILE:H	20:R:9:ILE:HD12	1.84	0.43
21:S:4:VAL:HG12	21:S:39:LEU:HB2	2.00	0.43
3:A:493:G:H2'	3:A:494:G:O4'	2.19	0.43
3:A:1473:G:H2'	3:A:1474:U:O4'	2.19	0.43
3:A:1517:G:C2	3:A:1732:C:N3	2.86	0.43
5:C:8:PRO:HB3	5:C:14:ARG:HG3	1.99	0.43
6:D:109:VAL:HG12	6:D:201:LEU:HD22	2.01	0.43
6:D:148:GLN:OE1	6:D:148:GLN:N	2.51	0.43
10:H:104:THR:HA	10:H:108:VAL:O	2.19	0.43
12:J:15:ALA:O	12:J:46:THR:OG1	2.30	0.43
13:K:26:GLY:O	13:K:30:THR:HG23	2.18	0.43
16:N:33:LEU:HD11	16:N:128:THR:HB	2.00	0.43
20:R:17:ILE:HD13	20:R:17:ILE:HA	1.63	0.43
25:W:29:ILE:O	25:W:91:PHE:HB2	2.19	0.43
26:X:47:ALA:HB1	26:X:51:VAL:O	2.19	0.43
3:A:1141:U:H4'	3:A:1142:A:O4'	2.19	0.43
3:A:1341:G:O2'	23:U:59:ASN:ND2	2.47	0.43
3:A:1501:G:H2'	3:A:1502:A:H8	1.84	0.43
3:A:2038:G:H2'	3:A:2039:U:O4'	2.17	0.43
3:A:2843:G:H2'	3:A:2844:G:C8	2.54	0.43
8:F:170:LEU:HD23	8:F:170:LEU:HA	1.75	0.43
9:G:44:LYS:HE3	9:G:44:LYS:HB2	1.80	0.43
12:J:33:VAL:HG13	12:J:67:PHE:CD2	2.54	0.43
17:O:72:ASP:OD1	17:O:73:ASN:N	2.51	0.43
23:U:34:VAL:HG11	23:U:43:ILE:HD13	2.01	0.43
25:W:21:ARG:HH21	25:W:87:GLN:C	2.22	0.43
3:A:5:A:H2'	3:A:6:A:C8	2.54	0.42
3:A:141:G:C8	3:A:142:A:O4'	2.72	0.42
3:A:195:A:H5''	15:M:47:ARG:HH22	1.84	0.42
3:A:675:A:OP1	7:E:58:LYS:NZ	2.52	0.42
3:A:1494:A:H2'	3:A:1495:A:H8	1.83	0.42
3:A:1759:A:H2'	3:A:1760:C:C6	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:2144:G:N2	3:A:2148:G:O6	2.52	0.42
3:A:2743:U:OP1	34:f:34:LYS:NZ	2.39	0.42
3:A:2771:C:H2'	3:A:2772:C:C6	2.54	0.42
5:C:245:VAL:HA	5:C:252:THR:HG22	2.01	0.42
35:i:413:VAL:HA	35:i:416:LEU:HD12	1.99	0.42
3:A:461:C:H2'	3:A:462:C:H6	1.84	0.42
3:A:464:U:C2	3:A:788:A:C6	3.07	0.42
3:A:573:U:O4	3:A:2029:G:O2'	2.36	0.42
3:A:1088:A:H61	12:J:135:SER:HB3	1.82	0.42
3:A:1614:A:H8	3:A:1614:A:O5'	2.02	0.42
3:A:2533:U:OP1	3:A:2665:A:O2'	2.34	0.42
3:A:2646:C:OP2	3:A:2732:G:O2'	2.35	0.42
5:C:210:ALA:HA	5:C:213:TRP:CE3	2.53	0.42
3:A:674:G:H2'	3:A:804:A:H61	1.83	0.42
3:A:1064:C:H5''	12:J:88:SER:HB2	2.01	0.42
3:A:1524:G:H2'	3:A:1525:A:O4'	2.20	0.42
3:A:1590:A:H2'	3:A:1591:A:C8	2.54	0.42
3:A:1736:U:H2'	3:A:1737:G:O4'	2.18	0.42
3:A:1922:G:H2'	3:A:1923:U:O4'	2.18	0.42
3:A:2184:A:H2'	3:A:2185:U:C6	2.53	0.42
3:A:2700:A:H2'	3:A:2701:U:C6	2.54	0.42
3:A:2790:U:H5'	3:A:2893:A:N7	2.34	0.42
4:B:66:A:H61	4:B:107:G:H2'	1.84	0.42
4:B:106:G:H2'	4:B:107:G:O4'	2.19	0.42
5:C:133:ARG:HD2	10:H:123:ARG:NH1	2.35	0.42
7:E:29:HIS:O	7:E:32:VAL:HG22	2.19	0.42
8:F:79:ILE:HG21	8:F:85:ILE:HD11	2.01	0.42
9:G:149:ARG:HG3	9:G:162:VAL:O	2.20	0.42
14:L:65:THR:HB	14:L:68:GLY:H	1.84	0.42
19:Q:34:GLU:CD	19:Q:39:ARG:HB2	2.44	0.42
1:1:48:G:H3'	1:1:49:G:C8	2.54	0.42
3:A:543:G:H5'	3:A:544:C:OP2	2.18	0.42
3:A:571:U:H3'	21:S:80:ARG:NH2	2.34	0.42
3:A:1387:A:H2'	3:A:1388:G:O4'	2.18	0.42
3:A:1637:A:H2'	3:A:1638:C:C6	2.54	0.42
5:C:24:LEU:HA	5:C:24:LEU:HD12	1.66	0.42
12:J:38:PHE:CD1	12:J:59:ILE:HD11	2.54	0.42
12:J:113:LYS:HA	12:J:116:ASP:HB2	2.01	0.42
16:N:36:VAL:HG13	25:W:82:TYR:CD2	2.55	0.42
20:R:24:TYR:N	20:R:24:TYR:HD1	2.17	0.42
24:V:61:LYS:HG2	24:V:62:GLU:H	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:123:G:N2	3:A:129:C:C2	2.87	0.42
3:A:653:U:C1'	3:A:654:A:H5''	2.49	0.42
3:A:729:G:H2'	3:A:1775:U:H1'	2.01	0.42
3:A:729:G:C5	5:C:207:LYS:HB2	2.55	0.42
3:A:1039:A:H2'	3:A:1040:A:O4'	2.20	0.42
3:A:1342:A:OP1	23:U:40:LYS:NZ	2.33	0.42
3:A:1751:U:H2'	3:A:1752:C:C6	2.54	0.42
3:A:1759:A:C2	3:A:2697:G:H1'	2.54	0.42
3:A:2518:A:H2'	3:A:2518:A:N3	2.34	0.42
8:F:48:LYS:HB2	8:F:48:LYS:HE2	1.85	0.42
12:J:103:ARG:H	12:J:103:ARG:HD2	1.83	0.42
3:A:307:G:N1	3:A:310:A:OP2	2.52	0.42
3:A:794:A:H2'	3:A:795:C:C6	2.55	0.42
3:A:812:C:C2	3:A:1250:G:N1	2.87	0.42
3:A:877:A:C6	3:A:899:A:C6	3.08	0.42
3:A:1798:U:OP2	5:C:271:ARG:NH2	2.52	0.42
3:A:1902:C:H4'	5:C:242:LYS:O	2.19	0.42
3:A:2304:G:H22	3:A:2312:U:H3	1.67	0.42
3:A:2322:A:C4	3:A:2323:G:C8	3.07	0.42
10:H:94:ILE:HG23	10:H:98:ASP:HB2	2.01	0.42
11:I:15:VAL:HG11	11:I:60:LEU:CD2	2.50	0.42
12:J:22:PRO:HB2	12:J:23:PRO:HD3	2.02	0.42
12:J:74:PRO:HA	12:J:75:PRO:HD3	1.89	0.42
19:Q:106:LYS:O	19:Q:109:ARG:HD3	2.20	0.42
20:R:47:TYR:CD2	20:R:47:TYR:C	2.98	0.42
20:R:117:LEU:HD23	20:R:117:LEU:HA	1.77	0.42
25:W:2:PHE:HE1	25:W:53:LYS:HD2	1.84	0.42
3:A:481:G:O2'	3:A:507:A:N1	2.45	0.42
3:A:819:A:N3	3:A:819:A:H2'	2.34	0.42
3:A:1110:G:HO2'	3:A:1111:A:P	2.43	0.42
3:A:1327:A:H2'	3:A:1328:A:O4'	2.19	0.42
3:A:1400:U:H2'	3:A:1401:G:O4'	2.19	0.42
4:B:57:A:C4	8:F:26:MET:HB3	2.54	0.42
10:H:1:MET:O	10:H:20:ASN:HA	2.20	0.42
11:I:85:VAL:HG21	11:I:90:GLY:O	2.20	0.42
17:O:75:ILE:HD12	17:O:75:ILE:HA	1.82	0.42
23:U:24:MET:HE2	23:U:24:MET:HB3	1.89	0.42
29:a:51:VAL:HG23	29:a:55:VAL:HG21	2.00	0.42
3:A:647:G:H2'	3:A:648:G:C8	2.55	0.42
3:A:1047:G:OP1	11:I:56:ARG:NH1	2.52	0.42
3:A:1463:C:H2'	3:A:1464:G:H8	1.85	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:O:103:ARG:HB3	17:O:106:ASP:OD1	2.20	0.42
35:i:354:UNK:HG1	36:k:39:LEU:HD13	2.02	0.42
3:A:669:G:N2	3:A:670:A:C2	2.88	0.42
3:A:910:A:C6	3:A:911:A:C6	3.08	0.42
3:A:1065:U:H2'	3:A:1066:U:O4'	2.19	0.42
3:A:1068:G:N2	3:A:1095:A:O3'	2.44	0.42
3:A:1324:G:C4	3:A:1328:A:N6	2.88	0.42
3:A:1509:A:O2'	3:A:1510:G:H8	2.03	0.42
3:A:2119:A:H62	3:A:2167:U:H1'	1.85	0.42
3:A:2433:A:H5'	3:A:2434:A:OP2	2.19	0.42
3:A:2776:A:C2	3:A:2778:A:C4	3.07	0.42
8:F:34:ILE:HB	8:F:96:MET:HG3	2.02	0.42
11:I:43:LYS:HE2	12:J:118:THR:HA	2.01	0.42
14:L:11:ALA:O	14:L:100:PHE:N	2.46	0.42
16:N:42:THR:N	16:N:45:GLN:OE1	2.47	0.42
20:R:31:VAL:HG12	20:R:34:VAL:H	1.85	0.42
3:A:565:C:H4'	3:A:1253:A:C6	2.55	0.42
3:A:948:C:O2'	3:A:984:A:O2'	2.35	0.42
3:A:1499:C:H2'	3:A:1500:G:H8	1.85	0.42
3:A:1880:U:H2'	3:A:1881:C:C6	2.55	0.42
8:F:4:LEU:HD23	8:F:4:LEU:HA	1.73	0.42
9:G:97:ALA:HB3	9:G:104:ASN:HB2	2.01	0.42
22:T:28:LYS:HB2	22:T:28:LYS:HE2	1.41	0.42
3:A:648:G:C2	3:A:649:G:C5	3.08	0.41
3:A:1417:C:H2'	3:A:1418:G:C8	2.55	0.41
3:A:1463:C:H2'	3:A:1464:G:C8	2.55	0.41
3:A:1607:C:O2'	3:A:1608:A:OP1	2.37	0.41
5:C:205:LEU:HD23	5:C:205:LEU:HA	1.68	0.41
7:E:109:LEU:HA	7:E:109:LEU:HD23	1.79	0.41
8:F:57:LEU:HD12	8:F:87:CYS:SG	2.60	0.41
8:F:79:ILE:HD12	8:F:79:ILE:O	2.20	0.41
35:i:422:ASP:HB2	35:i:423:MET:HE2	2.01	0.41
3:A:449:A:C4	3:A:450:G:C8	3.08	0.41
3:A:686:U:O4	32:d:12:ARG:NH1	2.52	0.41
3:A:1056:G:H5'	11:I:35:VAL:HG21	2.02	0.41
3:A:1449:G:N2	3:A:1463:C:C2	2.88	0.41
3:A:1770:G:C6	3:A:1983:G:C6	3.07	0.41
3:A:1877:A:H2'	3:A:1878:G:O4'	2.20	0.41
3:A:2466:C:OP1	34:f:4:ARG:HB2	2.20	0.41
3:A:2706:A:C2	3:A:2707:U:C2	3.08	0.41
9:G:73:ASN:O	9:G:77:ILE:HG13	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:53:A:H2'	3:A:54:G:O4'	2.20	0.41
3:A:118:A:N3	3:A:178:G:H1'	2.36	0.41
3:A:393:C:H2'	3:A:394:C:H6	1.85	0.41
3:A:1005:C:H2'	3:A:1006:C:H6	1.84	0.41
3:A:1484:U:H2'	3:A:1485:U:C6	2.55	0.41
3:A:1780:A:H3'	3:A:1781:U:H2'	2.01	0.41
3:A:1946:U:H2'	3:A:1947:C:H6	1.84	0.41
3:A:2209:G:C2	3:A:2216:G:C2	3.08	0.41
3:A:2339:C:O3'	4:B:41:G:N2	2.52	0.41
3:A:2838:G:H2'	3:A:2839:G:O4'	2.20	0.41
5:C:176:LEU:HB2	5:C:180:GLU:O	2.20	0.41
7:E:181:ILE:H	7:E:181:ILE:HG13	1.70	0.41
8:F:70:ALA:HB3	8:F:81:GLN:HA	2.02	0.41
9:G:76:VAL:O	9:G:80:THR:HG23	2.20	0.41
14:L:93:GLN:HA	14:L:94:PRO:HD3	1.88	0.41
3:A:335:C:H5''	24:V:82:ARG:HD2	2.02	0.41
3:A:848:C:H42	3:A:930:G:H1	1.68	0.41
3:A:1432:G:H2'	3:A:1433:A:C8	2.55	0.41
3:A:1482:G:H2'	3:A:1483:G:H8	1.84	0.41
3:A:2860:A:H5''	3:A:2861:U:OP2	2.21	0.41
3:A:2895:G:H2'	3:A:2896:C:C6	2.56	0.41
6:D:73:VAL:HG11	6:D:93:GLY:HA2	2.02	0.41
9:G:83:PHE:HB2	9:G:135:GLY:O	2.20	0.41
16:N:133:LYS:HB3	16:N:133:LYS:HE3	1.42	0.41
3:A:297:G:H2'	3:A:298:G:O4'	2.20	0.41
3:A:1078:U:O2	3:A:1088:A:H3'	2.21	0.41
3:A:1972:G:H2'	3:A:1973:G:C8	2.55	0.41
3:A:2267:A:H5''	3:A:2268:A:C5'	2.49	0.41
4:B:48:U:H4'	18:P:100:HIS:HD2	1.84	0.41
4:B:71:C:C2	4:B:106:G:C2	3.08	0.41
8:F:13:VAL:O	8:F:17:MET:HB2	2.21	0.41
14:L:71:ARG:HA	14:L:71:ARG:HD3	1.81	0.41
30:b:7:LYS:HA	30:b:8:PRO:HD3	1.91	0.41
32:d:22:MET:O	32:d:28:ARG:NH1	2.53	0.41
3:A:75:G:H4'	28:Z:48:ARG:NH2	2.35	0.41
3:A:528:A:C8	3:A:2042:A:C2	3.09	0.41
3:A:558:U:OP1	13:K:114:LEU:N	2.47	0.41
3:A:807:U:H2'	3:A:808:G:H8	1.84	0.41
3:A:1115:G:HO2'	3:A:1116:G:H5''	1.86	0.41
3:A:2102:G:C2	3:A:2187:U:O2	2.73	0.41
3:A:2352:A:N1	26:X:34:GLY:HA3	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:2365:G:H4'	26:X:60:PHE:CE2	2.55	0.41
3:A:2812:G:H2'	3:A:2813:A:O4'	2.20	0.41
27:Y:3:ARG:NE	27:Y:30:LEU:HD13	2.35	0.41
28:Z:21:LEU:HD23	28:Z:21:LEU:HA	1.82	0.41
30:b:37:LYS:HE3	30:b:37:LYS:HB2	1.86	0.41
2:2:74:C:O5'	2:2:74:C:H6	2.04	0.41
3:A:31:C:O3'	3:A:1238:G:H5'	2.21	0.41
3:A:678:C:H2'	3:A:679:C:H6	1.84	0.41
3:A:1073:A:H2'	3:A:1074:G:O4'	2.21	0.41
3:A:1709:U:H2'	3:A:1710:G:C8	2.55	0.41
3:A:1821:A:H2'	3:A:1822:C:C6	2.55	0.41
3:A:2286:G:C8	3:A:2287:A:N6	2.88	0.41
3:A:2550:G:C6	3:A:2551:C:C4	3.09	0.41
3:A:2682:A:C2	6:D:23:PRO:HB3	2.56	0.41
4:B:95:U:H2'	4:B:96:G:C8	2.56	0.41
15:M:78:ARG:HG2	15:M:113:ALA:HB3	2.03	0.41
22:T:33:LEU:HD23	22:T:33:LEU:HA	1.66	0.41
29:a:51:VAL:O	29:a:55:VAL:HG22	2.20	0.41
33:e:6:THR:O	33:e:8:ARG:HG2	2.21	0.41
3:A:561:G:H4'	20:R:48:ARG:HH22	1.86	0.41
3:A:799:G:C6	3:A:800:A:C6	3.08	0.41
3:A:1057:A:N7	3:A:1086:A:H2'	2.35	0.41
3:A:1275:A:OP2	3:A:1646:C:N4	2.52	0.41
3:A:1366:A:H2'	3:A:1367:A:O4'	2.21	0.41
3:A:1789:A:H2'	3:A:1790:C:O4'	2.21	0.41
3:A:2343:U:H2'	3:A:2344:U:C6	2.55	0.41
3:A:2785:C:H2'	3:A:2786:U:H6	1.85	0.41
8:F:36:LEU:HA	8:F:153:ASP:O	2.21	0.41
9:G:71:LEU:HA	9:G:71:LEU:HD23	1.83	0.41
9:G:154:PRO:HA	9:G:160:LYS:O	2.21	0.41
27:Y:54:LYS:O	27:Y:58:VAL:HG23	2.19	0.41
3:A:64:A:C6	3:A:65:U:C4	3.09	0.41
3:A:328:U:H4'	24:V:66:GLN:HE21	1.86	0.41
3:A:396:G:H1'	27:Y:29:PHE:HB3	2.02	0.41
3:A:465:G:C6	3:A:466:A:N6	2.89	0.41
3:A:520:G:H2'	3:A:521:U:C6	2.56	0.41
3:A:601:C:O2'	3:A:605:G:H5''	2.21	0.41
3:A:681:G:C2	3:A:797:G:C2	3.09	0.41
3:A:743:A:OP1	6:D:135:GLY:HA2	2.21	0.41
3:A:779:U:H2'	3:A:780:G:C8	2.56	0.41
3:A:997:G:OP1	20:R:92:ARG:HD2	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1341:G:C2	3:A:1398:C:H4'	2.56	0.41
3:A:1374:G:H8	3:A:1374:G:OP2	2.04	0.41
3:A:1423:G:N2	3:A:1576:U:O2	2.54	0.41
3:A:1869:G:N2	3:A:1871:A:HO2'	2.19	0.41
3:A:1869:G:C2	3:A:1873:G:C6	3.09	0.41
3:A:2061:G:H2'	3:A:2501:C:O2'	2.21	0.41
4:B:7:G:H5''	18:P:29:HIS:CE1	2.56	0.41
11:I:48:ALA:HB3	11:I:50:VAL:HG23	2.03	0.41
14:L:103:VAL:HB	14:L:107:LEU:HD12	2.02	0.41
15:M:81:ASP:HB3	15:M:100:ILE:HD13	2.02	0.41
16:N:6:ARG:CZ	16:N:6:ARG:HB2	2.50	0.41
18:P:115:LEU:HD23	18:P:117:PHE:CE2	2.56	0.41
26:X:41:ARG:HD3	26:X:41:ARG:HA	1.53	0.41
27:Y:72:ARG:HG3	27:Y:78:TYR:HE2	1.86	0.41
27:Y:74:ARG:HE	27:Y:74:ARG:HB3	1.45	0.41
28:Z:37:LEU:HD12	28:Z:37:LEU:HA	1.82	0.41
29:a:45:ARG:HH12	29:a:59:GLU:CD	2.29	0.41
3:A:141:G:C8	3:A:141:G:C3'	3.04	0.41
3:A:199:A:N6	3:A:2434:A:C5	2.89	0.41
3:A:948:C:H2'	3:A:949:G:H8	1.85	0.41
3:A:2578:G:OP2	3:A:2578:G:H4'	2.20	0.41
10:H:128:HIS:O	10:H:143:ILE:HA	2.20	0.41
11:I:61:ARG:HG2	11:I:73:LYS:HG2	2.02	0.41
16:N:38:ARG:HB2	16:N:98:PRO:HD3	2.03	0.41
21:S:85:LYS:HE2	21:S:85:LYS:HB3	1.80	0.41
28:Z:38:GLN:HG3	28:Z:39:GLN:H	1.85	0.41
1:l:62:C:HO2'	35:i:382:SER:C	2.22	0.40
3:A:778:G:H5''	3:A:779:U:OP2	2.21	0.40
3:A:811:U:C2	3:A:1251:C:C5	3.09	0.40
3:A:1045:C:OP1	3:A:1046:A:O2'	2.37	0.40
3:A:1818:U:C5	5:C:156:ARG:NH2	2.90	0.40
3:A:2229:U:H2'	3:A:2230:G:H8	1.85	0.40
3:A:2663:G:H2'	3:A:2664:G:O4'	2.21	0.40
3:A:2804:U:H2'	3:A:2805:C:C6	2.56	0.40
16:N:65:ILE:HG12	16:N:103:TYR:HD2	1.86	0.40
17:O:72:ASP:O	17:O:76:VAL:HG13	2.21	0.40
19:Q:40:LEU:HD23	19:Q:40:LEU:HA	1.75	0.40
27:Y:3:ARG:O	27:Y:12:PRO:HD3	2.21	0.40
3:A:42:A:C6	3:A:43:G:C5	3.10	0.40
3:A:118:A:C8	3:A:119:A:C8	3.09	0.40
3:A:277:G:H4'	3:A:278:A:C5	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:501:A:H2'	3:A:502:A:C8	2.56	0.40
3:A:1024:G:C6	3:A:1025:G:C6	3.09	0.40
3:A:1071:G:O2'	3:A:1089:A:OP2	2.36	0.40
3:A:2143:C:H2'	3:A:2144:G:O4'	2.21	0.40
3:A:2388:A:H5'	3:A:2389:G:OP2	2.21	0.40
3:A:2431:U:O2	3:A:2431:U:O4'	2.39	0.40
3:A:2603:G:C6	3:A:2604:U:C4	3.09	0.40
3:A:2847:U:C5	3:A:2848:G:C5	3.09	0.40
5:C:34:LEU:HD21	5:C:63:ARG:HG3	2.03	0.40
9:G:9:VAL:HG23	9:G:52:PHE:HE1	1.86	0.40
12:J:42:PHE:CE1	12:J:57:VAL:HB	2.56	0.40
22:T:109:ASP:OD1	22:T:110:ARG:N	2.54	0.40
26:X:70:GLU:HG3	26:X:72:LYS:HE2	2.04	0.40
3:A:719:C:H2'	3:A:720:U:C6	2.57	0.40
3:A:863:A:H2'	3:A:864:G:C8	2.57	0.40
3:A:863:A:H2'	3:A:864:G:H8	1.86	0.40
3:A:1127:A:N7	3:A:2488:G:O2'	2.55	0.40
3:A:1807:G:N2	3:A:1811:G:C5	2.89	0.40
3:A:1838:C:H4'	3:A:1839:G:H8	1.85	0.40
3:A:2421:G:H4'	3:A:2421:G:OP1	2.21	0.40
3:A:2600:A:H2'	3:A:2601:C:C6	2.56	0.40
3:A:2627:G:H1'	3:A:2777:G:N2	2.36	0.40
11:I:99:PHE:HD2	11:I:106:PHE:HZ	1.69	0.40
12:J:93:PRO:C	12:J:95:LYS:H	2.29	0.40
17:O:22:ARG:HG3	17:O:70:THR:HA	2.03	0.40
18:P:115:LEU:HD23	18:P:117:PHE:HE2	1.86	0.40
24:V:96:PHE:O	24:V:100:SER:HA	2.21	0.40
26:X:45:PHE:CD1	26:X:80:ILE:HD11	2.56	0.40
3:A:1:G:H2'	3:A:2:G:C8	2.57	0.40
3:A:445:C:H2'	3:A:446:G:O4'	2.22	0.40
3:A:822:G:H2'	3:A:823:C:C6	2.57	0.40
3:A:871:U:H4'	16:N:68:PHE:CD2	2.56	0.40
3:A:1672:A:N6	3:A:1673:G:C6	2.89	0.40
3:A:2423:U:H2'	3:A:2424:C:C1'	2.51	0.40
4:B:49:C:H2'	4:B:50:A:H8	1.87	0.40
5:C:157:SER:O	5:C:160:THR:OG1	2.38	0.40
7:E:148:ILE:H	7:E:148:ILE:HG12	1.64	0.40
8:F:65:PRO:HA	8:F:89:VAL:HG22	2.01	0.40
9:G:90:VAL:HG21	9:G:163:ARG:NH1	2.37	0.40
9:G:125:CYS:HB2	9:G:127:THR:O	2.22	0.40
11:I:13:ALA:O	11:I:17:GLU:HB2	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:K:99:ARG:HD2	13:K:102:GLU:OE1	2.22	0.40
15:M:79:LEU:HB2	15:M:113:ALA:O	2.21	0.40
18:P:28:VAL:HG12	18:P:93:ASP:O	2.21	0.40
28:Z:46:VAL:O	28:Z:50:VAL:HG23	2.21	0.40
33:e:38:THR:HA	33:e:41:LYS:HE3	2.04	0.40
3:A:339:U:H6	3:A:339:U:O5'	2.05	0.40
3:A:353:C:H2'	3:A:354:A:O4'	2.22	0.40
3:A:717:C:C5	3:A:718:A:C8	3.10	0.40
3:A:729:G:C6	5:C:207:LYS:HB2	2.56	0.40
3:A:991:C:H2'	3:A:992:C:H6	1.85	0.40
3:A:1139:G:H8	3:A:1139:G:OP2	2.05	0.40
3:A:1258:U:C2	3:A:1259:G:C8	3.09	0.40
3:A:1707:G:C5	3:A:1756:G:C6	3.10	0.40
3:A:2394:C:H42	3:A:2422:C:N4	2.19	0.40
3:A:2586:U:OP2	3:A:2608:G:N1	2.48	0.40
7:E:69:ARG:H	7:E:69:ARG:HG2	1.76	0.40
15:M:3:LEU:HD23	15:M:3:LEU:HA	1.77	0.40
17:O:65:LEU:HD12	17:O:65:LEU:HA	1.85	0.40
18:P:25:ARG:O	18:P:25:ARG:HG3	2.22	0.40
23:U:49:LYS:HG3	23:U:50:LEU:HD23	2.03	0.40
24:V:36:VAL:HB	24:V:39:ILE:HB	2.03	0.40
27:Y:36:HIS:O	27:Y:48:THR:HA	2.21	0.40
35:i:435:UNK:O	35:i:439:UNK:HB1	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	C	269/273 (98%)	261 (97%)	8 (3%)	0	100	100
6	D	207/209 (99%)	201 (97%)	6 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	E	199/201 (99%)	190 (96%)	9 (4%)	0	100	100
8	F	175/179 (98%)	166 (95%)	9 (5%)	0	100	100
9	G	174/177 (98%)	171 (98%)	3 (2%)	0	100	100
10	H	147/149 (99%)	138 (94%)	8 (5%)	1 (1%)	18	51
11	I	123/165 (74%)	113 (92%)	9 (7%)	1 (1%)	16	48
12	J	132/142 (93%)	126 (96%)	6 (4%)	0	100	100
13	K	140/142 (99%)	135 (96%)	5 (4%)	0	100	100
14	L	121/123 (98%)	117 (97%)	4 (3%)	0	100	100
15	M	142/144 (99%)	140 (99%)	2 (1%)	0	100	100
16	N	134/136 (98%)	131 (98%)	3 (2%)	0	100	100
17	O	123/127 (97%)	118 (96%)	5 (4%)	0	100	100
18	P	115/117 (98%)	112 (97%)	3 (3%)	0	100	100
19	Q	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
20	R	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
21	S	101/103 (98%)	99 (98%)	2 (2%)	0	100	100
22	T	108/110 (98%)	105 (97%)	3 (3%)	0	100	100
23	U	93/100 (93%)	90 (97%)	3 (3%)	0	100	100
24	V	100/104 (96%)	99 (99%)	1 (1%)	0	100	100
25	W	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
26	X	74/85 (87%)	73 (99%)	1 (1%)	0	100	100
27	Y	75/78 (96%)	72 (96%)	3 (4%)	0	100	100
28	Z	60/63 (95%)	58 (97%)	2 (3%)	0	100	100
29	a	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
30	b	54/57 (95%)	50 (93%)	4 (7%)	0	100	100
31	c	49/55 (89%)	48 (98%)	1 (2%)	0	100	100
32	d	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
33	e	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
34	f	36/38 (95%)	36 (100%)	0	0	100	100
35	i	84/453 (18%)	84 (100%)	0	0	100	100
36	k	16/18 (89%)	12 (75%)	4 (25%)	0	100	100
All	All	3532/4045 (87%)	3415 (97%)	115 (3%)	2 (0%)	49	79

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
10	H	118	PRO
11	I	108	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	C	216/218 (99%)	190 (88%)	26 (12%)	5	21
6	D	164/164 (100%)	148 (90%)	16 (10%)	7	29
7	E	165/165 (100%)	149 (90%)	16 (10%)	8	29
8	F	148/150 (99%)	127 (86%)	21 (14%)	3	17
9	G	137/138 (99%)	125 (91%)	12 (9%)	9	33
10	H	114/114 (100%)	100 (88%)	14 (12%)	4	21
11	I	95/123 (77%)	85 (90%)	10 (10%)	6	26
12	J	104/110 (94%)	88 (85%)	16 (15%)	2	15
13	K	116/116 (100%)	99 (85%)	17 (15%)	3	17
14	L	104/104 (100%)	96 (92%)	8 (8%)	12	37
15	M	103/103 (100%)	92 (89%)	11 (11%)	6	25
16	N	109/109 (100%)	99 (91%)	10 (9%)	8	31
17	O	102/103 (99%)	95 (93%)	7 (7%)	14	40
18	P	87/87 (100%)	70 (80%)	17 (20%)	1	9
19	Q	99/100 (99%)	88 (89%)	11 (11%)	6	24
20	R	89/90 (99%)	79 (89%)	10 (11%)	6	24
21	S	84/84 (100%)	73 (87%)	11 (13%)	4	20
22	T	93/93 (100%)	84 (90%)	9 (10%)	8	29
23	U	82/84 (98%)	77 (94%)	5 (6%)	17	43
24	V	83/85 (98%)	75 (90%)	8 (10%)	8	29
25	W	78/78 (100%)	72 (92%)	6 (8%)	12	37

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
26	X	57/63 (90%)	47 (82%)	10 (18%)	2	12
27	Y	67/68 (98%)	59 (88%)	8 (12%)	5	22
28	Z	54/55 (98%)	47 (87%)	7 (13%)	4	20
29	a	48/49 (98%)	45 (94%)	3 (6%)	16	42
30	b	47/48 (98%)	36 (77%)	11 (23%)	1	5
31	c	45/49 (92%)	40 (89%)	5 (11%)	6	24
32	d	38/38 (100%)	31 (82%)	7 (18%)	1	11
33	e	51/52 (98%)	47 (92%)	4 (8%)	11	36
34	f	34/34 (100%)	31 (91%)	3 (9%)	9	33
35	i	71/341 (21%)	64 (90%)	7 (10%)	7	28
36	k	17/17 (100%)	15 (88%)	2 (12%)	5	22
All	All	2901/3232 (90%)	2573 (89%)	328 (11%)	8	23

All (328) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	C	3	VAL
5	C	24	LEU
5	C	35	GLU
5	C	51	THR
5	C	72	ASP
5	C	74	ILE
5	C	120	VAL
5	C	130	LEU
5	C	134	ASN
5	C	147	LYS
5	C	156	ARG
5	C	172	VAL
5	C	180	GLU
5	C	185	GLU
5	C	189	ARG
5	C	192	LEU
5	C	195	VAL
5	C	203	ARG
5	C	204	VAL
5	C	228	VAL
5	C	242	LYS
5	C	250	VAL

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Mol	Chain	Res	Type
5	C	251	GLN
5	C	257	THR
5	C	261	LYS
5	C	271	ARG
6	D	12	THR
6	D	13	ARG
6	D	18	ASP
6	D	20	VAL
6	D	22	ILE
6	D	28	GLU
6	D	29	VAL
6	D	60	VAL
6	D	73	VAL
6	D	84	LEU
6	D	128	ARG
6	D	133	THR
6	D	139	SER
6	D	142	VAL
6	D	160	LYS
6	D	168	GLU
7	E	83	VAL
7	E	84	THR
7	E	94	GLN
7	E	96	VAL
7	E	97	ASN
7	E	105	LEU
7	E	119	ILE
7	E	127	GLU
7	E	138	LEU
7	E	148	ILE
7	E	169	VAL
7	E	173	THR
7	E	178	VAL
7	E	179	SER
7	E	184	ASP
7	E	196	VAL
8	F	3	LYS
8	F	4	LEU
8	F	14	LYS
8	F	25	VAL
8	F	49	LEU
8	F	51	ASP

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Mol	Chain	Res	Type
8	F	52	ASN
8	F	67	ILE
8	F	81	GLN
8	F	104	ILE
8	F	106	ILE
8	F	115	ARG
8	F	130	MET
8	F	141	ILE
8	F	144	ASP
8	F	149	VAL
8	F	150	ARG
8	F	153	ASP
8	F	156	ILE
8	F	162	SER
8	F	178	ARG
9	G	10	VAL
9	G	11	VAL
9	G	43	VAL
9	G	49	THR
9	G	87	LEU
9	G	114	ASP
9	G	124	GLU
9	G	125	CYS
9	G	127	THR
9	G	133	LEU
9	G	141	ILE
9	G	153	ARG
10	H	4	ILE
10	H	15	LEU
10	H	37	VAL
10	H	58	LEU
10	H	60	GLU
10	H	76	GLU
10	H	77	THR
10	H	78	VAL
10	H	86	ASP
10	H	87	GLU
10	H	108	VAL
10	H	110	VAL
10	H	112	LYS
10	H	142	VAL
11	I	16	SER

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Mol	Chain	Res	Type
11	I	36	ASP
11	I	54	VAL
11	I	55	VAL
11	I	58	THR
11	I	64	VAL
11	I	85	VAL
11	I	94	ARG
11	I	96	PHE
11	I	109	LYS
12	J	9	VAL
12	J	21	SER
12	J	28	LEU
12	J	31	GLN
12	J	35	ILE
12	J	55	ILE
12	J	61	VAL
12	J	66	SER
12	J	78	VAL
12	J	98	VAL
12	J	111	GLN
12	J	112	THR
12	J	113	LYS
12	J	116	ASP
12	J	128	SER
12	J	139	VAL
13	K	5	THR
13	K	7	LYS
13	K	17	VAL
13	K	28	LEU
13	K	31	GLU
13	K	34	ARG
13	K	40	HIS
13	K	57	LEU
13	K	69	ARG
13	K	70	THR
13	K	88	THR
13	K	90	GLU
13	K	101	ILE
13	K	103	ILE
13	K	122	LEU
13	K	131	ASN
13	K	142	ILE

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Mol	Chain	Res	Type
14	L	21	CYS
14	L	42	THR
14	L	49	ARG
14	L	56	ASP
14	L	58	LEU
14	L	65	THR
14	L	84	CYS
14	L	116	ILE
15	M	14	LYS
15	M	46	VAL
15	M	47	ARG
15	M	55	MET
15	M	59	ARG
15	M	86	GLU
15	M	91	ASP
15	M	101	ILE
15	M	126	ARG
15	M	141	LYS
15	M	143	GLU
16	N	6	ARG
16	N	7	THR
16	N	12	MET
16	N	25	ASP
16	N	54	THR
16	N	58	LYS
16	N	81	ARG
16	N	115	GLU
16	N	133	LYS
16	N	135	VAL
17	O	14	SER
17	O	33	ILE
17	O	36	THR
17	O	69	ARG
17	O	74	GLU
17	O	75	ILE
17	O	100	CYS
18	P	2	ASP
18	P	5	SER
18	P	16	ARG
18	P	18	LEU
18	P	19	GLN
18	P	20	GLU

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Mol	Chain	Res	Type
18	P	31	THR
18	P	36	TYR
18	P	43	ASN
18	P	49	VAL
18	P	55	GLU
18	P	56	LYS
18	P	58	ILE
18	P	61	GLN
18	P	69	ASP
18	P	78	VAL
18	P	98	GLN
19	Q	3	ASN
19	Q	7	GLN
19	Q	21	ARG
19	Q	26	VAL
19	Q	51	ARG
19	Q	65	SER
19	Q	68	GLU
19	Q	92	VAL
19	Q	94	LYS
19	Q	102	GLU
19	Q	115	ASN
20	R	6	ARG
20	R	17	ILE
20	R	24	TYR
20	R	31	VAL
20	R	39	VAL
20	R	40	ILE
20	R	51	ARG
20	R	74	ILE
20	R	80	ILE
20	R	109	LEU
21	S	4	VAL
21	S	10	LYS
21	S	20	VAL
21	S	25	LEU
21	S	38	VAL
21	S	45	GLU
21	S	60	LYS
21	S	72	VAL
21	S	83	TYR
21	S	85	LYS

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Mol	Chain	Res	Type
21	S	101	ILE
22	T	12	SER
22	T	20	VAL
22	T	28	LYS
22	T	55	ILE
22	T	68	ASP
22	T	74	ILE
22	T	95	ARG
22	T	96	ILE
22	T	98	LYS
23	U	7	LEU
23	U	16	VAL
23	U	17	SER
23	U	48	GLN
23	U	72	GLN
24	V	7	ARG
24	V	28	VAL
24	V	34	VAL
24	V	41	LEU
24	V	42	VAL
24	V	68	SER
24	V	83	VAL
24	V	102	THR
25	W	7	GLU
25	W	12	GLN
25	W	61	LEU
25	W	77	VAL
25	W	78	GLN
25	W	92	VAL
26	X	11	ARG
26	X	12	ASN
26	X	21	LEU
26	X	35	SER
26	X	38	VAL
26	X	41	ARG
26	X	56	ASP
26	X	58	THR
26	X	72	LYS
26	X	85	GLU
27	Y	2	SER
27	Y	4	VAL
27	Y	13	VAL

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Mol	Chain	Res	Type
27	Y	42	SER
27	Y	44	LYS
27	Y	71	LEU
27	Y	74	ARG
27	Y	77	LYS
28	Z	2	LYS
28	Z	16	THR
28	Z	28	LEU
28	Z	44	LYS
28	Z	45	GLN
28	Z	48	ARG
28	Z	56	LEU
29	a	30	ARG
29	a	36	VAL
29	a	56	LYS
30	b	4	GLN
30	b	9	THR
30	b	15	MET
30	b	18	SER
30	b	25	VAL
30	b	26	THR
30	b	28	LEU
30	b	36	GLU
30	b	40	ARG
30	b	46	ASP
30	b	52	ARG
31	c	5	ILE
31	c	6	ARG
31	c	22	THR
31	c	42	VAL
31	c	47	VAL
32	d	1	MET
32	d	12	ARG
32	d	24	THR
32	d	25	LYS
32	d	34	ARG
32	d	41	ARG
32	d	42	LEU
33	e	8	ARG
33	e	32	ILE
33	e	50	VAL
33	e	51	SER

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Mol	Chain	Res	Type
34	f	1	MET
34	f	2	LYS
34	f	12	ARG
35	i	333	ASP
35	i	369	ASP
35	i	374	VAL
35	i	379	ILE
35	i	386	LYS
35	i	397	SER
35	i	411	GLN
36	k	36	LEU
36	k	40	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (48) such sidechains are listed below:

Mol	Chain	Res	Type
5	C	86	ASN
5	C	90	ASN
5	C	251	GLN
6	D	136	ASN
6	D	140	HIS
7	E	24	ASN
7	E	165	HIS
8	F	37	ASN
8	F	63	GLN
8	F	81	GLN
8	F	127	ASN
9	G	30	ASN
9	G	48	ASN
10	H	33	GLN
12	J	31	GLN
13	K	76	HIS
13	K	80	HIS
13	K	86	GLN
14	L	3	GLN
14	L	89	ASN
15	M	104	GLN
16	N	3	GLN
18	P	43	ASN
18	P	100	HIS
19	Q	3	ASN
19	Q	52	ASN

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Mol	Chain	Res	Type
19	Q	56	HIS
19	Q	75	GLN
20	R	37	GLN
20	R	81	ASN
21	S	82	HIS
22	T	7	HIS
22	T	102	HIS
23	U	28	ASN
23	U	48	GLN
23	U	59	ASN
23	U	91	GLN
25	W	12	GLN
26	X	46	HIS
28	Z	25	GLN
28	Z	39	GLN
28	Z	58	ASN
29	a	20	HIS
30	b	6	ASN
32	d	29	GLN
35	i	332	ASN
35	i	381	ASN
35	i	411	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	42/113 (37%)	13 (30%)	0
2	2	2/3 (66%)	1 (50%)	0
3	A	2878/2903 (99%)	518 (17%)	19 (0%)
4	B	119/120 (99%)	13 (10%)	0
All	All	3041/3139 (96%)	545 (17%)	19 (0%)

All (545) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	33	C
1	1	36	U
1	1	37	U
1	1	38	U
1	1	39	A
1	1	41	C

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Mol	Chain	Res	Type
1	1	42	A
1	1	43	G
1	1	46	C
1	1	57	G
1	1	58	G
1	1	67	A
1	1	70	G
2	2	76	A
3	A	10	A
3	A	12	U
3	A	33	C
3	A	34	U
3	A	35	G
3	A	45	G
3	A	46	G
3	A	49	A
3	A	50	U
3	A	51	G
3	A	62	U
3	A	63	A
3	A	65	U
3	A	71	A
3	A	72	U
3	A	74	A
3	A	75	G
3	A	84	A
3	A	93	G
3	A	96	C
3	A	101	A
3	A	102	U
3	A	103	A
3	A	110	G
3	A	118	A
3	A	119	A
3	A	120	U
3	A	136	G
3	A	137	U
3	A	138	U
3	A	139	U
3	A	142	A
3	A	156	A
3	A	162	U

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Mol	Chain	Res	Type
3	A	181	A
3	A	188	G
3	A	196	A
3	A	199	A
3	A	215	G
3	A	216	A
3	A	220	G
3	A	221	A
3	A	222	A
3	A	226	A
3	A	248	G
3	A	266	G
3	A	272	A
3	A	275	C
3	A	276	U
3	A	285	G
3	A	291	G
3	A	302	C
3	A	311	A
3	A	329	G
3	A	330	A
3	A	335	C
3	A	349	U
3	A	353	C
3	A	356	G
3	A	361	G
3	A	362	A
3	A	372	G
3	A	386	G
3	A	396	G
3	A	399	U
3	A	411	G
3	A	419	U
3	A	424	G
3	A	454	A
3	A	455	C
3	A	475	C
3	A	477	A
3	A	479	A
3	A	480	A
3	A	481	G
3	A	491	G

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Mol	Chain	Res	Type
3	A	504	A
3	A	505	A
3	A	509	C
3	A	510	C
3	A	513	A
3	A	518	G
3	A	529	A
3	A	531	C
3	A	532	A
3	A	533	G
3	A	543	G
3	A	544	C
3	A	550	C
3	A	552	U
3	A	558	U
3	A	563	A
3	A	567	U
3	A	568	U
3	A	573	U
3	A	575	A
3	A	586	A
3	A	603	A
3	A	613	A
3	A	614	A
3	A	615	U
3	A	627	A
3	A	632	A
3	A	634	C
3	A	637	A
3	A	645	C
3	A	646	U
3	A	647	G
3	A	653	U
3	A	654	A
3	A	655	A
3	A	668	A
3	A	685	A
3	A	686	U
3	A	711	G
3	A	712	G
3	A	713	G
3	A	718	A

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Mol	Chain	Res	Type
3	A	730	A
3	A	747	U
3	A	753	A
3	A	757	G
3	A	763	G
3	A	764	A
3	A	765	C
3	A	775	G
3	A	777	G
3	A	782	A
3	A	784	G
3	A	785	G
3	A	788	A
3	A	789	A
3	A	790	U
3	A	791	C
3	A	793	A
3	A	794	A
3	A	801	G
3	A	805	G
3	A	812	C
3	A	827	U
3	A	828	U
3	A	831	G
3	A	846	U
3	A	859	G
3	A	865	C
3	A	869	G
3	A	878	A
3	A	896	A
3	A	897	C
3	A	899	A
3	A	907	G
3	A	910	A
3	A	914	G
3	A	915	C
3	A	932	U
3	A	933	A
3	A	946	C
3	A	953	G
3	A	957	C
3	A	961	C

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Mol	Chain	Res	Type
3	A	974	G
3	A	983	A
3	A	990	A
3	A	996	A
3	A	999	U
3	A	1005	C
3	A	1009	A
3	A	1012	U
3	A	1013	C
3	A	1022	G
3	A	1023	U
3	A	1027	A
3	A	1033	U
3	A	1040	A
3	A	1046	A
3	A	1056	G
3	A	1057	A
3	A	1070	A
3	A	1071	G
3	A	1073	A
3	A	1083	U
3	A	1087	G
3	A	1088	A
3	A	1090	A
3	A	1101	U
3	A	1111	A
3	A	1112	G
3	A	1116	G
3	A	1129	A
3	A	1130	U
3	A	1132	U
3	A	1133	A
3	A	1135	C
3	A	1136	G
3	A	1139	G
3	A	1142	A
3	A	1143	A
3	A	1155	A
3	A	1173	U
3	A	1179	G
3	A	1182	G
3	A	1206	G

Continued on next page...

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Mol	Chain	Res	Type
3	A	1212	G
3	A	1218	G
3	A	1236	G
3	A	1238	G
3	A	1247	A
3	A	1249	U
3	A	1252	G
3	A	1253	A
3	A	1256	G
3	A	1262	A
3	A	1271	G
3	A	1272	A
3	A	1294	U
3	A	1300	G
3	A	1301	A
3	A	1302	A
3	A	1308	A
3	A	1329	U
3	A	1332	G
3	A	1337	G
3	A	1338	G
3	A	1345	C
3	A	1346	G
3	A	1365	A
3	A	1379	U
3	A	1383	A
3	A	1395	A
3	A	1403	A
3	A	1416	G
3	A	1417	C
3	A	1424	G
3	A	1428	C
3	A	1434	A
3	A	1437	C
3	A	1449	G
3	A	1451	C
3	A	1452	G
3	A	1453	A
3	A	1482	G
3	A	1489	C
3	A	1491	G
3	A	1493	C

Continued on next page...

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Mol	Chain	Res	Type
3	A	1494	A
3	A	1495	A
3	A	1497	U
3	A	1498	C
3	A	1509	A
3	A	1510	G
3	A	1515	A
3	A	1524	G
3	A	1529	G
3	A	1533	C
3	A	1535	A
3	A	1536	C
3	A	1537	G
3	A	1554	U
3	A	1560	G
3	A	1566	A
3	A	1569	A
3	A	1576	U
3	A	1578	U
3	A	1581	G
3	A	1583	A
3	A	1585	C
3	A	1606	C
3	A	1607	C
3	A	1608	A
3	A	1616	A
3	A	1634	A
3	A	1639	C
3	A	1647	U
3	A	1648	U
3	A	1649	G
3	A	1660	G
3	A	1674	G
3	A	1677	A
3	A	1715	G
3	A	1722	A
3	A	1725	U
3	A	1729	U
3	A	1730	C
3	A	1738	G
3	A	1744	A
3	A	1757	A

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Mol	Chain	Res	Type
3	A	1764	C
3	A	1773	A
3	A	1782	U
3	A	1786	A
3	A	1791	A
3	A	1800	C
3	A	1801	A
3	A	1802	A
3	A	1808	A
3	A	1809	A
3	A	1811	G
3	A	1816	C
3	A	1829	A
3	A	1847	A
3	A	1849	G
3	A	1850	G
3	A	1870	C
3	A	1871	A
3	A	1872	A
3	A	1876	A
3	A	1896	G
3	A	1906	G
3	A	1920	C
3	A	1927	A
3	A	1929	G
3	A	1930	G
3	A	1931	U
3	A	1934	C
3	A	1936	A
3	A	1937	A
3	A	1939	U
3	A	1955	U
3	A	1956	U
3	A	1960	A
3	A	1962	C
3	A	1966	A
3	A	1967	C
3	A	1970	A
3	A	1971	U
3	A	1972	G
3	A	1974	C
3	A	1982	U

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Mol	Chain	Res	Type
3	A	1991	U
3	A	1992	G
3	A	1993	U
3	A	1997	C
3	A	2021	C
3	A	2023	C
3	A	2030	A
3	A	2031	A
3	A	2033	A
3	A	2043	C
3	A	2050	C
3	A	2054	A
3	A	2055	C
3	A	2056	G
3	A	2060	A
3	A	2061	G
3	A	2062	A
3	A	2069	G
3	A	2072	C
3	A	2093	G
3	A	2097	A
3	A	2101	A
3	A	2103	C
3	A	2104	C
3	A	2105	U
3	A	2106	U
3	A	2111	U
3	A	2112	G
3	A	2113	U
3	A	2116	G
3	A	2117	A
3	A	2118	U
3	A	2119	A
3	A	2120	G
3	A	2123	G
3	A	2126	A
3	A	2128	G
3	A	2131	U
3	A	2132	U
3	A	2133	G
3	A	2134	A
3	A	2145	C

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Mol	Chain	Res	Type
3	A	2146	C
3	A	2147	A
3	A	2148	G
3	A	2159	G
3	A	2160	C
3	A	2161	C
3	A	2163	A
3	A	2164	C
3	A	2165	C
3	A	2167	U
3	A	2168	G
3	A	2169	A
3	A	2170	A
3	A	2171	A
3	A	2172	U
3	A	2173	A
3	A	2174	C
3	A	2177	C
3	A	2178	C
3	A	2185	U
3	A	2187	U
3	A	2190	G
3	A	2198	A
3	A	2203	U
3	A	2204	G
3	A	2211	A
3	A	2212	A
3	A	2225	A
3	A	2238	G
3	A	2239	G
3	A	2250	G
3	A	2268	A
3	A	2278	A
3	A	2280	G
3	A	2283	C
3	A	2287	A
3	A	2288	A
3	A	2297	A
3	A	2305	U
3	A	2308	G
3	A	2322	A
3	A	2325	G

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Mol	Chain	Res	Type
3	A	2331	G
3	A	2336	A
3	A	2345	G
3	A	2347	C
3	A	2350	C
3	A	2354	C
3	A	2357	G
3	A	2366	A
3	A	2383	G
3	A	2385	C
3	A	2402	U
3	A	2403	C
3	A	2406	A
3	A	2420	C
3	A	2421	G
3	A	2422	C
3	A	2423	U
3	A	2424	C
3	A	2425	A
3	A	2427	C
3	A	2429	G
3	A	2430	A
3	A	2431	U
3	A	2432	A
3	A	2434	A
3	A	2435	A
3	A	2440	C
3	A	2441	U
3	A	2445	G
3	A	2448	A
3	A	2464	G
3	A	2475	C
3	A	2476	A
3	A	2478	A
3	A	2491	U
3	A	2492	U
3	A	2497	A
3	A	2502	G
3	A	2504	U
3	A	2505	G
3	A	2506	U
3	A	2507	C

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Mol	Chain	Res	Type
3	A	2513	A
3	A	2514	U
3	A	2518	A
3	A	2520	C
3	A	2529	G
3	A	2566	A
3	A	2567	G
3	A	2578	G
3	A	2582	G
3	A	2585	U
3	A	2586	U
3	A	2602	A
3	A	2603	G
3	A	2609	U
3	A	2613	U
3	A	2615	U
3	A	2621	G
3	A	2623	G
3	A	2624	G
3	A	2629	U
3	A	2630	G
3	A	2636	C
3	A	2638	G
3	A	2669	G
3	A	2682	A
3	A	2689	U
3	A	2690	U
3	A	2714	G
3	A	2716	C
3	A	2726	A
3	A	2733	A
3	A	2739	U
3	A	2744	G
3	A	2748	A
3	A	2757	A
3	A	2765	A
3	A	2778	A
3	A	2779	U
3	A	2780	G
3	A	2791	G
3	A	2792	A
3	A	2798	U

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Mol	Chain	Res	Type
3	A	2799	A
3	A	2801	G
3	A	2820	A
3	A	2821	A
3	A	2825	G
3	A	2833	U
3	A	2835	A
3	A	2836	U
3	A	2849	U
3	A	2860	A
3	A	2861	U
3	A	2867	G
3	A	2870	C
3	A	2873	A
3	A	2879	A
3	A	2880	C
3	A	2883	A
3	A	2884	U
3	A	2885	G
3	A	2886	A
3	A	2888	C
3	A	2891	U
4	B	24	G
4	B	25	U
4	B	35	C
4	B	41	G
4	B	45	A
4	B	56	G
4	B	66	A
4	B	67	G
4	B	71	C
4	B	88	C
4	B	89	U
4	B	90	C
4	B	109	A

All (19) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	A	100	U
3	A	613	A
3	A	645	C

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Mol	Chain	Res	Type
3	A	653	U
3	A	784	G
3	A	827	U
3	A	830	G
3	A	1110	G
3	A	1344	U
3	A	1494	A
3	A	1721	G
3	A	1939	U
3	A	2127	G
3	A	2158	A
3	A	2422	C
3	A	2424	C
3	A	2430	A
3	A	2602	A
3	A	2756	U

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 432 ligands modelled in this entry, 432 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

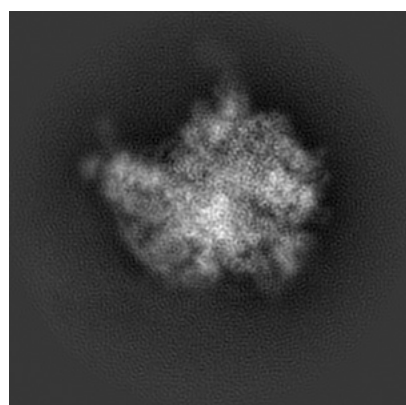
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-8004. These allow visual inspection of the internal detail of the map and identification of artifacts.

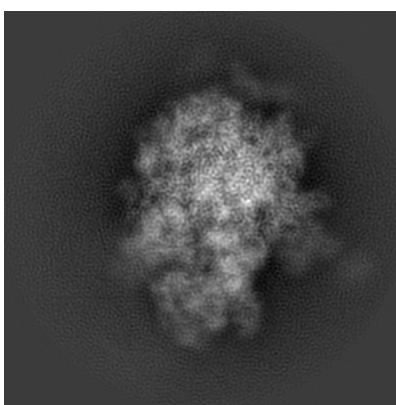
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

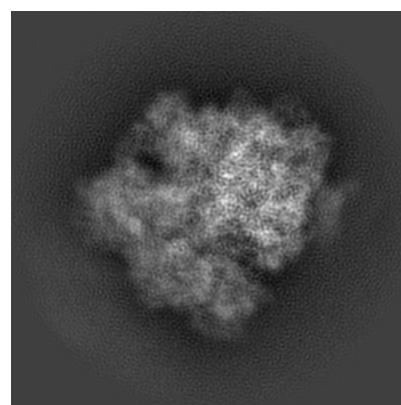
6.1.1 Primary map



X



Y

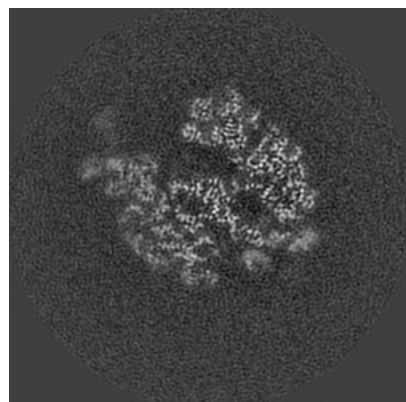


Z

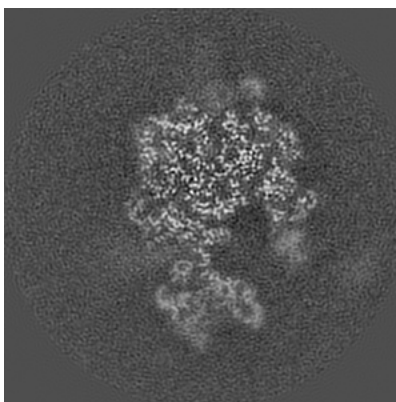
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

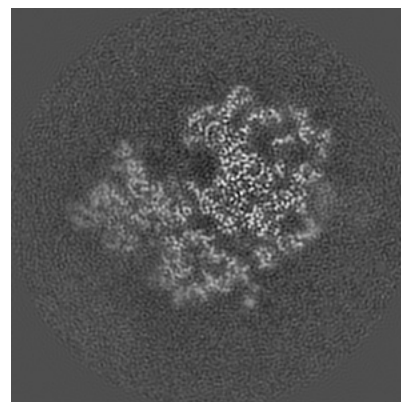
6.2.1 Primary map



X Index: 144



Y Index: 144

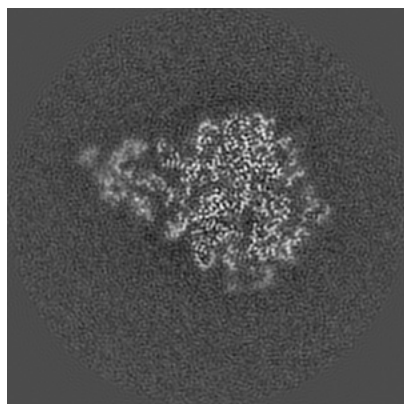


Z Index: 144

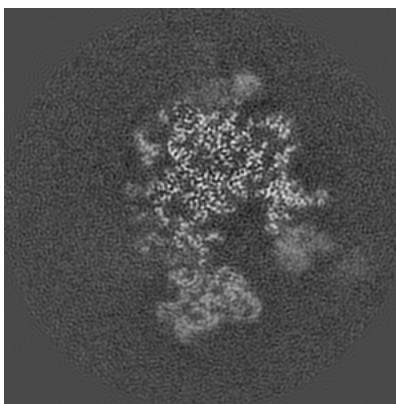
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

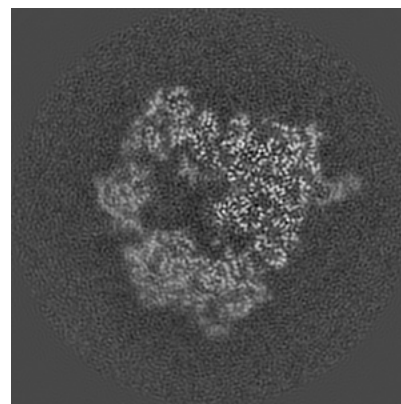
6.3.1 Primary map



X Index: 165



Y Index: 150

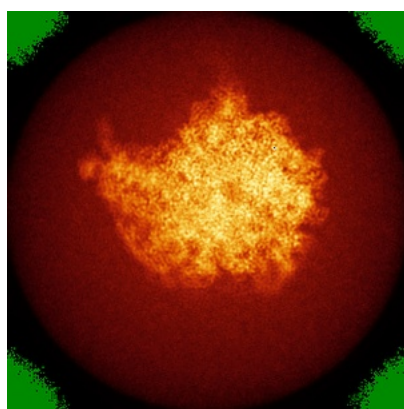


Z Index: 166

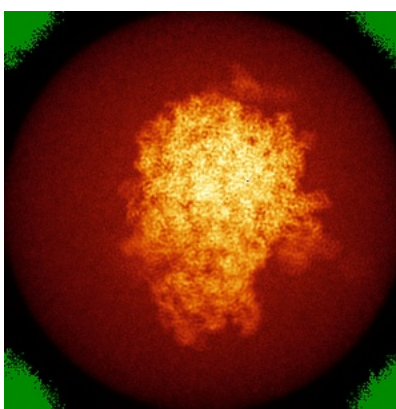
The images above show the largest variance slices of the map in three orthogonal directions.

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

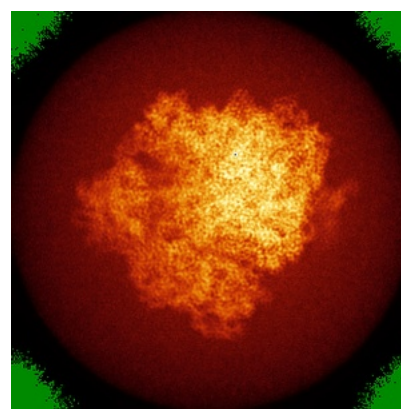
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

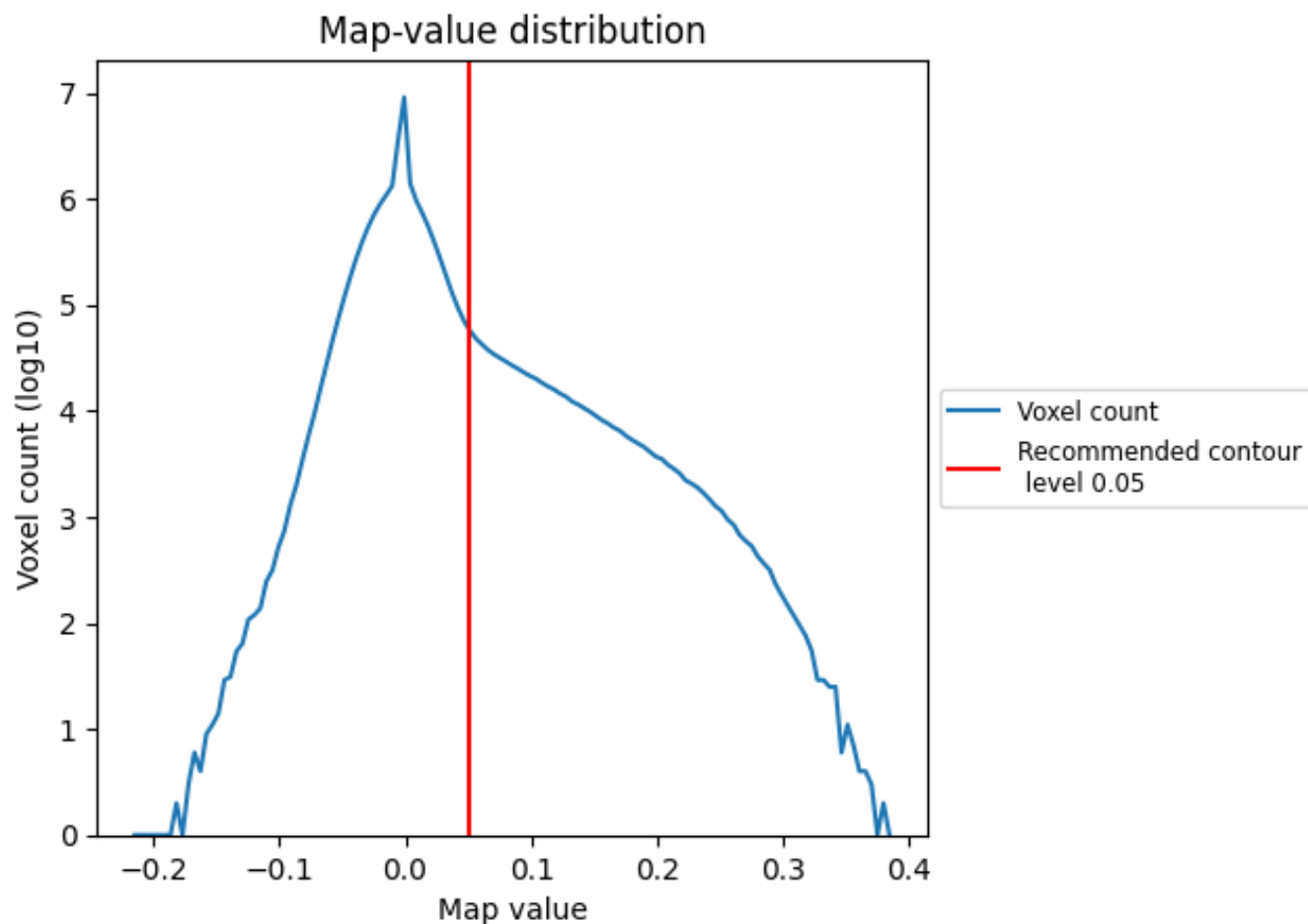
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

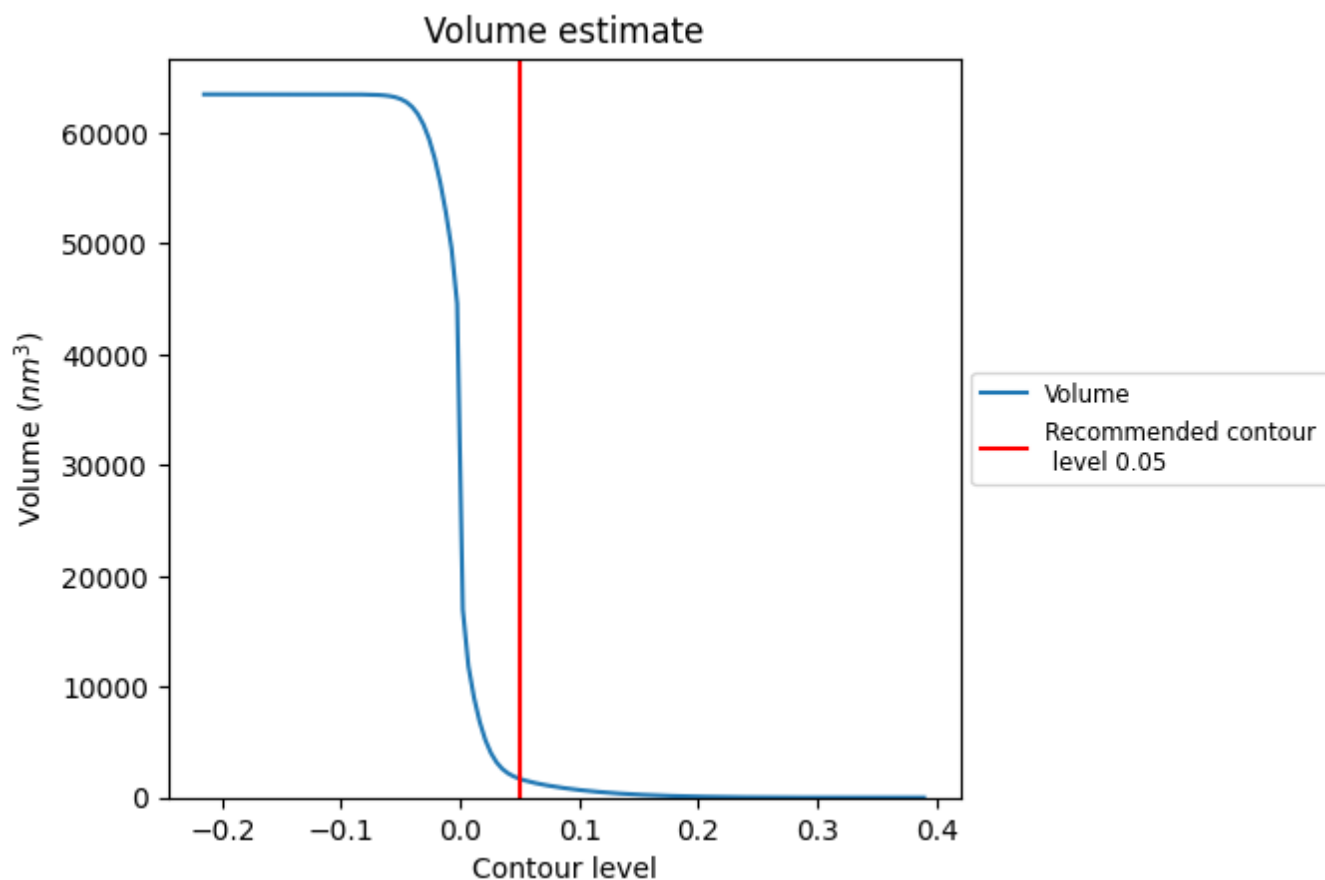
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

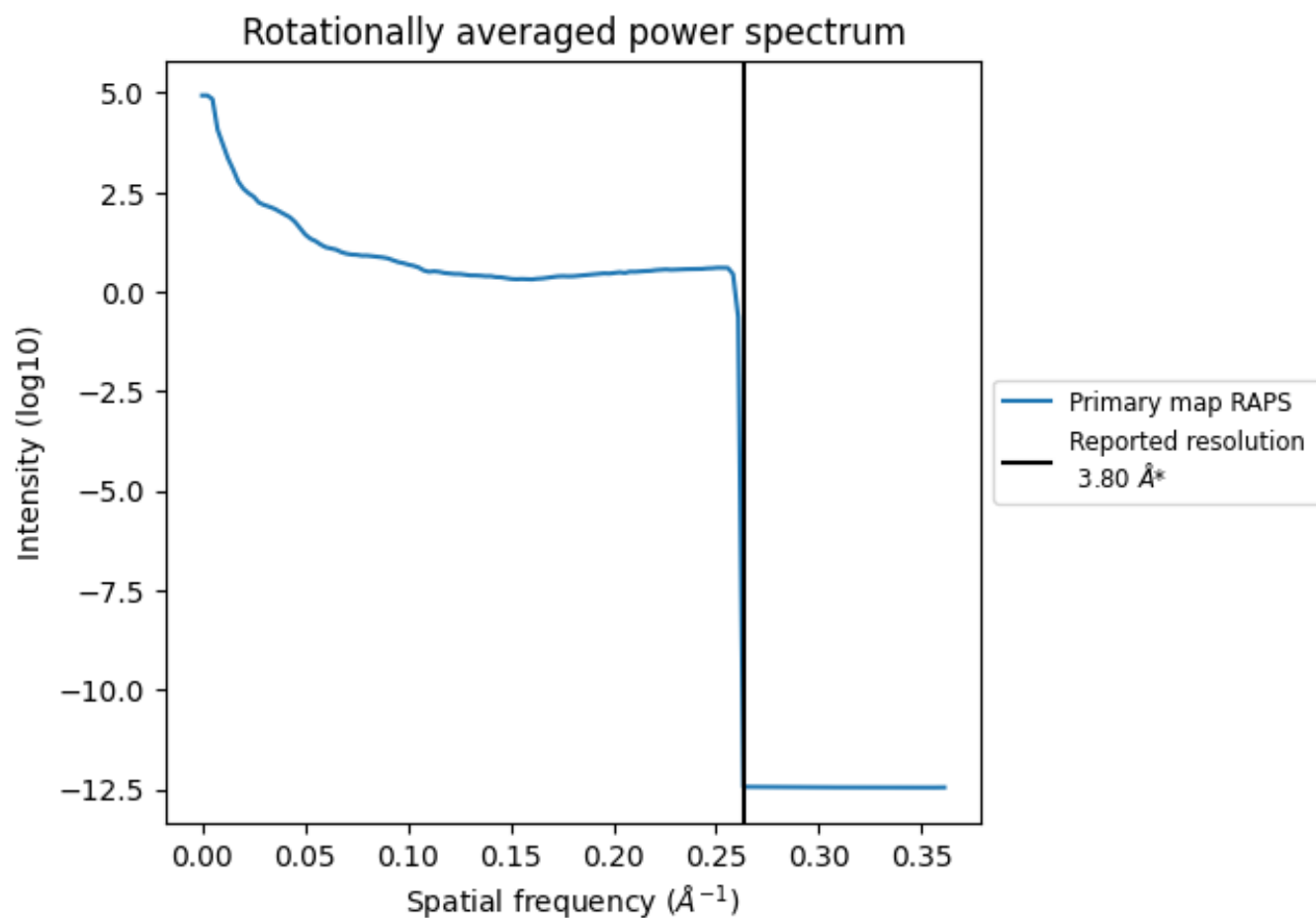
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1693 nm^3 ; this corresponds to an approximate mass of 1530 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 0.263 Å⁻¹

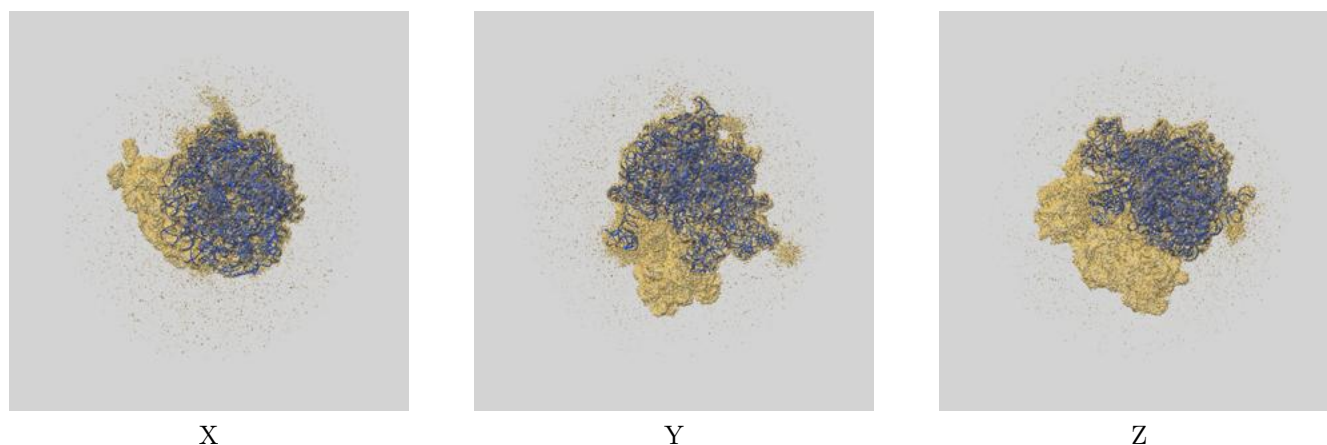
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

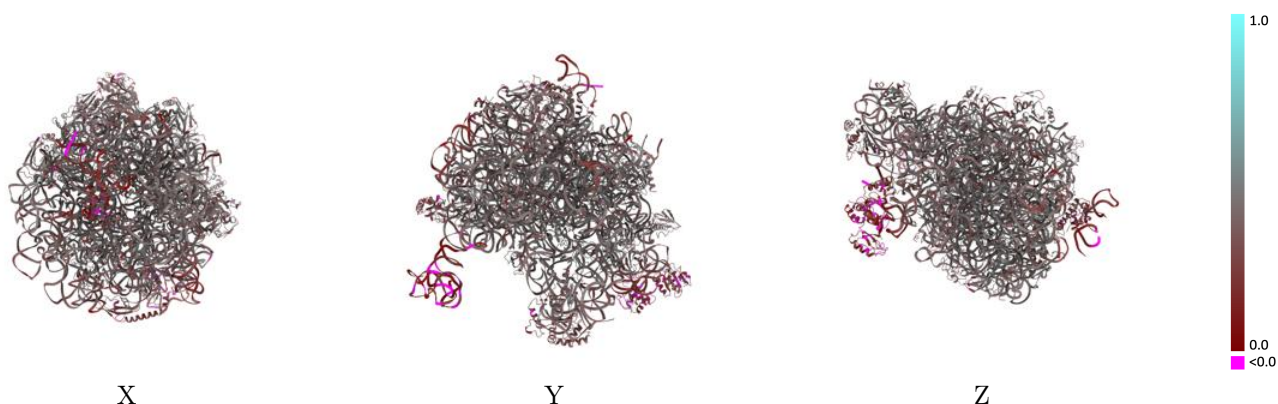
This section contains information regarding the fit between EMDB map EMD-8004 and PDB model 5GAH. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



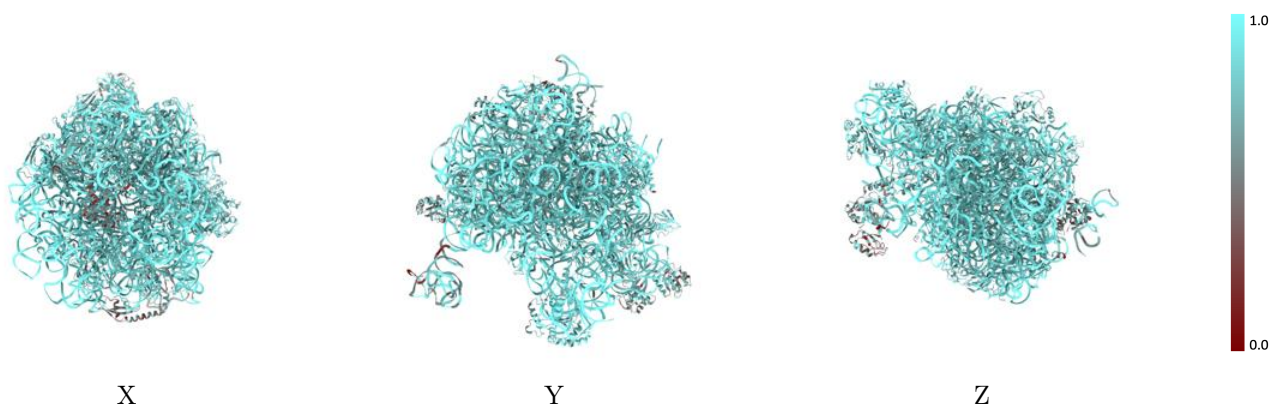
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



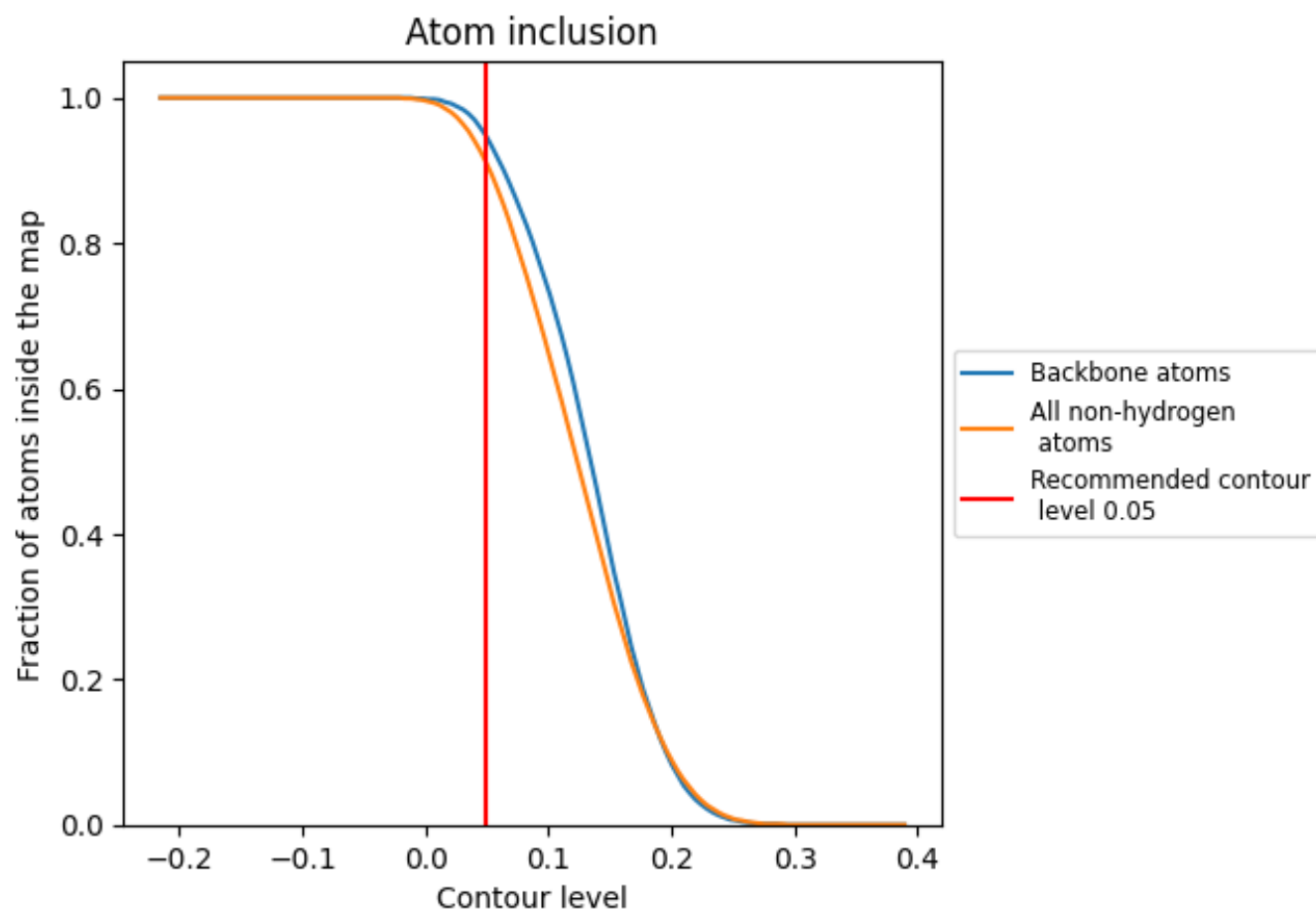
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 91% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9090	 0.3880
1	 0.7850	 0.1610
2	 0.9360	 0.4300
A	 0.9530	 0.3920
B	 0.9820	 0.3990
C	 0.8470	 0.4420
D	 0.8660	 0.4400
E	 0.8250	 0.4010
F	 0.8190	 0.3330
G	 0.8570	 0.3810
H	 0.5880	 0.2850
I	 0.6240	 0.1910
J	 0.5320	 0.1210
K	 0.8750	 0.4340
L	 0.7960	 0.4210
M	 0.8590	 0.4120
N	 0.8560	 0.4350
O	 0.8470	 0.4110
P	 0.8840	 0.4000
Q	 0.8260	 0.4050
R	 0.8740	 0.4190
S	 0.8770	 0.4320
T	 0.8130	 0.4270
U	 0.8080	 0.3860
V	 0.8360	 0.4030
W	 0.8740	 0.4250
X	 0.8650	 0.4480
Y	 0.8470	 0.4240
Z	 0.8020	 0.3690
a	 0.8700	 0.4200
b	 0.8390	 0.4110
c	 0.8180	 0.3950
d	 0.8650	 0.4380
e	 0.8720	 0.4570
f	 0.8800	 0.4360



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Chain	Atom inclusion	Q-score
i	 0.5820	 0.2390
k	 0.5330	 0.1660