



Full wwPDB EM Validation Report ⓘ

Mar 23, 2026 – 04:07 AM UTC

PDB ID : 8B6C / pdb_00008b6c
EMDB ID : EMD-15863
Title : Cryo-EM structure of ribosome-Sec61 in complex with cyclotriazadisulfonamide derivative CK147
Authors : Pauwels, E.; Shewakramani, N.R.; De Wijngaert, B.; Vermeire, K.; Das, K.
Deposited on : 2022-09-26
Resolution : 2.79 Å (reported)
Based on initial models : 6MTE, 3J7Q

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

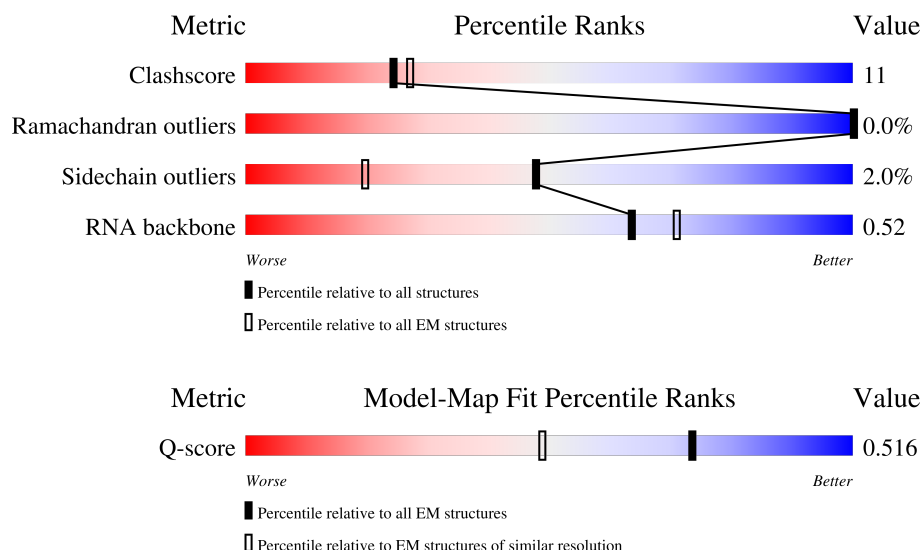
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 2.79 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	10811 (2.29 - 3.29)

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	T	159	
2	5	4808	
3	F	225	

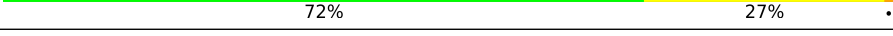
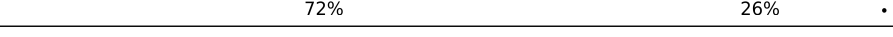
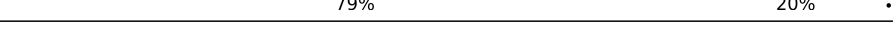
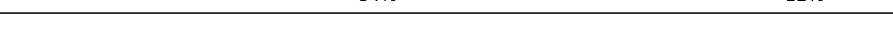
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Mol	Chain	Length	Quality of chain
4	D	293	
5	S	176	
6	b	245	
7	B	394	
8	d	107	
9	8	156	
10	G	319	
11	J	170	
12	c	98	
13	j	86	
14	A	257	
15	I	214	
16	q	68	
17	p	91	
18	V	131	
19	m	52	
20	l	50	
21	P	153	
22	E	291	
23	Q	188	
24	R	196	
25	W	157	
26	O	203	
27	K	476	
28	C	362	

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Mol	Chain	Length	Quality of chain
29	o	103	
30	r	124	
31	f	109	
32	e	128	
33	Z	135	
34	a	147	
35	g	114	
36	k	70	
37	H	190	
38	L	211	
39	7	120	
40	N	203	
41	i	105	
42	h	122	
43	M	138	
44	Y	134	
45	X	118	
46	U	99	
47	n	25	

2 Entry composition

There are 50 unique types of molecules in this entry. The entry contains 139959 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	T	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 2 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	5	3619	Total	C	N	O	P	0	0
			77665	34619	14204	25223	3619		

- Molecule 3 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	F	225	Total	C	N	O	S	0	0
			1875	1205	358	303	9		

- Molecule 4 is a protein called Ribosomal_L18_c domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	293	Total	C	N	O	S	0	0
			2391	1512	438	427	14		

- Molecule 5 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	S	176	Total	C	N	O	S	0	0
			1462	930	285	236	11		

- Molecule 6 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	b	104	Total	C	N	O	S	0	0
			848	527	189	129	3		

- Molecule 7 is a protein called Ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	394	Total	C	N	O	S	0	0
			3172	2020	597	542	13		

- Molecule 8 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	d	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 9 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	8	151	Total	C	N	O	P	0	0
			3208	1432	564	1062	150		

- Molecule 10 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	233	Total	C	N	O	S	0	0
			1879	1199	361	315	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	244	GLY	CYS	conflict	UNP G1STW0

- Molecule 11 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	J	170	Total	C	N	O	S	0	0
			1362	861	254	241	6		

- Molecule 12 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	c	98	Total	C	N	O	S	0	0
			761	481	134	140	6		

- Molecule 13 is a protein called Ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	j	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 14 is a protein called Ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	A	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 15 is a protein called Ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	I	205	Total	C	N	O	S	0	0
			1664	1056	321	274	13		

- Molecule 16 is a protein called Protein transport protein Sec61 subunit gamma.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	q	67	Total	C	N	O	S	0	0
			535	350	93	88	4		

- Molecule 17 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	p	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 18 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	V	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 19 is a protein called 60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	m	52	Total	C	N	O	S	0	0
			430	267	90	67	6		

- Molecule 20 is a protein called 60S ribosomal protein L39-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	l	50	Total	C	N	O	S	0	0
			447	286	96	64	1		

- Molecule 21 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	P	153	Total	C	N	O	S	0	0
			1242	777	241	215	9		

- Molecule 22 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	E	216	Total	C	N	O	S	0	0
			1729	1115	329	282	3		

- Molecule 23 is a protein called eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Q	187	Total	C	N	O	S	0	0
			1515	946	315	250	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Q	134	ARG	CYS	conflict	UNP F6QKI9

- Molecule 24 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	R	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 25 is a protein called Ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	W	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 26 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	O	199	Total	C	N	O	S	0	0
			1630	1051	319	255	5		

- Molecule 27 is a protein called Protein transport protein Sec61 subunit alpha isoform 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	K	444	Total	C	N	O	S	0	0
			3427	2243	555	607	22		

- Molecule 28 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	C	362	Total	C	N	O	S	0	0
			2884	1813	577	480	14		

- Molecule 29 is a protein called 60S ribosomal protein L36a-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	o	103	Total	C	N	O	S	0	0
			842	528	172	136	6		

- Molecule 30 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	r	124	Total	C	N	O	S	0	0
			994	616	205	167	6		

- Molecule 31 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	f	109	Total	C	N	O	S	0	0
			876	555	174	143	4		

- Molecule 32 is a protein called Ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	e	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 33 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Z	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 34 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	a	147	Total	C	N	O	S	0	0
			1162	734	239	185	4		

- Molecule 35 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	g	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 36 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	k	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k	24	LYS	ASN	conflict	UNP G1U001

- Molecule 37 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	H	190	Total	C	N	O	S	0	0
			1516	954	284	272	6		

- Molecule 38 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	L	210	Total	C	N	O	S	0	0
			1702	1065	354	279	4		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L	74	ARG	HIS	conflict	UNP G1TKB3

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Chain	Residue	Modelled	Actual	Comment	Reference
L	190	ARG	HIS	conflict	UNP G1TKB3

- Molecule 39 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 40 is a protein called Ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	N	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 41 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	i	102	Total	C	N	O	S	0	0
			830	520	176	129	5		

- Molecule 42 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	h	122	Total	C	N	O	S	0	0
			1013	640	204	168	1		

- Molecule 43 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	M	138	Total	C	N	O	S	0	0
			1137	727	221	182	7		

- Molecule 44 is a protein called Ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Y	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 45 is a protein called Ribosomal_L23eN domain-containing protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	X	118	Total	C	N	O	S	0	0
			967	618	181	167	1		

- Molecule 46 is a protein called 60S ribosomal protein L22 (Fragment).

Mol	Chain	Residues	Atoms					AltConf	Trace
46	U	99	Total	C	N	O	S	0	0
			809	519	141	147	2		

- Molecule 47 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	n	25	Total	C	N	O	S	0	0
			239	145	64	27	3		

- Molecule 48 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
48	5	161	Total	Mg	0
			161	161	
48	8	5	Total	Mg	0
			5	5	
48	A	1	Total	Mg	0
			1	1	
48	I	1	Total	Mg	0
			1	1	
48	V	1	Total	Mg	0
			1	1	
48	P	1	Total	Mg	0
			1	1	
48	a	1	Total	Mg	0
			1	1	
48	7	7	Total	Mg	0
			7	7	

- Molecule 49 is ZINC ION (CCD ID: ZN) (formula: Zn).

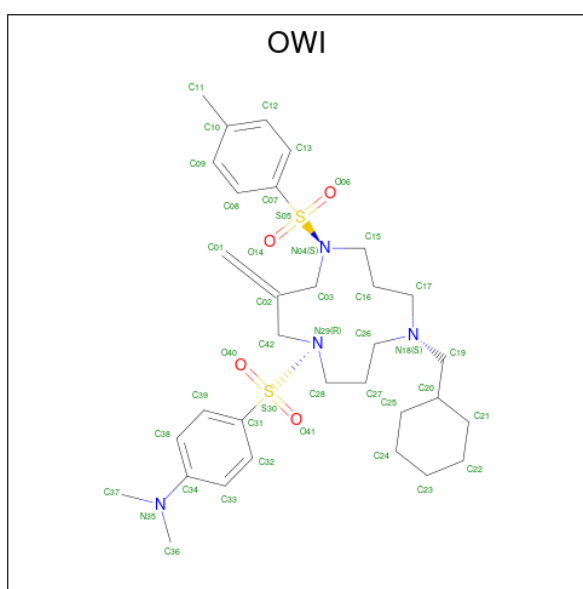
Mol	Chain	Residues	Atoms		AltConf
49	j	1	Total	Zn	0
			1	1	
49	p	1	Total	Zn	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
49	m	1	Total	Zn	0
			1	1	
49	o	1	Total	Zn	0
			1	1	
49	g	1	Total	Zn	0
			1	1	

- Molecule 50 is 4-[[9-(cyclohexylmethyl)-3-methylidene-5-(4-methylphenyl)sulfonyl-1,5,9-triazacyclododec-1-yl]sulfonyl]-{N}, {N}-dimethyl-aniline (CCD ID: OWI) (formula: $C_{32}H_{48}N_4O_4S_2$) (labeled as "Ligand of Interest" by depositor).

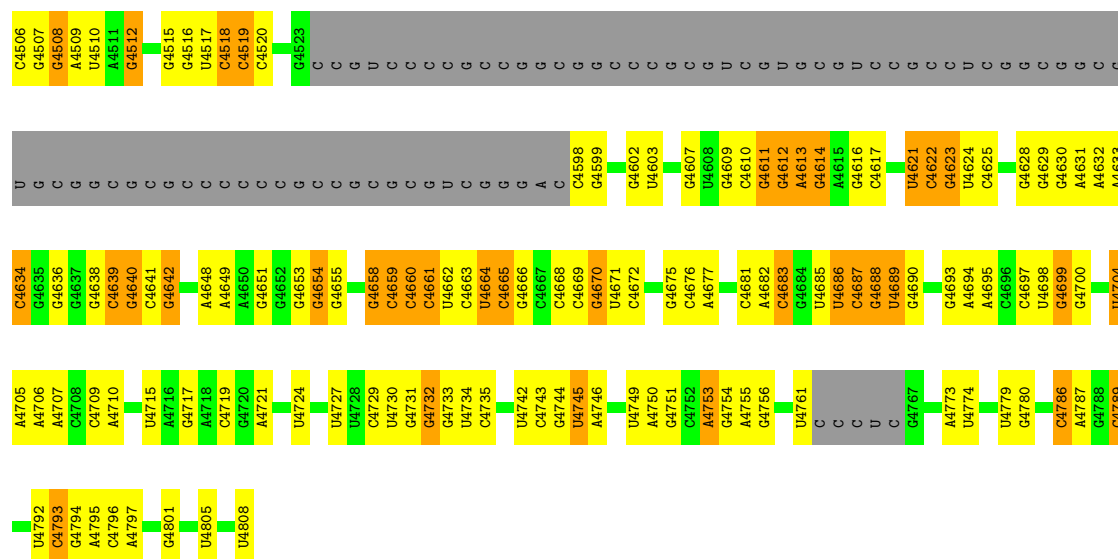


Mol	Chain	Residues	Atoms					AltConf
50	K	1	Total	C	N	O	S	0
			42	32	4	4	2	

G1742	G1658	G1554	G1456	A1375	G1306	G1224	U	G1103	C	G	G	G824	G759	G678
A1743	C1659	A1555	G1457	G1376	G1309	G1225	C	G1104	C	G	G	G825	C760	C679
A1744	U1557	A1458	A1458	C1384	C1309	G1227	C	C1105	U	C	C	A828	G761	A680
C1746	U1665	G1558	G1459	C1385	G1310	G1228	G	C1106	C	G	G	G829	U762	U681
G1750	U1666	G1559	C1460	C1386	G1311	U1229	G	G1107	U	C	C	C830	C763	G684
U1667	U1667	G1560	G1464	G1387	A1312	G1230	C	G1108	U	C	C	A831	G764	C685
U1670	C1670	G1567	C1464	A1388	C1313	G1231	G	G1109	C	G	G	G832	C765	A686
C1671	G1671	A1568	U1468	G1389	G1314	G1235	G	G1110	G	C	C	C833	C	G691
G1672	G1672	A1469	A1469	G1390	A1315	C1236	C	A	C	C	C	A834	C	G692
G1673	G1673	G1572	A1470	C	A1316	G1237	G	A	U	C	C	G835	U	G693
G1678	G1678	G1579	G1471	C1392	G1321	G1238	G	A	U	C	C	C838	C	G694
C1679	G1679	G1580	G1472	C1393	C1322	U1239	G	A	G	C	C	G839	C	C698
U1759	G1680	G1588	G1477	U1394	C1323	G1240	G	U	C	C	C	C840	G	G699
A1681	C1583	A1478	G1477	C1395	G1324	C1245	G	G1120	C	C	C	G841	U	C700
A1685	A1586	A1479	A1480	C1397	U1325	C1245	G	G1121	C	C	C	G842	C	G703
G1689	A1587	A1487	G1487	C1398	G1326	C1248	G	G1122	G	C	C	A844	C	G704
G1692	G1588	A1488	A1488	U1400	G1327	U1249	U	G1123	G	C	C	U845	G	A705
G1694	A1589	A1489	A1489	C1401	A1331	C1252	U	G1124	G	C	C	C846	C	C706
U1695	C1595	C1490	C1490	G1402	G1334	C1253	U	G1125	G	C	C	C847	C	C707
G1696	C1500	G1500	G1500	G1403	A1335	G1258	G	G1126	G	C	C	G851	G	G708
G1698	A1601	C1501	C1501	C1404	A1336	G1259	G	G1127	U	G	C	G852	C	C718
G1699	U1602	A1502	A1502	G1405	G1337	U1260	C	G1128	C	C	C	C853	C	C721
G1700	G1609	C1506	C1506	G1406	G1338	C1262	G	G1129	C	C	C	A856	G	G722
G1703	C1610	A1507	A1507	A1412	A1342	U1266	U	G1130	C	C	C	G857	G	U723
G1704	U1614	A1509	A1509	C1413	G1343	A1270	U	G1131	C	C	C	G858	G	G724
A1705	U1615	G1510	G1510	C1414	C1344	G1271	U	G1132	C	C	C	G859	G	G725
A1706	C1616	G1513	G1513	C1415	C1346	G1272	U	U1133	C	C	C	A860	C	A726
C1707	C1617	A1514	A1514	A1417	G1347	G1273	C	G1134	C	C	C	G861	C	G727
A1709	C1618	G1517	G1517	C1422	C1348	A1274	C	G1135	C	C	C	G862	C	G728
A1710	A1624	G1517	G1517	C1423	G1350	G1275	G	G1136	C	C	C	G863	C	G729
A1711	C1631	C1521	C1521	U1426	G	C1276	C	C	C	C	C	G864	C	C730
A1712	U1632	U1522	U1522	C1427	G	A1277	C	G1009	U	C	C	A866	C	C731
A1713	C1633	C1523	C1523	U1428	C	A1278	C	A1010	C	C	C	G867	C	C732
A1714	U1638	G1528	G1528	G1430	U	A1281	C	U1015	C	C	C	C868	C	G734
A1715	A1639	G1529	G1529	C1431	C	U1282	G	C	C	C	C	C869	C	G735
G1716	G1640	C1432	C1432	C1432	C	U1284	C	G1084	C	C	C	G870	C	U800
C1717	C1641	U1532	U1532	C1433	G	U1285	C	G1085	C	C	C	G871	C	G736
U1718	G1645	C1534	C1534	G1434	C	C1288	C	G1086	C	C	C	G872	C	G737
A1719	C1646	U1537	U1537	C1435	C	A1289	C	G1087	C	C	C	U873	C	G738
U1720	C1647	U1546	U1546	G1437	G	C1290	C	G1088	C	C	C	C874	C	G739
A1725	C1651	U1546	U1546	C1438	C	U1291	C	G1089	C	C	C	G875	C	G740
A1726	G1652	C1549	C1549	G1439	U1365	U1292	C	G1090	C	C	C	G876	C	A741
A1727	C	G1550	G1550	U1449	G1367	A1298	C	G1091	C	C	C	G877	C	G742
C1728	A	U1551	U1551	G1450	C1368	G1299	C	C1095	C	C	C	G878	C	G743
U1729	A	G1552	G1552	G1451	C1369	U1300	C	G1096	C	C	C	C879	C	G744
G1736	C	A1552	A1552	G1453	C1370	C1302	U	G1097	C	C	C	G880	C	G751
A1741	C1657	C1553	C1553	G1453	G1374	G1303	C	G1098	C	C	C	G881	C	G752
								G1099	C	C	C	U882	C	G753
								G1100	C	C	C	U884	C	G754
								C1101	C	C	C	C	C	G755
								G1102	C	C	C	U891	C	G756
												C	C	A757
												C	C	C821
												C	C	G822
												C	C	C823

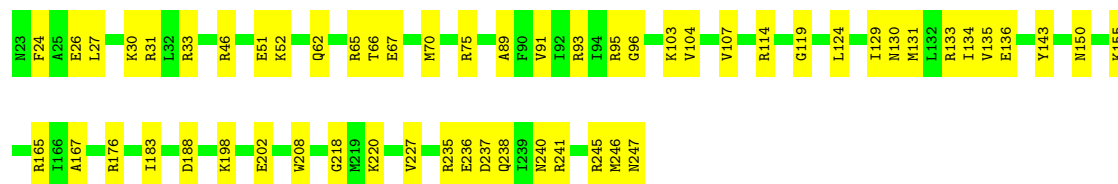






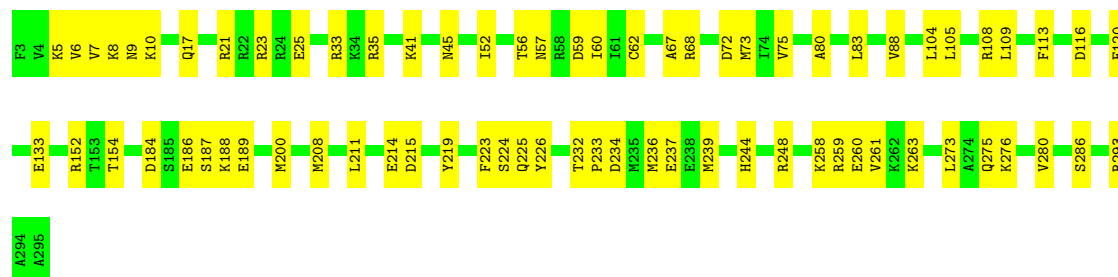
• Molecule 3: 60S ribosomal protein L7

Chain F:



• Molecule 4: Ribosomal_L18_c domain-containing protein

Chain D:

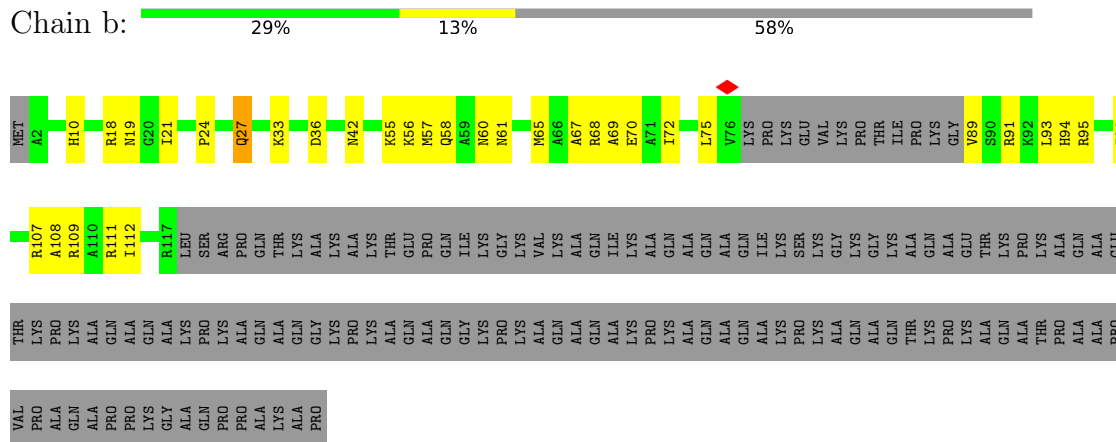


• Molecule 5: 60S ribosomal protein L18a

Chain S:



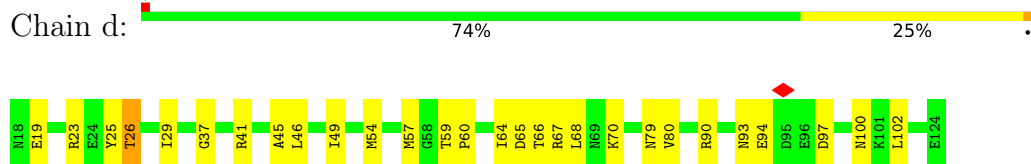
- Molecule 6: 60S ribosomal protein L29



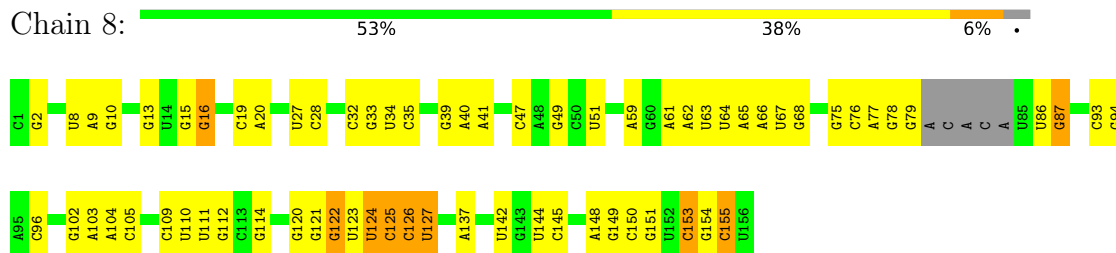
- Molecule 7: Ribosomal protein L3



- Molecule 8: 60S ribosomal protein L31

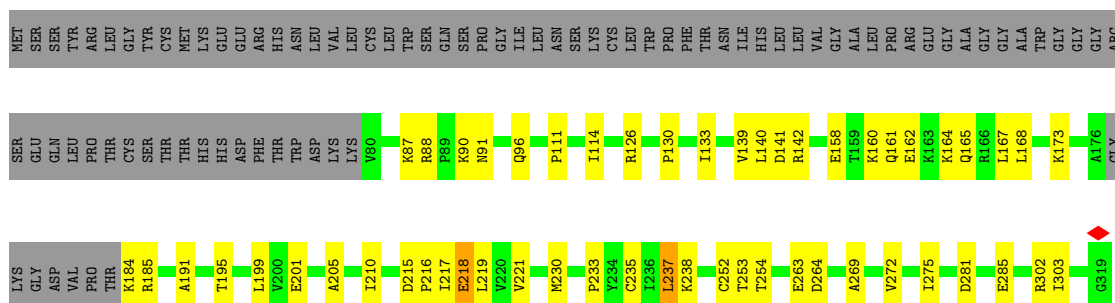


- Molecule 9: 5.8S rRNA

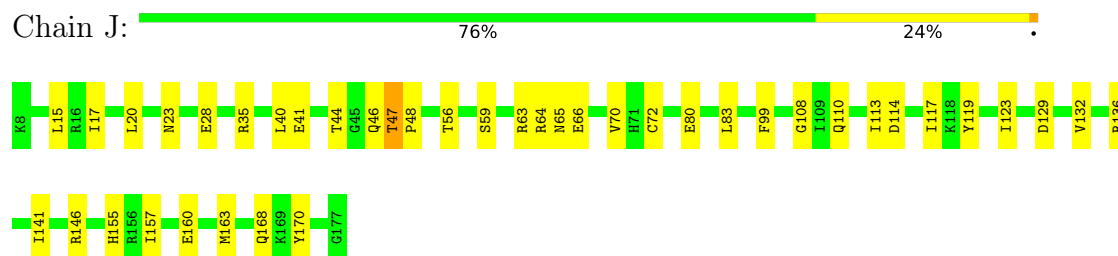


- Molecule 10: 60S ribosomal protein L7a

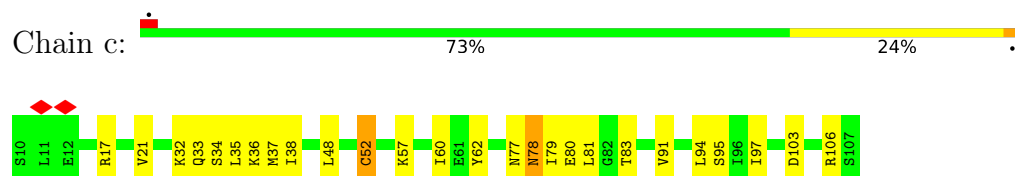




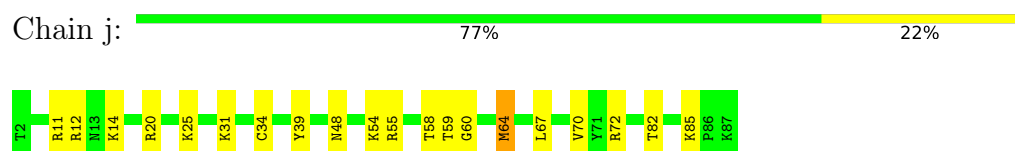
- Molecule 11: 60S ribosomal protein L11



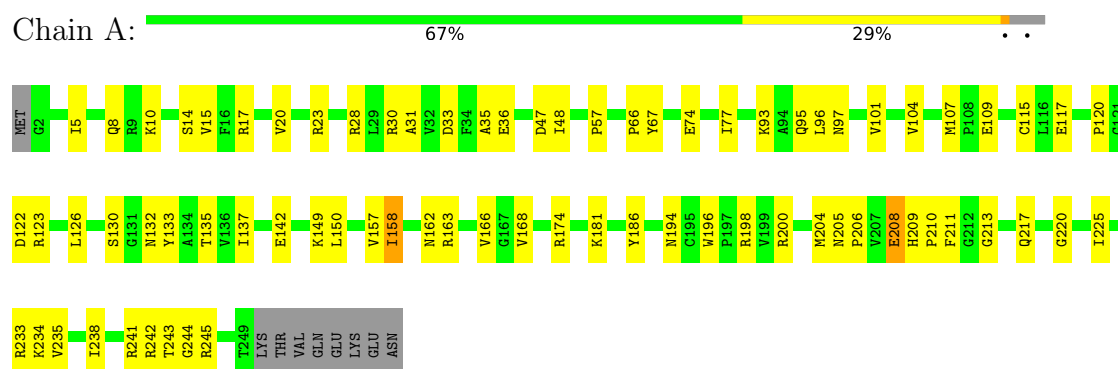
- Molecule 12: 60S ribosomal protein L30



- Molecule 13: Ribosomal protein L37

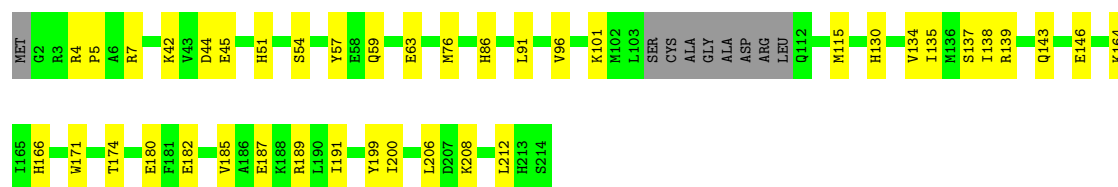


- Molecule 14: Ribosomal protein L8



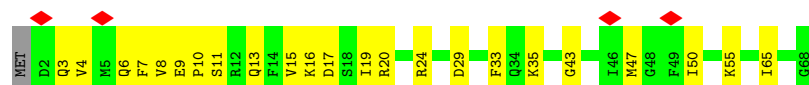
- Molecule 15: Ribosomal protein L10

Chain I:  77% 19%



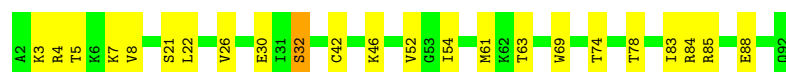
- Molecule 16: Protein transport protein Sec61 subunit gamma

Chain q:  6% 65% 34%



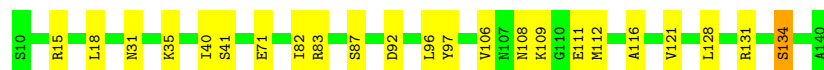
- Molecule 17: 60S ribosomal protein L37a

Chain p:  75% 24%



- Molecule 18: 60S ribosomal protein L23

Chain V:  82% 17%



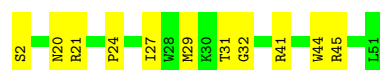
- Molecule 19: 60S ribosomal protein L40

Chain m:  75% 25%



- Molecule 20: 60S ribosomal protein L39-like

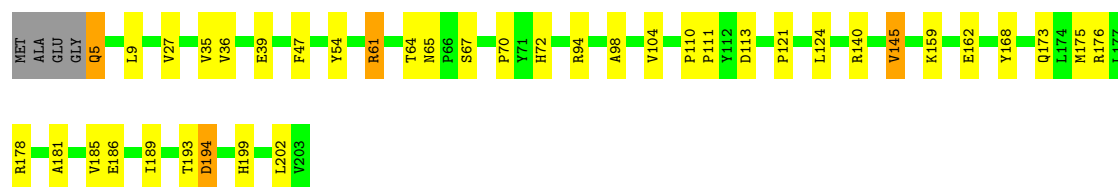
Chain l:  78% 22%



- Molecule 21: 60S ribosomal protein L17

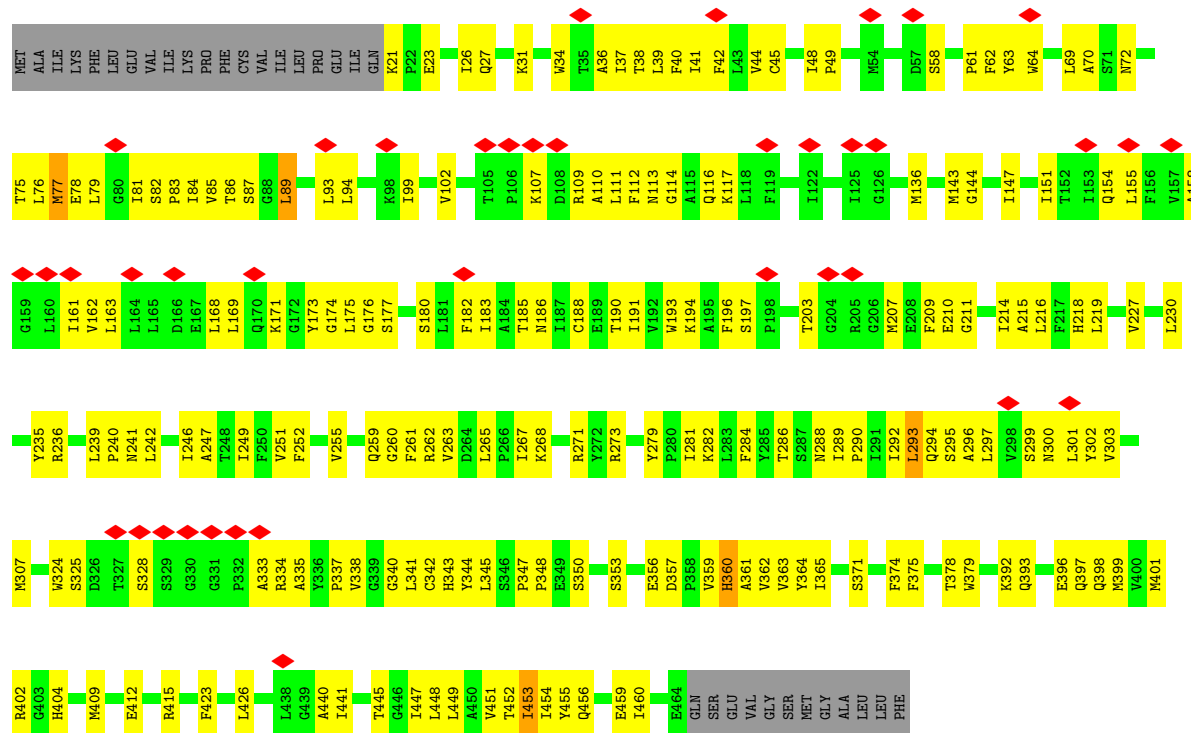
Chain P:  81% 19%

Chain O:  79% 17% ..



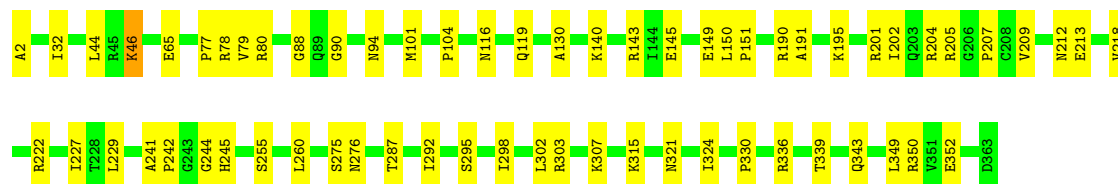
- Molecule 27: Protein transport protein Sec61 subunit alpha isoform 1

Chain K:  8% 52% 40% 7%



- Molecule 28: 60S ribosomal protein L4

Chain C:  83% 17%



- Molecule 29: 60S ribosomal protein L36a-like

Chain o:  85% 13% .



- Molecule 30: 60S ribosomal protein L28

Chain r: 64% 36%



- Molecule 31: 60S ribosomal protein L35a

Chain f: 75% 25%



- Molecule 32: Ribosomal protein L32

Chain e: 79% 21%



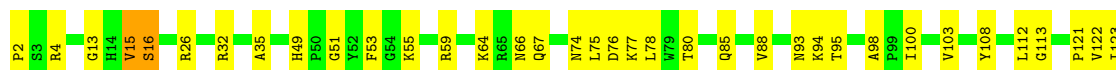
- Molecule 33: 60S ribosomal protein L27

Chain Z: 73% 26%



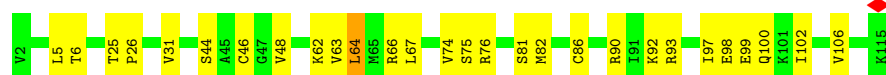
- Molecule 34: 60S ribosomal protein L27a

Chain a: 71% 27%



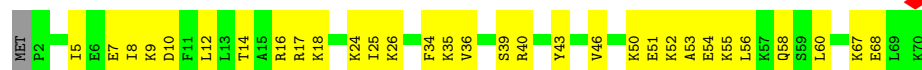
- Molecule 35: 60S ribosomal protein L34

Chain g:  75% 24%



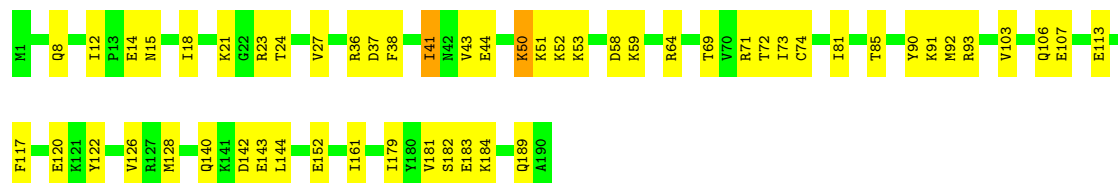
- Molecule 36: 60S ribosomal protein L38

Chain k:  54% 44%



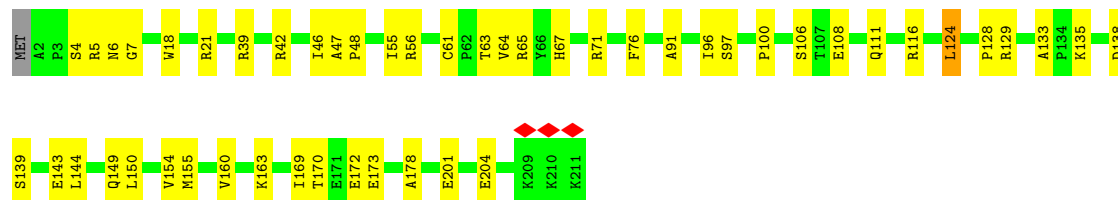
- Molecule 37: 60S ribosomal protein L9

Chain H:  72% 27%



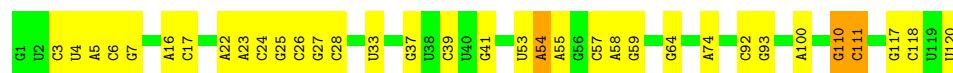
- Molecule 38: 60S ribosomal protein L13

Chain L:  76% 23%



- Molecule 39: 5S rRNA

Chain 7:  72% 26%



- Molecule 40: Ribosomal protein L15

Chain N:  74% 25%





- Molecule 41: 60S ribosomal protein L36

Chain i: 75% 21%



- Molecule 42: 60S ribosomal protein L35

Chain h: 79% 20%



- Molecule 43: 60S ribosomal protein L14

Chain M: 70% 30%



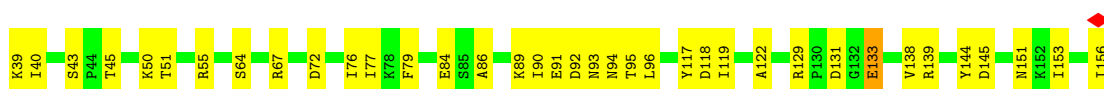
- Molecule 44: Ribosomal protein L26

Chain Y: 63% 35%



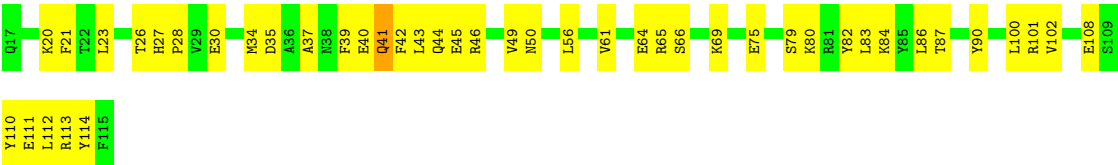
- Molecule 45: Ribosomal_L23eN domain-containing protein

Chain X: 69% 31%

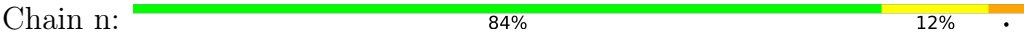


- Molecule 46: 60S ribosomal protein L22 (Fragment)

Chain U: 56% 43%



● Molecule 47: 60S ribosomal protein L41



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	132229	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	TFS GLACIOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	0.8	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	120000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.425	Depositor
Minimum map value	-0.156	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.01581	Depositor
Map size ($\text{\AA}$)	432.96002, 432.96002, 432.96002	wwPDB
Map dimensions	352, 352, 352	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.23, 1.23, 1.23	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: I4U, 1MA, PSU, A2M, MG, E7G, OWI, OMC, 5MC, E6G, P4U, OMG, MLZ, UR3, OMU, B8K, BGH, B8H, 7MG, P7G, ZN

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	T	0.24	0/1326	0.45	0/1770
2	5	0.25	4/85271 (0.0%)	0.32	8/132978 (0.0%)
3	F	0.20	0/1911	0.33	0/2549
4	D	0.24	0/2437	0.40	0/3264
5	S	0.23	0/1501	0.42	0/2012
6	b	0.27	0/861	0.53	0/1138
7	B	0.21	0/3240	0.34	0/4339
8	d	0.45	0/903	0.50	0/1216
9	8	0.20	0/3581	0.26	0/5577
10	G	0.32	0/1910	0.48	0/2569
11	J	0.21	0/1385	0.55	0/1852
12	c	0.20	0/771	0.42	0/1034
13	j	0.20	0/720	0.36	0/952
14	A	0.37	0/1936	0.48	0/2596
15	I	0.36	0/1702	0.48	0/2272
16	q	0.23	0/545	0.59	0/728
17	p	0.29	0/718	0.40	0/953
18	V	0.41	0/993	0.41	0/1332
19	m	0.25	0/425	0.49	0/561
20	l	0.19	0/459	0.36	0/608
21	P	0.31	0/1268	0.45	0/1700
22	E	0.22	0/1762	0.36	0/2362
23	Q	0.25	0/1539	0.40	0/2054
24	R	0.22	0/1524	0.41	0/2013
25	W	0.20	0/541	0.37	0/720
26	O	0.25	0/1662	0.41	0/2222
27	K	0.79	0/3502	1.15	4/4749 (0.1%)
28	C	0.36	0/2927	0.45	2/3932 (0.1%)
29	o	0.29	0/855	0.46	0/1128
30	r	0.40	0/1010	0.46	0/1354
31	f	0.21	0/895	0.39	0/1198

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	e	0.20	0/1071	0.35	0/1429
33	Z	0.31	0/1130	0.44	0/1507
34	a	0.20	0/1191	0.69	3/1590 (0.2%)
35	g	0.20	0/916	0.36	0/1220
36	k	0.23	0/575	0.66	2/761 (0.3%)
37	H	0.23	0/1535	0.44	0/2063
38	L	0.30	0/1733	0.44	0/2316
39	7	0.18	0/2858	0.22	0/4455
40	N	0.37	0/1746	0.45	1/2338 (0.0%)
41	i	0.17	0/841	0.34	0/1112
42	h	0.18	0/1021	0.37	0/1348
43	M	0.30	0/1158	0.47	0/1547
44	Y	0.22	0/1132	0.45	0/1504
45	X	0.24	0/984	0.48	0/1323
46	U	0.28	0/823	0.76	1/1104 (0.1%)
47	n	0.14	0/240	0.38	0/305
All	All	0.28	4/149034 (0.0%)	0.40	21/219654 (0.0%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	5	732	C	O3'-P	20.59	1.92	1.61
2	5	1390	G	O3'-P	18.62	1.89	1.61
2	5	1392	C	O3'-P	-13.69	1.40	1.61
2	5	731	C	O3'-P	-11.05	1.44	1.61

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5	731	C	OP1-P-O3'	-20.55	46.34	108.00
2	5	731	C	O3'-P-O5'	17.98	130.97	104.00
34	a	15	VAL	N-CA-C	-16.58	82.92	109.12
34	a	16	SER	N-CA-CB	15.16	136.11	110.49
2	5	732	C	O3'-P-O5'	8.28	116.42	104.00
2	5	732	C	P-O3'-C3'	-7.49	108.97	120.20
27	K	203	THR	N-CA-C	-7.31	103.96	113.17
28	C	244	GLY	N-CA-C	-7.23	105.52	114.92
34	a	15	VAL	CB-CA-C	-7.05	101.18	111.68
27	K	295	SER	N-CA-C	-7.01	104.46	112.87
27	K	340	GLY	CA-C-O	-6.03	118.07	122.23
46	U	41	GLN	CA-CB-CG	5.95	125.99	114.10
2	5	732	C	O4'-C4'-C3'	-5.82	98.18	104.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	k	53	ALA	CA-C-N	-5.48	112.47	122.38
36	k	53	ALA	C-N-CA	-5.48	112.47	122.38
2	5	2538	A	C2'-C3'-O3'	5.41	117.61	109.50
27	K	144	GLY	CA-C-O	-5.40	117.54	122.24
2	5	1392	C	O3'-P-O5'	-5.35	95.97	104.00
40	N	79	ALA	N-CA-C	5.33	122.15	110.80
2	5	732	C	C5'-C4'-O4'	-5.07	102.20	109.80
28	C	46	LYS	N-CA-C	-5.04	105.92	113.89

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	T	1298	0	1366	39	0
2	5	77665	0	39155	1279	0
3	F	1875	0	1995	46	0
4	D	2391	0	2424	53	0
5	S	1462	0	1508	37	0
6	b	848	0	920	35	0
7	B	3172	0	3310	68	0
8	d	888	0	930	18	0
9	8	3208	0	1629	48	0
10	G	1879	0	2027	50	0
11	J	1362	0	1399	29	0
12	c	761	0	794	19	0
13	j	705	0	737	16	0
14	A	1898	0	1993	60	0
15	I	1664	0	1712	29	0
16	q	535	0	565	25	0
17	p	708	0	756	18	0
18	V	979	0	1039	18	0
19	m	430	0	466	11	0
20	l	447	0	480	12	0
21	P	1242	0	1274	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
22	E	1729	0	1887	48	0
23	Q	1515	0	1634	40	0
24	R	1508	0	1664	43	0
25	W	528	0	541	4	0
26	O	1630	0	1778	37	0
27	K	3427	0	3530	223	0
28	C	2884	0	3054	48	0
29	o	842	0	912	10	0
30	r	994	0	1051	38	0
31	f	876	0	912	25	0
32	e	1053	0	1147	23	0
33	Z	1107	0	1182	31	0
34	a	1162	0	1209	41	0
35	g	906	0	998	20	0
36	k	569	0	637	31	0
37	H	1516	0	1597	50	0
38	L	1702	0	1820	44	0
39	7	2558	0	1296	20	0
40	N	1701	0	1749	39	0
41	i	830	0	916	17	0
42	h	1013	0	1147	22	0
43	M	1137	0	1211	34	0
44	Y	1115	0	1205	34	0
45	X	967	0	1040	38	0
46	U	809	0	833	43	0
47	n	239	0	289	3	0
48	5	161	0	0	0	0
48	7	7	0	0	0	0
48	8	5	0	0	0	0
48	A	1	0	0	0	0
48	I	1	0	0	0	0
48	P	1	0	0	0	0
48	V	1	0	0	0	0
48	a	1	0	0	0	0
49	g	1	0	0	0	0
49	j	1	0	0	0	0
49	m	1	0	0	0	0
49	o	1	0	0	0	0
49	p	1	0	0	0	0
50	K	42	0	0	0	0
All	All	139959	0	101718	2553	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including

hydrogen atoms). The all-atom clashscore for this structure is 11.

All (2553) 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)
27:K:239:LEU:CD1	27:K:240:PRO:HD2	1.67	1.22
26:O:5:GLN:N	26:O:5:GLN:HE21	1.34	1.22
27:K:239:LEU:HD12	27:K:240:PRO:HD2	1.29	1.13
27:K:210:GLU:O	27:K:239:LEU:HD11	1.57	1.04
27:K:21:LYS:HZ2	27:K:168:LEU:HD12	1.23	1.01
27:K:21:LYS:NZ	27:K:168:LEU:HD12	1.77	0.98
27:K:239:LEU:CG	27:K:240:PRO:HD2	1.92	0.98
26:O:5:GLN:N	26:O:5:GLN:NE2	2.12	0.97
27:K:21:LYS:NZ	27:K:168:LEU:CD1	2.29	0.95
2:5:1015:U:H3	2:5:1086:G:H1	1.04	0.95
2:5:1559:G:H2'	2:5:1560:7MG:H82	1.45	0.95
16:q:20:ARG:HG2	45:X:151:ASN:ND2	1.81	0.94
2:5:1698:G:H1	2:5:1712:U:H3	1.15	0.91
2:5:4486:G:H1	2:5:4698:U:H3	1.17	0.91
27:K:353:SER:HA	27:K:356:GLU:HG3	1.52	0.90
27:K:209:PHE:HB2	27:K:214:ILE:CG2	2.01	0.90
2:5:2400:G:H1	2:5:2413:U:H3	0.90	0.89
27:K:401:MET:HG3	27:K:409:MET:HE2	1.52	0.89
2:5:2364:G:H2'	2:5:2365:7MG:H82	1.52	0.89
27:K:169:LEU:HD21	27:K:176:GLY:O	1.72	0.89
43:M:32:ASP:OD1	43:M:33:GLN:N	2.04	0.88
2:5:1700:G:H1	2:5:1710:U:H3	0.90	0.88
2:5:4636:G:H1	2:5:4662:U:H3	1.22	0.87
27:K:344:TYR:HA	27:K:360:HIS:HB2	1.54	0.86
27:K:70:ALA:HB1	27:K:186:ASN:HD22	1.40	0.85
2:5:1399:G:H21	2:5:2049:G:H1	1.21	0.85
2:5:1928:G:H2'	2:5:1929:A:H8	1.41	0.85
2:5:4614:G:H5''	5:S:170:LYS:HZ1	1.41	0.85
21:P:41:ILE:HG23	21:P:42:ARG:HD2	1.59	0.84
2:5:3424:A:H62	2:5:3555:G:H21	1.22	0.84
2:5:3449:A:H2'	2:5:3450:A2M:H8	1.57	0.84
2:5:891:U:H3	2:5:979:G:H1	0.85	0.84
27:K:45:CYS:HA	27:K:76:LEU:HD12	1.57	0.84
27:K:239:LEU:HG	27:K:240:PRO:HD2	1.58	0.83
28:C:150:LEU:HD23	28:C:151:PRO:HD3	1.58	0.83
27:K:21:LYS:HZ2	27:K:168:LEU:CD1	1.85	0.83
27:K:239:LEU:HD12	27:K:240:PRO:CD	2.09	0.83
27:K:216:LEU:HD22	27:K:242:LEU:HD22	1.58	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:J:41:GLU:HB3	11:J:48:PRO:HD3	1.60	0.82
10:G:139:VAL:HG11	10:G:238:LYS:HE2	1.61	0.82
16:q:20:ARG:HG2	45:X:151:ASN:HD21	1.41	0.81
2:5:173:C:H5'	38:L:129:ARG:HH21	1.44	0.81
33:Z:59:LYS:HD3	33:Z:59:LYS:H	1.46	0.81
14:A:5:ILE:HG12	14:A:8:GLN:HG3	1.61	0.80
2:5:2276:G:OP1	27:K:268:LYS:HE3	1.81	0.80
11:J:35:ARG:HD2	11:J:123:ILE:HA	1.64	0.79
44:Y:38:LEU:HD11	44:Y:108:ARG:HA	1.62	0.79
27:K:215:ALA:HB2	27:K:239:LEU:CD2	2.12	0.79
2:5:2275:U:H5'	27:K:273:ARG:CD	2.12	0.79
27:K:215:ALA:HB2	27:K:239:LEU:HD21	1.64	0.79
14:A:28:ARG:HG3	14:A:123:ARG:HH21	1.45	0.79
2:5:4688:G:H4'	2:5:4689:U:H5'	1.63	0.79
38:L:64:VAL:HA	38:L:67:HIS:HD2	1.48	0.78
10:G:140:LEU:HD21	10:G:237:LEU:HD22	1.65	0.78
27:K:362:VAL:O	27:K:365:ILE:HG12	1.81	0.78
44:Y:30:MET:HB3	44:Y:101:PRO:HG2	1.66	0.78
41:i:70:LEU:HD23	41:i:87:ARG:HE	1.48	0.78
27:K:262:ARG:HG2	27:K:282:LYS:HG2	1.65	0.77
2:5:4614:G:H5''	5:S:170:LYS:NZ	1.98	0.77
10:G:164:LYS:HZ1	10:G:168:LEU:HB3	1.49	0.77
27:K:209:PHE:HB2	27:K:214:ILE:HG22	1.65	0.77
2:5:1406:G:H5'	2:5:2043:A:H8	1.49	0.77
26:O:181:ALA:HB1	43:M:126:GLU:HG3	1.67	0.76
40:N:160:GLU:OE1	40:N:160:GLU:N	2.18	0.76
27:K:215:ALA:CB	27:K:239:LEU:CD2	2.63	0.76
2:5:4381:A:H8	2:5:4787:A:H61	1.34	0.76
4:D:109:LEU:O	4:D:113:PHE:HB2	1.85	0.76
2:5:1214:A:C5	2:5:1395:U:H1'	2.20	0.76
38:L:63:THR:HG22	38:L:65:ARG:H	1.51	0.76
2:5:522:U:H3	2:5:632:G:H1	1.32	0.75
27:K:239:LEU:HG	27:K:240:PRO:CD	2.16	0.75
2:5:186:G:N2	2:5:186:G:OP2	2.18	0.75
46:U:66:SER:HB3	46:U:69:LYS:HB2	1.68	0.75
2:5:4117:G:H2'	2:5:4118:U:C6	2.21	0.75
7:B:89:ILE:HD11	7:B:150:PHE:HE1	1.52	0.75
4:D:261:VAL:HG22	4:D:263:LYS:H	1.51	0.75
2:5:761:C:N4	2:5:793:C:O2	2.20	0.75
2:5:3823:G:H1	2:5:3841:U:H3	1.35	0.75
9:8:94:G:OP2	13:j:72:ARG:NH1	2.20	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:K:21:LYS:HG2	27:K:168:LEU:HA	1.67	0.74
2:5:2426:C:OP2	35:g:76:ARG:NH2	2.20	0.74
3:F:202:GLU:N	3:F:202:GLU:OE1	2.20	0.74
4:D:120:GLU:O	4:D:248:ARG:NH2	2.20	0.74
27:K:191:ILE:HD12	27:K:441:ILE:HG22	1.69	0.74
11:J:160:GLU:OE1	11:J:160:GLU:N	2.20	0.74
27:K:42:PHE:CE2	27:K:185:THR:OG1	2.40	0.74
24:R:31:GLU:OE1	24:R:31:GLU:N	2.21	0.74
1:T:94:GLU:OE1	1:T:94:GLU:N	2.20	0.74
27:K:271:ARG:HG2	27:K:271:ARG:O	1.87	0.73
14:A:30:ARG:HG3	14:A:74:GLU:OE2	1.88	0.73
5:S:34:ALA:HB1	5:S:39:VAL:HG23	1.70	0.73
13:j:60:GLY:HA2	13:j:64:MET:HE1	1.70	0.73
44:Y:112:ASP:OD1	44:Y:113:LYS:N	2.21	0.73
10:G:263:GLU:OE1	10:G:263:GLU:N	2.17	0.73
2:5:4287:G:N2	2:5:4290:A:OP2	2.22	0.73
27:K:70:ALA:HB1	27:K:186:ASN:ND2	2.04	0.72
4:D:9:ASN:OD1	4:D:10:LYS:N	2.22	0.72
38:L:56:ARG:O	38:L:116:ARG:NH1	2.21	0.72
2:5:2390:G:H2'	2:5:2391:C:H6	1.54	0.72
2:5:1400:U:H2'	2:5:1401:C:C6	2.25	0.72
2:5:2032:G:OP1	30:r:101:LYS:NZ	2.22	0.72
23:Q:130:SER:HA	23:Q:134:ARG:HH22	1.54	0.72
29:o:51:GLN:HG2	29:o:55:ILE:HD11	1.70	0.72
14:A:104:VAL:HA	14:A:107:MET:HE2	1.70	0.72
38:L:21:ARG:HH21	40:N:196:ASN:HB3	1.54	0.72
1:T:159:MET:HA	1:T:159:MET:HE3	1.72	0.72
2:5:1928:G:H2'	2:5:1929:A:C8	2.25	0.72
2:5:2308:C:H1'	2:5:3404:G:H22	1.55	0.72
2:5:2490:A:H62	2:5:2529:G:H8	1.38	0.72
2:5:3953:C:C5'	2:5:4081:C:H5'	2.20	0.72
27:K:175:LEU:HD11	27:K:460:ILE:HG21	1.71	0.72
7:B:383:GLU:OE1	7:B:383:GLU:N	2.22	0.71
5:S:161:ARG:HH21	5:S:164:LYS:HG2	1.56	0.71
6:b:58:GLN:N	6:b:58:GLN:OE1	2.22	0.71
8:d:64:ILE:HG23	8:d:68:LEU:HD23	1.72	0.71
27:K:415:ARG:HD3	45:X:156:ILE:HG22	1.71	0.71
2:5:1312:A:H1'	44:Y:1:MET:HE2	1.71	0.71
37:H:41:ILE:HG21	37:H:73:ILE:HD11	1.71	0.71
2:5:4602:G:OP1	37:H:21:LYS:NZ	2.24	0.71
38:L:116:ARG:NH2	38:L:155:MET:O	2.23	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:304:C:O3'	41:i:76:ARG:NH1	2.24	0.71
11:J:110:GLN:OE1	11:J:110:GLN:N	2.21	0.71
2:5:2549:G:O2'	2:5:2552:C:N4	2.24	0.71
2:5:2687:A:O2'	2:5:4377:G:H4'	1.90	0.71
2:5:801:C:H2'	2:5:802:C:H6	1.56	0.70
2:5:3452:G:OP1	41:i:75:LYS:NZ	2.24	0.70
23:Q:50:ARG:HA	23:Q:53:MET:HG3	1.72	0.70
28:C:140:LYS:HE3	28:C:245:HIS:HB2	1.73	0.70
44:Y:88:GLU:OE1	44:Y:88:GLU:N	2.19	0.70
2:5:2105:G:OP2	30:r:98:ARG:NH2	2.24	0.70
10:G:164:LYS:O	10:G:164:LYS:NZ	2.23	0.70
1:T:32:ARG:O	4:D:41:LYS:NZ	2.24	0.70
2:5:1068:U:H2'	2:5:1069:G:H8	1.57	0.70
7:B:325:GLU:OE1	7:B:325:GLU:N	2.24	0.70
27:K:353:SER:HA	27:K:356:GLU:CG	2.20	0.70
27:K:415:ARG:NH2	45:X:91:GLU:OE2	2.24	0.70
2:5:852:G:OP1	31:f:73:LYS:NZ	2.25	0.70
2:5:4724:U:O2	7:B:174:ARG:NH1	2.25	0.70
27:K:207:MET:HG3	27:K:207:MET:O	1.91	0.70
2:5:2332:C:O2'	2:5:2334:C:N4	2.25	0.70
2:5:1214:A:C6	2:5:1395:U:H1'	2.27	0.69
20:l:24:PRO:HG2	20:l:27:ILE:HG12	1.71	0.69
2:5:2326:G:H22	2:5:2338:U:H3	1.38	0.69
27:K:209:PHE:HB2	27:K:214:ILE:HG21	1.74	0.69
2:5:2275:U:O3'	27:K:268:LYS:NZ	2.21	0.69
2:5:3400:C:OP1	14:A:8:GLN:NE2	2.25	0.69
4:D:293:ARG:NE	4:D:293:ARG:O	2.24	0.69
14:A:109:GLU:OE1	14:A:109:GLU:N	2.21	0.69
42:h:99:GLU:HA	42:h:102:LEU:HD22	1.73	0.69
2:5:3826:A:H61	2:5:3838:C:H42	1.40	0.69
2:5:188:G:N2	2:5:189:G:N7	2.40	0.69
2:5:1809:C:H2'	2:5:1810:A2M:H8	1.75	0.69
2:5:4399:C:OP1	8:d:79:ASN:ND2	2.21	0.69
7:B:329:ASP:OD1	7:B:329:ASP:N	2.26	0.69
46:U:80:LYS:HG2	46:U:110:TYR:CE2	2.28	0.69
2:5:847:C:OP1	28:C:336:ARG:NH2	2.25	0.69
27:K:21:LYS:NZ	27:K:168:LEU:CG	2.55	0.69
1:T:149:GLU:OE1	1:T:149:GLU:N	2.19	0.69
27:K:194:LYS:HG3	27:K:240:PRO:HB3	1.73	0.69
6:b:95:ARG:O	6:b:99:ILE:HD12	1.93	0.68
10:G:285:GLU:OE1	10:G:285:GLU:N	2.20	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
38:L:108:GLU:OE1	38:L:108:GLU:N	2.23	0.68
2:5:4706:A:H2'	2:5:4707:A:H8	1.58	0.68
2:5:2275:U:C5'	27:K:273:ARG:HD3	2.23	0.68
20:l:20:ASN:O	20:l:20:ASN:ND2	2.26	0.68
42:h:32:ARG:HG2	42:h:32:ARG:HH11	1.59	0.68
2:5:998:U:H3	2:5:1107:C:H42	1.42	0.68
37:H:43:VAL:HG12	37:H:59:LYS:HD3	1.75	0.68
2:5:661:A:N7	28:C:2:ALA:N	2.42	0.68
2:5:841:C:OP2	3:F:241:ARG:NH1	2.27	0.68
26:O:39:GLU:OE1	26:O:39:GLU:N	2.25	0.68
34:a:146:LEU:HD21	38:L:178:ALA:HB1	1.76	0.68
2:5:753:G:H2'	2:5:754:G:O4'	1.93	0.68
15:I:143:GLN:OE1	15:I:143:GLN:N	2.22	0.68
2:5:1276:C:H2'	2:5:1277:A:H8	1.59	0.68
13:j:20:ARG:NH2	13:j:39:TYR:OH	2.25	0.68
2:5:308:G:N2	2:5:308:G:OP2	2.27	0.68
46:U:111:GLU:OE2	46:U:113:ARG:NE	2.26	0.68
2:5:4269:A2M:H5''	2:5:4270:G:H5'	1.77	0.67
37:H:18:ILE:HG12	37:H:27:VAL:HG22	1.76	0.67
2:5:2165:G:OP1	32:e:36:ARG:NH2	2.27	0.67
2:5:2223:G:N2	2:5:2267:OMG:H5'	2.09	0.67
2:5:4381:A:H2	2:5:4409:G:H21	1.42	0.67
4:D:280:VAL:HG23	15:I:206:LEU:HD11	1.77	0.67
20:l:20:ASN:O	20:l:41:ARG:NH1	2.27	0.67
2:5:2249:G:N7	20:l:2:SER:N	2.43	0.67
2:5:4332:G:OP1	26:O:72:HIS:N	2.25	0.67
27:K:34:TRP:CZ2	27:K:168:LEU:HD21	2.30	0.67
30:r:56:ASP:OD1	30:r:57:GLY:N	2.28	0.67
2:5:4275:G:H2'	2:5:4276:UR3:H6	1.75	0.67
7:B:92:TYR:HB2	7:B:159:VAL:HB	1.77	0.67
30:r:28:GLU:OE1	30:r:28:GLU:N	2.22	0.67
46:U:37:ALA:O	46:U:40:GLU:HG2	1.93	0.67
2:5:1090:G:H2'	2:5:1091:G:H8	1.59	0.67
2:5:1342:A:H62	2:5:1374:G:H21	1.43	0.67
15:I:76:MET:HE3	15:I:138:ILE:HG21	1.75	0.67
45:X:50:LYS:HE2	45:X:50:LYS:HA	1.74	0.67
2:5:62:A:N3	2:5:77:U:O2'	2.26	0.67
2:5:245:C:O2'	2:5:246:G:OP2	2.12	0.67
2:5:3965:A:H2'	2:5:3966:A:C8	2.30	0.66
23:Q:89:ASP:OD1	23:Q:91:ARG:NH1	2.28	0.66
2:5:3449:A:OP2	2:5:3467:G:N2	2.27	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:K:300:ASN:O	27:K:301:LEU:C	2.39	0.66
32:e:85:LEU:HD21	32:e:115:ALA:HB2	1.77	0.66
2:5:2481:G:H22	2:5:2540:A:H61	1.40	0.66
27:K:21:LYS:NZ	27:K:168:LEU:HG	2.10	0.66
27:K:21:LYS:HZ1	27:K:168:LEU:CD1	2.08	0.66
2:5:2601:G:H2'	2:5:2602:G:C8	2.31	0.66
16:q:43:GLY:O	16:q:47:MET:HG3	1.96	0.66
2:5:2184:A:OP2	34:a:4:ARG:NH2	2.29	0.66
2:5:3852:G:N2	10:G:96:GLN:O	2.28	0.66
16:q:20:ARG:CG	45:X:151:ASN:HD21	2.09	0.66
2:5:1698:G:N2	2:5:1712:U:O2	2.23	0.66
2:5:2588:A:H2'	2:5:2589:A:H8	1.60	0.66
2:5:3486:G:N2	2:5:3502:U:O2	2.26	0.66
8:d:45:ALA:O	8:d:49:ILE:HG13	1.96	0.66
10:G:215:ASP:HB2	10:G:216:PRO:HD3	1.78	0.66
2:5:1464:C:H5''	34:a:2:PRO:HD3	1.78	0.66
46:U:42:PHE:CE1	46:U:46:ARG:HG3	2.31	0.66
2:5:664:G:H2'	2:5:665:G:H8	1.60	0.66
2:5:3836:G:H2'	2:5:3837:G:H8	1.61	0.66
2:5:1645:C:OP2	23:Q:11:ARG:NH2	2.28	0.65
2:5:3676:G:H1	2:5:3797:U:H3	1.45	0.65
2:5:4141:U:H6	2:5:4141:U:H5'	1.61	0.65
27:K:288:ASN:HB3	27:K:452:THR:HG21	1.77	0.65
27:K:347:PRO:O	27:K:360:HIS:HE1	1.79	0.65
43:M:27:ILE:HA	43:M:38:VAL:HG12	1.78	0.65
2:5:1758:G:C2	4:D:113:PHE:HE1	2.13	0.65
11:J:17:ILE:HD11	11:J:80:GLU:HG3	1.78	0.65
40:N:184:ILE:O	40:N:194:ARG:NH2	2.29	0.65
15:I:182:GLU:OE1	15:I:182:GLU:N	2.23	0.65
27:K:21:LYS:HZ2	27:K:168:LEU:CG	2.09	0.65
32:e:69:MET:HG2	32:e:75:ARG:HE	1.62	0.65
2:5:2275:U:H5'	27:K:273:ARG:HD3	1.79	0.65
2:5:3683:G:N1	2:5:3791:U:O2	2.28	0.65
2:5:4476:C:O2'	2:5:4479:C:N3	2.30	0.65
24:R:98:ARG:NH2	24:R:130:ASN:OD1	2.30	0.65
2:5:1403:G:H2'	2:5:1404:C:H6	1.61	0.65
2:5:1414:A:OP1	23:Q:65:ARG:NH1	2.29	0.65
21:P:50:ASP:OD2	21:P:56:GLN:NE2	2.29	0.65
2:5:1211:G:O6	6:b:111:ARG:NH2	2.29	0.65
2:5:1616:C:OP1	32:e:36:ARG:NH1	2.29	0.65
2:5:2276:G:P	27:K:268:LYS:HE3	2.37	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:2718:C:OP2	17:p:7:LYS:NZ	2.30	0.65
24:R:21:LYS:HE3	24:R:55:VAL:HA	1.79	0.65
42:h:16:GLU:OE1	42:h:16:GLU:N	2.20	0.65
22:E:247:GLU:OE1	22:E:247:GLU:N	2.21	0.65
2:5:4792:U:OP1	2:5:4793:C:N4	2.30	0.64
27:K:300:ASN:HA	27:K:303:VAL:HG12	1.79	0.64
2:5:4165:U:OP1	2:5:4167:C:N4	2.29	0.64
31:f:4:ARG:HH12	31:f:8:LYS:HE2	1.62	0.64
2:5:891:U:O2	2:5:979:G:N2	2.26	0.64
2:5:1406:G:H5'	2:5:2043:A:C8	2.33	0.64
27:K:169:LEU:CD2	27:K:176:GLY:O	2.45	0.64
8:d:19:GLU:OE1	8:d:19:GLU:N	2.28	0.64
2:5:1313:C:OP2	2:5:1314:G:O2'	2.14	0.64
26:O:193:THR:OG1	43:M:119:ARG:NH1	2.31	0.64
43:M:8:GLU:OE1	43:M:8:GLU:N	2.30	0.64
27:K:239:LEU:CG	27:K:240:PRO:CD	2.74	0.64
27:K:423:PHE:CE1	27:K:426:LEU:HD23	2.32	0.64
34:a:15:VAL:O	34:a:15:VAL:HG22	1.97	0.64
2:5:1741:A:H5''	2:5:1742:G:H5'	1.79	0.64
21:P:12:THR:OG1	21:P:13:LYS:NZ	2.30	0.64
33:Z:59:LYS:HA	33:Z:62:ILE:HB	1.80	0.64
7:B:222:VAL:O	7:B:343:ARG:NH1	2.31	0.64
22:E:169:LYS:HE3	22:E:211:ILE:HD11	1.80	0.64
38:L:46:ILE:O	38:L:149:GLN:NE2	2.31	0.64
2:5:3449:A:H2'	2:5:3450:A2M:C8	2.28	0.64
27:K:79:LEU:HD13	27:K:155:LEU:HB3	1.80	0.64
2:5:1346:C:H2'	2:5:1347:G:H8	1.63	0.63
12:c:17:ARG:NH1	12:c:103:ASP:OD1	2.30	0.63
14:A:30:ARG:HH21	14:A:36:GLU:HG3	1.62	0.63
17:p:85:ARG:HB3	17:p:85:ARG:NH1	2.12	0.63
27:K:344:TYR:HA	27:K:360:HIS:CB	2.26	0.63
46:U:83:LEU:O	46:U:87:THR:HG23	1.97	0.63
2:5:4699:G:H2'	2:5:4700:G:H8	1.62	0.63
2:5:663:C:HO2'	2:5:664:G:H8	1.46	0.63
2:5:1078:G:OP2	2:5:1078:G:N2	2.29	0.63
2:5:1335:A:OP1	23:Q:181:ARG:NH2	2.31	0.63
2:5:2335:C:H2'	2:5:2336:G:H8	1.61	0.63
24:R:13:SER:OG	24:R:38:ARG:NH2	2.31	0.63
2:5:303:C:OP2	40:N:68:ARG:NH2	2.32	0.63
2:5:4271:C:OP1	7:B:246:ARG:NH1	2.31	0.63
30:r:2:SER:OG	30:r:3:ALA:N	2.30	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:4735:C:H4'	8:d:26:THR:HG23	1.80	0.63
11:J:146:ARG:NH2	39:7:27:G:OP1	2.32	0.63
35:g:93:ARG:O	35:g:97:ILE:HG12	1.98	0.63
40:N:137:PRO:HA	40:N:142:ILE:HD11	1.80	0.63
2:5:2545:C:OP1	46:U:101:ARG:NH2	2.32	0.63
2:5:3843:G:OP1	14:A:93:LYS:NZ	2.31	0.63
23:Q:82:VAL:HG22	23:Q:84:GLY:H	1.63	0.63
27:K:169:LEU:HA	27:K:174:GLY:H	1.64	0.63
2:5:459:C:H4'	22:E:113:ARG:HH12	1.64	0.63
2:5:3953:C:H5'	2:5:4081:C:H5'	1.80	0.63
12:c:33:GLN:HA	12:c:36:LYS:HG3	1.79	0.63
21:P:153:LYS:HE2	21:P:153:LYS:HA	1.79	0.63
26:O:194:ASP:OD1	26:O:194:ASP:N	2.31	0.63
38:L:173:GLU:OE1	38:L:173:GLU:N	2.31	0.63
14:A:31:ALA:HB2	14:A:123:ARG:NH1	2.13	0.62
23:Q:93:GLN:OE1	23:Q:93:GLN:N	2.32	0.62
27:K:34:TRP:HZ2	27:K:168:LEU:HD21	1.62	0.62
27:K:168:LEU:HD23	27:K:173:TYR:HB2	1.82	0.62
2:5:1211:G:OP2	6:b:107:ARG:NH2	2.32	0.62
2:5:1458:A:H4'	2:5:1459:G:H5'	1.80	0.62
23:Q:76:GLU:N	23:Q:76:GLU:OE1	2.32	0.62
2:5:2243:G:H21	35:g:6:THR:HG22	1.64	0.62
2:5:2346:G:N2	2:5:3812:G:C6	2.63	0.62
2:5:3804:G:OP1	10:G:126:ARG:NE	2.32	0.62
14:A:31:ALA:HB2	14:A:123:ARG:HH11	1.64	0.62
2:5:4020:A:H2'	2:5:4021:G:C8	2.35	0.62
24:R:115:ILE:HG21	24:R:142:ILE:HD11	1.81	0.62
27:K:353:SER:CA	27:K:356:GLU:HG3	2.28	0.62
2:5:799:C:H2'	2:5:800:U:C6	2.35	0.62
2:5:1509:A:OP2	17:p:4:ARG:NH1	2.30	0.62
2:5:1610:C:OP2	34:a:26:ARG:NH1	2.32	0.62
3:F:237:ASP:OD1	3:F:238:GLN:NE2	2.31	0.62
45:X:67:ARG:HB2	45:X:67:ARG:HH11	1.64	0.62
2:5:1131:G:O2'	2:5:1209:G:N1	2.32	0.62
10:G:164:LYS:NZ	10:G:168:LEU:HB3	2.15	0.62
27:K:109:ARG:C	27:K:111:LEU:H	2.07	0.62
7:B:163:LEU:HD21	7:B:180:LEU:HD13	1.81	0.62
2:5:2400:G:O6	2:5:2413:U:O4	2.18	0.62
23:Q:178:ARG:H	34:a:51:GLY:HA2	1.64	0.62
27:K:169:LEU:HD21	27:K:177:SER:HA	1.82	0.62
21:P:94:MET:HE1	21:P:146:ILE:HB	1.80	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:1923:A:N7	2:5:1949:A:O2'	2.28	0.61
3:F:104:VAL:HG13	3:F:135:VAL:HG12	1.82	0.61
38:L:143:GLU:OE1	38:L:143:GLU:N	2.28	0.61
45:X:67:ARG:HB2	45:X:67:ARG:NH1	2.15	0.61
46:U:79:SER:OG	46:U:82:TYR:N	2.30	0.61
2:5:1924:G:N2	2:5:1942:G:O2'	2.32	0.61
2:5:2219:A:H2'	2:5:2220:C:C6	2.35	0.61
15:I:180:GLU:N	15:I:180:GLU:OE1	2.34	0.61
24:R:89:MET:HE1	24:R:97:ARG:HH12	1.66	0.61
28:C:101:MET:SD	28:C:104:PRO:HA	2.40	0.61
30:r:71:ARG:HG2	30:r:71:ARG:HH11	1.65	0.61
2:5:4516:G:H5'	26:O:176:ARG:HD3	1.82	0.61
23:Q:128:LEU:HD21	28:C:292:ILE:HD12	1.83	0.61
28:C:213:GLU:OE1	28:C:213:GLU:N	2.33	0.61
33:Z:59:LYS:H	33:Z:59:LYS:CD	2.13	0.61
37:H:8:GLN:HG2	37:H:74:CYS:SG	2.39	0.61
2:5:2161:G:N2	2:5:2164:G:OP2	2.31	0.61
2:5:2254:C:H2'	2:5:2255:A:H8	1.65	0.61
33:Z:14:LEU:HD21	35:g:92:LYS:HE3	1.83	0.61
2:5:263:G:H2'	2:5:264:C:H6	1.65	0.61
2:5:1717:C:OP1	4:D:5:LYS:NZ	2.28	0.61
2:5:3336:A:H8	24:R:71:ARG:HH22	1.48	0.61
10:G:201:GLU:HA	10:G:230:MET:HE1	1.82	0.61
2:5:4805:U:OP1	21:P:43:LYS:NZ	2.32	0.61
27:K:40:PHE:O	27:K:44:VAL:HG13	2.00	0.61
38:L:100:PRO:O	41:i:25:ARG:NH2	2.32	0.61
41:i:63:VAL:HG13	41:i:65:LYS:HG3	1.83	0.61
5:S:99:ASP:OD1	5:S:101:THR:N	2.25	0.61
34:a:76:ASP:OD1	34:a:76:ASP:N	2.33	0.61
2:5:800:U:H2'	2:5:801:C:C6	2.36	0.61
2:5:2363:C:O2	2:5:2483:G:N2	2.34	0.61
2:5:4068:G:N2	2:5:4071:A:OP2	2.32	0.61
16:q:47:MET:HE1	27:K:188:CYS:HB3	1.82	0.61
22:E:115:MET:O	30:r:87:ARG:NH1	2.31	0.61
27:K:151:ILE:HA	27:K:154:GLN:HG2	1.82	0.61
27:K:344:TYR:HA	27:K:360:HIS:HA	1.82	0.61
38:L:201:GLU:HA	38:L:204:GLU:HG3	1.82	0.61
44:Y:106:ILE:HG21	44:Y:109:LEU:HD12	1.83	0.61
2:5:4730:U:H2'	2:5:4731:G:H8	1.66	0.60
6:b:57:MET:O	6:b:61:ASN:ND2	2.27	0.60
9:8:96:C:H5''	42:h:66:LYS:HD2	1.81	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:K:398:GLN:OE1	27:K:398:GLN:N	2.35	0.60
2:5:728:G:H1	2:5:828:A:H62	1.49	0.60
22:E:48:ARG:HB2	22:E:64:MET:HE1	1.82	0.60
2:5:755:G:H2'	2:5:756:G:C8	2.37	0.60
2:5:2578:G:H2'	2:5:2579:G:H8	1.67	0.60
2:5:4117:G:H4'	2:5:4118:U:OP1	2.02	0.60
30:r:119:ARG:O	30:r:122:LYS:HG2	2.00	0.60
37:H:106:GLN:NE2	37:H:113:GLU:OE1	2.34	0.60
2:5:1101:C:N3	3:F:65:ARG:NH1	2.49	0.60
2:5:1210:C:OP1	6:b:107:ARG:NH1	2.34	0.60
2:5:1881:A:H2'	2:5:1882:A:C8	2.36	0.60
10:G:217:ILE:HG13	10:G:221:VAL:HG13	1.82	0.60
42:h:33:VAL:O	42:h:37:THR:HG22	2.02	0.60
2:5:1397:C:H2'	2:5:1398:A:C8	2.36	0.60
2:5:2335:C:H2'	2:5:2336:G:C8	2.36	0.60
2:5:3373:U:OP2	2:5:3378:A:N6	2.31	0.60
2:5:3862:C:H2'	2:5:3863:G:H8	1.67	0.60
2:5:4706:A:H2'	2:5:4707:A:C8	2.37	0.60
3:F:103:LYS:O	3:F:107:VAL:HG23	2.02	0.60
8:d:65:ASP:OD1	8:d:67:ARG:N	2.27	0.60
22:E:120:PRO:O	30:r:112:ARG:HD3	2.01	0.60
45:X:92:ASP:OD1	45:X:93:ASN:N	2.35	0.60
2:5:4000:G:H2'	2:5:4000:G:N3	2.15	0.60
7:B:165:HIS:ND1	7:B:166:THR:O	2.33	0.60
29:o:3:ASN:ND2	29:o:95:GLY:O	2.34	0.60
44:Y:2:LYS:HD2	44:Y:7:VAL:HG13	1.84	0.60
2:5:685:C:H2'	2:5:686:A:H8	1.67	0.60
27:K:302:TYR:HB3	27:K:324:TRP:HH2	1.67	0.60
27:K:393:GLN:HA	27:K:396:GLU:OE2	2.02	0.60
2:5:1806:A:H2'	2:5:1807:A:C8	2.37	0.60
2:5:3486:G:O6	2:5:3502:U:O4	2.20	0.60
2:5:3491:A:OP2	2:5:3497:G:N2	2.34	0.60
2:5:4205:U:H2'	2:5:4206:U:C6	2.37	0.60
2:5:4786:C:O2'	2:5:4787:A:H5''	2.02	0.60
5:S:95:ARG:NH2	5:S:112:ASP:OD2	2.33	0.60
2:5:125:C:H2'	2:5:126:C:H6	1.67	0.60
2:5:3337:C:OP2	24:R:71:ARG:NH2	2.28	0.60
2:5:4020:A:H2'	2:5:4021:G:H8	1.66	0.60
9:8:67:U:H2'	9:8:68:G:H8	1.67	0.60
27:K:62:PHE:CZ	27:K:302:TYR:HD2	2.19	0.60
27:K:328:SER:HA	27:K:333:ALA:HA	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:1436:C:O2'	2:5:1437:G:O5'	2.20	0.59
33:Z:90:PRO:O	33:Z:117:LYS:NZ	2.29	0.59
46:U:42:PHE:CD1	46:U:46:ARG:HG3	2.37	0.59
27:K:117:LYS:HD2	27:K:163:LEU:HB3	1.83	0.59
36:k:10:ASP:O	36:k:14:THR:HG23	2.02	0.59
37:H:92:MET:HB3	37:H:181:VAL:HA	1.85	0.59
1:T:112:ASN:HA	1:T:115:LYS:HG2	1.83	0.59
2:5:417:G:H1'	9:8:16:G:N2	2.17	0.59
2:5:4498:G:H1	2:5:4687:C:H5	1.48	0.59
14:A:142:GLU:OE1	14:A:142:GLU:N	2.25	0.59
16:q:24:ARG:HD3	45:X:156:ILE:HD13	1.82	0.59
27:K:348:PRO:HG3	27:K:361:ALA:HA	1.85	0.59
30:r:33:LYS:HA	32:e:90:MET:HG3	1.84	0.59
42:h:46:LYS:O	42:h:50:VAL:HG23	2.02	0.59
16:q:4:VAL:O	16:q:8:VAL:HG22	2.02	0.59
31:f:46:ARG:H	31:f:107:PRO:HG2	1.68	0.59
2:5:685:C:H2'	2:5:686:A:C8	2.36	0.59
2:5:2566:U:H2'	2:5:2567:G:C8	2.37	0.59
11:J:83:LEU:HD12	11:J:170:TYR:HE2	1.68	0.59
2:5:115:C:O2'	2:5:276:C:OP1	2.21	0.59
2:5:4432:G:OP2	19:m:86:LYS:NZ	2.36	0.59
24:R:162:ARG:HD2	24:R:163:ARG:N	2.18	0.59
2:5:1751:C:H5'	6:b:56:LYS:HE3	1.84	0.59
2:5:1757:G:O2'	2:5:1758:G:OP1	2.19	0.59
2:5:4426:G:H2'	2:5:4427:A:C8	2.38	0.59
41:i:68:ARG:HA	41:i:68:ARG:HH11	1.68	0.59
45:X:39:LYS:HG2	45:X:40:ILE:H	1.68	0.59
2:5:3516:A:H2'	2:5:3516:A:N3	2.17	0.59
22:E:122:GLU:HG3	32:e:7:LEU:HD22	1.84	0.59
1:T:27:LEU:O	1:T:31:MET:HG3	2.03	0.59
2:5:265:C:H1'	2:5:266:C:C5	2.37	0.59
2:5:801:C:H2'	2:5:802:C:C6	2.36	0.59
2:5:4340:U:H2'	2:5:4341:G:H8	1.67	0.59
2:5:4658:G:C4	2:5:4659:C:H1'	2.38	0.59
14:A:133:TYR:HB3	14:A:168:VAL:HG23	1.84	0.59
2:5:1283:U:H2'	2:5:1284:C:C6	2.38	0.58
2:5:3383:A:OP2	14:A:200:ARG:NH1	2.36	0.58
2:5:4598:C:H2'	2:5:4599:G:H8	1.68	0.58
6:b:21:ILE:H	6:b:21:ILE:HD12	1.68	0.58
2:5:684:C:H4'	30:r:85:ASN:HD22	1.67	0.58
2:5:1397:C:H2'	2:5:1398:A:H8	1.67	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:1924:G:H22	2:5:1943:U:H5	1.51	0.58
2:5:4498:G:N7	31:f:52:LYS:NZ	2.52	0.58
27:K:262:ARG:CG	27:K:282:LYS:HG2	2.32	0.58
28:C:78:ARG:HB3	28:C:88:GLY:HA2	1.84	0.58
30:r:58:LYS:HG3	30:r:83:ASN:HD21	1.68	0.58
2:5:478:G:H2'	2:5:479:G:H8	1.68	0.58
2:5:1400:U:H2'	2:5:1401:C:H6	1.65	0.58
10:G:111:PRO:HD2	10:G:114:ILE:HD12	1.85	0.58
30:r:31:ASN:ND2	30:r:40:TYR:O	2.36	0.58
31:f:46:ARG:NH1	31:f:46:ARG:HB2	2.19	0.58
2:5:1069:G:HO2'	4:D:286:SER:HG	1.51	0.58
2:5:1375:A:H5''	23:Q:68:ARG:HH12	1.67	0.58
27:K:86:THR:O	27:K:89:LEU:N	2.36	0.58
46:U:80:LYS:HG2	46:U:110:TYR:HE2	1.69	0.58
2:5:175:C:H2'	2:5:176:G:H8	1.68	0.58
2:5:1403:G:H2'	2:5:1404:C:C6	2.37	0.58
2:5:2390:G:H2'	2:5:2391:C:C6	2.37	0.58
2:5:4515:G:H4'	2:5:4612:G:C2	2.39	0.58
4:D:211:LEU:HB3	4:D:219:TYR:HB2	1.84	0.58
27:K:345:LEU:HD23	27:K:363:VAL:HG12	1.84	0.58
2:5:4006:U:H2'	2:5:4007:C:H6	1.69	0.58
2:5:4283:C:H2'	2:5:4284:G:C8	2.38	0.58
2:5:4731:G:H2'	2:5:4732:G:C8	2.37	0.58
7:B:147:ASP:OD1	7:B:148:LYS:N	2.37	0.58
14:A:20:VAL:HA	14:A:23:ARG:HG3	1.86	0.58
27:K:112:PHE:O	27:K:116:GLN:HG3	2.02	0.58
27:K:289:ILE:HA	27:K:292:ILE:HG12	1.85	0.58
32:e:90:MET:HE2	32:e:90:MET:HA	1.84	0.58
2:5:1436:C:O2'	2:5:1437:G:N3	2.36	0.58
27:K:21:LYS:HZ3	27:K:168:LEU:HG	1.67	0.58
2:5:1388:A:H3'	2:5:1389:G:H8	1.68	0.58
16:q:11:SER:O	16:q:15:VAL:HG22	2.04	0.58
2:5:1395:U:H2'	2:5:1396:C:H6	1.68	0.58
2:5:1750:G:H4'	6:b:60:ASN:HD22	1.69	0.58
2:5:4666:G:OP2	2:5:4666:G:N2	2.32	0.58
10:G:162:GLU:OE1	10:G:162:GLU:N	2.26	0.58
31:f:40:GLU:H	31:f:40:GLU:CD	2.12	0.58
33:Z:36:ARG:NH1	33:Z:38:TYR:OH	2.36	0.58
44:Y:130:LYS:NZ	44:Y:131:GLU:OE2	2.36	0.58
2:5:1401:C:H2'	2:5:1402:C:C6	2.38	0.58
2:5:4795:A:H2'	2:5:4796:C:C6	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:M:11:ARG:NH1	43:M:58:THR:O	2.36	0.58
2:5:3600:G:H22	2:5:3632:G:H1'	1.68	0.57
2:5:4476:C:H2'	2:5:4477:G:O4'	2.03	0.57
16:q:35:LYS:C	16:q:35:LYS:HD3	2.29	0.57
19:m:80:ARG:HG2	19:m:80:ARG:HH11	1.68	0.57
26:O:175:MET:SD	26:O:175:MET:C	2.87	0.57
37:H:14:GLU:N	37:H:14:GLU:OE1	2.34	0.57
2:5:2474:U:H1'	46:U:82:TYR:CD2	2.39	0.57
2:5:4194:G:H4'	2:5:4195:A:OP2	2.04	0.57
23:Q:109:ALA:O	23:Q:113:ILE:HG13	2.04	0.57
32:e:99:ILE:HG21	32:e:108:ARG:HG2	1.86	0.57
46:U:27:HIS:HB3	46:U:114:TYR:HE1	1.68	0.57
43:M:96:GLU:OE2	43:M:100:ARG:NE	2.38	0.57
2:5:645:C:H2'	2:5:646:G:H8	1.70	0.57
2:5:1398:A:C6	2:5:2051:G:C6	2.93	0.57
2:5:2300:G:OP1	40:N:65:ARG:NH2	2.36	0.57
36:k:10:ASP:N	36:k:10:ASP:OD1	2.36	0.57
44:Y:50:ARG:HD2	44:Y:115:ARG:HH11	1.69	0.57
2:5:1342:A:H62	2:5:1374:G:N2	2.03	0.57
2:5:2364:G:O3'	35:g:25:THR:OG1	2.23	0.57
2:5:3827:G:H1	2:5:3837:G:H1	1.53	0.57
24:R:90:PRO:HG2	24:R:93:VAL:HB	1.87	0.57
27:K:42:PHE:HZ	27:K:186:ASN:OD1	1.87	0.57
27:K:423:PHE:CD1	27:K:426:LEU:HD23	2.39	0.57
40:N:193:ARG:O	40:N:197:THR:HG23	2.05	0.57
5:S:35:PRO:HD2	5:S:39:VAL:HG21	1.85	0.57
15:I:51:HIS:ND1	15:I:137:SER:OG	2.37	0.57
19:m:54:PRO:O	19:m:58:GLN:HG3	2.04	0.57
27:K:38:THR:HA	27:K:41:ILE:HD12	1.86	0.57
27:K:196:PHE:HA	27:K:211:GLY:HA3	1.85	0.57
38:L:55:ILE:O	38:L:97:SER:OG	2.23	0.57
2:5:1343:G:H2'	2:5:1344:G:H8	1.70	0.57
2:5:2334:C:H2'	2:5:2335:C:C6	2.39	0.57
2:5:3424:A:H62	2:5:3555:G:N2	1.98	0.57
11:J:35:ARG:NH1	11:J:123:ILE:O	2.36	0.57
11:J:64:ARG:HG3	11:J:65:ASN:OD1	2.03	0.57
36:k:54:GLU:OE1	36:k:54:GLU:N	2.37	0.57
2:5:3395:A:N6	2:5:3914:G:O2'	2.37	0.57
2:5:4176:G:H4'	15:I:63:GLU:OE1	2.05	0.57
25:W:13:ILE:HD11	25:W:32:LEU:HA	1.86	0.57
46:U:41:GLN:HA	46:U:44:GLN:NE2	2.20	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:486:C:O2'	2:5:487:C:OP1	2.22	0.57
2:5:2539:A:H62	36:k:35:LYS:HE2	1.68	0.57
2:5:4721:A:OP1	21:P:74:LYS:NZ	2.36	0.57
4:D:184:ASP:OD1	4:D:186:GLU:HG2	2.05	0.57
16:q:10:PRO:HA	16:q:13:GLN:HE21	1.70	0.57
27:K:325:SER:HB2	27:K:338:VAL:HG21	1.87	0.57
2:5:364:G:O6	13:j:55:ARG:NH2	2.37	0.57
2:5:1407:A:H2'	2:5:1408:G:O4'	2.04	0.57
2:5:3857:G:H2'	2:5:3858:C:H6	1.69	0.57
2:5:4275:G:H2'	2:5:4276:UR3:C6	2.35	0.57
3:F:93:ARG:NH1	3:F:95:ARG:O	2.33	0.57
10:G:164:LYS:HZ1	10:G:168:LEU:HD23	1.70	0.57
27:K:64:TRP:CH2	27:K:347:PRO:HD3	2.40	0.57
27:K:197:SER:HB2	27:K:210:GLU:HB3	1.86	0.57
2:5:754:G:H4'	37:H:50:LYS:NZ	2.20	0.56
2:5:3396:G:H2'	2:5:3397:G:H8	1.70	0.56
6:b:91:ARG:HA	6:b:94:HIS:CD2	2.40	0.56
27:K:259:GLN:HA	27:K:284:PHE:CE2	2.40	0.56
30:r:90:LEU:HD13	30:r:111:ILE:HG23	1.86	0.56
43:M:39:ASP:N	43:M:39:ASP:OD1	2.36	0.56
2:5:3336:A:H3'	24:R:71:ARG:NH2	2.20	0.56
2:5:4337:U:H2'	2:5:4338:C:C6	2.40	0.56
2:5:4518:C:O2'	2:5:4520:C:OP2	2.22	0.56
16:q:20:ARG:CG	45:X:151:ASN:ND2	2.61	0.56
27:K:216:LEU:HD22	27:K:242:LEU:CD2	2.34	0.56
41:i:42:ASP:OD1	41:i:43:MET:N	2.38	0.56
2:5:150:U:OP2	10:G:253:THR:OG1	2.23	0.56
2:5:186:G:H22	2:5:189:G:P	2.29	0.56
2:5:660:G:N3	30:r:46:ARG:NH1	2.54	0.56
2:5:843:A:N7	3:F:150:ASN:ND2	2.53	0.56
2:5:1457:G:OP2	23:Q:65:ARG:NE	2.38	0.56
2:5:1930:A:O2'	2:5:1931:U:O5'	2.14	0.56
2:5:2040:A:C5	3:F:176:ARG:NH2	2.73	0.56
2:5:2588:A:H2'	2:5:2589:A:C8	2.39	0.56
2:5:3391:G:OP1	14:A:241:ARG:NH1	2.38	0.56
2:5:3858:C:H2'	2:5:3859:G:H8	1.70	0.56
7:B:153:MET:O	7:B:157:CYS:HB2	2.05	0.56
22:E:201:SER:N	22:E:291:PHE:O	2.30	0.56
2:5:759:G:H5'	2:5:760:C:H5	1.70	0.56
2:5:4486:G:N2	2:5:4698:U:O2	2.29	0.56
34:a:15:VAL:O	34:a:15:VAL:CG2	2.51	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:U:75:GLU:OE1	46:U:75:GLU:N	2.39	0.56
1:T:103:ASP:OD1	1:T:104:SER:N	2.38	0.56
2:5:2176:G:H5'	28:C:195:LYS:HE3	1.87	0.56
2:5:3863:G:H2'	2:5:3864:G:H8	1.71	0.56
2:5:3978:U:H4'	2:5:3979:A:O5'	2.04	0.56
26:O:113:ASP:OD1	26:O:113:ASP:N	2.34	0.56
27:K:180:SER:OG	27:K:453:ILE:HG12	2.06	0.56
27:K:209:PHE:CD2	27:K:214:ILE:HG21	2.40	0.56
27:K:404:HIS:HD2	45:X:84:GLU:HB2	1.71	0.56
2:5:164:G:H2'	2:5:165:A:H8	1.71	0.56
2:5:4634:C:H1'	43:M:132:ARG:HH12	1.70	0.56
11:J:20:LEU:HD12	11:J:132:VAL:HG12	1.87	0.56
2:5:4686:U:O2'	2:5:4687:C:OP1	2.23	0.56
12:c:17:ARG:O	12:c:21:VAL:HG12	2.06	0.56
30:r:105:ASP:OD1	30:r:105:ASP:N	2.38	0.56
2:5:1306:G:OP1	38:L:39:ARG:NH2	2.39	0.56
2:5:3816:C:H2'	2:5:3817:G:H8	1.71	0.56
2:5:4268:G:O2'	2:5:4271:C:OP2	2.21	0.56
2:5:4358:C:H1'	37:H:120:GLU:OE2	2.06	0.56
9:8:75:G:O2'	20:l:29:MET:HE1	2.06	0.56
31:f:4:ARG:HD2	31:f:6:TRP:H	1.70	0.56
41:i:51:ALA:HB3	41:i:54:GLU:HG3	1.87	0.56
2:5:1745:G:H2'	2:5:1746:C:H6	1.71	0.56
2:5:3857:G:H2'	2:5:3858:C:C6	2.41	0.56
2:5:2382:C:H2'	2:5:2383:C:C6	2.41	0.55
2:5:4796:C:H2'	2:5:4797:A:C8	2.40	0.55
9:8:126:C:O2'	9:8:127:U:O5'	2.19	0.55
1:T:43:LYS:NZ	2:5:1671:C:OP1	2.38	0.55
2:5:159:C:H5'	41:i:25:ARG:HH21	1.70	0.55
2:5:2430:A:H5'	2:5:2613:C:H5'	1.88	0.55
14:A:120:PRO:HA	14:A:162:ASN:HB3	1.87	0.55
32:e:113:GLU:CD	32:e:117:GLN:HE21	2.14	0.55
45:X:76:ILE:HG22	45:X:77:ILE:HD12	1.89	0.55
1:T:127:GLN:OE1	1:T:128:LEU:N	2.38	0.55
2:5:3863:G:H2'	2:5:3864:G:C8	2.41	0.55
2:5:4795:A:H2'	2:5:4796:C:H6	1.71	0.55
4:D:72:ASP:N	4:D:72:ASP:OD1	2.39	0.55
32:e:76:LYS:NZ	32:e:98:GLU:OE1	2.28	0.55
2:5:195:C:OP2	44:Y:28:LYS:NZ	2.30	0.55
2:5:2254:C:H2'	2:5:2255:A:C8	2.40	0.55
28:C:145:GLU:OE1	28:C:145:GLU:N	2.28	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:136:C:N4	42:h:76:LYS:O	2.40	0.55
2:5:162:A:H2'	2:5:163:A:H8	1.72	0.55
2:5:1758:G:N3	4:D:113:PHE:HE1	2.03	0.55
2:5:4006:U:H2'	2:5:4007:C:C6	2.41	0.55
2:5:4508:G:H2'	2:5:4509:A:H8	1.71	0.55
2:5:4515:G:OP1	26:O:168:TYR:OH	2.24	0.55
12:c:77:ASN:N	12:c:80:GLU:OE1	2.27	0.55
20:l:21:ARG:HD2	27:K:273:ARG:NH2	2.22	0.55
34:a:77:LYS:O	34:a:80:THR:OG1	2.24	0.55
2:5:1132:U:H1'	2:5:1134:G:C5	2.42	0.55
2:5:1277:A:H2'	2:5:1278:A:C8	2.42	0.55
19:m:92:THR:OG1	19:m:94:ASN:OD1	2.24	0.55
21:P:131:ARG:HG3	21:P:137:ASN:ND2	2.21	0.55
27:K:357:ASP:HB3	27:K:360:HIS:HD2	1.72	0.55
46:U:42:PHE:HD2	46:U:90:TYR:CD2	2.25	0.55
2:5:2328:U:H2'	2:5:2329:G:C8	2.41	0.55
2:5:2329:G:H2'	2:5:2330:G:C8	2.42	0.55
2:5:3502:U:H2'	2:5:3503:C:C6	2.41	0.55
2:5:4057:A:O2'	2:5:4058:U:H5'	2.07	0.55
9:8:75:G:H2'	9:8:76:C:C6	2.41	0.55
36:k:14:THR:HA	36:k:17:ARG:HG3	1.88	0.55
37:H:189:GLN:OE1	37:H:189:GLN:N	2.39	0.55
2:5:705:A:H2'	2:5:706:C:C6	2.42	0.55
2:5:881:C:OP1	22:E:48:ARG:HG2	2.07	0.55
2:5:1095:C:H2'	2:5:1096:G:H8	1.72	0.55
2:5:1124:A:O2'	3:F:51:GLU:OE2	2.24	0.55
2:5:4612:G:C4	26:O:175:MET:HE2	2.42	0.55
4:D:200:MET:HE3	4:D:237:GLU:HG3	1.88	0.55
7:B:189:THR:OG1	7:B:192:GLU:OE1	2.20	0.55
22:E:164:ARG:NH1	22:E:276:SER:OG	2.40	0.55
22:E:255:ALA:O	22:E:259:GLN:NE2	2.40	0.55
23:Q:184:ARG:NE	34:a:55:LYS:O	2.40	0.55
34:a:75:LEU:HG	34:a:113:GLY:HA2	1.87	0.55
2:5:756:G:H2'	2:5:757:A:H8	1.72	0.55
2:5:882:U:O2'	22:E:41:LYS:O	2.25	0.55
2:5:1743:A:H4'	2:5:1744:A:O5'	2.07	0.55
2:5:3680:C:C2	2:5:3681:A:C8	2.94	0.55
2:5:4439:C:OP1	37:H:64:ARG:NH2	2.40	0.55
22:E:165:VAL:HG12	22:E:178:VAL:HG22	1.89	0.55
23:Q:35:LEU:HD21	28:C:298:ILE:HD11	1.88	0.55
26:O:65:ASN:OD1	26:O:67:SER:OG	2.25	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:K:82:SER:HA	27:K:85:VAL:HG12	1.87	0.55
2:5:703:C:OP1	31:f:89:ARG:NH2	2.40	0.55
2:5:865:G:N2	2:5:866:A:N7	2.54	0.55
2:5:1872:G:H2'	2:5:1873:A:C8	2.42	0.55
2:5:4480:A:H2'	2:5:4481:G:C8	2.40	0.55
3:F:133:ARG:HA	3:F:136:GLU:HG3	1.89	0.55
6:b:65:MET:HE2	6:b:65:MET:HA	1.89	0.55
11:J:15:LEU:HD21	11:J:157:ILE:HG12	1.88	0.55
2:5:756:G:H8	2:5:756:G:OP2	1.90	0.54
2:5:1065:G:H2'	2:5:1066:A:C8	2.42	0.54
2:5:1098:C:H2'	2:5:1099:G:H8	1.71	0.54
2:5:1276:C:H2'	2:5:1277:A:C8	2.39	0.54
2:5:4662:U:H2'	2:5:4663:C:C6	2.41	0.54
2:5:4677:A:H1'	22:E:188:PRO:HG3	1.89	0.54
2:5:4693:G:H2'	2:5:4694:A:C8	2.43	0.54
5:S:164:LYS:HB3	5:S:165:PRO:HD3	1.88	0.54
15:I:189:ARG:HG2	15:I:199:TYR:HE1	1.71	0.54
2:5:2431:C:OP1	2:5:2611:C:O2'	2.24	0.54
2:5:2481:G:H22	2:5:2540:A:N6	2.05	0.54
2:5:3421:G:O2'	2:5:3550:U:OP2	2.21	0.54
2:5:3481:C:O2'	14:A:220:GLY:O	2.25	0.54
21:P:28:ASN:O	21:P:32:THR:HG22	2.06	0.54
28:C:77:PRO:O	28:C:90:GLY:HA2	2.08	0.54
33:Z:68:ILE:HG12	33:Z:119:GLU:HG2	1.89	0.54
37:H:14:GLU:HA	37:H:52:LYS:NZ	2.22	0.54
9:8:87:G:OP1	42:h:5:LYS:NZ	2.28	0.54
27:K:350:SER:H	27:K:353:SER:HB3	1.72	0.54
42:h:32:ARG:O	42:h:36:VAL:HG23	2.07	0.54
43:M:39:ASP:HB3	43:M:47:ARG:HA	1.88	0.54
2:5:1077:U:H2'	2:5:1078:G:N3	2.22	0.54
2:5:1403:G:C6	2:5:2045:G:C6	2.96	0.54
10:G:281:ASP:OD1	10:G:281:ASP:N	2.39	0.54
2:5:153:G:H2'	2:5:154:G:H8	1.73	0.54
2:5:891:U:O4	2:5:979:G:O6	2.25	0.54
5:S:168:THR:HG22	5:S:170:LYS:H	1.72	0.54
24:R:15:LEU:HD13	24:R:52:ARG:HB2	1.90	0.54
28:C:65:GLU:HG2	28:C:80:ARG:HE	1.73	0.54
30:r:85:ASN:O	30:r:89:THR:OG1	2.24	0.54
38:L:47:ALA:HB3	38:L:48:PRO:HD3	1.89	0.54
2:5:3826:A:H2'	2:5:3827:G:C8	2.42	0.54
2:5:3857:G:H1'	10:G:87:LYS:NZ	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:187:SER:O	4:D:189:GLU:HG3	2.08	0.54
2:5:1698:G:H2'	2:5:1699:G:H8	1.72	0.54
2:5:2275:U:OP1	27:K:273:ARG:CG	2.55	0.54
2:5:4049:C:H2'	2:5:4051:G:C8	2.43	0.54
4:D:88:VAL:HA	4:D:239:MET:HE1	1.88	0.54
12:c:48:LEU:HD21	12:c:60:ILE:HG21	1.89	0.54
2:5:3625:C:H2'	2:5:3626:A:C8	2.43	0.54
27:K:209:PHE:CB	27:K:214:ILE:HG21	2.38	0.54
29:o:4:VAL:O	29:o:94:GLY:N	2.39	0.54
2:5:3541:G:OP2	2:5:3541:G:N2	2.35	0.54
2:5:3605:G:H2'	2:5:3606:G:C8	2.42	0.54
2:5:3850:G:O2'	33:Z:136:PHE:OXT	2.25	0.54
5:S:1:MET:HE2	5:S:43:ARG:HG3	1.90	0.54
7:B:220:ILE:HG12	7:B:278:THR:HG23	1.89	0.54
27:K:36:ALA:O	27:K:39:LEU:HG	2.08	0.54
28:C:204:ARG:NH1	28:C:205:ARG:O	2.40	0.54
2:5:754:G:H4'	37:H:50:LYS:HE2	1.90	0.54
2:5:3858:C:H2'	2:5:3859:G:C8	2.43	0.54
27:K:207:MET:HE2	27:K:218:HIS:CD2	2.43	0.54
36:k:51:GLU:O	36:k:55:LYS:HG2	2.08	0.54
42:h:15:GLU:H	42:h:15:GLU:CD	2.15	0.54
46:U:28:PRO:HG3	46:U:100:LEU:HD11	1.89	0.54
2:5:1068:U:H2'	2:5:1069:G:C8	2.40	0.53
2:5:3625:C:H2'	2:5:3626:A:H8	1.72	0.53
2:5:4431:U:OP1	19:m:88:LYS:NZ	2.37	0.53
27:K:64:TRP:HH2	27:K:347:PRO:HD3	1.73	0.53
2:5:1125:C:H2'	2:5:1126:G:C8	2.43	0.53
2:5:2143:A:N7	28:C:143:ARG:NH1	2.55	0.53
2:5:2385:G:H2'	2:5:2386:A:C8	2.44	0.53
2:5:3788:C:H2'	2:5:3789:G:C8	2.44	0.53
4:D:52:ILE:HD13	39:7:6:C:H4'	1.89	0.53
4:D:83:LEU:HB3	4:D:88:VAL:HB	1.90	0.53
7:B:103:LYS:HG2	7:B:149:ASP:OD1	2.08	0.53
10:G:195:THR:O	10:G:199:LEU:HG	2.09	0.53
17:p:5:THR:OG1	17:p:8:VAL:O	2.20	0.53
27:K:401:MET:H	27:K:409:MET:HE1	1.73	0.53
31:f:8:LYS:HD3	31:f:100:ARG:NH1	2.24	0.53
37:H:92:MET:HA	37:H:182:SER:H	1.72	0.53
2:5:291:U:O4	29:o:43:ARG:NH2	2.42	0.53
2:5:1955:C:H2'	2:5:1956:A:H8	1.73	0.53
11:J:28:GLU:OE1	11:J:28:GLU:N	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:c:34:SER:O	12:c:38:ILE:HG22	2.08	0.53
40:N:98:LEU:HD23	40:N:128:LYS:HD2	1.89	0.53
2:5:48:G:HO2'	2:5:49:U:P	2.31	0.53
2:5:263:G:H2'	2:5:264:C:C6	2.42	0.53
2:5:1487:G:OP2	13:j:31:LYS:NZ	2.41	0.53
14:A:204:MET:HB3	14:A:208:GLU:HG3	1.89	0.53
23:Q:132:LYS:HB2	23:Q:134:ARG:HH11	1.74	0.53
24:R:162:ARG:NH1	24:R:163:ARG:HB2	2.22	0.53
37:H:14:GLU:HA	37:H:52:LYS:HZ2	1.73	0.53
45:X:119:ILE:HA	45:X:144:TYR:HE2	1.74	0.53
2:5:275:C:H2'	2:5:276:C:C6	2.44	0.53
2:5:522:U:H2'	2:5:523:C:H6	1.73	0.53
2:5:737:G:H22	2:5:819:C:H2'	1.72	0.53
2:5:1395:U:H2'	2:5:1396:C:C6	2.44	0.53
2:5:1700:G:O6	2:5:1711:C:N4	2.42	0.53
2:5:3941:G:H5''	2:5:3941:G:N3	2.23	0.53
4:D:5:LYS:N	4:D:5:LYS:HE2	2.23	0.53
21:P:25:HIS:O	21:P:29:THR:OG1	2.25	0.53
27:K:302:TYR:HB3	27:K:324:TRP:CH2	2.44	0.53
2:5:2678:A:O2'	7:B:228:TYR:O	2.25	0.53
2:5:3998:C:OP2	2:5:3999:A:O2'	2.25	0.53
36:k:51:GLU:OE1	36:k:51:GLU:N	2.41	0.53
43:M:11:ARG:CZ	43:M:61:ILE:HD11	2.39	0.53
45:X:122:ALA:N	45:X:139:ARG:O	2.40	0.53
2:5:462:G:H2'	2:5:463:A:C8	2.43	0.53
2:5:478:G:H2'	2:5:479:G:C8	2.43	0.53
2:5:1392:C:H2'	2:5:1393:C:OP1	2.08	0.53
2:5:3894:C:C5'	33:Z:59:LYS:HZ1	2.21	0.53
2:5:4745:U:H4'	2:5:4746:A:H5'	1.90	0.53
3:F:167:ALA:HB1	28:C:315:LYS:HD2	1.90	0.53
9:8:124:U:H4'	9:8:125:C:O5'	2.08	0.53
12:c:78:ASN:N	12:c:78:ASN:OD1	2.42	0.53
22:E:68:LYS:HE3	22:E:70:LEU:HD11	1.89	0.53
27:K:215:ALA:CB	27:K:239:LEU:HD23	2.37	0.53
33:Z:71:PHE:HA	33:Z:111:ARG:HD2	1.91	0.53
44:Y:4:ASN:HB3	44:Y:7:VAL:HG12	1.91	0.53
47:n:10:MET:O	47:n:10:MET:HE3	2.08	0.53
2:5:257:C:H2'	2:5:258:G:H8	1.74	0.53
2:5:667:C:H2'	2:5:668:G:H8	1.73	0.53
2:5:3593:A:H2'	2:5:3594:A:H8	1.74	0.53
4:D:223:PHE:HB3	4:D:226:TYR:HB2	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:R:2:SER:OG	24:R:3:MET:N	2.42	0.53
24:R:95:TRP:CZ2	24:R:99:MET:HE2	2.43	0.53
28:C:218:VAL:O	28:C:222:ARG:HB2	2.09	0.53
2:5:2275:U:H5'	27:K:273:ARG:HD2	1.88	0.53
2:5:2704:OMC:H2'	2:5:2705:G:O4'	2.09	0.53
2:5:4611:G:H4'	2:5:4613:A:P	2.48	0.53
4:D:67:ALA:HA	4:D:72:ASP:HB3	1.91	0.53
18:V:82:ILE:HD12	18:V:121:VAL:HG22	1.90	0.53
2:5:85:G:O2'	2:5:97:G:O6	2.20	0.53
2:5:718:C:H1'	28:C:343:GLN:HG2	1.90	0.53
7:B:45:ALA:HB3	7:B:183:ILE:HG23	1.91	0.53
9:8:75:G:H2'	9:8:76:C:H6	1.74	0.53
46:U:39:PHE:O	46:U:43:LEU:HD23	2.10	0.53
1:T:87:LYS:HZ2	2:5:4051:G:H22	1.56	0.52
2:5:262:G:H2'	2:5:263:G:H8	1.73	0.52
2:5:1127:G:H2'	2:5:1128:C:H6	1.74	0.52
2:5:1235:G:O2'	2:5:1236:C:OP1	2.26	0.52
2:5:1405:C:O4'	2:5:2044:A:O2'	2.27	0.52
2:5:2219:A:H2'	2:5:2220:C:H6	1.73	0.52
2:5:2370:A:OP1	24:R:38:ARG:NH1	2.42	0.52
22:E:180:GLY:HA3	22:E:185:ASN:HD21	1.74	0.52
46:U:49:VAL:HG12	46:U:50:ASN:OD1	2.09	0.52
2:5:1079:C:H2'	2:5:1080:G:H8	1.73	0.52
2:5:4019:A:H2'	2:5:4020:A:C8	2.43	0.52
4:D:56:THR:HG21	39:7:26:C:H5''	1.91	0.52
26:O:121:PRO:HA	26:O:124:LEU:HD12	1.90	0.52
27:K:107:LYS:O	27:K:111:LEU:HG	2.08	0.52
34:a:93:ASN:OD1	34:a:94:LYS:N	2.42	0.52
2:5:1079:C:H2'	2:5:1080:G:C8	2.45	0.52
2:5:1546:U:N3	2:5:4301:U:OP1	2.37	0.52
2:5:2565:G:H2'	2:5:2566:U:C6	2.45	0.52
2:5:2616:OMG:OP1	36:k:39:SER:OG	2.28	0.52
2:5:4623:G:N7	22:E:275:ARG:NH2	2.56	0.52
2:5:4786:C:H5'	2:5:4789:C:H5	1.75	0.52
2:5:758:C:C2	2:5:795:A:N6	2.77	0.52
2:5:1130:C:N3	2:5:1131:G:O2'	2.40	0.52
7:B:306:ASP:OD1	7:B:306:ASP:N	2.39	0.52
14:A:95:GLN:OE1	14:A:95:GLN:N	2.41	0.52
2:5:1881:A:H2'	2:5:1882:A:H8	1.72	0.52
2:5:2518:G:H1	12:c:33:GLN:NE2	2.07	0.52
2:5:4172:C:H2'	2:5:4173:G:O4'	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
17:p:74:THR:O	17:p:78:THR:HG23	2.10	0.52
20:l:44:TRP:CZ3	20:l:45:ARG:HD3	2.44	0.52
30:r:119:ARG:HB3	30:r:119:ARG:CZ	2.39	0.52
32:e:101:HIS:HA	32:e:108:ARG:HH22	1.74	0.52
39:7:58:A:H2'	39:7:59:G:H8	1.75	0.52
7:B:112:ASP:O	7:B:116:ARG:HG2	2.09	0.52
27:K:151:ILE:HG23	27:K:154:GLN:HE21	1.75	0.52
27:K:415:ARG:HD3	45:X:156:ILE:CG2	2.39	0.52
42:h:32:ARG:HG2	42:h:32:ARG:NH1	2.25	0.52
43:M:9:VAL:HG11	43:M:66:HIS:HA	1.92	0.52
2:5:785:G:H2'	2:5:786:G:C8	2.44	0.52
2:5:2363:C:H2'	2:5:2364:G:H8	1.75	0.52
5:S:95:ARG:HD2	5:S:113:MET:HE3	1.92	0.52
15:I:191:ILE:HD13	15:I:200:ILE:HG13	1.90	0.52
36:k:18:LYS:HB2	36:k:18:LYS:NZ	2.25	0.52
2:5:1423:C:OP1	34:a:132:ARG:NH2	2.40	0.52
2:5:1785:G:H2'	2:5:1786:C:C6	2.45	0.52
2:5:2422:G:N2	2:5:2425:A:OP2	2.33	0.52
2:5:3577:A:OP2	7:B:249:ARG:NH2	2.42	0.52
2:5:3593:A:H2'	2:5:3594:A:C8	2.44	0.52
2:5:4047:U:OP2	2:5:4049:C:N4	2.43	0.52
17:p:26:VAL:HG22	17:p:30:GLU:HG3	1.91	0.52
28:C:44:LEU:C	28:C:46:LYS:H	2.18	0.52
46:U:41:GLN:O	46:U:45:GLU:HG2	2.09	0.52
2:5:206:U:O2'	2:5:208:A:N7	2.39	0.52
2:5:280:G:OP2	40:N:44:ARG:NH2	2.40	0.52
2:5:1700:G:N2	2:5:1710:U:O2	2.25	0.52
2:5:3503:C:H2'	2:5:3504:U:C6	2.45	0.52
2:5:3854:C:H5''	2:5:3855:A:H5''	1.91	0.52
2:5:3932:A:H2'	2:5:3933:G:C8	2.45	0.52
2:5:4625:C:H42	2:5:4672:C:H42	1.58	0.52
2:5:4660:C:H2'	2:5:4661:C:C6	2.45	0.52
12:c:37:MET:HG3	12:c:97:ILE:HD11	1.91	0.52
14:A:126:LEU:HD23	14:A:150:LEU:HD21	1.92	0.52
17:p:22:LEU:O	17:p:26:VAL:HG12	2.09	0.52
22:E:165:VAL:HG13	22:E:180:GLY:N	2.25	0.52
2:5:4512:G:OP1	37:H:23:ARG:NH1	2.43	0.52
4:D:208:MET:HE3	4:D:233:PRO:HG3	1.92	0.52
10:G:140:LEU:HD23	10:G:140:LEU:H	1.74	0.52
14:A:36:GLU:OE1	14:A:163:ARG:NE	2.43	0.52
14:A:117:GLU:HB2	14:A:122:ASP:OD1	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:H:107:GLU:OE1	37:H:107:GLU:N	2.43	0.52
1:T:70:HIS:NE2	2:5:4073:C:OP1	2.43	0.51
2:5:1135:C:N4	2:5:1205:G:N7	2.58	0.51
2:5:1288:C:H2'	2:5:1289:A:H8	1.74	0.51
2:5:1387:G:H1'	2:5:1407:A:H61	1.74	0.51
2:5:2430:A:O2'	2:5:2431:C:O4'	2.26	0.51
2:5:2538:A:OP1	36:k:35:LYS:NZ	2.42	0.51
2:5:4253:A:H2'	2:5:4254:C:C6	2.46	0.51
14:A:130:SER:OG	14:A:174:ARG:NH2	2.40	0.51
24:R:50:ILE:C	24:R:51:ILE:HD13	2.34	0.51
34:a:121:PRO:HA	34:a:141:GLY:O	2.11	0.51
39:7:110:G:H2'	39:7:111:C:C6	2.45	0.51
2:5:1745:G:H2'	2:5:1746:C:C6	2.45	0.51
2:5:2270:G:OP1	24:R:5:ARG:NH2	2.44	0.51
2:5:3603:A:H2'	2:5:3604:A:C8	2.46	0.51
4:D:35:ARG:HH11	4:D:35:ARG:HG3	1.75	0.51
12:c:81:LEU:HG	12:c:91:VAL:HG13	1.92	0.51
26:O:5:GLN:HE21	26:O:5:GLN:CA	2.21	0.51
2:5:229:G:OP1	44:Y:11:ARG:NH1	2.42	0.51
2:5:2001:C:O2'	5:S:111:ARG:NH2	2.44	0.51
2:5:3669:C:H1'	40:N:125:SER:HB3	1.91	0.51
2:5:3803:U:OP1	10:G:302:ARG:NH2	2.42	0.51
2:5:4445:U:H1'	2:5:4446:A:H5''	1.92	0.51
2:5:4640:G:H2'	2:5:4641:C:C6	2.46	0.51
4:D:133:GLU:OE1	4:D:133:GLU:N	2.43	0.51
27:K:42:PHE:CZ	27:K:186:ASN:OD1	2.64	0.51
27:K:297:LEU:HD21	27:K:371:SER:OG	2.10	0.51
2:5:642:G:H2'	2:5:643:A:H8	1.75	0.51
2:5:2481:G:N2	2:5:2540:A:H61	2.05	0.51
3:F:24:PHE:HB2	3:F:27:LEU:HB3	1.92	0.51
9:8:102:G:OP2	9:8:104:A:O2'	2.25	0.51
10:G:158:GLU:OE2	10:G:162:GLU:HG2	2.10	0.51
14:A:117:GLU:HB2	14:A:122:ASP:CG	2.36	0.51
27:K:89:LEU:O	27:K:93:LEU:HG	2.11	0.51
2:5:1834:G:OP1	3:F:95:ARG:NH2	2.42	0.51
2:5:3357:G:O2'	2:5:3358:G:OP1	2.28	0.51
6:b:108:ALA:O	6:b:112:ILE:HG22	2.11	0.51
7:B:57:VAL:HG22	7:B:73:VAL:HG12	1.91	0.51
22:E:48:ARG:O	22:E:67:ARG:NH2	2.36	0.51
2:5:180:C:H2'	2:5:181:C:C6	2.46	0.51
2:5:1065:G:H2'	2:5:1066:A:H8	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:1390:G:C2	2:5:1405:C:C2	2.99	0.51
2:5:1658:C:H2'	2:5:1659:C:H6	1.73	0.51
2:5:3797:U:H2'	2:5:3798:U:C6	2.46	0.51
8:d:54:MET:HA	8:d:54:MET:HE3	1.92	0.51
10:G:139:VAL:HG21	10:G:238:LYS:HG3	1.92	0.51
23:Q:38:ARG:NH2	28:C:303:ARG:O	2.28	0.51
24:R:159:ALA:HB1	24:R:162:ARG:HH21	1.75	0.51
27:K:34:TRP:O	27:K:37:ILE:HD12	2.11	0.51
27:K:215:ALA:CB	27:K:239:LEU:HD21	2.36	0.51
27:K:392:LYS:HG2	27:K:396:GLU:OE1	2.11	0.51
37:H:12:ILE:HD11	37:H:52:LYS:HD3	1.92	0.51
1:T:40:VAL:HG11	1:T:96:ILE:HD11	1.93	0.51
2:5:164:G:H2'	2:5:165:A:C8	2.46	0.51
2:5:1678:G:H2'	2:5:1679:C:C6	2.45	0.51
2:5:2549:G:N2	2:5:2552:C:OP2	2.44	0.51
2:5:3464:A:H2'	2:5:3465:A:C8	2.46	0.51
2:5:3934:U:H2'	2:5:3935:U:C6	2.45	0.51
3:F:89:ALA:HB2	3:F:124:LEU:HD21	1.92	0.51
7:B:107:ALA:HB2	7:B:201:LEU:HG	1.93	0.51
28:C:287:THR:HG23	30:r:2:SER:HB3	1.92	0.51
46:U:28:PRO:HB2	46:U:34:MET:SD	2.50	0.51
2:5:3580:U:H2'	2:5:3581:A:H8	1.76	0.51
3:F:235:ARG:HD3	3:F:238:GLN:HB2	1.93	0.51
6:b:91:ARG:HA	6:b:94:HIS:HD2	1.74	0.51
9:8:153:C:OP1	10:G:238:LYS:NZ	2.27	0.51
14:A:200:ARG:NH2	14:A:217:GLN:OE1	2.44	0.51
30:r:10:VAL:HG22	30:r:14:SER:HB2	1.92	0.51
38:L:128:PRO:HD3	38:L:144:LEU:HD21	1.93	0.51
2:5:1386:C:H2'	2:5:1387:G:O4'	2.11	0.51
2:5:3373:U:H5	2:5:3378:A:N7	2.09	0.51
22:E:152:ILE:HD12	22:E:274:LEU:HD21	1.93	0.51
26:O:94:ARG:HD2	31:f:97:ILE:HG21	1.91	0.51
26:O:185:VAL:HG21	43:M:126:GLU:HG2	1.93	0.51
27:K:207:MET:O	27:K:218:HIS:HB3	2.11	0.51
46:U:37:ALA:O	46:U:41:GLN:OE1	2.28	0.51
2:5:510:G:H21	34:a:85:GLN:HE22	1.58	0.51
2:5:725:G:HO2'	2:5:726:A:H8	1.58	0.51
2:5:1289:A:H2'	2:5:1290:C:C6	2.46	0.51
2:5:1583:C:OP1	14:A:14:SER:OG	2.27	0.51
2:5:1617:C:H2'	2:5:1618:C:C6	2.45	0.51
2:5:2310:U:H4'	2:5:2311:U:H5'	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:3816:C:H2'	2:5:3817:G:C8	2.46	0.51
27:K:21:LYS:O	27:K:171:LYS:HG3	2.11	0.51
28:C:32:ILE:HD12	28:C:130:ALA:HB2	1.93	0.51
2:5:175:C:H2'	2:5:176:G:C8	2.46	0.50
2:5:754:G:H1	2:5:801:C:H42	1.58	0.50
2:5:756:G:H2'	2:5:757:A:C8	2.46	0.50
2:5:784:C:H2'	2:5:785:G:C8	2.46	0.50
2:5:3504:U:O2'	2:5:3505:U:H2'	2.11	0.50
2:5:3890:G:H2'	2:5:3891:G:H8	1.76	0.50
2:5:3894:C:O5'	33:Z:59:LYS:NZ	2.41	0.50
2:5:4661:C:H2'	2:5:4662:U:C6	2.45	0.50
4:D:224:SER:OG	4:D:225:GLN:OE1	2.27	0.50
10:G:199:LEU:HD13	10:G:205:ALA:HB2	1.93	0.50
10:G:201:GLU:OE2	40:N:6:TYR:OH	2.21	0.50
11:J:113:ILE:HA	11:J:117:ILE:HB	1.93	0.50
16:q:9:GLU:HG3	16:q:10:PRO:HD3	1.93	0.50
18:V:82:ILE:HG13	18:V:83:ARG:HG3	1.93	0.50
24:R:106:LEU:HD21	24:R:138:LEU:HD21	1.94	0.50
27:K:58:SER:HB3	27:K:136:MET:SD	2.52	0.50
27:K:415:ARG:CD	45:X:156:ILE:HG22	2.40	0.50
44:Y:55:VAL:HG13	44:Y:104:VAL:HG13	1.91	0.50
2:5:2536:G:OP1	36:k:35:LYS:HE3	2.11	0.50
2:5:3330:C:H2'	2:5:3331:A:H8	1.76	0.50
2:5:4371:C:O2'	2:5:4372:A:H5'	2.11	0.50
2:5:4681:C:H4'	22:E:157:THR:HG23	1.92	0.50
2:5:4730:U:H2'	2:5:4731:G:C8	2.45	0.50
7:B:116:ARG:HD3	7:B:122:TRP:CD2	2.46	0.50
7:B:233:SER:O	7:B:272:LYS:NZ	2.39	0.50
15:I:51:HIS:HB3	15:I:134:VAL:HG13	1.92	0.50
16:q:29:ASP:O	16:q:33:PHE:N	2.41	0.50
24:R:7:GLN:N	24:R:7:GLN:OE1	2.42	0.50
27:K:344:TYR:HA	27:K:360:HIS:CA	2.40	0.50
38:L:64:VAL:HA	38:L:67:HIS:CD2	2.38	0.50
2:5:735:G:H2'	2:5:736:C:O4'	2.12	0.50
2:5:754:G:H1	2:5:801:C:N4	2.10	0.50
2:5:1277:A:H2'	2:5:1278:A:H8	1.75	0.50
2:5:1416:C:H2'	2:5:1417:A:H8	1.76	0.50
2:5:1510:G:O6	17:p:4:ARG:NH2	2.45	0.50
2:5:4316:G:H2'	2:5:4317:A:H8	1.77	0.50
3:F:27:LEU:O	3:F:31:ARG:HG2	2.11	0.50
5:S:150:ILE:HG12	43:M:30:VAL:HG21	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:153:MET:HE3	7:B:194:LEU:HD11	1.92	0.50
31:f:33:VAL:HG23	31:f:38:GLU:HB2	1.92	0.50
38:L:128:PRO:HA	38:L:138:ASP:OD2	2.11	0.50
46:U:100:LEU:HD12	46:U:112:LEU:HB3	1.94	0.50
5:S:9:GLU:OE2	5:S:31:ARG:NH1	2.44	0.50
7:B:224:LYS:HG2	7:B:340:THR:HB	1.92	0.50
10:G:158:GLU:OE1	10:G:158:GLU:HA	2.10	0.50
16:q:20:ARG:HA	45:X:151:ASN:HD21	1.76	0.50
27:K:247:ALA:HB3	27:K:440:ALA:HA	1.94	0.50
33:Z:66:SER:O	33:Z:66:SER:OG	2.27	0.50
38:L:124:LEU:HA	42:h:121:VAL:HA	1.93	0.50
39:7:23:A:N3	39:7:118:C:O2'	2.39	0.50
2:5:1415:C:H2'	2:5:1416:C:H6	1.76	0.50
44:Y:102:SER:OG	44:Y:103:LYS:NZ	2.44	0.50
2:5:119:G:H3'	2:5:120:A:H5''	1.94	0.50
2:5:469:C:N3	22:E:108:ARG:NH2	2.48	0.50
2:5:2396:A:H2	2:5:2608:A:H62	1.59	0.50
2:5:4253:A:O2'	18:V:41:SER:OG	2.24	0.50
5:S:20:PRO:HA	5:S:23:ARG:HH12	1.76	0.50
10:G:165:GLN:O	10:G:168:LEU:HG	2.12	0.50
14:A:17:ARG:HH11	14:A:17:ARG:HG3	1.77	0.50
18:V:71:GLU:H	18:V:71:GLU:CD	2.16	0.50
40:N:46:ASP:OD2	40:N:50:ARG:NH2	2.44	0.50
2:5:35:U:O2'	2:5:1480:A:N1	2.44	0.50
2:5:1089:G:H2'	2:5:1090:G:C8	2.47	0.50
2:5:2122:A:O2'	32:e:48:ARG:NH2	2.45	0.50
2:5:2328:U:H3	2:5:2336:G:H1	1.59	0.50
2:5:2482:U:H2'	2:5:2537:G:H1	1.76	0.50
2:5:3900:G:H2'	2:5:3901:C:C6	2.46	0.50
2:5:4141:U:H5'	2:5:4141:U:C6	2.44	0.50
2:5:4743:C:H2'	2:5:4744:G:O4'	2.12	0.50
2:5:4786:C:C5'	2:5:4789:C:H5	2.25	0.50
23:Q:132:LYS:H	23:Q:134:ARG:NH1	2.10	0.50
27:K:62:PHE:CE2	27:K:64:TRP:HB2	2.47	0.50
27:K:72:ASN:H	27:K:78:GLU:HA	1.77	0.50
27:K:151:ILE:O	27:K:154:GLN:HG2	2.12	0.50
27:K:207:MET:HE2	27:K:218:HIS:HD2	1.76	0.50
44:Y:62:TYR:CE2	44:Y:97:VAL:HG11	2.47	0.50
2:5:799:C:O2'	2:5:800:U:H5'	2.12	0.50
2:5:1271:C:H2'	2:5:1272:G:H8	1.77	0.50
2:5:1471:G:O2'	38:L:18:TRP:NE1	2.39	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:2434:A:H2'	2:5:2435:U:H6	1.77	0.50
14:A:104:VAL:HA	14:A:107:MET:CE	2.40	0.50
28:C:207:PRO:HG2	28:C:227:ILE:HD13	1.93	0.50
35:g:46:CYS:HB2	35:g:86:CYS:SG	2.50	0.50
36:k:67:LYS:C	36:k:67:LYS:HD3	2.37	0.50
1:T:5:LYS:HD2	2:5:4048:U:H4'	1.94	0.50
2:5:152:U:P	40:N:49:ARG:HH21	2.35	0.50
2:5:217:C:H4'	2:5:218:A:O5'	2.11	0.50
2:5:417:G:N3	9:8:16:G:C2	2.80	0.50
2:5:753:G:C5	2:5:754:G:C8	3.00	0.50
2:5:1288:C:H2'	2:5:1289:A:C8	2.47	0.50
2:5:1385:C:OP1	23:Q:134:ARG:HB3	2.11	0.50
2:5:1929:A:H3'	2:5:1930:A:N3	2.27	0.50
2:5:3335:G:N2	2:5:3336:A:N1	2.60	0.50
2:5:3489:G:N1	2:5:3500:U:C2	2.80	0.50
9:8:67:U:H2'	9:8:68:G:C8	2.47	0.50
10:G:218:GLU:CD	40:N:11:TRP:HE1	2.20	0.50
45:X:94:ASN:O	45:X:94:ASN:ND2	2.42	0.50
2:5:162:A:H2'	2:5:163:A:C8	2.46	0.49
2:5:181:C:H2'	2:5:182:G:C8	2.47	0.49
2:5:186:G:H21	2:5:186:G:P	2.34	0.49
2:5:1103:G:H5''	3:F:62:GLN:OE1	2.11	0.49
2:5:1866:U:OP1	2:5:1888:U:O2'	2.20	0.49
2:5:4206:U:H2'	2:5:4207:C:H6	1.77	0.49
2:5:4649:A:H4'	7:B:95:THR:HG22	1.93	0.49
5:S:13:VAL:HG22	5:S:63:TYR:HB3	1.92	0.49
16:q:65:ILE:HG13	27:K:49:PRO:HG2	1.93	0.49
33:Z:29:ILE:HD11	33:Z:98:LYS:HD2	1.93	0.49
36:k:7:GLU:CD	36:k:9:LYS:H	2.20	0.49
37:H:41:ILE:HG21	37:H:73:ILE:CD1	2.41	0.49
2:5:394:G:N2	2:5:397:G:OP2	2.33	0.49
2:5:456:C:H2'	2:5:457:G:C8	2.47	0.49
2:5:804:C:H2'	2:5:805:G:C8	2.48	0.49
2:5:1434:G:H2'	2:5:1435:C:C6	2.47	0.49
2:5:2334:C:H2'	2:5:2335:C:H6	1.75	0.49
2:5:2391:C:H2'	2:5:2392:G:H8	1.76	0.49
2:5:3854:C:OP1	10:G:90:LYS:NZ	2.43	0.49
2:5:4440:G:H4'	37:H:71:ARG:HH12	1.77	0.49
28:C:116:ASN:HB2	28:C:119:GLN:HG3	1.94	0.49
40:N:124:ASP:OD1	40:N:126:THR:N	2.38	0.49
2:5:1100:U:O2'	2:5:1102:G:H5'	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:3652:U:H2'	2:5:3653:U:C6	2.48	0.49
2:5:4408:C:O2'	2:5:4743:C:OP1	2.30	0.49
4:D:258:LYS:NZ	4:D:259:ARG:O	2.42	0.49
25:W:47:ARG:HG2	25:W:47:ARG:HH11	1.76	0.49
27:K:23:GLU:HA	27:K:173:TYR:CE1	2.47	0.49
27:K:263:VAL:HB	27:K:281:ILE:HB	1.93	0.49
27:K:282:LYS:HZ3	27:K:455:TYR:HE2	1.59	0.49
30:r:85:ASN:N	30:r:85:ASN:OD1	2.45	0.49
45:X:129:ARG:NH2	45:X:131:ASP:OD2	2.45	0.49
2:5:99:A:H2'	2:5:100:C:O2	2.13	0.49
2:5:233:U:H2'	2:5:234:G:C8	2.46	0.49
2:5:660:G:OP2	30:r:67:ARG:NH2	2.45	0.49
2:5:1271:C:H2'	2:5:1272:G:C8	2.47	0.49
2:5:2573:U:H2'	2:5:2574:C:C6	2.47	0.49
2:5:2602:G:O2'	2:5:2603:G:O4'	2.19	0.49
2:5:3984:G:H2'	2:5:3985:A:H8	1.78	0.49
8:d:59:THR:HG22	8:d:102:LEU:HB2	1.94	0.49
9:8:49:G:OP1	42:h:48:ARG:NH1	2.46	0.49
28:C:79:VAL:O	28:C:88:GLY:N	2.40	0.49
31:f:14:TYR:OH	31:f:92:LEU:O	2.26	0.49
37:H:81:ILE:O	37:H:85:THR:HG23	2.12	0.49
38:L:42:ARG:O	38:L:46:ILE:HG12	2.12	0.49
2:5:469:C:H2'	2:5:470:A:H8	1.77	0.49
2:5:882:U:H2'	2:5:883:C:C6	2.47	0.49
2:5:3940:U:H4'	2:5:3941:G:OP1	2.11	0.49
11:J:66:GLU:OE1	11:J:66:GLU:N	2.45	0.49
16:q:55:LYS:HE2	27:K:193:TRP:HA	1.95	0.49
27:K:169:LEU:CD2	27:K:177:SER:HA	2.43	0.49
40:N:138:PHE:HA	40:N:143:ARG:HD2	1.94	0.49
2:5:406:C:O2'	2:5:407:A:OP1	2.27	0.49
2:5:804:C:H2'	2:5:805:G:H8	1.77	0.49
2:5:1387:G:H1'	2:5:1407:A:N6	2.28	0.49
2:5:1392:C:C2'	2:5:1393:C:OP1	2.60	0.49
2:5:2654:G:N1	2:5:2657:C:OP2	2.31	0.49
2:5:3588:A:OP1	21:P:82:ARG:HG2	2.12	0.49
2:5:4081:C:H2'	2:5:4082:A:C8	2.48	0.49
2:5:4434:C:H2'	2:5:4435:U:C6	2.47	0.49
2:5:4687:C:H2'	2:5:4688:G:N2	2.27	0.49
16:q:47:MET:HA	16:q:50:ILE:HG22	1.95	0.49
17:p:61:MET:HG2	35:g:48:VAL:O	2.12	0.49
24:R:151:ARG:HE	24:R:151:ARG:C	2.19	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:K:448:LEU:O	27:K:452:THR:HG22	2.12	0.49
41:i:68:ARG:HA	41:i:68:ARG:NH1	2.27	0.49
2:5:718:C:OP1	28:C:350:ARG:NH1	2.41	0.49
2:5:4383:OMG:H2'	2:5:4384:U:C6	2.48	0.49
7:B:189:THR:N	7:B:192:GLU:OE2	2.45	0.49
9:8:142:U:OP1	40:N:38:ARG:NH2	2.42	0.49
10:G:235:CYS:HB3	10:G:275:ILE:HD13	1.94	0.49
14:A:47:ASP:OD1	14:A:48:ILE:N	2.44	0.49
26:O:199:HIS:NE2	43:M:108:ASP:HB3	2.28	0.49
27:K:86:THR:O	27:K:87:SER:C	2.56	0.49
27:K:113:ASN:O	27:K:117:LYS:HG2	2.13	0.49
27:K:337:PRO:O	27:K:343:HIS:HB2	2.13	0.49
32:e:89:LEU:HD13	32:e:118:LEU:HD22	1.93	0.49
2:5:1299:G:OP1	23:Q:108:ARG:NH2	2.45	0.49
2:5:1457:G:H22	34:a:77:LYS:NZ	2.11	0.49
2:5:4733:G:H2'	2:5:4734:U:C6	2.48	0.49
8:d:93:ASN:OD1	8:d:94:GLU:N	2.46	0.49
26:O:9:LEU:HB2	26:O:35:VAL:HG23	1.95	0.49
26:O:185:VAL:CG2	43:M:126:GLU:HG2	2.43	0.49
27:K:251:VAL:HG21	27:K:447:ILE:HD13	1.95	0.49
27:K:289:ILE:N	27:K:290:PRO:HD2	2.28	0.49
31:f:10:ILE:HD11	31:f:100:ARG:HH21	1.78	0.49
33:Z:115:LYS:NZ	33:Z:119:GLU:OE2	2.34	0.49
37:H:44:GLU:OE1	43:M:2:VAL:HA	2.13	0.49
1:T:87:LYS:HZ2	2:5:4051:G:H1	1.61	0.49
2:5:645:C:H2'	2:5:646:G:C8	2.47	0.49
2:5:1641:C:O3'	6:b:18:ARG:HD2	2.13	0.49
2:5:1785:G:H2'	2:5:1786:C:H6	1.77	0.49
2:5:2190:A:C5	32:e:31:ILE:HD11	2.48	0.49
2:5:4254:C:N3	2:5:4258:U:H5	2.11	0.49
2:5:4598:C:H2'	2:5:4599:G:C8	2.46	0.49
7:B:138:GLN:OE1	7:B:138:GLN:N	2.43	0.49
16:q:16:LYS:O	16:q:19:ILE:HD12	2.12	0.49
34:a:85:GLN:HA	34:a:88:VAL:HG12	1.95	0.49
39:7:23:A:H2'	39:7:24:C:C6	2.47	0.49
43:M:59:ASP:OD1	43:M:59:ASP:N	2.37	0.49
2:5:424:U:H2'	2:5:425:U:C6	2.48	0.49
2:5:1325:U:O2	2:5:1325:U:O4'	2.31	0.49
2:5:4278:U:OP2	2:5:4300:G:N1	2.39	0.49
2:5:4660:C:H2'	2:5:4661:C:H6	1.77	0.49
4:D:104:LEU:HD11	4:D:108:ARG:HH21	1.78	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:Q:178:ARG:N	34:a:51:GLY:HA2	2.27	0.49
27:K:271:ARG:O	27:K:271:ARG:CG	2.58	0.49
38:L:61:CYS:SG	38:L:71:ARG:HG3	2.53	0.49
45:X:55:ARG:HB2	45:X:55:ARG:HH11	1.78	0.49
2:5:1346:C:H2'	2:5:1347:G:C8	2.46	0.48
2:5:3620:G:O2'	2:5:3621:G:OP1	2.28	0.48
2:5:4309:U:H2'	2:5:4310:A:C8	2.48	0.48
3:F:218:GLY:O	3:F:245:ARG:NH2	2.46	0.48
6:b:89:VAL:N	6:b:94:HIS:HE1	2.11	0.48
9:8:66:A:H2'	9:8:67:U:C6	2.48	0.48
14:A:137:ILE:HD11	14:A:149:LYS:HB2	1.95	0.48
16:q:3:GLN:O	16:q:6:GLN:HG3	2.12	0.48
28:C:275:SER:OG	28:C:276:ASN:N	2.46	0.48
33:Z:115:LYS:O	33:Z:119:GLU:HG3	2.12	0.48
37:H:24:THR:HA	37:H:37:ASP:HA	1.95	0.48
38:L:5:ARG:HB2	38:L:5:ARG:NH1	2.28	0.48
44:Y:55:VAL:HG11	44:Y:104:VAL:HG22	1.94	0.48
2:5:422:C:H2'	2:5:423:G:H8	1.77	0.48
2:5:511:A:O3'	38:L:163:LYS:NZ	2.41	0.48
2:5:1624:A:H4'	2:5:1640:G:N2	2.28	0.48
2:5:2029:U:OP2	28:C:307:LYS:NZ	2.46	0.48
2:5:2639:G:H5'	20:l:45:ARG:HH21	1.78	0.48
2:5:3866:C:H2'	2:5:3867:C:C6	2.48	0.48
2:5:4508:G:H2'	2:5:4509:A:C8	2.48	0.48
14:A:57:PRO:HB3	17:p:54:ILE:HD11	1.94	0.48
15:I:208:LYS:HB2	15:I:208:LYS:NZ	2.28	0.48
16:q:47:MET:CE	27:K:188:CYS:HB3	2.43	0.48
27:K:109:ARG:C	27:K:111:LEU:N	2.71	0.48
27:K:267:ILE:HG13	27:K:279:TYR:HB2	1.95	0.48
34:a:98:ALA:HB2	34:a:121:PRO:HB2	1.95	0.48
2:5:271:C:H2'	2:5:272:U:H6	1.77	0.48
2:5:398:A2M:O5'	2:5:398:A2M:H8	2.14	0.48
2:5:3836:G:H2'	2:5:3837:G:C8	2.45	0.48
2:5:3953:C:H5''	2:5:4081:C:H5'	1.92	0.48
2:5:4519:C:O2	2:5:4519:C:O4'	2.29	0.48
2:5:4660:C:O2'	2:5:4661:C:OP1	2.30	0.48
3:F:46:ARG:HH21	28:C:330:PRO:HD3	1.79	0.48
17:p:84:ARG:O	17:p:88:GLU:HG2	2.13	0.48
26:O:110:PRO:N	26:O:111:PRO:HD2	2.28	0.48
27:K:72:ASN:HB3	27:K:75:THR:OG1	2.14	0.48
30:r:47:LYS:HG2	30:r:102:TYR:CE1	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:251:C:H2'	2:5:252:C:C6	2.48	0.48
2:5:271:C:H2'	2:5:272:U:C6	2.49	0.48
2:5:664:G:H2'	2:5:665:G:C8	2.44	0.48
2:5:1134:G:N2	2:5:1207:G:O6	2.46	0.48
2:5:2266:A:H2'	2:5:2267:OMG:C8	2.48	0.48
2:5:2291:G:H2'	2:5:2292:A:C8	2.49	0.48
2:5:3445:U:H3'	2:5:3446:G:H5''	1.95	0.48
2:5:3817:G:H2'	2:5:3818:G:H8	1.77	0.48
2:5:4661:C:H2'	2:5:4662:U:H6	1.79	0.48
11:J:44:THR:HG23	11:J:46:GLN:HG2	1.94	0.48
18:V:108:ASN:OD1	18:V:109:LYS:N	2.46	0.48
22:E:202:THR:HG21	43:M:107:PHE:HB2	1.95	0.48
27:K:302:TYR:CE1	27:K:342:CYS:HB3	2.48	0.48
37:H:91:LYS:HD2	37:H:143:GLU:OE2	2.13	0.48
44:Y:22:PRO:O	44:Y:26:ARG:HG2	2.12	0.48
44:Y:47:MET:HE3	44:Y:48:PRO:HD2	1.95	0.48
1:T:119:ALA:HA	1:T:122:LYS:HB2	1.94	0.48
2:5:1750:G:H2'	2:5:1751:C:H6	1.77	0.48
8:d:94:GLU:HB2	8:d:97:ASP:OD2	2.12	0.48
10:G:91:ASN:ND2	10:G:96:GLN:OE1	2.47	0.48
17:p:32:SER:OG	17:p:69:TRP:O	2.31	0.48
19:m:56:LEU:HD11	37:H:93:ARG:HE	1.78	0.48
43:M:105:THR:OG1	43:M:106:ASP:N	2.37	0.48
45:X:89:LYS:HG3	45:X:95:THR:CG2	2.43	0.48
1:T:36:LYS:HB2	1:T:36:LYS:NZ	2.28	0.48
2:5:693:C:H2'	2:5:694:G:H8	1.79	0.48
2:5:754:G:H4'	37:H:50:LYS:CE	2.43	0.48
2:5:1300:U:H2'	2:5:1301:C:C6	2.49	0.48
2:5:1408:G:O2'	2:5:1409:G:H5'	2.14	0.48
2:5:1916:C:C2	2:5:1929:A:N6	2.81	0.48
2:5:2026:C:OP2	23:Q:37:ARG:NH1	2.44	0.48
2:5:2444:A:N6	2:5:2587:A:OP2	2.46	0.48
2:5:4249:A:H2'	2:5:4250:C:C6	2.48	0.48
8:d:70:LYS:HB2	8:d:70:LYS:HE3	1.58	0.48
14:A:225:ILE:HD11	14:A:233:ARG:HG3	1.94	0.48
15:I:86:HIS:HB3	15:I:139:ARG:HG2	1.95	0.48
20:I:31:THR:OG1	20:I:32:GLY:N	2.46	0.48
23:Q:40:ASN:OD1	23:Q:132:LYS:NZ	2.47	0.48
24:R:39:GLN:OE1	24:R:42:ARG:NH1	2.47	0.48
30:r:58:LYS:HB3	30:r:58:LYS:HE3	1.64	0.48
34:a:103:VAL:HB	34:a:108:TYR:HB2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:M:24:LEU:HD11	43:M:86:TRP:CG	2.48	0.48
43:M:86:TRP:O	43:M:89:THR:HG22	2.14	0.48
1:T:102:ARG:HH21	1:T:105:PHE:HE2	1.62	0.48
2:5:93:G:H2'	2:5:94:A:C8	2.49	0.48
2:5:667:C:H2'	2:5:668:G:C8	2.48	0.48
2:5:799:C:C4	2:5:800:U:C4	3.01	0.48
2:5:2265:OMC:H1'	2:5:2265:OMC:HM23	1.61	0.48
2:5:2538:A:H4'	2:5:2539:A:O5'	2.14	0.48
2:5:2680:U:OP1	7:B:249:ARG:NH1	2.45	0.48
28:C:209:VAL:HB	28:C:229:LEU:HD13	1.96	0.48
30:r:36:ASN:HD22	30:r:36:ASN:C	2.20	0.48
34:a:122:VAL:C	34:a:123:ILE:HD13	2.38	0.48
37:H:103:VAL:HG11	37:H:144:LEU:HD11	1.95	0.48
2:5:2360:A:O2'	35:g:66:ARG:NH2	2.47	0.48
2:5:3895:C:P	33:Z:60:LYS:HZ3	2.37	0.48
2:5:4515:G:O2'	2:5:4612:G:O6	2.31	0.48
2:5:4630:G:O6	2:5:4631:A:N6	2.47	0.48
3:F:198:LYS:NZ	3:F:198:LYS:HB3	2.29	0.48
5:S:96:GLU:OE2	5:S:139:ARG:N	2.44	0.48
11:J:56:THR:HG23	11:J:63:ARG:HA	1.95	0.48
44:Y:52:ASP:OD1	44:Y:110:LYS:HD2	2.14	0.48
2:5:295:A:OP2	29:o:39:ARG:NH2	2.27	0.48
2:5:3343:A:H2	2:5:4755:A:H8	1.61	0.48
2:5:3890:G:H2'	2:5:3891:G:C8	2.49	0.48
2:5:3931:G:O2'	2:5:3932:A:H5'	2.13	0.48
2:5:4149:PSU:O2'	2:5:4150:U:H5'	2.13	0.48
2:5:4517:U:H2'	2:5:4518:C:C5	2.49	0.48
15:I:146:GLU:OE1	15:I:146:GLU:N	2.47	0.48
27:K:158:ALA:O	27:K:161:ILE:HG13	2.14	0.48
27:K:359:VAL:O	27:K:363:VAL:HG23	2.14	0.48
27:K:412:GLU:CD	27:K:415:ARG:HH12	2.21	0.48
2:5:426:A:H2'	2:5:427:A:H8	1.79	0.48
2:5:1088:C:H2'	2:5:1089:G:C8	2.49	0.48
2:5:2581:C:O2'	2:5:2583:U:O2	2.31	0.48
2:5:3468:A:H2'	2:5:3469:A:C8	2.49	0.48
2:5:3857:G:H1'	10:G:87:LYS:HZ3	1.78	0.48
2:5:4206:U:H2'	2:5:4207:C:C6	2.49	0.48
2:5:4213:A:O2'	2:5:4256:A:N3	2.39	0.48
2:5:4664:U:H4'	2:5:4665:C:O5'	2.14	0.48
24:R:97:ARG:O	24:R:101:ILE:HG13	2.13	0.48
27:K:207:MET:O	27:K:207:MET:CG	2.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:k:51:GLU:HA	36:k:54:GLU:OE1	2.14	0.48
39:7:57:C:H2'	39:7:58:A:H8	1.79	0.48
45:X:55:ARG:HB2	45:X:55:ARG:NH1	2.28	0.48
2:5:728:G:C2	2:5:729:G:C8	3.01	0.47
2:5:757:A:H3'	2:5:758:C:C5'	2.43	0.47
2:5:1127:G:H2'	2:5:1128:C:C6	2.48	0.47
2:5:1457:G:H1	34:a:77:LYS:HE2	1.79	0.47
2:5:3636:G:O2'	2:5:3637:A:OP1	2.31	0.47
7:B:74:GLU:OE1	7:B:285:TYR:OH	2.32	0.47
24:R:159:ALA:HB1	24:R:162:ARG:NH2	2.29	0.47
1:T:87:LYS:HZ2	2:5:4051:G:N2	2.12	0.47
2:5:6:C:H2'	2:5:7:C:H6	1.79	0.47
2:5:1572:G:H1'	2:5:2356:A:N6	2.28	0.47
2:5:1929:A:C5	2:5:1930:A:C6	3.01	0.47
2:5:4205:U:H2'	2:5:4206:U:H6	1.78	0.47
2:5:4227:U:H2'	2:5:4228:U:H6	1.79	0.47
3:F:220:LYS:HD2	3:F:220:LYS:HA	1.59	0.47
4:D:21:ARG:O	4:D:25:GLU:HG3	2.13	0.47
5:S:76:LYS:NZ	5:S:100:LEU:O	2.38	0.47
9:8:75:G:OP2	44:Y:74:TYR:OH	2.25	0.47
15:I:171:TRP:O	15:I:174:THR:OG1	2.26	0.47
33:Z:13:VAL:HG12	33:Z:21:ARG:O	2.14	0.47
35:g:82:MET:HE1	35:g:90:ARG:CZ	2.43	0.47
44:Y:69:LYS:N	44:Y:83:GLU:OE1	2.47	0.47
46:U:37:ALA:HA	46:U:40:GLU:OE2	2.14	0.47
1:T:72:VAL:HG12	1:T:74:ILE:HG23	1.96	0.47
2:5:132:G:N2	2:5:137:G:C2	2.83	0.47
2:5:699:G:H2'	2:5:700:C:C6	2.49	0.47
2:5:805:G:H2'	2:5:806:G:H8	1.79	0.47
2:5:871:U:H2'	2:5:872:G:C8	2.49	0.47
2:5:1343:G:H2'	2:5:1344:G:C8	2.48	0.47
2:5:1666:U:H2'	2:5:1667:U:C6	2.50	0.47
2:5:2477:C:H2'	2:5:2478:U:H6	1.79	0.47
2:5:4090:U:H2'	2:5:4091:C:C6	2.49	0.47
2:5:4648:A:H2'	7:B:156:TYR:CD2	2.49	0.47
14:A:158:ILE:HG23	14:A:162:ASN:HD21	1.79	0.47
18:V:131:ARG:O	18:V:134:SER:OG	2.31	0.47
22:E:257:ASP:OD1	22:E:258:SER:N	2.47	0.47
27:K:72:ASN:ND2	27:K:75:THR:HG21	2.29	0.47
2:5:134:G:H4'	2:5:135:G:O5'	2.13	0.47
2:5:639:G:H2'	2:5:640:G:H8	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:821:C:H2'	2:5:822:C:C6	2.48	0.47
2:5:1095:C:H2'	2:5:1096:G:C8	2.49	0.47
2:5:2018:G:H2'	2:5:2019:U:C6	2.49	0.47
2:5:2433:G:H2'	2:5:2597:G:N2	2.30	0.47
2:5:2503:A:OP1	24:R:117:ARG:NH2	2.47	0.47
2:5:4639:C:OP2	2:5:4640:G:H3'	2.14	0.47
11:J:47:THR:HG23	39:7:39:C:H4'	1.96	0.47
26:O:186:GLU:OE1	26:O:186:GLU:N	2.48	0.47
2:5:858:G:O2'	22:E:126:ARG:O	2.33	0.47
2:5:1210:C:H5''	6:b:107:ARG:HH22	1.79	0.47
2:5:1398:A:H3'	2:5:1399:G:C8	2.50	0.47
2:5:3556:A:H2'	2:5:3557:A2M:H8	1.96	0.47
2:5:4388:U:H2'	2:5:4389:G:H8	1.79	0.47
26:O:61:ARG:HA	26:O:70:PRO:HD2	1.95	0.47
36:k:8:ILE:HD11	36:k:56:LEU:HD12	1.95	0.47
43:M:42:CYS:SG	43:M:74:ARG:HG3	2.55	0.47
2:5:877:C:H5''	3:F:46:ARG:NH1	2.30	0.47
2:5:884:U:OP1	22:E:75:TYR:OH	2.22	0.47
2:5:3459:A:H2'	2:5:3460:A:C8	2.48	0.47
2:5:4517:U:H2'	2:5:4518:C:C6	2.50	0.47
14:A:234:LYS:HG2	14:A:238:ILE:HG12	1.96	0.47
27:K:456:GLN:O	27:K:459:GLU:HG3	2.13	0.47
31:f:6:TRP:HB3	31:f:104:MET:HG3	1.97	0.47
33:Z:66:SER:HB2	33:Z:122:TYR:HE2	1.79	0.47
34:a:100:ILE:HG12	34:a:123:ILE:HB	1.96	0.47
2:5:37:U:H4'	34:a:32:ARG:HD2	1.97	0.47
2:5:647:C:H2'	2:5:648:C:C6	2.50	0.47
2:5:800:U:H2'	2:5:801:C:C5	2.50	0.47
2:5:1102:G:H2'	2:5:1103:G:H8	1.78	0.47
2:5:1744:A:N1	6:b:27:GLN:HA	2.30	0.47
2:5:2011:C:OP1	23:Q:2:GLY:N	2.48	0.47
2:5:2217:A:H2'	2:5:2218:A:C8	2.50	0.47
2:5:3450:A2M:H2	2:5:3666:G:O4'	2.15	0.47
2:5:4733:G:H2'	2:5:4734:U:H6	1.80	0.47
3:F:227:VAL:HA	5:S:39:VAL:HG12	1.96	0.47
3:F:237:ASP:O	3:F:240:ASN:ND2	2.48	0.47
4:D:236:MET:HA	4:D:239:MET:HG2	1.97	0.47
7:B:43:LEU:HB2	7:B:210:VAL:HG22	1.97	0.47
14:A:30:ARG:O	14:A:163:ARG:NH2	2.48	0.47
15:I:54:SER:HB2	15:I:135:ILE:HD11	1.97	0.47
21:P:6:LEU:HD12	21:P:6:LEU:HA	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
26:O:202:LEU:HD23	26:O:202:LEU:HA	1.79	0.47
27:K:246:ILE:O	27:K:249:ILE:HG12	2.15	0.47
27:K:294:GLN:O	27:K:297:LEU:HG	2.15	0.47
37:H:117:PHE:O	37:H:120:GLU:HB2	2.15	0.47
46:U:20:LYS:O	46:U:108:GLU:HB2	2.15	0.47
2:5:125:C:H2'	2:5:126:C:C6	2.48	0.47
2:5:1086:G:H2'	2:5:1087:G:C8	2.49	0.47
2:5:2512:C:H2'	2:5:2513:C:O4'	2.15	0.47
2:5:4090:U:H2'	2:5:4091:C:H6	1.80	0.47
2:5:4116:OMG:HM23	2:5:4116:OMG:H1'	1.46	0.47
2:5:4364:G:H5''	18:V:15:ARG:HB2	1.96	0.47
2:5:4381:A:H8	2:5:4787:A:N6	2.06	0.47
2:5:4709:C:C2	2:5:4710:A:C8	3.03	0.47
7:B:199:GLU:OE1	7:B:199:GLU:N	2.39	0.47
9:8:76:C:C2	9:8:77:A:C8	3.03	0.47
22:E:216:THR:H	22:E:219:TYR:HB3	1.80	0.47
24:R:165:LYS:O	24:R:168:GLU:HG3	2.14	0.47
27:K:399:MET:HA	27:K:399:MET:HE3	1.96	0.47
43:M:41:PRO:HG3	43:M:73:VAL:HG12	1.96	0.47
2:5:23:C:H2'	2:5:24:G:O4'	2.15	0.47
2:5:253:G:H2'	2:5:254:G:H8	1.80	0.47
2:5:1387:G:C6	2:5:1406:G:C6	3.02	0.47
2:5:1632:PSU:O2'	2:5:1633:C:H5'	2.15	0.47
2:5:2109:C:H4'	2:5:2110:U:O5'	2.14	0.47
2:5:4685:U:O2'	31:f:2:SER:O	2.26	0.47
27:K:21:LYS:HZ1	27:K:168:LEU:HD12	1.68	0.47
35:g:46:CYS:HB3	35:g:86:CYS:SG	2.54	0.47
38:L:55:ILE:HG23	38:L:76:PHE:HE2	1.80	0.47
2:5:184:U:H3	2:5:253:G:H1	1.63	0.47
2:5:1500:G:H2'	2:5:1501:C:C6	2.49	0.47
2:5:1911:G:H2'	2:5:1912:G:C8	2.50	0.47
2:5:2221:G:O2'	2:5:2223:G:N7	2.44	0.47
2:5:3386:G:O2'	2:5:3425:U:OP1	2.27	0.47
2:5:3892:G:H2'	2:5:3893:G:H8	1.79	0.47
2:5:3984:G:H2'	2:5:3985:A:C8	2.49	0.47
2:5:4414:U:OP1	7:B:226:LYS:HE2	2.15	0.47
3:F:143:TYR:HE2	3:F:236:GLU:HG3	1.80	0.47
7:B:56:ILE:O	7:B:73:VAL:HA	2.15	0.47
15:I:45:GLU:OE1	15:I:45:GLU:N	2.48	0.47
16:q:19:ILE:HD12	16:q:20:ARG:N	2.30	0.47
27:K:168:LEU:HD23	27:K:173:TYR:CB	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
33:Z:103:ASP:C	33:Z:103:ASP:OD1	2.58	0.47
2:5:429:A:H2'	2:5:430:G:C8	2.50	0.46
2:5:2019:U:H2'	2:5:2020:C:C6	2.50	0.46
2:5:3380:A:H1'	2:5:3517:A:H61	1.79	0.46
4:D:59:ASP:OD1	4:D:60:ILE:N	2.48	0.46
4:D:234:ASP:N	4:D:234:ASP:OD1	2.47	0.46
5:S:100:LEU:HD21	43:M:31:ILE:HD11	1.96	0.46
2:5:798:C:H2'	2:5:799:C:C6	2.50	0.46
2:5:1334:G:N2	2:5:1337:G:OP2	2.34	0.46
2:5:1394:U:O2	3:F:33:ARG:NH2	2.48	0.46
2:5:1600:C:OP1	28:C:80:ARG:NH1	2.46	0.46
2:5:2518:G:N7	12:c:32:LYS:HG3	2.30	0.46
2:5:3380:A:C4	2:5:3517:A:N6	2.83	0.46
2:5:3580:U:H2'	2:5:3581:A:C8	2.51	0.46
2:5:3666:G:H2'	2:5:3667:C:C6	2.50	0.46
2:5:3862:C:H2'	2:5:3863:G:C8	2.48	0.46
9:8:153:C:H2'	9:8:154:G:H8	1.80	0.46
22:E:113:ARG:NE	22:E:113:ARG:HA	2.30	0.46
27:K:62:PHE:CE2	27:K:299:SER:HA	2.50	0.46
44:Y:56:GLN:HB2	44:Y:105:VAL:HG13	1.96	0.46
2:5:257:C:H2'	2:5:258:G:C8	2.50	0.46
2:5:522:U:H2'	2:5:523:C:C6	2.51	0.46
2:5:2217:A:H2'	2:5:2218:A:H8	1.80	0.46
2:5:2338:U:H2'	2:5:2339:G:H8	1.80	0.46
2:5:3602:C:O3'	7:B:261:ARG:NH2	2.49	0.46
2:5:3682:U:O4	2:5:3792:C:H1'	2.15	0.46
2:5:4792:U:H3'	2:5:4793:C:C6	2.50	0.46
5:S:15:ARG:HG3	5:S:16:CYS:O	2.14	0.46
9:8:51:U:H4'	20:l:21:ARG:NH1	2.30	0.46
37:H:92:MET:HE2	37:H:179:ILE:HG22	1.96	0.46
39:7:4:U:H2'	39:7:5:A:H8	1.80	0.46
39:7:92:C:H2'	39:7:93:G:H8	1.80	0.46
44:Y:26:ARG:O	44:Y:30:MET:HG3	2.15	0.46
2:5:7:C:H2'	2:5:8:U:C6	2.51	0.46
2:5:1098:C:H2'	2:5:1099:G:C8	2.50	0.46
2:5:1449:U:H2'	2:5:1450:G:H8	1.79	0.46
2:5:1647:C:H5''	23:Q:53:MET:SD	2.55	0.46
2:5:2101:C:H5''	2:5:2102:G:C8	2.51	0.46
2:5:2222:A:H2'	2:5:2223:G:O4'	2.15	0.46
2:5:2382:C:H2'	2:5:2383:C:H6	1.79	0.46
2:5:2391:C:H2'	2:5:2392:G:C8	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:2712:U:O2'	2:5:2724:A:N7	2.43	0.46
2:5:3500:U:H2'	2:5:3501:C:H6	1.80	0.46
2:5:3929:G:H2'	2:5:3929:G:N3	2.31	0.46
2:5:4687:C:H3'	2:5:4688:G:H5''	1.96	0.46
2:5:4794:G:H2'	2:5:4795:A:C8	2.51	0.46
5:S:99:ASP:OD1	5:S:100:LEU:N	2.49	0.46
10:G:217:ILE:HG13	10:G:221:VAL:CG1	2.43	0.46
16:q:9:GLU:O	16:q:13:GLN:HG3	2.16	0.46
26:O:54:TYR:CE2	26:O:145:VAL:HG11	2.50	0.46
27:K:343:HIS:NE2	27:K:357:ASP:OD2	2.43	0.46
40:N:35:ALA:HA	40:N:65:ARG:HG2	1.97	0.46
40:N:158:HIS:HB3	40:N:161:MET:HB2	1.96	0.46
1:T:22:HIS:O	4:D:17:GLN:NE2	2.39	0.46
1:T:121:GLU:OE2	1:T:122:LYS:NZ	2.36	0.46
2:5:757:A:N6	2:5:759:G:O6	2.48	0.46
2:5:1713:C:H2'	2:5:1714:A:O4'	2.16	0.46
2:5:1845:U:H2'	2:5:1846:A:H8	1.79	0.46
2:5:2362:U:H1'	2:5:2363:C:C6	2.51	0.46
2:5:2517:A:N6	17:p:42:CYS:HA	2.30	0.46
2:5:3683:G:O2'	2:5:3684:A:H5'	2.16	0.46
2:5:4117:G:O2'	2:5:4118:U:P	2.74	0.46
2:5:4218:G:O2'	19:m:74:TYR:O	2.34	0.46
2:5:4340:U:H2'	2:5:4341:G:C8	2.50	0.46
2:5:4773:A:H2'	2:5:4774:U:O4'	2.16	0.46
11:J:23:ASN:OD1	11:J:129:ASP:HB2	2.15	0.46
14:A:17:ARG:HG3	14:A:17:ARG:NH1	2.30	0.46
17:p:84:ARG:HB3	17:p:84:ARG:CZ	2.46	0.46
23:Q:35:LEU:HB3	23:Q:44:ASN:ND2	2.31	0.46
27:K:345:LEU:O	27:K:364:TYR:HD1	1.98	0.46
2:5:263:G:O2'	2:5:264:C:H5'	2.15	0.46
2:5:512:U:O4'	34:a:85:GLN:NE2	2.47	0.46
2:5:1397:C:O2	2:5:2051:G:N1	2.43	0.46
2:5:1891:G:OP1	5:S:139:ARG:NE	2.49	0.46
2:5:2360:A:N3	2:5:2382:C:O2'	2.48	0.46
2:5:2433:G:H2'	2:5:2597:G:H22	1.81	0.46
2:5:2737:A:H2'	2:5:2738:A:C8	2.50	0.46
2:5:4124:A:O2'	2:5:4125:A:H2'	2.15	0.46
7:B:300:LYS:HG2	7:B:313:SER:HB3	1.98	0.46
7:B:310:SER:OG	7:B:311:ASP:N	2.49	0.46
22:E:70:LEU:HA	22:E:73:ARG:HB2	1.97	0.46
23:Q:39:THR:HG21	23:Q:132:LYS:HG2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:K:23:GLU:HA	27:K:173:TYR:HE1	1.81	0.46
27:K:267:ILE:HG22	27:K:399:MET:HE2	1.98	0.46
40:N:33:LEU:HD13	40:N:37:HIS:CE1	2.51	0.46
2:5:299:C:H2'	2:5:300:A:C8	2.51	0.46
2:5:1128:C:H2'	2:5:1129:G:O4'	2.16	0.46
2:5:1415:C:H2'	2:5:1416:C:C6	2.50	0.46
2:5:1758:G:C4	4:D:113:PHE:CE1	3.04	0.46
2:5:2107:C:OP1	30:r:112:ARG:NH1	2.49	0.46
2:5:2258:U:H2'	2:5:2259:G:C8	2.51	0.46
2:5:2568:A:N6	24:R:88:ARG:O	2.48	0.46
2:5:3331:A:H2'	2:5:3332:G:H8	1.81	0.46
2:5:3506:A:H2'	2:5:3507:A:N3	2.30	0.46
2:5:3866:C:H2'	2:5:3867:C:H6	1.80	0.46
2:5:3982:G:H2'	2:5:3983:C:H6	1.81	0.46
5:S:84:TYR:HE1	5:S:93:MET:HE3	1.81	0.46
7:B:312:LYS:NZ	7:B:368:ILE:O	2.49	0.46
10:G:184:LYS:NZ	10:G:185:ARG:O	2.48	0.46
2:5:275:C:O2'	2:5:276:C:O5'	2.30	0.46
2:5:370:U:O3'	13:j:25:LYS:NZ	2.47	0.46
2:5:851:G:H2'	2:5:852:G:H8	1.81	0.46
2:5:1427:C:H2'	2:5:1428:U:C6	2.51	0.46
2:5:2255:A:H2'	2:5:2256:U:C6	2.51	0.46
2:5:2287:U:O2'	9:8:112:G:O2'	2.32	0.46
2:5:2444:A:N6	2:5:2586:A:H3'	2.31	0.46
2:5:3419:A:OP2	14:A:10:LYS:NZ	2.49	0.46
2:5:3508:G:OP2	2:5:3508:G:N2	2.45	0.46
2:5:3932:A:H2'	2:5:3933:G:H8	1.79	0.46
2:5:4365:U:H2'	2:5:4366:OMU:H6	1.97	0.46
2:5:4686:U:HO2'	2:5:4687:C:P	2.37	0.46
9:8:148:A:H2'	9:8:149:G:C8	2.51	0.46
13:j:67:LEU:HA	13:j:70:VAL:HG12	1.97	0.46
14:A:206:PRO:HD3	14:A:213:GLY:CA	2.45	0.46
23:Q:88:ASP:OD2	23:Q:108:ARG:HD2	2.16	0.46
27:K:94:LEU:HD23	27:K:99:ILE:HD12	1.98	0.46
28:C:275:SER:OG	28:C:276:ASN:OD1	2.34	0.46
29:o:30:LYS:NZ	29:o:30:LYS:HB3	2.30	0.46
33:Z:5:MET:O	33:Z:28:ASN:ND2	2.49	0.46
2:5:161:G:H2'	2:5:162:A:H8	1.81	0.46
2:5:172:C:O3'	38:L:129:ARG:NH2	2.49	0.46
2:5:884:U:C5	22:E:73:ARG:HD3	2.50	0.46
2:5:998:U:H3	2:5:1107:C:N4	2.12	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:1064:G:H2'	2:5:1065:G:C8	2.51	0.46
2:5:1102:G:H2'	2:5:1103:G:C8	2.51	0.46
2:5:1326:G:H2'	2:5:1327:G:H8	1.81	0.46
2:5:1807:A:H61	15:I:115:MET:HE2	1.80	0.46
2:5:1931:U:O2'	2:5:1941:A:O5'	2.33	0.46
2:5:3454:G:H2'	2:5:3455:A2M:H8	1.97	0.46
2:5:3609:A:N3	2:5:4147:G:O2'	2.44	0.46
2:5:4476:C:OP2	2:5:4704:U:O2'	2.29	0.46
5:S:81:TRP:O	5:S:127:MET:HB2	2.16	0.46
7:B:47:LEU:HB2	7:B:84:MET:HE3	1.97	0.46
14:A:33:ASP:OD1	14:A:35:ALA:N	2.49	0.46
28:C:201:ARG:CZ	28:C:201:ARG:HB2	2.46	0.46
36:k:51:GLU:HG2	36:k:55:LYS:NZ	2.31	0.46
38:L:173:GLU:H	38:L:173:GLU:CD	2.23	0.46
46:U:34:MET:HE2	46:U:35:ASP:N	2.31	0.46
2:5:187:U:O2'	2:5:188:G:H3'	2.15	0.46
2:5:678:G:H5'	2:5:679:C:OP2	2.16	0.46
2:5:856:A:H1'	2:5:2015:G:H5''	1.98	0.46
2:5:1389:G:H2'	2:5:1389:G:N3	2.31	0.46
2:5:1796:C:H2'	2:5:1797:A:C8	2.51	0.46
2:5:4664:U:H1'	2:5:4665:C:OP2	2.16	0.46
3:F:143:TYR:CE2	3:F:236:GLU:HG3	2.50	0.46
6:b:33:LYS:HE2	6:b:33:LYS:HB3	1.80	0.46
18:V:71:GLU:OE1	18:V:71:GLU:N	2.23	0.46
27:K:168:LEU:HG	27:K:173:TYR:CD2	2.51	0.46
27:K:282:LYS:NZ	27:K:455:TYR:HE2	2.14	0.46
28:C:260:LEU:HD23	28:C:260:LEU:HA	1.76	0.46
34:a:127:LYS:NZ	34:a:148:ALA:O	2.49	0.46
37:H:93:ARG:HG3	37:H:182:SER:HB3	1.98	0.46
40:N:84:PRO:HA	40:N:87:HIS:CD2	2.51	0.46
45:X:86:ALA:O	45:X:90:ILE:HG13	2.16	0.46
2:5:187:U:OP2	2:5:245:C:N4	2.49	0.45
2:5:1210:C:H5''	6:b:107:ARG:HH12	1.81	0.45
2:5:1427:C:H2'	2:5:1428:U:H6	1.81	0.45
2:5:1468:U:H4'	38:L:4:SER:HB2	1.99	0.45
2:5:2327:A:H2'	2:5:2328:U:C6	2.51	0.45
2:5:2381:U:OP2	36:k:40:ARG:NH1	2.49	0.45
2:5:2599:G:C6	2:5:2600:A:N6	2.84	0.45
2:5:4347:U:H2'	2:5:4348:A:H8	1.82	0.45
2:5:4654:G:H2'	2:5:4655:G:H8	1.81	0.45
7:B:141:ALA:HA	7:B:144:ARG:NH2	2.30	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
23:Q:124:ASP:OD1	23:Q:124:ASP:N	2.46	0.45
31:f:106:TYR:CD1	31:f:107:PRO:HD3	2.51	0.45
44:Y:54:GLU:OE1	44:Y:108:ARG:HD2	2.16	0.45
2:5:239:C:OP1	44:Y:33:PRO:HB3	2.16	0.45
2:5:759:G:C5	2:5:795:A:N7	2.84	0.45
2:5:828:A:H3'	2:5:829:G:H8	1.81	0.45
2:5:3489:G:N1	2:5:3500:U:N3	2.64	0.45
2:5:3919:G:H2'	2:5:3920:U:C6	2.52	0.45
2:5:4751:G:O2'	2:5:4753:A:OP1	2.28	0.45
4:D:60:ILE:HB	4:D:80:ALA:HB2	1.98	0.45
7:B:173:LEU:HD22	7:B:342:LYS:HD3	1.98	0.45
28:C:321:ASN:HB3	28:C:324:ILE:HB	1.97	0.45
2:5:787:C:H2'	2:5:788:G:C8	2.52	0.45
2:5:4117:G:H2'	2:5:4118:U:O4'	2.16	0.45
2:5:4612:G:N3	26:O:175:MET:HE2	2.32	0.45
2:5:4634:C:O2	43:M:132:ARG:NH2	2.39	0.45
9:8:40:A:H2'	9:8:41:A:C8	2.52	0.45
22:E:196:PHE:CD2	31:f:106:TYR:HB2	2.52	0.45
26:O:27:VAL:HG12	26:O:98:ALA:HB1	1.97	0.45
26:O:173:GLN:OE1	26:O:176:ARG:NH1	2.49	0.45
42:h:29:SER:O	42:h:33:VAL:HG12	2.16	0.45
2:5:417:G:H1'	9:8:16:G:H22	1.82	0.45
2:5:756:G:C2	2:5:757:A:C4	3.05	0.45
2:5:1403:G:H1'	2:5:2045:G:N2	2.31	0.45
2:5:1449:U:H2'	2:5:1450:G:C8	2.51	0.45
2:5:3416:G:H2'	2:5:3417:C:C6	2.51	0.45
2:5:3432:C:O2'	2:5:3506:A:N3	2.42	0.45
2:5:4070:A:H2'	2:5:4071:A:C8	2.51	0.45
2:5:4431:U:P	19:m:86:LYS:HE2	2.57	0.45
4:D:41:LYS:HD3	4:D:41:LYS:HA	1.52	0.45
22:E:112:LEU:HD23	22:E:112:LEU:H	1.81	0.45
37:H:140:GLN:HG2	37:H:143:GLU:OE1	2.17	0.45
40:N:115:VAL:O	40:N:159:ARG:NH1	2.49	0.45
2:5:65:A:N6	2:5:75:G:H1'	2.31	0.45
2:5:1521:C:H2'	2:5:1522:U:C6	2.52	0.45
2:5:2327:A:H2'	2:5:2328:U:H6	1.82	0.45
2:5:4633:A:H5''	2:5:4634:C:C6	2.52	0.45
2:5:4671:U:H2'	2:5:4672:C:C6	2.52	0.45
7:B:90:VAL:HG23	7:B:104:THR:HG22	1.98	0.45
27:K:34:TRP:HE1	27:K:168:LEU:CD2	2.30	0.45
33:Z:47:ASP:N	33:Z:69:LYS:O	2.40	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:M:34:ASN:HA	43:M:52:PHE:HD2	1.81	0.45
45:X:94:ASN:OD1	45:X:145:ASP:HA	2.17	0.45
2:5:681:U:C4	22:E:98:PRO:HG2	2.51	0.45
2:5:728:G:H1	2:5:828:A:N6	2.13	0.45
2:5:1078:G:H1'	4:D:275:GLN:NE2	2.32	0.45
2:5:4469:A:H2'	2:5:4470:A:C8	2.51	0.45
2:5:4518:C:H1'	2:5:4519:C:C2	2.52	0.45
8:d:37:GLY:O	8:d:41:ARG:HG3	2.16	0.45
9:8:122:G:H2'	9:8:123:U:O4'	2.17	0.45
24:R:78:ILE:C	24:R:78:ILE:HD12	2.42	0.45
27:K:169:LEU:HD21	27:K:176:GLY:C	2.41	0.45
28:C:190:ARG:HB2	28:C:202:ILE:HG23	1.98	0.45
37:H:23:ARG:HG3	37:H:23:ARG:HH11	1.81	0.45
38:L:91:ALA:HB1	38:L:96:ILE:HB	1.98	0.45
41:i:43:MET:O	41:i:47:VAL:HG12	2.16	0.45
1:T:42:ILE:HD11	1:T:74:ILE:HD11	1.98	0.45
2:5:286:U:H2'	2:5:287:U:C6	2.52	0.45
2:5:299:C:H2'	2:5:300:A:H8	1.80	0.45
2:5:300:A:H2'	2:5:301:G:H8	1.81	0.45
2:5:657:G:H2'	2:5:658:G:H8	1.82	0.45
2:5:1403:G:C4	2:5:2045:G:N1	2.84	0.45
2:5:1416:C:H2'	2:5:1417:A:C8	2.52	0.45
2:5:1439:G:N3	2:5:1439:G:H2'	2.32	0.45
2:5:2223:G:H22	2:5:2267:OMG:H5'	1.82	0.45
2:5:2477:C:H2'	2:5:2478:U:C6	2.52	0.45
2:5:2742:C:H2'	2:5:2743:U:C6	2.52	0.45
2:5:4012:G:H2'	2:5:4012:G:N3	2.32	0.45
4:D:62:CYS:HB3	4:D:105:LEU:HD22	1.99	0.45
7:B:181:MET:HE3	7:B:181:MET:HB2	1.81	0.45
12:c:77:ASN:ND2	12:c:80:GLU:OE1	2.50	0.45
18:V:111:GLU:H	18:V:111:GLU:CD	2.25	0.45
28:C:212:ASN:HD22	28:C:255:SER:HB2	1.82	0.45
2:5:143:C:O4'	10:G:161:GLN:NE2	2.49	0.45
2:5:475:G:H2'	2:5:476:G:H8	1.82	0.45
2:5:676:G:H2'	2:5:677:C:O4'	2.16	0.45
2:5:1102:G:O2'	2:5:1103:G:OP1	2.30	0.45
2:5:1252:C:H2'	2:5:1253:C:C6	2.52	0.45
2:5:2229:U:H2'	2:5:2230:G:H8	1.81	0.45
2:5:2665:G:N7	24:R:20:LYS:NZ	2.51	0.45
2:5:3531:A:C5	18:V:40:ILE:HD12	2.52	0.45
2:5:3797:U:H2'	2:5:3798:U:H6	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:3817:G:H2'	2:5:3818:G:C8	2.52	0.45
2:5:3823:G:H2'	2:5:3824:C:C6	2.52	0.45
9:8:120:G:C2	9:8:121:G:C8	3.05	0.45
15:I:200:ILE:HG21	15:I:212:LEU:HD21	1.99	0.45
27:K:61:PRO:HD3	27:K:136:MET:HE3	1.99	0.45
27:K:293:LEU:O	27:K:296:ALA:HB3	2.17	0.45
30:r:28:GLU:HB2	30:r:29:PRO:HD2	1.99	0.45
34:a:93:ASN:OD1	34:a:95:THR:N	2.43	0.45
38:L:170:THR:OG1	38:L:173:GLU:OE1	2.35	0.45
39:7:58:A:H2'	39:7:59:G:C8	2.51	0.45
1:T:119:ALA:HA	1:T:122:LYS:HD3	1.98	0.45
2:5:1403:G:C4	2:5:2045:G:C2	3.05	0.45
2:5:1678:G:N3	2:5:1681:A:N6	2.64	0.45
2:5:1911:G:N1	2:5:1934:G:C6	2.85	0.45
2:5:2165:G:OP2	32:e:34:ASN:ND2	2.50	0.45
2:5:2575:G:H2'	2:5:2576:C:C6	2.52	0.45
2:5:3856:A:H1'	10:G:88:ARG:HB2	1.97	0.45
2:5:4094:A:O2'	2:5:4096:C:OP2	2.28	0.45
24:R:171:LYS:O	24:R:175:GLU:HG3	2.17	0.45
25:W:9:SER:HA	25:W:52:THR:HG23	1.98	0.45
27:K:294:GLN:C	27:K:296:ALA:N	2.72	0.45
31:f:45:LYS:NZ	31:f:108:SER:HA	2.32	0.45
36:k:16:ARG:HB3	36:k:16:ARG:NH1	2.32	0.45
38:L:133:ALA:O	38:L:135:LYS:NZ	2.49	0.45
1:T:27:LEU:HD23	4:D:33:ARG:HH11	1.82	0.45
2:5:135:G:O2'	42:h:96:ASN:HB2	2.17	0.45
2:5:406:C:HO2'	2:5:407:A:P	2.39	0.45
2:5:725:G:C6	2:5:831:A:C4	3.05	0.45
2:5:759:G:N3	2:5:759:G:H2'	2.31	0.45
2:5:1638:PSU:H2'	2:5:1639:A:H8	1.82	0.45
2:5:1854:C:OP2	26:O:94:ARG:NH2	2.50	0.45
2:5:3330:C:H2'	2:5:3331:A:C8	2.52	0.45
2:5:3369:U:O4	2:5:3383:A:H2	2.00	0.45
2:5:3643:C:H2'	2:5:3644:U:C6	2.52	0.45
2:5:4324:G:H2'	2:5:4325:U:C6	2.52	0.45
2:5:4366:OMU:H1'	2:5:4366:OMU:HM23	1.59	0.45
2:5:4369:OMG:HM23	2:5:4369:OMG:H1'	1.58	0.45
7:B:340:THR:OG1	7:B:341:LYS:N	2.47	0.45
10:G:219:LEU:HD21	40:N:45:PRO:HG2	1.98	0.45
14:A:205:ASN:O	14:A:208:GLU:HG2	2.17	0.45
21:P:50:ASP:C	21:P:50:ASP:OD1	2.60	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:K:286:THR:HG22	27:K:379:TRP:HD1	1.82	0.45
31:f:36:ARG:HG3	31:f:80:ASN:HA	1.99	0.45
34:a:64:LYS:HE3	34:a:67:GLN:HE21	1.81	0.45
38:L:21:ARG:NH2	40:N:196:ASN:HB3	2.27	0.45
38:L:172:GLU:HG3	41:i:3:LEU:HD21	1.99	0.45
46:U:42:PHE:HD2	46:U:90:TYR:HD2	1.64	0.45
1:T:102:ARG:HA	1:T:102:ARG:HD2	1.88	0.44
2:5:152:U:OP2	40:N:49:ARG:NH2	2.50	0.44
2:5:318:A:H2'	2:5:319:A:C8	2.53	0.44
2:5:1260:OMG:HM23	2:5:1260:OMG:H1'	1.60	0.44
2:5:1757:G:HO2'	2:5:1758:G:P	2.38	0.44
2:5:2363:C:H2'	2:5:2364:G:C8	2.52	0.44
2:5:2518:G:H1	12:c:33:GLN:HE21	1.66	0.44
2:5:2601:G:H2'	2:5:2602:G:N7	2.32	0.44
2:5:4088:C:H2'	2:5:4089:U:H6	1.83	0.44
27:K:107:LYS:HD2	27:K:107:LYS:HA	1.77	0.44
27:K:347:PRO:C	27:K:360:HIS:HE1	2.25	0.44
41:i:42:ASP:OD1	41:i:42:ASP:C	2.61	0.44
43:M:44:ARG:HA	43:M:44:ARG:HD2	1.39	0.44
44:Y:10:ASP:OD1	44:Y:12:SER:N	2.50	0.44
46:U:40:GLU:OE2	46:U:65:ARG:NH2	2.50	0.44
2:5:657:G:H2'	2:5:658:G:C8	2.51	0.44
2:5:1388:A:N6	2:5:1406:G:O2'	2.50	0.44
2:5:1617:C:H2'	2:5:1618:C:H6	1.83	0.44
2:5:2475:U:H2'	2:5:2476:U:C6	2.52	0.44
2:5:3342:A:H2'	2:5:3343:A:H8	1.82	0.44
2:5:3662:U:H2'	2:5:3663:C:C6	2.52	0.44
7:B:232:THR:HG21	7:B:249:ARG:HB3	2.00	0.44
13:j:14:LYS:HE2	13:j:14:LYS:HB3	1.87	0.44
21:P:9:GLU:CD	21:P:10:ASN:HD22	2.25	0.44
24:R:167:LYS:O	24:R:170:ARG:HG3	2.17	0.44
26:O:181:ALA:O	26:O:185:VAL:HG23	2.17	0.44
27:K:82:SER:O	27:K:85:VAL:HG12	2.17	0.44
2:5:158:A:N1	2:5:276:C:O2'	2.42	0.44
2:5:266:C:O3'	42:h:109:ARG:NH2	2.50	0.44
2:5:475:G:H2'	2:5:476:G:C8	2.52	0.44
2:5:798:C:N3	2:5:799:C:C4	2.86	0.44
2:5:866:A:O4'	2:5:868:C:N4	2.50	0.44
2:5:1532:G:C5	14:A:181:LYS:HB2	2.52	0.44
2:5:3789:G:H2'	2:5:3790:A:O4'	2.17	0.44
2:5:4515:G:H2'	2:5:4516:G:H8	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:S:82:LEU:HD23	5:S:83:ARG:N	2.33	0.44
7:B:31:SER:O	7:B:348:ARG:NH1	2.50	0.44
8:d:57:MET:CE	8:d:90:ARG:HB2	2.46	0.44
40:N:44:ARG:NH1	40:N:120:TRP:O	2.51	0.44
40:N:155:VAL:O	40:N:162:ARG:NH2	2.51	0.44
42:h:36:VAL:HG21	45:X:79:PHE:HB2	1.99	0.44
46:U:90:TYR:CD1	46:U:90:TYR:C	2.96	0.44
1:T:121:GLU:HG2	1:T:122:LYS:HD2	1.98	0.44
2:5:382:G:N1	2:5:385:A:OP2	2.41	0.44
2:5:1009:G:H2'	2:5:1010:A:H8	1.82	0.44
2:5:1290:C:H2'	2:5:1291:G:H8	1.81	0.44
2:5:1532:G:O2'	2:5:1567:G:H4'	2.18	0.44
2:5:1757:G:H2'	2:5:1759:U:OP2	2.17	0.44
2:5:1816:G:O6	6:b:10:HIS:NE2	2.44	0.44
2:5:2514:C:OP1	17:p:46:LYS:HE2	2.18	0.44
2:5:2737:A:H2'	2:5:2738:A:H8	1.81	0.44
2:5:4669:C:H5'	22:E:269:GLN:HG3	1.99	0.44
15:I:42:LYS:O	15:I:139:ARG:NH2	2.44	0.44
21:P:42:ARG:HD2	21:P:42:ARG:N	2.32	0.44
26:O:47:PHE:CE1	26:O:140:ARG:HG2	2.52	0.44
40:N:6:TYR:CD1	41:i:40:VAL:HG13	2.52	0.44
2:5:425:U:H2'	2:5:426:A:H8	1.82	0.44
2:5:497:G:O2'	2:5:498:G:H5'	2.18	0.44
2:5:881:C:OP2	22:E:68:LYS:HD3	2.17	0.44
2:5:1698:G:H2'	2:5:1699:G:C8	2.52	0.44
2:5:1948:A:H2'	2:5:1949:A:C8	2.53	0.44
2:5:2255:A:H2'	2:5:2256:U:H6	1.82	0.44
2:5:3331:A:H2'	2:5:3332:G:C8	2.52	0.44
2:5:3368:C:H4'	2:5:3557:A2M:H2	1.99	0.44
2:5:4026:A:OP2	4:D:23:ARG:NH2	2.47	0.44
2:5:4510:U:O2'	5:S:174:THR:OG1	2.34	0.44
27:K:63:TYR:CD2	27:K:334:ARG:HD3	2.52	0.44
27:K:143:MET:O	27:K:147:ILE:HB	2.17	0.44
27:K:348:PRO:HD3	27:K:364:TYR:CD2	2.53	0.44
27:K:375:PHE:HA	27:K:378:THR:HG22	1.98	0.44
29:o:36:GLN:HE21	34:a:59:ARG:NH2	2.16	0.44
34:a:75:LEU:HA	34:a:78:LEU:HB2	1.99	0.44
35:g:98:GLU:OE1	35:g:98:GLU:HA	2.16	0.44
37:H:41:ILE:CG2	37:H:43:VAL:HG13	2.47	0.44
38:L:138:ASP:OD1	38:L:139:SER:N	2.51	0.44
40:N:159:ARG:HB3	40:N:164:LEU:HB2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:U:26:THR:O	46:U:30:GLU:HG3	2.18	0.44
2:5:132:G:H2'	2:5:133:C:O4'	2.18	0.44
2:5:759:G:C5'	2:5:760:C:H5	2.30	0.44
2:5:788:G:H2'	2:5:789:G:H8	1.82	0.44
2:5:798:C:H2'	2:5:799:C:C1'	2.47	0.44
2:5:993:A:H3'	2:5:994:C:H5''	2.00	0.44
2:5:1015:U:O4	2:5:1086:G:O6	2.36	0.44
2:5:1222:C:H2'	2:5:1223:A:O4'	2.18	0.44
2:5:1651:C:H2'	2:5:1652:G:H8	1.81	0.44
2:5:1832:C:H1'	2:5:1876:C:O2	2.17	0.44
2:5:2232:A:H5'	8:d:70:LYS:HE2	1.98	0.44
2:5:2364:G:O2'	35:g:26:PRO:HG2	2.17	0.44
2:5:4321:G:O2'	2:5:4808:U:OP1	2.35	0.44
2:5:4507:G:H2'	2:5:4508:G:O4'	2.17	0.44
3:F:31:ARG:HG3	3:F:31:ARG:NH1	2.33	0.44
3:F:91:VAL:O	3:F:119:GLY:HA2	2.17	0.44
14:A:196:TRP:O	14:A:198:ARG:N	2.50	0.44
18:V:106:VAL:HG12	18:V:112:MET:HA	1.98	0.44
27:K:26:ILE:HG21	27:K:31:LYS:HD3	1.98	0.44
27:K:307:MET:HE3	27:K:307:MET:HB3	1.84	0.44
44:Y:22:PRO:HG2	44:Y:25:ILE:HG12	2.00	0.44
1:T:13:TYR:OH	2:5:1729:U:OP2	2.27	0.44
2:5:38:A:H5''	34:a:35:ALA:HB2	2.00	0.44
2:5:1087:G:H2'	2:5:1088:C:C6	2.51	0.44
2:5:1401:C:C2	2:5:1402:C:C5	3.05	0.44
2:5:1403:G:C6	2:5:1404:C:C4	3.05	0.44
2:5:1513:A:H2'	2:5:1514:G:H8	1.83	0.44
2:5:2602:G:H2'	2:5:2603:G:C8	2.53	0.44
2:5:4000:G:O3'	2:5:4001:A:H3'	2.18	0.44
3:F:67:GLU:OE1	3:F:67:GLU:N	2.50	0.44
3:F:246:MET:HE2	3:F:246:MET:HB3	1.75	0.44
7:B:261:ARG:HB2	26:O:64:THR:HG21	1.99	0.44
9:8:27:U:H2'	9:8:28:C:C6	2.53	0.44
11:J:119:TYR:CD1	11:J:119:TYR:C	2.96	0.44
24:R:78:ILE:HG22	24:R:81:ARG:NH1	2.33	0.44
1:T:87:LYS:CE	2:5:4051:G:H22	2.31	0.44
2:5:163:A:H2'	2:5:164:G:H8	1.83	0.44
2:5:272:U:H2'	2:5:273:U:C6	2.53	0.44
2:5:426:A:H2'	2:5:427:A:C8	2.53	0.44
2:5:668:G:H2'	2:5:669:C:C6	2.52	0.44
2:5:797:C:H2'	2:5:799:C:OP2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:797:C:H2'	2:5:799:C:P	2.58	0.44
2:5:856:A:N6	2:5:1227:G:H1'	2.33	0.44
2:5:1398:A:C5	2:5:1399:G:C5	3.06	0.44
2:5:1506:C:H2'	2:5:1507:G:H5'	2.00	0.44
2:5:1710:U:H2'	2:5:1711:C:C6	2.53	0.44
2:5:2360:A:H5'	35:g:62:LYS:HE3	2.00	0.44
2:5:2599:G:H2'	2:5:2600:A:C8	2.53	0.44
2:5:3867:C:H2'	2:5:3868:C:C6	2.52	0.44
9:8:13:G:H1'	21:P:120:ASN:HD22	1.82	0.44
27:K:37:ILE:HD12	27:K:38:THR:N	2.32	0.44
37:H:128:MET:HE2	37:H:128:MET:HA	2.00	0.44
39:7:24:C:H2'	39:7:25:G:O4'	2.18	0.44
2:5:50:C:C2	2:5:51:A:C8	3.06	0.44
2:5:264:C:H2'	2:5:265:C:C6	2.52	0.44
2:5:1133:C:O2	2:5:1208:C:O2'	2.32	0.44
2:5:1755:C:C6	6:b:42:ASN:ND2	2.86	0.44
2:5:3900:G:H2'	2:5:3901:C:H6	1.83	0.44
2:5:4622:C:N4	22:E:184:LEU:O	2.40	0.44
2:5:4677:A:N6	22:E:250:LYS:HG2	2.33	0.44
4:D:152:ARG:HG3	4:D:154:THR:HG23	2.00	0.44
6:b:55:LYS:HA	6:b:58:GLN:HE22	1.82	0.44
9:8:154:G:O3'	10:G:142:ARG:NH1	2.51	0.44
35:g:63:VAL:HG13	35:g:66:ARG:NH1	2.33	0.44
36:k:52:LYS:HA	36:k:55:LYS:HZ3	1.83	0.44
46:U:42:PHE:HE1	46:U:46:ARG:HG3	1.78	0.44
2:5:268:G:H2'	2:5:269:G:H8	1.83	0.43
2:5:324:A:H2'	2:5:325:U:C6	2.53	0.43
2:5:636:G:H2'	2:5:637:C:C6	2.53	0.43
2:5:707:C:H2'	2:5:708:G:H8	1.83	0.43
2:5:987:C:O2'	2:5:988:G:O5'	2.32	0.43
2:5:1108:G:H2'	2:5:1109:G:H8	1.83	0.43
2:5:2018:G:H2'	2:5:2019:U:H6	1.83	0.43
2:5:2381:U:H2'	2:5:2382:C:C6	2.53	0.43
2:5:2596:G:H3'	2:5:2597:G:C8	2.52	0.43
2:5:3687:A:H2	2:5:3787:C:H42	1.66	0.43
2:5:4312:U:O2'	7:B:234:ARG:NH1	2.49	0.43
2:5:4754:G:H2'	2:5:4755:A:C2	2.52	0.43
11:J:40:LEU:HD23	11:J:70:VAL:HG12	1.99	0.43
14:A:166:VAL:HG13	17:p:83:ILE:HD13	1.99	0.43
15:I:86:HIS:HB3	15:I:139:ARG:CG	2.48	0.43
15:I:91:LEU:HD12	15:I:135:ILE:HG23	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:K:21:LYS:HB3	27:K:171:LYS:HG3	2.00	0.43
27:K:262:ARG:HG2	27:K:282:LYS:CG	2.42	0.43
37:H:15:ASN:N	37:H:15:ASN:OD1	2.51	0.43
39:7:28:C:H1'	39:7:54:A:H61	1.82	0.43
45:X:43:SER:OG	45:X:45:THR:HG22	2.17	0.43
1:T:17:ARG:HB2	1:T:22:HIS:CE1	2.53	0.43
2:5:37:U:H2'	2:5:38:A:O4'	2.18	0.43
2:5:663:C:O2'	2:5:664:G:H8	1.98	0.43
2:5:1270:A2M:HM'3	2:5:1270:A2M:H1'	1.45	0.43
2:5:3339:U:H2'	2:5:3340:A:C8	2.53	0.43
2:5:3414:A:H3'	14:A:132:ASN:HD21	1.83	0.43
2:5:3517:A:H2'	2:5:3517:A:N3	2.34	0.43
2:5:3898:G:H2'	2:5:3899:C:H6	1.83	0.43
2:5:4204:C:H2'	2:5:4205:U:C6	2.53	0.43
2:5:4272:U:O2'	2:5:4273:G:H5'	2.18	0.43
2:5:4509:A:O2'	2:5:4510:U:H5'	2.18	0.43
2:5:4683:C:N4	31:f:59:THR:HA	2.33	0.43
6:b:58:GLN:HA	6:b:61:ASN:HB2	2.00	0.43
7:B:137:TRP:O	7:B:143:LYS:NZ	2.40	0.43
18:V:96:LEU:HD12	18:V:97:TYR:H	1.83	0.43
23:Q:22:ASP:C	23:Q:22:ASP:OD1	2.61	0.43
30:r:38:PHE:O	30:r:45:HIS:NE2	2.35	0.43
34:a:49:HIS:NE2	38:L:7:GLY:O	2.38	0.43
38:L:150:LEU:HD11	38:L:154:VAL:HG12	1.99	0.43
45:X:117:TYR:CE2	45:X:153:ILE:HD11	2.52	0.43
46:U:35:ASP:C	46:U:35:ASP:OD1	2.61	0.43
2:5:671:G:H2'	2:5:672:C:C6	2.54	0.43
2:5:1398:A:H2'	2:5:1399:G:C8	2.53	0.43
2:5:1615:U:H3'	34:a:13:GLY:HA2	2.00	0.43
2:5:2450:C:H2'	2:5:2451:G:H8	1.83	0.43
2:5:4144:C:H2'	2:5:4145:U:O4'	2.18	0.43
15:I:44:ASP:OD1	15:I:44:ASP:N	2.44	0.43
16:q:17:ASP:OD1	16:q:17:ASP:C	2.62	0.43
24:R:95:TRP:CH2	24:R:99:MET:HE2	2.53	0.43
27:K:61:PRO:CD	27:K:136:MET:HE3	2.48	0.43
35:g:44:SER:OG	35:g:46:CYS:SG	2.63	0.43
36:k:36:VAL:HG13	36:k:43:TYR:HB2	2.01	0.43
41:i:3:LEU:HD12	41:i:5:TYR:CE1	2.53	0.43
43:M:74:ARG:HG2	43:M:74:ARG:HH11	1.83	0.43
1:T:86:ALA:HB2	6:b:24:PRO:HG3	2.00	0.43
2:5:1086:G:C2	2:5:1087:G:C5	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:1929:A:H3'	2:5:1930:A:C2	2.54	0.43
2:5:2363:C:H1'	2:5:2483:G:H21	1.83	0.43
2:5:2704:OMC:HM23	2:5:2704:OMC:H1'	1.52	0.43
2:5:4018:G:OP2	2:5:4018:G:N2	2.35	0.43
2:5:4654:G:H2'	2:5:4655:G:C8	2.53	0.43
3:F:183:ILE:HG23	3:F:188:ASP:HB2	2.00	0.43
5:S:161:ARG:HG3	5:S:161:ARG:O	2.18	0.43
6:b:72:ILE:HA	6:b:75:LEU:HG	2.00	0.43
10:G:173:LYS:HA	10:G:173:LYS:HD2	1.90	0.43
11:J:99:PHE:HE2	11:J:163:MET:HA	1.83	0.43
14:A:66:PRO:HG2	14:A:67:TYR:CE1	2.53	0.43
14:A:210:PRO:HG2	14:A:235:VAL:HG21	1.99	0.43
27:K:445:THR:O	27:K:449:LEU:HG	2.18	0.43
30:r:54:ALA:HA	30:r:61:VAL:HG23	1.99	0.43
34:a:74:ASN:HA	34:a:112:LEU:O	2.19	0.43
2:5:6:C:H2'	2:5:7:C:C6	2.52	0.43
2:5:460:C:H2'	2:5:461:G:H8	1.84	0.43
2:5:740:G:H2'	2:5:741:A:C8	2.53	0.43
2:5:757:A:H3'	2:5:758:C:H5''	1.99	0.43
2:5:1398:A:H2'	2:5:1399:G:O4'	2.18	0.43
2:5:1506:C:C2'	2:5:1507:G:H5'	2.48	0.43
2:5:2586:A:H2'	2:5:2587:A:C8	2.52	0.43
2:5:2700:A:H2'	2:5:2701:A:O4'	2.18	0.43
2:5:3396:G:H2'	2:5:3397:G:C8	2.51	0.43
2:5:3892:G:H2'	2:5:3893:G:C8	2.54	0.43
2:5:4193:5MC:H6	2:5:4193:5MC:H2'	1.65	0.43
2:5:4616:G:H2'	2:5:4617:C:H6	1.84	0.43
2:5:4621:U:OP1	43:M:117:LYS:NZ	2.52	0.43
6:b:36:ASP:OD1	6:b:36:ASP:C	2.62	0.43
6:b:99:ILE:O	6:b:109:ARG:NH1	2.51	0.43
7:B:192:GLU:HA	7:B:195:ASP:OD1	2.18	0.43
9:8:94:G:H1'	13:j:82:THR:O	2.18	0.43
10:G:141:ASP:C	10:G:141:ASP:OD1	2.61	0.43
27:K:81:ILE:O	27:K:84:ILE:HG22	2.17	0.43
36:k:24:LYS:C	36:k:25:ILE:HD13	2.43	0.43
46:U:23:LEU:HD13	46:U:110:TYR:HB2	2.00	0.43
2:5:221:C:H2'	2:5:222:C:H6	1.83	0.43
2:5:739:G:N1	2:5:818:C:N3	2.67	0.43
2:5:790:G:N2	2:5:792:G:H21	2.17	0.43
2:5:1387:G:H2'	2:5:1406:G:N2	2.33	0.43
2:5:1903:A:H3'	2:5:1904:G:H8	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:1931:U:H3'	2:5:1931:U:OP2	2.19	0.43
2:5:4219:A:P	19:m:76:ARG:HH21	2.41	0.43
2:5:4622:C:H2'	2:5:4623:G:H8	1.84	0.43
3:F:107:VAL:HG13	3:F:131:MET:HG2	2.00	0.43
4:D:273:LEU:HA	4:D:276:LYS:HG2	1.99	0.43
6:b:68:ARG:HH11	6:b:69:ALA:N	2.17	0.43
9:8:19:C:H2'	9:8:20:A:C8	2.54	0.43
22:E:243:TYR:OH	22:E:249:ARG:NH1	2.52	0.43
23:Q:63:LEU:O	23:Q:67:ILE:HG23	2.17	0.43
33:Z:11:VAL:HG11	33:Z:80:LEU:HB3	2.00	0.43
38:L:135:LYS:HD3	38:L:135:LYS:HA	1.78	0.43
46:U:56:LEU:HB3	46:U:61:VAL:HG13	2.00	0.43
2:5:165:A:H2'	2:5:166:C:C6	2.54	0.43
2:5:874:C:H2'	2:5:875:G:H8	1.84	0.43
2:5:881:C:H2'	2:5:882:U:H6	1.84	0.43
2:5:1375:A:OP1	23:Q:68:ARG:NH2	2.51	0.43
2:5:4341:G:H2'	2:5:4342:C:H6	1.83	0.43
2:5:4456:C:H2'	2:5:4457:C:C6	2.53	0.43
2:5:4640:G:H2'	2:5:4641:C:H6	1.84	0.43
5:S:24:THR:O	5:S:24:THR:OG1	2.29	0.43
7:B:112:ASP:N	7:B:112:ASP:OD1	2.52	0.43
8:d:60:PRO:HB2	8:d:100:ASN:HD22	1.84	0.43
9:8:154:G:H5''	10:G:142:ARG:HH12	1.83	0.43
12:c:79:ILE:O	12:c:83:THR:HG22	2.19	0.43
18:V:31:ASN:HD21	18:V:116:ALA:N	2.17	0.43
33:Z:12:LEU:HD12	33:Z:12:LEU:HA	1.86	0.43
45:X:117:TYR:C	45:X:118:ASP:OD1	2.62	0.43
1:T:111:GLU:OE2	1:T:115:LYS:HD2	2.19	0.43
2:5:250:C:O3'	13:j:85:LYS:NZ	2.35	0.43
2:5:644:C:H2'	2:5:645:C:H6	1.83	0.43
2:5:684:C:H2'	2:5:685:C:C6	2.53	0.43
2:5:1290:C:H2'	2:5:1291:G:C8	2.54	0.43
2:5:1400:U:O2'	2:5:1401:C:OP1	2.35	0.43
2:5:2445:G:H2'	2:5:2446:C:C6	2.53	0.43
3:F:52:LYS:HG2	6:b:93:LEU:HD22	2.01	0.43
4:D:214:GLU:HG2	4:D:215:ASP:N	2.34	0.43
5:S:147:ASP:OD1	5:S:147:ASP:C	2.61	0.43
9:8:32:C:H2'	9:8:33:G:O4'	2.18	0.43
15:I:143:GLN:H	15:I:143:GLN:CD	2.16	0.43
18:V:96:LEU:HD12	18:V:97:TYR:N	2.34	0.43
19:m:67:LYS:HD2	19:m:76:ARG:HG2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
25:W:57:ARG:HH11	25:W:57:ARG:HG3	1.83	0.43
27:K:194:LYS:HD2	27:K:194:LYS:HA	1.90	0.43
27:K:341:LEU:HA	27:K:344:TYR:HD2	1.84	0.43
33:Z:29:ILE:HD12	33:Z:40:HIS:NE2	2.34	0.43
37:H:92:MET:SD	37:H:161:ILE:HD11	2.59	0.43
38:L:111:GLN:OE1	38:L:111:GLN:HA	2.19	0.43
39:7:16:A:H2'	39:7:17:C:C6	2.53	0.43
39:7:37:G:N2	39:7:41:G:N3	2.66	0.43
40:N:145:ASN:C	40:N:145:ASN:OD1	2.61	0.43
44:Y:66:GLN:CD	44:Y:66:GLN:N	2.76	0.43
2:5:801:C:O2'	2:5:802:C:H5'	2.18	0.43
2:5:1064:G:H2'	2:5:1065:G:H8	1.84	0.43
2:5:1248:C:H2'	2:5:1249:C:C6	2.54	0.43
2:5:2691:G:O2'	2:5:3570:U:O4	2.36	0.43
2:5:3464:A:H2'	2:5:3465:A:H8	1.84	0.43
2:5:3543:G:O2'	2:5:3546:U:OP2	2.37	0.43
2:5:3674:A:H2'	2:5:3675:A:C8	2.54	0.43
2:5:4085:A:H2'	2:5:4086:U:C6	2.53	0.43
2:5:4496:C:H2'	2:5:4497:G:O4'	2.18	0.43
2:5:4518:C:N4	2:5:4602:G:H1	2.17	0.43
2:5:4628:G:C6	2:5:4670:G:C6	3.06	0.43
12:c:106:ARG:CZ	12:c:106:ARG:HA	2.49	0.43
21:P:108:ASP:C	21:P:108:ASP:OD1	2.62	0.43
24:R:119:MET:O	24:R:123:LEU:HG	2.19	0.43
28:C:150:LEU:CD2	28:C:151:PRO:HD3	2.39	0.43
28:C:190:ARG:HG2	28:C:191:ALA:N	2.33	0.43
33:Z:92:ASP:C	33:Z:92:ASP:OD1	2.61	0.43
33:Z:92:ASP:OD1	33:Z:94:THR:N	2.52	0.43
36:k:5:ILE:HD11	36:k:43:TYR:HD1	1.83	0.43
36:k:9:LYS:HB3	36:k:9:LYS:HE3	1.80	0.43
37:H:51:LYS:O	37:H:52:LYS:HD2	2.19	0.43
40:N:79:ALA:HB1	40:N:81:TYR:CZ	2.54	0.43
40:N:114:ARG:NH1	40:N:151:ILE:O	2.52	0.43
46:U:23:LEU:HD21	46:U:83:LEU:HD13	2.01	0.43
46:U:87:THR:OG1	46:U:102:VAL:HG21	2.19	0.43
2:5:385:A:H4'	2:5:386:A:OP1	2.18	0.43
2:5:1401:C:H2'	2:5:1402:C:H6	1.82	0.43
2:5:2390:G:C5	2:5:2391:C:C5	3.06	0.43
2:5:2568:A:H1'	24:R:93:VAL:HG21	1.99	0.43
2:5:3793:G:O2'	2:5:3794:U:O5'	2.28	0.43
2:5:3985:A:H2'	2:5:3986:G:C8	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:4699:G:H2'	2:5:4700:G:C8	2.49	0.43
7:B:36:ASP:OD1	7:B:36:ASP:N	2.51	0.43
7:B:46:PHE:CZ	7:B:84:MET:HG3	2.54	0.43
16:q:3:GLN:HG2	16:q:7:PHE:CE2	2.53	0.43
22:E:216:THR:OG1	22:E:217:ASP:N	2.51	0.43
26:O:159:LYS:O	26:O:162:GLU:HG2	2.19	0.43
30:r:114:ALA:O	30:r:118:LEU:HG	2.19	0.43
37:H:43:VAL:HB	37:H:58:ASP:O	2.19	0.43
2:5:267:G:H2'	2:5:268:G:H8	1.84	0.42
2:5:427:A:H2'	2:5:428:G:C8	2.54	0.42
2:5:1387:G:H2'	2:5:1406:G:H22	1.83	0.42
2:5:1400:U:O2'	2:5:1401:C:P	2.76	0.42
2:5:1725:A:H2'	2:5:1728:C:C5	2.54	0.42
2:5:1752:U:C2	2:5:1765:G:N2	2.87	0.42
2:5:1937:A:N7	2:5:1938:A:N6	2.66	0.42
2:5:1938:A:H2'	2:5:1939:G:C4	2.54	0.42
2:5:2616:OMG:HM23	2:5:2616:OMG:H1'	1.60	0.42
2:5:3524:OMG:HM23	2:5:3524:OMG:H1'	1.89	0.42
2:5:3806:C:OP1	40:N:31:ARG:NH1	2.51	0.42
2:5:3838:C:H2'	2:5:3839:U:H6	1.84	0.42
2:5:4000:G:H3'	2:5:4002:A:OP2	2.19	0.42
4:D:56:THR:HG22	4:D:57:ASN:H	1.84	0.42
5:S:81:TRP:HB2	5:S:128:LYS:HB2	2.01	0.42
9:8:47:C:H1'	9:8:61:A:H2'	2.00	0.42
10:G:191:ALA:HB1	10:G:252:CYS:SG	2.59	0.42
10:G:264:ASP:OD1	10:G:264:ASP:N	2.52	0.42
13:j:58:THR:OG1	13:j:59:THR:N	2.50	0.42
23:Q:125:GLN:H	23:Q:125:GLN:HG3	1.62	0.42
24:R:144:LYS:HD2	24:R:144:LYS:C	2.44	0.42
27:K:193:TRP:CD2	27:K:197:SER:OG	2.60	0.42
35:g:5:LEU:H	35:g:5:LEU:HD23	1.84	0.42
39:7:3:C:H2'	39:7:4:U:C6	2.54	0.42
46:U:84:LYS:HD2	46:U:110:TYR:CE1	2.53	0.42
2:5:648:C:H2'	2:5:649:C:H6	1.84	0.42
2:5:666:C:H2'	2:5:667:C:H6	1.84	0.42
2:5:2431:C:H5''	2:5:2432:C:H5''	2.00	0.42
2:5:3790:A:H2'	2:5:3791:U:O4'	2.19	0.42
2:5:3982:G:H2'	2:5:3983:C:C6	2.54	0.42
2:5:4489:G:N3	2:5:4489:G:H2'	2.33	0.42
11:J:114:ASP:N	11:J:114:ASP:OD1	2.52	0.42
14:A:186:TYR:HB2	14:A:196:TRP:CZ3	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:I:182:GLU:HA	15:I:185:VAL:HG12	2.01	0.42
22:E:206:ILE:O	22:E:209:VAL:HG22	2.19	0.42
30:r:113:ARG:O	30:r:117:ILE:HG12	2.18	0.42
35:g:102:ILE:HD13	35:g:102:ILE:HA	1.86	0.42
41:i:59:GLU:OE1	41:i:59:GLU:HA	2.19	0.42
44:Y:80:ILE:HG23	44:Y:101:PRO:HG3	2.01	0.42
1:T:93:ILE:O	1:T:96:ILE:HG22	2.20	0.42
2:5:881:C:H2'	2:5:882:U:C6	2.54	0.42
2:5:1957:C:H2'	2:5:1958:C:C6	2.55	0.42
2:5:2450:C:H2'	2:5:2451:G:C8	2.54	0.42
2:5:2482:U:H2'	2:5:2537:G:N1	2.34	0.42
2:5:2539:A:H5'	36:k:26:LYS:HE2	2.01	0.42
2:5:3457:G:N2	2:5:3460:A:OP2	2.41	0.42
2:5:3990:A:H2'	2:5:3991:G:O4'	2.19	0.42
6:b:99:ILE:HD12	6:b:99:ILE:H	1.84	0.42
7:B:80:GLU:HG2	7:B:82:PRO:HD3	2.01	0.42
7:B:86:VAL:O	7:B:202:GLU:N	2.53	0.42
12:c:52:CYS:SG	12:c:57:LYS:HB2	2.59	0.42
27:K:151:ILE:HA	27:K:154:GLN:CG	2.49	0.42
27:K:267:ILE:HD13	27:K:401:MET:HG2	2.01	0.42
34:a:66:ASN:HB3	38:L:63:THR:CG2	2.49	0.42
37:H:69:THR:O	37:H:72:THR:HG22	2.18	0.42
2:5:459:C:H4'	22:E:113:ARG:HH22	1.81	0.42
2:5:1124:A:H5''	22:E:61:ARG:HB2	2.01	0.42
2:5:1398:A:H3'	2:5:1399:G:H8	1.84	0.42
2:5:1533:U:H2'	2:5:1534:C:H6	1.82	0.42
2:5:1666:U:H2'	2:5:1667:U:H6	1.83	0.42
2:5:1756:U:H2'	2:5:1757:G:O4'	2.19	0.42
2:5:1918:A:O2'	2:5:1919:U:OP1	2.27	0.42
2:5:2434:A:H2'	2:5:2435:U:C6	2.55	0.42
3:F:165:ARG:HD2	3:F:208:TRP:CE2	2.55	0.42
9:8:27:U:H2'	9:8:28:C:H6	1.85	0.42
27:K:236:ARG:HD3	27:K:239:LEU:HD23	2.01	0.42
27:K:397:GLN:OE1	27:K:397:GLN:N	2.52	0.42
29:o:10:THR:OG1	29:o:11:PHE:N	2.53	0.42
39:7:3:C:H2'	39:7:4:U:H6	1.84	0.42
42:h:46:LYS:O	42:h:49:VAL:HG22	2.19	0.42
2:5:1067:C:H2'	2:5:1068:U:H6	1.83	0.42
2:5:1432:C:H2'	2:5:1433:C:H6	1.84	0.42
2:5:2331:C:H3'	2:5:2333:U:O4	2.19	0.42
2:5:2573:U:H2'	2:5:2574:C:H6	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:3620:G:HO2'	2:5:3621:G:P	2.41	0.42
2:5:4136:A:H2'	2:5:4137:G:O4'	2.19	0.42
2:5:4602:G:H2'	2:5:4603:U:C6	2.54	0.42
2:5:4687:C:H3'	2:5:4688:G:C5'	2.50	0.42
5:S:112:ASP:OD1	5:S:116:ARG:NH1	2.53	0.42
6:b:67:ALA:O	6:b:70:GLU:HG2	2.19	0.42
9:8:66:A:H2'	9:8:67:U:H6	1.84	0.42
28:C:292:ILE:O	28:C:298:ILE:HG21	2.20	0.42
32:e:35:TRP:CZ2	32:e:56:PRO:HD2	2.55	0.42
32:e:75:ARG:HB2	32:e:95:TYR:CD1	2.54	0.42
40:N:48:ALA:HB1	40:N:53:TYR:HB3	2.01	0.42
46:U:69:LYS:HE2	46:U:69:LYS:HA	2.01	0.42
1:T:28:ALA:O	1:T:32:ARG:HG3	2.19	0.42
2:5:828:A:H3'	2:5:829:G:C8	2.54	0.42
2:5:864:A:H2'	2:5:865:G:C8	2.55	0.42
2:5:1392:C:O5'	2:5:2044:A:N6	2.52	0.42
2:5:2440:G:H2'	2:5:2441:A:C8	2.55	0.42
2:5:2477:C:C2	2:5:2478:U:C5	3.08	0.42
2:5:2707:A:H2'	2:5:2708:U:C6	2.54	0.42
2:5:2743:U:H2'	2:5:2744:G:C8	2.54	0.42
2:5:3934:U:H2'	2:5:3935:U:H6	1.85	0.42
2:5:4250:C:H2'	2:5:4251:C:C6	2.55	0.42
2:5:4270:G:C2	7:B:252:ALA:HB1	2.54	0.42
2:5:4346:G:O2'	2:5:4347:U:P	2.77	0.42
15:I:187:GLU:OE1	15:I:189:ARG:HB2	2.20	0.42
22:E:133:LYS:N	22:E:133:LYS:HD2	2.33	0.42
27:K:61:PRO:HG3	27:K:136:MET:HE3	2.01	0.42
27:K:361:ALA:O	27:K:364:TYR:HB3	2.20	0.42
28:C:336:ARG:HA	28:C:339:THR:HG22	2.00	0.42
34:a:123:ILE:HD12	38:L:169:ILE:HD11	2.02	0.42
2:5:460:C:H2'	2:5:461:G:C8	2.54	0.42
2:5:734:G:C6	2:5:825:G:C5	3.07	0.42
2:5:1215:G:N2	2:5:1394:U:C2	2.88	0.42
2:5:1248:C:H2'	2:5:1249:C:H6	1.84	0.42
2:5:1859:C:H3'	2:5:1860:C:H5''	2.01	0.42
2:5:2308:C:H2'	2:5:2309:G:O4'	2.20	0.42
2:5:3339:U:H2'	2:5:3340:A:H8	1.85	0.42
2:5:3587:C:H2'	2:5:3588:A:H8	1.84	0.42
2:5:3679:A:H2'	2:5:3680:C:C6	2.54	0.42
2:5:4322:U:H2'	2:5:4323:U:C6	2.55	0.42
8:d:23:ARG:NH1	8:d:25:TYR:OH	2.47	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:8:154:G:H2'	9:8:155:C:C6	2.55	0.42
10:G:210:ILE:HG23	10:G:254:THR:HG22	2.01	0.42
10:G:269:ALA:O	10:G:272:VAL:HG12	2.19	0.42
26:O:35:VAL:HG12	26:O:104:VAL:HG12	2.02	0.42
27:K:454:ILE:HD12	27:K:454:ILE:HA	1.90	0.42
28:C:149:GLU:OE2	30:r:71:ARG:NE	2.53	0.42
30:r:68:SER:OG	30:r:69:GLY:N	2.53	0.42
30:r:71:ARG:HG2	30:r:71:ARG:NH1	2.33	0.42
37:H:23:ARG:NH1	37:H:23:ARG:HG3	2.35	0.42
37:H:120:GLU:HG3	37:H:122:TYR:H	1.85	0.42
44:Y:30:MET:SD	44:Y:78:TYR:HA	2.59	0.42
45:X:131:ASP:OD1	45:X:131:ASP:C	2.62	0.42
46:U:56:LEU:HD23	46:U:61:VAL:HG13	2.02	0.42
1:T:87:LYS:NZ	2:5:4051:G:H22	2.18	0.42
2:5:253:G:H2'	2:5:254:G:C8	2.55	0.42
2:5:300:A:H2'	2:5:301:G:C8	2.55	0.42
2:5:379:G:O2'	2:5:380:U:H5'	2.19	0.42
2:5:726:A:H2'	2:5:727:A:O4'	2.19	0.42
2:5:863:G:O2'	2:5:864:A:H5'	2.20	0.42
2:5:1397:C:H1'	2:5:2052:G:N2	2.35	0.42
2:5:1398:A:C6	2:5:1399:G:C4	3.07	0.42
2:5:1666:U:OP1	3:F:130:ASN:ND2	2.53	0.42
2:5:2247:A:O2'	13:j:12:ARG:O	2.30	0.42
2:5:2311:U:C2	2:5:2349:G:N7	2.87	0.42
2:5:2475:U:C2	2:5:2476:U:C5	3.07	0.42
2:5:2510:C:OP1	24:R:100:ARG:NE	2.39	0.42
2:5:3439:U:H2'	2:5:3440:C:C6	2.55	0.42
2:5:4357:A:H2'	2:5:4358:C:H6	1.83	0.42
2:5:4465:G:O2'	2:5:4466:C:O5'	2.26	0.42
2:5:4519:C:C5	2:5:4603:U:O2	2.73	0.42
5:S:13:VAL:HA	5:S:28:TYR:O	2.20	0.42
9:8:15:G:H2'	9:8:16:G:O4'	2.19	0.42
9:8:144:U:H2'	9:8:145:C:C6	2.55	0.42
14:A:14:SER:OG	14:A:15:VAL:N	2.51	0.42
15:I:57:TYR:HD1	15:I:130:HIS:HA	1.83	0.42
23:Q:48:LEU:HD11	23:Q:52:PHE:CZ	2.54	0.42
31:f:37:ASP:OD1	31:f:37:ASP:N	2.51	0.42
37:H:36:ARG:HD3	37:H:38:PHE:CZ	2.54	0.42
37:H:51:LYS:HZ2	37:H:53:LYS:HG2	1.85	0.42
37:H:142:ASP:OD1	37:H:142:ASP:O	2.38	0.42
40:N:178:HIS:HA	40:N:181:HIS:NE2	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:M:77:TRP:NE1	43:M:82:ILE:HB	2.35	0.42
44:Y:55:VAL:CG1	44:Y:104:VAL:HG13	2.49	0.42
45:X:89:LYS:HG3	45:X:95:THR:HG22	2.01	0.42
45:X:95:THR:HG1	45:X:138:VAL:C	2.23	0.42
1:T:117:LYS:HB3	1:T:117:LYS:HE3	1.80	0.42
2:5:131:C:H2'	2:5:132:G:C8	2.55	0.42
2:5:184:U:O2'	2:5:189:G:O4'	2.38	0.42
2:5:763:C:H2'	2:5:764:G:H8	1.84	0.42
2:5:1223:A:O2'	2:5:1225:G:N7	2.52	0.42
2:5:1284:C:H2'	2:5:1285:U:H6	1.85	0.42
2:5:1554:G:H21	2:5:1556:A:C4'	2.33	0.42
2:5:1696:U:P	2:5:1707:C:H42	2.42	0.42
2:5:2582:C:H4'	17:p:52:VAL:HG21	2.02	0.42
2:5:4091:C:H2'	2:5:4092:U:H6	1.85	0.42
2:5:4362:A:O3'	7:B:65:SER:HB3	2.20	0.42
3:F:93:ARG:NH1	3:F:96:GLY:O	2.45	0.42
7:B:17:LEU:O	7:B:19:ARG:N	2.53	0.42
14:A:33:ASP:OD1	14:A:33:ASP:C	2.62	0.42
19:m:82:VAL:HG12	19:m:83:ASN:OD1	2.20	0.42
21:P:96:LYS:NZ	21:P:96:LYS:HB2	2.34	0.42
23:Q:35:LEU:HA	23:Q:35:LEU:HD23	1.86	0.42
27:K:227:VAL:O	27:K:230:LEU:HG	2.20	0.42
27:K:252:PHE:O	27:K:255:VAL:HG12	2.20	0.42
45:X:117:TYR:O	45:X:119:ILE:HG23	2.19	0.42
2:5:263:G:C4	2:5:264:C:C5	3.08	0.42
2:5:729:G:H4'	43:M:70:GLN:HE22	1.84	0.42
2:5:994:C:H2'	2:5:995:C:O4'	2.19	0.42
2:5:1132:U:H1'	2:5:1134:G:C4	2.54	0.42
2:5:2275:U:H5''	27:K:273:ARG:HD3	1.99	0.42
2:5:3798:U:H2'	2:5:3799:U:C6	2.55	0.42
2:5:4049:C:H2'	2:5:4051:G:H8	1.82	0.42
4:D:68:ARG:HG3	4:D:73:MET:HE3	2.00	0.42
4:D:187:SER:O	4:D:188:LYS:C	2.63	0.42
4:D:259:ARG:HD3	4:D:260:GLU:O	2.20	0.42
7:B:37:PRO:HA	7:B:187:GLY:O	2.20	0.42
7:B:184:GLN:NE2	7:B:186:ASN:OD1	2.53	0.42
9:8:51:U:H4'	20:l:21:ARG:HH12	1.83	0.42
10:G:233:PRO:HG2	10:G:272:VAL:HG22	2.02	0.42
12:c:62:TYR:HE2	35:g:99:GLU:HG3	1.85	0.42
23:Q:59:PRO:HG3	23:Q:143:ARG:HA	2.02	0.42
24:R:41:ILE:HD13	24:R:41:ILE:HA	1.88	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
27:K:268:LYS:HD2	27:K:402:ARG:CZ	2.49	0.42
36:k:51:GLU:HG2	36:k:55:LYS:HZ2	1.85	0.42
45:X:133:GLU:OE1	45:X:133:GLU:N	2.53	0.42
2:5:251:C:H2'	2:5:252:C:H6	1.84	0.41
2:5:260:C:H2'	2:5:261:G:C8	2.55	0.41
2:5:353:A:C4	2:5:379:G:N7	2.88	0.41
2:5:486:C:HO2'	2:5:487:C:P	2.43	0.41
2:5:1413:C:H2'	2:5:1414:A:H8	1.85	0.41
2:5:1478:A:N3	2:5:4135:C:O2'	2.47	0.41
2:5:1934:G:H2'	2:5:1935:C:C6	2.55	0.41
2:5:2383:C:H2'	2:5:2384:G:H8	1.84	0.41
2:5:2599:G:C6	2:5:2600:A:C6	3.08	0.41
2:5:2604:U:H4'	2:5:2605:G:O4'	2.19	0.41
2:5:2607:A:H2'	2:5:2608:A:H8	1.85	0.41
2:5:3603:A:H2'	2:5:3604:A:H8	1.82	0.41
2:5:4481:G:H2'	2:5:4482:C:O4'	2.21	0.41
2:5:4602:G:H2'	2:5:4603:U:H6	1.84	0.41
6:b:21:ILE:HD12	6:b:21:ILE:N	2.34	0.41
15:I:4:ARG:HG3	15:I:5:PRO:HD2	2.02	0.41
30:r:8:MET:HE3	30:r:8:MET:HB3	1.80	0.41
31:f:104:MET:HE2	31:f:106:TYR:OH	2.20	0.41
44:Y:10:ASP:OD1	44:Y:10:ASP:C	2.63	0.41
2:5:40:G:N2	2:5:4126:A:H62	2.18	0.41
2:5:91:G:H5'	2:5:92:C:H5''	2.02	0.41
2:5:106:A:H2'	2:5:107:G:O4'	2.20	0.41
2:5:153:G:H2'	2:5:154:G:C8	2.55	0.41
2:5:173:C:H2'	2:5:174:C:C6	2.56	0.41
2:5:197:A:N1	2:5:225:G:O2'	2.42	0.41
2:5:1426:U:H2'	2:5:1427:C:H6	1.85	0.41
2:5:2275:U:OP1	27:K:273:ARG:HG2	2.19	0.41
2:5:4151:G:P	15:I:7:ARG:HH21	2.43	0.41
8:d:65:ASP:OD1	8:d:66:THR:N	2.52	0.41
14:A:209:HIS:C	14:A:211:PHE:H	2.28	0.41
28:C:241:ALA:O	28:C:242:PRO:C	2.62	0.41
42:h:103:LYS:O	42:h:108:GLN:NE2	2.51	0.41
2:5:269:G:H2'	2:5:270:U:C6	2.55	0.41
2:5:473:C:C2	2:5:676:G:N2	2.88	0.41
2:5:1398:A:C2	2:5:1399:G:H1'	2.55	0.41
2:5:1422:C:H2'	2:5:1423:C:H6	1.84	0.41
2:5:1430:G:H2'	2:5:1431:C:C6	2.55	0.41
2:5:1528:G:OP1	24:R:92:LYS:NZ	2.52	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:1718:U:OP1	4:D:6:VAL:HG12	2.20	0.41
2:5:2658:A:H2'	2:5:2659:G:C8	2.55	0.41
2:5:3565:C:H2'	2:5:3566:C:H6	1.85	0.41
2:5:3679:A:H2'	2:5:3680:C:H6	1.86	0.41
2:5:3794:U:H2'	2:5:3795:U:O4'	2.20	0.41
2:5:4000:G:H1	2:5:4003:A:H62	1.68	0.41
2:5:4052:OMU:HM23	2:5:4052:OMU:H1'	1.58	0.41
2:5:4328:C:OP2	7:B:28:LYS:NZ	2.31	0.41
2:5:4519:C:O2	2:5:4519:C:H5'	2.20	0.41
5:S:82:LEU:HD21	5:S:84:TYR:HB3	2.02	0.41
11:J:141:ILE:HD13	11:J:141:ILE:HA	1.83	0.41
27:K:44:VAL:O	27:K:48:ILE:HD13	2.20	0.41
27:K:182:PHE:O	27:K:186:ASN:CG	2.63	0.41
27:K:347:PRO:HA	27:K:364:TYR:CG	2.55	0.41
2:5:1261:U:H2'	2:5:1262:C:C6	2.55	0.41
2:5:4203:U:O2	7:B:252:ALA:HB3	2.21	0.41
2:5:4490:G:H2'	2:5:4491:A:H8	1.86	0.41
13:j:48:ASN:HA	13:j:54:LYS:HD3	2.01	0.41
14:A:122:ASP:OD1	14:A:122:ASP:C	2.63	0.41
30:r:116:ALA:O	30:r:117:ILE:C	2.63	0.41
32:e:63:ASN:OD1	32:e:63:ASN:C	2.63	0.41
36:k:60:LEU:HD22	36:k:60:LEU:H	1.85	0.41
36:k:67:LYS:HD3	36:k:68:GLU:N	2.36	0.41
39:7:4:U:H2'	39:7:5:A:C8	2.55	0.41
40:N:136:ASP:OD1	40:N:136:ASP:C	2.63	0.41
2:5:808:U:H2'	2:5:809:G:O4'	2.20	0.41
2:5:1859:C:O2'	2:5:1861:G:H5''	2.20	0.41
2:5:2186:G:C5	28:C:101:MET:HE1	2.55	0.41
2:5:3424:A:N6	2:5:3555:G:H21	2.03	0.41
2:5:3961:C:C2	2:5:3962:G:C8	3.08	0.41
2:5:4717:G:O2'	2:5:4719:C:OP2	2.35	0.41
4:D:232:THR:OG1	4:D:234:ASP:OD1	2.28	0.41
7:B:54:THR:OG1	7:B:55:HIS:N	2.54	0.41
11:J:41:GLU:HA	11:J:44:THR:HG22	2.02	0.41
26:O:186:GLU:HA	26:O:189:ILE:HG13	2.02	0.41
27:K:219:LEU:HD11	27:K:236:ARG:HE	1.86	0.41
31:f:4:ARG:NH1	31:f:8:LYS:HE2	2.31	0.41
35:g:100:GLN:OE1	35:g:100:GLN:HA	2.20	0.41
45:X:90:ILE:HD13	45:X:96:LEU:HD23	2.02	0.41
1:T:84:ILE:HG22	6:b:24:PRO:HD3	2.03	0.41
1:T:129:LYS:NZ	2:5:1775:G:O5'	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:756:G:C8	2:5:756:G:OP2	2.72	0.41
2:5:1072:C:H1'	2:5:1074:C:C2	2.55	0.41
2:5:1350:G:O3'	2:5:1366:C:H5''	2.21	0.41
2:5:1665:U:H5'	3:F:134:ILE:HD11	2.02	0.41
2:5:2028:G:H1'	2:5:2029:U:OP2	2.21	0.41
2:5:2592:C:H4'	35:g:64:LEU:HB3	2.02	0.41
2:5:2608:A:H2'	2:5:2609:A:C8	2.56	0.41
2:5:3519:G:H1'	2:5:3521:C:N4	2.36	0.41
2:5:3655:A:H2'	2:5:3656:C:C6	2.55	0.41
2:5:3686:A:N6	2:5:3787:C:N3	2.68	0.41
2:5:3855:A:O2'	2:5:3856:A:H8	2.04	0.41
2:5:4658:G:C6	2:5:4659:C:C2	3.09	0.41
2:5:4786:C:O2'	2:5:4789:C:OP2	2.30	0.41
5:S:99:ASP:CG	5:S:100:LEU:N	2.79	0.41
10:G:130:PRO:HG2	10:G:133:ILE:HD12	2.02	0.41
14:A:77:ILE:HD11	14:A:115:CYS:HB2	2.02	0.41
14:A:242:ARG:HG2	14:A:243:THR:N	2.36	0.41
21:P:84:PRO:HB2	21:P:87:SER:OG	2.19	0.41
27:K:77:MET:C	27:K:79:LEU:N	2.76	0.41
27:K:292:ILE:HG13	27:K:293:LEU:N	2.36	0.41
27:K:449:LEU:O	27:K:453:ILE:HB	2.20	0.41
28:C:295:SER:OG	28:C:298:ILE:HG22	2.20	0.41
30:r:17:LEU:HD12	30:r:17:LEU:HA	1.93	0.41
32:e:21:ILE:HD13	32:e:21:ILE:HA	1.81	0.41
44:Y:91:ASN:OD1	44:Y:91:ASN:C	2.64	0.41
2:5:262:G:N3	2:5:263:G:C8	2.89	0.41
2:5:381:U:H4'	2:5:415:G:H5'	2.03	0.41
2:5:637:C:H2'	2:5:638:G:C8	2.55	0.41
2:5:839:G:H2'	2:5:840:C:C6	2.55	0.41
2:5:1125:C:O2'	2:5:1126:G:O5'	2.32	0.41
2:5:1270:A2M:OP2	2:5:4191:U:O2'	2.34	0.41
2:5:1416:C:C2	2:5:1417:A:C8	3.09	0.41
2:5:1513:A:H2'	2:5:1514:G:C8	2.56	0.41
2:5:1601:A:H2'	2:5:1602:U:C6	2.55	0.41
2:5:1750:G:H2'	2:5:1751:C:C6	2.55	0.41
2:5:1758:G:N3	4:D:113:PHE:CE1	2.87	0.41
2:5:1995:G:C8	2:5:1997:G:C8	3.08	0.41
2:5:2218:A:H2'	2:5:2219:A:H8	1.85	0.41
2:5:2345:A:O2'	2:5:2346:G:O5'	2.35	0.41
2:5:3384:A:H2'	2:5:3385:A:C8	2.55	0.41
2:5:4088:C:H2'	2:5:4089:U:C6	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:4388:U:H2'	2:5:4389:G:C8	2.54	0.41
2:5:4436:B8K:O2'	37:H:72:THR:OG1	2.29	0.41
3:F:114:ARG:NH1	23:Q:4:ASP:O	2.46	0.41
11:J:136:ARG:HB3	11:J:155:HIS:CE1	2.54	0.41
12:c:35:LEU:HD23	12:c:35:LEU:HA	1.85	0.41
14:A:97:ASN:OD1	14:A:97:ASN:C	2.63	0.41
14:A:158:ILE:CG2	14:A:162:ASN:HD21	2.33	0.41
24:R:99:MET:HE1	24:R:127:VAL:O	2.21	0.41
27:K:114:GLY:O	27:K:117:LYS:N	2.54	0.41
27:K:265:LEU:HA	27:K:265:LEU:HD23	1.82	0.41
37:H:36:ARG:NH2	37:H:152:GLU:OE2	2.52	0.41
38:L:55:ILE:HG12	38:L:56:ARG:N	2.36	0.41
45:X:72:ASP:O	45:X:76:ILE:HG12	2.20	0.41
46:U:82:TYR:HE1	46:U:86:LEU:HD11	1.85	0.41
2:5:108:A:N1	2:5:333:U:O2'	2.52	0.41
2:5:260:C:H2'	2:5:261:G:H8	1.85	0.41
2:5:423:G:H2'	2:5:424:U:C6	2.55	0.41
2:5:1400:U:H3	2:5:2048:A:H61	1.68	0.41
2:5:1405:C:C4'	2:5:2044:A:O2'	2.69	0.41
2:5:1588:G:H5'	2:5:1589:A:OP1	2.20	0.41
2:5:1805:U:H2'	2:5:1806:A:O4'	2.20	0.41
2:5:1948:A:H8	2:5:1948:A:OP1	2.04	0.41
2:5:2476:U:H2'	2:5:2477:C:H6	1.85	0.41
2:5:2681:G:OP1	7:B:248:LEU:N	2.52	0.41
2:5:3478:A:H5''	14:A:244:GLY:HA3	2.02	0.41
2:5:3601:OMC:HM23	2:5:3601:OMC:H1'	1.85	0.41
2:5:3997:A:H5''	11:J:108:GLY:HA3	2.02	0.41
2:5:4430:A:H2'	2:5:4431:U:O4'	2.21	0.41
2:5:4628:G:H2'	2:5:4629:G:H8	1.86	0.41
3:F:26:GLU:O	3:F:30:LYS:HG2	2.21	0.41
6:b:65:MET:O	6:b:68:ARG:HD3	2.20	0.41
7:B:155:LYS:HE2	7:B:156:TYR:CE1	2.55	0.41
8:d:29:ILE:H	8:d:29:ILE:HG12	1.67	0.41
11:J:168:GLN:C	11:J:168:GLN:OE1	2.64	0.41
24:R:115:ILE:CG2	24:R:142:ILE:HD11	2.49	0.41
27:K:62:PHE:HE2	27:K:299:SER:HA	1.84	0.41
27:K:168:LEU:HG	27:K:173:TYR:HD2	1.86	0.41
37:H:183:GLU:C	37:H:183:GLU:OE1	2.64	0.41
47:n:8:LYS:HB3	47:n:8:LYS:HE2	1.83	0.41
2:5:369:G:N2	2:5:372:A:OP2	2.41	0.41
2:5:422:C:H2'	2:5:423:G:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:450:G:H8	2:5:450:G:OP2	2.03	0.41
2:5:704:G:H2'	2:5:705:A:H8	1.85	0.41
2:5:751:G:C6	2:5:805:G:C6	3.09	0.41
2:5:880:G:OP1	22:E:64:MET:HG3	2.21	0.41
2:5:1399:G:N2	2:5:2049:G:H1	2.02	0.41
2:5:1489:A2M:N3	13:j:11:ARG:HB2	2.35	0.41
2:5:1715:A:N3	2:5:1715:A:H2'	2.35	0.41
2:5:1796:C:H2'	2:5:1797:A:H8	1.86	0.41
2:5:1871:A:H2'	2:5:1872:G:C8	2.55	0.41
2:5:1912:G:H2'	2:5:1913:U:C5	2.55	0.41
2:5:1946:G:C2	2:5:1952:A:N6	2.89	0.41
2:5:3496:PSU:H2'	2:5:3497:G:O4'	2.21	0.41
2:5:3864:G:H2'	2:5:3865:C:C6	2.56	0.41
2:5:4004:C:H2'	2:5:4005:C:H6	1.86	0.41
2:5:4239:U:O2'	2:5:4240:OMG:H5'	2.20	0.41
2:5:4476:C:C5	2:5:4704:U:C2	3.09	0.41
2:5:4518:C:O2'	2:5:4519:C:OP2	2.39	0.41
2:5:4622:C:H2'	2:5:4623:G:C8	2.55	0.41
3:F:66:THR:O	3:F:70:MET:HG2	2.20	0.41
3:F:124:LEU:HD12	3:F:129:ILE:CD1	2.51	0.41
5:S:20:PRO:HA	5:S:23:ARG:NH1	2.35	0.41
9:8:8:U:H2'	9:8:9:A:C8	2.55	0.41
9:8:78:G:H2'	9:8:79:G:C8	2.55	0.41
11:J:15:LEU:HD23	11:J:15:LEU:HA	1.86	0.41
11:J:155:HIS:HB2	39:7:55:A:H4'	2.02	0.41
14:A:96:LEU:HD21	17:p:83:ILE:HG23	2.03	0.41
18:V:35:LYS:HE3	18:V:35:LYS:HB3	1.94	0.41
18:V:108:ASN:OD1	18:V:108:ASN:C	2.64	0.41
22:E:215:LEU:HD12	22:E:215:LEU:O	2.21	0.41
24:R:103:ARG:HD2	24:R:124:TYR:CZ	2.56	0.41
26:O:175:MET:O	26:O:178:ARG:HB3	2.21	0.41
27:K:42:PHE:HE2	27:K:185:THR:HG1	1.56	0.41
27:K:186:ASN:O	27:K:190:THR:HG23	2.21	0.41
31:f:63:LYS:NZ	31:f:63:LYS:HB3	2.35	0.41
32:e:23:HIS:HA	32:e:53:ILE:HD12	2.03	0.41
33:Z:11:VAL:HG11	33:Z:80:LEU:HD22	2.01	0.41
34:a:123:ILE:HD13	34:a:123:ILE:N	2.36	0.41
34:a:134:GLU:OE2	38:L:178:ALA:N	2.54	0.41
36:k:25:ILE:HD12	36:k:34:PHE:CD2	2.56	0.41
36:k:58:GLN:H	36:k:58:GLN:CD	2.22	0.41
40:N:90:ASN:O	40:N:90:ASN:ND2	2.47	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:N:124:ASP:OD1	40:N:124:ASP:C	2.64	0.41
42:h:22:ASP:O	42:h:26:VAL:HG13	2.21	0.41
42:h:69:LEU:HD13	45:X:64:SER:HB2	2.01	0.41
46:U:84:LYS:HB2	46:U:110:TYR:CZ	2.55	0.41
2:5:161:G:H2'	2:5:162:A:C8	2.56	0.41
2:5:429:A:H2'	2:5:430:G:H8	1.86	0.41
2:5:459:C:C4'	22:E:113:ARG:HH22	2.34	0.41
2:5:516:U:H2'	2:5:517:C:H4'	2.03	0.41
2:5:699:G:H2'	2:5:700:C:H6	1.85	0.41
2:5:751:G:O2'	2:5:752:G:H5'	2.21	0.41
2:5:1208:C:H5'	6:b:95:ARG:CZ	2.51	0.41
2:5:1556:A:N7	2:5:3375:A:C4	2.89	0.41
2:5:2405:G:N2	2:5:2407:G:H3'	2.36	0.41
2:5:2707:A:H2'	2:5:2708:U:H6	1.86	0.41
2:5:3451:A:C4	2:5:3452:G:C8	3.09	0.41
2:5:3453:U:H2'	2:5:3454:G:H8	1.86	0.41
2:5:4668:C:OP1	43:M:114:LYS:NZ	2.49	0.41
9:8:9:A:H2'	9:8:10:G:H8	1.86	0.41
9:8:77:A:C6	9:8:78:G:C6	3.08	0.41
14:A:242:ARG:NH2	14:A:245:ARG:O	2.49	0.41
16:q:15:VAL:O	16:q:19:ILE:HG13	2.21	0.41
23:Q:178:ARG:HB2	34:a:53:PHE:O	2.21	0.41
27:K:27:GLN:O	27:K:31:LYS:N	2.53	0.41
27:K:69:LEU:HA	27:K:81:ILE:HG12	2.02	0.41
27:K:151:ILE:CA	27:K:154:GLN:HG2	2.50	0.41
27:K:260:GLY:O	27:K:261:PHE:C	2.64	0.41
29:o:66:ILE:O	29:o:66:ILE:HD12	2.21	0.41
33:Z:9:LYS:NZ	33:Z:83:THR:O	2.36	0.41
36:k:36:VAL:CG1	36:k:43:TYR:HB2	2.51	0.41
36:k:50:LYS:O	36:k:54:GLU:OE1	2.39	0.41
37:H:126:VAL:HG11	37:H:161:ILE:HG22	2.03	0.41
46:U:20:LYS:NZ	46:U:21:PHE:C	2.79	0.41
46:U:64:GLU:C	46:U:64:GLU:OE1	2.64	0.41
1:T:114:GLN:OE1	1:T:115:LYS:N	2.54	0.40
2:5:32:G:OP1	40:N:73:ARG:NH1	2.55	0.40
2:5:223:G:H4'	2:5:225:G:N7	2.36	0.40
2:5:259:C:H2'	2:5:260:C:H6	1.86	0.40
2:5:852:G:H2'	2:5:853:C:C6	2.56	0.40
2:5:1387:G:O2'	2:5:1407:A:N6	2.55	0.40
2:5:1403:G:C2	2:5:1404:C:C2	3.10	0.40
2:5:1600:C:H2'	2:5:1601:A:C8	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:1658:C:H2'	2:5:1659:C:C6	2.54	0.40
2:5:1943:U:C2	2:5:1955:C:H1'	2.56	0.40
2:5:2647:OMC:HM23	2:5:2647:OMC:H1'	1.66	0.40
2:5:3342:A:H2'	2:5:3343:A:C8	2.56	0.40
2:5:3466:U:H2'	2:5:3467:G:O4'	2.22	0.40
2:5:4007:C:H2'	2:5:4008:C:H6	1.86	0.40
2:5:4010:G:OP1	4:D:8:LYS:NZ	2.37	0.40
2:5:4225:A:H2'	2:5:4226:A:O4'	2.21	0.40
2:5:4451:A:H2'	2:5:4452:G:O4'	2.21	0.40
2:5:4698:U:H2'	2:5:4699:G:O4'	2.21	0.40
2:5:4742:U:H2'	2:5:4743:C:C6	2.56	0.40
9:8:64:U:C2	9:8:65:A:C8	3.09	0.40
9:8:93:C:O2'	9:8:94:G:H8	2.03	0.40
14:A:157:VAL:O	14:A:158:ILE:HD13	2.21	0.40
27:K:109:ARG:HA	27:K:112:PHE:CE2	2.56	0.40
38:L:6:ASN:OD1	38:L:7:GLY:N	2.54	0.40
2:5:273:U:H2'	2:5:274:C:C6	2.57	0.40
2:5:325:U:H2'	2:5:326:C:C6	2.57	0.40
2:5:419:A:N6	9:8:15:G:H1'	2.36	0.40
2:5:673:C:H2'	2:5:674:G:C8	2.56	0.40
2:5:1413:C:H2'	2:5:1414:A:C8	2.56	0.40
2:5:1549:C:O2'	2:5:1552:G:H1'	2.21	0.40
2:5:2186:G:C4	28:C:101:MET:HE1	2.56	0.40
2:5:2420:C:OP1	33:Z:111:ARG:NH2	2.53	0.40
2:5:3891:G:H2'	2:5:3892:G:H8	1.85	0.40
3:F:247:ASN:OD1	3:F:247:ASN:C	2.64	0.40
4:D:244:HIS:O	4:D:248:ARG:HG3	2.21	0.40
5:S:100:LEU:HD11	43:M:49:ALA:HB2	2.03	0.40
10:G:164:LYS:O	10:G:167:LEU:HG	2.21	0.40
10:G:201:GLU:HA	10:G:230:MET:CE	2.49	0.40
12:c:94:LEU:HD22	12:c:95:SER:H	1.86	0.40
13:j:34:CYS:HB3	13:j:39:TYR:H	1.87	0.40
18:V:109:LYS:HE2	18:V:109:LYS:HB2	1.74	0.40
27:K:151:ILE:CD1	27:K:154:GLN:NE2	2.84	0.40
27:K:294:GLN:C	27:K:296:ALA:H	2.29	0.40
27:K:325:SER:O	27:K:335:ALA:HA	2.22	0.40
29:o:36:GLN:HE21	34:a:59:ARG:HH22	1.68	0.40
32:e:85:LEU:HD12	32:e:85:LEU:HA	1.86	0.40
32:e:105:SER:HA	32:e:108:ARG:HB2	2.03	0.40
2:5:137:G:N1	2:5:138:G:C5	2.89	0.40
2:5:1459:G:H2'	2:5:1460:C:C6	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:1971:U:H2'	2:5:1972:A:C8	2.57	0.40
2:5:2116:G:H2'	2:5:2117:C:H6	1.86	0.40
2:5:2514:C:H2'	2:5:2515:C:C6	2.57	0.40
2:5:2570:C:H2'	2:5:2571:U:C6	2.57	0.40
2:5:3982:G:H4'	2:5:4074:G:O2'	2.20	0.40
2:5:4339:C:H2'	2:5:4340:U:H6	1.87	0.40
2:5:4487:A:C4	2:5:4639:C:N4	2.88	0.40
2:5:4631:A:N7	2:5:4632:A:N6	2.69	0.40
2:5:4670:G:C6	2:5:4671:U:C4	3.09	0.40
3:F:155:LYS:NZ	3:F:247:ASN:OXT	2.49	0.40
7:B:189:THR:HG1	7:B:192:GLU:CD	2.23	0.40
14:A:66:PRO:HG2	14:A:67:TYR:CD1	2.56	0.40
20:l:44:TRP:H	20:l:44:TRP:CD1	2.39	0.40
22:E:144:ARG:NH2	31:f:110:ILE:OXT	2.54	0.40
23:Q:34:PHE:CE1	28:C:302:LEU:HD21	2.56	0.40
27:K:345:LEU:HD23	27:K:363:VAL:CG1	2.52	0.40
27:K:374:PHE:O	27:K:378:THR:HG22	2.21	0.40
30:r:26:SER:OG	30:r:28:GLU:OE1	2.34	0.40
37:H:90:TYR:CE1	37:H:184:LYS:HB3	2.56	0.40
1:T:160:ALA:O	15:I:166:HIS:ND1	2.55	0.40
2:5:231:U:H4'	44:Y:100:HIS:CD2	2.56	0.40
2:5:1522:U:H2'	2:5:1523:C:H6	1.87	0.40
2:5:1947:U:H5'	2:5:1948:A:OP2	2.21	0.40
2:5:2178:C:H2'	2:5:2179:G:H8	1.87	0.40
2:5:3455:A2M:HM'3	2:5:3455:A2M:H1'	1.84	0.40
2:5:3670:G:H4'	2:5:3671:G:O5'	2.21	0.40
2:5:4139:G:O4'	2:5:4193:5MC:HM53	2.22	0.40
2:5:4384:U:H2'	2:5:4385:G:N3	2.36	0.40
2:5:4642:G:C6	2:5:4658:G:C6	3.09	0.40
2:5:4659:C:C4	2:5:4660:C:N4	2.88	0.40
22:E:281:THR:O	22:E:284:VAL:HG22	2.21	0.40
32:e:99:ILE:N	32:e:99:ILE:HD13	2.36	0.40
41:i:57:ALA:HB1	41:i:73:ILE:HD11	2.03	0.40
46:U:37:ALA:O	46:U:40:GLU:N	2.55	0.40
2:5:172:C:O2	42:h:112:ARG:NH2	2.54	0.40
2:5:275:C:H4'	2:5:276:C:OP1	2.21	0.40
2:5:684:C:H2'	2:5:685:C:H6	1.85	0.40
2:5:724:G:OP2	3:F:75:ARG:NH2	2.42	0.40
2:5:821:C:H2'	2:5:822:C:H6	1.85	0.40
2:5:1341:A:H5'	34:a:113:GLY:O	2.22	0.40
2:5:1405:C:H2'	2:5:1406:G:C8	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:5:3894:C:O3'	33:Z:60:LYS:NZ	2.53	0.40
2:5:4163:C:H2'	2:5:4164:G:O4'	2.22	0.40
2:5:4190:C:H2'	2:5:4191:U:H6	1.87	0.40
2:5:4612:G:C2	26:O:175:MET:CE	3.04	0.40
2:5:4640:G:C2	2:5:4641:C:C2	3.10	0.40
2:5:4749:U:H2'	2:5:4750:A:H8	1.86	0.40
13:j:67:LEU:HA	13:j:70:VAL:CG1	2.50	0.40
18:V:92:ASP:OD1	18:V:92:ASP:C	2.65	0.40
27:K:48:ILE:HG22	27:K:76:LEU:HD21	2.03	0.40
27:K:82:SER:N	27:K:83:PRO:HD2	2.36	0.40
27:K:267:ILE:HD13	27:K:267:ILE:HA	1.89	0.40
28:C:349:LEU:O	28:C:352:GLU:HG3	2.22	0.40
33:Z:89:ILE:HD11	33:Z:117:LYS:HB3	2.04	0.40
47:n:16:LYS:NZ	47:n:16:LYS:HB2	2.36	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	
1	T	157/159 (99%)	153 (98%)	4 (2%)	0	100	100
3	F	223/225 (99%)	215 (96%)	8 (4%)	0	100	100
4	D	291/293 (99%)	284 (98%)	7 (2%)	0	100	100
5	S	174/176 (99%)	168 (97%)	6 (3%)	0	100	100
6	b	100/245 (41%)	97 (97%)	3 (3%)	0	100	100
7	B	392/394 (100%)	382 (97%)	10 (3%)	0	100	100
8	d	105/107 (98%)	102 (97%)	3 (3%)	0	100	100
10	G	229/319 (72%)	219 (96%)	10 (4%)	0	100	100
11	J	168/170 (99%)	159 (95%)	9 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	c	96/98 (98%)	96 (100%)	0	0	100	100
13	j	84/86 (98%)	84 (100%)	0	0	100	100
14	A	246/257 (96%)	229 (93%)	17 (7%)	0	100	100
15	I	201/214 (94%)	193 (96%)	8 (4%)	0	100	100
16	q	65/68 (96%)	65 (100%)	0	0	100	100
17	p	89/91 (98%)	85 (96%)	4 (4%)	0	100	100
18	V	129/131 (98%)	128 (99%)	1 (1%)	0	100	100
19	m	49/52 (94%)	46 (94%)	3 (6%)	0	100	100
20	l	48/50 (96%)	44 (92%)	4 (8%)	0	100	100
21	P	151/153 (99%)	148 (98%)	3 (2%)	0	100	100
22	E	208/291 (72%)	198 (95%)	9 (4%)	1 (0%)	24	55
23	Q	185/188 (98%)	175 (95%)	10 (5%)	0	100	100
24	R	178/196 (91%)	174 (98%)	4 (2%)	0	100	100
25	W	61/157 (39%)	58 (95%)	3 (5%)	0	100	100
26	O	197/203 (97%)	192 (98%)	5 (2%)	0	100	100
27	K	442/476 (93%)	430 (97%)	11 (2%)	1 (0%)	43	72
28	C	359/362 (99%)	343 (96%)	16 (4%)	0	100	100
29	o	101/103 (98%)	93 (92%)	8 (8%)	0	100	100
30	r	122/124 (98%)	120 (98%)	2 (2%)	0	100	100
31	f	107/109 (98%)	104 (97%)	3 (3%)	0	100	100
32	e	126/128 (98%)	122 (97%)	4 (3%)	0	100	100
33	Z	133/135 (98%)	130 (98%)	3 (2%)	0	100	100
34	a	145/147 (99%)	138 (95%)	6 (4%)	1 (1%)	18	47
35	g	112/114 (98%)	110 (98%)	2 (2%)	0	100	100
36	k	67/70 (96%)	65 (97%)	2 (3%)	0	100	100
37	H	188/190 (99%)	184 (98%)	4 (2%)	0	100	100
38	L	208/211 (99%)	201 (97%)	7 (3%)	0	100	100
40	N	201/203 (99%)	193 (96%)	8 (4%)	0	100	100
41	i	100/105 (95%)	95 (95%)	5 (5%)	0	100	100
42	h	120/122 (98%)	119 (99%)	1 (1%)	0	100	100
43	M	136/138 (99%)	131 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
44	Y	132/134 (98%)	130 (98%)	2 (2%)	0	100	100
45	X	116/118 (98%)	112 (97%)	4 (3%)	0	100	100
46	U	97/99 (98%)	88 (91%)	9 (9%)	0	100	100
47	n	23/25 (92%)	23 (100%)	0	0	100	100
All	All	6861/7436 (92%)	6625 (97%)	233 (3%)	3 (0%)	100	100

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
34	a	16	SER
22	E	118	TYR
27	K	110	ALA

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	T	139/139 (100%)	136 (98%)	3 (2%)	45	78
3	F	196/196 (100%)	196 (100%)	0	100	100
4	D	247/247 (100%)	243 (98%)	4 (2%)	55	83
5	S	157/157 (100%)	155 (99%)	2 (1%)	61	86
6	b	84/184 (46%)	82 (98%)	2 (2%)	43	77
7	B	342/342 (100%)	339 (99%)	3 (1%)	70	89
8	d	98/98 (100%)	95 (97%)	3 (3%)	35	70
10	G	200/272 (74%)	196 (98%)	4 (2%)	48	80
11	J	143/143 (100%)	140 (98%)	3 (2%)	47	79
12	c	84/84 (100%)	82 (98%)	2 (2%)	43	77
13	j	73/73 (100%)	72 (99%)	1 (1%)	59	85
14	A	190/199 (96%)	185 (97%)	5 (3%)	40	75
15	I	175/181 (97%)	171 (98%)	4 (2%)	44	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	q	58/59 (98%)	58 (100%)	0	100	100
17	p	74/74 (100%)	70 (95%)	4 (5%)	20	51
18	V	101/101 (100%)	97 (96%)	4 (4%)	28	63
19	m	47/47 (100%)	47 (100%)	0	100	100
20	l	47/47 (100%)	47 (100%)	0	100	100
21	P	134/134 (100%)	131 (98%)	3 (2%)	45	78
22	E	190/251 (76%)	188 (99%)	2 (1%)	65	87
23	Q	164/165 (99%)	158 (96%)	6 (4%)	30	65
24	R	159/175 (91%)	155 (98%)	4 (2%)	42	76
25	W	55/126 (44%)	53 (96%)	2 (4%)	31	66
26	O	171/173 (99%)	166 (97%)	5 (3%)	37	73
27	K	370/398 (93%)	359 (97%)	11 (3%)	36	72
28	C	301/301 (100%)	300 (100%)	1 (0%)	86	95
29	o	91/91 (100%)	87 (96%)	4 (4%)	25	59
30	r	108/108 (100%)	107 (99%)	1 (1%)	70	89
31	f	88/88 (100%)	88 (100%)	0	100	100
32	e	114/114 (100%)	114 (100%)	0	100	100
33	Z	117/117 (100%)	114 (97%)	3 (3%)	40	75
34	a	119/119 (100%)	119 (100%)	0	100	100
35	g	98/98 (100%)	91 (93%)	7 (7%)	13	39
36	k	64/65 (98%)	62 (97%)	2 (3%)	35	70
37	H	169/169 (100%)	167 (99%)	2 (1%)	63	87
38	L	175/176 (99%)	172 (98%)	3 (2%)	53	83
40	N	171/171 (100%)	169 (99%)	2 (1%)	63	87
41	i	86/89 (97%)	81 (94%)	5 (6%)	18	49
42	h	109/109 (100%)	107 (98%)	2 (2%)	51	82
43	M	117/117 (100%)	115 (98%)	2 (2%)	53	83
44	Y	124/124 (100%)	119 (96%)	5 (4%)	28	63
45	X	106/106 (100%)	104 (98%)	2 (2%)	50	81
46	U	89/89 (100%)	89 (100%)	0	100	100
47	n	24/24 (100%)	22 (92%)	2 (8%)	10	32

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	5968/6340 (94%)	5848 (98%)	120 (2%)	48 80

All (120) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	T	40	VAL
1	T	43	LYS
1	T	69	GLN
4	D	7	VAL
4	D	45	ASN
4	D	75	VAL
4	D	116	ASP
5	S	67	VAL
5	S	90	THR
6	b	19	ASN
6	b	27	GLN
7	B	194	LEU
7	B	329	ASP
7	B	353	VAL
8	d	26	THR
8	d	46	LEU
8	d	80	VAL
10	G	160	LYS
10	G	218	GLU
10	G	237	LEU
10	G	303	ILE
11	J	47	THR
11	J	59	SER
11	J	72	CYS
12	c	52	CYS
12	c	78	ASN
13	j	64	MET
14	A	101	VAL
14	A	135	THR
14	A	158	ILE
14	A	194	ASN
14	A	208	GLU
15	I	59	GLN
15	I	96	VAL
15	I	101	LYS
15	I	164	LYS
17	p	3	LYS

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Mol	Chain	Res	Type
17	p	21	SER
17	p	32	SER
17	p	63	THR
18	V	18	LEU
18	V	87	SER
18	V	128	LEU
18	V	134	SER
21	P	54	LYS
21	P	100	SER
21	P	111	SER
22	E	64	MET
22	E	264	ILE
23	Q	8	ASN
23	Q	79	THR
23	Q	95	VAL
23	Q	148	VAL
23	Q	154	LYS
23	Q	183	SER
24	R	12	SER
24	R	44	LEU
24	R	59	SER
24	R	122	SER
25	W	41	LEU
25	W	48	GLN
26	O	5	GLN
26	O	36	VAL
26	O	61	ARG
26	O	145	VAL
26	O	194	ASP
27	K	77	MET
27	K	89	LEU
27	K	102	VAL
27	K	162	VAL
27	K	183	ILE
27	K	235	TYR
27	K	241	ASN
27	K	293	LEU
27	K	360	HIS
27	K	451	VAL
27	K	453	ILE
28	C	94	ASN
29	o	2	VAL

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Mol	Chain	Res	Type
29	o	33	LEU
29	o	55	ILE
29	o	66	ILE
30	r	76	SER
33	Z	12	LEU
33	Z	26	VAL
33	Z	53	VAL
35	g	31	VAL
35	g	64	LEU
35	g	67	LEU
35	g	74	VAL
35	g	75	SER
35	g	81	SER
35	g	106	VAL
36	k	12	LEU
36	k	46	VAL
37	H	41	ILE
37	H	50	LYS
38	L	106	SER
38	L	124	LEU
38	L	160	VAL
40	N	80	THR
40	N	98	LEU
41	i	33	LEU
41	i	34	THR
41	i	76	ARG
41	i	89	GLU
41	i	91	SER
42	h	49	VAL
42	h	88	THR
43	M	44	ARG
43	M	62	LEU
44	Y	20	ASN
44	Y	34	LEU
44	Y	104	VAL
44	Y	113	LYS
44	Y	125	SER
45	X	51	THR
45	X	133	GLU
47	n	8	LYS
47	n	17	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (53)

such sidechains are listed below:

Mol	Chain	Res	Type
1	T	77	ASN
3	F	62	GLN
3	F	118	ASN
4	D	122	GLN
4	D	202	GLN
4	D	229	ASN
4	D	282	GLN
5	S	37	HIS
6	b	94	HIS
7	B	123	HIS
7	B	184	GLN
7	B	204	GLN
7	B	209	GLN
8	d	121	ASN
10	G	161	GLN
10	G	165	GLN
12	c	33	GLN
13	j	66	HIS
14	A	38	HIS
14	A	162	ASN
14	A	205	ASN
15	I	73	ASN
17	p	72	ASN
20	l	25	GLN
21	P	21	ASN
21	P	137	ASN
22	E	248	GLN
23	Q	160	HIS
23	Q	188	ASN
27	K	154	GLN
27	K	186	ASN
27	K	218	HIS
27	K	360	HIS
27	K	404	HIS
28	C	116	ASN
28	C	215	ASN
28	C	286	ASN
30	r	4	HIS
30	r	31	ASN
30	r	36	ASN
30	r	83	ASN
32	e	34	ASN

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Mol	Chain	Res	Type
33	Z	127	ASN
34	a	34	ASN
34	a	39	HIS
34	a	85	GLN
38	L	19	GLN
40	N	15	GLN
40	N	57	GLN
40	N	156	HIS
40	N	182	HIS
42	h	98	HIS
45	X	151	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	5	3602/4808 (74%)	700 (19%)	55 (1%)
39	7	119/120 (99%)	12 (10%)	0
9	8	149/156 (95%)	26 (17%)	1 (0%)
All	All	3870/5084 (76%)	738 (19%)	56 (1%)

All (738) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	5	12	A
2	5	13	U
2	5	25	A
2	5	30	C
2	5	39	A
2	5	42	A
2	5	58	G
2	5	59	A
2	5	64	A
2	5	65	A
2	5	73	A
2	5	76	A
2	5	91	G
2	5	104	G
2	5	108	A
2	5	109	G
2	5	110	C
2	5	119	G

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Mol	Chain	Res	Type
2	5	120	A
2	5	126	C
2	5	134	G
2	5	135	G
2	5	136	C
2	5	137	G
2	5	142	G
2	5	152	U
2	5	157	U
2	5	159	C
2	5	172	C
2	5	173	C
2	5	182	G
2	5	185	C
2	5	187	U
2	5	188	G
2	5	189	G
2	5	200	U
2	5	201	C
2	5	209	U
2	5	216	C
2	5	217	C
2	5	218	A
2	5	220	C
2	5	224	U
2	5	233	U
2	5	234	G
2	5	246	G
2	5	265	C
2	5	266	C
2	5	274	C
2	5	275	C
2	5	276	C
2	5	280	G
2	5	297	U
2	5	306	A
2	5	309	C
2	5	315	G
2	5	316	U
2	5	322	C
2	5	334	A
2	5	340	C

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Mol	Chain	Res	Type
2	5	350	C
2	5	362	A
2	5	373	G
2	5	386	A
2	5	387	G
2	5	406	C
2	5	407	A
2	5	408	A
2	5	409	G
2	5	410	A
2	5	412	G
2	5	418	A
2	5	449	C
2	5	450	G
2	5	452	A
2	5	453	G
2	5	454	U
2	5	457	G
2	5	463	A
2	5	464	G
2	5	467	U
2	5	468	U
2	5	487	C
2	5	493	U
2	5	494	G
2	5	498	G
2	5	499	C
2	5	502	U
2	5	505	C
2	5	506	G
2	5	507	G
2	5	515	U
2	5	517	C
2	5	660	G
2	5	663	C
2	5	678	G
2	5	679	C
2	5	680	A
2	5	691	G
2	5	698	C
2	5	699	G
2	5	721	C

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Mol	Chain	Res	Type
2	5	722	U
2	5	723	G
2	5	724	G
2	5	725	G
2	5	726	A
2	5	732	C
2	5	734	G
2	5	738	G
2	5	742	A
2	5	744	G
2	5	753	G
2	5	756	G
2	5	758	C
2	5	763	C
2	5	787	C
2	5	790	G
2	5	791	C
2	5	792	G
2	5	793	C
2	5	795	A
2	5	797	C
2	5	798	C
2	5	799	C
2	5	800	U
2	5	814	A
2	5	824	C
2	5	825	G
2	5	828	A
2	5	830	C
2	5	831	A
2	5	832	G
2	5	833	C
2	5	834	A
2	5	835	G
2	5	838	C
2	5	839	G
2	5	841	C
2	5	844	A
2	5	845	U
2	5	856	A
2	5	859	G
2	5	860	A

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Mol	Chain	Res	Type
2	5	861	G
2	5	864	A
2	5	866	A
2	5	867	C
2	5	868	C
2	5	869	U
2	5	872	G
2	5	879	C
2	5	884	U
2	5	987	C
2	5	988	G
2	5	994	C
2	5	996	C
2	5	1066	A
2	5	1070	U
2	5	1071	C
2	5	1072	C
2	5	1073	C
2	5	1074	C
2	5	1084	C
2	5	1086	G
2	5	1101	C
2	5	1102	G
2	5	1103	G
2	5	1105	C
2	5	1106	C
2	5	1107	C
2	5	1121	G
2	5	1122	C
2	5	1123	C
2	5	1124	A
2	5	1126	G
2	5	1127	G
2	5	1129	G
2	5	1131	G
2	5	1132	U
2	5	1133	C
2	5	1135	C
2	5	1136	G
2	5	1206	C
2	5	1208	C
2	5	1209	G

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Mol	Chain	Res	Type
2	5	1210	C
2	5	1214	A
2	5	1215	G
2	5	1216	C
2	5	1217	G
2	5	1219	G
2	5	1220	C
2	5	1224	C
2	5	1228	G
2	5	1229	U
2	5	1231	G
2	5	1236	C
2	5	1237	G
2	5	1239	U
2	5	1240	G
2	5	1245	C
2	5	1248	C
2	5	1258	C
2	5	1270	A2M
2	5	1274	A
2	5	1281	A
2	5	1292	P4U
2	5	1298	A
2	5	1302	G
2	5	1303	G
2	5	1309	C
2	5	1310	G
2	5	1315	A
2	5	1316	A
2	5	1321	G
2	5	1323	C
2	5	1324	G
2	5	1331	A
2	5	1338	G
2	5	1341	A
2	5	1342	A
2	5	1346	C
2	5	1348	G
2	5	1349	C
2	5	1350	G
2	5	1366	C
2	5	1367	G

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Mol	Chain	Res	Type
2	5	1369	C
2	5	1370	G
2	5	1376	G
2	5	1384	C
2	5	1389	G
2	5	1393	C
2	5	1394	U
2	5	1395	U
2	5	1400	U
2	5	1401	C
2	5	1402	C
2	5	1412	G
2	5	1437	G
2	5	1438	C
2	5	1439	G
2	5	1452	A
2	5	1453	G
2	5	1456	C
2	5	1457	G
2	5	1469	U
2	5	1472	G
2	5	1478	A
2	5	1479	A2M
2	5	1489	A2M
2	5	1490	C
2	5	1502	A
2	5	1517	G
2	5	1521	C
2	5	1529	G
2	5	1533	U
2	5	1537	PSU
2	5	1546	U
2	5	1551	U
2	5	1557	U
2	5	1567	G
2	5	1568	A
2	5	1579	G
2	5	1580	OMG
2	5	1586	A
2	5	1588	G
2	5	1589	A
2	5	1595	C

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Mol	Chain	Res	Type
2	5	1609	G
2	5	1616	C
2	5	1631	C
2	5	1632	PSU
2	5	1633	C
2	5	1660	G
2	5	1670	C
2	5	1673	G
2	5	1680	G
2	5	1681	A
2	5	1685	A
2	5	1689	G
2	5	1692	G
2	5	1694	C
2	5	1695	U
2	5	1696	U
2	5	1699	G
2	5	1700	G
2	5	1703	G
2	5	1707	C
2	5	1711	C
2	5	1712	U
2	5	1714	A
2	5	1715	A
2	5	1720	U
2	5	1726	A
2	5	1736	E7G
2	5	1743	A
2	5	1744	A
2	5	1746	C
2	5	1751	C
2	5	1754	G
2	5	1758	G
2	5	1760	G
2	5	1767	C
2	5	1774	G
2	5	1775	G
2	5	1776	A
2	5	1781	G
2	5	1794	G
2	5	1808	G
2	5	1821	U

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Mol	Chain	Res	Type
2	5	1828	U
2	5	1829	G
2	5	1836	A
2	5	1838	G
2	5	1857	U
2	5	1859	C
2	5	1860	C
2	5	1861	G
2	5	1869	U
2	5	1870	C
2	5	1871	A
2	5	1887	G
2	5	1890	G
2	5	1896	U
2	5	1897	A
2	5	1900	G
2	5	1901	A
2	5	1903	A
2	5	1910	U
2	5	1913	U
2	5	1919	U
2	5	1923	A
2	5	1924	G
2	5	1926	C
2	5	1929	A
2	5	1930	A
2	5	1931	U
2	5	1933	C
2	5	1936	U
2	5	1940	G
2	5	1941	A
2	5	1942	G
2	5	1946	G
2	5	1947	U
2	5	1965	A
2	5	1968	A
2	5	1969	A
2	5	1986	A
2	5	1987	U
2	5	1991	G
2	5	1994	G
2	5	1995	G

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Mol	Chain	Res	Type
2	5	2008	A
2	5	2023	U
2	5	2029	U
2	5	2031	G
2	5	2032	G
2	5	2036	A
2	5	2037	G
2	5	2039	G
2	5	2041	G
2	5	2044	A
2	5	2045	G
2	5	2047	G
2	5	2048	A
2	5	2049	G
2	5	2102	G
2	5	2103	C
2	5	2110	U
2	5	2111	A
2	5	2118	G
2	5	2122	A
2	5	2132	C
2	5	2143	A
2	5	2144	G
2	5	2149	G
2	5	2156	A
2	5	2174	G
2	5	2176	G
2	5	2191	G
2	5	2194	C
2	5	2203	A
2	5	2238	A
2	5	2241	U
2	5	2260	A
2	5	2265	OMC
2	5	2267	OMG
2	5	2268	U
2	5	2276	G
2	5	2284	C
2	5	2293	G
2	5	2314	G
2	5	2318	G
2	5	2331	C

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Mol	Chain	Res	Type
2	5	2332	C
2	5	2333	U
2	5	2334	C
2	5	2338	U
2	5	2346	G
2	5	2347	C
2	5	2348	C
2	5	2349	G
2	5	2356	A
2	5	2363	C
2	5	2372	A
2	5	2380	A
2	5	2387	G
2	5	2389	G
2	5	2390	G
2	5	2396	A
2	5	2403	C
2	5	2426	C
2	5	2429	G
2	5	2432	C
2	5	2444	A
2	5	2461	G
2	5	2462	G
2	5	2463	G
2	5	2470	C
2	5	2481	G
2	5	2483	G
2	5	2492	G
2	5	2496	C
2	5	2504	U
2	5	2505	G
2	5	2512	C
2	5	2529	G
2	5	2530	U
2	5	2538	A
2	5	2539	A
2	5	2550	U
2	5	2551	U
2	5	2554	G
2	5	2558	G
2	5	2559	C
2	5	2564	G

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Mol	Chain	Res	Type
2	5	2566	U
2	5	2568	A
2	5	2569	G
2	5	2583	U
2	5	2586	A
2	5	2587	A
2	5	2596	G
2	5	2597	G
2	5	2598	A
2	5	2602	G
2	5	2606	U
2	5	2607	A
2	5	2612	U
2	5	2630	A
2	5	2631	U
2	5	2633	U
2	5	2657	C
2	5	2669	U
2	5	2670	G
2	5	2685	G
2	5	2688	A
2	5	2698	G
2	5	2741	G
2	5	3330	C
2	5	3336	A
2	5	3337	C
2	5	3338	U
2	5	3349	G
2	5	3357	G
2	5	3358	G
2	5	3367	A
2	5	3380	A
2	5	3389	U
2	5	3394	A
2	5	3396	G
2	5	3405	C
2	5	3443	A
2	5	3444	A
2	5	3446	G
2	5	3461	PSU
2	5	3480	A
2	5	3485	G

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Mol	Chain	Res	Type
2	5	3488	A
2	5	3491	A
2	5	3492	A
2	5	3493	C
2	5	3494	B8H
2	5	3495	A
2	5	3496	PSU
2	5	3505	U
2	5	3506	A
2	5	3509	G
2	5	3510	U
2	5	3516	A
2	5	3517	A
2	5	3519	G
2	5	3520	C
2	5	3524	OMG
2	5	3542	C
2	5	3543	G
2	5	3544	C
2	5	3546	U
2	5	3549	A
2	5	3551	G
2	5	3570	U
2	5	3572	U
2	5	3609	A
2	5	3610	C
2	5	3611	G
2	5	3612	P7G
2	5	3621	G
2	5	3629	B8K
2	5	3633	A
2	5	3637	A
2	5	3638	A
2	5	3639	G
2	5	3640	A
2	5	3647	U
2	5	3648	G
2	5	3649	A
2	5	3659	U
2	5	3670	G
2	5	3671	G
2	5	3683	G

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Mol	Chain	Res	Type
2	5	3684	A
2	5	3687	A
2	5	3788	C
2	5	3789	G
2	5	3794	U
2	5	3801	A
2	5	3804	G
2	5	3812	G
2	5	3814	G
2	5	3816	C
2	5	3825	G
2	5	3844	C
2	5	3847	C
2	5	3848	U
2	5	3849	G
2	5	3853	C
2	5	3855	A
2	5	3904	C
2	5	3908	C
2	5	3909	U
2	5	3910	C
2	5	3912	G
2	5	3916	A
2	5	3929	G
2	5	3930	G
2	5	3937	G
2	5	3940	U
2	5	3941	G
2	5	3942	G
2	5	3944	G
2	5	3949	A
2	5	3971	G
2	5	3975	U
2	5	3979	A
2	5	3997	A
2	5	4000	G
2	5	4001	A
2	5	4012	G
2	5	4014	A
2	5	4017	A
2	5	4019	A
2	5	4027	A

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Mol	Chain	Res	Type
2	5	4037	G
2	5	4039	PSU
2	5	4051	G
2	5	4052	OMU
2	5	4053	A
2	5	4060	C
2	5	4064	C
2	5	4065	C
2	5	4076	G
2	5	4078	C
2	5	4081	C
2	5	4085	A
2	5	4095	C
2	5	4096	C
2	5	4117	G
2	5	4118	U
2	5	4119	G
2	5	4123	G
2	5	4124	A
2	5	4126	A
2	5	4133	C
2	5	4140	A
2	5	4141	U
2	5	4142	A
2	5	4144	C
2	5	4165	U
2	5	4167	C
2	5	4168	A
2	5	4176	G
2	5	4186	G
2	5	4194	G
2	5	4195	A
2	5	4196	PSU
2	5	4198	U
2	5	4210	A
2	5	4240	OMG
2	5	4246	PSU
2	5	4256	A
2	5	4257	A
2	5	4258	U
2	5	4259	A
2	5	4264	A

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Mol	Chain	Res	Type
2	5	4265	C
2	5	4266	G
2	5	4268	G
2	5	4269	A2M
2	5	4270	G
2	5	4294	A
2	5	4295	G
2	5	4306	C
2	5	4313	G
2	5	4319	G
2	5	4321	G
2	5	4332	G
2	5	4335	A
2	5	4336	A
2	5	4373	U
2	5	4382	PSU
2	5	4383	OMG
2	5	4398	G
2	5	4402	A
2	5	4416	C
2	5	4418	A
2	5	4423	U
2	5	4441	C
2	5	4446	A
2	5	4455	U
2	5	4465	G
2	5	4466	C
2	5	4476	C
2	5	4479	C
2	5	4480	A
2	5	4482	C
2	5	4487	A
2	5	4490	G
2	5	4492	G
2	5	4498	G
2	5	4501	G
2	5	4503	C
2	5	4504	C
2	5	4506	C
2	5	4508	G
2	5	4512	G
2	5	4518	C

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Mol	Chain	Res	Type
2	5	4519	C
2	5	4607	G
2	5	4609	G
2	5	4610	C
2	5	4611	G
2	5	4612	G
2	5	4613	A
2	5	4614	G
2	5	4621	U
2	5	4622	C
2	5	4624	U
2	5	4634	C
2	5	4638	G
2	5	4639	C
2	5	4640	G
2	5	4642	G
2	5	4651	G
2	5	4653	G
2	5	4654	G
2	5	4658	G
2	5	4659	C
2	5	4660	C
2	5	4661	C
2	5	4664	U
2	5	4665	C
2	5	4670	G
2	5	4676	C
2	5	4682	A
2	5	4683	C
2	5	4687	C
2	5	4688	G
2	5	4689	U
2	5	4690	G
2	5	4695	A
2	5	4697	C
2	5	4699	G
2	5	4704	U
2	5	4705	A
2	5	4715	U
2	5	4727	U
2	5	4729	C
2	5	4732	G

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Mol	Chain	Res	Type
2	5	4745	U
2	5	4753	A
2	5	4756	G
2	5	4761	U
2	5	4779	U
2	5	4780	G
2	5	4786	C
2	5	4789	C
2	5	4793	C
2	5	4801	G
9	8	2	G
9	8	16	G
9	8	34	U
9	8	35	C
9	8	39	G
9	8	59	A
9	8	62	A
9	8	63	U
9	8	86	U
9	8	87	G
9	8	103	A
9	8	105	C
9	8	109	C
9	8	110	U
9	8	111	U
9	8	114	G
9	8	122	G
9	8	124	U
9	8	125	C
9	8	126	C
9	8	127	U
9	8	137	A
9	8	150	C
9	8	151	G
9	8	153	C
9	8	155	C
39	7	7	G
39	7	22	A
39	7	33	U
39	7	53	U
39	7	54	A
39	7	64	G

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Mol	Chain	Res	Type
39	7	74	A
39	7	100	A
39	7	110	G
39	7	111	C
39	7	117	G
39	7	120	U

All (56) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	5	12	A
2	5	125	C
2	5	134	G
2	5	217	C
2	5	245	C
2	5	275	C
2	5	385	A
2	5	406	C
2	5	417	G
2	5	486	C
2	5	493	U
2	5	829	G
2	5	987	C
2	5	1065	G
2	5	1102	G
2	5	1123	C
2	5	1125	C
2	5	1207	G
2	5	1235	G
2	5	1273	G
2	5	1314	G
2	5	1400	U
2	5	1588	G
2	5	1743	A
2	5	1757	G
2	5	1918	A
2	5	1929	A
2	5	1985	G
2	5	2028	G
2	5	2109	C
2	5	2345	A
2	5	2482	U

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Mol	Chain	Res	Type
2	5	2504	U
2	5	2538	A
2	5	2597	G
2	5	3335	G
2	5	3357	G
2	5	3620	G
2	5	3636	G
2	5	3793	G
2	5	3847	C
2	5	3940	U
2	5	3978	U
2	5	4000	G
2	5	4117	G
2	5	4141	U
2	5	4194	G
2	5	4445	U
2	5	4465	G
2	5	4623	G
2	5	4660	C
2	5	4664	U
2	5	4675	G
2	5	4686	U
2	5	4786	C
9	8	124	U

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

66 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	OMC	5	2704	2	19,22,23	2.22	5 (26%)	25,31,34	0.98	2 (8%)
2	PSU	5	4039	2	18,21,22	2.02	5 (27%)	21,30,33	2.06	4 (19%)
2	PSU	5	4149	2	18,21,22	1.60	5 (27%)	21,30,33	2.26	6 (28%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PSU	5	1537	2	18,21,22	2.06	5 (27%)	21,30,33	2.01	4 (19%)
2	A2M	5	398	2	22,25,26	4.01	8 (36%)	30,36,39	2.05	8 (26%)
2	1MA	5	1266	2	21,25,26	2.02	3 (14%)	30,37,40	1.96	7 (23%)
2	PSU	5	1638	2	18,21,22	2.03	5 (27%)	21,30,33	2.06	4 (19%)
2	PSU	5	3447	2	18,21,22	2.00	5 (27%)	21,30,33	2.00	4 (19%)
2	A2M	5	1489	48,2	22,25,26	4.03	8 (36%)	30,36,39	2.03	9 (30%)
2	A2M	5	4269	48,2	22,25,26	4.00	8 (36%)	30,36,39	2.02	9 (30%)
2	E6G	5	4101	2	24,27,28	1.65	5 (20%)	34,39,42	2.49	13 (38%)
2	UR3	5	4276	2	19,22,23	1.01	1 (5%)	26,32,35	1.82	5 (19%)
2	OMC	5	3601	2	19,22,23	2.24	5 (26%)	25,31,34	0.97	3 (12%)
2	OMG	5	1260	2	23,26,27	2.54	5 (21%)	32,38,41	1.96	9 (28%)
2	B8H	5	1799	2	19,22,23	2.06	8 (42%)	21,32,35	2.20	3 (14%)
2	OMG	5	4383	2	23,26,27	2.57	5 (21%)	32,38,41	2.02	10 (31%)
2	OMU	5	4366	2	19,22,23	3.11	7 (36%)	25,31,34	1.94	6 (24%)
2	P4U	5	1292	2	21,24,25	2.42	7 (33%)	28,33,36	1.61	3 (10%)
2	OMG	5	1580	48,2	23,26,27	1.34	4 (17%)	32,38,41	2.00	6 (18%)
2	OMC	5	2208	2	19,22,23	2.24	5 (26%)	25,31,34	0.97	3 (12%)
2	OMC	5	4282	2	19,22,23	0.95	1 (5%)	25,31,34	1.08	1 (4%)
2	B8H	5	3494	2	19,22,23	2.03	7 (36%)	21,32,35	2.06	3 (14%)
2	OMG	5	3524	2	23,26,27	2.58	5 (21%)	32,38,41	1.96	9 (28%)
2	P7G	5	3612	2	24,28,29	5.12	6 (25%)	25,41,44	1.13	1 (4%)
2	PSU	5	4382	2	18,21,22	2.02	5 (27%)	21,30,33	2.11	5 (23%)
2	A2M	5	3557	2	22,25,26	4.00	8 (36%)	30,36,39	2.07	8 (26%)
2	5MC	5	4193	2	19,22,23	1.43	3 (15%)	26,32,35	1.38	4 (15%)
2	OMG	5	4369	2	23,26,27	2.56	5 (21%)	32,38,41	1.98	10 (31%)
2	OMG	5	4240	2	23,26,27	2.57	5 (21%)	32,38,41	1.97	8 (25%)
2	PSU	5	3496	2	18,21,22	2.02	6 (33%)	21,30,33	1.92	5 (23%)
2	OMC	5	2647	2	19,22,23	2.24	5 (26%)	25,31,34	0.97	2 (8%)
2	B8K	5	4436	2	24,28,29	5.11	7 (29%)	29,42,45	2.41	7 (24%)
2	OMG	5	2267	2	23,26,27	1.28	4 (17%)	32,38,41	2.10	7 (21%)
2	PSU	5	4374	2	18,21,22	2.04	5 (27%)	21,30,33	2.10	4 (19%)
2	PSU	5	4277	2	18,21,22	1.98	5 (27%)	21,30,33	2.03	4 (19%)
2	OMG	5	2207	2	23,26,27	2.57	5 (21%)	32,38,41	1.94	7 (21%)
2	A2M	5	1270	2	22,25,26	1.49	5 (22%)	30,36,39	2.14	8 (26%)
2	PSU	5	4246	2	18,21,22	2.02	5 (27%)	21,30,33	2.10	5 (23%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	B8K	5	3629	2	24,28,29	5.17	7 (29%)	29,42,45	2.36	7 (24%)
2	1MA	5	4161	2	21,25,26	2.01	3 (14%)	30,37,40	1.94	7 (23%)
2	E7G	5	1736	2	24,27,28	4.30	7 (29%)	28,40,43	2.25	8 (28%)
2	OMC	5	2265	48,2	19,22,23	2.22	5 (26%)	25,31,34	0.97	2 (8%)
2	A2M	5	1479	2	22,25,26	3.97	8 (36%)	30,36,39	2.18	11 (36%)
2	OMG	5	1477	2	23,26,27	2.57	6 (26%)	32,38,41	1.98	10 (31%)
2	7MG	5	1560	2	23,26,27	4.56	6 (26%)	27,39,42	2.23	8 (29%)
2	7MG	5	2365	2	23,26,27	1.41	4 (17%)	27,39,42	2.80	8 (29%)
2	OMC	5	3433	2	19,22,23	2.23	4 (21%)	25,31,34	0.97	2 (8%)
2	A2M	5	3450	2	22,25,26	4.01	8 (36%)	30,36,39	2.02	8 (26%)
2	OMG	5	4116	2	23,26,27	1.29	4 (17%)	32,38,41	2.19	8 (25%)
2	PSU	5	4196	48,2	18,21,22	1.99	6 (33%)	21,30,33	2.06	4 (19%)
28	MLZ	C	333	28	8,9,10	0.46	0	4,9,11	0.65	0
2	A2M	5	3455	2	22,25,26	4.00	8 (36%)	30,36,39	2.04	8 (26%)
2	P7G	5	1848	2	24,28,29	5.05	6 (25%)	25,41,44	1.13	1 (4%)
2	OMU	5	4052	2	19,22,23	3.12	7 (36%)	25,31,34	1.91	6 (24%)
2	BGH	5	3631	2	25,29,30	5.73	12 (48%)	30,43,46	2.44	10 (33%)
2	OMG	5	2616	2	23,26,27	2.57	4 (17%)	32,38,41	1.97	10 (31%)
2	I4U	5	1614	2	20,24,25	2.44	5 (25%)	27,34,37	1.95	2 (7%)
2	PSU	5	4188	2	18,21,22	2.06	6 (33%)	21,30,33	2.11	5 (23%)
19	MLZ	m	72	19	8,9,10	0.49	0	4,9,11	0.53	0
2	A2M	5	1810	48,2	22,25,26	1.48	5 (22%)	30,36,39	2.15	10 (33%)
2	5MC	5	3514	2	19,22,23	2.96	5 (26%)	26,32,35	1.37	3 (11%)
2	B8H	5	4042	2	19,22,23	2.05	8 (42%)	21,32,35	2.20	3 (14%)
2	OMC	5	3619	2	19,22,23	2.23	5 (26%)	25,31,34	0.98	3 (12%)
2	PSU	5	2351	2	18,21,22	2.02	5 (27%)	21,30,33	1.95	4 (19%)
2	PSU	5	1632	2	18,21,22	2.00	5 (27%)	21,30,33	2.11	4 (19%)
2	PSU	5	3461	2	18,21,22	2.05	5 (27%)	21,30,33	1.97	4 (19%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	OMC	5	2704	2	-	1/9/27/28	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PSU	5	4039	2	-	2/7/25/26	0/2/2/2
2	PSU	5	4149	2	-	2/7/25/26	0/2/2/2
2	PSU	5	1537	2	-	2/7/25/26	0/2/2/2
2	A2M	5	398	2	-	1/9/27/28	0/3/3/3
2	1MA	5	1266	2	-	1/7/25/26	0/3/3/3
2	PSU	5	1638	2	-	0/7/25/26	0/2/2/2
2	PSU	5	3447	2	-	0/7/25/26	0/2/2/2
2	A2M	5	1489	48,2	-	2/9/27/28	0/3/3/3
2	A2M	5	4269	48,2	-	3/9/27/28	0/3/3/3
2	E6G	5	4101	2	-	4/10/28/29	0/3/3/3
2	UR3	5	4276	2	-	0/7/25/26	0/2/2/2
2	OMC	5	3601	2	-	0/9/27/28	0/2/2/2
2	OMG	5	1260	2	-	1/9/27/28	0/3/3/3
2	B8H	5	1799	2	-	0/7/25/26	0/2/2/2
2	OMG	5	4383	2	-	3/9/27/28	0/3/3/3
2	OMU	5	4366	2	-	1/9/27/28	0/2/2/2
2	P4U	5	1292	2	-	4/10/29/30	0/2/2/2
2	OMG	5	1580	48,2	-	0/9/27/28	0/3/3/3
2	OMC	5	2208	2	-	0/9/27/28	0/2/2/2
2	OMC	5	4282	2	-	2/9/27/28	0/2/2/2
2	B8H	5	3494	2	-	2/7/25/26	0/2/2/2
2	OMG	5	3524	2	-	2/9/27/28	0/3/3/3
2	P7G	5	3612	2	-	3/10/40/41	0/3/3/3
2	PSU	5	4382	2	-	3/7/25/26	0/2/2/2
2	A2M	5	3557	2	-	1/9/27/28	0/3/3/3
2	5MC	5	4193	2	-	4/7/25/26	0/2/2/2
2	OMG	5	4369	2	-	1/9/27/28	0/3/3/3
2	OMG	5	4240	2	-	3/9/27/28	0/3/3/3
2	PSU	5	3496	2	-	3/7/25/26	0/2/2/2
2	OMC	5	2647	2	-	1/9/27/28	0/2/2/2
2	B8K	5	4436	2	-	0/11/41/42	0/3/3/3
2	OMG	5	2267	2	-	2/9/27/28	0/3/3/3
2	PSU	5	4374	2	-	0/7/25/26	0/2/2/2
2	PSU	5	4277	2	-	0/7/25/26	0/2/2/2
2	OMG	5	2207	2	-	2/9/27/28	0/3/3/3
2	A2M	5	1270	2	-	3/9/27/28	0/3/3/3
2	PSU	5	4246	2	-	5/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	B8K	5	3629	2	-	3/11/41/42	0/3/3/3
2	1MA	5	4161	2	-	1/7/25/26	0/3/3/3
2	E7G	5	1736	2	-	3/9/39/40	0/3/3/3
2	OMC	5	2265	48,2	-	2/9/27/28	0/2/2/2
2	A2M	5	1479	2	-	2/9/27/28	0/3/3/3
2	OMG	5	1477	2	-	0/9/27/28	0/3/3/3
2	7MG	5	1560	2	-	0/7/37/38	0/3/3/3
2	7MG	5	2365	2	-	0/7/37/38	0/3/3/3
2	OMC	5	3433	2	-	4/9/27/28	0/2/2/2
2	A2M	5	3450	2	-	0/9/27/28	0/3/3/3
2	OMG	5	4116	2	-	1/9/27/28	0/3/3/3
2	PSU	5	4196	48,2	-	4/7/25/26	0/2/2/2
28	MLZ	C	333	28	-	0/7/8/10	-
2	A2M	5	3455	2	-	0/9/27/28	0/3/3/3
2	P7G	5	1848	2	-	0/10/40/41	0/3/3/3
2	OMU	5	4052	2	-	3/9/27/28	0/2/2/2
2	BGH	5	3631	2	-	2/13/43/44	0/3/3/3
2	OMG	5	2616	2	-	1/9/27/28	0/3/3/3
2	I4U	5	1614	2	-	1/9/29/30	0/2/2/2
2	PSU	5	4188	2	-	0/7/25/26	0/2/2/2
19	MLZ	m	72	19	-	1/7/8/10	-
2	A2M	5	1810	48,2	-	0/9/27/28	0/3/3/3
2	5MC	5	3514	2	-	0/7/25/26	0/2/2/2
2	B8H	5	4042	2	-	2/7/25/26	0/2/2/2
2	OMC	5	3619	2	-	1/9/27/28	0/2/2/2
2	PSU	5	2351	2	-	0/7/25/26	0/2/2/2
2	PSU	5	1632	2	-	1/7/25/26	0/2/2/2
2	PSU	5	3461	2	-	2/7/25/26	0/2/2/2

All (355) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	5	3629	B8K	C8-N9	-22.47	1.31	1.45
2	5	3631	BGH	C8-N9	-22.39	1.31	1.45
2	5	4436	B8K	C8-N9	-22.15	1.31	1.45
2	5	3612	P7G	C8-N9	-21.39	1.32	1.45
2	5	1848	P7G	C8-N9	-21.09	1.32	1.45
2	5	1560	7MG	C8-N9	-18.20	1.34	1.45
2	5	1736	E7G	C8-N9	-16.58	1.35	1.45
2	5	4052	OMU	O4-C4	11.23	1.46	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	5	4366	OMU	O4-C4	11.16	1.46	1.24
2	5	1489	A2M	C2'-C1'	-10.42	1.27	1.53
2	5	3557	A2M	C2'-C1'	-10.34	1.27	1.53
2	5	398	A2M	C2'-C1'	-10.31	1.27	1.53
2	5	4269	A2M	C2'-C1'	-10.29	1.27	1.53
2	5	3455	A2M	C2'-C1'	-10.28	1.27	1.53
2	5	3450	A2M	C2'-C1'	-10.22	1.27	1.53
2	5	1479	A2M	C3'-C4'	-10.17	1.27	1.53
2	5	4269	A2M	C3'-C4'	-10.14	1.27	1.53
2	5	1489	A2M	C3'-C4'	-10.14	1.27	1.53
2	5	398	A2M	C3'-C4'	-10.11	1.27	1.53
2	5	3450	A2M	C3'-C4'	-10.10	1.27	1.53
2	5	1479	A2M	C2'-C1'	-10.05	1.28	1.53
2	5	3557	A2M	C3'-C4'	-10.05	1.27	1.53
2	5	3455	A2M	C3'-C4'	-9.98	1.27	1.53
2	5	3514	5MC	C5-C4	-9.63	1.36	1.44
2	5	2616	OMG	O6-C6	9.38	1.41	1.23
2	5	4240	OMG	O6-C6	9.36	1.41	1.23
2	5	3524	OMG	O6-C6	9.36	1.41	1.23
2	5	4369	OMG	O6-C6	9.32	1.41	1.23
2	5	2207	OMG	O6-C6	9.32	1.41	1.23
2	5	4383	OMG	O6-C6	9.30	1.41	1.23
2	5	1560	7MG	O6-C6	9.29	1.41	1.23
2	5	1477	OMG	O6-C6	9.28	1.41	1.23
2	5	3631	BGH	C3'-C4'	-9.24	1.29	1.53
2	5	1260	OMG	O6-C6	9.21	1.41	1.23
2	5	3612	P7G	O6-C6	9.03	1.40	1.23
2	5	1848	P7G	O6-C6	9.00	1.40	1.23
2	5	1614	I4U	O2-C2	8.76	1.40	1.23
2	5	1736	E7G	O6-C6	8.51	1.39	1.23
2	5	3631	BGH	O6-C6	8.44	1.39	1.23
2	5	3629	B8K	O6-C6	8.42	1.39	1.23
2	5	4436	B8K	O6-C6	8.34	1.39	1.23
2	5	1292	P4U	O2-C2	8.33	1.39	1.23
2	5	4161	1MA	C6-N6	8.02	1.47	1.28
2	5	1266	1MA	C6-N6	8.00	1.47	1.28
2	5	3631	BGH	O4'-C4'	7.55	1.61	1.45
2	5	3612	P7G	C8-N7	-6.65	1.32	1.45
2	5	2208	OMC	C4-N4	6.53	1.49	1.33
2	5	2704	OMC	C4-N4	6.52	1.49	1.33
2	5	3433	OMC	C4-N4	6.52	1.49	1.33
2	5	3619	OMC	C4-N4	6.51	1.49	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	5	3601	OMC	C4-N4	6.50	1.49	1.33
2	5	2265	OMC	C4-N4	6.50	1.49	1.33
2	5	2647	OMC	C4-N4	6.49	1.49	1.33
2	5	1848	P7G	C8-N7	-6.46	1.32	1.45
2	5	2616	OMG	C2-N2	6.38	1.49	1.34
2	5	4383	OMG	C2-N2	6.32	1.49	1.34
2	5	3524	OMG	C2-N2	6.32	1.49	1.34
2	5	2207	OMG	C2-N2	6.30	1.48	1.34
2	5	1477	OMG	C2-N2	6.28	1.48	1.34
2	5	4369	OMG	C2-N2	6.27	1.48	1.34
2	5	4240	OMG	C2-N2	6.26	1.48	1.34
2	5	1260	OMG	C2-N2	6.15	1.48	1.34
2	5	1736	E7G	C8-N7	-6.11	1.33	1.45
2	5	1489	A2M	O4'-C1'	6.04	1.56	1.42
2	5	3450	A2M	O4'-C1'	6.04	1.55	1.42
2	5	398	A2M	O4'-C1'	6.01	1.55	1.42
2	5	3455	A2M	O4'-C1'	5.99	1.55	1.42
2	5	1479	A2M	C3'-C2'	5.98	1.66	1.53
2	5	3557	A2M	O4'-C1'	5.97	1.55	1.42
2	5	4269	A2M	O4'-C1'	5.97	1.55	1.42
2	5	3455	A2M	C3'-C2'	5.97	1.66	1.53
2	5	398	A2M	C3'-C2'	5.92	1.65	1.53
2	5	1479	A2M	O4'-C1'	5.92	1.55	1.42
2	5	1489	A2M	C3'-C2'	5.90	1.65	1.53
2	5	3450	A2M	C3'-C2'	5.89	1.65	1.53
2	5	3557	A2M	C3'-C2'	5.80	1.65	1.53
2	5	4269	A2M	C3'-C2'	5.78	1.65	1.53
2	5	3455	A2M	O4'-C4'	5.01	1.56	1.45
2	5	3514	5MC	C4-N4	4.98	1.46	1.34
2	5	3450	A2M	O4'-C4'	4.97	1.56	1.45
2	5	398	A2M	O4'-C4'	4.93	1.55	1.45
2	5	3447	PSU	C6-C5	4.93	1.40	1.35
2	5	3496	PSU	C6-C5	4.91	1.40	1.35
2	5	4277	PSU	C6-C5	4.89	1.40	1.35
2	5	4246	PSU	C6-C5	4.87	1.40	1.35
2	5	1537	PSU	C6-C5	4.86	1.40	1.35
2	5	1489	A2M	O4'-C4'	4.85	1.55	1.45
2	5	3461	PSU	C6-C5	4.83	1.40	1.35
2	5	3514	5MC	C2-N1	-4.81	1.30	1.40
2	5	3557	A2M	O4'-C4'	4.80	1.55	1.45
2	5	3631	BGH	C2-N2	4.77	1.45	1.34
2	5	4188	PSU	C6-C5	4.77	1.40	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	5	4269	A2M	O4'-C4'	4.76	1.55	1.45
2	5	1736	E7G	C2-N2	4.76	1.45	1.34
2	5	1632	PSU	C6-C5	4.74	1.40	1.35
2	5	4436	B8K	C2-N2	4.73	1.45	1.34
2	5	4382	PSU	C6-C5	4.71	1.40	1.35
2	5	3612	P7G	C2-N2	4.70	1.45	1.34
2	5	4039	PSU	C6-C5	4.70	1.40	1.35
2	5	1848	P7G	C2-N2	4.70	1.45	1.34
2	5	3631	BGH	O4'-C1'	-4.69	1.31	1.42
2	5	4374	PSU	C6-C5	4.68	1.40	1.35
2	5	2351	PSU	C6-C5	4.67	1.40	1.35
2	5	3629	B8K	C2-N2	4.67	1.45	1.34
2	5	1479	A2M	O4'-C4'	4.63	1.55	1.45
2	5	1638	PSU	C6-C5	4.56	1.40	1.35
2	5	4193	5MC	C5-C4	4.55	1.47	1.44
2	5	4052	OMU	C2-N1	-4.55	1.31	1.38
2	5	4196	PSU	C6-C5	4.51	1.40	1.35
2	5	4366	OMU	C2-N1	-4.43	1.31	1.38
2	5	3601	OMC	C2-N1	-4.41	1.30	1.40
2	5	398	A2M	C6-N6	4.38	1.45	1.34
2	5	3433	OMC	C2-N1	-4.37	1.30	1.40
2	5	4269	A2M	C6-N6	4.37	1.45	1.34
2	5	3455	A2M	C6-N6	4.37	1.45	1.34
2	5	3619	OMC	C2-N1	-4.37	1.30	1.40
2	5	3450	A2M	C6-N6	4.36	1.45	1.34
2	5	1489	A2M	C6-N6	4.36	1.45	1.34
2	5	2208	OMC	C2-N1	-4.35	1.31	1.40
2	5	3557	A2M	C6-N6	4.32	1.45	1.34
2	5	1479	A2M	C6-N6	4.30	1.45	1.34
2	5	2647	OMC	C2-N1	-4.29	1.31	1.40
2	5	2265	OMC	C2-N1	-4.27	1.31	1.40
2	5	2704	OMC	C2-N1	-4.24	1.31	1.40
2	5	1560	7MG	C2-N2	4.16	1.43	1.34
2	5	1270	A2M	C5-C4	4.12	1.46	1.39
2	5	1799	B8H	C2-N1	-3.98	1.31	1.38
2	5	1614	I4U	C2-N1	-3.95	1.31	1.40
2	5	4042	B8H	C2-N1	-3.92	1.31	1.38
2	5	4101	E6G	C2-N2	3.91	1.41	1.33
2	5	1560	7MG	C4-N9	-3.91	1.33	1.37
2	5	1810	A2M	C5-C4	3.86	1.46	1.39
2	5	3494	B8H	C2-N1	-3.86	1.32	1.38
2	5	2647	OMC	O2-C2	-3.85	1.16	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	5	3619	OMC	O2-C2	-3.84	1.16	1.23
2	5	2265	OMC	O2-C2	-3.83	1.16	1.23
2	5	4101	E6G	O6-C6	3.80	1.40	1.34
2	5	3601	OMC	O2-C2	-3.80	1.16	1.23
2	5	2704	OMC	O2-C2	-3.76	1.16	1.23
2	5	4374	PSU	C4-N3	-3.76	1.31	1.38
2	5	2208	OMC	O2-C2	-3.75	1.16	1.23
2	5	1736	E7G	C6-N1	-3.74	1.31	1.38
2	5	3433	OMC	O2-C2	-3.73	1.16	1.23
2	5	3514	5MC	C6-C5	3.72	1.40	1.34
2	5	1560	7MG	C6-N1	-3.67	1.32	1.38
2	5	2365	7MG	C4-N9	-3.67	1.33	1.37
2	5	4382	PSU	C4-N3	-3.66	1.32	1.38
2	5	4366	OMU	C4-N3	-3.66	1.32	1.38
2	5	1632	PSU	C4-N3	-3.66	1.32	1.38
2	5	4196	PSU	C4-N3	-3.63	1.32	1.38
2	5	1537	PSU	C4-N3	-3.61	1.32	1.38
2	5	4039	PSU	C4-N3	-3.61	1.32	1.38
2	5	4188	PSU	C4-N3	-3.61	1.32	1.38
2	5	4052	OMU	C4-N3	-3.61	1.32	1.38
2	5	2351	PSU	C4-N3	-3.60	1.32	1.38
2	5	1638	PSU	C4-N3	-3.56	1.32	1.38
2	5	1799	B8H	C4-N3	-3.56	1.32	1.38
2	5	4246	PSU	C4-N3	-3.55	1.32	1.38
2	5	4042	B8H	C2-N3	-3.54	1.31	1.38
2	5	3447	PSU	C4-N3	-3.54	1.32	1.38
2	5	3631	BGH	C4-N9	-3.53	1.33	1.37
2	5	4042	B8H	C4-N3	-3.52	1.32	1.38
2	5	4277	PSU	C4-N3	-3.52	1.32	1.38
2	5	1292	P4U	O4-C41	-3.51	1.35	1.45
2	5	1799	B8H	C2-N3	-3.51	1.31	1.38
2	5	3461	PSU	C4-N3	-3.48	1.32	1.38
2	5	3631	BGH	C6-N1	-3.42	1.32	1.38
2	5	3494	B8H	C2-N3	-3.41	1.32	1.38
2	5	3496	PSU	C4-N3	-3.41	1.32	1.38
2	5	3629	B8K	C6-N1	-3.38	1.32	1.38
2	5	3494	B8H	C1'-C5	3.35	1.57	1.50
2	5	4101	E6G	C8-N9	-3.32	1.31	1.37
2	5	1638	PSU	C2-N1	-3.32	1.32	1.36
2	5	1848	P7G	C6-N1	-3.32	1.32	1.38
2	5	4436	B8K	C6-N1	-3.31	1.32	1.38
2	5	4149	PSU	C4-N3	-3.31	1.32	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	5	3631	BGH	C71-N7	3.30	1.47	1.39
2	5	4436	B8K	C71-N7	3.30	1.47	1.39
2	5	3494	B8H	C4-N3	-3.30	1.32	1.38
2	5	4039	PSU	C2-N1	-3.29	1.32	1.36
2	5	3629	B8K	C4-N9	-3.29	1.33	1.37
2	5	4436	B8K	C4-N9	-3.29	1.33	1.37
2	5	2351	PSU	C2-N1	-3.27	1.32	1.36
2	5	3629	B8K	C71-N7	3.27	1.46	1.39
2	5	3612	P7G	C6-N1	-3.26	1.32	1.38
2	5	4188	PSU	C2-N1	-3.26	1.32	1.36
2	5	3450	A2M	C8-N9	-3.25	1.32	1.37
2	5	3461	PSU	C2-N1	-3.24	1.32	1.36
2	5	3557	A2M	C8-N9	-3.22	1.32	1.37
2	5	1537	PSU	C2-N1	-3.22	1.32	1.36
2	5	4374	PSU	C2-N1	-3.20	1.32	1.36
2	5	3496	PSU	C2-N1	-3.17	1.32	1.36
2	5	4196	PSU	C2-N1	-3.13	1.32	1.36
2	5	3447	PSU	C2-N1	-3.12	1.32	1.36
2	5	1489	A2M	C8-N9	-3.11	1.32	1.37
2	5	1580	OMG	C6-N1	-3.06	1.33	1.38
2	5	1479	A2M	C8-N9	-3.06	1.32	1.37
2	5	1477	OMG	C6-N1	-3.06	1.33	1.38
2	5	4269	A2M	C8-N9	-3.04	1.32	1.37
2	5	4382	PSU	C2-N1	-3.03	1.32	1.36
2	5	4383	OMG	C6-N1	-3.03	1.33	1.38
2	5	398	A2M	C8-N9	-3.02	1.32	1.37
2	5	4246	PSU	C2-N1	-3.02	1.32	1.36
2	5	2207	OMG	C6-N1	-3.01	1.33	1.38
2	5	1260	OMG	C6-N1	-2.99	1.33	1.38
2	5	3631	BGH	O2'-C2'	-2.99	1.35	1.42
2	5	4369	OMG	C6-N1	-2.98	1.33	1.38
2	5	3494	B8H	C6-C5	2.96	1.39	1.35
2	5	3524	OMG	C6-N1	-2.96	1.33	1.38
2	5	1292	P4U	C6-C5	2.95	1.41	1.35
2	5	4116	OMG	C6-N1	-2.94	1.33	1.38
2	5	4240	OMG	C6-N1	-2.94	1.33	1.38
2	5	3455	A2M	C8-N9	-2.93	1.32	1.37
2	5	1632	PSU	C2-N1	-2.92	1.32	1.36
2	5	4277	PSU	C2-N1	-2.92	1.32	1.36
2	5	3461	PSU	C6-N1	-2.92	1.31	1.36
2	5	2365	7MG	C6-N1	-2.91	1.33	1.38
2	5	1292	P4U	O4-C4	2.89	1.38	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	5	1799	B8H	C1'-C5	2.88	1.56	1.50
2	5	2365	7MG	C5-C4	2.87	1.46	1.37
2	5	2616	OMG	C6-N1	-2.87	1.33	1.38
2	5	4196	PSU	C6-N1	-2.86	1.31	1.36
2	5	1270	A2M	C5-N7	-2.84	1.33	1.39
2	5	2267	OMG	C6-N1	-2.82	1.33	1.38
2	5	4366	OMU	C2-N3	-2.81	1.33	1.38
2	5	1580	OMG	C5-C4	2.80	1.46	1.38
2	5	4042	B8H	C1'-C5	2.80	1.56	1.50
2	5	4382	PSU	C6-N1	-2.80	1.31	1.36
2	5	4188	PSU	C6-N1	-2.78	1.31	1.36
2	5	3450	A2M	C5-N7	-2.77	1.34	1.39
2	5	1638	PSU	C6-N1	-2.76	1.31	1.36
2	5	2267	OMG	C5-C4	2.75	1.46	1.38
2	5	4052	OMU	C2-N3	-2.73	1.33	1.38
2	5	4039	PSU	C6-N1	-2.73	1.31	1.36
2	5	4193	5MC	C6-N1	-2.73	1.33	1.38
2	5	1479	A2M	C5-N7	-2.73	1.34	1.39
2	5	2351	PSU	C6-N1	-2.72	1.31	1.36
2	5	4269	A2M	C5-N7	-2.72	1.34	1.39
2	5	1799	B8H	C6-C5	2.72	1.39	1.35
2	5	4246	PSU	C6-N1	-2.71	1.31	1.36
2	5	4374	PSU	C6-N1	-2.71	1.31	1.36
2	5	3496	PSU	C6-N1	-2.70	1.31	1.36
2	5	398	A2M	C5-N7	-2.69	1.34	1.39
2	5	1537	PSU	C6-N1	-2.69	1.31	1.36
2	5	1266	1MA	C5-N7	-2.69	1.33	1.39
2	5	1632	PSU	C6-N1	-2.69	1.31	1.36
2	5	3557	A2M	C5-N7	-2.68	1.34	1.39
2	5	4277	PSU	C6-N1	-2.68	1.31	1.36
2	5	3447	PSU	C6-N1	-2.67	1.31	1.36
2	5	4116	OMG	C5-C4	2.67	1.46	1.38
2	5	1810	A2M	C5-N7	-2.65	1.34	1.39
2	5	1614	I4U	O4-C41	-2.64	1.41	1.47
2	5	1489	A2M	C5-N7	-2.64	1.34	1.39
2	5	4042	B8H	C6-C5	2.64	1.38	1.35
2	5	3455	A2M	C5-N7	-2.63	1.34	1.39
2	5	4042	B8H	O4-C4	-2.62	1.18	1.23
2	5	4161	1MA	C5-N7	-2.60	1.33	1.39
2	5	1560	7MG	C8-N7	-2.58	1.29	1.42
2	5	1292	P4U	C42-C41	2.58	1.65	1.49
2	5	1292	P4U	C4-N3	2.57	1.34	1.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	5	4101	E6G	C5-N7	-2.56	1.34	1.39
2	5	4149	PSU	C6-C5	2.56	1.38	1.35
2	5	1799	B8H	O4-C4	-2.55	1.18	1.23
2	5	4193	5MC	C6-C5	2.53	1.38	1.34
2	5	4042	B8H	O2-C2	-2.52	1.18	1.23
2	5	1614	I4U	C6-N1	-2.52	1.32	1.38
2	5	4116	OMG	C5-N7	-2.51	1.34	1.39
2	5	4149	PSU	C2-N3	-2.50	1.33	1.37
2	5	1799	B8H	O2-C2	-2.49	1.18	1.23
2	5	2365	7MG	C5-N7	-2.48	1.32	1.35
2	5	1580	OMG	C5-N7	-2.48	1.34	1.39
2	5	2704	OMC	C6-C5	2.48	1.40	1.35
2	5	2208	OMC	C6-C5	2.47	1.40	1.35
2	5	2351	PSU	C2-N3	-2.47	1.33	1.37
2	5	2265	OMC	C6-C5	2.46	1.40	1.35
2	5	3601	OMC	C6-C5	2.46	1.40	1.35
2	5	4161	1MA	C8-N9	-2.44	1.32	1.37
2	5	1266	1MA	C8-N9	-2.44	1.32	1.37
2	5	3433	OMC	C6-C5	2.43	1.40	1.35
2	5	2647	OMC	C6-C5	2.43	1.40	1.35
2	5	2267	OMG	C5-N7	-2.43	1.34	1.39
2	5	3494	B8H	O4-C4	-2.41	1.19	1.23
2	5	3494	B8H	O2-C2	-2.41	1.18	1.23
2	5	1810	A2M	C4-N9	-2.41	1.32	1.37
2	5	4039	PSU	C2-N3	-2.40	1.33	1.37
2	5	3619	OMC	C6-C5	2.40	1.40	1.35
2	5	4374	PSU	C2-N3	-2.39	1.33	1.37
2	5	3631	BGH	C2-N1	-2.39	1.31	1.37
2	5	1638	PSU	C2-N3	-2.38	1.33	1.37
2	5	4436	B8K	C2-N1	-2.38	1.31	1.37
2	5	1477	OMG	C8-N9	-2.37	1.32	1.37
2	5	1260	OMG	C8-N9	-2.37	1.32	1.37
2	5	3629	B8K	C2-N1	-2.36	1.31	1.37
2	5	4149	PSU	C2'-C1'	-2.35	1.50	1.53
2	5	1736	E7G	C72-C71	2.34	1.62	1.50
2	5	1537	PSU	C2-N3	-2.34	1.33	1.37
2	5	4240	OMG	C8-N9	-2.33	1.32	1.37
2	5	3524	OMG	C8-N9	-2.33	1.32	1.37
2	5	4383	OMG	C8-N9	-2.32	1.32	1.37
2	5	3514	5MC	C6-N1	-2.32	1.34	1.38
2	5	1292	P4U	C6-N1	-2.32	1.32	1.38
2	5	2207	OMG	C8-N9	-2.32	1.32	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	5	1270	A2M	C4-N9	-2.32	1.32	1.37
2	5	4369	OMG	C8-N9	-2.31	1.32	1.37
2	5	4196	PSU	C2-N3	-2.29	1.33	1.37
2	5	4101	E6G	C2-N1	-2.28	1.31	1.35
2	5	1270	A2M	C5-C6	2.28	1.47	1.41
2	5	1848	P7G	C2-N3	-2.28	1.32	1.37
2	5	4382	PSU	C2-N3	-2.27	1.33	1.37
2	5	4188	PSU	O4'-C1'	-2.27	1.40	1.43
2	5	1810	A2M	C5-C6	2.26	1.47	1.41
2	5	3461	PSU	C2-N3	-2.26	1.33	1.37
2	5	3631	BGH	O3'-C3'	2.25	1.48	1.43
2	5	3612	P7G	C2-N3	-2.24	1.32	1.37
2	5	4188	PSU	C2-N3	-2.24	1.33	1.37
2	5	4149	PSU	C2-N1	-2.24	1.33	1.36
2	5	1632	PSU	C2-N3	-2.24	1.33	1.37
2	5	2616	OMG	C8-N9	-2.22	1.32	1.37
2	5	4366	OMU	C6-C5	2.21	1.40	1.35
2	5	3496	PSU	C1'-C5	2.21	1.55	1.50
2	5	3496	PSU	C2-N3	-2.20	1.33	1.37
2	5	4366	OMU	C6-N1	-2.19	1.32	1.38
2	5	3447	PSU	C2-N3	-2.18	1.33	1.37
2	5	4246	PSU	C2-N3	-2.18	1.33	1.37
2	5	4276	UR3	C5-C4	-2.17	1.38	1.43
2	5	3524	OMG	C5-N7	-2.15	1.34	1.39
2	5	4052	OMU	C5-C4	-2.12	1.39	1.43
2	5	2647	OMC	C5-C4	-2.11	1.38	1.42
2	5	4366	OMU	C5-C4	-2.10	1.39	1.43
2	5	4052	OMU	C6-N1	-2.10	1.33	1.38
2	5	1614	I4U	C2-N3	-2.10	1.32	1.36
2	5	4052	OMU	C6-C5	2.09	1.39	1.35
2	5	4277	PSU	C2-N3	-2.09	1.34	1.37
2	5	1260	OMG	C5-N7	-2.08	1.34	1.39
2	5	2704	OMC	C5-C4	-2.08	1.38	1.42
2	5	2208	OMC	C5-C4	-2.08	1.38	1.42
2	5	3601	OMC	C5-C4	-2.08	1.38	1.42
2	5	1477	OMG	C5-N7	-2.08	1.34	1.39
2	5	4240	OMG	C5-N7	-2.08	1.34	1.39
2	5	4116	OMG	C4-N9	-2.08	1.32	1.38
2	5	4369	OMG	C5-N7	-2.07	1.34	1.39
2	5	4383	OMG	C5-N7	-2.07	1.34	1.39
2	5	2265	OMC	C5-C4	-2.07	1.38	1.42
2	5	2207	OMG	C5-N7	-2.07	1.34	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	5	2267	OMG	C4-N9	-2.07	1.32	1.38
2	5	4282	OMC	C6-N1	-2.06	1.33	1.38
2	5	1270	A2M	C8-N9	-2.05	1.34	1.37
2	5	4042	B8H	C4-C5	-2.03	1.38	1.44
2	5	1799	B8H	C4-C5	-2.02	1.38	1.44
2	5	1810	A2M	C8-N9	-2.02	1.34	1.37
2	5	1477	OMG	C2-N1	-2.02	1.32	1.37
2	5	1736	E7G	C4-N9	-2.02	1.35	1.37
2	5	3619	OMC	C5-C4	-2.01	1.38	1.42
2	5	1580	OMG	C4-N9	-2.01	1.33	1.38
2	5	4196	PSU	C4-C5	-2.00	1.38	1.44

All (372) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5	2365	7MG	N9-C4-N3	9.54	139.43	125.46
2	5	1614	I4U	O4-C4-C5	8.34	121.37	115.45
2	5	4101	E6G	C5-C4-N3	-7.28	119.51	127.18
2	5	4149	PSU	N1-C2-N3	6.94	122.49	115.17
2	5	1799	B8H	N3-C2-N1	6.72	121.71	115.22
2	5	4276	UR3	C4-N3-C2	-6.64	119.23	124.58
2	5	4042	B8H	N3-C2-N1	6.64	121.64	115.22
2	5	4383	OMG	C5-C4-N3	-6.43	118.15	128.39
2	5	3494	B8H	N3-C2-N1	6.40	121.41	115.22
2	5	4161	1MA	C5-C4-N3	-6.37	117.90	127.27
2	5	1266	1MA	C5-C4-N3	-6.36	117.90	127.27
2	5	2207	OMG	C5-C4-N3	-6.30	118.36	128.39
2	5	3524	OMG	C5-C4-N3	-6.28	118.40	128.39
2	5	1580	OMG	C5-C4-N3	-6.25	118.44	128.39
2	5	4369	OMG	C5-C4-N3	-6.22	118.49	128.39
2	5	4116	OMG	C5-C4-N3	-6.22	118.49	128.39
2	5	4240	OMG	C5-C4-N3	-6.22	118.49	128.39
2	5	1477	OMG	C5-C4-N3	-6.16	118.58	128.39
2	5	1260	OMG	C5-C4-N3	-6.15	118.61	128.39
2	5	2267	OMG	C5-C4-N3	-6.13	118.63	128.39
2	5	2616	OMG	C5-C4-N3	-6.08	118.72	128.39
2	5	4374	PSU	N1-C2-N3	6.07	121.58	115.17
2	5	4188	PSU	N1-C2-N3	6.03	121.53	115.17
2	5	4246	PSU	N1-C2-N3	6.02	121.52	115.17
2	5	1270	A2M	C5-C4-N3	-6.02	118.43	126.72
2	5	4101	E6G	N3-C4-N9	5.92	134.51	126.99
2	5	4039	PSU	N1-C2-N3	5.91	121.41	115.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5	1292	P4U	O4-C4-C5	5.91	119.64	115.45
2	5	4196	PSU	N1-C2-N3	5.89	121.39	115.17
2	5	4277	PSU	N1-C2-N3	5.89	121.38	115.17
2	5	1537	PSU	N1-C2-N3	5.89	121.38	115.17
2	5	1632	PSU	N1-C2-N3	5.86	121.34	115.17
2	5	1638	PSU	N1-C2-N3	5.84	121.33	115.17
2	5	4382	PSU	N1-C2-N3	5.83	121.32	115.17
2	5	3461	PSU	N1-C2-N3	5.83	121.31	115.17
2	5	3447	PSU	N1-C2-N3	5.78	121.27	115.17
2	5	3557	A2M	C5-C4-N3	-5.78	118.77	126.72
2	5	3450	A2M	C5-C4-N3	-5.74	118.82	126.72
2	5	2351	PSU	N1-C2-N3	5.67	121.15	115.17
2	5	3629	B8K	N9-C8-N7	5.65	110.77	103.31
2	5	2365	7MG	N9-C8-N7	-5.65	95.37	103.37
2	5	1479	A2M	C5-C4-N3	-5.62	118.98	126.72
2	5	2365	7MG	C5-C4-N3	-5.62	117.59	128.13
2	5	1489	A2M	C5-C4-N3	-5.60	119.00	126.72
2	5	398	A2M	C5-C4-N3	-5.60	119.01	126.72
2	5	3496	PSU	N1-C2-N3	5.57	121.04	115.17
2	5	1810	A2M	C5-C4-N3	-5.56	119.06	126.72
2	5	4269	A2M	C5-C4-N3	-5.44	119.23	126.72
2	5	3455	A2M	C5-C4-N3	-5.41	119.26	126.72
2	5	3631	BGH	N9-C8-N7	5.40	110.43	103.31
2	5	4436	B8K	N9-C8-N7	5.38	110.40	103.31
2	5	1799	B8H	C4-N3-C2	-5.37	120.30	127.34
2	5	4042	B8H	C4-N3-C2	-5.34	120.34	127.34
2	5	4436	B8K	C5-C6-N1	5.24	120.17	110.94
2	5	1560	7MG	N9-C4-N3	5.20	133.08	125.46
2	5	4366	OMU	N3-C2-N1	5.18	121.64	114.89
2	5	4383	OMG	C2-N3-C4	5.08	121.05	112.30
2	5	1736	E7G	N9-C4-N3	5.06	132.88	125.46
2	5	4116	OMG	C2-N3-C4	5.05	120.99	112.30
2	5	4366	OMU	C4-N3-C2	-5.05	120.35	126.61
2	5	3629	B8K	C5-C6-N1	5.03	119.79	110.94
2	5	4052	OMU	N3-C2-N1	4.99	121.38	114.89
2	5	4052	OMU	C4-N3-C2	-4.98	120.43	126.61
2	5	1477	OMG	C2-N3-C4	4.97	120.85	112.30
2	5	1736	E7G	C2-N3-C4	4.96	120.84	112.30
2	5	1260	OMG	C2-N3-C4	4.94	120.82	112.30
2	5	3631	BGH	C5-C6-N1	4.94	119.64	110.94
2	5	4436	B8K	C2-N3-C4	4.94	120.81	112.30
2	5	4240	OMG	C2-N3-C4	4.92	120.78	112.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5	2267	OMG	C2-N3-C4	4.92	120.78	112.30
2	5	4369	OMG	C2-N3-C4	4.92	120.77	112.30
2	5	2616	OMG	C2-N3-C4	4.90	120.74	112.30
2	5	3494	B8H	C4-N3-C2	-4.89	120.93	127.34
2	5	3524	OMG	C2-N3-C4	4.88	120.70	112.30
2	5	1580	OMG	C2-N3-C4	4.87	120.68	112.30
2	5	2207	OMG	C2-N3-C4	4.85	120.65	112.30
2	5	1270	A2M	N3-C4-N9	4.76	135.26	127.17
2	5	4116	OMG	N9-C4-N3	4.72	135.39	125.95
2	5	1266	1MA	C2-N3-C4	4.71	121.77	112.53
2	5	3629	B8K	C2-N3-C4	4.71	120.41	112.30
2	5	1580	OMG	N9-C4-N3	4.68	135.31	125.95
2	5	1736	E7G	C5-C4-N3	-4.67	119.37	128.13
2	5	3631	BGH	C2-N3-C4	4.65	120.30	112.30
2	5	1560	7MG	C2-N3-C4	4.64	120.28	112.30
2	5	4161	1MA	C2-N3-C4	4.63	121.61	112.53
2	5	1736	E7G	N9-C8-N7	4.57	109.84	103.37
2	5	2267	OMG	N9-C4-N3	4.56	135.07	125.95
2	5	1560	7MG	C5-C6-N1	4.55	118.94	110.94
2	5	1736	E7G	C5-C6-N1	4.54	118.92	110.94
2	5	1810	A2M	N3-C4-N9	4.53	134.87	127.17
2	5	3631	BGH	C72-C71-N7	4.51	125.45	118.80
2	5	4436	B8K	C72-C71-N7	4.49	125.42	118.80
2	5	3557	A2M	N3-C4-N9	4.49	134.80	127.17
2	5	398	A2M	N3-C4-N9	4.46	134.76	127.17
2	5	1479	A2M	N3-C4-N9	4.44	134.72	127.17
2	5	3450	A2M	N3-C4-N9	4.44	134.72	127.17
2	5	1632	PSU	C4-N3-C2	-4.44	120.26	126.37
2	5	4382	PSU	C4-N3-C2	-4.43	120.27	126.37
2	5	3629	B8K	C72-C71-N7	4.41	125.31	118.80
2	5	1614	I4U	C5-C4-N3	-4.41	118.39	124.86
2	5	4101	E6G	C61-O6-C6	-4.40	113.20	117.57
2	5	4116	OMG	C2'-C1'-N9	-4.39	105.91	114.24
2	5	4149	PSU	C4-N3-C2	-4.38	120.33	126.37
2	5	4246	PSU	C4-N3-C2	-4.37	120.35	126.37
2	5	1848	P7G	N9-C8-N7	4.36	109.55	103.37
2	5	4196	PSU	C4-N3-C2	-4.35	120.37	126.37
2	5	3455	A2M	N3-C4-N9	4.35	134.57	127.17
2	5	3612	P7G	N9-C8-N7	4.34	109.52	103.37
2	5	1638	PSU	C4-N3-C2	-4.34	120.39	126.37
2	5	3631	BGH	N9-C4-N3	4.31	131.77	125.46
2	5	4039	PSU	C4-N3-C2	-4.30	120.45	126.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5	1489	A2M	N3-C4-N9	4.29	134.46	127.17
2	5	4269	A2M	N3-C4-N9	4.27	134.44	127.17
2	5	4374	PSU	C4-N3-C2	-4.27	120.49	126.37
2	5	4383	OMG	N9-C4-N3	4.24	134.44	125.95
2	5	2365	7MG	C2-N3-C4	4.23	119.58	112.30
2	5	4277	PSU	C4-N3-C2	-4.23	120.55	126.37
2	5	4188	PSU	C4-N3-C2	-4.21	120.58	126.37
2	5	3524	OMG	N9-C4-N3	4.21	134.36	125.95
2	5	1537	PSU	C4-N3-C2	-4.19	120.60	126.37
2	5	2207	OMG	N9-C4-N3	4.17	134.29	125.95
2	5	1560	7MG	C5-C4-N3	-4.17	120.30	128.13
2	5	3447	PSU	C4-N3-C2	-4.14	120.67	126.37
2	5	4193	5MC	C5-C6-N1	-4.12	118.84	123.31
2	5	4369	OMG	N9-C4-N3	4.11	134.17	125.95
2	5	1260	OMG	N9-C4-N3	4.07	134.09	125.95
2	5	3629	B8K	C6-C5-C4	-4.07	115.25	122.40
2	5	4436	B8K	C6-C5-C4	-4.07	115.25	122.40
2	5	2351	PSU	C4-N3-C2	-4.06	120.78	126.37
2	5	3461	PSU	C4-N3-C2	-4.05	120.80	126.37
2	5	4240	OMG	N9-C4-N3	4.00	133.96	125.95
2	5	3514	5MC	C5-C6-N1	-4.00	118.97	123.31
2	5	2267	OMG	C2'-C1'-N9	-3.98	106.68	114.24
2	5	1477	OMG	N9-C4-N3	3.97	133.90	125.95
2	5	3455	A2M	N3-C2-N1	-3.95	122.60	128.58
2	5	4436	B8K	N9-C4-N3	3.92	131.21	125.46
2	5	1489	A2M	N3-C2-N1	-3.92	122.64	128.58
2	5	4269	A2M	N3-C2-N1	-3.91	122.67	128.58
2	5	2616	OMG	N9-C4-N3	3.90	133.75	125.95
2	5	4101	E6G	C2-N1-C6	3.89	121.37	115.96
2	5	398	A2M	N3-C2-N1	-3.89	122.69	128.58
2	5	3496	PSU	C4-N3-C2	-3.89	121.02	126.37
2	5	3631	BGH	C5-C4-N3	-3.87	120.86	128.13
2	5	4161	1MA	N9-C4-N3	3.87	135.71	126.90
2	5	1479	A2M	N3-C2-N1	-3.84	122.77	128.58
2	5	1292	P4U	C5-C4-N3	-3.81	119.27	124.86
2	5	1266	1MA	N1-C2-N3	-3.80	121.48	126.00
2	5	1560	7MG	N9-C8-N7	3.80	108.75	103.37
2	5	1810	A2M	C2'-C1'-N9	-3.75	107.57	113.75
2	5	3557	A2M	N3-C2-N1	-3.74	122.92	128.58
2	5	1266	1MA	N9-C4-N3	3.73	135.39	126.90
2	5	3450	A2M	N3-C2-N1	-3.70	122.98	128.58
2	5	1810	A2M	C2-N3-C4	3.70	120.86	111.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5	4042	B8H	O2-C2-N1	-3.69	119.05	122.78
2	5	3514	5MC	C5-C4-N3	-3.69	117.97	121.75
2	5	4436	B8K	C5-C4-N3	-3.69	121.21	128.13
2	5	3629	B8K	N9-C4-N3	3.68	130.86	125.46
2	5	3631	BGH	C6-C5-C4	-3.64	115.99	122.40
2	5	1799	B8H	O2-C2-N1	-3.62	119.12	122.78
2	5	1270	A2M	C2-N3-C4	3.61	120.64	111.83
2	5	1638	PSU	O2-C2-N1	-3.61	119.07	122.79
2	5	4161	1MA	N1-C2-N3	-3.61	121.71	126.00
2	5	4277	PSU	O2-C2-N1	-3.60	119.07	122.79
2	5	1270	A2M	C2'-C1'-N9	-3.58	107.86	113.75
2	5	3629	B8K	C5-C4-N3	-3.53	121.50	128.13
2	5	4374	PSU	O2-C2-N1	-3.51	119.17	122.79
2	5	4282	OMC	C2'-C1'-N1	-3.50	107.61	114.24
2	5	4382	PSU	C5-C6-N1	-3.49	117.29	122.14
2	5	4246	PSU	O2-C2-N1	-3.49	119.19	122.79
2	5	4039	PSU	O2-C2-N1	-3.48	119.20	122.79
2	5	3461	PSU	O2-C2-N1	-3.47	119.21	122.79
2	5	4188	PSU	O2-C2-N1	-3.47	119.21	122.79
2	5	4149	PSU	O2-C2-N1	-3.46	119.22	122.79
2	5	4276	UR3	C5-C4-N3	3.42	119.54	115.04
2	5	1537	PSU	O2-C2-N1	-3.40	119.28	122.79
2	5	1810	A2M	N3-C2-N1	-3.39	123.44	128.58
2	5	3496	PSU	O2-C2-N1	-3.39	119.30	122.79
2	5	1489	A2M	C2-N3-C4	3.39	120.10	111.83
2	5	4101	E6G	N9-C8-N7	-3.38	109.14	113.94
2	5	3557	A2M	C2-N3-C4	3.37	120.07	111.83
2	5	398	A2M	C2-N3-C4	3.35	120.00	111.83
2	5	1479	A2M	C2-N3-C4	3.34	120.00	111.83
2	5	4149	PSU	C3'-C2'-C1'	3.34	105.63	101.69
2	5	4196	PSU	O2-C2-N1	-3.34	119.35	122.79
2	5	4052	OMU	C5-C4-N3	3.33	119.47	114.80
2	5	1632	PSU	O2-C2-N1	-3.32	119.37	122.79
2	5	3447	PSU	O2-C2-N1	-3.31	119.37	122.79
2	5	4196	PSU	C5-C6-N1	-3.31	117.55	122.14
2	5	1632	PSU	C5-C6-N1	-3.30	117.57	122.14
2	5	4269	A2M	C2-N3-C4	3.29	119.88	111.83
2	5	1270	A2M	C4-C5-N7	-3.29	106.82	110.58
2	5	3450	A2M	C2-N3-C4	3.29	119.87	111.83
2	5	3494	B8H	O2-C2-N1	-3.29	119.45	122.78
2	5	1479	A2M	C4'-O4'-C1'	-3.29	102.21	109.47
2	5	4366	OMU	C5-C4-N3	3.28	119.39	114.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5	3455	A2M	C2-N3-C4	3.26	119.79	111.83
2	5	4101	E6G	C5-C6-N1	-3.25	119.14	123.49
2	5	4101	E6G	C4-N9-C8	3.23	109.13	105.74
2	5	1810	A2M	C4-C5-N7	-3.20	106.92	110.58
2	5	2351	PSU	O2-C2-N1	-3.19	119.50	122.79
2	5	4382	PSU	O2-C2-N1	-3.18	119.51	122.79
2	5	4277	PSU	C5-C6-N1	-3.17	117.74	122.14
2	5	4116	OMG	C6-C5-N7	3.11	135.94	130.29
2	5	4039	PSU	C5-C6-N1	-3.11	117.83	122.14
2	5	1810	A2M	C4-N9-C8	3.10	108.99	105.74
2	5	4374	PSU	C5-C6-N1	-3.08	117.86	122.14
2	5	1560	7MG	C6-C5-C4	-3.06	117.02	122.40
2	5	4246	PSU	C5-C6-N1	-3.06	117.90	122.14
2	5	4101	E6G	N3-C2-N1	-3.03	120.84	125.48
2	5	2267	OMG	C6-C5-N7	3.02	135.79	130.29
2	5	4188	PSU	C5-C6-N1	-3.01	117.96	122.14
2	5	1638	PSU	C5-C6-N1	-3.00	117.98	122.14
2	5	3631	BGH	C2'-C1'-N9	-2.98	108.08	114.14
2	5	1580	OMG	C6-C5-N7	2.96	135.68	130.29
2	5	3455	A2M	N9-C8-N7	-2.95	109.74	113.94
2	5	3447	PSU	C5-C6-N1	-2.95	118.04	122.14
2	5	2351	PSU	C5-C6-N1	-2.94	118.06	122.14
2	5	1489	A2M	N9-C8-N7	-2.92	109.80	113.94
2	5	4101	E6G	C2-N3-C4	2.91	121.30	113.51
2	5	1537	PSU	C5-C6-N1	-2.91	118.11	122.14
2	5	4269	A2M	N9-C8-N7	-2.90	109.82	113.94
2	5	1270	A2M	N3-C2-N1	-2.89	124.20	128.58
2	5	398	A2M	N9-C8-N7	-2.88	109.85	113.94
2	5	3557	A2M	N9-C8-N7	-2.88	109.85	113.94
2	5	4101	E6G	C5-N7-C8	2.88	107.97	103.45
2	5	1479	A2M	N9-C8-N7	-2.87	109.87	113.94
2	5	1560	7MG	C6-C5-N7	2.86	136.36	131.93
2	5	4052	OMU	O4-C4-C5	-2.80	120.33	125.16
2	5	2365	7MG	C5-C6-N1	2.77	115.82	110.94
2	5	4366	OMU	O2-C2-N1	-2.75	119.22	122.80
2	5	2616	OMG	C4-C5-N7	-2.74	106.33	110.67
2	5	1489	A2M	C5-N7-C8	2.74	107.75	103.45
2	5	3557	A2M	C5-N7-C8	2.73	107.75	103.45
2	5	3455	A2M	C4-N9-C8	2.73	108.60	105.74
2	5	4240	OMG	C4-C5-N7	-2.72	106.36	110.67
2	5	1479	A2M	C5-N7-C8	2.71	107.72	103.45
2	5	4052	OMU	O2-C2-N1	-2.71	119.27	122.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5	1477	OMG	C4-C5-N7	-2.70	106.39	110.67
2	5	4383	OMG	C4-C5-N7	-2.69	106.41	110.67
2	5	398	A2M	C5-N7-C8	2.69	107.67	103.45
2	5	4366	OMU	C5-C6-N1	-2.68	117.48	121.84
2	5	4101	E6G	C4-C5-C6	2.67	117.84	115.22
2	5	4366	OMU	O4-C4-C5	-2.67	120.57	125.16
2	5	3461	PSU	C5-C6-N1	-2.66	118.44	122.14
2	5	4369	OMG	C4-C5-N7	-2.66	106.45	110.67
2	5	3557	A2M	C4-C5-N7	-2.66	107.54	110.58
2	5	1489	A2M	C4-C5-N7	-2.64	107.56	110.58
2	5	1560	7MG	O6-C6-C5	-2.63	121.17	127.62
2	5	4193	5MC	C5-C4-N3	-2.62	119.06	121.75
2	5	2365	7MG	C5-C4-N9	-2.62	102.98	106.33
2	5	3455	A2M	C5-N7-C8	2.62	107.57	103.45
2	5	4269	A2M	C4-N9-C8	2.61	108.48	105.74
2	5	4052	OMU	C5-C6-N1	-2.61	117.59	121.84
2	5	4269	A2M	C5-N7-C8	2.60	107.54	103.45
2	5	398	A2M	C4-N9-C8	2.60	108.47	105.74
2	5	1260	OMG	C4-C5-N7	-2.58	106.59	110.67
2	5	3557	A2M	C4-N9-C8	2.56	108.43	105.74
2	5	1736	E7G	C6-C5-C4	-2.56	117.90	122.40
2	5	2207	OMG	C4-C5-N7	-2.55	106.63	110.67
2	5	3524	OMG	C4-C5-N7	-2.55	106.63	110.67
2	5	1270	A2M	C4-N9-C8	2.54	108.40	105.74
2	5	4101	E6G	O6-C6-C5	2.52	120.06	116.73
2	5	1736	E7G	O6-C6-C5	-2.52	121.44	127.62
2	5	1479	A2M	C4-N9-C8	2.52	108.38	105.74
2	5	1489	A2M	C4-N9-C8	2.49	108.35	105.74
2	5	2616	OMG	C8-N7-C5	2.49	108.69	104.26
2	5	1479	A2M	C4-C5-N7	-2.49	107.74	110.58
2	5	4383	OMG	C8-N7-C5	2.48	108.68	104.26
2	5	4369	OMG	C8-N7-C5	2.47	108.65	104.26
2	5	4101	E6G	C4-C5-N7	-2.46	107.77	110.58
2	5	398	A2M	C4-C5-N7	-2.45	107.78	110.58
2	5	1266	1MA	C8-N7-C5	2.44	108.61	104.26
2	5	1477	OMG	C8-N7-C5	2.44	108.61	104.26
2	5	4240	OMG	C8-N7-C5	2.44	108.61	104.26
2	5	4116	OMG	O6-C6-C5	-2.44	120.09	126.53
2	5	3450	A2M	C4-C5-N7	-2.44	107.80	110.58
2	5	3496	PSU	C5-C6-N1	-2.43	118.77	122.14
2	5	4116	OMG	C4-C5-N7	-2.43	106.82	110.67
2	5	1810	A2M	C5-N7-C8	2.42	107.25	103.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5	3450	A2M	C5-N7-C8	2.42	107.25	103.45
2	5	4269	A2M	C4-C5-N7	-2.42	107.82	110.58
2	5	2267	OMG	C4-C5-N7	-2.42	106.84	110.67
2	5	3524	OMG	C8-N7-C5	2.41	108.56	104.26
2	5	1580	OMG	C4-C5-N7	-2.41	106.85	110.67
2	5	2704	OMC	O2-C2-N3	-2.41	118.53	122.33
2	5	4149	PSU	C5-C6-N1	-2.41	118.79	122.14
2	5	4161	1MA	N9-C8-N7	-2.41	108.94	113.40
2	5	2265	OMC	O2-C2-N3	-2.40	118.54	122.33
2	5	3450	A2M	N9-C8-N7	-2.39	110.55	113.94
2	5	2365	7MG	O6-C6-C5	-2.39	121.76	127.62
2	5	4161	1MA	C8-N7-C5	2.38	108.50	104.26
2	5	1266	1MA	N9-C8-N7	-2.38	109.00	113.40
2	5	1266	1MA	C4-C5-N7	-2.36	106.92	110.67
2	5	4383	OMG	C2-N1-C6	-2.36	120.83	125.11
2	5	1260	OMG	C8-N7-C5	2.36	108.46	104.26
2	5	1270	A2M	C5-N7-C8	2.36	107.15	103.45
2	5	4188	PSU	O4'-C1'-C2'	2.35	108.41	105.15
2	5	3524	OMG	C2-N1-C6	-2.35	120.85	125.11
2	5	3433	OMC	C5-C6-N1	-2.34	118.04	121.84
2	5	2616	OMG	C6-C5-N7	2.33	134.53	130.29
2	5	3455	A2M	C4-C5-N7	-2.33	107.92	110.58
2	5	1479	A2M	C3'-C2'-C1'	2.32	107.25	102.81
2	5	2207	OMG	C8-N7-C5	2.31	108.37	104.26
2	5	2208	OMC	O2-C2-N3	-2.30	118.70	122.33
2	5	1477	OMG	C6-C5-N7	2.29	134.45	130.29
2	5	2207	OMG	C2-N1-C6	-2.28	120.97	125.11
2	5	2208	OMC	N1-C2-N3	2.28	122.76	118.80
2	5	3514	5MC	O2-C2-N3	-2.28	118.74	122.33
2	5	2647	OMC	O2-C2-N3	-2.27	118.75	122.33
2	5	2704	OMC	N1-C2-N3	2.26	122.73	118.80
2	5	3601	OMC	O2-C2-N3	-2.26	118.76	122.33
2	5	4369	OMG	C2-N1-C6	-2.26	121.02	125.11
2	5	2365	7MG	O4'-C1'-N9	2.25	112.36	109.30
2	5	4161	1MA	C4-C5-N7	-2.25	107.11	110.67
2	5	4269	A2M	C4'-O4'-C1'	-2.24	104.51	109.47
2	5	1810	A2M	N9-C8-N7	-2.24	110.75	113.94
2	5	4383	OMG	O6-C6-C5	-2.24	120.61	126.53
2	5	1477	OMG	C2-N1-C6	-2.24	121.05	125.11
2	5	4276	UR3	C1'-N1-C2	2.24	120.70	117.04
2	5	4240	OMG	C2-N1-C6	-2.23	121.06	125.11
2	5	3619	OMC	N1-C2-N3	2.22	122.66	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5	2265	OMC	N1-C2-N3	2.22	122.66	118.80
2	5	2616	OMG	C2-N1-C6	-2.22	121.09	125.11
2	5	2267	OMG	O6-C6-C5	-2.22	120.68	126.53
2	5	1489	A2M	C4'-O4'-C1'	-2.21	104.58	109.47
2	5	1292	P4U	C41-O4-C4	-2.21	112.73	117.09
2	5	4193	5MC	C3'-C2'-C1'	2.21	105.64	101.46
2	5	3524	OMG	O6-C6-C5	-2.20	120.72	126.53
2	5	4240	OMG	C6-C5-N7	2.20	134.29	130.29
2	5	2647	OMC	N1-C2-N3	2.20	122.62	118.80
2	5	3601	OMC	N1-C2-N3	2.19	122.60	118.80
2	5	1260	OMG	C2-N1-C6	-2.18	121.15	125.11
2	5	2616	OMG	O6-C6-C5	-2.18	120.77	126.53
2	5	1260	OMG	O6-C6-C5	-2.17	120.81	126.53
2	5	4369	OMG	C6-C5-N7	2.16	134.23	130.29
2	5	4369	OMG	O6-C6-C5	-2.16	120.82	126.53
2	5	2207	OMG	O6-C6-C5	-2.16	120.83	126.53
2	5	4383	OMG	C6-C5-N7	2.16	134.21	130.29
2	5	1477	OMG	O6-C6-C5	-2.15	120.85	126.53
2	5	1810	A2M	C6-C5-N7	2.14	136.21	132.09
2	5	4240	OMG	O6-C6-C5	-2.13	120.90	126.53
2	5	1736	E7G	C2-N1-C6	-2.13	121.24	125.11
2	5	3619	OMC	O2-C2-N3	-2.13	118.97	122.33
2	5	4383	OMG	C5-C6-N1	2.13	118.68	113.25
2	5	1580	OMG	O6-C6-C5	-2.12	120.93	126.53
2	5	3496	PSU	O4'-C1'-C2'	2.12	108.09	105.15
2	5	3433	OMC	N1-C2-N3	2.12	122.48	118.80
2	5	3450	A2M	C4-N9-C8	2.11	107.95	105.74
2	5	3619	OMC	C5-C6-N1	-2.10	118.42	121.84
2	5	3631	BGH	C2-N1-C6	-2.10	121.31	125.11
2	5	4116	OMG	C5-C6-N1	2.09	118.58	113.25
2	5	2616	OMG	N9-C8-N7	-2.09	109.52	113.40
2	5	4382	PSU	O4'-C1'-C2'	2.09	108.04	105.15
2	5	3524	OMG	C5-C6-N1	2.08	118.56	113.25
2	5	4383	OMG	N9-C8-N7	-2.07	109.56	113.40
2	5	4276	UR3	C6-N1-C2	-2.06	120.11	121.80
2	5	1260	OMG	C6-C5-N7	2.06	134.04	130.29
2	5	4369	OMG	N9-C8-N7	-2.06	109.58	113.40
2	5	1477	OMG	C5-C6-N1	2.06	118.49	113.25
2	5	1477	OMG	N9-C8-N7	-2.05	109.60	113.40
2	5	4276	UR3	C3U-N3-C4	2.05	120.71	117.87
2	5	4193	5MC	N1-C2-N3	2.04	122.35	118.80
2	5	4246	PSU	O4'-C1'-C2'	2.04	107.98	105.15

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	5	4369	OMG	C5-C6-N1	2.04	118.45	113.25
2	5	1260	OMG	N9-C8-N7	-2.04	109.62	113.40
2	5	2616	OMG	C5-C6-N1	2.03	118.42	113.25
2	5	3601	OMC	C5-C6-N1	-2.02	118.55	121.84
2	5	3524	OMG	N9-C8-N7	-2.01	109.67	113.40
2	5	4149	PSU	O2-C2-N3	-2.01	118.29	121.86
2	5	2208	OMC	C5-C6-N1	-2.01	118.57	121.84
2	5	1479	A2M	C2'-C1'-N9	-2.00	110.45	113.75
2	5	3631	BGH	C5'-C4'-C3'	-2.00	108.01	115.21

There are no chirality outliers.

All (98) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	5	1260	OMG	C1'-C2'-O2'-CM2
2	5	1270	A2M	C1'-C2'-O2'-CM'
2	5	1292	P4U	N3-C4-O4-C41
2	5	1292	P4U	O4'-C4'-C5'-O5'
2	5	1537	PSU	C3'-C4'-C5'-O5'
2	5	1537	PSU	O4'-C4'-C5'-O5'
2	5	1736	E7G	O4'-C4'-C5'-O5'
2	5	2207	OMG	C1'-C2'-O2'-CM2
2	5	2265	OMC	C1'-C2'-O2'-CM2
2	5	2267	OMG	O4'-C4'-C5'-O5'
2	5	2267	OMG	C3'-C4'-C5'-O5'
2	5	2616	OMG	C1'-C2'-O2'-CM2
2	5	2647	OMC	C1'-C2'-O2'-CM2
2	5	2704	OMC	C1'-C2'-O2'-CM2
2	5	3433	OMC	C2'-C1'-N1-C2
2	5	3433	OMC	C2'-C1'-N1-C6
2	5	3461	PSU	O4'-C4'-C5'-O5'
2	5	3494	B8H	O4'-C4'-C5'-O5'
2	5	3496	PSU	O4'-C4'-C5'-O5'
2	5	3524	OMG	O4'-C4'-C5'-O5'
2	5	3557	A2M	C1'-C2'-O2'-CM'
2	5	3612	P7G	O4'-C4'-C5'-O5'
2	5	3629	B8K	O4'-C4'-C5'-O5'
2	5	4052	OMU	C1'-C2'-O2'-CM2
2	5	4101	E6G	C5-C6-O6-C61
2	5	4101	E6G	N1-C6-O6-C61
2	5	4116	OMG	C1'-C2'-O2'-CM2
2	5	4149	PSU	O4'-C1'-C5-C4

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Mol	Chain	Res	Type	Atoms
2	5	4149	PSU	O4'-C1'-C5-C6
2	5	4193	5MC	C2'-C1'-N1-C6
2	5	4196	PSU	C2'-C1'-C5-C4
2	5	4196	PSU	O4'-C4'-C5'-O5'
2	5	4246	PSU	C3'-C4'-C5'-O5'
2	5	4246	PSU	O4'-C4'-C5'-O5'
2	5	4269	A2M	O4'-C4'-C5'-O5'
2	5	4282	OMC	C1'-C2'-O2'-CM2
2	5	4366	OMU	C1'-C2'-O2'-CM2
2	5	4369	OMG	C1'-C2'-O2'-CM2
2	5	4383	OMG	O4'-C4'-C5'-O5'
2	5	4383	OMG	C1'-C2'-O2'-CM2
19	m	72	MLZ	C-CA-CB-CG
2	5	1292	P4U	C3'-C4'-C5'-O5'
2	5	3461	PSU	C3'-C4'-C5'-O5'
2	5	3496	PSU	C3'-C4'-C5'-O5'
2	5	3631	BGH	C3'-C4'-C5'-O5'
2	5	4039	PSU	C3'-C4'-C5'-O5'
2	5	4052	OMU	C3'-C4'-C5'-O5'
2	5	4196	PSU	C3'-C4'-C5'-O5'
2	5	4382	PSU	C3'-C4'-C5'-O5'
2	5	4382	PSU	O4'-C4'-C5'-O5'
2	5	1292	P4U	O4-C41-C42-C43
2	5	3631	BGH	O4'-C4'-C5'-O5'
2	5	4039	PSU	O4'-C4'-C5'-O5'
2	5	4240	OMG	O4'-C4'-C5'-O5'
2	5	4240	OMG	C3'-C4'-C5'-O5'
2	5	4193	5MC	C2'-C1'-N1-C2
2	5	1736	E7G	C3'-C4'-C5'-O5'
2	5	3524	OMG	C3'-C4'-C5'-O5'
2	5	3612	P7G	C3'-C4'-C5'-O5'
2	5	4269	A2M	C3'-C4'-C5'-O5'
2	5	3494	B8H	C3'-C4'-C5'-O5'
2	5	3629	B8K	C3'-C4'-C5'-O5'
2	5	4383	OMG	C3'-C4'-C5'-O5'
2	5	4052	OMU	O4'-C4'-C5'-O5'
2	5	1736	E7G	C72-C71-N7-C8
2	5	4101	E6G	C62-C61-O6-C6
2	5	4161	1MA	C3'-C4'-C5'-O5'
2	5	2207	OMG	O4'-C4'-C5'-O5'
2	5	1479	A2M	C3'-C4'-C5'-O5'
2	5	1489	A2M	C3'-C2'-O2'-CM'

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Mol	Chain	Res	Type	Atoms
2	5	1270	A2M	C3'-C4'-C5'-O5'
2	5	4193	5MC	O4'-C1'-N1-C2
2	5	4193	5MC	O4'-C1'-N1-C6
2	5	4240	OMG	C3'-C2'-O2'-CM2
2	5	1270	A2M	C4'-C5'-O5'-P
2	5	1489	A2M	C4'-C5'-O5'-P
2	5	3629	B8K	C4'-C5'-O5'-P
2	5	4246	PSU	C4'-C5'-O5'-P
2	5	4042	B8H	O4'-C1'-C5-C4
2	5	4196	PSU	O4'-C1'-C5-C4
2	5	4246	PSU	O4'-C1'-C5-C4
2	5	4282	OMC	C3'-C4'-C5'-O5'
2	5	3433	OMC	O4'-C1'-N1-C6
2	5	3496	PSU	C4'-C5'-O5'-P
2	5	3433	OMC	O4'-C1'-N1-C2
2	5	4269	A2M	C3'-C2'-O2'-CM'
2	5	398	A2M	O4'-C4'-C5'-O5'
2	5	1632	PSU	O4'-C1'-C5-C6
2	5	4042	B8H	O4'-C1'-C5-C6
2	5	4246	PSU	O4'-C1'-C5-C6
2	5	4382	PSU	O4'-C1'-C5-C6
2	5	3612	P7G	C72-C71-N7-C8
2	5	1614	I4U	C42-C41-O4-C4
2	5	2265	OMC	O4'-C4'-C5'-O5'
2	5	4101	E6G	O4'-C4'-C5'-O5'
2	5	1266	1MA	C2'-C1'-N9-C8
2	5	3619	OMC	C4'-C5'-O5'-P
2	5	1479	A2M	O4'-C4'-C5'-O5'

There are no ring outliers.

31 monomers are involved in 43 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	5	2704	OMC	2	0
2	5	4149	PSU	1	0
2	5	398	A2M	1	0
2	5	1638	PSU	1	0
2	5	1489	A2M	1	0
2	5	4269	A2M	1	0
2	5	4276	UR3	2	0
2	5	3601	OMC	1	0
2	5	1260	OMG	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	5	4383	OMG	1	0
2	5	4366	OMU	2	0
2	5	3524	OMG	1	0
2	5	3557	A2M	2	0
2	5	4193	5MC	2	0
2	5	4369	OMG	1	0
2	5	4240	OMG	1	0
2	5	3496	PSU	1	0
2	5	2647	OMC	1	0
2	5	4436	B8K	1	0
2	5	2267	OMG	3	0
2	5	1270	A2M	2	0
2	5	2265	OMC	1	0
2	5	1560	7MG	1	0
2	5	2365	7MG	1	0
2	5	3450	A2M	3	0
2	5	4116	OMG	1	0
2	5	3455	A2M	2	0
2	5	4052	OMU	1	0
2	5	2616	OMG	2	0
2	5	1810	A2M	1	0
2	5	1632	PSU	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 184 ligands modelled in this entry, 183 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
50	OWI	K	501	-	45,45,45	2.20	12 (26%)	62,64,64	2.87	14 (22%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
50	OWI	K	501	-	-	26/52/60/60	0/3/4/4

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
50	K	501	OWI	S05-N04	6.76	1.72	1.63
50	K	501	OWI	S30-N29	6.53	1.72	1.63
50	K	501	OWI	C31-S30	5.60	1.84	1.76
50	K	501	OWI	C07-S05	4.87	1.83	1.76
50	K	501	OWI	C34-N35	3.84	1.46	1.37
50	K	501	OWI	O41-S30	3.13	1.46	1.43
50	K	501	OWI	O06-S05	2.72	1.46	1.43
50	K	501	OWI	O40-S30	2.66	1.46	1.43
50	K	501	OWI	C03-N04	-2.57	1.43	1.47
50	K	501	OWI	O14-S05	2.53	1.46	1.43
50	K	501	OWI	C03-C02	2.33	1.52	1.50
50	K	501	OWI	C42-C02	2.31	1.52	1.50

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
50	K	501	OWI	O41-S30-O40	-12.28	100.43	119.59
50	K	501	OWI	O14-S05-O06	-11.97	100.91	119.59
50	K	501	OWI	O41-S30-N29	7.07	113.34	106.69
50	K	501	OWI	O14-S05-N04	6.19	112.52	106.69
50	K	501	OWI	O06-S05-N04	4.63	111.04	106.69
50	K	501	OWI	C31-S30-N29	4.04	112.15	107.28
50	K	501	OWI	O14-S05-C07	3.50	112.45	108.10
50	K	501	OWI	O40-S30-N29	3.45	109.94	106.69
50	K	501	OWI	C20-C19-N18	-2.90	109.45	114.06
50	K	501	OWI	C42-C02-C03	2.47	120.76	116.15
50	K	501	OWI	O40-S30-C31	2.46	111.16	108.10
50	K	501	OWI	C07-S05-N04	2.38	110.15	107.28
50	K	501	OWI	C26-N18-C19	-2.21	106.74	111.89
50	K	501	OWI	C03-C02-C01	-2.11	119.08	122.00

There are no chirality outliers.

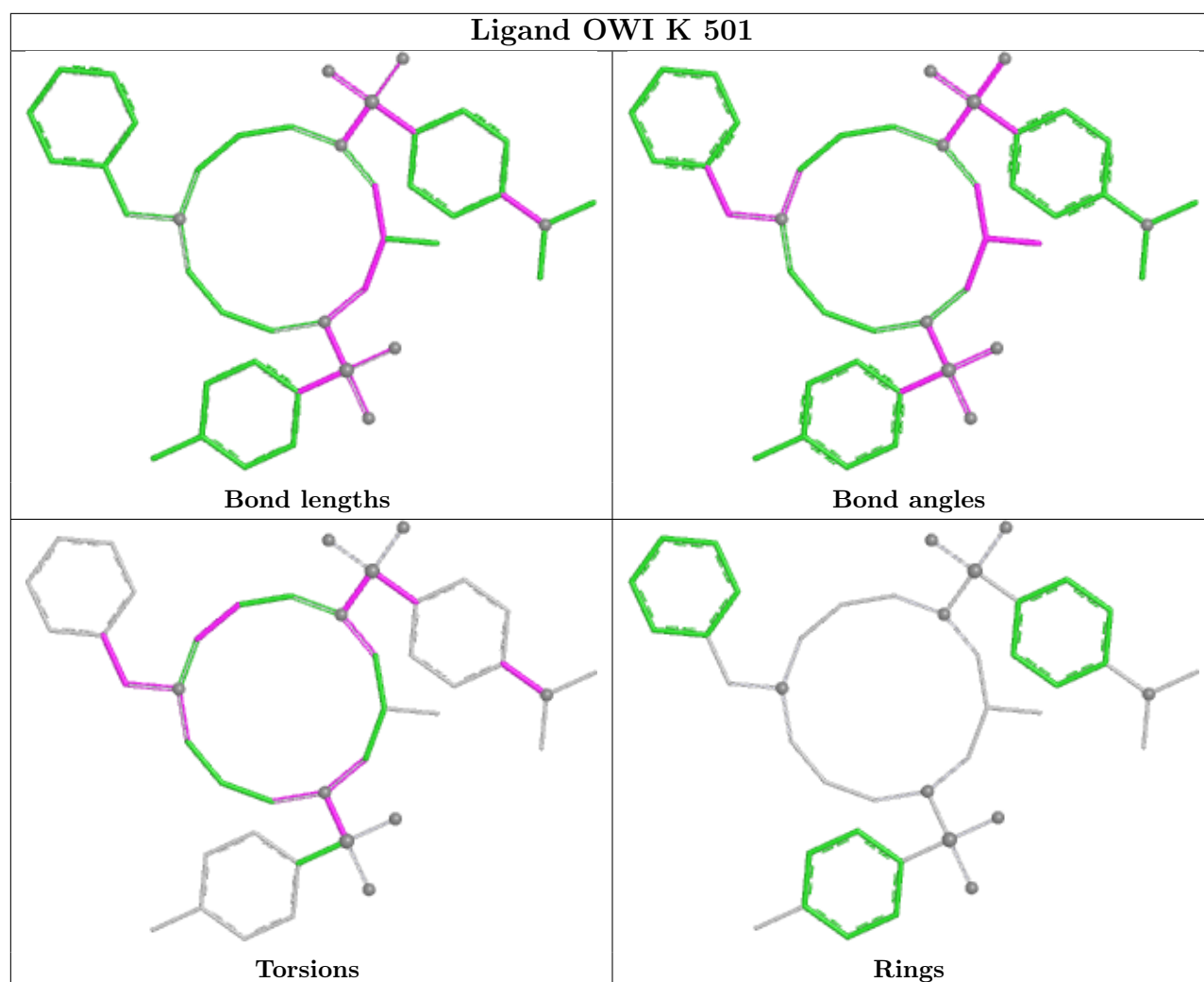
All (26) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
50	K	501	OWI	C16-C15-N04-S05
50	K	501	OWI	N18-C19-C20-C21
50	K	501	OWI	N18-C19-C20-C25
50	K	501	OWI	C20-C19-N18-C26
50	K	501	OWI	C02-C42-N29-C28
50	K	501	OWI	C02-C42-N29-S30
50	K	501	OWI	C03-N04-S05-C07
50	K	501	OWI	C39-C31-S30-N29
50	K	501	OWI	C32-C31-S30-N29
50	K	501	OWI	C33-C34-N35-C36
50	K	501	OWI	C38-C34-N35-C37
50	K	501	OWI	C33-C34-N35-C37
50	K	501	OWI	C38-C34-N35-C36
50	K	501	OWI	N18-C26-C27-C28
50	K	501	OWI	C03-N04-S05-O14
50	K	501	OWI	C16-C17-N18-C26
50	K	501	OWI	C15-N04-S05-O14
50	K	501	OWI	C32-C31-S30-O41
50	K	501	OWI	C39-C31-S30-O41
50	K	501	OWI	C02-C03-N04-C15
50	K	501	OWI	C15-N04-S05-O06
50	K	501	OWI	C16-C17-N18-C19
50	K	501	OWI	C15-N04-S05-C07
50	K	501	OWI	C42-N29-S30-O40
50	K	501	OWI	C28-N29-S30-O40
50	K	501	OWI	C03-N04-S05-O06

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

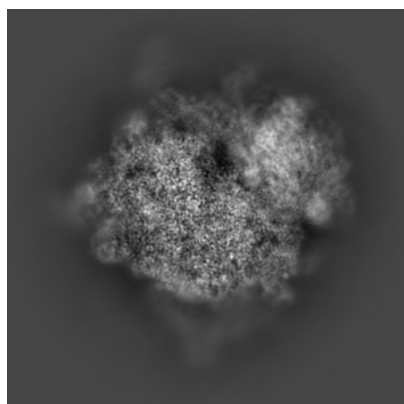
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-15863. These allow visual inspection of the internal detail of the map and identification of artifacts.

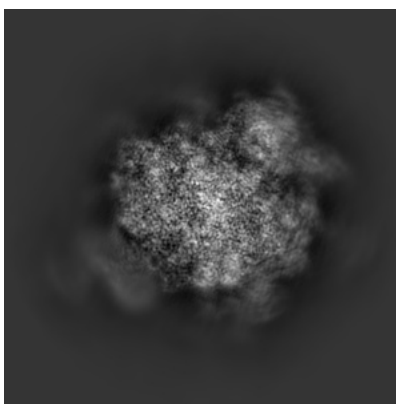
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

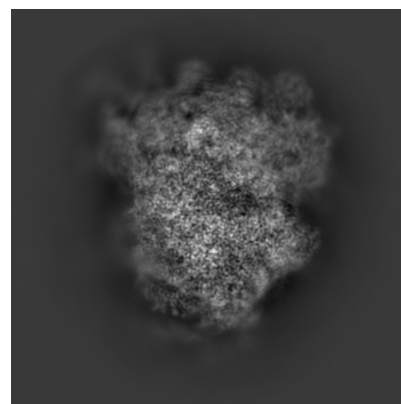
6.1.1 Primary map



X

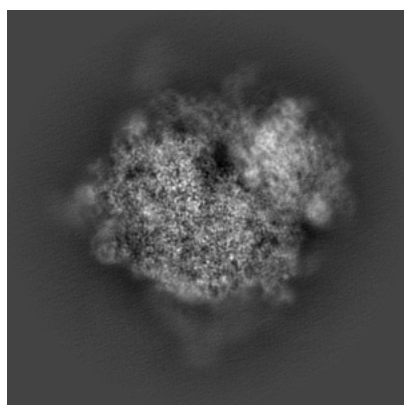


Y

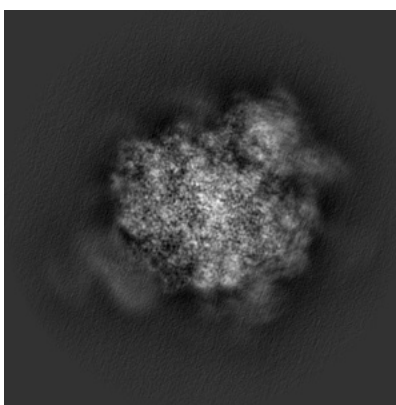


Z

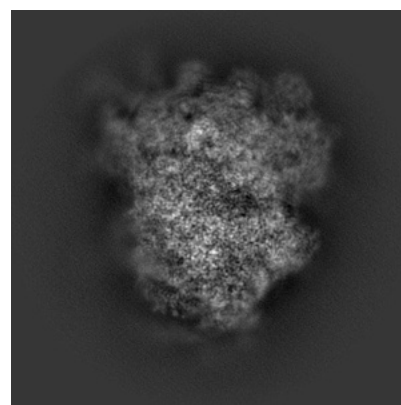
6.1.2 Raw map



X



Y

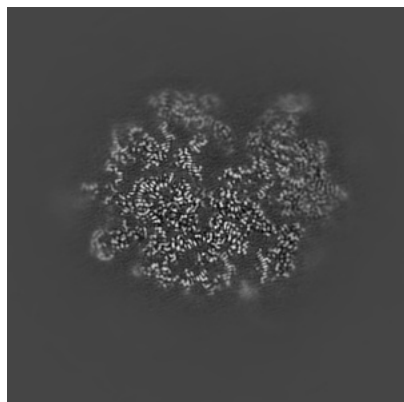


Z

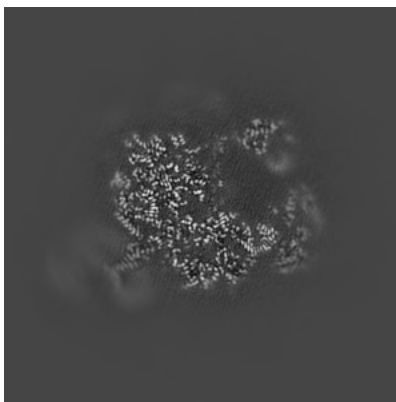
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

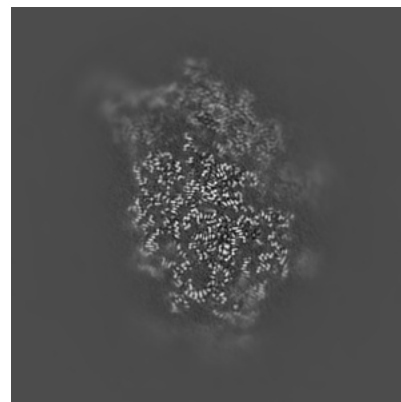
6.2.1 Primary map



X Index: 176

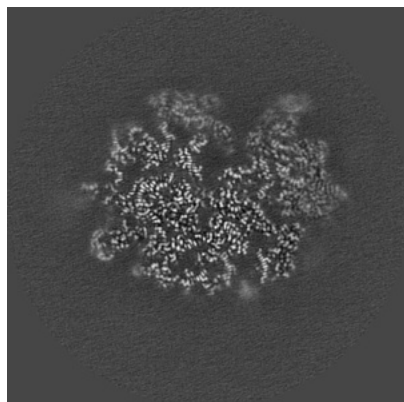


Y Index: 176

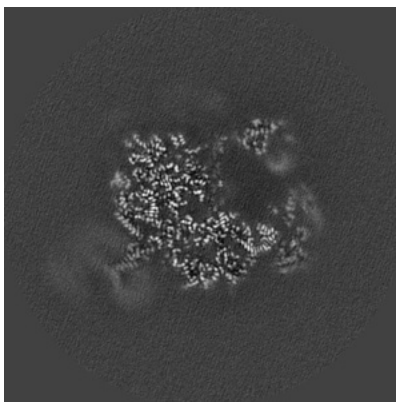


Z Index: 176

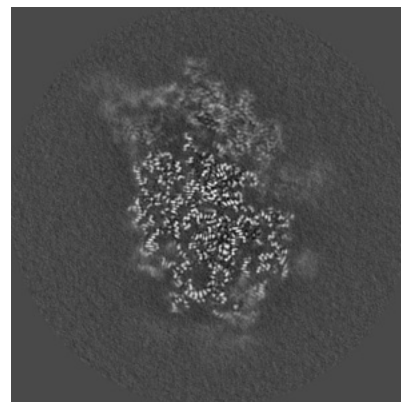
6.2.2 Raw map



X Index: 176



Y Index: 176

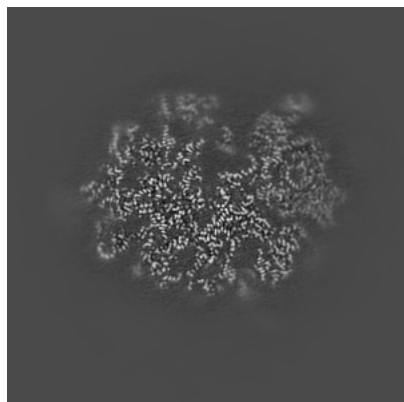


Z Index: 176

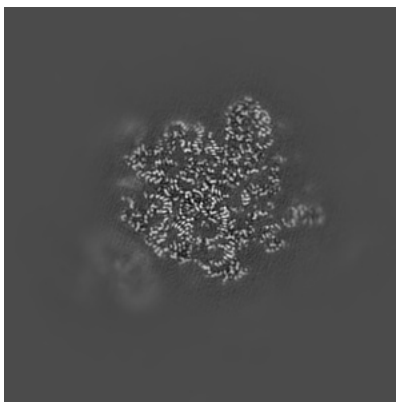
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

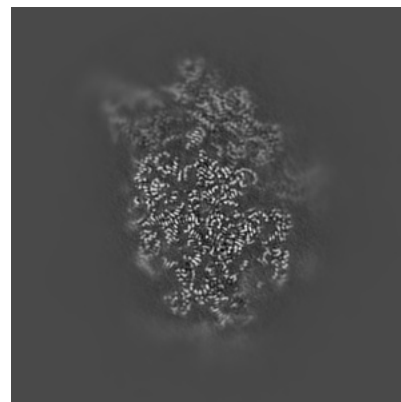
6.3.1 Primary map



X Index: 179

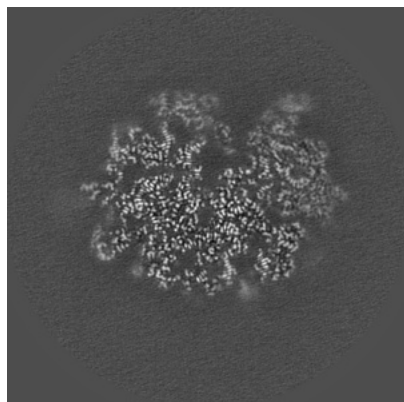


Y Index: 147

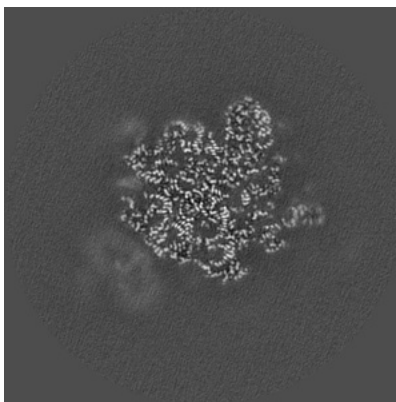


Z Index: 180

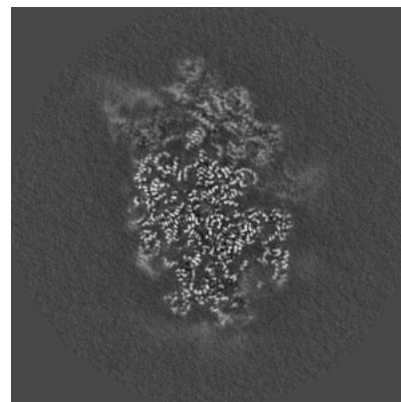
6.3.2 Raw map



X Index: 177



Y Index: 147

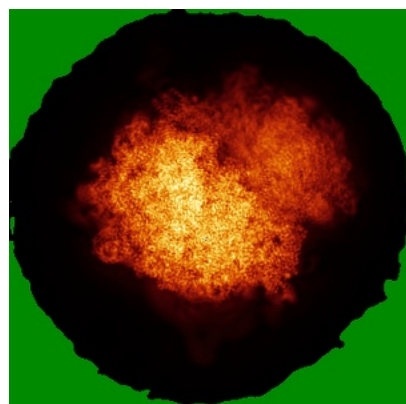


Z Index: 180

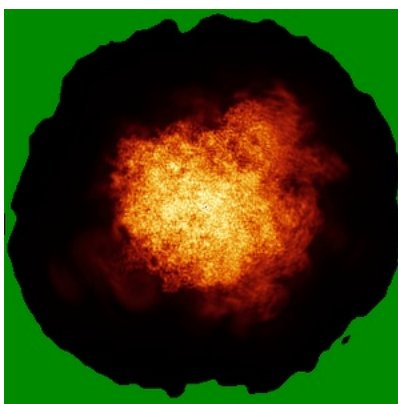
The images above show the largest variance slices of the map in three orthogonal directions.

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

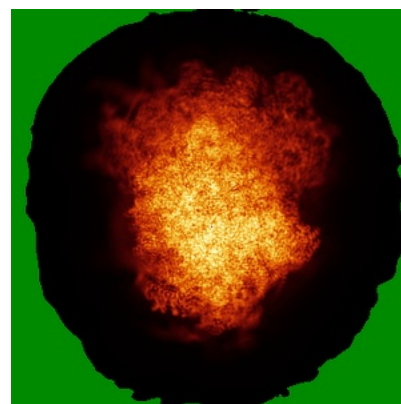
6.4.1 Primary map



X

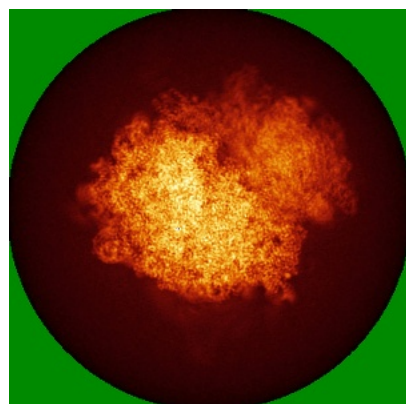


Y

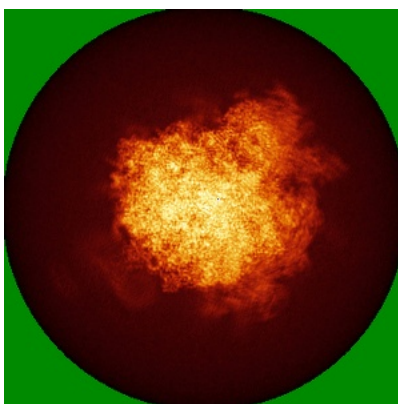


Z

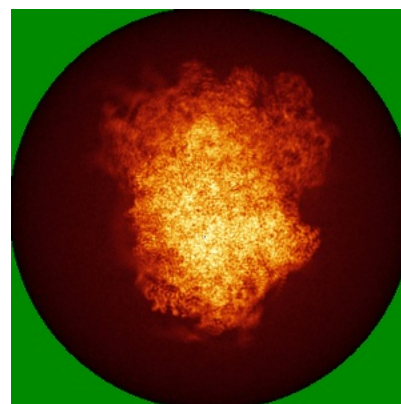
6.4.2 Raw map



X



Y

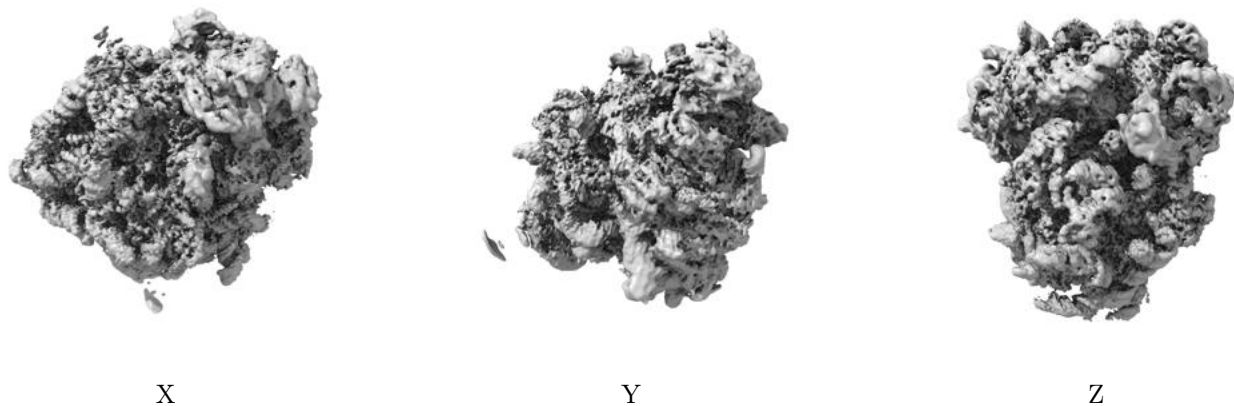


Z

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

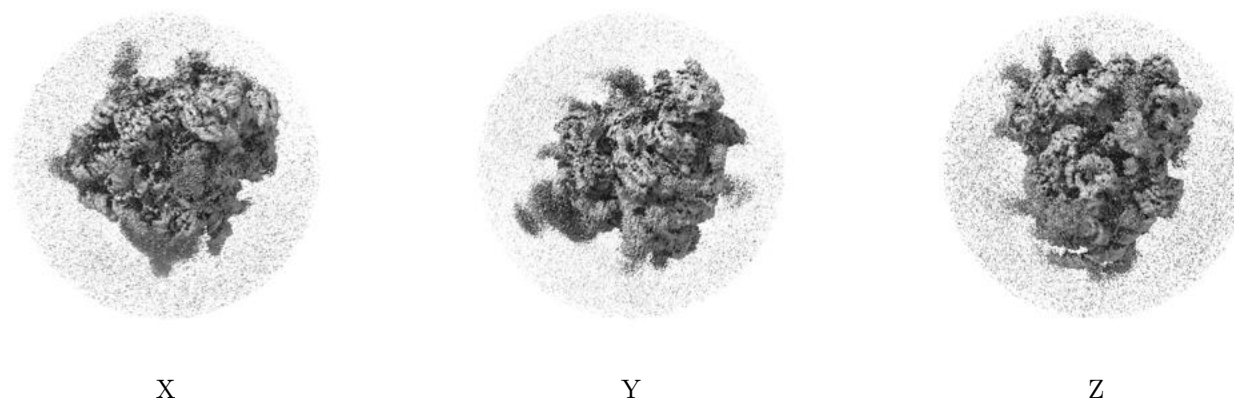
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01581. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

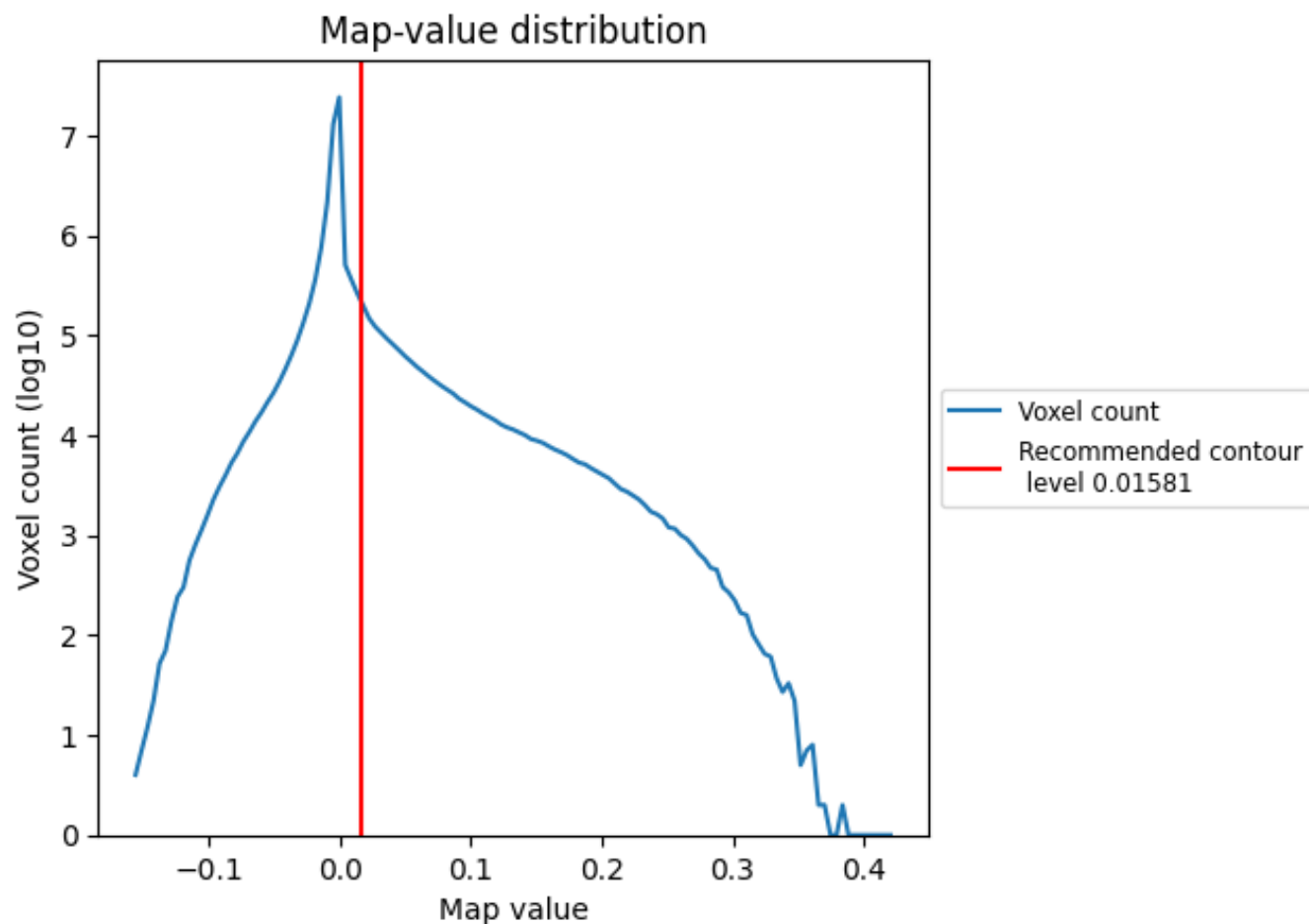
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

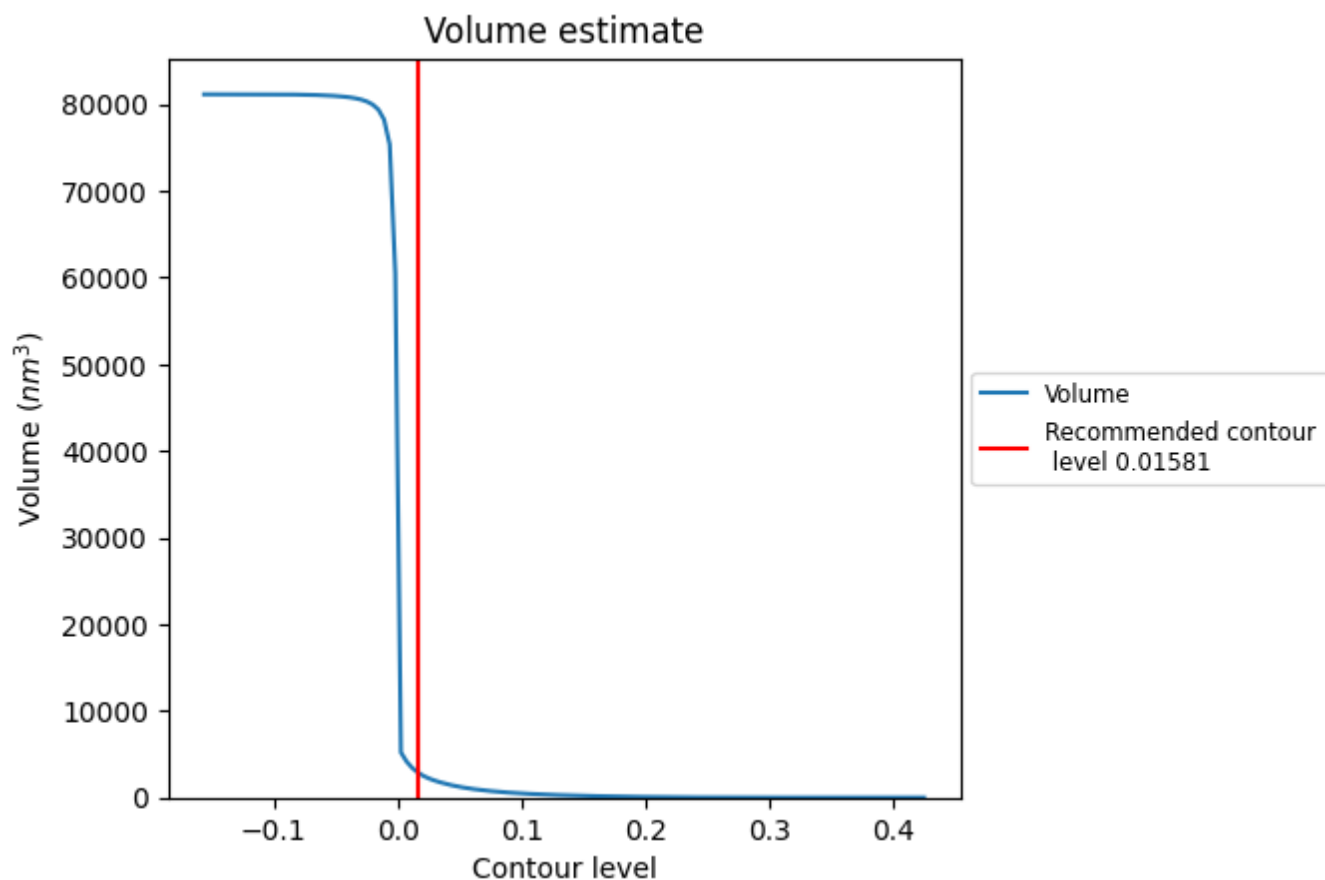
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

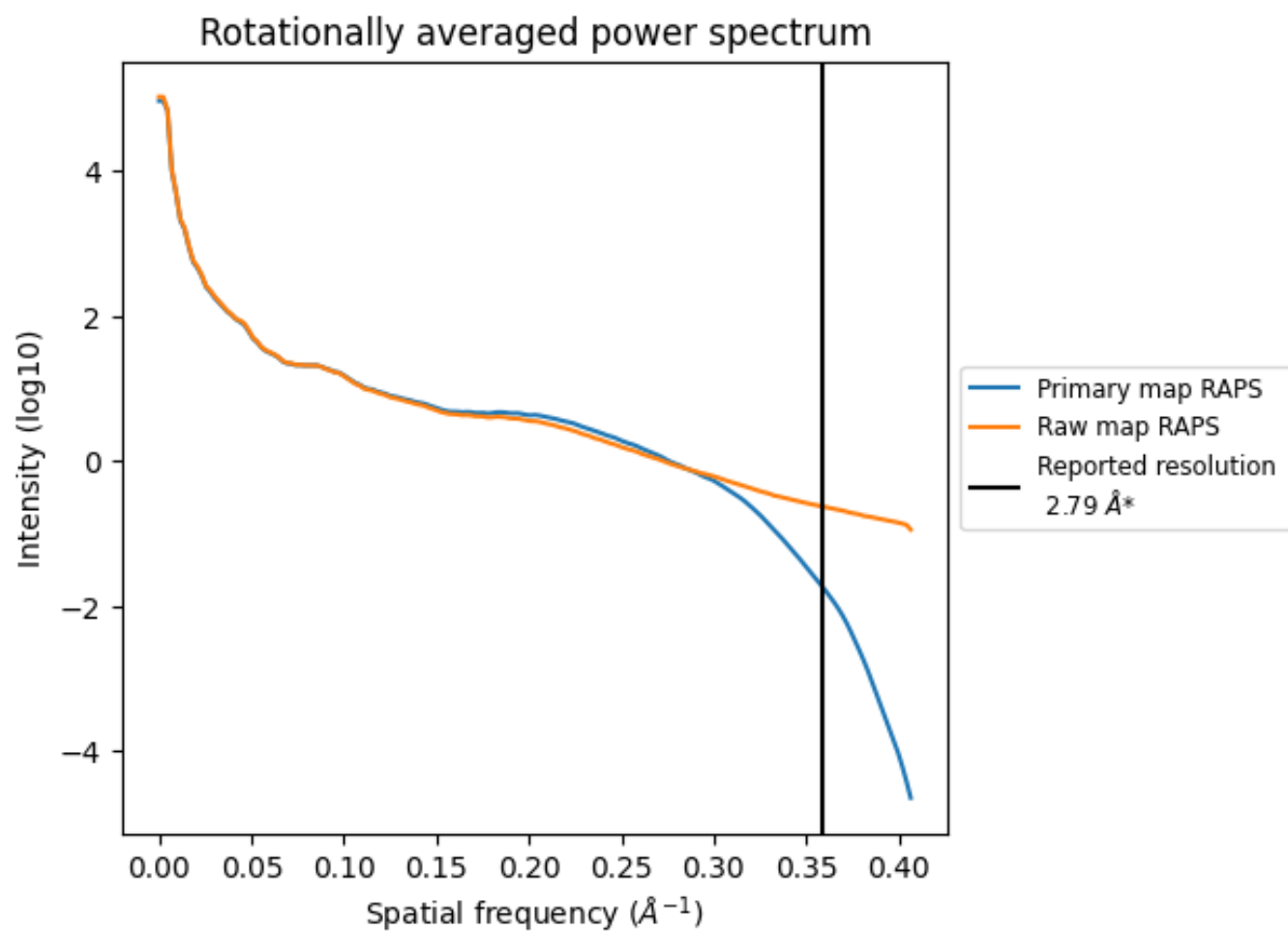
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2951 nm³; this corresponds to an approximate mass of 2665 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 ⓘ

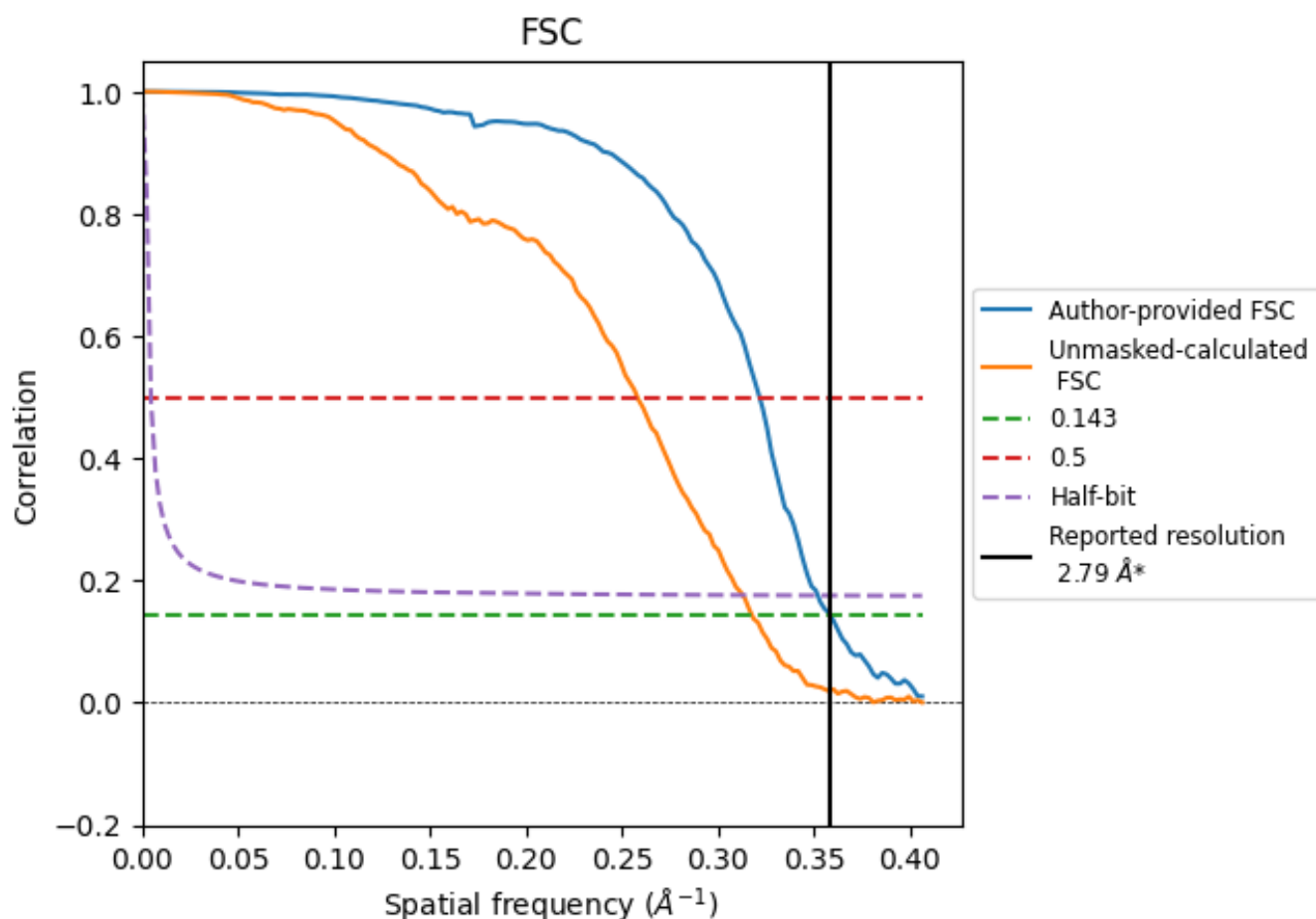


*Reported resolution corresponds to spatial frequency of 0.358 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.358 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

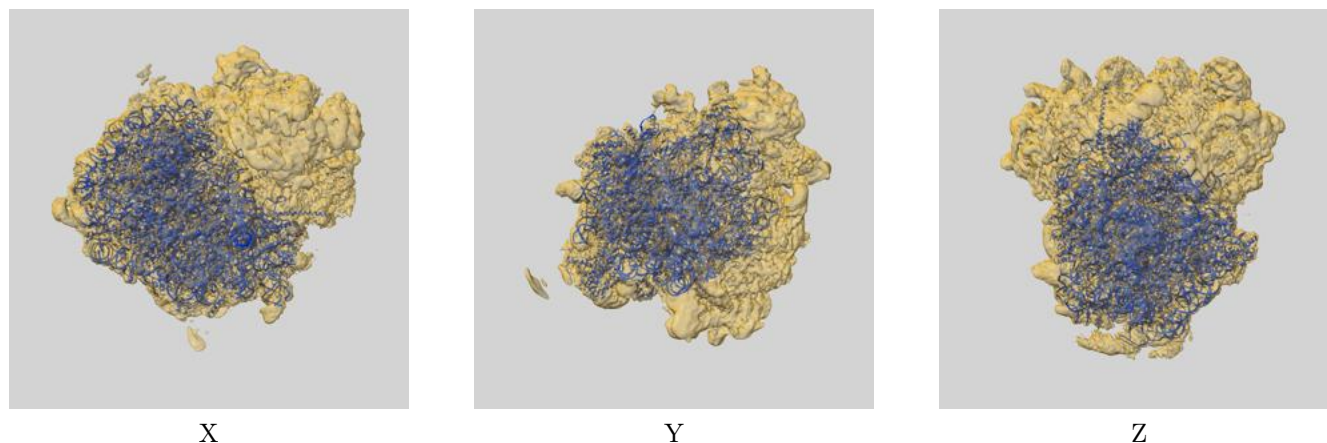
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.79	-	-
Author-provided FSC curve	2.79	3.11	2.84
Unmasked-calculated*	3.15	3.87	3.19

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.15 differs from the reported value 2.79 by more than 10 %

9 Map-model fit [i](#)

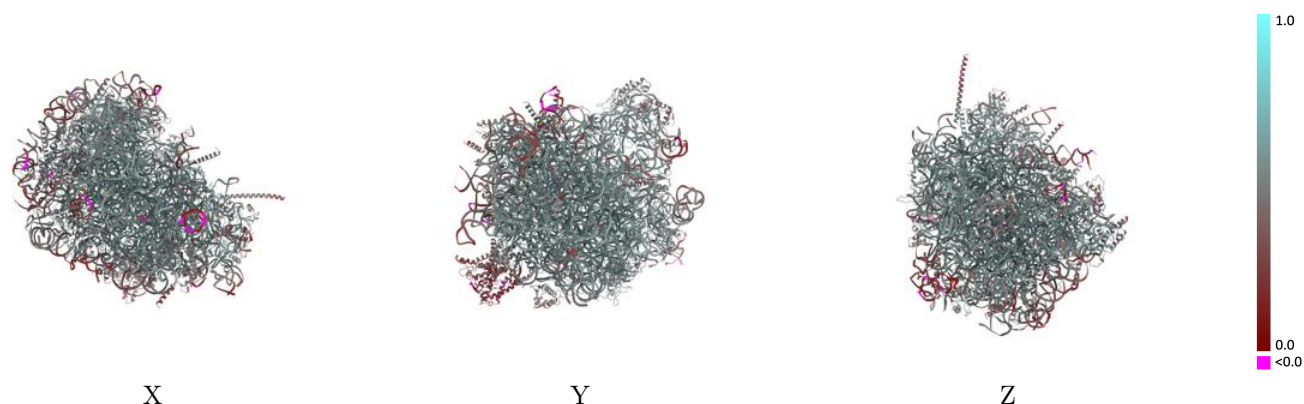
This section contains information regarding the fit between EMDB map EMD-15863 and PDB model 8B6C. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

9.1 Map-model overlay [i](#)



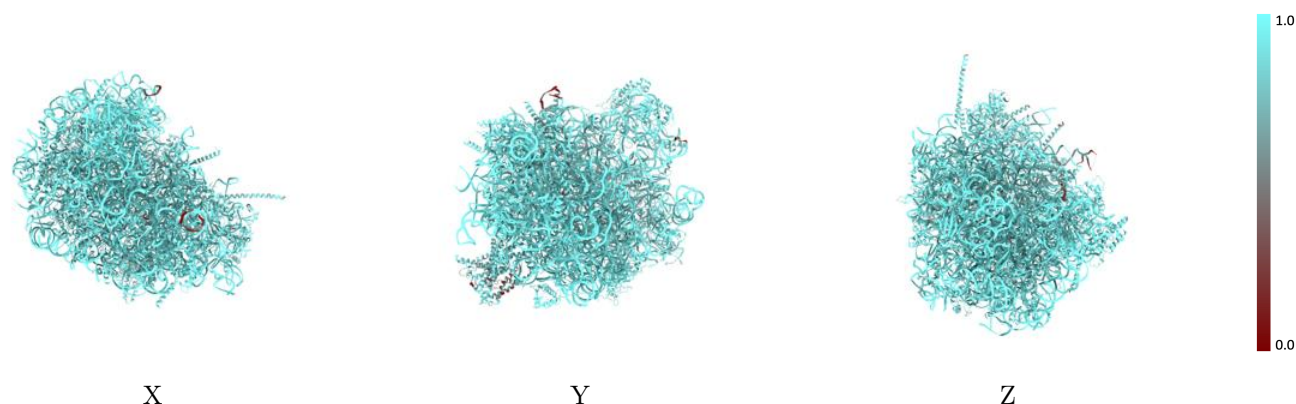
The images above show the 3D surface view of the map at the recommended contour level 0.01581 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



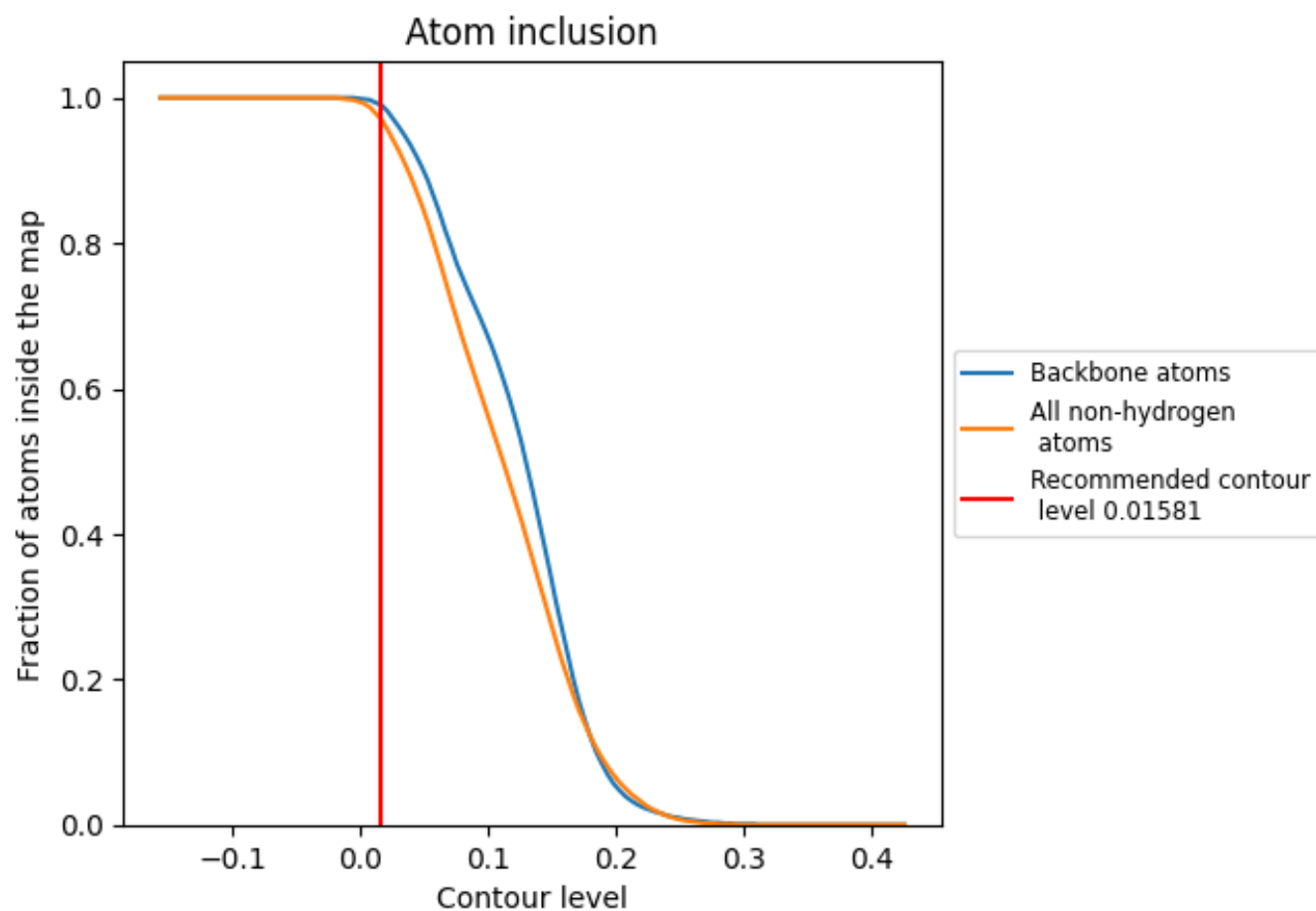
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01581).

9.4 Atom inclusion ⓘ



At the recommended contour level, 99% of all backbone atoms, 97% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.01581) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9710	 0.5160
5	 0.9870	 0.5160
7	 0.9980	 0.5520
8	 0.9950	 0.5410
A	 0.9700	 0.5720
B	 0.9690	 0.5500
C	 0.9660	 0.5490
D	 0.9720	 0.5050
E	 0.9710	 0.5230
F	 0.9590	 0.5510
G	 0.9560	 0.4800
H	 0.9550	 0.5320
I	 0.9590	 0.5400
J	 0.9500	 0.4670
K	 0.7720	 0.2550
L	 0.9370	 0.5110
M	 0.9720	 0.5320
N	 0.9720	 0.5760
O	 0.9750	 0.5530
P	 0.9620	 0.5550
Q	 0.9580	 0.5600
R	 0.9400	 0.4920
S	 0.9720	 0.5580
T	 0.9600	 0.5390
U	 0.9440	 0.4390
V	 0.9560	 0.5610
W	 0.9570	 0.5450
X	 0.9310	 0.5240
Y	 0.9450	 0.5250
Z	 0.9700	 0.5140
a	 0.9750	 0.5680
b	 0.9320	 0.4730
c	 0.9400	 0.4970
d	 0.9510	 0.5230
e	 0.9660	 0.5670



Continued on next page...

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Chain	Atom inclusion	Q-score
f	 0.9670	 0.5760
g	 0.9450	 0.5440
h	 0.9370	 0.5150
i	 0.9470	 0.4970
j	 0.9780	 0.5790
k	 0.9170	 0.4660
l	 0.9560	 0.5470
m	 0.9520	 0.5540
n	 0.8850	 0.4620
o	 0.9620	 0.5470
p	 0.9420	 0.5400
q	 0.8050	 0.2950
r	 0.9770	 0.5530