



Full wwPDB EM Validation Report ⓘ

Jun 18, 2026 – 03:50 am BST

PDB ID : 7PJS / pdb_00007pjs
EMDB ID : EMD-13458
Title : Structure of the 70S ribosome with tRNAs in the classical pre-translocation state and apramycin (C)
Authors : Petrychenko, V.; Peng, B.Z.; Schwarzer, A.C.; Peske, F.; Rodnina, M.V.; Fischer, N.
Deposited on : 2021-08-24
Resolution : 2.35 Å (reported)
Based on initial models : 4AQY, 6YSS, 5LZD

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:

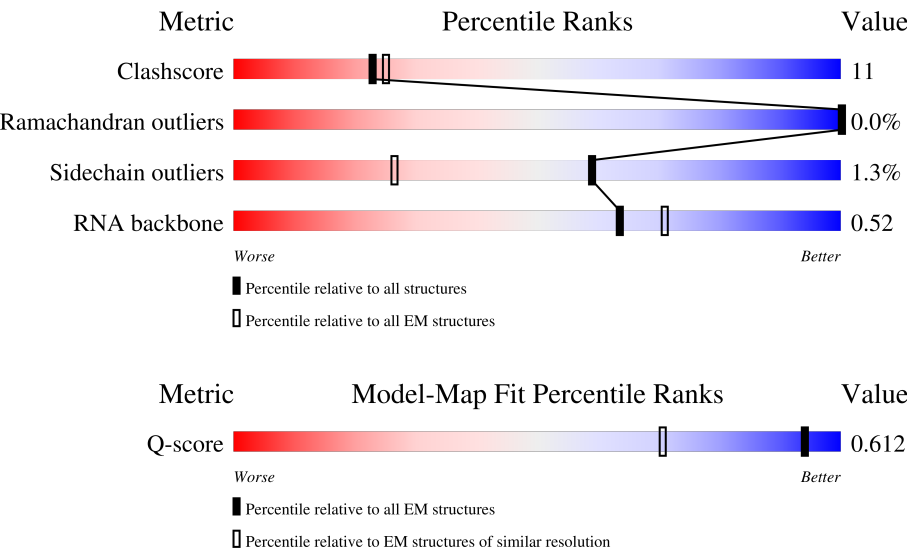
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 i

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

The reported resolution of this entry is 2.35 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.



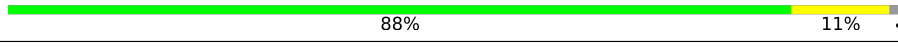
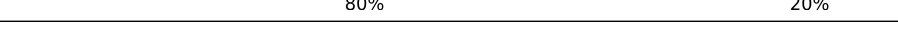
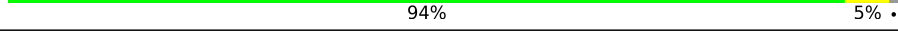
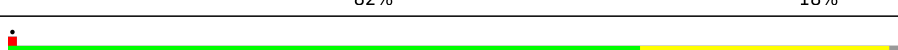
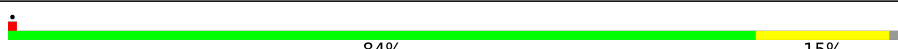
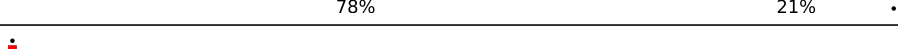
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	4607 (1.85 - 2.85)

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	0	57	79% 19% .
2	1	55	64% 27% 9%

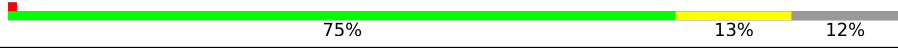
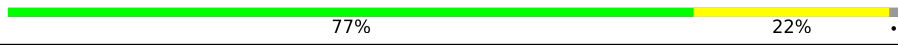
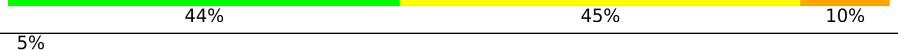
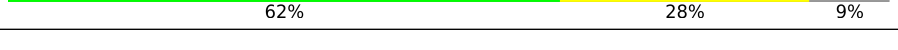
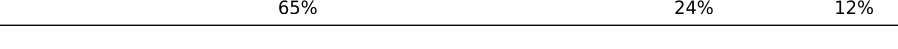
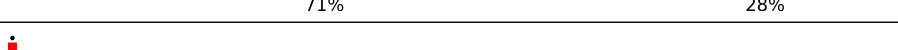
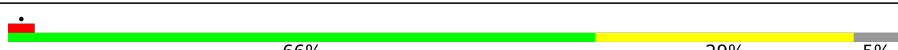
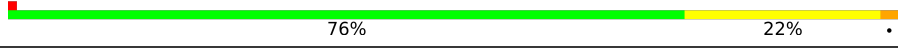
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Mol	Chain	Length	Quality of chain
3	2	46	
4	3	65	
5	4	38	
6	5	165	
7	6	70	
8	A	2903	
9	B	120	
10	C	273	
11	D	209	
12	E	201	
13	F	179	
14	G	177	
15	H	149	
16	I	142	
17	J	142	
18	K	123	
19	L	144	
20	M	136	
21	N	127	
22	O	117	
23	P	115	
24	Q	118	
25	R	103	
26	S	110	
27	T	100	

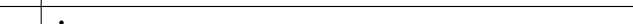
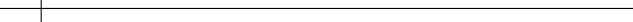
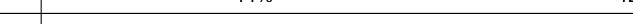
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Mol	Chain	Length	Quality of chain
28	U	104	
29	V	94	
30	W	85	
31	X	78	
32	Y	63	
33	Z	59	
34	a	1542	
35	b	240	
36	c	233	
37	d	206	
38	e	167	
39	f	135	
40	g	179	
41	h	130	
42	i	130	
43	j	103	
44	k	129	
45	l	124	
46	m	118	
47	n	102	
48	o	89	
49	p	82	
50	q	84	
51	r	75	
52	s	92	

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Mol	Chain	Length	Quality of chain
53	t	87	
54	u	71	
55	v	77	
56	w	76	
57	y	2	
58	z	33	

2 Entry composition

There are 63 unique types of molecules in this entry. The entry contains 147741 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L32.

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

- Molecule 2 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	1	50	Total	C	N	O	0	0
			409	263	75	71		

- Molecule 3 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 4 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 5 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 6 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms				AltConf	Trace
6	5	131	Total	C	N	O	0	0
			647	385	131	131		

- Molecule 7 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	66	Total	C	N	O	S	0	0
			522	323	99	94	6		

- Molecule 8 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A	2903	Total	C	N	O	P	0	0
			62338	27816	11471	20148	2903		

- Molecule 9 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	B	120	Total	C	N	O	P	0	0
			2570	1144	468	838	120		

- Molecule 10 is a protein called 50S ribosomal protein L2.

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

- Molecule 11 is a protein called 50S ribosomal protein L3.

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

- Molecule 12 is a protein called 50S ribosomal protein L4.

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

- Molecule 13 is a protein called 50S ribosomal protein L5.

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

- Molecule 14 is a protein called 50S ribosomal protein L6.

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

- Molecule 15 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	H	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

- Molecule 16 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	I	141	Total	C	N	O	S	0	0
			693	411	141	141			

- Molecule 17 is a protein called 50S ribosomal protein L13.

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

- Molecule 18 is a protein called 50S ribosomal protein L14.

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

- Molecule 19 is a protein called 50S ribosomal protein L15.

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

- Molecule 20 is a protein called 50S ribosomal protein L16.

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

- Molecule 21 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	N	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 22 is a protein called 50S ribosomal protein L18.

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

- Molecule 23 is a protein called 50S ribosomal protein L19.

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

- Molecule 24 is a protein called 50S ribosomal protein L20.

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

- Molecule 25 is a protein called 50S ribosomal protein L21.

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

- Molecule 26 is a protein called 50S ribosomal protein L22.

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

- Molecule 27 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	T	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 28 is a protein called 50S ribosomal protein L24.

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

- Molecule 29 is a protein called 50S ribosomal protein L25.

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

- Molecule 30 is a protein called 50S ribosomal protein L27.

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

- Molecule 31 is a protein called 50S ribosomal protein L28.

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

- Molecule 32 is a protein called 50S ribosomal protein L29.

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

- Molecule 33 is a protein called 50S ribosomal protein L30.

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

- Molecule 34 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	a	1540	Total	C	N	O	P	0	0
			33050	14748	6057	10705	1540		

- Molecule 35 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	b	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 36 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	c	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 37 is a protein called 30S ribosomal protein S4.

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

- Molecule 38 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	e	157	Total	C	N	O	S	0	0
			1141	709	218	208	6		

- Molecule 39 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	f	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 40 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	g	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 41 is a protein called 30S ribosomal protein S8.

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

- Molecule 42 is a protein called 30S ribosomal protein S9.

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

- Molecule 43 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	j	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 44 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	k	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

- Molecule 45 is a protein called 30S ribosomal protein S12.

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

- Molecule 46 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	m	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 47 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	n	101	Total	C	N	O	S	0	0
			799	498	165	133	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
n	35	ALA	-	insertion	UNP C3SR07

- Molecule 48 is a protein called 30S ribosomal protein S15.

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

- Molecule 49 is a protein called 30S ribosomal protein S16.

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

- Molecule 50 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	q	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 51 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	r	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 52 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	s	82	Total	C	N	O	S	0	0
			658	421	125	110	2		

- Molecule 53 is a protein called 30S ribosomal protein S20.

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

- Molecule 54 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	u	65	Total	C	N	O	S	0	0
			506	313	105	87	1		

- Molecule 55 is a RNA chain called P-site tRNA(fMet).

Mol	Chain	Residues	Atoms						AltConf	Trace
55	v	77	Total	C	N	O	P	S	0	0
			1642	733	297	534	77	1		

- Molecule 56 is a RNA chain called P-site fMet-Phe-tRNA(Phe).

Mol	Chain	Residues	Atoms					AltConf	Trace	
56	w	76	Total	C	N	O	P	S	0	0
			1631	731	291	531	76	2		

- Molecule 57 is a protein called Dipeptide (FME-PHE).

Mol	Chain	Residues	Atoms					AltConf	Trace
57	y	2	Total	C	N	O	S	0	0
			21	15	2	3	1		

- Molecule 58 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	z	11	Total	C	N	O	P	0	0
			230	103	35	81	11		

- Molecule 59 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
59	0	1	Total	Mg	0
			1	1	
59	A	258	Total	Mg	0
			258	258	
59	B	4	Total	Mg	0
			4	4	
59	C	2	Total	Mg	0
			2	2	
59	D	1	Total	Mg	0
			1	1	
59	N	1	Total	Mg	0
			1	1	
59	O	1	Total	Mg	0
			1	1	
59	P	1	Total	Mg	0
			1	1	
59	a	92	Total	Mg	0
			92	92	

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Mol	Chain	Residues	Atoms		AltConf
59	m	1	Total	Mg	0
			1	1	
59	n	1	Total	Mg	0
			1	1	

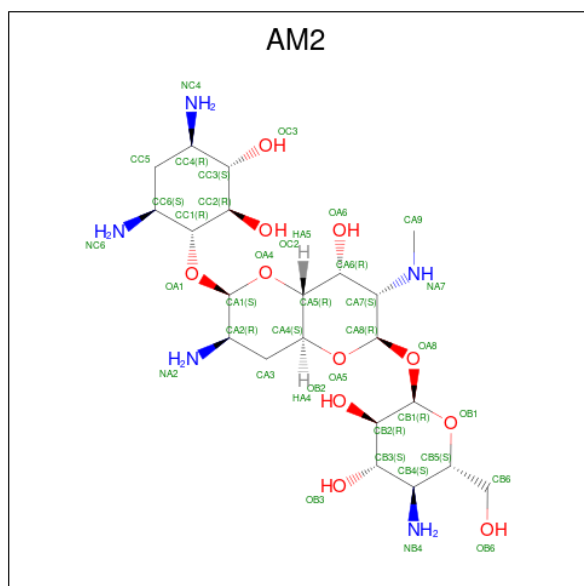
- Molecule 60 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
60	4	1	Total	Zn	0
			1	1	
60	6	1	Total	Zn	0
			1	1	

- Molecule 61 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		AltConf
61	A	1	Total	Na	0
			1	1	
61	B	1	Total	Na	0
			1	1	

- Molecule 62 is APRAMYCIN (CCD ID: AM2) (formula: C₂₁H₄₁N₅O₁₁).



Mol	Chain	Residues	Atoms				AltConf
62	a	1	Total	C	N	O	0
			37	21	5	11	

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Mol	Chain	Residues	Atoms				AltConf
62	a	1	Total	C	N	O	0
			37	21	5	11	
62	a	1	Total	C	N	O	0
			37	21	5	11	
62	a	1	Total	C	N	O	0
			37	21	5	11	

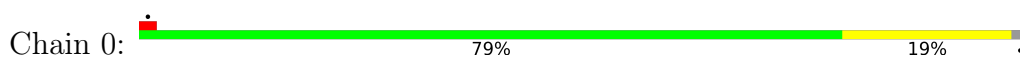
- Molecule 63 is water.

Mol	Chain	Residues	Atoms		AltConf
63	A	5	Total	O	0
			5	5	
63	a	15	Total	O	0
			15	15	
63	z	2	Total	O	0
			2	2	

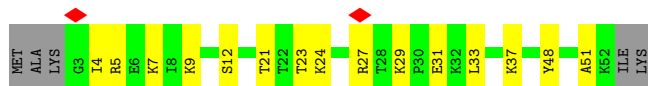
3 Residue-property plots [i](#)

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

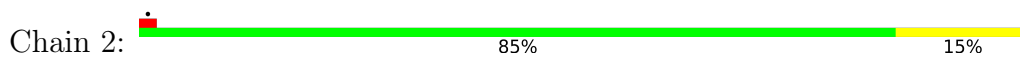
- Molecule 1: 50S ribosomal protein L32



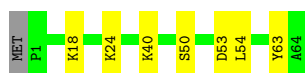
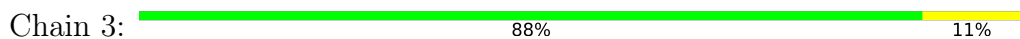
- Molecule 2: 50S ribosomal protein L33



- Molecule 3: 50S ribosomal protein L34



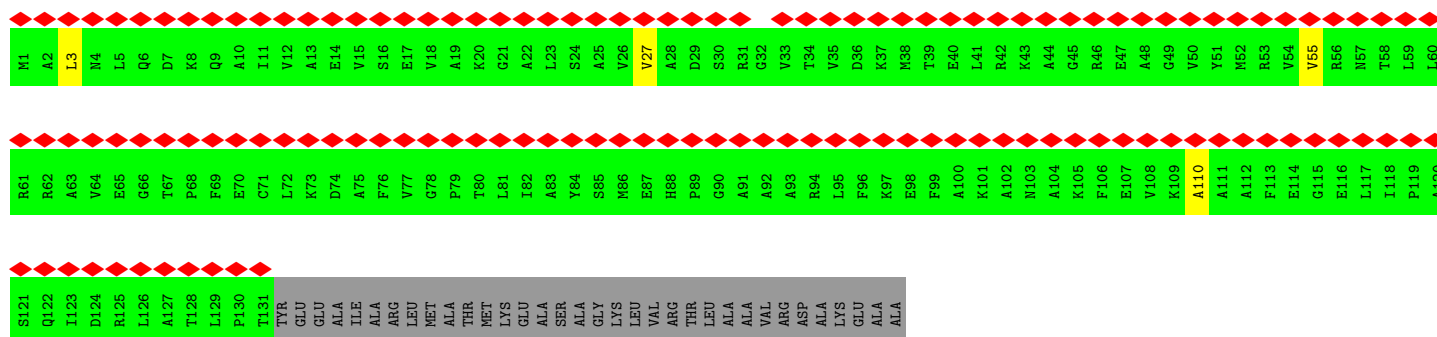
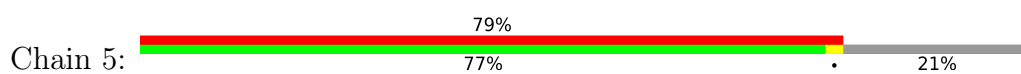
- Molecule 4: 50S ribosomal protein L35



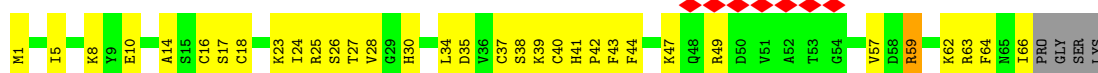
- Molecule 5: 50S ribosomal protein L36



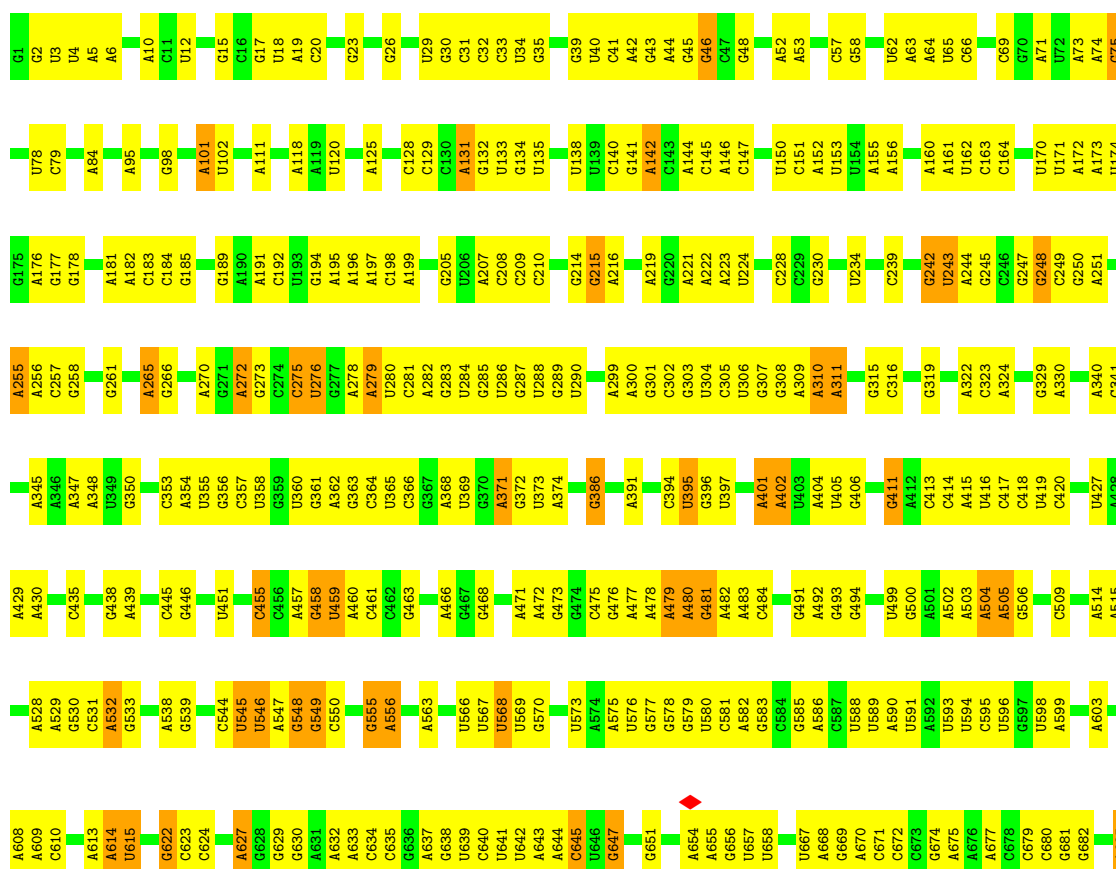
- Molecule 6: 50S ribosomal protein L10



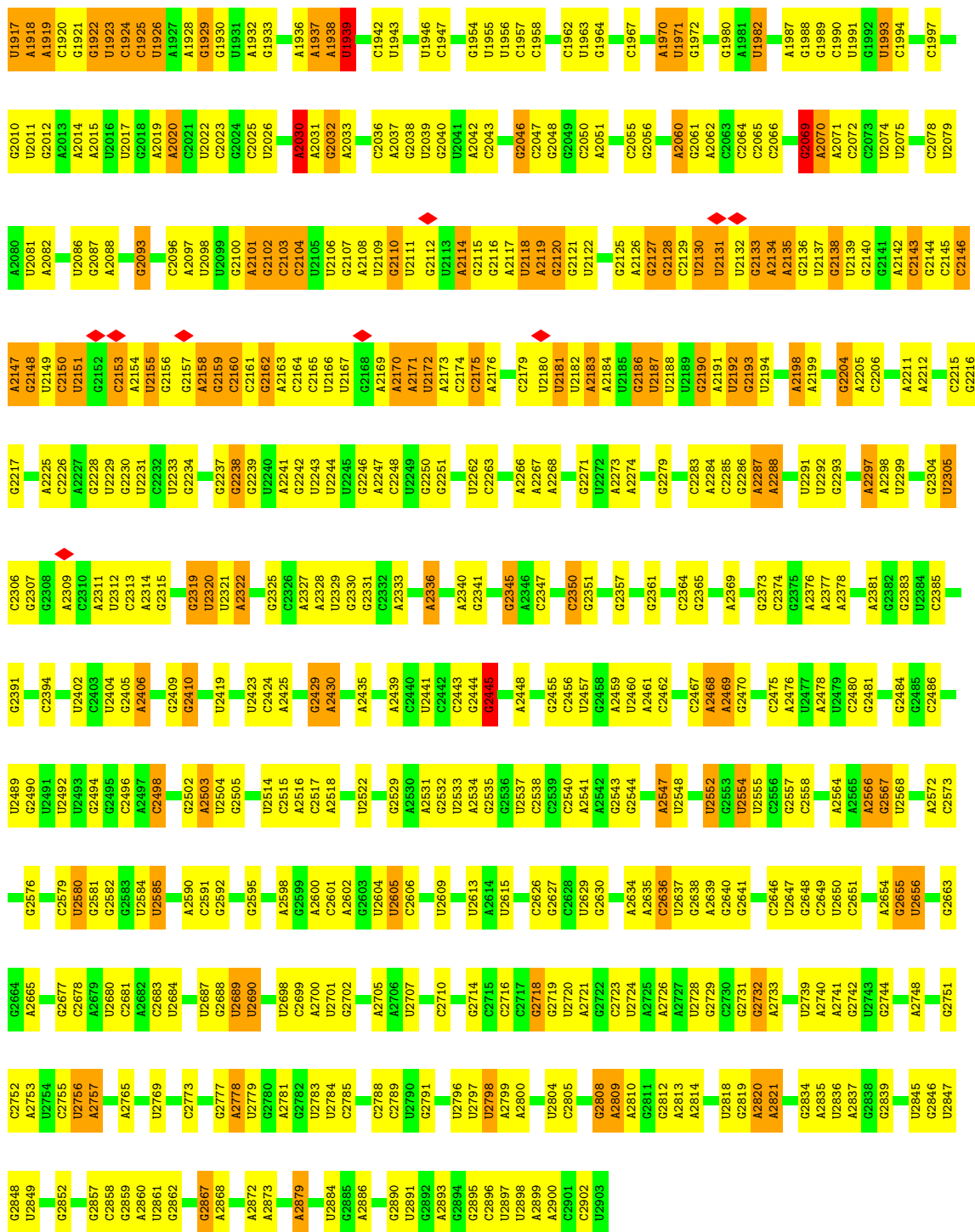
• Molecule 7: 50S ribosomal protein L31



• Molecule 8: 23S ribosomal RNA



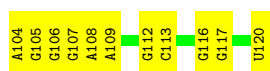
U1818	A1717	U1618	C1533	G1363	A1272	A1175	A1088	G1022	A927	U847	C765	U686
A1819	G1720	A1618	U1534	G1364	A1275	U1176	A1089	U1023	A928	C848	U766	C657
U1820	G1721	A1626	A1536	A1365	A1276	C1177	A1090	G1026	U929	A849	U767	U688
U1826	A1722	A1626	G1537	G1368	C1278	G1179	C1092	A1027	U931	U850	G774	A689
G1827	C1726	G1631	G1538	G1369	G1279	U1180	G1093	A1028	U932	C851	G775	G690
G1828	C1727	A1632	U1539	C1370	G1280	U1181	U1094	A1029	A933	U852	G776	A693
A1829	G1728	G1633	G1540	G1371	G1281	G1182	A1095	C1030	U934	C853	G776	U694
C1830	A1729	A1634	U1541	U1372	U1282	U1183	U1096	G1031	C935	C856	G782	A697
G1831	C1730	U1635	G1542	G1376	G1283	U1184	U1097	U1032	A936	G857	G783	C698
C1832	U1731	A1637	U1543	A1377	A1284	U1187	U1098	U1033	C937	G858	G784	A699
G1835	C1732	A1641	A1544	G1378	A1285	G1187	G1099	G1036	A941	G859	G785	G700
C1838	G1739	G1642	U1545	U1378	C1289	G1197	C1100	G1037	G942	A863	C786	G700
G1842	A1744	C1646	G1546	U1379	C1290	U1198	U1101	G1038	C946	G864	C787	U703
C1843	U1745	A1647	A1548	A1383	C1291	U1199	C1102	A1039	A947	U871	A788	G704
U1746	U1746	U1648	A1549	A1384	G1292	C1200	A1103	G1041	C948	U872	A789	U709
U1747	U1747	G1649	U1554	A1385	C1293	U1203	G1105	G1044	G949	C876	A793	U710
A1848	C1748	A1650	U1563	G1387	C1297	U1204	G1106	G1045	G954	A877	C796	G711
A1853	G1753	G1651	C1564	A1388	G1300	A1205	G1107	A1046	U955	A878	G797	U714
U1854	C1760	G1653	G1565	A1389	A1301	G1206	U1108	A1048	C961	G879	A802	A715
A1855	U1764	A1654	G1566	A1393	C1306	G1212	A1111	G1053	A959	G880	G805	A716
U1856	C1764	A1655	A1569	A1394	A1307	U1219	G1112	A1054	U967	G881	C806	C717
G1857	U1773	U1657	A1570	A1395	A1307	G1224	G1115	G1055	U967	G882	C806	U720
A1858	U1773	G1658	A1571	A1396	A1307	G1225	G1120	A1056	C968	G883	G808	A721
U1866	U1779	A1672	A1572	U1405	A1307	G1226	G1123	A1057	G969	G884	G809	C723
G1867	C1782	G1673	A1573	G1407	A1307	G1227	G1124	U1058	U970	G885	U810	U726
G1868	A1782	A1674	U1578	U1411	G1315	U1231	G1125	U1059	A973	G886	U811	A727
A1783	C1783	G1674	A1579	U1412	G1316	G1232	A1126	U1061	G974	C889	C812	G728
U1784	U1784	U1680	A1580	U1413	G1317	C1233	A1126	G1062	A975	U884	C814	G729
A1785	U1785	G1681	U1584	C1414	U1318	G1234	U1130	G1063	G976	A886	C817	A730
U1786	C1786	G1682	C1585	U1415	G1319	G1235	G1131	U1064	A983	A887	G818	A734
A1884	C1790	G1683	A1586	G1416	U1320	G1236	U1132	U1065	A984	C888	A819	A739
A1885	U1791	G1684	G1587	C1417	U1321	G1236	U1133	U1066	A989	U894	C823	C740
A1889	C1792	U1688	A1591	U1418	A1327	A1247	A1134	A1067	A990	C897	G822	U741
A1890	U1793	U1688	C1592	U1419	A1328	G1248	A1135	G1068	C993	C898	C823	A742
A1901	C1795	U1693	A1593	A1420	U1329	U1249	U1141	A1069	C994	A899	U827	A743
A1902	U1796	C1694	C1595	G1421	G1334	C1251	A1142	A1070	C995	A900	U828	U744
G1903	G1797	G1697	A1596	A1427	G1339	G1252	U1149	G1071	A996	C903	A829	G745
G1904	U1798	A1698	U1597	G1428	U1340	A1253	C1150	G1072	A1000	G907	U832	U746
C1905	G1799	G1699	A1598	G1430	G1341	U1254	C1154	A1073	A1001	C908	G748	C747
G1906	C1800	A1700	U1599	A1431	U1362	G1255	G1153	G1075	G1002	A909	A833	A749
A1801	A1801	G1703	C1600	G1432	A1353	G1256	C1154	A1077	A910	A910	G834	A749
G1907	A1802	C1704	A1601	A1433	A1354	A1262	G1155	U1078	C1005	A911	C837	A753
C1908	A1803	G1704	U1602	G1434	A1354	U1263	A1156	C1079	A1009	C912	C838	U754
G1909	G1807	U1709	A1603	G1435	G1355	A1264	U1168	A1080	G914	U913	U839	U755
C1910	A1808	G1710	C1604	G1436	C1357	A1265	A1169	U1081	C915	G914	C840	G760
U1911	A1809	C1606	U1523	C1437	A1358	G1266	C1170	U1082	G1012	G916	G843	A761
A1912	A1810	C1607	G1524	U1438	A1359	A1269	G1171	U1083	C1013	C917	A844	U762
A1913	C1816	A1608	A1528	A1439	A1360	C1270	U1172	A1084	A1014	A918	G763	G763
3TD1915	A1916	A1609	A1532	U1440	G1361	G1271	U1173	A1085	A1021	A918	U846	A764
A1916	A1916	A1610	A1532	U1442	C1362	G1271	U1174	A1086				



• Molecule 9: 5S ribosomal RNA

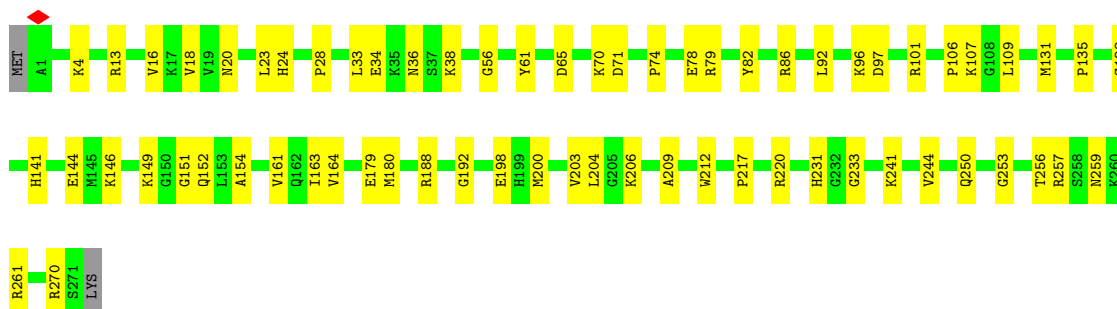
Chain B: 57% 32% 12%





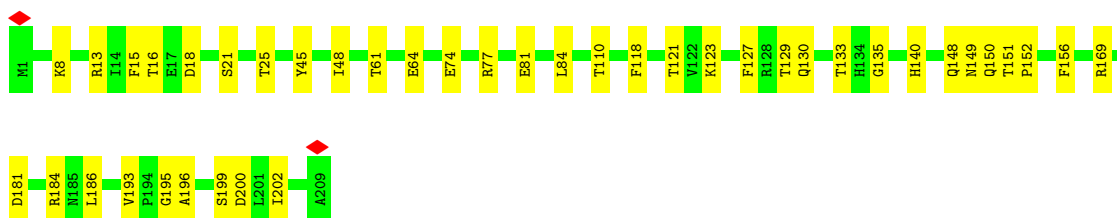
- Molecule 10: 50S ribosomal protein L2

Chain C: 75% 24%



- Molecule 11: 50S ribosomal protein L3

Chain D: 80% 20%



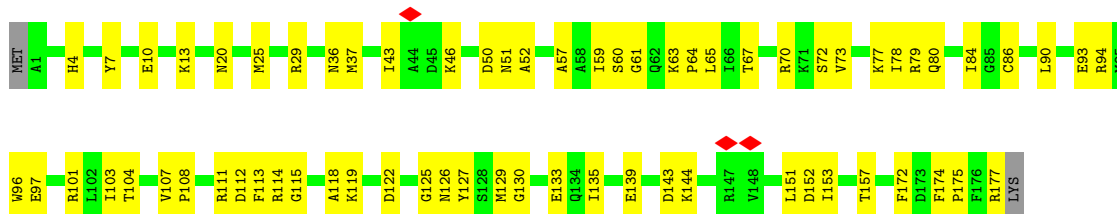
- Molecule 12: 50S ribosomal protein L4

Chain E: 88% 12%



- Molecule 13: 50S ribosomal protein L5

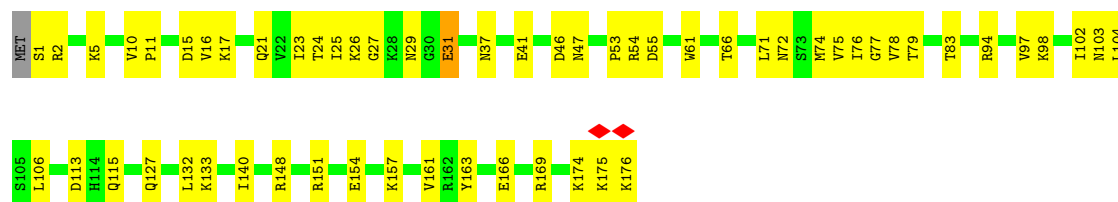
Chain F: 61% 37%



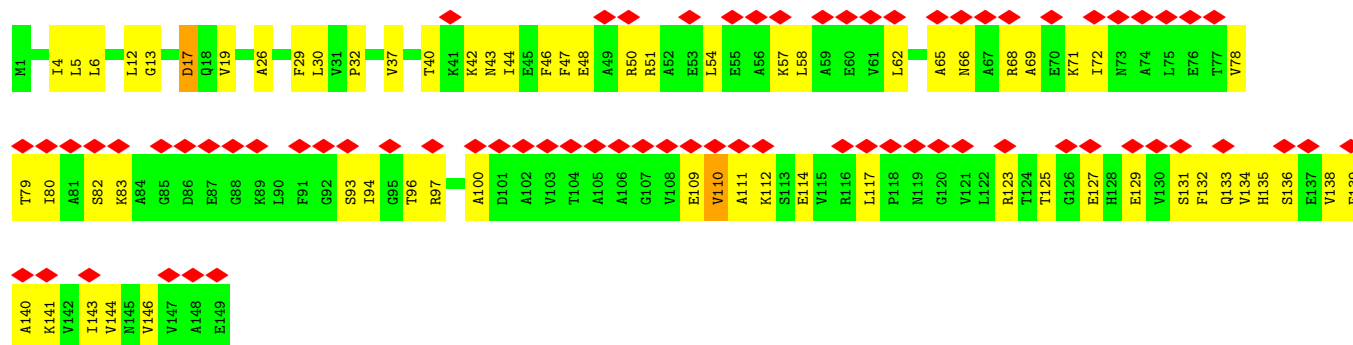
- Molecule 14: 50S ribosomal protein L6

Chain G: 67% 32%

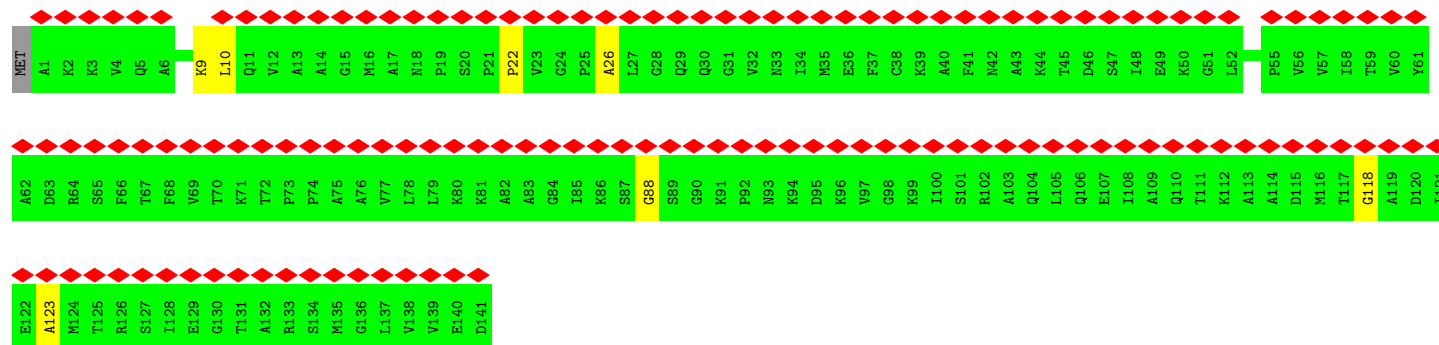




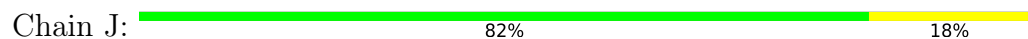
• Molecule 15: 50S ribosomal protein L9



• Molecule 16: 50S ribosomal protein L11



• Molecule 17: 50S ribosomal protein L13

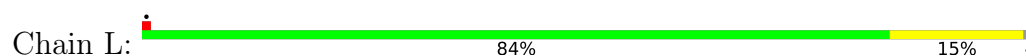


• Molecule 18: 50S ribosomal protein L14





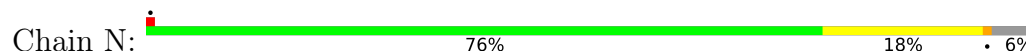
- Molecule 19: 50S ribosomal protein L15



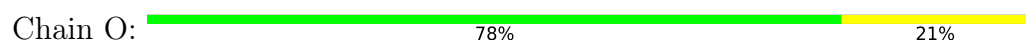
- Molecule 20: 50S ribosomal protein L16



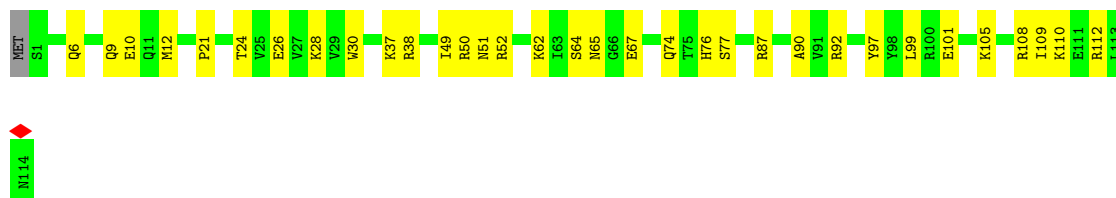
- Molecule 21: 50S ribosomal protein L17



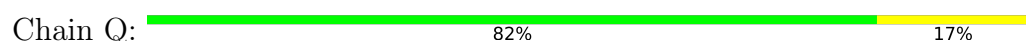
- Molecule 22: 50S ribosomal protein L18



- Molecule 23: 50S ribosomal protein L19

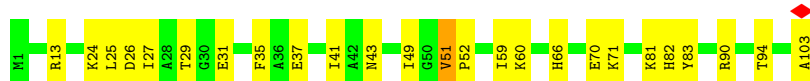
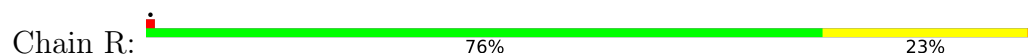


- Molecule 24: 50S ribosomal protein L20

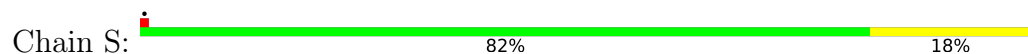




- Molecule 25: 50S ribosomal protein L21



- Molecule 26: 50S ribosomal protein L22



- Molecule 27: 50S ribosomal protein L23



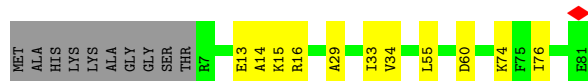
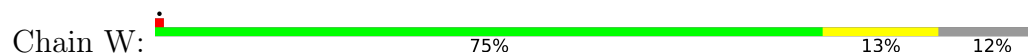
- Molecule 28: 50S ribosomal protein L24



- Molecule 29: 50S ribosomal protein L25



- Molecule 30: 50S ribosomal protein L27



- Molecule 31: 50S ribosomal protein L28

Chain X:  77% 22% .



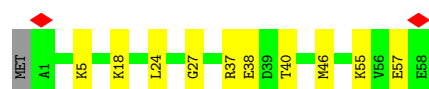
- Molecule 32: 50S ribosomal protein L29

Chain Y:  75% 25%

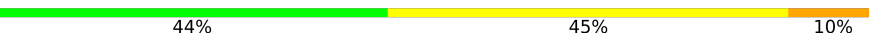


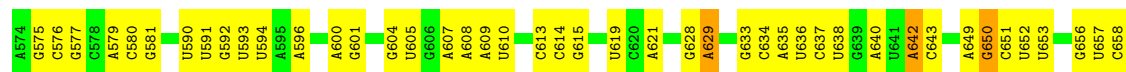
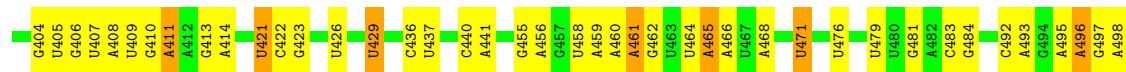
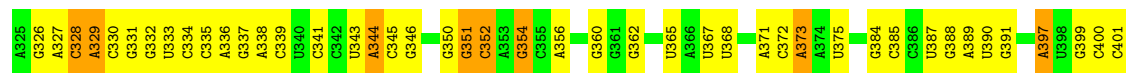
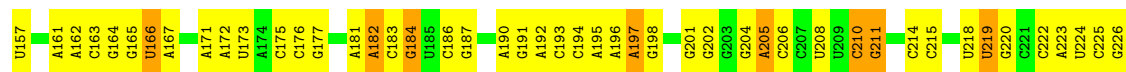
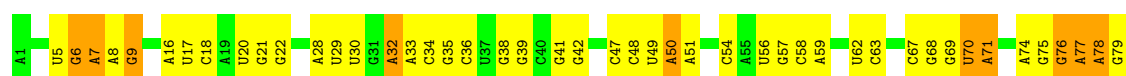
- Molecule 33: 50S ribosomal protein L30

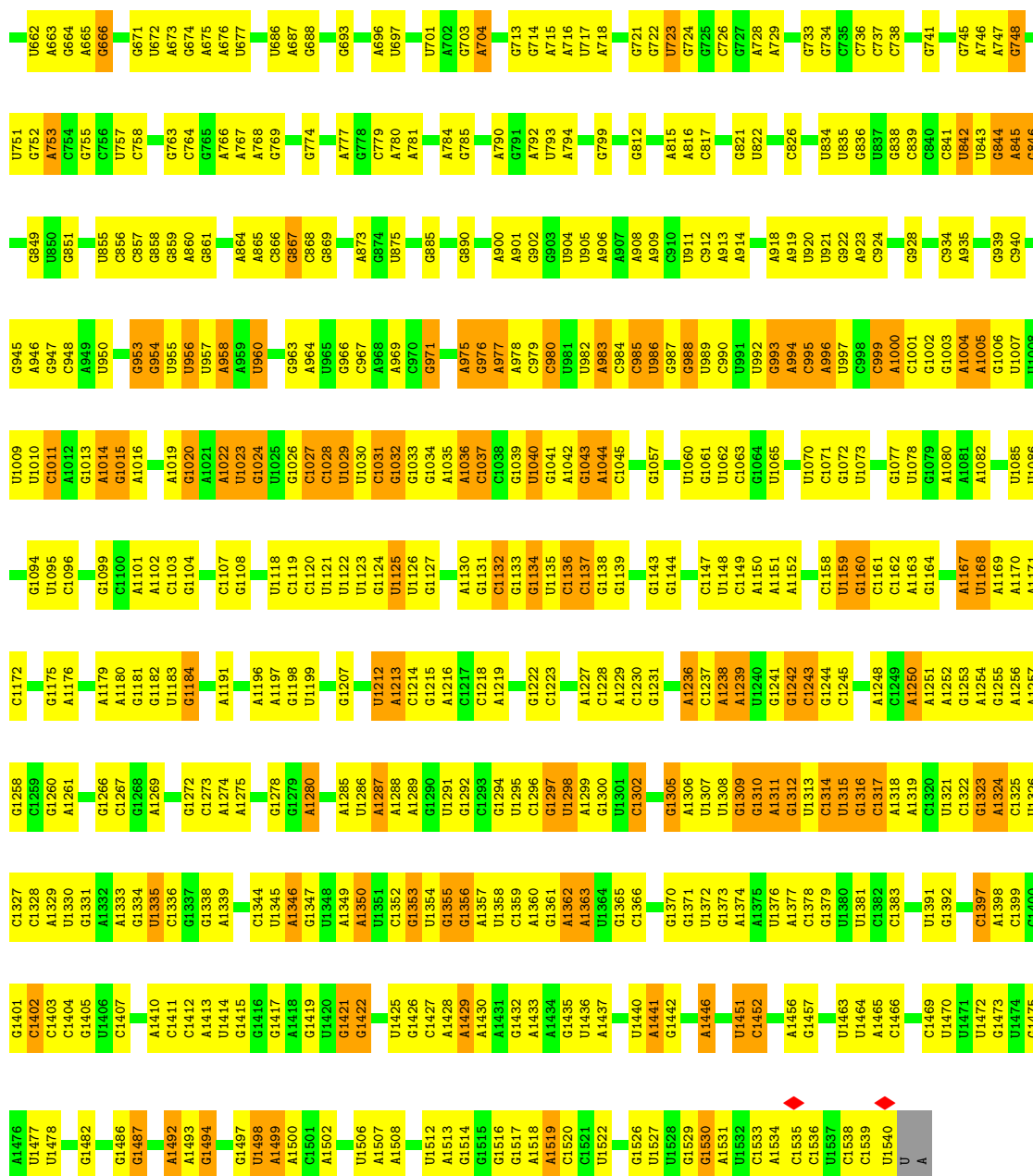
Chain Z:  81% 17% .



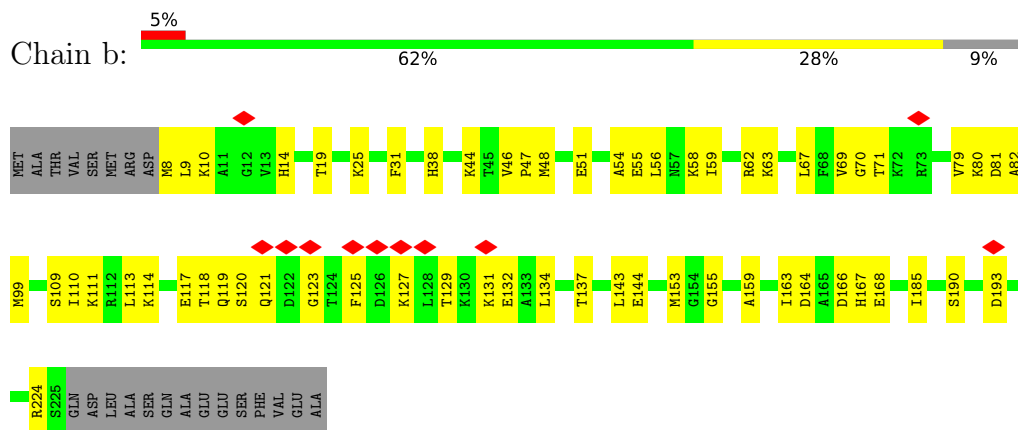
- Molecule 34: 16S ribosomal RNA

Chain a:  44% 45% 10%



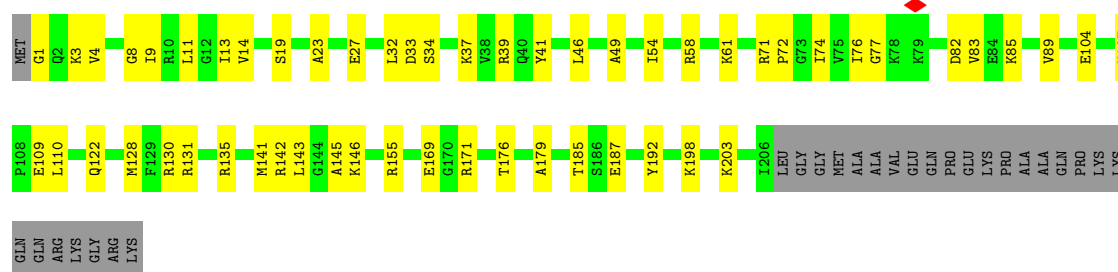


• Molecule 35: 30S ribosomal protein S2



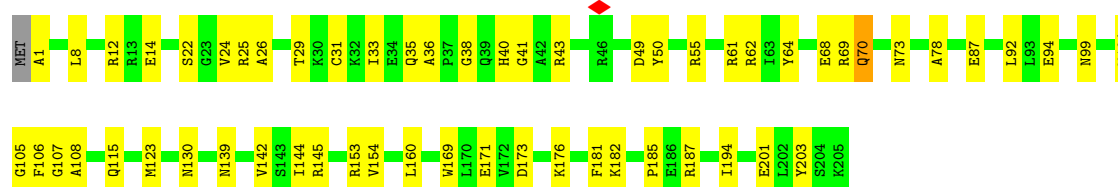
- Molecule 36: 30S ribosomal protein S3

Chain c:  65% 24% 12%



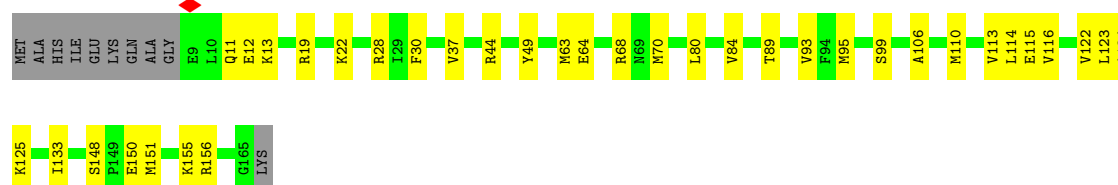
- Molecule 37: 30S ribosomal protein S4

Chain d:  71% 28%



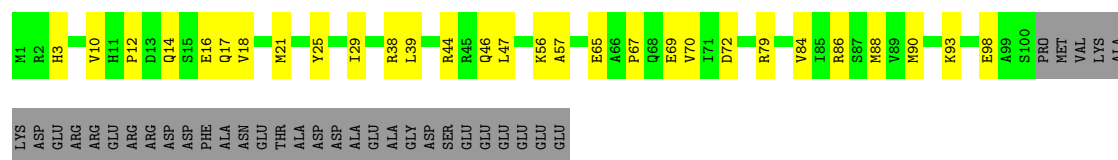
- Molecule 38: 30S ribosomal protein S5

Chain e:  72% 22% 6%



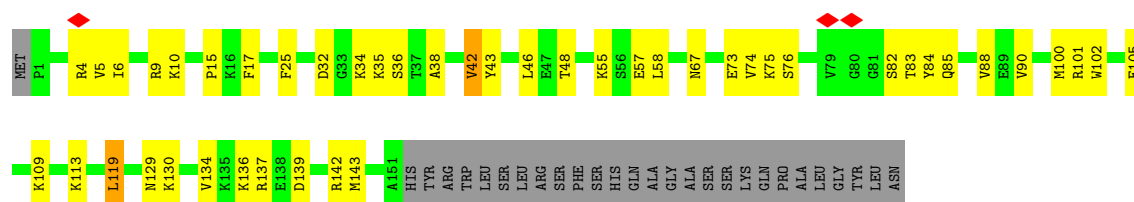
- Molecule 39: 30S ribosomal protein S6

Chain f:  53% 21% 26%



- Molecule 40: 30S ribosomal protein S7

Chain g:  59% 25% 16%



- Molecule 41: 30S ribosomal protein S8

Chain h: 79% 20% .



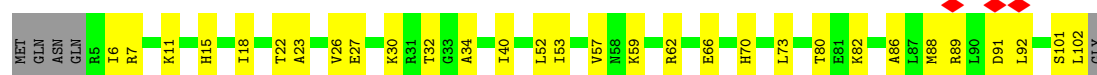
- Molecule 42: 30S ribosomal protein S9

Chain i: 58% 35% 5% .



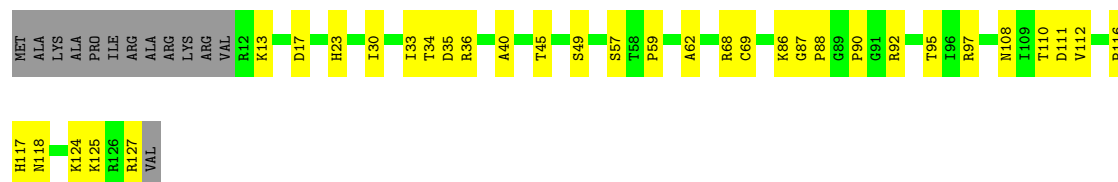
- Molecule 43: 30S ribosomal protein S10

Chain j: 66% 29% 5% .



- Molecule 44: 30S ribosomal protein S11

Chain k: 64% 26% 10% .



- Molecule 45: 30S ribosomal protein S12

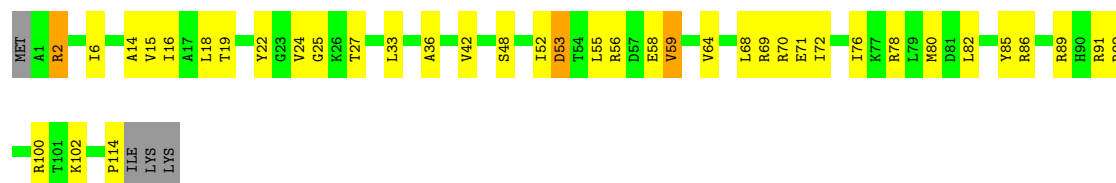
Chain l: 73% 25% .





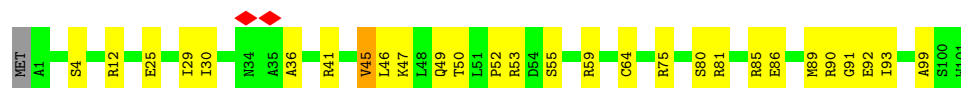
- Molecule 46: 30S ribosomal protein S13

Chain m: 64% 31% . .



- Molecule 47: 30S ribosomal protein S14

Chain n: 72% 26% ..



- Molecule 48: 30S ribosomal protein S15

Chain o: 78% 20% ..



- Molecule 49: 30S ribosomal protein S16

Chain p: 76% 22% .



- Molecule 50: 30S ribosomal protein S17

Chain q: 75% 19% . 5%



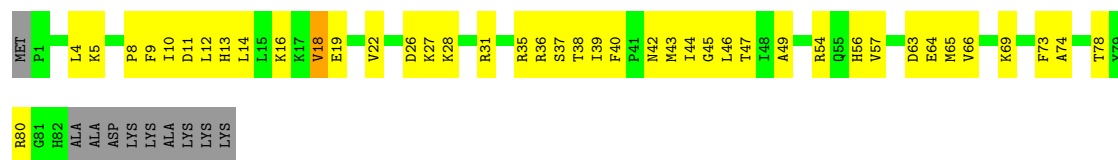
- Molecule 51: 30S ribosomal protein S18

Chain r: 68% 19% 13%



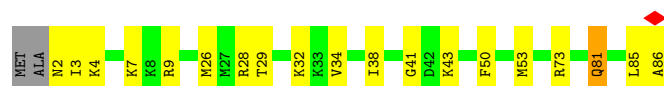
- Molecule 52: 30S ribosomal protein S19

Chain s: 



- Molecule 53: 30S ribosomal protein S20

Chain t: 

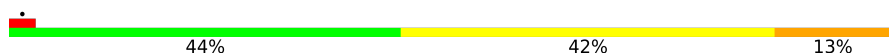


- Molecule 54: 30S ribosomal protein S21

Chain u: 



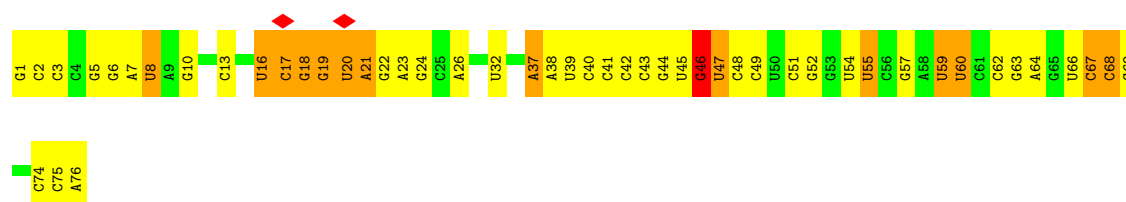
- Molecule 55: P-site tRNA(fMet)

Chain v: 

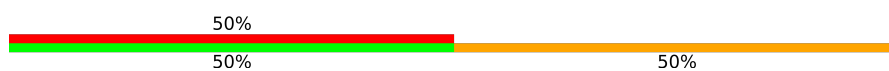


- Molecule 56: P-site fMet-Phe-tRNA(Phe)

Chain w: 

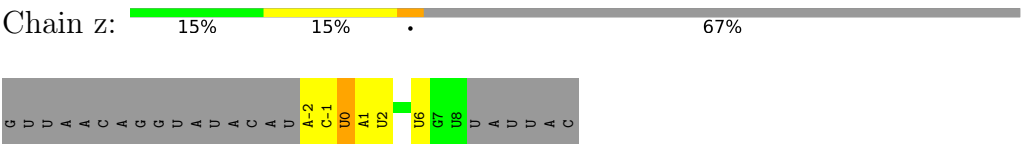


- Molecule 57: Dipeptide (FME-PHE)

Chain y: 



● Molecule 58: mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	537761	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1200	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	21.985	Depositor
Minimum map value	-5.122	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2	Depositor
Map size (Å)	334.08, 334.08, 334.08	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.6525, 0.6525, 0.6525	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 2MG, MG, H2U, AM2, MIA, 4OC, 1MG, OMC, 3TD, UR3, OMU, 5MC, ZN, MA6, OMG, G7M, 4SU, FME, PSU, 6MZ, 2MA, NA, 5MU

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	0	0.23	0/450	0.38	0/599
2	1	0.19	0/416	0.31	0/554
3	2	0.23	0/380	0.29	0/498
4	3	0.22	0/513	0.29	0/676
5	4	0.22	0/303	0.42	0/397
6	5	0.08	0/646	0.27	0/898
7	6	0.21	0/531	0.59	0/709
8	A	0.28	0/69266	0.30	0/108055
9	B	0.23	0/2873	0.28	0/4478
10	C	0.24	0/2121	0.35	0/2852
11	D	0.23	0/1586	0.34	0/2134
12	E	0.21	0/1571	0.29	0/2113
13	F	0.20	0/1434	0.41	0/1926
14	G	0.16	0/1343	0.32	0/1816
15	H	0.21	0/1122	0.57	0/1515
16	I	0.08	0/692	0.25	0/960
17	J	0.22	0/1152	0.30	0/1551
18	K	0.23	0/947	0.36	0/1268
19	L	0.23	0/1054	0.37	0/1403
20	M	0.23	0/1093	0.31	0/1460
21	N	0.22	0/973	0.33	0/1301
22	O	0.20	0/902	0.38	0/1209
23	P	0.23	0/929	0.30	0/1242
24	Q	0.22	0/960	0.26	0/1278
25	R	0.25	0/829	0.40	0/1107
26	S	0.22	0/864	0.30	0/1156
27	T	0.21	0/744	0.35	0/994
28	U	0.20	0/787	0.36	0/1051
29	V	0.21	0/766	0.38	0/1025
30	W	0.22	0/582	0.30	0/769
31	X	0.25	0/635	0.34	0/848

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Y	0.21	0/510	0.40	0/677
33	Z	0.21	0/453	0.28	0/605
34	a	0.25	0/36725	0.32	0/57285
35	b	0.17	0/1735	0.40	0/2338
36	c	0.21	0/1651	0.34	0/2225
37	d	0.18	0/1665	0.34	0/2227
38	e	0.22	0/1154	0.34	0/1554
39	f	0.20	0/835	0.42	0/1128
40	g	0.18	0/1195	0.40	0/1602
41	h	0.18	0/989	0.27	0/1326
42	i	0.21	0/1034	0.42	0/1375
43	j	0.23	0/796	0.54	0/1077
44	k	0.21	0/885	0.40	0/1195
45	l	0.24	0/969	0.41	0/1300
46	m	0.20	0/892	0.41	0/1193
47	n	0.20	0/811	0.31	0/1081
48	o	0.18	0/722	0.30	0/964
49	p	0.20	0/659	0.35	0/884
50	q	0.21	0/657	0.38	0/881
51	r	0.20	0/544	0.35	0/731
52	s	0.23	0/675	0.43	0/908
53	t	0.17	0/671	0.28	0/888
54	u	0.20	0/512	0.37	0/683
55	v	0.23	0/1745	0.29	0/2716
56	w	0.24	1/1650 (0.1%)	0.28	0/2569
57	y	0.20	0/11	0.17	0/13
58	z	0.25	0/255	0.73	2/394 (0.5%)
All	All	0.25	1/158864 (0.0%)	0.32	2/237661 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	w	46	G7M	O3'-P	5.18	1.61	1.56

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	z	-1	C	OP2-P-O3'	-8.79	81.61	108.00
58	z	-1	C	OP1-P-O3'	-8.78	81.67	108.00

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	0	444	0	461	8	0
2	1	409	0	440	15	0
3	2	377	0	418	6	0
4	3	504	0	574	7	0
5	4	302	0	340	8	0
6	5	647	0	336	3	0
7	6	522	0	521	37	0
8	A	62338	0	31372	1050	0
9	B	2570	0	1301	33	0
10	C	2082	0	2157	52	0
11	D	1565	0	1616	35	0
12	E	1552	0	1619	21	0
13	F	1410	0	1447	59	0
14	G	1323	0	1374	39	0
15	H	1111	0	1148	48	0
16	I	693	0	347	8	0
17	J	1129	0	1162	26	0
18	K	938	0	1012	29	0
19	L	1045	0	1117	18	0
20	M	1074	0	1157	31	0
21	N	960	0	1000	17	0
22	O	892	0	923	22	0
23	P	917	0	965	27	0
24	Q	947	0	1022	18	0
25	R	816	0	839	18	0
26	S	857	0	922	13	0
27	T	738	0	807	17	0
28	U	779	0	834	21	0
29	V	753	0	780	23	0
30	W	575	0	592	10	0
31	X	625	0	655	14	0
32	Y	509	0	543	19	0
33	Z	449	0	491	7	0
34	a	33050	0	16654	628	0
35	b	1704	0	1732	51	0
36	c	1624	0	1699	37	0
37	d	1643	0	1710	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	e	1141	0	1170	27	0
39	f	817	0	808	21	0
40	g	1181	0	1240	38	0
41	h	979	0	1034	18	0
42	i	1022	0	1070	44	0
43	j	786	0	828	27	0
44	k	869	0	878	28	0
45	l	955	0	1019	29	0
46	m	883	0	944	34	0
47	n	799	0	841	24	0
48	o	714	0	737	15	0
49	p	649	0	666	15	0
50	q	648	0	691	15	0
51	r	535	0	552	11	0
52	s	658	0	685	33	0
53	t	665	0	714	17	0
54	u	506	0	502	23	0
55	v	1642	0	839	26	0
56	w	1631	0	836	40	0
57	y	21	0	19	1	0
58	z	230	0	116	4	0
59	0	1	0	0	0	0
59	A	258	0	0	0	0
59	B	4	0	0	0	0
59	C	2	0	0	0	0
59	D	1	0	0	0	0
59	N	1	0	0	0	0
59	O	1	0	0	0	0
59	P	1	0	0	0	0
59	a	92	0	0	0	0
59	m	1	0	0	0	0
59	n	1	0	0	0	0
60	4	1	0	0	0	0
60	6	1	0	0	0	0
61	A	1	0	0	0	0
61	B	1	0	0	0	0
62	a	148	0	164	3	0
63	A	5	0	0	0	0
63	a	15	0	0	2	0
63	z	2	0	0	0	0
All	All	147741	0	98440	2674	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 (2674) 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)
43:j:88:MET:HE3	43:j:89:ARG:H	1.20	1.02
34:a:1310:G:H1	34:a:1327:C:H5	1.15	0.92
8:A:1478:G:H1	8:A:1513:U:H3	1.17	0.91
8:A:881:G:H1	8:A:895:U:H3	1.15	0.90
56:w:5:G:N2	56:w:68:C:O2	2.04	0.89
8:A:1936:A:H2	8:A:1943:U:H3	1.22	0.88
8:A:1053:C:O2	8:A:1106:G:N2	2.07	0.87
34:a:1027:C:H42	34:a:1034:G:H22	1.22	0.86
34:a:982:U:H3	34:a:1223:C:H5	1.25	0.85
8:A:1053:C:N3	8:A:1106:G:N1	2.24	0.85
34:a:664:G:H22	34:a:741:G:H1	1.21	0.85
8:A:1415:U:H3	8:A:1587:G:H1	1.26	0.84
32:Y:34:SER:OG	32:Y:36:GLN:NE2	2.11	0.83
8:A:1900:A:H1'	8:A:1970:A:H2'	1.59	0.82
56:w:6:G:N1	56:w:67:C:N3	2.26	0.82
8:A:585:G:N7	24:Q:5:ARG:NH2	2.28	0.81
55:v:20:H2U:H2'	55:v:21:A:H5'	1.62	0.81
56:w:6:G:N2	56:w:67:C:O2	2.14	0.80
34:a:673:A:H2'	34:a:674:G:C8	2.16	0.80
52:s:40:PHE:H	52:s:43:MET:HE2	1.45	0.79
2:1:4:ILE:HG22	2:1:27:ARG:HH12	1.46	0.79
40:g:73:GLU:HG2	40:g:90:VAL:HG22	1.64	0.79
8:A:848:C:H2'	8:A:849:A:H8	1.47	0.78
34:a:1151:A:HO2'	34:a:1152:A:H8	1.30	0.78
7:6:16:CYS:SG	7:6:37:CYS:HB2	2.21	0.78
14:G:103:ASN:ND2	14:G:113:ASP:OD1	2.16	0.78
8:A:1102:C:H3'	8:A:1103:A:H8	1.48	0.78
34:a:1218:C:H2'	34:a:1219:A:C8	2.18	0.78
7:6:28:VAL:HG12	13:F:139:GLU:HA	1.65	0.77
56:w:26:A:H61	56:w:44:G:H1	1.32	0.77
34:a:1086:U:H3	34:a:1099:G:H22	1.29	0.77
8:A:84:A:H62	8:A:101:A:H2	1.33	0.77
8:A:2639:A:O3'	17:J:96:ARG:NH2	2.17	0.76
3:2:39:ARG:NH2	8:A:468:G:N7	2.34	0.75
17:J:125:TYR:HH	17:J:132:HIS:HE2	1.35	0.75
8:A:475:C:O2	8:A:479:A:N6	2.18	0.75
8:A:1802:A:H2'	8:A:1803:A:C8	2.22	0.74
8:A:284:U:H3	8:A:356:G:H1	1.33	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2117:A:N6	8:A:2166:U:O2	2.17	0.74
36:c:39:ARG:NH1	36:c:54:ILE:O	2.20	0.74
44:k:17:ASP:HB3	44:k:36:ARG:HD3	1.70	0.74
8:A:627:A:OP1	19:L:78:ARG:NH1	2.18	0.74
42:i:29:ILE:HG22	42:i:64:ILE:HB	1.68	0.74
8:A:1907:G:O2'	8:A:1908:C:O5'	2.06	0.73
34:a:1030:U:H5''	34:a:1031:C:H5'	1.69	0.73
34:a:946:A:H2'	34:a:947:G:C8	2.22	0.73
43:j:59:LYS:HE2	43:j:62:ARG:HH21	1.53	0.73
13:F:43:ILE:HD11	13:F:78:ILE:HG13	1.69	0.73
15:H:43:ASN:O	15:H:47:PHE:N	2.22	0.73
8:A:568:U:H1'	8:A:2030:6MZ:H9C1	1.71	0.72
35:b:8:MET:HE3	35:b:9:LEU:H	1.54	0.72
8:A:1925:C:O2'	8:A:1926:U:O2	2.06	0.72
8:A:2142:A:N6	8:A:2150:C:O2	2.21	0.72
34:a:1522:U:OP1	44:k:127:ARG:NH1	2.22	0.72
14:G:29:ASN:ND2	14:G:77:GLY:O	2.23	0.72
14:G:174:LYS:HG2	14:G:175:LYS:HE3	1.72	0.72
34:a:458:U:H2'	34:a:459:A:H8	1.54	0.72
15:H:26:ALA:HA	15:H:30:LEU:HB2	1.72	0.72
56:w:22:G:O6	56:w:46:G7M:N2	2.17	0.72
11:D:77:ARG:NH1	11:D:200:ASP:OD1	2.23	0.72
26:S:82:MET:HB2	26:S:98:LYS:HB2	1.72	0.71
8:A:270:A:N1	8:A:369:U:O2'	2.21	0.71
34:a:461:A:N6	34:a:471:U:O4	2.18	0.71
34:a:1152:A:OP1	43:j:70:HIS:ND1	2.23	0.71
38:e:13:LYS:NZ	38:e:115:GLU:OE1	2.21	0.71
14:G:106:LEU:O	14:G:151:ARG:NH1	2.23	0.70
8:A:882:G:H1	8:A:894:U:H3	1.36	0.70
34:a:1137:C:O2'	34:a:1138:G:N2	2.23	0.70
40:g:4:ARG:NH1	40:g:5:VAL:O	2.24	0.70
15:H:139:PHE:HB3	15:H:141:LYS:HE3	1.73	0.70
35:b:25:LYS:NZ	35:b:193:ASP:OD2	2.23	0.70
9:B:37:C:O2	22:O:100:HIS:NE2	2.22	0.70
23:P:101:GLU:OE1	23:P:101:GLU:N	2.24	0.70
34:a:1027:C:N3	34:a:1034:G:N1	2.38	0.70
34:a:1319:A:O2'	34:a:1323:G:N2	2.24	0.70
7:6:59:ARG:HG2	7:6:59:ARG:HH11	1.56	0.70
56:w:43:C:H2'	56:w:44:G:C8	2.27	0.70
15:H:71:LYS:NZ	15:H:109:GLU:OE1	2.23	0.70
42:i:27:ILE:HG22	42:i:62:LEU:HB2	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:261:U:OP2	53:t:73:ARG:NH2	2.25	0.70
14:G:15:ASP:OD1	14:G:17:LYS:NZ	2.24	0.70
34:a:845:A:O2'	51:r:47:ARG:NH1	2.25	0.69
34:a:1253:G:N2	34:a:1356:G:OP1	2.24	0.69
32:Y:11:VAL:O	32:Y:15:ASN:ND2	2.25	0.69
8:A:1171:G:H1	8:A:1177:G:H22	1.38	0.69
25:R:24:LYS:HA	25:R:94:THR:HG23	1.72	0.69
42:i:90:ASP:HB3	42:i:93:LEU:HD12	1.74	0.69
13:F:36:ASN:HB3	13:F:152:ASP:HB2	1.75	0.69
8:A:319:G:H1	8:A:323:C:H5	1.40	0.69
34:a:77:A:H2'	34:a:78:A:C8	2.28	0.69
42:i:20:ILE:HD11	42:i:89:TYR:HB2	1.74	0.69
14:G:26:LYS:NZ	14:G:27:GLY:O	2.24	0.69
52:s:11:ASP:OD2	52:s:13:HIS:NE2	2.26	0.69
45:l:53:ARG:HH11	45:l:63:THR:HG23	1.57	0.69
8:A:1858:A:N6	8:A:1884:G:O2'	2.26	0.69
54:u:3:ILE:N	54:u:21:SER:HG	1.91	0.68
8:A:2127:G:N2	8:A:2128:G:O6	2.27	0.68
36:c:34:SER:OG	36:c:58:ARG:NH2	2.25	0.68
44:k:112:VAL:HG12	51:r:72:ARG:HD3	1.75	0.68
8:A:1918:A:O2'	8:A:1919:A:N7	2.26	0.68
8:A:2391:G:O2'	8:A:2429:G:N2	2.27	0.68
34:a:76:G:O6	34:a:93:U:O2	2.12	0.68
34:a:977:A:O2'	34:a:979:C:OP2	2.11	0.68
8:A:1028:A:H2'	8:A:1029:A:C8	2.29	0.68
8:A:1980:G:O2'	8:A:1982:U:OP2	2.11	0.68
8:A:2130:U:O4'	8:A:2159:G:N2	2.26	0.68
35:b:10:LYS:HG3	35:b:14:HIS:HE1	1.59	0.68
7:6:8:LYS:HE2	7:6:8:LYS:N	2.09	0.67
8:A:2469:A:N6	8:A:2481:G:O2'	2.27	0.67
8:A:2140:G:N2	8:A:2151:U:O2	2.25	0.67
27:T:56:GLU:HG2	27:T:88:LYS:HG2	1.76	0.67
35:b:80:LYS:HB2	35:b:92:ASN:HD22	1.59	0.67
34:a:677:U:H3	34:a:713:G:H22	1.42	0.67
48:o:13:GLU:O	48:o:83:ARG:NH2	2.26	0.67
9:B:90:C:H5''	20:M:18:ARG:HG2	1.75	0.67
15:H:57:LYS:HD2	15:H:58:LEU:N	2.10	0.67
8:A:1798:U:OP2	10:C:270:ARG:NH2	2.27	0.67
23:P:105:LYS:O	23:P:108:ARG:NH1	2.27	0.67
7:6:37:CYS:HB3	7:6:40:CYS:SG	2.34	0.67
17:J:49:ASP:OD1	17:J:121:LYS:NZ	2.24	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2847:U:H2'	8:A:2848:G:O4'	1.95	0.67
18:K:88:ASN:ND2	18:K:91:SER:O	2.28	0.67
45:l:109:ARG:HB3	45:l:118:VAL:HG21	1.77	0.67
2:1:31:GLU:OE2	2:1:31:GLU:N	2.20	0.66
8:A:2144:G:O2'	8:A:2147:A:N6	2.26	0.66
10:C:28:PRO:HG2	10:C:33:LEU:HD11	1.77	0.66
34:a:1014:A:H2'	34:a:1015:G:C8	2.30	0.66
8:A:994:C:OP1	24:Q:52:ARG:NH2	2.28	0.66
8:A:2777:G:H5''	8:A:2778:A:H5'	1.77	0.66
37:d:173:ASP:OD2	37:d:176:LYS:NZ	2.25	0.66
8:A:2328:A:H2'	8:A:2329:U:C6	2.29	0.66
34:a:1030:U:HO2'	34:a:1032:G:H1	1.43	0.66
8:A:714:U:O2'	8:A:716:A:N7	2.28	0.66
34:a:38:G:H22	34:a:397:A:H5'	1.60	0.66
34:a:1060:U:OP1	47:n:85:ARG:NH2	2.27	0.66
8:A:301:G:OP2	28:U:81:ARG:NH2	2.29	0.66
8:A:1072:C:OP1	8:A:1088:A:O2'	2.09	0.66
8:A:2636:C:O2'	11:D:45:TYR:OH	2.11	0.66
40:g:35:LYS:HG2	42:i:40:ARG:HH22	1.61	0.66
7:6:18:CYS:HB2	7:6:40:CYS:HB3	1.77	0.66
8:A:1826:G:O2'	8:A:1971:U:OP2	2.13	0.66
34:a:337:G:H2'	34:a:338:A:C8	2.30	0.66
8:A:837:C:N3	8:A:941:A:N6	2.43	0.66
12:E:21:ARG:HD3	12:E:106:LYS:HB3	1.78	0.66
29:V:51:GLN:OE1	29:V:57:TYR:OH	2.14	0.66
34:a:985:C:O2'	34:a:986:U:O2	2.08	0.66
36:c:19:SER:OG	36:c:39:ARG:NH2	2.28	0.66
48:o:1:SER:HB2	48:o:34:GLN:HE22	1.60	0.66
55:v:22:G:OP2	55:v:46:A:N6	2.28	0.66
5:4:1:MET:HE2	5:4:34:LYS:HE3	1.77	0.65
8:A:2131:U:O2	8:A:2158:A:N6	2.29	0.65
8:A:2172:U:O2'	8:A:2174:C:OP2	2.14	0.65
34:a:459:A:H2'	34:a:460:A:H8	1.60	0.65
8:A:1386:C:H2'	8:A:1387:A:C8	2.31	0.65
8:A:1799:G:O2'	10:C:179:GLU:OE2	2.11	0.65
9:B:1:U:H2'	9:B:2:G:H8	1.60	0.65
10:C:106:PRO:HD2	10:C:109:LEU:HD22	1.75	0.65
28:U:25:LYS:HE2	28:U:25:LYS:HA	1.77	0.65
18:K:102:PRO:HB3	18:K:121:GLU:HB3	1.78	0.65
34:a:81:A:N7	34:a:89:U:O2'	2.28	0.65
8:A:774:G:N2	8:A:787:C:O2'	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:1779:U:H5	8:A:1784:A:N7	1.94	0.65
34:a:50:A:O2'	34:a:360:G:N2	2.28	0.65
49:p:4:ILE:HG12	49:p:21:VAL:HG22	1.76	0.65
8:A:75:G:H22	8:A:111:A:H2	1.45	0.65
34:a:1071:C:H2'	34:a:1072:G:H8	1.62	0.65
17:J:31:GLU:HB3	17:J:142:ILE:HD12	1.79	0.65
52:s:49:ALA:HB1	52:s:56:HIS:HB3	1.79	0.65
8:A:2638:G:H1'	8:A:2778:A:H61	1.61	0.65
34:a:544:G:OP1	37:d:55:ARG:NH2	2.29	0.65
8:A:191:A:H2'	8:A:192:C:C6	2.32	0.65
8:A:1434:A:H2'	8:A:1435:G:C8	2.31	0.65
18:K:63:VAL:HG12	18:K:107:LEU:HD21	1.79	0.65
8:A:481:G:H1'	8:A:506:G:N2	2.12	0.65
8:A:639:U:H2'	8:A:640:C:C6	2.31	0.65
11:D:74:GLU:OE1	11:D:74:GLU:N	2.30	0.65
21:N:56:LYS:NZ	21:N:90:ARG:O	2.26	0.65
8:A:2183:A:H2'	8:A:2184:A:C8	2.32	0.64
17:J:96:ARG:HD2	17:J:99:ARG:HG2	1.78	0.64
34:a:713:G:H2'	34:a:714:G:C8	2.33	0.64
34:a:458:U:H2'	34:a:459:A:C8	2.31	0.64
37:d:123:MET:HG3	37:d:145:ARG:HG2	1.80	0.64
8:A:1084:A:H1'	8:A:1106:G:H1'	1.79	0.64
11:D:45:TYR:OH	11:D:81:GLU:OE2	2.16	0.64
12:E:170:ARG:NH1	12:E:176:ASP:OD1	2.29	0.64
34:a:310:G:H5''	49:p:31:ARG:HB2	1.77	0.64
34:a:1027:C:O2	34:a:1034:G:O6	2.14	0.64
34:a:8:A:N6	37:d:201:GLU:O	2.28	0.64
34:a:426:U:OP1	37:d:35:GLN:NE2	2.30	0.64
4:3:18:LYS:HG3	8:A:651:G:H5'	1.79	0.64
15:H:132:PHE:HB3	15:H:140:ALA:HB3	1.80	0.64
23:P:90:ALA:HB2	23:P:112:ARG:HA	1.78	0.64
39:f:69:GLU:CD	39:f:69:GLU:H	2.06	0.64
5:4:31:PRO:HD3	14:G:169:ARG:HH22	1.63	0.64
34:a:555:U:H2'	34:a:556:C:C6	2.33	0.64
36:c:110:LEU:O	36:c:203:LYS:NZ	2.31	0.64
43:j:86:ALA:HA	43:j:89:ARG:HH12	1.63	0.64
45:l:98:ARG:HB2	45:l:116:TYR:HA	1.80	0.64
8:A:555:G:HO2'	8:A:556:A:H8	1.46	0.64
34:a:953:G:OP1	34:a:964:A:N6	2.30	0.64
14:G:21:GLN:NE2	14:G:37:ASN:O	2.31	0.64
14:G:46:ASP:O	14:G:47:ASN:ND2	2.32	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:d:70:GLN:HA	37:d:73:ASN:HB2	1.80	0.64
34:a:1222:G:OP2	34:a:1322:C:N4	2.28	0.63
40:g:17:PHE:HB3	40:g:58:LEU:HD21	1.80	0.63
8:A:639:U:H2'	8:A:640:C:H6	1.63	0.63
34:a:202:G:H21	34:a:466:A:H61	1.46	0.63
36:c:141:MET:HG3	36:c:169:GLU:HG3	1.81	0.63
54:u:6:ARG:NH1	54:u:8:ASN:OD1	2.31	0.63
34:a:147:G:H2'	34:a:148:G:C8	2.34	0.63
40:g:15:PRO:HA	42:i:45:MET:HE2	1.80	0.63
8:A:887:A:H1'	8:A:888:C:H5''	1.81	0.63
8:A:1509:A:H2'	8:A:1510:G:C8	2.33	0.63
8:A:2117:A:N1	8:A:2170:A:N6	2.47	0.63
34:a:946:A:H2'	34:a:947:G:H8	1.62	0.63
41:h:42:GLU:HG3	41:h:100:ILE:HG21	1.79	0.63
14:G:94:ARG:HG3	14:G:127:GLN:HB2	1.78	0.63
34:a:714:G:H2'	34:a:715:A:C8	2.34	0.63
34:a:769:G:H4'	34:a:1513:A:H4'	1.81	0.63
8:A:993:G:OP2	24:Q:50:ARG:NH2	2.32	0.63
34:a:459:A:H2'	34:a:460:A:C8	2.34	0.63
34:a:1391:U:H2'	34:a:1392:G:C8	2.34	0.63
42:i:64:ILE:HG21	42:i:78:ILE:HG12	1.80	0.63
54:u:7:GLU:HA	54:u:17:ARG:HH22	1.64	0.63
8:A:476:G:N1	8:A:479:A:OP2	2.30	0.62
8:A:2138:G:O6	8:A:2154:A:O2'	2.16	0.62
8:A:2584:U:H3'	8:A:2585:U:H5''	1.79	0.62
48:o:5:GLU:H	48:o:5:GLU:CD	2.08	0.62
13:F:50:ASP:OD1	13:F:51:ASN:N	2.33	0.62
34:a:344:A:H5''	34:a:345:C:H5	1.63	0.62
34:a:405:U:O4	37:d:1:ALA:N	2.32	0.62
8:A:2327:A:H2'	8:A:2328:A:C8	2.34	0.62
56:w:16:U:O2'	56:w:60:U:O2	2.15	0.62
8:A:481:G:H1'	8:A:506:G:H21	1.62	0.62
34:a:492:C:H2'	34:a:493:A:C8	2.34	0.62
8:A:5:A:H2'	8:A:6:A:C8	2.35	0.62
8:A:310:A:O2'	8:A:311:A:O5'	2.15	0.62
8:A:1061:U:H2'	8:A:1068:G:H1'	1.81	0.62
8:A:1109:C:H2'	8:A:1110:G:C8	2.35	0.62
9:B:7:G:OP1	22:O:4:LYS:NZ	2.31	0.62
29:V:51:GLN:OE1	29:V:79:ARG:NH2	2.33	0.62
34:a:202:G:H22	34:a:215:C:H5	1.47	0.62
8:A:2032:G:N2	11:D:151:THR:OG1	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2120:G:H2'	8:A:2121:G:C8	2.35	0.62
8:A:2291:U:H2'	8:A:2292:U:C6	2.35	0.62
35:b:46:VAL:HG23	35:b:47:PRO:HD3	1.80	0.62
8:A:2120:G:H2'	8:A:2121:G:H8	1.63	0.62
40:g:139:ASP:OD2	40:g:142:ARG:NH2	2.33	0.62
8:A:181:A:H2'	8:A:182:A:C8	2.35	0.62
10:C:74:PRO:HB2	10:C:96:LYS:HE2	1.81	0.62
25:R:41:ILE:HD13	25:R:103:ALA:HA	1.82	0.61
34:a:1036:A:O2'	34:a:1037:C:O5'	2.18	0.61
42:i:115:VAL:HG13	43:j:62:ARG:HH11	1.65	0.61
8:A:813:U:H2'	8:A:814:C:C6	2.34	0.61
8:A:1178:C:H4'	8:A:1179:G:C5	2.35	0.61
8:A:1405:U:H2'	8:A:1406:U:C6	2.35	0.61
53:t:2:ASN:HB2	53:t:7:LYS:HG2	1.82	0.61
42:i:18:VAL:HG22	42:i:64:ILE:HG12	1.82	0.61
8:A:1528:A:N6	8:A:1543:G:O2'	2.34	0.61
8:A:1796:U:H2'	8:A:1797:G:H8	1.65	0.61
34:a:1009:U:H3	34:a:1020:G:H1	1.47	0.61
8:A:698:C:O2'	8:A:734:A:N6	2.33	0.61
8:A:910:A:H2'	8:A:911:A:C8	2.36	0.61
34:a:1130:A:H2'	34:a:1131:G:H8	1.65	0.61
42:i:44:ARG:HH11	42:i:44:ARG:HG3	1.65	0.61
8:A:704:G:H2'	8:A:726:G:H22	1.64	0.61
8:A:1794:A:H2'	8:A:1795:C:C6	2.36	0.61
8:A:2320:U:O2'	8:A:2322:A:N7	2.31	0.61
17:J:17:VAL:HG23	17:J:137:PRO:HB2	1.82	0.61
37:d:8:LEU:HD13	37:d:31:CYS:HB3	1.83	0.61
32:Y:34:SER:HG	32:Y:36:GLN:HE21	1.47	0.61
34:a:1430:A:N6	62:a:1684:AM2:OB6	2.33	0.61
8:A:848:C:H2'	8:A:849:A:C8	2.33	0.61
34:a:401:C:O2'	34:a:621:A:N3	2.33	0.61
34:a:1028:C:O2'	34:a:1029:U:O2	2.14	0.61
34:a:1326:U:H2'	34:a:1327:C:O2	2.00	0.61
37:d:40:HIS:HB3	37:d:43:ARG:HD3	1.83	0.61
39:f:44:ARG:HG2	39:f:56:LYS:HD3	1.83	0.61
3:2:24:THR:HG23	3:2:27:GLY:H	1.66	0.61
8:A:2243:U:H2'	8:A:2244:U:C6	2.35	0.61
8:A:2312:U:H5'	13:F:84:ILE:HD11	1.83	0.61
55:v:1:C:H2'	55:v:2:G:H8	1.66	0.61
10:C:198:GLU:CD	10:C:198:GLU:H	2.08	0.61
34:a:481:G:O2'	34:a:483:C:N4	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
42:i:54:VAL:HG12	42:i:93:LEU:HD22	1.83	0.61
49:p:48:GLU:OE1	49:p:51:ARG:NH2	2.31	0.61
5:4:23:ILE:HD13	8:A:1032:A:H1'	1.83	0.60
8:A:1061:U:O2'	16:I:9:LYS:O	2.19	0.60
34:a:82:G:N2	34:a:88:U:OP2	2.34	0.60
34:a:986:U:H5	34:a:1219:A:N1	1.97	0.60
42:i:26:LYS:HE3	42:i:61:ASP:HB3	1.83	0.60
44:k:13:LYS:HE2	44:k:13:LYS:N	2.16	0.60
13:F:25:MET:O	13:F:29:ARG:NH1	2.32	0.60
15:H:42:LYS:O	15:H:46:PHE:HB3	2.01	0.60
54:u:6:ARG:C	54:u:6:ARG:HD3	2.25	0.60
14:G:16:VAL:HG12	14:G:25:ILE:HG12	1.82	0.60
8:A:310:A:O2'	8:A:311:A:H2'	2.00	0.60
8:A:1817:G:OP1	10:C:86:ARG:NH2	2.33	0.60
8:A:1469:A:H2'	8:A:1470:A:C8	2.36	0.60
34:a:542:G:H5'	37:d:38:GLY:HA2	1.84	0.60
11:D:149:ASN:OD1	11:D:150:GLN:N	2.33	0.60
4:3:24:LYS:HB3	19:L:62:PRO:HG2	1.82	0.60
15:H:114:GLU:HB3	15:H:133:GLN:O	2.01	0.60
7:6:25:ARG:O	13:F:101:ARG:NH1	2.35	0.60
34:a:460:A:H2'	34:a:461:A:C8	2.36	0.60
37:d:49:ASP:OD1	37:d:50:TYR:N	2.34	0.60
7:6:1:MET:HB3	9:B:43:C:H5''	1.84	0.60
7:6:25:ARG:NH1	13:F:97:GLU:OE2	2.35	0.60
11:D:148:GLN:HB2	11:D:152:PRO:HG2	1.83	0.60
34:a:499:A:H61	34:a:547:A:H5''	1.66	0.60
34:a:718:A:O2'	54:u:34:ARG:NH2	2.35	0.60
8:A:272:A:H2'	8:A:273:G:C8	2.37	0.59
8:A:1071:G:H2'	8:A:1089:A:H62	1.67	0.59
8:A:2186:G:OP1	8:A:2186:G:H4'	2.01	0.59
34:a:1149:C:H2'	34:a:1150:A:H8	1.66	0.59
5:4:11:CYS:SG	5:4:33:HIS:CE1	2.94	0.59
8:A:593:U:H2'	8:A:594:U:C6	2.36	0.59
8:A:2637:U:H2'	8:A:2638:G:O4'	2.02	0.59
34:a:1362:A:O2'	34:a:1363:A:OP1	2.12	0.59
8:A:272:A:H2'	8:A:273:G:H8	1.67	0.59
8:A:1432:G:H2'	8:A:1433:A:C8	2.37	0.59
8:A:2153:C:H2'	8:A:2154:A:H8	1.66	0.59
8:A:2720:U:OP1	23:P:52:ARG:NH2	2.34	0.59
13:F:7:TYR:HB2	13:F:172:PHE:HZ	1.67	0.59
20:M:66:ARG:NH1	20:M:104:GLU:OE2	2.33	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:1363:A:O2'	34:a:1365:G:N7	2.34	0.59
34:a:17:U:H2'	34:a:18:C:C6	2.36	0.59
8:A:483:A:O2'	28:U:56:GLY:N	2.35	0.59
8:A:2246:G:H2'	8:A:2247:A:H8	1.68	0.59
8:A:2848:G:H2'	8:A:2867:G:N2	2.17	0.59
20:M:20:LEU:HD13	29:V:81:PRO:HG2	1.84	0.59
34:a:335:C:H2'	34:a:336:A:H8	1.67	0.59
56:w:26:A:N6	56:w:44:G:H1	2.01	0.59
8:A:2636:C:HO2'	11:D:45:TYR:HH	1.42	0.59
34:a:945:G:C2	34:a:946:A:C8	2.91	0.59
34:a:963:G:H21	43:j:57:VAL:HG11	1.68	0.59
34:a:1412:C:H2'	34:a:1413:A:C8	2.38	0.59
8:A:1506:U:H2'	8:A:1507:C:C6	2.38	0.59
8:A:2131:U:H4'	8:A:2133:G:H4'	1.84	0.59
8:A:2469:A:H4'	20:M:55:ARG:HD2	1.84	0.59
8:A:2514:U:H2'	8:A:2515:C:C6	2.38	0.59
8:A:171:U:H2'	8:A:172:A:H8	1.68	0.59
11:D:181:ASP:HB3	11:D:186:LEU:HB2	1.82	0.59
31:X:43:LYS:HE2	31:X:43:LYS:HA	1.84	0.59
34:a:264:C:O2'	50:q:65:PRO:O	2.17	0.59
34:a:429:U:H3'	37:d:8:LEU:HD12	1.83	0.59
34:a:1004:A:O2'	34:a:1005:A:OP1	2.15	0.59
46:m:82:LEU:HD11	52:s:65:MET:HB3	1.85	0.59
8:A:500:G:N1	8:A:503:A:OP2	2.31	0.59
8:A:833:A:H2'	8:A:834:G:C8	2.38	0.59
8:A:1028:A:N3	8:A:2486:C:O2'	2.36	0.59
8:A:1779:U:OP2	8:A:1784:A:N6	2.32	0.59
8:A:2638:G:H1'	8:A:2778:A:N6	2.17	0.59
8:A:2683:C:O2	18:K:70:ARG:NH2	2.36	0.59
22:O:34:HIS:ND1	22:O:53:THR:OG1	2.36	0.59
34:a:1493:A:OP2	63:a:1701:HOH:O	2.17	0.59
44:k:97:ARG:NH1	44:k:97:ARG:HB2	2.17	0.59
47:n:46:LEU:HD13	52:s:12:LEU:HD23	1.83	0.59
8:A:1799:G:OP1	10:C:257:ARG:NH1	2.28	0.59
15:H:134:VAL:HB	15:H:138:VAL:HG11	1.85	0.59
8:A:1170:C:H3'	8:A:1171:G:H8	1.68	0.58
10:C:71:ASP:OD1	10:C:188:ARG:NH2	2.34	0.58
15:H:54:LEU:HA	15:H:57:LYS:HG3	1.84	0.58
34:a:78:A:H2'	34:a:79:G:C8	2.38	0.58
34:a:790:A:OP1	55:v:38:A:O2'	2.17	0.58
34:a:826:C:O2	41:h:15:ASN:ND2	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:q:7:LEU:HD23	50:q:24:ILE:HD13	1.84	0.58
8:A:1141:U:H4'	8:A:1142:A:O4'	2.03	0.58
8:A:1796:U:H2'	8:A:1797:G:C8	2.37	0.58
8:A:2070:A:H2'	8:A:2071:A:C8	2.38	0.58
20:M:56:ALA:HB2	20:M:119:LEU:HD12	1.84	0.58
8:A:581:C:H2'	8:A:582:A:C8	2.38	0.58
8:A:796:C:OP1	12:E:57:LYS:HE2	2.04	0.58
8:A:1053:C:N4	8:A:1106:G:O6	2.31	0.58
8:A:2107:G:H3'	8:A:2108:A:H8	1.66	0.58
8:A:2445:2MG:OP1	12:E:69:ARG:NH2	2.34	0.58
9:B:1:U:H2'	9:B:2:G:C8	2.37	0.58
8:A:1509:A:H2'	8:A:1510:G:H8	1.68	0.58
8:A:2329:U:H2'	8:A:2330:G:C8	2.39	0.58
34:a:266:G:H3'	50:q:68:LYS:HB2	1.86	0.58
8:A:5:A:H2'	8:A:6:A:H8	1.69	0.58
8:A:1168:G:H2'	8:A:1169:A:C8	2.38	0.58
8:A:2182:U:H2'	8:A:2183:A:C8	2.38	0.58
46:m:72:ILE:O	46:m:76:ILE:HG13	2.03	0.58
47:n:52:PRO:O	47:n:55:SER:OG	2.19	0.58
8:A:1062:G:N2	8:A:1064:C:O2'	2.36	0.58
23:P:90:ALA:HB3	23:P:110:LYS:HG3	1.86	0.58
8:A:742:A:H2'	8:A:743:A:C8	2.38	0.58
8:A:2591:C:H2'	8:A:2592:G:C8	2.38	0.58
8:A:2788:C:O2'	8:A:2809:A:N3	2.34	0.58
34:a:1287:A:H2'	34:a:1288:A:C8	2.39	0.58
34:a:1323:G:HO2'	34:a:1324:A:H8	1.47	0.58
7:6:16:CYS:SG	7:6:17:SER:N	2.77	0.58
8:A:300:A:OP2	28:U:81:ARG:NH1	2.35	0.58
8:A:2071:A:H2'	8:A:2072:C:C6	2.38	0.58
15:H:5:LEU:HD13	15:H:13:GLY:HA2	1.85	0.58
18:K:43:ILE:HD12	18:K:56:ASP:HB2	1.86	0.58
34:a:501:C:H2'	34:a:502:A:C8	2.38	0.58
3:2:29:GLN:NE2	8:A:210:C:OP1	2.31	0.58
7:6:43:PHE:HA	7:6:47:LYS:HB3	1.86	0.58
8:A:1746:A:H2'	8:A:1747:U:C6	2.38	0.58
8:A:1922:G:H8	8:A:1922:G:OP1	1.86	0.58
8:A:2086:U:H2'	8:A:2087:G:C8	2.39	0.58
10:C:154:ALA:HB2	10:C:161:VAL:HG23	1.84	0.58
34:a:890:G:O2'	34:a:906:A:N6	2.36	0.58
34:a:1310:G:OP2	46:m:86:ARG:NH2	2.36	0.58
56:w:18:G:O6	56:w:55:PSU:HI'	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2271:G:H5'	30:W:16:ARG:HD3	1.84	0.57
9:B:117:G:P	22:O:56:LYS:HZ3	2.27	0.57
34:a:674:G:H2'	34:a:675:A:H8	1.69	0.57
34:a:1212:U:H5''	34:a:1213:A:N7	2.19	0.57
34:a:1305:G:N2	34:a:1331:G:H1'	2.19	0.57
48:o:11:VAL:HG21	48:o:21:THR:HG22	1.86	0.57
56:w:16:U:H3'	56:w:17:C:H5'	1.86	0.57
8:A:141:G:O2'	8:A:142:A:O5'	2.22	0.57
8:A:1797:G:O2'	10:C:256:THR:OG1	2.20	0.57
8:A:1936:A:N6	8:A:1963:U:O2	2.37	0.57
10:C:164:VAL:HG21	10:C:180:MET:HE1	1.84	0.57
12:E:125:SER:O	12:E:137:LYS:NZ	2.38	0.57
34:a:746:A:H2'	34:a:747:A:C8	2.39	0.57
11:D:48:ILE:HG23	11:D:84:LEU:HD21	1.84	0.57
34:a:375:U:H5''	49:p:70:ARG:HG3	1.86	0.57
42:i:40:ARG:HG3	42:i:42:THR:HG22	1.87	0.57
56:w:37:MIA:H2'	56:w:38:A:O4'	2.03	0.57
8:A:151:C:H2'	8:A:152:A:H8	1.69	0.57
8:A:1334:G:H5''	27:T:69:ARG:HH12	1.69	0.57
9:B:8:C:O3'	22:O:25:ARG:NH2	2.37	0.57
11:D:8:LYS:NZ	11:D:195:GLY:O	2.32	0.57
20:M:136:MET:O	29:V:79:ARG:NH1	2.37	0.57
28:U:96:LYS:C	28:U:98:ASN:H	2.12	0.57
44:k:116:PRO:HG2	54:u:34:ARG:HH11	1.70	0.57
34:a:1310:G:N1	34:a:1327:C:H5	1.95	0.57
38:e:93:VAL:HB	38:e:110:MET:HE3	1.87	0.57
8:A:503:A:H5''	8:A:504:A:H3'	1.86	0.57
8:A:1000:A:H2'	8:A:1001:A:C8	2.39	0.57
21:N:72:ASP:HB3	21:N:75:ILE:HB	1.85	0.57
34:a:69:G:H2'	34:a:70:U:C6	2.39	0.57
34:a:995:C:H3'	34:a:996:A:H5''	1.85	0.57
34:a:1071:C:H2'	34:a:1072:G:C8	2.40	0.57
34:a:1149:C:H2'	34:a:1150:A:C8	2.40	0.57
8:A:2391:G:H2'	8:A:2424:C:H41	1.70	0.57
8:A:2788:C:H2'	8:A:2789:C:C6	2.40	0.57
34:a:509:A:N3	34:a:543:U:O2'	2.34	0.57
34:a:741:G:OP1	48:o:34:GLN:NE2	2.38	0.57
8:A:340:A:O2'	12:E:162:ARG:NH2	2.38	0.57
8:A:1070:A:N7	8:A:1095:A:O2'	2.30	0.57
13:F:112:ASP:CG	46:m:70:ARG:HH12	2.13	0.57
15:H:97:ARG:HH22	15:H:112:LYS:HB3	1.70	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
24:Q:111:LYS:HD2	25:R:49:ILE:HG21	1.86	0.57
46:m:2:ARG:HG2	46:m:2:ARG:HH11	1.68	0.57
8:A:1168:G:H2'	8:A:1169:A:H8	1.70	0.57
8:A:1936:A:H62	8:A:1963:U:H3	1.51	0.57
8:A:2137:U:N3	8:A:2155:U:O2	2.38	0.57
8:A:859:G:O2'	8:A:916:G:O6	2.22	0.56
8:A:1437:C:H2'	8:A:1438:U:C6	2.40	0.56
8:A:1715:G:O2'	8:A:1716:U:O5'	2.23	0.56
8:A:2175:C:H2'	8:A:2176:A:H8	1.70	0.56
8:A:2804:U:H2'	8:A:2805:C:C6	2.40	0.56
34:a:1039:G:H2'	34:a:1040:U:C6	2.40	0.56
34:a:1132:C:H2'	34:a:1133:G:H8	1.70	0.56
34:a:1373:G:N7	42:i:12:LYS:NZ	2.53	0.56
7:6:47:LYS:HE3	13:F:114:ARG:HE	1.69	0.56
8:A:2079:U:O2'	31:X:22:ASN:OD1	2.23	0.56
8:A:2246:G:H2'	8:A:2247:A:C8	2.40	0.56
24:Q:48:ASP:HA	24:Q:51:GLN:HB2	1.87	0.56
46:m:76:ILE:O	46:m:80:MET:HG3	2.05	0.56
8:A:545:U:H3'	8:A:546:U:C6	2.40	0.56
8:A:995:C:O2	17:J:3:THR:OG1	2.20	0.56
8:A:1703:G:H2'	8:A:1704:C:C6	2.40	0.56
32:Y:11:VAL:HG12	32:Y:15:ASN:HD21	1.70	0.56
34:a:127:G:O2'	50:q:5:ARG:NH1	2.39	0.56
34:a:662:U:H2'	34:a:663:A:C8	2.40	0.56
34:a:1273:C:H2'	34:a:1274:A:O4'	2.05	0.56
36:c:176:THR:HG22	36:c:179:ALA:H	1.70	0.56
56:w:21:A:N6	56:w:46:G7M:H2'	2.21	0.56
8:A:580:U:H2'	8:A:581:C:C6	2.40	0.56
8:A:1853:A:H2'	8:A:1854:A:C8	2.40	0.56
28:U:25:LYS:HD2	28:U:36:GLU:CD	2.31	0.56
34:a:842:U:H4'	34:a:846:G:N1	2.21	0.56
34:a:1014:A:O2'	34:a:1015:G:OP1	2.22	0.56
34:a:1421:G:H8	34:a:1421:G:OP1	1.87	0.56
34:a:1513:A:H2'	34:a:1514:G:C8	2.41	0.56
34:a:191:G:H2'	34:a:192:A:H8	1.69	0.56
34:a:993:G:O2'	34:a:994:A:N7	2.38	0.56
49:p:4:ILE:HB	49:p:67:ILE:HD13	1.88	0.56
8:A:1818:U:O2'	10:C:152:GLN:O	2.22	0.56
34:a:1297:G:H4'	34:a:1298:U:O5'	2.04	0.56
37:d:94:GLU:HA	37:d:99:ASN:HD22	1.70	0.56
40:g:82:SER:HB2	40:g:84:TYR:CE2	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
55:v:23:C:H2'	55:v:24:U:C6	2.41	0.56
55:v:50:U:H2'	55:v:51:C:C6	2.41	0.56
56:w:5:G:H2'	56:w:6:G:H8	1.70	0.56
8:A:594:U:H2'	8:A:595:C:C6	2.41	0.56
8:A:871:U:H2'	8:A:872:U:C6	2.40	0.56
8:A:1816:C:N4	10:C:34:GLU:OE2	2.28	0.56
34:a:501:C:H2'	34:a:502:A:H8	1.71	0.56
34:a:1078:U:C2	38:e:89:THR:HG21	2.41	0.56
34:a:1327:C:H2'	34:a:1328:C:H6	1.71	0.56
35:b:67:LEU:HD21	35:b:91:VAL:HG23	1.87	0.56
8:A:555:G:O2'	8:A:556:A:H8	1.89	0.56
20:M:57:VAL:O	20:M:59:ARG:N	2.38	0.56
25:R:51:VAL:HB	25:R:52:PRO:CD	2.35	0.56
31:X:2:ARG:O	31:X:11:PRO:HD3	2.06	0.56
38:e:37:VAL:HG11	38:e:113:VAL:HG22	1.87	0.56
43:j:40:ILE:N	43:j:73:LEU:O	2.30	0.56
55:v:20:H2U:H61	55:v:21:A:H5'	1.88	0.56
8:A:1079:C:H42	8:A:1083:U:H3	1.54	0.56
8:A:2199:A:OP1	31:X:36:ARG:NH2	2.39	0.56
8:A:2547:A:H2'	8:A:2548:U:C6	2.41	0.56
13:F:77:LYS:O	13:F:77:LYS:HG2	2.06	0.56
34:a:1119:C:H2'	34:a:1120:C:H6	1.71	0.56
34:a:1328:C:H5''	46:m:27:THR:HG21	1.88	0.56
52:s:44:ILE:HD13	52:s:63:ASP:HA	1.87	0.56
8:A:1794:A:H2'	8:A:1795:C:H6	1.71	0.56
8:A:2011:U:OP1	26:S:42:LYS:NZ	2.37	0.56
15:H:40:THR:OG1	15:H:43:ASN:OD1	2.24	0.56
22:O:2:ASP:OD2	22:O:3:LYS:N	2.38	0.56
34:a:56:U:H2'	34:a:57:G:C8	2.41	0.56
34:a:1031:C:O3'	34:a:1032:G:H2'	2.06	0.56
40:g:75:LYS:HB2	40:g:75:LYS:HZ3	1.71	0.56
54:u:6:ARG:O	54:u:17:ARG:NH2	2.39	0.56
8:A:743:A:O2'	8:A:1659:G:OP1	2.20	0.55
8:A:856:G:H2'	8:A:857:G:C8	2.40	0.55
8:A:2468:A:O2'	8:A:2469:A:O5'	2.20	0.55
10:C:36:ASN:HB2	10:C:61:TYR:HB2	1.87	0.55
34:a:77:A:H2'	34:a:78:A:H8	1.68	0.55
34:a:1376:U:O4	40:g:9:ARG:NH2	2.32	0.55
36:c:46:LEU:HB3	36:c:49:ALA:HB3	1.86	0.55
41:h:28:SER:HB3	41:h:56:PRO:HB2	1.87	0.55
55:v:33:U:O2'	55:v:34:C:O5'	2.23	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2162:G:P	8:A:2171:A:H62	2.30	0.55
8:A:2705:A:O2'	8:A:2852:G:OP1	2.22	0.55
13:F:57:ALA:HB2	13:F:64:PRO:HD3	1.87	0.55
34:a:526:C:OP2	45:l:87:LYS:HE3	2.06	0.55
4:3:40:LYS:NZ	8:A:2419:U:OP1	2.28	0.55
8:A:704:G:O2'	8:A:727:A:N6	2.38	0.55
8:A:2108:A:N1	8:A:2183:A:N6	2.54	0.55
8:A:2233:U:H2'	8:A:2234:G:C8	2.41	0.55
34:a:41:G:H2'	34:a:42:G:H8	1.70	0.55
34:a:1530:G:H2'	34:a:1531:A:C8	2.41	0.55
15:H:135:HIS:H	15:H:138:VAL:HB	1.71	0.55
34:a:1359:C:OP2	47:n:75:ARG:NH1	2.36	0.55
53:t:34:VAL:HG21	53:t:53:MET:HG2	1.89	0.55
48:o:25:GLU:OE2	48:o:76:ARG:NH1	2.39	0.55
50:q:24:ILE:HB	50:q:41:THR:HG23	1.88	0.55
8:A:247:G:OP2	8:A:249:C:N4	2.36	0.55
8:A:883:G:C2	8:A:884:U:H1'	2.42	0.55
14:G:98:LYS:HD2	14:G:98:LYS:N	2.22	0.55
20:M:42:THR:HG22	20:M:93:VAL:HG12	1.89	0.55
34:a:71:A:H61	34:a:99:C:H1'	1.72	0.55
8:A:1078:U:H5	8:A:1088:A:H5''	1.70	0.55
8:A:2297:A:N1	8:A:2321:U:H5	2.05	0.55
34:a:56:U:H2'	34:a:57:G:H8	1.72	0.55
34:a:235:C:H2'	34:a:236:A:C8	2.41	0.55
36:c:76:ILE:HA	36:c:83:VAL:HG13	1.87	0.55
7:6:59:ARG:HG2	7:6:59:ARG:NH1	2.21	0.55
8:A:64:A:H2'	8:A:65:U:C6	2.42	0.55
8:A:807:U:OP2	19:L:41:ARG:NH2	2.39	0.55
8:A:881:G:H2'	8:A:882:G:C8	2.42	0.55
15:H:12:LEU:HD13	15:H:19:VAL:HG21	1.89	0.55
29:V:4:ILE:HG12	29:V:50:MET:HE1	1.89	0.55
49:p:52:LEU:HD11	49:p:74:LEU:HB3	1.89	0.55
8:A:1353:A:H2'	8:A:1354:A:C8	2.42	0.55
8:A:1913:A:C6	34:a:1494:G:H5'	2.42	0.55
8:A:2186:G:C2	8:A:2187:U:H1'	2.42	0.55
34:a:323:U:H2'	34:a:324:G:O4'	2.06	0.55
34:a:920:U:H2'	34:a:921:U:C6	2.42	0.55
34:a:922:G:H2'	34:a:923:A:C8	2.42	0.55
34:a:1003:G:N2	34:a:1005:A:OP1	2.39	0.55
34:a:1010:U:H2'	34:a:1011:C:C6	2.41	0.55
34:a:1530:G:O6	54:u:45:LYS:NZ	2.39	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:324:A:OP2	8:A:1205:A:N6	2.40	0.55
8:A:463:G:N2	8:A:466:A:OP2	2.37	0.55
8:A:1567:G:OP2	10:C:82:TYR:OH	2.24	0.55
18:K:113:MET:HE3	18:K:113:MET:HA	1.88	0.55
34:a:1266:G:N2	34:a:1269:A:OP2	2.33	0.55
8:A:581:C:H2'	8:A:582:A:H8	1.71	0.54
8:A:675:A:N3	8:A:2443:C:O2'	2.38	0.54
8:A:739:A:H1'	8:A:740:C:H5	1.72	0.54
8:A:1843:C:O2'	10:C:253:GLY:O	2.21	0.54
9:B:31:C:O2'	9:B:53:A:N1	2.37	0.54
34:a:85:U:H4'	34:a:86:G:H8	1.72	0.54
34:a:144:G:H2'	34:a:145:G:O4'	2.06	0.54
34:a:384:G:H2'	34:a:385:C:C6	2.42	0.54
34:a:455:G:H2'	34:a:456:A:C8	2.42	0.54
34:a:674:G:H21	44:k:117:HIS:HB2	1.72	0.54
34:a:1312:G:H2'	34:a:1313:U:O2	2.07	0.54
36:c:61:LYS:HE3	36:c:61:LYS:HA	1.88	0.54
37:d:14:GLU:OE2	37:d:62:ARG:NH1	2.40	0.54
1:0:42:ILE:HG22	1:0:48:TYR:HB2	1.88	0.54
13:F:115:GLY:O	13:F:177:ARG:NH1	2.38	0.54
14:G:23:ILE:HD12	14:G:24:THR:H	1.72	0.54
15:H:100:ALA:HB3	15:H:112:LYS:HD3	1.89	0.54
34:a:512:U:H2'	34:a:513:C:C6	2.42	0.54
34:a:1355:G:O2'	34:a:1356:G:H8	1.91	0.54
34:a:1494:G:OP1	63:a:1702:HOH:O	2.18	0.54
7:6:10:GLU:H	7:6:10:GLU:CD	2.14	0.54
8:A:181:A:H2'	8:A:182:A:H8	1.72	0.54
8:A:504:A:C2	8:A:1234:U:H5''	2.42	0.54
26:S:73:LYS:HB2	26:S:106:VAL:HB	1.89	0.54
40:g:143:MET:HA	40:g:143:MET:HE2	1.90	0.54
8:A:504:A:H4'	8:A:505:A:O5'	2.06	0.54
8:A:528:A:C2	8:A:2042:A:H2'	2.43	0.54
12:E:176:ASP:OD1	12:E:179:SER:OG	2.25	0.54
27:T:54:GLU:HG2	27:T:88:LYS:HB2	1.88	0.54
8:A:395:U:H2'	8:A:396:G:C8	2.43	0.54
8:A:1693:U:H5''	8:A:1694:C:H5	1.72	0.54
34:a:1036:A:O2'	34:a:1037:C:O4'	2.25	0.54
37:d:8:LEU:O	37:d:12:ARG:HG2	2.06	0.54
7:6:37:CYS:SG	7:6:38:SER:N	2.81	0.54
8:A:849:A:H2'	8:A:850:U:C6	2.43	0.54
8:A:1874:C:H2'	8:A:1875:G:O4'	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2839:G:N2	21:N:91:ALA:O	2.31	0.54
8:A:2848:G:O2'	8:A:2868:A:N6	2.41	0.54
23:P:24:THR:HB	23:P:87:ARG:HB3	1.89	0.54
27:T:92:ASN:OD1	27:T:93:LEU:N	2.41	0.54
34:a:640:A:O2'	41:h:107:LYS:NZ	2.35	0.54
8:A:1490:A:C8	10:C:97:ASP:HB3	2.42	0.54
8:A:1913:A:C5	34:a:1494:G:H5'	2.43	0.54
17:J:125:TYR:OH	17:J:132:HIS:NE2	2.29	0.54
34:a:1451:U:H5''	34:a:1452:C:H5	1.72	0.54
34:a:1494:G:N7	62:a:1682:AM2:NC6	2.55	0.54
35:b:56:LEU:HD13	35:b:216:VAL:HG13	1.90	0.54
35:b:129:THR:HG23	35:b:132:GLU:HB3	1.89	0.54
38:e:150:GLU:CD	38:e:150:GLU:H	2.16	0.54
42:i:50:PRO:O	42:i:54:VAL:HG22	2.07	0.54
47:n:30:ILE:HG12	47:n:45:VAL:HG12	1.90	0.54
1:0:51:ARG:HD2	1:0:53:VAL:HG12	1.89	0.54
8:A:634:C:H2'	8:A:635:C:C6	2.43	0.54
8:A:1442:U:H2'	8:A:1443:U:C6	2.43	0.54
8:A:2144:G:HO2'	8:A:2147:A:H62	1.53	0.54
8:A:2683:C:H4'	11:D:13:ARG:NH2	2.22	0.54
14:G:83:THR:HG22	14:G:133:LYS:HG2	1.89	0.54
34:a:67:C:H2'	34:a:68:G:C8	2.43	0.54
34:a:736:C:H2'	34:a:737:C:H6	1.73	0.54
34:a:1004:A:N6	34:a:1026:G:H1'	2.23	0.54
39:f:12:PRO:HB3	39:f:56:LYS:O	2.07	0.54
8:A:545:U:O2	8:A:548:G:O6	2.25	0.54
8:A:1013:C:H2'	8:A:1014:A:H8	1.73	0.54
8:A:1111:A:N3	8:A:1112:G:H1'	2.23	0.54
8:A:2159:G:O2'	8:A:2160:C:O4'	2.25	0.54
8:A:2627:G:O2'	8:A:2781:A:N1	2.39	0.54
32:Y:5:GLU:HA	32:Y:8:GLU:HG2	1.90	0.54
34:a:96:U:H2'	34:a:97:G:H8	1.73	0.54
34:a:335:C:H2'	34:a:336:A:C8	2.43	0.54
34:a:728:A:H2'	34:a:729:A:C8	2.43	0.54
34:a:1323:G:O2'	34:a:1324:A:H8	1.90	0.54
35:b:59:ILE:HD12	35:b:159:ALA:HB2	1.90	0.54
44:k:86:LYS:HB2	44:k:112:VAL:HG23	1.90	0.54
44:k:108:ASN:HA	54:u:7:GLU:OE2	2.08	0.54
48:o:42:PHE:HB3	48:o:52:ARG:HH21	1.73	0.54
56:w:21:A:H61	56:w:46:G7M:H2'	1.72	0.54
8:A:832:U:H2'	8:A:833:A:C8	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:1028:A:N6	8:A:1125:G:H2'	2.23	0.54
8:A:2241:A:H2'	8:A:2242:G:C8	2.43	0.54
34:a:1014:A:C2	34:a:1219:A:H1'	2.43	0.54
39:f:46:GLN:OE1	39:f:56:LYS:HE3	2.08	0.54
7:6:28:VAL:HG23	7:6:30:HIS:H	1.71	0.53
8:A:704:G:H2'	8:A:726:G:N2	2.21	0.53
8:A:1682:G:H2'	8:A:1683:U:C6	2.42	0.53
8:A:1744:A:H3'	8:A:1745:A:H8	1.73	0.53
8:A:1747:U:H2'	8:A:1748:C:C6	2.43	0.53
34:a:35:G:H2'	34:a:36:C:C6	2.42	0.53
34:a:501:C:OP1	45:l:113:ARG:NH2	2.32	0.53
34:a:515:G:O2'	34:a:516:PSU:O4'	2.26	0.53
52:s:35:ARG:NH2	52:s:74:ALA:O	2.40	0.53
7:6:14:ALA:HB1	7:6:34:LEU:HD21	1.88	0.53
8:A:17:G:H2'	8:A:18:U:C6	2.43	0.53
8:A:851:C:H2'	8:A:852:U:C6	2.44	0.53
8:A:909:A:H2'	8:A:912:C:H5	1.73	0.53
8:A:1171:G:H1	8:A:1177:G:H1	1.57	0.53
8:A:1198:U:H2'	8:A:1199:U:C6	2.43	0.53
8:A:2834:G:H2'	8:A:2879:A:H61	1.73	0.53
52:s:26:ASP:OD1	52:s:28:LYS:N	2.35	0.53
56:w:59:U:H2'	56:w:60:U:O4'	2.07	0.53
8:A:2144:G:H1'	8:A:2148:G:H22	1.74	0.53
8:A:2331:G:O2'	8:A:2336:A:N1	2.37	0.53
8:A:2635:A:O2'	11:D:81:GLU:OE1	2.18	0.53
20:M:50:ARG:HA	20:M:53:MET:HE3	1.90	0.53
6:5:55:VAL:HA	8:A:1084:A:H5'	1.88	0.53
8:A:849:A:H2'	8:A:850:U:H6	1.72	0.53
8:A:947:A:H2'	8:A:948:C:C6	2.43	0.53
8:A:1441:G:H2'	8:A:1442:U:C6	2.44	0.53
8:A:2698:U:H2'	8:A:2699:C:C6	2.43	0.53
34:a:715:A:H2'	34:a:716:A:C8	2.43	0.53
34:a:1062:U:H2'	34:a:1063:C:C6	2.42	0.53
34:a:1313:U:C2'	34:a:1314:C:H5'	2.38	0.53
52:s:31:ARG:HA	52:s:49:ALA:HB3	1.90	0.53
34:a:41:G:H2'	34:a:42:G:C8	2.44	0.53
47:n:36:ALA:HB1	47:n:41:ARG:HH11	1.72	0.53
52:s:27:LYS:NZ	52:s:45:GLY:O	2.41	0.53
8:A:700:G:O2'	8:A:1632:A:N3	2.38	0.53
8:A:1469:A:H2'	8:A:1470:A:H8	1.72	0.53
8:A:2134:A:N6	8:A:2156:G:O2'	2.30	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2567:G:H2'	8:A:2568:U:C6	2.44	0.53
8:A:2757:A:N1	14:G:66:THR:OG1	2.35	0.53
17:J:11:VAL:HG11	17:J:50:THR:HA	1.91	0.53
34:a:1498:UR3:H6	34:a:1499:A:H62	1.74	0.53
2:1:37:LYS:HB2	2:1:48:TYR:CD1	2.43	0.53
8:A:630:G:N2	8:A:633:A:OP2	2.34	0.53
8:A:1720:U:H2'	8:A:1721:G:O4'	2.09	0.53
8:A:2649:C:H2'	8:A:2650:U:H6	1.74	0.53
34:a:85:U:H5'	34:a:86:G:H5'	1.91	0.53
8:A:1820:U:C2	10:C:200:MET:HG2	2.44	0.53
8:A:2149:U:OP2	8:A:2150:C:N4	2.42	0.53
21:N:8:ARG:HD2	21:N:43:GLU:HG2	1.91	0.53
29:V:25:LYS:NZ	29:V:41:GLU:OE2	2.38	0.53
34:a:1297:G:N2	34:a:1298:U:O4	2.42	0.53
34:a:1314:C:O2'	34:a:1315:U:OP2	2.24	0.53
46:m:14:ALA:HB3	46:m:33:LEU:HD11	1.91	0.53
2:1:12:SER:HB3	2:1:48:TYR:CZ	2.43	0.53
8:A:645:C:H2'	8:A:647:G:C8	2.44	0.53
8:A:1149:G:H2'	8:A:1150:C:C6	2.44	0.53
8:A:1532:A:N6	8:A:1540:G:O6	2.42	0.53
8:A:1594:U:H2'	8:A:1595:C:C6	2.43	0.53
13:F:118:ALA:C	13:F:119:LYS:HE2	2.34	0.53
36:c:23:ALA:HB1	36:c:27:GLU:HG2	1.89	0.53
42:i:56:MET:HB3	42:i:60:LEU:HD23	1.91	0.53
56:w:6:G:O6	56:w:67:C:N4	2.23	0.53
10:C:131:MET:HG2	10:C:163:ILE:HD11	1.91	0.53
19:L:9:ALA:O	19:L:12:SER:OG	2.24	0.53
20:M:17:ASN:O	20:M:38:ARG:NH1	2.37	0.53
21:N:24:MET:HE1	21:N:40:LYS:HD3	1.90	0.53
25:R:66:HIS:ND1	25:R:94:THR:HG22	2.23	0.53
35:b:81:ASP:OD1	35:b:82:ALA:N	2.42	0.53
8:A:608:A:H2'	8:A:609:A:C8	2.44	0.52
8:A:721:A:H2'	8:A:722:A:C8	2.44	0.52
8:A:883:G:H2'	8:A:884:U:O4'	2.10	0.52
14:G:27:GLY:HA3	14:G:78:VAL:HB	1.91	0.52
34:a:984:C:O2'	34:a:985:C:H5'	2.09	0.52
34:a:1437:A:OP1	53:t:28:ARG:NH2	2.35	0.52
2:1:27:ARG:HD3	2:1:27:ARG:H	1.74	0.52
8:A:589:U:H2'	8:A:590:A:C8	2.45	0.52
8:A:1340:U:OP2	27:T:82:LYS:NZ	2.42	0.52
8:A:1475:G:H1'	8:A:1732:C:H41	1.72	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:1548:A:H2'	8:A:1549:A:C8	2.44	0.52
8:A:1907:G:O2'	8:A:1908:C:H6	1.92	0.52
8:A:2532:G:N2	8:A:2663:G:O2'	2.43	0.52
26:S:80:PRO:O	26:S:100:THR:OG1	2.26	0.52
34:a:191:G:H2'	34:a:192:A:C8	2.45	0.52
34:a:539:A:H2'	34:a:540:G:C8	2.44	0.52
34:a:1013:G:N2	34:a:1016:A:OP2	2.29	0.52
34:a:1289:A:O3'	40:g:34:LYS:NZ	2.42	0.52
35:b:47:PRO:O	35:b:51:GLU:HG2	2.09	0.52
8:A:2:G:H2'	8:A:3:U:C6	2.43	0.52
8:A:657:U:H2'	8:A:658:U:C6	2.45	0.52
8:A:1386:C:H2'	8:A:1387:A:H8	1.70	0.52
34:a:62:U:H2'	34:a:63:C:C6	2.45	0.52
34:a:171:A:H2'	34:a:172:A:C8	2.44	0.52
34:a:662:U:O2'	34:a:836:G:OP1	2.27	0.52
6:5:27:VAL:HA	6:5:110:ALA:HA	1.92	0.52
8:A:171:U:H2'	8:A:172:A:C8	2.43	0.52
8:A:371:A:H61	8:A:401:A:H3'	1.73	0.52
8:A:1062:G:H4'	8:A:1063:G:OP1	2.10	0.52
8:A:1125:G:OP2	8:A:1126:A:O2'	2.22	0.52
8:A:1171:G:H1	8:A:1177:G:N2	2.06	0.52
8:A:2037:A:H2'	8:A:2038:G:C8	2.44	0.52
8:A:2097:A:H2'	8:A:2098:U:C6	2.45	0.52
8:A:2229:U:H2'	8:A:2230:G:H8	1.74	0.52
8:A:2809:A:OP2	8:A:2890:G:N1	2.33	0.52
13:F:78:ILE:HD11	13:F:84:ILE:HG21	1.90	0.52
14:G:41:GLU:HB3	14:G:54:ARG:HH21	1.73	0.52
14:G:72:ASN:O	14:G:76:ILE:HG13	2.09	0.52
34:a:1027:C:N4	34:a:1034:G:H22	2.01	0.52
36:c:109:GLU:HB2	36:c:143:LEU:HD12	1.90	0.52
8:A:153:U:OP1	31:X:76:LYS:NZ	2.43	0.52
8:A:1248:G:OP1	12:E:44:ARG:NH1	2.43	0.52
8:A:2074:U:H2'	8:A:2075:U:C6	2.45	0.52
18:K:102:PRO:HD2	23:P:67:GLU:OE2	2.09	0.52
34:a:59:A:H5''	34:a:387:U:H5''	1.91	0.52
34:a:62:U:OP1	34:a:385:C:O2'	2.27	0.52
34:a:96:U:H2'	34:a:97:G:C8	2.45	0.52
34:a:148:G:O2'	34:a:1446:A:N3	2.42	0.52
34:a:1057:G:O2'	36:c:187:GLU:OE1	2.27	0.52
34:a:1295:U:H2'	34:a:1296:C:C6	2.45	0.52
34:a:1325:C:H2'	34:a:1326:U:O2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
37:d:106:PHE:HB3	37:d:144:ILE:HD11	1.92	0.52
1:0:15:ARG:HA	8:A:2046:G:H5'	1.91	0.52
8:A:578:G:OP1	8:A:1255:U:O2'	2.21	0.52
8:A:586:A:N1	8:A:809:G:O2'	2.41	0.52
8:A:644:A:H2'	8:A:645:C:O4'	2.10	0.52
8:A:813:U:H2'	8:A:814:C:H6	1.72	0.52
8:A:1183:U:H2'	8:A:1184:U:C6	2.45	0.52
8:A:1416:G:H2'	8:A:1417:C:H6	1.75	0.52
8:A:2014:A:H2'	8:A:2015:A:C8	2.44	0.52
8:A:2319:G:O2'	8:A:2320:U:O5'	2.21	0.52
14:G:97:VAL:C	14:G:98:LYS:HD2	2.35	0.52
14:G:97:VAL:HG22	14:G:102:ILE:HG13	1.90	0.52
28:U:33:VAL:HG13	28:U:66:VAL:HG12	1.91	0.52
34:a:269:C:H2'	34:a:270:A:C8	2.45	0.52
34:a:526:C:P	45:l:87:LYS:HE3	2.50	0.52
34:a:1120:C:H2'	34:a:1121:U:C6	2.44	0.52
34:a:1319:A:C8	34:a:1323:G:C6	2.97	0.52
37:d:106:PHE:HA	37:d:154:VAL:HG23	1.90	0.52
42:i:51:LEU:HD13	42:i:57:VAL:HA	1.90	0.52
56:w:18:G:O2'	56:w:57:G:N2	2.38	0.52
8:A:45:G:H5'	8:A:46:G:OP1	2.10	0.52
8:A:347:A:H2'	8:A:348:A:C8	2.45	0.52
8:A:1365:A:OP1	31:X:27:ARG:NH2	2.31	0.52
8:A:1790:C:H2'	8:A:1791:A:C5	2.44	0.52
8:A:2025:C:H2'	8:A:2026:U:C6	2.45	0.52
35:b:58:LYS:HB3	35:b:62:ARG:HH12	1.75	0.52
37:d:64:TYR:OH	37:d:94:GLU:OE2	2.21	0.52
8:A:155:A:H2'	8:A:156:A:C8	2.45	0.52
8:A:394:C:H2'	8:A:395:U:O4'	2.10	0.52
8:A:878:A:H3'	8:A:879:G:H8	1.74	0.52
8:A:1187:G:H5''	25:R:83:TYR:CE1	2.44	0.52
8:A:1224:U:H2'	8:A:1225:G:C8	2.44	0.52
10:C:56:GLY:HA2	10:C:212:TRP:HA	1.92	0.52
20:M:53:MET:HG3	20:M:120:ALA:HB2	1.92	0.52
34:a:509:A:H2'	34:a:510:A:C8	2.45	0.52
34:a:1132:C:H2'	34:a:1133:G:C8	2.45	0.52
42:i:5:TYR:HB2	42:i:20:ILE:HG12	1.91	0.52
54:u:20:ARG:O	54:u:24:LYS:HG2	2.10	0.52
8:A:310:A:HO2'	8:A:311:A:P	2.33	0.52
8:A:395:U:H2'	8:A:396:G:N7	2.24	0.52
8:A:1061:U:H1'	16:I:10:LEU:HA	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2273:A:H2'	8:A:2274:A:C8	2.45	0.52
8:A:2773:C:OP1	11:D:169:ARG:NH1	2.42	0.52
23:P:87:ARG:NH2	23:P:109:ILE:O	2.39	0.52
34:a:686:U:O2'	34:a:687:A:O4'	2.28	0.52
34:a:1350:A:O2'	40:g:32:ASP:OD1	2.24	0.52
52:s:22:VAL:HG12	52:s:46:LEU:HD21	1.90	0.52
8:A:793:A:OP2	8:A:2071:A:O2'	2.23	0.52
8:A:885:C:O2'	8:A:886:A:OP2	2.28	0.52
8:A:1055:G:H2'	8:A:1056:G:C8	2.45	0.52
8:A:1172:C:H2'	8:A:1173:U:O4'	2.10	0.52
8:A:1315:C:O2'	8:A:1392:A:N3	2.42	0.52
8:A:2153:C:H2'	8:A:2154:A:C8	2.44	0.52
8:A:2312:U:O3'	13:F:67:THR:HG21	2.09	0.52
26:S:59:GLU:HB3	26:S:66:ILE:HD11	1.92	0.52
27:T:76:ARG:HH11	27:T:76:ARG:HG3	1.74	0.52
34:a:33:A:H2'	34:a:34:C:C6	2.45	0.52
34:a:613:C:H2'	34:a:614:C:C6	2.45	0.52
37:d:22:SER:HB2	37:d:108:ALA:HB1	1.90	0.52
8:A:499:U:H2'	8:A:500:G:O4'	2.10	0.51
8:A:1171:G:H22	8:A:1177:G:H22	1.56	0.51
8:A:2377:A:H2'	8:A:2378:A:C8	2.46	0.51
34:a:500:G:H2'	34:a:501:C:C6	2.45	0.51
34:a:821:G:H2'	34:a:822:U:C6	2.45	0.51
53:t:43:LYS:HD2	53:t:86:ALA:HB2	1.91	0.51
8:A:1538:G:H2'	8:A:1539:U:C6	2.44	0.51
8:A:2143:C:H2'	8:A:2144:G:O4'	2.10	0.51
8:A:2809:A:H2'	8:A:2810:A:C8	2.45	0.51
34:a:1239:A:O2'	40:g:113:LYS:O	2.29	0.51
4:3:63:TYR:CE2	8:A:242:G:H5''	2.44	0.51
8:A:306:U:H2'	8:A:307:G:O4'	2.10	0.51
8:A:1809:A:H2'	8:A:1810:A:C8	2.45	0.51
44:k:33:ILE:HG12	44:k:69:CYS:SG	2.51	0.51
47:n:49:GLN:HE22	52:s:11:ASP:HA	1.75	0.51
7:6:47:LYS:HA	7:6:49:ARG:NH2	2.26	0.51
8:A:1063:G:H2'	16:I:88:GLY:HA3	1.93	0.51
8:A:1068:G:H2'	8:A:1069:A:H4'	1.92	0.51
8:A:1433:A:H2'	8:A:1434:A:O4'	2.11	0.51
8:A:1923:U:O2'	55:v:12:G:H1'	2.10	0.51
8:A:2687:U:H2'	8:A:2688:G:O4'	2.10	0.51
32:Y:39:GLN:HB3	32:Y:41:HIS:CE1	2.46	0.51
34:a:736:C:H2'	34:a:737:C:C6	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
40:g:75:LYS:HB2	40:g:75:LYS:NZ	2.25	0.51
47:n:90:ARG:NH1	47:n:92:GLU:OE1	2.44	0.51
55:v:75:C:H2'	55:v:76:A:N7	2.25	0.51
1:0:23:ALA:HB2	26:S:23:LEU:HD22	1.93	0.51
8:A:672:C:OP2	19:L:42:SER:OG	2.22	0.51
8:A:1889:A:H2'	8:A:1890:A:C8	2.45	0.51
10:C:70:LYS:NZ	10:C:97:ASP:OD2	2.42	0.51
34:a:1435:G:H2'	34:a:1436:U:C6	2.45	0.51
8:A:876:C:H2'	8:A:877:A:O4'	2.11	0.51
8:A:1068:G:N2	16:I:22:PRO:O	2.44	0.51
8:A:1447:C:O2'	8:A:1544:A:N3	2.41	0.51
8:A:1654:A:O2'	11:D:118:PHE:O	2.25	0.51
8:A:2537:U:H2'	8:A:2538:C:C6	2.45	0.51
19:L:81:ASP:HB3	19:L:100:ILE:HD13	1.93	0.51
34:a:95:C:O2'	34:a:96:U:OP1	2.27	0.51
34:a:197:A:N1	34:a:220:G:O2'	2.35	0.51
34:a:460:A:H2'	34:a:461:A:H8	1.75	0.51
34:a:1010:U:H2'	34:a:1011:C:H6	1.75	0.51
34:a:1028:C:H1'	34:a:1029:U:H5'	1.92	0.51
34:a:1410:A:H2'	34:a:1411:C:C6	2.45	0.51
34:a:1500:A:H5''	34:a:1508:A:H5''	1.93	0.51
34:a:1527:U:OP2	54:u:41:THR:HG22	2.11	0.51
39:f:47:LEU:HD21	39:f:57:ALA:HB3	1.92	0.51
44:k:116:PRO:O	54:u:34:ARG:NH1	2.40	0.51
8:A:850:U:H3	8:A:927:A:H61	1.58	0.51
8:A:1429:G:H2'	8:A:1430:G:H8	1.75	0.51
21:N:55:ALA:HA	21:N:80:PHE:CE1	2.45	0.51
34:a:1238:A:OP1	34:a:1335:U:O2'	2.22	0.51
34:a:1244:G:H2'	34:a:1245:C:C6	2.45	0.51
43:j:92:LEU:HD23	43:j:92:LEU:H	1.74	0.51
8:A:2247:A:H2'	8:A:2248:C:H6	1.75	0.51
9:B:48:U:H4'	22:O:100:HIS:HD2	1.75	0.51
34:a:987:G:O2'	34:a:988:G:H8	1.94	0.51
46:m:16:ILE:O	46:m:19:THR:HG22	2.10	0.51
46:m:53:ASP:HA	46:m:56:ARG:HG3	1.93	0.51
50:q:31:PRO:HB2	50:q:32:ILE:HD12	1.92	0.51
8:A:1570:A:H2'	8:A:1571:A:C8	2.45	0.51
13:F:129:MET:HG3	13:F:153:ILE:HB	1.92	0.51
19:L:78:ARG:HG2	19:L:113:ALA:HB3	1.93	0.51
25:R:26:ASP:C	25:R:27:ILE:HD13	2.35	0.51
34:a:656:G:O2'	48:o:27:GLN:OE1	2.23	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:1120:C:H2'	34:a:1121:U:H6	1.76	0.51
34:a:1125:U:H2'	34:a:1126:U:H2'	1.92	0.51
34:a:1308:U:H2'	34:a:1309:G:H8	1.76	0.51
8:A:172:A:H2'	8:A:173:A:H8	1.76	0.51
8:A:494:G:H4'	26:S:6:LYS:HB2	1.93	0.51
34:a:333:U:P	53:t:2:ASN:HD21	2.34	0.51
2:l:4:ILE:HB	8:A:2284:A:OP1	2.11	0.50
8:A:1361:G:H2'	8:A:1362:C:C6	2.45	0.50
8:A:1478:G:N2	8:A:1513:U:O2	2.29	0.50
8:A:1946:U:H2'	8:A:1947:C:C6	2.46	0.50
10:C:24:HIS:CG	10:C:79:ARG:HD2	2.47	0.50
34:a:911:U:H2'	34:a:912:C:C6	2.46	0.50
35:b:71:THR:OG1	35:b:168:GLU:OE2	2.26	0.50
42:i:56:MET:HG2	42:i:59:LYS:HE2	1.94	0.50
8:A:1710:G:H2'	8:A:1711:A:C8	2.46	0.50
8:A:1920:C:H2'	8:A:1921:G:O4'	2.12	0.50
8:A:2181:U:H2'	8:A:2182:U:O4'	2.12	0.50
8:A:2898:U:H2'	8:A:2899:A:C8	2.46	0.50
13:F:111:ARG:HH21	46:m:2:ARG:HH21	1.58	0.50
13:F:143:ASP:C	13:F:144:LYS:HD3	2.35	0.50
15:H:131:SER:OG	15:H:132:PHE:N	2.44	0.50
34:a:553:A:H5''	45:l:20:VAL:HG21	1.92	0.50
34:a:636:U:H2'	34:a:637:C:C6	2.46	0.50
34:a:696:A:H2'	34:a:697:U:H6	1.76	0.50
34:a:976:G:N2	34:a:1362:A:H2'	2.26	0.50
51:r:56:ARG:HB3	51:r:60:ARG:HH21	1.76	0.50
8:A:219:A:N3	8:A:234:U:O2'	2.38	0.50
8:A:1954:G:O2'	8:A:1956:U:O4	2.22	0.50
8:A:2584:U:H3'	8:A:2585:U:C5'	2.41	0.50
25:R:29:THR:O	25:R:29:THR:OG1	2.28	0.50
34:a:628:G:H2'	34:a:629:A:C8	2.46	0.50
34:a:859:G:H2'	34:a:860:A:C8	2.46	0.50
34:a:1327:C:H2'	34:a:1328:C:C6	2.46	0.50
39:f:25:TYR:O	39:f:29:ILE:HD12	2.11	0.50
44:k:110:THR:HG23	54:u:4:LYS:HG2	1.93	0.50
8:A:3:U:H2'	8:A:4:U:C6	2.46	0.50
8:A:58:G:O2'	8:A:73:A:N1	2.39	0.50
8:A:84:A:N1	8:A:98:G:O2'	2.34	0.50
8:A:144:A:H2'	8:A:145:C:C6	2.46	0.50
8:A:279:A:H62	8:A:361:G:H1'	1.76	0.50
8:A:355:U:H2'	8:A:356:G:H8	1.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:414:C:H2'	8:A:415:A:C8	2.46	0.50
8:A:839:U:H2'	8:A:840:C:C6	2.46	0.50
8:A:1311:G:H21	8:A:1603:A:H62	1.59	0.50
8:A:2100:G:H2'	8:A:2101:A:C8	2.46	0.50
8:A:2646:C:OP2	8:A:2732:G:O2'	2.27	0.50
10:C:106:PRO:HG2	10:C:109:LEU:HB2	1.93	0.50
11:D:13:ARG:HD2	11:D:15:PHE:CE2	2.47	0.50
29:V:86:LEU:HD13	29:V:89:ILE:HD11	1.93	0.50
34:a:235:C:H2'	34:a:236:A:H8	1.75	0.50
34:a:294:U:OP1	34:a:610:U:O2'	2.21	0.50
51:r:19:GLU:OE1	51:r:19:GLU:N	2.44	0.50
8:A:151:C:H2'	8:A:152:A:C8	2.46	0.50
8:A:353:C:H2'	8:A:354:A:H8	1.77	0.50
8:A:753:A:H2'	8:A:754:U:H6	1.76	0.50
8:A:1585:C:H3'	8:A:1586:A:H8	1.77	0.50
8:A:2070:A:H2'	8:A:2071:A:H8	1.75	0.50
9:B:2:G:H2'	9:B:3:C:C6	2.47	0.50
34:a:91:U:H2'	34:a:92:U:C6	2.46	0.50
34:a:337:G:H2'	34:a:338:A:H8	1.74	0.50
34:a:600:A:OP2	41:h:87:ARG:NH1	2.44	0.50
35:b:58:LYS:HB3	35:b:62:ARG:NH1	2.26	0.50
36:c:8:GLY:HA3	47:n:89:MET:HE3	1.94	0.50
38:e:64:GLU:OE1	38:e:68:ARG:HD3	2.12	0.50
7:6:62:LYS:HZ2	7:6:63:ARG:N	2.09	0.50
8:A:632:A:H2'	8:A:633:A:C8	2.47	0.50
8:A:948:C:H2'	8:A:949:G:H8	1.76	0.50
8:A:1038:G:H2'	8:A:1039:A:C8	2.46	0.50
8:A:1039:A:H2'	8:A:1040:A:O4'	2.11	0.50
8:A:1484:U:H2'	8:A:1485:U:C6	2.47	0.50
9:B:79:G:N7	29:V:14:LYS:NZ	2.60	0.50
11:D:184:ARG:NH2	23:P:6:GLN:HB3	2.27	0.50
18:K:34:GLY:N	18:K:37:ASP:OD2	2.33	0.50
29:V:58:SER:O	29:V:73:LYS:NZ	2.45	0.50
34:a:71:A:N1	34:a:99:C:O2'	2.40	0.50
34:a:579:A:H2'	34:a:580:C:C6	2.47	0.50
34:a:674:G:H2'	34:a:675:A:C8	2.46	0.50
34:a:908:A:H2'	34:a:909:A:C8	2.46	0.50
34:a:1167:A:H4'	34:a:1168:U:H5	1.76	0.50
35:b:117:GLU:HA	35:b:117:GLU:OE2	2.11	0.50
48:o:34:GLN:HA	48:o:34:GLN:OE1	2.12	0.50
54:u:46:ARG:HH11	54:u:46:ARG:HG3	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:57:C:H2'	8:A:58:G:O4'	2.12	0.50
8:A:458:G:O2'	8:A:459:U:P	2.70	0.50
8:A:566:U:H5''	19:L:29:LYS:HE3	1.94	0.50
8:A:715:A:O2'	8:A:716:A:OP1	2.27	0.50
8:A:743:A:OP1	11:D:135:GLY:HA2	2.12	0.50
8:A:1197:G:H2'	8:A:1198:U:H6	1.76	0.50
8:A:2047:C:H2'	8:A:2048:G:H8	1.76	0.50
8:A:2595:G:N2	8:A:2598:A:OP2	2.38	0.50
10:C:231:HIS:HA	10:C:241:LYS:HE3	1.92	0.50
20:M:4:PRO:HG3	20:M:70:ASP:HA	1.93	0.50
27:T:8:LEU:O	32:Y:29:ARG:NH2	2.37	0.50
34:a:953:G:N7	46:m:102:LYS:NZ	2.59	0.50
34:a:1346:A:OP1	42:i:121:ARG:NH1	2.44	0.50
35:b:166:ASP:OD2	35:b:190:SER:OG	2.30	0.50
39:f:90:MET:HE1	51:r:22:TYR:CZ	2.47	0.50
3:2:2:LYS:HE2	8:A:687:C:H5''	1.94	0.50
8:A:843:G:H2'	8:A:844:A:C8	2.47	0.50
8:A:1069:A:H2'	8:A:1073:A:N7	2.27	0.50
8:A:1178:C:H2'	8:A:1180:U:C6	2.46	0.50
8:A:1292:G:H2'	8:A:1293:C:C6	2.47	0.50
8:A:1542:U:H2'	8:A:1543:G:O4'	2.12	0.50
8:A:1672:A:C2	8:A:2582:G:H5'	2.47	0.50
8:A:2640:G:P	17:J:96:ARG:HH21	2.33	0.50
45:l:49:ARG:NE	45:l:88:ASP:OD2	2.40	0.50
51:r:42:ARG:HG3	51:r:43:ILE:HD13	1.93	0.50
7:6:24:ILE:HD12	7:6:24:ILE:O	2.11	0.50
8:A:182:A:H2'	8:A:183:C:H6	1.77	0.50
8:A:275:C:H3'	8:A:276:U:H5''	1.92	0.50
8:A:397:U:OP2	31:X:9:LYS:NZ	2.41	0.50
8:A:784:G:H5'	8:A:785:G:OP1	2.12	0.50
8:A:2605:PSU:H2'	8:A:2606:C:C6	2.46	0.50
14:G:154:GLU:OE1	14:G:157:LYS:N	2.45	0.50
34:a:202:G:H1	34:a:215:C:H41	1.58	0.50
34:a:1000:A:H2'	34:a:1001:C:C6	2.46	0.50
34:a:1250:A:H2'	34:a:1251:A:C8	2.47	0.50
34:a:1404:C:H2'	34:a:1405:G:C8	2.47	0.50
38:e:106:ALA:HB2	38:e:124:ALA:HB3	1.94	0.50
42:i:96:GLU:CD	42:i:96:GLU:H	2.20	0.50
8:A:192:C:O2'	8:A:802:A:N3	2.44	0.49
8:A:397:U:H5''	31:X:31:ASN:HB2	1.92	0.49
8:A:927:A:H2'	8:A:928:A:C8	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:1394:U:H2'	8:A:1395:A:O4'	2.12	0.49
8:A:1651:G:H5'	21:N:39:PRO:HG2	1.94	0.49
8:A:2179:C:O2'	8:A:2181:U:OP2	2.27	0.49
8:A:2439:A:N6	8:A:2585:U:O2'	2.45	0.49
8:A:2557:G:H2'	8:A:2558:C:C6	2.47	0.49
10:C:198:GLU:OE1	10:C:198:GLU:N	2.32	0.49
14:G:21:GLN:OE1	14:G:54:ARG:NH2	2.44	0.49
15:H:65:ALA:HB1	15:H:68:ARG:HH21	1.77	0.49
17:J:13:ARG:NH2	17:J:49:ASP:O	2.33	0.49
20:M:53:MET:HE1	20:M:103:TYR:CD1	2.47	0.49
34:a:521:G:H4'	45:l:69:GLU:HG3	1.94	0.49
34:a:978:A:C2	34:a:1319:A:C4	3.00	0.49
55:v:8:4SU:O2'	55:v:21:A:N1	2.36	0.49
8:A:1130:U:C2	8:A:2025:C:H5''	2.48	0.49
13:F:112:ASP:OD2	46:m:70:ARG:NH1	2.45	0.49
15:H:32:PRO:HA	31:X:38:TRP:CD1	2.47	0.49
18:K:99:ILE:HD12	18:K:118:LEU:HB2	1.93	0.49
30:W:55:LEU:HD12	30:W:76:ILE:HD12	1.94	0.49
34:a:501:C:OP2	45:l:120:ARG:NH1	2.45	0.49
34:a:559:A:H4'	34:a:560:A:H3'	1.94	0.49
34:a:1181:G:H1'	34:a:1182:G:C4	2.47	0.49
36:c:122:GLN:OE1	36:c:135:ARG:NH1	2.45	0.49
38:e:49:TYR:CE1	38:e:133:ILE:HD11	2.46	0.49
39:f:3:HIS:CE1	39:f:65:GLU:HG3	2.47	0.49
40:g:57:GLU:OE1	40:g:57:GLU:N	2.45	0.49
40:g:76:SER:OG	40:g:85:GLN:OE1	2.22	0.49
5:4:16:ILE:HD13	5:4:25:VAL:HG22	1.94	0.49
8:A:289:G:H2'	8:A:290:U:C6	2.47	0.49
8:A:1902:C:H4'	10:C:241:LYS:O	2.13	0.49
10:C:135:PRO:O	10:C:138:SER:OG	2.26	0.49
34:a:81:A:H3'	34:a:82:G:H8	1.78	0.49
34:a:868:C:H2'	34:a:869:G:O4'	2.13	0.49
43:j:66:GLU:HB3	47:n:99:ALA:HB2	1.93	0.49
55:v:37:A:H3'	55:v:38:A:H8	1.76	0.49
56:w:68:C:H2'	56:w:69:G:C8	2.46	0.49
7:6:26:SER:OG	7:6:27:THR:N	2.45	0.49
8:A:69:C:O2	8:A:73:A:O2'	2.30	0.49
8:A:1081:U:H1'	16:I:123:ALA:HB1	1.93	0.49
8:A:1266:G:O2'	8:A:2012:G:O6	2.21	0.49
8:A:2297:A:N6	8:A:2319:G:H1'	2.27	0.49
8:A:2394:C:H5''	19:L:63:LYS:HE2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2812:G:H2'	8:A:2813:A:C8	2.46	0.49
10:C:244:VAL:HG12	10:C:250:GLN:HA	1.94	0.49
13:F:111:ARG:HH21	46:m:2:ARG:NH2	2.10	0.49
13:F:133:GLU:OE1	13:F:135:ILE:HG22	2.13	0.49
15:H:50:ARG:HH11	15:H:54:LEU:HD21	1.77	0.49
15:H:83:LYS:HD2	15:H:83:LYS:C	2.38	0.49
34:a:236:A:H2'	34:a:237:G:C8	2.47	0.49
34:a:524:G:H2'	34:a:525:C:C6	2.47	0.49
56:w:5:G:H2'	56:w:6:G:C8	2.47	0.49
8:A:78:U:H2'	8:A:79:C:C6	2.48	0.49
8:A:208:C:H2'	8:A:209:C:H6	1.77	0.49
8:A:415:A:H2'	8:A:416:U:C6	2.47	0.49
8:A:2590:A:H2'	8:A:2591:C:C6	2.48	0.49
13:F:103:ILE:HG23	13:F:104:THR:HG23	1.94	0.49
25:R:25:LEU:H	25:R:94:THR:HG21	1.77	0.49
34:a:496:A:O2'	34:a:497:G:C8	2.65	0.49
36:c:71:ARG:HG2	36:c:74:ILE:HD13	1.94	0.49
40:g:129:ASN:HA	40:g:134:VAL:HG21	1.95	0.49
41:h:10:LEU:HD22	41:h:74:ILE:HD11	1.94	0.49
47:n:49:GLN:NE2	52:s:12:LEU:H	2.11	0.49
8:A:959:A:H2'	8:A:960:A:C8	2.47	0.49
8:A:1081:U:H3	16:I:118:GLY:HA3	1.76	0.49
8:A:1231:U:H2'	8:A:1232:G:H8	1.77	0.49
8:A:1359:A:OP2	8:A:1371:G:N1	2.33	0.49
8:A:1599:U:H2'	8:A:1600:C:C6	2.47	0.49
8:A:1753:G:H5''	23:P:92:ARG:HD3	1.94	0.49
8:A:2119:A:H1'	8:A:2170:A:C2	2.47	0.49
8:A:2175:C:H2'	8:A:2176:A:C8	2.48	0.49
8:A:2328:A:H2'	8:A:2329:U:H6	1.74	0.49
12:E:176:ASP:OD1	12:E:176:ASP:N	2.45	0.49
13:F:72:SER:OG	13:F:79:ARG:HA	2.13	0.49
17:J:7:LYS:O	17:J:11:VAL:HG23	2.12	0.49
34:a:1004:A:O2'	34:a:1005:A:H5'	2.13	0.49
34:a:1137:C:H4'	34:a:1138:G:C2	2.47	0.49
34:a:1175:G:H2'	34:a:1176:A:H8	1.77	0.49
34:a:1477:U:H2'	34:a:1478:U:C6	2.48	0.49
37:d:69:ARG:O	37:d:70:GLN:HB3	2.12	0.49
3:2:1:MET:HA	3:2:1:MET:HE3	1.94	0.49
8:A:504:A:H2	8:A:1234:U:H5''	1.78	0.49
8:A:1434:A:H2'	8:A:1435:G:H8	1.75	0.49
8:A:2345:G:N3	8:A:2381:A:H2'	2.26	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2700:A:H2'	8:A:2701:U:C6	2.48	0.49
8:A:2845:U:H5''	23:P:51:ASN:O	2.12	0.49
10:C:4:LYS:NZ	10:C:13:ARG:O	2.46	0.49
15:H:79:THR:C	15:H:80:ILE:HD13	2.37	0.49
29:V:2:PHE:HB2	29:V:61:LEU:HD22	1.94	0.49
34:a:1005:A:N6	34:a:1024:G:O2'	2.46	0.49
34:a:1338:G:H2'	34:a:1339:A:C8	2.48	0.49
52:s:65:MET:HB2	52:s:73:PHE:CZ	2.48	0.49
8:A:150:U:H2'	8:A:151:C:C6	2.48	0.49
8:A:250:G:H2'	8:A:251:A:C8	2.47	0.49
8:A:1022:G:N2	8:A:1023:U:O4	2.36	0.49
8:A:1437:C:H2'	8:A:1438:U:H6	1.76	0.49
8:A:2250:G:O2'	8:A:2496:C:OP1	2.19	0.49
8:A:2305:U:H5''	13:F:130:GLY:HA3	1.95	0.49
18:K:70:ARG:HG2	18:K:76:VAL:HG22	1.95	0.49
33:Z:27:GLY:HA3	33:Z:37:ARG:HH21	1.78	0.49
34:a:1328:C:C2	34:a:1329:A:C8	3.01	0.49
36:c:128:MET:SD	36:c:130:ARG:HB2	2.53	0.49
49:p:45:GLU:N	49:p:45:GLU:OE2	2.46	0.49
7:6:64:PHE:CG	52:s:8:PRO:HD3	2.48	0.49
8:A:285:G:H2'	8:A:286:U:C6	2.48	0.49
8:A:909:A:H2'	8:A:912:C:C5	2.47	0.49
8:A:1169:A:H2'	8:A:1170:C:O4'	2.11	0.49
18:K:102:PRO:HD3	23:P:65:ASN:HB2	1.95	0.49
21:N:87:PHE:HD1	21:N:90:ARG:HG3	1.78	0.49
22:O:63:LYS:HG3	22:O:64:TYR:H	1.77	0.49
29:V:45:ASP:N	29:V:45:ASP:OD1	2.45	0.49
33:Z:38:GLU:HG2	33:Z:40:THR:HG23	1.95	0.49
34:a:673:A:H2'	34:a:674:G:H8	1.74	0.49
34:a:1027:C:H5'	34:a:1028:C:C5	2.48	0.49
34:a:1060:U:H4'	43:j:53:ILE:HG13	1.95	0.49
44:k:62:ALA:HB1	44:k:95:THR:HG23	1.95	0.49
54:u:38:GLU:HA	54:u:38:GLU:OE2	2.13	0.49
56:w:23:A:H2'	56:w:24:G:C8	2.47	0.49
7:6:41:HIS:HB3	7:6:44:PHE:HD2	1.78	0.49
8:A:753:A:H2'	8:A:754:U:C6	2.48	0.49
8:A:850:U:O2	33:Z:46:MET:HE3	2.13	0.49
8:A:1387:A:H2'	8:A:1388:G:C8	2.48	0.49
8:A:1791:A:N6	8:A:1828:G:O2'	2.37	0.49
8:A:1857:G:O2'	8:A:1885:A:N6	2.46	0.49
8:A:2064:C:H2'	8:A:2065:C:C6	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2728:U:O2'	8:A:2729:G:H8	1.95	0.49
8:A:2895:G:H2'	8:A:2896:C:C6	2.48	0.49
10:C:209:ALA:HA	10:C:212:TRP:CE2	2.48	0.49
24:Q:96:ASP:OD2	25:R:13:ARG:NE	2.46	0.49
34:a:34:C:H2'	34:a:35:G:H8	1.76	0.49
34:a:1158:C:C4	34:a:1160:G:C8	3.01	0.49
34:a:1358:U:OP1	47:n:75:ARG:HB2	2.13	0.49
36:c:110:LEU:HD11	36:c:145:ALA:HB2	1.94	0.49
38:e:19:ARG:HD3	38:e:30:PHE:HB3	1.94	0.49
39:f:44:ARG:HB2	39:f:44:ARG:CZ	2.43	0.49
56:w:62:C:H2'	56:w:63:G:H8	1.77	0.49
8:A:32:C:H2'	8:A:33:C:C6	2.48	0.48
8:A:2804:U:H2'	8:A:2805:C:H6	1.78	0.48
15:H:40:THR:O	15:H:44:ILE:HG13	2.13	0.48
22:O:61:GLN:OE1	22:O:61:GLN:N	2.46	0.48
34:a:90:C:H2'	34:a:91:U:C6	2.48	0.48
34:a:455:G:H2'	34:a:456:A:H8	1.77	0.48
34:a:1040:U:H2'	34:a:1041:G:C8	2.48	0.48
41:h:95:MET:HE3	41:h:98:LEU:HB2	1.94	0.48
8:A:172:A:H2'	8:A:173:A:C8	2.46	0.48
8:A:207:A:H2'	8:A:208:C:O4'	2.13	0.48
8:A:307:G:N1	8:A:310:A:OP2	2.40	0.48
8:A:355:U:H2'	8:A:356:G:C8	2.48	0.48
8:A:720:U:H2'	8:A:721:A:C8	2.48	0.48
8:A:1528:A:OP2	8:A:1543:G:N2	2.44	0.48
8:A:2649:C:H2'	8:A:2650:U:C6	2.48	0.48
17:J:9:GLU:H	17:J:9:GLU:CD	2.21	0.48
34:a:745:G:H2'	34:a:746:A:C8	2.47	0.48
34:a:1507:A:H2'	34:a:1508:A:C8	2.49	0.48
40:g:75:LYS:HD3	40:g:88:VAL:HG21	1.95	0.48
43:j:6:ILE:HG22	43:j:102:LEU:HD23	1.96	0.48
2:1:29:LYS:NZ	8:A:2286:G:OP1	2.39	0.48
8:A:134:G:H2'	8:A:135:U:C6	2.47	0.48
8:A:483:A:H5''	28:U:46:LYS:HD2	1.95	0.48
8:A:1055:G:H2'	8:A:1056:G:H8	1.78	0.48
8:A:1802:A:H2'	8:A:1803:A:H8	1.76	0.48
8:A:2848:G:H2'	8:A:2867:G:H22	1.78	0.48
27:T:4:GLU:HG3	27:T:49:LYS:HE3	1.95	0.48
31:X:5:GLN:O	31:X:73:ARG:NH2	2.46	0.48
34:a:75:G:H2'	34:a:76:G:O4'	2.14	0.48
34:a:195:A:H2'	34:a:196:A:C8	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:464:U:O2'	34:a:466:A:N7	2.43	0.48
34:a:465:A:H2'	34:a:466:A:O4'	2.12	0.48
34:a:751:U:H2'	34:a:752:G:O4'	2.13	0.48
34:a:918:A:H2'	34:a:919:A:C8	2.49	0.48
34:a:1118:U:O3'	42:i:84:ARG:NH2	2.39	0.48
36:c:131:ARG:HB3	36:c:135:ARG:HH21	1.79	0.48
37:d:94:GLU:HA	37:d:99:ASN:ND2	2.29	0.48
43:j:23:ALA:O	43:j:27:GLU:HG2	2.13	0.48
44:k:88:PRO:HD3	54:u:31:VAL:HG11	1.94	0.48
7:6:25:ARG:HG3	7:6:25:ARG:HH11	1.77	0.48
8:A:191:A:H2'	8:A:192:C:H6	1.78	0.48
8:A:588:U:H2'	8:A:589:U:C6	2.48	0.48
8:A:936:A:H2'	8:A:937:C:C6	2.48	0.48
8:A:1059:G:N1	8:A:1080:A:H1'	2.28	0.48
8:A:1269:A:H2'	8:A:1270:C:C6	2.48	0.48
8:A:1545:A:H2'	8:A:1546:G:O4'	2.13	0.48
8:A:1656:C:H2'	8:A:1657:U:H6	1.78	0.48
11:D:16:THR:OG1	11:D:18:ASP:OD1	2.16	0.48
14:G:53:PRO:HG3	14:G:61:TRP:CE2	2.48	0.48
15:H:69:ALA:C	15:H:71:LYS:H	2.20	0.48
18:K:98:ARG:HH21	34:a:341:C:H5	1.60	0.48
53:t:41:GLY:HA2	53:t:85:LEU:HD11	1.96	0.48
7:6:5:ILE:HB	13:F:63:LYS:HD2	1.96	0.48
8:A:1057:A:N6	8:A:1086:A:H2'	2.28	0.48
8:A:1716:U:H2'	8:A:1717:A:H8	1.79	0.48
8:A:2134:A:H5'	8:A:2156:G:N2	2.29	0.48
9:B:66:A:H5''	9:B:67:G:OP1	2.14	0.48
20:M:21:ALA:HB1	20:M:100:LYS:HD3	1.94	0.48
34:a:205:A:H3'	34:a:206:C:H6	1.78	0.48
34:a:608:A:H2'	34:a:609:A:O4'	2.14	0.48
35:b:119:GLN:HA	35:b:123:GLY:HA3	1.94	0.48
8:A:208:C:H2'	8:A:209:C:C6	2.48	0.48
8:A:411:G:OP2	8:A:2406:A:O2'	2.28	0.48
8:A:576:U:H2'	8:A:577:G:C8	2.49	0.48
8:A:614:A:O2'	8:A:615:U:OP1	2.31	0.48
8:A:709:U:H2'	8:A:710:U:C6	2.49	0.48
8:A:1199:U:H2'	8:A:1200:C:C6	2.48	0.48
8:A:1486:U:H2'	8:A:1487:U:H6	1.78	0.48
29:V:57:TYR:OH	29:V:79:ARG:NH2	2.47	0.48
34:a:411:A:OP1	37:d:25:ARG:NH1	2.46	0.48
38:e:11:GLN:HB3	38:e:116:VAL:HG12	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:m:58:GLU:HA	46:m:58:GLU:OE2	2.14	0.48
8:A:189:G:P	31:X:13:THR:HG21	2.54	0.48
8:A:396:G:H1'	31:X:28:PHE:HB3	1.96	0.48
8:A:577:G:O2'	8:A:1254:A:OP1	2.31	0.48
8:A:918:A:H5''	9:B:97:C:O2'	2.13	0.48
8:A:1009:A:N3	8:A:1153:C:O2'	2.44	0.48
8:A:1412:U:H2'	8:A:1413:A:C8	2.49	0.48
8:A:2899:A:H2'	8:A:2900:A:C8	2.49	0.48
29:V:40:ILE:HD12	29:V:42:LEU:HD21	1.96	0.48
37:d:12:ARG:HH21	37:d:35:GLN:HG3	1.78	0.48
38:e:114:LEU:HD13	38:e:122:VAL:HG11	1.95	0.48
2:1:21:THR:HG21	8:A:2419:U:H4'	1.96	0.48
7:6:23:LYS:HA	7:6:23:LYS:HE2	1.96	0.48
8:A:18:U:OP1	24:Q:29:ARG:NH1	2.34	0.48
8:A:514:A:H2'	8:A:515:A:C8	2.48	0.48
8:A:1061:U:N3	8:A:1068:G:OP1	2.42	0.48
8:A:1486:U:H2'	8:A:1487:U:C6	2.49	0.48
8:A:2114:A:C5	8:A:2115:G:H1'	2.48	0.48
8:A:2314:A:H2'	8:A:2315:G:C8	2.47	0.48
8:A:2533:U:OP1	8:A:2665:A:O2'	2.31	0.48
10:C:146:LYS:HB2	10:C:149:LYS:HB2	1.95	0.48
13:F:114:ARG:HA	13:F:114:ARG:NE	2.29	0.48
34:a:634:C:H2'	34:a:635:A:C8	2.49	0.48
34:a:737:C:H2'	34:a:738:C:H6	1.78	0.48
34:a:999:C:O2	34:a:999:C:H2'	2.14	0.48
34:a:1148:U:H2'	34:a:1149:C:O4'	2.13	0.48
34:a:1421:G:P	34:a:1421:G:O4'	2.71	0.48
7:6:18:CYS:HB2	7:6:40:CYS:SG	2.54	0.48
8:A:413:C:H2'	8:A:414:C:C6	2.48	0.48
8:A:775:G:H4'	8:A:776:G:H5'	1.95	0.48
8:A:1532:A:H2'	8:A:1533:C:C6	2.49	0.48
34:a:224:U:H2'	34:a:225:C:C6	2.48	0.48
34:a:928:G:O2'	34:a:1533:C:OP1	2.31	0.48
35:b:110:ILE:HD12	35:b:111:LYS:N	2.28	0.48
7:6:18:CYS:HB2	7:6:40:CYS:CB	2.44	0.48
8:A:365:U:H2'	8:A:366:C:C6	2.49	0.48
8:A:401:A:H2'	8:A:402:A:C8	2.49	0.48
8:A:2121:G:H2'	8:A:2122:U:H6	1.78	0.48
8:A:2143:C:H3'	8:A:2144:G:C8	2.49	0.48
9:B:29:A:H2'	9:B:30:C:C6	2.48	0.48
13:F:125:GLY:O	13:F:157:THR:OG1	2.24	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:399:G:H2'	34:a:400:C:C6	2.49	0.48
34:a:737:C:H2'	34:a:738:C:C6	2.49	0.48
34:a:1130:A:OP1	42:i:17:ARG:NH2	2.34	0.48
34:a:1238:A:H2	34:a:1241:G:N3	2.11	0.48
36:c:107:LYS:HG3	36:c:110:LEU:HB2	1.96	0.48
40:g:25:PHE:HD2	40:g:100:MET:HG2	1.78	0.48
8:A:414:C:H2'	8:A:415:A:H8	1.79	0.47
8:A:642:U:O2'	8:A:644:A:N7	2.39	0.47
8:A:667:U:H2'	8:A:668:A:O4'	2.14	0.47
8:A:1091:G:H2'	8:A:1092:C:O4'	2.14	0.47
8:A:2128:G:N3	8:A:2128:G:H2'	2.29	0.47
13:F:127:TYR:HE2	13:F:129:MET:HB3	1.78	0.47
13:F:133:GLU:CD	13:F:135:ILE:H	2.22	0.47
15:H:62:LEU:HD22	15:H:66:ASN:ND2	2.29	0.47
15:H:97:ARG:NH2	15:H:112:LYS:HB3	2.28	0.47
17:J:31:GLU:HG3	17:J:142:ILE:HB	1.96	0.47
34:a:1425:U:H2'	34:a:1426:G:H8	1.78	0.47
53:t:50:PHE:O	53:t:53:MET:HG3	2.13	0.47
56:w:5:G:N1	56:w:68:C:N3	2.35	0.47
8:A:242:G:O2'	8:A:243:U:P	2.72	0.47
8:A:357:C:H2'	8:A:358:U:C6	2.49	0.47
8:A:364:C:H2'	8:A:365:U:C6	2.49	0.47
8:A:419:U:H2'	8:A:420:C:C6	2.50	0.47
8:A:484:C:OP1	28:U:47:PRO:HG3	2.13	0.47
8:A:643:A:N1	8:A:2369:A:O2'	2.44	0.47
8:A:1604:C:O2'	8:A:1610:A:N1	2.39	0.47
11:D:156:PHE:CE1	17:J:81:ILE:HD13	2.49	0.47
13:F:7:TYR:HB2	13:F:172:PHE:CZ	2.46	0.47
18:K:110:GLU:HA	18:K:113:MET:HG2	1.96	0.47
28:U:53:GLN:N	28:U:54:PRO:HD3	2.29	0.47
34:a:404:G:O2'	34:a:498:A:N1	2.38	0.47
34:a:407:U:H2'	34:a:408:A:C8	2.49	0.47
34:a:693:G:C8	58:z:-2:A:H1'	2.49	0.47
8:A:197:A:H62	8:A:2430:A:H2'	1.80	0.47
8:A:1641:A:H2'	8:A:1642:G:O4'	2.13	0.47
8:A:1853:A:N1	8:A:2087:G:H1'	2.29	0.47
8:A:2121:G:H2'	8:A:2122:U:C6	2.49	0.47
8:A:2143:C:H3'	8:A:2144:G:H8	1.79	0.47
34:a:28:A:O2'	34:a:296:U:OP1	2.19	0.47
34:a:161:A:H2'	34:a:162:A:O4'	2.14	0.47
34:a:687:A:C2	34:a:704:A:C5	3.03	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:1151:A:O2'	34:a:1152:A:H8	1.95	0.47
34:a:1169:A:H2'	34:a:1170:A:C8	2.49	0.47
36:c:33:ASP:OD2	36:c:37:LYS:NZ	2.46	0.47
52:s:26:ASP:OD1	52:s:27:LYS:N	2.47	0.47
7:6:43:PHE:HD1	7:6:47:LYS:HD2	1.79	0.47
8:A:30:G:H2'	8:A:31:C:C6	2.49	0.47
8:A:48:G:N1	8:A:177:G:OP2	2.43	0.47
8:A:373:U:H2'	8:A:374:A:H8	1.79	0.47
8:A:492:A:H2'	8:A:493:G:O4'	2.14	0.47
8:A:892:A:H2'	8:A:893:C:O4'	2.14	0.47
8:A:1327:A:H2'	8:A:1328:A:O4'	2.14	0.47
8:A:2100:G:C6	8:A:2190:G:C6	3.03	0.47
8:A:2140:G:H1	8:A:2151:U:H3	1.62	0.47
30:W:34:VAL:HG12	30:W:55:LEU:HB2	1.96	0.47
34:a:635:A:H2'	34:a:636:U:C6	2.48	0.47
34:a:766:A:OP2	34:a:812:G:N2	2.47	0.47
34:a:908:A:H2'	34:a:909:A:H8	1.79	0.47
34:a:1060:U:H2'	34:a:1061:G:H8	1.79	0.47
36:c:185:THR:HG22	36:c:198:LYS:HG2	1.95	0.47
39:f:67:PRO:HG2	39:f:70:VAL:HG23	1.96	0.47
40:g:67:ASN:O	40:g:137:ARG:NH2	2.47	0.47
40:g:82:SER:O	40:g:83:THR:OG1	2.32	0.47
49:p:70:ARG:HD2	49:p:70:ARG:HA	1.70	0.47
50:q:24:ILE:HD11	50:q:60:ILE:HD11	1.96	0.47
8:A:1108:U:H3'	8:A:1109:C:C5	2.50	0.47
12:E:118:LEU:HD11	12:E:188:MET:HG3	1.95	0.47
20:M:75:GLU:HB2	20:M:90:GLU:HG3	1.96	0.47
34:a:958:A:OP1	52:s:54:ARG:NH1	2.46	0.47
34:a:1077:G:N2	34:a:1080:A:OP2	2.40	0.47
34:a:1147:C:O2'	42:i:17:ARG:HD2	2.15	0.47
35:b:8:MET:SD	35:b:9:LEU:N	2.87	0.47
44:k:34:THR:HG22	44:k:40:ALA:HA	1.97	0.47
8:A:285:G:C6	8:A:356:G:C6	3.03	0.47
8:A:476:G:H4'	8:A:502:A:N1	2.29	0.47
8:A:582:A:H2'	8:A:583:G:C8	2.50	0.47
8:A:1068:G:O6	8:A:1070:A:N6	2.48	0.47
8:A:1170:C:H41	8:A:1178:C:H42	1.61	0.47
8:A:1866:A:H2'	8:A:1867:G:O4'	2.14	0.47
8:A:2292:U:H2'	8:A:2293:G:C8	2.50	0.47
12:E:10:SER:OG	12:E:11:ALA:N	2.47	0.47
26:S:2:GLU:HG2	26:S:108:SER:HB3	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
32:Y:5:GLU:OE1	32:Y:5:GLU:N	2.40	0.47
34:a:324:G:N1	34:a:327:A:OP2	2.48	0.47
34:a:983:A:H5''	34:a:984:C:OP2	2.13	0.47
34:a:1060:U:C5	36:c:1:GLY:HA3	2.50	0.47
34:a:1242:G:HO2'	34:a:1243:C:H6	1.59	0.47
46:m:85:TYR:O	46:m:89:ARG:HG2	2.15	0.47
8:A:242:G:N2	8:A:255:A:OP2	2.37	0.47
8:A:609:A:H2'	8:A:610:C:O4'	2.15	0.47
8:A:729:G:C6	10:C:206:LYS:HB2	2.49	0.47
8:A:1544:A:H2'	8:A:1545:A:C8	2.49	0.47
8:A:1786:A:H1'	8:A:1938:A:N6	2.29	0.47
8:A:1842:G:H2'	8:A:1843:C:C6	2.49	0.47
8:A:1856:U:H2'	8:A:1857:G:O4'	2.15	0.47
8:A:2108:A:H2	8:A:2182:U:H3	1.61	0.47
8:A:2598:A:H5''	10:C:233:GLY:HA3	1.97	0.47
12:E:7:ASP:OD1	12:E:7:ASP:N	2.45	0.47
12:E:127:GLU:H	12:E:127:GLU:CD	2.22	0.47
13:F:60:SER:HB2	13:F:90:LEU:HD21	1.96	0.47
13:F:78:ILE:HD11	13:F:84:ILE:HD13	1.97	0.47
13:F:114:ARG:HE	13:F:114:ARG:HA	1.79	0.47
14:G:16:VAL:HB	14:G:23:ILE:HD11	1.96	0.47
14:G:55:ASP:OD1	14:G:55:ASP:N	2.43	0.47
21:N:54:LEU:HD21	21:N:65:LEU:HB3	1.96	0.47
34:a:270:A:H2'	34:a:271:C:C6	2.49	0.47
34:a:580:C:H2'	34:a:581:G:O4'	2.14	0.47
34:a:1032:G:H3'	34:a:1033:G:C8	2.49	0.47
35:b:31:PHE:O	35:b:31:PHE:CD1	2.67	0.47
35:b:54:ALA:O	35:b:58:LYS:HG2	2.14	0.47
36:c:110:LEU:HD21	36:c:143:LEU:HB2	1.96	0.47
38:e:84:VAL:HG23	38:e:95:MET:HB2	1.96	0.47
40:g:74:VAL:HB	40:g:85:GLN:HB3	1.97	0.47
41:h:51:GLU:OE2	41:h:51:GLU:N	2.44	0.47
42:i:35:GLU:H	42:i:35:GLU:CD	2.22	0.47
56:w:2:C:H2'	56:w:3:C:C6	2.50	0.47
8:A:155:A:H2'	8:A:156:A:H8	1.78	0.47
8:A:1281:G:H2'	8:A:1282:U:C6	2.49	0.47
8:A:1937:A:H1'	8:A:1939:5MU:H72	1.96	0.47
8:A:2304:G:H22	8:A:2312:U:H3	1.63	0.47
34:a:279:A:H5''	34:a:281:G:O4'	2.14	0.47
34:a:1236:A:H2'	34:a:1237:C:C6	2.50	0.47
44:k:23:HIS:HB3	44:k:30:ILE:HB	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:m:55:LEU:O	46:m:59:VAL:HG13	2.14	0.47
1:0:28:SER:OG	1:0:39:ARG:HD3	2.15	0.47
8:A:580:U:H2'	8:A:581:C:H6	1.80	0.47
8:A:589:U:H2'	8:A:590:A:H8	1.80	0.47
8:A:851:C:H2'	8:A:852:U:H6	1.78	0.47
8:A:1171:G:H22	8:A:1177:G:N2	2.13	0.47
8:A:1181:U:H2'	8:A:1182:G:C8	2.50	0.47
8:A:1416:G:H2'	8:A:1417:C:C6	2.50	0.47
8:A:1857:G:N2	8:A:1884:G:H2'	2.30	0.47
8:A:2078:C:H2'	8:A:2079:U:C6	2.50	0.47
8:A:2460:U:C2	8:A:2461:A:C8	3.03	0.47
17:J:131:ASN:OD1	17:J:131:ASN:N	2.40	0.47
23:P:30:TRP:CE3	23:P:37:LYS:HD3	2.49	0.47
45:l:53:ARG:HE	45:l:61:GLU:HG3	1.80	0.47
55:v:76:A:OP1	57:y:101:FME:HCN	2.15	0.47
8:A:286:U:H2'	8:A:287:G:H8	1.80	0.47
8:A:2081:U:H2'	8:A:2082:A:H8	1.80	0.47
13:F:93:GLU:OE1	13:F:93:GLU:HA	2.15	0.47
34:a:1311:A:N1	34:a:1326:U:H5	2.13	0.47
42:i:114:LYS:HB2	42:i:117:LEU:HD12	1.96	0.47
46:m:68:LEU:O	46:m:71:GLU:HG2	2.15	0.47
52:s:9:PHE:O	52:s:38:THR:HG23	2.15	0.47
8:A:239:C:HO2'	8:A:622:G:HO2'	1.61	0.46
8:A:322:A:OP2	12:E:163:ASN:HB2	2.15	0.46
8:A:704:G:H1'	8:A:727:A:H61	1.79	0.46
8:A:1226:A:OP1	24:Q:15:LYS:NZ	2.33	0.46
8:A:2655:G:H1'	8:A:2656:U:OP2	2.14	0.46
13:F:78:ILE:CD1	13:F:84:ILE:HD13	2.45	0.46
14:G:104:LEU:HD13	14:G:106:LEU:HD11	1.97	0.46
23:P:38:ARG:HD2	34:a:345:C:OP1	2.15	0.46
24:Q:71:ASN:HB3	24:Q:109:VAL:HG11	1.96	0.46
34:a:334:C:H2'	34:a:335:C:H6	1.80	0.46
34:a:671:G:O2'	39:f:79:ARG:NH2	2.48	0.46
34:a:673:A:O3'	39:f:86:ARG:NH1	2.48	0.46
34:a:1513:A:H2'	34:a:1514:G:H8	1.78	0.46
35:b:44:LYS:O	35:b:48:MET:HG3	2.14	0.46
36:c:142:ARG:NH1	36:c:143:LEU:HD21	2.30	0.46
8:A:1387:A:H2'	8:A:1388:G:H8	1.80	0.46
8:A:1496:A:H2'	8:A:1498:C:C5	2.50	0.46
8:A:1710:G:H4'	8:A:2858:C:O2	2.15	0.46
8:A:2039:U:H2'	8:A:2040:G:C8	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2186:G:N3	8:A:2187:U:H1'	2.30	0.46
8:A:2292:U:H2'	8:A:2293:G:H8	1.80	0.46
8:A:2756:U:H1'	8:A:2757:A:H5''	1.97	0.46
9:B:48:U:H2'	9:B:49:C:C6	2.50	0.46
34:a:6:G:O6	38:e:99:SER:N	2.39	0.46
34:a:1302:C:C2	46:m:16:ILE:HG13	2.50	0.46
36:c:41:TYR:OH	36:c:89:VAL:HG11	2.14	0.46
39:f:72:ASP:OD2	39:f:72:ASP:N	2.48	0.46
49:p:40:ASN:HB3	49:p:43:ALA:HB2	1.97	0.46
55:v:64:G:H2'	55:v:65:C:C6	2.51	0.46
8:A:641:U:O2'	8:A:2350:C:OP1	2.32	0.46
8:A:1059:G:H1	8:A:1080:A:H1'	1.80	0.46
8:A:1282:U:H2'	8:A:1283:G:O4'	2.15	0.46
8:A:1649:G:O2'	21:N:106:ASP:OD2	2.21	0.46
8:A:2107:G:H3'	8:A:2108:A:C8	2.49	0.46
8:A:2198:A:C4	15:H:29:PHE:HB2	2.51	0.46
8:A:2297:A:H61	8:A:2319:G:H1'	1.81	0.46
13:F:59:ILE:HD13	13:F:151:LEU:HD11	1.97	0.46
18:K:99:ILE:HD13	18:K:115:ILE:HG23	1.98	0.46
34:a:76:G:O6	34:a:93:U:C2	2.68	0.46
34:a:512:U:H2'	34:a:513:C:H6	1.79	0.46
34:a:867:G:O2'	34:a:873:A:N1	2.40	0.46
36:c:146:LYS:H	36:c:146:LYS:HE2	1.80	0.46
45:l:74:GLN:OE1	45:l:74:GLN:HA	2.16	0.46
6:5:3:LEU:HA	8:A:1044:C:OP1	2.15	0.46
8:A:39:G:H2'	8:A:40:U:C6	2.51	0.46
8:A:102:U:C4	32:Y:2:LYS:HE3	2.49	0.46
8:A:438:G:H2'	8:A:439:A:C8	2.51	0.46
8:A:1922:G:P	8:A:1922:G:O4'	2.74	0.46
8:A:2515:C:H2'	8:A:2516:A:H8	1.79	0.46
8:A:2576:G:O2'	8:A:2579:C:OP2	2.24	0.46
14:G:115:GLN:OE1	14:G:115:GLN:HA	2.15	0.46
15:H:42:LYS:C	15:H:42:LYS:HD3	2.40	0.46
15:H:50:ARG:HH22	15:H:51:ARG:NE	2.14	0.46
19:L:76:GLU:C	19:L:77:ILE:HD13	2.40	0.46
33:Z:5:LYS:HB2	33:Z:57:GLU:HB2	1.97	0.46
34:a:176:C:H2'	34:a:177:G:N3	2.30	0.46
34:a:718:A:C2	51:r:37:LYS:HG2	2.51	0.46
34:a:1027:C:O2	34:a:1034:G:C6	2.69	0.46
34:a:1163:A:H2'	34:a:1164:G:C8	2.51	0.46
34:a:1251:A:H2'	34:a:1252:A:C8	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:j:91:ASP:N	43:j:91:ASP:OD1	2.48	0.46
50:q:16:MET:HE3	50:q:16:MET:HB2	1.78	0.46
8:A:514:A:N3	8:A:581:C:O2'	2.44	0.46
8:A:1357:C:H2'	8:A:1358:G:O4'	2.15	0.46
8:A:1727:C:H2'	8:A:1728:C:C6	2.50	0.46
8:A:2065:C:H2'	8:A:2066:C:H6	1.81	0.46
8:A:2228:G:H2'	8:A:2229:U:C6	2.50	0.46
8:A:2627:G:N2	8:A:2777:G:OP2	2.48	0.46
9:B:2:G:H2'	9:B:3:C:H6	1.80	0.46
15:H:72:ILE:HD12	15:H:72:ILE:H	1.81	0.46
20:M:59:ARG:HH22	56:w:57:G:P	2.38	0.46
34:a:214:C:H2'	34:a:215:C:O2	2.15	0.46
34:a:1082:A:OP1	38:e:22:LYS:NZ	2.46	0.46
34:a:1218:C:H2'	34:a:1219:A:H8	1.75	0.46
45:l:87:LYS:HG2	45:l:87:LYS:O	2.15	0.46
47:n:64:CYS:HB2	47:n:80:SER:HB3	1.98	0.46
7:6:57:VAL:HG22	52:s:66:VAL:HG21	1.98	0.46
7:6:62:LYS:HZ2	7:6:62:LYS:C	2.23	0.46
8:A:65:U:H2'	8:A:66:C:H6	1.80	0.46
8:A:146:A:H2'	8:A:147:C:C6	2.51	0.46
8:A:161:A:OP2	8:A:162:U:O2'	2.27	0.46
8:A:255:A:H2'	8:A:256:A:O4'	2.15	0.46
8:A:353:C:H2'	8:A:354:A:C8	2.51	0.46
8:A:538:A:O2'	17:J:9:GLU:OE2	2.28	0.46
8:A:579:G:O2'	8:A:2019:A:OP1	2.32	0.46
8:A:1411:U:H2'	8:A:1412:U:C6	2.51	0.46
8:A:1683:U:H2'	8:A:1684:G:C8	2.50	0.46
8:A:2065:C:H2'	8:A:2066:C:C6	2.51	0.46
8:A:2690:U:OP1	21:N:14:SER:OG	2.31	0.46
13:F:64:PRO:HB2	13:F:86:CYS:SG	2.55	0.46
14:G:148:ARG:HA	14:G:161:VAL:HB	1.98	0.46
34:a:1313:U:O2'	34:a:1314:C:H5'	2.15	0.46
48:o:47:LYS:HA	48:o:47:LYS:HD3	1.68	0.46
50:q:44:HIS:HB3	50:q:70:LYS:HG2	1.97	0.46
7:6:39:LYS:C	7:6:41:HIS:H	2.24	0.46
8:A:4:U:H2'	8:A:5:A:C8	2.51	0.46
8:A:689:A:H2'	8:A:690:G:C8	2.51	0.46
8:A:703:U:H2'	8:A:704:G:O4'	2.15	0.46
8:A:1563:U:H2'	8:A:1564:C:C6	2.51	0.46
8:A:1932:A:H2'	8:A:1933:G:O4'	2.16	0.46
8:A:2461:A:H2'	8:A:2462:C:C6	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2896:C:H2'	8:A:2897:U:C6	2.50	0.46
34:a:855:U:H2'	34:a:856:C:C6	2.50	0.46
34:a:971:G:OP2	34:a:1231:G:N2	2.43	0.46
35:b:196:ASP:OD1	35:b:196:ASP:N	2.49	0.46
37:d:43:ARG:HH11	37:d:43:ARG:HB2	1.81	0.46
37:d:87:GLU:HG3	37:d:187:ARG:HB2	1.98	0.46
39:f:17:GLN:O	39:f:21:MET:HG3	2.16	0.46
43:j:32:THR:O	43:j:82:LYS:NZ	2.33	0.46
45:l:9:LYS:HB3	45:l:9:LYS:HE3	1.71	0.46
45:l:80:LEU:HD13	45:l:101:LEU:HD22	1.96	0.46
52:s:38:THR:HG22	52:s:69:LYS:HE2	1.97	0.46
56:w:1:G:H2'	56:w:2:C:C6	2.50	0.46
8:A:475:C:N3	8:A:479:A:N7	2.64	0.46
8:A:590:A:H2'	8:A:591:U:C6	2.51	0.46
8:A:671:C:H2'	8:A:672:C:H6	1.81	0.46
8:A:685:A:O2'	8:A:773:U:O4	2.29	0.46
8:A:766:U:H2'	8:A:767:U:C6	2.51	0.46
8:A:1831:G:H2'	8:A:1832:C:C6	2.51	0.46
8:A:2313:C:H2'	8:A:2314:A:H8	1.81	0.46
8:A:2329:U:H2'	8:A:2330:G:H8	1.79	0.46
8:A:2689:U:OP1	8:A:2719:G:N1	2.36	0.46
8:A:2784:U:H2'	8:A:2785:C:C6	2.51	0.46
34:a:113:G:H2'	34:a:114:U:C6	2.51	0.46
34:a:1171:A:H2'	34:a:1172:C:C6	2.51	0.46
54:u:12:ASP:O	54:u:16:ARG:HG2	2.16	0.46
56:w:40:C:H2'	56:w:41:C:H6	1.81	0.46
2:1:7:LYS:HA	2:1:23:THR:HA	1.97	0.46
8:A:95:A:O2'	32:Y:41:HIS:ND1	2.30	0.46
8:A:594:U:H2'	8:A:595:C:H6	1.79	0.46
8:A:2205:A:H2'	8:A:2206:C:C6	2.51	0.46
11:D:13:ARG:NH1	11:D:21:SER:OG	2.46	0.46
15:H:71:LYS:HD3	15:H:71:LYS:HA	1.66	0.46
24:Q:57:ARG:HA	24:Q:60:TRP:CE3	2.51	0.46
34:a:5:U:H4'	34:a:6:G:C8	2.51	0.46
34:a:276:G:OP1	50:q:13:SER:OG	2.21	0.46
34:a:343:U:O2'	34:a:346:G:O6	2.34	0.46
34:a:745:G:H2'	34:a:746:A:H8	1.79	0.46
34:a:1318:A:H2'	34:a:1319:A:H5''	1.98	0.46
41:h:86:LYS:HB2	41:h:124:ILE:HD11	1.97	0.46
2:1:24:LYS:NZ	2:1:31:GLU:O	2.44	0.46
5:4:18:LYS:HG3	5:4:23:ILE:HG13	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:948:C:H2'	8:A:949:G:C8	2.51	0.46
8:A:1370:C:H2'	8:A:1371:G:O4'	2.16	0.46
8:A:1504:A:H2'	8:A:1505:A:C8	2.51	0.46
8:A:2097:A:H2'	8:A:2098:U:H6	1.79	0.46
8:A:2114:A:H3'	8:A:2115:G:O4'	2.15	0.46
8:A:2404:U:H2'	8:A:2405:G:O4'	2.15	0.46
8:A:2514:U:H2'	8:A:2515:C:H6	1.78	0.46
20:M:47:GLU:HA	20:M:47:GLU:OE2	2.15	0.46
27:T:69:ARG:HG2	27:T:74:ILE:HD12	1.98	0.46
29:V:51:GLN:HG2	29:V:86:LEU:HD11	1.98	0.46
34:a:522:C:H41	45:l:49:ARG:NH2	2.14	0.46
34:a:953:G:H5'	34:a:954:G:OP2	2.16	0.46
34:a:1163:A:H2'	34:a:1164:G:H8	1.81	0.46
35:b:153:MET:HG2	35:b:155:GLY:O	2.16	0.46
8:A:299:A:N3	8:A:319:G:O2'	2.43	0.45
8:A:934:U:H2'	8:A:935:C:C6	2.50	0.45
8:A:1523:U:H5''	8:A:1524:G:C8	2.51	0.45
8:A:1842:G:H2'	8:A:1843:C:H6	1.80	0.45
8:A:1993:U:H4'	11:D:133:THR:OG1	2.15	0.45
8:A:2700:A:H2'	8:A:2701:U:H6	1.81	0.45
22:O:76:LYS:O	22:O:80:GLU:HG2	2.16	0.45
34:a:74:A:H2'	34:a:75:G:H8	1.81	0.45
34:a:126:G:OP1	34:a:605:U:O2'	2.22	0.45
36:c:32:LEU:HD11	47:n:93:ILE:HG12	1.98	0.45
40:g:4:ARG:HH22	40:g:6:ILE:HA	1.80	0.45
41:h:49:LYS:HG3	41:h:51:GLU:OE2	2.15	0.45
54:u:5:VAL:HG21	54:u:18:PHE:HA	1.97	0.45
55:v:50:U:H2'	55:v:51:C:H6	1.79	0.45
55:v:65:C:H2'	55:v:66:C:H6	1.80	0.45
8:A:671:C:H2'	8:A:672:C:C6	2.50	0.45
8:A:1289:C:H2'	8:A:1290:C:H6	1.81	0.45
9:B:106:G:H2'	9:B:107:G:O4'	2.16	0.45
11:D:110:THR:HB	11:D:202:ILE:HB	1.97	0.45
15:H:78:VAL:HG13	15:H:144:VAL:HG23	1.97	0.45
29:V:10:LYS:H	29:V:10:LYS:HE2	1.81	0.45
30:W:13:GLU:O	30:W:15:LYS:NZ	2.49	0.45
34:a:201:G:H2'	34:a:202:G:C8	2.51	0.45
34:a:332:G:O3'	53:t:2:ASN:ND2	2.35	0.45
34:a:407:U:H2'	34:a:408:A:H8	1.82	0.45
34:a:651:C:H2'	34:a:652:U:C6	2.51	0.45
34:a:779:C:H2'	34:a:780:A:O4'	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:904:U:H2'	34:a:905:U:C6	2.51	0.45
34:a:1242:G:H2'	34:a:1242:G:OP2	2.16	0.45
34:a:1329:A:H5''	46:m:25:GLY:H	1.81	0.45
37:d:115:GLN:HG2	37:d:153:ARG:HH12	1.81	0.45
49:p:71:VAL:O	49:p:75:ILE:HD12	2.16	0.45
51:r:71:ASP:HB2	54:u:4:LYS:HE2	1.98	0.45
3:2:12:ARG:NH1	8:A:686:U:O4	2.45	0.45
8:A:181:A:H1'	8:A:435:C:H5'	1.97	0.45
8:A:184:C:H2'	8:A:185:G:C8	2.52	0.45
8:A:638:G:H2'	8:A:639:U:C6	2.51	0.45
8:A:704:G:H1'	8:A:727:A:N6	2.30	0.45
8:A:1182:G:H2'	8:A:1183:U:O4'	2.15	0.45
8:A:2731:G:H2'	8:A:2732:G:C8	2.52	0.45
8:A:2819:G:H2'	8:A:2821:A:N7	2.31	0.45
12:E:15:SER:N	12:E:197:GLU:OE2	2.49	0.45
13:F:73:VAL:HB	13:F:78:ILE:HG22	1.97	0.45
18:K:1:MET:HG2	18:K:32:TYR:CD2	2.52	0.45
32:Y:6:LEU:HA	32:Y:9:LYS:HD2	1.98	0.45
34:a:619:U:N3	37:d:130:ASN:OD1	2.46	0.45
34:a:1135:U:H2'	34:a:1137:C:H1'	1.99	0.45
43:j:30:LYS:HA	43:j:34:ALA:HA	1.99	0.45
51:r:24:ASP:OD2	51:r:27:THR:HG23	2.16	0.45
56:w:63:G:H2'	56:w:64:A:H8	1.82	0.45
8:A:832:U:H2'	8:A:833:A:H8	1.81	0.45
8:A:1102:C:H3'	8:A:1103:A:C8	2.39	0.45
8:A:1278:C:H2'	8:A:1279:G:H8	1.81	0.45
8:A:1536:C:H4'	8:A:1537:G:C4	2.51	0.45
8:A:1923:U:H5'	8:A:1924:C:OP2	2.16	0.45
8:A:2096:C:H2'	8:A:2097:A:H8	1.81	0.45
8:A:2461:A:H1'	8:A:2492:U:C2	2.52	0.45
8:A:2684:U:O4'	18:K:70:ARG:NH1	2.49	0.45
20:M:117:PHE:HD2	20:M:130:PHE:CD2	2.35	0.45
27:T:30:ILE:HG13	27:T:85:VAL:HB	1.97	0.45
32:Y:5:GLU:H	32:Y:5:GLU:CD	2.22	0.45
34:a:575:G:O2'	34:a:821:G:H5'	2.17	0.45
34:a:635:A:H2'	34:a:636:U:H6	1.82	0.45
34:a:780:A:H5''	44:k:124:LYS:HD3	1.99	0.45
34:a:1486:G:H2'	34:a:1487:G:O4'	2.16	0.45
35:b:224:ARG:HG2	35:b:224:ARG:HH11	1.81	0.45
8:A:128:C:H2'	8:A:129:C:C6	2.52	0.45
8:A:131:A:H2'	8:A:132:G:C8	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:679:C:H2'	8:A:680:C:C6	2.52	0.45
13:F:107:VAL:N	13:F:108:PRO:HD2	2.31	0.45
18:K:97:THR:O	18:K:98:ARG:HD2	2.17	0.45
32:Y:19:LEU:HD23	32:Y:19:LEU:HA	1.83	0.45
34:a:9:G:OP2	38:e:125:LYS:NZ	2.37	0.45
34:a:34:C:H2'	34:a:35:G:C8	2.52	0.45
34:a:1182:G:H4'	34:a:1184:G:H5''	1.97	0.45
34:a:1361:G:O2'	34:a:1362:A:OP1	2.31	0.45
35:b:69:VAL:HG12	35:b:168:GLU:HG2	1.99	0.45
40:g:113:LYS:HD3	40:g:113:LYS:HA	1.66	0.45
41:h:101:ALA:HB3	41:h:112:ASP:HB3	1.98	0.45
42:i:48:ARG:O	42:i:52:GLU:HG2	2.16	0.45
48:o:1:SER:HB2	48:o:34:GLN:NE2	2.30	0.45
8:A:184:C:H2'	8:A:185:G:H8	1.81	0.45
8:A:623:C:H2'	8:A:624:C:C6	2.52	0.45
8:A:739:A:N3	8:A:740:C:N4	2.57	0.45
8:A:742:A:H2'	8:A:743:A:H8	1.80	0.45
8:A:995:C:OP2	24:Q:53:LYS:NZ	2.46	0.45
8:A:2836:U:H2'	8:A:2837:A:C8	2.52	0.45
10:C:23:LEU:HD13	10:C:82:TYR:HB2	1.99	0.45
11:D:121:THR:HB	11:D:127:PHE:CD2	2.52	0.45
15:H:17:ASP:OD1	15:H:17:ASP:N	2.50	0.45
15:H:93:SER:HB2	15:H:123:ARG:HD3	1.99	0.45
20:M:54:THR:HG22	20:M:59:ARG:HG2	1.98	0.45
34:a:107:G:O6	53:t:9:ARG:HD3	2.17	0.45
34:a:246:A:C2	34:a:282:A:C5	3.03	0.45
38:e:12:GLU:HG2	38:e:63:MET:SD	2.57	0.45
40:g:109:LYS:HB2	40:g:109:LYS:HE2	1.74	0.45
44:k:125:LYS:HB2	44:k:125:LYS:HE2	1.59	0.45
8:A:52:A:H2'	8:A:53:A:C8	2.52	0.45
8:A:242:G:H1'	8:A:243:U:H5	1.82	0.45
8:A:1564:C:H2'	8:A:1565:C:C6	2.52	0.45
8:A:2114:A:H2'	8:A:2167:U:H4'	1.99	0.45
8:A:2564:A:OP1	8:A:2648:G:O2'	2.21	0.45
8:A:2718:G:H5'	23:P:97:TYR:HD2	1.82	0.45
9:B:44:G:H4'	9:B:45:A:OP2	2.16	0.45
34:a:74:A:H2'	34:a:75:G:C8	2.52	0.45
34:a:676:A:H2'	34:a:677:U:H6	1.81	0.45
34:a:1181:G:H1'	34:a:1182:G:N9	2.32	0.45
38:e:44:ARG:HB3	38:e:70:MET:HE1	1.99	0.45
8:A:194:G:H2'	8:A:195:A:O4'	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:302:C:H2'	8:A:303:G:H8	1.81	0.45
8:A:1057:A:N1	8:A:1082:U:N3	2.65	0.45
8:A:1064:C:N4	8:A:1068:G:O2'	2.46	0.45
8:A:1443:U:H2'	8:A:1444:G:C8	2.52	0.45
8:A:1710:G:H2'	8:A:1711:A:H8	1.81	0.45
8:A:1857:G:H22	8:A:1884:G:H2'	1.82	0.45
8:A:2298:A:OP1	13:F:70:ARG:NH1	2.46	0.45
8:A:2590:A:H2'	8:A:2591:C:H6	1.81	0.45
13:F:61:GLY:C	13:F:94:ARG:HH22	2.24	0.45
27:T:53:VAL:HG12	27:T:91:GLN:CD	2.42	0.45
34:a:362:G:N1	34:a:365:U:OP2	2.49	0.45
34:a:513:C:H2'	34:a:514:C:C6	2.52	0.45
34:a:523:A:H61	45:l:88:ASP:CG	2.25	0.45
50:q:49:ASN:O	50:q:51:GLU:N	2.50	0.45
55:v:15:G:H22	55:v:48:C:H42	1.63	0.45
8:A:128:C:H2'	8:A:129:C:H6	1.81	0.45
8:A:282:A:H2'	8:A:283:G:H8	1.82	0.45
8:A:1385:A:O2'	8:A:1396:U:O2	2.35	0.45
8:A:1438:U:H2'	8:A:1439:A:H8	1.81	0.45
8:A:2552:OMU:H2'	8:A:2554:U:OP2	2.16	0.45
28:U:39:ASN:HB3	28:U:62:ALA:HB3	1.98	0.45
32:Y:12:GLU:H	32:Y:12:GLU:CD	2.23	0.45
34:a:81:A:H61	34:a:86:G:N2	2.15	0.45
34:a:223:A:H2'	34:a:224:U:C6	2.52	0.45
34:a:1107:C:OP1	36:c:171:ARG:HG3	2.17	0.45
34:a:1297:G:H1'	34:a:1298:U:OP2	2.16	0.45
34:a:1352:C:H2'	34:a:1353:G:C8	2.52	0.45
35:b:120:SER:HA	35:b:125:PHE:CG	2.52	0.45
55:v:10:G:N2	55:v:26:G:H1'	2.31	0.45
8:A:722:A:H2'	8:A:723:C:O4'	2.17	0.45
8:A:1278:C:H2'	8:A:1279:G:C8	2.52	0.45
8:A:1680:U:H2'	8:A:1681:G:O4'	2.17	0.45
13:F:122:ASP:OD2	13:F:126:ASN:HB2	2.16	0.45
15:H:4:ILE:HD12	15:H:17:ASP:O	2.16	0.45
20:M:62:LYS:HD3	20:M:64:TRP:CZ2	2.52	0.45
23:P:12:MET:HG2	23:P:76:HIS:CE1	2.52	0.45
28:U:36:GLU:HA	28:U:36:GLU:OE2	2.17	0.45
34:a:131:A:H2'	34:a:132:C:C6	2.52	0.45
34:a:210:C:O2'	34:a:211:G:H5''	2.17	0.45
34:a:1175:G:H2'	34:a:1176:A:C8	2.53	0.45
34:a:1191:A:H5''	36:c:3:LYS:HE3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:1355:G:O2'	34:a:1356:G:OP2	2.31	0.45
35:b:8:MET:CE	35:b:9:LEU:H	2.27	0.45
35:b:109:SER:OG	35:b:143:LEU:HD11	2.17	0.45
45:l:84:GLY:O	45:l:95:HIS:ND1	2.42	0.45
48:o:23:SER:OG	48:o:25:GLU:OE1	2.35	0.45
52:s:14:LEU:O	52:s:18:VAL:HG13	2.17	0.45
56:w:1:G:H2'	56:w:2:C:H6	1.80	0.45
8:A:1251:C:OP2	24:Q:5:ARG:HD2	2.17	0.44
8:A:2591:C:H2'	8:A:2592:G:H8	1.80	0.44
8:A:2654:A:N1	8:A:2665:A:H5''	2.33	0.44
8:A:2783:U:H2'	8:A:2784:U:C6	2.52	0.44
8:A:2859:G:H2'	8:A:2860:A:C8	2.53	0.44
8:A:2898:U:H2'	8:A:2899:A:H8	1.82	0.44
9:B:104:A:H2'	9:B:105:G:O4'	2.17	0.44
11:D:74:GLU:CD	11:D:74:GLU:H	2.24	0.44
22:O:39:VAL:HB	22:O:49:VAL:HG22	1.99	0.44
25:R:60:LYS:HE2	25:R:60:LYS:HB2	1.68	0.44
34:a:222:C:H2'	34:a:223:A:H8	1.82	0.44
34:a:299:G:H2'	34:a:300:A:C8	2.53	0.44
34:a:551:U:H2'	34:a:552:U:C6	2.52	0.44
34:a:634:C:H2'	34:a:635:A:H8	1.81	0.44
34:a:1492:A:OP1	45:l:43:LYS:N	2.50	0.44
46:m:36:ALA:HB2	46:m:58:GLU:HG3	1.97	0.44
53:t:38:ILE:HD13	53:t:81:GLN:HB3	1.98	0.44
8:A:569:U:H2'	8:A:570:G:O4'	2.17	0.44
8:A:697:G:H2'	8:A:698:C:C6	2.53	0.44
8:A:2038:G:H2'	8:A:2039:U:O4'	2.17	0.44
8:A:2106:U:H2'	8:A:2107:G:H8	1.82	0.44
8:A:2262:U:H2'	8:A:2263:C:H6	1.81	0.44
8:A:2531:A:OP1	14:G:174:LYS:HE3	2.17	0.44
14:G:163:TYR:HB2	14:G:166:GLU:HB2	1.99	0.44
15:H:65:ALA:O	15:H:68:ARG:NH2	2.51	0.44
15:H:125:THR:HA	15:H:146:VAL:HG13	1.98	0.44
17:J:90:GLU:HA	17:J:90:GLU:OE2	2.18	0.44
23:P:6:GLN:O	23:P:10:GLU:HG2	2.17	0.44
34:a:81:A:H3'	34:a:82:G:C8	2.52	0.44
34:a:672:U:H2'	34:a:673:A:C8	2.52	0.44
34:a:864:A:H2'	34:a:865:A:C8	2.53	0.44
37:d:78:ALA:HB2	37:d:92:LEU:HD22	1.99	0.44
40:g:38:ALA:O	40:g:42:VAL:HG13	2.17	0.44
43:j:88:MET:HE3	43:j:89:ARG:N	2.05	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:n:86:GLU:HG3	47:n:90:ARG:NH2	2.32	0.44
58:z:0:U:H2'	58:z:1:A:C8	2.52	0.44
8:A:248:G:O5'	8:A:249:C:H5''	2.17	0.44
8:A:1199:U:H1'	24:Q:3:VAL:HG22	1.98	0.44
8:A:1289:C:H2'	8:A:1290:C:C6	2.52	0.44
8:A:1592:C:H2'	8:A:1593:A:H8	1.82	0.44
8:A:1597:A:H5''	8:A:1598:A:H5'	1.98	0.44
8:A:2103:C:H5'	8:A:2104:C:OP2	2.17	0.44
8:A:2723:C:H2'	8:A:2724:U:O4'	2.16	0.44
13:F:129:MET:HE3	13:F:129:MET:HB2	1.81	0.44
14:G:1:SER:O	14:G:5:LYS:HG2	2.17	0.44
34:a:328:C:H4'	34:a:329:A:H5''	1.98	0.44
34:a:1313:U:H5	34:a:1324:A:N1	2.16	0.44
34:a:1456:A:H2'	34:a:1457:G:O4'	2.17	0.44
35:b:114:LYS:O	35:b:118:THR:HG23	2.17	0.44
7:6:42:PRO:CB	7:6:47:LYS:HB2	2.47	0.44
8:A:613:A:H2'	8:A:614:A:O4'	2.18	0.44
8:A:1156:A:C8	24:Q:50:ARG:HG2	2.53	0.44
8:A:1179:G:H2'	8:A:1179:G:N3	2.32	0.44
8:A:1602:U:OP2	27:T:64:LYS:NZ	2.38	0.44
8:A:2229:U:H2'	8:A:2230:G:C8	2.51	0.44
8:A:2266:A:H4'	8:A:2267:A:N3	2.33	0.44
8:A:2646:C:H2'	8:A:2647:U:O4'	2.18	0.44
8:A:2677:G:H2'	8:A:2678:C:C6	2.53	0.44
26:S:20:VAL:HG11	26:S:44:ALA:HA	1.99	0.44
31:X:6:VAL:HG21	31:X:58:ILE:HD11	1.98	0.44
4:3:50:SER:OG	4:3:53:ASP:OD2	2.35	0.44
8:A:532:A:H4'	8:A:533:G:C8	2.52	0.44
8:A:640:C:H2'	8:A:641:U:C6	2.52	0.44
8:A:890:C:N4	8:A:891:G:O6	2.50	0.44
8:A:1341:G:OP2	8:A:1394:U:O2'	2.27	0.44
8:A:1592:C:H2'	8:A:1593:A:C8	2.52	0.44
8:A:2137:U:H2'	8:A:2138:G:C8	2.53	0.44
8:A:2287:A:HO2'	8:A:2288:A:P	2.39	0.44
8:A:2455:G:H2'	8:A:2456:C:C6	2.53	0.44
8:A:2572:A:N7	11:D:150:GLN:HB2	2.32	0.44
10:C:18:VAL:HG13	10:C:198:GLU:HG2	2.00	0.44
23:P:99:LEU:HD11	23:P:109:ILE:HD11	1.99	0.44
34:a:333:U:H2'	34:a:334:C:H6	1.82	0.44
34:a:834:U:H2'	34:a:835:U:C6	2.53	0.44
34:a:1291:U:H2'	34:a:1292:G:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:c:77:GLY:HA3	36:c:82:ASP:OD2	2.18	0.44
37:d:104:MET:HE1	37:d:142:VAL:HB	1.99	0.44
56:w:41:C:H2'	56:w:42:C:H6	1.83	0.44
8:A:857:G:H2'	8:A:858:G:O4'	2.17	0.44
8:A:1263:U:H2'	8:A:1264:A:C8	2.53	0.44
8:A:1709:U:H2'	8:A:1710:G:C8	2.52	0.44
8:A:1936:A:H2	8:A:1943:U:N3	2.03	0.44
8:A:2193:G:H2'	8:A:2194:U:C6	2.52	0.44
8:A:2271:G:OP1	30:W:14:ALA:HB1	2.17	0.44
8:A:2298:A:H2'	8:A:2299:U:O4'	2.16	0.44
18:K:2:ILE:HD12	18:K:6:THR:HG21	2.00	0.44
34:a:182:A:C4	34:a:184:G:C8	3.06	0.44
34:a:338:A:H2'	34:a:339:C:C6	2.52	0.44
34:a:1135:U:H4'	34:a:1136:C:C5	2.52	0.44
35:b:19:THR:HA	35:b:38:HIS:CD2	2.53	0.44
36:c:4:VAL:HG21	36:c:9:ILE:HD13	1.99	0.44
36:c:82:ASP:HA	36:c:85:LYS:HG2	1.98	0.44
42:i:17:ARG:HG3	42:i:65:THR:HG22	1.99	0.44
42:i:105:ARG:NH1	42:i:106:ASP:O	2.51	0.44
1:0:53:VAL:HG23	1:0:54:ILE:HG12	2.00	0.44
8:A:12:U:O2	8:A:2626:C:H4'	2.18	0.44
8:A:1485:U:H2'	8:A:1486:U:H6	1.81	0.44
8:A:2364:C:H2'	8:A:2365:G:O4'	2.18	0.44
8:A:2543:G:H2'	8:A:2544:G:C8	2.53	0.44
10:C:141:HIS:ND1	10:C:192:GLY:O	2.39	0.44
11:D:129:THR:HG23	11:D:140:HIS:O	2.18	0.44
23:P:38:ARG:NH1	34:a:346:G:OP1	2.39	0.44
34:a:838:G:H2'	34:a:839:C:C6	2.52	0.44
34:a:923:A:H2'	34:a:924:C:C6	2.52	0.44
34:a:971:G:H1'	34:a:1365:G:O2'	2.18	0.44
35:b:55:GLU:O	35:b:59:ILE:HG12	2.17	0.44
35:b:134:LEU:HA	35:b:137:THR:HB	2.00	0.44
37:d:36:ALA:HB3	37:d:41:GLY:HA2	2.00	0.44
44:k:30:ILE:HG23	44:k:45:THR:HG22	1.99	0.44
46:m:48:SER:O	46:m:52:ILE:HG13	2.18	0.44
56:w:51:C:H2'	56:w:52:G:H8	1.83	0.44
8:A:132:G:H2'	8:A:133:U:C6	2.53	0.44
8:A:1989:G:H2'	8:A:1990:C:O4'	2.18	0.44
8:A:2142:A:H61	8:A:2150:C:H1'	1.83	0.44
8:A:2581:G:OP2	8:A:2581:G:N2	2.48	0.44
11:D:184:ARG:HH21	23:P:6:GLN:HB3	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
13:F:144:LYS:HD3	13:F:144:LYS:N	2.33	0.44
18:K:23:LYS:HB3	18:K:40:LYS:HB3	2.00	0.44
19:L:23:ILE:HG12	25:R:82:HIS:CD2	2.53	0.44
34:a:77:A:O2'	34:a:78:A:OP1	2.29	0.44
34:a:202:G:H1	34:a:215:C:H5	1.63	0.44
34:a:351:G:OP1	53:t:3:ILE:HD11	2.18	0.44
34:a:723:U:H2'	34:a:855:U:H4'	2.00	0.44
34:a:1253:G:O2'	34:a:1356:G:H5''	2.17	0.44
34:a:1376:U:H2'	34:a:1377:A:C8	2.53	0.44
34:a:1441:A:N3	34:a:1441:A:H2'	2.32	0.44
35:b:96:LEU:HB2	35:b:99:MET:HG3	2.00	0.44
37:d:171:GLU:HB2	37:d:182:LYS:HD3	2.00	0.44
40:g:42:VAL:O	40:g:46:LEU:HB2	2.18	0.44
42:i:54:VAL:CG1	42:i:93:LEU:HD22	2.46	0.44
52:s:16:LYS:HA	52:s:19:GLU:HB2	1.99	0.44
4:3:53:ASP:HB3	19:L:57:LEU:HD22	2.00	0.44
8:A:391:A:H1'	8:A:411:G:O4'	2.18	0.44
8:A:455:C:N3	8:A:472:A:H2'	2.33	0.44
8:A:577:G:H2'	8:A:578:G:C8	2.53	0.44
8:A:598:U:H2'	8:A:599:A:C8	2.53	0.44
8:A:933:A:H5'	8:A:934:U:OP2	2.18	0.44
8:A:1197:G:H2'	8:A:1198:U:C6	2.53	0.44
8:A:1429:G:H2'	8:A:1430:G:C8	2.52	0.44
8:A:1443:U:H2'	8:A:1444:G:H8	1.82	0.44
8:A:1594:U:H2'	8:A:1595:C:H6	1.83	0.44
8:A:1858:A:C2	8:A:1885:A:H1'	2.53	0.44
8:A:2109:U:H2'	8:A:2110:G:C4	2.52	0.44
8:A:2650:U:H2'	8:A:2651:C:H6	1.82	0.44
8:A:2680:U:O2'	8:A:2681:C:H5'	2.18	0.44
15:H:66:ASN:HB3	15:H:135:HIS:HB2	1.99	0.44
34:a:321:A:H2'	34:a:322:C:C6	2.53	0.44
34:a:958:A:OP1	52:s:54:ARG:NH2	2.50	0.44
34:a:1095:U:H2'	34:a:1096:C:C6	2.52	0.44
35:b:117:GLU:O	35:b:121:GLN:HG2	2.18	0.44
44:k:35:ASP:C	44:k:35:ASP:OD1	2.60	0.44
5:4:1:MET:HE3	8:A:2742:G:H5''	2.01	0.43
8:A:244:A:H2'	8:A:245:G:O4'	2.18	0.43
8:A:368:A:H2'	8:A:369:U:O4'	2.17	0.43
8:A:538:A:H2'	8:A:539:G:O4'	2.17	0.43
8:A:807:U:O2'	8:A:2060:A:N1	2.45	0.43
8:A:1484:U:H2'	8:A:1485:U:H6	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:1715:G:HO2'	8:A:1716:U:P	2.39	0.43
8:A:2011:U:H2'	8:A:2012:G:O4'	2.19	0.43
9:B:5:U:OP1	9:B:61:G:O2'	2.31	0.43
14:G:1:SER:OG	14:G:2:ARG:N	2.49	0.43
14:G:71:LEU:HA	14:G:74:MET:HB2	2.00	0.43
18:K:17:ARG:HB2	18:K:45:GLU:HG2	2.00	0.43
23:P:50:ARG:CZ	23:P:52:ARG:HG3	2.47	0.43
34:a:763:G:H2'	34:a:764:C:C6	2.53	0.43
34:a:865:A:H2'	34:a:866:C:C6	2.52	0.43
34:a:1323:G:O2'	34:a:1324:A:C8	2.60	0.43
34:a:1399:C:O2	34:a:1502:A:N6	2.51	0.43
36:c:11:LEU:HD23	36:c:11:LEU:HA	1.89	0.43
37:d:14:GLU:OE2	37:d:55:ARG:NH1	2.51	0.43
40:g:4:ARG:NH2	40:g:6:ILE:HA	2.32	0.43
49:p:67:ILE:HD13	49:p:67:ILE:HA	1.91	0.43
55:v:49:G:H2'	55:v:50:U:C6	2.53	0.43
4:3:63:TYR:CD2	8:A:242:G:H5''	2.53	0.43
8:A:356:G:H2'	8:A:357:C:C6	2.54	0.43
8:A:935:C:H2'	8:A:936:A:H8	1.83	0.43
8:A:1028:A:H2'	8:A:1029:A:H8	1.78	0.43
8:A:1571:A:H2'	8:A:1572:A:C8	2.53	0.43
8:A:2104:C:N4	8:A:2186:G:N7	2.66	0.43
8:A:2204:G:H4'	10:C:149:LYS:HD3	1.99	0.43
8:A:2314:A:H2'	8:A:2315:G:H8	1.83	0.43
8:A:2468:A:O2'	8:A:2469:A:H8	2.00	0.43
9:B:39:A:H2'	9:B:40:U:C6	2.53	0.43
20:M:69:PRO:HA	20:M:94:ALA:HB2	2.00	0.43
28:U:85:ARG:HH22	28:U:99:SER:C	2.26	0.43
34:a:246:A:N1	34:a:278:G:O2'	2.45	0.43
34:a:268:U:H2'	34:a:269:C:C6	2.52	0.43
34:a:356:A:N3	34:a:368:U:O2'	2.39	0.43
34:a:555:U:H2'	34:a:556:C:H6	1.82	0.43
34:a:687:A:C8	34:a:701:U:C4	3.06	0.43
34:a:994:A:O2'	34:a:995:C:O4'	2.35	0.43
34:a:1162:C:H2'	34:a:1163:A:H8	1.82	0.43
34:a:1402:4OC:H2'	34:a:1403:C:O4'	2.17	0.43
36:c:72:PRO:HG3	36:c:104:GLU:HG3	2.00	0.43
39:f:88:MET:CG	39:f:90:MET:HE2	2.48	0.43
41:h:102:VAL:HG12	41:h:125:ILE:HD12	1.99	0.43
42:i:58:GLU:H	42:i:58:GLU:CD	2.26	0.43
45:l:107:LYS:HA	45:l:107:LYS:HE2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
49:p:19:VAL:HB	49:p:36:VAL:O	2.18	0.43
2:1:33:LEU:HD11	8:A:2286:G:C2	2.53	0.43
8:A:303:G:H2'	8:A:304:U:C6	2.53	0.43
8:A:460:A:H2'	8:A:461:C:O4'	2.19	0.43
8:A:634:C:H2'	8:A:635:C:H6	1.82	0.43
8:A:828:U:H2'	8:A:829:A:C8	2.53	0.43
8:A:899:A:H5'	8:A:900:A:OP1	2.18	0.43
8:A:1176:U:H2'	8:A:1177:G:C8	2.53	0.43
8:A:2243:U:H2'	8:A:2244:U:H6	1.82	0.43
15:H:82:SER:HB2	15:H:94:ILE:HD11	2.00	0.43
27:T:5:GLU:H	27:T:5:GLU:CD	2.26	0.43
32:Y:10:SER:OG	32:Y:13:GLU:OE1	2.27	0.43
32:Y:36:GLN:CD	32:Y:36:GLN:N	2.77	0.43
34:a:20:U:H2'	34:a:21:G:O4'	2.18	0.43
34:a:29:U:O2'	34:a:30:U:H5'	2.18	0.43
34:a:49:U:O4	34:a:365:U:H5	2.01	0.43
34:a:767:A:H2'	34:a:768:A:O4'	2.18	0.43
34:a:1401:G:H2'	34:a:1402:4OC:O4'	2.18	0.43
35:b:212:TYR:O	35:b:216:VAL:HG23	2.17	0.43
50:q:32:ILE:HD12	50:q:32:ILE:N	2.33	0.43
8:A:340:A:H2'	8:A:341:C:O4'	2.17	0.43
8:A:493:G:H2'	8:A:494:G:O4'	2.17	0.43
8:A:754:U:H2'	8:A:755:U:C6	2.54	0.43
8:A:1405:U:H2'	8:A:1406:U:H6	1.81	0.43
8:A:1428:C:C5	8:A:1569:A:H5''	2.54	0.43
8:A:1440:U:H2'	8:A:1441:G:C8	2.54	0.43
8:A:1495:A:H2'	8:A:1496:A:C8	2.54	0.43
8:A:2636:C:H2'	8:A:2637:U:C6	2.54	0.43
9:B:42:C:C6	13:F:65:LEU:HB2	2.53	0.43
10:C:144:GLU:HA	10:C:151:GLY:HA2	2.00	0.43
21:N:28:LEU:HD23	21:N:48:VAL:HG21	2.00	0.43
34:a:143:A:H5''	34:a:144:G:H5''	2.00	0.43
34:a:757:U:OP1	34:a:822:U:O2'	2.31	0.43
34:a:1134:G:H3'	34:a:1135:U:H6	1.83	0.43
34:a:1159:U:H5'	35:b:131:LYS:NZ	2.33	0.43
34:a:1436:U:H2'	34:a:1437:A:C8	2.53	0.43
35:b:119:GLN:O	35:b:125:PHE:HB2	2.18	0.43
56:w:19:G:H5'	56:w:20:U:C6	2.54	0.43
8:A:4:U:H2'	8:A:5:A:H8	1.82	0.43
8:A:40:U:H2'	8:A:41:C:C6	2.54	0.43
8:A:305:C:H2'	8:A:306:U:C6	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:362:A:H5'	8:A:363:G:OP2	2.19	0.43
8:A:479:A:H1'	8:A:480:A:H5''	1.99	0.43
8:A:1319:C:O2'	8:A:1320:C:H5'	2.18	0.43
8:A:1419:A:O2'	8:A:1421:G:N7	2.48	0.43
8:A:1427:A:H4'	8:A:1428:C:O4'	2.19	0.43
8:A:1626:A:OP2	8:A:1626:A:H8	2.01	0.43
8:A:1715:G:O2'	8:A:1716:U:P	2.76	0.43
8:A:1924:C:O2'	55:v:13:C:H4'	2.18	0.43
8:A:1946:U:H2'	8:A:1947:C:H6	1.82	0.43
8:A:2047:C:H2'	8:A:2048:G:C8	2.53	0.43
13:F:114:ARG:HD3	46:m:70:ARG:NH1	2.33	0.43
18:K:71:ARG:HB2	18:K:75:SER:OG	2.19	0.43
19:L:37:GLY:O	19:L:41:ARG:HG2	2.18	0.43
20:M:109:PRO:HD2	20:M:112:LEU:HD23	2.00	0.43
22:O:63:LYS:HG3	22:O:64:TYR:N	2.33	0.43
28:U:40:LEU:HB3	28:U:59:GLU:OE1	2.18	0.43
34:a:373:A:H1'	34:a:481:G:C8	2.54	0.43
34:a:1043:G:O2'	34:a:1044:A:OP1	2.32	0.43
34:a:1198:G:H2'	34:a:1199:U:C6	2.53	0.43
34:a:1417:G:N2	34:a:1482:G:H2'	2.34	0.43
35:b:164:ASP:HB3	35:b:167:HIS:HB3	2.01	0.43
38:e:148:SER:HB3	38:e:151:MET:HE3	2.00	0.43
45:l:53:ARG:NE	45:l:61:GLU:HG3	2.33	0.43
46:m:80:MET:HE2	46:m:80:MET:HB3	1.87	0.43
49:p:46:LYS:HE2	49:p:46:LYS:HB2	1.59	0.43
8:A:75:G:N3	8:A:75:G:H2'	2.34	0.43
8:A:290:U:H3	8:A:350:G:H1	1.66	0.43
8:A:1264:A:H8	8:A:1264:A:OP2	2.02	0.43
8:A:1297:C:OP1	8:A:2710:C:H4'	2.18	0.43
8:A:1315:C:H2'	8:A:1316:U:C6	2.53	0.43
8:A:1464:G:H2'	8:A:1465:G:C8	2.53	0.43
8:A:1688:U:O2'	8:A:1700:A:N7	2.38	0.43
15:H:47:PHE:HA	15:H:51:ARG:HH11	1.84	0.43
25:R:71:LYS:HA	25:R:90:ARG:HG2	2.00	0.43
34:a:86:G:O2'	34:a:87:C:H3'	2.18	0.43
34:a:1000:A:H2'	34:a:1001:C:H6	1.83	0.43
34:a:1167:A:H5''	34:a:1168:U:OP1	2.19	0.43
34:a:1414:U:H2'	34:a:1415:G:H8	1.84	0.43
35:b:63:LYS:HE2	35:b:63:LYS:HB2	1.82	0.43
37:d:105:GLY:C	37:d:107:GLY:H	2.27	0.43
40:g:130:LYS:HB2	40:g:130:LYS:HZ2	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:k:97:ARG:HB2	44:k:97:ARG:HH11	1.84	0.43
45:l:61:GLU:HA	45:l:61:GLU:OE2	2.17	0.43
56:w:41:C:H2'	56:w:42:C:C6	2.54	0.43
8:A:289:G:H2'	8:A:290:U:H6	1.84	0.43
8:A:471:A:H2'	8:A:472:A:O4'	2.19	0.43
8:A:1073:A:H5''	8:A:1075:C:H41	1.83	0.43
8:A:2237:G:H5''	8:A:2238:G:OP1	2.18	0.43
8:A:2373:G:H2'	8:A:2374:C:C6	2.53	0.43
28:U:40:LEU:HA	28:U:60:LYS:O	2.19	0.43
34:a:255:G:H2'	34:a:256:U:C6	2.53	0.43
34:a:354:G:O2'	34:a:389:A:OP1	2.35	0.43
34:a:552:U:H2'	34:a:553:A:H8	1.83	0.43
34:a:642:A:N7	41:h:106:SER:HA	2.34	0.43
34:a:1267:C:O2	34:a:1327:C:H4'	2.18	0.43
34:a:1464:U:H2'	34:a:1465:A:H8	1.84	0.43
36:c:155:ARG:HD3	36:c:192:TYR:O	2.19	0.43
49:p:6:LEU:HB3	49:p:17:TYR:HB3	2.01	0.43
7:6:62:LYS:NZ	7:6:63:ARG:HG3	2.34	0.43
8:A:1354:A:H2'	8:A:1355:G:O4'	2.19	0.43
8:A:2813:A:H2'	8:A:2814:A:C8	2.53	0.43
9:B:116:G:O3'	22:O:56:LYS:NZ	2.49	0.43
20:M:117:PHE:HD2	20:M:130:PHE:HD2	1.66	0.43
34:a:54:C:H2'	34:a:352:C:H41	1.83	0.43
34:a:81:A:H61	34:a:86:G:H21	1.67	0.43
34:a:186:C:H2'	34:a:187:G:O4'	2.18	0.43
34:a:264:C:H2'	34:a:265:G:O4'	2.18	0.43
34:a:331:G:H2'	53:t:4:LYS:HE3	2.01	0.43
34:a:816:A:OP1	34:a:1526:G:O2'	2.30	0.43
34:a:1070:U:H2'	34:a:1071:C:C6	2.54	0.43
34:a:1072:G:H2'	34:a:1073:U:C6	2.54	0.43
34:a:1102:A:H2'	34:a:1103:C:C6	2.54	0.43
34:a:1118:U:H2'	34:a:1119:C:C6	2.53	0.43
35:b:113:LEU:HB2	35:b:143:LEU:HG	2.00	0.43
37:d:187:ARG:NH2	37:d:194:ILE:O	2.52	0.43
40:g:25:PHE:HZ	40:g:119:LEU:HD21	1.84	0.43
44:k:57:SER:O	44:k:90:PRO:HG3	2.18	0.43
46:m:14:ALA:O	46:m:18:LEU:HB2	2.19	0.43
7:6:16:CYS:SG	7:6:37:CYS:CB	3.01	0.43
8:A:69:C:H4'	8:A:75:G:N7	2.33	0.43
8:A:308:G:H2'	8:A:309:A:C8	2.54	0.43
8:A:315:G:H2'	8:A:316:C:C6	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:679:C:H2'	8:A:680:C:H6	1.84	0.43
8:A:749:A:H4'	8:A:1271:G:N3	2.34	0.43
8:A:822:G:H2'	8:A:823:C:C6	2.54	0.43
8:A:1316:U:H2'	8:A:1317:G:H8	1.83	0.43
8:A:1727:C:H2'	8:A:1728:C:H6	1.82	0.43
8:A:2069:G7M:HO2'	8:A:2070:A:P	2.42	0.43
8:A:2215:C:H2'	8:A:2216:G:C8	2.54	0.43
8:A:2216:G:H2'	8:A:2217:G:C8	2.53	0.43
8:A:2229:U:O2	31:X:33:HIS:HE1	2.01	0.43
8:A:2566:A:N1	18:K:28:SER:OG	2.46	0.43
8:A:2688:G:H1'	8:A:2721:A:N6	2.33	0.43
9:B:36:C:O2'	9:B:37:C:OP1	2.30	0.43
23:P:62:LYS:HD3	23:P:64:SER:HB2	2.01	0.43
34:a:110:C:O2'	49:p:25:ARG:O	2.27	0.43
34:a:421:U:H5''	34:a:422:C:H5	1.84	0.43
34:a:642:A:H2'	34:a:643:C:H6	1.83	0.43
34:a:900:A:H2'	34:a:901:A:C8	2.54	0.43
34:a:912:C:H2'	34:a:913:A:C8	2.54	0.43
34:a:1179:A:H2'	34:a:1180:A:O4'	2.19	0.43
34:a:1324:A:H2'	34:a:1325:C:O4'	2.18	0.43
39:f:38:ARG:HD3	39:f:98:GLU:O	2.18	0.43
50:q:19:SER:HB3	50:q:70:LYS:HD3	2.01	0.43
7:6:25:ARG:NH1	7:6:25:ARG:HG3	2.33	0.43
8:A:687:C:H2'	8:A:688:U:O4'	2.19	0.43
8:A:1001:A:H2'	8:A:1002:G:O4'	2.19	0.43
8:A:2114:A:H5'	8:A:2115:G:C8	2.54	0.43
8:A:2134:A:H2'	8:A:2135:A:O4'	2.19	0.43
8:A:2230:G:H2'	8:A:2231:U:C6	2.54	0.43
8:A:2641:G:H5''	17:J:78:THR:HB	2.01	0.43
11:D:61:THR:OG1	11:D:64:GLU:HG2	2.19	0.43
15:H:129:GLU:OE1	15:H:129:GLU:HA	2.19	0.43
17:J:31:GLU:OE2	17:J:34:ARG:HD3	2.19	0.43
34:a:859:G:H2'	34:a:860:A:H8	1.83	0.43
34:a:1228:C:H4'	46:m:114:PRO:HG2	2.01	0.43
34:a:1296:C:O2'	34:a:1297:G:OP1	2.33	0.43
34:a:1410:A:H2'	34:a:1411:C:H6	1.82	0.43
34:a:1421:G:H2'	34:a:1422:G:O4'	2.19	0.43
35:b:8:MET:C	35:b:9:LEU:HD23	2.44	0.43
35:b:70:GLY:HA3	35:b:79:VAL:HG21	2.01	0.43
43:j:15:HIS:HB3	43:j:70:HIS:CE1	2.54	0.43
51:r:31:TYR:HB3	51:r:54:LEU:HD21	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:417:C:H2'	8:A:418:C:C6	2.54	0.42
8:A:811:U:H2'	19:L:21:ARG:HA	2.01	0.42
8:A:967:U:H2'	8:A:968:C:C6	2.54	0.42
8:A:974:G:H8	8:A:990:A:H62	1.62	0.42
8:A:1361:G:H2'	8:A:1362:C:H6	1.84	0.42
8:A:1637:A:H5'	8:A:1760:C:O2'	2.19	0.42
8:A:1904:G:O2'	8:A:1928:A:N1	2.46	0.42
8:A:2144:G:H2'	8:A:2146:C:O2'	2.19	0.42
8:A:2813:A:H2'	8:A:2814:A:H8	1.84	0.42
8:A:2820:A:OP2	21:N:2:ARG:NH2	2.51	0.42
13:F:46:LYS:HE3	13:F:46:LYS:HB3	1.79	0.42
13:F:77:LYS:O	13:F:77:LYS:NZ	2.51	0.42
18:K:106:GLU:OE1	18:K:106:GLU:N	2.51	0.42
19:L:96:LYS:HG3	19:L:101:ILE:HD11	2.00	0.42
20:M:35:ALA:HB2	20:M:102:LEU:HD11	2.01	0.42
34:a:545:C:P	37:d:61:ARG:HH12	2.42	0.42
34:a:590:U:H2'	34:a:591:U:C6	2.54	0.42
34:a:838:G:C6	34:a:849:G:C6	3.07	0.42
34:a:842:U:N3	34:a:844:G:OP2	2.51	0.42
34:a:1143:G:H2'	34:a:1144:G:H8	1.83	0.42
38:e:150:GLU:CD	38:e:150:GLU:N	2.76	0.42
41:h:88:LYS:HE3	41:h:88:LYS:HB3	1.61	0.42
54:u:48:LYS:NZ	54:u:48:LYS:HB3	2.33	0.42
56:w:66:U:H2'	56:w:67:C:O4'	2.18	0.42
2:l:9:LYS:O	2:l:51:ALA:N	2.51	0.42
8:A:138:U:H2'	8:A:140:C:C5	2.54	0.42
8:A:760:G:H2'	8:A:761:A:O4'	2.18	0.42
8:A:1316:U:H2'	8:A:1317:G:C8	2.54	0.42
8:A:1830:C:H2'	8:A:1831:G:H8	1.83	0.42
8:A:2050:C:H2'	8:A:2051:A:O4'	2.20	0.42
8:A:2115:G:H4'	8:A:2166:U:O2'	2.19	0.42
8:A:2216:G:H2'	8:A:2217:G:H8	1.84	0.42
8:A:2522:U:O2'	8:A:2647:U:OP1	2.23	0.42
22:O:27:VAL:N	22:O:38:GLN:O	2.51	0.42
28:U:52:ASN:C	28:U:54:PRO:HD3	2.44	0.42
29:V:57:TYR:HE1	29:V:77:VAL:HG21	1.83	0.42
34:a:16:A:N1	34:a:919:A:H2	2.17	0.42
34:a:515:G:O2'	34:a:516:PSU:H6	2.02	0.42
34:a:527:G7M:O2'	34:a:535:A:N1	2.38	0.42
34:a:607:A:H2'	34:a:608:A:C8	2.53	0.42
34:a:1321:U:H3'	34:a:1322:C:H2'	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:1362:A:HO2'	34:a:1363:A:P	2.32	0.42
36:c:13:ILE:HG22	36:c:14:VAL:HG13	2.01	0.42
38:e:80:LEU:HD11	38:e:95:MET:HB3	2.01	0.42
44:k:59:PRO:HD3	44:k:90:PRO:HB2	2.01	0.42
8:A:19:A:H2'	8:A:20:C:C6	2.55	0.42
8:A:413:C:H2'	8:A:414:C:H6	1.84	0.42
8:A:593:U:H2'	8:A:594:U:H6	1.82	0.42
8:A:1100:C:N4	8:A:1101:U:O2	2.52	0.42
8:A:1693:U:H5''	8:A:1694:C:C5	2.53	0.42
8:A:1792:G:H5'	10:C:203:VAL:HG13	2.02	0.42
8:A:1913:A:C8	34:a:1494:G:H4'	2.54	0.42
8:A:2247:A:H2'	8:A:2248:C:C6	2.54	0.42
8:A:2751:G:C4	14:G:2:ARG:HD3	2.53	0.42
14:G:176:LYS:HE2	14:G:176:LYS:HB2	1.84	0.42
29:V:71:LYS:O	29:V:94:ALA:N	2.50	0.42
32:Y:12:GLU:CD	32:Y:12:GLU:N	2.77	0.42
34:a:958:A:C6	52:s:54:ARG:HD2	2.55	0.42
34:a:1216:A:H5''	47:n:4:SER:HB3	1.99	0.42
34:a:1427:C:H2'	34:a:1428:A:C8	2.55	0.42
35:b:224:ARG:HG2	35:b:224:ARG:NH1	2.33	0.42
42:i:50:PRO:HD3	42:i:79:ARG:HD3	2.01	0.42
45:l:34:THR:N	45:l:53:ARG:O	2.52	0.42
8:A:171:U:C2	8:A:172:A:C8	3.07	0.42
8:A:323:C:O2	8:A:1205:A:H2	2.02	0.42
8:A:451:U:H4'	12:E:47:LYS:HE2	2.02	0.42
8:A:881:G:H2'	8:A:882:G:H8	1.85	0.42
8:A:1095:A:C8	16:I:26:ALA:HB1	2.55	0.42
8:A:1534:U:O2	8:A:1538:G:N2	2.51	0.42
8:A:2205:A:H2'	8:A:2206:C:H6	1.84	0.42
10:C:4:LYS:HD2	10:C:16:VAL:HG22	2.00	0.42
10:C:259:ASN:C	10:C:261:ARG:H	2.25	0.42
11:D:129:THR:HG22	11:D:130:GLN:O	2.20	0.42
14:G:26:LYS:HB2	14:G:31:GLU:OE1	2.19	0.42
18:K:1:MET:HG2	18:K:32:TYR:CG	2.54	0.42
22:O:61:GLN:N	22:O:61:GLN:CD	2.77	0.42
26:S:86:MET:HB2	26:S:96:ILE:HG12	2.01	0.42
28:U:46:LYS:HE3	28:U:47:PRO:HD2	2.00	0.42
30:W:74:LYS:HB2	30:W:74:LYS:HE2	1.74	0.42
34:a:35:G:H21	45:l:114:SER:HB2	1.84	0.42
34:a:123:U:H2'	34:a:124:C:H6	1.85	0.42
34:a:253:A:H2'	34:a:254:G:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:995:C:H3'	34:a:996:A:C5'	2.49	0.42
34:a:1019:A:H2'	34:a:1020:G:O4'	2.19	0.42
34:a:1167:A:H4'	34:a:1168:U:C5	2.54	0.42
34:a:1391:U:H2'	34:a:1392:G:H8	1.83	0.42
35:b:163:ILE:O	35:b:185:ILE:HB	2.19	0.42
43:j:52:LEU:HD21	43:j:59:LYS:HD2	2.02	0.42
43:j:80:THR:C	43:j:82:LYS:H	2.27	0.42
45:l:26:CYS:SG	45:l:29:LYS:NZ	2.86	0.42
46:m:22:TYR:CE2	46:m:69:ARG:HB2	2.55	0.42
46:m:78:ARG:NH1	52:s:64:GLU:OE2	2.52	0.42
53:t:53:MET:HE2	53:t:53:MET:HB2	1.77	0.42
8:A:538:A:H61	8:A:555:G:H1'	1.85	0.42
8:A:627:A:H5''	19:L:78:ARG:HH22	1.84	0.42
8:A:1521:G:OP2	8:A:1522:A:O2'	2.29	0.42
8:A:1709:U:H2'	8:A:1710:G:H8	1.83	0.42
8:A:2467:C:H2'	8:A:2468:A:O4'	2.19	0.42
8:A:2683:C:H4'	11:D:13:ARG:HH22	1.83	0.42
10:C:38:LYS:HB2	10:C:38:LYS:HE3	1.79	0.42
17:J:4:PHE:O	24:Q:63:ARG:NH1	2.42	0.42
34:a:123:U:H2'	34:a:124:C:C6	2.54	0.42
34:a:218:U:H2'	34:a:219:U:O4'	2.19	0.42
34:a:384:G:H2'	34:a:385:C:H6	1.81	0.42
34:a:456:A:N1	34:a:476:U:H5	2.17	0.42
34:a:642:A:C5	41:h:106:SER:HA	2.54	0.42
34:a:921:U:H2'	34:a:922:G:O4'	2.19	0.42
34:a:956:U:H5	34:a:960:U:O2	2.02	0.42
34:a:1044:A:C5	34:a:1045:C:H1'	2.55	0.42
34:a:1118:U:H2'	34:a:1119:C:H6	1.83	0.42
44:k:49:SER:CB	44:k:68:ARG:HE	2.32	0.42
52:s:36:ARG:O	52:s:69:LYS:NZ	2.52	0.42
8:A:1081:U:N3	16:I:118:GLY:HA3	2.35	0.42
8:A:1171:G:N2	8:A:1177:G:H22	2.18	0.42
8:A:1176:U:H2'	8:A:1177:G:O4'	2.19	0.42
8:A:1504:A:H2'	8:A:1505:A:H8	1.85	0.42
8:A:1631:G:H1'	8:A:1635:A:H61	1.84	0.42
20:M:69:PRO:O	20:M:70:ASP:OD2	2.37	0.42
23:P:21:PRO:HD3	23:P:49:ILE:HD12	2.01	0.42
25:R:37:GLU:O	25:R:37:GLU:HG2	2.19	0.42
27:T:54:GLU:H	27:T:54:GLU:CD	2.27	0.42
34:a:6:G:C4	38:e:123:LEU:HD11	2.53	0.42
34:a:175:C:H2'	34:a:176:C:C6	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:193:C:H2'	34:a:194:C:C6	2.54	0.42
34:a:389:A:H3'	34:a:390:U:H6	1.84	0.42
34:a:753:A:OP1	48:o:68:TYR:OH	2.25	0.42
34:a:784:A:H2'	34:a:785:G:C8	2.55	0.42
34:a:1413:A:H2	34:a:1487:G:H22	1.67	0.42
62:a:1685:AM2:HA1	62:a:1685:AM2:HC2	1.79	0.42
35:b:55:GLU:HG2	35:b:197:PHE:CZ	2.55	0.42
37:d:26:ALA:HB3	37:d:29:THR:HG23	2.02	0.42
40:g:101:ARG:O	40:g:105:GLU:HG2	2.20	0.42
43:j:11:LYS:HA	43:j:70:HIS:O	2.20	0.42
48:o:81:ILE:HD12	48:o:87:ARG:HG2	2.01	0.42
8:A:29:U:H2'	8:A:30:G:C8	2.55	0.42
8:A:716:A:H2'	8:A:717:C:O4'	2.20	0.42
8:A:1068:G:N7	8:A:1069:A:H1'	2.35	0.42
8:A:1341:G:H1'	27:T:59:ASN:HB3	2.01	0.42
8:A:2081:U:H2'	8:A:2082:A:C8	2.54	0.42
8:A:2114:A:H2'	8:A:2114:A:N3	2.35	0.42
8:A:2193:G:H2'	8:A:2194:U:H6	1.85	0.42
10:C:78:GLU:HG2	10:C:92:LEU:O	2.19	0.42
11:D:25:THR:HG21	11:D:193:VAL:HG22	2.02	0.42
13:F:113:PHE:HZ	13:F:175:PRO:HG2	1.85	0.42
20:M:4:PRO:CG	20:M:70:ASP:HA	2.48	0.42
26:S:11:ARG:HA	26:S:11:ARG:HD2	1.82	0.42
34:a:747:A:H2'	34:a:748:G:O4'	2.20	0.42
34:a:857:C:H2'	34:a:858:G:O4'	2.20	0.42
34:a:950:U:OP2	46:m:100:ARG:HD2	2.20	0.42
34:a:1512:U:H2'	34:a:1513:A:C8	2.54	0.42
37:d:33:ILE:HD12	37:d:33:ILE:HA	1.84	0.42
40:g:102:TRP:NE1	40:g:136:LYS:HE3	2.34	0.42
42:i:29:ILE:HA	42:i:64:ILE:O	2.19	0.42
43:j:15:HIS:O	43:j:18:ILE:HG22	2.20	0.42
52:s:39:ILE:HB	52:s:66:VAL:O	2.19	0.42
2:1:4:ILE:HD12	2:1:4:ILE:N	2.34	0.42
5:4:12:ARG:CZ	5:4:12:ARG:HB2	2.50	0.42
8:A:26:G:H1'	8:A:514:A:N6	2.35	0.42
8:A:478:A:H61	8:A:500:G:HO2'	1.63	0.42
8:A:567:U:H2'	8:A:568:U:O4'	2.20	0.42
8:A:1107:G:H2'	8:A:1108:U:O4'	2.19	0.42
8:A:1827:U:H2'	8:A:1828:G:O4'	2.20	0.42
8:A:1847:G:H8	8:A:1847:G:OP2	2.03	0.42
8:A:2845:U:H2'	8:A:2846:G:C8	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:B:48:U:H4'	22:O:100:HIS:CD2	2.53	0.42
13:F:37:MET:HE1	13:F:52:ALA:O	2.20	0.42
13:F:114:ARG:HD3	46:m:70:ARG:CZ	2.50	0.42
18:K:17:ARG:HD3	18:K:17:ARG:HA	1.86	0.42
18:K:116:ILE:HD12	18:K:117:SER:N	2.35	0.42
33:Z:55:LYS:HE3	33:Z:55:LYS:HB3	1.65	0.42
34:a:500:G:H2'	34:a:501:C:H6	1.85	0.42
34:a:636:U:H2'	34:a:637:C:H6	1.85	0.42
34:a:718:A:H2	51:r:37:LYS:HG2	1.83	0.42
34:a:939:G:H2'	34:a:940:C:C6	2.55	0.42
34:a:1002:G:C6	34:a:1003:G:C5	3.08	0.42
34:a:1134:G:C2	34:a:1135:U:H1'	2.55	0.42
37:d:24:VAL:HG12	37:d:160:LEU:HD21	2.00	0.42
42:i:26:LYS:HD2	42:i:26:LYS:C	2.45	0.42
8:A:176:A:O2'	8:A:177:G:H5'	2.19	0.42
8:A:629:G:N3	8:A:639:U:O2'	2.52	0.42
8:A:1306:C:H2'	8:A:1307:A:H8	1.85	0.42
8:A:1318:U:H2'	8:A:1319:C:C6	2.54	0.42
8:A:1505:A:H2'	8:A:1506:U:C6	2.54	0.42
8:A:1942:C:H2'	8:A:1943:U:C5	2.55	0.42
8:A:2469:A:H2'	8:A:2470:G:O4'	2.20	0.42
15:H:110:VAL:HG13	15:H:111:ALA:O	2.20	0.42
17:J:96:ARG:HH11	17:J:99:ARG:HD3	1.85	0.42
34:a:57:G:H2'	34:a:58:C:C6	2.55	0.42
34:a:95:C:HO2'	34:a:96:U:P	2.42	0.42
34:a:637:C:H2'	34:a:638:U:C6	2.55	0.42
34:a:875:U:O2'	41:h:14:ARG:HD2	2.20	0.42
34:a:1161:C:H2'	34:a:1162:C:H6	1.85	0.42
34:a:1269:A:H1'	34:a:1326:U:H1'	2.02	0.42
35:b:113:LEU:HD11	35:b:144:GLU:HB2	2.01	0.42
35:b:127:LYS:H	35:b:127:LYS:HD2	1.84	0.42
35:b:131:LYS:O	35:b:134:LEU:HD23	2.19	0.42
47:n:41:ARG:NH2	52:s:5:LYS:O	2.53	0.42
8:A:247:G:H4'	8:A:386:G:C5	2.54	0.42
8:A:265:A:N1	8:A:427:U:O2'	2.50	0.42
8:A:353:C:C2	8:A:354:A:C8	3.07	0.42
8:A:580:U:O3'	24:Q:30:VAL:HG13	2.20	0.42
8:A:729:G:O2'	8:A:763:G:H4'	2.20	0.42
8:A:1021:A:O2'	8:A:1123:C:OP1	2.31	0.42
8:A:1722:A:N6	8:A:1738:G:H1'	2.35	0.42
8:A:2350:C:H2'	8:A:2351:G:O4'	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2552:OMU:HM23	8:A:2552:OMU:H1'	1.49	0.42
8:A:2846:G:H2'	8:A:2847:U:C6	2.55	0.42
9:B:113:C:H1'	22:O:46:GLU:HA	2.01	0.42
10:C:107:LYS:NZ	10:C:107:LYS:HB3	2.34	0.42
13:F:127:TYR:CE2	13:F:129:MET:HB3	2.53	0.42
17:J:99:ARG:HA	17:J:99:ARG:HD2	1.87	0.42
18:K:116:ILE:HD12	18:K:116:ILE:C	2.45	0.42
19:L:89:VAL:HG21	19:L:123:ARG:NH1	2.35	0.42
21:N:57:THR:HG23	21:N:62:ASN:ND2	2.35	0.42
28:U:73:ASN:C	28:U:75:ALA:H	2.27	0.42
29:V:21:ARG:HA	29:V:25:LYS:O	2.20	0.42
34:a:109:A:H5'	34:a:110:C:C5	2.55	0.42
34:a:855:U:H2'	34:a:856:C:H6	1.85	0.42
34:a:947:G:H2'	34:a:948:C:C6	2.55	0.42
34:a:1001:C:H2'	34:a:1002:G:C8	2.54	0.42
34:a:1022:A:C2'	34:a:1023:U:H5'	2.50	0.42
34:a:1291:U:H2'	34:a:1292:G:H8	1.85	0.42
36:c:11:LEU:HD11	47:n:91:GLY:HA2	2.02	0.42
38:e:44:ARG:HH11	38:e:44:ARG:HG2	1.85	0.42
38:e:44:ARG:HG2	38:e:44:ARG:NH1	2.35	0.42
44:k:13:LYS:HE2	44:k:13:LYS:H	1.84	0.42
44:k:87:GLY:O	44:k:92:ARG:NH1	2.53	0.42
48:o:7:THR:O	48:o:11:VAL:HG12	2.20	0.42
55:v:32:C:N4	55:v:33:U:O4	2.52	0.42
8:A:150:U:H2'	8:A:151:C:H6	1.85	0.41
8:A:478:A:N1	8:A:500:G:H4'	2.35	0.41
8:A:568:U:O4	25:R:81:LYS:NZ	2.52	0.41
8:A:624:C:O2'	8:A:657:U:OP1	2.34	0.41
8:A:741:U:H2'	8:A:742:A:C8	2.55	0.41
8:A:1219:U:H2'	8:A:1220:G:C8	2.55	0.41
8:A:1363:C:O2'	8:A:1809:A:N3	2.50	0.41
8:A:1385:A:H1'	8:A:1386:C:C6	2.55	0.41
8:A:2305:U:H2'	8:A:2306:C:C6	2.55	0.41
8:A:2409:G:H2'	8:A:2410:G:O4'	2.20	0.41
8:A:2533:U:H2'	8:A:2534:A:O4'	2.20	0.41
8:A:2724:U:OP1	11:D:123:LYS:NZ	2.46	0.41
10:C:70:LYS:HG3	10:C:101:ARG:NH1	2.35	0.41
13:F:10:GLU:O	13:F:13:LYS:HG3	2.20	0.41
15:H:96:THR:HG22	15:H:117:LEU:HD13	2.01	0.41
34:a:309:A:O2'	34:a:607:A:N1	2.42	0.41
34:a:757:U:H2'	34:a:758:C:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:a:821:G:H2'	34:a:822:U:H6	1.84	0.41
34:a:1314:C:OP1	52:s:5:LYS:NZ	2.50	0.41
34:a:1411:C:H2'	34:a:1412:C:C6	2.55	0.41
34:a:1463:U:H2'	34:a:1464:U:C6	2.55	0.41
34:a:1498:UR3:H3U2	58:z:2:U:H4'	2.02	0.41
37:d:169:TRP:CD2	37:d:185:PRO:HB3	2.55	0.41
42:i:20:ILE:HG22	42:i:62:LEU:CD2	2.49	0.41
43:j:22:THR:O	43:j:26:VAL:HG13	2.19	0.41
7:6:64:PHE:CD1	52:s:8:PRO:HD3	2.55	0.41
8:A:2:G:H2'	8:A:3:U:H6	1.82	0.41
8:A:279:A:N6	8:A:361:G:H1'	2.34	0.41
8:A:280:U:H2'	8:A:281:C:C6	2.55	0.41
8:A:429:A:H2'	8:A:430:A:C8	2.55	0.41
8:A:595:C:H2'	8:A:596:U:C6	2.55	0.41
8:A:764:A:H2	10:C:217:PRO:HG3	1.85	0.41
8:A:969:G:H2'	8:A:970:U:C6	2.55	0.41
8:A:1028:A:H61	8:A:1125:G:H2'	1.83	0.41
8:A:1153:C:H2'	8:A:1154:G:O4'	2.20	0.41
8:A:1794:A:O2'	8:A:1900:A:H2'	2.19	0.41
8:A:2087:G:H2'	8:A:2088:A:H8	1.84	0.41
17:J:96:ARG:HD2	17:J:99:ARG:CG	2.48	0.41
26:S:66:ILE:N	26:S:66:ILE:HD13	2.35	0.41
27:T:48:GLN:HA	27:T:53:VAL:O	2.19	0.41
34:a:32:A:H2'	34:a:33:A:C8	2.55	0.41
34:a:109:A:C6	34:a:326:G:C6	3.08	0.41
34:a:255:G:H4'	50:q:18:LYS:HD3	2.02	0.41
34:a:436:C:H2'	34:a:437:U:C6	2.55	0.41
34:a:591:U:H2'	34:a:592:G:H8	1.85	0.41
34:a:980:C:O3'	47:n:12:ARG:NH2	2.54	0.41
34:a:994:A:O2'	34:a:995:C:O5'	2.38	0.41
34:a:1122:U:H2'	34:a:1123:U:C6	2.54	0.41
34:a:1354:U:C2'	34:a:1355:G:H5'	2.50	0.41
34:a:1530:G:H2'	34:a:1531:A:H8	1.85	0.41
40:g:10:LYS:HE2	40:g:10:LYS:HB2	1.94	0.41
56:w:8:4SU:O2'	56:w:21:A:N1	2.45	0.41
56:w:46:G7M:O2'	56:w:47:U:OP1	2.34	0.41
8:A:549:G:H2'	8:A:550:C:C6	2.55	0.41
8:A:833:A:H2'	8:A:834:G:H8	1.84	0.41
8:A:930:G:H1'	33:Z:24:LEU:HD11	2.02	0.41
8:A:1444:G:H2'	8:A:1445:G:H8	1.86	0.41
8:A:1541:C:H2'	8:A:1542:U:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:1987:A:H2'	8:A:1988:G:C8	2.55	0.41
8:A:2638:G:O2'	8:A:2639:A:H8	2.03	0.41
23:P:26:GLU:OE2	23:P:28:LYS:HD3	2.18	0.41
24:Q:75:TYR:CZ	24:Q:79:ILE:HG13	2.56	0.41
32:Y:34:SER:O	32:Y:36:GLN:NE2	2.53	0.41
34:a:155:A:H2'	34:a:156:C:C6	2.55	0.41
34:a:530:G:O6	58:z:6:U:H1'	2.20	0.41
34:a:600:A:H2'	34:a:601:G:C8	2.55	0.41
34:a:1095:U:P	34:a:1108:G:H1	2.44	0.41
34:a:1241:G:O2'	34:a:1242:G:H5'	2.20	0.41
34:a:1317:C:C5	47:n:53:ARG:HD3	2.56	0.41
37:d:68:GLU:OE2	37:d:203:TYR:OH	2.28	0.41
39:f:14:GLN:OE1	39:f:14:GLN:N	2.54	0.41
39:f:21:MET:HE1	39:f:84:VAL:HG23	2.01	0.41
43:j:52:LEU:HB2	47:n:81:ARG:HD2	2.02	0.41
56:w:40:C:H2'	56:w:41:C:C6	2.55	0.41
56:w:75:C:H2'	56:w:76:A:C8	2.56	0.41
8:A:282:A:H2'	8:A:283:G:C8	2.55	0.41
8:A:329:G:O4'	8:A:477:A:H1'	2.20	0.41
8:A:347:A:H2'	8:A:348:A:H8	1.85	0.41
8:A:595:C:H2'	8:A:596:U:H6	1.86	0.41
8:A:1993:U:H2'	8:A:1994:C:O4'	2.20	0.41
8:A:2165:C:H2'	8:A:2166:U:O4'	2.20	0.41
8:A:2376:A:H2'	8:A:2377:A:O4'	2.19	0.41
8:A:2405:G:HO2'	8:A:2406:A:P	2.43	0.41
8:A:2752:C:H2'	8:A:2753:A:O4'	2.20	0.41
9:B:116:G:H2'	9:B:117:G:C8	2.54	0.41
12:E:3:LEU:HD12	12:E:14:VAL:HG11	2.02	0.41
30:W:15:LYS:HA	30:W:15:LYS:HD3	1.85	0.41
33:Z:55:LYS:HD2	33:Z:57:GLU:OE2	2.19	0.41
34:a:975:A:N1	34:a:1366:C:O2'	2.45	0.41
34:a:1316:G:H22	34:a:1319:A:H5'	1.85	0.41
42:i:29:ILE:HD11	42:i:37:TYR:HB3	2.02	0.41
47:n:25:GLU:O	47:n:29:ILE:HG13	2.20	0.41
2:l:5:ARG:NH1	8:A:2285:C:OP2	2.44	0.41
8:A:640:C:H2'	8:A:641:U:H6	1.84	0.41
8:A:680:C:H2'	8:A:681:G:C8	2.55	0.41
8:A:858:G:H3'	8:A:859:G:C8	2.55	0.41
8:A:1326:U:O2'	8:A:2010:G:O2'	2.35	0.41
8:A:1651:G:H4'	21:N:39:PRO:HG2	2.02	0.41
8:A:1652:A:N6	21:N:11:ASN:OD1	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:1889:A:H2'	8:A:1890:A:H8	1.84	0.41
8:A:2808:G:O2'	8:A:2809:A:H8	2.03	0.41
12:E:105:LEU:HD23	12:E:105:LEU:HA	1.92	0.41
20:M:53:MET:HE3	20:M:53:MET:HB2	1.98	0.41
21:N:1:MET:HB3	21:N:1:MET:HE2	1.79	0.41
25:R:35:PHE:HB2	25:R:59:ILE:HB	2.03	0.41
30:W:33:ILE:HG21	30:W:76:ILE:HG21	2.03	0.41
34:a:696:A:H2'	34:a:697:U:C6	2.55	0.41
34:a:1465:A:H2'	34:a:1466:C:C6	2.55	0.41
37:d:49:ASP:OD1	37:d:49:ASP:C	2.63	0.41
40:g:43:TYR:HD1	40:g:43:TYR:HA	1.78	0.41
42:i:127:SER:OG	42:i:129:ARG:OXT	2.38	0.41
45:l:31:GLY:HA3	45:l:54:VAL:CG1	2.51	0.41
46:m:24:VAL:HG23	46:m:64:VAL:HG11	2.03	0.41
54:u:7:GLU:HA	54:u:17:ARG:NH2	2.33	0.41
8:A:173:A:H2'	8:A:174:U:C6	2.56	0.41
8:A:693:A:H2'	8:A:694:U:C6	2.55	0.41
8:A:864:G:O2'	8:A:914:G:O6	2.36	0.41
8:A:984:A:H2'	8:A:984:A:N3	2.36	0.41
8:A:1205:A:H5''	8:A:1206:G:C8	2.55	0.41
8:A:1987:A:H2'	8:A:1988:G:H8	1.85	0.41
8:A:2313:C:H2'	8:A:2314:A:C8	2.56	0.41
8:A:2600:A:H2'	8:A:2601:C:C6	2.56	0.41
8:A:2655:G:N2	8:A:2656:U:O4	2.33	0.41
8:A:2740:A:H2'	8:A:2741:A:C8	2.56	0.41
9:B:24:G:N7	9:B:56:G:H2'	2.35	0.41
9:B:51:G:OP1	22:O:63:LYS:NZ	2.31	0.41
9:B:65:U:H3'	9:B:108:A:N6	2.35	0.41
34:a:134:G:H2'	34:a:135:C:O4'	2.21	0.41
34:a:838:G:H2'	34:a:839:C:H6	1.85	0.41
34:a:1256:A:O2'	34:a:1278:G:O6	2.27	0.41
34:a:1329:A:C5	34:a:1330:U:C5	3.08	0.41
37:d:43:ARG:HB2	37:d:43:ARG:NH1	2.36	0.41
8:A:817:C:O2'	8:A:839:U:H5''	2.20	0.41
8:A:1605:C:H2'	8:A:1606:C:O4'	2.20	0.41
8:A:1697:G:OP2	8:A:1698:A:O2'	2.32	0.41
8:A:1827:U:OP2	10:C:220:ARG:HD2	2.21	0.41
8:A:1928:A:H2'	8:A:1929:G:O4'	2.21	0.41
18:K:26:GLY:O	18:K:30:ARG:HD2	2.21	0.41
20:M:57:VAL:HG22	20:M:112:LEU:HG	2.02	0.41
22:O:50:ALA:O	22:O:81:ARG:NH1	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:O:51:ALA:HB3	22:O:78:VAL:HB	2.03	0.41
25:R:31:GLU:CD	25:R:31:GLU:N	2.79	0.41
28:U:32:LYS:HB3	28:U:63:ALA:HB1	2.01	0.41
29:V:53:LYS:HB3	29:V:55:GLU:CD	2.46	0.41
34:a:181:A:H61	34:a:194:C:H2'	1.86	0.41
34:a:505:G:H2'	34:a:506:G:C8	2.56	0.41
34:a:593:U:H2'	34:a:594:U:C6	2.55	0.41
34:a:604:G:H2'	34:a:605:U:O4'	2.21	0.41
34:a:666:G:H5'	34:a:726:C:H1'	2.01	0.41
34:a:717:U:H4'	44:k:118:ASN:HD22	1.86	0.41
34:a:1323:G:O2'	34:a:1324:A:P	2.79	0.41
34:a:1346:A:H2'	40:g:9:ARG:NH1	2.36	0.41
40:g:130:LYS:HB2	40:g:130:LYS:NZ	2.36	0.41
8:A:363:G:H2'	8:A:364:C:C6	2.56	0.41
8:A:445:C:H2'	8:A:446:G:O4'	2.21	0.41
8:A:598:U:H2'	8:A:599:A:H8	1.84	0.41
8:A:699:A:H2'	8:A:700:G:O4'	2.20	0.41
8:A:1013:C:H2'	8:A:1014:A:C8	2.52	0.41
8:A:2093:G:O2'	8:A:2198:A:N1	2.49	0.41
8:A:2118:U:C5	8:A:2148:G:H1'	2.56	0.41
8:A:2489:U:H2'	8:A:2490:G:O4'	2.21	0.41
34:a:7:A:H5'	34:a:298:A:O4'	2.20	0.41
34:a:148:G:H2'	34:a:149:A:O4'	2.20	0.41
34:a:410:G:OP1	37:d:25:ARG:HD2	2.21	0.41
34:a:996:A:OP1	34:a:996:A:H4'	2.21	0.41
42:i:5:TYR:HB2	42:i:20:ILE:CG1	2.51	0.41
42:i:86:LEU:HD23	42:i:86:LEU:HA	1.88	0.41
42:i:99:LYS:HE2	42:i:99:LYS:HB2	1.57	0.41
42:i:115:VAL:HG13	43:j:62:ARG:NH1	2.32	0.41
55:v:18:G:H1	55:v:55:PSU:H6	1.68	0.41
55:v:20:H2U:H61	55:v:21:A:C5'	2.50	0.41
1:0:39:ARG:HG3	1:0:40:HIS:ND1	2.36	0.41
8:A:257:C:H2'	8:A:258:G:O4'	2.21	0.41
8:A:850:U:H2'	8:A:851:C:C6	2.55	0.41
8:A:975:A:H1'	8:A:990:A:C2	2.56	0.41
8:A:1275:A:OP2	8:A:1646:C:N4	2.42	0.41
8:A:1283:G:N2	8:A:1285:A:H3'	2.35	0.41
8:A:1485:U:H2'	8:A:1486:U:C6	2.55	0.41
8:A:1914:C:H2'	8:A:1915:3TD:O4'	2.21	0.41
8:A:1957:C:H2'	8:A:1958:C:C6	2.55	0.41
8:A:2096:C:H2'	8:A:2097:A:C8	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2110:G:N1	8:A:2120:G:N7	2.69	0.41
8:A:2191:A:H2'	8:A:2192:U:C6	2.56	0.41
9:B:52:A:O2'	9:B:53:A:P	2.78	0.41
9:B:112:G:H2'	9:B:113:C:C6	2.56	0.41
10:C:65:ASP:OD1	10:C:101:ARG:NH1	2.47	0.41
13:F:4:HIS:HB2	13:F:96:TRP:CG	2.56	0.41
13:F:72:SER:HB2	13:F:80:GLN:HB2	2.03	0.41
15:H:135:HIS:CG	15:H:136:SER:H	2.39	0.41
17:J:36:LEU:HG	17:J:54:ILE:HD12	2.03	0.41
22:O:79:ALA:O	22:O:83:LEU:HG	2.21	0.41
29:V:10:LYS:NZ	29:V:41:GLU:OE1	2.52	0.41
29:V:28:ALA:HB3	29:V:40:ILE:HG13	2.03	0.41
34:a:154:U:H2'	34:a:155:A:C8	2.55	0.41
34:a:156:C:H2'	34:a:157:U:O4'	2.20	0.41
34:a:234:C:H4'	50:q:65:PRO:HG3	2.02	0.41
34:a:257:G:H2'	34:a:258:G:H8	1.86	0.41
34:a:350:G:H2'	34:a:351:G:C8	2.56	0.41
34:a:390:U:H2'	34:a:391:G:C8	2.56	0.41
34:a:613:C:H2'	34:a:614:C:H6	1.84	0.41
34:a:718:A:O2'	54:u:30:GLU:OE2	2.39	0.41
34:a:979:C:C6	47:n:59:ARG:HD2	2.56	0.41
34:a:984:C:C2'	34:a:985:C:H5'	2.50	0.41
34:a:1130:A:H2'	34:a:1131:G:C8	2.51	0.41
34:a:1333:A:H2'	34:a:1334:G:O4'	2.21	0.41
34:a:1428:A:H2'	34:a:1429:A:O4'	2.20	0.41
35:b:44:LYS:C	35:b:47:PRO:HD2	2.46	0.41
39:f:10:VAL:HG21	39:f:18:VAL:HG22	2.03	0.41
39:f:16:GLU:OE2	39:f:16:GLU:N	2.42	0.41
41:h:1:SER:O	41:h:1:SER:OG	2.32	0.41
43:j:59:LYS:HE2	43:j:62:ARG:NH2	2.28	0.41
52:s:10:ILE:HG13	52:s:37:SER:HB3	2.03	0.41
53:t:26:MET:HE3	53:t:26:MET:HB3	1.96	0.41
55:v:11:A:H2'	55:v:12:G:C8	2.56	0.41
55:v:56:C:H2'	55:v:57:A:C8	2.56	0.41
8:A:78:U:H2'	8:A:79:C:H6	1.85	0.41
8:A:247:G:H4'	8:A:386:G:C4	2.56	0.41
8:A:852:U:H2'	8:A:853:C:C6	2.56	0.41
8:A:887:A:H2'	46:m:91:ARG:HD3	2.03	0.41
8:A:1490:A:H62	10:C:96:LYS:HB2	1.86	0.41
8:A:2101:A:H5'	8:A:2102:G:OP2	2.21	0.41
8:A:2340:A:H2'	8:A:2341:G:H8	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2554:U:H2'	8:A:2555:U:C6	2.55	0.41
8:A:2895:G:H2'	8:A:2896:C:H6	1.86	0.41
11:D:196:ALA:O	11:D:199:SER:OG	2.35	0.41
13:F:4:HIS:HB2	13:F:96:TRP:CD1	2.56	0.41
34:a:440:C:C2	34:a:441:A:C8	3.09	0.41
34:a:592:G:H2'	34:a:593:U:C6	2.56	0.41
34:a:657:U:H2'	34:a:658:C:H6	1.85	0.41
34:a:721:G:H4'	34:a:722:G:O4'	2.20	0.41
34:a:860:A:H2'	34:a:861:G:O4'	2.21	0.41
34:a:1135:U:H4'	34:a:1136:C:H5	1.85	0.41
34:a:1241:G:C2'	34:a:1242:G:H5'	2.51	0.41
34:a:1244:G:H2'	34:a:1245:C:H6	1.85	0.41
34:a:1315:U:O2	34:a:1360:A:H2	2.03	0.41
34:a:1397:C:OP2	38:e:28:ARG:NH2	2.54	0.41
34:a:1469:C:H2'	34:a:1470:U:O4'	2.21	0.41
35:b:110:ILE:HD12	35:b:110:ILE:C	2.46	0.41
37:d:139:ASN:N	37:d:181:PHE:O	2.44	0.41
38:e:155:LYS:HG3	38:e:156:ARG:HG3	2.03	0.41
42:i:96:GLU:OE2	42:i:96:GLU:N	2.49	0.41
53:t:29:THR:HA	53:t:32:LYS:HE2	2.02	0.41
1:0:4:GLN:O	8:A:2017:U:H4'	2.21	0.40
2:1:7:LYS:HB3	2:1:7:LYS:HE3	1.66	0.40
8:A:1406:U:H2'	8:A:1407:G:H8	1.86	0.40
8:A:1418:G:H1'	8:A:1580:A:H61	1.86	0.40
8:A:1482:G:H2'	8:A:1483:G:H8	1.86	0.40
8:A:1716:U:H2'	8:A:1717:A:C8	2.56	0.40
8:A:2312:U:OP1	13:F:70:ARG:N	2.42	0.40
8:A:2540:C:H2'	8:A:2541:A:O4'	2.22	0.40
8:A:2857:G:N2	8:A:2860:A:OP2	2.32	0.40
12:E:21:ARG:HD3	12:E:106:LYS:CB	2.50	0.40
23:P:74:GLN:HB2	23:P:77:SER:HB2	2.03	0.40
34:a:269:C:H2'	34:a:270:A:H8	1.86	0.40
34:a:322:C:H2'	34:a:323:U:C6	2.56	0.40
34:a:409:U:OP1	37:d:22:SER:HB3	2.21	0.40
34:a:545:C:H2'	34:a:546:A:O4'	2.21	0.40
34:a:649:A:H2'	34:a:650:G:O4'	2.21	0.40
34:a:672:U:H2'	34:a:673:A:H8	1.86	0.40
34:a:1127:G:H5'	34:a:1280:A:O2'	2.20	0.40
34:a:1135:U:O2'	34:a:1138:G:O6	2.37	0.40
40:g:35:LYS:HG2	42:i:40:ARG:NH2	2.31	0.40
41:h:50:VAL:HG12	41:h:50:VAL:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
46:m:92:ARG:HA	46:m:92:ARG:HD3	1.82	0.40
52:s:42:ASN:OD1	52:s:42:ASN:C	2.63	0.40
53:t:2:ASN:HB3	53:t:3:ILE:H	1.73	0.40
8:A:195:A:H61	8:A:198:C:H3'	1.84	0.40
8:A:197:A:N6	8:A:2430:A:H2'	2.35	0.40
8:A:1029:A:H2'	8:A:1030:C:O4'	2.22	0.40
8:A:1036:G:C6	8:A:1120:G:C6	3.09	0.40
8:A:1203:U:H5'	19:L:3:LEU:HD23	2.02	0.40
8:A:1321:A:C4	8:A:1322:A:C8	3.08	0.40
8:A:1451:C:H4'	8:A:1452:G:O5'	2.21	0.40
8:A:2087:G:H2'	8:A:2088:A:C8	2.56	0.40
8:A:2443:C:H2'	8:A:2444:G:C8	2.56	0.40
10:C:20:ASN:HB3	10:C:23:LEU:HG	2.02	0.40
14:G:10:VAL:HA	14:G:11:PRO:HD3	1.88	0.40
14:G:132:LEU:HB3	14:G:140:ILE:HD11	2.03	0.40
15:H:6:LEU:HD11	15:H:37:VAL:HG13	2.03	0.40
15:H:135:HIS:CG	15:H:136:SER:N	2.89	0.40
18:K:71:ARG:HD3	18:K:71:ARG:HA	1.84	0.40
20:M:53:MET:HE1	20:M:103:TYR:CG	2.56	0.40
22:O:88:LYS:HA	22:O:88:LYS:HD3	1.97	0.40
23:P:108:ARG:NH2	34:a:1464:U:OP2	2.54	0.40
24:Q:107:ALA:HB1	25:R:49:ILE:HD11	2.03	0.40
29:V:71:LYS:HD2	29:V:71:LYS:N	2.37	0.40
30:W:29:ALA:N	30:W:60:ASP:OD1	2.51	0.40
34:a:128:G:H2'	34:a:129:A:C8	2.57	0.40
34:a:320:A:H2'	34:a:321:A:O4'	2.21	0.40
34:a:1313:U:C5	34:a:1324:A:N1	2.89	0.40
34:a:1313:U:OP1	52:s:4:LEU:HB2	2.21	0.40
34:a:1349:A:O2'	34:a:1350:A:OP1	2.37	0.40
45:l:81:ILE:HG23	45:l:94:TYR:HB3	2.03	0.40
56:w:2:C:H2'	56:w:3:C:H6	1.86	0.40
8:A:44:A:H2'	8:A:45:G:O4'	2.21	0.40
8:A:214:G:H2'	8:A:215:G:C8	2.56	0.40
8:A:532:A:N1	8:A:2020:A:H1'	2.36	0.40
8:A:1055:G:OP2	8:A:1055:G:H8	2.03	0.40
8:A:1339:G:P	27:T:15:HIS:HE2	2.44	0.40
8:A:2131:U:H1'	8:A:2158:A:N6	2.36	0.40
8:A:2516:A:O2'	8:A:2517:C:H5'	2.20	0.40
8:A:2808:G:H2'	8:A:2890:G:O6	2.20	0.40
8:A:2861:U:H2'	8:A:2862:G:H8	1.86	0.40
14:G:75:VAL:O	14:G:79:THR:HG23	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
15:H:68:ARG:O	15:H:68:ARG:HD2	2.21	0.40
17:J:17:VAL:HG22	17:J:55:ILE:HB	2.03	0.40
28:U:27:VAL:HG22	28:U:33:VAL:HG12	2.03	0.40
34:a:335:C:C2	34:a:336:A:C8	3.10	0.40
34:a:371:A:O2'	34:a:373:A:N7	2.49	0.40
34:a:1302:C:N3	46:m:16:ILE:HG13	2.37	0.40
43:j:7:ARG:HB2	43:j:101:SER:OG	2.21	0.40
56:w:37:MIA:H163	56:w:37:MIA:H121	1.82	0.40
8:A:177:G:H3'	8:A:178:G:H8	1.86	0.40
8:A:674:G:H1'	12:E:69:ARG:HD3	2.03	0.40
8:A:710:U:H2'	8:A:711:G:H8	1.87	0.40
8:A:863:A:H2'	8:A:864:G:C8	2.57	0.40
8:A:1057:A:C6	8:A:1086:A:H2'	2.57	0.40
8:A:1372:U:O2'	8:A:2212:A:N3	2.52	0.40
8:A:1436:G:H2'	8:A:1437:C:O4'	2.21	0.40
8:A:2107:G:N3	8:A:2107:G:H2'	2.36	0.40
8:A:2646:C:O5'	8:A:2646:C:H6	2.04	0.40
8:A:2718:G:H5'	23:P:97:TYR:CD2	2.57	0.40
8:A:2798:U:P	8:A:2798:U:H6	2.44	0.40
10:C:204:LEU:HB3	10:C:209:ALA:HB3	2.02	0.40
15:H:143:ILE:HD13	15:H:143:ILE:HA	2.00	0.40
20:M:108:VAL:HG13	20:M:112:LEU:HD23	2.04	0.40
26:S:48:LYS:HG2	26:S:52:GLU:OE1	2.21	0.40
32:Y:10:SER:H	32:Y:13:GLU:CD	2.30	0.40
34:a:190:A:H2'	34:a:191:G:O4'	2.22	0.40
34:a:204:G:C6	34:a:205:A:C8	3.10	0.40
34:a:963:G:N2	43:j:57:VAL:HG11	2.35	0.40
38:e:64:GLU:OE2	38:e:68:ARG:NH1	2.54	0.40
38:e:70:MET:HB3	38:e:70:MET:HE2	1.74	0.40
39:f:93:LYS:HB3	39:f:93:LYS:HE2	1.85	0.40
44:k:111:ASP:H	54:u:3:ILE:HG23	1.85	0.40
45:l:102:ASP:OD1	45:l:102:ASP:C	2.64	0.40
8:A:656:G:H2'	8:A:657:U:C6	2.56	0.40
8:A:796:C:H2'	8:A:797:G:C8	2.57	0.40
8:A:858:G:OP1	30:W:74:LYS:HD2	2.22	0.40
8:A:911:A:N6	20:M:11:LYS:O	2.50	0.40
8:A:941:A:H2'	8:A:942:G:O4'	2.21	0.40
8:A:1086:A:H4'	8:A:1087:G:C5	2.56	0.40
8:A:1537:G:N3	8:A:1537:G:H3'	2.36	0.40
8:A:2233:U:H2'	8:A:2234:G:H8	1.85	0.40
8:A:2340:A:H2'	8:A:2341:G:C8	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:2580:PSU:H5'	11:D:135:GLY:O	2.22	0.40
12:E:15:SER:HG	12:E:17:THR:HG1	1.69	0.40
28:U:13:LEU:HD11	28:U:70:ALA:HB2	2.04	0.40
29:V:44:HIS:CE1	29:V:85:LYS:HE2	2.57	0.40
34:a:166:U:H2'	34:a:167:A:H8	1.87	0.40
34:a:521:G:OP2	45:l:50:LYS:NZ	2.39	0.40
34:a:1160:G:C2	34:a:1161:C:C6	3.10	0.40
40:g:46:LEU:HA	40:g:46:LEU:HD12	1.86	0.40
42:i:18:VAL:HG11	42:i:82:ILE:HA	2.02	0.40
47:n:47:LYS:O	47:n:50:THR:OG1	2.36	0.40
55:v:21:A:N6	55:v:46:A:H1'	2.37	0.40
56:w:6:G:H2'	56:w:7:A:C8	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	54/57 (95%)	54 (100%)	0	0	100	100
2	1	48/55 (87%)	48 (100%)	0	0	100	100
3	2	44/46 (96%)	43 (98%)	1 (2%)	0	100	100
4	3	62/65 (95%)	59 (95%)	3 (5%)	0	100	100
5	4	36/38 (95%)	33 (92%)	3 (8%)	0	100	100
6	5	129/165 (78%)	116 (90%)	13 (10%)	0	100	100
7	6	64/70 (91%)	57 (89%)	7 (11%)	0	100	100
10	C	269/273 (98%)	256 (95%)	13 (5%)	0	100	100
11	D	207/209 (99%)	197 (95%)	10 (5%)	0	100	100
12	E	199/201 (99%)	197 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
13	F	175/179 (98%)	161 (92%)	14 (8%)	0	100	100
14	G	174/177 (98%)	172 (99%)	2 (1%)	0	100	100
15	H	147/149 (99%)	128 (87%)	19 (13%)	0	100	100
16	I	139/142 (98%)	130 (94%)	9 (6%)	0	100	100
17	J	140/142 (99%)	138 (99%)	2 (1%)	0	100	100
18	K	120/123 (98%)	116 (97%)	4 (3%)	0	100	100
19	L	141/144 (98%)	133 (94%)	8 (6%)	0	100	100
20	M	134/136 (98%)	129 (96%)	5 (4%)	0	100	100
21	N	118/127 (93%)	113 (96%)	5 (4%)	0	100	100
22	O	114/117 (97%)	112 (98%)	2 (2%)	0	100	100
23	P	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
24	Q	115/118 (98%)	113 (98%)	2 (2%)	0	100	100
25	R	101/103 (98%)	95 (94%)	5 (5%)	1 (1%)	12	12
26	S	108/110 (98%)	106 (98%)	2 (2%)	0	100	100
27	T	91/100 (91%)	91 (100%)	0	0	100	100
28	U	100/104 (96%)	92 (92%)	8 (8%)	0	100	100
29	V	92/94 (98%)	90 (98%)	2 (2%)	0	100	100
30	W	73/85 (86%)	69 (94%)	4 (6%)	0	100	100
31	X	75/78 (96%)	74 (99%)	1 (1%)	0	100	100
32	Y	61/63 (97%)	61 (100%)	0	0	100	100
33	Z	56/59 (95%)	56 (100%)	0	0	100	100
35	b	216/240 (90%)	203 (94%)	13 (6%)	0	100	100
36	c	204/233 (88%)	195 (96%)	9 (4%)	0	100	100
37	d	203/206 (98%)	190 (94%)	13 (6%)	0	100	100
38	e	155/167 (93%)	152 (98%)	3 (2%)	0	100	100
39	f	98/135 (73%)	94 (96%)	4 (4%)	0	100	100
40	g	149/179 (83%)	145 (97%)	4 (3%)	0	100	100
41	h	127/130 (98%)	125 (98%)	2 (2%)	0	100	100
42	i	125/130 (96%)	122 (98%)	3 (2%)	0	100	100
43	j	96/103 (93%)	85 (88%)	11 (12%)	0	100	100
44	k	114/129 (88%)	106 (93%)	8 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
45	l	121/124 (98%)	116 (96%)	5 (4%)	0	100	100
46	m	112/118 (95%)	108 (96%)	4 (4%)	0	100	100
47	n	99/102 (97%)	98 (99%)	1 (1%)	0	100	100
48	o	86/89 (97%)	80 (93%)	6 (7%)	0	100	100
49	p	80/82 (98%)	76 (95%)	4 (5%)	0	100	100
50	q	78/84 (93%)	76 (97%)	2 (3%)	0	100	100
51	r	63/75 (84%)	61 (97%)	2 (3%)	0	100	100
52	s	80/92 (87%)	79 (99%)	1 (1%)	0	100	100
53	t	83/87 (95%)	81 (98%)	2 (2%)	0	100	100
54	u	63/71 (89%)	61 (97%)	2 (3%)	0	100	100
All	All	5850/6220 (94%)	5602 (96%)	247 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
25	R	51	VAL

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	47/48 (98%)	47 (100%)	0	100	100
2	1	45/49 (92%)	45 (100%)	0	100	100
3	2	38/38 (100%)	38 (100%)	0	100	100
4	3	51/52 (98%)	50 (98%)	1 (2%)	48	63
5	4	34/34 (100%)	34 (100%)	0	100	100
7	6	59/62 (95%)	56 (95%)	3 (5%)	21	26
10	C	216/218 (99%)	216 (100%)	0	100	100
11	D	164/164 (100%)	164 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	E	165/165 (100%)	165 (100%)	0	100	100
13	F	148/150 (99%)	146 (99%)	2 (1%)	59	73
14	G	137/138 (99%)	136 (99%)	1 (1%)	76	86
15	H	114/114 (100%)	110 (96%)	4 (4%)	32	42
17	J	116/116 (100%)	115 (99%)	1 (1%)	70	82
18	K	103/104 (99%)	103 (100%)	0	100	100
19	L	102/103 (99%)	102 (100%)	0	100	100
20	M	109/109 (100%)	108 (99%)	1 (1%)	70	82
21	N	100/103 (97%)	99 (99%)	1 (1%)	68	81
22	O	86/87 (99%)	86 (100%)	0	100	100
23	P	99/100 (99%)	98 (99%)	1 (1%)	68	81
24	Q	89/90 (99%)	89 (100%)	0	100	100
25	R	84/84 (100%)	82 (98%)	2 (2%)	43	57
26	S	93/93 (100%)	93 (100%)	0	100	100
27	T	80/84 (95%)	79 (99%)	1 (1%)	61	76
28	U	83/85 (98%)	83 (100%)	0	100	100
29	V	78/78 (100%)	78 (100%)	0	100	100
30	W	57/63 (90%)	57 (100%)	0	100	100
31	X	67/68 (98%)	67 (100%)	0	100	100
32	Y	55/55 (100%)	55 (100%)	0	100	100
33	Z	48/49 (98%)	47 (98%)	1 (2%)	47	61
35	b	180/198 (91%)	180 (100%)	0	100	100
36	c	170/190 (90%)	170 (100%)	0	100	100
37	d	172/173 (99%)	171 (99%)	1 (1%)	78	87
38	e	114/126 (90%)	114 (100%)	0	100	100
39	f	87/116 (75%)	86 (99%)	1 (1%)	65	79
40	g	124/147 (84%)	119 (96%)	5 (4%)	28	37
41	h	104/105 (99%)	102 (98%)	2 (2%)	50	65
42	i	105/107 (98%)	94 (90%)	11 (10%)	6	6
43	j	86/90 (96%)	86 (100%)	0	100	100
44	k	89/99 (90%)	89 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	l	103/104 (99%)	102 (99%)	1 (1%)	68	81
46	m	92/96 (96%)	86 (94%)	6 (6%)	15	18
47	n	79/84 (94%)	78 (99%)	1 (1%)	61	76
48	o	76/77 (99%)	74 (97%)	2 (3%)	40	54
49	p	65/65 (100%)	63 (97%)	2 (3%)	35	47
50	q	74/78 (95%)	73 (99%)	1 (1%)	59	73
51	r	56/65 (86%)	56 (100%)	0	100	100
52	s	72/79 (91%)	67 (93%)	5 (7%)	14	16
53	t	65/66 (98%)	64 (98%)	1 (2%)	57	72
54	u	46/61 (75%)	45 (98%)	1 (2%)	45	59
57	y	1/1 (100%)	1 (100%)	0	100	100
All	All	4627/4830 (96%)	4568 (99%)	59 (1%)	59	76

All (59) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	3	54	LEU
7	6	35	ASP
7	6	59	ARG
7	6	66	ILE
13	F	20	ASN
13	F	174	PHE
14	G	31	GLU
15	H	17	ASP
15	H	48	GLU
15	H	110	VAL
15	H	127	GLU
17	J	129	GLU
20	M	78	LEU
21	N	57	THR
23	P	9	GLN
25	R	43	ASN
25	R	70	GLU
27	T	93	LEU
33	Z	18	LYS
37	d	70	GLN
39	f	39	LEU
40	g	36	SER

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Mol	Chain	Res	Type
40	g	42	VAL
40	g	48	THR
40	g	55	LYS
40	g	119	LEU
41	h	37	ASN
41	h	117	GLN
42	i	13	SER
42	i	27	ILE
42	i	28	VAL
42	i	29	ILE
42	i	47	VAL
42	i	65	THR
42	i	71	ILE
42	i	79	ARG
42	i	84	ARG
42	i	104	THR
42	i	115	VAL
45	l	101	LEU
46	m	2	ARG
46	m	6	ILE
46	m	15	VAL
46	m	42	VAL
46	m	53	ASP
46	m	59	VAL
47	n	45	VAL
48	o	13	GLU
48	o	39	GLN
49	p	46	LYS
49	p	74	LEU
50	q	41	THR
52	s	18	VAL
52	s	47	THR
52	s	57	VAL
52	s	78	THR
52	s	80	ARG
53	t	81	GLN
54	u	13	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (51) such sidechains are listed below:

Mol	Chain	Res	Type
5	4	13	ASN

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Mol	Chain	Res	Type
10	C	52	HIS
10	C	89	ASN
11	D	42	ASN
11	D	58	ASN
12	E	9	GLN
12	E	90	GLN
12	E	92	HIS
12	E	136	GLN
15	H	2	GLN
17	J	47	HIS
17	J	58	ASN
18	K	5	GLN
20	M	13	HIS
21	N	9	GLN
21	N	31	HIS
21	N	62	ASN
22	O	116	GLN
23	P	6	GLN
23	P	40	GLN
23	P	65	ASN
24	Q	70	GLN
27	T	70	HIS
27	T	72	GLN
28	U	39	ASN
29	V	5	ASN
30	W	8	ASN
32	Y	15	ASN
32	Y	36	GLN
32	Y	39	GLN
32	Y	45	GLN
35	b	108	GLN
36	c	99	GLN
37	d	197	HIS
38	e	69	ASN
38	e	77	ASN
38	e	131	ASN
38	e	147	ASN
39	f	3	HIS
41	h	3	GLN
41	h	20	ASN
43	j	58	ASN
44	k	21	HIS

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Mol	Chain	Res	Type
44	k	100	ASN
47	n	49	GLN
48	o	49	HIS
49	p	9	HIS
49	p	59	HIS
53	t	19	HIS
53	t	60	GLN
54	u	55	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	a	1539/1542 (99%)	314 (20%)	0
55	v	76/77 (98%)	18 (23%)	0
56	w	75/76 (98%)	18 (24%)	0
58	z	10/33 (30%)	1 (10%)	0
8	A	2902/2903 (99%)	518 (17%)	37 (1%)
9	B	119/120 (99%)	23 (19%)	4 (3%)
All	All	4721/4751 (99%)	892 (18%)	41 (0%)

All (892) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	A	10	A
8	A	15	G
8	A	23	G
8	A	34	U
8	A	35	G
8	A	42	A
8	A	43	G
8	A	46	G
8	A	62	U
8	A	63	A
8	A	71	A
8	A	74	A
8	A	75	G
8	A	101	A
8	A	118	A
8	A	120	U
8	A	125	A
8	A	131	A

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Mol	Chain	Res	Type
8	A	142	A
8	A	160	A
8	A	163	C
8	A	164	C
8	A	170	U
8	A	196	A
8	A	199	A
8	A	205	G
8	A	215	G
8	A	216	A
8	A	221	A
8	A	222	A
8	A	223	A
8	A	224	U
8	A	228	C
8	A	230	G
8	A	242	G
8	A	243	U
8	A	248	G
8	A	255	A
8	A	261	G
8	A	265	A
8	A	266	G
8	A	272	A
8	A	275	C
8	A	276	U
8	A	278	A
8	A	279	A
8	A	288	U
8	A	311	A
8	A	330	A
8	A	345	A
8	A	360	U
8	A	371	A
8	A	372	G
8	A	386	G
8	A	395	U
8	A	401	A
8	A	402	A
8	A	404	A
8	A	405	U
8	A	406	G

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Mol	Chain	Res	Type
8	A	411	G
8	A	455	C
8	A	457	A
8	A	458	G
8	A	459	U
8	A	473	G
8	A	480	A
8	A	481	G
8	A	482	A
8	A	491	G
8	A	504	A
8	A	505	A
8	A	509	C
8	A	529	A
8	A	530	G
8	A	531	C
8	A	532	A
8	A	544	C
8	A	545	U
8	A	546	U
8	A	547	A
8	A	548	G
8	A	549	G
8	A	556	A
8	A	563	A
8	A	568	U
8	A	573	U
8	A	575	A
8	A	603	A
8	A	614	A
8	A	615	U
8	A	622	G
8	A	627	A
8	A	637	A
8	A	645	C
8	A	647	G
8	A	654	A
8	A	655	A
8	A	669	G
8	A	670	A
8	A	677	A
8	A	682	G

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Mol	Chain	Res	Type
8	A	685	A
8	A	686	U
8	A	715	A
8	A	716	A
8	A	717	C
8	A	729	G
8	A	730	A
8	A	747	5MC
8	A	764	A
8	A	775	G
8	A	782	A
8	A	784	G
8	A	785	G
8	A	789	A
8	A	805	G
8	A	812	C
8	A	819	A
8	A	827	U
8	A	828	U
8	A	846	U
8	A	847	U
8	A	856	G
8	A	858	G
8	A	859	G
8	A	885	C
8	A	887	A
8	A	888	C
8	A	891	G
8	A	892	A
8	A	894	U
8	A	895	U
8	A	896	A
8	A	898	C
8	A	903	C
8	A	907	G
8	A	910	A
8	A	931	U
8	A	941	A
8	A	946	C
8	A	961	C
8	A	973	A
8	A	974	G

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Mol	Chain	Res	Type
8	A	975	A
8	A	983	A
8	A	995	C
8	A	996	A
8	A	1005	C
8	A	1012	U
8	A	1013	C
8	A	1026	G
8	A	1033	U
8	A	1041	G
8	A	1046	A
8	A	1047	G
8	A	1048	A
8	A	1053	C
8	A	1054	A
8	A	1056	G
8	A	1057	A
8	A	1058	U
8	A	1059	G
8	A	1060	U
8	A	1061	U
8	A	1062	G
8	A	1063	G
8	A	1064	C
8	A	1066	U
8	A	1067	A
8	A	1068	G
8	A	1069	A
8	A	1070	A
8	A	1072	C
8	A	1073	A
8	A	1074	G
8	A	1075	C
8	A	1077	A
8	A	1078	U
8	A	1079	C
8	A	1080	A
8	A	1081	U
8	A	1082	U
8	A	1083	U
8	A	1084	A
8	A	1085	A

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Mol	Chain	Res	Type
8	A	1086	A
8	A	1087	G
8	A	1088	A
8	A	1090	A
8	A	1091	G
8	A	1093	G
8	A	1094	U
8	A	1096	A
8	A	1098	A
8	A	1100	C
8	A	1101	U
8	A	1102	C
8	A	1103	A
8	A	1105	U
8	A	1109	C
8	A	1111	A
8	A	1112	G
8	A	1115	G
8	A	1132	U
8	A	1133	A
8	A	1134	A
8	A	1135	C
8	A	1142	A
8	A	1171	G
8	A	1174	U
8	A	1175	A
8	A	1176	U
8	A	1179	G
8	A	1180	U
8	A	1212	G
8	A	1225	G
8	A	1227	G
8	A	1236	G
8	A	1247	A
8	A	1250	G
8	A	1253	A
8	A	1256	G
8	A	1262	A
8	A	1264	A
8	A	1271	G
8	A	1272	A
8	A	1300	G

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Mol	Chain	Res	Type
8	A	1301	A
8	A	1306	C
8	A	1329	U
8	A	1352	U
8	A	1365	A
8	A	1368	G
8	A	1376	C
8	A	1378	A
8	A	1379	U
8	A	1383	A
8	A	1395	A
8	A	1415	U
8	A	1416	G
8	A	1420	A
8	A	1421	G
8	A	1428	C
8	A	1432	G
8	A	1452	G
8	A	1453	A
8	A	1460	U
8	A	1461	C
8	A	1475	G
8	A	1482	G
8	A	1490	A
8	A	1491	G
8	A	1493	C
8	A	1494	A
8	A	1497	U
8	A	1508	A
8	A	1509	A
8	A	1515	A
8	A	1524	G
8	A	1532	A
8	A	1534	U
8	A	1536	C
8	A	1554	U
8	A	1563	U
8	A	1566	A
8	A	1569	A
8	A	1578	U
8	A	1584	U
8	A	1591	A

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Mol	Chain	Res	Type
8	A	1608	A
8	A	1610	A
8	A	1626	A
8	A	1634	A
8	A	1635	A
8	A	1647	U
8	A	1648	U
8	A	1649	G
8	A	1651	G
8	A	1674	G
8	A	1693	U
8	A	1715	G
8	A	1716	U
8	A	1726	C
8	A	1730	C
8	A	1731	G
8	A	1738	G
8	A	1764	C
8	A	1773	A
8	A	1782	U
8	A	1784	A
8	A	1786	A
8	A	1791	A
8	A	1800	C
8	A	1801	A
8	A	1807	G
8	A	1808	A
8	A	1816	C
8	A	1829	A
8	A	1838	C
8	A	1847	G
8	A	1848	A
8	A	1857	G
8	A	1869	G
8	A	1884	G
8	A	1900	A
8	A	1901	A
8	A	1906	G
8	A	1908	C
8	A	1910	G
8	A	1916	A
8	A	1917	PSU

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Mol	Chain	Res	Type
8	A	1918	A
8	A	1919	A
8	A	1922	G
8	A	1923	U
8	A	1924	C
8	A	1925	C
8	A	1926	U
8	A	1929	G
8	A	1930	G
8	A	1937	A
8	A	1938	A
8	A	1939	5MU
8	A	1955	U
8	A	1964	G
8	A	1967	C
8	A	1970	A
8	A	1971	U
8	A	1972	G
8	A	1982	U
8	A	1991	U
8	A	1993	U
8	A	1997	C
8	A	2020	A
8	A	2022	U
8	A	2023	C
8	A	2030	6MZ
8	A	2031	A
8	A	2032	G
8	A	2033	A
8	A	2036	C
8	A	2043	C
8	A	2046	G
8	A	2055	C
8	A	2056	G
8	A	2060	A
8	A	2061	G
8	A	2062	A
8	A	2069	G7M
8	A	2070	A
8	A	2093	G
8	A	2101	A
8	A	2102	G

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Mol	Chain	Res	Type
8	A	2103	C
8	A	2104	C
8	A	2110	G
8	A	2111	U
8	A	2112	G
8	A	2114	A
8	A	2116	G
8	A	2118	U
8	A	2119	A
8	A	2120	G
8	A	2125	G
8	A	2126	A
8	A	2127	G
8	A	2128	G
8	A	2129	C
8	A	2130	U
8	A	2131	U
8	A	2132	U
8	A	2133	G
8	A	2134	A
8	A	2135	A
8	A	2136	G
8	A	2138	G
8	A	2139	U
8	A	2143	C
8	A	2145	C
8	A	2146	C
8	A	2147	A
8	A	2148	G
8	A	2150	C
8	A	2151	U
8	A	2153	C
8	A	2155	U
8	A	2157	G
8	A	2159	G
8	A	2160	C
8	A	2161	C
8	A	2162	G
8	A	2163	A
8	A	2164	C
8	A	2169	A
8	A	2170	A

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Mol	Chain	Res	Type
8	A	2171	A
8	A	2172	U
8	A	2173	A
8	A	2175	C
8	A	2180	U
8	A	2181	U
8	A	2183	A
8	A	2186	G
8	A	2187	U
8	A	2188	U
8	A	2190	G
8	A	2193	G
8	A	2198	A
8	A	2204	G
8	A	2211	A
8	A	2225	A
8	A	2226	C
8	A	2238	G
8	A	2239	G
8	A	2268	A
8	A	2279	G
8	A	2283	C
8	A	2287	A
8	A	2288	A
8	A	2297	A
8	A	2305	U
8	A	2307	G
8	A	2309	A
8	A	2311	A
8	A	2320	U
8	A	2322	A
8	A	2325	G
8	A	2333	A
8	A	2336	A
8	A	2345	G
8	A	2347	C
8	A	2350	C
8	A	2357	G
8	A	2361	G
8	A	2383	G
8	A	2385	C
8	A	2402	U

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Mol	Chain	Res	Type
8	A	2406	A
8	A	2410	G
8	A	2423	U
8	A	2425	A
8	A	2429	G
8	A	2430	A
8	A	2435	A
8	A	2441	U
8	A	2445	2MG
8	A	2448	A
8	A	2459	A
8	A	2469	A
8	A	2475	C
8	A	2476	A
8	A	2478	A
8	A	2480	C
8	A	2484	G
8	A	2494	G
8	A	2498	OMC
8	A	2502	G
8	A	2503	2MA
8	A	2505	G
8	A	2518	A
8	A	2529	G
8	A	2535	G
8	A	2547	A
8	A	2554	U
8	A	2566	A
8	A	2567	G
8	A	2573	C
8	A	2585	U
8	A	2602	A
8	A	2609	U
8	A	2613	U
8	A	2615	U
8	A	2629	U
8	A	2630	G
8	A	2634	A
8	A	2636	C
8	A	2656	U
8	A	2689	U
8	A	2690	U

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Mol	Chain	Res	Type
8	A	2702	G
8	A	2707	U
8	A	2714	G
8	A	2716	C
8	A	2718	G
8	A	2726	A
8	A	2732	G
8	A	2733	A
8	A	2739	U
8	A	2744	G
8	A	2748	A
8	A	2755	C
8	A	2757	A
8	A	2765	A
8	A	2769	U
8	A	2778	A
8	A	2779	U
8	A	2791	G
8	A	2796	U
8	A	2797	U
8	A	2798	U
8	A	2799	A
8	A	2800	A
8	A	2809	A
8	A	2818	U
8	A	2820	A
8	A	2821	A
8	A	2835	A
8	A	2849	U
8	A	2867	G
8	A	2872	A
8	A	2873	A
8	A	2879	A
8	A	2884	U
8	A	2886	A
8	A	2891	U
8	A	2893	A
8	A	2902	C
9	B	13	G
9	B	24	G
9	B	32	U
9	B	33	G

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Mol	Chain	Res	Type
9	B	35	C
9	B	37	C
9	B	42	C
9	B	44	G
9	B	45	A
9	B	51	G
9	B	53	A
9	B	56	G
9	B	62	C
9	B	65	U
9	B	67	G
9	B	73	A
9	B	88	C
9	B	89	U
9	B	90	C
9	B	91	C
9	B	101	A
9	B	109	A
9	B	120	U
34	a	6	G
34	a	7	A
34	a	9	G
34	a	22	G
34	a	32	A
34	a	39	G
34	a	47	C
34	a	48	C
34	a	50	A
34	a	51	A
34	a	70	U
34	a	71	A
34	a	76	G
34	a	77	A
34	a	78	A
34	a	80	A
34	a	81	A
34	a	83	C
34	a	84	U
34	a	85	U
34	a	86	G
34	a	89	U
34	a	90	C

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Mol	Chain	Res	Type
34	a	94	G
34	a	96	U
34	a	119	A
34	a	121	U
34	a	130	A
34	a	141	G
34	a	144	G
34	a	163	C
34	a	164	G
34	a	165	G
34	a	166	U
34	a	173	U
34	a	182	A
34	a	183	C
34	a	184	G
34	a	197	A
34	a	198	G
34	a	205	A
34	a	208	U
34	a	210	C
34	a	211	G
34	a	219	U
34	a	226	G
34	a	240	G
34	a	245	U
34	a	247	G
34	a	251	G
34	a	266	G
34	a	267	C
34	a	271	C
34	a	289	G
34	a	299	G
34	a	306	A
34	a	321	A
34	a	328	C
34	a	329	A
34	a	330	C
34	a	344	A
34	a	351	G
34	a	352	C
34	a	354	G
34	a	367	U

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Mol	Chain	Res	Type
34	a	372	C
34	a	373	A
34	a	388	G
34	a	397	A
34	a	406	G
34	a	411	A
34	a	413	G
34	a	414	A
34	a	421	U
34	a	423	G
34	a	429	U
34	a	461	A
34	a	462	G
34	a	465	A
34	a	468	A
34	a	471	U
34	a	479	U
34	a	484	G
34	a	495	A
34	a	496	A
34	a	509	A
34	a	510	A
34	a	511	C
34	a	516	PSU
34	a	518	C
34	a	521	G
34	a	531	U
34	a	535	A
34	a	536	C
34	a	547	A
34	a	550	G
34	a	559	A
34	a	562	U
34	a	564	C
34	a	572	A
34	a	573	A
34	a	576	C
34	a	577	G
34	a	596	A
34	a	615	G
34	a	629	A
34	a	633	G

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Mol	Chain	Res	Type
34	a	642	A
34	a	650	G
34	a	653	U
34	a	665	A
34	a	666	G
34	a	688	G
34	a	703	G
34	a	704	A
34	a	723	U
34	a	724	G
34	a	733	G
34	a	734	G
34	a	748	G
34	a	753	A
34	a	755	G
34	a	774	G
34	a	777	A
34	a	781	A
34	a	792	A
34	a	793	U
34	a	794	A
34	a	799	G
34	a	815	A
34	a	817	C
34	a	841	C
34	a	842	U
34	a	843	U
34	a	844	G
34	a	845	A
34	a	846	G
34	a	851	G
34	a	867	G
34	a	885	G
34	a	902	G
34	a	914	A
34	a	934	C
34	a	935	A
34	a	953	G
34	a	954	G
34	a	955	U
34	a	956	U
34	a	957	U

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Mol	Chain	Res	Type
34	a	958	A
34	a	960	U
34	a	969	A
34	a	971	G
34	a	975	A
34	a	976	G
34	a	977	A
34	a	980	C
34	a	983	A
34	a	985	C
34	a	986	U
34	a	988	G
34	a	989	U
34	a	990	C
34	a	992	U
34	a	993	G
34	a	994	A
34	a	995	C
34	a	996	A
34	a	997	U
34	a	999	C
34	a	1000	A
34	a	1004	A
34	a	1005	A
34	a	1006	G
34	a	1007	U
34	a	1011	C
34	a	1014	A
34	a	1015	G
34	a	1020	G
34	a	1022	A
34	a	1023	U
34	a	1024	G
34	a	1027	C
34	a	1028	C
34	a	1029	U
34	a	1031	C
34	a	1032	G
34	a	1035	A
34	a	1036	A
34	a	1037	C
34	a	1040	U

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Mol	Chain	Res	Type
34	a	1042	A
34	a	1043	G
34	a	1044	A
34	a	1065	U
34	a	1085	U
34	a	1094	G
34	a	1101	A
34	a	1104	G
34	a	1124	G
34	a	1125	U
34	a	1132	C
34	a	1134	G
34	a	1136	C
34	a	1137	C
34	a	1139	G
34	a	1159	U
34	a	1160	G
34	a	1167	A
34	a	1168	U
34	a	1183	U
34	a	1184	G
34	a	1196	A
34	a	1197	A
34	a	1212	U
34	a	1213	A
34	a	1214	C
34	a	1215	G
34	a	1227	A
34	a	1229	A
34	a	1230	C
34	a	1236	A
34	a	1238	A
34	a	1239	A
34	a	1242	G
34	a	1243	C
34	a	1248	A
34	a	1250	A
34	a	1254	A
34	a	1255	G
34	a	1257	A
34	a	1258	G
34	a	1260	G

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Mol	Chain	Res	Type
34	a	1261	A
34	a	1272	G
34	a	1275	A
34	a	1280	A
34	a	1285	A
34	a	1286	U
34	a	1287	A
34	a	1294	G
34	a	1297	G
34	a	1298	U
34	a	1299	A
34	a	1300	G
34	a	1302	C
34	a	1305	G
34	a	1306	A
34	a	1307	U
34	a	1309	G
34	a	1310	G
34	a	1311	A
34	a	1312	G
34	a	1314	C
34	a	1315	U
34	a	1316	G
34	a	1317	C
34	a	1323	G
34	a	1324	A
34	a	1335	U
34	a	1336	C
34	a	1344	C
34	a	1345	U
34	a	1346	A
34	a	1347	G
34	a	1350	A
34	a	1353	G
34	a	1355	G
34	a	1356	G
34	a	1357	A
34	a	1362	A
34	a	1363	A
34	a	1370	G
34	a	1371	G
34	a	1372	U

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Mol	Chain	Res	Type
34	a	1374	A
34	a	1378	C
34	a	1379	G
34	a	1381	U
34	a	1383	C
34	a	1397	C
34	a	1398	A
34	a	1419	G
34	a	1421	G
34	a	1422	G
34	a	1429	A
34	a	1432	G
34	a	1433	A
34	a	1440	U
34	a	1441	A
34	a	1442	G
34	a	1446	A
34	a	1451	U
34	a	1452	C
34	a	1472	U
34	a	1473	G
34	a	1475	G
34	a	1487	G
34	a	1492	A
34	a	1494	G
34	a	1497	G
34	a	1499	A
34	a	1506	U
34	a	1517	G
34	a	1519	MA6
34	a	1520	C
34	a	1529	G
34	a	1530	G
34	a	1534	A
34	a	1535	C
34	a	1536	C
34	a	1538	C
34	a	1539	C
34	a	1540	U
55	v	9	G
55	v	18	G
55	v	19	G

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Mol	Chain	Res	Type
55	v	20	H2U
55	v	21	A
55	v	30	G
55	v	33	U
55	v	34	C
55	v	37	A
55	v	44	A
55	v	45	G
55	v	47	U
55	v	48	C
55	v	52	G
55	v	56	C
55	v	70	G
55	v	74	C
55	v	76	A
56	w	10	G
56	w	13	C
56	w	16	U
56	w	17	C
56	w	18	G
56	w	19	G
56	w	20	U
56	w	21	A
56	w	45	U
56	w	46	G7M
56	w	47	U
56	w	48	C
56	w	49	C
56	w	59	U
56	w	60	U
56	w	67	C
56	w	68	C
56	w	74	C
58	z	0	U

All (41) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
8	A	242	G
8	A	310	A
8	A	458	G
8	A	479	A

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Mol	Chain	Res	Type
8	A	481	G
8	A	504	A
8	A	545	U
8	A	555	G
8	A	715	A
8	A	774	G
8	A	784	G
8	A	887	A
8	A	954	G
8	A	976	G
8	A	1014	A
8	A	1023	U
8	A	1062	G
8	A	1082	U
8	A	1090	A
8	A	1093	G
8	A	1361	G
8	A	1432	G
8	A	1451	C
8	A	1490	A
8	A	1715	G
8	A	1730	C
8	A	1847	G
8	A	2150	C
8	A	2158	A
8	A	2192	U
8	A	2287	A
8	A	2319	G
8	A	2468	A
8	A	2655	G
8	A	2756	U
8	A	2796	U
8	A	2808	G
9	B	36	C
9	B	44	G
9	B	52	A
9	B	66	A

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

46 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$
34	MA6	a	1518	34	23,26,27	1.45	4 (17%)	34,38,41	2.75	12 (35%)
34	2MG	a	1207	34	23,26,27	2.93	8 (34%)	32,38,41	2.22	11 (34%)
8	OMC	A	2498	8,59	19,22,23	2.86	7 (36%)	26,31,34	0.75	0
8	PSU	A	955	8	18,21,22	1.03	1 (5%)	22,30,33	1.86	5 (22%)
8	PSU	A	1917	8	18,21,22	1.03	1 (5%)	22,30,33	1.75	5 (22%)
8	2MG	A	2445	8	23,26,27	2.88	9 (39%)	32,38,41	2.22	12 (37%)
8	PSU	A	2457	8	18,21,22	1.06	1 (5%)	22,30,33	1.86	5 (22%)
56	5MU	w	54	56	19,22,23	4.79	7 (36%)	28,32,35	3.65	9 (32%)
56	G7M	w	46	56	23,26,27	2.62	8 (34%)	35,39,42	2.24	10 (28%)
8	6MZ	A	1618	8	22,25,26	2.98	5 (22%)	30,36,39	4.28	13 (43%)
56	PSU	w	32	56	18,21,22	1.02	1 (5%)	22,30,33	1.70	4 (18%)
34	MA6	a	1519	34	23,26,27	1.45	5 (21%)	34,38,41	2.78	12 (35%)
56	PSU	w	55	56	18,21,22	1.06	1 (5%)	22,30,33	1.97	5 (22%)
8	PSU	A	746	8,59	18,21,22	1.05	1 (5%)	22,30,33	1.71	4 (18%)
55	H2U	v	20	55	18,21,22	3.08	5 (27%)	21,30,33	1.98	5 (23%)
34	4OC	a	1402	34	20,23,24	2.97	8 (40%)	26,32,35	0.90	1 (3%)
8	PSU	A	2605	8	18,21,22	1.04	1 (5%)	22,30,33	1.81	4 (18%)
8	OMU	A	2552	8,59	19,22,23	2.89	8 (42%)	26,31,34	1.76	5 (19%)
55	4SU	v	8	55	18,21,22	3.59	7 (38%)	26,30,33	2.22	4 (15%)
34	2MG	a	966	34	23,26,27	2.92	8 (34%)	32,38,41	2.24	11 (34%)
34	5MC	a	967	34	18,22,23	3.68	7 (38%)	26,32,35	1.00	2 (7%)
34	UR3	a	1498	34	19,22,23	2.68	7 (36%)	26,32,35	1.37	3 (11%)
34	2MG	a	1516	34	23,26,27	2.90	8 (34%)	32,38,41	2.28	12 (37%)
8	2MG	A	1835	8	23,26,27	2.92	8 (34%)	32,38,41	2.25	11 (34%)
8	5MC	A	1962	8	18,22,23	3.65	7 (38%)	26,32,35	1.04	2 (7%)
56	4SU	w	8	56	18,21,22	3.56	7 (38%)	26,30,33	2.20	4 (15%)
34	G7M	a	527	34	23,26,27	2.60	8 (34%)	35,39,42	2.29	10 (28%)
8	1MG	A	745	8	22,26,27	2.64	5 (22%)	33,39,42	2.01	8 (24%)
8	2MA	A	2503	8,59	22,25,26	3.76	8 (36%)	33,37,40	2.24	7 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
56	MIA	w	37	56	28,31,32	2.54	6 (21%)	40,44,47	3.05	16 (40%)
8	OMG	A	2251	8,59,55	23,26,27	2.38	9 (39%)	33,38,41	1.83	8 (24%)
55	PSU	v	55	55	18,21,22	1.06	1 (5%)	22,30,33	1.68	4 (18%)
8	5MU	A	1939	8	19,22,23	4.76	7 (36%)	28,32,35	3.79	10 (35%)
8	PSU	A	1911	8	18,21,22	1.06	1 (5%)	22,30,33	1.80	4 (18%)
8	PSU	A	2580	8	18,21,22	1.10	2 (11%)	22,30,33	1.90	6 (27%)
34	PSU	a	516	34,59	18,21,22	0.98	1 (5%)	22,30,33	1.70	5 (22%)
8	6MZ	A	2030	8	22,25,26	2.89	5 (22%)	30,36,39	4.36	14 (46%)
55	5MU	v	54	55	19,22,23	4.81	7 (36%)	28,32,35	3.66	9 (32%)
8	PSU	A	2604	8	18,21,22	1.01	1 (5%)	22,30,33	1.85	4 (18%)
56	PSU	w	39	56	18,21,22	1.09	1 (5%)	22,30,33	1.71	3 (13%)
8	5MC	A	747	8	18,22,23	3.65	7 (38%)	26,32,35	1.09	2 (7%)
8	G7M	A	2069	8	23,26,27	2.56	8 (34%)	35,39,42	2.38	11 (31%)
8	PSU	A	2504	8	18,21,22	1.09	1 (5%)	22,30,33	1.78	4 (18%)
57	FME	y	101	57	8,9,10	0.88	0	7,9,11	1.81	2 (28%)
8	3TD	A	1915	8	18,22,23	4.25	5 (27%)	22,32,35	1.65	2 (9%)
34	5MC	a	1407	34	18,22,23	3.69	7 (38%)	26,32,35	1.03	2 (7%)

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
34	MA6	a	1518	34	-	0/11/29/30	0/3/3/3
34	2MG	a	1207	34	-	0/9/27/28	0/3/3/3
8	OMC	A	2498	8,59	-	2/9/27/28	0/2/2/2
8	PSU	A	955	8	-	0/7/25/26	0/2/2/2
8	PSU	A	1917	8	-	1/7/25/26	0/2/2/2
8	2MG	A	2445	8	-	2/9/27/28	0/3/3/3
8	PSU	A	2457	8	-	0/7/25/26	0/2/2/2
56	5MU	w	54	56	-	0/7/25/26	0/2/2/2
56	G7M	w	46	56	-	0/7/25/26	0/3/3/3
8	6MZ	A	1618	8	-	0/9/27/28	0/3/3/3
56	PSU	w	32	56	-	3/7/25/26	0/2/2/2
34	MA6	a	1519	34	-	1/11/29/30	0/3/3/3
56	PSU	w	55	56	-	1/7/25/26	0/2/2/2
8	PSU	A	746	8,59	-	2/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
55	H2U	v	20	55	-	3/7/38/39	0/2/2/2
34	4OC	a	1402	34	-	2/9/29/30	0/2/2/2
8	PSU	A	2605	8	-	0/7/25/26	0/2/2/2
8	OMU	A	2552	8,59	-	3/9/27/28	0/2/2/2
55	4SU	v	8	55	-	0/7/25/26	0/2/2/2
34	2MG	a	966	34	-	0/9/27/28	0/3/3/3
34	5MC	a	967	34	-	0/7/25/26	0/2/2/2
34	UR3	a	1498	34	-	2/7/25/26	0/2/2/2
34	2MG	a	1516	34	-	0/9/27/28	0/3/3/3
8	2MG	A	1835	8	-	2/9/27/28	0/3/3/3
8	5MC	A	1962	8	-	2/7/25/26	0/2/2/2
56	4SU	w	8	56	-	0/7/25/26	0/2/2/2
34	G7M	a	527	34	-	1/7/25/26	0/3/3/3
8	1MG	A	745	8	-	0/7/25/26	0/3/3/3
8	2MA	A	2503	8,59	-	2/7/25/26	0/3/3/3
56	MIA	w	37	56	-	2/15/33/34	0/3/3/3
8	OMG	A	2251	8,59,55	-	1/9/27/28	0/3/3/3
55	PSU	v	55	55	-	2/7/25/26	0/2/2/2
8	5MU	A	1939	8	-	2/7/25/26	0/2/2/2
8	PSU	A	1911	8	-	0/7/25/26	0/2/2/2
8	PSU	A	2580	8	-	0/7/25/26	0/2/2/2
34	PSU	a	516	34,59	-	0/7/25/26	0/2/2/2
8	6MZ	A	2030	8	-	2/9/27/28	0/3/3/3
55	5MU	v	54	55	-	0/7/25/26	0/2/2/2
8	PSU	A	2604	8	-	0/7/25/26	0/2/2/2
56	PSU	w	39	56	-	3/7/25/26	0/2/2/2
8	5MC	A	747	8	-	0/7/25/26	0/2/2/2
8	G7M	A	2069	8	-	1/7/25/26	0/3/3/3
8	PSU	A	2504	8	-	2/7/25/26	0/2/2/2
57	FME	y	101	57	-	5/7/9/11	-
8	3TD	A	1915	8	-	3/7/25/26	0/2/2/2
34	5MC	a	1407	34	-	0/7/25/26	0/2/2/2

All (230) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	1915	3TD	C6-C5	12.88	1.50	1.35
8	A	1618	6MZ	C6-N6	12.29	1.47	1.34
8	A	2503	2MA	C4-N3	11.97	1.49	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	A	2030	6MZ	C6-N6	11.67	1.46	1.34
55	v	54	5MU	C2-N1	11.06	1.56	1.38
56	w	54	5MU	C2-N1	10.96	1.56	1.38
55	v	54	5MU	C6-N1	10.38	1.55	1.38
8	A	1939	5MU	C2-N1	10.36	1.55	1.38
56	w	54	5MU	C6-N1	10.36	1.55	1.38
8	A	1939	5MU	C6-N1	10.27	1.55	1.38
55	v	54	5MU	C4-C5	10.10	1.61	1.44
8	A	1939	5MU	C4-C5	9.87	1.61	1.44
56	w	54	5MU	C4-C5	9.86	1.61	1.44
55	v	20	H2U	C2-N1	9.43	1.49	1.35
34	a	1407	5MC	C6-C5	9.38	1.50	1.34
8	A	1915	3TD	C2-N1	9.23	1.49	1.37
34	a	967	5MC	C6-C5	9.19	1.49	1.34
8	A	1962	5MC	C6-C5	9.18	1.49	1.34
8	A	747	5MC	C6-C5	9.17	1.49	1.34
8	A	1939	5MU	C4-N3	-8.16	1.23	1.38
55	v	8	4SU	C4-N3	7.95	1.46	1.37
56	w	8	4SU	C4-N3	7.90	1.46	1.37
56	w	54	5MU	C4-N3	-7.86	1.24	1.38
55	v	54	5MU	C4-N3	-7.72	1.24	1.38
34	a	966	2MG	C2-N3	7.44	1.46	1.31
34	a	1207	2MG	C2-N3	7.41	1.46	1.31
8	A	1835	2MG	C2-N3	7.34	1.45	1.31
55	v	8	4SU	C2-N1	7.34	1.50	1.38
34	a	1516	2MG	C2-N3	7.27	1.45	1.31
56	w	8	4SU	C2-N1	7.25	1.50	1.38
56	w	37	MIA	C13-C14	7.19	1.53	1.32
8	A	745	1MG	C2-N2	7.18	1.47	1.34
8	A	2445	2MG	C2-N3	7.13	1.45	1.31
56	w	37	MIA	C2-S10	7.01	1.81	1.75
8	A	1962	5MC	C4-N3	6.83	1.45	1.34
34	a	1498	UR3	C2-N1	6.82	1.48	1.38
34	a	967	5MC	C4-N3	6.81	1.45	1.34
8	A	2503	2MA	C2-N3	6.79	1.46	1.34
8	A	2552	OMU	C2-N1	6.74	1.49	1.38
8	A	747	5MC	C4-N3	6.69	1.45	1.34
34	a	1407	5MC	C4-N3	6.67	1.45	1.34
56	w	37	MIA	C6-N6	6.57	1.44	1.34
34	a	1402	4OC	C4-N3	6.56	1.44	1.32
55	v	20	H2U	C2-N3	6.49	1.49	1.38
8	A	1835	2MG	C4-N3	6.38	1.49	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	a	966	2MG	C4-N3	6.37	1.49	1.34
34	a	1207	2MG	C4-N3	6.36	1.49	1.34
34	a	527	G7M	C4-N3	6.35	1.49	1.34
8	A	745	1MG	C4-N3	6.30	1.49	1.34
8	A	2552	OMU	C2-N3	6.30	1.49	1.38
56	w	46	G7M	C4-N3	6.28	1.49	1.34
34	a	1207	2MG	C2-N2	6.27	1.47	1.33
34	a	1516	2MG	C2-N2	6.25	1.47	1.33
34	a	1516	2MG	C4-N3	6.24	1.49	1.34
34	a	967	5MC	C2-N3	6.23	1.49	1.36
8	A	2069	G7M	C4-N3	6.21	1.49	1.34
8	A	2498	OMC	C6-C5	6.21	1.49	1.35
8	A	1835	2MG	C2-N2	6.20	1.47	1.33
8	A	2445	2MG	C4-N3	6.19	1.49	1.34
8	A	1962	5MC	C2-N3	6.17	1.48	1.36
34	a	966	2MG	C2-N2	6.14	1.47	1.33
8	A	2251	OMG	C4-N3	6.14	1.48	1.34
8	A	2445	2MG	C2-N2	6.12	1.47	1.33
34	a	1498	UR3	C6-C5	6.10	1.49	1.35
8	A	747	5MC	C2-N3	6.10	1.48	1.36
34	a	1407	5MC	C2-N3	6.07	1.48	1.36
34	a	1402	4OC	C6-C5	6.02	1.49	1.35
8	A	1939	5MU	C6-C5	5.94	1.44	1.34
56	w	8	4SU	C6-C5	5.88	1.48	1.35
8	A	2498	OMC	C2-N3	5.87	1.48	1.36
55	v	8	4SU	C6-C5	5.83	1.48	1.35
55	v	54	5MU	C6-C5	5.77	1.44	1.34
56	w	46	G7M	C2-N3	5.70	1.46	1.33
8	A	2503	2MA	C2-N1	5.69	1.44	1.34
8	A	2503	2MA	C6-N1	5.68	1.43	1.35
56	w	54	5MU	C6-C5	5.67	1.43	1.34
8	A	1915	3TD	C6-N1	5.66	1.45	1.36
34	a	527	G7M	C2-N3	5.64	1.46	1.33
34	a	1402	4OC	C2-N3	5.60	1.47	1.36
8	A	745	1MG	C2-N3	5.58	1.44	1.34
55	v	8	4SU	C2-N3	5.57	1.47	1.38
8	A	2552	OMU	C6-C5	5.53	1.47	1.35
8	A	2498	OMC	C4-N3	5.52	1.45	1.34
56	w	8	4SU	C2-N3	5.44	1.47	1.38
8	A	2069	G7M	C2-N3	5.36	1.46	1.33
8	A	2251	OMG	C2-N3	5.22	1.45	1.33
56	w	8	4SU	C4-S4	-5.16	1.58	1.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	v	8	4SU	C4-S4	-5.13	1.58	1.68
34	a	527	G7M	C5-N7	-5.09	1.33	1.39
55	v	20	H2U	C4-N3	4.97	1.46	1.37
8	A	1915	3TD	C2-N3	4.92	1.49	1.38
8	A	2069	G7M	C5-N7	-4.84	1.33	1.39
34	a	967	5MC	C4-N4	4.79	1.46	1.34
56	w	46	G7M	C5-N7	-4.78	1.33	1.39
8	A	747	5MC	C4-N4	4.74	1.46	1.34
8	A	1962	5MC	C4-N4	4.73	1.46	1.34
34	a	1407	5MC	C4-N4	4.73	1.46	1.34
34	a	1498	UR3	C2-N3	4.61	1.47	1.39
34	a	1407	5MC	C6-N1	4.56	1.45	1.38
8	A	2251	OMG	C2-N2	4.49	1.44	1.34
34	a	967	5MC	C6-N1	4.49	1.45	1.38
8	A	747	5MC	C6-N1	4.41	1.45	1.38
8	A	2503	2MA	C5-C6	4.40	1.53	1.41
34	a	966	2MG	C2-N1	4.40	1.43	1.36
34	a	1516	2MG	C2-N1	4.39	1.43	1.36
34	a	1207	2MG	C2-N1	4.38	1.43	1.36
8	A	1835	2MG	C2-N1	4.33	1.43	1.36
56	w	46	G7M	C2-N2	4.29	1.44	1.34
8	A	1962	5MC	C6-N1	4.28	1.45	1.38
8	A	2445	2MG	C2-N1	4.27	1.43	1.36
34	a	527	G7M	C2-N2	4.23	1.44	1.34
34	a	1407	5MC	C2-N1	4.19	1.49	1.40
8	A	2069	G7M	C2-N2	4.13	1.44	1.34
8	A	747	5MC	C2-N1	4.11	1.48	1.40
34	a	967	5MC	C2-N1	4.08	1.48	1.40
8	A	1962	5MC	C2-N1	4.06	1.48	1.40
34	a	1402	4OC	C4-N4	4.02	1.44	1.35
56	w	46	G7M	C5-C6	3.96	1.54	1.43
34	a	1402	4OC	C5-C4	3.80	1.48	1.40
34	a	527	G7M	C5-C6	3.79	1.54	1.43
34	a	1402	4OC	C2-N1	3.78	1.48	1.40
8	A	2498	OMC	C4-N4	3.73	1.42	1.33
8	A	2069	G7M	C5-C6	3.71	1.53	1.43
8	A	2498	OMC	C2-N1	3.57	1.47	1.40
8	A	2503	2MA	C6-N6	-3.55	1.25	1.34
8	A	2445	2MG	O6-C6	-3.54	1.16	1.23
8	A	1835	2MG	O6-C6	-3.53	1.16	1.23
55	v	55	PSU	C6-C5	3.53	1.39	1.35
8	A	1835	2MG	C5-N7	-3.52	1.32	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	a	966	2MG	C5-N7	-3.51	1.32	1.39
8	A	2498	OMC	C6-N1	3.50	1.46	1.38
34	a	1207	2MG	C5-N7	-3.45	1.32	1.39
34	a	966	2MG	O6-C6	-3.44	1.17	1.23
8	A	747	5MC	O2-C2	-3.44	1.17	1.23
8	A	2445	2MG	C5-N7	-3.43	1.32	1.39
34	a	1207	2MG	O6-C6	-3.42	1.17	1.23
34	a	1407	5MC	O2-C2	-3.40	1.17	1.23
34	a	1516	2MG	O6-C6	-3.40	1.17	1.23
8	A	2504	PSU	C6-C5	3.40	1.39	1.35
8	A	2552	OMU	C4-N3	3.36	1.44	1.38
8	A	745	1MG	C5-N7	-3.35	1.32	1.39
8	A	2030	6MZ	C5-C4	-3.34	1.32	1.39
34	a	1516	2MG	C5-N7	-3.31	1.32	1.39
8	A	1962	5MC	O2-C2	-3.29	1.17	1.23
34	a	1518	MA6	C6-N6	3.29	1.46	1.36
56	w	55	PSU	C6-C5	3.28	1.39	1.35
8	A	1911	PSU	C6-C5	3.26	1.39	1.35
56	w	39	PSU	C6-C5	3.26	1.39	1.35
55	v	8	4SU	C5-C4	3.25	1.46	1.42
34	a	967	5MC	O2-C2	-3.24	1.17	1.23
34	a	1519	MA6	C6-N6	3.23	1.46	1.36
56	w	32	PSU	C6-C5	3.22	1.39	1.35
56	w	8	4SU	C5-C4	3.19	1.46	1.42
8	A	2251	OMG	C5-N7	-3.19	1.32	1.39
8	A	1618	6MZ	C5-C4	-3.14	1.33	1.39
8	A	2030	6MZ	C8-N9	-3.14	1.31	1.37
8	A	2552	OMU	O4-C4	-3.14	1.18	1.24
8	A	2498	OMC	O2-C2	-3.13	1.17	1.23
8	A	746	PSU	C6-C5	3.11	1.38	1.35
8	A	1618	6MZ	C8-N9	-3.11	1.32	1.37
34	a	1402	4OC	O2-C2	-3.10	1.18	1.23
8	A	1917	PSU	C6-C5	3.10	1.38	1.35
8	A	2457	PSU	C6-C5	3.07	1.38	1.35
8	A	2605	PSU	C6-C5	3.07	1.38	1.35
8	A	1915	3TD	C4-N3	3.06	1.47	1.40
8	A	2503	2MA	C5-N7	-3.04	1.33	1.39
8	A	2580	PSU	C6-C5	3.02	1.38	1.35
56	w	37	MIA	C5-C4	-3.00	1.33	1.39
8	A	2604	PSU	C6-C5	3.00	1.38	1.35
34	a	1402	4OC	C6-N1	3.00	1.45	1.38
34	a	1519	MA6	C5-N7	-3.00	1.33	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	a	1518	MA6	C8-N9	-2.99	1.32	1.37
8	A	955	PSU	C6-C5	2.98	1.38	1.35
34	a	1519	MA6	C8-N9	-2.91	1.32	1.37
34	a	1498	UR3	C6-N1	2.91	1.45	1.38
34	a	1518	MA6	C5-N7	-2.90	1.33	1.39
34	a	516	PSU	C6-C5	2.88	1.38	1.35
8	A	1939	5MU	O4-C4	-2.87	1.18	1.23
8	A	1939	5MU	O2-C2	-2.86	1.17	1.23
8	A	2069	G7M	O6-C6	-2.83	1.18	1.23
8	A	2552	OMU	O2-C2	-2.81	1.17	1.23
34	a	527	G7M	O6-C6	-2.81	1.18	1.23
34	a	1518	MA6	C5-C4	-2.79	1.33	1.39
8	A	2251	OMG	O6-C6	-2.78	1.18	1.23
56	w	37	MIA	C5-N7	-2.77	1.33	1.39
56	w	54	5MU	O4-C4	-2.77	1.18	1.23
8	A	2030	6MZ	C4-N9	-2.76	1.31	1.37
56	w	46	G7M	C2-N1	2.76	1.44	1.37
34	a	1519	MA6	C5-C4	-2.71	1.33	1.39
55	v	8	4SU	O2-C2	-2.69	1.18	1.23
55	v	54	5MU	O4-C4	-2.64	1.18	1.23
8	A	2552	OMU	C6-N1	2.57	1.44	1.38
56	w	46	G7M	O6-C6	-2.56	1.18	1.23
8	A	2069	G7M	C2-N1	2.55	1.44	1.37
56	w	46	G7M	C6-N1	2.55	1.43	1.38
56	w	8	4SU	O2-C2	-2.54	1.18	1.23
34	a	1498	UR3	O2-C2	-2.51	1.17	1.22
56	w	54	5MU	O2-C2	-2.50	1.18	1.23
34	a	527	G7M	C2-N1	2.50	1.43	1.37
8	A	2251	OMG	C2-N1	2.47	1.43	1.37
8	A	745	1MG	C5-C6	2.44	1.51	1.45
34	a	1498	UR3	O4-C4	-2.43	1.18	1.23
34	a	1207	2MG	C5-C6	2.42	1.53	1.44
8	A	1618	6MZ	C4-N9	-2.42	1.32	1.37
8	A	2445	2MG	C5-C6	2.41	1.53	1.44
34	a	1516	2MG	C5-C6	2.40	1.53	1.44
8	A	2251	OMG	C5-C6	2.34	1.53	1.44
8	A	2069	G7M	C6-N1	2.34	1.43	1.38
55	v	54	5MU	O2-C2	-2.34	1.18	1.23
8	A	1835	2MG	C5-C6	2.33	1.53	1.44
55	v	20	H2U	O4-C4	-2.31	1.18	1.23
34	a	966	2MG	C5-C6	2.30	1.53	1.44
8	A	2030	6MZ	C6-N1	-2.29	1.31	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	v	20	H2U	O2-C2	-2.27	1.18	1.23
8	A	2580	PSU	O4'-C1'	-2.24	1.40	1.43
34	a	527	G7M	C6-N1	2.22	1.43	1.38
8	A	1618	6MZ	C6-N1	-2.20	1.31	1.35
8	A	2251	OMG	C4-N9	-2.19	1.32	1.38
56	w	37	MIA	C8-N9	-2.19	1.33	1.37
34	a	1516	2MG	C6-N1	2.17	1.42	1.38
8	A	2503	2MA	C4-N9	-2.16	1.32	1.37
8	A	2552	OMU	C5-C4	2.13	1.48	1.43
8	A	2251	OMG	C6-N1	2.13	1.42	1.38
34	a	966	2MG	C6-N1	2.12	1.42	1.38
34	a	1519	MA6	C8-N7	2.11	1.35	1.31
8	A	1835	2MG	C6-N1	2.08	1.42	1.38
8	A	2445	2MG	C6-N1	2.05	1.42	1.38
34	a	1207	2MG	C6-N1	2.05	1.42	1.38
34	a	1498	UR3	C5-C4	2.03	1.49	1.43
8	A	2445	2MG	C4-N9	-2.02	1.32	1.38

All (302) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	2030	6MZ	C4-N9-C8	13.24	120.08	105.73
8	A	1618	6MZ	C4-N9-C8	13.13	119.95	105.73
8	A	1939	5MU	C5-C4-N3	12.47	125.95	115.31
55	v	54	5MU	C5-C4-N3	12.28	125.80	115.31
56	w	54	5MU	C5-C4-N3	12.28	125.79	115.31
8	A	1939	5MU	C5-C6-N1	-11.03	111.99	123.34
8	A	2030	6MZ	N9-C8-N7	-10.65	99.35	113.91
8	A	1618	6MZ	N9-C8-N7	-10.45	99.62	113.91
55	v	54	5MU	C5-C6-N1	-10.10	112.95	123.34
56	w	54	5MU	C5-C6-N1	-9.80	113.25	123.34
34	a	1519	MA6	N1-C6-N6	-9.68	106.50	117.08
34	a	1518	MA6	N1-C6-N6	-9.40	106.81	117.08
56	w	37	MIA	C12-C13-C14	-9.05	109.52	127.14
56	w	37	MIA	C11-S10-C2	8.78	108.82	102.27
8	A	2030	6MZ	C5-C6-N1	8.35	127.09	118.20
8	A	1618	6MZ	C5-C6-N1	8.31	127.06	118.20
55	v	8	4SU	C4-N3-C2	-7.73	119.83	127.34
56	w	8	4SU	C4-N3-C2	-7.67	119.89	127.34
8	A	1618	6MZ	N3-C4-N9	6.76	138.22	127.08
8	A	1835	2MG	C2-N3-C4	6.73	120.38	112.04
56	w	37	MIA	C5-C4-N3	-6.68	119.67	127.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
55	v	20	H2U	C4-N3-C2	-6.66	120.27	125.79
34	a	1516	2MG	C2-N3-C4	6.61	120.23	112.04
8	A	2445	2MG	C2-N3-C4	6.57	120.19	112.04
34	a	1207	2MG	C2-N3-C4	6.52	120.12	112.04
34	a	966	2MG	C2-N3-C4	6.38	119.95	112.04
8	A	2503	2MA	C5-C4-N3	-6.24	120.18	127.19
8	A	2030	6MZ	N3-C4-N9	6.17	137.24	127.08
8	A	2030	6MZ	C9-N6-C6	-5.88	117.81	122.87
34	a	527	G7M	CN7-N7-C5	5.69	133.84	126.77
8	A	2503	2MA	N9-C8-N7	-5.66	106.17	113.91
8	A	2030	6MZ	N1-C2-N3	-5.65	119.76	128.60
8	A	2069	G7M	CN7-N7-C5	5.64	133.78	126.77
34	a	1518	MA6	N1-C2-N3	-5.63	119.79	128.60
8	A	1835	2MG	C5-C4-N3	-5.58	119.41	128.46
56	w	8	4SU	C5-C4-N3	5.54	119.83	114.69
34	a	1519	MA6	N1-C2-N3	-5.51	119.98	128.60
34	a	966	2MG	C5-C4-N3	-5.43	119.65	128.46
55	v	8	4SU	C5-C4-N3	5.40	119.70	114.69
8	A	1618	6MZ	N1-C2-N3	-5.35	120.23	128.60
34	a	1207	2MG	C5-C4-N3	-5.35	119.79	128.46
8	A	1939	5MU	C4-N3-C2	-5.29	120.50	127.35
8	A	2445	2MG	C5-C4-N3	-5.27	119.92	128.46
8	A	2552	OMU	C4-N3-C2	-5.25	119.66	126.58
8	A	1915	3TD	N1-C2-N3	5.24	120.27	116.14
56	w	46	G7M	CN7-N7-C5	5.20	133.23	126.77
56	w	54	5MU	O4-C4-C5	-5.15	118.93	124.90
55	v	54	5MU	O4-C4-C5	-5.12	118.97	124.90
8	A	745	1MG	C5-C4-N3	-5.12	120.16	128.46
34	a	1516	2MG	C5-C4-N3	-5.05	120.27	128.46
8	A	2251	OMG	C5-C4-N3	-4.97	120.40	128.46
56	w	55	PSU	N1-C2-N3	4.94	120.73	115.13
8	A	1618	6MZ	C5-C4-N9	-4.91	100.08	105.78
8	A	1939	5MU	O4-C4-C5	-4.88	119.24	124.90
8	A	2604	PSU	C4-N3-C2	-4.88	119.31	126.34
8	A	2457	PSU	C4-N3-C2	-4.87	119.31	126.34
8	A	745	1MG	C1'-N9-C4	-4.86	112.06	126.50
56	w	54	5MU	C4-N3-C2	-4.86	121.06	127.35
34	a	1519	MA6	C5-C4-N3	-4.83	120.45	126.75
55	v	54	5MU	C4-N3-C2	-4.81	121.12	127.35
8	A	955	PSU	N1-C2-N3	4.78	120.55	115.13
8	A	955	PSU	C4-N3-C2	-4.78	119.45	126.34
34	a	966	2MG	C2-N1-C6	-4.76	119.00	124.48

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	a	1519	MA6	C5-C6-N6	4.74	133.56	125.30
34	a	527	G7M	C5-C4-N3	-4.73	119.07	128.15
8	A	2604	PSU	N1-C2-N3	4.73	120.49	115.13
34	a	1518	MA6	C5-C4-N3	-4.73	120.58	126.75
8	A	2605	PSU	C4-N3-C2	-4.72	119.53	126.34
8	A	2457	PSU	N1-C2-N3	4.71	120.47	115.13
8	A	1939	5MU	N3-C2-N1	4.71	121.15	114.89
8	A	2580	PSU	N1-C2-N3	4.70	120.45	115.13
34	a	527	G7M	C2-N3-C4	4.67	120.61	112.30
56	w	46	G7M	C1'-N9-C4	-4.66	112.67	126.50
56	w	37	MIA	C15-C14-C13	-4.65	109.22	122.65
8	A	1911	PSU	N1-C2-N3	4.64	120.38	115.13
8	A	1911	PSU	C4-N3-C2	-4.63	119.67	126.34
8	A	2030	6MZ	C5-N7-C8	4.62	110.08	103.51
8	A	2503	2MA	N3-C4-N9	4.62	133.40	126.99
8	A	2504	PSU	C4-N3-C2	-4.62	119.69	126.34
56	w	37	MIA	C16-C14-C13	-4.60	109.35	122.65
34	a	1518	MA6	N9-C8-N7	-4.60	107.62	113.91
8	A	2605	PSU	N1-C2-N3	4.60	120.34	115.13
56	w	39	PSU	C4-N3-C2	-4.59	119.72	126.34
8	A	746	PSU	C4-N3-C2	-4.59	119.72	126.34
8	A	2504	PSU	N1-C2-N3	4.58	120.32	115.13
8	A	2580	PSU	C4-N3-C2	-4.58	119.75	126.34
8	A	2069	G7M	C2-N3-C4	4.55	120.41	112.30
8	A	1917	PSU	N1-C2-N3	4.55	120.29	115.13
34	a	1518	MA6	C5-C6-N6	4.55	133.22	125.30
8	A	2069	G7M	C1'-N9-C4	-4.53	113.03	126.50
8	A	2030	6MZ	C5-C4-N9	-4.53	100.52	105.78
8	A	1618	6MZ	C5-N7-C8	4.53	109.94	103.51
34	a	1519	MA6	N9-C8-N7	-4.52	107.73	113.91
55	v	55	PSU	C4-N3-C2	-4.50	119.86	126.34
56	w	39	PSU	N1-C2-N3	4.49	120.22	115.13
8	A	1835	2MG	C2-N1-C6	-4.47	119.33	124.48
56	w	32	PSU	C4-N3-C2	-4.47	119.90	126.34
34	a	1207	2MG	C2-N1-C6	-4.47	119.34	124.48
8	A	2445	2MG	C2-N1-C6	-4.45	119.36	124.48
8	A	746	PSU	N1-C2-N3	4.44	120.16	115.13
56	w	32	PSU	N1-C2-N3	4.42	120.13	115.13
34	a	516	PSU	C4-N3-C2	-4.42	119.98	126.34
34	a	527	G7M	CN7-N7-C8	-4.39	118.07	124.84
56	w	55	PSU	C4-N3-C2	-4.39	120.02	126.34
8	A	1618	6MZ	C1'-N9-C8	-4.38	117.24	127.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	w	54	5MU	N3-C2-N1	4.38	120.70	114.89
8	A	1917	PSU	C4-N3-C2	-4.38	120.03	126.34
34	a	1516	2MG	C2-N1-C6	-4.37	119.45	124.48
56	w	46	G7M	C2-N3-C4	4.35	120.05	112.30
55	v	55	PSU	N1-C2-N3	4.33	120.03	115.13
8	A	2251	OMG	C2-N3-C4	4.32	119.99	112.30
8	A	2503	2MA	C4-N9-C8	4.31	110.39	105.73
8	A	745	1MG	C1'-N9-C8	4.29	138.92	126.70
8	A	2069	G7M	CN7-N7-C8	-4.28	118.23	124.84
34	a	516	PSU	N1-C2-N3	4.26	119.96	115.13
56	w	37	MIA	N9-C8-N7	-4.24	108.12	113.91
56	w	54	5MU	C5M-C5-C4	4.23	123.42	118.77
8	A	2552	OMU	N3-C2-N1	4.22	120.49	114.89
56	w	37	MIA	N3-C4-N9	4.20	132.82	126.99
34	a	1498	UR3	C4-N3-C2	-4.19	120.62	124.56
56	w	46	G7M	C5-C4-N3	-4.15	120.20	128.15
56	w	54	5MU	C5M-C5-C6	-4.14	117.32	122.85
55	v	54	5MU	N3-C2-N1	4.12	120.36	114.89
55	v	54	5MU	C5M-C5-C4	4.11	123.30	118.77
8	A	2069	G7M	C5-C4-N3	-4.10	120.30	128.15
55	v	54	5MU	C5M-C5-C6	-4.09	117.39	122.85
34	a	527	G7M	C5-C6-N1	4.08	120.31	111.79
56	w	46	G7M	CN7-N7-C8	-4.07	118.56	124.84
8	A	2069	G7M	C5-C6-N1	4.06	120.26	111.79
56	w	37	MIA	C4-C5-C6	4.05	119.94	116.81
56	w	46	G7M	C5-C6-N1	4.01	120.16	111.79
8	A	1915	3TD	C4-N3-C2	-3.92	120.35	124.61
8	A	1618	6MZ	C5-C4-N3	-3.88	121.69	126.75
8	A	1618	6MZ	C9-N6-C6	-3.81	119.59	122.87
55	v	8	4SU	N3-C2-N1	3.77	119.89	114.89
8	A	2503	2MA	C5-N7-C8	3.71	108.78	103.51
56	w	46	G7M	C1'-N9-C8	3.70	139.23	126.74
8	A	2069	G7M	O6-C6-C5	-3.68	119.75	128.06
56	w	8	4SU	N3-C2-N1	3.66	119.75	114.89
8	A	2030	6MZ	C2-N3-C4	3.65	120.37	111.75
8	A	1939	5MU	C5M-C5-C6	-3.65	117.98	122.85
8	A	747	5MC	C5-C6-N1	-3.64	119.59	123.34
8	A	1835	2MG	N9-C4-N3	3.64	133.25	125.94
34	a	1518	MA6	C2-N1-C6	3.64	120.35	111.75
34	a	527	G7M	N9-C4-N3	3.64	133.24	125.94
8	A	745	1MG	C2-N3-C4	3.63	120.13	111.98
34	a	527	G7M	C1'-N9-C4	-3.62	115.74	126.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	a	1519	MA6	C2-N1-C6	3.61	120.29	111.75
56	w	37	MIA	N3-C2-N1	-3.61	120.34	126.95
56	w	55	PSU	O2-C2-N1	-3.60	118.82	122.79
8	A	1618	6MZ	C2-N3-C4	3.60	120.24	111.75
34	a	527	G7M	O6-C6-C5	-3.57	120.01	128.06
55	v	8	4SU	C5-C4-S4	-3.56	119.88	124.47
34	a	966	2MG	N9-C4-N3	3.53	133.03	125.94
56	w	8	4SU	C5-C4-S4	-3.48	119.98	124.47
8	A	2069	G7M	C1'-N9-C8	3.46	138.43	126.74
8	A	2030	6MZ	C5-C4-N3	-3.46	122.24	126.75
34	a	1519	MA6	C2-N3-C4	3.44	119.89	111.75
34	a	1518	MA6	C2-N3-C4	3.43	119.86	111.75
8	A	1962	5MC	C5-C6-N1	-3.43	119.81	123.34
56	w	46	G7M	O6-C6-C5	-3.43	120.33	128.06
8	A	745	1MG	N9-C4-N3	3.37	132.71	125.94
34	a	967	5MC	C5-C6-N1	-3.34	119.91	123.34
8	A	2030	6MZ	C1'-N9-C8	-3.32	119.64	127.14
34	a	527	G7M	C2-N1-C6	-3.30	119.09	125.10
34	a	1207	2MG	N9-C4-N3	3.29	132.54	125.94
34	a	1516	2MG	C1'-N9-C4	-3.28	116.75	126.50
34	a	1407	5MC	C5-C6-N1	-3.27	119.98	123.34
8	A	1939	5MU	O2-C2-N1	-3.25	118.47	122.79
56	w	55	PSU	C6-C5-C4	3.25	120.47	118.20
56	w	46	G7M	C2-N1-C6	-3.25	119.18	125.10
8	A	745	1MG	N9-C8-N7	-3.24	107.29	113.39
8	A	2251	OMG	N9-C8-N7	-3.23	107.31	113.39
8	A	2552	OMU	C5-C4-N3	3.23	119.67	114.84
55	v	20	H2U	N3-C2-N1	3.23	120.07	116.65
34	a	1519	MA6	C4-C5-C6	3.21	119.47	115.88
57	y	101	FME	CA-N-CN	3.21	127.75	122.82
34	a	1518	MA6	C5-N7-C8	3.20	108.05	103.51
8	A	2030	6MZ	C4-C5-C6	-3.19	114.33	116.81
34	a	1519	MA6	C5-N7-C8	3.19	108.05	103.51
34	a	1518	MA6	C4-C5-C6	3.19	119.45	115.88
8	A	2445	2MG	N9-C4-N3	3.19	132.35	125.94
8	A	1939	5MU	C5M-C5-C4	3.18	122.27	118.77
8	A	2503	2MA	N3-C2-N1	-3.16	119.90	125.72
57	y	101	FME	C-CA-N	3.11	115.35	109.73
8	A	2251	OMG	C2-N1-C6	-3.11	119.44	125.10
8	A	2251	OMG	N9-C4-N3	3.07	132.11	125.94
34	a	1516	2MG	N9-C8-N7	-3.07	107.60	113.39
56	w	37	MIA	C5-N7-C8	3.06	107.85	103.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	2030	6MZ	C6-C5-N7	3.05	135.69	132.39
8	A	2069	G7M	N9-C4-N3	3.02	132.01	125.94
8	A	2069	G7M	C2-N1-C6	-3.02	119.59	125.10
34	a	1516	2MG	N9-C4-N3	2.98	131.92	125.94
34	a	966	2MG	N9-C8-N7	-2.93	107.87	113.39
34	a	1498	UR3	C1'-N1-C2	2.92	121.92	116.99
34	a	1518	MA6	N3-C4-N9	2.92	131.89	127.08
56	w	37	MIA	C2-N3-C4	2.89	119.95	112.35
8	A	2445	2MG	N9-C8-N7	-2.85	108.03	113.39
8	A	1917	PSU	O2-C2-N1	-2.84	119.66	122.79
34	a	527	G7M	C1'-N9-C8	2.84	136.33	126.74
34	a	1516	2MG	C1'-N9-C8	2.84	134.78	126.70
55	v	20	H2U	C5-C6-N1	2.83	120.95	111.61
34	a	1498	UR3	C6-N1-C2	-2.83	119.25	121.79
34	a	1207	2MG	N9-C8-N7	-2.83	108.07	113.39
56	w	46	G7M	N9-C4-N3	2.82	131.59	125.94
8	A	1835	2MG	N9-C8-N7	-2.80	108.12	113.39
34	a	1519	MA6	N3-C4-N9	2.79	131.69	127.08
34	a	966	2MG	C5-C6-N1	2.78	120.25	113.19
34	a	1516	2MG	C5-C6-N1	2.78	120.24	113.19
8	A	1939	5MU	O4-C4-N3	-2.77	114.81	120.12
8	A	2251	OMG	C5-C6-N1	2.76	120.20	113.19
34	a	1518	MA6	C4-N9-C8	2.74	108.70	105.73
34	a	1207	2MG	C5-C6-N1	2.74	120.16	113.19
8	A	1835	2MG	C5-C6-N1	2.73	120.12	113.19
8	A	2580	PSU	O2-C2-N1	-2.72	119.80	122.79
8	A	2504	PSU	O2-C2-N1	-2.70	119.81	122.79
8	A	955	PSU	O2-C2-N1	-2.70	119.82	122.79
8	A	2445	2MG	C5-C6-N1	2.69	120.02	113.19
56	w	55	PSU	C6-N1-C2	-2.68	119.94	122.68
34	a	516	PSU	O2-C2-N1	-2.68	119.84	122.79
55	v	20	H2U	C5-C4-N3	2.67	119.65	116.65
8	A	745	1MG	C5-C6-N1	2.67	120.06	114.91
8	A	2030	6MZ	C4-N9-C1'	-2.65	120.28	126.59
8	A	2445	2MG	C1'-N9-C4	-2.61	118.75	126.50
34	a	1516	2MG	N1-C2-N3	-2.59	119.94	123.95
34	a	1207	2MG	C1'-N9-C4	-2.59	118.80	126.50
34	a	966	2MG	O6-C6-C5	-2.59	119.72	126.60
8	A	2580	PSU	O4'-C1'-C2'	2.57	108.78	105.14
8	A	2251	OMG	O6-C6-C5	-2.56	119.81	126.60
55	v	54	5MU	O4-C4-N3	-2.55	115.24	120.12
8	A	1835	2MG	O6-C6-C5	-2.54	119.85	126.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
56	w	54	5MU	O4-C4-N3	-2.52	115.28	120.12
8	A	2552	OMU	O4-C4-C5	-2.51	120.75	125.16
8	A	2604	PSU	O2-C2-N1	-2.50	120.03	122.79
34	a	1516	2MG	O6-C6-C5	-2.49	119.99	126.60
34	a	1519	MA6	C4-N9-C8	2.48	108.42	105.73
55	v	20	H2U	O2-C2-N1	-2.47	120.00	123.11
8	A	1962	5MC	CM5-C5-C6	-2.47	119.55	122.85
8	A	2457	PSU	O2-C2-N1	-2.46	120.08	122.79
8	A	746	PSU	O2-C2-N1	-2.46	120.08	122.79
8	A	1911	PSU	O2-C2-N1	-2.45	120.09	122.79
34	a	1207	2MG	O6-C6-C5	-2.44	120.12	126.60
8	A	1835	2MG	N1-C2-N3	-2.44	120.18	123.95
8	A	2445	2MG	O6-C6-C5	-2.43	120.16	126.60
8	A	1618	6MZ	C4-C5-C6	-2.42	114.93	116.81
34	a	516	PSU	C6-N1-C2	-2.42	120.21	122.68
56	w	37	MIA	C16-C14-C15	-2.41	109.27	114.60
56	w	37	MIA	S10-C2-N1	2.40	124.31	116.01
8	A	2069	G7M	O3'-C3'-C2'	2.39	119.57	111.82
34	a	966	2MG	CM2-N2-C2	-2.39	118.59	123.86
8	A	1917	PSU	C6-N1-C2	-2.38	120.25	122.68
8	A	2552	OMU	C1'-N1-C2	2.38	121.87	117.57
56	w	54	5MU	O2-C2-N1	-2.38	119.63	122.79
34	a	1207	2MG	N1-C2-N3	-2.38	120.28	123.95
56	w	32	PSU	O2-C2-N1	-2.37	120.18	122.79
8	A	2445	2MG	N1-C2-N3	-2.37	120.29	123.95
8	A	2580	PSU	C6-C5-C4	2.35	119.84	118.20
8	A	2580	PSU	C6-N1-C2	-2.33	120.30	122.68
34	a	966	2MG	C1'-N9-C4	-2.30	119.66	126.50
8	A	2445	2MG	CM2-N2-C2	-2.28	118.83	123.86
8	A	2504	PSU	C6-N1-C2	-2.26	120.38	122.68
34	a	1402	4OC	C6-C5-C4	2.25	119.72	116.96
34	a	1207	2MG	C1'-N9-C8	2.25	133.10	126.70
8	A	747	5MC	CM5-C5-C6	-2.25	119.85	122.85
8	A	1835	2MG	C1'-N9-C4	-2.24	119.85	126.50
8	A	1911	PSU	C6-N1-C2	-2.22	120.41	122.68
8	A	2445	2MG	C1'-N9-C8	2.21	132.99	126.70
55	v	55	PSU	O2-C2-N1	-2.21	120.36	122.79
8	A	2251	OMG	C8-N7-C5	2.20	108.23	104.24
34	a	1519	MA6	C4-C5-N7	-2.20	107.94	110.62
8	A	955	PSU	C6-N1-C2	-2.19	120.44	122.68
56	w	37	MIA	C12-N6-C6	-2.19	119.30	122.55
34	a	966	2MG	N1-C2-N3	-2.19	120.57	123.95

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
8	A	2457	PSU	C6-C5-C4	2.18	119.72	118.20
56	w	37	MIA	C4-N9-C8	2.18	108.09	105.73
8	A	2605	PSU	O2-C2-N1	-2.18	120.39	122.79
8	A	745	1MG	C8-N7-C5	2.17	108.17	104.24
56	w	32	PSU	C6-N1-C2	-2.17	120.47	122.68
34	a	1407	5MC	CM5-C5-C6	-2.16	119.96	122.85
8	A	1618	6MZ	C6-C5-N7	2.13	134.69	132.39
8	A	1835	2MG	CM2-N2-C2	-2.12	119.18	123.86
34	a	1516	2MG	C8-N7-C5	2.11	108.06	104.24
55	v	54	5MU	O2-C2-N1	-2.11	119.98	122.79
34	a	1516	2MG	CM2-N2-C2	-2.11	119.21	123.86
8	A	2503	2MA	N6-C6-N1	2.10	120.01	117.03
56	w	39	PSU	C6-N1-C2	-2.10	120.53	122.68
55	v	55	PSU	C6-N1-C2	-2.10	120.54	122.68
56	w	37	MIA	N6-C6-N1	-2.09	115.84	118.50
34	a	1518	MA6	C4-C5-N7	-2.07	108.10	110.62
8	A	1939	5MU	C6-C5-C4	2.06	119.75	118.03
34	a	516	PSU	O4'-C1'-C2'	2.05	108.04	105.14
34	a	967	5MC	CM5-C5-C6	-2.05	120.11	122.85
34	a	966	2MG	C8-N7-C5	2.04	107.94	104.24
8	A	955	PSU	C6-C5-C4	2.04	119.63	118.20
8	A	1835	2MG	C8-N7-C5	2.04	107.93	104.24
34	a	1207	2MG	C8-N7-C5	2.03	107.92	104.24
8	A	746	PSU	C6-N1-C2	-2.03	120.61	122.68
8	A	1917	PSU	O4'-C1'-C2'	2.02	107.99	105.14
8	A	2604	PSU	C6-N1-C2	-2.01	120.63	122.68
8	A	2605	PSU	C6-C5-C4	2.01	119.60	118.20
8	A	2445	2MG	C8-N7-C5	2.01	107.88	104.24
8	A	2457	PSU	O4'-C1'-C2'	2.01	107.97	105.14

There are no chirality outliers.

All (52) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
55	v	20	H2U	O4'-C4'-C5'-O5'
55	v	55	PSU	O4'-C1'-C5-C4
55	v	55	PSU	O4'-C1'-C5-C6
8	A	746	PSU	C2'-C1'-C5-C4
8	A	1915	3TD	C2'-C1'-C5-C4
8	A	1915	3TD	O4'-C1'-C5-C4
8	A	1915	3TD	O4'-C1'-C5-C6
8	A	2251	OMG	C1'-C2'-O2'-CM2

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Mol	Chain	Res	Type	Atoms
8	A	2445	2MG	C3'-C4'-C5'-O5'
8	A	2498	OMC	O4'-C4'-C5'-O5'
8	A	2552	OMU	O4'-C1'-N1-C2
8	A	2552	OMU	O4'-C1'-N1-C6
8	A	2552	OMU	C1'-C2'-O2'-CM2
34	a	1498	UR3	O4'-C1'-N1-C2
56	w	32	PSU	O4'-C1'-C5-C4
56	w	32	PSU	C2'-C1'-C5-C6
56	w	32	PSU	O4'-C1'-C5-C6
56	w	37	MIA	C12-C13-C14-C15
56	w	37	MIA	C12-C13-C14-C16
56	w	39	PSU	C2'-C1'-C5-C4
56	w	39	PSU	O4'-C1'-C5-C4
56	w	39	PSU	O4'-C1'-C5-C6
57	y	101	FME	CB-CA-N-CN
57	y	101	FME	N-CA-CB-CG
57	y	101	FME	C-CA-CB-CG
34	a	1498	UR3	O4'-C1'-N1-C6
8	A	1939	5MU	O4'-C4'-C5'-O5'
8	A	2030	6MZ	O4'-C4'-C5'-O5'
8	A	2030	6MZ	C3'-C4'-C5'-O5'
8	A	2503	2MA	O4'-C4'-C5'-O5'
8	A	2503	2MA	C3'-C4'-C5'-O5'
8	A	2498	OMC	C3'-C4'-C5'-O5'
8	A	2445	2MG	O4'-C4'-C5'-O5'
8	A	1939	5MU	C3'-C4'-C5'-O5'
55	v	20	H2U	C4'-C5'-O5'-P
8	A	1835	2MG	O4'-C4'-C5'-O5'
8	A	2504	PSU	O4'-C4'-C5'-O5'
34	a	1402	4OC	O4'-C4'-C5'-O5'
57	y	101	FME	CA-CB-CG-SD
57	y	101	FME	CB-CG-SD-CE
8	A	1835	2MG	C3'-C4'-C5'-O5'
34	a	527	G7M	C4'-C5'-O5'-P
56	w	55	PSU	O4'-C1'-C5-C4
8	A	746	PSU	O4'-C1'-C5-C6
8	A	1917	PSU	C4'-C5'-O5'-P
8	A	2504	PSU	C3'-C4'-C5'-O5'
55	v	20	H2U	C2'-C1'-N1-C6
8	A	1962	5MC	C2'-C1'-N1-C6
8	A	2069	G7M	O4'-C4'-C5'-O5'
34	a	1402	4OC	C3'-C4'-C5'-O5'

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Mol	Chain	Res	Type	Atoms
8	A	1962	5MC	O4'-C1'-N1-C6
34	a	1519	MA6	C4'-C5'-O5'-P

There are no ring outliers.

20 monomers are involved in 30 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	2445	2MG	1	0
56	w	46	G7M	4	0
56	w	55	PSU	1	0
55	v	20	H2U	3	0
34	a	1402	4OC	2	0
8	A	2605	PSU	1	0
8	A	2552	OMU	2	0
55	v	8	4SU	1	0
34	a	1498	UR3	2	0
56	w	8	4SU	1	0
34	a	527	G7M	1	0
56	w	37	MIA	2	0
55	v	55	PSU	1	0
8	A	1939	5MU	1	0
8	A	2580	PSU	1	0
34	a	516	PSU	2	0
8	A	2030	6MZ	1	0
8	A	2069	G7M	1	0
57	y	101	FME	1	0
8	A	1915	3TD	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 371 ligands modelled in this entry, 367 are monoatomic - leaving 4 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	$\# Z > 2$
62	AM2	a	1682	-	40,40,40	1.61	9 (22%)	53,60,60	1.05	3 (5%)
62	AM2	a	1684	-	40,40,40	1.62	8 (20%)	53,60,60	1.10	3 (5%)
62	AM2	a	1689	-	40,40,40	1.64	8 (20%)	53,60,60	1.09	4 (7%)
62	AM2	a	1685	-	40,40,40	1.67	7 (17%)	53,60,60	1.08	5 (9%)

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
62	AM2	a	1682	-	-	1/12/84/84	0/4/4/4
62	AM2	a	1684	-	-	4/12/84/84	0/4/4/4
62	AM2	a	1689	-	-	3/12/84/84	0/4/4/4
62	AM2	a	1685	-	-	4/12/84/84	0/4/4/4

All (32) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
62	a	1685	AM2	OA4-CA1	4.60	1.53	1.41
62	a	1689	AM2	OA4-CA1	4.58	1.53	1.41
62	a	1684	AM2	OA4-CA1	4.49	1.53	1.41
62	a	1682	AM2	OA4-CA1	4.32	1.52	1.41
62	a	1685	AM2	OA4-CA5	3.77	1.49	1.44
62	a	1685	AM2	OA5-CA8	3.76	1.51	1.41
62	a	1689	AM2	OA4-CA5	3.73	1.49	1.44
62	a	1685	AM2	OB1-CB1	3.69	1.51	1.41
62	a	1684	AM2	OA4-CA5	3.62	1.49	1.44
62	a	1689	AM2	OA5-CA8	3.52	1.50	1.41
62	a	1684	AM2	OA5-CA8	3.49	1.50	1.41
62	a	1689	AM2	OB1-CB1	3.49	1.50	1.41
62	a	1684	AM2	OB1-CB1	3.48	1.50	1.41
62	a	1682	AM2	OB1-CB1	3.43	1.50	1.41
62	a	1685	AM2	OA5-CA4	3.41	1.52	1.44
62	a	1682	AM2	OA5-CA8	3.34	1.50	1.41
62	a	1682	AM2	OA4-CA5	3.15	1.48	1.44
62	a	1689	AM2	OA5-CA4	3.14	1.52	1.44
62	a	1684	AM2	OA5-CA4	3.09	1.51	1.44

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
62	a	1682	AM2	OA5-CA4	2.92	1.51	1.44
62	a	1682	AM2	CB3-CB4	-2.90	1.49	1.53
62	a	1684	AM2	CB3-CB4	-2.79	1.50	1.53
62	a	1685	AM2	CB3-CB4	-2.63	1.50	1.53
62	a	1689	AM2	CB3-CB4	-2.58	1.50	1.53
62	a	1682	AM2	OA1-CA1	-2.47	1.34	1.41
62	a	1684	AM2	OA1-CA1	-2.37	1.35	1.41
62	a	1682	AM2	OA8-CA8	-2.32	1.35	1.41
62	a	1689	AM2	OA1-CA1	-2.31	1.35	1.41
62	a	1685	AM2	OA1-CA1	-2.27	1.35	1.41
62	a	1689	AM2	OA8-CA8	-2.15	1.35	1.41
62	a	1682	AM2	OA8-CB1	-2.09	1.35	1.41
62	a	1684	AM2	OA8-CA8	-2.01	1.36	1.41

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	a	1684	AM2	CA9-NA7-CA7	-3.48	109.32	114.38
62	a	1682	AM2	CA9-NA7-CA7	-3.46	109.35	114.38
62	a	1684	AM2	CA1-OA1-CC1	-3.28	109.83	117.96
62	a	1689	AM2	CA9-NA7-CA7	-3.19	109.74	114.38
62	a	1689	AM2	CA1-OA1-CC1	-3.08	110.35	117.96
62	a	1682	AM2	CA1-OA1-CC1	-2.97	110.61	117.96
62	a	1685	AM2	CA1-OA1-CC1	-2.96	110.64	117.96
62	a	1685	AM2	OA4-CA5-CA4	2.76	113.07	108.88
62	a	1682	AM2	CB1-OA8-CA8	-2.68	109.64	114.42
62	a	1684	AM2	CB1-OA8-CA8	-2.61	109.75	114.42
62	a	1685	AM2	CB1-OA8-CA8	-2.55	109.86	114.42
62	a	1689	AM2	CB1-OA8-CA8	-2.55	109.87	114.42
62	a	1685	AM2	CC5-CC4-CC3	2.34	113.57	110.04
62	a	1685	AM2	CC3-CC2-CC1	2.29	114.92	109.68
62	a	1689	AM2	OA4-CA5-CA4	2.29	112.35	108.88

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
62	a	1684	AM2	CA6-CA7-NA7-CA9
62	a	1684	AM2	CA8-CA7-NA7-CA9
62	a	1685	AM2	CA8-CA7-NA7-CA9
62	a	1684	AM2	OB1-CB5-CB6-OB6
62	a	1684	AM2	CB4-CB5-CB6-OB6

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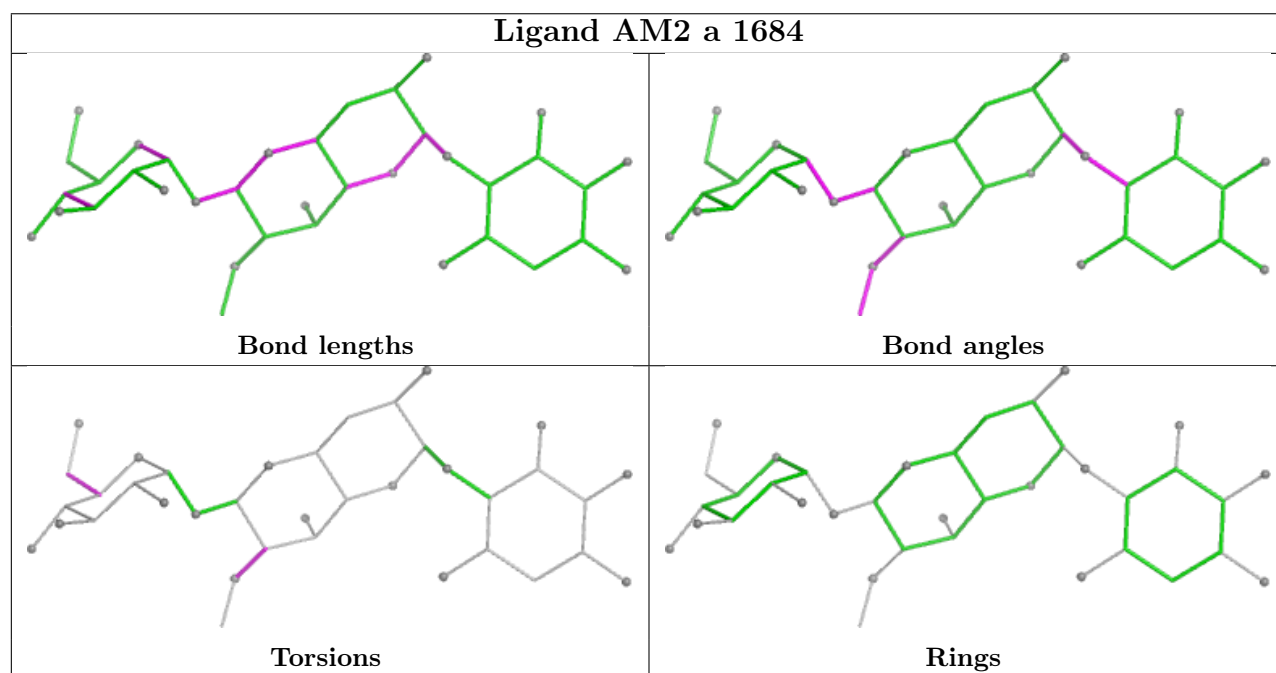
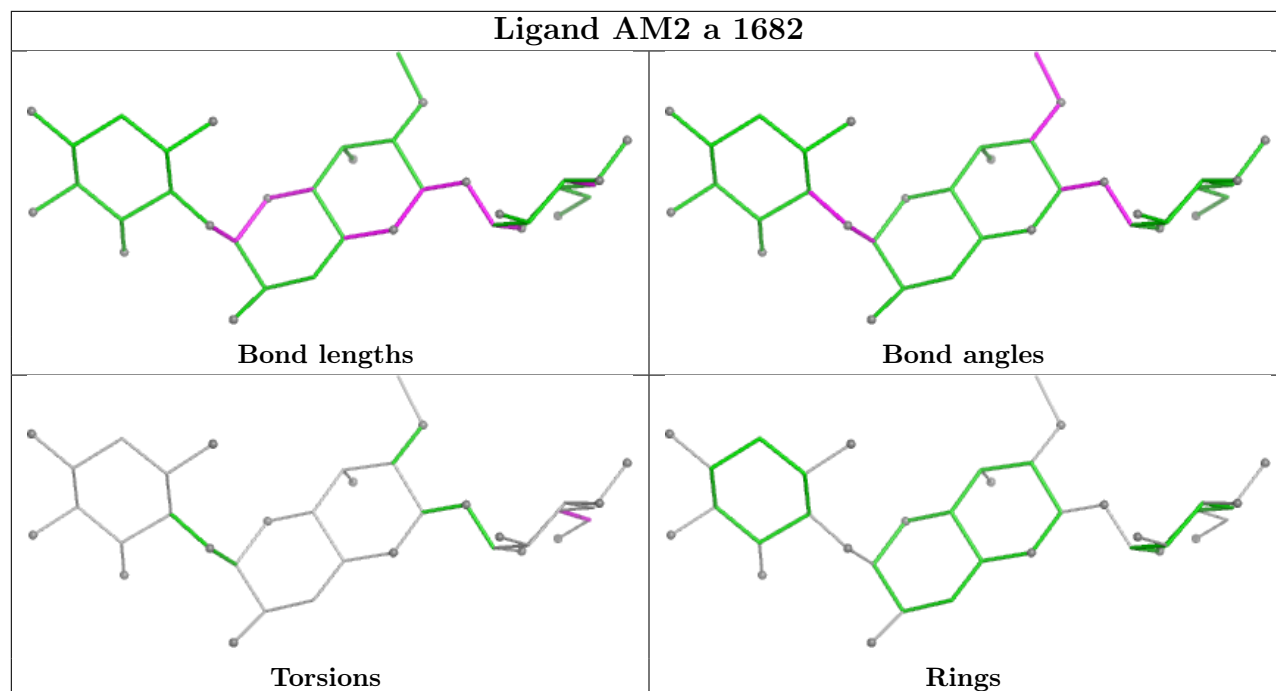
Mol	Chain	Res	Type	Atoms
62	a	1685	AM2	OB1-CB1-OA8-CA8
62	a	1685	AM2	CC2-CC1-OA1-CA1
62	a	1689	AM2	OB1-CB5-CB6-OB6
62	a	1682	AM2	OB1-CB5-CB6-OB6
62	a	1685	AM2	OA4-CA1-OA1-CC1
62	a	1689	AM2	CA6-CA7-NA7-CA9
62	a	1689	AM2	CA8-CA7-NA7-CA9

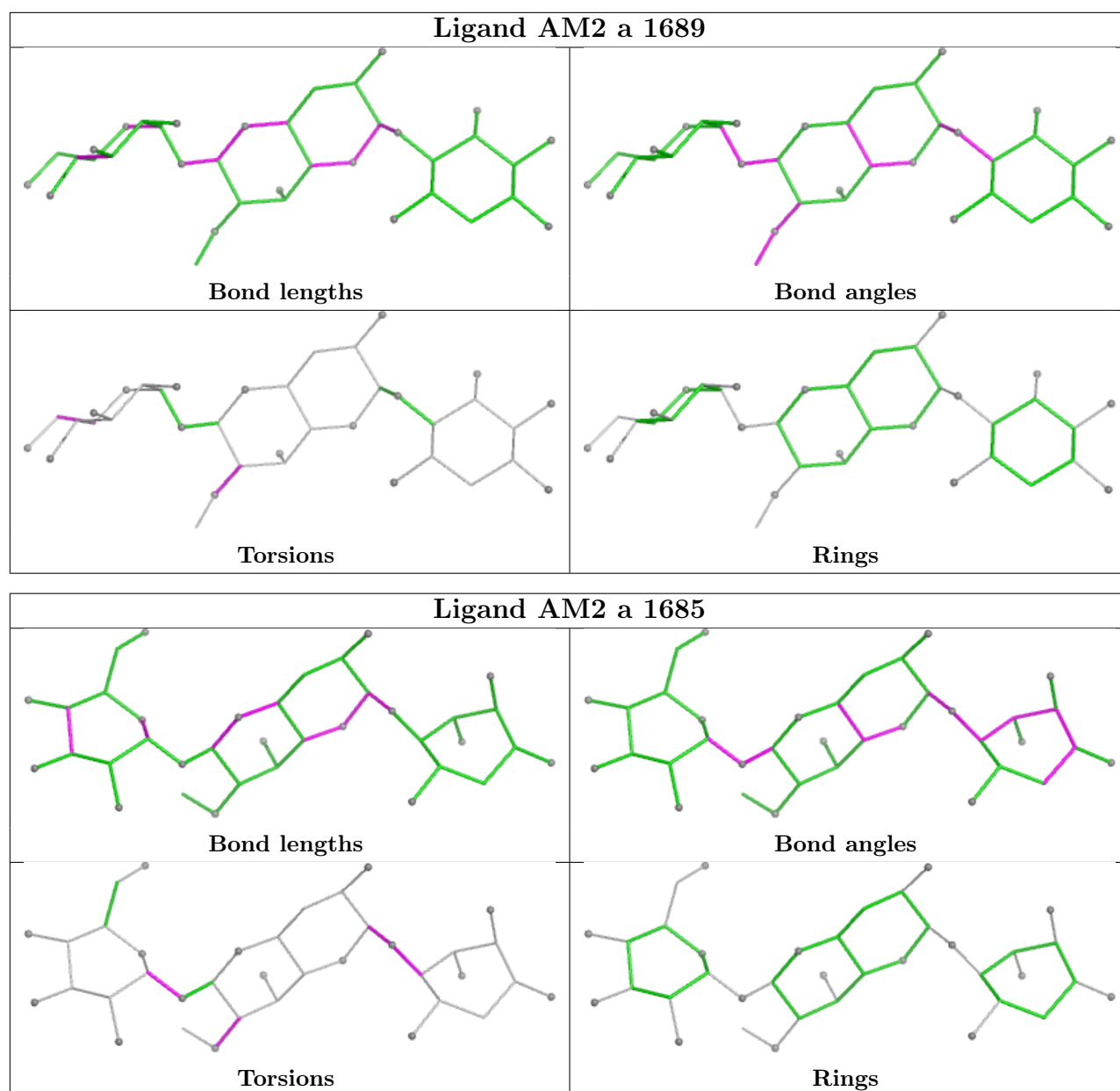
There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
62	a	1682	AM2	1	0
62	a	1684	AM2	1	0
62	a	1685	AM2	1	0

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.

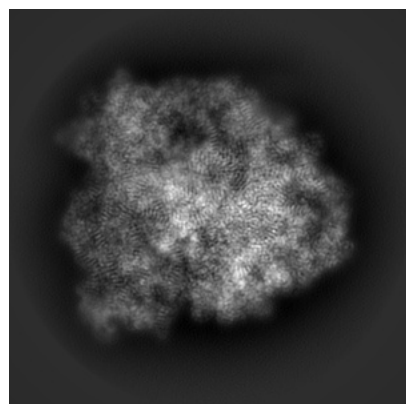
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13458. These allow visual inspection of the internal detail of the map and identification of artifacts.

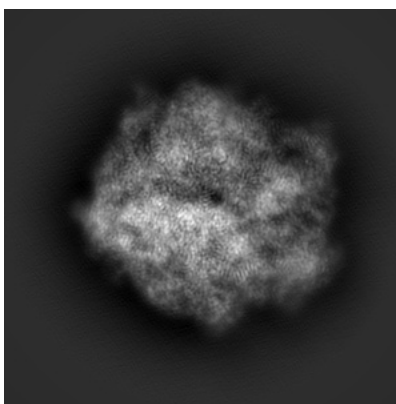
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

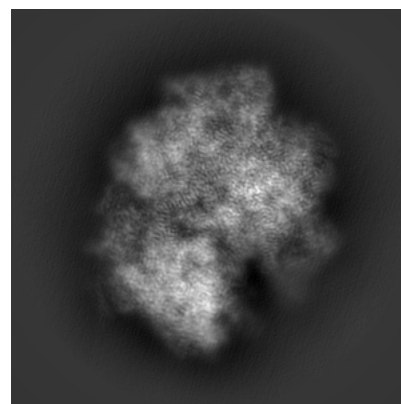
6.1.1 Primary map



X

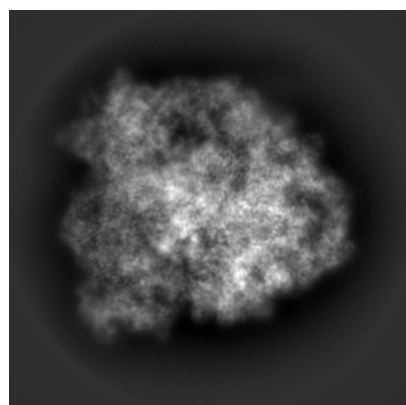


Y

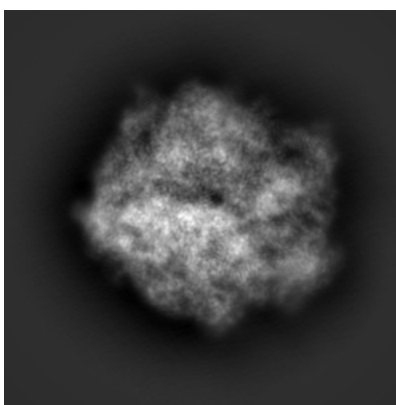


Z

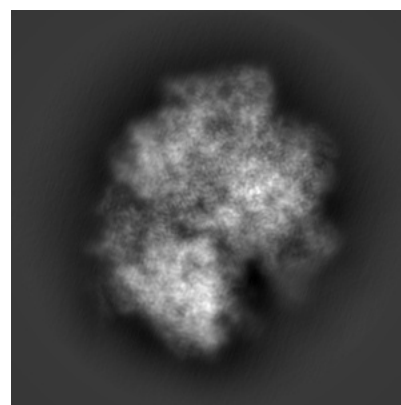
6.1.2 Raw map



X



Y

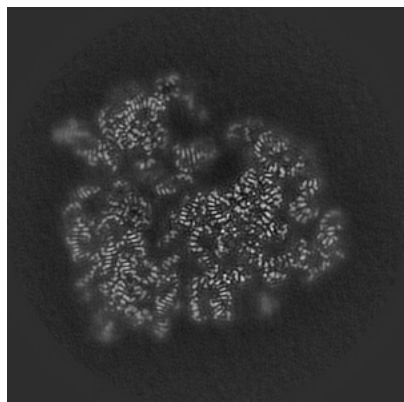


Z

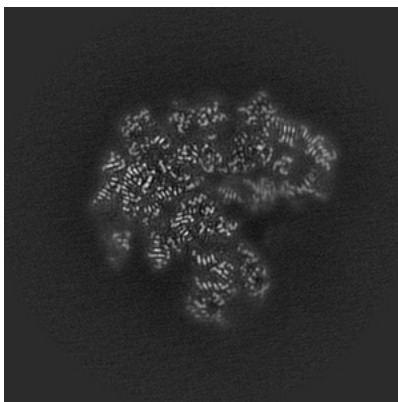
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

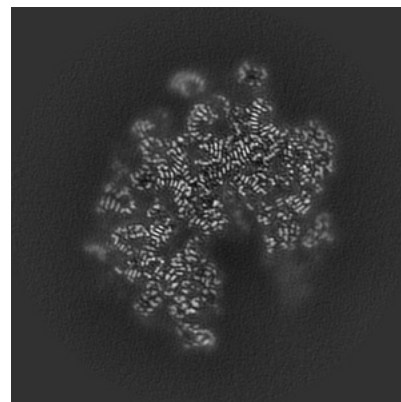
6.2.1 Primary map



X Index: 256

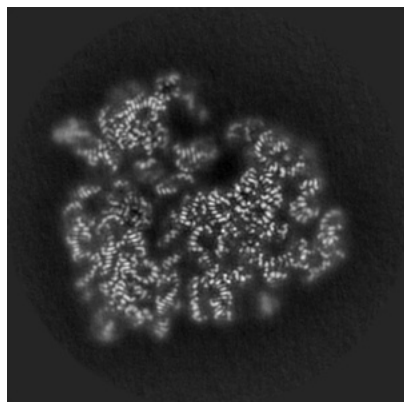


Y Index: 256

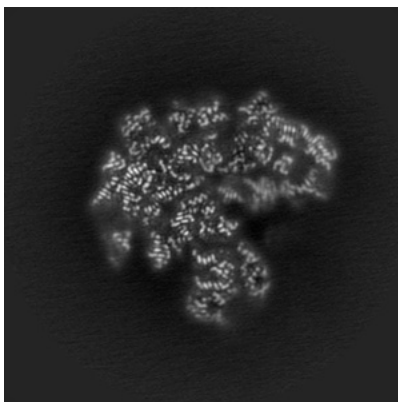


Z Index: 256

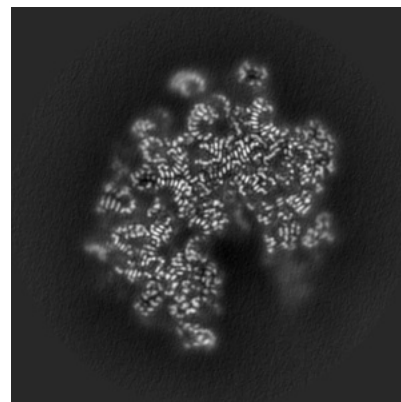
6.2.2 Raw map



X Index: 144



Y Index: 144

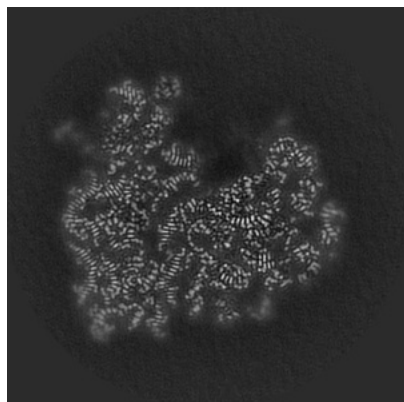


Z Index: 144

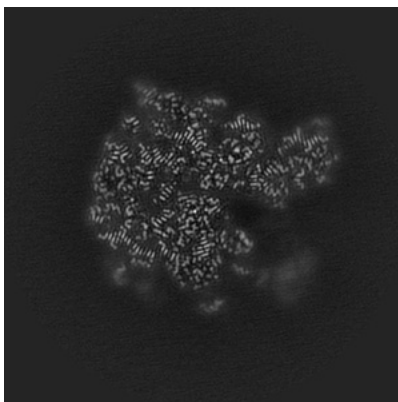
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

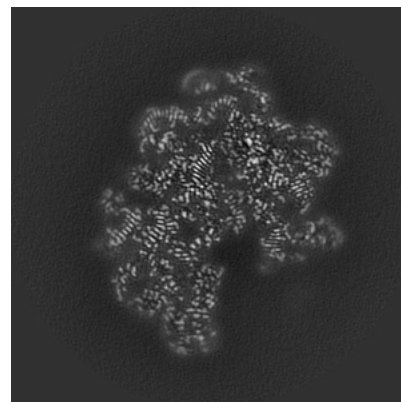
6.3.1 Primary map



X Index: 246

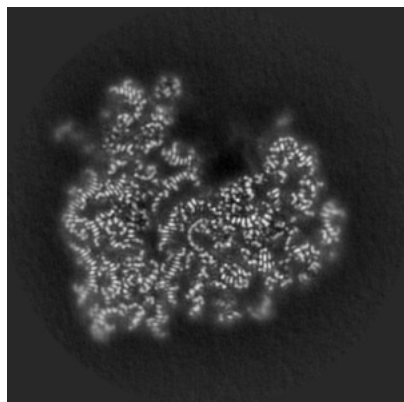


Y Index: 285

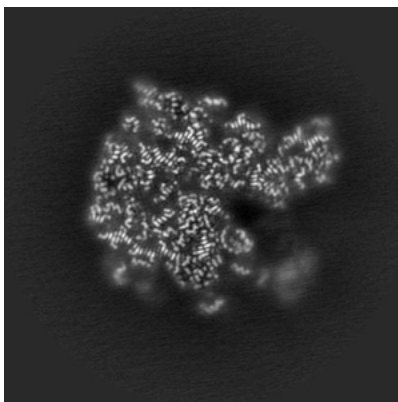


Z Index: 242

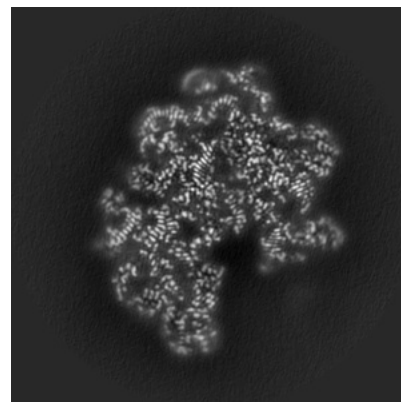
6.3.2 Raw map



X Index: 138



Y Index: 160

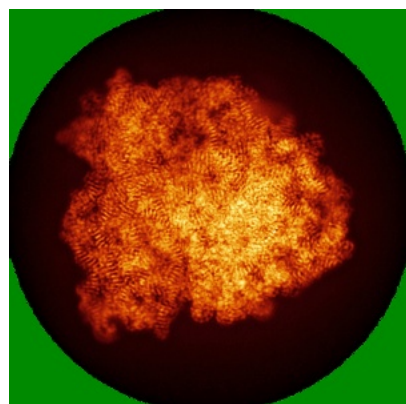


Z Index: 136

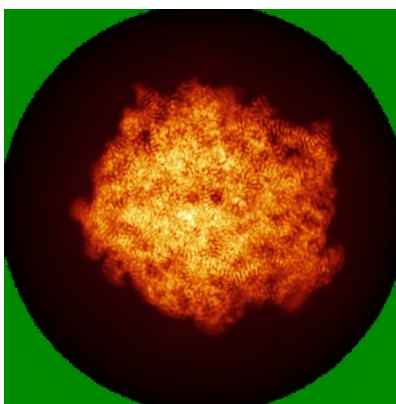
The images above show the largest variance slices of the map in three orthogonal directions.

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

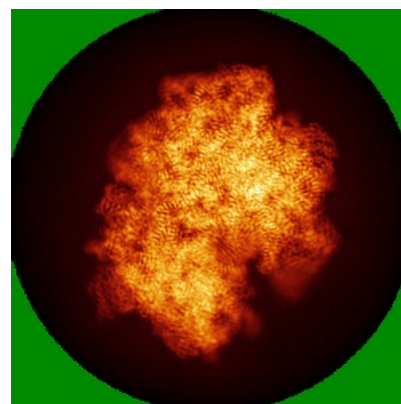
6.4.1 Primary map



X

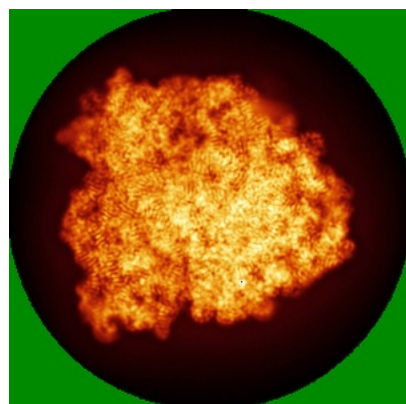


Y

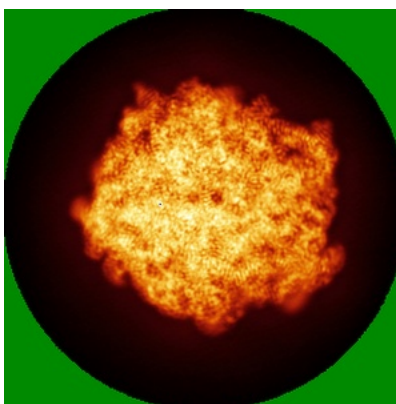


Z

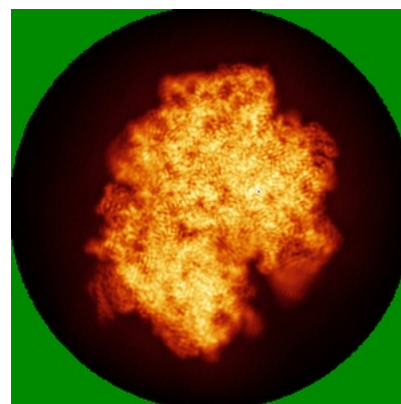
6.4.2 Raw map



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](#)

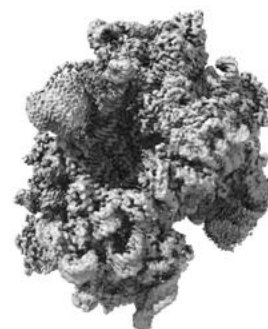
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 2.0. 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



X



Y



Z

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.

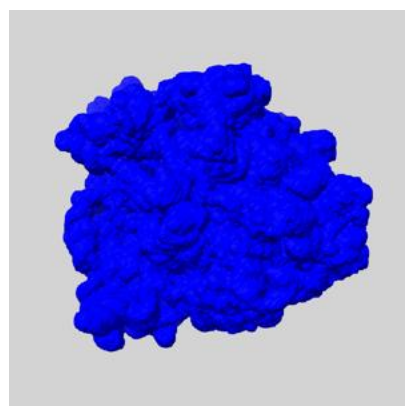
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

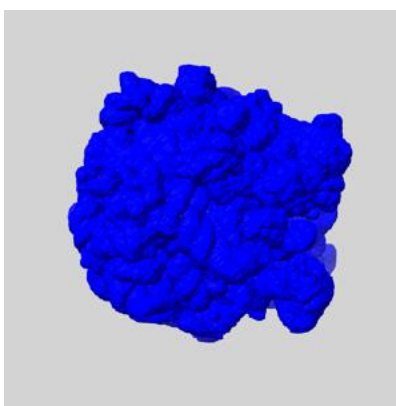
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

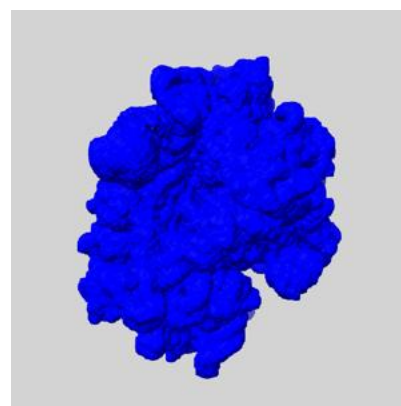
6.6.1 emd_13458_msk_1.map [i](#)



X



Y

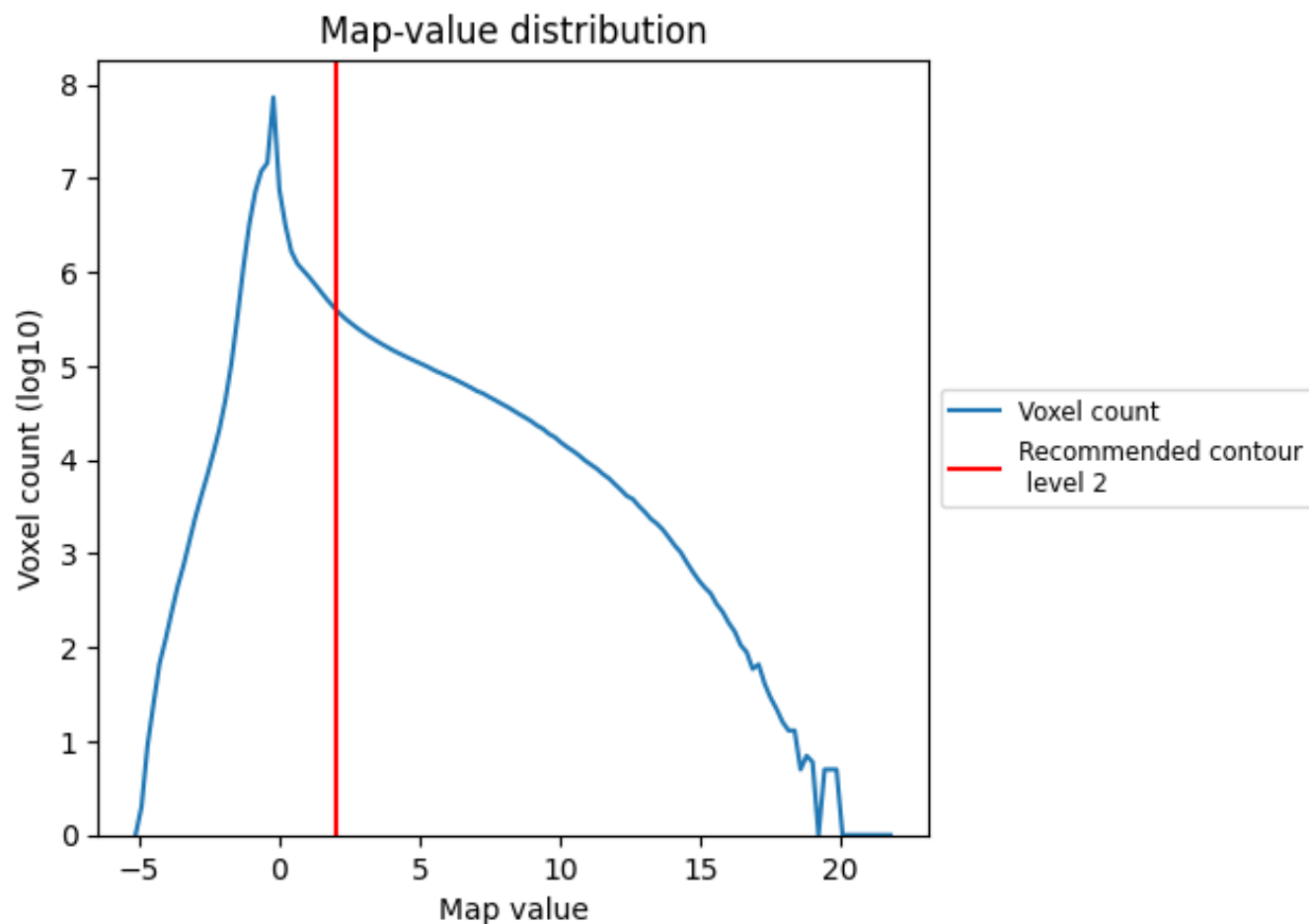


Z

7 Map analysis [i](#)

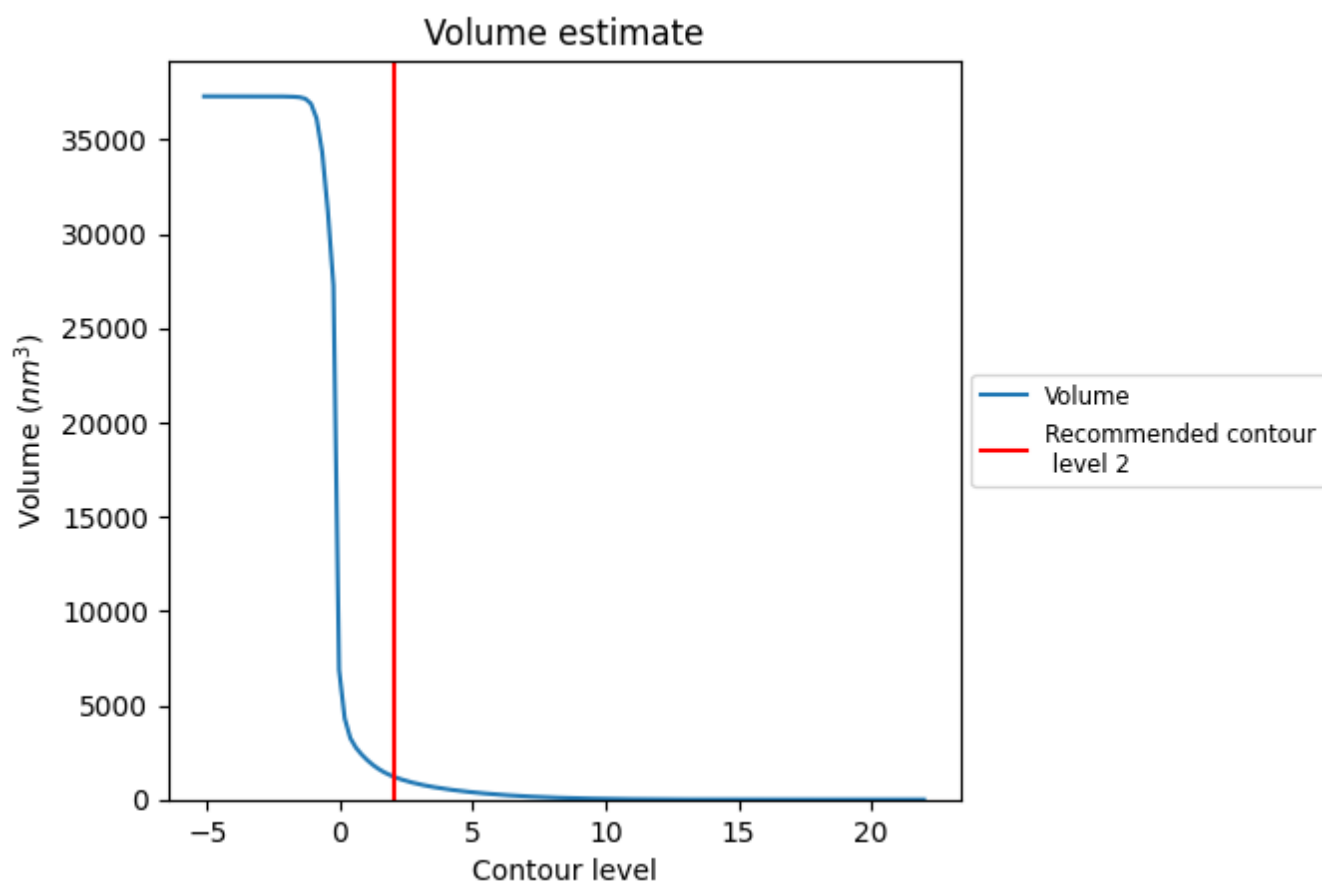
This section contains the results of statistical analysis of the map.

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.

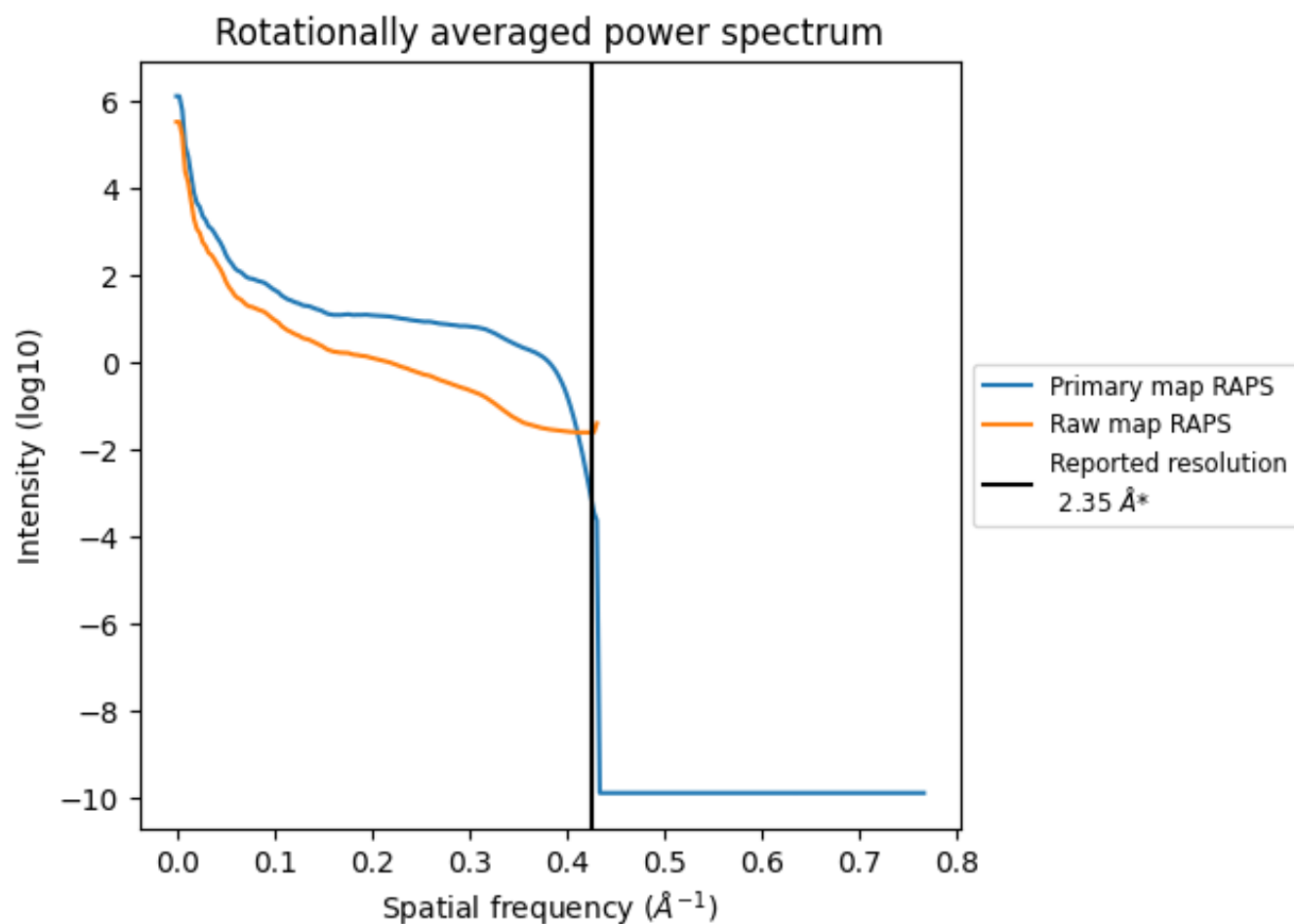
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1226 nm³; this corresponds to an approximate mass of 1108 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 ⓘ

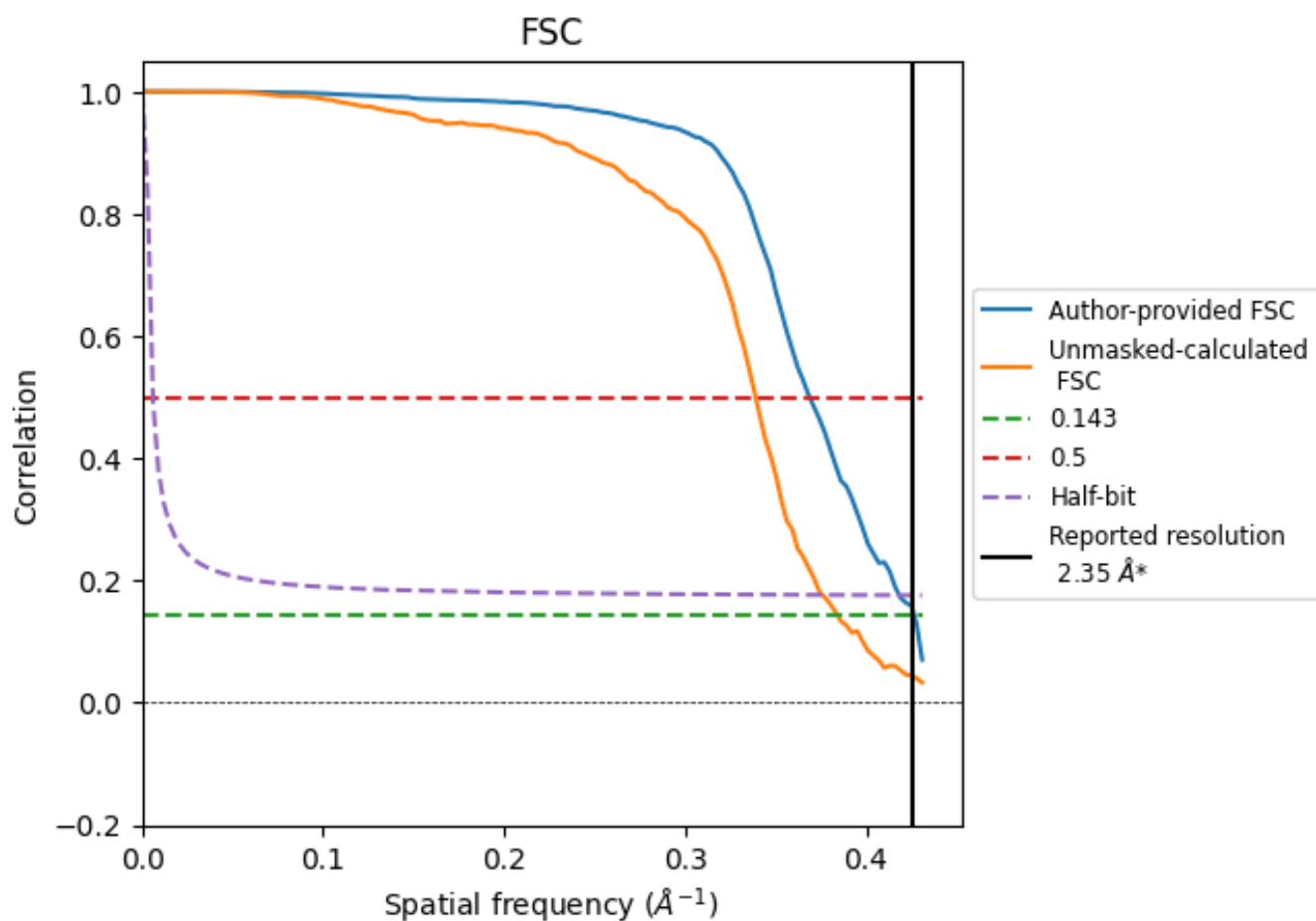


*Reported resolution corresponds to spatial frequency of 0.426 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.426 Å⁻¹

8.2 Resolution estimates [i](#)

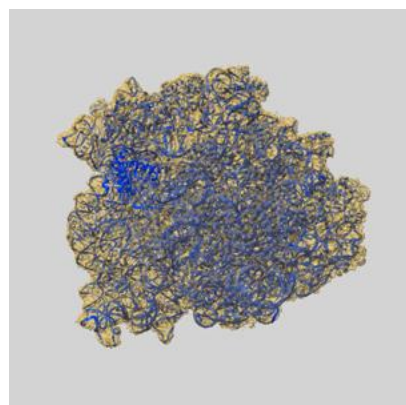
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.35	-	-
Author-provided FSC curve	2.34	2.71	2.39
Unmasked-calculated*	2.60	2.95	2.66

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 2.60 differs from the reported value 2.35 by more than 10 %

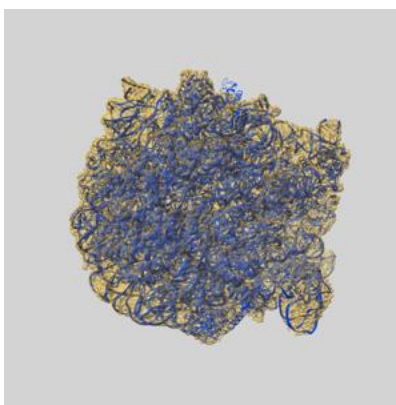
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13458 and PDB model 7PJS. Per-residue inclusion information can be found in [section 3](#) on [page 17](#).

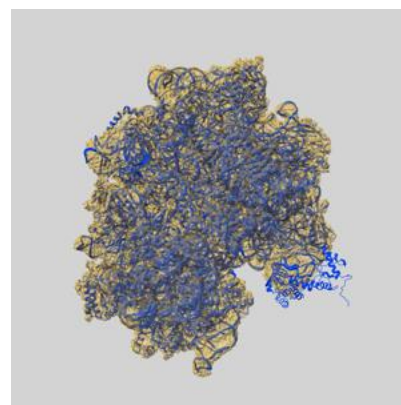
9.1 Map-model overlay [i](#)



X



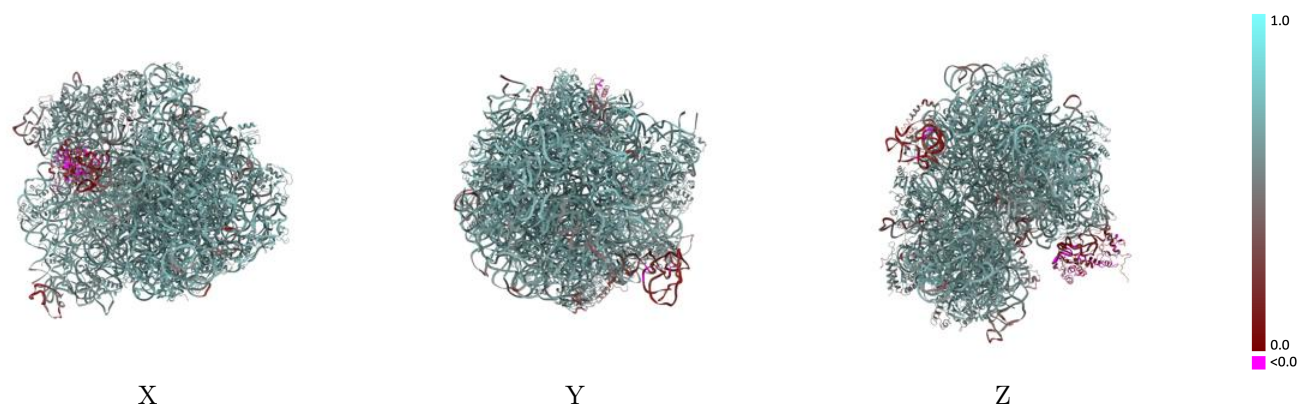
Y



Z

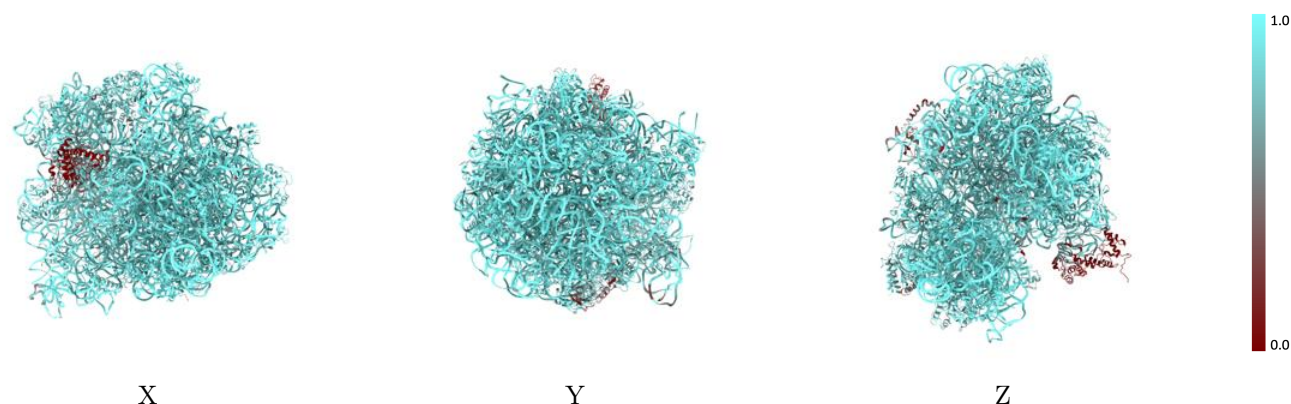
The images above show the 3D surface view of the map at the recommended contour level 2.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



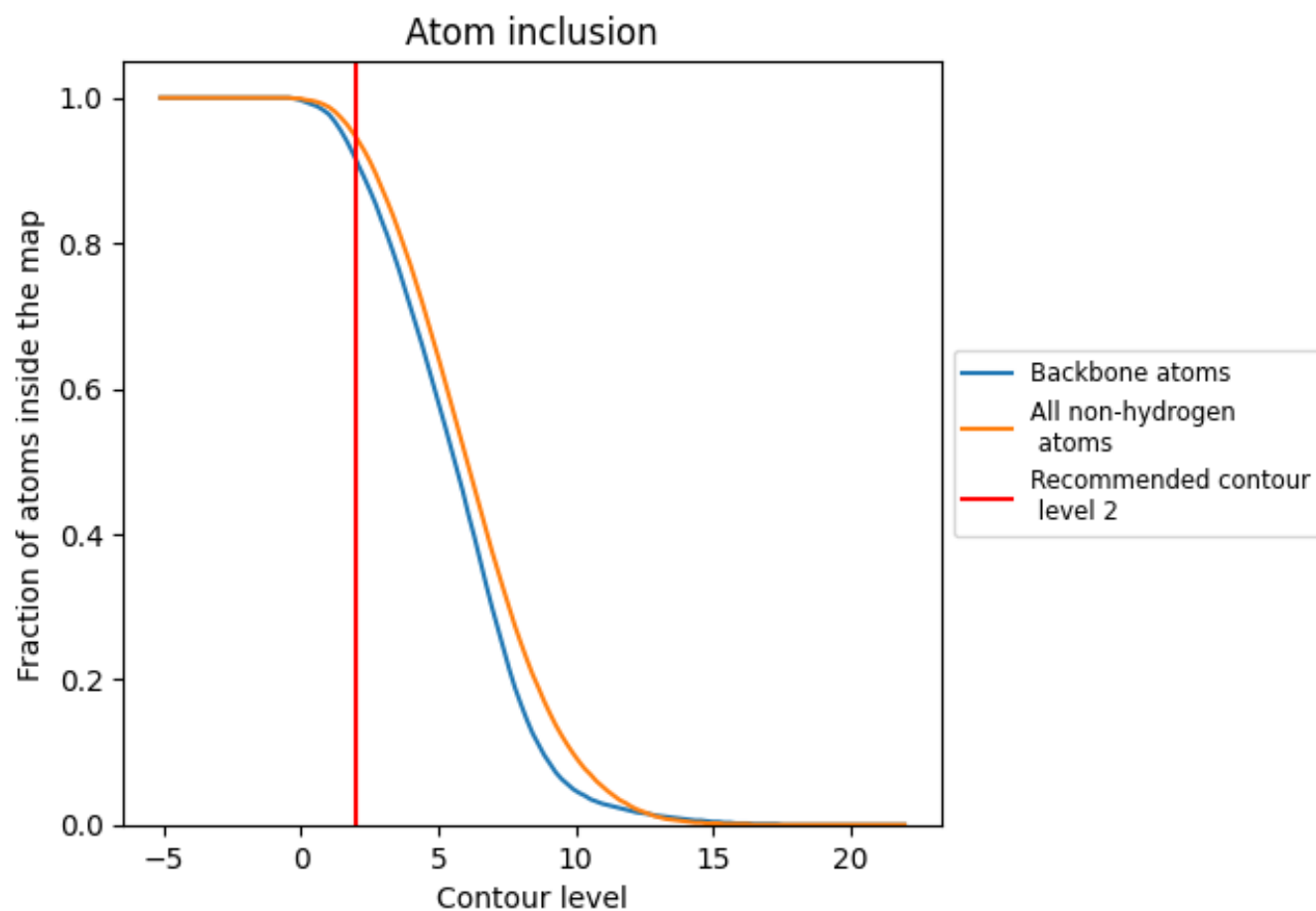
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 95% 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 (2) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9460	 0.6120
0	 0.9420	 0.6510
1	 0.8880	 0.6290
2	 0.9690	 0.6800
3	 0.9700	 0.6790
4	 0.9450	 0.6330
5	 0.0110	 0.1310
6	 0.7910	 0.4950
A	 0.9770	 0.6210
B	 0.9860	 0.6220
C	 0.9530	 0.6650
D	 0.9430	 0.6540
E	 0.9280	 0.6360
F	 0.8580	 0.5430
G	 0.8690	 0.5500
H	 0.4660	 0.4410
I	 0.0660	 0.1220
J	 0.9510	 0.6580
K	 0.9170	 0.6450
L	 0.9490	 0.6460
M	 0.9430	 0.6570
N	 0.9630	 0.6610
O	 0.9490	 0.6180
P	 0.9230	 0.6460
Q	 0.9780	 0.6770
R	 0.9220	 0.6350
S	 0.9230	 0.6500
T	 0.9210	 0.6280
U	 0.9180	 0.6050
V	 0.9050	 0.6210
W	 0.9520	 0.6680
X	 0.9350	 0.6560
Y	 0.9130	 0.5980
Z	 0.9290	 0.6480
a	 0.9860	 0.6170



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Chain	Atom inclusion	Q-score
b	 0.7670	 0.5510
c	 0.9110	 0.6110
d	 0.9090	 0.5930
e	 0.9430	 0.6420
f	 0.8910	 0.5810
g	 0.8710	 0.5700
h	 0.9390	 0.6410
i	 0.9370	 0.6050
j	 0.8540	 0.5490
k	 0.9210	 0.6120
l	 0.9210	 0.6400
m	 0.9340	 0.5990
n	 0.9580	 0.6230
o	 0.9170	 0.6100
p	 0.9270	 0.6120
q	 0.9070	 0.6170
r	 0.9300	 0.6120
s	 0.9170	 0.5940
t	 0.9290	 0.6080
u	 0.8120	 0.5500
v	 0.9140	 0.5720
w	 0.8880	 0.5260
y	 0.5240	 0.5310
z	 0.9390	 0.5990