



Full wwPDB EM Validation Report ⓘ

Jul 3, 2025 – 11:55 AM EDT

PDB ID : 8UX8 / pdb_00008ux8
EMDB ID : EMD-42714
Title : E. coli 70S ribosome with unmodified Lys-tRNA^{Pro}(GGG) bound to slippery P-site CCC-C codon in the +1 mRNA reading frame
Authors : Kimbrough, E.M.; Dunham, C.M.; Nguyen, H.A.
Deposited on : 2023-11-09
Resolution : 3.60 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev118
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.44

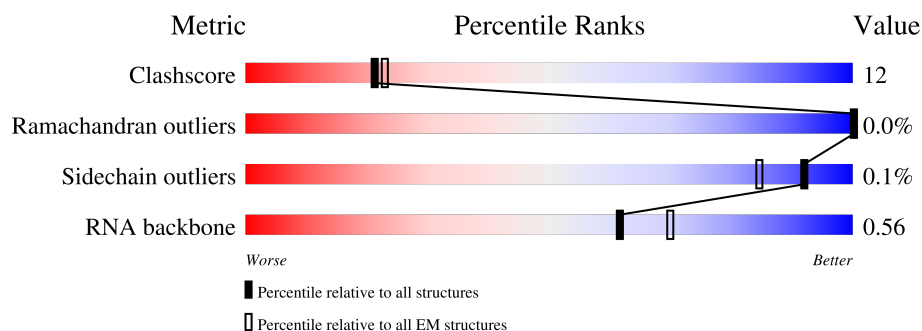
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.60 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)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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

Mol	Chain	Length	Quality of chain
1	1	2904	
2	2	1540	
3	3	120	
4	4	18	
5	5	77	
6	A	229	
7	B	273	

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Mol	Chain	Length	Quality of chain
8	C	209	
9	D	201	
10	E	179	
11	F	177	
12	G	149	
13	J	142	
14	K	123	
15	L	144	
16	M	136	
17	N	127	
18	O	117	
19	P	115	
20	Q	118	
21	R	103	
22	S	110	
23	T	100	
24	U	104	
25	V	94	
26	W	84	
27	X	78	
28	Y	63	
29	Z	59	
30	a	70	
31	b	57	
32	c	55	

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Mol	Chain	Length	Quality of chain
33	d	46	
34	e	65	
35	f	38	
36	g	241	
37	h	233	
38	i	206	
39	j	167	
40	k	135	
41	l	179	
42	m	130	
43	n	130	
44	o	103	
45	p	129	
46	q	124	
47	r	118	
48	s	101	
49	t	89	
50	u	82	
51	v	84	
52	w	75	
53	x	92	
54	y	87	
55	z	71	

2 Entry composition

There are 58 unique types of molecules in this entry. The entry contains 146547 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	2903	Total	C	N	O	P	0	0
			62334	27814	11470	20147	2903		

- Molecule 2 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	1534	Total	C	N	O	P	0	0
			32929	14693	6041	10661	1534		

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	120	Total	C	N	O	P	0	0
			2569	1144	468	837	120		

- Molecule 4 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	11	Total	C	N	O	P	0	0
			230	103	38	78	11		

- Molecule 5 is a RNA chain called Lys-tRNA^{pro}L.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	77	Total	C	N	O	P	0	0
			1648	733	297	541	77		

- Molecule 6 is a protein called Large ribosomal subunit protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	A	67	Total	C	N	O	S	0	0
			507	321	90	95	1		

- Molecule 7 is a protein called 50S ribosomal protein L2.

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

- Molecule 8 is a protein called 50S ribosomal protein L3.

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

- Molecule 9 is a protein called 50S ribosomal protein L4.

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

- Molecule 10 is a protein called 50S ribosomal protein L5.

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

- Molecule 11 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	F	175	Total	C	N	O	S	0	0
			1313	826	241	244	2		

- Molecule 12 is a protein called 50S ribosomal protein L9.

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

- Molecule 13 is a protein called Large ribosomal subunit protein uL13.

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	N	119	Total	C	N	O	S	0	0
			951	588	195	163	5		

- Molecule 18 is a protein called Large ribosomal subunit protein uL18.

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

- Molecule 19 is a protein called Large ribosomal subunit protein bL19.

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

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

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

- Molecule 21 is a protein called Ribosomal protein L21.

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	T	94	Total	C	N	O	S	0	0
			746	470	140	134	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	U	103	Total	C	N	O		0	0
			788	498	148	142			

- Molecule 25 is a protein called Large ribosomal subunit protein bL25.

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

- Molecule 26 is a protein called Large ribosomal subunit protein bL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	W	76	Total	C	N	O	S	0	0
			582	360	117	104	1		

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

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

- Molecule 28 is a protein called Large ribosomal subunit protein uL29.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Z	58	Total	C	N	O	S	0	0
			448	281	87	78	2		

- Molecule 30 is a protein called 50S ribosomal protein L31.

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

- Molecule 31 is a protein called 50S ribosomal protein L32.

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

- Molecule 32 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
32	c	52	Total	C	N	O	0	0
			426	275	78	73		

- Molecule 33 is a protein called 50S ribosomal protein L34.

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

- Molecule 34 is a protein called 50S ribosomal protein L35.

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

- Molecule 35 is a protein called 50S ribosomal protein L36.

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

- Molecule 36 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	g	225	Total	C	N	O	S	0	0
			1760	1113	316	323	8		

- Molecule 37 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	h	208	Total	C	N	O	S	0	0
			1636	1036	307	290	3		

- Molecule 38 is a protein called 30S ribosomal protein S4.

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

- Molecule 39 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	j	156	Total	C	N	O	S	0	0
			1152	717	217	212	6		

- Molecule 40 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	k	104	Total	C	N	O	S	0	0
			848	536	153	152	7		

- Molecule 41 is a protein called 30S ribosomal protein S7.

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

- Molecule 42 is a protein called Small ribosomal subunit protein uS8.

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

- Molecule 43 is a protein called Small ribosomal subunit protein uS9.

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

- Molecule 44 is a protein called Small ribosomal subunit protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	o	99	Total	C	N	O	S	0	0
			790	495	151	143	1		

- Molecule 45 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	p	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 46 is a protein called Small ribosomal subunit protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	q	123	Total	C	N	O	S	0	0
			957	591	196	165	5		

- Molecule 47 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	r	116	Total	C	N	O	S	0	0
			900	558	181	158	3		

- Molecule 48 is a protein called Small ribosomal subunit protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	s	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 49 is a protein called Small ribosomal subunit protein uS15.

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

- Molecule 50 is a protein called 30S ribosomal protein S16.

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

- Molecule 51 is a protein called Small ribosomal subunit protein uS17.

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

- Molecule 52 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	w	66	Total	C	N	O	S	0	0
			544	344	102	97	1		

- Molecule 53 is a protein called Small ribosomal subunit protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	x	83	Total	C	N	O	S	0	0
			663	424	126	111	2		

- Molecule 54 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	y	86	Total	C	N	O	S	0	0
			669	414	138	114	3		

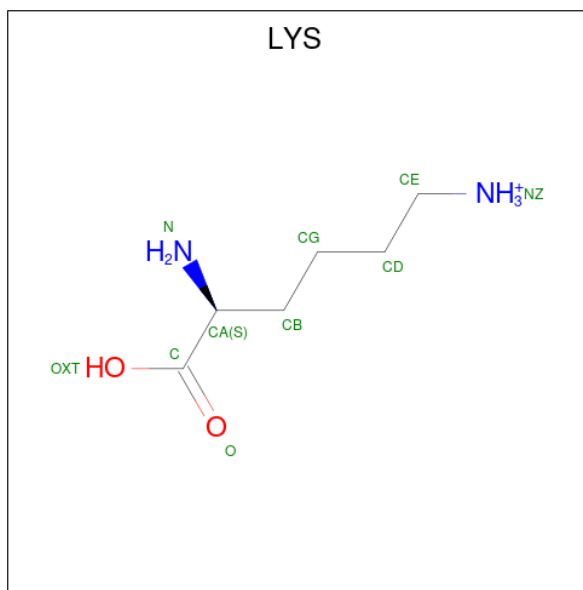
- Molecule 55 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	z	70	Total	C	N	O	S	0	0
			589	366	125	97	1		

- Molecule 56 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
56	1	262	Total 262	Mg 262	0
56	2	111	Total 111	Mg 111	0
56	3	10	Total 10	Mg 10	0
56	5	1	Total 1	Mg 1	0
56	B	3	Total 3	Mg 3	0
56	L	2	Total 2	Mg 2	0
56	M	1	Total 1	Mg 1	0
56	Q	1	Total 1	Mg 1	0
56	X	1	Total 1	Mg 1	0
56	b	1	Total 1	Mg 1	0
56	l	1	Total 1	Mg 1	0
56	z	1	Total 1	Mg 1	0

- Molecule 57 is LYSINE (CCD ID: LYS) (formula: $C_6H_{15}N_2O_2$).



Mol	Chain	Residues	Atoms				AltConf
57	5	1	Total	C	N	O	0
			9	6	2	1	

- Molecule 58 is water.

Mol	Chain	Residues	Atoms		AltConf
58	1	700	Total	O	0
			700	700	
58	2	341	Total	O	0
			341	341	
58	3	7	Total	O	0
			7	7	
58	4	1	Total	O	0
			1	1	
58	5	10	Total	O	0
			10	10	
58	B	2	Total	O	0
			2	2	
58	C	7	Total	O	0
			7	7	
58	D	10	Total	O	0
			10	10	
58	E	4	Total	O	0
			4	4	
58	F	6	Total	O	0
			6	6	
58	G	12	Total	O	0
			12	12	
58	J	7	Total	O	0
			7	7	
58	K	4	Total	O	0
			4	4	
58	L	3	Total	O	0
			3	3	
58	M	2	Total	O	0
			2	2	
58	N	2	Total	O	0
			2	2	
58	O	6	Total	O	0
			6	6	
58	P	6	Total	O	0
			6	6	
58	Q	7	Total	O	0
			7	7	

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Mol	Chain	Residues	Atoms		AltConf
58	R	7	Total 7	O 7	0
58	S	4	Total 4	O 4	0
58	T	2	Total 2	O 2	0
58	U	6	Total 6	O 6	0
58	V	1	Total 1	O 1	0
58	W	2	Total 2	O 2	0
58	Y	8	Total 8	O 8	0
58	Z	2	Total 2	O 2	0
58	a	2	Total 2	O 2	0
58	b	2	Total 2	O 2	0
58	f	1	Total 1	O 1	0
58	g	20	Total 20	O 20	0
58	h	14	Total 14	O 14	0
58	i	8	Total 8	O 8	0
58	j	3	Total 3	O 3	0
58	k	7	Total 7	O 7	0
58	l	5	Total 5	O 5	0
58	m	3	Total 3	O 3	0
58	n	4	Total 4	O 4	0
58	o	3	Total 3	O 3	0
58	p	5	Total 5	O 5	0

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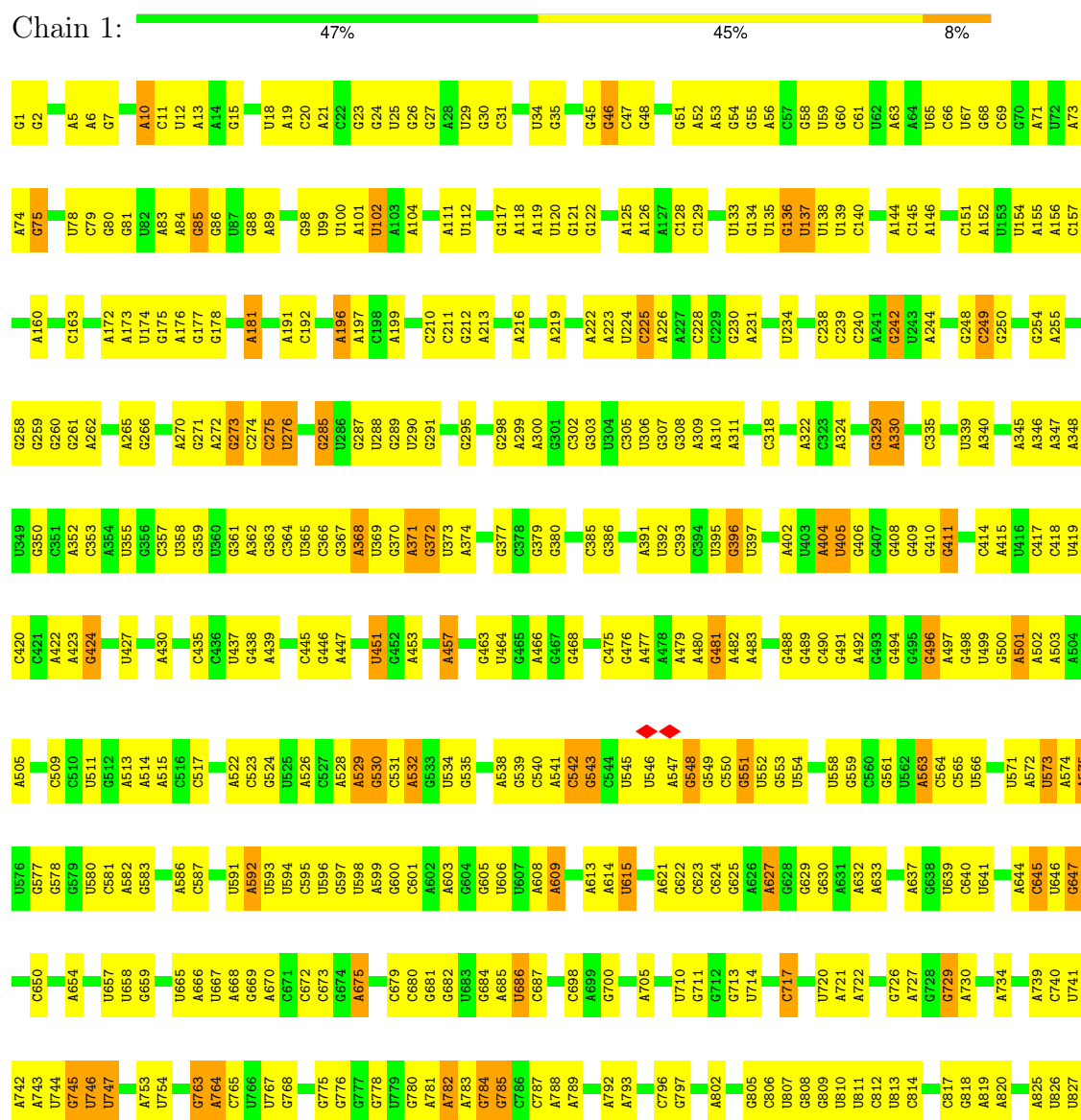
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Mol	Chain	Residues	Atoms		AltConf
58	q	1	Total 1	O 1	0
58	r	4	Total 4	O 4	0
58	t	1	Total 1	O 1	0
58	u	4	Total 4	O 4	0
58	v	3	Total 3	O 3	0
58	w	3	Total 3	O 3	0
58	x	1	Total 1	O 1	0
58	z	4	Total 4	O 4	0

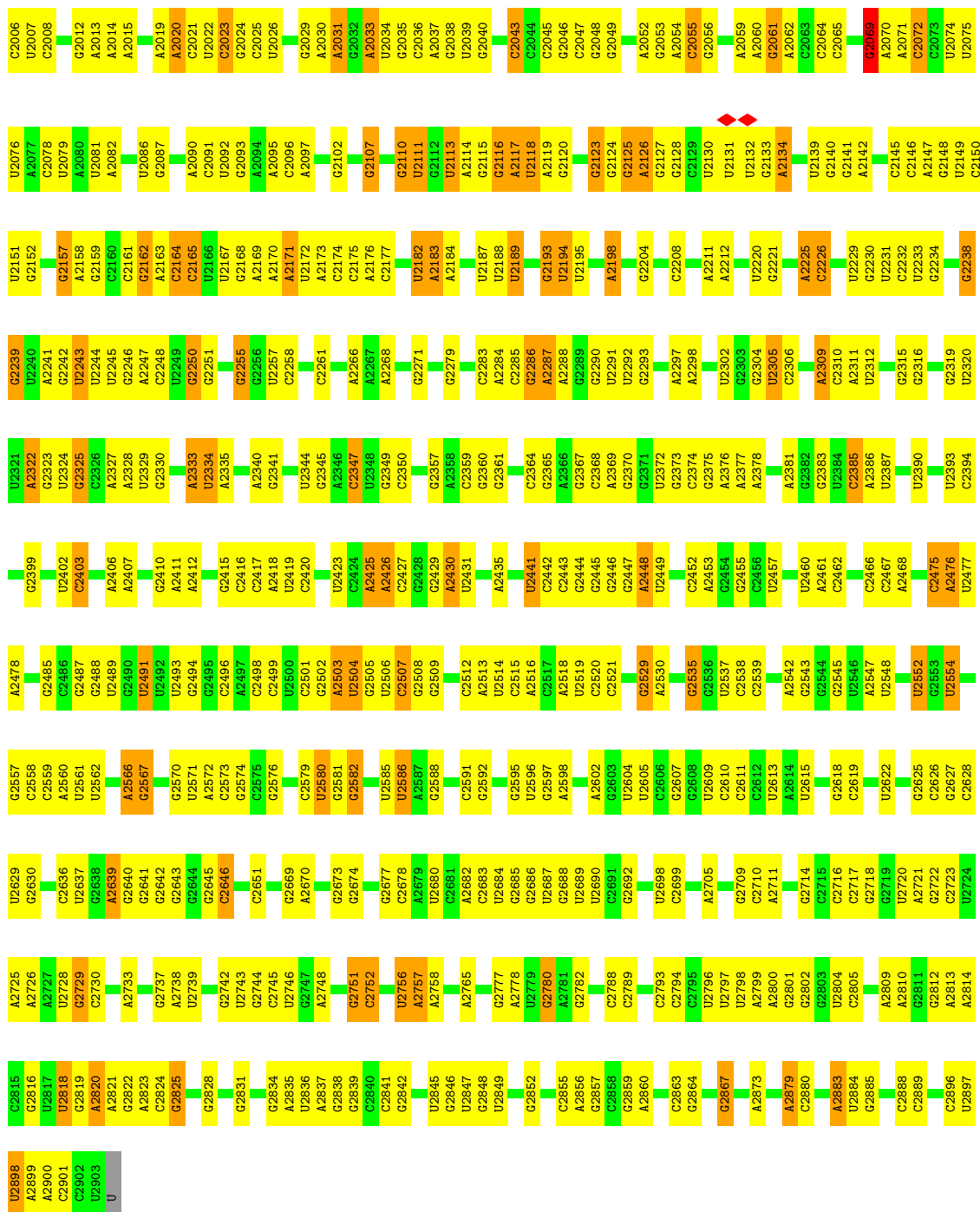
3 Residue-property plots

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

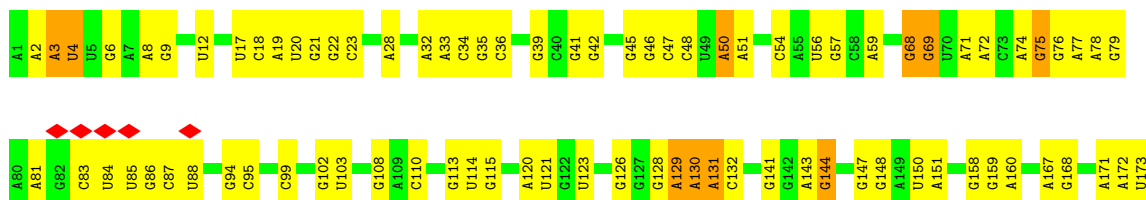
• Molecule 1: 23S rRNA



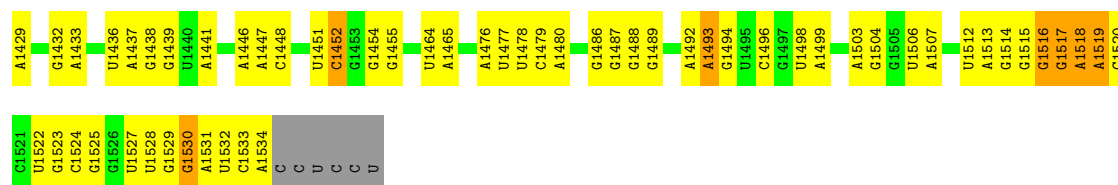
G1906	G1907	C1816	A1739	G1663	C1577	A1490	U1415	G1238	A1165	A1073	C992	G907	U828
G1907	A1744	U1817	A1744	G1666	U1578	A1494	C1417	A1241	A1169	G1074	G992	A910	A829
G1910	A1745	A1819	A1746	G1667	G1581	A1495	C1417	A1241	A1169	C1075	G993	A910	G830
U1911	A1746	U1820	A1746	G1667	C1582	A1496	A1420	G1245	G1171	C1076	G994	C994	U831
A1912	U1747	A1821	A1668	A1668	A1583	U1497	G1421	A1246	G1171	A1077	C995	G914	U832
A1913	C1748	C1822	A1669	A1669	A1583	U1497	G1422	A1246	U1173	U1078	A996	C915	A833
A1914	A1749	A1822	A1670	U1670	U1589	G1501	G1423	U1249	U1174	C1079	A1000	G916	C834
A1915	G1750	U1825	U1671	U1671	A1590	A1502	G1424	C1330	U1174	A1080	A1000	A917	C835
A1916	A1751	G1826	A1672	A1672	A1591	A1503	G1425	C1251	U1176	A1084	A1001	U919	C836
U1917	C1752	U1827	G1673	G1673	C1592	A1508	A1426	G1253	G1177	A1085	C1007	A920	U839
A1918	G1753	G1828	G1674	G1674	A1593	A1509	G1427	A1253	C1177	A1086	A1008	A920	U839
A1918	A1754	A1829	G1675	G1675	U1594	A1509	G1428	A1254	G1179	G1087	A1009	A920	U839
G1921	A1755	C1830	A1676	A1676	C1595	G1510	G1429	U1255	G1179	A1088	A1009	A920	U839
G1921	G1756	G1831	A1677	A1677	A1596	A1596	G1430	G1256	G1182	G1093	A1099	A920	U839
C1924	A1757	C1832	A1678	A1678	A1597	U1513	A1431	C1351	U1183	A1010	A1099	A927	G843
C1925	A1757	C1833	A1679	A1679	A1598	G1514	G1432	A1352	U1183	A1010	G1011	A927	A844
U1926	U1680	U1834	U1680	U1680	U1599	A1515	A1433	A1354	U1184	U1094	U1012	A928	U846
A1927	C1760	G1835	G1681	G1681	U1600	A1515	A1434	A1354	G1185	A1095	C1013	G930	U847
A1928	C1761	G1836	G1682	G1682	C1600	A1518	A1434	A1354	G1185	A1096	G1016	U931	C848
A1928	A1762	C1837	G1683	G1683	G1601	G1519	G1435	A1285	G1187	U097	G1016	U931	C848
G1930	C1763	C1837	G1684	G1684	C1604	G1519	G1436	A1285	G1187	A1096	G1016	U931	C848
U1931	C1764	C1837	G1684	G1684	C1605	G1524	A1439	A1285	G1187	A1096	G1016	U931	C848
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G1844	C1771	G1845	G1687	U1688	C1604	A1528	U1440	G1271	G1192	U1105	A1028	A941	G858
G1845	A1772	A1773	U1688	U1688	C1605	A1528	U1440	G1271	G1192	U1105	A1028	A941	G858
A1837	A1773	A1773	G1696	G1696	A1610	A1532	G1441	U1273	G1193	A1111	A1029	G942	C859
A1838	U1778	U1778	G1706	G1706	A1614	A1532	G1442	U1273	G1193	A1111	A1029	G942	C859
G1849	U1778	U1778	C1533	C1533	A1614	A1532	G1442	U1273	G1193	A1111	A1029	G942	C859
G1850	A1779	U1779	C1534	C1534	A1615	A1532	G1443	G1368	G1196	G1112	A1030	A943	A863
U1851	U1779	U1779	A1616	A1616	C1615	C1533	G1443	G1368	G1196	G1112	A1030	A943	A863
U1852	A1780	G1702	A1617	A1617	C1616	C1534	G1444	G1371	G1197	G1115	C946	A947	C865
A1853	U1781	G1702	A1618	A1618	C1617	A1535	G1445	G1371	G1197	G1115	C946	A947	C865
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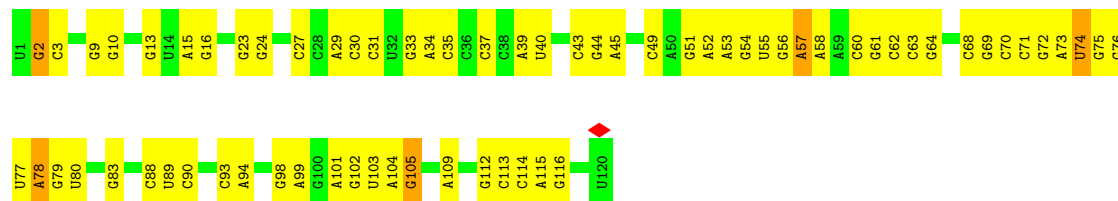
• Molecule 2: 16S ribosomal RNA



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G1334	A1254	C1161	U1083	A1004	A923	U842	G752	A673	A573	Q497	A412	C335	G255	C175
G1338	G1255	A1162	G1084	A1005	C924	U843	A753	G674	A574	C501	A413	A336	G256	G176
G1342	A1256	A1167	U1085	A1006	G925	U844	G755	A675	G575	A502	A414	A337	G257	C177
G1343	C1257	U1168	G1086	U1007	G926	G845	G756	A676	C576	G505	U421	A338	G258	C178
G1347	C1258	U1169	U1008	U1008	G927	G846	A759	U677	G577	G506	G422	A339	G259	U179
A1350	G1259	A1170	U1009	U1009	C932	G849	G763	U678	A579	G507	G423	G347	G260	U180
U1351	G1260	U1171	U1010	C1011	G933	U850	G764	C679	C580	U508	G424	C348	U261	A181
C1352	A1261	C1172	U1011	G1012	C934	G851	G765	U684	C581	G425	U425	A182	C264	A182
G1353	U1173	U1173	G1013	G1013	A935	G852	G769	A687	U591	A509	U426	G351	G265	G184
G1355	A1176	A1176	A1014	A1015	A938	U855	G773	G688	G592	A510	U427	G352	G266	U185
U1356	G1177	G1177	A1016	A1016	G939	U859	G773	C689	U593	A511	G428	A353	G267	C186
A1357	G1178	G1178	U1017	U1017	C944	G860	G778	G690	U594	C513	U429	C354	U268	G187
A1363	A1179	A1179	A1018	A1018	G945	U865	C779	A695	A596	U515	G436	G357	C271	C193
C1367	A1180	A1180	G1108	G1109	G947	U866	A780	A696	U597	G516	U437	U358	G275	C194
G1370	G1181	G1181	C1109	A1021	C947	C866	G786	U697	C599	G517	U438	G359	A196	A196
A1374	U1182	U1182	U1115	A1022	U952	C869	G787	G700	A600	C519	U439	G360	A197	A197
A1375	U1116	U1116	U1116	U1023	U953	U871	A790	A704	A602	A520	G454	A362	G281	G202
A1376	U1183	U1183	C1119	A1024	G953	U875	U793	A705	U603	G522	G455	U367	G285	G203
A1377	G1184	G1184	G945	U1025	G954	C876	A794	A706	U604	A523	G456	U368	C286	G204
C1378	G1185	G1185	U955	U1026	G955	U877	G797	G707	G601	C524	G457	C372	G289	U209
G1379	G1187	G1187	U956	C1027	U956	U878	C798	A708	U605	A525	U458	A374	G292	G211
C1383	G1188	G1188	U957	U1028	U957	U879	G799	G713	G614	A532	A459	U375	G296	G212
G1384	G1189	G1189	A958	A1029	A958	U880	G800	G714	G615	C536	A460	G376	G297	G213
G1385	A1196	A1196	A959	U1030	A959	U881	A715	A716	U619	G537	G462	C381	A300	C214
U1390	A1197	A1197	U960	C1031	U960	U882	U801	A717	C620	G538	U463	G382	A306	C215
U1391	G1198	G1198	U961	U1032	C962	U883	G807	G721	A621	A539	U464	A383	G310	U216
C1393	G1207	G1207	G963	G1033	G963	U884	C811	G722	A629	G540	U467	A384	C311	C222
C1394	C1208	C1208	U965	U1034	U965	U885	C812	U723	A630	G541	A468	C385	C312	A223
G1395	C1209	C1209	U966	G1035	U966	U886	A815	G727	G633	G542	C469	C386	A313	U224
U1398	A1213	A1213	A968	G1041	A968	U887	A816	G730	C634	U543	C470	U387	C314	G225
U1399	G1214	G1214	C970	A1042	C970	U888	C817	G731	A635	A544	U472	A388	G314	G226
C1400	G1215	G1215	G971	G1043	A969	U889	A817	G732	A642	G545	U473	A389	U317	
G1401	A1216	A1216	A975	A1044	C971	U890	U820	C732	A643	C546	G474	U390	U318	
C1402	C1217	C1217	G976	G1045	A976	U891	G821	G733	C647	G547	A478	G391	G319	G230
U1409	A1218	A1218	C979	C1046	C979	U892	U822	G734	U648	U552	U479	C392	G318	U229
G1410	C1219	C1219	U981	G1053	U981	U893	C823	G735	A649	A553	U480	A393	G319	G231
C1411	G1220	G1220	C984	A1055	U981	U894	G824	C736	G650	A554	G481	A320	A321	U231
A1412	U1146	U1146	C985	A1056	C985	U895	A825	C737	G651	A555	A482	A321	A321	G232
A1413	C1147	C1147	U989	U1065	U989	U896	U827	C738	U653	A559	C483	U398	U323	C235
A1414	U1148	U1148	U990	U1066	C985	U897	U828	C739	C660	A560	G484	G399	U324	A236
A1415	C1149	C1149	U991	C1066	U989	U898	U829	U740	G661	A563	U485	C401	G327	G240
G1416	A1150	A1150	U992	U1070	U989	U899	G832	G745	U662	C564	C489	U405	A329	
C1419	U1151	U1151	U993	C1071	U992	U900	G833	A746	A663	G567	C490	G406	A329	C350
A1428	A1152	A1152	A994	G1072	A994	U901	U834	A747	G664	G570	G491	U407	A329	G247
	U1157	U1157	U995	U1073	A995	U902	U835	G748	A665	U571	C492	A408	C350	G247
	C1158	C1158	U996	G1074	A996	U903	U836	G749	A666		C493	U409	G332	G251
	U1159	U1159		G1077		U904	U837	C750	G667		A493	G410	U333	



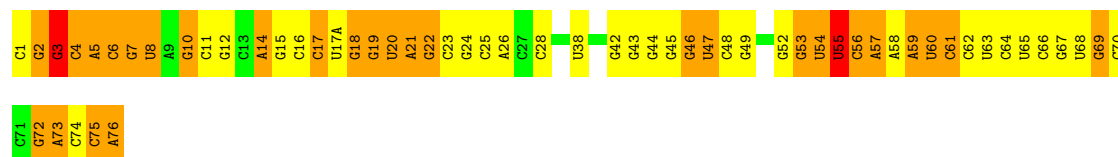
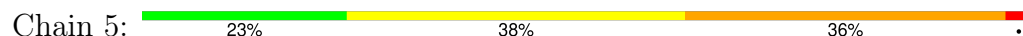
• Molecule 3: 5S ribosomal RNA



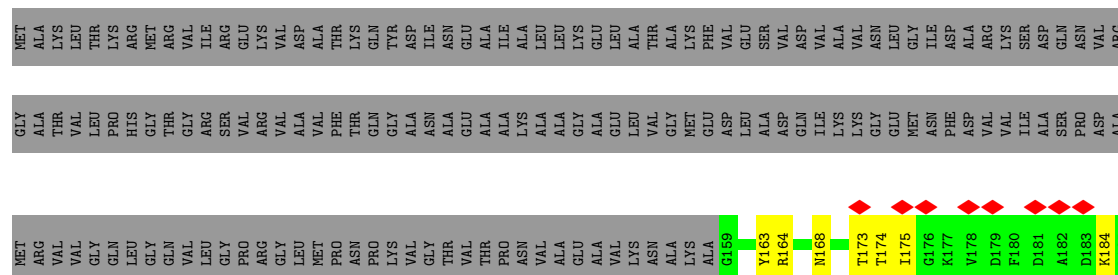
• Molecule 4: mRNA



• Molecule 5: Lys-tRNA^{proL}

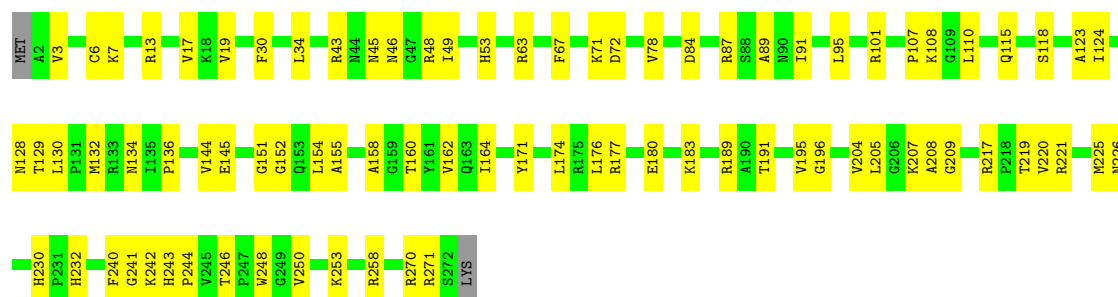


• Molecule 6: Large ribosomal subunit protein uL1



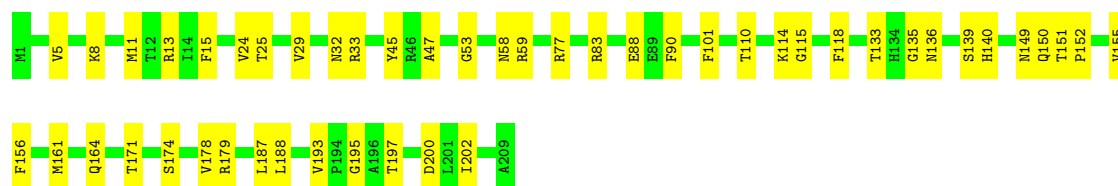
• Molecule 7: 50S ribosomal protein L2

Chain B: 



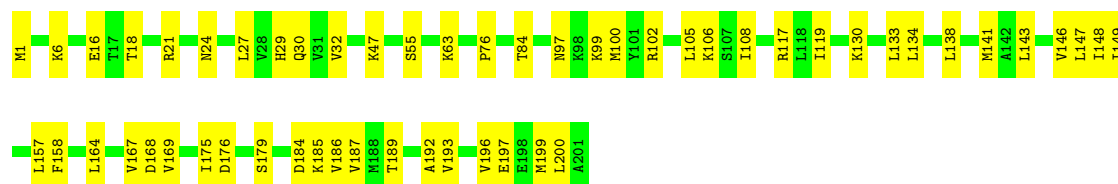
- Molecule 8: 50S ribosomal protein L3

Chain C: 



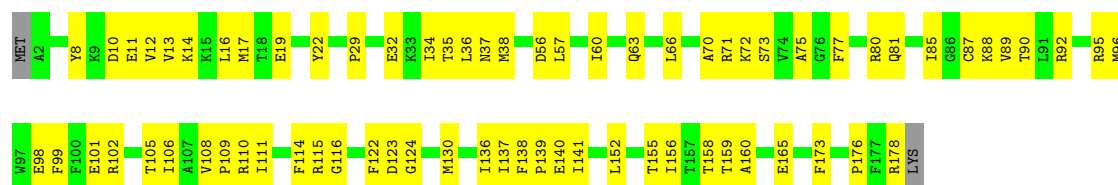
- Molecule 9: 50S ribosomal protein L4

Chain D: 



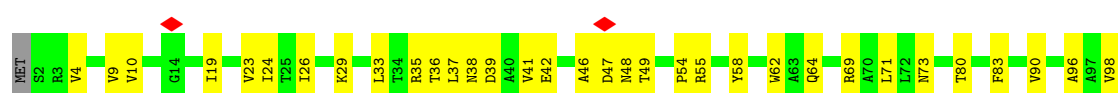
- Molecule 10: 50S ribosomal protein L5

Chain E: 



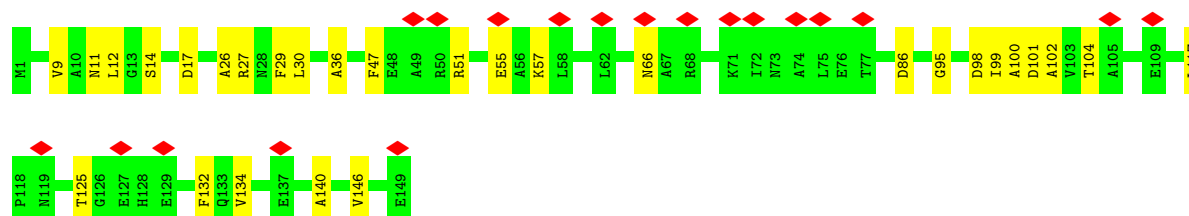
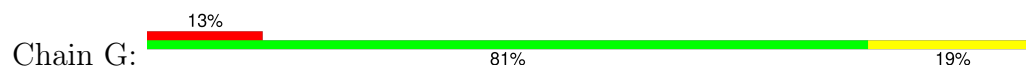
- Molecule 11: 50S ribosomal protein L6

Chain F: 

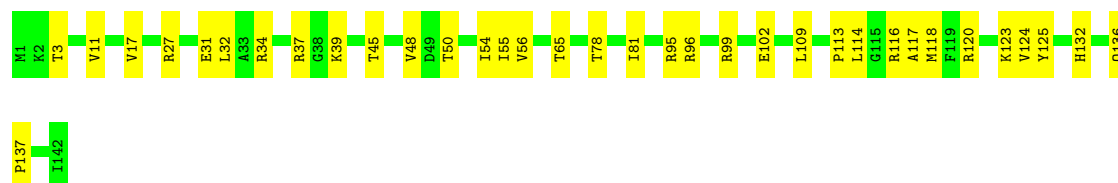




- Molecule 12: 50S ribosomal protein L9



- Molecule 13: Large ribosomal subunit protein uL13



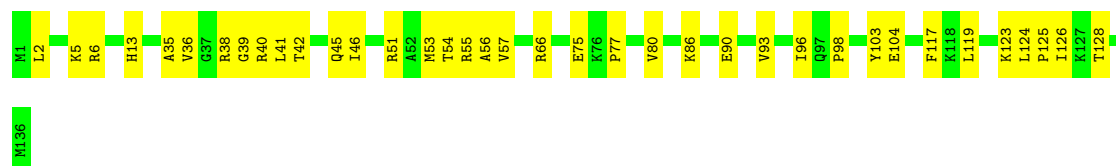
- Molecule 14: 50S ribosomal protein L14



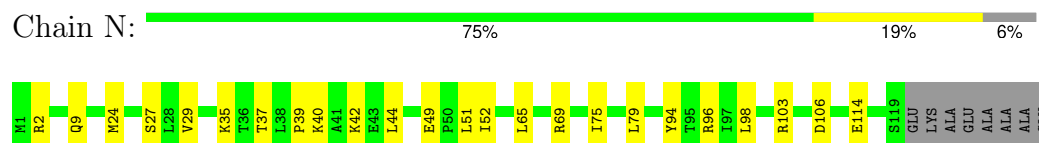
- Molecule 15: 50S ribosomal protein L15



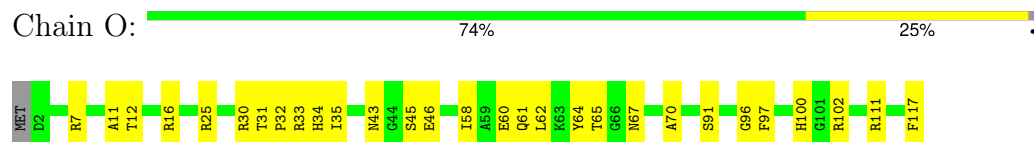
- Molecule 16: 50S ribosomal protein L16



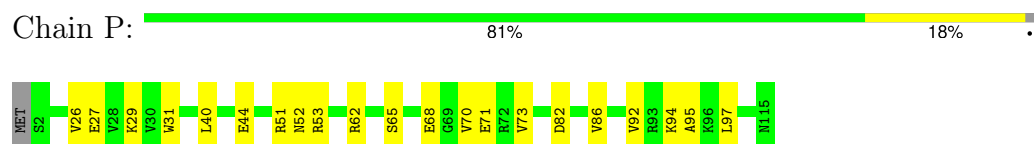
- Molecule 17: 50S ribosomal protein L17



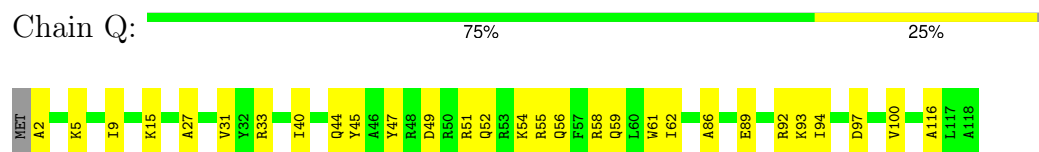
- Molecule 18: Large ribosomal subunit protein uL18



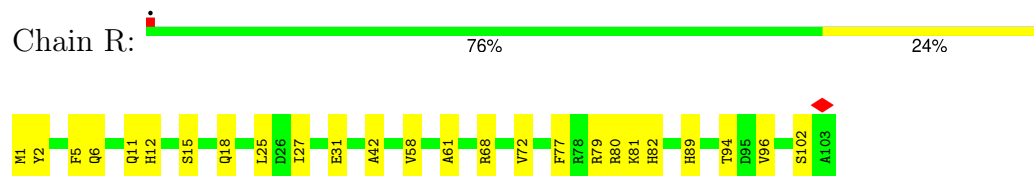
- Molecule 19: Large ribosomal subunit protein bL19



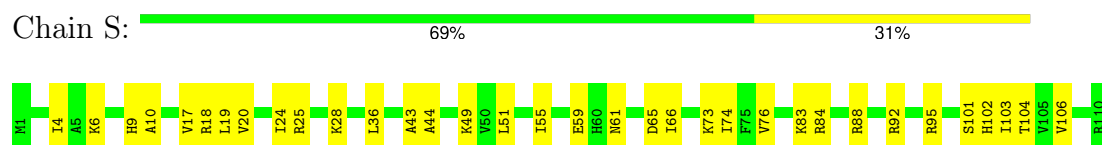
- Molecule 20: 50S ribosomal protein L20



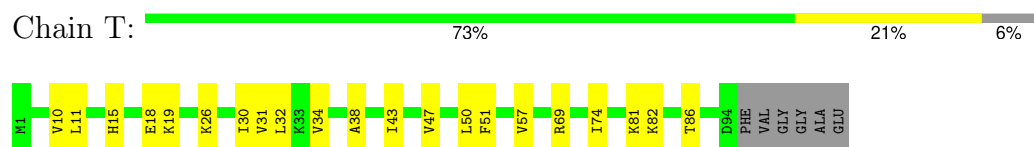
- Molecule 21: Ribosomal protein L21




- Molecule 22: 50S ribosomal protein L22

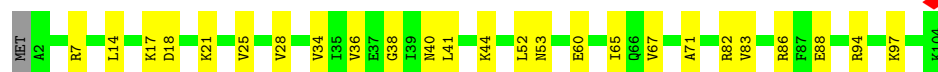


- Molecule 23: 50S ribosomal protein L23




- Molecule 24: 50S ribosomal protein L24

Chain U:  75% 24%



- Molecule 25: Large ribosomal subunit protein bL25

Chain V:  81% 19%




- Molecule 26: Large ribosomal subunit protein bL27

Chain W:  67% 24% 10%




- Molecule 27: 50S ribosomal protein L28

Chain X:  79% 19%



- Molecule 28: Large ribosomal subunit protein uL29

Chain Y:  84% 14%



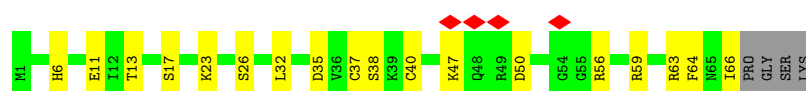
- Molecule 29: 50S ribosomal protein L30

Chain Z:  75% 24%



- Molecule 30: 50S ribosomal protein L31

Chain a:  6% 69% 26% 6%



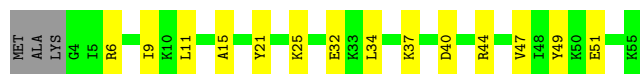
- Molecule 31: 50S ribosomal protein L32

Chain b:  74% 25% .



- Molecule 32: 50S ribosomal protein L33

Chain c:  69% 25% 5%



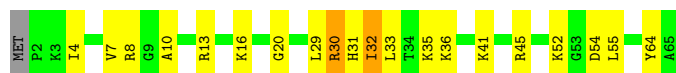
- Molecule 33: 50S ribosomal protein L34

Chain d:  70% 30%



- Molecule 34: 50S ribosomal protein L35

Chain e:  68% 28% . .



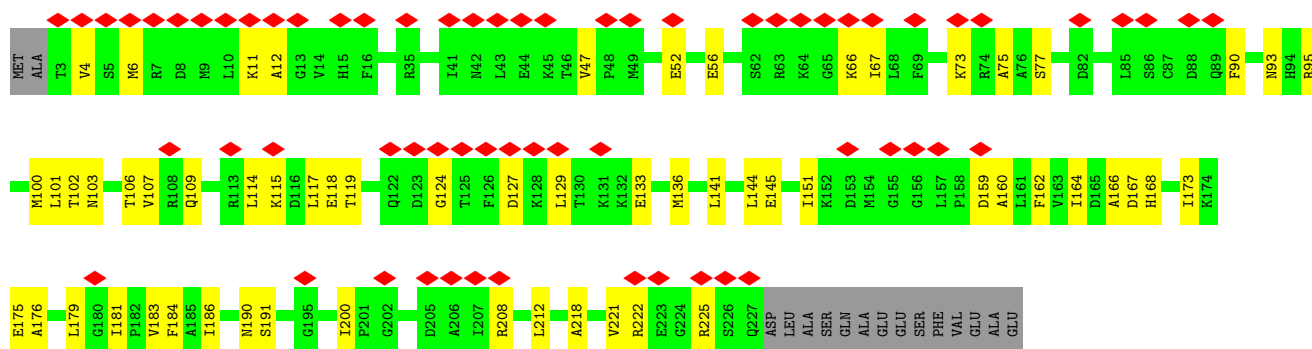
- Molecule 35: 50S ribosomal protein L36

Chain f:  74% 26%



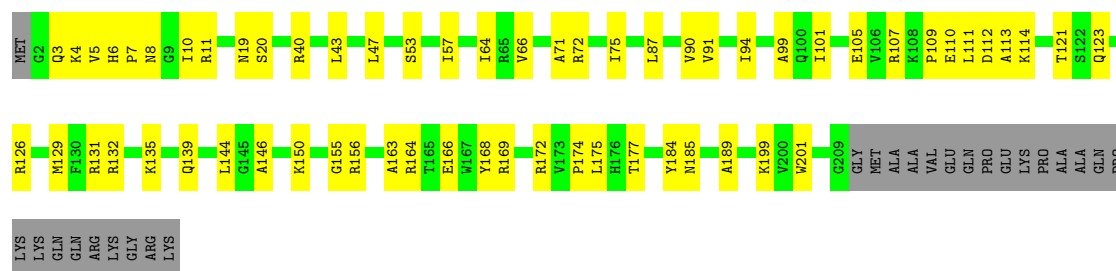
- Molecule 36: 30S ribosomal protein S2

Chain g:  27% 68% 25% 7%



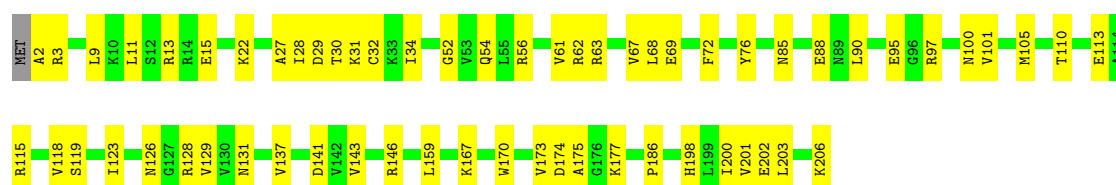
- Molecule 37: 30S ribosomal protein S3

Chain h:  63% 26% 11%



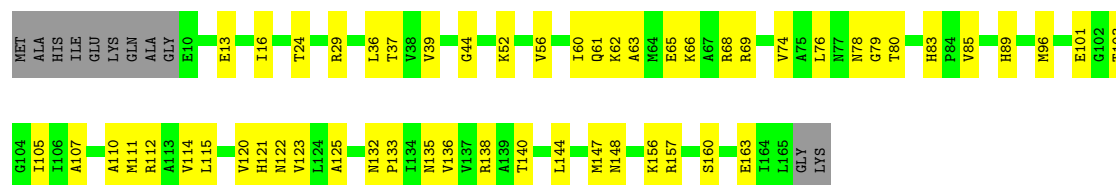
• Molecule 38: 30S ribosomal protein S4

Chain i:  70% 30%



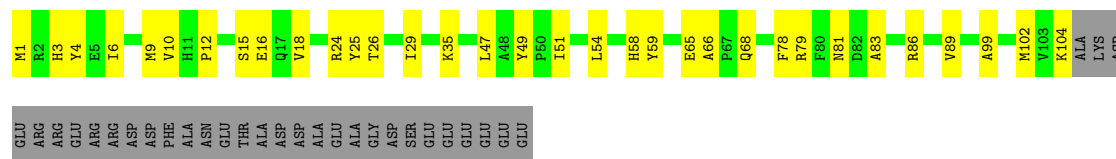
• Molecule 39: 30S ribosomal protein S5

Chain j:  61% 32% 7%



• Molecule 40: 30S ribosomal protein S6

Chain k:  53% 24% 23%

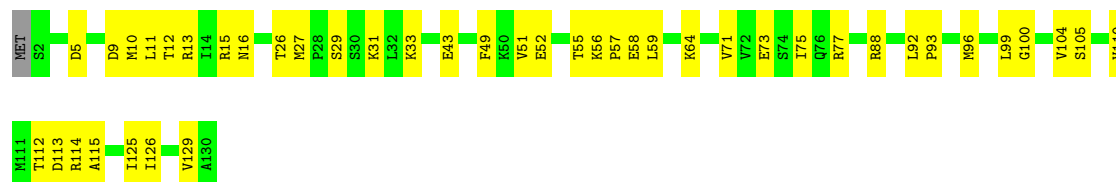


• Molecule 41: 30S ribosomal protein S7

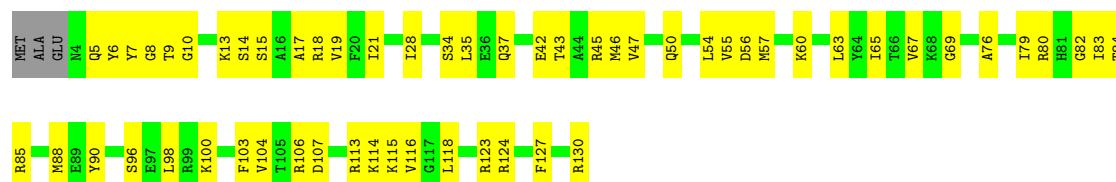
Chain l:  58% 26% 16%



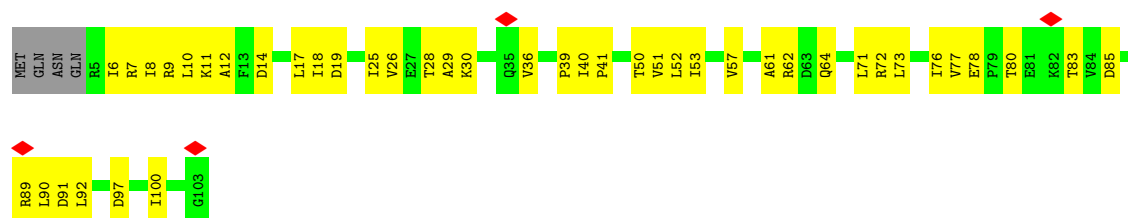
- Molecule 42: Small ribosomal subunit protein uS8



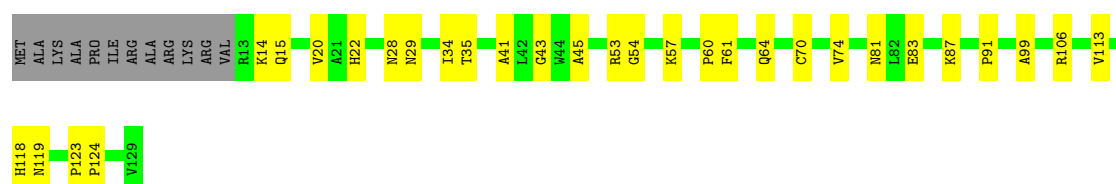
- Molecule 43: Small ribosomal subunit protein uS9



- Molecule 44: Small ribosomal subunit protein uS10

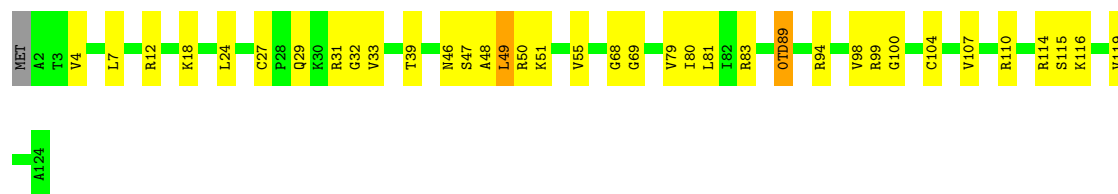


- Molecule 45: 30S ribosomal protein S11

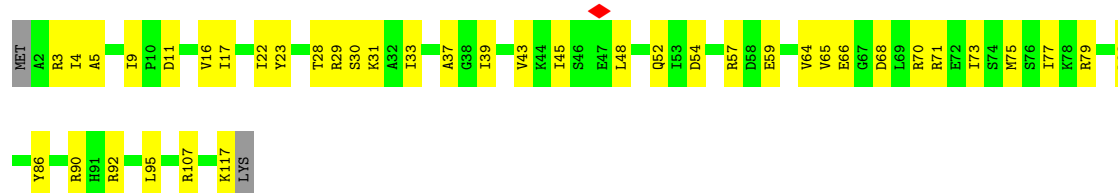


- Molecule 46: Small ribosomal subunit protein uS12





- Molecule 47: 30S ribosomal protein S13



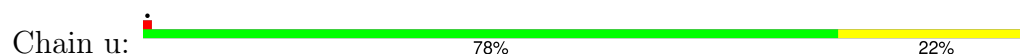
- Molecule 48: Small ribosomal subunit protein uS14



- Molecule 49: Small ribosomal subunit protein uS15



- Molecule 50: 30S ribosomal protein S16

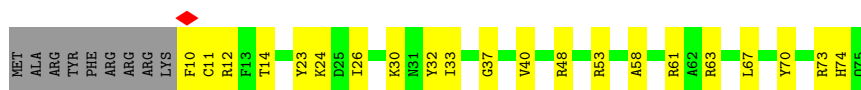


- Molecule 51: Small ribosomal subunit protein uS17



- Molecule 52: 30S ribosomal protein S18





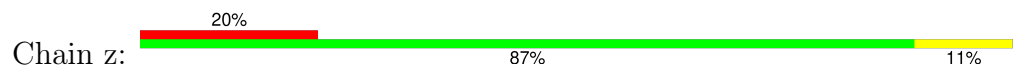
- Molecule 53: Small ribosomal subunit protein uS19



- Molecule 54: 30S ribosomal protein S20



- Molecule 55: 30S ribosomal protein S21



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	69316	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	61.23	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2700	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.056	Depositor
Minimum map value	-0.009	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.012	Depositor
Map size (Å)	547.328, 547.328, 547.328	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.069, 1.069, 1.069	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: OMG, MA6, MG, OMC, 2MG, 2MA, 5MC, OMU, PSU, 1MG, UR3, 5MU, G7M, 7MG, 4OC, 0TD, 6MZ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	1	0.14	0/69335	0.25	0/108168
2	2	0.13	0/36590	0.23	0/57074
3	3	0.11	0/2872	0.23	0/4478
4	4	0.34	0/255	0.55	0/394
5	5	0.30	0/1841	0.54	2/2870 (0.1%)
6	A	0.10	0/511	0.28	0/685
7	B	0.14	0/2121	0.29	0/2852
8	C	0.14	0/1586	0.32	0/2134
9	D	0.15	0/1571	0.35	0/2113
10	E	0.14	0/1434	0.38	0/1926
11	F	0.12	0/1333	0.28	0/1805
12	G	0.13	0/1122	0.33	0/1515
13	J	0.16	0/1152	0.34	0/1551
14	K	0.12	0/955	0.25	0/1279
15	L	0.14	0/1062	0.28	0/1413
16	M	0.14	0/1093	0.29	0/1460
17	N	0.15	0/964	0.34	0/1289
18	O	0.13	0/902	0.31	0/1209
19	P	0.14	0/929	0.28	0/1242
20	Q	0.17	0/960	0.33	0/1278
21	R	0.14	0/829	0.34	0/1107
22	S	0.16	0/864	0.35	0/1156
23	T	0.13	0/752	0.29	0/1005
24	U	0.14	0/796	0.32	0/1062
25	V	0.15	0/766	0.36	0/1025
26	W	0.13	0/589	0.25	0/779
27	X	0.15	0/635	0.31	0/848
28	Y	0.13	0/502	0.33	0/667
29	Z	0.13	0/452	0.27	0/605
30	a	0.12	0/531	0.30	0/709
31	b	0.13	0/450	0.29	0/599

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	c	0.13	0/433	0.26	0/576
33	d	0.14	0/380	0.26	0/498
34	e	0.39	0/513	0.62	1/676 (0.1%)
35	f	0.13	0/303	0.33	0/397
36	g	0.14	0/1791	0.39	0/2413
37	h	0.14	0/1663	0.36	0/2241
38	i	0.12	0/1665	0.26	0/2227
39	j	0.16	0/1165	0.36	0/1568
40	k	0.15	0/867	0.37	0/1171
41	l	0.14	0/1195	0.37	0/1602
42	m	0.16	0/989	0.39	0/1326
43	n	0.22	0/1034	0.50	0/1375
44	o	0.15	0/800	0.38	0/1082
45	p	0.19	0/893	0.37	0/1205
46	q	0.27	0/960	0.40	0/1286
47	r	0.13	0/909	0.35	0/1215
48	s	0.12	0/817	0.27	0/1088
49	t	0.13	0/722	0.31	0/964
50	u	0.16	0/659	0.33	0/884
51	v	0.12	0/657	0.31	0/881
52	w	0.17	0/553	0.29	0/743
53	x	0.12	0/680	0.28	0/915
54	y	0.16	0/675	0.34	0/895
55	z	0.10	0/597	0.24	0/792
All	All	0.14	0/156674	0.28	3/234317 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	e	30	ARG	N-CA-C	-11.61	92.49	108.86
5	5	55	U	C3'-C2'-O2'	6.24	120.05	110.70
5	5	3	G	C4'-C3'-O3'	5.85	118.18	109.40

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	1	62334	0	31367	1170	0
2	2	32929	0	16587	576	0
3	3	2569	0	1301	46	0
4	4	230	0	119	8	0
5	5	1648	0	833	73	0
6	A	507	0	542	10	0
7	B	2082	0	2154	58	0
8	C	1565	0	1616	40	0
9	D	1552	0	1619	50	0
10	E	1410	0	1444	53	0
11	F	1313	0	1358	32	0
12	G	1111	0	1148	18	0
13	J	1129	0	1162	34	0
14	K	946	0	1023	25	0
15	L	1053	0	1129	30	0
16	M	1074	0	1157	29	0
17	N	951	0	994	17	0
18	O	892	0	923	26	0
19	P	917	0	962	18	0
20	Q	947	0	1019	30	0
21	R	816	0	839	25	0
22	S	857	0	922	26	0
23	T	746	0	811	15	0
24	U	788	0	844	18	0
25	V	753	0	780	17	0
26	W	582	0	599	15	0
27	X	625	0	652	11	0
28	Y	501	0	531	10	0
29	Z	448	0	488	11	0
30	a	522	0	524	19	0
31	b	444	0	458	16	0
32	c	426	0	464	11	0
33	d	377	0	418	16	0
34	e	504	0	572	25	0
35	f	302	0	343	9	0
36	g	1760	0	1787	39	0
37	h	1636	0	1710	42	0
38	i	1643	0	1707	45	0
39	j	1152	0	1196	40	0
40	k	848	0	846	27	0
41	l	1181	0	1238	35	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	m	979	0	1031	35	0
43	n	1022	0	1070	44	0
44	o	790	0	831	36	0
45	p	877	0	887	28	0
46	q	957	0	1017	34	0
47	r	900	0	965	31	0
48	s	805	0	844	27	0
49	t	714	0	734	23	0
50	u	649	0	666	16	0
51	v	648	0	691	18	0
52	w	544	0	560	15	0
53	x	663	0	688	32	0
54	y	669	0	719	19	0
55	z	589	0	629	6	0
56	1	262	0	0	0	0
56	2	111	0	0	0	0
56	3	10	0	0	0	0
56	5	1	0	0	0	0
56	B	3	0	0	0	0
56	L	2	0	0	0	0
56	M	1	0	0	0	0
56	Q	1	0	0	0	0
56	X	1	0	0	0	0
56	b	1	0	0	0	0
56	l	1	0	0	0	0
56	z	1	0	0	0	0
57	5	9	0	12	0	0
58	1	700	0	0	22	0
58	2	341	0	0	5	0
58	3	7	0	0	0	0
58	4	1	0	0	0	0
58	5	10	0	0	3	0
58	B	2	0	0	0	0
58	C	7	0	0	0	0
58	D	10	0	0	2	0
58	E	4	0	0	1	0
58	F	6	0	0	1	0
58	G	12	0	0	0	0
58	J	7	0	0	3	0
58	K	4	0	0	2	0
58	L	3	0	0	3	0
58	M	2	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
58	N	2	0	0	0	0
58	O	6	0	0	1	0
58	P	6	0	0	0	0
58	Q	7	0	0	1	0
58	R	7	0	0	5	0
58	S	4	0	0	1	0
58	T	2	0	0	0	0
58	U	6	0	0	0	0
58	V	1	0	0	0	0
58	W	2	0	0	0	0
58	Y	8	0	0	2	0
58	Z	2	0	0	1	0
58	a	2	0	0	0	0
58	b	2	0	0	0	0
58	f	1	0	0	0	0
58	g	20	0	0	1	0
58	h	14	0	0	2	0
58	i	8	0	0	2	0
58	j	3	0	0	0	0
58	k	7	0	0	1	0
58	l	5	0	0	1	0
58	m	3	0	0	0	0
58	n	4	0	0	0	0
58	o	3	0	0	0	0
58	p	5	0	0	1	0
58	q	1	0	0	0	0
58	r	4	0	0	0	0
58	t	1	0	0	0	0
58	u	4	0	0	0	0
58	v	3	0	0	0	0
58	w	3	0	0	1	0
58	x	1	0	0	0	0
58	z	4	0	0	0	0
All	All	146547	0	97530	2747	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 12.

All (2747) 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)
5:5:67:G:H5'	58:5:206:HOH:O	1.65	0.95
1:1:408:G:H1	1:1:419:U:H3	1.16	0.94
5:5:18:G:H1	5:5:57:A:N6	1.68	0.91
54:y:57:ILE:HG13	54:y:61:GLN:HE22	1.36	0.89
1:1:1270:C:H5''	1:1:1271:G:H5'	1.55	0.88
2:2:246:A:H62	2:2:281:G:N2	1.70	0.88
1:1:377:G:H1	1:1:397:U:H3	1.18	0.87
2:2:458:U:H3	2:2:474:G:H1	0.87	0.86
1:1:572:A:H61	1:1:2029:G:H21	1.21	0.85
1:1:1039:A:C2	1:1:1116:G:N1	2.46	0.84
1:1:586:A:H5'	9:D:84:THR:HG21	1.59	0.83
1:1:2491:U:H5'	1:1:2570:G:H5''	1.62	0.82
44:o:51:VAL:HG23	48:s:81:ARG:HB2	1.63	0.81
1:1:274:C:O2	1:1:363:G:N2	2.14	0.80
8:C:156:PHE:HB3	13:J:81:ILE:HD11	1.64	0.80
5:5:18:G:N1	5:5:57:A:N6	2.28	0.80
36:g:100:MET:HA	36:g:107:VAL:HG21	1.64	0.79
2:2:20:U:O2'	2:2:573:A:N6	2.17	0.78
10:E:38:MET:HG2	10:E:57:LEU:HD22	1.66	0.78
2:2:875:U:O2'	42:m:15:ARG:NH1	2.17	0.77
43:n:96:SER:OG	43:n:100:LYS:NZ	2.17	0.77
1:1:1202:G:N2	15:L:4:ASN:OD1	2.17	0.77
49:t:29:VAL:HG11	49:t:81:LEU:HD21	1.67	0.77
38:i:129:VAL:HG21	38:i:146:ARG:HH21	1.48	0.77
2:2:246:A:N6	2:2:281:G:N2	2.32	0.77
1:1:26:G:H1'	1:1:515:A:H61	1.48	0.77
2:2:335:C:H2'	2:2:336:A:H8	1.50	0.77
3:3:71:C:H42	3:3:105:G:H1	1.33	0.77
2:2:1124:G:O2'	2:2:1145:A:N6	2.17	0.76
17:N:37:THR:HG22	17:N:39:PRO:HD2	1.67	0.76
2:2:673:A:H2'	2:2:674:G:C8	2.21	0.76
1:1:475:C:O2	1:1:479:A:N6	2.19	0.76
13:J:34:ARG:HG3	13:J:39:LYS:HB2	1.68	0.76
2:2:438:U:H3	2:2:496:A:H62	1.34	0.76
7:B:225:MET:HG2	7:B:230:HIS:HB2	1.67	0.76
5:5:54:U:H3	5:5:58:A:H62	1.34	0.75
2:2:826:C:O2	42:m:16:ASN:ND2	2.19	0.75
1:1:1047:G:H21	1:1:1111:A:H62	1.34	0.75
1:1:497:A:H2'	1:1:498:G:H8	1.52	0.74
1:1:1779:U:OP2	1:1:1784:A:N6	2.21	0.74
1:1:698:C:O2'	1:1:734:A:N6	2.19	0.74
53:x:18:LYS:NZ	53:x:32:ARG:O	2.21	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:45:G:H5''	1:1:46:G:H5'	1.70	0.74
34:e:32:ILE:HD11	34:e:35:LYS:HG2	1.69	0.74
1:1:447:A:OP1	20:Q:5:LYS:NZ	2.20	0.74
1:1:2117:A:N1	1:1:2171:A:N6	2.35	0.74
47:r:4:ILE:HG23	47:r:57:ARG:HG2	1.70	0.74
5:5:56:C:O2'	10:E:75:ALA:HB2	1.89	0.73
43:n:43:THR:HA	43:n:46:MET:HE3	1.70	0.73
1:1:848:C:H2'	1:1:849:A:H8	1.52	0.73
13:J:114:LEU:O	13:J:118:MET:HB3	1.87	0.73
37:h:11:ARG:NH1	37:h:177:THR:O	2.21	0.73
1:1:2333:A:H4'	1:1:2334:U:H5''	1.70	0.73
2:2:927:G:OP2	4:4:11:A:N6	2.22	0.73
34:e:16:LYS:HE2	34:e:20:GLY:HA2	1.71	0.73
1:1:1215:G:H1	1:1:1234:U:H3	1.34	0.73
1:1:155:A:H2'	1:1:156:A:H8	1.54	0.72
1:1:1868:C:N4	1:1:1869:G:O6	2.22	0.72
36:g:4:VAL:HG11	36:g:212:LEU:HD21	1.69	0.72
43:n:13:LYS:HG3	43:n:14:SER:H	1.55	0.72
12:G:66:ASN:ND2	12:G:134:VAL:O	2.23	0.72
1:1:111:A:O2'	28:Y:58:ASN:ND2	2.23	0.72
1:1:2102:G:N2	1:1:2187:U:O2	2.22	0.72
13:J:27:ARG:NH1	58:J:201:HOH:O	2.23	0.72
1:1:1039:A:N1	1:1:1116:G:O6	2.23	0.71
25:V:48:MET:SD	25:V:51:GLN:NE2	2.62	0.71
27:X:45:ARG:HH21	27:X:47:VAL:HG12	1.55	0.71
54:y:57:ILE:O	54:y:61:GLN:NE2	2.23	0.71
1:1:2188:U:O4	1:1:2189:U:O4	2.07	0.71
2:2:180:U:H3	2:2:195:A:H62	1.36	0.71
1:1:242:G:H5'	34:e:64:TYR:HE2	1.55	0.71
43:n:56:ASP:O	43:n:60:LYS:NZ	2.24	0.71
58:1:3302:HOH:O	17:N:2:ARG:NH1	2.23	0.71
1:1:309:A:N3	1:1:329:G:O2'	2.24	0.70
2:2:981:U:OP1	48:s:9:ARG:NH1	2.25	0.70
1:1:572:A:H61	1:1:2029:G:N2	1.89	0.70
44:o:29:ALA:HB1	44:o:36:VAL:HG21	1.72	0.70
1:1:177:G:N2	1:1:177:G:OP2	2.24	0.70
2:2:297:G:N2	2:2:300:A:OP2	2.25	0.70
2:2:671:G:O2'	40:k:79:ARG:NH2	2.24	0.70
43:n:28:ILE:HG12	43:n:63:LEU:HD21	1.73	0.70
50:u:4:ILE:HG12	50:u:21:VAL:HG22	1.72	0.70
1:1:2758:A:H1'	11:F:38:ASN:HD21	1.56	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:429:U:H5'	38:i:9:LEU:HD11	1.74	0.70
10:E:13:VAL:O	10:E:17:MET:HG2	1.92	0.70
38:i:61:VAL:HG21	38:i:200:ILE:HD11	1.73	0.70
9:D:119:ILE:HB	9:D:187:VAL:HG12	1.74	0.70
1:1:274:C:N3	1:1:363:G:N1	2.40	0.70
10:E:105:THR:HG23	10:E:106:ILE:HG13	1.74	0.70
37:h:172:ARG:HG2	37:h:174:PRO:HD3	1.74	0.69
5:5:49:G:H1	5:5:65:U:H3	1.39	0.69
13:J:17:VAL:HG12	13:J:55:ILE:HB	1.74	0.69
1:1:2134:A:N6	1:1:2157:G:O2'	2.26	0.69
14:K:30:ARG:NH2	14:K:37:ASP:OD2	2.25	0.69
1:1:686:U:OP1	33:d:11:LYS:NZ	2.19	0.69
41:l:47:LEU:HD21	41:l:58:GLU:HB3	1.75	0.69
1:1:464:U:H1'	1:1:686:U:H5	1.57	0.69
1:1:497:A:H2'	1:1:498:G:C8	2.28	0.69
2:2:674:G:H2'	2:2:675:A:H8	1.57	0.69
5:5:60:U:OP2	5:5:61:C:N4	2.25	0.69
1:1:196:A:H61	1:1:831:G:N2	1.90	0.69
1:1:463:G:N2	1:1:466:A:OP2	2.24	0.69
2:2:310:G:H5''	50:u:31:ARG:HB2	1.75	0.69
2:2:1261:A:N6	2:2:1274:A:O2'	2.26	0.69
7:B:6:CYS:SG	7:B:13:ARG:NH1	2.66	0.69
9:D:164:LEU:HD22	9:D:167:VAL:HG22	1.75	0.69
1:1:2378:A:HO2'	18:O:91:SER:HG	1.40	0.69
16:M:75:GLU:HB2	16:M:90:GLU:HG3	1.75	0.69
30:a:35:ASP:OD2	47:r:3:ARG:NH1	2.25	0.69
39:j:13:GLU:OE2	39:j:68:ARG:NH1	2.25	0.69
2:2:673:A:H2'	2:2:674:G:H8	1.58	0.69
48:s:54:ASP:HA	48:s:59:ARG:HG3	1.74	0.69
1:1:2515:C:H2'	1:1:2516:A:H8	1.58	0.68
47:r:23:TYR:HB3	47:r:66:GLU:HB3	1.74	0.68
1:1:1047:G:N2	1:1:1111:A:H62	1.90	0.68
37:h:57:ILE:HG23	37:h:64:ILE:HD11	1.74	0.68
2:2:1447:A:OP1	2:2:1448:C:N4	2.25	0.68
11:F:38:ASN:ND2	11:F:64:GLN:OE1	2.27	0.68
1:1:2140:G:N1	1:1:2151:U:N3	2.41	0.68
2:2:946:A:O2'	2:2:1333:A:N3	2.26	0.68
41:l:113:ASP:HB2	41:l:119:ARG:HG3	1.75	0.68
1:1:1429:G:H2'	1:1:1430:G:H8	1.58	0.68
1:1:2530:A:N7	11:F:172:LYS:NZ	2.42	0.68
8:C:5:VAL:H	8:C:32:ASN:HD21	1.41	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:581:C:H2'	1:1:582:A:H8	1.58	0.68
1:1:1668:A:N3	1:1:1670:C:N4	2.42	0.68
3:3:104:A:C5	3:3:105:G:H1'	2.28	0.68
1:1:2312:U:O2	10:E:37:ASN:ND2	2.27	0.68
1:1:2031:A:N3	1:1:2455:G:O2'	2.27	0.67
2:2:1266:G:N2	2:2:1269:A:OP2	2.26	0.67
43:n:106:ARG:NH1	43:n:107:ASP:O	2.27	0.67
1:1:2069:G7M:N2	1:1:2442:C:O2	2.21	0.67
2:2:1312:G:OP2	30:a:63:ARG:NH2	2.27	0.67
1:1:535:G:H1	1:1:558:U:H3	1.42	0.67
1:1:1830:C:H2'	1:1:1831:G:H8	1.58	0.67
1:1:2595:G:N2	1:1:2598:A:OP2	2.27	0.67
1:1:2640:G:OP1	13:J:95:ARG:NH1	2.27	0.67
20:Q:49:ASP:HA	20:Q:52:GLN:HB2	1.77	0.67
1:1:1074:G:N2	58:1:3321:HOH:O	2.27	0.67
1:1:2061:G:OP2	9:D:63:LYS:NZ	2.26	0.67
1:1:2188:U:C4	1:1:2189:U:O4	2.47	0.67
10:E:63:GLN:HE21	10:E:89:VAL:HG13	1.58	0.67
1:1:468:G:OP2	33:d:37:LYS:NZ	2.26	0.67
2:2:150:U:H3	2:2:171:A:H62	1.42	0.67
10:E:158:THR:HG22	10:E:160:ALA:H	1.58	0.67
44:o:40:ILE:HD11	44:o:73:LEU:HD23	1.76	0.67
1:1:2220:U:H2'	1:1:2221:G:H8	1.60	0.67
9:D:21:ARG:NH2	58:D:302:HOH:O	2.26	0.67
1:1:219:A:N3	1:1:234:U:O2'	2.26	0.67
21:R:15:SER:H	21:R:18:GLN:HE22	1.42	0.67
1:1:528:A:H5''	13:J:113:PRO:HG3	1.75	0.67
2:2:1054:C:H42	4:4:21:U:H5	1.43	0.67
1:1:270:A:H5'	1:1:271:G:H5''	1.77	0.66
1:1:2376:A:N3	18:O:111:ARG:NH2	2.43	0.66
1:1:2857:G:N2	1:1:2860:A:OP2	2.21	0.66
21:R:72:VAL:O	58:R:201:HOH:O	2.13	0.66
1:1:2076:U:OP2	1:1:2238:G:N2	2.28	0.66
1:1:2796:U:H3	1:1:2799:A:H61	1.43	0.66
43:n:84:THR:HG23	43:n:98:LEU:HD23	1.76	0.66
2:2:1072:G:H21	36:g:106:THR:HG21	1.60	0.66
2:2:246:A:N6	2:2:281:G:H21	1.92	0.66
47:r:86:TYR:OH	47:r:90:ARG:NH1	2.29	0.66
41:l:15:ASP:OD1	41:l:20:SER:N	2.25	0.66
46:q:68:GLY:O	46:q:99:ARG:NH1	2.29	0.66
1:1:572:A:N6	1:1:2029:G:H21	1.92	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1255:G:O2'	2:2:1258:G:N3	2.24	0.66
25:V:69:GLU:OE1	25:V:69:GLU:N	2.28	0.66
2:2:405:U:O4	38:i:2:ALA:N	2.29	0.66
2:2:1027:C:N4	2:2:1034:G:O6	2.29	0.66
45:p:113:VAL:O	52:w:73:ARG:NH1	2.29	0.66
1:1:539:G:H1	1:1:554:U:H3	1.44	0.66
1:1:1287:A:N1	1:1:1649:G:O2'	2.26	0.66
7:B:3:VAL:HG12	7:B:19:VAL:HG22	1.77	0.66
15:L:1:MET:O	58:L:301:HOH:O	2.14	0.66
42:m:43:GLU:OE2	42:m:114:ARG:NH2	2.29	0.66
1:1:302:C:H2'	1:1:303:G:H8	1.62	0.65
1:1:2848:G:O2'	1:1:2867:G:N2	2.29	0.65
8:C:179:ARG:HB3	8:C:188:LEU:HD12	1.79	0.65
1:1:514:A:N3	1:1:581:C:O2'	2.27	0.65
2:2:938:A:N3	2:2:1376:U:O2'	2.25	0.65
26:W:37:ILE:HD11	26:W:82:ILE:HD11	1.77	0.65
7:B:232:HIS:HA	7:B:242:LYS:HD2	1.78	0.65
2:2:1119:C:OP1	43:n:85:ARG:NH2	2.30	0.65
14:K:58:LEU:HD11	14:K:86:LEU:HD23	1.77	0.65
20:Q:33:ARG:NH1	58:Q:301:HOH:O	2.25	0.65
40:k:16:GLU:OE2	40:k:16:GLU:N	2.27	0.65
43:n:42:GLU:HA	43:n:45:ARG:HD2	1.77	0.65
1:1:2460:U:O2	1:1:2493:U:N3	2.30	0.65
2:2:410:G:OP2	38:i:31:LYS:NZ	2.28	0.65
1:1:820:A:H4'	1:1:836:G:H22	1.60	0.65
1:1:1190:G:H5''	15:L:32:GLY:HA2	1.79	0.65
1:1:2258:C:O2'	1:1:2427:C:OP2	2.14	0.65
1:1:747:5MU:O2'	22:S:92:ARG:NH2	2.29	0.65
1:1:1597:A:H5''	1:1:1598:A:H5'	1.77	0.65
17:N:96:ARG:NH1	17:N:114:GLU:OE2	2.30	0.65
41:l:133:THR:HA	41:l:136:LYS:HG2	1.79	0.65
1:1:380:G:N1	1:1:395:U:N3	2.44	0.65
1:1:1016:G:O6	1:1:1147:A:N6	2.29	0.65
2:2:1005:A:H3'	2:2:1006:G:H8	1.61	0.65
7:B:144:VAL:HB	7:B:154:LEU:HB2	1.79	0.65
22:S:25:ARG:NH1	22:S:74:ILE:O	2.27	0.65
25:V:48:MET:HA	25:V:51:GLN:HG3	1.79	0.65
30:a:37:CYS:SG	30:a:38:SER:N	2.66	0.65
2:2:358:U:H2'	2:2:359:G:H8	1.61	0.64
11:F:98:VAL:HG12	11:F:103:ILE:HG12	1.80	0.64
1:1:993:G:OP2	20:Q:51:ARG:NH2	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1055:A:O2'	37:h:156:ARG:NH1	2.30	0.64
15:L:2:ARG:NH1	58:L:301:HOH:O	2.25	0.64
30:a:50:ASP:CG	47:r:71:ARG:HH22	2.06	0.64
1:1:1434:A:H2'	1:1:1435:G:H8	1.61	0.64
2:2:501:C:OP1	46:q:114:ARG:NH2	2.23	0.64
2:2:689:C:OP2	45:p:53:ARG:NH2	2.30	0.64
2:2:958:A:OP1	53:x:55:ARG:NH1	2.30	0.64
1:1:411:G:OP2	1:1:2406:A:O2'	2.16	0.64
1:1:2183:A:H2'	1:1:2184:A:C8	2.31	0.64
2:2:246:A:N6	2:2:281:G:C2	2.65	0.64
2:2:393:A:OP2	50:u:12:LYS:NZ	2.20	0.64
1:1:517:C:OP1	31:b:13:ARG:NH2	2.30	0.64
1:1:877:A:O2'	1:1:900:A:N6	2.30	0.64
1:1:918:A:N3	3:3:80:U:O2'	2.28	0.64
42:m:96:MET:HB3	42:m:100:GLY:H	1.61	0.64
1:1:244:A:OP2	34:e:8:ARG:NH2	2.30	0.64
1:1:2250:G:O2'	1:1:2496:C:OP1	2.15	0.64
2:2:335:C:O2'	2:2:1433:A:N3	2.27	0.64
5:5:19:G:OP1	5:5:60:U:N3	2.30	0.64
7:B:225:MET:HG3	7:B:226:ASN:H	1.63	0.64
52:w:37:GLY:O	52:w:63:ARG:NH2	2.31	0.64
1:1:887:A:O2'	1:1:889:C:OP2	2.14	0.64
1:1:2279:G:N7	26:W:14:ARG:NH2	2.46	0.64
1:1:2581:G:N2	1:1:2581:G:OP2	2.30	0.64
38:i:11:LEU:HB3	38:i:63:ARG:HD3	1.78	0.64
38:i:202:GLU:OE1	39:j:112:ARG:NH2	2.30	0.64
1:1:2720:U:OP1	19:P:53:ARG:NH2	2.31	0.64
2:2:222:C:H2'	2:2:223:A:H8	1.63	0.64
11:F:41:VAL:O	11:F:55:ARG:NH2	2.29	0.64
43:n:7:TYR:CG	43:n:8:GLY:N	2.66	0.64
49:t:32:LEU:HD11	49:t:59:MET:HB3	1.80	0.64
1:1:1030:C:N3	58:1:3338:HOH:O	2.30	0.64
1:1:1789:A:OP2	7:B:221:ARG:NH1	2.30	0.64
1:1:2304:G:H22	1:1:2312:U:H3	1.46	0.64
13:J:37:ARG:HA	13:J:118:MET:HE2	1.79	0.64
34:e:32:ILE:HG23	34:e:36:LYS:HZ1	1.62	0.64
2:2:842:U:O3'	2:2:844:G:N2	2.32	0.63
1:1:818:G:N1	1:1:1188:U:OP2	2.27	0.63
1:1:1992:G:N2	1:1:1996:C:O2'	2.31	0.63
37:h:112:ASP:OD1	37:h:113:ALA:N	2.31	0.63
1:1:102:U:O4	28:Y:2:LYS:N	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:298:G:N1	1:1:339:U:OP2	2.26	0.63
1:1:1807:G:N2	1:1:1810:A:OP2	2.30	0.63
1:1:2116:G:N2	1:1:2161:C:OP1	2.31	0.63
1:1:2618:G:H21	8:C:155:VAL:HG21	1.63	0.63
1:1:1042:G:N2	58:1:3318:HOH:O	2.31	0.63
1:1:1363:C:O2'	1:1:1809:A:N3	2.28	0.63
1:1:2075:U:H1'	1:1:2597:G:H21	1.64	0.63
2:2:103:U:OP2	54:y:9:LYS:NZ	2.28	0.63
5:5:19:G:H3'	5:5:20:U:H5	1.63	0.63
15:L:19:LEU:HD23	15:L:27:LEU:HD13	1.80	0.63
17:N:51:LEU:HB3	17:N:79:LEU:HD21	1.80	0.63
23:T:15:HIS:HB3	23:T:31:VAL:HG23	1.80	0.63
2:2:1356:G:H2'	2:2:1357:A:C8	2.33	0.63
1:1:210:C:OP1	33:d:29:GLN:NE2	2.32	0.63
19:P:26:VAL:HG12	19:P:86:VAL:HG12	1.81	0.63
2:2:1073:U:O2	36:g:103:ASN:ND2	2.31	0.63
41:l:113:ASP:OD2	41:l:122:ASN:ND2	2.32	0.63
2:2:1124:G:O2'	2:2:1127:G:O6	2.17	0.63
8:C:33:ARG:NH2	8:C:53:GLY:O	2.31	0.63
49:t:29:VAL:HG23	49:t:63:ARG:HG3	1.81	0.63
1:1:5:A:H2'	1:1:6:A:H8	1.64	0.62
2:2:844:G:O2'	52:w:12:ARG:NH2	2.32	0.62
8:C:24:VAL:HG12	8:C:178:VAL:HG21	1.79	0.62
9:D:168:ASP:OD1	58:D:301:HOH:O	2.16	0.62
22:S:55:ILE:O	22:S:59:GLU:HG2	1.99	0.62
41:l:138:ARG:NH2	41:l:139:GLU:OE2	2.32	0.62
18:O:43:ASN:ND2	58:O:202:HOH:O	2.33	0.62
36:g:167:ASP:OD1	36:g:168:HIS:N	2.32	0.62
47:r:65:VAL:HG22	47:r:66:GLU:H	1.64	0.62
1:1:1193:G:OP1	15:L:14:LYS:NZ	2.28	0.62
1:1:2107:G:O6	1:1:2182:U:O2	2.17	0.62
2:2:1496:C:H1'	2:2:1517:G:H22	1.65	0.62
9:D:176:ASP:OD1	9:D:179:SER:OG	2.16	0.62
2:2:337:G:H2'	2:2:338:A:H8	1.64	0.62
5:5:3:G:H3'	5:5:3:G:OP2	1.98	0.62
6:A:193:LEU:HG	6:A:197:LYS:HE2	1.79	0.62
53:x:36:ARG:NH2	53:x:75:ALA:O	2.33	0.62
2:2:1396:A:O2'	39:j:29:ARG:NH2	2.32	0.62
10:E:22:TYR:OH	10:E:165:GLU:OE1	2.17	0.62
16:M:103:TYR:HE2	16:M:124:LEU:HD11	1.64	0.62
1:1:2006:C:O2'	1:1:2823:A:N3	2.32	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2788:C:O2'	1:1:2809:A:N3	2.29	0.62
1:1:2831:G:OP2	8:C:59:ARG:NH2	2.32	0.62
2:2:12:U:H4'	2:2:526:C:H4'	1.82	0.62
3:3:9:G:O2'	18:O:45:SER:OG	2.18	0.62
10:E:38:MET:HB2	10:E:87:CYS:HB2	1.80	0.62
39:j:107:ALA:HB1	39:j:111:MET:HG2	1.82	0.62
1:1:535:G:N2	58:1:3350:HOH:O	2.33	0.62
2:2:841:C:H2'	2:2:843:U:H5'	1.80	0.62
10:E:72:LYS:NZ	58:E:201:HOH:O	2.30	0.62
29:Z:9:GLN:HB2	29:Z:29:LEU:HD23	1.82	0.62
40:k:29:ILE:HD11	40:k:66:ALA:HB2	1.81	0.62
1:1:529:A:OP2	13:J:116:ARG:NH2	2.30	0.62
1:1:559:G:N3	20:Q:56:GLN:NE2	2.48	0.62
1:1:2548:U:O2	14:K:23:LYS:NZ	2.32	0.62
1:1:2820:A:OP1	58:1:3302:HOH:O	2.16	0.62
2:2:451:A:OP2	50:u:70:ARG:NH2	2.31	0.62
2:2:642:A:N3	42:m:105:SER:OG	2.31	0.62
9:D:147:LEU:HB3	9:D:186:VAL:HG12	1.81	0.62
24:U:41:LEU:HD12	24:U:60:GLU:HG2	1.80	0.62
36:g:167:ASP:OD2	36:g:190:ASN:ND2	2.33	0.62
50:u:6:LEU:HG	50:u:17:TYR:HB3	1.82	0.62
1:1:882:G:O6	1:1:894:U:O4	2.18	0.62
2:2:689:C:OP1	45:p:29:ASN:ND2	2.33	0.62
17:N:49:GLU:HG2	17:N:94:TYR:HB2	1.82	0.62
18:O:30:ARG:HA	18:O:35:ILE:HG22	1.82	0.62
39:j:114:VAL:HG11	39:j:140:THR:HG21	1.80	0.62
53:x:50:ALA:HB1	53:x:57:HIS:HB3	1.80	0.62
1:1:2359:C:O2'	34:e:54:ASP:OD2	2.16	0.62
2:2:458:U:O4	2:2:474:G:O6	2.18	0.62
2:2:516:PSU:O2'	2:2:519:C:N4	2.29	0.62
2:2:1377:A:OP1	41:l:92:ARG:NH2	2.33	0.62
2:2:1522:U:H2'	2:2:1523:G:H8	1.63	0.62
10:E:111:ILE:HD13	10:E:137:ILE:HG21	1.82	0.62
1:1:489:G:N7	22:S:49:LYS:NZ	2.47	0.61
1:1:517:C:OP2	31:b:10:ARG:NH1	2.33	0.61
2:2:1127:G:H22	2:2:1147:C:H42	1.46	0.61
2:2:1317:C:H3'	2:2:1318:A:H8	1.65	0.61
30:a:13:THR:OG1	30:a:23:LYS:NZ	2.25	0.61
6:A:163:TYR:HB2	6:A:173:THR:HG22	1.81	0.61
9:D:106:LYS:HD3	9:D:200:LEU:HD13	1.82	0.61
1:1:250:G:OP2	34:e:13:ARG:NH2	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:981:A:OP2	1:1:982:C:N4	2.33	0.61
2:2:1005:A:N6	2:2:1024:G:O2'	2.30	0.61
2:2:1241:G:H2'	2:2:1242:G:H8	1.66	0.61
7:B:123:ALA:O	7:B:128:ASN:ND2	2.31	0.61
1:1:2372:U:H2'	1:1:2373:G:H8	1.65	0.61
2:2:1219:A:H2'	2:2:1220:G:H8	1.64	0.61
3:3:75:G:H2'	3:3:76:G:C8	2.35	0.61
7:B:71:LYS:O	7:B:118:SER:OG	2.18	0.61
10:E:29:PRO:HB3	10:E:160:ALA:HB2	1.82	0.61
11:F:90:VAL:O	11:F:160:LYS:HA	1.99	0.61
1:1:242:G:H5'	34:e:64:TYR:CE2	2.36	0.61
1:1:1629:U:O4	1:1:1630:A:N6	2.33	0.61
1:1:2420:C:OP2	34:e:33:LEU:N	2.33	0.61
2:2:385:C:N4	2:2:386:C:N4	2.47	0.61
2:2:714:G:H2'	2:2:715:A:C8	2.36	0.61
24:U:40:ASN:HD21	24:U:65:ILE:HB	1.65	0.61
37:h:72:ARG:HB3	37:h:75:ILE:HG22	1.81	0.61
51:v:76:VAL:HG23	51:v:77:ARG:HG2	1.82	0.61
9:D:149:ILE:HD11	9:D:175:ILE:HG12	1.83	0.61
33:d:34:ARG:NH2	33:d:41:ARG:O	2.25	0.61
47:r:79:ARG:NH2	53:x:65:GLU:OE2	2.33	0.61
52:w:30:LYS:HA	52:w:33:ILE:HG22	1.81	0.61
1:1:2467:C:OP1	35:f:8:LYS:NZ	2.33	0.61
2:2:662:U:O2'	2:2:836:G:OP1	2.18	0.61
2:2:1077:G:N2	2:2:1080:A:OP2	2.29	0.61
38:i:177:LYS:N	58:i:301:HOH:O	2.32	0.61
1:1:196:A:H61	1:1:831:G:H21	1.47	0.61
1:1:806:C:O2	1:1:2444:G:O2'	2.19	0.61
2:2:41:G:H2'	2:2:42:G:H8	1.64	0.61
38:i:27:ALA:HB3	38:i:30:THR:HG23	1.83	0.61
42:m:10:MET:HG3	42:m:27:MET:HE1	1.81	0.61
42:m:104:VAL:HG12	42:m:125:ILE:HA	1.82	0.61
1:1:75:G:H22	1:1:111:A:H2	1.48	0.61
36:g:119:THR:O	36:g:124:GLY:N	2.30	0.61
37:h:8:ASN:ND2	48:s:89:MET:O	2.31	0.61
37:h:20:SER:OG	37:h:40:ARG:NH2	2.34	0.61
19:P:31:TRP:NE1	19:P:82:ASP:OD2	2.34	0.60
1:1:482:A:OP1	58:1:3301:HOH:O	2.16	0.60
58:1:3330:HOH:O	23:T:26:LYS:NZ	2.34	0.60
2:2:352:C:O2	2:2:355:C:N4	2.34	0.60
2:2:490:C:H2'	2:2:491:G:H8	1.66	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:946:A:H2'	2:2:947:G:H8	1.66	0.60
11:F:29:LYS:NZ	11:F:80:THR:O	2.34	0.60
1:1:881:G:H22	1:1:895:U:H3	1.49	0.60
1:1:2107:G:O6	1:1:2182:U:C2	2.54	0.60
2:2:380:G:N2	2:2:383:A:OP2	2.30	0.60
2:2:946:A:H2'	2:2:947:G:C8	2.36	0.60
40:k:35:LYS:NZ	58:k:202:HOH:O	2.35	0.60
44:o:8:ILE:HG22	44:o:100:ILE:HG22	1.82	0.60
1:1:686:U:O2	33:d:8:SER:OG	2.16	0.60
1:1:2818:U:OP2	17:N:42:LYS:NZ	2.33	0.60
2:2:401:C:O2'	2:2:621:A:N3	2.32	0.60
2:2:1143:G:H2'	2:2:1144:G:C8	2.37	0.60
2:2:1218:C:H2'	2:2:1219:A:H8	1.65	0.60
7:B:180:GLU:OE2	7:B:270:ARG:NH1	2.35	0.60
41:l:14:PRO:HB2	41:l:19:GLY:HA2	1.84	0.60
44:o:9:ARG:HH12	44:o:71:LEU:HD21	1.67	0.60
1:1:1009:A:O4'	20:Q:59:GLN:NE2	2.34	0.60
2:2:333:U:OP1	54:y:2:ALA:N	2.35	0.60
2:2:1060:U:H2'	2:2:1061:G:H8	1.64	0.60
2:2:1219:A:H2'	2:2:1220:G:C8	2.36	0.60
1:1:212:G:H2'	1:1:213:A:C8	2.37	0.60
1:1:1048:A:H1'	1:1:1112:G:H21	1.65	0.60
1:1:2079:U:O2'	27:X:23:ASN:OD1	2.19	0.60
2:2:28:A:O2'	2:2:296:U:OP1	2.19	0.60
2:2:921:U:O2	39:j:24:THR:OG1	2.19	0.60
2:2:1167:A:O2'	2:2:1169:A:N7	2.35	0.60
1:1:742:A:H2'	1:1:743:A:C8	2.37	0.60
1:1:1443:U:H2'	1:1:1444:G:H8	1.66	0.60
1:1:2111:U:H3	1:1:2145:C:HO2'	1.49	0.60
1:1:2596:U:O2'	7:B:241:GLY:O	2.19	0.60
2:2:375:U:H4'	50:u:6:LEU:HD23	1.83	0.60
1:1:1201:U:H2'	1:1:1202:G:H8	1.67	0.60
1:1:1266:G:OP1	31:b:16:ARG:NE	2.35	0.60
1:1:1447:C:H2'	1:1:1448:G:H8	1.65	0.60
1:1:2304:G:N2	1:1:2312:U:H3	2.00	0.60
43:n:88:MET:HE3	43:n:98:LEU:HD22	1.84	0.60
48:s:41:ARG:NH2	53:x:6:LYS:O	2.27	0.60
1:1:155:A:H2'	1:1:156:A:C8	2.35	0.59
1:1:581:C:H2'	1:1:582:A:C8	2.38	0.59
1:1:1724:G:O6	1:1:1737:G:N2	2.34	0.59
1:1:2684:U:OP2	19:P:51:ARG:NH1	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:691:G:O6	45:p:53:ARG:NH1	2.35	0.59
2:2:1162:C:H2'	2:2:1163:A:H8	1.66	0.59
5:5:23:C:H2'	5:5:24:G:C8	2.37	0.59
22:S:73:LYS:HB2	22:S:106:VAL:HB	1.83	0.59
1:1:1039:A:N1	1:1:1116:G:C6	2.70	0.59
1:1:1386:C:H2'	1:1:1387:A:H8	1.67	0.59
2:2:460:A:H2'	2:2:461:A:H8	1.67	0.59
3:3:43:C:O2	10:E:92:ARG:NH1	2.35	0.59
17:N:24:MET:HE1	17:N:40:LYS:HB3	1.84	0.59
30:a:56:ARG:HH21	53:x:68:GLY:HA3	1.68	0.59
44:o:53:ILE:HD11	44:o:61:ALA:HB1	1.84	0.59
1:1:239:C:H2'	1:1:240:C:O4'	2.01	0.59
1:1:1009:A:H5'	20:Q:59:GLN:HG3	1.85	0.59
1:1:1788:C:OP1	7:B:221:ARG:NH2	2.35	0.59
1:1:1798:U:H5''	7:B:258:ARG:HB2	1.84	0.59
2:2:519:C:H5'	46:q:48:ALA:HA	1.84	0.59
2:2:740:U:H4'	49:t:39:LEU:HD21	1.83	0.59
21:R:12:HIS:N	58:R:202:HOH:O	2.36	0.59
1:1:1065:U:O2'	1:1:1066:U:O4'	2.20	0.59
1:1:1857:G:N2	1:1:1884:G:O2'	2.27	0.59
1:1:2126:A:O2'	1:1:2162:G:N2	2.34	0.59
1:1:2419:U:OP1	34:e:41:LYS:NZ	2.33	0.59
2:2:34:C:H2'	2:2:35:G:H8	1.68	0.59
2:2:160:A:H61	2:2:347:G:N2	1.99	0.59
52:w:10:PHE:N	58:w:101:HOH:O	2.35	0.59
1:1:494:G:N3	22:S:61:ASN:ND2	2.46	0.59
1:1:500:G:N1	1:1:503:A:OP2	2.31	0.59
1:1:781:A:OP1	7:B:217:ARG:NH2	2.34	0.59
1:1:1143:A:N7	58:J:201:HOH:O	2.31	0.59
1:1:2049:G:N2	8:C:161:MET:SD	2.75	0.59
2:2:979:C:O2	48:s:59:ARG:NE	2.36	0.59
34:e:31:HIS:O	34:e:32:ILE:C	2.45	0.59
37:h:10:ILE:HG23	37:h:11:ARG:HG3	1.85	0.59
1:1:807:U:OP2	15:L:41:ARG:NH2	2.35	0.59
2:2:1092:A:OP2	41:l:4:ARG:NH2	2.35	0.59
7:B:124:ILE:HD13	7:B:136:PRO:HD3	1.84	0.59
29:Z:16:ARG:O	29:Z:21:LYS:NZ	2.36	0.59
42:m:9:ASP:OD1	42:m:13:ARG:NH1	2.34	0.59
1:1:2092:U:OP2	12:G:27:ARG:NH1	2.34	0.59
1:1:2682:A:C8	8:C:11:MET:HE3	2.38	0.59
2:2:993:G:O2'	2:2:994:A:N7	2.35	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:5:17:C:H3'	5:5:17(A):U:H2'	1.84	0.59
16:M:66:ARG:NH1	16:M:104:GLU:OE2	2.33	0.59
2:2:619:U:H3	38:i:131:ASN:HB3	1.68	0.59
2:2:1157:A:N7	2:2:1180:A:N6	2.50	0.59
2:2:1451:U:OP2	2:2:1452:C:N4	2.36	0.59
10:E:122:PHE:O	10:E:124:GLY:N	2.36	0.59
30:a:17:SER:OG	47:r:54:ASP:OD1	2.19	0.59
33:d:34:ARG:NE	33:d:42:LEU:O	2.36	0.59
1:1:86:G:HO2'	1:1:104:A:HO2'	1.51	0.59
1:1:605:G:OP1	9:D:99:LYS:NZ	2.36	0.59
1:1:630:G:N2	1:1:633:A:OP2	2.31	0.59
1:1:1571:A:H2'	1:1:1572:A:H8	1.68	0.59
3:3:112:G:N2	18:O:45:SER:O	2.29	0.59
30:a:11:GLU:OE1	30:a:23:LYS:HD2	2.03	0.59
37:h:131:ARG:NH2	37:h:168:TYR:OH	2.34	0.59
1:1:917:A:H5''	1:1:2268:A:H61	1.67	0.59
1:1:2812:G:H2'	1:1:2813:A:H8	1.68	0.59
1:1:2845:U:O3'	19:P:53:ARG:NH1	2.36	0.59
2:2:21:G:H2'	2:2:22:G:C8	2.38	0.59
2:2:269:C:H2'	2:2:270:A:C8	2.38	0.59
2:2:677:U:O2	2:2:777:A:O2'	2.21	0.59
8:C:77:ARG:NH2	8:C:200:ASP:OD1	2.35	0.59
1:1:2193:G:O2'	1:1:2194:U:OP1	2.17	0.58
2:2:1253:G:H2'	2:2:1254:A:H8	1.68	0.58
2:2:1384:C:H2'	2:2:1385:G:H8	1.67	0.58
14:K:71:ARG:NH2	14:K:123:LEU:O	2.36	0.58
1:1:563:A:OP2	21:R:79:ARG:NH1	2.36	0.58
1:1:764:A:H5'	7:B:209:GLY:HA2	1.84	0.58
1:1:2475:C:H42	1:1:2529:G:N2	2.01	0.58
14:K:7:MET:HE2	14:K:7:MET:HA	1.85	0.58
45:p:14:LYS:NZ	45:p:15:GLN:O	2.36	0.58
1:1:832:U:H2'	1:1:833:A:H8	1.67	0.58
1:1:870:U:OP1	16:M:6:ARG:NH1	2.36	0.58
1:1:2081:U:H2'	1:1:2082:A:H8	1.69	0.58
1:1:2194:U:H2'	1:1:2195:U:H6	1.67	0.58
2:2:1148:U:H2'	2:2:1149:C:O4'	2.02	0.58
2:2:1513:A:H2'	2:2:1514:G:H8	1.67	0.58
5:5:20:U:H2'	5:5:21:A:H5'	1.83	0.58
9:D:97:ASN:HB2	9:D:100:MET:HG3	1.86	0.58
1:1:358:U:H2'	1:1:359:G:H8	1.68	0.58
1:1:1007:C:H5''	13:J:37:ARG:NH1	2.18	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1416:G:O2'	1:1:1417:C:O5'	2.21	0.58
1:1:1434:A:H2'	1:1:1435:G:C8	2.38	0.58
43:n:57:MET:HG2	43:n:60:LYS:HD2	1.85	0.58
46:q:46:ASN:ND2	46:q:89:OTD:SB	2.75	0.58
46:q:114:ARG:HB3	46:q:119:VAL:HB	1.84	0.58
53:x:3:ARG:NH1	53:x:8:GLY:O	2.36	0.58
53:x:31:LEU:HB2	53:x:49:ILE:HG22	1.86	0.58
1:1:1433:A:H2'	1:1:1434:A:H8	1.68	0.58
1:1:2139:U:O2	1:1:2152:G:O6	2.20	0.58
43:n:6:TYR:HB2	43:n:21:ILE:HB	1.84	0.58
1:1:99:U:O2	24:U:7:ARG:NH2	2.35	0.58
9:D:189:THR:H	9:D:192:ALA:HB3	1.69	0.58
45:p:119:ASN:ND2	58:p:201:HOH:O	2.35	0.58
1:1:1048:A:H1'	1:1:1112:G:N2	2.18	0.58
1:1:1386:C:H2'	1:1:1387:A:C8	2.39	0.58
1:1:1432:G:H2'	1:1:1433:A:C8	2.39	0.58
1:1:2045:C:H5''	31:b:15:MET:SD	2.44	0.58
2:2:385:C:C4	2:2:386:C:N4	2.72	0.58
5:5:18:G:N1	5:5:57:A:C6	2.70	0.58
13:J:125:TYR:OH	13:J:132:HIS:NE2	2.34	0.58
1:1:926:G:H2'	1:1:927:A:H8	1.68	0.58
1:1:2816:G:N3	1:1:2883:A:O2'	2.33	0.58
2:2:564:C:OP2	46:q:12:ARG:NH1	2.37	0.58
13:J:31:GLU:OE2	13:J:34:ARG:NH1	2.37	0.58
42:m:5:ASP:OD1	42:m:77:ARG:NH1	2.36	0.58
45:p:87:LYS:HB2	45:p:113:VAL:HG13	1.86	0.58
1:1:632:A:N3	1:1:2403:C:O2'	2.35	0.58
1:1:711:G:H1	1:1:720:U:H3	1.50	0.58
2:2:322:C:H2'	2:2:323:U:C6	2.38	0.58
2:2:438:U:H3	2:2:496:A:N6	2.02	0.58
2:2:727:G:N2	2:2:730:G:OP2	2.33	0.58
39:j:78:ASN:OD1	39:j:79:GLY:N	2.36	0.58
40:k:99:ALA:O	40:k:104:LYS:NZ	2.37	0.58
1:1:2475:C:H42	1:1:2529:G:H22	1.52	0.58
1:1:196:A:N6	1:1:831:G:H21	2.01	0.57
1:1:729:G:O2'	1:1:763:G:H4'	2.04	0.57
1:1:1654:A:N1	1:1:2048:G:O2'	2.36	0.57
2:2:619:U:H4'	38:i:128:ARG:HH22	1.69	0.57
3:3:27:C:OP1	18:O:34:HIS:NE2	2.33	0.57
3:3:37:C:O2	18:O:100:HIS:NE2	2.35	0.57
37:h:155:GLY:HA2	37:h:163:ALA:HB1	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
43:n:47:VAL:HA	43:n:50:GLN:OE1	2.04	0.57
1:1:5:A:H2'	1:1:6:A:C8	2.39	0.57
1:1:582:A:H2'	1:1:583:G:H8	1.69	0.57
1:1:1858:A:H61	1:1:1884:G:H1'	1.70	0.57
9:D:6:LYS:HG3	9:D:119:ILE:HG23	1.84	0.57
13:J:96:ARG:HH12	13:J:99:ARG:HD3	1.69	0.57
16:M:42:THR:OG1	16:M:45:GLN:HG3	2.04	0.57
47:r:5:ALA:HB1	47:r:65:VAL:HG21	1.87	0.57
47:r:83:LEU:HD11	53:x:65:GLU:HG3	1.86	0.57
1:1:615:U:H3	9:D:176:ASP:HB3	1.70	0.57
37:h:132:ARG:NH2	58:h:303:HOH:O	2.37	0.57
1:1:863:A:H2'	1:1:864:G:H8	1.69	0.57
1:1:948:C:H2'	1:1:949:G:H8	1.69	0.57
1:1:1532:A:N7	58:1:3347:HOH:O	2.32	0.57
2:2:537:G:H5''	46:q:110:ARG:HH12	1.69	0.57
1:1:324:A:OP2	1:1:1205:A:N6	2.37	0.57
1:1:1024:G:HO2'	1:1:1144:A:HO2'	1.44	0.57
1:1:2229:U:H2'	1:1:2230:G:H8	1.70	0.57
2:2:390:U:H2'	2:2:391:G:C8	2.39	0.57
9:D:158:PHE:HA	9:D:169:VAL:HG21	1.85	0.57
10:E:63:GLN:NE2	10:E:90:THR:O	2.36	0.57
37:h:87:LEU:HA	37:h:90:VAL:HG22	1.86	0.57
45:p:20:VAL:HA	45:p:83:GLU:O	2.05	0.57
45:p:29:ASN:HB2	45:p:57:LYS:HE3	1.87	0.57
1:1:2591:C:H2'	1:1:2592:G:H8	1.69	0.57
1:1:2737:G:H2'	1:1:2738:A:C8	2.40	0.57
2:2:292:G:O2'	2:2:609:A:N6	2.37	0.57
3:3:60:C:H2'	3:3:61:G:H8	1.69	0.57
40:k:1:MET:SD	40:k:1:MET:N	2.74	0.57
48:s:90:ARG:NE	48:s:92:GLU:OE2	2.35	0.57
1:1:30:G:O2'	1:1:1214:A:N3	2.27	0.57
1:1:2039:U:H2'	1:1:2040:G:H8	1.69	0.57
1:1:2123:G:H5'	6:A:174:THR:HA	1.87	0.57
2:2:1384:C:H2'	2:2:1385:G:C8	2.39	0.57
5:5:28:C:O2'	47:r:117:LYS:NZ	2.31	0.57
44:o:26:VAL:HG11	44:o:39:PRO:HD3	1.86	0.57
53:x:52:HIS:CD2	53:x:54:GLY:H	2.22	0.57
1:1:793:A:OP2	1:1:2071:A:O2'	2.23	0.57
2:2:320:A:H2'	2:2:321:A:C8	2.40	0.57
2:2:1145:A:O2'	2:2:1146:A:H8	1.88	0.57
49:t:23:GLY:O	49:t:28:GLN:NE2	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:498:G:H2'	1:1:499:U:O4'	2.05	0.57
1:1:2576:G:O2'	1:1:2579:C:OP2	2.23	0.57
2:2:206:C:N4	2:2:213:G:H1	2.03	0.57
2:2:713:G:H2'	2:2:714:G:C8	2.39	0.57
2:2:754:C:O5'	49:t:72:ARG:NH2	2.38	0.57
15:L:79:LEU:HD11	15:L:112:LEU:HD12	1.86	0.57
46:q:80:ILE:HG23	46:q:104:CYS:HB2	1.87	0.57
48:s:9:ARG:O	48:s:13:ARG:HG2	2.05	0.57
1:1:83:A:N7	1:1:101:A:N6	2.52	0.57
1:1:639:U:H2'	1:1:640:C:C6	2.40	0.57
1:1:1093:G:H21	1:1:1098:A:H62	1.51	0.57
1:1:1263:U:OP1	31:b:13:ARG:NH1	2.35	0.57
1:1:1288:G:OP1	1:1:1289:C:N4	2.35	0.57
1:1:1433:A:H2'	1:1:1434:A:C8	2.40	0.57
1:1:2328:A:H2'	1:1:2329:U:C6	2.39	0.57
2:2:459:A:H2'	2:2:460:A:H8	1.69	0.57
7:B:246:THR:HG23	7:B:248:TRP:H	1.69	0.57
1:1:1039:A:H2	1:1:1116:G:N1	1.99	0.56
1:1:1539:U:H2'	1:1:1540:G:H8	1.70	0.56
2:2:490:C:H2'	2:2:491:G:C8	2.40	0.56
2:2:1187:G:N3	48:s:100:SER:OG	2.32	0.56
7:B:130:LEU:HD13	7:B:134:ASN:HB2	1.86	0.56
10:E:11:GLU:OE1	10:E:14:LYS:NZ	2.33	0.56
18:O:64:TYR:HB3	18:O:67:ASN:HD22	1.70	0.56
42:m:96:MET:HG3	42:m:99:LEU:HB2	1.86	0.56
51:v:14:SER:HA	51:v:55:ILE:HG22	1.87	0.56
1:1:23:G:H2'	1:1:24:G:H8	1.70	0.56
1:1:464:U:O2	33:d:16:HIS:NE2	2.37	0.56
1:1:1364:G:OP1	27:X:3:ARG:NH1	2.38	0.56
1:1:1962:5MC:H4'	1:1:1963:U:OP1	2.06	0.56
1:1:2591:C:H2'	1:1:2592:G:C8	2.40	0.56
2:2:1412:C:H2'	2:2:1413:A:C8	2.40	0.56
5:5:67:G:C5'	58:5:206:HOH:O	2.38	0.56
1:1:371:A:N6	1:1:402:A:OP2	2.37	0.56
1:1:559:G:N2	20:Q:52:GLN:OE1	2.37	0.56
1:1:1202:G:H2'	1:1:1203:U:C6	2.41	0.56
1:1:1528:A:OP2	1:1:1543:G:N2	2.39	0.56
1:1:1666:G:O2'	14:K:6:THR:OG1	2.21	0.56
1:1:2291:U:O2'	1:1:2374:C:O2	2.22	0.56
1:1:2822:G:OP1	8:C:164:GLN:NE2	2.38	0.56
2:2:738:C:OP1	40:k:4:TYR:OH	2.20	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1094:G:N2	58:2:1825:HOH:O	2.36	0.56
2:2:1236:A:H4'	2:2:1304:G:H4'	1.87	0.56
7:B:162:VAL:HG12	7:B:176:LEU:HA	1.87	0.56
9:D:157:LEU:HG	9:D:169:VAL:HG11	1.87	0.56
23:T:38:ALA:O	23:T:81:LYS:NZ	2.31	0.56
32:c:40:ASP:OD1	32:c:49:TYR:OH	2.23	0.56
34:e:31:HIS:CG	34:e:32:ILE:H	2.23	0.56
1:1:160:A:N3	1:1:2208:C:O2'	2.35	0.56
2:2:970:C:N4	43:n:130:ARG:OXT	2.38	0.56
5:5:8:U:O2'	5:5:21:A:N1	2.34	0.56
8:C:25:THR:HG21	8:C:193:VAL:HG22	1.88	0.56
9:D:21:ARG:HE	9:D:106:LYS:HB2	1.70	0.56
12:G:51:ARG:NH2	12:G:55:GLU:OE2	2.39	0.56
22:S:95:ARG:NH2	58:S:201:HOH:O	2.37	0.56
26:W:41:ARG:O	26:W:57:HIS:ND1	2.36	0.56
39:j:115:LEU:HD13	39:j:123:VAL:HG11	1.87	0.56
46:q:80:ILE:HD12	46:q:104:CYS:HB2	1.86	0.56
1:1:1202:G:OP2	1:1:1204:A:O2'	2.23	0.56
1:1:1495:A:N3	1:1:1578:U:O2'	2.36	0.56
1:1:1954:G:O2'	1:1:1956:U:O4	2.21	0.56
2:2:673:A:H4'	40:k:86:ARG:NH1	2.21	0.56
16:M:56:ALA:HB2	16:M:119:LEU:HD12	1.87	0.56
46:q:50:ARG:NE	46:q:89:0TD:OD1	2.35	0.56
51:v:59:VAL:HG12	51:v:78:VAL:HG12	1.86	0.56
1:1:659:G:N2	9:D:30:GLN:OE1	2.39	0.56
1:1:2680:U:O2'	8:C:11:MET:HE1	2.05	0.56
5:5:2:G:H4'	5:5:3:G:OP1	2.05	0.56
5:5:59:A:O2'	5:5:60:U:OP1	2.23	0.56
38:i:11:LEU:HD13	38:i:63:ARG:HG2	1.86	0.56
44:o:80:THR:HG1	44:o:83:THR:HG1	1.52	0.56
45:p:54:GLY:H	45:p:57:LYS:HD3	1.71	0.56
1:1:370:G:O2'	1:1:424:G:OP1	2.23	0.56
1:1:1469:A:H2'	1:1:1470:A:H8	1.70	0.56
1:1:2037:A:H2'	1:1:2038:G:C8	2.40	0.56
1:1:2127:G:H21	1:1:2173:A:H1'	1.70	0.56
2:2:1342:C:H2'	2:2:1343:G:H8	1.71	0.56
5:5:18:G:C6	5:5:57:A:N6	2.74	0.56
1:1:1681:G:H21	1:1:1762:A:H3'	1.69	0.56
1:1:2311:A:N6	58:1:3385:HOH:O	2.39	0.56
1:1:2349:G:OP1	34:e:45:ARG:NH2	2.39	0.56
10:E:32:GLU:OE2	10:E:159:THR:OG1	2.18	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
22:S:6:LYS:HG2	22:S:104:THR:HG23	1.87	0.56
45:p:64:GLN:HB2	45:p:99:ALA:HB2	1.86	0.56
1:1:552:U:H2'	1:1:553:G:H8	1.71	0.56
1:1:1131:G:HO2'	1:1:2025:C:HO2'	1.43	0.56
1:1:2037:A:H2'	1:1:2038:G:H8	1.71	0.56
37:h:129:MET:HB2	37:h:132:ARG:HD2	1.87	0.56
1:1:2039:U:H2'	1:1:2040:G:C8	2.41	0.56
2:2:910:C:OP2	46:q:18:LYS:NZ	2.31	0.55
19:P:29:LYS:HB3	19:P:40:LEU:HD12	1.87	0.55
37:h:123:GLN:OE1	37:h:126:ARG:NH1	2.39	0.55
1:1:742:A:H2'	1:1:743:A:H8	1.71	0.55
1:1:887:A:OP1	47:r:92:ARG:NH2	2.38	0.55
1:1:2285:C:OP2	32:c:6:ARG:NE	2.27	0.55
2:2:1375:A:H5''	41:l:25:LYS:HD2	1.87	0.55
10:E:111:ILE:HB	10:E:114:PHE:HB2	1.88	0.55
44:o:11:LYS:HG3	44:o:97:ASP:HB3	1.88	0.55
1:1:782:A:N7	7:B:220:VAL:HG21	2.22	0.55
2:2:1041:G:H2'	2:2:1042:A:C8	2.42	0.55
2:2:1250:A:N3	2:2:1370:G:O2'	2.36	0.55
1:1:358:U:H2'	1:1:359:G:C8	2.41	0.55
1:1:851:C:H2'	1:1:852:U:C6	2.41	0.55
3:3:114:C:H2'	3:3:115:A:H8	1.72	0.55
5:5:4:C:O2'	5:5:5:A:OP2	2.24	0.55
13:J:17:VAL:HG13	13:J:137:PRO:HB2	1.88	0.55
15:L:75:ALA:HB2	15:L:105:ILE:HD12	1.88	0.55
1:1:446:G:H5''	20:Q:5:LYS:HE3	1.88	0.55
1:1:629:G:H1'	1:1:639:U:H1'	1.87	0.55
2:2:17:U:H2'	2:2:18:C:C6	2.42	0.55
2:2:660:C:N3	2:2:746:A:N6	2.54	0.55
2:2:1145:A:H2	2:2:1146:A:H62	1.53	0.55
7:B:72:ASP:OD2	7:B:189:ARG:NH2	2.30	0.55
1:1:2286:G:OP2	32:c:6:ARG:NH2	2.39	0.55
2:2:1218:C:H2'	2:2:1219:A:C8	2.42	0.55
22:S:19:LEU:HB3	31:b:22:LEU:HD13	1.89	0.55
41:l:79:ARG:NH1	41:l:81:GLY:O	2.40	0.55
42:m:52:GLU:N	42:m:52:GLU:OE2	2.40	0.55
50:u:21:VAL:HG21	50:u:60:TRP:CD1	2.41	0.55
1:1:1798:U:OP2	7:B:271:ARG:NH1	2.31	0.55
36:g:173:ILE:HG22	36:g:183:VAL:HG11	1.89	0.55
53:x:39:THR:HG22	53:x:70:LYS:HG2	1.89	0.55
1:1:112:U:H5'	28:Y:58:ASN:ND2	2.22	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:307:G:N1	1:1:310:A:OP2	2.26	0.55
1:1:668:A:H2'	1:1:670:A:H62	1.72	0.55
1:1:721:A:H2'	1:1:722:A:H8	1.72	0.55
1:1:843:G:H2'	1:1:844:A:C8	2.42	0.55
1:1:992:C:OP1	20:Q:47:TYR:OH	2.25	0.55
1:1:1447:C:H2'	1:1:1448:G:C8	2.41	0.55
7:B:67:PHE:HB3	7:B:152:GLY:H	1.71	0.55
10:E:16:LEU:HD23	10:E:29:PRO:HD2	1.89	0.55
39:j:13:GLU:HG2	39:j:39:VAL:HG12	1.89	0.55
45:p:81:ASN:OD1	45:p:106:ARG:NE	2.39	0.55
1:1:372:G:H5''	27:X:61:LYS:HD2	1.89	0.55
1:1:2036:C:H2'	1:1:2037:A:H8	1.71	0.55
1:1:2446:G:N2	1:1:2449:U:O2	2.38	0.55
2:2:459:A:H2'	2:2:460:A:C8	2.42	0.55
2:2:460:A:H2'	2:2:461:A:C8	2.42	0.55
2:2:923:A:O2'	2:2:1399:C:OP2	2.21	0.55
5:5:1:C:O2	5:5:72:G:N1	2.39	0.55
48:s:10:GLU:HG3	48:s:63:ARG:HD2	1.89	0.55
1:1:1065:U:O2'	1:1:1066:U:O5'	2.25	0.55
1:1:2127:G:HO2'	1:1:2128:G:H8	1.54	0.55
1:1:2255:G:O2'	5:5:3:G:OP1	2.25	0.55
2:2:21:G:H2'	2:2:22:G:H8	1.72	0.55
2:2:143:A:H2	2:2:220:G:H1	1.55	0.55
2:2:739:C:O2'	49:t:42:HIS:ND1	2.37	0.55
11:F:96:ALA:HB3	11:F:131:ILE:HD11	1.89	0.55
18:O:61:GLN:OE1	18:O:61:GLN:N	2.40	0.55
35:f:25:VAL:HG12	35:f:35:GLN:HB2	1.89	0.55
41:l:75:VAL:HG11	41:l:148:ASN:HD21	1.72	0.55
2:2:398:U:H2'	2:2:399:G:H8	1.71	0.54
5:5:62:C:H2'	5:5:63:U:C6	2.42	0.54
13:J:32:LEU:HD22	13:J:54:ILE:HG21	1.90	0.54
16:M:53:MET:HE3	16:M:117:PHE:HE1	1.71	0.54
43:n:34:SER:HB3	43:n:37:GLN:OE1	2.06	0.54
51:v:46:VAL:HG21	51:v:61:ILE:HG21	1.89	0.54
1:1:55:G:H2'	1:1:56:A:H8	1.71	0.54
2:2:356:A:N3	2:2:368:U:O2'	2.32	0.54
2:2:859:G:N2	58:2:1835:HOH:O	2.39	0.54
2:2:1513:A:H2'	2:2:1514:G:C8	2.42	0.54
44:o:52:LEU:HD21	44:o:62:ARG:HH21	1.72	0.54
1:1:1752:C:H2'	1:1:1753:G:C8	2.43	0.54
1:1:2562:U:H4'	14:K:25:LEU:HD22	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:514:C:H2'	2:2:515:G:C8	2.42	0.54
2:2:1439:G:OP2	54:y:33:LYS:NZ	2.35	0.54
36:g:218:ALA:O	36:g:222:ARG:HG2	2.08	0.54
1:1:99:U:H5''	1:1:100:U:H5'	1.89	0.54
1:1:574:A:N6	1:1:2034:U:OP1	2.41	0.54
2:2:337:G:H2'	2:2:338:A:C8	2.41	0.54
3:3:51:G:H2'	3:3:52:A:C8	2.42	0.54
18:O:60:GLU:HG2	18:O:61:GLN:OE1	2.08	0.54
24:U:25:VAL:HA	24:U:36:VAL:HA	1.88	0.54
24:U:40:ASN:ND2	24:U:65:ILE:HB	2.21	0.54
28:Y:14:LEU:HB3	28:Y:57:LEU:HD21	1.90	0.54
1:1:826:U:O2	1:1:831:G:O6	2.25	0.54
1:1:2241:A:H2'	1:1:2242:G:C8	2.42	0.54
13:J:37:ARG:HA	13:J:118:MET:CE	2.37	0.54
21:R:25:LEU:HG	21:R:94:THR:HG21	1.90	0.54
43:n:10:GLY:HA3	43:n:82:GLY:N	2.23	0.54
1:1:946:C:H2'	1:1:947:A:H8	1.72	0.54
2:2:842:U:H4'	2:2:846:G:C6	2.42	0.54
36:g:102:THR:HA	36:g:179:LEU:HD11	1.90	0.54
41:l:35:LYS:HB3	41:l:38:THR:HG22	1.90	0.54
1:1:258:G:H2'	1:1:259:G:C8	2.43	0.54
1:1:629:G:N3	1:1:639:U:O2'	2.40	0.54
1:1:2096:C:H2'	1:1:2097:A:C8	2.42	0.54
1:1:2140:G:O6	1:1:2151:U:O4	2.26	0.54
2:2:1071:C:H2'	2:2:1072:G:H8	1.72	0.54
41:l:71:PRO:HG3	41:l:99:LEU:HD11	1.90	0.54
1:1:2123:G:N2	6:A:215:SER:OG	2.41	0.54
1:1:2162:G:O2'	1:1:2163:A:N7	2.39	0.54
1:1:2743:U:HO2'	11:F:153:ARG:HH22	1.55	0.54
2:2:1151:A:HO2'	2:2:1152:A:H8	1.55	0.54
2:2:1171:A:H2'	2:2:1172:C:H6	1.73	0.54
5:5:53:G:H2'	5:5:54:U:C5	2.42	0.54
7:B:78:VAL:HG21	7:B:110:LEU:HD11	1.88	0.54
12:G:86:ASP:OD2	40:k:24:ARG:NH1	2.41	0.54
25:V:72:VAL:HG11	25:V:91:PHE:HB3	1.90	0.54
1:1:285:G:O6	1:1:355:U:O2	2.25	0.54
1:1:1063:G:N2	58:1:3369:HOH:O	2.36	0.54
1:1:1141:U:OP1	13:J:27:ARG:NH2	2.40	0.54
1:1:1224:U:OP2	21:R:68:ARG:NH2	2.41	0.54
2:2:895:G:H2'	2:2:896:C:C6	2.43	0.54
7:B:108:LYS:HA	7:B:196:GLY:HA2	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:R:5:PHE:N	58:R:202:HOH:O	2.41	0.54
44:o:10:LEU:HB3	44:o:18:ILE:HD11	1.90	0.54
51:v:17:MET:HE2	51:v:20:SER:HB3	1.89	0.54
53:x:40:ILE:HG12	53:x:71:LEU:HD23	1.90	0.54
1:1:1085:A:N7	1:1:1086:A:N6	2.56	0.54
1:1:2898:U:O3'	13:J:136:GLN:NE2	2.41	0.54
2:2:8:A:N6	38:i:202:GLU:O	2.40	0.54
2:2:1074:G:OP1	39:j:69:ARG:NH2	2.40	0.54
2:2:1209:C:O2'	2:2:1214:C:N4	2.41	0.54
5:5:55:U:O2'	5:5:56:C:H3'	2.08	0.54
8:C:136:ASN:ND2	8:C:139:SER:O	2.41	0.54
9:D:102:ARG:O	9:D:106:LYS:HG2	2.08	0.54
9:D:117:ARG:NH1	9:D:184:ASP:O	2.41	0.54
9:D:146:VAL:H	9:D:167:VAL:HG12	1.72	0.54
12:G:14:SER:N	12:G:17:ASP:OD2	2.41	0.54
13:J:45:THR:HB	13:J:48:VAL:HB	1.89	0.54
21:R:1:MET:HA	21:R:42:ALA:O	2.08	0.54
38:i:13:ARG:HG2	38:i:34:ILE:HA	1.88	0.54
1:1:408:G:H2'	1:1:409:G:H8	1.73	0.53
1:1:565:C:P	21:R:80:ARG:H	2.30	0.53
1:1:797:G:OP1	9:D:55:SER:OG	2.22	0.53
1:1:947:A:H2'	1:1:948:C:C6	2.44	0.53
1:1:1278:C:O2'	17:N:27:SER:OG	2.24	0.53
1:1:1421:G:H2'	1:1:1422:G:H8	1.73	0.53
1:1:2095:A:H5'	12:G:11:ASN:HD22	1.72	0.53
2:2:521:G:O2'	2:2:536:C:O2'	2.25	0.53
2:2:662:U:H2'	2:2:663:A:C8	2.43	0.53
14:K:17:ARG:NH1	58:K:201:HOH:O	2.40	0.53
1:1:863:A:H2'	1:1:864:G:C8	2.42	0.53
1:1:2074:U:H2'	1:1:2075:U:C6	2.43	0.53
1:1:2292:U:H2'	1:1:2293:G:H8	1.74	0.53
2:2:81:A:N6	2:2:88:U:O4	2.41	0.53
2:2:501:C:H2'	2:2:502:A:H8	1.74	0.53
2:2:1515:G:H2'	2:2:1516:2MG:C8	2.43	0.53
12:G:9:VAL:HG11	12:G:12:LEU:HB3	1.90	0.53
24:U:86:ARG:NH2	24:U:88:GLU:OE2	2.36	0.53
37:h:19:ASN:HB3	37:h:40:ARG:HH22	1.73	0.53
44:o:50:THR:HB	44:o:62:ARG:HD3	1.90	0.53
44:o:78:GLU:OE1	44:o:78:GLU:N	2.41	0.53
1:1:145:C:H2'	1:1:146:A:H8	1.73	0.53
1:1:136:G:O6	1:1:144:A:N6	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:414:C:H2'	1:1:415:A:C8	2.43	0.53
1:1:451:U:H4'	9:D:47:LYS:HE3	1.90	0.53
1:1:1197:G:H22	1:1:1249:U:H1'	1.73	0.53
1:1:1576:U:H2'	1:1:1577:C:C6	2.43	0.53
1:1:2487:G:H2'	1:1:2488:G:H8	1.73	0.53
1:1:2626:C:H2'	1:1:2627:G:H8	1.74	0.53
2:2:1342:C:H2'	2:2:1343:G:C8	2.44	0.53
1:1:741:U:H2'	1:1:742:A:C8	2.44	0.53
1:1:1710:G:H2'	1:1:1711:A:C8	2.44	0.53
3:3:83:G:O6	3:3:94:A:N6	2.42	0.53
11:F:23:VAL:HA	11:F:36:THR:HA	1.89	0.53
15:L:28:GLY:HA3	21:R:82:HIS:NE2	2.24	0.53
26:W:47:ALA:HB1	26:W:51:VAL:HG13	1.91	0.53
42:m:75:ILE:CD1	42:m:129:VAL:HG22	2.38	0.53
1:1:858:G:H3'	1:1:859:G:C8	2.44	0.53
1:1:2102:G:H1	1:1:2187:U:H3	1.51	0.53
2:2:1176:A:H2'	2:2:1177:G:H8	1.74	0.53
2:2:1287:A:H2'	2:2:1288:A:C8	2.44	0.53
5:5:53:G:H2'	5:5:54:U:H5	1.74	0.53
14:K:121:GLU:OE1	19:P:65:SER:OG	2.21	0.53
22:S:18:ARG:HG3	22:S:76:VAL:HB	1.91	0.53
37:h:135:LYS:NZ	37:h:139:GLN:HE22	2.07	0.53
1:1:230:G:H2'	1:1:231:A:H8	1.74	0.53
1:1:582:A:H2'	1:1:583:G:C8	2.43	0.53
1:1:1995:U:O2	14:K:3:GLN:NE2	2.37	0.53
1:1:2636:C:O2'	8:C:45:TYR:OH	2.27	0.53
2:2:977:A:OP1	48:s:61:ARG:NH1	2.42	0.53
2:2:1041:G:H2'	2:2:1042:A:H8	1.73	0.53
37:h:135:LYS:NZ	58:h:301:HOH:O	2.24	0.53
1:1:627:A:H5''	15:L:78:ARG:HH21	1.74	0.53
1:1:1746:A:H2'	1:1:1747:U:C6	2.44	0.53
1:1:2113:U:N3	1:1:2114:A:N7	2.56	0.53
2:2:113:G:H2'	2:2:114:U:C6	2.44	0.53
2:2:674:G:H2'	2:2:675:A:C8	2.42	0.53
2:2:1179:A:H2'	2:2:1180:A:C8	2.44	0.53
2:2:1253:G:H2'	2:2:1254:A:C8	2.43	0.53
2:2:1314:C:H2'	2:2:1315:U:H6	1.73	0.53
5:5:62:C:H2'	5:5:63:U:H6	1.74	0.53
24:U:34:VAL:HG13	24:U:67:VAL:HG22	1.91	0.53
43:n:15:SER:OG	43:n:69:GLY:O	2.24	0.53
1:1:1962:5MC:O2'	1:1:1963:U:O5'	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2113:U:O4	1:1:2114:A:N6	2.41	0.53
2:2:1320:C:H1'	53:x:73:GLU:HG2	1.91	0.53
18:O:33:ARG:O	18:O:65:THR:OG1	2.21	0.53
26:W:75:LYS:HE2	26:W:77:ARG:HH22	1.74	0.53
38:i:85:ASN:HB3	38:i:88:GLU:HB2	1.91	0.53
1:1:1548:A:H2'	1:1:1549:A:C8	2.43	0.53
1:1:2261:C:OP1	26:W:19:LYS:NZ	2.35	0.53
1:1:2286:G:H4'	1:1:2287:A:O5'	2.08	0.53
2:2:390:U:H2'	2:2:391:G:H8	1.74	0.53
2:2:1029:U:H2'	2:2:1031:C:H1'	1.91	0.53
2:2:1321:U:H3'	2:2:1322:C:H2'	1.89	0.53
2:2:1518:MA6:O5'	2:2:1518:MA6:H8	2.07	0.53
39:j:148:ASN:ND2	42:m:73:GLU:OE1	2.37	0.53
41:l:97:ASN:O	41:l:101:MET:HE2	2.09	0.53
1:1:135:U:H2'	1:1:136:G:C8	2.44	0.52
1:1:2357:G:N2	1:1:2360:G:OP2	2.33	0.52
1:1:2547:A:H2'	1:1:2548:U:C6	2.43	0.52
2:2:821:G:H2'	2:2:822:U:C6	2.43	0.52
13:J:56:VAL:HB	13:J:124:VAL:HG23	1.90	0.52
44:o:77:VAL:HG23	44:o:78:GLU:OE1	2.10	0.52
49:t:80:GLN:HE22	49:t:84:ARG:HE	1.57	0.52
1:1:483:A:N6	1:1:496:G:H22	2.06	0.52
1:1:545:U:HO2'	1:1:548:G:H1	1.57	0.52
1:1:946:C:H2'	1:1:947:A:C8	2.44	0.52
1:1:1000:A:H2'	1:1:1001:A:C8	2.43	0.52
1:1:1278:C:H2'	1:1:1279:G:H8	1.74	0.52
1:1:1424:G:H2'	1:1:1425:G:C8	2.44	0.52
1:1:1443:U:H2'	1:1:1444:G:C8	2.44	0.52
1:1:2698:U:H2'	1:1:2699:C:C6	2.45	0.52
2:2:1009:U:H2'	2:2:1020:G:H22	1.75	0.52
25:V:6:ALA:HB1	25:V:40:ILE:HB	1.91	0.52
47:r:9:ILE:HD11	47:r:22:ILE:HD11	1.92	0.52
1:1:48:G:N2	1:1:177:G:OP2	2.42	0.52
1:1:151:C:H2'	1:1:152:A:H8	1.74	0.52
1:1:1152:C:H2'	1:1:1153:C:H6	1.74	0.52
2:2:790:A:OP1	5:5:38:U:O2'	2.16	0.52
2:2:1130:A:H62	2:2:1144:G:H21	1.55	0.52
3:3:54:G:H2'	3:3:55:U:C6	2.44	0.52
20:Q:58:ARG:O	20:Q:62:ILE:HG12	2.09	0.52
43:n:28:ILE:HB	43:n:35:LEU:HD22	1.91	0.52
1:1:308:G:H1'	1:1:501:A:OP1	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:550:C:N4	1:1:551:G:O6	2.43	0.52
1:1:1068:G:N2	1:1:1095:A:O3'	2.43	0.52
1:1:1306:C:H2'	1:1:1307:A:H8	1.73	0.52
1:1:2047:C:H2'	1:1:2048:G:H8	1.74	0.52
2:2:385:C:N4	2:2:386:C:H41	2.07	0.52
12:G:30:LEU:HB3	12:G:36:ALA:HB3	1.91	0.52
29:Z:16:ARG:HG3	29:Z:54:MET:HE1	1.91	0.52
43:n:19:VAL:HG22	43:n:65:ILE:HG23	1.89	0.52
1:1:408:G:H2'	1:1:409:G:C8	2.45	0.52
1:1:523:C:H2'	1:1:524:G:C8	2.45	0.52
1:1:727:A:OP2	1:1:1431:A:O2'	2.26	0.52
1:1:1702:G:N2	2:2:1428:A:O2'	2.42	0.52
2:2:21:G:H1'	2:2:915:A:H61	1.74	0.52
2:2:545:C:H5'	38:i:69:GLU:HB2	1.91	0.52
2:2:773:G:O6	2:2:807:A:N6	2.43	0.52
8:C:29:VAL:HG21	8:C:187:LEU:HD12	1.92	0.52
31:b:29:SER:HB3	31:b:40:ARG:HD3	1.91	0.52
45:p:34:ILE:HG13	45:p:74:VAL:HG11	1.90	0.52
1:1:228:C:N4	1:1:2407:A:N3	2.57	0.52
2:2:41:G:H2'	2:2:42:G:C8	2.43	0.52
5:5:10:G:C2	5:5:26:A:H1'	2.45	0.52
10:E:73:SER:HB2	10:E:81:GLN:H	1.74	0.52
40:k:47:LEU:HD23	40:k:51:ILE:HD13	1.92	0.52
51:v:80:GLU:OE2	51:v:80:GLU:N	2.42	0.52
54:y:5:LYS:O	54:y:9:LYS:HG2	2.09	0.52
1:1:878:A:N6	58:1:3403:HOH:O	2.43	0.52
1:1:1264:A:OP1	31:b:16:ARG:NH2	2.28	0.52
1:1:1278:C:H2'	1:1:1279:G:C8	2.44	0.52
1:1:2639:A:O3'	13:J:96:ARG:NH2	2.43	0.52
1:1:2720:U:C2	1:1:2721:A:C8	2.98	0.52
2:2:895:G:H2'	2:2:896:C:H6	1.74	0.52
2:2:932:C:H5''	41:l:4:ARG:HD3	1.91	0.52
2:2:1330:U:H4'	47:r:23:TYR:CZ	2.44	0.52
11:F:130:GLU:OE2	58:F:201:HOH:O	2.19	0.52
15:L:85:VAL:HG21	15:L:90:VAL:HG12	1.91	0.52
22:S:51:LEU:O	22:S:55:ILE:HG12	2.10	0.52
23:T:69:ARG:HG2	23:T:74:ILE:HD12	1.91	0.52
1:1:1869:G:N2	1:1:1871:A:O2'	2.43	0.52
1:1:1924:C:H2'	1:1:1925:C:C6	2.45	0.52
1:1:2571:U:O2'	8:C:151:THR:O	2.27	0.52
1:1:2642:G:H2'	1:1:2643:G:H8	1.75	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:229:U:H5''	50:u:33:ILE:HD13	1.92	0.52
2:2:876:C:H1'	42:m:12:THR:HG21	1.92	0.52
10:E:140:GLU:OE1	30:a:26:SER:OG	2.26	0.52
38:i:15:GLU:OE2	38:i:56:ARG:NH2	2.35	0.52
38:i:159:LEU:HD13	38:i:175:ALA:HB1	1.91	0.52
1:1:675:A:N3	1:1:2443:C:O2'	2.40	0.52
1:1:995:C:O2	13:J:3:THR:OG1	2.22	0.52
1:1:2291:U:H2'	1:1:2292:U:C6	2.45	0.52
2:2:160:A:H61	2:2:347:G:H21	1.56	0.52
2:2:363:A:H5'	46:q:81:LEU:HD11	1.92	0.52
3:3:93:C:OP2	25:V:18:ARG:NH1	2.41	0.52
5:5:23:C:H2'	5:5:24:G:H8	1.75	0.52
23:T:47:VAL:HG23	23:T:51:PHE:HD2	1.75	0.52
41:l:26:PHE:HD1	41:l:101:MET:HB3	1.73	0.52
1:1:523:C:H2'	1:1:524:G:H8	1.75	0.52
1:1:1044:C:O2'	1:1:1111:A:N1	2.42	0.52
1:1:2046:G:H5'	31:b:16:ARG:HG3	1.90	0.52
1:1:2074:U:H2'	1:1:2075:U:H6	1.75	0.52
2:2:736:C:H2'	2:2:737:C:H6	1.73	0.52
2:2:1083:U:O2'	2:2:1102:A:OP2	2.27	0.52
2:2:1486:G:H2'	2:2:1487:G:O4'	2.10	0.52
17:N:29:VAL:HG21	17:N:75:ILE:HG23	1.92	0.52
39:j:61:GLN:O	39:j:65:GLU:HG2	2.10	0.52
1:1:1:G:H2'	1:1:2:G:H8	1.75	0.51
1:1:191:A:H2'	1:1:192:C:H6	1.75	0.51
1:1:796:C:H2'	1:1:797:G:C8	2.45	0.51
1:1:1387:A:H2'	1:1:1388:G:H8	1.74	0.51
1:1:1713:A:N6	1:1:1746:A:N1	2.58	0.51
2:2:126:G:OP1	2:2:605:U:O2'	2.24	0.51
38:i:101:VAL:HG21	38:i:137:VAL:HG11	1.91	0.51
41:l:57:SER:HB3	41:l:60:GLU:HG2	1.92	0.51
1:1:468:G:H5''	9:D:55:SER:HB2	1.93	0.51
1:1:641:U:O4	1:1:647:G:O6	2.27	0.51
1:1:713:G:OP2	49:t:89:ARG:NH2	2.42	0.51
1:1:2013:A:N6	1:1:2014:A:N1	2.57	0.51
1:1:2328:A:H2'	1:1:2329:U:H6	1.76	0.51
1:1:2625:G:OP2	58:1:3303:HOH:O	2.19	0.51
2:2:363:A:OP1	46:q:31:ARG:N	2.30	0.51
2:2:1012:A:N6	2:2:1018:G:O6	2.43	0.51
2:2:1151:A:O2'	2:2:1152:A:H8	1.92	0.51
7:B:155:ALA:HB2	7:B:162:VAL:HG13	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:F:104:ASN:ND2	11:F:114:ASP:OD1	2.42	0.51
39:j:16:ILE:HG21	39:j:110:ALA:HB2	1.92	0.51
1:1:30:G:H2'	1:1:31:C:H6	1.74	0.51
1:1:261:G:H2'	1:1:262:A:H8	1.76	0.51
1:1:1478:G:H1	1:1:1513:U:H3	1.59	0.51
1:1:2055:C:H5'	1:1:2056:G:H5''	1.91	0.51
2:2:811:C:O2'	2:2:901:A:N1	2.43	0.51
10:E:8:TYR:HB2	10:E:173:PHE:HZ	1.75	0.51
37:h:53:SER:OG	37:h:112:ASP:OD2	2.17	0.51
38:i:15:GLU:OE2	38:i:63:ARG:NH1	2.44	0.51
39:j:62:LYS:O	39:j:66:LYS:HG2	2.09	0.51
1:1:395:U:O2'	1:1:396:G:N7	2.29	0.51
1:1:2834:G:H2'	1:1:2879:A:H61	1.75	0.51
2:2:269:C:H2'	2:2:270:A:H8	1.74	0.51
47:r:64:VAL:HG13	47:r:68:ASP:HB2	1.92	0.51
1:1:1494:A:H2'	1:1:1495:A:C8	2.46	0.51
1:1:1738:G:HO2'	1:1:1739:A:H8	1.58	0.51
1:1:2743:U:O2'	11:F:153:ARG:NH2	2.31	0.51
2:2:22:G:H2'	2:2:23:C:H6	1.76	0.51
2:2:1317:C:H3'	2:2:1318:A:C8	2.45	0.51
7:B:246:THR:HG22	7:B:250:VAL:H	1.75	0.51
17:N:24:MET:HE2	17:N:44:LEU:HD22	1.93	0.51
20:Q:51:ARG:O	20:Q:55:ARG:HG3	2.11	0.51
36:g:167:ASP:HB3	36:g:191:SER:HA	1.93	0.51
43:n:113:ARG:HE	48:s:101:TRP:CD1	2.29	0.51
1:1:226:A:H1'	1:1:230:G:N2	2.25	0.51
2:2:255:G:H4'	51:v:19:LYS:HD3	1.92	0.51
2:2:1350:A:H2'	2:2:1351:U:O4'	2.10	0.51
12:G:26:ALA:HA	12:G:30:LEU:HD12	1.92	0.51
16:M:40:ARG:HB2	16:M:93:VAL:HG21	1.91	0.51
36:g:6:MET:HE1	36:g:47:VAL:HG21	1.93	0.51
40:k:10:VAL:HB	40:k:58:HIS:HB3	1.92	0.51
42:m:26:THR:HG23	42:m:58:GLU:OE2	2.10	0.51
1:1:2013:A:H2	22:S:88:ARG:HH22	1.57	0.51
1:1:2170:A:H1'	1:1:2171:A:O4'	2.11	0.51
1:1:2692:G:H1'	1:1:2847:U:H1'	1.93	0.51
2:2:514:C:H2'	2:2:515:G:H8	1.76	0.51
2:2:904:U:H2'	2:2:905:U:H6	1.75	0.51
2:2:1130:A:H62	2:2:1144:G:N2	2.08	0.51
5:5:6:C:H2'	5:5:7:G:C8	2.46	0.51
15:L:57:LEU:HD22	34:e:54:ASP:HB3	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:746:PSU:O2'	1:1:2611:C:O2'	2.13	0.51
2:2:384:G:H2'	2:2:385:C:C6	2.46	0.51
2:2:471:U:H2'	2:2:472:U:C6	2.46	0.51
2:2:883:C:H2'	2:2:884:U:C6	2.45	0.51
3:3:16:G:N2	3:3:69:G:H1'	2.26	0.51
3:3:104:A:N7	3:3:105:G:H1'	2.25	0.51
36:g:133:GLU:HA	36:g:136:MET:HG3	1.93	0.51
38:i:105:MET:HG3	38:i:173:VAL:HG22	1.91	0.51
48:s:88:ALA:HB2	48:s:96:LEU:HD23	1.92	0.51
1:1:288:U:H2'	1:1:289:G:C8	2.45	0.51
1:1:601:C:O2'	9:D:99:LYS:NZ	2.42	0.51
1:1:1153:C:OP1	20:Q:92:ARG:NH2	2.43	0.51
1:1:2899:A:H2'	1:1:2900:A:C8	2.46	0.51
2:2:275:G:H5'	51:v:16:LYS:HD2	1.91	0.51
5:5:67:G:H2'	5:5:68:U:C6	2.46	0.51
9:D:146:VAL:HA	9:D:185:LYS:O	2.10	0.51
52:w:70:TYR:HB2	52:w:74:HIS:NE2	2.26	0.51
1:1:608:A:H2'	1:1:609:A:H8	1.75	0.51
32:c:11:LEU:HD21	32:c:34:LEU:HD23	1.93	0.51
39:j:89:HIS:NE2	39:j:138:ARG:HD2	2.25	0.51
40:k:49:TYR:HB3	52:w:74:HIS:CE1	2.46	0.51
48:s:49:GLN:OE1	53:x:13:LEU:N	2.44	0.51
1:1:30:G:H2'	1:1:31:C:C6	2.46	0.50
1:1:191:A:H2'	1:1:192:C:C6	2.46	0.50
1:1:591:U:O4	1:1:592:A:N6	2.43	0.50
1:1:843:G:H2'	1:1:844:A:H8	1.74	0.50
1:1:2119:A:N6	1:1:2167:U:O2'	2.44	0.50
2:2:599:C:H2'	2:2:600:A:H8	1.76	0.50
2:2:613:C:H2'	2:2:614:C:C6	2.46	0.50
2:2:1162:C:H2'	2:2:1163:A:C8	2.46	0.50
2:2:1532:U:O4	2:2:1533:C:N4	2.44	0.50
6:A:193:LEU:O	6:A:197:LYS:HG3	2.11	0.50
40:k:49:TYR:OH	40:k:86:ARG:NH2	2.44	0.50
1:1:542:C:N4	1:1:543:G:O6	2.45	0.50
1:1:820:A:C2	1:1:943:A:H4'	2.46	0.50
1:1:851:C:H2'	1:1:852:U:H6	1.76	0.50
1:1:1124:G:O2'	35:f:37:GLN:O	2.28	0.50
1:1:2140:G:N2	1:1:2151:U:O2	2.41	0.50
1:1:2758:A:O2'	11:F:38:ASN:OD1	2.29	0.50
2:2:407:U:H2'	2:2:408:A:C8	2.46	0.50
2:2:501:C:H2'	2:2:502:A:C8	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:E:38:MET:HE2	10:E:38:MET:HA	1.93	0.50
34:e:32:ILE:O	34:e:36:LYS:NZ	2.43	0.50
46:q:39:THR:HG22	46:q:49:LEU:HD22	1.93	0.50
1:1:571:U:OP1	21:R:80:ARG:NH2	2.36	0.50
1:1:744:U:H2'	1:1:745:1MG:O4'	2.11	0.50
1:1:2595:G:O2'	1:1:2597:G:O6	2.28	0.50
2:2:912:C:H2'	2:2:913:A:C8	2.46	0.50
2:2:1439:G:OP1	54:y:33:LYS:HD3	2.11	0.50
25:V:1:MET:HE1	25:V:59:GLU:HB3	1.92	0.50
38:i:95:GLU:HA	38:i:100:ASN:ND2	2.26	0.50
38:i:118:VAL:HG22	38:i:123:ILE:HG13	1.94	0.50
42:m:113:ASP:OD1	42:m:114:ARG:N	2.44	0.50
1:1:673:C:H5'	9:D:76:PRO:HD2	1.93	0.50
1:1:767:U:H2'	1:1:768:G:H8	1.77	0.50
1:1:2521:C:C2	1:1:2545:G:N2	2.79	0.50
1:1:2863:C:H2'	1:1:2864:G:C8	2.47	0.50
3:3:39:A:H2'	3:3:40:U:C6	2.47	0.50
12:G:95:GLY:H	12:G:98:ASP:HB2	1.76	0.50
1:1:262:A:N3	1:1:430:A:O2'	2.44	0.50
1:1:832:U:H2'	1:1:833:A:C8	2.45	0.50
1:1:2246:G:H2'	1:1:2247:A:H8	1.77	0.50
1:1:2390:U:OP2	34:e:35:LYS:NZ	2.35	0.50
2:2:33:A:H2'	2:2:34:C:C6	2.46	0.50
38:i:97:ARG:HH21	38:i:115:ARG:HH21	1.59	0.50
47:r:39:ILE:HD11	47:r:52:GLN:HB3	1.93	0.50
49:t:21:ASP:OD1	49:t:21:ASP:N	2.44	0.50
1:1:306:U:H2'	1:1:307:G:O4'	2.11	0.50
1:1:476:G:H2'	58:1:3309:HOH:O	2.11	0.50
1:1:1329:U:OP2	1:1:1330:C:N4	2.39	0.50
1:1:1750:G:H2'	1:1:1751:U:C6	2.46	0.50
1:1:2194:U:H2'	1:1:2195:U:C6	2.46	0.50
1:1:2330:G:H21	26:W:42:GLY:HA2	1.77	0.50
1:1:2579:C:O2'	8:C:136:ASN:OD1	2.29	0.50
2:2:318:G:O6	2:2:336:A:N6	2.45	0.50
2:2:925:G:C2	2:2:927:G:C8	3.00	0.50
12:G:47:PHE:HD1	12:G:51:ARG:HB2	1.77	0.50
1:1:172:A:H2'	1:1:173:A:H8	1.76	0.50
1:1:535:G:N2	58:1:3349:HOH:O	2.33	0.50
1:1:624:C:O2'	1:1:657:U:OP1	2.29	0.50
1:1:2425:A:H5''	1:1:2427:C:O4'	2.12	0.50
2:2:216:U:H4'	2:2:464:U:H4'	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:747:A:H2'	2:2:748:G:C8	2.46	0.50
2:2:1003:G:N2	2:2:1005:A:O5'	2.44	0.50
2:2:1124:G:N2	2:2:1125:U:O4	2.44	0.50
10:E:34:ILE:HG13	10:E:96:MET:HE3	1.93	0.50
51:v:8:LEU:HD12	51:v:25:ILE:HG21	1.92	0.50
1:1:20:C:H2'	1:1:21:A:H8	1.77	0.50
1:1:175:G:H2'	1:1:176:A:C8	2.46	0.50
1:1:927:A:H2'	1:1:928:A:H8	1.77	0.50
1:1:1361:G:H2'	1:1:1362:C:H6	1.77	0.50
1:1:2673:G:H2'	1:1:2674:G:H8	1.77	0.50
2:2:1524:C:H2'	2:2:1525:G:H8	1.77	0.50
24:U:28:VAL:HG12	24:U:34:VAL:HG12	1.93	0.50
36:g:162:PHE:HA	36:g:184:PHE:O	2.12	0.50
36:g:221:VAL:O	36:g:225:ARG:HG2	2.12	0.50
39:j:107:ALA:HB2	39:j:125:ALA:HB3	1.94	0.50
45:p:60:PRO:HD3	45:p:91:PRO:HB3	1.93	0.50
49:t:35:GLN:HG3	49:t:59:MET:HE1	1.94	0.50
1:1:288:U:H2'	1:1:289:G:H8	1.76	0.50
1:1:807:U:H2'	1:1:808:G:H8	1.76	0.50
1:1:809:G:H2'	1:1:810:U:C6	2.47	0.50
1:1:833:A:H2'	1:1:834:G:H8	1.77	0.50
1:1:1790:C:O2'	7:B:208:ALA:HB2	2.12	0.50
1:1:1794:A:H2'	1:1:1795:C:C6	2.47	0.50
1:1:1864:U:OP1	1:1:2410:G:O2'	2.28	0.50
1:1:2756:U:H1'	1:1:2757:A:H5''	1.93	0.50
2:2:113:G:H1'	2:2:354:G:H5'	1.94	0.50
2:2:714:G:H1'	2:2:777:A:C8	2.47	0.50
2:2:1414:U:H2'	2:2:1415:G:H8	1.77	0.50
21:R:58:VAL:HG12	21:R:102:SER:HB3	1.94	0.50
24:U:14:LEU:HD21	24:U:71:ALA:HB3	1.94	0.50
39:j:79:GLY:O	39:j:121:HIS:N	2.39	0.50
1:1:154:U:H2'	1:1:155:A:C8	2.47	0.49
2:2:579:A:H2'	2:2:580:C:C6	2.48	0.49
2:2:684:U:O2'	45:p:41:ALA:O	2.30	0.49
2:2:1228:C:OP1	47:r:107:ARG:NH2	2.45	0.49
10:E:35:THR:HB	10:E:155:THR:OG1	2.11	0.49
15:L:79:LEU:HB3	15:L:116:VAL:HG13	1.94	0.49
21:R:89:HIS:O	58:R:201:HOH:O	2.19	0.49
42:m:112:THR:HG23	42:m:115:ALA:H	1.77	0.49
1:1:242:G:H22	1:1:255:A:P	2.34	0.49
1:1:379:G:N1	1:1:396:G:C6	2.81	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2233:U:H2'	1:1:2234:G:H8	1.76	0.49
2:2:513:C:H2'	2:2:514:C:C6	2.47	0.49
2:2:1120:C:H2'	2:2:1121:U:C6	2.47	0.49
10:E:115:ARG:O	30:a:47:LYS:NZ	2.45	0.49
50:u:44:SER:N	50:u:47:GLU:OE2	2.45	0.49
54:y:4:ILE:HG23	54:y:7:ALA:H	1.76	0.49
1:1:532:A:N7	1:1:2021:C:O2'	2.45	0.49
1:1:828:U:H2'	1:1:829:A:C8	2.47	0.49
1:1:2048:G:H21	8:C:118:PHE:HZ	1.60	0.49
1:1:2309:A:N6	58:1:3412:HOH:O	2.45	0.49
1:1:2443:C:H2'	1:1:2444:G:H8	1.77	0.49
1:1:2705:A:O2'	1:1:2852:G:OP1	2.22	0.49
2:2:392:C:H2'	2:2:393:A:H8	1.76	0.49
7:B:107:PRO:HA	7:B:195:VAL:HA	1.94	0.49
8:C:11:MET:HB2	8:C:24:VAL:O	2.12	0.49
45:p:34:ILE:N	45:p:43:GLY:O	2.40	0.49
49:t:6:GLU:OE1	49:t:6:GLU:N	2.44	0.49
1:1:587:C:OP2	15:L:21:ARG:NH1	2.45	0.49
1:1:1031:G:H22	1:1:1122:G:H1	1.58	0.49
1:1:1539:U:H2'	1:1:1540:G:C8	2.48	0.49
1:1:1615:C:OP2	1:1:1617:C:N4	2.43	0.49
1:1:2360:G:H1'	15:L:60:ARG:HD2	1.94	0.49
2:2:358:U:H2'	2:2:359:G:C8	2.46	0.49
2:2:676:A:H2'	2:2:677:U:H6	1.77	0.49
2:2:835:U:OP1	52:w:53:ARG:NH2	2.45	0.49
5:5:54:U:H2'	5:5:55:U:H5'	1.92	0.49
20:Q:44:GLN:NE2	21:R:77:PHE:HB3	2.28	0.49
40:k:3:HIS:ND1	40:k:65:GLU:OE1	2.45	0.49
40:k:6:ILE:HG22	40:k:89:VAL:HG13	1.93	0.49
52:w:26:ILE:HG21	52:w:67:LEU:HD12	1.94	0.49
1:1:197:A:H62	1:1:2430:A:H2'	1.76	0.49
1:1:936:A:H2'	1:1:937:C:C6	2.48	0.49
1:1:2888:C:H2'	1:1:2889:C:H6	1.76	0.49
2:2:141:G:OP2	58:2:1801:HOH:O	2.19	0.49
2:2:1128:C:O2'	43:n:18:ARG:NH2	2.44	0.49
2:2:1147:C:O2'	43:n:18:ARG:HD3	2.12	0.49
26:W:59:LEU:HD12	26:W:80:ILE:HD12	1.94	0.49
36:g:117:LEU:HD23	36:g:141:LEU:HD13	1.93	0.49
1:1:299:A:N1	1:1:322:A:O2'	2.34	0.49
1:1:417:C:H2'	1:1:418:C:C6	2.47	0.49
1:1:684:G:N2	1:1:788:A:OP2	2.40	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:796:C:H2'	1:1:797:G:H8	1.78	0.49
1:1:1000:A:OP2	1:1:1154:G:N1	2.28	0.49
1:1:1734:G:H2'	1:1:1735:A:H8	1.77	0.49
1:1:1844:C:H2'	1:1:1845:G:H8	1.76	0.49
1:1:2543:G:H21	1:1:2646:C:H5''	1.78	0.49
1:1:2824:C:OP2	1:1:2825:G:N2	2.46	0.49
2:2:552:U:O2'	46:q:83:ARG:O	2.26	0.49
2:2:581:G:N1	2:2:759:A:OP2	2.29	0.49
10:E:66:LEU:HG	10:E:88:LYS:HE3	1.94	0.49
10:E:102:ARG:NH2	30:a:26:SER:HA	2.28	0.49
36:g:52:GLU:O	36:g:56:GLU:HG2	2.13	0.49
47:r:90:ARG:HH21	47:r:95:LEU:HB3	1.76	0.49
1:1:414:C:H1'	1:1:1864:U:H1'	1.95	0.49
1:1:639:U:H2'	1:1:640:C:H6	1.77	0.49
1:1:1475:G:O2'	1:1:1514:G:O6	2.30	0.49
2:2:413:G:H22	2:2:429:U:P	2.36	0.49
2:2:520:A:OP2	46:q:48:ALA:HB1	2.13	0.49
2:2:1005:A:H3'	2:2:1006:G:C8	2.44	0.49
5:5:72:G:P	5:5:72:G:H8	2.35	0.49
10:E:110:ARG:NE	10:E:137:ILE:O	2.46	0.49
38:i:28:ILE:HD12	38:i:34:ILE:HD13	1.94	0.49
1:1:1441:G:H2'	1:1:1442:U:C6	2.47	0.49
1:1:2302:U:O2'	10:E:123:ASP:O	2.17	0.49
1:1:2591:C:N4	1:1:2592:G:O6	2.45	0.49
2:2:859:G:OP2	2:2:869:G:N1	2.43	0.49
2:2:1060:U:OP1	48:s:85:ARG:NH2	2.46	0.49
2:2:1287:A:H2	2:2:1353:G:H1'	1.78	0.49
22:S:17:VAL:HB	22:S:76:VAL:HG11	1.95	0.49
45:p:35:THR:HG23	45:p:41:ALA:HA	1.95	0.49
54:y:36:TYR:CZ	54:y:79:LEU:HD21	2.48	0.49
1:1:580:U:H2'	1:1:581:C:C6	2.48	0.49
1:1:833:A:H2'	1:1:834:G:C8	2.48	0.49
1:1:1133:A:H4'	1:1:1134:A:H5''	1.95	0.49
1:1:1175:A:H4'	1:1:1176:U:H5'	1.94	0.49
1:1:2291:U:H2'	1:1:2292:U:H6	1.76	0.49
2:2:855:U:OP2	2:2:871:U:N3	2.38	0.49
2:2:1100:C:OP2	36:g:95:ARG:HD3	2.12	0.49
2:2:1302:C:C5	47:r:17:ILE:HD11	2.48	0.49
8:C:5:VAL:HG22	8:C:202:ILE:HG12	1.95	0.49
11:F:105:LEU:HB2	11:F:113:VAL:HB	1.93	0.49
26:W:53:CYS:SG	26:W:57:HIS:HA	2.53	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
36:g:186:ILE:HD13	36:g:200:ILE:HB	1.94	0.49
47:r:11:ASP:HA	47:r:45:ILE:HB	1.94	0.49
49:t:32:LEU:HD23	49:t:63:ARG:HB2	1.95	0.49
1:1:598:U:H2'	1:1:599:A:H8	1.78	0.49
1:1:1281:G:H2'	1:1:1282:U:C6	2.48	0.49
1:1:1392:A:N6	23:T:18:GLU:HG3	2.27	0.49
1:1:1915:U:H2'	1:1:1916:A:C8	2.48	0.49
1:1:2245:U:H5''	1:1:2246:G:H5'	1.95	0.49
1:1:2310:C:H2'	10:E:77:PHE:HE2	1.77	0.49
1:1:2475:C:N4	1:1:2529:G:H22	2.11	0.49
1:1:2812:G:H2'	1:1:2813:A:C8	2.47	0.49
2:2:131:A:H2'	2:2:132:C:C6	2.48	0.49
2:2:602:A:H2'	2:2:603:U:C6	2.48	0.49
2:2:955:U:H2'	2:2:956:U:C6	2.48	0.49
2:2:1304:G:N2	2:2:1334:G:C6	2.81	0.49
5:5:20:U:C2'	5:5:21:A:H5'	2.43	0.49
8:C:101:PHE:CD2	8:C:187:LEU:HD11	2.48	0.49
13:J:81:ILE:HD12	13:J:81:ILE:H	1.78	0.49
27:X:49:LEU:HB3	27:X:51:VAL:HG13	1.93	0.49
38:i:170:TRP:CD2	38:i:186:PRO:HB3	2.47	0.49
51:v:10:GLY:HA3	51:v:25:ILE:HD13	1.94	0.49
54:y:54:MET:O	54:y:57:ILE:HG22	2.13	0.49
1:1:145:C:H2'	1:1:146:A:C8	2.48	0.48
1:1:174:U:H2'	1:1:175:G:H8	1.77	0.48
1:1:511:U:H4'	1:1:1235:G:H4'	1.94	0.48
1:1:1115:G:O2'	1:1:1116:G:H5''	2.13	0.48
1:1:2020:A:H5'	31:b:9:THR:HB	1.94	0.48
1:1:2374:C:N4	1:1:2375:G:O6	2.46	0.48
2:2:780:A:N6	2:2:801:U:OP2	2.38	0.48
19:P:92:VAL:HG11	19:P:97:LEU:HD11	1.94	0.48
43:n:113:ARG:HE	48:s:101:TRP:NE1	2.11	0.48
1:1:871:U:H2'	1:1:872:U:C6	2.48	0.48
1:1:1438:U:H2'	1:1:1439:A:H8	1.77	0.48
1:1:1939:5MU:OP1	1:1:2604:U:O2'	2.31	0.48
1:1:2514:U:H2'	1:1:2515:C:C6	2.48	0.48
2:2:339:C:H2'	2:2:340:U:C6	2.48	0.48
2:2:427:U:O2'	2:2:541:G:OP1	2.29	0.48
2:2:1311:A:OP1	30:a:59:ARG:NH1	2.45	0.48
2:2:1493:A:C1'	4:4:19:G:H1'	2.43	0.48
2:2:1512:U:H2'	2:2:1513:A:C8	2.47	0.48
36:g:118:GLU:OE1	58:g:301:HOH:O	2.20	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:665:U:H2'	1:1:666:A:H8	1.78	0.48
1:1:741:U:H2'	1:1:742:A:H8	1.76	0.48
1:1:1042:G:H1'	1:1:1043:C:O4'	2.12	0.48
1:1:1604:C:O2'	1:1:1610:A:N1	2.38	0.48
2:2:1314:C:H2'	2:2:1315:U:C6	2.49	0.48
38:i:62:ARG:HH21	38:i:68:LEU:HA	1.78	0.48
1:1:81:G:O2'	1:1:295:G:O2'	2.30	0.48
1:1:347:A:H2'	1:1:348:A:C8	2.48	0.48
1:1:644:A:H2'	1:1:645:C:O4'	2.12	0.48
1:1:1771:C:H2'	1:1:1772:A:C8	2.49	0.48
1:1:2716:C:H2'	1:1:2717:C:H6	1.78	0.48
2:2:22:G:H2'	2:2:23:C:C6	2.47	0.48
2:2:258:G:H1	2:2:268:U:H3	1.59	0.48
2:2:944:G:N1	2:2:1338:G:OP2	2.39	0.48
2:2:1133:G:H2'	2:2:1134:G:C8	2.48	0.48
2:2:1176:A:H2'	2:2:1177:G:C8	2.47	0.48
2:2:1237:C:H5''	2:2:1238:A:C8	2.47	0.48
21:R:61:ALA:HB1	21:R:96:VAL:HG22	1.94	0.48
39:j:76:LEU:HD11	39:j:120:VAL:HG12	1.95	0.48
1:1:489:G:N3	1:1:1284:A:N6	2.61	0.48
1:1:564:C:OP1	58:1:3304:HOH:O	2.20	0.48
1:1:575:A:OP2	1:1:2499:C:O2'	2.25	0.48
1:1:2372:U:H2'	1:1:2373:G:C8	2.48	0.48
1:1:2509:G:N1	1:1:2580:PSU:O2	2.47	0.48
5:5:15:G:H22	5:5:48:C:N4	2.11	0.48
9:D:184:ASP:OD1	15:L:2:ARG:NH2	2.46	0.48
22:S:20:VAL:HG11	22:S:44:ALA:HA	1.94	0.48
27:X:43:GLU:OE2	27:X:45:ARG:HB3	2.12	0.48
36:g:101:LEU:HD11	36:g:175:GLU:HB3	1.94	0.48
36:g:114:LEU:HD12	36:g:144:LEU:HD23	1.96	0.48
1:1:370:G:P	1:1:423:A:H62	2.37	0.48
1:1:437:U:H2'	1:1:438:G:H8	1.78	0.48
1:1:2176:A:H2'	1:1:2177:C:C6	2.49	0.48
1:1:2677:G:H2'	1:1:2678:C:C6	2.49	0.48
1:1:2799:A:O2'	1:1:2800:A:H5''	2.14	0.48
2:2:18:C:OP1	39:j:132:ASN:ND2	2.45	0.48
2:2:19:A:OP1	39:j:135:ASN:ND2	2.45	0.48
2:2:224:U:OP1	54:y:69:LYS:NZ	2.46	0.48
2:2:1269:A:O2'	2:2:1325:C:O2'	2.22	0.48
3:3:23:G:H2'	3:3:24:G:C5	2.48	0.48
5:5:72:G:C2	5:5:73:A:C5	3.02	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:E:56:ASP:O	10:E:60:ILE:HG12	2.14	0.48
22:S:65:ASP:OD1	22:S:66:ILE:N	2.45	0.48
48:s:46:LEU:HB2	53:x:13:LEU:HD13	1.95	0.48
54:y:39:ILE:HG23	54:y:86:LEU:HD12	1.95	0.48
1:1:445:C:OP1	20:Q:2:ALA:N	2.46	0.48
1:1:587:C:O2	15:L:33:ARG:NH1	2.47	0.48
1:1:641:U:H3	1:1:647:G:H1	1.61	0.48
1:1:948:C:H2'	1:1:949:G:C8	2.48	0.48
1:1:1287:A:C2	1:1:1649:G:H4'	2.49	0.48
1:1:1962:5MC:O2'	1:1:1963:U:H3'	2.13	0.48
1:1:2023:C:H2'	1:1:2024:G:H8	1.78	0.48
1:1:2375:G:N2	1:1:2378:A:OP2	2.42	0.48
2:2:68:G:N2	2:2:151:A:C2	2.79	0.48
2:2:335:C:H2'	2:2:336:A:C8	2.39	0.48
2:2:539:A:H2'	2:2:540:G:H8	1.78	0.48
2:2:1031:C:H4'	2:2:1032:G:C2	2.48	0.48
2:2:1181:G:H1'	2:2:1182:G:C4	2.49	0.48
5:5:56:C:O2'	10:E:75:ALA:CB	2.61	0.48
7:B:225:MET:HG3	7:B:226:ASN:N	2.28	0.48
12:G:132:PHE:HB2	12:G:140:ALA:HB3	1.96	0.48
41:l:53:ARG:NH1	41:l:122:ASN:OD1	2.47	0.48
41:l:79:ARG:HD3	41:l:84:THR:HG22	1.95	0.48
43:n:17:ALA:HB2	43:n:67:VAL:HG23	1.96	0.48
54:y:28:MET:HE1	54:y:67:ILE:HG21	1.95	0.48
1:1:980:A:H8	1:1:980:A:OP1	1.97	0.48
1:1:1987:A:H2'	1:1:1988:G:H8	1.79	0.48
1:1:2061:G:H2'	1:1:2501:C:O2'	2.14	0.48
1:1:2552:OMU:H2'	1:1:2554:U:OP2	2.14	0.48
2:2:78:A:H2'	2:2:79:G:H8	1.78	0.48
2:2:393:A:C2	2:2:394:G:C8	3.02	0.48
2:2:405:U:OP2	38:i:3:ARG:NH1	2.47	0.48
3:3:74:U:H3	25:V:29:ILE:HD11	1.79	0.48
5:5:17:C:OP1	5:5:60:U:O2'	2.27	0.48
5:5:69:G:C2	5:5:70:C:C2	3.02	0.48
7:B:160:THR:HG22	7:B:177:ARG:HG2	1.94	0.48
37:h:3:GLN:HB2	37:h:4:LYS:HD3	1.96	0.48
41:l:26:PHE:HZ	41:l:120:LEU:HD11	1.79	0.48
1:1:600:G:N2	1:1:605:G:O3'	2.47	0.48
1:1:2086:U:H2'	1:1:2087:G:C8	2.49	0.48
1:1:2687:U:H2'	1:1:2688:G:O4'	2.12	0.48
2:2:339:C:H2'	2:2:340:U:H6	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:373:A:N3	2:2:482:A:N6	2.61	0.48
2:2:965:U:H1'	2:2:969:A:C2	2.49	0.48
3:3:2:G:H2'	3:3:3:C:H6	1.79	0.48
5:5:59:A:H2'	5:5:60:U:N1	2.29	0.48
7:B:145:GLU:HG2	7:B:151:GLY:H	1.78	0.48
9:D:105:LEU:HD12	9:D:108:ILE:HD11	1.94	0.48
39:j:157:ARG:HD3	42:m:43:GLU:HG3	1.95	0.48
46:q:100:GLY:N	46:q:104:CYS:O	2.45	0.48
47:r:75:MET:HE3	47:r:79:ARG:HB3	1.95	0.48
52:w:23:TYR:HA	52:w:58:ALA:HB1	1.95	0.48
1:1:685:A:N1	1:1:787:C:H1'	2.29	0.48
1:1:714:U:OP2	49:t:88:ARG:NH1	2.33	0.48
1:1:1105:U:H2'	1:1:1106:G:H8	1.79	0.48
1:1:1858:A:N6	1:1:1884:G:H1'	2.29	0.48
1:1:1953:A:O2'	1:1:2559:C:O2	2.31	0.48
1:1:2007:U:H2'	1:1:2008:C:C6	2.49	0.48
1:1:2271:G:H5'	26:W:20:ARG:HG3	1.95	0.48
1:1:2329:U:H2'	1:1:2330:G:C8	2.48	0.48
1:1:2683:C:OP1	19:P:51:ARG:NH2	2.47	0.48
2:2:68:G:H3'	2:2:69:G:H5''	1.96	0.48
2:2:78:A:H2'	2:2:79:G:C8	2.49	0.48
2:2:496:A:H2'	2:2:496:A:N3	2.27	0.48
2:2:1183:U:O2'	2:2:1185:G:OP2	2.32	0.48
2:2:1216:A:H5''	48:s:5:SER:OG	2.13	0.48
33:d:16:HIS:HB2	33:d:44:VAL:HG11	1.96	0.48
36:g:114:LEU:HG	36:g:145:GLU:OE2	2.14	0.48
1:1:69:C:O2	1:1:73:A:O2'	2.26	0.47
1:1:780:G:C2	1:1:782:A:C2	3.02	0.47
1:1:1427:A:H4'	1:1:1428:C:O4'	2.14	0.47
1:1:2025:C:H2'	1:1:2026:U:C6	2.49	0.47
1:1:2036:C:H2'	1:1:2037:A:C8	2.49	0.47
2:2:634:C:H2'	2:2:635:A:C8	2.49	0.47
2:2:886:G:O6	2:2:912:C:N4	2.47	0.47
7:B:30:PHE:O	7:B:34:LEU:HD23	2.13	0.47
16:M:41:LEU:HD13	16:M:96:ILE:HG13	1.96	0.47
16:M:42:THR:HA	16:M:93:VAL:HA	1.96	0.47
16:M:77:PRO:HD2	16:M:80:VAL:HG11	1.96	0.47
17:N:65:LEU:O	17:N:69:ARG:HG2	2.14	0.47
20:Q:40:ILE:O	20:Q:44:GLN:HG3	2.14	0.47
1:1:1571:A:H2'	1:1:1572:A:C8	2.49	0.47
1:1:1914:C:H2'	1:1:1915:U:H6	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2788:C:H2'	1:1:2789:C:C6	2.49	0.47
1:1:2896:C:H2'	1:1:2897:U:C6	2.50	0.47
2:2:963:G:N2	44:o:57:VAL:HG11	2.30	0.47
2:2:1326:U:H2'	2:2:1327:C:H6	1.78	0.47
2:2:1464:U:H2'	2:2:1465:A:H8	1.79	0.47
5:5:69:G:H2'	5:5:70:C:C6	2.49	0.47
9:D:141:MET:HE1	9:D:143:LEU:HD12	1.95	0.47
10:E:139:PRO:HB2	30:a:32:LEU:HD11	1.96	0.47
23:T:10:VAL:HG13	23:T:11:LEU:HD12	1.95	0.47
24:U:18:ASP:HB2	24:U:21:LYS:HD2	1.97	0.47
38:i:174:ASP:OD2	58:i:301:HOH:O	2.19	0.47
39:j:44:GLY:O	39:j:74:VAL:N	2.48	0.47
1:1:848:C:H2'	1:1:849:A:C8	2.40	0.47
1:1:918:A:H2'	1:1:919:U:O4'	2.15	0.47
1:1:1054:A:H2'	1:1:1055:G:C8	2.49	0.47
1:1:1266:G:OP2	31:b:17:ARG:NH2	2.41	0.47
1:1:1771:C:H2'	1:1:1772:A:H8	1.79	0.47
1:1:1819:A:H5''	7:B:160:THR:HG21	1.96	0.47
2:2:167:A:N6	2:2:168:G:O6	2.47	0.47
2:2:1095:U:P	2:2:1108:G:H1	2.37	0.47
43:n:47:VAL:HG11	43:n:76:ALA:HB1	1.96	0.47
43:n:79:ILE:O	43:n:83:ILE:HG13	2.13	0.47
1:1:418:C:H2'	1:1:419:U:C6	2.50	0.47
1:1:813:U:H2'	1:1:814:C:H6	1.79	0.47
1:1:927:A:O2'	29:Z:39:GLU:OE2	2.32	0.47
1:1:2651:C:N4	58:1:3406:HOH:O	2.43	0.47
2:2:769:G:H4'	2:2:1513:A:H4'	1.95	0.47
2:2:824:G:H2'	2:2:825:A:H8	1.78	0.47
2:2:927:G:P	4:4:11:A:H61	2.37	0.47
2:2:1120:C:H2'	2:2:1121:U:H6	1.80	0.47
5:5:3:G:H1'	5:5:4:C:O5'	2.14	0.47
25:V:32:GLY:O	25:V:93:ARG:NH1	2.46	0.47
31:b:13:ARG:O	31:b:17:ARG:HG2	2.14	0.47
41:l:126:ASP:O	41:l:131:LYS:N	2.41	0.47
1:1:265:A:N1	1:1:427:U:O2'	2.41	0.47
1:1:633:A:H5''	15:L:70:LYS:HD2	1.97	0.47
1:1:729:G:OP2	7:B:207:LYS:NZ	2.42	0.47
1:1:927:A:H2'	1:1:928:A:C8	2.48	0.47
1:1:1361:G:H2'	1:1:1362:C:C6	2.49	0.47
1:1:1431:A:H2'	1:1:1432:G:C8	2.49	0.47
1:1:1509:A:O2'	1:1:1510:G:O5'	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1668:A:O2'	1:1:1674:G:N7	2.36	0.47
1:1:2292:U:H2'	1:1:2293:G:C8	2.49	0.47
1:1:2530:A:OP2	1:1:2535:G:N2	2.47	0.47
3:3:30:C:H1'	3:3:57:A:H61	1.79	0.47
5:5:11:C:H2'	5:5:12:G:C8	2.50	0.47
5:5:22:G:N7	5:5:46:G:N2	2.55	0.47
20:Q:97:ASP:HA	20:Q:100:VAL:HG12	1.97	0.47
1:1:1:G:H2'	1:1:2:G:C8	2.50	0.47
1:1:13:A:O2'	1:1:15:G:N7	2.41	0.47
1:1:417:C:H2'	1:1:418:C:H6	1.80	0.47
1:1:1389:G:N1	1:1:1399:C:N3	2.63	0.47
1:1:1830:C:H2'	1:1:1831:G:C8	2.46	0.47
1:1:2508:G:H1	1:1:2580:PSU:HN3	1.62	0.47
2:2:259:G:H2'	2:2:260:G:H8	1.80	0.47
2:2:715:A:H2'	2:2:716:A:C8	2.49	0.47
37:h:121:THR:HG23	37:h:189:ALA:HB2	1.97	0.47
54:y:57:ILE:HG13	54:y:61:GLN:NE2	2.18	0.47
1:1:365:U:H2'	1:1:366:C:C6	2.49	0.47
1:1:391:A:O2'	1:1:410:G:OP1	2.30	0.47
1:1:1085:A:H2'	1:1:1086:A:C8	2.50	0.47
1:1:1751:U:H2'	1:1:1752:C:C6	2.50	0.47
1:1:2246:G:H2'	1:1:2247:A:C8	2.50	0.47
1:1:2452:C:H2'	1:1:2453:A:O4'	2.15	0.47
1:1:2514:U:H2'	1:1:2515:C:H6	1.80	0.47
2:2:216:U:H2'	2:2:217:C:C6	2.49	0.47
2:2:270:A:H2'	2:2:271:C:C6	2.49	0.47
2:2:454:G:H2'	2:2:455:G:H8	1.79	0.47
2:2:714:G:N2	2:2:777:A:N3	2.52	0.47
2:2:747:A:H2'	2:2:748:G:H8	1.80	0.47
2:2:935:A:O2'	2:2:1383:C:N3	2.47	0.47
2:2:945:G:C2	2:2:946:A:C8	3.03	0.47
2:2:1323:G:H2'	2:2:1324:A:H8	1.80	0.47
2:2:1493:A:H1'	4:4:19:G:H1'	1.96	0.47
10:E:138:PHE:HE2	10:E:152:LEU:HD21	1.79	0.47
15:L:79:LEU:HA	15:L:82:LEU:HD13	1.97	0.47
16:M:36:VAL:HG22	25:V:82:TYR:HB2	1.97	0.47
36:g:106:THR:O	36:g:109:GLN:HG2	2.14	0.47
38:i:54:GLN:HB3	38:i:203:LEU:HB2	1.96	0.47
42:m:55:THR:HG23	42:m:56:LYS:HG2	1.96	0.47
1:1:1234:U:C4	1:1:1235:G:C5	3.03	0.47
1:1:1252:G:N2	20:Q:33:ARG:HB3	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2845:U:H2'	1:1:2846:G:C8	2.49	0.47
1:1:2845:U:H5''	19:P:52:ASN:O	2.15	0.47
1:1:2899:A:H2'	1:1:2900:A:H8	1.80	0.47
2:2:695:A:H2'	2:2:696:A:C8	2.50	0.47
2:2:1127:G:H2'	2:2:1128:C:H6	1.79	0.47
14:K:24:VAL:HG13	14:K:33:ALA:HB2	1.96	0.47
16:M:2:LEU:HD22	16:M:46:ILE:HG21	1.97	0.47
37:h:105:GLU:OE1	37:h:107:ARG:NE	2.48	0.47
44:o:36:VAL:HG22	44:o:76:ILE:HG22	1.96	0.47
53:x:36:ARG:HH21	53:x:75:ALA:HB3	1.80	0.47
1:1:1196:C:C2	1:1:1197:G:C8	3.03	0.47
1:1:1817:G:OP1	7:B:87:ARG:NH2	2.39	0.47
1:1:2081:U:H2'	1:1:2082:A:C8	2.49	0.47
1:1:2324:U:H5''	1:1:2325:G:H5''	1.97	0.47
1:1:2340:A:H2'	1:1:2341:G:H8	1.80	0.47
1:1:2347:C:O2'	32:c:21:TYR:OH	2.25	0.47
1:1:2468:A:OP2	1:1:2476:A:N6	2.42	0.47
1:1:2836:U:H2'	1:1:2837:A:H8	1.80	0.47
2:2:382:A:H2'	2:2:383:A:C8	2.49	0.47
2:2:501:C:O2	2:2:549:C:O2'	2.32	0.47
2:2:539:A:H2'	2:2:540:G:C8	2.50	0.47
2:2:575:G:H4'	2:2:576:C:H5''	1.97	0.47
2:2:1171:A:H2'	2:2:1172:C:C6	2.50	0.47
2:2:1414:U:O2	2:2:1487:G:N2	2.47	0.47
5:5:21:A:N7	5:5:47:U:H1'	2.30	0.47
9:D:130:LYS:HB2	9:D:133:LEU:HG	1.97	0.47
13:J:116:ARG:O	13:J:120:ARG:HG3	2.14	0.47
32:c:25:LYS:NZ	32:c:32:GLU:O	2.46	0.47
1:1:1060:U:C2	1:1:1062:G:H5'	2.50	0.47
1:1:1486:U:H2'	1:1:1487:U:H6	1.79	0.47
1:1:1696:G:N2	1:1:1977:A:O2'	2.46	0.47
1:1:1734:G:H2'	1:1:1735:A:C8	2.50	0.47
1:1:2344:U:H3'	32:c:37:LYS:O	2.15	0.47
2:2:777:A:H2'	2:2:778:G:H8	1.79	0.47
2:2:1028:C:N4	58:2:1846:HOH:O	2.44	0.47
2:2:1479:C:H2'	2:2:1480:A:H8	1.80	0.47
5:5:14:A:C2	5:5:15:G:H1'	2.50	0.47
21:R:89:HIS:N	58:R:201:HOH:O	2.39	0.47
36:g:176:ALA:HB1	36:g:181:ILE:HB	1.97	0.47
37:h:110:GLU:HG2	37:h:144:LEU:HD22	1.97	0.47
38:i:110:THR:HG23	38:i:113:GLU:H	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
54:y:79:LEU:O	54:y:83:ILE:HG13	2.15	0.47
1:1:175:G:H2'	1:1:176:A:H8	1.80	0.46
1:1:481:G:OP2	24:U:44:LYS:HD2	2.14	0.46
1:1:608:A:H2'	1:1:609:A:C8	2.50	0.46
1:1:1097:U:H3'	1:1:1098:A:H8	1.80	0.46
1:1:1413:A:H2'	1:1:1414:C:C6	2.50	0.46
1:1:1667:G:O2'	1:1:1991:U:O4	2.22	0.46
1:1:2233:U:H2'	1:1:2234:G:C8	2.49	0.46
2:2:436:C:H2'	2:2:437:U:C6	2.50	0.46
2:2:594:U:H2'	2:2:595:A:O4'	2.15	0.46
2:2:1226:C:O2	53:x:83:HIS:NE2	2.47	0.46
36:g:67:ILE:HG22	36:g:160:ALA:HB3	1.97	0.46
37:h:150:LYS:HG3	37:h:201:TRP:CE3	2.50	0.46
1:1:1042:G:O2'	1:1:1043:C:H5''	2.14	0.46
1:1:1056:G:H21	1:1:1104:C:H41	1.61	0.46
1:1:1476:U:H2'	1:1:1477:A:H8	1.79	0.46
1:1:2345:G:N3	1:1:2381:A:H2'	2.30	0.46
2:2:952:U:H4'	2:2:964:A:H61	1.81	0.46
2:2:1391:U:H2'	2:2:1392:G:C8	2.50	0.46
2:2:1454:G:H2'	2:2:1455:G:H8	1.80	0.46
7:B:232:HIS:CG	7:B:240:PHE:HE1	2.33	0.46
22:S:24:ILE:HD13	22:S:36:LEU:HD11	1.96	0.46
23:T:11:LEU:HA	23:T:34:VAL:HG12	1.97	0.46
36:g:115:LYS:HE2	36:g:118:GLU:OE2	2.15	0.46
37:h:11:ARG:NH2	37:h:175:LEU:O	2.40	0.46
39:j:83:HIS:CE1	42:m:96:MET:HE1	2.50	0.46
39:j:133:PRO:HA	39:j:136:VAL:HG22	1.97	0.46
40:k:18:VAL:HG11	40:k:58:HIS:CE1	2.50	0.46
1:1:367:G:H2'	1:1:367:G:N3	2.29	0.46
1:1:494:G:H5''	22:S:4:ILE:HG23	1.98	0.46
1:1:871:U:H2'	1:1:872:U:H6	1.81	0.46
1:1:2477:U:O2	35:f:4:ARG:NH2	2.48	0.46
2:2:264:C:O2'	51:v:66:PRO:O	2.31	0.46
2:2:360:G:H2'	2:2:361:G:C8	2.50	0.46
2:2:510:A:N3	2:2:543:U:H1'	2.31	0.46
2:2:976:G:H5'	48:s:61:ARG:HH22	1.79	0.46
2:2:1343:G:H1'	43:n:123:ARG:NH1	2.31	0.46
2:2:1355:G:H2'	2:2:1356:G:H8	1.80	0.46
58:K:202:HOH:O	19:P:70:VAL:HG13	2.15	0.46
19:P:27:GLU:HB2	19:P:44:GLU:HG2	1.97	0.46
43:n:124:ARG:HH12	43:n:127:PHE:HB2	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
44:o:12:ALA:HB3	44:o:18:ILE:HB	1.96	0.46
47:r:37:ALA:HB2	47:r:59:GLU:OE2	2.15	0.46
49:t:57:LEU:HA	49:t:60:VAL:HG22	1.97	0.46
1:1:586:A:N1	1:1:809:G:O2'	2.39	0.46
1:1:1233:C:C2	1:1:1234:U:C5	3.03	0.46
1:1:1287:A:O5'	17:N:103:ARG:NH2	2.45	0.46
1:1:1917:PSU:O2	1:1:1918:A:N6	2.49	0.46
2:2:59:A:H3'	2:2:331:G:H22	1.81	0.46
2:2:1326:U:C2	2:2:1327:C:C5	3.03	0.46
39:j:144:LEU:O	39:j:147:MET:HG2	2.16	0.46
40:k:26:THR:HA	40:k:29:ILE:HG22	1.97	0.46
1:1:879:G:H2'	1:1:880:G:H8	1.80	0.46
1:1:1501:G:OP1	7:B:101:ARG:NH2	2.33	0.46
1:1:1794:A:H2'	1:1:1795:C:H6	1.80	0.46
1:1:2071:A:H2'	1:1:2072:C:C6	2.49	0.46
1:1:2091:C:H4'	27:X:56:MET:HE1	1.98	0.46
5:5:52:G:H2'	5:5:53:G:C8	2.49	0.46
5:5:52:G:H2'	5:5:53:G:H8	1.79	0.46
12:G:99:ILE:HD11	12:G:117:LEU:HD11	1.97	0.46
43:n:47:VAL:HG22	43:n:80:ARG:HB2	1.97	0.46
1:1:414:C:H2'	1:1:415:A:H8	1.81	0.46
1:1:453:A:N3	1:1:457:A:O2'	2.46	0.46
1:1:935:C:H2'	1:1:936:A:C8	2.50	0.46
1:1:935:C:H2'	1:1:936:A:H8	1.81	0.46
1:1:1117:C:H2'	1:1:1118:C:C6	2.51	0.46
1:1:1359:A:OP2	1:1:1371:G:N1	2.38	0.46
1:1:1569:A:H2'	1:1:1570:A:C8	2.50	0.46
1:1:2610:C:N4	58:1:3396:HOH:O	2.41	0.46
2:2:231:U:H2'	2:2:232:G:H8	1.80	0.46
2:2:674:G:N2	45:p:118:HIS:HB2	2.31	0.46
2:2:745:G:OP1	2:2:851:G:O2'	2.32	0.46
18:O:7:ARG:HD2	18:O:97:PHE:CZ	2.51	0.46
22:S:28:LYS:HE3	22:S:28:LYS:HB3	1.78	0.46
30:a:56:ARG:NH2	53:x:68:GLY:HA3	2.31	0.46
41:l:40:GLU:HA	41:l:43:VAL:HG12	1.96	0.46
49:t:26:GLU:HA	49:t:29:VAL:HG12	1.97	0.46
1:1:272:A:H2'	1:1:273:G:H8	1.81	0.46
1:1:345:A:N3	1:1:347:A:N6	2.63	0.46
1:1:813:U:H2'	1:1:814:C:C6	2.51	0.46
1:1:1141:U:H4'	1:1:1142:A:O4'	2.16	0.46
1:1:1326:U:N3	1:1:1648:U:O2'	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1655:A:N6	1:1:2005:A:O2'	2.48	0.46
1:1:2298:A:OP1	10:E:71:ARG:NH1	2.39	0.46
2:2:71:A:H61	2:2:99:C:H1'	1.81	0.46
2:2:114:U:H2'	2:2:115:G:C8	2.51	0.46
2:2:147:G:H2'	2:2:148:G:C8	2.50	0.46
2:2:751:U:H2'	2:2:752:G:O4'	2.15	0.46
2:2:826:C:H1'	42:m:16:ASN:HD22	1.80	0.46
2:2:1530:G:H2'	2:2:1531:A:C8	2.51	0.46
9:D:29:HIS:HA	9:D:32:VAL:HG22	1.97	0.46
10:E:10:ASP:O	10:E:14:LYS:NZ	2.46	0.46
10:E:136:ILE:HD12	10:E:141:ILE:HG23	1.98	0.46
15:L:41:ARG:NH1	58:L:303:HOH:O	2.47	0.46
20:Q:86:ALA:HB2	20:Q:116:ALA:HB2	1.98	0.46
38:i:85:ASN:HD22	39:j:101:GLU:HG3	1.79	0.46
49:t:12:VAL:HG21	49:t:22:THR:HG22	1.97	0.46
1:1:1812:U:H2'	1:1:1813:G:H8	1.80	0.46
2:2:707:U:H4'	45:p:22:HIS:ND1	2.31	0.46
3:3:77:U:O2	25:V:78:GLN:NE2	2.36	0.46
9:D:1:MET:HE2	9:D:16:GLU:HG2	1.98	0.46
37:h:66:VAL:HB	37:h:101:ILE:HD13	1.98	0.46
44:o:52:LEU:O	48:s:81:ARG:NH1	2.48	0.46
50:u:52:LEU:HD22	50:u:57:ILE:HD11	1.98	0.46
1:1:329:G:O6	24:U:17:LYS:N	2.49	0.46
1:1:959:A:H2'	1:1:960:A:C8	2.51	0.46
1:1:1710:G:H2'	1:1:1711:A:H8	1.81	0.46
1:1:1850:G:H2'	1:1:1851:U:H6	1.81	0.46
1:1:2054:A:H2'	31:b:5:GLN:OE1	2.16	0.46
2:2:1147:C:O2	43:n:18:ARG:NH1	2.49	0.46
2:2:1323:G:H2'	2:2:1324:A:C8	2.51	0.46
3:3:74:U:C4	25:V:37:PRO:HG2	2.50	0.46
5:5:15:G:C2	5:5:59:A:C6	3.03	0.46
10:E:16:LEU:HA	10:E:19:GLU:HG2	1.98	0.46
31:b:53:LYS:HD2	31:b:55:ILE:O	2.16	0.46
53:x:40:ILE:HD11	53:x:74:PHE:HE2	1.81	0.46
1:1:174:U:H2'	1:1:175:G:C8	2.51	0.46
1:1:522:A:H2'	1:1:523:C:C6	2.51	0.46
1:1:1501:G:H4'	7:B:95:LEU:HD11	1.98	0.46
1:1:2029:G:N1	1:1:2033:A:OP2	2.37	0.46
2:2:707:U:H2'	2:2:708:C:C6	2.51	0.46
2:2:865:A:H2'	2:2:866:C:C6	2.51	0.46
11:F:35:ARG:NH2	11:F:71:LEU:HB3	2.31	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
20:Q:94:ILE:HA	20:Q:97:ASP:OD2	2.16	0.46
38:i:126:ASN:HD21	38:i:141:ASP:CG	2.24	0.46
42:m:93:PRO:HG3	42:m:125:ILE:HD13	1.98	0.46
1:1:88:G:O6	1:1:89:A:N6	2.49	0.45
1:1:121:G:H2'	1:1:122:G:H8	1.80	0.45
1:1:565:C:OP2	21:R:80:ARG:N	2.48	0.45
1:1:807:U:H2'	1:1:808:G:C8	2.51	0.45
1:1:2641:G:H5''	13:J:78:THR:HB	1.98	0.45
2:2:1130:A:N6	2:2:1144:G:H21	2.14	0.45
2:2:1375:A:OP1	41:l:25:LYS:NZ	2.46	0.45
3:3:73:A:N6	3:3:103:U:C2	2.84	0.45
15:L:63:LYS:HA	34:e:13:ARG:HG2	1.97	0.45
44:o:26:VAL:O	44:o:30:LYS:HG2	2.16	0.45
1:1:55:G:H2'	1:1:56:A:C8	2.51	0.45
1:1:291:G:C6	1:1:350:G:C6	3.04	0.45
1:1:357:C:H2'	1:1:358:U:C6	2.51	0.45
1:1:971:G:H2'	1:1:972:A:O4'	2.16	0.45
1:1:1024:G:C6	1:1:1025:G:C6	3.04	0.45
1:1:1030:C:N3	1:1:1124:G:N1	2.64	0.45
2:2:8:A:N7	38:i:206:LYS:HA	2.31	0.45
2:2:748:G:H2'	2:2:749:A:C8	2.52	0.45
18:O:35:ILE:HG21	18:O:102:ARG:HD2	1.98	0.45
35:f:14:CYS:SG	35:f:33:HIS:ND1	2.85	0.45
43:n:47:VAL:CG1	43:n:76:ALA:HB1	2.46	0.45
1:1:305:C:H2'	1:1:306:U:C6	2.51	0.45
1:1:480:A:O2'	1:1:498:G:N2	2.50	0.45
1:1:526:A:O2'	1:1:2043:C:O2	2.26	0.45
1:1:575:A:OP2	1:1:2055:C:N4	2.50	0.45
1:1:1130:U:N3	1:1:2025:C:OP1	2.45	0.45
1:1:1429:G:H2'	1:1:1430:G:C8	2.45	0.45
1:1:1518:C:H2'	1:1:1519:G:H8	1.80	0.45
1:1:1688:U:O2'	1:1:1700:A:N7	2.34	0.45
1:1:2286:G:H5''	1:1:2287:A:OP1	2.17	0.45
1:1:2290:G:H2'	1:1:2291:U:C6	2.52	0.45
1:1:2804:U:H2'	1:1:2805:C:C6	2.51	0.45
2:2:513:C:H2'	2:2:514:C:H6	1.80	0.45
2:2:523:A:H61	46:q:89:0TD:CG	2.28	0.45
2:2:634:C:H2'	2:2:635:A:H8	1.80	0.45
2:2:678:U:H2'	2:2:679:C:H6	1.81	0.45
2:2:704:A:C4	2:2:705:G:C8	3.05	0.45
3:3:101:A:H2'	3:3:102:G:C8	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
11:F:35:ARG:HG2	11:F:35:ARG:HH11	1.81	0.45
37:h:111:LEU:HD22	37:h:146:ALA:HB2	1.99	0.45
44:o:53:ILE:HG22	48:s:85:ARG:HE	1.80	0.45
49:t:88:ARG:HD2	49:t:89:ARG:HH11	1.81	0.45
1:1:19:A:H2'	1:1:20:C:C6	2.51	0.45
1:1:1712:U:OP2	1:1:1713:A:O2'	2.27	0.45
1:1:1791:A:H4'	7:B:205:LEU:HB2	1.98	0.45
1:1:2320:U:H1'	1:1:2322:A:N7	2.32	0.45
2:2:110:C:O2'	50:u:25:ARG:O	2.33	0.45
2:2:113:G:H2'	2:2:114:U:H6	1.78	0.45
2:2:407:U:H2'	2:2:408:A:H8	1.82	0.45
2:2:409:U:OP2	38:i:22:LYS:HD2	2.16	0.45
2:2:1493:A:H1'	4:4:19:G:N3	2.31	0.45
5:5:11:C:H2'	5:5:12:G:H8	1.82	0.45
5:5:18:G:N2	5:5:57:A:C5	2.85	0.45
5:5:63:U:H2'	5:5:64:C:C6	2.51	0.45
11:F:10:VAL:HA	11:F:49:THR:HA	1.98	0.45
14:K:59:LYS:NZ	14:K:89:ASN:O	2.40	0.45
14:K:78:ARG:N	19:P:71:GLU:O	2.48	0.45
37:h:64:ILE:O	37:h:99:ALA:HA	2.17	0.45
45:p:34:ILE:HG12	45:p:70:CYS:SG	2.55	0.45
1:1:65:U:H2'	1:1:66:C:H6	1.81	0.45
1:1:1065:U:O4	1:1:1069:A:O2'	2.33	0.45
1:1:1322:A:O3'	22:S:84:ARG:NH2	2.48	0.45
1:1:1614:A:H61	22:S:88:ARG:H	1.64	0.45
1:1:2315:G:H2'	1:1:2316:G:H8	1.82	0.45
1:1:2385:C:H2'	1:1:2386:A:C8	2.51	0.45
1:1:2519:U:H5'	1:1:2567:G:N2	2.32	0.45
1:1:2836:U:H2'	1:1:2837:A:C8	2.50	0.45
2:2:123:U:H5''	2:2:311:C:O2'	2.17	0.45
2:2:579:A:H2'	2:2:580:C:H6	1.81	0.45
2:2:1437:A:H2'	2:2:1438:G:H8	1.81	0.45
3:3:49:C:OP1	18:O:102:ARG:N	2.49	0.45
3:3:62:C:H2'	3:3:63:C:H6	1.81	0.45
7:B:34:LEU:HD11	7:B:63:ARG:NH1	2.31	0.45
7:B:84:ASP:HB2	7:B:91:ILE:HG23	1.99	0.45
11:F:42:GLU:OE1	11:F:55:ARG:NH1	2.49	0.45
12:G:57:LYS:HD3	12:G:57:LYS:C	2.41	0.45
42:m:11:LEU:HG	42:m:75:ILE:HG13	1.99	0.45
44:o:19:ASP:OD1	44:o:72:ARG:NH2	2.49	0.45
46:q:29:GLN:HB3	46:q:81:LEU:HG	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
47:r:31:LYS:HB3	47:r:31:LYS:HE2	1.87	0.45
1:1:154:U:H2'	1:1:155:A:H8	1.80	0.45
1:1:287:G:H2'	1:1:288:U:C6	2.51	0.45
1:1:368:A:H2'	1:1:369:U:C6	2.52	0.45
1:1:419:U:H2'	1:1:420:C:C6	2.51	0.45
1:1:1297:C:H2'	1:1:1298:C:C6	2.51	0.45
1:1:2377:A:O2'	18:O:117:PHE:O	2.30	0.45
1:1:2415:G:H2'	1:1:2416:C:C6	2.52	0.45
2:2:175:C:H2'	2:2:176:C:C6	2.52	0.45
2:2:1328:C:H5''	47:r:28:THR:HG21	1.98	0.45
2:2:1351:U:H4'	41:l:33:ASP:OD1	2.16	0.45
3:3:74:U:C4	3:3:75:G:C5	3.05	0.45
10:E:36:LEU:HD21	10:E:99:PHE:CE2	2.52	0.45
14:K:7:MET:HE3	14:K:20:MET:HE3	1.98	0.45
24:U:53:ASN:O	24:U:53:ASN:ND2	2.47	0.45
43:n:116:VAL:HG21	44:o:62:ARG:HB3	1.98	0.45
48:s:24:ARG:HH11	48:s:51:LEU:HD23	1.81	0.45
1:1:627:A:H5''	15:L:78:ARG:NH2	2.32	0.45
1:1:1638:C:O2	1:1:2698:U:O2'	2.35	0.45
1:1:1789:A:H2'	1:1:1790:C:O4'	2.17	0.45
1:1:2467:C:O2	16:M:123:LYS:NZ	2.39	0.45
2:2:1014:A:C2	2:2:1219:A:H1'	2.52	0.45
2:2:1014:A:H2'	2:2:1015:G:C4	2.51	0.45
7:B:53:HIS:CE1	7:B:219:THR:HA	2.52	0.45
10:E:108:VAL:HG21	10:E:176:PRO:HG2	1.98	0.45
11:F:54:PRO:HG3	11:F:62:TRP:CE2	2.52	0.45
18:O:11:ALA:HB2	18:O:96:GLY:N	2.31	0.45
45:p:123:PRO:HD2	55:z:38:TYR:HD1	1.82	0.45
1:1:18:U:O4	1:1:19:A:N6	2.50	0.45
1:1:78:U:H2'	1:1:79:C:C6	2.52	0.45
1:1:79:C:O2'	1:1:346:A:N3	2.45	0.45
1:1:289:G:H2'	1:1:290:U:C6	2.51	0.45
1:1:753:A:H2'	1:1:754:U:C6	2.52	0.45
1:1:1085:A:N1	58:1:3367:HOH:O	2.36	0.45
1:1:1141:U:OP2	13:J:65:THR:OG1	2.29	0.45
1:1:1733:G:H2'	1:1:1734:G:C8	2.52	0.45
1:1:1853:A:N7	1:1:1889:A:N6	2.64	0.45
2:2:472:U:H2'	2:2:473:U:C6	2.52	0.45
2:2:1409:C:H2'	2:2:1410:A:H8	1.82	0.45
3:3:30:C:H2'	3:3:31:C:O4'	2.16	0.45
6:A:184:LYS:O	6:A:187:GLU:HG3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
18:O:31:THR:O	18:O:102:ARG:NH1	2.50	0.45
31:b:12:LYS:HA	31:b:12:LYS:HD2	1.83	0.45
1:1:374:A:H4'	1:1:422:A:H2	1.81	0.45
1:1:743:A:OP1	8:C:135:GLY:HA2	2.17	0.45
1:1:1495:A:H2'	1:1:1496:A:C8	2.52	0.45
1:1:1858:A:H2'	1:1:1859:U:O4'	2.17	0.45
1:1:2114:A:H2'	1:1:2167:U:H5'	1.99	0.45
1:1:2387:U:OP1	26:W:55:ARG:NH2	2.50	0.45
1:1:2508:G:H2'	1:1:2509:G:H8	1.81	0.45
1:1:2515:C:H2'	1:1:2516:A:C8	2.47	0.45
1:1:2686:G:H2'	1:1:2687:U:C6	2.51	0.45
1:1:2751:G:OP1	1:1:2751:G:N2	2.50	0.45
2:2:542:G:H2'	2:2:543:U:H6	1.82	0.45
2:2:1287:A:H2'	2:2:1288:A:H8	1.82	0.45
5:5:24:G:H2'	5:5:25:C:C6	2.52	0.45
9:D:148:ILE:HB	9:D:169:VAL:HG12	1.98	0.45
25:V:61:LEU:HB2	25:V:72:VAL:O	2.16	0.45
29:Z:24:LEU:HD11	29:Z:54:MET:SD	2.56	0.45
41:l:30:LEU:HD23	41:l:43:VAL:HB	1.98	0.45
1:1:223:A:N6	1:1:422:A:N1	2.65	0.45
1:1:302:C:H2'	1:1:303:G:C8	2.48	0.45
1:1:499:U:H2'	1:1:500:G:H8	1.82	0.45
1:1:559:G:N2	20:Q:49:ASP:OD2	2.30	0.45
1:1:882:G:O6	1:1:894:U:C4	2.70	0.45
1:1:1298:C:H2'	1:1:1299:G:O4'	2.17	0.45
1:1:1431:A:H2'	1:1:1432:G:H8	1.81	0.45
1:1:1721:G:O2'	1:1:1739:A:N6	2.50	0.45
1:1:2257:U:H2'	1:1:2258:C:C6	2.52	0.45
1:1:2488:G:H2'	1:1:2489:U:C6	2.52	0.45
1:1:2645:G:OP2	1:1:2645:G:N2	2.33	0.45
1:1:2717:C:O2'	19:P:94:LYS:NZ	2.32	0.45
2:2:323:U:H2'	2:2:324:G:O4'	2.16	0.45
2:2:505:G:H2'	2:2:506:G:H8	1.82	0.45
2:2:939:G:O2'	2:2:1375:A:N3	2.47	0.45
5:5:15:G:N2	5:5:59:A:C5	2.85	0.45
1:1:6:A:H2'	1:1:7:G:C8	2.52	0.44
1:1:404:A:H1'	1:1:405:U:OP2	2.17	0.44
1:1:1296:G:OP1	1:1:2709:G:O2'	2.27	0.44
1:1:1315:C:O2'	1:1:1392:A:H1'	2.16	0.44
1:1:1604:C:H2'	1:1:1605:C:C6	2.51	0.44
1:1:1726:C:H2'	1:1:1727:C:C6	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2090:A:N6	1:1:2230:G:O6	2.50	0.44
1:1:2284:A:HO2'	1:1:2288:A:N6	2.16	0.44
1:1:2466:C:C2	1:1:2485:G:C2	3.05	0.44
2:2:197:A:N1	2:2:220:G:O2'	2.50	0.44
2:2:235:C:H2'	2:2:236:A:H8	1.82	0.44
2:2:509:A:H5'	38:i:52:GLY:HA2	1.99	0.44
2:2:559:A:H4'	2:2:560:A:H3'	1.98	0.44
2:2:570:G:H5'	2:2:820:U:O4'	2.17	0.44
2:2:740:U:H2'	2:2:741:G:H8	1.82	0.44
2:2:1367:C:OP2	43:n:114:LYS:NZ	2.47	0.44
3:3:75:G:N2	25:V:29:ILE:HG21	2.32	0.44
5:5:15:G:H2'	5:5:59:A:N1	2.32	0.44
19:P:68:GLU:OE1	19:P:68:GLU:N	2.50	0.44
41:l:93:PRO:HA	41:l:96:ARG:CD	2.47	0.44
1:1:1071:G:O2'	1:1:1072:C:O4'	2.24	0.44
1:1:1299:G:O6	1:1:1639:C:H5''	2.18	0.44
1:1:1387:A:H2'	1:1:1388:G:C8	2.51	0.44
1:1:2081:U:H3	1:1:2239:G:H1	1.65	0.44
1:1:2728:U:O2'	1:1:2729:G:H8	2.01	0.44
2:2:763:G:H2'	2:2:764:C:C6	2.53	0.44
2:2:1356:G:H2'	2:2:1357:A:H8	1.82	0.44
5:5:59:A:O2'	5:5:60:U:P	2.74	0.44
44:o:6:ILE:HD12	44:o:76:ILE:HD11	1.99	0.44
44:o:85:ASP:O	44:o:89:ARG:HG2	2.18	0.44
47:r:66:GLU:HB2	47:r:70:ARG:HE	1.81	0.44
1:1:58:G:H2'	1:1:59:U:C6	2.52	0.44
1:1:239:C:HO2'	1:1:622:G:HO2'	1.63	0.44
1:1:299:A:OP1	24:U:97:LYS:NZ	2.35	0.44
1:1:632:A:H2'	1:1:633:A:C8	2.52	0.44
1:1:679:C:H2'	1:1:680:C:H6	1.82	0.44
1:1:955:PSU:OP1	16:M:86:LYS:NZ	2.41	0.44
1:1:994:C:OP2	20:Q:54:LYS:NZ	2.36	0.44
1:1:1079:C:H2'	1:1:1080:A:H8	1.81	0.44
1:1:1245:G:O6	1:1:1246:A:N6	2.51	0.44
1:1:1581:G:H2'	1:1:1582:C:C6	2.52	0.44
2:2:318:G:C6	2:2:336:A:C6	3.05	0.44
2:2:750:C:H2'	2:2:751:U:C6	2.52	0.44
21:R:15:SER:H	21:R:18:GLN:NE2	2.11	0.44
42:m:51:VAL:HA	42:m:58:GLU:O	2.17	0.44
43:n:65:ILE:HG21	43:n:79:ILE:HG23	1.99	0.44
49:t:55:GLY:O	49:t:59:MET:HG3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:126:A:H61	33:d:42:LEU:HB3	1.82	0.44
1:1:392:U:H2'	1:1:393:C:C6	2.53	0.44
1:1:593:U:H2'	1:1:594:U:C6	2.52	0.44
1:1:623:C:H2'	1:1:624:C:C6	2.52	0.44
1:1:817:C:O2'	1:1:839:U:H5''	2.17	0.44
1:1:888:C:N4	47:r:92:ARG:HG2	2.32	0.44
1:1:929:U:H1'	29:Z:26:GLY:O	2.16	0.44
1:1:1030:C:O2	35:f:37:GLN:NE2	2.51	0.44
1:1:1310:G:N2	1:1:1313:U:C4	2.85	0.44
1:1:1747:U:H2'	1:1:1748:C:C6	2.52	0.44
1:1:1853:A:N3	1:1:2233:U:O2'	2.43	0.44
2:2:144:G:N1	2:2:179:A:N7	2.66	0.44
2:2:411:A:H1'	2:2:413:G:H5''	2.00	0.44
2:2:458:U:O2	2:2:474:G:N2	2.35	0.44
2:2:777:A:H2'	2:2:778:G:C8	2.53	0.44
2:2:1095:U:H2'	2:2:1096:C:C6	2.52	0.44
3:3:78:A:N6	3:3:98:G:O2'	2.49	0.44
7:B:107:PRO:HD2	7:B:110:LEU:HD22	1.98	0.44
36:g:77:SER:OG	36:g:93:ASN:HB2	2.18	0.44
40:k:81:ASN:HD21	40:k:83:ALA:HB3	1.82	0.44
44:o:14:ASP:HB3	44:o:17:LEU:HB3	2.00	0.44
46:q:81:LEU:HB3	46:q:98:VAL:HG22	2.00	0.44
48:s:49:GLN:NE2	53:x:11:ILE:O	2.46	0.44
1:1:479:A:O2'	1:1:481:G:H5'	2.17	0.44
1:1:623:C:H2'	1:1:624:C:H6	1.82	0.44
1:1:1142:A:C4	1:1:1144:A:N7	2.86	0.44
1:1:1201:U:N3	1:1:1202:G:N7	2.66	0.44
1:1:1837:C:C2	1:1:1904:G:N2	2.85	0.44
1:1:2247:A:H2'	1:1:2248:C:H6	1.82	0.44
1:1:2566:A:N1	14:K:28:SER:OG	2.39	0.44
2:2:1250:A:H2	2:2:1370:G:H1'	1.82	0.44
11:F:175:LYS:HD2	11:F:175:LYS:HA	1.77	0.44
46:q:49:LEU:HD23	46:q:49:LEU:HA	1.50	0.44
1:1:46:G:H2'	1:1:47:C:C6	2.52	0.44
1:1:210:C:H2'	1:1:211:C:C6	2.53	0.44
1:1:418:C:H2'	1:1:419:U:H6	1.83	0.44
1:1:532:A:H2	1:1:2019:A:H2	1.64	0.44
1:1:1039:A:C2	1:1:1116:G:C6	3.04	0.44
1:1:1152:C:H2'	1:1:1153:C:C6	2.52	0.44
1:1:2096:C:H2'	1:1:2097:A:H8	1.83	0.44
1:1:2140:G:H2'	1:1:2141:G:C8	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:176:C:H2'	2:2:177:G:N3	2.33	0.44
2:2:285:C:H2'	2:2:286:C:H6	1.83	0.44
2:2:613:C:H2'	2:2:614:C:H6	1.83	0.44
9:D:176:ASP:OD1	9:D:176:ASP:N	2.50	0.44
21:R:6:GLN:HG3	21:R:11:GLN:HG2	2.00	0.44
21:R:79:ARG:O	21:R:80:ARG:HG2	2.16	0.44
45:p:34:ILE:HG21	45:p:74:VAL:HG21	2.00	0.44
1:1:479:A:H4'	1:1:480:A:H5'	2.00	0.44
1:1:534:U:O2'	20:Q:49:ASP:OD1	2.35	0.44
1:1:594:U:H2'	1:1:595:C:C6	2.53	0.44
1:1:858:G:H1	1:1:920:A:H61	1.66	0.44
1:1:882:G:H1	1:1:894:U:H3	1.65	0.44
1:1:1117:C:H2'	1:1:1118:C:H6	1.83	0.44
1:1:1353:A:C8	1:1:1354:A:N7	2.85	0.44
1:1:1385:A:H1'	1:1:1386:C:C6	2.53	0.44
1:1:1392:A:H61	23:T:18:GLU:HG3	1.83	0.44
2:2:35:G:N3	46:q:115:SER:HB2	2.32	0.44
2:2:102:G:H2'	2:2:103:U:C6	2.52	0.44
2:2:180:U:C2'	2:2:181:A:H5'	2.47	0.44
2:2:222:C:H2'	2:2:223:A:C8	2.48	0.44
2:2:375:U:O2'	50:u:6:LEU:O	2.35	0.44
2:2:604:G:H2'	2:2:605:U:O4'	2.17	0.44
2:2:1042:A:H2'	2:2:1043:G:O4'	2.18	0.44
8:C:152:PRO:HG3	8:C:156:PHE:CZ	2.53	0.44
9:D:146:VAL:HG21	9:D:187:VAL:HG13	1.99	0.44
9:D:149:ILE:HG22	9:D:187:VAL:O	2.18	0.44
17:N:96:ARG:HD3	17:N:98:LEU:HD21	1.98	0.44
22:S:9:HIS:H	22:S:102:HIS:CE1	2.36	0.44
37:h:184:TYR:HE1	37:h:199:LYS:HB3	1.83	0.44
54:y:76:LYS:O	54:y:80:THR:OG1	2.32	0.44
55:z:11:PRO:HB2	55:z:14:VAL:HG22	1.99	0.44
1:1:6:A:H2'	1:1:7:G:H8	1.83	0.44
1:1:259:G:H2'	1:1:260:G:H8	1.83	0.44
1:1:623:C:C2	1:1:624:C:C5	3.06	0.44
1:1:831:G:O2'	15:L:38:GLN:OE1	2.28	0.44
1:1:1600:C:H2'	1:1:1601:G:H8	1.82	0.44
1:1:1635:A:H2'	1:1:1636:U:O4'	2.18	0.44
1:1:1654:A:O2'	8:C:118:PHE:O	2.28	0.44
1:1:1733:G:H2'	1:1:1734:G:H8	1.83	0.44
1:1:2171:A:O2'	1:1:2173:A:OP1	2.32	0.44
2:2:75:G:H2'	2:2:76:G:H8	1.83	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:424:G:H2'	2:2:425:G:H8	1.82	0.44
2:2:1083:U:H3'	2:2:1084:G:C8	2.52	0.44
2:2:1354:U:H2'	2:2:1355:G:H8	1.81	0.44
15:L:132:ARG:O	15:L:136:GLU:HG2	2.18	0.44
42:m:105:SER:HB2	42:m:126:ILE:HD11	1.99	0.44
43:n:56:ASP:N	43:n:56:ASP:OD1	2.48	0.44
43:n:84:THR:HG21	43:n:104:VAL:HA	2.00	0.44
51:v:8:LEU:O	51:v:60:GLU:HA	2.18	0.44
55:z:32:VAL:O	55:z:36:GLU:HG2	2.18	0.44
1:1:895:U:O4	1:1:897:C:N4	2.51	0.44
1:1:979:A:H2'	1:1:982:C:H42	1.82	0.44
1:1:2243:U:H2'	1:1:2244:U:C6	2.52	0.44
1:1:2539:C:H5'	35:f:3:VAL:HG21	2.00	0.44
2:2:254:G:O2'	51:v:18:GLU:O	2.35	0.44
2:2:355:C:H1'	2:2:388:G:H1'	1.99	0.44
2:2:859:G:H2'	2:2:860:A:C8	2.53	0.44
2:2:1140:C:HO2'	2:2:1141:C:H6	1.64	0.44
2:2:1193:G:O6	37:h:3:GLN:NE2	2.51	0.44
2:2:1321:U:O4	53:x:36:ARG:NH1	2.50	0.44
7:B:17:VAL:HB	7:B:204:VAL:HG22	1.99	0.44
16:M:35:ALA:HA	16:M:128:THR:HG22	1.99	0.44
1:1:363:G:H2'	1:1:364:C:C6	2.52	0.43
1:1:499:U:C2	1:1:500:G:C8	3.06	0.43
1:1:577:G:H2'	1:1:578:G:C8	2.53	0.43
1:1:687:C:H5''	33:d:2:LYS:HE2	2.00	0.43
1:1:1201:U:H2'	1:1:1202:G:C8	2.49	0.43
1:1:1351:C:HO2'	1:1:1571:A:HO2'	1.65	0.43
1:1:1853:A:H2'	1:1:1854:A:C8	2.53	0.43
1:1:2417:C:H2'	1:1:2418:A:H8	1.83	0.43
1:1:2425:A:H4'	1:1:2426:A:O5'	2.18	0.43
1:1:2557:G:H2'	1:1:2558:C:H6	1.83	0.43
1:1:2745:C:H2'	1:1:2746:U:C6	2.53	0.43
2:2:323:U:O4	2:2:327:A:N7	2.51	0.43
2:2:563:A:H2'	2:2:567:G:C8	2.53	0.43
2:2:1347:G:N2	2:2:1374:A:OP2	2.40	0.43
2:2:1401:G:O6	2:2:1504:G:N2	2.51	0.43
5:5:19:G:H3'	5:5:20:U:C5	2.49	0.43
5:5:54:U:C2'	5:5:55:U:H5'	2.47	0.43
10:E:108:VAL:HG12	10:E:109:PRO:HD3	1.98	0.43
14:K:8:LEU:HB2	14:K:19:VAL:HG23	2.00	0.43
16:M:39:GLY:HA3	16:M:126:ILE:HD11	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
21:R:2:TYR:CE1	21:R:42:ALA:HB3	2.52	0.43
36:g:73:LYS:C	36:g:75:ALA:H	2.26	0.43
36:g:166:ALA:HB1	36:g:173:ILE:HD13	2.00	0.43
41:l:78:ARG:NH1	58:l:302:HOH:O	2.51	0.43
44:o:41:PRO:HA	44:o:72:ARG:HD3	2.00	0.43
1:1:10:A:H2'	1:1:11:C:O4'	2.18	0.43
1:1:271:G:N1	1:1:367:G:N7	2.66	0.43
1:1:592:A:C2	34:e:4:ILE:HD11	2.53	0.43
1:1:1600:C:H2'	1:1:1601:G:C8	2.52	0.43
1:1:2636:C:H2'	1:1:2637:U:C6	2.52	0.43
2:2:505:G:H2'	2:2:506:G:C8	2.53	0.43
2:2:591:U:P	42:m:31:LYS:HD3	2.58	0.43
2:2:908:A:H2'	2:2:909:A:H8	1.82	0.43
2:2:1268:G:O2'	2:2:1326:U:O2'	2.26	0.43
2:2:1315:U:H2'	2:2:1316:G:O4'	2.18	0.43
3:3:71:C:H2'	3:3:72:G:O4'	2.18	0.43
38:i:119:SER:HA	38:i:131:ASN:O	2.18	0.43
47:r:16:VAL:HA	47:r:30:SER:OG	2.18	0.43
1:1:644:A:C2	1:1:2369:A:H1'	2.53	0.43
1:1:1219:U:H2'	1:1:1220:G:H8	1.83	0.43
1:1:2821:A:OP2	8:C:115:GLY:N	2.31	0.43
2:2:436:C:H2'	2:2:437:U:H6	1.82	0.43
2:2:887:G:H2'	2:2:888:G:O4'	2.18	0.43
2:2:1319:A:O2'	2:2:1323:G:N7	2.45	0.43
2:2:1355:G:H2'	2:2:1356:G:C8	2.53	0.43
3:3:2:G:H2'	3:3:3:C:C6	2.53	0.43
3:3:70:C:H2'	3:3:71:C:C6	2.53	0.43
7:B:154:LEU:HD12	7:B:176:LEU:HD22	2.00	0.43
13:J:55:ILE:HA	13:J:123:LYS:O	2.19	0.43
21:R:27:ILE:HG22	21:R:31:GLU:HB3	1.99	0.43
30:a:56:ARG:HD2	30:a:56:ARG:HA	1.71	0.43
34:e:29:LEU:HD12	34:e:33:LEU:HD21	2.00	0.43
34:e:32:ILE:O	34:e:33:LEU:HG	2.19	0.43
37:h:150:LYS:HB3	37:h:169:ARG:HG3	2.00	0.43
39:j:52:LYS:HB3	39:j:52:LYS:HE3	1.91	0.43
40:k:15:SER:O	40:k:18:VAL:HG12	2.19	0.43
40:k:29:ILE:HD11	40:k:66:ALA:CB	2.47	0.43
46:q:4:VAL:HG23	51:v:34:TYR:HB3	1.99	0.43
1:1:500:G:H1'	1:1:505:A:H61	1.83	0.43
1:1:561:G:O2'	20:Q:45:TYR:OH	2.20	0.43
1:1:1011:G:C6	1:1:1151:A:C6	3.06	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1197:G:C2	1:1:1198:U:C5	3.07	0.43
1:1:1199:U:H2'	1:1:1200:C:C6	2.54	0.43
1:1:1715:G:N2	1:1:1744:A:OP2	2.50	0.43
1:1:2751:G:H5''	1:1:2752:C:H5	1.84	0.43
2:2:647:C:H2'	2:2:648:A:H8	1.82	0.43
2:2:1017:U:O2'	2:2:1018:G:H8	2.01	0.43
3:3:9:G:OP1	18:O:25:ARG:NH2	2.51	0.43
5:5:10:G:H2'	5:5:11:C:C6	2.54	0.43
5:5:61:C:H2'	5:5:62:C:C6	2.54	0.43
8:C:8:LYS:NZ	8:C:195:GLY:O	2.43	0.43
16:M:54:THR:HA	16:M:57:VAL:HG12	2.01	0.43
19:P:62:ARG:HB2	19:P:71:GLU:HG2	2.00	0.43
20:Q:27:ALA:O	20:Q:31:VAL:HG22	2.19	0.43
22:S:83:LYS:HD2	22:S:95:ARG:NH1	2.33	0.43
1:1:138:U:H2'	1:1:140:C:N3	2.34	0.43
1:1:307:G:N2	1:1:309:A:H3'	2.33	0.43
1:1:322:A:H5'	1:1:340:A:H1'	2.00	0.43
1:1:330:A:N7	1:1:1210:G:O2'	2.44	0.43
1:1:681:G:H2'	1:1:682:G:H8	1.83	0.43
1:1:864:G:H2'	1:1:865:C:C6	2.53	0.43
1:1:1501:G:P	7:B:101:ARG:HH22	2.40	0.43
1:1:2033:A:O2'	1:1:2035:G:OP2	2.26	0.43
1:1:2118:U:O4	1:1:2148:G:N2	2.51	0.43
1:1:2134:A:O2'	1:1:2159:G:N3	2.49	0.43
1:1:2461:A:H2'	1:1:2462:C:C6	2.54	0.43
1:1:2557:G:H2'	1:1:2558:C:C6	2.53	0.43
1:1:2837:A:H2'	1:1:2838:G:H8	1.83	0.43
2:2:3:A:H5''	2:2:4:U:O4'	2.19	0.43
2:2:337:G:C2	2:2:338:A:C5	3.06	0.43
2:2:552:U:H2'	2:2:553:A:C8	2.53	0.43
2:2:731:G:H2'	2:2:732:C:C6	2.54	0.43
2:2:1126:U:OP1	44:o:7:ARG:NH2	2.51	0.43
2:2:1313:U:H2'	2:2:1314:C:C6	2.53	0.43
8:C:13:ARG:HD2	8:C:15:PHE:CZ	2.53	0.43
13:J:96:ARG:NH1	13:J:99:ARG:HD3	2.33	0.43
38:i:198:HIS:HA	38:i:201:VAL:HG12	2.00	0.43
47:r:73:ILE:O	47:r:77:ILE:HG13	2.19	0.43
51:v:27:ARG:N	51:v:40:ARG:O	2.41	0.43
52:w:11:CYS:SG	52:w:14:THR:HG23	2.58	0.43
1:1:20:C:H2'	1:1:21:A:C8	2.52	0.43
1:1:438:G:H2'	1:1:439:A:C8	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:820:A:H2	1:1:943:A:H4'	1.84	0.43
1:1:1030:C:N4	1:1:1124:G:O6	2.52	0.43
1:1:1365:A:P	27:X:28:ARG:HH22	2.41	0.43
1:1:1541:C:H2'	1:1:1542:U:C6	2.53	0.43
1:1:1727:C:N3	1:1:1734:G:N1	2.66	0.43
1:1:1825:U:H2'	1:1:1826:G:C8	2.53	0.43
1:1:1910:G:C2	1:1:1921:G:C2	3.07	0.43
1:1:2284:A:O2'	1:1:2288:A:N6	2.52	0.43
1:1:2537:U:H2'	1:1:2538:C:C6	2.53	0.43
2:2:102:G:H2'	2:2:103:U:H6	1.84	0.43
2:2:953:G:C6	2:2:1229:A:C6	3.07	0.43
2:2:1135:U:O2'	2:2:1136:C:O2	2.22	0.43
10:E:101:GLU:O	10:E:105:THR:HG22	2.18	0.43
11:F:39:ASP:OD1	11:F:58:TYR:OH	2.20	0.43
14:K:75:SER:HB2	19:P:73:VAL:O	2.19	0.43
15:L:79:LEU:HG	15:L:111:ILE:O	2.18	0.43
17:N:35:LYS:HB3	17:N:35:LYS:HE2	1.74	0.43
29:Z:45:ARG:HD3	29:Z:45:ARG:HA	1.85	0.43
34:e:31:HIS:CD2	34:e:32:ILE:HG22	2.53	0.43
35:f:18:LYS:HB2	35:f:18:LYS:HE3	1.83	0.43
37:h:91:VAL:HA	37:h:94:ILE:HG12	1.99	0.43
47:r:43:VAL:HG21	47:r:48:LEU:HD21	2.01	0.43
55:z:10:GLU:OE1	55:z:14:VAL:HG23	2.18	0.43
1:1:275:C:H3'	1:1:276:U:H5''	2.01	0.43
1:1:290:U:H3	1:1:350:G:H1	1.67	0.43
1:1:910:A:H62	16:M:13:HIS:N	2.17	0.43
1:1:1219:U:H2'	1:1:1220:G:C8	2.53	0.43
1:1:2685:G:H2'	1:1:2686:G:H8	1.84	0.43
2:2:158:G:H2'	2:2:159:G:O4'	2.18	0.43
2:2:236:A:H2'	2:2:237:G:C8	2.54	0.43
2:2:376:G:H5''	50:u:5:ARG:HB2	2.00	0.43
6:A:201:PRO:HG2	6:A:204:ALA:HB2	2.01	0.43
24:U:38:GLY:HA2	24:U:41:LEU:HD21	2.00	0.43
1:1:24:G:H2'	1:1:25:U:C6	2.53	0.43
1:1:172:A:H2'	1:1:173:A:C8	2.53	0.43
1:1:192:C:O2'	1:1:802:A:N3	2.45	0.43
1:1:577:G:O2'	1:1:1254:A:OP1	2.37	0.43
1:1:624:C:H2'	1:1:625:G:C8	2.54	0.43
1:1:888:C:H2'	1:1:889:C:C6	2.54	0.43
1:1:976:G:O2'	1:1:1155:A:O2'	2.18	0.43
1:1:1352:U:H1'	1:1:1570:A:H2	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1754:A:N1	1:1:2716:C:O2'	2.52	0.43
1:1:1907:G:O6	1:1:1924:C:N4	2.52	0.43
1:1:2588:G:C6	1:1:2607:G:C2	3.07	0.43
2:2:195:A:H1'	2:2:222:C:O2'	2.18	0.43
2:2:470:C:H2'	2:2:471:U:C6	2.54	0.43
2:2:838:G:C6	2:2:849:G:C6	3.07	0.43
2:2:1391:U:H2'	2:2:1392:G:H8	1.82	0.43
2:2:1476:A:H2'	2:2:1477:U:C6	2.53	0.43
2:2:1488:G:H2'	2:2:1489:G:C8	2.54	0.43
20:Q:61:TRP:CH2	20:Q:93:LYS:HB2	2.54	0.43
20:Q:89:GLU:O	21:R:11:GLN:NE2	2.40	0.43
27:X:17:ASN:OD1	27:X:27:ARG:HD2	2.19	0.43
32:c:15:ALA:HB2	32:c:47:VAL:HG21	2.01	0.43
37:h:6:HIS:CD2	48:s:89:MET:HB3	2.54	0.43
40:k:49:TYR:O	40:k:51:ILE:HD12	2.19	0.43
42:m:10:MET:HE1	42:m:33:LYS:HA	2.01	0.43
1:1:156:A:H2'	1:1:157:C:C6	2.54	0.43
1:1:705:A:H4'	7:B:7:LYS:HD2	2.00	0.43
1:1:1353:A:H2'	1:1:1354:A:C8	2.54	0.43
1:1:1645:G:H5''	1:1:1646:C:O4'	2.19	0.43
1:1:1656:C:H2'	1:1:1657:U:H6	1.84	0.43
1:1:1668:A:N1	1:1:1676:A:N6	2.67	0.43
1:1:1882:U:H2'	1:1:1883:U:C6	2.53	0.43
1:1:2002:G:OP2	17:N:9:GLN:NE2	2.52	0.43
1:1:2441:U:OP2	1:1:2586:U:O2'	2.34	0.43
1:1:2780:G:N1	13:J:102:GLU:OE2	2.44	0.43
1:1:2845:U:H2'	1:1:2846:G:H8	1.84	0.43
5:5:10:G:N2	5:5:26:A:H1'	2.34	0.43
16:M:40:ARG:HB2	16:M:93:VAL:CG2	2.49	0.43
22:S:17:VAL:HA	22:S:43:ALA:HB1	2.00	0.43
32:c:15:ALA:HB2	32:c:47:VAL:HG11	2.01	0.43
33:d:46:LYS:HE2	33:d:46:LYS:HB2	1.89	0.43
1:1:177:G:H3'	1:1:178:G:H8	1.84	0.43
1:1:581:C:P	20:Q:33:ARG:HG3	2.59	0.43
1:1:679:C:H2'	1:1:680:C:C6	2.53	0.43
1:1:926:G:H2'	1:1:927:A:C8	2.52	0.43
1:1:1043:C:H2'	1:1:1044:C:O4'	2.19	0.43
1:1:1209:U:H2'	1:1:1210:G:H21	1.83	0.43
1:1:1339:G:OP1	23:T:82:LYS:NZ	2.48	0.43
1:1:2485:G:H5''	16:M:45:GLN:NE2	2.34	0.43
1:1:2723:C:OP1	8:C:114:LYS:NZ	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:45:G:H2'	2:2:46:G:H8	1.84	0.43
11:F:9:VAL:HG11	11:F:73:ASN:HB2	2.00	0.43
16:M:5:LYS:NZ	58:M:301:HOH:O	2.51	0.43
39:j:37:THR:HG22	39:j:63:ALA:HB1	2.01	0.43
1:1:274:C:N4	1:1:363:G:O6	2.52	0.42
1:1:573:U:O2'	1:1:575:A:OP1	2.28	0.42
1:1:666:A:H2'	1:1:667:U:C6	2.54	0.42
1:1:825:A:H2'	1:1:826:U:O4'	2.19	0.42
1:1:872:U:H2'	1:1:873:C:C6	2.54	0.42
1:1:954:G:O3'	16:M:13:HIS:ND1	2.52	0.42
1:1:1707:G:C8	1:1:1756:G:C5	3.07	0.42
1:1:1821:A:H2'	1:1:1822:C:C6	2.54	0.42
1:1:1996:C:P	14:K:31:ARG:HH21	2.41	0.42
1:1:2399:G:C6	1:1:2418:A:C6	3.07	0.42
1:1:2399:G:O6	1:1:2418:A:N6	2.52	0.42
1:1:2552:OMU:O5'	1:1:2552:OMU:H6	2.19	0.42
1:1:2559:C:H2'	1:1:2560:A:H8	1.84	0.42
1:1:2716:C:H2'	1:1:2717:C:C6	2.54	0.42
2:2:34:C:H2'	2:2:35:G:C8	2.51	0.42
2:2:216:U:H2'	2:2:217:C:H6	1.83	0.42
2:2:676:A:H2'	2:2:677:U:C6	2.53	0.42
2:2:736:C:H2'	2:2:737:C:C6	2.53	0.42
2:2:922:G:H2'	2:2:923:A:C8	2.53	0.42
2:2:1250:A:H4'	43:n:69:GLY:HA2	2.01	0.42
2:2:1258:G:H2'	2:2:1259:C:C6	2.54	0.42
2:2:1313:U:H2'	2:2:1314:C:H6	1.83	0.42
36:g:66:LYS:N	36:g:159:ASP:OD2	2.39	0.42
38:i:167:LYS:HE2	38:i:167:LYS:HB2	1.91	0.42
44:o:28:THR:HG21	44:o:90:LEU:HD22	2.02	0.42
1:1:48:G:H22	1:1:177:G:P	2.41	0.42
1:1:102:U:C4	28:Y:4:LYS:HE2	2.54	0.42
1:1:225:C:H2'	1:1:226:A:O4'	2.19	0.42
1:1:592:A:H2	34:e:4:ILE:HD11	1.83	0.42
1:1:1266:G:O2'	1:1:2012:G:O6	2.36	0.42
1:1:1447:C:O2'	1:1:1544:A:N3	2.47	0.42
1:1:1663:G:O6	1:1:1998:A:N6	2.52	0.42
1:1:1914:C:H2'	1:1:1915:U:C6	2.54	0.42
2:2:285:C:H2'	2:2:286:C:C6	2.54	0.42
2:2:313:A:H2'	2:2:314:C:C6	2.54	0.42
2:2:389:A:H3'	2:2:390:U:H6	1.84	0.42
2:2:507:C:OP2	2:2:508:U:O2'	2.24	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1236:A:H2'	2:2:1237:C:C6	2.53	0.42
2:2:1326:U:H2'	2:2:1327:C:C6	2.54	0.42
6:A:175:ILE:HD12	6:A:189:LEU:HG	2.02	0.42
9:D:130:LYS:HA	9:D:130:LYS:HD2	1.89	0.42
9:D:193:VAL:O	9:D:197:GLU:HG3	2.19	0.42
30:a:37:CYS:N	30:a:40:CYS:SG	2.83	0.42
30:a:64:PHE:HE1	30:a:66:ILE:HD13	1.84	0.42
36:g:12:ALA:HA	36:g:208:ARG:HE	1.84	0.42
41:l:131:LYS:HA	41:l:131:LYS:HD2	1.80	0.42
43:n:43:THR:O	43:n:46:MET:HG2	2.18	0.42
46:q:116:LYS:HE3	46:q:116:LYS:HB3	1.87	0.42
48:s:47:LYS:O	48:s:50:THR:OG1	2.35	0.42
1:1:1297:C:OP1	1:1:2710:C:H4'	2.19	0.42
1:1:1469:A:H2'	1:1:1470:A:C8	2.52	0.42
1:1:1518:C:H2'	1:1:1519:G:C8	2.54	0.42
1:1:2230:G:H2'	1:1:2231:U:C6	2.54	0.42
1:1:2820:A:N1	8:C:197:THR:HB	2.35	0.42
2:2:186:C:H2'	2:2:187:G:O4'	2.20	0.42
2:2:438:U:O2'	2:2:439:U:OP2	2.36	0.42
4:4:15:C:H2'	4:4:16:C:C6	2.53	0.42
5:5:3:G:C8	5:5:4:C:C5	3.07	0.42
9:D:196:VAL:HA	9:D:199:MET:HG2	2.00	0.42
12:G:101:ASP:OD1	12:G:102:ALA:N	2.53	0.42
16:M:38:ARG:HB2	16:M:98:PRO:HD3	2.01	0.42
28:Y:56:LEU:HD23	28:Y:56:LEU:HA	1.85	0.42
34:e:52:LYS:HA	34:e:55:LEU:HD12	2.02	0.42
37:h:5:VAL:HG11	37:h:10:ILE:HD12	2.01	0.42
37:h:71:ALA:HB1	37:h:109:PRO:HB3	2.00	0.42
39:j:156:LYS:HD2	42:m:71:VAL:HA	2.01	0.42
43:n:115:LYS:HB2	43:n:118:LEU:HD12	2.00	0.42
49:t:70:LEU:HD12	49:t:70:LEU:HA	1.85	0.42
51:v:22:VAL:HG12	51:v:45:HIS:CD2	2.55	0.42
1:1:84:A:N6	1:1:101:A:H8	2.17	0.42
1:1:438:G:H2'	1:1:439:A:H8	1.84	0.42
1:1:1105:U:H2'	1:1:1106:G:C8	2.54	0.42
1:1:1174:U:H4'	1:1:1177:G:N1	2.34	0.42
1:1:1901:A:OP2	7:B:253:LYS:NZ	2.36	0.42
1:1:2538:C:H2'	1:1:2539:C:H6	1.84	0.42
2:2:21:G:H5'	2:2:573:A:H61	1.83	0.42
2:2:212:G:C4	2:2:213:G:C8	3.07	0.42
2:2:306:A:N6	58:2:1864:HOH:O	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:859:G:H2'	2:2:860:A:H8	1.84	0.42
2:2:958:A:N1	53:x:55:ARG:N	2.68	0.42
2:2:1115:U:H2'	2:2:1116:U:C6	2.54	0.42
2:2:1121:U:H2'	2:2:1122:U:C6	2.55	0.42
22:S:76:VAL:HG22	22:S:103:ILE:HG23	2.01	0.42
38:i:76:TYR:HA	38:i:90:LEU:HD12	2.00	0.42
40:k:25:TYR:CZ	40:k:78:PHE:HE1	2.36	0.42
41:l:40:GLU:O	41:l:44:TYR:HD2	2.02	0.42
1:1:61:C:H5'	58:Y:102:HOH:O	2.20	0.42
1:1:784:G:H5'	1:1:785:G:OP1	2.19	0.42
1:1:1047:G:H21	1:1:1111:A:N6	2.09	0.42
1:1:1204:A:O4'	1:1:1206:G:C8	2.72	0.42
1:1:1658:C:OP1	8:C:140:HIS:NE2	2.42	0.42
1:1:2070:A:H2'	1:1:2071:A:H8	1.84	0.42
1:1:2078:C:H2'	1:1:2079:U:C6	2.54	0.42
1:1:2188:U:C4	1:1:2189:U:C4	3.07	0.42
1:1:2373:G:H2'	1:1:2374:C:C6	2.54	0.42
1:1:2626:C:H2'	1:1:2627:G:C8	2.54	0.42
1:1:2636:C:H2'	1:1:2637:U:H6	1.83	0.42
2:2:851:G:C2	2:2:852:G:C8	3.06	0.42
3:3:63:C:H2'	3:3:64:G:H8	1.84	0.42
3:3:113:C:O2'	18:O:46:GLU:OE2	2.34	0.42
9:D:134:LEU:O	9:D:138:LEU:HD23	2.20	0.42
11:F:24:ILE:HG12	11:F:37:LEU:HD13	2.02	0.42
11:F:46:ALA:O	11:F:48:ASN:N	2.51	0.42
18:O:12:THR:O	18:O:16:ARG:HG2	2.20	0.42
31:b:11:SER:O	31:b:15:MET:HB2	2.19	0.42
46:q:32:GLY:O	46:q:79:VAL:HA	2.19	0.42
47:r:29:ARG:O	47:r:33:ILE:HG12	2.18	0.42
50:u:52:LEU:HD23	50:u:52:LEU:HA	1.94	0.42
54:y:19:LYS:HB2	54:y:19:LYS:HE2	1.86	0.42
1:1:67:U:C2	1:1:68:G:C8	3.08	0.42
1:1:238:C:H1'	1:1:608:A:C2	2.54	0.42
1:1:477:A:H3'	58:1:3309:HOH:O	2.20	0.42
1:1:488:G:N2	1:1:492:A:N7	2.68	0.42
1:1:987:C:O2'	1:1:1000:A:N3	2.41	0.42
1:1:1026:G:OP1	1:1:1134:A:O2'	2.34	0.42
1:1:1060:U:H4'	1:1:1061:U:H2'	2.02	0.42
1:1:1164:C:H2'	1:1:1165:A:H8	1.85	0.42
1:1:1996:C:OP2	14:K:31:ARG:NH2	2.50	0.42
1:1:2411:A:H2'	1:1:2412:A:H8	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2420:C:OP2	34:e:33:LEU:HB2	2.19	0.42
1:1:2507:C:C2	1:1:2508:G:C8	3.08	0.42
1:1:2628:C:O2'	1:1:2782:G:OP1	2.27	0.42
2:2:837:U:H2'	2:2:838:G:H8	1.85	0.42
2:2:958:A:C2	53:x:55:ARG:HG3	2.55	0.42
2:2:971:G:P	2:2:1231:G:H21	2.41	0.42
2:2:1297:G:O2'	41:l:114:LYS:NZ	2.29	0.42
7:B:43:ARG:NH2	7:B:49:ILE:HD11	2.34	0.42
10:E:115:ARG:HH22	30:a:47:LYS:HA	1.84	0.42
11:F:83:PHE:CE2	11:F:138:LYS:HB2	2.54	0.42
13:J:117:ALA:HA	13:J:120:ARG:HD2	2.01	0.42
37:h:164:ARG:NH2	37:h:166:GLU:OE2	2.50	0.42
39:j:80:THR:OG1	39:j:122:ASN:O	2.24	0.42
1:1:125:A:OP2	33:d:19:ARG:HD3	2.20	0.42
1:1:224:U:O4	1:1:419:U:O2'	2.37	0.42
1:1:930:G:H1'	29:Z:25:LEU:HD21	2.00	0.42
1:1:947:A:H2'	1:1:948:C:H6	1.83	0.42
1:1:1201:U:C2	1:1:1202:G:N7	2.88	0.42
1:1:1286:A:N6	1:1:1329:U:O2	2.52	0.42
1:1:1380:G:H2'	1:1:1381:G:H8	1.85	0.42
1:1:1441:G:H2'	1:1:1442:U:H6	1.84	0.42
1:1:1476:U:H2'	1:1:1477:A:C8	2.54	0.42
1:1:1486:U:H2'	1:1:1487:U:C6	2.54	0.42
1:1:1637:A:H5'	1:1:1760:C:O2'	2.20	0.42
1:1:1867:G:H2'	1:1:1868:C:C6	2.54	0.42
1:1:2618:G:H2'	1:1:2619:C:C6	2.54	0.42
1:1:2899:A:C2	1:1:2900:A:C5	3.07	0.42
2:2:33:A:H2'	2:2:34:C:H6	1.85	0.42
2:2:35:G:H2'	2:2:36:C:H6	1.85	0.42
2:2:317:U:N3	2:2:318:G:N7	2.68	0.42
2:2:514:C:C2	2:2:515:G:N7	2.87	0.42
2:2:553:A:H2'	2:2:554:A:C8	2.55	0.42
2:2:598:U:H2'	2:2:599:C:C6	2.55	0.42
2:2:647:C:H2'	2:2:648:A:C8	2.54	0.42
2:2:739:C:HO2'	49:t:42:HIS:CE1	2.37	0.42
2:2:779:C:H4'	45:p:124:PRO:HA	2.02	0.42
2:2:1402:4OC:H2'	2:2:1403:C:O4'	2.19	0.42
5:5:1:C:H6	5:5:1:C:P	2.43	0.42
5:5:63:U:H2'	5:5:64:C:H6	1.84	0.42
5:5:67:G:C4'	58:5:206:HOH:O	2.68	0.42
6:A:168:ASN:O	6:A:168:ASN:ND2	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:45:ASN:OD1	7:B:46:ASN:N	2.53	0.42
8:C:47:ALA:HB2	8:C:83:ARG:HD2	2.00	0.42
11:F:19:ILE:HD12	11:F:24:ILE:HD12	2.01	0.42
13:J:109:LEU:HD23	13:J:109:LEU:HA	1.87	0.42
14:K:103:VAL:O	14:K:122:VAL:HA	2.19	0.42
37:h:43:LEU:O	37:h:47:LEU:HG	2.18	0.42
49:t:32:LEU:O	49:t:36:ILE:HG12	2.20	0.42
1:1:498:G:C6	1:1:499:U:C2	3.08	0.42
1:1:983:A:N6	1:1:984:A:H62	2.18	0.42
1:1:1282:U:H3	1:1:1286:A:H62	1.67	0.42
1:1:1297:C:H2'	1:1:1298:C:H6	1.85	0.42
1:1:1321:A:C4	1:1:1322:A:C8	3.07	0.42
1:1:1387:A:C6	1:1:1401:G:N1	2.88	0.42
1:1:1562:U:H2'	1:1:1563:U:C6	2.55	0.42
1:1:1805:A:H2'	1:1:1806:C:C6	2.55	0.42
1:1:2168:G:H2'	1:1:2169:A:C8	2.54	0.42
1:1:2225:A:H4'	1:1:2226:C:H6	1.83	0.42
1:1:2231:U:H2'	1:1:2232:C:C6	2.55	0.42
1:1:2250:G:H5'	1:1:2250:G:N3	2.33	0.42
2:2:56:U:H2'	2:2:57:G:C8	2.55	0.42
2:2:412:A:H62	2:2:431:A:H61	1.66	0.42
2:2:708:C:H2'	2:2:709:U:C6	2.54	0.42
2:2:891:U:H2'	2:2:892:A:H8	1.85	0.42
2:2:1415:G:H2'	2:2:1416:G:H8	1.85	0.42
3:3:51:G:H3'	18:O:64:TYR:CE1	2.54	0.42
7:B:171:TYR:HD2	7:B:183:LYS:HB3	1.84	0.42
36:g:141:LEU:O	36:g:145:GLU:HG2	2.19	0.42
39:j:160:SER:O	39:j:163:GLU:HG2	2.19	0.42
40:k:12:PRO:HG3	40:k:54:LEU:HD11	2.02	0.42
41:l:102:ARG:HA	41:l:105:VAL:HG12	2.02	0.42
45:p:61:PHE:O	45:p:64:GLN:HG3	2.19	0.42
47:r:45:ILE:O	47:r:45:ILE:HG22	2.19	0.42
52:w:32:TYR:O	52:w:40:VAL:HG12	2.19	0.42
1:1:1095:A:HO2'	1:1:1096:A:H8	1.66	0.42
1:1:1182:G:H2'	1:1:1183:U:O4'	2.20	0.42
1:1:1268:A:H2'	1:1:1269:A:O4'	2.20	0.42
1:1:1548:A:H2'	1:1:1549:A:H8	1.84	0.42
1:1:1672:A:C2	1:1:2582:G:H5'	2.55	0.42
1:1:1904:G:H2'	1:1:1905:C:O4'	2.19	0.42
2:2:673:A:H4'	40:k:86:ARG:HH11	1.85	0.42
2:2:684:U:O2	45:p:41:ALA:HB3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1070:U:H2'	2:2:1071:C:C6	2.55	0.42
2:2:1152:A:H4'	44:o:19:ASP:OD2	2.20	0.42
3:3:33:G:H2'	3:3:34:A:O4'	2.19	0.42
7:B:129:THR:OG1	7:B:191:THR:HG22	2.19	0.42
17:N:103:ARG:HD3	17:N:106:ASP:HB3	2.02	0.42
38:i:67:VAL:HG21	38:i:72:PHE:HD2	1.85	0.42
54:y:33:LYS:HE3	54:y:33:LYS:HB2	1.89	0.42
1:1:409:G:H2'	1:1:410:G:C8	2.55	0.42
1:1:720:U:H2'	1:1:721:A:C8	2.54	0.42
1:1:835:C:H2'	1:1:836:G:H8	1.84	0.42
1:1:885:C:H2'	1:1:886:A:C8	2.55	0.42
1:1:947:A:C6	1:1:971:G:N1	2.88	0.42
1:1:1422:G:C6	1:1:1577:C:N3	2.88	0.42
1:1:1592:C:H2'	1:1:1593:A:C8	2.55	0.42
1:1:1687:G:N2	1:1:1702:G:C6	2.88	0.42
1:1:1996:C:H5	14:K:32:TYR:OH	2.03	0.42
1:1:2014:A:H2'	1:1:2015:A:C8	2.55	0.42
1:1:2742:G:OP1	35:f:24:ARG:NH1	2.52	0.42
1:1:2818:U:H2'	1:1:2819:G:C8	2.55	0.42
2:2:50:A:O2'	2:2:360:G:N2	2.51	0.42
2:2:202:G:O2'	2:2:468:A:H8	2.03	0.42
2:2:598:U:H2'	2:2:599:C:H6	1.84	0.42
2:2:932:C:H5''	41:l:4:ARG:CD	2.49	0.42
6:A:164:ARG:HA	6:A:164:ARG:HD3	1.92	0.42
9:D:24:ASN:HB3	9:D:27:LEU:HG	2.02	0.42
10:E:95:ARG:O	10:E:98:GLU:HG3	2.20	0.42
14:K:18:ARG:HB2	14:K:45:GLU:HG2	2.02	0.42
32:c:9:ILE:HD12	32:c:51:GLU:HB2	2.01	0.42
37:h:129:MET:HA	37:h:129:MET:HE3	2.01	0.42
37:h:135:LYS:HD2	37:h:135:LYS:HA	1.87	0.42
38:i:9:LEU:HD13	38:i:32:CYS:SG	2.59	0.42
39:j:56:VAL:O	39:j:60:ILE:HG12	2.19	0.42
39:j:85:VAL:HG11	39:j:147:MET:HB3	2.02	0.42
46:q:24:LEU:O	46:q:27:CYS:HB3	2.20	0.42
55:z:5:LYS:HE2	55:z:5:LYS:HB2	1.88	0.42
1:1:289:G:H2'	1:1:290:U:H6	1.84	0.41
1:1:596:U:H2'	1:1:597:G:H8	1.84	0.41
1:1:700:G:O2'	1:1:1632:A:N3	2.35	0.41
1:1:764:A:O2'	1:1:765:C:H5'	2.20	0.41
1:1:969:G:H2'	1:1:970:U:C6	2.55	0.41
1:1:1298:C:C2	1:1:1643:G:N2	2.88	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1351:C:O2'	1:1:1571:A:O2'	2.31	0.41
1:1:1405:U:H2'	1:1:1406:U:C6	2.54	0.41
1:1:1442:U:H2'	1:1:1443:U:C6	2.55	0.41
1:1:1651:G:H2'	1:1:1652:A:H8	1.85	0.41
1:1:1710:G:C6	1:1:1749:A:C6	3.08	0.41
1:1:2164:C:H3'	1:1:2165:C:H6	1.85	0.41
1:1:2247:A:H2'	1:1:2248:C:C6	2.55	0.41
1:1:2304:G:H4'	10:E:130:MET:HA	2.01	0.41
1:1:2519:U:H5'	1:1:2567:G:H21	1.85	0.41
2:2:193:C:H2'	2:2:194:C:C6	2.55	0.41
2:2:323:U:H3	2:2:327:A:H62	1.68	0.41
2:2:958:A:H1'	2:2:985:C:O2'	2.19	0.41
2:2:1530:G:H2'	2:2:1531:A:H8	1.84	0.41
11:F:109:PHE:CZ	11:F:152:ARG:HD3	2.55	0.41
39:j:16:ILE:HD13	39:j:36:LEU:HG	2.01	0.41
39:j:96:MET:HE1	39:j:144:LEU:HG	2.01	0.41
46:q:89:0TD:H8	46:q:89:0TD:H4	1.75	0.41
1:1:117:G:OP2	1:1:119:A:O2'	2.21	0.41
1:1:682:G:H5'	33:d:26:ASN:CG	2.45	0.41
1:1:792:A:N3	1:1:2072:C:O2'	2.49	0.41
1:1:1276:A:N6	1:1:1645:G:O6	2.53	0.41
1:1:1590:A:H2'	1:1:1591:A:C8	2.54	0.41
1:1:1748:C:H2'	1:1:1749:A:H8	1.86	0.41
1:1:2140:G:O6	1:1:2151:U:C4	2.73	0.41
1:1:2322:A:H2'	1:1:2323:G:C8	2.55	0.41
1:1:2365:G:H4'	26:W:60:PHE:CE1	2.54	0.41
1:1:2547:A:H2'	1:1:2548:U:H6	1.84	0.41
1:1:2669:G:H2'	1:1:2670:A:H8	1.86	0.41
2:2:35:G:H2'	2:2:36:C:C6	2.55	0.41
2:2:214:C:C2	2:2:215:C:C5	3.07	0.41
2:2:765:G:N1	2:2:812:G:O2'	2.41	0.41
2:2:1287:A:N3	2:2:1353:G:O2'	2.39	0.41
2:2:1401:G:H2'	2:2:1402:4OC:O4'	2.18	0.41
2:2:1477:U:H2'	2:2:1478:U:C6	2.55	0.41
2:2:1527:U:H2'	2:2:1528:U:C6	2.55	0.41
16:M:51:ARG:HD2	16:M:55:ARG:HH22	1.85	0.41
23:T:50:LEU:HD11	28:Y:26:PHE:CE2	2.55	0.41
40:k:102:MET:HE3	52:w:24:LYS:HB3	2.00	0.41
42:m:29:SER:OG	42:m:57:PRO:HB2	2.20	0.41
1:1:624:C:H2'	1:1:625:G:H8	1.86	0.41
1:1:2149:U:H2'	1:1:2150:C:C6	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2813:A:C4	1:1:2814:A:C8	3.08	0.41
1:1:2859:G:H2'	1:1:2860:A:C8	2.55	0.41
2:2:1412:C:H2'	2:2:1413:A:H8	1.83	0.41
7:B:89:ALA:HB2	7:B:158:ALA:HA	2.01	0.41
11:F:26:ILE:HG23	11:F:33:LEU:HB2	2.03	0.41
18:O:7:ARG:HD2	18:O:97:PHE:CE1	2.55	0.41
28:Y:53:VAL:O	28:Y:57:LEU:HD23	2.20	0.41
42:m:64:LYS:HB3	42:m:71:VAL:HG21	2.02	0.41
46:q:7:LEU:HD22	46:q:12:ARG:HD3	2.03	0.41
53:x:29:LYS:HD2	53:x:30:PRO:HD2	2.02	0.41
1:1:85:G:C6	1:1:98:G:N1	2.88	0.41
1:1:686:U:H5''	33:d:11:LYS:NZ	2.34	0.41
1:1:783:A:H8	1:1:1778:U:O2'	2.04	0.41
1:1:826:U:H2'	1:1:828:U:O4'	2.20	0.41
1:1:1464:G:H2'	1:1:1465:G:C8	2.56	0.41
1:1:1537:G:C2	1:1:1538:G:C8	3.09	0.41
1:1:1679:A:H2'	1:1:1680:U:H6	1.86	0.41
1:1:2110:G:OP2	1:1:2110:G:H8	2.02	0.41
1:1:2622:U:O2'	1:1:2825:G:N7	2.52	0.41
58:1:3335:HOH:O	8:C:58:ASN:ND2	2.52	0.41
2:2:959:A:O2'	2:2:984:C:O2'	2.25	0.41
15:L:37:GLY:N	15:L:40:SER:OG	2.52	0.41
26:W:72:LYS:HE2	26:W:79:PHE:CG	2.55	0.41
42:m:92:LEU:HD23	42:m:92:LEU:HA	1.93	0.41
43:n:6:TYR:CD2	43:n:90:TYR:HA	2.55	0.41
51:v:79:VAL:HB	51:v:80:GLU:OE2	2.20	0.41
53:x:4:SER:OG	53:x:6:LYS:HG2	2.21	0.41
53:x:5:LEU:HD23	53:x:5:LEU:H	1.86	0.41
1:1:258:G:H2'	1:1:259:G:H8	1.86	0.41
1:1:605:G:H2'	1:1:606:U:O4'	2.20	0.41
1:1:883:G:N2	1:1:884:U:H5	2.19	0.41
1:1:902:C:H2'	1:1:903:C:C6	2.55	0.41
1:1:1076:C:H2'	1:1:1077:A:C8	2.56	0.41
1:1:1437:C:H2'	1:1:1438:U:C6	2.55	0.41
1:1:1570:A:H2'	1:1:1571:A:C8	2.56	0.41
1:1:1750:G:H2'	1:1:1751:U:H6	1.84	0.41
1:1:2305:U:H2'	1:1:2306:C:C6	2.54	0.41
2:2:20:U:H2'	2:2:21:G:O4'	2.19	0.41
2:2:1308:U:H2'	2:2:1309:G:C8	2.55	0.41
5:5:14:A:C2	5:5:22:G:H1'	2.55	0.41
8:C:88:GLU:HB3	8:C:90:PHE:HE1	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:C:110:THR:HG22	8:C:171:THR:HG23	2.02	0.41
10:E:34:ILE:HG12	10:E:156:ILE:HG13	2.02	0.41
12:G:125:THR:HA	12:G:146:VAL:HG21	2.03	0.41
14:K:63:VAL:HG12	14:K:107:LEU:HD11	2.02	0.41
16:M:77:PRO:O	16:M:80:VAL:HG12	2.20	0.41
21:R:79:ARG:O	21:R:81:LYS:HG2	2.21	0.41
22:S:17:VAL:HG11	22:S:103:ILE:HG12	2.02	0.41
24:U:83:VAL:CG2	24:U:94:ARG:HB3	2.51	0.41
36:g:93:ASN:OD1	36:g:93:ASN:N	2.51	0.41
41:l:15:ASP:OD1	41:l:15:ASP:N	2.52	0.41
50:u:15:PRO:HG2	50:u:41:PRO:HG2	2.02	0.41
50:u:42:ILE:O	50:u:42:ILE:HG23	2.19	0.41
1:1:29:U:H2'	1:1:30:G:H8	1.85	0.41
1:1:78:U:H2'	1:1:79:C:H6	1.86	0.41
1:1:121:G:H2'	1:1:122:G:C8	2.55	0.41
1:1:249:C:O5'	1:1:2394:C:O2'	2.39	0.41
1:1:272:A:H2'	1:1:273:G:C8	2.55	0.41
1:1:1203:U:O2	1:1:1241:A:N6	2.53	0.41
1:1:1283:G:H22	1:1:1286:A:P	2.43	0.41
1:1:1436:G:H2'	1:1:1437:C:O4'	2.21	0.41
1:1:1649:G:H2'	1:1:1650:A:C8	2.56	0.41
1:1:1744:A:H3'	1:1:1745:A:H8	1.85	0.41
1:1:1874:C:H2'	1:1:1875:G:O4'	2.21	0.41
1:1:2466:C:H2'	1:1:2467:C:H6	1.86	0.41
2:2:592:G:H2'	2:2:593:U:C6	2.56	0.41
2:2:763:G:H2'	2:2:764:C:H6	1.86	0.41
2:2:1160:G:C6	2:2:1161:C:C4	3.08	0.41
2:2:1376:U:H2'	2:2:1377:A:C8	2.56	0.41
5:5:44:G:H2'	5:5:45:G:C8	2.55	0.41
9:D:148:ILE:HD13	9:D:187:VAL:HG21	2.03	0.41
10:E:116:GLY:O	10:E:178:ARG:NH2	2.53	0.41
14:K:23:LYS:HD3	14:K:23:LYS:HA	1.96	0.41
29:Z:58:GLU:O	58:Z:101:HOH:O	2.21	0.41
36:g:114:LEU:HD23	36:g:118:GLU:OE2	2.20	0.41
44:o:9:ARG:NH1	44:o:71:LEU:HD21	2.34	0.41
1:1:18:U:H2'	1:1:19:A:C8	2.55	0.41
1:1:84:A:H4'	1:1:85:G:H5'	2.03	0.41
1:1:500:G:H2'	1:1:502:A:N7	2.35	0.41
1:1:672:C:H2'	1:1:673:C:C6	2.55	0.41
1:1:739:A:H1'	1:1:740:C:H5	1.85	0.41
1:1:983:A:H62	1:1:984:A:H62	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:1130:U:C2	8:C:152:PRO:HB3	2.56	0.41
1:1:1183:U:H2'	1:1:1184:U:C6	2.56	0.41
1:1:1993:U:H4'	8:C:133:THR:CG2	2.51	0.41
1:1:2730:C:O3'	8:C:174:SER:OG	2.38	0.41
1:1:2819:G:C6	1:1:2828:G:C6	3.08	0.41
1:1:2838:G:C4	1:1:2839:G:C8	3.08	0.41
2:2:19:A:N1	2:2:917:G:C6	2.89	0.41
2:2:521:G:N7	46:q:50:ARG:NH2	2.65	0.41
2:2:736:C:OP1	52:w:61:ARG:NH1	2.53	0.41
2:2:875:U:HO2'	42:m:15:ARG:NH1	2.18	0.41
2:2:1053:G:N2	2:2:1058:G:O6	2.54	0.41
2:2:1352:C:H2'	2:2:1353:G:C8	2.56	0.41
2:2:1488:G:H2'	2:2:1489:G:H8	1.86	0.41
5:5:6:C:H2'	5:5:7:G:H8	1.85	0.41
29:Z:44:ILE:O	29:Z:48:ILE:HG12	2.19	0.41
34:e:7:VAL:HG23	34:e:10:ALA:HB3	2.03	0.41
36:g:164:ILE:O	36:g:186:ILE:HB	2.20	0.41
37:h:7:PRO:HD2	37:h:184:TYR:CD2	2.55	0.41
39:j:105:ILE:HG22	39:j:123:VAL:HG12	2.03	0.41
42:m:105:SER:HB2	42:m:110:VAL:HG12	2.02	0.41
43:n:54:LEU:HD11	43:n:103:PHE:CD2	2.56	0.41
43:n:55:VAL:O	43:n:57:MET:N	2.52	0.41
44:o:25:ILE:HD11	44:o:92:LEU:HD11	2.02	0.41
46:q:49:LEU:O	46:q:51:LYS:HD3	2.21	0.41
1:1:24:G:H2'	1:1:25:U:H6	1.85	0.41
1:1:54:G:H1'	33:d:35:ARG:HE	1.86	0.41
1:1:126:A:H5'	33:d:19:ARG:HG3	2.02	0.41
1:1:615:U:N3	9:D:176:ASP:HB3	2.34	0.41
1:1:629:G:OP1	1:1:650:C:O2'	2.31	0.41
1:1:641:U:O2'	1:1:2350:C:OP1	2.39	0.41
1:1:778:G:H5''	7:B:48:ARG:HD2	2.03	0.41
1:1:1010:A:N3	1:1:1153:C:H1'	2.35	0.41
1:1:1561:C:H2'	1:1:1562:U:C6	2.56	0.41
1:1:1582:C:H2'	1:1:1583:A:C8	2.56	0.41
1:1:2519:U:O4'	1:1:2542:A:N6	2.54	0.41
1:1:2801:G:H2'	1:1:2802:G:H8	1.86	0.41
2:2:18:C:H5''	39:j:132:ASN:ND2	2.36	0.41
2:2:235:C:H2'	2:2:236:A:C8	2.56	0.41
2:2:1161:C:H2'	2:2:1162:C:H6	1.84	0.41
3:3:70:C:H2'	3:3:71:C:H6	1.86	0.41
5:5:75:C:H2'	5:5:76:A:O4'	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
12:G:100:ALA:O	12:G:104:THR:HG23	2.21	0.41
13:J:114:LEU:O	13:J:118:MET:CB	2.64	0.41
16:M:46:ILE:HA	16:M:103:TYR:OH	2.21	0.41
26:W:19:LYS:HA	26:W:19:LYS:HD3	1.84	0.41
39:j:111:MET:HE2	39:j:140:THR:HB	2.02	0.41
48:s:64:CYS:HB2	48:s:80:SER:HB3	2.02	0.41
1:1:112:U:H5'	28:Y:58:ASN:HD21	1.86	0.41
1:1:133:U:H2'	1:1:134:G:H8	1.84	0.41
1:1:181:A:H1'	1:1:435:C:H5'	2.03	0.41
1:1:380:G:OP1	27:X:18:ARG:HB2	2.21	0.41
1:1:464:U:H1'	1:1:686:U:C5	2.47	0.41
1:1:530:G:H4'	1:1:532:A:H62	1.86	0.41
1:1:600:G:H5'	9:D:27:LEU:HD23	2.03	0.41
1:1:645:C:H2'	1:1:647:G:C8	2.56	0.41
1:1:934:U:H2'	1:1:935:C:C6	2.56	0.41
1:1:1069:A:C2	1:1:1096:A:H4'	2.56	0.41
1:1:1071:G:H2'	1:1:1072:C:C6	2.56	0.41
1:1:1287:A:H2'	1:1:1288:G:C4	2.56	0.41
1:1:1295:C:C2	1:1:1296:G:C8	3.08	0.41
1:1:1401:G:H2'	1:1:1402:U:C6	2.56	0.41
1:1:1582:C:O2'	1:1:1583:A:O4'	2.36	0.41
1:1:1594:U:H2'	1:1:1595:C:C6	2.55	0.41
1:1:1637:A:H2'	1:1:1638:C:C6	2.56	0.41
1:1:1678:A:C4	1:1:1679:A:C8	3.09	0.41
1:1:1788:C:H2'	1:1:1789:A:O4'	2.21	0.41
1:1:1802:A:H2'	1:1:1803:A:C8	2.56	0.41
1:1:2291:U:H1'	1:1:2374:C:H1'	2.03	0.41
1:1:2722:G:H2'	1:1:2723:C:C6	2.56	0.41
1:1:2745:C:H2'	1:1:2746:U:H6	1.85	0.41
1:1:2804:U:H2'	1:1:2805:C:H6	1.86	0.41
2:2:171:A:H2'	2:2:172:A:C8	2.56	0.41
2:2:261:U:OP2	54:y:74:ARG:NH1	2.46	0.41
2:2:489:C:H2'	2:2:490:C:H6	1.85	0.41
2:2:542:G:H2'	2:2:543:U:C6	2.55	0.41
2:2:672:U:H2'	2:2:673:A:H8	1.85	0.41
2:2:674:G:H21	45:p:118:HIS:HB2	1.86	0.41
2:2:1318:A:H4'	53:x:10:PHE:CG	2.56	0.41
2:2:1321:U:O2'	53:x:78:ARG:NH2	2.54	0.41
3:3:77:U:H5'	25:V:21:ARG:HH22	1.86	0.41
7:B:132:MET:SD	7:B:164:ILE:HD11	2.61	0.41
7:B:144:VAL:HG11	7:B:174:LEU:HD21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:D:6:LYS:HB3	9:D:6:LYS:HE3	1.85	0.41
10:E:8:TYR:HA	10:E:12:VAL:HB	2.03	0.41
10:E:70:ALA:HB2	10:E:85:ILE:HG13	2.02	0.41
11:F:117:LEU:HD12	11:F:144:VAL:HG21	2.02	0.41
13:J:11:VAL:HG21	13:J:50:THR:HA	2.03	0.41
13:J:118:MET:HG3	58:J:203:HOH:O	2.20	0.41
14:K:116:ILE:HD11	14:K:122:VAL:HG13	2.03	0.41
17:N:52:ILE:HB	17:N:94:TYR:CD2	2.56	0.41
18:O:32:PRO:HA	18:O:102:ARG:HH22	1.86	0.41
18:O:62:LEU:HD21	18:O:70:ALA:CB	2.50	0.41
23:T:18:GLU:HG2	23:T:19:LYS:N	2.36	0.41
23:T:30:ILE:HD12	23:T:32:LEU:HD21	2.03	0.41
24:U:52:LEU:HD23	24:U:52:LEU:O	2.21	0.41
25:V:72:VAL:CG1	25:V:91:PHE:HB3	2.51	0.41
29:Z:56:LYS:HE2	29:Z:58:GLU:HG2	2.03	0.41
36:g:11:LYS:HG3	36:g:208:ARG:NH2	2.36	0.41
38:i:28:ILE:HG13	38:i:29:ASP:N	2.36	0.41
38:i:105:MET:HE1	38:i:143:VAL:HB	2.02	0.41
39:j:24:THR:HG22	39:j:29:ARG:HG3	2.02	0.41
40:k:9:MET:HE2	40:k:59:TYR:CE2	2.55	0.41
44:o:53:ILE:HG22	48:s:85:ARG:NE	2.36	0.41
46:q:39:THR:HG21	46:q:49:LEU:HB3	2.03	0.41
49:t:71:LYS:HG3	49:t:78:TYR:CD2	2.55	0.41
53:x:50:ALA:HA	53:x:59:PRO:HA	2.02	0.41
1:1:12:U:O2	1:1:2626:C:H4'	2.20	0.41
1:1:254:G:O2'	1:1:255:A:O4'	2.35	0.41
1:1:287:G:H2'	1:1:288:U:H6	1.86	0.41
1:1:335:C:H5''	24:U:82:ARG:HD2	2.02	0.41
1:1:659:G:H21	9:D:30:GLN:CD	2.27	0.41
1:1:714:U:H1'	1:1:717:C:H5	1.86	0.41
1:1:1016:G:C6	1:1:1147:A:C6	3.09	0.41
1:1:2125:G:N2	1:1:2171:A:O5'	2.40	0.41
1:1:2364:C:H2'	1:1:2365:G:O4'	2.21	0.41
1:1:2478:A:C8	1:1:2529:G:N7	2.89	0.41
1:1:2834:G:H2'	1:1:2879:A:N6	2.36	0.41
2:2:56:U:H2'	2:2:57:G:H8	1.86	0.41
2:2:129:A:O2'	2:2:130:A:H2'	2.21	0.41
2:2:144:G:N2	2:2:179:A:C8	2.89	0.41
2:2:713:G:H2'	2:2:714:G:H8	1.83	0.41
2:2:1161:C:H2'	2:2:1162:C:C6	2.56	0.41
2:2:1506:U:O2'	2:2:1507:A:H5'	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:1524:C:H2'	2:2:1525:G:C8	2.54	0.41
2:2:1527:U:P	55:z:45:ARG:HH21	2.44	0.41
3:3:60:C:H2'	3:3:61:G:C8	2.54	0.41
37:h:6:HIS:CE1	37:h:8:ASN:HB3	2.56	0.41
42:m:88:ARG:H	42:m:88:ARG:HG3	1.71	0.41
43:n:84:THR:O	43:n:88:MET:HG2	2.21	0.41
44:o:91:ASP:OD1	44:o:91:ASP:N	2.48	0.41
46:q:33:VAL:C	46:q:55:VAL:HG23	2.46	0.41
52:w:14:THR:HG22	52:w:48:ARG:HE	1.85	0.41
1:1:128:C:H2'	1:1:129:C:H6	1.86	0.40
1:1:223:A:C6	1:1:422:A:C6	3.09	0.40
1:1:477:A:H61	1:1:500:G:H5''	1.85	0.40
1:1:565:C:H2'	1:1:566:U:C6	2.56	0.40
1:1:657:U:H2'	1:1:658:U:C6	2.56	0.40
1:1:1203:U:O5'	1:1:1204:A:H5''	2.20	0.40
1:1:1283:G:N2	1:1:1286:A:OP2	2.54	0.40
1:1:1379:U:O2'	1:1:1380:G:OP1	2.38	0.40
1:1:1413:A:H2'	1:1:1414:C:H6	1.86	0.40
1:1:1735:A:C6	1:1:1736:U:C4	3.09	0.40
1:1:1788:C:H2'	1:1:1789:A:C8	2.56	0.40
1:1:2370:G:H4'	32:c:44:ARG:HH21	1.86	0.40
1:1:2446:G:H4'	1:1:2448:A:N7	2.35	0.40
1:1:2669:G:H2'	1:1:2670:A:C8	2.57	0.40
1:1:2848:G:N7	19:P:95:ALA:HB2	2.36	0.40
2:2:6:G:H22	39:j:103:THR:HG22	1.85	0.40
2:2:745:G:H2'	2:2:746:A:H8	1.86	0.40
2:2:1415:G:C6	2:2:1486:G:C6	3.09	0.40
9:D:18:THR:HA	9:D:106:LYS:HD2	2.02	0.40
16:M:36:VAL:HG13	25:V:82:TYR:CD2	2.56	0.40
36:g:127:ASP:O	36:g:129:LEU:HD22	2.22	0.40
37:h:114:LYS:HB2	37:h:185:ASN:ND2	2.36	0.40
38:i:126:ASN:ND2	38:i:141:ASP:OD1	2.42	0.40
42:m:49:PHE:HB2	42:m:59:LEU:HD11	2.03	0.40
53:x:17:LYS:HD3	53:x:17:LYS:HA	1.89	0.40
1:1:300:A:O2'	1:1:318:C:O2	2.29	0.40
1:1:513:A:H2'	1:1:514:A:C8	2.56	0.40
1:1:1217:U:OP1	20:Q:15:LYS:HD2	2.21	0.40
1:1:1378:A:N3	1:1:1379:U:H2'	2.37	0.40
1:1:1709:U:O2'	1:1:2859:G:N3	2.47	0.40
1:1:1727:C:H2'	1:1:1728:C:O4'	2.20	0.40
1:1:1826:G:H2'	1:1:1827:U:C6	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:2198:A:C4	12:G:29:PHE:HB2	2.56	0.40
1:1:2393:U:H5''	15:L:62:PRO:HB3	2.02	0.40
2:2:1149:C:H2'	2:2:1150:A:C8	2.56	0.40
2:2:1172:C:C2	2:2:1173:U:C5	3.09	0.40
4:4:16:C:H2'	4:4:17:C:C6	2.56	0.40
5:5:72:G:N2	5:5:73:A:C4	2.90	0.40
5:5:72:G:N3	5:5:73:A:C8	2.89	0.40
9:D:105:LEU:HD23	9:D:200:LEU:HD21	2.03	0.40
15:L:29:LYS:HG3	15:L:30:THR:HG23	2.03	0.40
20:Q:9:ILE:H	20:Q:9:ILE:HD12	1.86	0.40
23:T:34:VAL:HG21	23:T:43:ILE:HD11	2.03	0.40
27:X:39:TRP:NE1	27:X:41:GLU:OE2	2.51	0.40
28:Y:32:ALA:O	58:Y:101:HOH:O	2.22	0.40
36:g:90:PHE:HB3	36:g:151:ILE:HD13	2.04	0.40
44:o:50:THR:HG22	44:o:64:GLN:HG3	2.03	0.40
53:x:40:ILE:HD12	53:x:66:MET:O	2.22	0.40
1:1:571:U:H3'	21:R:80:ARG:NH2	2.37	0.40
1:1:1178:C:H2'	1:1:1179:G:H5''	2.02	0.40
1:1:1299:G:O2'	1:1:1301:A:N7	2.52	0.40
1:1:2053:G:H5'	8:C:150:GLN:H	1.85	0.40
1:1:2130:U:O2'	1:1:2134:A:O5'	2.30	0.40
1:1:2290:G:H2'	1:1:2291:U:H6	1.85	0.40
1:1:2560:A:C6	1:1:2561:U:C4	3.10	0.40
1:1:2841:C:H2'	1:1:2842:G:H8	1.86	0.40
1:1:2855:C:H2'	1:1:2856:A:H8	1.85	0.40
2:2:678:U:H2'	2:2:679:C:C6	2.56	0.40
2:2:696:A:H2'	2:2:697:U:C6	2.56	0.40
2:2:836:G:C6	2:2:851:G:C5	3.10	0.40
2:2:911:U:OP2	46:q:94:ARG:NH2	2.54	0.40
2:2:1515:G:H2'	2:2:1516:2MG:H8	1.86	0.40
3:3:29:A:O2'	3:3:58:A:N1	2.48	0.40
8:C:149:ASN:C	8:C:151:THR:H	2.29	0.40
10:E:63:GLN:HA	30:a:6:HIS:HD2	1.86	0.40
11:F:4:VAL:HB	11:F:69:ARG:HD2	2.02	0.40
11:F:26:ILE:CG2	11:F:33:LEU:HB2	2.51	0.40
1:1:52:A:H2'	1:1:53:A:C8	2.57	0.40
1:1:627:A:C6	15:L:111:ILE:HD11	2.57	0.40
1:1:1190:G:H2'	1:1:1191:G:H8	1.87	0.40
1:1:1542:U:H2'	1:1:1543:G:O4'	2.21	0.40
1:1:1684:G:O6	1:1:1705:A:N6	2.55	0.40
1:1:2174:C:H2'	1:1:2175:C:C6	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:2:34:C:C2	2:2:35:G:N7	2.89	0.40
2:2:185:U:H2'	2:2:186:C:C6	2.57	0.40
2:2:373:A:C2	2:2:374:A:C8	3.09	0.40
2:2:691:G:OP2	45:p:28:ASN:ND2	2.50	0.40
2:2:799:G:H2'	2:2:800:G:O4'	2.21	0.40
2:2:1152:A:OP1	44:o:72:ARG:NH1	2.39	0.40
3:3:9:G:H2'	3:3:10:G:H8	1.87	0.40
7:B:243:HIS:HA	7:B:244:PRO:HD3	1.97	0.40
23:T:57:VAL:O	23:T:86:THR:HG22	2.21	0.40
41:l:140:ASP:OD1	41:l:143:ARG:NH2	2.36	0.40
1:1:136:G:C5	1:1:137:U:C4	3.10	0.40
1:1:532:A:N3	1:1:532:A:H2'	2.37	0.40
1:1:597:G:H2'	1:1:598:U:C6	2.57	0.40
1:1:886:A:H2'	1:1:887:A:O4'	2.22	0.40
1:1:962:G:H2'	1:1:963:U:H6	1.86	0.40
1:1:980:A:C6	1:1:1136:G:H5'	2.57	0.40
1:1:1409:U:H2'	1:1:1410:G:C8	2.56	0.40
1:1:1445:G:H2'	1:1:1446:C:H6	1.86	0.40
1:1:1473:G:C6	1:1:1519:G:C6	3.10	0.40
1:1:2064:C:H2'	1:1:2065:C:H6	1.86	0.40
1:1:2367:G:C2	1:1:2368:C:C5	3.09	0.40
1:1:2485:G:O3'	16:M:125:PRO:HB3	2.21	0.40
1:1:2710:C:H2'	1:1:2711:A:C8	2.57	0.40
1:1:2809:A:H2'	1:1:2810:A:C8	2.57	0.40
2:2:76:G:H2'	2:2:77:A:H8	1.86	0.40
2:2:629:A:H2'	2:2:630:A:O4'	2.20	0.40
2:2:738:C:H5''	40:k:68:GLN:HG2	2.03	0.40
2:2:786:G:C2	2:2:797:C:C2	3.10	0.40
2:2:1375:A:H2'	2:2:1376:U:O4'	2.21	0.40
2:2:1436:U:O4	2:2:1437:A:N6	2.55	0.40
3:3:62:C:H2'	3:3:63:C:C6	2.56	0.40
10:E:73:SER:OG	10:E:80:ARG:HA	2.21	0.40
10:E:106:ILE:O	10:E:109:PRO:HD2	2.21	0.40
18:O:58:ILE:O	18:O:62:LEU:HB2	2.22	0.40
22:S:10:ALA:N	22:S:101:SER:O	2.50	0.40
26:W:44:LYS:HB3	26:W:44:LYS:HE2	1.94	0.40
44:o:40:ILE:CG1	44:o:73:LEU:HB3	2.51	0.40
45:p:45:ALA:HB3	45:p:70:CYS:HB2	2.03	0.40
46:q:69:GLY:HA3	46:q:107:VAL:HG11	2.03	0.40
51:v:49:GLU:H	51:v:49:GLU:CD	2.30	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	
6	A	65/229 (28%)	63 (97%)	2 (3%)	0	100	100
7	B	269/273 (98%)	257 (96%)	12 (4%)	0	100	100
8	C	207/209 (99%)	196 (95%)	11 (5%)	0	100	100
9	D	199/201 (99%)	196 (98%)	3 (2%)	0	100	100
10	E	175/179 (98%)	165 (94%)	10 (6%)	0	100	100
11	F	173/177 (98%)	168 (97%)	4 (2%)	1 (1%)	22	55
12	G	147/149 (99%)	142 (97%)	5 (3%)	0	100	100
13	J	140/142 (99%)	138 (99%)	2 (1%)	0	100	100
14	K	121/123 (98%)	118 (98%)	3 (2%)	0	100	100
15	L	142/144 (99%)	138 (97%)	4 (3%)	0	100	100
16	M	134/136 (98%)	132 (98%)	2 (2%)	0	100	100
17	N	117/127 (92%)	112 (96%)	5 (4%)	0	100	100
18	O	114/117 (97%)	109 (96%)	5 (4%)	0	100	100
19	P	112/115 (97%)	112 (100%)	0	0	100	100
20	Q	115/118 (98%)	115 (100%)	0	0	100	100
21	R	101/103 (98%)	95 (94%)	6 (6%)	0	100	100
22	S	108/110 (98%)	103 (95%)	5 (5%)	0	100	100
23	T	92/100 (92%)	89 (97%)	3 (3%)	0	100	100
24	U	101/104 (97%)	98 (97%)	3 (3%)	0	100	100
25	V	92/94 (98%)	91 (99%)	1 (1%)	0	100	100
26	W	74/84 (88%)	70 (95%)	4 (5%)	0	100	100
27	X	75/78 (96%)	73 (97%)	2 (3%)	0	100	100
28	Y	60/63 (95%)	56 (93%)	4 (7%)	0	100	100
29	Z	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
30	a	64/70 (91%)	59 (92%)	5 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
31	b	54/57 (95%)	52 (96%)	2 (4%)	0	100	100
32	c	50/55 (91%)	50 (100%)	0	0	100	100
33	d	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
34	e	62/65 (95%)	57 (92%)	5 (8%)	0	100	100
35	f	36/38 (95%)	36 (100%)	0	0	100	100
36	g	223/241 (92%)	214 (96%)	9 (4%)	0	100	100
37	h	206/233 (88%)	196 (95%)	10 (5%)	0	100	100
38	i	203/206 (98%)	196 (97%)	7 (3%)	0	100	100
39	j	154/167 (92%)	145 (94%)	9 (6%)	0	100	100
40	k	102/135 (76%)	100 (98%)	2 (2%)	0	100	100
41	l	149/179 (83%)	142 (95%)	7 (5%)	0	100	100
42	m	127/130 (98%)	126 (99%)	1 (1%)	0	100	100
43	n	125/130 (96%)	120 (96%)	5 (4%)	0	100	100
44	o	97/103 (94%)	89 (92%)	8 (8%)	0	100	100
45	p	115/129 (89%)	114 (99%)	1 (1%)	0	100	100
46	q	120/124 (97%)	108 (90%)	12 (10%)	0	100	100
47	r	114/118 (97%)	107 (94%)	7 (6%)	0	100	100
48	s	98/101 (97%)	96 (98%)	2 (2%)	0	100	100
49	t	86/89 (97%)	83 (96%)	3 (4%)	0	100	100
50	u	80/82 (98%)	77 (96%)	3 (4%)	0	100	100
51	v	78/84 (93%)	74 (95%)	4 (5%)	0	100	100
52	w	64/75 (85%)	62 (97%)	2 (3%)	0	100	100
53	x	81/92 (88%)	80 (99%)	1 (1%)	0	100	100
54	y	84/87 (97%)	83 (99%)	1 (1%)	0	100	100
55	z	68/71 (96%)	68 (100%)	0	0	100	100
All	All	5673/6141 (92%)	5465 (96%)	207 (4%)	1 (0%)	100	100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
11	F	47	ASP

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	
6	A	54/177 (30%)	54 (100%)	0	100	100
7	B	216/218 (99%)	215 (100%)	1 (0%)	86	93
8	C	164/164 (100%)	164 (100%)	0	100	100
9	D	165/165 (100%)	165 (100%)	0	100	100
10	E	148/150 (99%)	148 (100%)	0	100	100
11	F	136/138 (99%)	136 (100%)	0	100	100
12	G	114/114 (100%)	114 (100%)	0	100	100
13	J	116/116 (100%)	116 (100%)	0	100	100
14	K	104/104 (100%)	104 (100%)	0	100	100
15	L	103/103 (100%)	103 (100%)	0	100	100
16	M	109/109 (100%)	109 (100%)	0	100	100
17	N	99/103 (96%)	99 (100%)	0	100	100
18	O	86/87 (99%)	86 (100%)	0	100	100
19	P	99/100 (99%)	99 (100%)	0	100	100
20	Q	89/90 (99%)	89 (100%)	0	100	100
21	R	84/84 (100%)	84 (100%)	0	100	100
22	S	93/93 (100%)	93 (100%)	0	100	100
23	T	81/84 (96%)	81 (100%)	0	100	100
24	U	84/85 (99%)	84 (100%)	0	100	100
25	V	78/78 (100%)	78 (100%)	0	100	100
26	W	58/62 (94%)	58 (100%)	0	100	100
27	X	67/68 (98%)	67 (100%)	0	100	100
28	Y	54/55 (98%)	54 (100%)	0	100	100
29	Z	48/49 (98%)	48 (100%)	0	100	100
30	a	59/62 (95%)	59 (100%)	0	100	100
31	b	47/48 (98%)	47 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
32	c	47/49 (96%)	47 (100%)	0	100	100
33	d	38/38 (100%)	38 (100%)	0	100	100
34	e	51/52 (98%)	49 (96%)	2 (4%)	27	57
35	f	34/34 (100%)	34 (100%)	0	100	100
36	g	187/199 (94%)	187 (100%)	0	100	100
37	h	171/190 (90%)	171 (100%)	0	100	100
38	i	172/173 (99%)	172 (100%)	0	100	100
39	j	119/126 (94%)	119 (100%)	0	100	100
40	k	91/116 (78%)	91 (100%)	0	100	100
41	l	124/147 (84%)	124 (100%)	0	100	100
42	m	104/105 (99%)	104 (100%)	0	100	100
43	n	105/107 (98%)	103 (98%)	2 (2%)	52	73
44	o	86/90 (96%)	86 (100%)	0	100	100
45	p	90/99 (91%)	90 (100%)	0	100	100
46	q	102/103 (99%)	100 (98%)	2 (2%)	50	72
47	r	94/96 (98%)	94 (100%)	0	100	100
48	s	83/84 (99%)	83 (100%)	0	100	100
49	t	76/77 (99%)	76 (100%)	0	100	100
50	u	65/65 (100%)	65 (100%)	0	100	100
51	v	74/78 (95%)	74 (100%)	0	100	100
52	w	57/65 (88%)	57 (100%)	0	100	100
53	x	72/79 (91%)	72 (100%)	0	100	100
54	y	65/66 (98%)	65 (100%)	0	100	100
55	z	60/61 (98%)	60 (100%)	0	100	100
All	All	4722/5005 (94%)	4715 (100%)	7 (0%)	92	97

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
7	B	115	GLN
34	e	30	ARG
34	e	32	ILE
43	n	5	GLN
43	n	9	THR

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Mol	Chain	Res	Type
46	q	47	SER
46	q	49	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (40) such sidechains are listed below:

Mol	Chain	Res	Type
6	A	203	GLN
7	B	53	HIS
7	B	153	GLN
7	B	226	ASN
7	B	260	ASN
11	F	22	GLN
11	F	38	ASN
12	G	11	ASN
13	J	58	ASN
13	J	80	HIS
15	L	104	GLN
16	M	88	ASN
17	N	107	ASN
18	O	29	HIS
19	P	66	ASN
21	R	66	HIS
23	T	48	GLN
24	U	40	ASN
25	V	75	GLN
25	V	87	GLN
28	Y	36	GLN
28	Y	58	ASN
36	g	42	ASN
36	g	122	GLN
36	g	168	HIS
37	h	102	ASN
37	h	139	GLN
38	i	126	ASN
38	i	136	GLN
40	k	14	GLN
40	k	46	GLN
41	l	52	GLN
41	l	148	ASN
44	o	70	HIS
48	s	66	GLN
49	t	80	GLN

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Mol	Chain	Res	Type
50	u	40	ASN
53	x	52	HIS
54	y	48	GLN
54	y	61	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	2902/2904 (99%)	456 (15%)	10 (0%)
2	2	1532/1540 (99%)	228 (14%)	3 (0%)
3	3	119/120 (99%)	20 (16%)	0
4	4	10/18 (55%)	8 (80%)	0
5	5	76/77 (98%)	34 (44%)	5 (6%)
All	All	4639/4659 (99%)	746 (16%)	18 (0%)

All (746) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	10	A
1	1	27	G
1	1	34	U
1	1	35	G
1	1	46	G
1	1	51	G
1	1	60	G
1	1	63	A
1	1	71	A
1	1	74	A
1	1	75	G
1	1	80	G
1	1	85	G
1	1	102	U
1	1	118	A
1	1	120	U
1	1	136	G
1	1	137	U
1	1	139	U
1	1	163	C
1	1	181	A
1	1	196	A
1	1	199	A

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Mol	Chain	Res	Type
1	1	216	A
1	1	222	A
1	1	225	C
1	1	242	G
1	1	248	G
1	1	249	C
1	1	266	G
1	1	273	G
1	1	275	C
1	1	276	U
1	1	285	G
1	1	311	A
1	1	329	G
1	1	330	A
1	1	352	A
1	1	353	C
1	1	361	G
1	1	362	A
1	1	368	A
1	1	371	A
1	1	372	G
1	1	373	U
1	1	385	C
1	1	386	G
1	1	396	G
1	1	405	U
1	1	406	G
1	1	411	G
1	1	424	G
1	1	451	U
1	1	457	A
1	1	481	G
1	1	490	C
1	1	491	G
1	1	496	G
1	1	501	A
1	1	509	C
1	1	529	A
1	1	530	G
1	1	531	C
1	1	532	A
1	1	538	A

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Mol	Chain	Res	Type
1	1	540	C
1	1	541	A
1	1	542	C
1	1	543	G
1	1	546	U
1	1	547	A
1	1	548	G
1	1	549	G
1	1	551	G
1	1	563	A
1	1	573	U
1	1	575	A
1	1	592	A
1	1	603	A
1	1	609	A
1	1	613	A
1	1	614	A
1	1	615	U
1	1	621	A
1	1	627	A
1	1	637	A
1	1	645	C
1	1	646	U
1	1	647	G
1	1	654	A
1	1	669	G
1	1	675	A
1	1	686	U
1	1	710	U
1	1	717	C
1	1	726	G
1	1	729	G
1	1	730	A
1	1	747	5MU
1	1	763	G
1	1	764	A
1	1	775	G
1	1	776	G
1	1	782	A
1	1	784	G
1	1	785	G
1	1	789	A

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Mol	Chain	Res	Type
1	1	805	G
1	1	811	U
1	1	812	C
1	1	819	A
1	1	827	U
1	1	828	U
1	1	845	A
1	1	846	U
1	1	858	G
1	1	859	G
1	1	877	A
1	1	878	A
1	1	884	U
1	1	885	C
1	1	893	C
1	1	895	U
1	1	896	A
1	1	907	G
1	1	910	A
1	1	914	G
1	1	915	C
1	1	919	U
1	1	931	U
1	1	941	A
1	1	946	C
1	1	953	G
1	1	961	C
1	1	973	A
1	1	974	G
1	1	980	A
1	1	983	A
1	1	995	C
1	1	996	A
1	1	1009	A
1	1	1012	U
1	1	1013	C
1	1	1026	G
1	1	1028	A
1	1	1029	A
1	1	1030	C
1	1	1033	U
1	1	1042	G

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Mol	Chain	Res	Type
1	1	1043	C
1	1	1046	A
1	1	1047	G
1	1	1051	G
1	1	1061	U
1	1	1065	U
1	1	1066	U
1	1	1068	G
1	1	1070	A
1	1	1071	G
1	1	1073	A
1	1	1084	A
1	1	1087	G
1	1	1088	A
1	1	1096	A
1	1	1097	U
1	1	1111	A
1	1	1112	G
1	1	1116	G
1	1	1130	U
1	1	1132	U
1	1	1133	A
1	1	1134	A
1	1	1135	C
1	1	1142	A
1	1	1155	A
1	1	1169	A
1	1	1171	G
1	1	1172	C
1	1	1174	U
1	1	1175	A
1	1	1179	G
1	1	1186	G
1	1	1199	U
1	1	1200	C
1	1	1201	U
1	1	1204	A
1	1	1212	G
1	1	1225	G
1	1	1236	G
1	1	1238	G
1	1	1250	G

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Mol	Chain	Res	Type
1	1	1253	A
1	1	1255	U
1	1	1256	G
1	1	1266	G
1	1	1271	G
1	1	1272	A
1	1	1273	U
1	1	1300	G
1	1	1301	A
1	1	1302	A
1	1	1314	C
1	1	1325	U
1	1	1345	C
1	1	1365	A
1	1	1368	G
1	1	1378	A
1	1	1379	U
1	1	1380	G
1	1	1383	A
1	1	1386	C
1	1	1408	G
1	1	1416	G
1	1	1417	C
1	1	1420	A
1	1	1428	C
1	1	1437	C
1	1	1453	A
1	1	1458	U
1	1	1459	G
1	1	1460	U
1	1	1467	U
1	1	1482	G
1	1	1490	A
1	1	1494	A
1	1	1497	U
1	1	1503	A
1	1	1508	A
1	1	1510	G
1	1	1515	A
1	1	1524	G
1	1	1534	U
1	1	1535	A

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Mol	Chain	Res	Type
1	1	1536	C
1	1	1537	G
1	1	1555	G
1	1	1558	C
1	1	1559	U
1	1	1566	A
1	1	1569	A
1	1	1578	U
1	1	1581	G
1	1	1583	A
1	1	1589	U
1	1	1590	A
1	1	1610	A
1	1	1617	C
1	1	1618	6MZ
1	1	1619	G
1	1	1647	U
1	1	1648	U
1	1	1649	G
1	1	1674	G
1	1	1715	G
1	1	1729	U
1	1	1730	C
1	1	1732	C
1	1	1735	A
1	1	1738	G
1	1	1756	G
1	1	1757	A
1	1	1764	C
1	1	1773	A
1	1	1781	U
1	1	1800	C
1	1	1801	A
1	1	1808	A
1	1	1815	A
1	1	1816	C
1	1	1829	A
1	1	1833	C
1	1	1835	2MG
1	1	1848	A
1	1	1858	A
1	1	1864	U

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Mol	Chain	Res	Type
1	1	1865	U
1	1	1866	A
1	1	1869	G
1	1	1872	A
1	1	1906	G
1	1	1913	A
1	1	1916	A
1	1	1924	C
1	1	1927	A
1	1	1929	G
1	1	1930	G
1	1	1931	U
1	1	1937	A
1	1	1955	U
1	1	1963	U
1	1	1964	G
1	1	1967	C
1	1	1970	A
1	1	1971	U
1	1	1972	G
1	1	1991	U
1	1	1992	G
1	1	1993	U
1	1	1997	C
1	1	2020	A
1	1	2022	U
1	1	2023	C
1	1	2030	A
1	1	2031	A
1	1	2033	A
1	1	2043	C
1	1	2052	A
1	1	2055	C
1	1	2059	A
1	1	2060	A
1	1	2061	G
1	1	2062	A
1	1	2069	G7M
1	1	2072	C
1	1	2093	G
1	1	2107	G
1	1	2110	G

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Mol	Chain	Res	Type
1	1	2111	U
1	1	2113	U
1	1	2115	G
1	1	2116	G
1	1	2117	A
1	1	2118	U
1	1	2120	G
1	1	2123	G
1	1	2124	G
1	1	2125	G
1	1	2126	A
1	1	2131	U
1	1	2132	U
1	1	2133	G
1	1	2134	A
1	1	2142	A
1	1	2146	C
1	1	2147	A
1	1	2157	G
1	1	2158	A
1	1	2162	G
1	1	2164	C
1	1	2165	C
1	1	2171	A
1	1	2172	U
1	1	2182	U
1	1	2183	A
1	1	2189	U
1	1	2193	G
1	1	2194	U
1	1	2198	A
1	1	2204	G
1	1	2211	A
1	1	2212	A
1	1	2226	C
1	1	2238	G
1	1	2239	G
1	1	2243	U
1	1	2250	G
1	1	2255	G
1	1	2266	A
1	1	2283	C

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Mol	Chain	Res	Type
1	1	2287	A
1	1	2297	A
1	1	2305	U
1	1	2309	A
1	1	2319	G
1	1	2322	A
1	1	2325	G
1	1	2327	A
1	1	2333	A
1	1	2334	U
1	1	2335	A
1	1	2347	C
1	1	2361	G
1	1	2383	G
1	1	2385	C
1	1	2402	U
1	1	2403	C
1	1	2423	U
1	1	2425	A
1	1	2426	A
1	1	2429	G
1	1	2430	A
1	1	2431	U
1	1	2435	A
1	1	2441	U
1	1	2447	G
1	1	2448	A
1	1	2475	C
1	1	2476	A
1	1	2491	U
1	1	2494	G
1	1	2498	OMC
1	1	2502	G
1	1	2503	2MA
1	1	2504	PSU
1	1	2505	G
1	1	2506	U
1	1	2507	C
1	1	2512	C
1	1	2513	A
1	1	2518	A
1	1	2520	C

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Mol	Chain	Res	Type
1	1	2529	G
1	1	2535	G
1	1	2554	U
1	1	2566	A
1	1	2567	G
1	1	2572	A
1	1	2573	C
1	1	2574	G
1	1	2582	G
1	1	2585	U
1	1	2586	U
1	1	2602	A
1	1	2609	U
1	1	2613	U
1	1	2615	U
1	1	2629	U
1	1	2630	G
1	1	2639	A
1	1	2646	C
1	1	2689	U
1	1	2690	U
1	1	2714	G
1	1	2718	G
1	1	2725	A
1	1	2726	A
1	1	2729	G
1	1	2733	A
1	1	2739	U
1	1	2744	G
1	1	2748	A
1	1	2751	G
1	1	2752	C
1	1	2757	A
1	1	2765	A
1	1	2777	G
1	1	2778	A
1	1	2780	G
1	1	2793	C
1	1	2794	C
1	1	2797	U
1	1	2798	U
1	1	2818	U

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Mol	Chain	Res	Type
1	1	2820	A
1	1	2825	G
1	1	2835	A
1	1	2849	U
1	1	2867	G
1	1	2873	A
1	1	2879	A
1	1	2880	C
1	1	2883	A
1	1	2884	U
1	1	2885	G
1	1	2898	U
1	1	2901	C
2	2	2	A
2	2	3	A
2	2	4	U
2	2	9	G
2	2	32	A
2	2	39	G
2	2	47	C
2	2	48	C
2	2	50	A
2	2	51	A
2	2	54	C
2	2	68	G
2	2	69	G
2	2	72	A
2	2	74	A
2	2	75	G
2	2	83	C
2	2	84	U
2	2	85	U
2	2	86	G
2	2	87	C
2	2	94	G
2	2	95	C
2	2	108	G
2	2	120	A
2	2	121	U
2	2	128	G
2	2	129	A
2	2	130	A

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Mol	Chain	Res	Type
2	2	131	A
2	2	144	G
2	2	173	U
2	2	177	G
2	2	181	A
2	2	183	C
2	2	197	A
2	2	204	G
2	2	209	U
2	2	211	G
2	2	212	G
2	2	226	G
2	2	240	G
2	2	247	G
2	2	251	G
2	2	266	G
2	2	267	C
2	2	279	A
2	2	280	C
2	2	281	G
2	2	289	G
2	2	328	C
2	2	330	C
2	2	332	G
2	2	347	G
2	2	351	G
2	2	352	C
2	2	354	G
2	2	367	U
2	2	372	C
2	2	373	A
2	2	406	G
2	2	412	A
2	2	413	G
2	2	414	A
2	2	421	U
2	2	422	C
2	2	424	G
2	2	429	U
2	2	451	A
2	2	456	A
2	2	457	G

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Mol	Chain	Res	Type
2	2	458	U
2	2	463	U
2	2	464	U
2	2	467	U
2	2	468	A
2	2	478	A
2	2	479	U
2	2	481	G
2	2	484	G
2	2	485	U
2	2	493	A
2	2	496	A
2	2	497	G
2	2	509	A
2	2	511	C
2	2	512	U
2	2	517	G
2	2	518	C
2	2	519	C
2	2	521	G
2	2	527	7MG
2	2	532	A
2	2	547	A
2	2	559	A
2	2	564	C
2	2	572	A
2	2	573	A
2	2	576	C
2	2	577	G
2	2	596	A
2	2	633	G
2	2	650	G
2	2	653	U
2	2	665	A
2	2	687	A
2	2	700	G
2	2	721	G
2	2	723	U
2	2	731	G
2	2	734	G
2	2	747	A
2	2	755	G

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Mol	Chain	Res	Type
2	2	777	A
2	2	793	U
2	2	794	A
2	2	815	A
2	2	817	C
2	2	821	G
2	2	828	U
2	2	829	G
2	2	832	G
2	2	841	C
2	2	844	G
2	2	846	G
2	2	851	G
2	2	889	A
2	2	902	G
2	2	914	A
2	2	926	G
2	2	934	C
2	2	935	A
2	2	960	U
2	2	961	U
2	2	966	2MG
2	2	967	5MC
2	2	968	A
2	2	969	A
2	2	971	G
2	2	975	A
2	2	976	G
2	2	977	A
2	2	989	U
2	2	992	U
2	2	993	G
2	2	996	A
2	2	1004	A
2	2	1008	U
2	2	1009	U
2	2	1010	U
2	2	1018	G
2	2	1021	A
2	2	1023	U
2	2	1026	G
2	2	1030	U

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Mol	Chain	Res	Type
2	2	1032	G
2	2	1044	A
2	2	1045	C
2	2	1064	G
2	2	1065	U
2	2	1066	C
2	2	1085	U
2	2	1094	G
2	2	1095	U
2	2	1101	A
2	2	1108	G
2	2	1124	G
2	2	1132	C
2	2	1133	G
2	2	1135	U
2	2	1136	C
2	2	1137	C
2	2	1139	G
2	2	1140	C
2	2	1141	C
2	2	1142	G
2	2	1147	C
2	2	1149	C
2	2	1151	A
2	2	1152	A
2	2	1158	C
2	2	1159	U
2	2	1167	A
2	2	1176	A
2	2	1184	G
2	2	1196	A
2	2	1197	A
2	2	1213	A
2	2	1214	C
2	2	1227	A
2	2	1228	C
2	2	1239	A
2	2	1257	A
2	2	1261	A
2	2	1269	A
2	2	1275	A
2	2	1279	G

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Mol	Chain	Res	Type
2	2	1280	A
2	2	1286	U
2	2	1287	A
2	2	1299	A
2	2	1300	G
2	2	1302	C
2	2	1305	G
2	2	1317	C
2	2	1320	C
2	2	1322	C
2	2	1363	A
2	2	1379	G
2	2	1384	C
2	2	1398	A
2	2	1419	G
2	2	1429	A
2	2	1432	G
2	2	1441	A
2	2	1446	A
2	2	1452	C
2	2	1492	A
2	2	1493	A
2	2	1494	G
2	2	1499	A
2	2	1503	A
2	2	1517	G
2	2	1519	MA6
2	2	1520	C
2	2	1529	G
2	2	1530	G
2	2	1534	A
3	3	2	G
3	3	13	G
3	3	15	A
3	3	35	C
3	3	44	G
3	3	45	A
3	3	53	A
3	3	56	G
3	3	57	A
3	3	68	C
3	3	74	U

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Mol	Chain	Res	Type
3	3	78	A
3	3	79	G
3	3	88	C
3	3	89	U
3	3	90	C
3	3	99	A
3	3	105	G
3	3	109	A
3	3	116	G
4	4	12	A
4	4	13	U
4	4	15	C
4	4	16	C
4	4	18	C
4	4	19	G
4	4	20	U
4	4	21	U
5	5	2	G
5	5	3	G
5	5	4	C
5	5	5	A
5	5	6	C
5	5	7	G
5	5	8	U
5	5	10	G
5	5	14	A
5	5	16	C
5	5	17	C
5	5	18	G
5	5	19	G
5	5	20	U
5	5	21	A
5	5	22	G
5	5	42	G
5	5	43	G
5	5	46	G
5	5	47	U
5	5	53	G
5	5	54	U
5	5	55	U
5	5	56	C
5	5	57	A

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Mol	Chain	Res	Type
5	5	60	U
5	5	61	C
5	5	66	C
5	5	69	G
5	5	72	G
5	5	73	A
5	5	74	C
5	5	75	C
5	5	76	A

All (18) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	404	A
1	1	784	G
1	1	894	U
1	1	1379	U
1	1	1962	5MC
1	1	2193	G
1	1	2225	A
1	1	2286	G
1	1	2425	A
1	1	2756	U
2	2	516	PSU
2	2	1109	C
2	2	1383	C
5	5	2	G
5	5	3	G
5	5	19	G
5	5	59	A
5	5	72	G

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

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

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

RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	2MG	2	966	2	18,26,27	1.05	1 (5%)	16,38,41	1.42	3 (18%)
1	PSU	1	746	1,56	18,21,22	1.09	1 (5%)	21,30,33	1.87	5 (23%)
2	PSU	2	516	2	18,21,22	1.08	1 (5%)	21,30,33	1.87	5 (23%)
1	PSU	1	955	1	18,21,22	1.13	1 (5%)	21,30,33	1.85	4 (19%)
1	PSU	1	2580	1	18,21,22	1.10	2 (11%)	21,30,33	2.17	6 (28%)
1	PSU	1	1917	1	18,21,22	1.10	1 (5%)	21,30,33	1.96	5 (23%)
1	2MG	1	2445	1	18,26,27	1.19	2 (11%)	16,38,41	0.92	1 (6%)
1	OMU	1	2552	1	19,22,23	3.07	8 (42%)	25,31,34	1.82	5 (20%)
2	UR3	2	1498	2	19,22,23	2.80	8 (42%)	26,32,35	1.58	4 (15%)
46	0TD	q	89	46	8,9,10	1.78	2 (25%)	6,11,13	1.77	1 (16%)
2	2MG	2	1207	2	18,26,27	1.17	2 (11%)	16,38,41	0.86	1 (6%)
1	5MC	1	1962	1	19,22,23	0.57	0	26,32,35	0.58	0
2	MA6	2	1519	2	19,26,27	1.80	3 (15%)	18,38,41	3.47	3 (16%)
1	5MU	1	1939	1,56	19,22,23	0.42	0	27,32,35	0.49	0
1	1MG	1	745	1	19,26,27	3.11	7 (36%)	18,39,42	1.61	4 (22%)
1	G7M	1	2069	1	20,26,27	2.67	7 (35%)	16,39,42	1.17	1 (6%)
1	OMG	1	2251	1,5	19,26,27	1.16	2 (10%)	21,38,41	0.81	1 (4%)
2	MA6	2	1518	2	19,26,27	1.81	3 (15%)	18,38,41	3.37	3 (16%)
1	2MA	1	2503	1,56	18,25,26	4.77	11 (61%)	20,37,40	2.53	4 (20%)
1	PSU	1	2457	1	18,21,22	1.07	1 (5%)	21,30,33	1.92	6 (28%)
1	PSU	1	2605	1	18,21,22	1.13	1 (5%)	21,30,33	1.96	5 (23%)
1	OMC	1	2498	1	19,22,23	0.55	0	25,31,34	0.67	0
2	5MC	2	1407	2	19,22,23	0.55	0	26,32,35	0.63	0
1	6MZ	1	1618	1	17,25,26	3.88	6 (35%)	15,36,39	4.52	6 (40%)
1	2MG	1	1835	1	18,26,27	1.18	2 (11%)	16,38,41	0.83	1 (6%)
1	5MU	1	747	1	19,22,23	0.43	0	27,32,35	0.57	0
2	5MC	2	967	2	19,22,23	1.53	3 (15%)	26,32,35	1.35	4 (15%)
1	PSU	1	1911	1	18,21,22	1.13	1 (5%)	21,30,33	1.95	5 (23%)
2	2MG	2	1516	2	18,26,27	1.21	2 (11%)	16,38,41	0.91	1 (6%)
2	7MG	2	527	2	23,26,27	1.09	1 (4%)	27,39,42	0.89	2 (7%)
2	4OC	2	1402	2	20,23,24	3.20	8 (40%)	25,32,35	0.88	1 (4%)
1	PSU	1	2504	1	18,21,22	1.57	5 (27%)	21,30,33	2.11	4 (19%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the

Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns.
'-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	2MG	2	966	2	-	0/5/27/28	0/3/3/3
1	PSU	1	746	1,56	-	0/7/25/26	0/2/2/2
2	PSU	2	516	2	-	2/7/25/26	0/2/2/2
1	PSU	1	955	1	-	0/7/25/26	0/2/2/2
1	PSU	1	2580	1	-	0/7/25/26	0/2/2/2
1	PSU	1	1917	1	-	0/7/25/26	0/2/2/2
1	2MG	1	2445	1	-	0/5/27/28	0/3/3/3
1	OMU	1	2552	1	-	0/9/27/28	0/2/2/2
2	UR3	2	1498	2	-	2/7/25/26	0/2/2/2
46	0TD	q	89	46	-	3/7/12/14	-
2	2MG	2	1207	2	-	0/5/27/28	0/3/3/3
1	5MC	1	1962	1	-	0/7/25/26	0/2/2/2
2	MA6	2	1519	2	-	3/7/29/30	0/3/3/3
1	5MU	1	1939	1,56	-	0/7/25/26	0/2/2/2
1	1MG	1	745	1	-	0/3/25/26	0/3/3/3
1	G7M	1	2069	1	-	0/3/25/26	0/3/3/3
1	OMG	1	2251	1,5	-	0/5/27/28	0/3/3/3
2	MA6	2	1518	2	-	0/7/29/30	0/3/3/3
1	2MA	1	2503	1,56	-	3/3/25/26	0/3/3/3
1	PSU	1	2457	1	-	0/7/25/26	0/2/2/2
1	PSU	1	2605	1	-	0/7/25/26	0/2/2/2
1	OMC	1	2498	1	-	0/9/27/28	0/2/2/2
2	5MC	2	1407	2	-	0/7/25/26	0/2/2/2
1	6MZ	1	1618	1	-	1/5/27/28	0/3/3/3
1	2MG	1	1835	1	-	2/5/27/28	0/3/3/3
1	5MU	1	747	1	-	0/7/25/26	0/2/2/2
2	5MC	2	967	2	-	2/7/25/26	0/2/2/2
1	PSU	1	1911	1	-	0/7/25/26	0/2/2/2
2	2MG	2	1516	2	-	0/5/27/28	0/3/3/3
2	7MG	2	527	2	-	3/7/37/38	0/3/3/3
2	4OC	2	1402	2	-	1/9/29/30	0/2/2/2
1	PSU	1	2504	1	-	2/7/25/26	0/2/2/2

All (92) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	1618	6MZ	C3'-C4'	-9.25	1.29	1.53
1	1	2503	2MA	C3'-C4'	-9.14	1.29	1.53
1	1	745	1MG	C2-N3	8.85	1.47	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	2503	2MA	C4-N3	8.41	1.48	1.35
1	1	2503	2MA	O4'-C1'	-7.88	1.30	1.40
2	2	1498	UR3	C2-N1	7.45	1.48	1.38
1	1	1618	6MZ	O4'-C1'	-7.41	1.31	1.40
2	2	1402	4OC	C4-N3	7.37	1.45	1.32
1	1	2503	2MA	O4'-C4'	7.30	1.61	1.45
1	1	1618	6MZ	O4'-C4'	7.17	1.60	1.45
1	1	2552	OMU	C2-N1	7.15	1.49	1.38
1	1	2552	OMU	C2-N3	6.97	1.50	1.38
1	1	2503	2MA	C2-N3	6.86	1.45	1.34
1	1	745	1MG	C2-N2	6.35	1.45	1.34
2	2	1402	4OC	C2-N3	6.31	1.48	1.36
2	2	1402	4OC	C6-C5	6.22	1.49	1.35
2	2	1498	UR3	C6-C5	6.14	1.49	1.35
1	1	2069	G7M	C2-N2	5.83	1.47	1.34
2	2	1518	MA6	C6-N6	5.73	1.50	1.37
2	2	1519	MA6	C6-N6	5.72	1.50	1.37
1	1	2552	OMU	C6-C5	5.71	1.48	1.35
1	1	2503	2MA	C2-N1	5.67	1.43	1.34
1	1	1618	6MZ	C6-C5	-5.64	1.36	1.44
1	1	745	1MG	C4-N3	5.17	1.49	1.37
1	1	2069	G7M	C2-N3	5.17	1.45	1.33
1	1	2069	G7M	C4-N3	5.07	1.49	1.37
2	2	967	5MC	C5-C4	4.96	1.47	1.44
2	2	1498	UR3	C2-N3	4.95	1.48	1.39
1	1	2503	2MA	C6-N1	4.85	1.42	1.33
2	2	1402	4OC	C4-N4	4.66	1.45	1.36
2	2	527	7MG	C5-N7	4.50	1.41	1.35
2	2	1402	4OC	C2-N1	4.33	1.49	1.40
1	1	2552	OMU	C4-N3	4.19	1.45	1.38
1	1	2069	G7M	C6-N1	3.90	1.43	1.37
2	2	1518	MA6	C6-C5	-3.85	1.38	1.44
2	2	1519	MA6	C6-C5	-3.74	1.39	1.44
2	2	516	PSU	C6-C5	3.72	1.39	1.35
1	1	955	PSU	C6-C5	3.72	1.39	1.35
1	1	2605	PSU	C6-C5	3.70	1.39	1.35
2	2	1402	4OC	C5-C4	3.67	1.49	1.41
1	1	1911	PSU	C6-C5	3.66	1.39	1.35
1	1	2069	G7M	C2-N1	3.65	1.46	1.37
1	1	2069	G7M	C5-C6	3.59	1.54	1.45
1	1	1917	PSU	C6-C5	3.58	1.39	1.35
1	1	745	1MG	C2-N1	3.46	1.43	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	1	745	1MG	C5-C4	-3.44	1.34	1.43
1	1	746	PSU	C6-C5	3.41	1.39	1.35
1	1	2457	PSU	C6-C5	3.40	1.39	1.35
1	1	2504	PSU	C4-N3	-3.23	1.32	1.38
1	1	2580	PSU	C6-C5	3.20	1.38	1.35
2	2	1402	4OC	C6-N1	3.18	1.45	1.38
1	1	1835	2MG	C8-N7	-3.11	1.30	1.34
1	1	1618	6MZ	O2'-C2'	-3.09	1.35	1.43
1	1	2445	2MG	C8-N7	-3.05	1.30	1.34
1	1	2503	2MA	O2'-C2'	-3.05	1.35	1.43
2	2	1498	UR3	C6-N1	3.01	1.45	1.38
2	2	1516	2MG	C8-N7	-2.98	1.30	1.34
2	2	1207	2MG	C8-N7	-2.97	1.30	1.34
46	q	89	0TD	CB-CA	-2.91	1.53	1.54
1	1	2552	OMU	O4-C4	-2.90	1.18	1.24
1	1	2251	OMG	C8-N7	-2.87	1.30	1.34
2	2	1519	MA6	C2-N3	2.83	1.36	1.32
1	1	2552	OMU	C6-N1	2.82	1.44	1.38
2	2	1518	MA6	C2-N3	2.80	1.36	1.32
1	1	2503	2MA	O3'-C3'	2.79	1.49	1.43
2	2	967	5MC	C6-N1	-2.76	1.33	1.38
1	1	2504	PSU	C6-C5	2.75	1.38	1.35
1	1	745	1MG	C5-C6	2.75	1.55	1.47
2	2	966	2MG	C6-N1	-2.73	1.33	1.37
1	1	1618	6MZ	O3'-C3'	2.68	1.49	1.43
2	2	1402	4OC	O2-C2	-2.64	1.18	1.23
2	2	1516	2MG	C5-C6	-2.54	1.42	1.47
1	1	2251	OMG	C5-C6	-2.52	1.42	1.47
1	1	2503	2MA	C6-N6	-2.50	1.25	1.34
1	1	1835	2MG	C5-C6	-2.49	1.42	1.47
2	2	1207	2MG	C5-C6	-2.48	1.42	1.47
1	1	2504	PSU	C2-N3	-2.48	1.33	1.37
1	1	2445	2MG	C5-C6	-2.47	1.42	1.47
2	2	1498	UR3	C4-N3	2.44	1.45	1.40
1	1	2503	2MA	C6-C5	2.42	1.52	1.43
1	1	2552	OMU	C5-C4	2.39	1.48	1.43
1	1	2552	OMU	O2-C2	-2.36	1.18	1.23
1	1	2069	G7M	O6-C6	-2.35	1.17	1.23
2	2	967	5MC	C6-C5	2.34	1.38	1.34
1	1	2504	PSU	C2-N1	-2.27	1.33	1.36
2	2	1498	UR3	O4-C4	-2.27	1.18	1.23
1	1	2504	PSU	C2'-C1'	-2.25	1.50	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	1498	UR3	C5-C4	2.24	1.49	1.43
1	1	2580	PSU	O4'-C1'	-2.19	1.40	1.43
2	2	1498	UR3	O2-C2	-2.14	1.18	1.22
1	1	745	1MG	C6-N1	2.05	1.43	1.39
46	q	89	0TD	OD1-CG	2.02	1.28	1.22

All (91) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	1618	6MZ	C1'-N9-C4	13.56	150.46	126.64
2	2	1519	MA6	N1-C6-N6	-12.61	102.26	116.83
2	2	1518	MA6	N1-C6-N6	-12.20	102.74	116.83
1	1	2503	2MA	C1'-N9-C4	8.71	141.94	126.64
1	1	2504	PSU	N1-C2-N3	6.66	122.19	115.17
1	1	1618	6MZ	N3-C2-N1	-6.44	119.93	128.67
2	2	1519	MA6	N3-C2-N1	-6.31	120.10	128.67
2	2	1518	MA6	N3-C2-N1	-6.24	120.20	128.67
1	1	2552	OMU	C4-N3-C2	-5.67	119.57	126.61
2	2	1498	UR3	C4-N3-C2	-5.37	120.25	124.58
1	1	2580	PSU	N1-C2-N3	5.18	120.63	115.17
1	1	2580	PSU	C4-N3-C2	-4.99	119.49	126.37
1	1	1917	PSU	C4-N3-C2	-4.92	119.59	126.37
1	1	1911	PSU	C4-N3-C2	-4.91	119.61	126.37
1	1	746	PSU	C4-N3-C2	-4.90	119.61	126.37
1	1	1911	PSU	N1-C2-N3	4.85	120.28	115.17
1	1	1917	PSU	N1-C2-N3	4.85	120.28	115.17
1	1	2605	PSU	C4-N3-C2	-4.82	119.73	126.37
1	1	1618	6MZ	C9-N6-C6	-4.82	118.38	122.85
1	1	2605	PSU	N1-C2-N3	4.78	120.21	115.17
1	1	2457	PSU	N1-C2-N3	4.77	120.20	115.17
1	1	2457	PSU	C4-N3-C2	-4.71	119.89	126.37
1	1	746	PSU	N1-C2-N3	4.65	120.07	115.17
1	1	955	PSU	C4-N3-C2	-4.61	120.02	126.37
2	2	516	PSU	C4-N3-C2	-4.58	120.06	126.37
1	1	2503	2MA	C2-N3-C4	4.57	119.15	115.46
1	1	955	PSU	N1-C2-N3	4.56	119.97	115.17
2	2	516	PSU	N1-C2-N3	4.54	119.95	115.17
1	1	2504	PSU	C4-N3-C2	-4.33	120.41	126.37
1	1	1618	6MZ	C2-N1-C6	4.25	119.90	116.60
1	1	745	1MG	C5-C6-N1	4.09	119.88	113.96
1	1	1618	6MZ	O4'-C1'-N9	3.98	114.02	108.75
1	1	2552	OMU	N3-C2-N1	3.95	120.03	114.89

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	1618	6MZ	C4'-O4'-C1'	-3.80	106.44	109.92
2	2	967	5MC	C5-C6-N1	-3.64	119.36	123.31
1	1	2552	OMU	C5-C4-N3	3.63	119.88	114.80
1	1	2504	PSU	O2-C2-N1	-3.59	119.09	122.79
1	1	745	1MG	C8-N7-C5	3.58	108.65	102.55
2	2	1498	UR3	C5-C4-N3	3.57	119.74	115.04
1	1	2580	PSU	O2-C2-N1	-3.50	119.17	122.79
2	2	1518	MA6	C2-N1-C6	3.32	120.10	116.84
2	2	1519	MA6	C2-N1-C6	3.32	120.09	116.84
1	1	2457	PSU	O2-C2-N1	-3.15	119.54	122.79
46	q	89	0TD	OD2-CG-CB	3.12	119.89	113.15
1	1	2069	G7M	C2-N1-C6	-3.08	119.47	125.11
1	1	955	PSU	O2-C2-N1	-2.99	119.70	122.79
1	1	2552	OMU	O4-C4-C5	-2.93	120.10	125.16
1	1	1917	PSU	O2-C2-N1	-2.89	119.81	122.79
1	1	2580	PSU	C6-C5-C4	2.89	120.12	118.17
1	1	2503	2MA	N3-C2-N1	-2.85	120.78	125.77
2	2	966	2MG	C8-N7-C5	2.85	107.40	102.55
1	1	2605	PSU	O2-C2-N1	-2.83	119.86	122.79
1	1	2503	2MA	C4'-O4'-C1'	-2.76	107.40	109.92
1	1	746	PSU	O2-C2-N1	-2.75	119.95	122.79
1	1	1911	PSU	O2-C2-N1	-2.75	119.95	122.79
1	1	2580	PSU	C6-N1-C2	-2.74	120.15	122.69
1	1	2580	PSU	O4'-C1'-C2'	2.66	108.83	105.15
2	2	967	5MC	C5-C4-N3	-2.56	119.13	121.75
1	1	955	PSU	C6-N1-C2	-2.54	120.33	122.69
2	2	516	PSU	C6-N1-C2	-2.54	120.34	122.69
2	2	516	PSU	O2-C2-N1	-2.48	120.23	122.79
1	1	745	1MG	O6-C6-C5	-2.46	120.14	124.18
1	1	2605	PSU	C6-N1-C2	-2.46	120.41	122.69
1	1	1911	PSU	C6-N1-C2	-2.45	120.42	122.69
1	1	2457	PSU	C6-N1-C2	-2.43	120.43	122.69
2	2	527	7MG	C4-C5-N7	2.40	108.21	105.38
1	1	1917	PSU	C6-N1-C2	-2.37	120.49	122.69
2	2	967	5MC	C2'-C1'-N1	-2.37	106.67	113.25
2	2	1402	4OC	C6-C5-C4	2.36	119.85	117.00
2	2	1498	UR3	C6-N1-C2	-2.34	119.89	121.80
1	1	2445	2MG	O6-C6-C5	2.32	128.91	124.32
2	2	967	5MC	O2-C2-N3	-2.28	118.74	122.33
2	2	966	2MG	C5-C6-N1	2.28	118.41	114.07
2	2	1207	2MG	O6-C6-C5	2.24	128.75	124.32
1	1	2552	OMU	O2-C2-N1	-2.23	119.90	122.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	1498	UR3	C1'-N1-C2	2.21	120.65	117.04
2	2	966	2MG	CM2-N2-C2	-2.19	118.94	123.65
2	2	1516	2MG	O6-C6-C5	2.18	128.65	124.32
1	1	1835	2MG	O6-C6-C5	2.18	128.64	124.32
2	2	527	7MG	C5-C4-N9	2.17	109.11	106.33
1	1	746	PSU	C6-N1-C2	-2.17	120.68	122.69
1	1	746	PSU	C6-C5-C4	2.16	119.63	118.17
1	1	2605	PSU	C6-C5-C4	2.15	119.62	118.17
1	1	2251	OMG	O6-C6-C5	2.15	128.58	124.32
1	1	1917	PSU	C6-C5-C4	2.10	119.59	118.17
2	2	516	PSU	C3'-C2'-C1'	2.06	104.12	101.69
1	1	2457	PSU	C6-C5-C4	2.05	119.56	118.17
1	1	1911	PSU	C6-C5-C4	2.02	119.54	118.17
1	1	745	1MG	CM1-N1-C6	2.02	120.28	117.54
1	1	2504	PSU	C5-C6-N1	-2.02	119.34	122.14
1	1	2457	PSU	O4'-C1'-C2'	2.01	107.94	105.15

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	2	516	PSU	O4'-C1'-C5-C4
2	2	516	PSU	O4'-C1'-C5-C6
1	1	2504	PSU	O4'-C4'-C5'-O5'
2	2	967	5MC	O4'-C4'-C5'-O5'
2	2	1519	MA6	O4'-C4'-C5'-O5'
1	1	2504	PSU	C3'-C4'-C5'-O5'
2	2	527	7MG	C3'-C4'-C5'-O5'
1	1	1835	2MG	O4'-C4'-C5'-O5'
1	1	1835	2MG	C3'-C4'-C5'-O5'
1	1	2503	2MA	O4'-C4'-C5'-O5'
1	1	2503	2MA	C3'-C4'-C5'-O5'
2	2	1519	MA6	C3'-C4'-C5'-O5'
2	2	527	7MG	O4'-C4'-C5'-O5'
2	2	967	5MC	C3'-C4'-C5'-O5'
2	2	1498	UR3	O4'-C4'-C5'-O5'
2	2	1498	UR3	C3'-C4'-C5'-O5'
46	q	89	0TD	CG-CB-SB-CSB
2	2	1519	MA6	C5-C6-N6-C9
46	q	89	0TD	SB-CB-CG-OD1
2	2	527	7MG	C4'-C5'-O5'-P
46	q	89	0TD	CA-CB-SB-CSB

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Mol	Chain	Res	Type	Atoms
2	2	1402	4OC	O4'-C4'-C5'-O5'
1	1	2503	2MA	C4'-C5'-O5'-P
1	1	1618	6MZ	N1-C6-N6-C9

There are no ring outliers.

15 monomers are involved in 24 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	1	746	PSU	1	0
2	2	516	PSU	1	0
1	1	955	PSU	1	0
1	1	2580	PSU	2	0
1	1	1917	PSU	1	0
1	1	2552	OMU	2	0
46	q	89	0TD	4	0
1	1	1962	5MC	3	0
1	1	1939	5MU	1	0
1	1	745	1MG	1	0
1	1	2069	G7M	1	0
2	2	1518	MA6	1	0
1	1	747	5MU	1	0
2	2	1516	2MG	2	0
2	2	1402	4OC	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 396 ligands modelled in this entry, 395 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
57	LYS	5	101	5	7,8,9	1.10	1 (14%)	3,8,10	0.54	0

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
57	LYS	5	101	5	-	3/6/7/9	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
57	5	101	LYS	O-C	2.61	1.29	1.20

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
57	5	101	LYS	CE-CD-CG-CB
57	5	101	LYS	CG-CD-CE-NZ
57	5	101	LYS	CA-CB-CG-CD

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

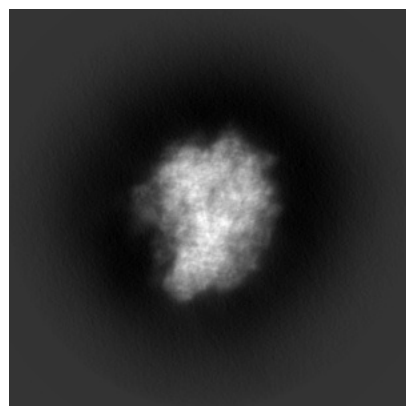
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-42714. These allow visual inspection of the internal detail of the map and identification of artifacts.

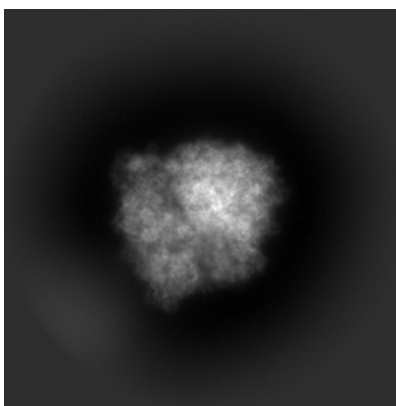
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

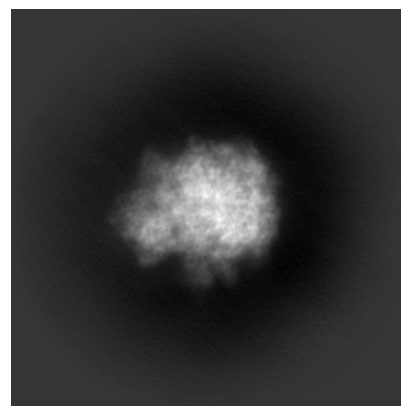
6.1.1 Primary map



X

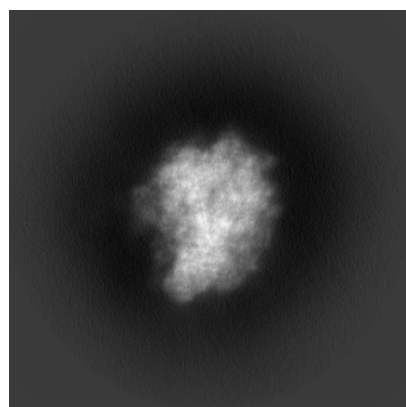


Y

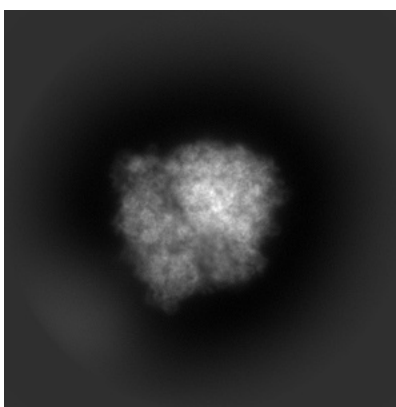


Z

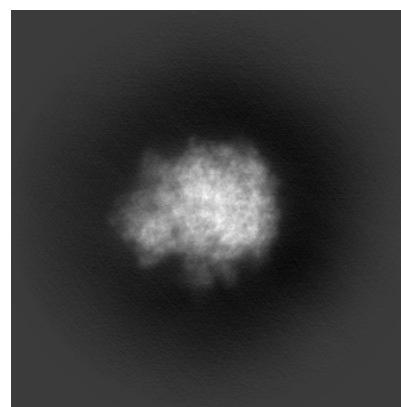
6.1.2 Raw map



X



Y

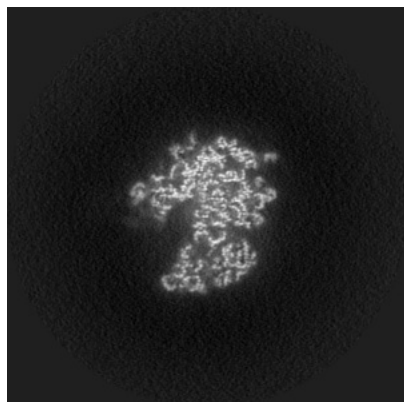


Z

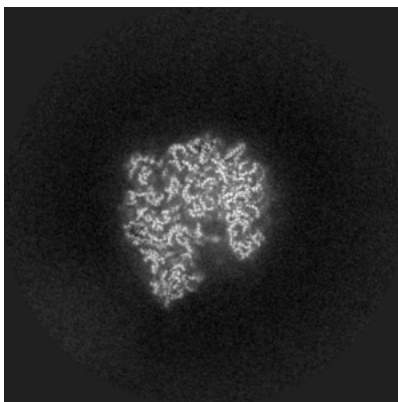
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

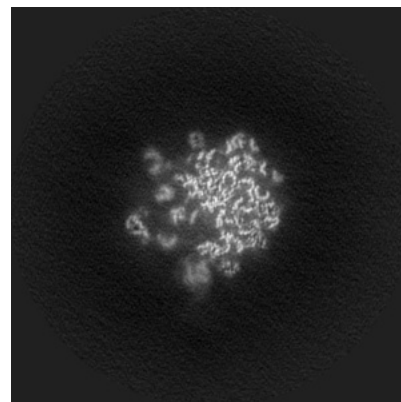
6.2.1 Primary map



X Index: 256

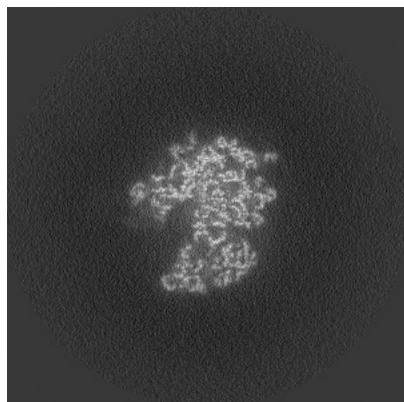


Y Index: 256

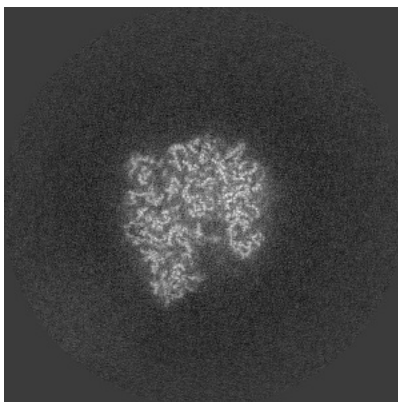


Z Index: 256

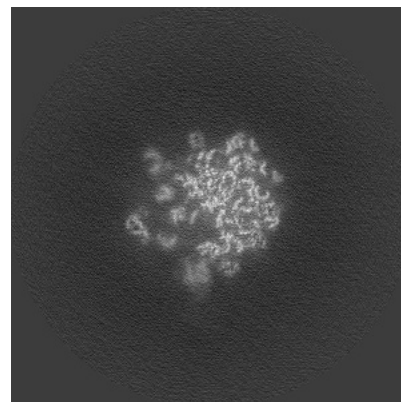
6.2.2 Raw map



X Index: 256



Y Index: 256

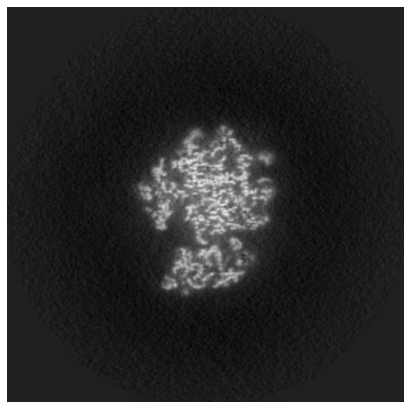


Z Index: 256

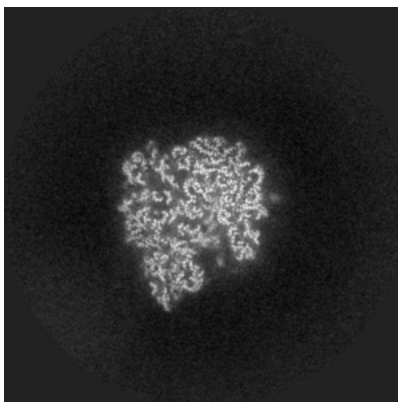
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

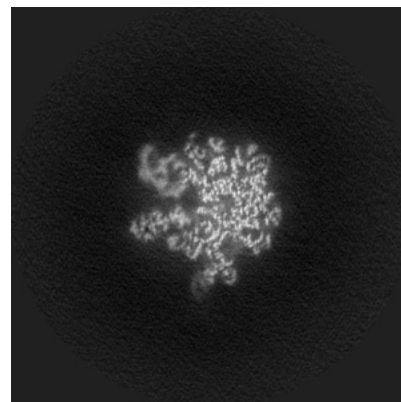
6.3.1 Primary map



X Index: 264

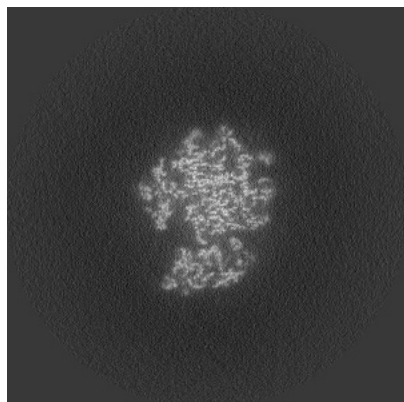


Y Index: 250

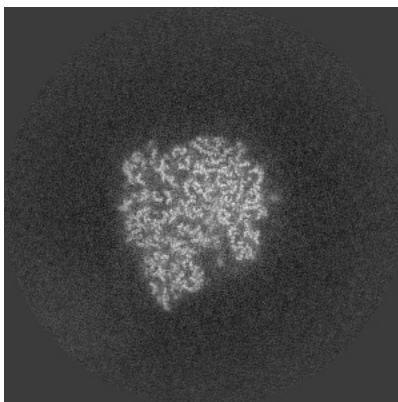


Z Index: 274

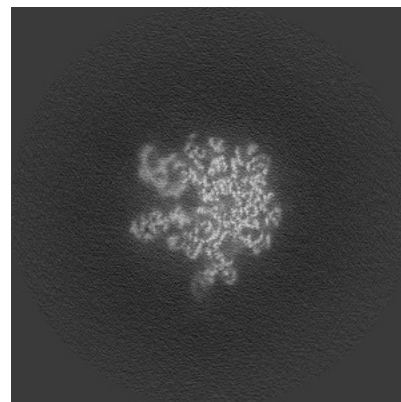
6.3.2 Raw map



X Index: 264



Y Index: 250

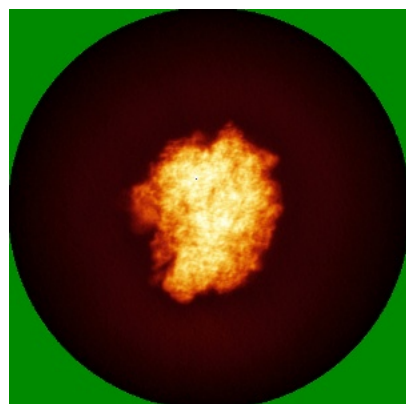


Z Index: 274

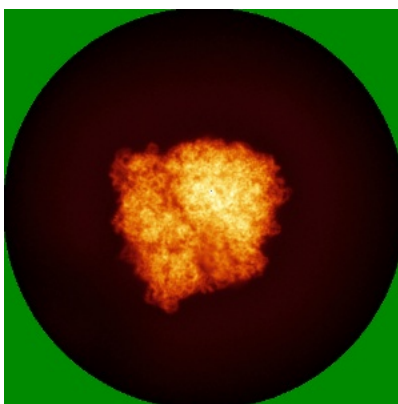
The images above show the largest variance slices of the map in three orthogonal directions.

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

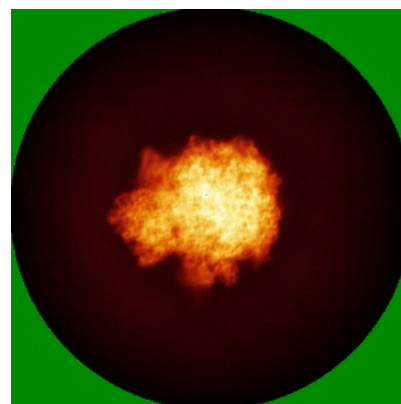
6.4.1 Primary map



X

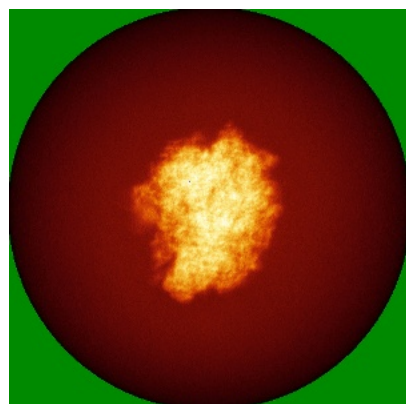


Y

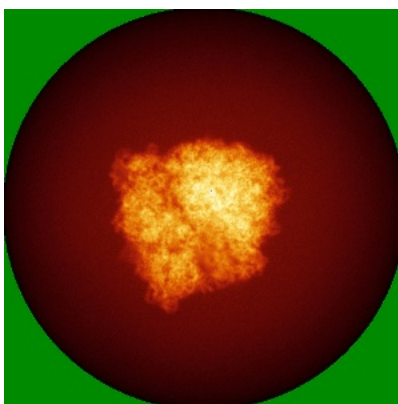


Z

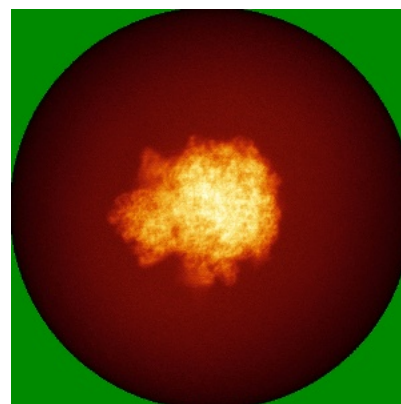
6.4.2 Raw map



X



Y

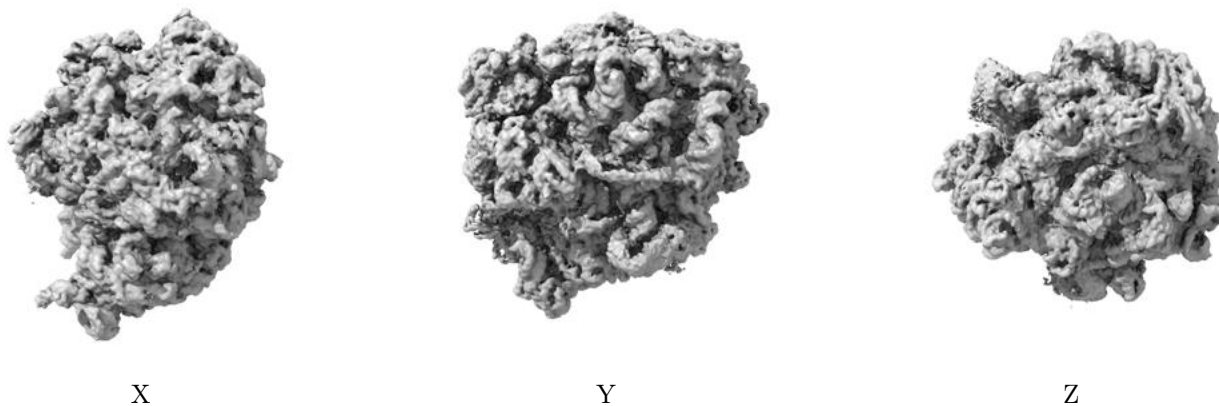


Z

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

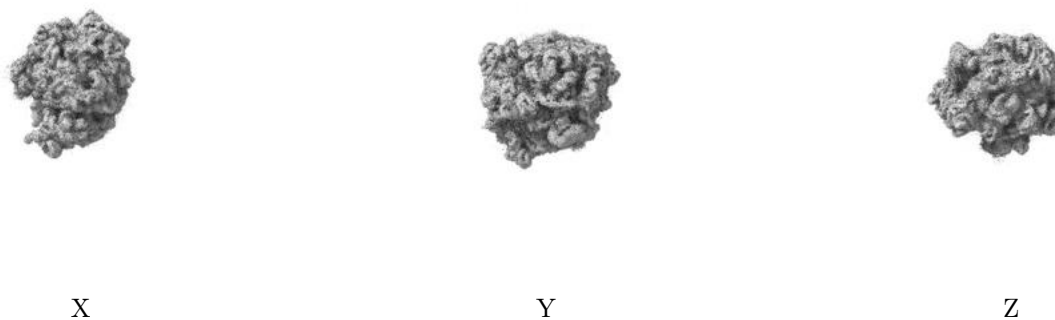
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.012. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



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

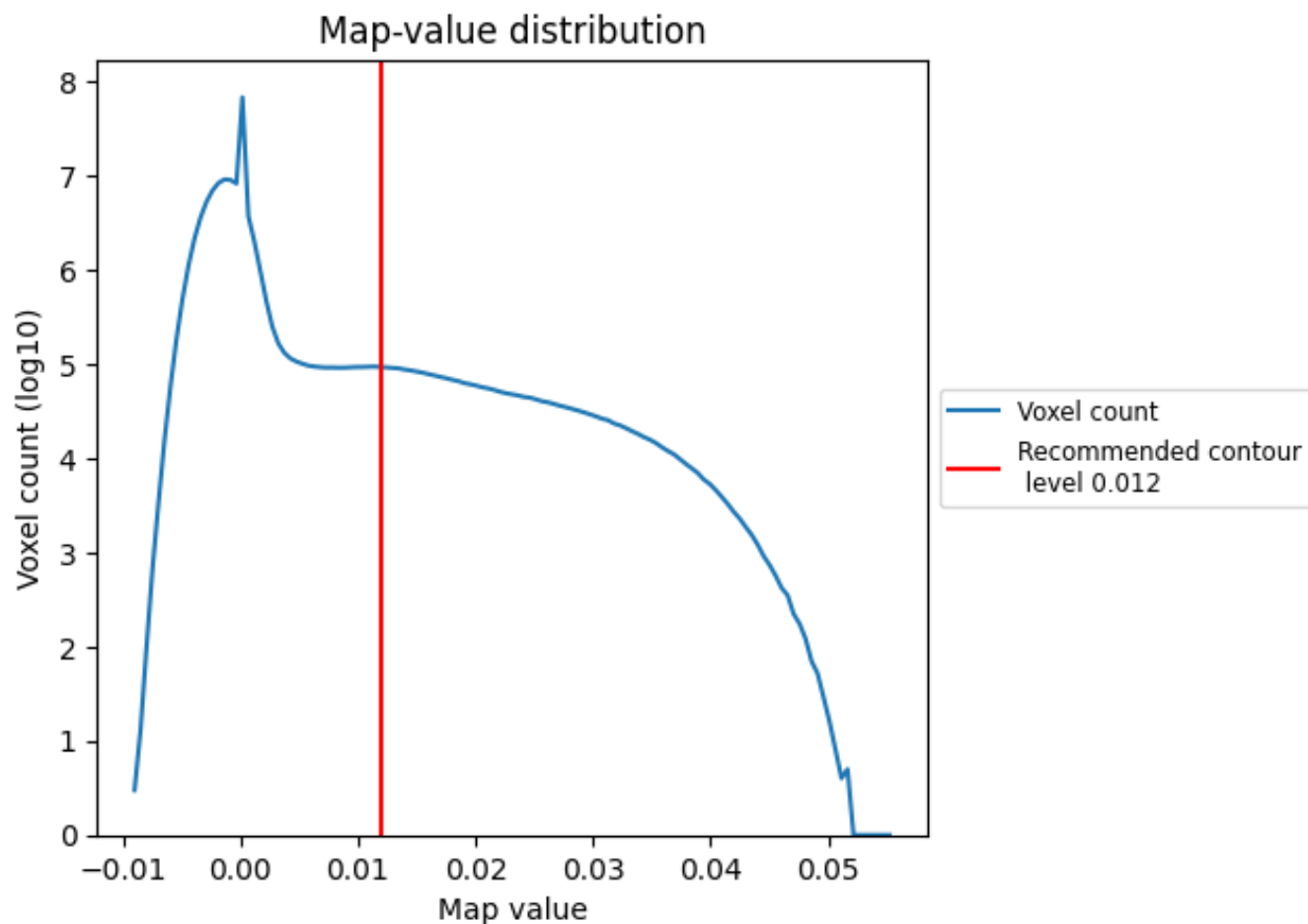
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

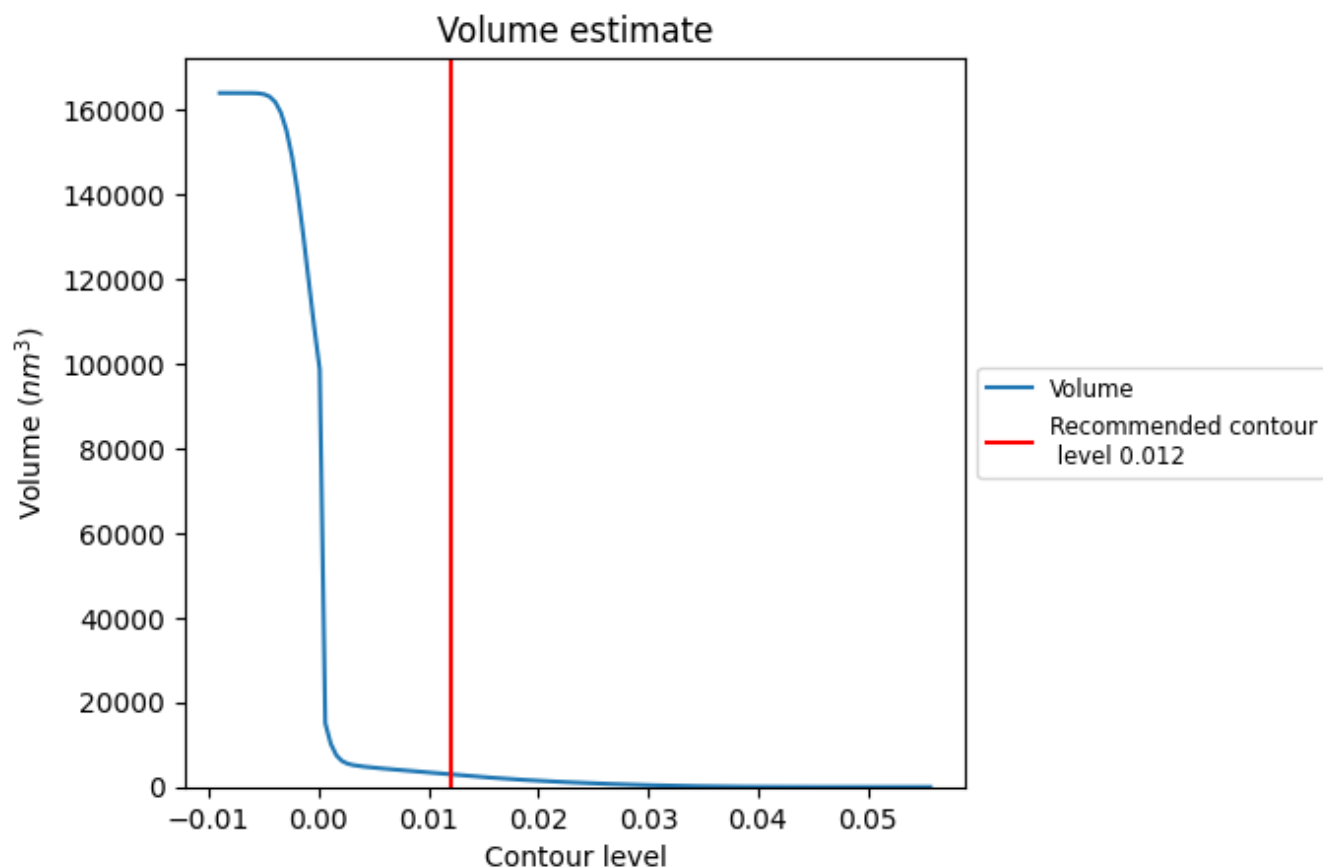
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

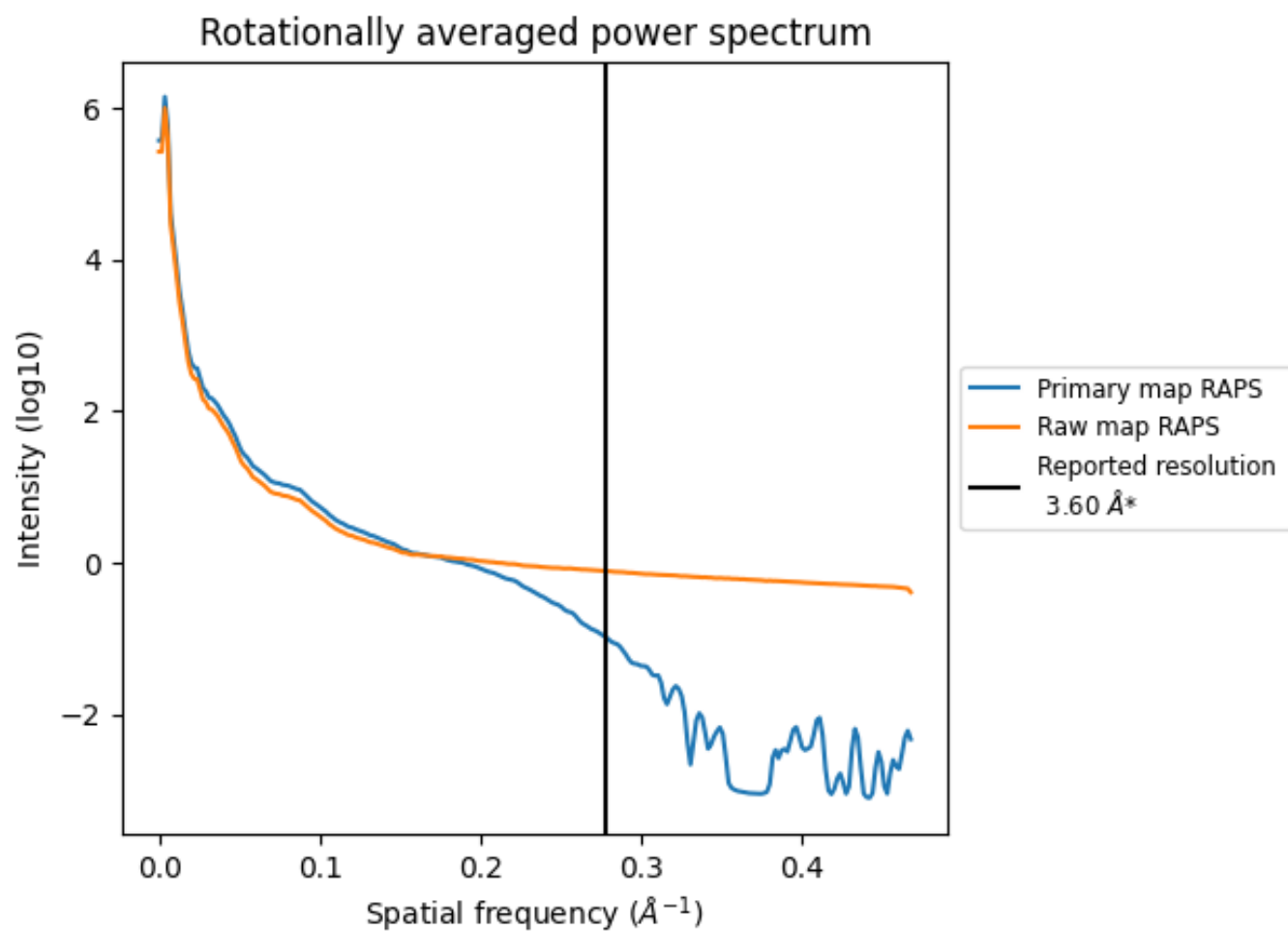
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2984 nm³; this corresponds to an approximate mass of 2696 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 ⓘ

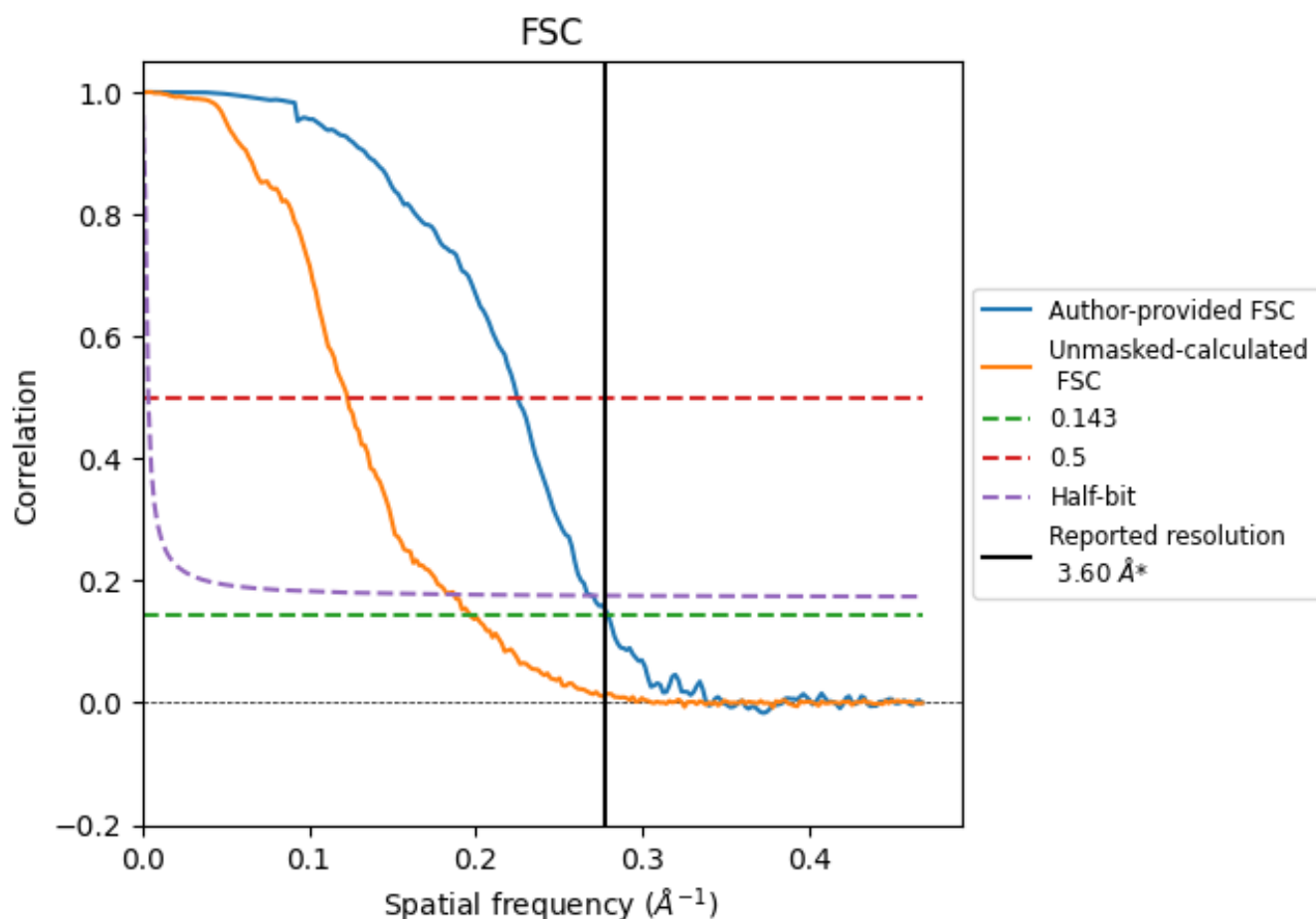


*Reported resolution corresponds to spatial frequency of 0.278 Å⁻¹

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 0.278 Å⁻¹

8.2 Resolution estimates [i](#)

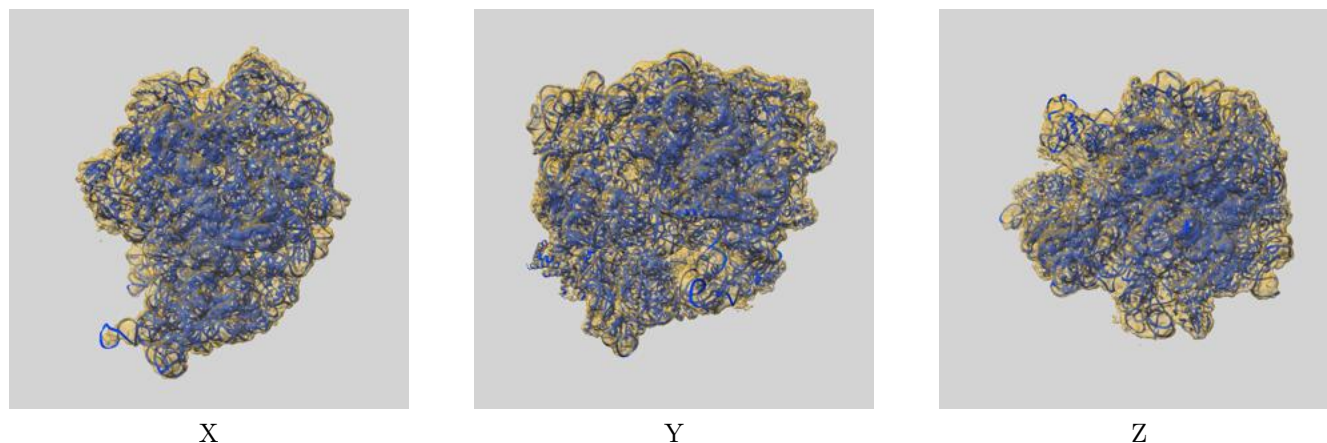
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.60	-	-
Author-provided FSC curve	3.58	4.44	3.71
Unmasked-calculated*	5.08	8.13	5.35

*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 5.08 differs from the reported value 3.6 by more than 10 %

9 Map-model fit [i](#)

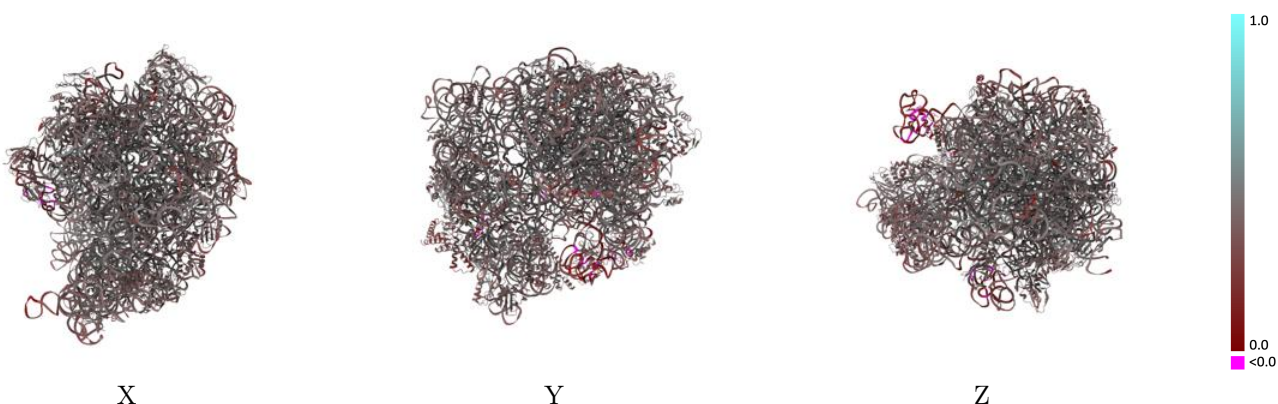
This section contains information regarding the fit between EMDB map EMD-42714 and PDB model 8UX8. Per-residue inclusion information can be found in section [3](#) on page [17](#).

9.1 Map-model overlay [i](#)



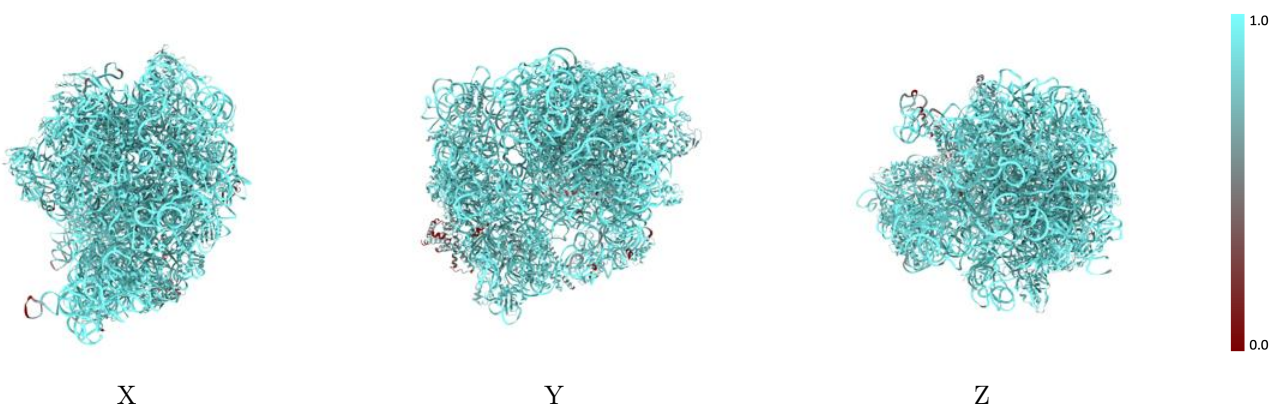
The images above show the 3D surface view of the map at the recommended contour level 0.012 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



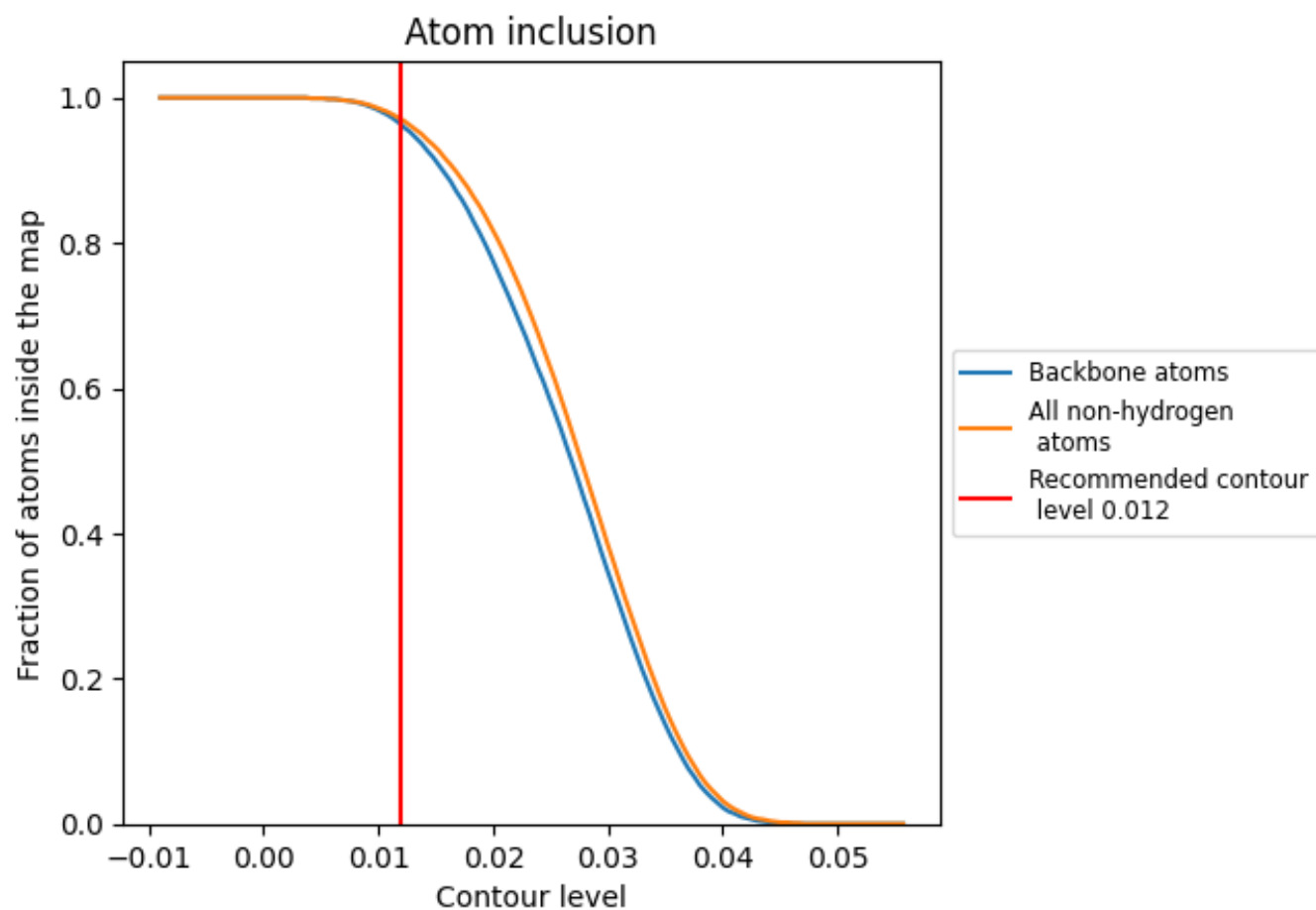
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.012).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 97% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ











































The table lists the average atom inclusion at the recommended contour level (0.012) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9700	 0.4060
1	 0.9890	 0.4060
2	 0.9870	 0.4080
3	 0.9770	 0.3810
4	 1.0000	 0.3440
5	 1.0000	 0.3840
A	 0.7680	 0.1920
B	 0.9980	 0.4600
C	 0.9680	 0.4520
D	 0.9180	 0.4220
E	 0.9290	 0.3660
F	 0.9180	 0.3970
G	 0.7430	 0.3310
J	 0.9860	 0.4350
K	 0.9970	 0.4530
L	 0.9570	 0.4370
M	 0.9920	 0.4400
N	 0.9950	 0.4330
O	 0.9470	 0.4010
P	 0.9800	 0.4490
Q	 0.9770	 0.4080
R	 0.9320	 0.4390
S	 0.9870	 0.4400
T	 0.9600	 0.4270
U	 0.9250	 0.4120
V	 0.9270	 0.4140
W	 0.9950	 0.4500
X	 0.9870	 0.4330
Y	 0.9280	 0.3600
Z	 0.9470	 0.4310
a	 0.8200	 0.3530
b	 0.9860	 0.4470
c	 0.9950	 0.4220
d	 1.0000	 0.4510
e	 1.0000	 0.4430



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Chain	Atom inclusion	Q-score
f	 1.0000	 0.4460
g	 0.5550	 0.3390
h	 0.9580	 0.4090
i	 0.9280	 0.3870
j	 0.9780	 0.4190
k	 0.9380	 0.4030
l	 0.9550	 0.3640
m	 0.9540	 0.4270
n	 0.9350	 0.4010
o	 0.8710	 0.3690
p	 0.9730	 0.4190
q	 0.9890	 0.4310
r	 0.9230	 0.3740
s	 0.9700	 0.3920
t	 0.9830	 0.3800
u	 0.9390	 0.4220
v	 0.9830	 0.4110
w	 0.9430	 0.3650
x	 0.9400	 0.3940
y	 0.9760	 0.3600
z	 0.7110	 0.3290