



Full wwPDB EM Validation Report ⓘ

Mar 3, 2024 – 11:28 AM EST

PDB ID : 6BY7
EMDB ID : EMD-7304
Title : Folding DNA into a lipid-conjugated nano-barrel for controlled reconstitution of membrane proteins
Authors : Dong, Y.; Chen, S.; Zhang, S.; Sodroski, J.; Yang, Z.; Liu, D.; Mao, Y.
Deposited on : 2017-12-20
Resolution : 7.50 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:

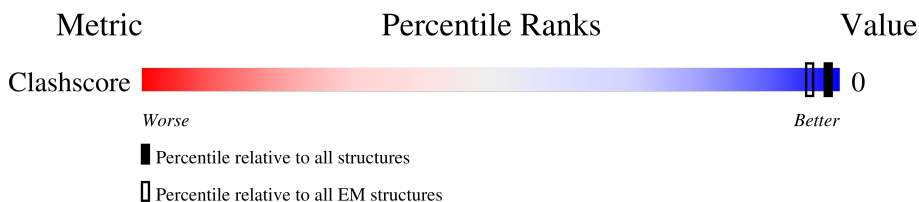
EMDB validation analysis : 0.0.1.dev70
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance i

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


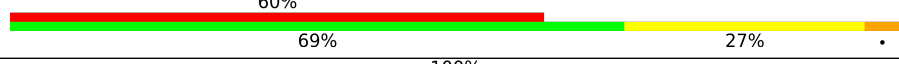
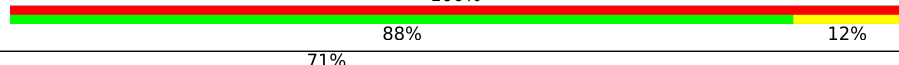







The reported resolution of this entry is 7.50 Å.

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	158937	4297

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	1A	52	
2	1B	55	
3	1C	16	
4	1D	59	
5	1E	51	
6	1F	46	
7	1G	16	
8	1H	48	
9	1I	47	
10	1J	24	

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Mol	Chain	Length	Quality of chain
11	1K	46	100% 67% 28%
12	1L	16	100% 81% 19%
13	1M	32	50% 88% 9%
14	1O	40	58% 75% 25%
15	1P	46	100% 72% 24%
16	1Q	37	78% 84% 16%
17	1R	48	58% 73% 25%
18	1S	37	65% 76% 22%
19	1T	16	100% 94% 6%
20	1U	40	38% 90% 8%
21	1V	26	100% 85% 15%
22	1W	40	80% 85% 15%
23	1X	48	56% 85% 12%
24	1Y	27	85% 89% 11%
25	1Z	26	100% 88% 8%
26	1a	47	85% 85% 15%
27	1b	32	41% 75% 25%
28	1c	40	32% 92% 8%
29	1d	40	75% 92% 8%
30	1e	26	100% 92% 8%
31	1f	40	38% 85% 15%
32	1g	48	44% 92% 6%
33	1h	48	31% 83% 17%
34	1i	48	98% 90% 10%
35	1j	32	53% 91% 9%

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Mol	Chain	Length	Quality of chain
36	1k	40	48% 80% 20%
37	1l	48	100% 88% 12%
38	1m	16	100% 81% 19%
39	1n	56	36% 91% 7%
40	1o	40	95% 82% 18%
41	1p	40	65% 80% 20%
42	1q	48	94% 85% 10%
43	1r	32	34% 88% 12%
44	1s	32	69% 75% 25%
45	1t	32	47% 88% 12%
46	1u	48	100% 73% 27%
47	1v	16	100% 94% 6%
48	1w	40	40% 85% 10% 5%
49	1x	16	94% 69% 31%
50	2N	36	47% 86% 11%
51	2A	32	94% 72% 25%
52	2B	48	65% 81% 15%
53	2C	26	88% 85% 12%
54	2D	32	50% 94% ..
55	2E	40	50% 88% 12%
56	2F	48	42% 85% 10%
57	2G	40	78% 88% 12%
58	2H	40	98% 85% 15%
59	2I	16	100% 94% 6%
60	2J	29	83% 86% 14%

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Mol	Chain	Length	Quality of chain
61	2K	24	38% 83% 17%
62	2L	32	69% 91% 9%
63	2M	24	92% 96%
64	2O	26	88% 77% 12% 8%
65	2P	40	35% 75% 25%
66	2Q	40	58% 92% 5%
67	2R	40	42% 82% 18%
68	2S	58	86% 81% 19%
69	2T	24	96% 96%
70	2U	52	48% 88% 12%
71	2V	40	40% 88% 12%
72	2W	48	46% 88% 12%
73	2X	48	40% 85% 15%
74	2Y	32	16% 91% 6%
75	2Z	40	58% 82% 18%
76	2a	58	83% 88% 12%
77	2b	56	32% 84% 14%
78	2c	45	84% 93%
79	2d	52	35% 88% 10%
80	2e	37	97% 84% 14%
81	2f	48	48% 90% 10%
82	2g	48	60% 90% 10%
83	2h	56	34% 91% 5%
84	2i	32	47% 78% 22%
85	2j	16	100% 81% 19%

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Mol	Chain	Length	Quality of chain
86	2k	32	44% 91% 9%
87	2l	48	40% 88% 10%
88	2m	48	81% 94% 6%
89	2n	16	100% 81% 19%
90	2o	32	88% 91% 9%
91	2p	32	44% 88% 12%
92	2q	40	55% 80% 20%
93	2r	24	71% 79% 12% 8%
94	2s	32	56% 91% 9%
95	2t	40	100% 78% 22%
96	2u	32	72% 88% 12%
97	2v	32	50% 81% 19%
98	2w	47	74% 77% 23%
99	2x	16	100% 94% 6%
100	3N	4346	66% 83% 16%
101	3A	40	82% 88% 12%
102	3B	40	42% 80% 15% 5%
103	3C	48	46% 83% 17%
104	3D	48	46% 81% 15%
105	3E	48	54% 85% 15%
106	3F	56	32% 88% 9%
107	3G	16	100% 88% 12%
108	3H	56	71% 79% 20%
109	3I	36	42% 78% 19%
110	3J	35	100% 83% 14%

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Mol	Chain	Length	Quality of chain
111	3S	32	<p>78% 88% 12%</p>
112	3K	48	<p>63% 90% 8%</p>
113	3L	37	<p>65% 95% 5%</p>
114	3M	55	<p>65% 80% 20%</p>
115	3O	48	<p>75% 83% 15%</p>
116	3P	38	<p>100% 97%</p>
117	3Q	26	<p>88% 81% 15%</p>
118	3R	32	<p>22% 84% 16%</p>

2 Entry composition [i](#)

There are 118 unique types of molecules in this entry. The entry contains 180167 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 DNA chain called DNA (52-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	1A	52	1082	516	213	302	51	0	0

- Molecule 2 is a DNA chain called DNA (55-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	1B	55	1137	540	219	324	54	0	0

- Molecule 3 is a DNA chain called DNA (5'-D(*AP*AP*TP*AP*AP*CP*GP*GP*CP*TP*CP*AP*GP*AP*GP*C)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	1C	16	327	156	66	90	15	0	0

- Molecule 4 is a DNA chain called DNA (59-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	1D	59	1220	584	229	349	58	0	0

- Molecule 5 is a DNA chain called DNA (51-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
5	1E	51	1052	502	206	294	50	0	0

- Molecule 6 is a DNA chain called DNA (46-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
6	1F	46	950	455	181	269	45	0	0

- Molecule 7 is a DNA chain called DNA (5'-D(*TP*CP*AP*AP*CP*CP*GP*AP*GP*CP*TP*TP*GP*CP*TP*T)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
7	1G	16	321	155	55	96	15	0	0

- Molecule 8 is a DNA chain called DNA (48-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
8	1H	48	970	465	177	281	47	0	0

- Molecule 9 is a DNA chain called DNA (47-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
9	1I	47	971	462	183	280	46	0	0

- Molecule 10 is a DNA chain called DNA (5'-D(*TP*AP*TP*TP*AP*GP*CP*GP*AP*GP*AP*TP*GP*GP*TP*TP*TP*TP*AP*TP*TP*AP*CP*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
10	1J	24	492	238	86	145	23	0	0

- Molecule 11 is a DNA chain called DNA (46-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
11	1K	46	945	450	177	273	45	0	0

- Molecule 12 is a DNA chain called DNA (5'-D(*CP*GP*AP*CP*AP*GP*AP*AP*TP*GP*AP*AP*AP*GP*AP*G)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
12	1L	16	333	158	73	87	15	0	0

- Molecule 13 is a DNA chain called DNA (32-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
13	1M	32	645	306	120	188	31	0	0

- Molecule 14 is a DNA chain called DNA (40-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
14	1O	40	808	386	154	229	39	0	0

- Molecule 15 is a DNA chain called DNA (46-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
15	1P	46	948	451	182	270	45	0	0

- Molecule 16 is a DNA chain called DNA (37-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
16	1Q	37	752	358	149	209	36	0	0

- Molecule 17 is a DNA chain called DNA (48-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
17	1R	48	976	464	181	284	47	0	0

- Molecule 18 is a DNA chain called DNA (37-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
18	1S	37	763	365	145	217	36	0	0

- Molecule 19 is a DNA chain called DNA (5'-D(*CP*GP*CP*CP*AP*CP*CP*AP*GP*AP*TP*TP*CP*AP*TP*C)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
19	1T	16	318	153	57	93	15	0	0

- Molecule 20 is a DNA chain called DNA (40-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
20	1U	40	826	393	168	226	39	0	0

- Molecule 21 is a DNA chain called DNA (26-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
21	1V	26	521	252	84	160	25	0	0

- Molecule 22 is a DNA chain called DNA (40-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
22	1W	40	830	397	158	236	39	0	0

- Molecule 23 is a DNA chain called DNA (48-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
23	1X	48	983	468	192	276	47	0	0

- Molecule 24 is a DNA chain called DNA (27-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
24	1Y	27	544	262	92	164	26	0	0

- Molecule 25 is a DNA chain called DNA (26-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
25	1Z	26	531	254	100	152	25	0	0

- Molecule 26 is a DNA chain called DNA (47-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
26	1a	47	965	465	183	271	46	0	0

- Molecule 27 is a DNA chain called DNA (32-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
27	1b	32	Total	C	N	O	P	0	0
			665	317	133	184	31		

- Molecule 28 is a DNA chain called DNA (40-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
28	1c	40	Total	C	N	O	P	0	0
			820	395	151	235	39		

- Molecule 29 is a DNA chain called DNA (40-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
29	1d	40	Total	C	N	O	P	0	0
			826	396	162	229	39		

- Molecule 30 is a DNA chain called DNA (26-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
30	1e	26	Total	C	N	O	P	0	0
			524	252	96	151	25		

- Molecule 31 is a DNA chain called DNA (40-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
31	1f	40	Total	C	N	O	P	0	0
			804	387	141	237	39		

- Molecule 32 is a DNA chain called DNA (48-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
32	1g	48	Total	C	N	O	P	0	0
			982	469	191	275	47		

- Molecule 33 is a DNA chain called DNA (48-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
33	1h	48	Total	C	N	O	P	0	0
			993	474	192	280	47		

- Molecule 34 is a DNA chain called DNA (48-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
34	li	48	986	473	184	282	47	0	0

- Molecule 35 is a DNA chain called DNA (32-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
35	lj	32	659	314	130	184	31	0	0

- Molecule 36 is a DNA chain called DNA (40-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
36	lk	40	827	397	152	239	39	0	0

- Molecule 37 is a DNA chain called DNA (48-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
37	ll	48	980	470	175	288	47	0	0

- Molecule 38 is a DNA chain called DNA (5'-D(P*TP*CP*GP*AP*GP*GP*TP*GP*AP*T P*TP*CP*GP*CP*GP*T)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
38	lm	16	328	157	59	97	15	0	0

- Molecule 39 is a DNA chain called DNA (56-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
39	ln	56	1148	548	217	328	55	0	0

- Molecule 40 is a DNA chain called DNA (40-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
40	lo	40	821	390	156	236	39	0	0

- Molecule 41 is a DNA chain called DNA (40-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
41	1p	40	Total	C	N	O	P	0	0
			816	389	157	231	39		

- Molecule 42 is a DNA chain called DNA (48-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
42	1q	48	Total	C	N	O	P	0	0
			981	468	183	283	47		

- Molecule 43 is a DNA chain called DNA (32-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
43	1r	32	Total	C	N	O	P	0	0
			654	310	125	188	31		

- Molecule 44 is a DNA chain called DNA (32-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
44	1s	32	Total	C	N	O	P	0	0
			649	312	117	189	31		

- Molecule 45 is a DNA chain called DNA (32-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
45	1t	32	Total	C	N	O	P	0	0
			651	310	119	191	31		

- Molecule 46 is a DNA chain called DNA (48-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
46	1u	48	Total	C	N	O	P	0	0
			982	469	176	290	47		

- Molecule 47 is a DNA chain called DNA (5'-D(P*CP*CP*CP*CP*CP*AP*GP*CP*TP*GP*GP*TP*CP*AP*TP*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
47	1v	16	Total	C	N	O	P	0	0
			319	153	57	94	15		

- Molecule 48 is a DNA chain called DNA (40-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
48	1w	40	808	387	144	238	39	0	0

- Molecule 49 is a DNA chain called DNA (5'-D(P*GP*AP*CP*AP*GP*AP*TP*GP*CP*GP*TP*GP*CP*CP*AP*G)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
49	1x	16	329	156	66	92	15	0	0

- Molecule 50 is a DNA chain called DNA (48-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
50	2N	36	736	353	133	215	35	0	0

- Molecule 51 is a DNA chain called DNA (40-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
51	2A	32	665	315	135	184	31	0	0

- Molecule 52 is a DNA chain called DNA (48-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
52	2B	48	975	465	186	277	47	0	0

- Molecule 53 is a DNA chain called DNA (40-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
53	2C	26	527	256	83	163	25	0	0

- Molecule 54 is a DNA chain called DNA (29-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
54	2D	32	652	314	124	183	31	0	0

- Molecule 55 is a DNA chain called DNA (5'-D(P*CP*AP*TP*AP*AP*CP*GP*CP*AP*T*P*AP*AP*AP*AP*CP*GP*AP*GP*GP*AP*GP*GP*TP*T)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
55	2E	40	Total	C	N	O	P	0	0
			816	393	147	237	39		

- Molecule 56 is a DNA chain called DNA (32-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
56	2F	48	Total	C	N	O	P	0	0
			988	473	181	287	47		

- Molecule 57 is a DNA chain called DNA (26-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
57	2G	40	Total	C	N	O	P	0	0
			820	393	147	241	39		

- Molecule 58 is a DNA chain called DNA (40-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
58	2H	40	Total	C	N	O	P	0	0
			807	389	148	231	39		

- Molecule 59 is a DNA chain called DNA (40-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
59	2I	16	Total	C	N	O	P	0	0
			328	158	61	94	15		

- Molecule 60 is a DNA chain called DNA (58-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
60	2J	29	Total	C	N	O	P	0	0
			599	285	117	169	28		

- Molecule 61 is a DNA chain called DNA (52-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
61	2K	24	Total	C	N	O	P	0	0
			495	236	100	136	23		

- Molecule 62 is a DNA chain called DNA (40-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
62	2L	32	653	314	121	187	31	0	0

- Molecule 63 is a DNA chain called DNA (48-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
63	2M	24	488	233	94	138	23	0	0

- Molecule 64 is a DNA chain called DNA (48-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
64	2O	26	532	257	97	153	25	0	0

- Molecule 65 is a DNA chain called DNA (32-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
65	2P	40	822	390	162	231	39	0	0

- Molecule 66 is a DNA chain called DNA (58-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
66	2Q	40	818	392	151	236	39	0	0

- Molecule 67 is a DNA chain called DNA (56-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
67	2R	40	822	394	155	234	39	0	0

- Molecule 68 is a DNA chain called DNA (52-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
68	2S	58	1192	566	232	337	57	0	0

- Molecule 69 is a DNA chain called DNA (37-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
69	2T	24	Total	C	N	O	P	0	0
			494	236	94	141	23		

- Molecule 70 is a DNA chain called DNA (48-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
70	2U	52	Total	C	N	O	P	0	0
			1059	508	191	309	51		

- Molecule 71 is a DNA chain called DNA (48-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
71	2V	40	Total	C	N	O	P	0	0
			815	393	141	242	39		

- Molecule 72 is a DNA chain called DNA (32-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
72	2W	48	Total	C	N	O	P	0	0
			987	472	185	283	47		

- Molecule 73 is a DNA chain called DNA (32-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
73	2X	48	Total	C	N	O	P	0	0
			974	463	179	285	47		

- Molecule 74 is a DNA chain called DNA (48-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
74	2Y	32	Total	C	N	O	P	0	0
			656	312	126	187	31		

- Molecule 75 is a DNA chain called DNA (48-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
75	2Z	40	Total	C	N	O	P	0	0
			818	394	146	239	39		

- Molecule 76 is a DNA chain called DNA (5'-D(P*TP*TP*TP*GP*TP*TP*AP*AP*AP*A P*CP*CP*GP*AP*TP*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
76	2a	58	1179	566	214	342	57	0	0

- Molecule 77 is a DNA chain called DNA (32-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
77	2b	56	1149	549	213	332	55	0	0

- Molecule 78 is a DNA chain called DNA (32-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
78	2c	45	914	441	165	264	44	0	0

- Molecule 79 is a DNA chain called DNA (40-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
79	2d	52	1075	508	218	298	51	0	0

- Molecule 80 is a DNA chain called DNA (5'-D(P*CP*TP*GP*GP*CP*CP*TP*TP*CP*C P*TP*GP*TP*AP*GP*CP*CP*AP*AP*AP*AP*AP*TP*A)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
80	2e	37	766	367	143	220	36	0	0

- Molecule 81 is a DNA chain called DNA (32-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
81	2f	48	976	467	184	278	47	0	0

- Molecule 82 is a DNA chain called DNA (40-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
82	2g	48	972	464	184	277	47	0	0

- Molecule 83 is a DNA chain called DNA (32-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
83	2h	56	Total	C	N	O	P	0	0
			1156	551	223	327	55		

- Molecule 84 is a DNA chain called DNA (32-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
84	2i	32	Total	C	N	O	P	0	0
			661	315	135	180	31		

- Molecule 85 is a DNA chain called DNA (47-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
85	2j	16	Total	C	N	O	P	0	0
			326	157	59	95	15		

- Molecule 86 is a DNA chain called DNA (5'-D(P*CP*CP*AP*GP*TP*GP*CP*CP*AP*A P*AP*TP*CP*CP*GP*C)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
86	2k	32	Total	C	N	O	P	0	0
			652	312	123	186	31		

- Molecule 87 is a DNA chain called DNA (40-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
87	2l	48	Total	C	N	O	P	0	0
			980	466	191	276	47		

- Molecule 88 is a DNA chain called DNA (48-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
88	2m	48	Total	C	N	O	P	0	0
			984	472	185	280	47		

- Molecule 89 is a DNA chain called DNA (48-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
89	2n	16	Total	C	N	O	P	0	0
			325	158	58	94	15		

- Molecule 90 is a DNA chain called DNA (48-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
90	2o	32	Total	C	N	O	P	0	0
			653	314	112	196	31		

- Molecule 91 is a DNA chain called DNA (56-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
91	2p	32	Total	C	N	O	P	0	0
			656	312	120	193	31		

- Molecule 92 is a DNA chain called DNA (56-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
92	2q	40	Total	C	N	O	P	0	0
			805	386	136	244	39		

- Molecule 93 is a DNA chain called DNA (32-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
93	2r	24	Total	C	N	O	P	0	0
			485	233	88	141	23		

- Molecule 94 is a DNA chain called DNA (48-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
94	2s	32	Total	C	N	O	P	0	0
			655	311	130	183	31		

- Molecule 95 is a DNA chain called DNA (37-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
95	2t	40	Total	C	N	O	P	0	0
			824	391	164	230	39		

- Molecule 96 is a DNA chain called DNA (55-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
96	2u	32	Total	C	N	O	P	0	0
			652	311	121	189	31		

- Molecule 97 is a DNA chain called DNA (48-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
97	2v	32	Total	C	N	O	P	0	0
			651	313	107	200	31		

- Molecule 98 is a DNA chain called DNA (38-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
98	2w	47	Total	C	N	O	P	0	0
			974	464	202	262	46		

- Molecule 99 is a DNA chain called DNA (32-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
99	2x	16	Total	C	N	O	P	0	0
			320	153	60	92	15		

- Molecule 100 is a DNA chain called DNA (4346-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
100	3N	4346	Total	C	N	O	P	0	0
			88890	42499	15686	26368	4337		

- Molecule 101 is a DNA chain called DNA (40-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
101	3A	40	Total	C	N	O	P	0	0
			841	395	175	232	39		

- Molecule 102 is a DNA chain called DNA (40-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
102	3B	40	Total	C	N	O	P	0	0
			818	389	157	233	39		

- Molecule 103 is a DNA chain called DNA (48-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
103	3C	48	Total	C	N	O	P	0	0
			982	469	185	281	47		

- Molecule 104 is a DNA chain called DNA (48-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
104	3D	48	999	473	193	286	47	0	0

- Molecule 105 is a DNA chain called DNA (48-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
105	3E	48	991	468	198	278	47	0	0

- Molecule 106 is a DNA chain called DNA (56-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
106	3F	56	1131	544	197	335	55	0	0

- Molecule 107 is a DNA chain called DNA (5'-D(*GP*TP*GP*CP*CP*TP*AP*AP*GP*GP*AP*TP*AP*TP*TP*C)-3').

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
107	3G	16	326	157	59	95	15	0	0

- Molecule 108 is a DNA chain called DNA (56-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
108	3H	56	1142	546	210	331	55	0	0

- Molecule 109 is a DNA chain called DNA (36-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
109	3I	36	736	350	139	212	35	0	0

- Molecule 110 is a DNA chain called DNA (35-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
110	3J	35	714	341	133	206	34	0	0

- Molecule 111 is a DNA chain called DNA (32-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
111	3S	32	Total	C	N	O	P	0	0
			655	314	121	189	31		

- Molecule 112 is a DNA chain called DNA (48-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
112	3K	48	Total	C	N	O	P	0	0
			988	469	197	275	47		

- Molecule 113 is a DNA chain called DNA (37-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
113	3L	37	Total	C	N	O	P	0	0
			760	358	146	220	36		

- Molecule 114 is a DNA chain called DNA (55-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
114	3M	55	Total	C	N	O	P	0	0
			1129	539	214	322	54		

- Molecule 115 is a DNA chain called DNA (48-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
115	3O	48	Total	C	N	O	P	0	0
			985	471	189	278	47		

- Molecule 116 is a DNA chain called DNA (38-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
116	3P	38	Total	C	N	O	P	0	0
			785	375	150	223	37		

- Molecule 117 is a DNA chain called DNA (26-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
117	3Q	26	Total	C	N	O	P	0	0
			539	255	114	145	25		

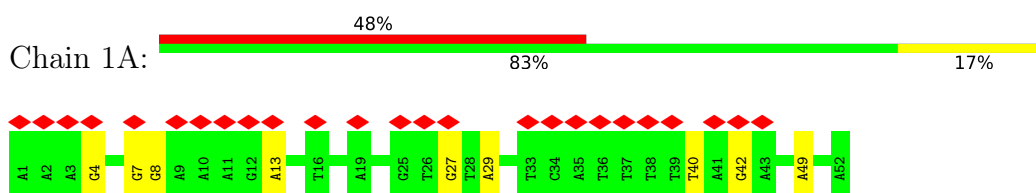
- Molecule 118 is a DNA chain called DNA (32-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
118	3R	32	666	317	127	191	31	0	0

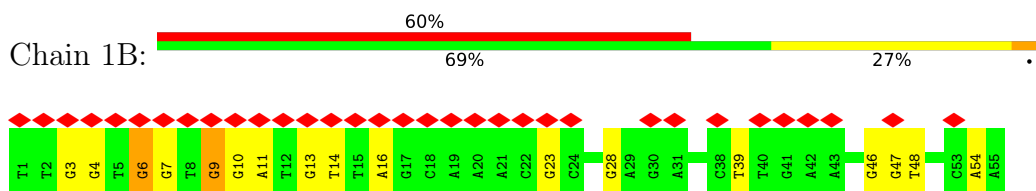
3 Residue-property plots [i](#)

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

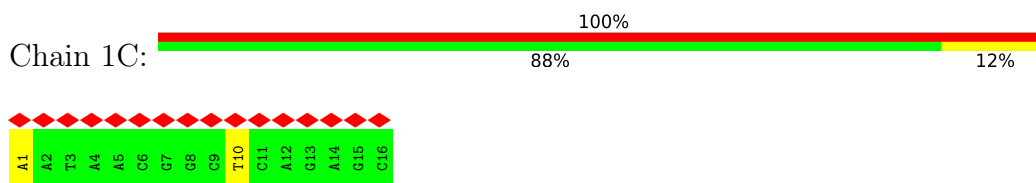
- Molecule 1: DNA (52-MER)



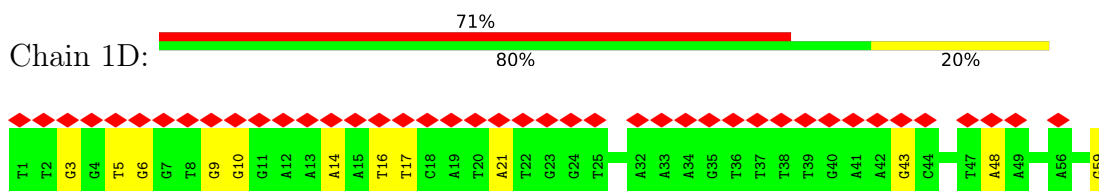
- Molecule 2: DNA (55-MER)



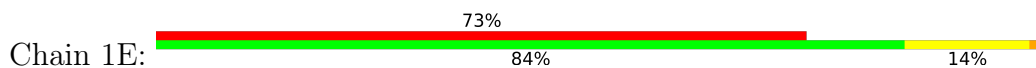
- Molecule 3: DNA (5'-D(*AP*AP*TP*AP*AP*CP*GP*GP*CP*TP*CP*AP*GP*AP*GP*C)-3')

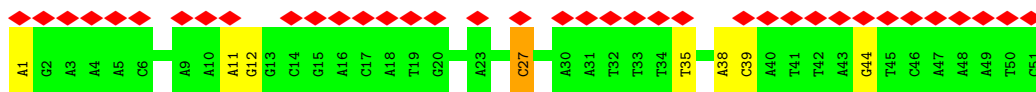


- Molecule 4: DNA (59-MER)



- Molecule 5: DNA (51-MER)

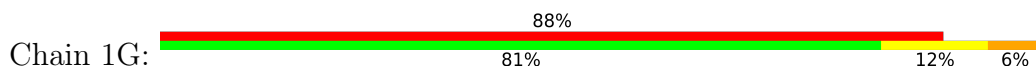




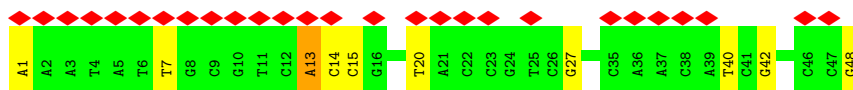
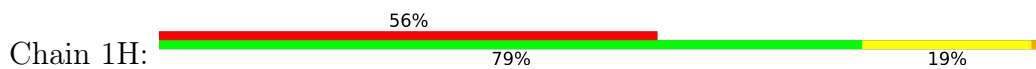
- Molecule 6: DNA (46-MER)



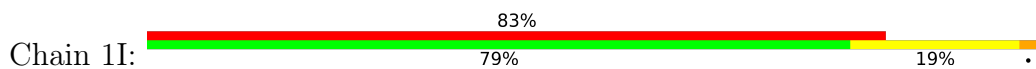
- Molecule 7: DNA (5'-D(*TP*CP*AP*AP*CP*CP*GP*AP*GP*CP*TP*TP*GP*CP*TP*T)-3')



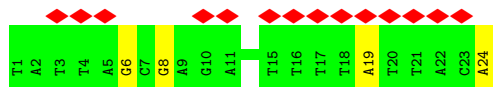
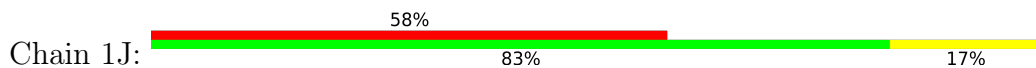
- Molecule 8: DNA (48-MER)



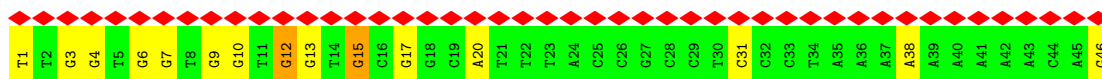
- Molecule 9: DNA (47-MER)



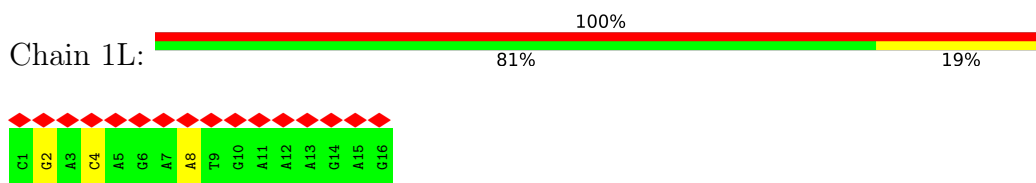
- Molecule 10: DNA (5'-D(*TP*AP*TP*TP*AP*GP*CP*GP*AP*GP*AP*TP*GP*GP*TP*TP*TP*TP*AP*TP*TP*AP*CP*A)-3')



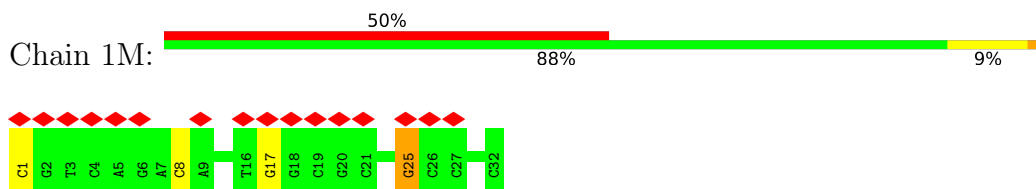
- Molecule 11: DNA (46-MER)



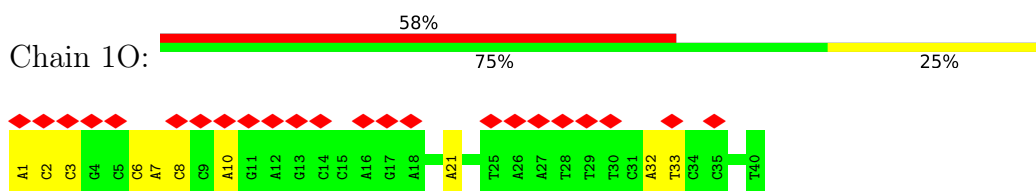
- Molecule 12: DNA (5'-D(*CP*GP*AP*CP*AP*GP*AP*AP*TP*GP*AP*AP*AP*GP*AP*G)-3')



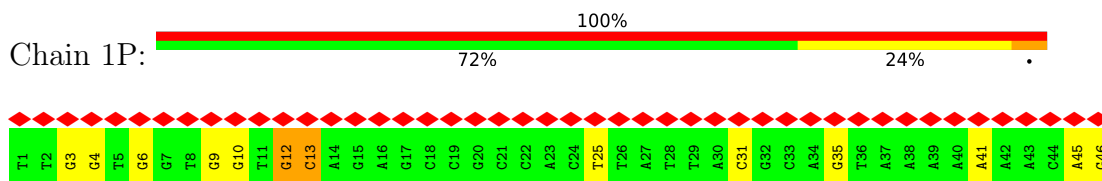
- Molecule 13: DNA (32-MER)



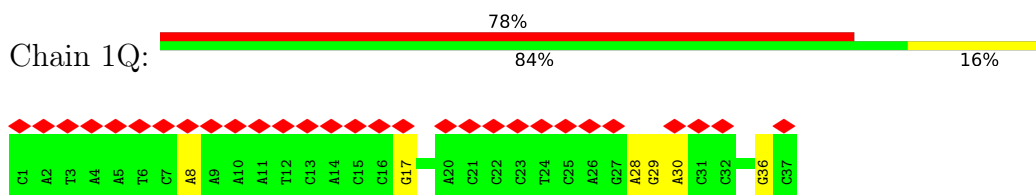
- Molecule 14: DNA (40-MER)



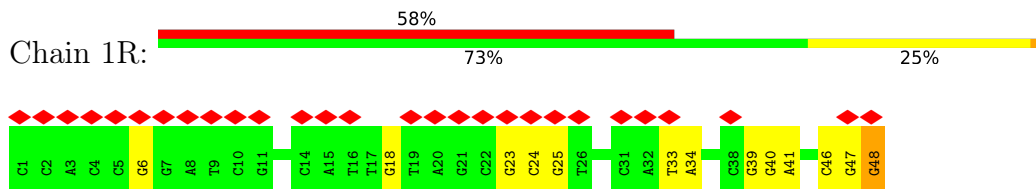
- Molecule 15: DNA (46-MER)



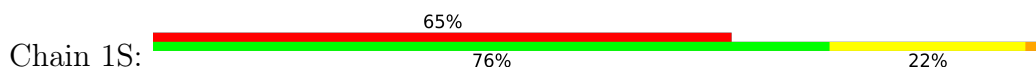
- Molecule 16: DNA (37-MER)

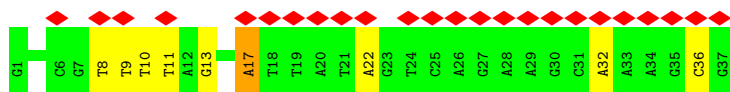


- Molecule 17: DNA (48-MER)

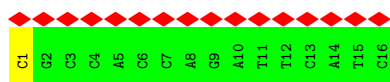


- Molecule 18: DNA (37-MER)

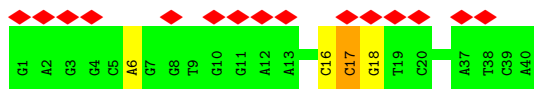
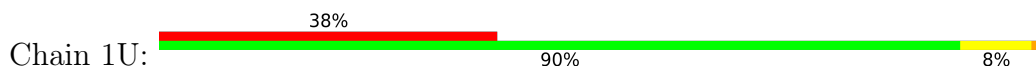




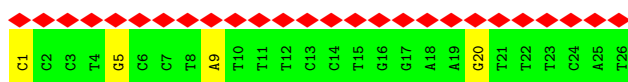
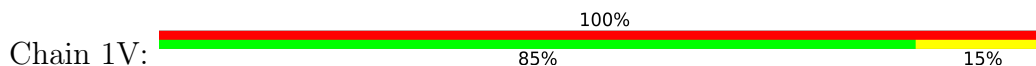
- Molecule 19: DNA (5'-D(*CP*GP*CP*CP*AP*CP*CP*AP*GP*AP*TP*TP*CP*AP*TP*C)-3')



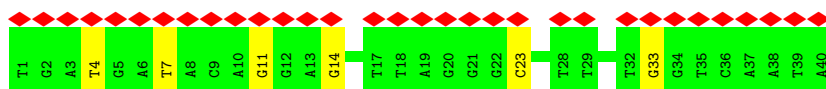
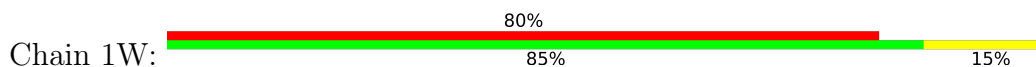
- Molecule 20: DNA (40-MER)



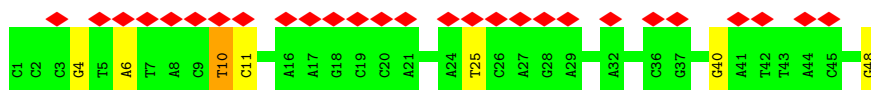
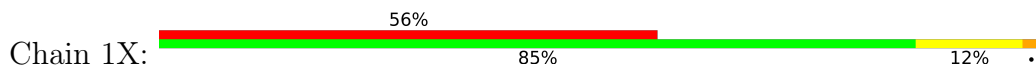
- Molecule 21: DNA (26-MER)



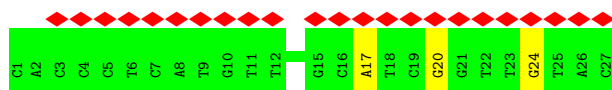
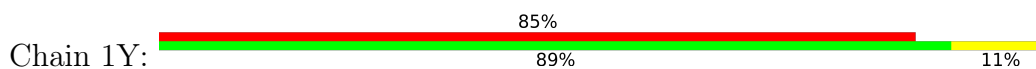
- Molecule 22: DNA (40-MER)



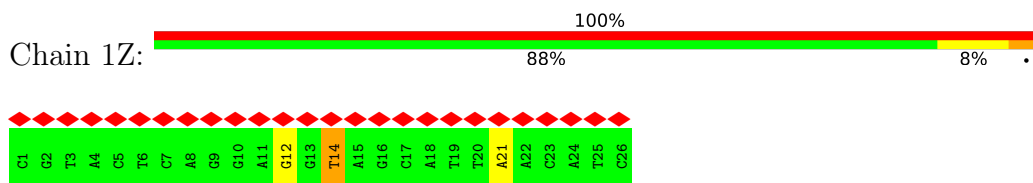
- Molecule 23: DNA (48-MER)



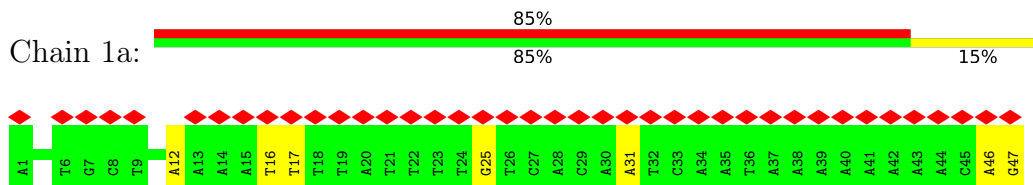
- Molecule 24: DNA (27-MER)



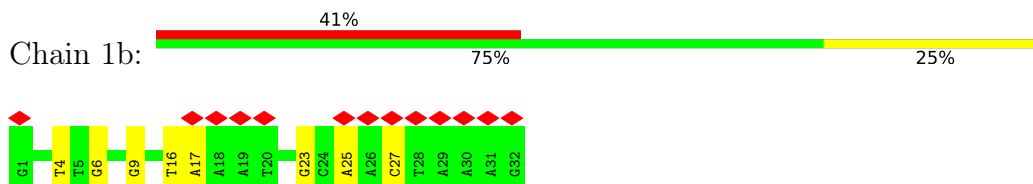
• Molecule 25: DNA (26-MER)



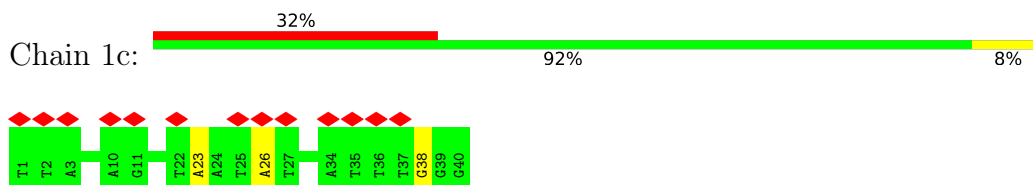
• Molecule 26: DNA (47-MER)



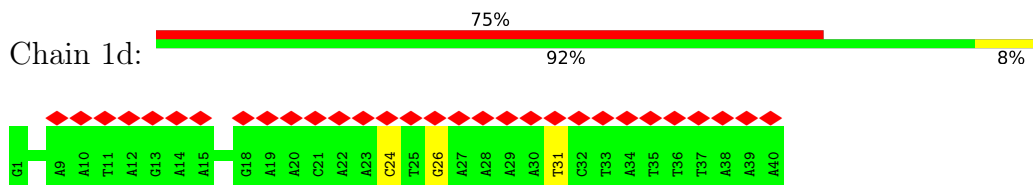
• Molecule 27: DNA (32-MER)



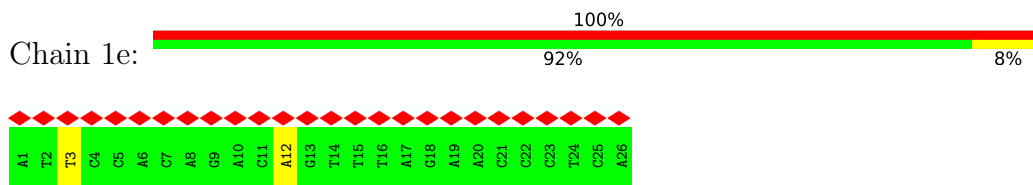
• Molecule 28: DNA (40-MER)



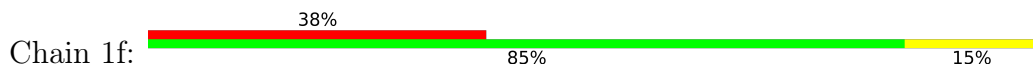
• Molecule 29: DNA (40-MER)

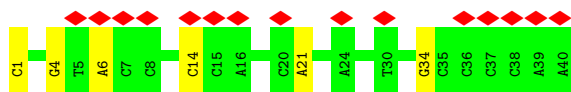


• Molecule 30: DNA (26-MER)

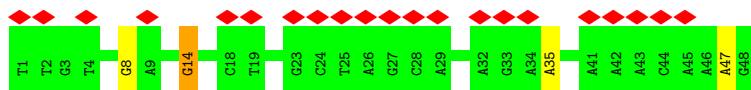
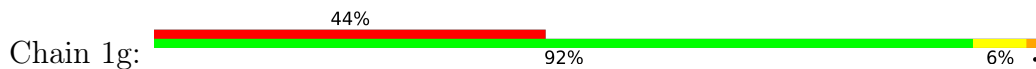


• Molecule 31: DNA (40-MER)

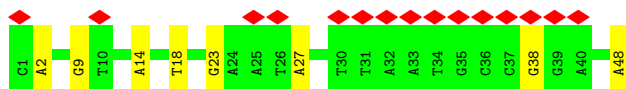
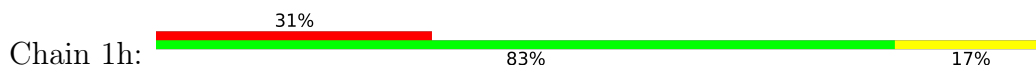




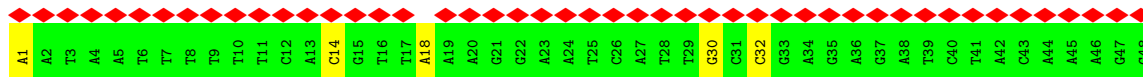
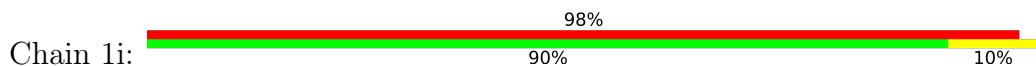
- Molecule 32: DNA (48-MER)



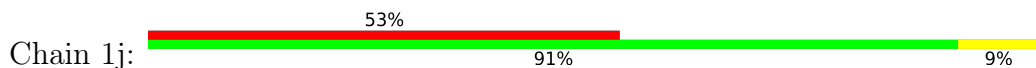
- Molecule 33: DNA (48-MER)



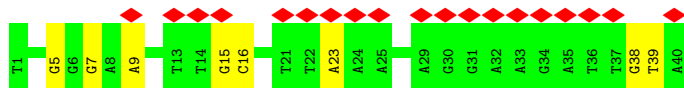
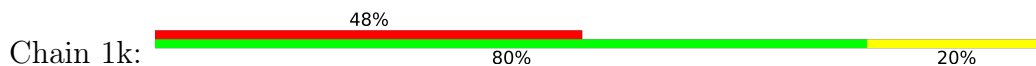
- Molecule 34: DNA (48-MER)



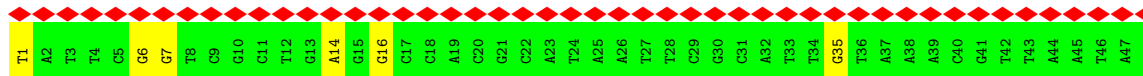
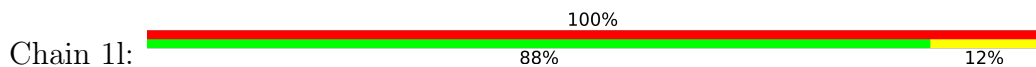
- Molecule 35: DNA (32-MER)



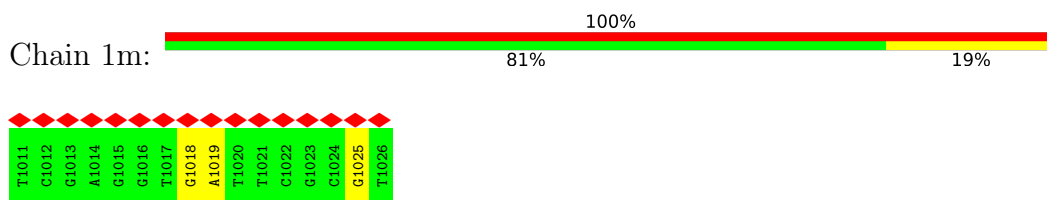
- Molecule 36: DNA (40-MER)



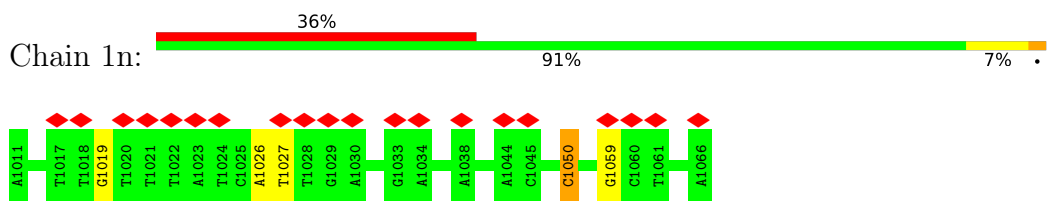
- Molecule 37: DNA (48-MER)



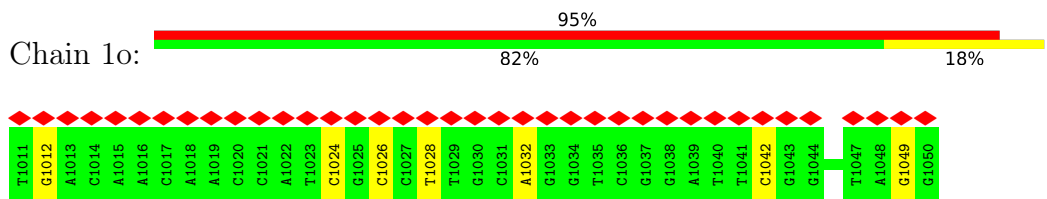
- Molecule 38: DNA (5'-D(P*TP*CP*GP*AP*GP*GP*TP*GP*AP*TP*TP*CP*GP*CP*GP*T)-3')



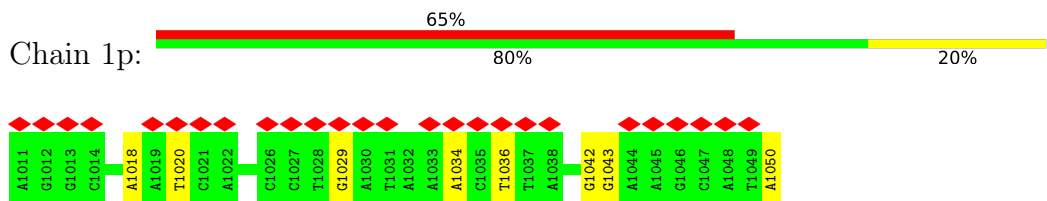
- Molecule 39: DNA (56-MER)



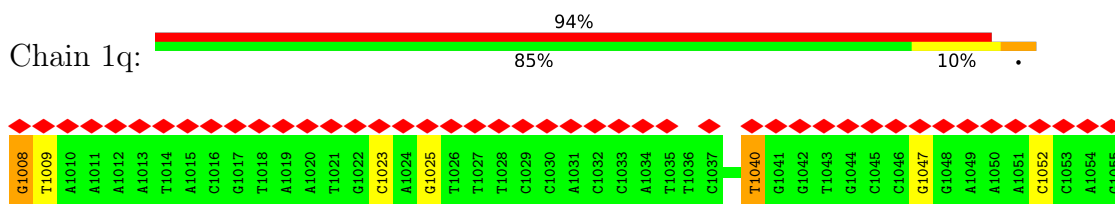
- Molecule 40: DNA (40-MER)



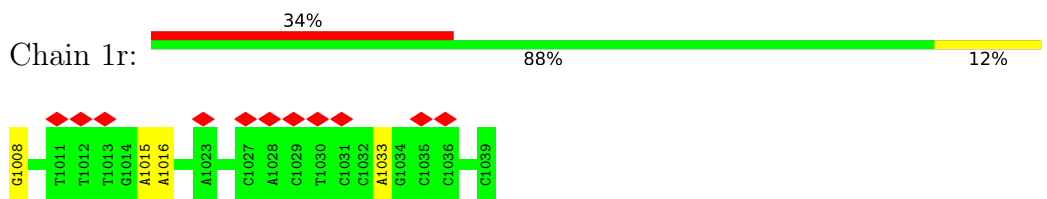
- Molecule 41: DNA (40-MER)



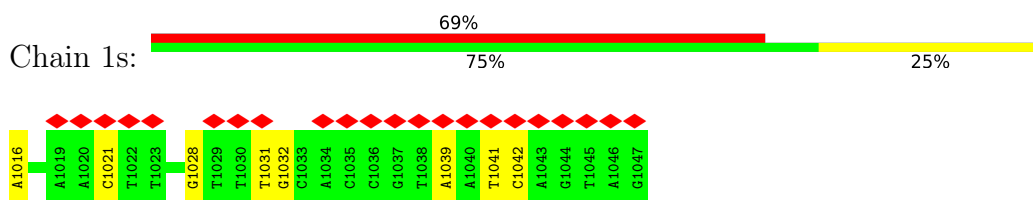
- Molecule 42: DNA (48-MER)



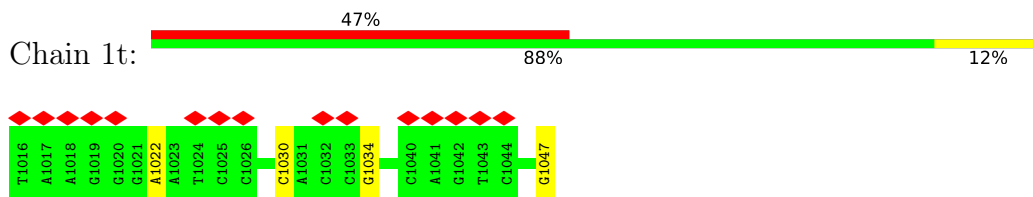
- Molecule 43: DNA (32-MER)



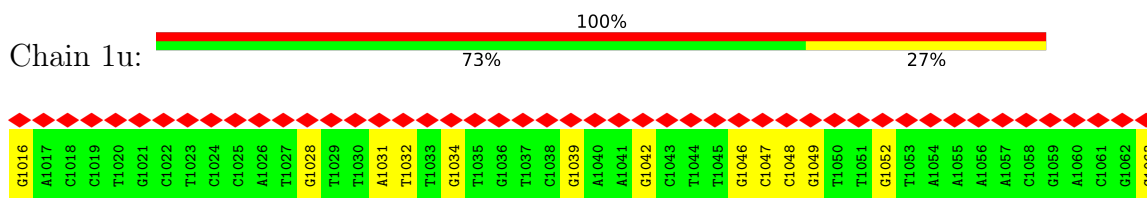
- Molecule 44: DNA (32-MER)



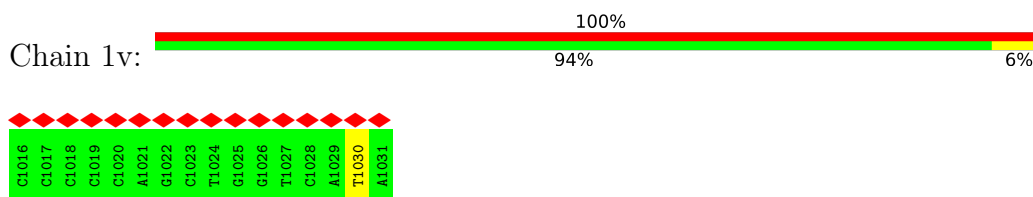
- Molecule 45: DNA (32-MER)



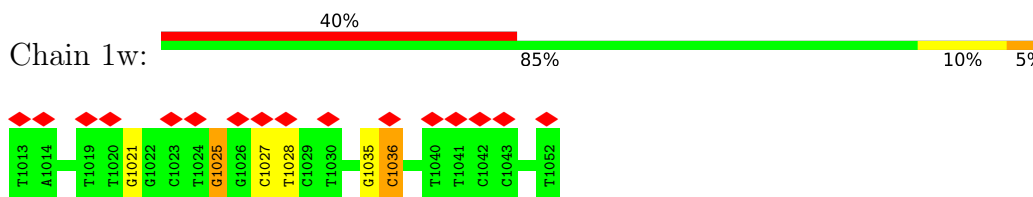
- Molecule 46: DNA (48-MER)



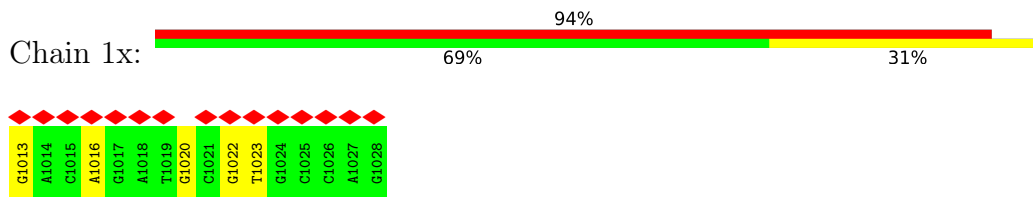
- Molecule 47: DNA (5'-D(P*CP*CP*CP*CP*CP*AP*GP*CP*TP*GP*GP*TP*CP*AP*TP*A)-3')



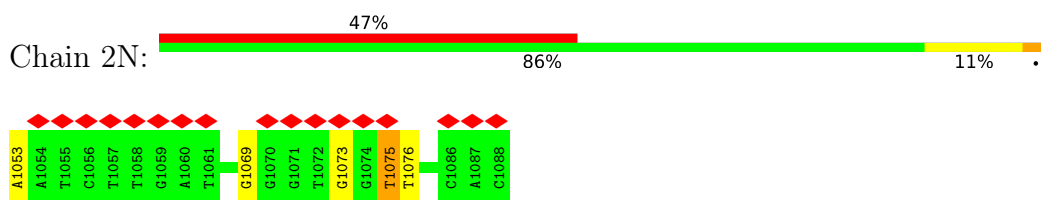
- Molecule 48: DNA (40-MER)



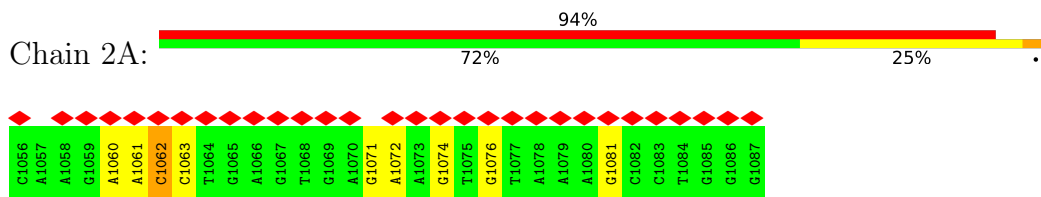
- Molecule 49: DNA (5'-D(P*GP*AP*CP*AP*GP*AP*TP*GP*CP*GP*TP*GP*CP*CP*AP*G)-3')



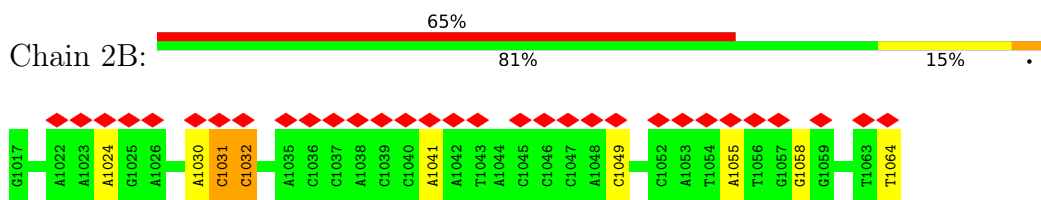
- Molecule 50: DNA (48-MER)



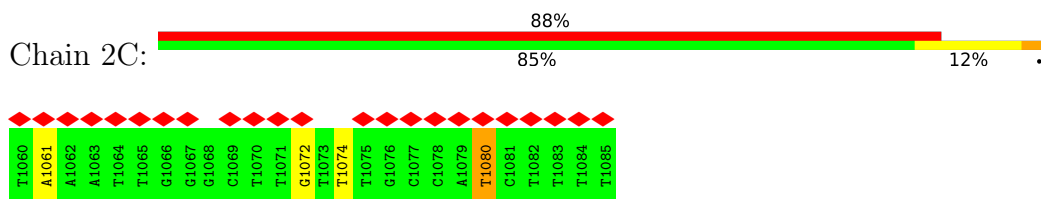
- Molecule 51: DNA (40-MER)



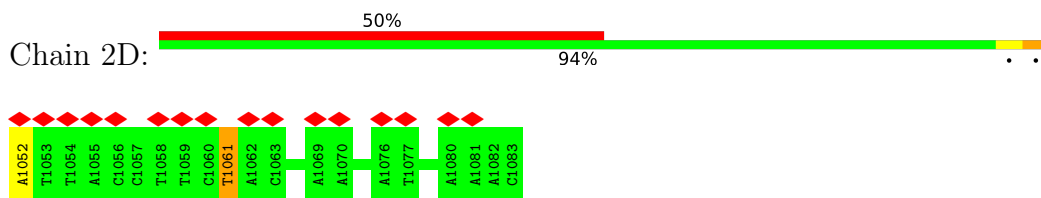
- Molecule 52: DNA (48-MER)



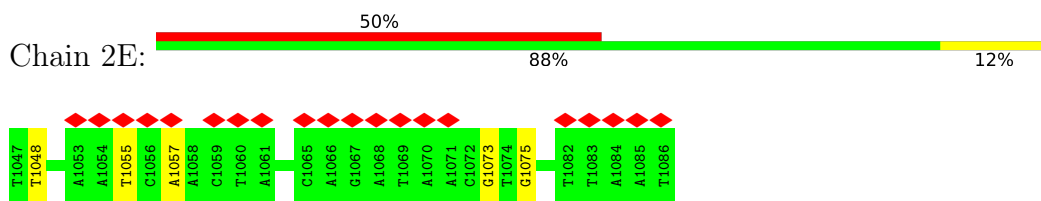
- Molecule 53: DNA (40-MER)



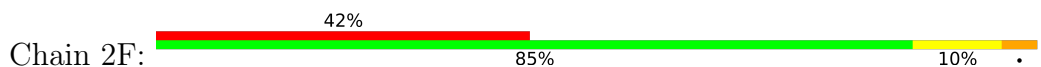
- Molecule 54: DNA (29-MER)

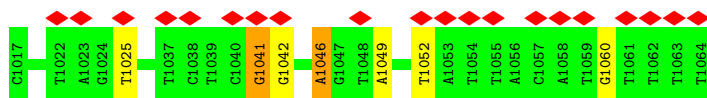


- Molecule 55: DNA (5'-D(P*CP*AP*TP*AP*AP*CP*GP*CP*AP*TP*AP*AP*AP*AP*CP*GP*AP*GP*GP*AP*GP*GP*TP*T)-3')

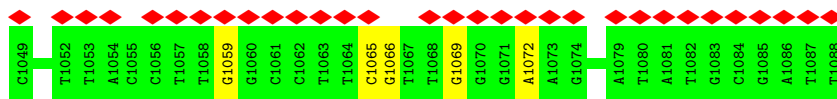
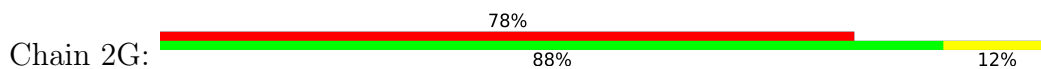


- Molecule 56: DNA (32-MER)

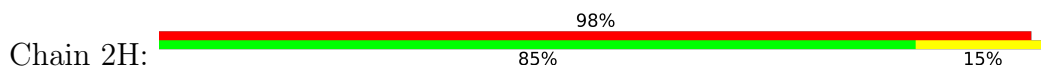




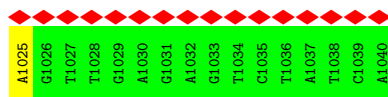
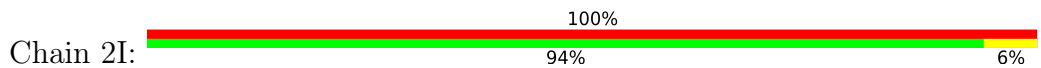
- Molecule 57: DNA (26-MER)



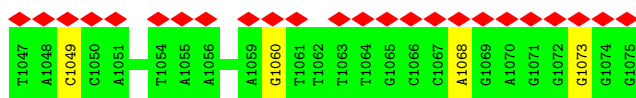
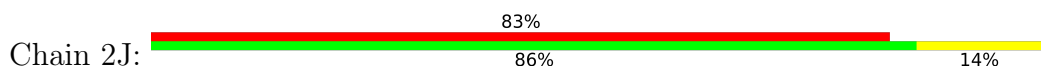
- Molecule 58: DNA (40-MER)



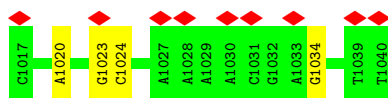
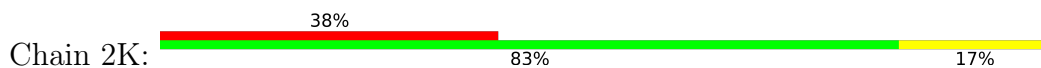
- Molecule 59: DNA (40-MER)



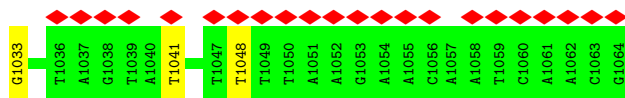
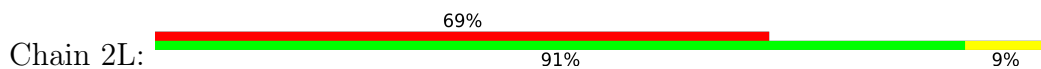
- Molecule 60: DNA (58-MER)



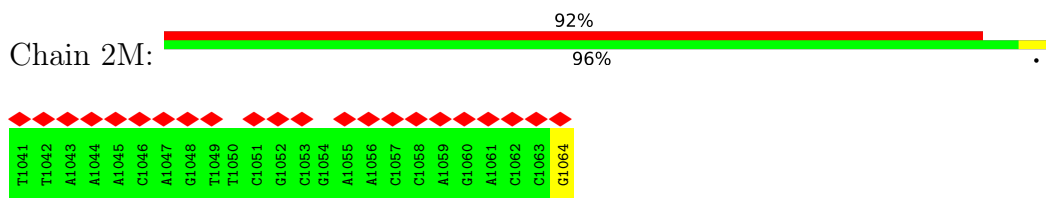
- Molecule 61: DNA (52-MER)



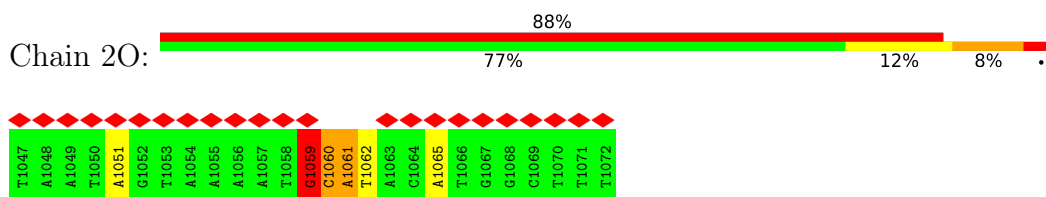
- Molecule 62: DNA (40-MER)



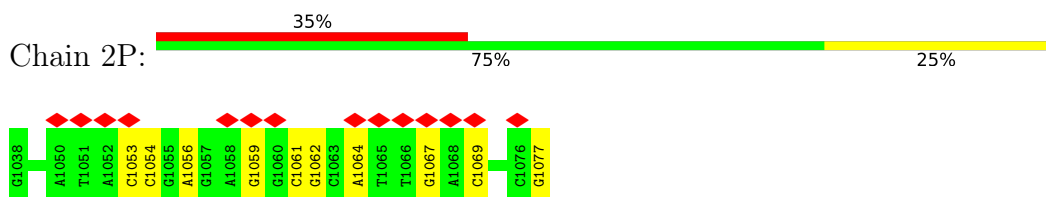
- Molecule 63: DNA (48-MER)



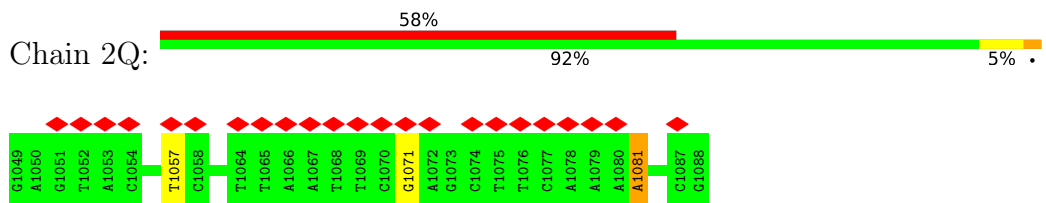
- Molecule 64: DNA (48-MER)



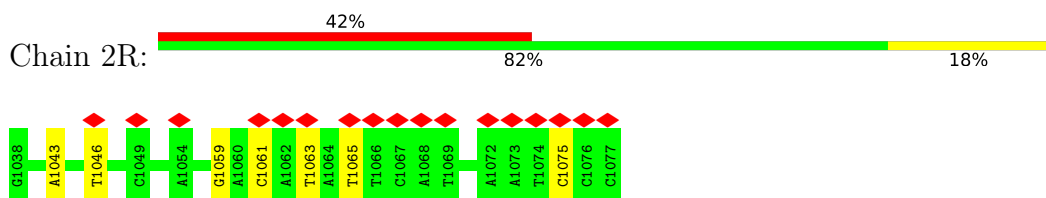
- Molecule 65: DNA (32-MER)



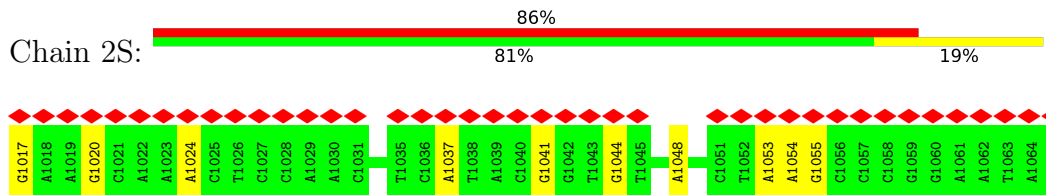
- Molecule 66: DNA (58-MER)



- Molecule 67: DNA (56-MER)

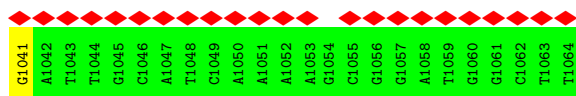


- Molecule 68: DNA (52-MER)

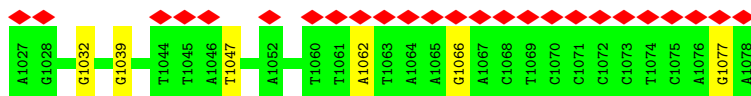
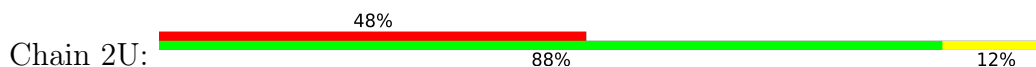


- Molecule 69: DNA (37-MER)

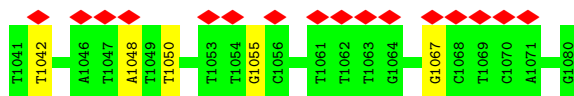
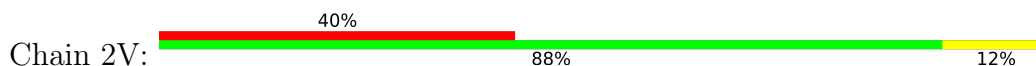




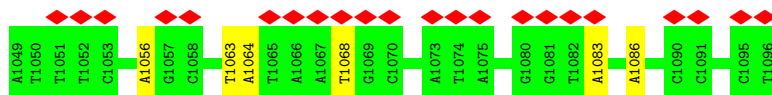
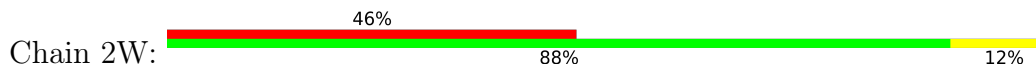
- Molecule 70: DNA (48-MER)



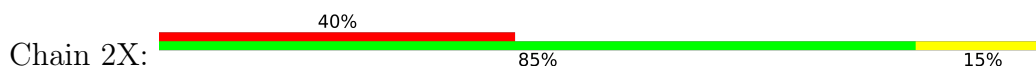
- Molecule 71: DNA (48-MER)



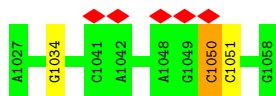
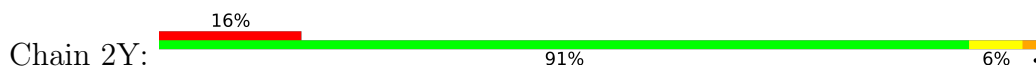
- Molecule 72: DNA (32-MER)



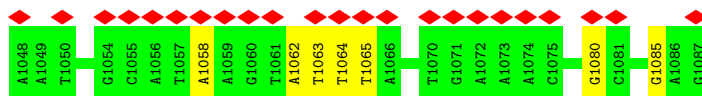
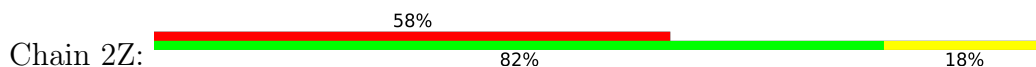
- Molecule 73: DNA (32-MER)



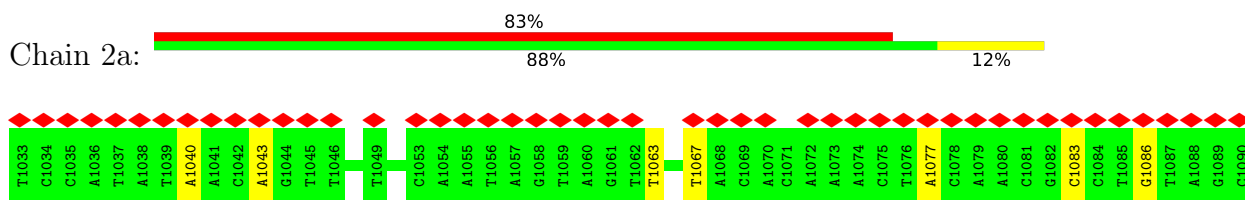
- Molecule 74: DNA (48-MER)



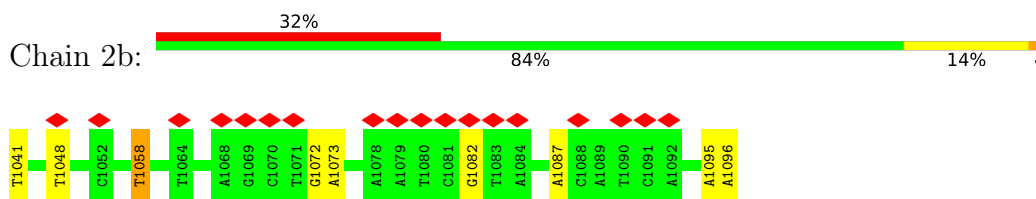
- Molecule 75: DNA (48-MER)



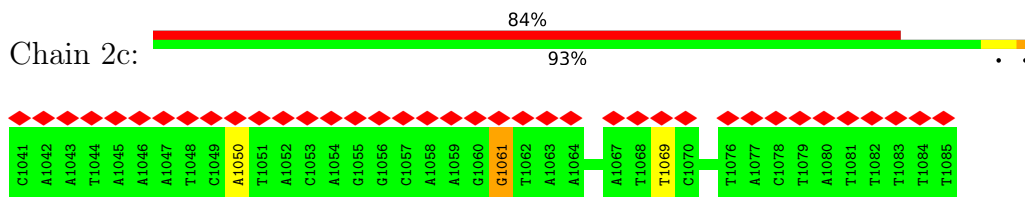
- Molecule 76: DNA (5'-D(P*TP*TP*TP*GP*TP*TP*AP*AP*AP*AP*CP*CP*GP*AP*TP*A)-3')



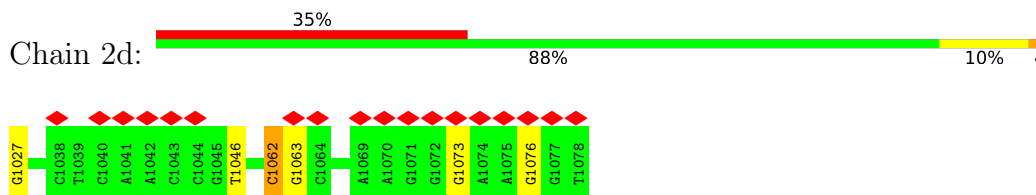
- Molecule 77: DNA (32-MER)



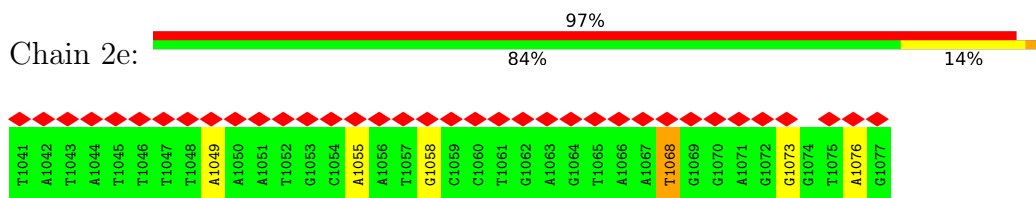
- Molecule 78: DNA (32-MER)



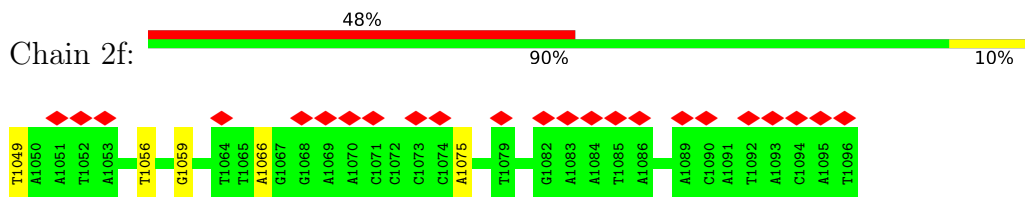
- Molecule 79: DNA (40-MER)



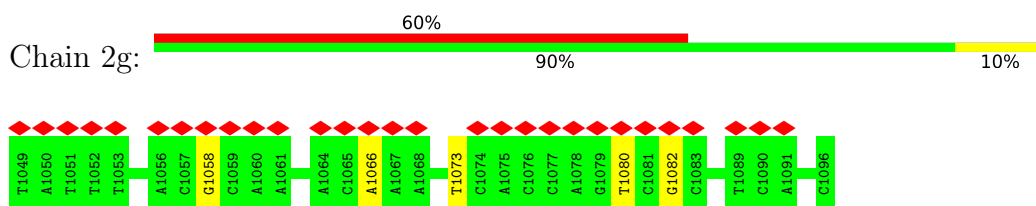
- Molecule 80: DNA (5'-D(P*CP*TP*GP*GP*CP*CP*TP*TP*CP*CP*TP*GP*TP*AP*GP*CP*CP*AP*AP*AP*AP*TP*A)-3')



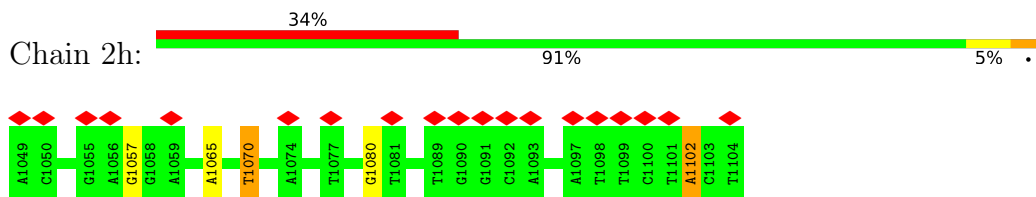
- Molecule 81: DNA (32-MER)



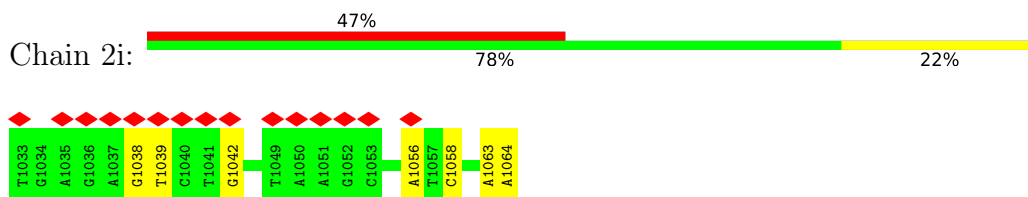
- Molecule 82: DNA (40-MER)



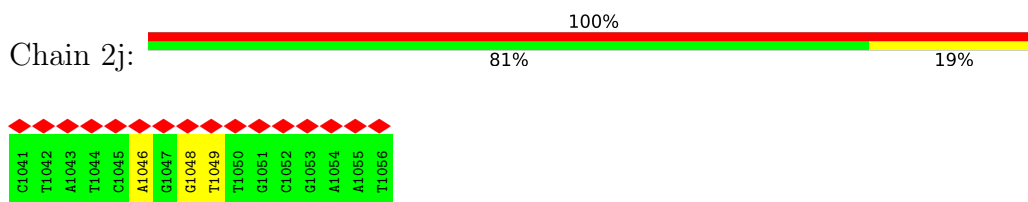
- Molecule 83: DNA (32-MER)



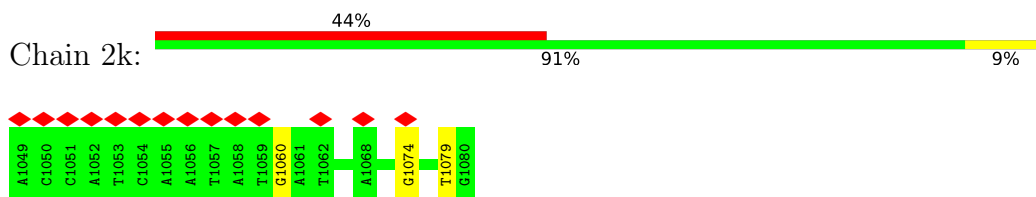
- Molecule 84: DNA (32-MER)



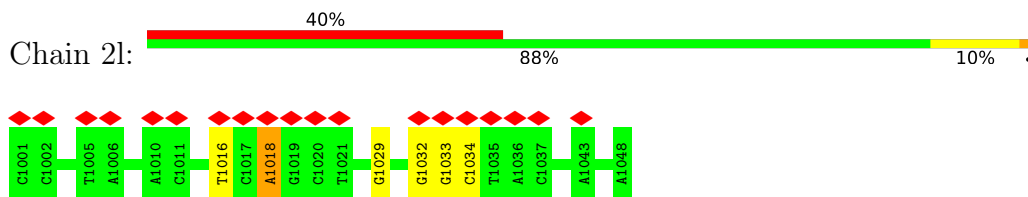
- Molecule 85: DNA (47-MER)



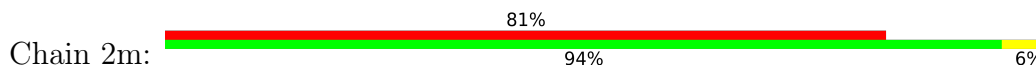
- Molecule 86: DNA (5'-D(P*CP*CP*AP*GP*TP*GP*CP*CP*AP*AP*AP*TP*CP*CP*GP*C)-3')

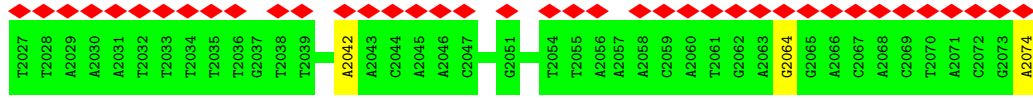


- Molecule 87: DNA (40-MER)

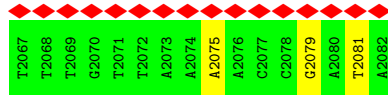
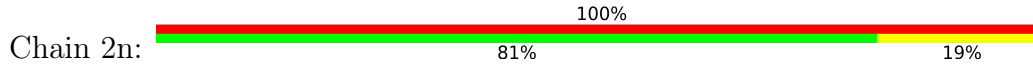


- Molecule 88: DNA (48-MER)

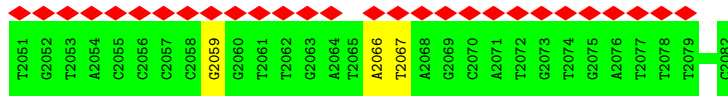
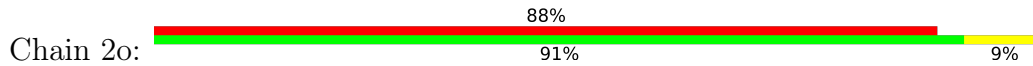




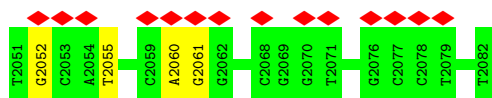
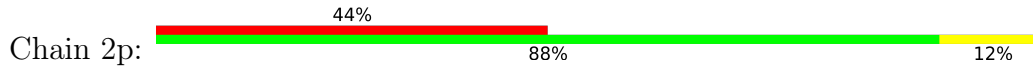
• Molecule 89: DNA (48-MER)



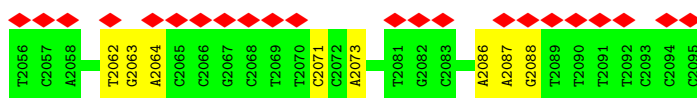
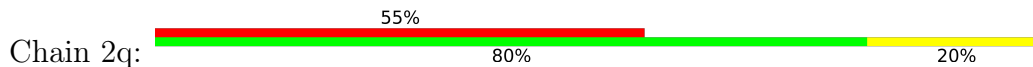
• Molecule 90: DNA (48-MER)



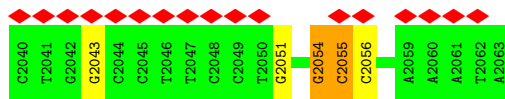
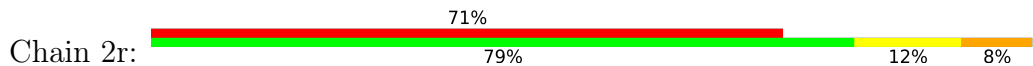
• Molecule 91: DNA (56-MER)



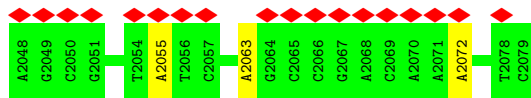
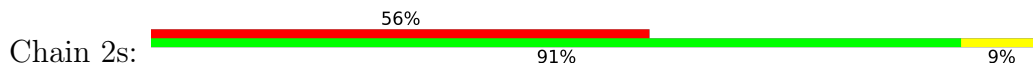
• Molecule 92: DNA (56-MER)



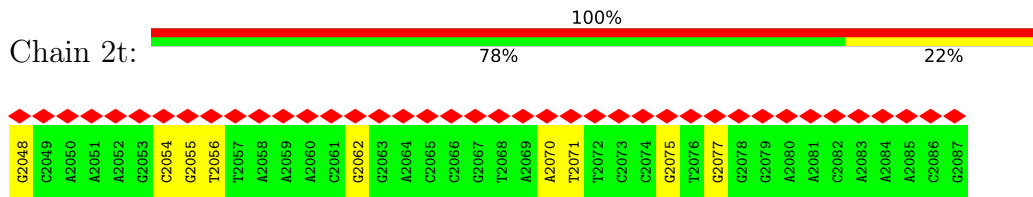
• Molecule 93: DNA (32-MER)



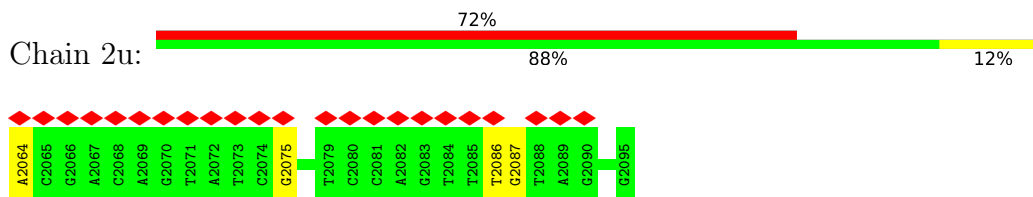
• Molecule 94: DNA (48-MER)



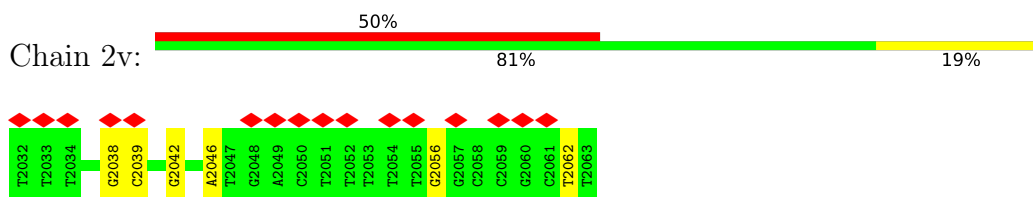
• Molecule 95: DNA (37-MER)



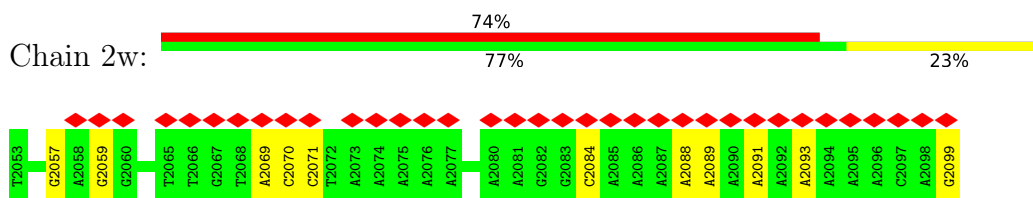
• Molecule 96: DNA (55-MER)



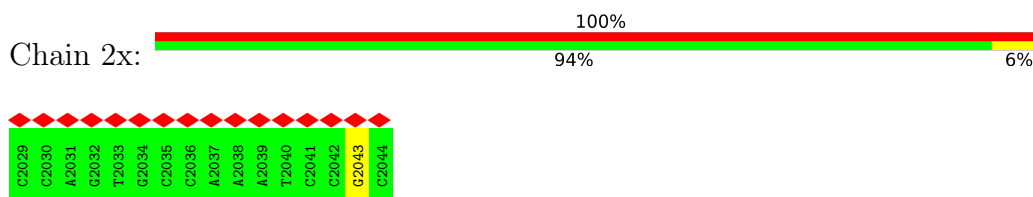
• Molecule 97: DNA (48-MER)



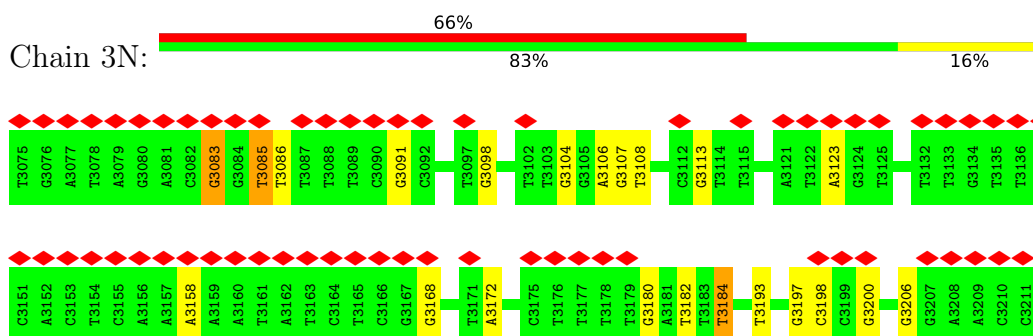
• Molecule 98: DNA (38-MER)

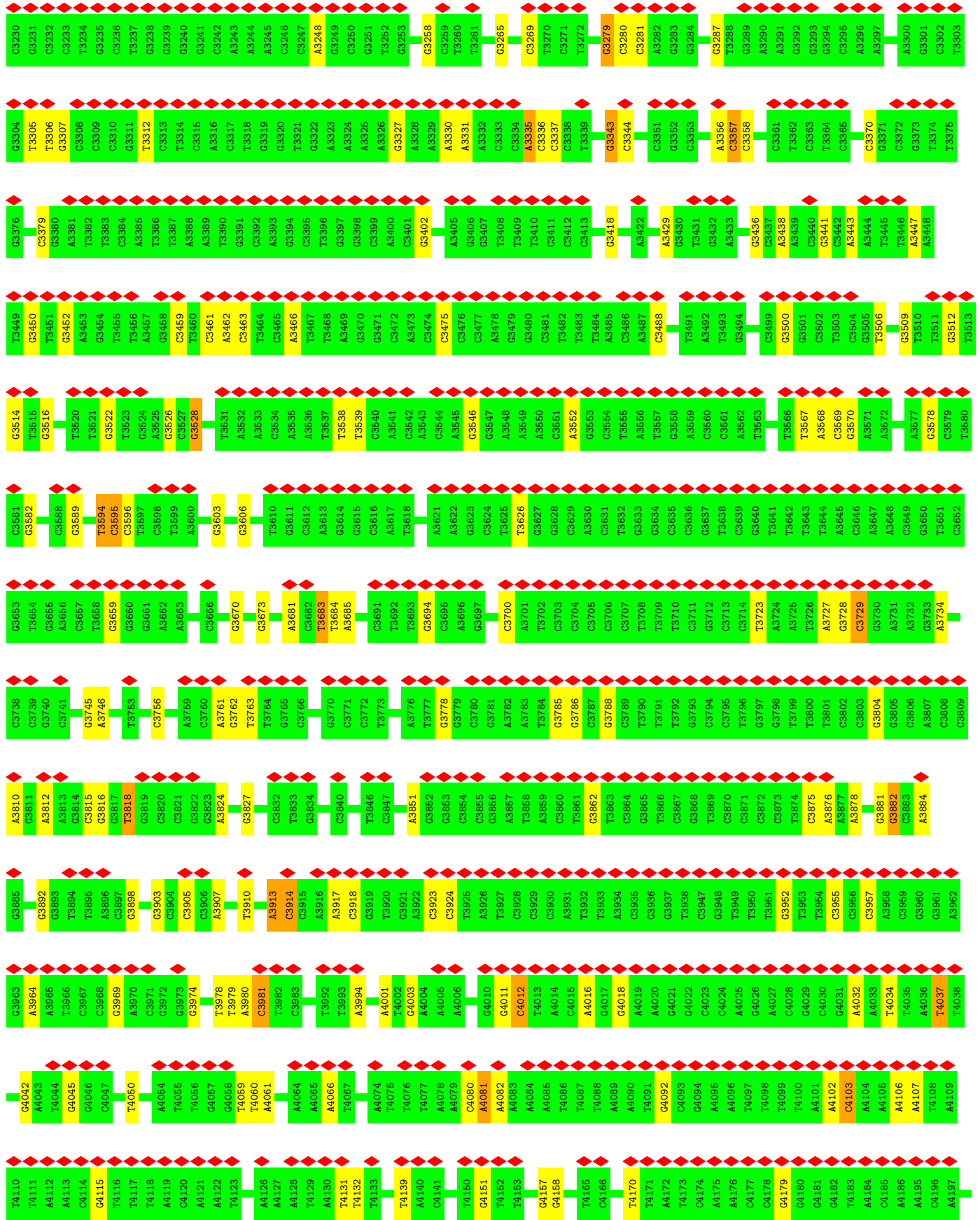


• Molecule 99: DNA (32-MER)

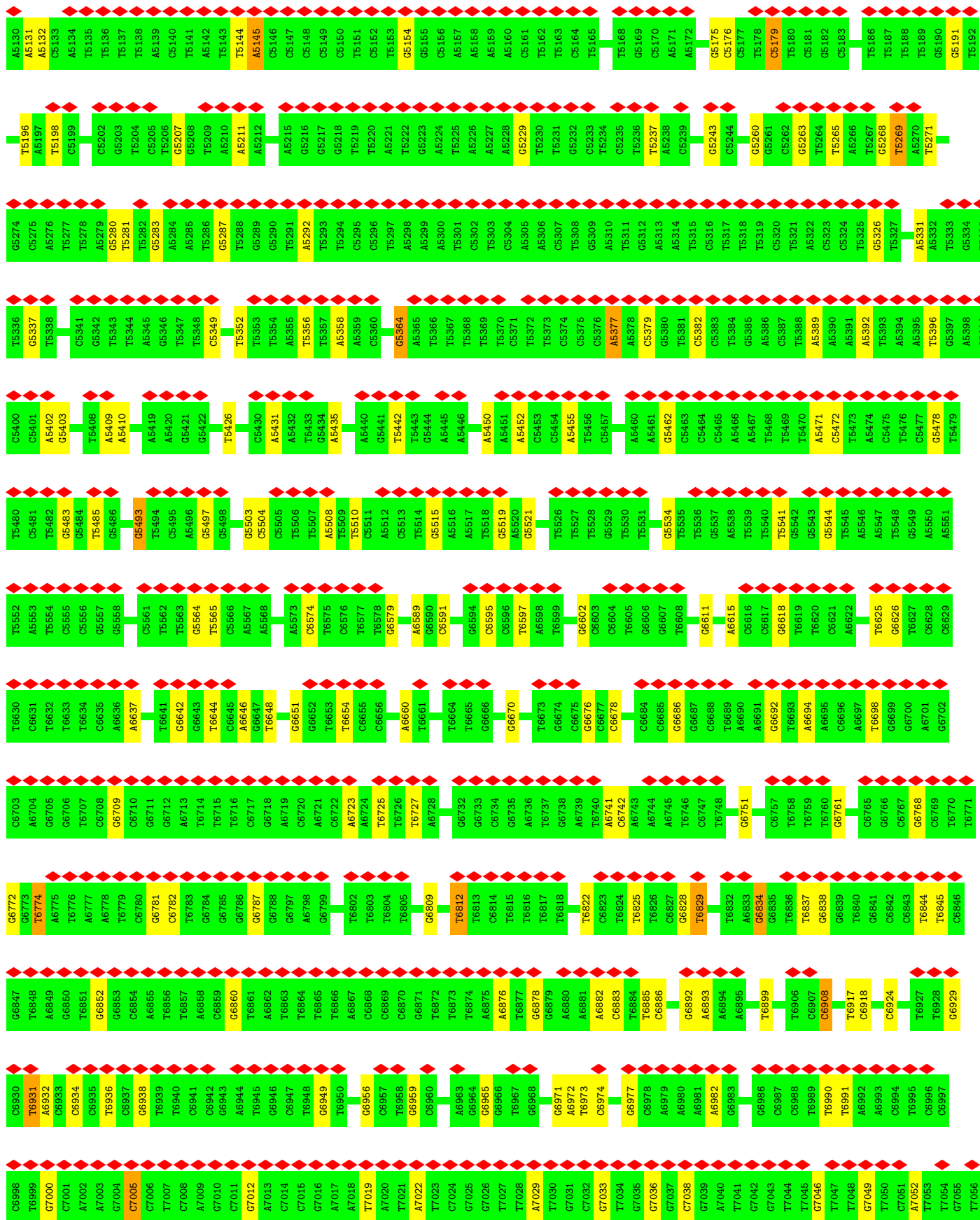


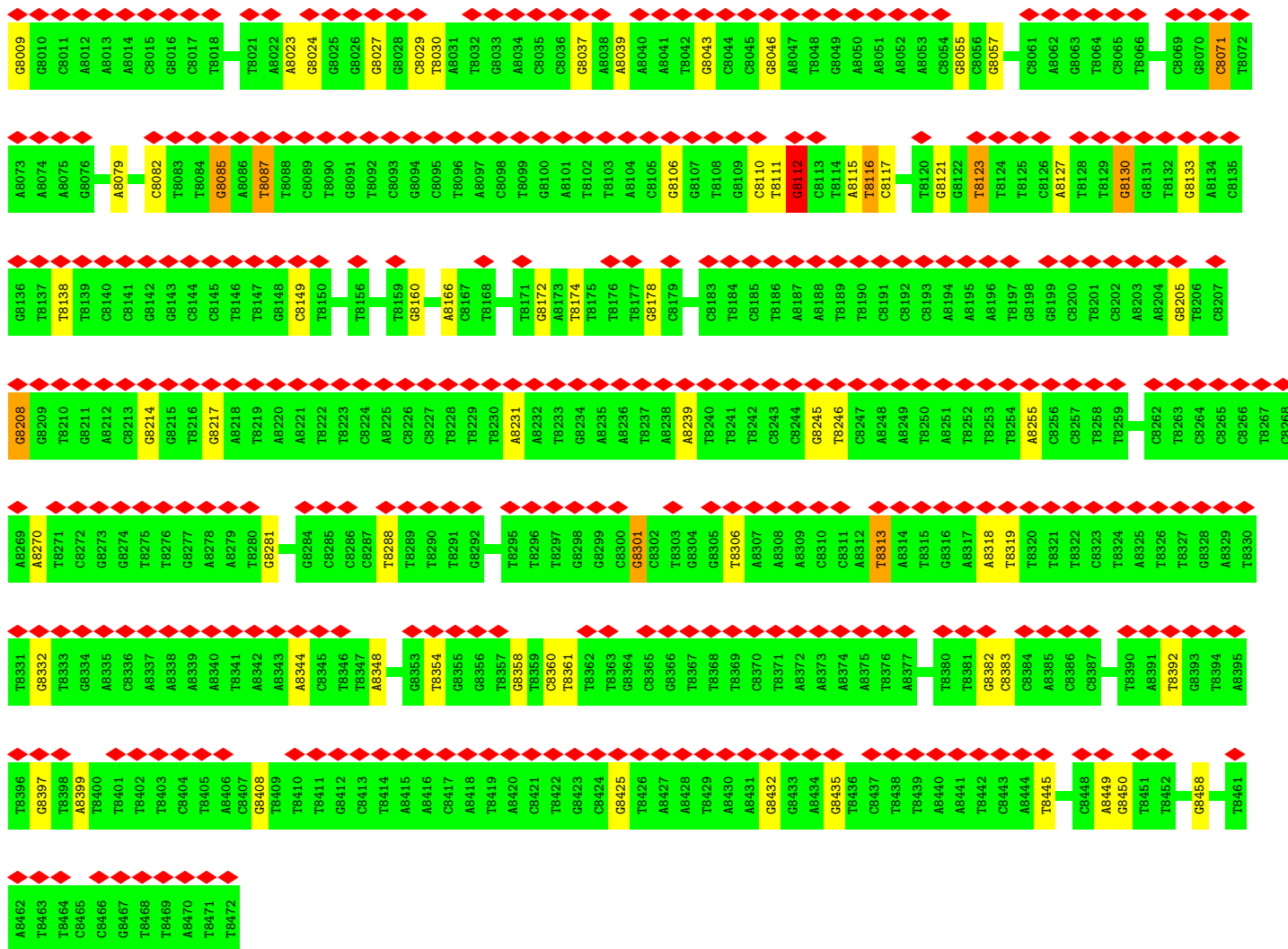
• Molecule 100: DNA (4346-MER)



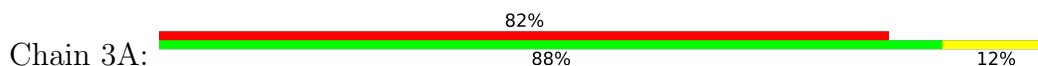


T4201	A4202	G4203	T4204	T4205	T4206	T4207	A4208	C4209	G4210	A4211	T4212	T4213	A4214	C4215	C4216	T4217	T4218	T4219	T4222	C4223	G4224	A4225	T4226	T4227	C4228	T4229	C4230	T4231	T4232	G4233	T4236	C4237	T4238	T4239	C4240	C4241	A4242	G4243	A4244	C4245	T4246	A4322	C4247	T4248	C4249	A4250	G4251	C4252	G4253	A4254	A4255	T4256	G4257	A4258	C4259	C4260	T4261	G4262
A4263	T4264	A4265	G4266	C4267	C4268	T4269	T4270	T4271	G4272	T4273	A4274	G4275	A4276	T4277	C4278	T4279	C4280	T4281	C4282	A4283	C4284	A4285	A4286	T4287	C4288	A4289	G4290	C4291	T4292	A4293	C4298	T4299	C4300	A4308	A4309	C4310	T4311	A4312	A4313	G4321	A4322	A4323	G4329	A4330	A4331	T4332	A4333	T4334	C4335	A4336	T4337	A4338	T4339	T4340	G4341			
A4342	T4343	G4344	C4345	T4346	C4347	A4348	T4349	T4350	G4352	A4353	C4354	T4355	C4356	T4357	C4358	T4359	C4360	G4361	G4362	G4363	C4364	C4365	T4366	T4367	T4368	C4369	T4370	A4371	A4372	C4373	C4374	C4375	T4376	T4377	T4378	T4379	G4380	A4381	A4382	T4383	C4384	T4387	A4388	C4389	C4390	T4391	A4392	C4393	A4394	C4395	T4396	T4397	T4398	A4399	C4400	T4401	C4402	
A4403	G4404	G4405	C4406	T4407	T4408	T4409	G4410	C4411	A4412	T4413	T4414	T4415	A4416	A4417	A4418	A4419	T4420	A4421	T4422	A4423	T4424	G4425	A4426	G4427	G4428	G4429	T4430	T4431	C4432	T4433	A4434	A4435	A4436	A4437	A4438	T4439	T4442	T4443	T4444	A4445	C4446	G4452	A4462	C4463	C4464	T4467	C4468	T4469	A4470	C4471	A4476	A4477	A4478	C4479				
T4480	A4486	G4487	G4488	G4489	C4490	C4491	A4492	T4493	T4496	G4497	T4498	T4499	A4500	A4501	A4502	A4503	G4504	T4505	A4506	C4507	A4508	A4509	C4510	C4511	G4512	A4513	T4514	A4515	T4516	A4517	A4523	T4524	G4525	C4526	T4527	C4528	T4529	C4534	T4535	T4536	T4537	A4538	T4539	T4540	G4541	C4542	T4543	T4544	A4545	A4546	T4547	T4548	T4549	A4550	C4551			
C4552	T4553	A4554	A4555	T4556	T4557	C4558	C4562	C4563	C4564	T4565	T4566	G4567	C4568	C4569	T4570	G4571	T4572	A4573	T4574	G4575	A4576	T4577	T4578	T4579	A4580	T4581	T4582	G4583	C4584	A4585	T4586	G4587	T4588	T4589	A4590	A4591	T4592	G4593	C4594	T4595	A4596	C4597	T4598	A4599	C4600	T4601	A4602	T4603	T4604	A4605	G4606	C4607	T4607	A4608	G4609	T4612	T4613	C4614
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A4697	A4698	A4701	A4702	A4703	T4704	C4705	T4706	A4707	C4708	T4709	T4712	T4713	C4714	C4715	C4716	A4717	C4718	A4719	A4720	T4721	T4722	G4723	G4724	G4725	A4726	A4727	T4728	C4729	A4730	A4731	C4732	T4733	C4734	T4736	T4737	A4738	A4739	T4740	T4741	G4742	A4743	A4744	T4745	G4746	T4747	A4748	A4749	C4750	T4751	T4752	C4753	C4754	A4755	G4756	A4757	C4758		
A4759	C4760	C4761	G4762	T4763	A4764	C4765	T4766	T4767	T4768	A4769	G4770	C4773	C4774	A4775	T4776	A4781	G4788	C4791	A4792	G4793	C4794	T4795	A4796	C4797	A4798	G4799	T4803	A4804	T4805	A4806	T4807	T4808	C4809	A4813	A4814	T4815	T4816	A4817	A4818	G4819	A4820	A4821	A4822	A4823	A4824	A4825	A4826	C4827	A4828	A4829	T4830	C4831	C4832					
G4833	C4834	A4835	A4836	G4841	A4842	C4843	C4844	T4845	C4846	T4847	T4848	T4849	T4850	A4855	C4856	G4857	A4858	G4859	T4863	T4864	A4865	A4866	A4867	G4868	T4873	C4874	T4875	C4876	T4877	A4878	A4879	T4880	C4881	C4882	T4883	C4884	A4885	C4886	C4887	T4888	C4889	T4890	T4891	G4892	C4895	T4896	A4897	C4898	A4899	T4900	C4901	T4902	C4903	C4904				
G4905	C4906	T4907	C4908	T4909	G4910	C4911	T4912	T4913	C4914	G4915	C4916	T4917	T4918	A4922	G4923	C4924	T4925	C4926	A4928	A4932	A4935	C4936	G4937	C4938	G4939	A4943	T4944	T4945	G4946	A4947	T4954	C4955	G4956	G4957	G4958	C4959	T4960	T4961	C4962	C4965	T4966	T4967	A4968	A4969	T4970	C4971	T4972	C4973	T4974	T4975	T4976							
G4977	A4978	T4979	C4980	A4981	A4982	A4983	T4984	C4985	C4986	G4987	C4988	T4989	T4990	T4991	C4992	C4993	T4994	T4995	C4996	T4997	C4998	A4999	C5000	T5001	A5002	T5003	A5004	G5008	T5009	C5010	G5013	G5014	A5020	C5021	C5022	T5023	G5024	T5028	T5029	T5030	G5031	A5032	T5033	T5034	T5035	A5036	T5037	G5038	G5039	T5040	C5041	A5042	T5043	T5044	C5045			
G5048	T5049	T5050	T5051	T5052	C5053	T5054	G5055	A5056	A5057	C5058	T5059	G5060	T5061	T5062	T5063	A5064	A5065	A5067	A5068	A5069	T5070	T5071	T5072	G5073	A5074	G5075	G5076	G5077	T5081	T5082	C5083	A5084	A5101	C5104	C5105	G5106	C5107	A5108	A5111	T5112	T5113	G5114	A5115	A5116	C5117	T5122	C5123	C5124	T5127	C5128	T5129							

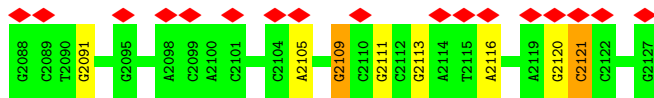
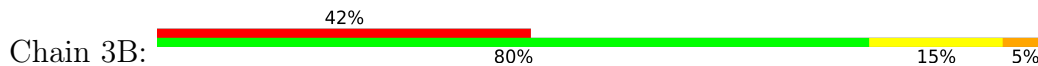




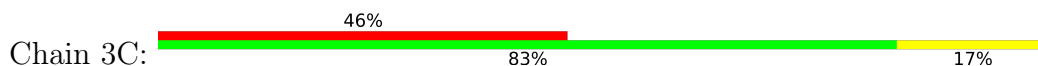
• Molecule 101: DNA (40-MER)

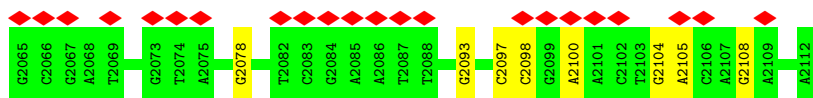


• Molecule 102: DNA (40-MER)

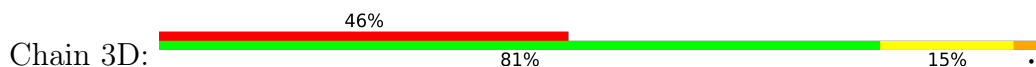


• Molecule 103: DNA (48-MER)

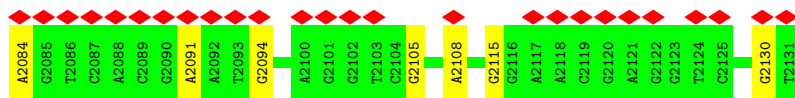
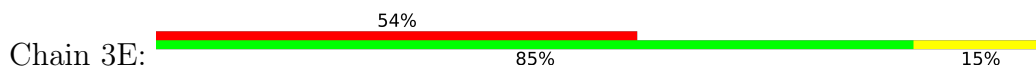




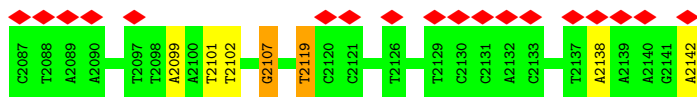
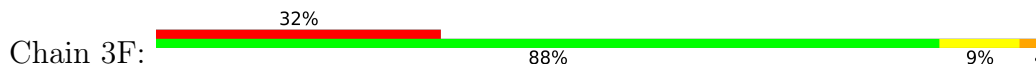
- Molecule 104: DNA (48-MER)



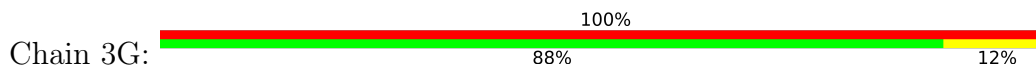
- Molecule 105: DNA (48-MER)



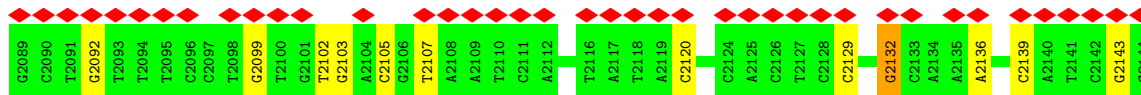
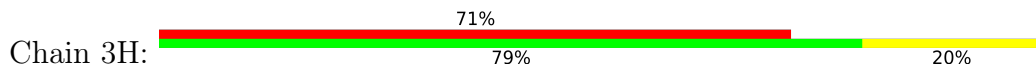
- Molecule 106: DNA (56-MER)



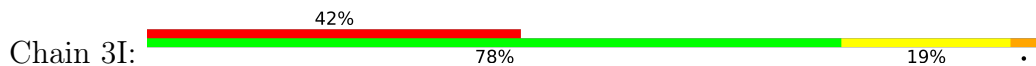
- Molecule 107: DNA (5'-D(*GP*TP*GP*CP*CP*TP*AP*AP*GP*GP*AP*TP*AP*TP*TP*C)-3')

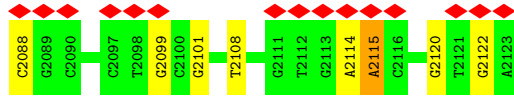


- Molecule 108: DNA (56-MER)

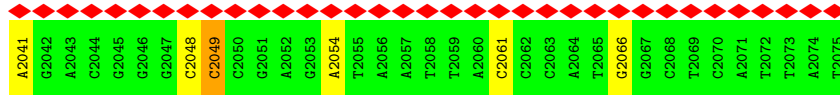
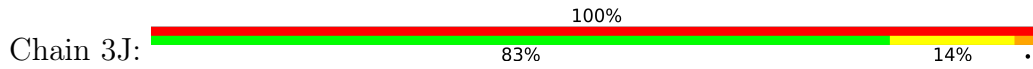


- Molecule 109: DNA (36-MER)

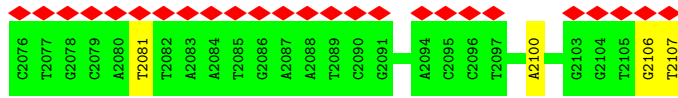
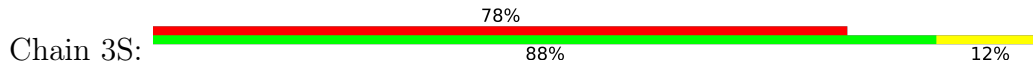




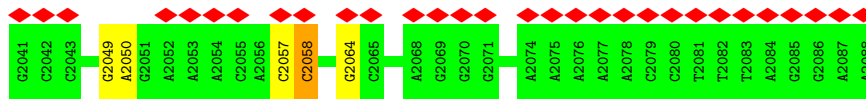
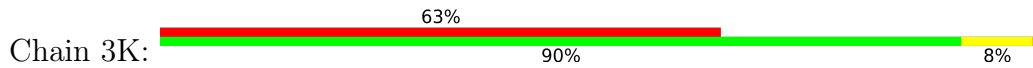
• Molecule 110: DNA (35-MER)



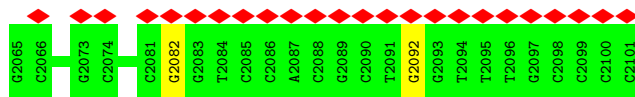
• Molecule 111: DNA (32-MER)



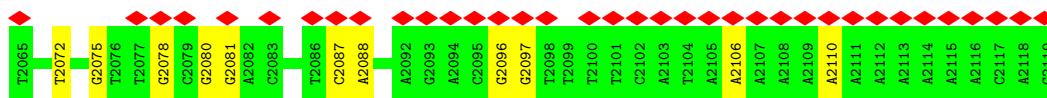
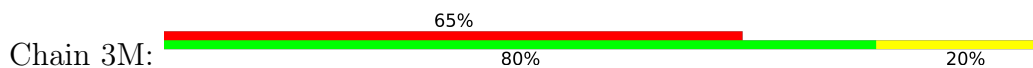
• Molecule 112: DNA (48-MER)



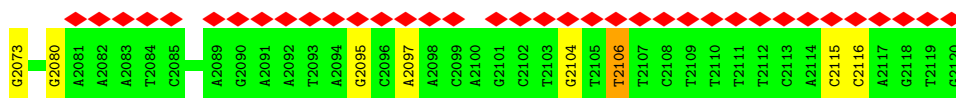
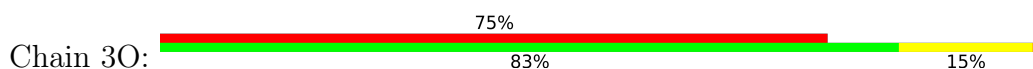
• Molecule 113: DNA (37-MER)



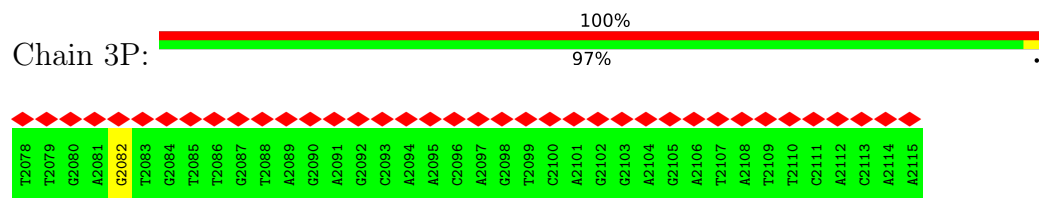
• Molecule 114: DNA (55-MER)



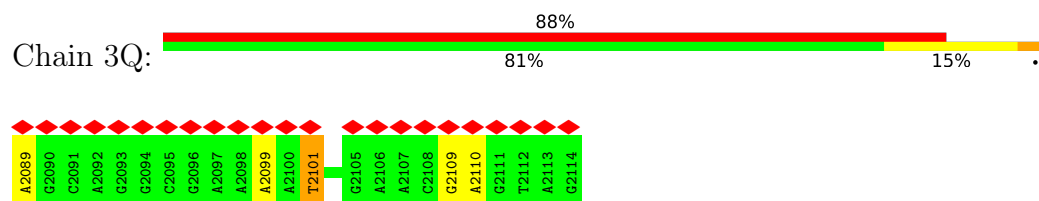
• Molecule 115: DNA (48-MER)



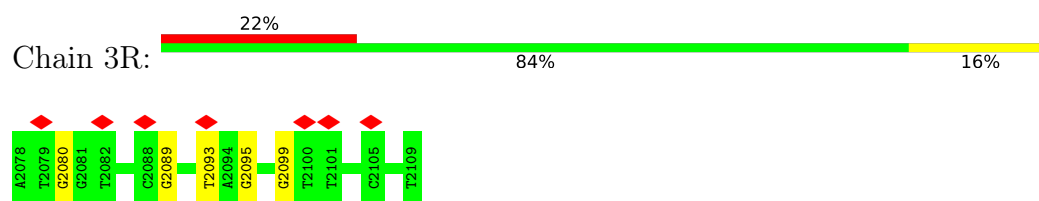
- Molecule 116: DNA (38-MER)



- Molecule 117: DNA (26-MER)



- Molecule 118: DNA (32-MER)



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	108931	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	48	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	23500	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.005	Depositor
Minimum map value	-0.001	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.001	Depositor
Recommended contour level	0.003	Depositor
Map size (Å)	456.0, 456.0, 456.0	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.76, 0.76, 0.76	Depositor

5 Model quality i

5.1 Standard geometry i

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	1A	1.12	0/1220	1.18	9/1885 (0.5%)
2	1B	1.16	0/1279	1.27	12/1975 (0.6%)
3	1C	1.13	0/368	1.28	5/566 (0.9%)
4	1D	1.12	0/1372	1.16	9/2119 (0.4%)
5	1E	1.12	0/1185	1.14	5/1828 (0.3%)
6	1F	1.15	0/1069	1.43	15/1650 (0.9%)
7	1G	1.10	0/358	1.30	4/550 (0.7%)
8	1H	1.11	0/1087	1.29	10/1671 (0.6%)
9	1I	1.19	0/1091	1.27	6/1685 (0.4%)
10	1J	1.10	0/551	1.13	3/850 (0.4%)
11	1K	1.18	0/1061	1.39	12/1637 (0.7%)
12	1L	1.11	0/377	1.18	2/581 (0.3%)
13	1M	1.15	0/722	1.31	7/1110 (0.6%)
14	1O	1.13	0/907	1.20	3/1394 (0.2%)
15	1P	1.15	0/1066	1.36	13/1645 (0.8%)
16	1Q	1.09	0/846	1.23	5/1301 (0.4%)
17	1R	1.17	0/1094	1.35	13/1685 (0.8%)
18	1S	1.16	0/858	1.27	9/1324 (0.7%)
19	1T	1.08	0/355	1.28	2/544 (0.4%)
20	1U	1.14	1/932 (0.1%)	1.73	9/1437 (0.6%)
21	1V	1.11	0/580	1.19	6/892 (0.7%)
22	1W	1.12	0/934	1.18	7/1443 (0.5%)
23	1X	1.13	0/1106	1.18	2/1704 (0.1%)
24	1Y	1.11	0/607	1.15	3/934 (0.3%)
25	1Z	1.10	0/596	1.23	5/918 (0.5%)
26	1a	1.08	0/1086	1.19	4/1674 (0.2%)
27	1b	1.12	0/750	1.27	9/1158 (0.8%)
28	1c	1.10	0/921	1.14	5/1420 (0.4%)
29	1d	1.10	0/931	1.15	2/1436 (0.1%)
30	1e	1.09	0/587	1.13	2/902 (0.2%)
31	1f	1.14	0/899	1.27	9/1382 (0.7%)
32	1g	1.11	0/1105	1.19	6/1702 (0.4%)
33	1h	1.11	0/1118	1.16	6/1726 (0.3%)
34	1i	1.10	0/1108	1.18	6/1709 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	1j	1.13	0/742	1.15	4/1144 (0.3%)
36	1k	1.10	0/929	1.15	7/1435 (0.5%)
37	1l	1.12	0/1098	1.16	7/1693 (0.4%)
38	1m	1.15	0/367	1.35	4/566 (0.7%)
39	1n	1.12	0/1290	1.23	6/1989 (0.3%)
40	1o	1.16	0/922	1.25	5/1422 (0.4%)
41	1p	1.14	0/917	1.34	10/1412 (0.7%)
42	1q	1.12	0/1101	1.18	10/1697 (0.6%)
43	1r	1.12	0/734	1.26	5/1131 (0.4%)
44	1s	1.11	0/727	1.34	8/1119 (0.7%)
45	1t	1.15	0/729	1.28	7/1123 (0.6%)
46	1u	1.15	0/1100	1.35	17/1697 (1.0%)
47	1v	1.12	0/356	1.10	0/546
48	1w	1.12	0/904	1.32	7/1391 (0.5%)
49	1x	1.17	0/370	1.29	5/570 (0.9%)
50	2N	1.11	0/825	1.20	7/1272 (0.6%)
51	2A	1.16	0/750	1.32	10/1158 (0.9%)
52	2B	1.14	0/1095	1.28	5/1685 (0.3%)
53	2C	1.11	0/587	1.20	5/905 (0.6%)
54	2D	1.09	0/733	1.19	5/1128 (0.4%)
55	2E	1.10	0/915	1.22	9/1410 (0.6%)
56	2F	1.12	0/1109	1.11	4/1712 (0.2%)
57	2G	1.10	0/919	1.16	5/1418 (0.4%)
58	2H	1.09	0/905	1.27	8/1391 (0.6%)
59	2I	1.07	0/368	1.16	3/567 (0.5%)
60	2J	1.13	0/674	1.22	5/1040 (0.5%)
61	2K	1.12	0/558	1.15	3/860 (0.3%)
62	2L	1.10	0/733	1.18	5/1129 (0.4%)
63	2M	1.10	0/548	1.14	1/843 (0.1%)
64	2O	1.18	2/597 (0.3%)	1.48	10/920 (1.1%)
65	2P	1.12	0/925	1.64	12/1426 (0.8%)
66	2Q	1.10	0/918	1.21	5/1415 (0.4%)
67	2R	1.11	0/924	1.23	8/1425 (0.6%)
68	2S	1.12	0/1341	1.51	18/2068 (0.9%)
69	2T	1.10	0/555	1.16	4/856 (0.5%)
70	2U	1.10	1/1187 (0.1%)	1.15	4/1829 (0.2%)
71	2V	1.11	0/912	1.15	5/1406 (0.4%)
72	2W	1.11	0/1109	1.10	4/1711 (0.2%)
73	2X	1.13	0/1091	1.23	6/1680 (0.4%)
74	2Y	1.13	0/737	1.19	4/1136 (0.4%)
75	2Z	1.11	0/917	1.24	7/1414 (0.5%)
76	2a	1.09	0/1322	1.23	11/2036 (0.5%)
77	2b	1.12	0/1290	1.55	15/1990 (0.8%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	2c	1.07	0/1025	1.08	3/1578 (0.2%)
79	2d	1.13	0/1212	1.24	9/1870 (0.5%)
80	2e	1.08	0/861	1.11	6/1330 (0.5%)
81	2f	1.11	0/1096	1.24	7/1687 (0.4%)
82	2g	1.12	0/1091	1.27	7/1678 (0.4%)
83	2h	1.12	0/1301	1.18	6/2008 (0.3%)
84	2i	1.12	0/746	1.21	4/1150 (0.3%)
85	2j	1.14	0/365	1.11	1/562 (0.2%)
86	2k	1.11	0/732	1.15	3/1127 (0.3%)
87	2l	1.11	0/1102	1.18	6/1697 (0.4%)
88	2m	1.10	0/1106	1.10	2/1705 (0.1%)
89	2n	1.11	0/364	1.23	2/560 (0.4%)
90	2o	1.10	0/730	1.10	2/1126 (0.2%)
91	2p	1.13	0/735	1.25	4/1134 (0.4%)
92	2q	1.12	0/898	1.24	8/1382 (0.6%)
93	2r	1.15	0/543	1.48	10/835 (1.2%)
94	2s	1.14	0/737	1.24	3/1135 (0.3%)
95	2t	1.14	0/928	1.44	14/1431 (1.0%)
96	2u	1.13	0/731	1.27	6/1126 (0.5%)
97	2v	1.14	0/726	1.31	5/1120 (0.4%)
98	2w	1.14	0/1101	1.33	14/1698 (0.8%)
99	2x	1.10	0/358	1.17	1/549 (0.2%)
100	3N	1.12	0/99584	1.25	838/153695 (0.5%)
101	3A	1.14	0/950	1.14	4/1470 (0.3%)
102	3B	1.13	0/919	1.22	8/1416 (0.6%)
103	3C	1.12	0/1103	1.22	7/1700 (0.4%)
104	3D	1.15	0/1124	1.28	12/1738 (0.7%)
105	3E	1.14	0/1116	1.34	15/1722 (0.9%)
106	3F	1.09	0/1265	1.21	7/1947 (0.4%)
107	3G	1.12	0/365	1.15	1/562 (0.2%)
108	3H	1.14	0/1281	1.30	12/1974 (0.6%)
109	3I	1.15	0/826	1.30	9/1273 (0.7%)
110	3J	1.14	0/801	1.26	7/1234 (0.6%)
111	3S	1.11	0/735	1.25	4/1133 (0.4%)
112	3K	1.12	0/1113	1.14	1/1716 (0.1%)
113	3L	1.13	0/853	1.21	3/1316 (0.2%)
114	3M	1.13	0/1269	1.29	11/1957 (0.6%)
115	3O	1.09	0/1108	1.19	11/1708 (0.6%)
116	3P	1.10	0/883	1.10	2/1363 (0.1%)
117	3Q	1.12	0/609	1.25	3/939 (0.3%)
118	3R	1.13	0/749	1.29	8/1158 (0.7%)
All	All	1.12	4/202097 (0.0%)	1.25	1601/311711 (0.5%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	1A	0	2
2	1B	0	9
4	1D	0	5
5	1E	0	3
6	1F	0	5
7	1G	0	1
8	1H	0	4
9	1I	0	6
10	1J	0	1
11	1K	0	8
12	1L	0	1
13	1M	0	1
14	1O	0	5
15	1P	0	9
16	1Q	0	1
17	1R	0	3
18	1S	0	2
20	1U	0	1
22	1W	0	1
23	1X	0	4
25	1Z	0	1
26	1a	0	4
27	1b	0	2
29	1d	0	1
31	1f	0	1
32	1g	0	1
33	1h	0	3
34	1i	0	1
35	1j	0	1
36	1k	0	3
37	1l	0	2
39	1n	0	1
40	1o	0	2
41	1p	0	2
42	1q	0	3
44	1s	0	3
46	1u	0	1
47	1v	0	1
48	1w	0	4

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Mol	Chain	#Chirality outliers	#Planarity outliers
50	2N	0	2
52	2B	0	4
53	2C	0	1
54	2D	0	1
56	2F	0	5
57	2G	0	2
58	2H	0	1
60	2J	0	1
64	2O	0	3
65	2P	0	3
66	2Q	0	2
67	2R	0	2
68	2S	0	2
70	2U	0	1
71	2V	0	1
72	2W	0	2
73	2X	0	1
74	2Y	0	1
75	2Z	0	1
77	2b	0	3
78	2c	0	2
79	2d	0	1
80	2e	0	1
82	2g	0	1
83	2h	0	4
84	2i	0	3
85	2j	0	2
87	2l	0	2
88	2m	0	1
89	2n	0	1
90	2o	0	1
91	2p	0	1
92	2q	0	4
93	2r	0	2
95	2t	0	1
96	2u	0	1
97	2v	0	2
98	2w	0	3
100	3N	0	176
101	3A	0	2
102	3B	0	1
103	3C	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
104	3D	0	3
106	3F	0	4
107	3G	0	1
108	3H	0	5
109	3I	0	2
110	3J	0	2
111	3S	0	1
112	3K	0	3
114	3M	0	2
115	3O	0	1
117	3Q	0	4
All	All	0	390

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
64	2O	1059	DG	C5'-C4'	5.71	1.57	1.51
20	1U	17	DC	N1-C6	5.49	1.40	1.37
64	2O	1060	DC	C5'-C4'	5.38	1.57	1.51
70	2U	1047	DT	C5'-C4'	5.03	1.56	1.51

All (1601) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
20	1U	17	DC	C6-N1-C2	-42.12	103.45	120.30
77	2b	1073	DA	O5'-P-OP1	-26.14	79.33	110.70
65	2P	1062	DG	O5'-P-OP1	-24.68	81.09	110.70
68	2S	1054	DA	O5'-P-OP1	-24.15	81.72	110.70
77	2b	1073	DA	O5'-P-OP2	-23.92	81.99	110.70
65	2P	1062	DG	O5'-P-OP2	-23.65	82.33	110.70
68	2S	1054	DA	O5'-P-OP2	-21.22	85.24	110.70
20	1U	17	DC	C6-N1-C1'	-18.79	98.25	120.80
29	1d	31	DT	P-O3'-C3'	16.19	139.13	119.70
100	3N	4563	DC	P-O3'-C3'	15.88	138.75	119.70
100	3N	8344	DA	P-O3'-C3'	15.85	138.72	119.70
100	3N	7738	DC	P-O3'-C3'	15.82	138.69	119.70
48	1w	1027	DC	P-O3'-C3'	15.60	138.42	119.70
100	3N	7785	DG	P-O3'-C3'	15.60	138.41	119.70
77	2b	1072	DG	O3'-P-O5'	15.49	133.44	104.00
51	2A	1063	DC	P-O3'-C3'	15.41	138.19	119.70
100	3N	7981	DG	P-O3'-C3'	15.35	138.12	119.70
39	1n	1027	DT	P-O3'-C3'	15.30	138.06	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
44	1s	1032	DG	P-O3'-C3'	15.09	137.80	119.70
95	2t	2062	DG	P-O3'-C3'	15.04	137.75	119.70
100	3N	4708	DC	P-O3'-C3'	15.01	137.71	119.70
111	3S	2100	DA	P-O3'-C3'	14.68	137.31	119.70
64	2O	1060	DC	P-O3'-C3'	14.59	137.20	119.70
100	3N	3461	DC	P-O3'-C3'	14.56	137.17	119.70
93	2r	2056	DC	P-O3'-C3'	14.56	137.17	119.70
26	1a	31	DA	P-O3'-C3'	14.52	137.13	119.70
100	3N	6829	DT	P-O3'-C3'	14.43	137.02	119.70
100	3N	7325	DC	P-O3'-C3'	14.41	136.99	119.70
100	3N	5124	DC	P-O3'-C3'	14.41	136.99	119.70
6	1F	16	DA	P-O3'-C3'	14.35	136.92	119.70
100	3N	3746	DA	P-O3'-C3'	14.31	136.87	119.70
100	3N	4375	DC	P-O3'-C3'	14.30	136.87	119.70
68	2S	1054	DA	OP1-P-OP2	14.27	141.00	119.60
100	3N	3459	DC	P-O3'-C3'	14.26	136.81	119.70
100	3N	5292	DA	P-O3'-C3'	14.24	136.79	119.70
100	3N	7022	DA	P-O3'-C3'	14.22	136.77	119.70
98	2w	2089	DA	P-O3'-C3'	14.19	136.73	119.70
100	3N	7793	DT	P-O3'-C3'	14.11	136.63	119.70
100	3N	8319	DT	P-O3'-C3'	14.08	136.60	119.70
65	2P	1062	DG	OP1-P-OP2	14.07	140.71	119.60
100	3N	4139	DT	P-O3'-C3'	14.07	136.59	119.70
100	3N	3957	DC	P-O3'-C3'	14.02	136.53	119.70
68	2S	1044	DG	P-O3'-C3'	13.95	136.44	119.70
100	3N	8172	DG	P-O3'-C3'	13.95	136.44	119.70
64	2O	1062	DT	P-O3'-C3'	13.94	136.43	119.70
100	3N	3923	DC	P-O3'-C3'	13.93	136.41	119.70
73	2X	1052	DG	P-O3'-C3'	13.87	136.35	119.70
114	3M	2110	DA	P-O3'-C3'	13.83	136.30	119.70
43	1r	1016	DA	P-O3'-C3'	13.81	136.27	119.70
100	3N	7060	DC	P-O3'-C3'	13.77	136.22	119.70
100	3N	8087	DT	P-O3'-C3'	13.76	136.21	119.70
100	3N	4356	DG	P-O3'-C3'	13.73	136.18	119.70
67	2R	1065	DT	P-O3'-C3'	13.70	136.15	119.70
52	2B	1041	DA	P-O3'-C3'	13.69	136.13	119.70
100	3N	3827	DG	P-O3'-C3'	13.64	136.07	119.70
95	2t	2054	DC	P-O3'-C3'	13.63	136.06	119.70
100	3N	3193	DT	P-O3'-C3'	13.61	136.03	119.70
100	3N	5269	DT	P-O3'-C3'	13.60	136.02	119.70
100	3N	7005	DC	P-O3'-C3'	13.57	135.99	119.70
100	3N	7696	DC	P-O3'-C3'	13.56	135.97	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
100	3N	3528	DG	P-O3'-C3'	13.54	135.94	119.70
9	1I	41	DG	P-O3'-C3'	13.52	135.92	119.70
100	3N	4865	DA	P-O3'-C3'	13.51	135.92	119.70
100	3N	6931	DT	P-O3'-C3'	13.44	135.83	119.70
100	3N	3570	DG	P-O3'-C3'	13.38	135.75	119.70
93	2r	2055	DC	P-O3'-C3'	13.37	135.75	119.70
100	3N	3700	DC	P-O3'-C3'	13.28	135.63	119.70
100	3N	7062	DC	P-O3'-C3'	13.27	135.63	119.70
100	3N	7778	DA	P-O3'-C3'	13.26	135.62	119.70
100	3N	7777	DG	P-O3'-C3'	13.25	135.60	119.70
89	2n	2075	DA	P-O3'-C3'	13.23	135.57	119.70
100	3N	7533	DC	P-O3'-C3'	13.22	135.57	119.70
110	3J	2061	DC	P-O3'-C3'	13.21	135.56	119.70
113	3L	2092	DG	P-O3'-C3'	13.17	135.51	119.70
77	2b	1041	DT	O4'-C4'-C3'	-13.16	98.10	106.00
58	2H	1074	DC	O4'-C4'-C3'	-13.11	98.13	106.00
100	3N	5377	DA	P-O3'-C3'	13.10	135.42	119.70
11	1K	15	DG	P-O3'-C3'	13.08	135.40	119.70
100	3N	7645	DG	P-O3'-C3'	13.06	135.37	119.70
98	2w	2093	DA	P-O3'-C3'	13.04	135.35	119.70
100	3N	3370	DC	P-O3'-C3'	13.04	135.34	119.70
18	1S	9	DT	P-O3'-C3'	13.02	135.32	119.70
20	1U	16	DC	P-O3'-C3'	13.01	135.32	119.70
100	3N	4283	DA	P-O3'-C3'	12.97	135.27	119.70
100	3N	7278	DG	P-O3'-C3'	12.96	135.26	119.70
100	3N	4726	DA	P-O3'-C3'	12.90	135.18	119.70
100	3N	6709	DG	P-O3'-C3'	12.83	135.09	119.70
65	2P	1061	DC	O3'-P-O5'	12.82	128.36	104.00
11	1K	20	DA	P-O3'-C3'	12.78	135.04	119.70
100	3N	4633	DG	P-O3'-C3'	12.77	135.02	119.70
20	1U	17	DC	C2-N3-C4	-12.76	113.52	119.90
100	3N	3659	DG	P-O3'-C3'	12.71	134.95	119.70
100	3N	4968	DA	P-O3'-C3'	12.64	134.87	119.70
97	2v	2046	DA	P-O3'-C3'	12.63	134.85	119.70
6	1F	24	DA	P-O3'-C3'	12.62	134.85	119.70
100	3N	8039	DA	P-O3'-C3'	12.61	134.83	119.70
100	3N	5392	DA	O4'-C4'-C3'	-12.53	98.48	106.00
45	1t	1022	DA	P-O3'-C3'	12.48	134.68	119.70
68	2S	1053	DA	OP2-P-O3'	-12.48	77.75	105.20
114	3M	2087	DC	P-O3'-C3'	12.48	134.67	119.70
100	3N	4701	DA	P-O3'-C3'	12.38	134.56	119.70
11	1K	38	DA	P-O3'-C3'	12.38	134.56	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
81	2f	1049	DT	O4'-C4'-C3'	-12.37	98.58	106.00
15	1P	13	DC	P-O3'-C3'	12.35	134.53	119.70
100	3N	7635	DA	P-O3'-C3'	12.34	134.51	119.70
100	3N	6698	DT	P-O3'-C3'	12.33	134.50	119.70
100	3N	5191	DG	P-O3'-C3'	12.27	134.43	119.70
100	3N	5493	DG	P-O3'-C3'	12.23	134.37	119.70
97	2v	2039	DC	P-O3'-C3'	12.22	134.37	119.70
100	3N	3673	DG	P-O3'-C3'	12.20	134.34	119.70
100	3N	3875	DC	P-O3'-C3'	12.17	134.30	119.70
105	3E	2108	DA	P-O3'-C3'	12.16	134.30	119.70
11	1K	10	DG	P-O3'-C3'	12.16	134.29	119.70
100	3N	6934	DC	P-O3'-C3'	12.15	134.28	119.70
40	1o	1028	DT	P-O3'-C3'	12.11	134.23	119.70
100	3N	3994	DA	P-O3'-C3'	12.10	134.22	119.70
106	3F	2101	DT	O4'-C4'-C3'	-12.10	98.74	106.00
15	1P	12	DG	P-O3'-C3'	12.10	134.22	119.70
52	2B	1031	DC	P-O3'-C3'	12.09	134.21	119.70
8	1H	1	DA	O4'-C4'-C3'	-12.09	98.75	106.00
100	3N	7944	DG	P-O3'-C3'	12.09	134.20	119.70
100	3N	4082	DA	O4'-C4'-C3'	-12.08	98.75	106.00
100	3N	7180	DT	P-O3'-C3'	12.04	134.15	119.70
100	3N	4818	DA	P-O3'-C3'	12.04	134.15	119.70
108	3H	2139	DC	P-O3'-C3'	12.02	134.12	119.70
27	1b	6	DG	P-O3'-C3'	12.01	134.11	119.70
76	2a	1086	DG	P-O3'-C3'	11.99	134.08	119.70
100	3N	4939	DG	P-O3'-C3'	11.96	134.05	119.70
100	3N	3248	DA	P-O3'-C3'	11.94	134.03	119.70
100	3N	3589	DG	P-O3'-C3'	11.86	133.93	119.70
79	2d	1027	DG	P-O3'-C3'	11.80	133.85	119.70
100	3N	8071	DC	P-O3'-C3'	11.79	133.84	119.70
100	3N	8288	DT	P-O3'-C3'	11.78	133.83	119.70
100	3N	4210	DG	P-O3'-C3'	11.78	133.83	119.70
105	3E	2084	DA	O4'-C4'-C3'	-11.77	98.94	106.00
100	3N	6637	DA	P-O3'-C3'	11.73	133.77	119.70
100	3N	6837	DT	O4'-C4'-C3'	-11.72	98.97	106.00
100	3N	5237	DT	P-O3'-C3'	11.70	133.74	119.70
118	3R	2089	DG	P-O3'-C3'	11.64	133.67	119.70
6	1F	9	DA	P-O3'-C3'	11.63	133.66	119.70
2	1B	47	DG	O4'-C4'-C3'	-11.63	99.02	106.00
100	3N	3123	DA	P-O3'-C3'	11.61	133.63	119.70
117	3Q	2101	DT	P-O3'-C3'	11.54	133.54	119.70
77	2b	1073	DA	OP1-P-OP2	11.52	136.89	119.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
100	3N	4972	DT	P-O3'-C3'	11.51	133.51	119.70
100	3N	3216	DT	P-O3'-C3'	11.50	133.50	119.70
100	3N	8458	DG	P-O3'-C3'	11.49	133.49	119.70
68	2S	1053	DA	OP1-P-O3'	-11.42	80.07	105.20
100	3N	5131	DA	P-O3'-C3'	11.40	133.38	119.70
100	3N	3379	DC	P-O3'-C3'	11.38	133.36	119.70
17	1R	41	DA	O4'-C4'-C3'	-11.38	99.17	106.00
100	3N	6924	DC	P-O3'-C3'	11.34	133.31	119.70
100	3N	8313	DT	P-O3'-C3'	11.33	133.29	119.70
60	2J	1068	DA	P-O3'-C3'	11.29	133.25	119.70
100	3N	7085	DA	P-O3'-C3'	11.28	133.24	119.70
100	3N	3418	DG	P-O3'-C3'	11.25	133.20	119.70
104	3D	2102	DC	O4'-C4'-C3'	-11.24	99.26	106.00
6	1F	8	DA	P-O3'-C3'	11.22	133.16	119.70
100	3N	4452	DG	P-O3'-C3'	11.21	133.15	119.70
104	3D	2086	DG	O4'-C4'-C3'	-11.17	99.30	106.00
96	2u	2086	DT	P-O3'-C3'	11.12	133.04	119.70
100	3N	5131	DA	O4'-C4'-C3'	-11.07	99.36	106.00
25	1Z	14	DT	O4'-C4'-C3'	-11.04	99.38	106.00
100	3N	7809	DG	O4'-C4'-C3'	-11.04	99.38	106.00
76	2a	1063	DT	O4'-C4'-C3'	-11.03	99.38	106.00
68	2S	1053	DA	O3'-P-O5'	11.03	124.95	104.00
34	1i	14	DC	P-O3'-C3'	11.02	132.92	119.70
100	3N	4092	DG	P-O3'-C3'	10.98	132.87	119.70
100	3N	7809	DG	P-O3'-C3'	10.97	132.87	119.70
65	2P	1061	DC	OP2-P-O3'	-10.96	81.09	105.20
100	3N	3085	DT	O4'-C4'-C3'	-10.94	99.43	106.00
100	3N	5379	DC	P-O3'-C3'	10.94	132.83	119.70
100	3N	7805	DT	P-O3'-C3'	10.91	132.80	119.70
46	1u	1046	DG	O4'-C4'-C3'	-10.89	99.47	106.00
19	1T	1	DC	O4'-C4'-C3'	-10.84	99.50	106.00
100	3N	5115	DG	O4'-C4'-C3'	-10.82	99.51	106.00
100	3N	7052	DA	P-O3'-C3'	10.82	132.68	119.70
66	2Q	1071	DG	P-O3'-C3'	10.79	132.65	119.70
46	1u	1046	DG	P-O3'-C3'	10.71	132.56	119.70
41	1p	1042	DG	P-O3'-C3'	10.69	132.53	119.70
82	2g	1082	DG	P-O3'-C3'	10.66	132.49	119.70
100	3N	3974	DG	O4'-C4'-C3'	-10.65	99.61	106.00
65	2P	1061	DC	OP1-P-O3'	-10.63	81.82	105.20
31	1f	21	DA	P-O3'-C3'	10.63	132.45	119.70
39	1n	1050	DC	P-O3'-C3'	10.62	132.45	119.70
83	2h	1065	DA	O4'-C4'-C3'	-10.60	99.64	106.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
100	3N	6990	DT	P-O3'-C3'	10.57	132.39	119.70
58	2H	1075	DA	O4'-C4'-C3'	-10.53	99.68	106.00
100	3N	7911	DG	O4'-C4'-C3'	-10.52	99.69	106.00
100	3N	7052	DA	O4'-C4'-C3'	-10.51	99.69	106.00
100	3N	7725	DA	P-O3'-C3'	10.51	132.31	119.70
100	3N	4212	DT	O4'-C4'-C3'	-10.50	99.70	106.00
77	2b	1072	DG	OP1-P-O3'	-10.46	82.18	105.20
100	3N	4663	DA	P-O3'-C3'	10.46	132.25	119.70
28	1c	23	DA	P-O3'-C3'	10.43	132.21	119.70
117	3Q	2089	DA	O4'-C4'-C3'	-10.39	99.77	106.00
100	3N	4850	DT	O4'-C4'-C3'	-10.39	99.77	106.00
100	3N	7166	DC	P-O3'-C3'	10.39	132.16	119.70
100	3N	3509	DG	O4'-C4'-C3'	-10.38	99.77	106.00
100	3N	8450	DG	O4'-C4'-C3'	-10.33	99.80	106.00
100	3N	4151	DG	O4'-C4'-C3'	-10.29	99.83	106.00
52	2B	1024	DA	P-O3'-C3'	10.28	132.04	119.70
75	2Z	1062	DA	O4'-C4'-C3'	-10.26	99.85	106.00
110	3J	2041	DA	O4'-C4'-C3'	-10.21	99.87	106.00
100	3N	4917	DT	P-O3'-C3'	10.20	131.94	119.70
100	3N	3683	DT	O4'-C1'-C2'	-10.18	97.75	105.90
44	1s	1016	DA	O4'-C4'-C3'	-10.18	99.89	106.00
114	3M	2075	DG	O4'-C4'-C3'	-10.16	99.90	106.00
100	3N	4338	DA	O4'-C4'-C3'	-10.14	99.92	106.00
100	3N	7683	DG	O4'-C4'-C3'	-10.14	99.92	106.00
100	3N	6611	DG	O4'-C4'-C3'	-10.10	99.94	106.00
21	1V	1	DC	O4'-C4'-C3'	-10.10	99.94	106.00
82	2g	1080	DT	P-O3'-C3'	10.10	131.81	119.70
100	3N	7211	DT	P-O3'-C3'	10.08	131.80	119.70
100	3N	7915	DG	O4'-C4'-C3'	-10.07	99.96	106.00
100	3N	7911	DG	P-O3'-C3'	10.05	131.76	119.70
77	2b	1072	DG	OP2-P-O3'	-10.02	83.17	105.20
106	3F	2101	DT	P-O3'-C3'	9.99	131.69	119.70
95	2t	2055	DG	P-O3'-C3'	9.97	131.67	119.70
7	1G	8	DA	O4'-C4'-C3'	-9.94	100.03	106.00
100	3N	4290	DG	O4'-C4'-C3'	-9.91	100.05	106.00
13	1M	1	DC	P-O3'-C3'	9.91	131.59	119.70
100	3N	6990	DT	O4'-C4'-C3'	-9.89	100.06	106.00
108	3H	2120	DC	P-O3'-C3'	9.89	131.57	119.70
46	1u	1047	DC	P-O3'-C3'	9.89	131.56	119.70
27	1b	6	DG	O4'-C4'-C3'	-9.85	100.09	106.00
97	2v	2038	DG	P-O3'-C3'	9.84	131.51	119.70
100	3N	3994	DA	O4'-C4'-C3'	-9.84	100.10	106.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
100	3N	5033	DT	O4'-C4'-C3'	-9.81	100.12	106.00
100	3N	7081	DG	O4'-C4'-C3'	-9.80	100.12	106.00
52	2B	1032	DC	P-O3'-C3'	9.77	131.42	119.70
100	3N	7768	DG	O4'-C4'-C3'	-9.75	100.15	106.00
103	3C	2105	DA	P-O3'-C3'	9.75	131.40	119.70
97	2v	2038	DG	O4'-C4'-C3'	-9.74	100.15	106.00
100	3N	5280	DG	O4'-C4'-C3'	-9.74	100.15	106.00
98	2w	2084	DC	P-O3'-C3'	9.73	131.38	119.70
100	3N	4865	DA	O4'-C4'-C3'	-9.72	100.17	106.00
100	3N	4942	DA	O4'-C4'-C3'	-9.72	100.17	106.00
100	3N	4603	DT	O4'-C4'-C3'	-9.71	100.17	106.00
100	3N	5268	DG	P-O3'-C3'	9.71	131.36	119.70
100	3N	4233	DG	O4'-C4'-C3'	-9.68	100.19	106.00
7	1G	8	DA	P-O3'-C3'	9.67	131.31	119.70
109	3I	2088	DC	O4'-C4'-C3'	-9.66	100.20	106.00
100	3N	5352	DT	O4'-C4'-C3'	-9.66	100.20	106.00
95	2t	2071	DT	P-O3'-C3'	9.66	131.29	119.70
100	3N	4725	DG	O4'-C4'-C3'	-9.66	100.21	106.00
69	2T	1041	DG	O4'-C4'-C3'	-9.65	100.21	106.00
100	3N	3330	DA	O4'-C4'-C3'	-9.64	100.21	106.00
26	1a	16	DT	P-O3'-C3'	9.62	131.24	119.70
100	3N	7625	DG	O4'-C4'-C3'	-9.60	100.24	106.00
100	3N	4452	DG	O4'-C4'-C3'	-9.59	100.24	106.00
100	3N	8332	DG	O4'-C4'-C3'	-9.59	100.24	106.00
100	3N	4770	DG	O4'-C4'-C3'	-9.58	100.25	106.00
100	3N	3223	DG	O4'-C4'-C3'	-9.57	100.26	106.00
8	1H	15	DC	O4'-C4'-C3'	-9.54	100.28	106.00
13	1M	1	DC	O4'-C4'-C3'	-9.53	100.28	106.00
108	3H	2103	DG	P-O3'-C3'	9.52	131.13	119.70
100	3N	3327	DG	O4'-C4'-C3'	-9.52	100.29	106.00
100	3N	7526	DT	O4'-C4'-C3'	-9.52	100.29	106.00
100	3N	4623	DT	O4'-C4'-C3'	-9.47	100.32	106.00
100	3N	8313	DT	O4'-C4'-C3'	-9.47	100.32	106.00
100	3N	5077	DG	P-O3'-C3'	9.46	131.05	119.70
38	1m	1018	DG	P-O3'-C3'	9.45	131.04	119.70
96	2u	2064	DA	O4'-C4'-C3'	-9.44	100.33	106.00
100	3N	5108	DA	P-O3'-C3'	9.44	131.03	119.70
104	3D	2106	DT	O4'-C4'-C3'	-9.41	100.35	106.00
100	3N	5410	DA	O4'-C4'-C3'	-9.41	100.36	106.00
100	3N	3745	DG	O4'-C4'-C3'	-9.39	100.36	106.00
55	2E	1048	DT	O4'-C4'-C3'	-9.38	100.37	106.00
100	3N	4514	DT	O4'-C4'-C3'	-9.37	100.38	106.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
100	3N	4973	DT	O4'-C4'-C3'	-9.35	100.39	106.00
100	3N	7166	DC	O4'-C4'-C3'	-9.35	100.39	106.00
100	3N	3522	DG	O4'-C4'-C3'	-9.35	100.39	106.00
77	2b	1096	DA	O4'-C4'-C3'	-9.34	100.39	106.00
39	1n	1026	DA	P-O3'-C3'	9.34	130.90	119.70
100	3N	4034	DT	O4'-C4'-C3'	-9.29	100.43	106.00
55	2E	1055	DT	O4'-C1'-C2'	-9.29	98.47	105.90
100	3N	6828	DG	P-O3'-C3'	9.26	130.82	119.70
51	2A	1062	DC	P-O3'-C3'	9.25	130.81	119.70
22	1W	4	DT	O4'-C4'-C3'	-9.24	100.45	106.00
111	3S	2106	DG	O4'-C4'-C3'	-9.24	100.46	106.00
50	2N	1075	DT	P-O3'-C3'	9.23	130.78	119.70
100	3N	3786	DG	O4'-C4'-C3'	-9.22	100.47	106.00
100	3N	7112	DT	O4'-C4'-C3'	-9.21	100.47	106.00
46	1u	1032	DT	P-O3'-C3'	9.21	130.75	119.70
100	3N	5471	DA	O4'-C4'-C3'	-9.18	100.49	106.00
100	3N	4066	DA	O4'-C4'-C3'	-9.17	100.50	106.00
16	1Q	29	DG	P-O3'-C3'	9.14	130.67	119.70
17	1R	33	DT	P-O3'-C3'	9.13	130.65	119.70
75	2Z	1063	DT	P-O3'-C3'	9.12	130.65	119.70
43	1r	1015	DA	P-O3'-C3'	9.12	130.64	119.70
100	3N	3172	DA	O4'-C4'-C3'	-9.08	100.55	106.00
100	3N	7337	DT	P-O3'-C3'	9.06	130.58	119.70
100	3N	7981	DG	O4'-C1'-C2'	-9.06	98.65	105.90
100	3N	5145	DA	P-O3'-C3'	9.05	130.56	119.70
100	3N	7109	DT	O4'-C4'-C3'	-9.04	100.57	106.00
91	2p	2061	DG	O4'-C4'-C3'	-9.04	100.58	106.00
98	2w	2057	DG	O4'-C4'-C3'	-9.03	100.58	106.00
11	1K	31	DC	O4'-C4'-C3'	-9.02	100.59	106.00
46	1u	1048	DC	P-O3'-C3'	9.00	130.50	119.70
100	3N	3528	DG	O4'-C1'-C2'	-8.96	98.73	105.90
104	3D	2116	DA	P-O3'-C3'	8.93	130.42	119.70
59	2I	1025	DA	O4'-C4'-C3'	-8.91	100.65	106.00
100	3N	8046	DG	P-O3'-C3'	8.85	130.32	119.70
31	1f	21	DA	O4'-C4'-C3'	-8.79	100.72	106.00
100	3N	5175	DG	O4'-C1'-C2'	-8.79	98.87	105.90
100	3N	8046	DG	O4'-C4'-C3'	-8.79	100.73	106.00
79	2d	1027	DG	O4'-C1'-C2'	-8.79	98.87	105.90
74	2Y	1034	DG	O4'-C4'-C3'	-8.78	100.73	106.00
81	2f	1056	DT	O4'-C4'-C3'	-8.76	100.74	106.00
75	2Z	1064	DT	P-O3'-C3'	8.76	130.21	119.70
82	2g	1073	DT	O4'-C1'-C2'	-8.74	98.91	105.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
100	3N	4283	DA	O4'-C1'-C2'	-8.73	98.92	105.90
95	2t	2056	DT	O4'-C1'-C2'	-8.72	98.93	105.90
54	2D	1052	DA	O4'-C1'-C2'	-8.71	98.93	105.90
15	1P	13	DC	O4'-C1'-C2'	-8.71	98.93	105.90
67	2R	1065	DT	O4'-C1'-C2'	-8.66	98.97	105.90
64	2O	1062	DT	O4'-C1'-C2'	-8.66	98.97	105.90
100	3N	7696	DC	O4'-C1'-C2'	-8.65	98.98	105.90
105	3E	2091	DA	P-O3'-C3'	8.65	130.08	119.70
100	3N	3659	DG	O4'-C1'-C2'	-8.62	99.00	105.90
58	2H	1079	DG	O4'-C4'-C3'	-8.61	100.84	106.00
66	2Q	1071	DG	O4'-C4'-C3'	-8.55	100.87	106.00
6	1F	7	DG	O4'-C1'-C2'	-8.55	99.06	105.90
100	3N	5191	DG	O4'-C1'-C2'	-8.54	99.07	105.90
100	3N	6837	DT	P-O3'-C3'	8.54	129.94	119.70
100	3N	6825	DT	O4'-C4'-C3'	-8.53	100.88	106.00
62	2L	1033	DG	O4'-C1'-C2'	-8.53	99.08	105.90
93	2r	2054	DG	P-O3'-C3'	8.52	129.92	119.70
100	3N	7211	DT	O4'-C4'-C3'	-8.52	100.89	106.00
100	3N	7784	DC	P-O3'-C3'	8.51	129.92	119.70
100	3N	5493	DG	O4'-C1'-C2'	-8.49	99.11	105.90
100	3N	6908	DC	P-O3'-C3'	8.49	129.88	119.70
17	1R	25	DG	P-O3'-C3'	8.47	129.87	119.70
100	3N	6698	DT	O4'-C1'-C2'	-8.47	99.12	105.90
100	3N	4701	DA	O4'-C1'-C2'	-8.45	99.14	105.90
100	3N	4633	DG	O4'-C1'-C2'	-8.44	99.14	105.90
100	3N	5084	DA	N1-C6-N6	-8.39	113.57	118.60
45	1t	1022	DA	O4'-C4'-C3'	-8.36	100.99	106.00
53	2C	1072	DG	O4'-C4'-C3'	-8.31	101.01	106.00
76	2a	1086	DG	O4'-C4'-C3'	-8.29	101.03	106.00
100	3N	3603	DG	O4'-C1'-C2'	-8.29	99.27	105.90
100	3N	4968	DA	O4'-C1'-C2'	-8.27	99.28	105.90
100	3N	3875	DC	O4'-C4'-C3'	-8.27	101.04	106.00
100	3N	5077	DG	O4'-C4'-C3'	-8.26	101.04	106.00
31	1f	14	DC	P-O3'-C3'	8.25	129.60	119.70
100	3N	4939	DG	O4'-C1'-C2'	-8.24	99.31	105.90
100	3N	4945	DT	O4'-C4'-C3'	-8.24	101.06	106.00
3	1C	1	DA	O4'-C1'-C2'	-8.22	99.33	105.90
100	3N	3168	DG	P-O3'-C3'	8.21	129.56	119.70
114	3M	2097	DG	P-O3'-C3'	8.19	129.53	119.70
50	2N	1053	DA	O4'-C1'-C2'	-8.18	99.36	105.90
100	3N	5377	DA	O4'-C1'-C2'	-8.17	99.36	105.90
98	2w	2069	DA	P-O3'-C3'	8.16	129.49	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
82	2g	1073	DT	O4'-C4'-C3'	-8.14	101.12	106.00
100	3N	8071	DC	O4'-C1'-C2'	-8.13	99.40	105.90
92	2q	2088	DG	O4'-C1'-C2'	-8.11	99.41	105.90
100	3N	3418	DG	O4'-C1'-C2'	-8.09	99.43	105.90
50	2N	1075	DT	O4'-C4'-C3'	-8.07	101.16	106.00
91	2p	2052	DG	O4'-C1'-C2'	-8.06	99.45	105.90
92	2q	2062	DT	O4'-C4'-C3'	-8.05	101.17	106.00
100	3N	8425	DG	O4'-C1'-C2'	-8.05	99.46	105.90
100	3N	7278	DG	O4'-C1'-C2'	-8.05	99.46	105.90
2	1B	47	DG	P-O3'-C3'	8.04	129.35	119.70
13	1M	1	DC	O4'-C1'-C2'	-8.02	99.48	105.90
5	1E	1	DA	O4'-C1'-C2'	-8.01	99.49	105.90
42	1q	1008	DG	O4'-C1'-C2'	-7.99	99.51	105.90
51	2A	1074	DG	O4'-C1'-C2'	-7.99	99.51	105.90
24	1Y	17	DA	P-O3'-C3'	7.98	129.27	119.70
100	3N	3673	DG	O4'-C1'-C2'	-7.97	99.52	105.90
100	3N	5471	DA	P-O3'-C3'	7.96	129.25	119.70
100	3N	8239	DA	O4'-C4'-C3'	-7.93	101.24	106.00
105	3E	2091	DA	O4'-C1'-C2'	-7.93	99.56	105.90
41	1p	1042	DG	O4'-C4'-C3'	-7.92	101.25	106.00
105	3E	2108	DA	O4'-C1'-C2'	-7.92	99.56	105.90
100	3N	3123	DA	O4'-C1'-C2'	-7.91	99.57	105.90
60	2J	1068	DA	O4'-C1'-C2'	-7.91	99.57	105.90
100	3N	3827	DG	O4'-C1'-C2'	-7.90	99.58	105.90
100	3N	7975	DG	O4'-C1'-C2'	-7.89	99.59	105.90
100	3N	7635	DA	O4'-C1'-C2'	-7.87	99.61	105.90
108	3H	2103	DG	O4'-C1'-C2'	-7.87	99.61	105.90
100	3N	3589	DG	O4'-C1'-C2'	-7.86	99.61	105.90
118	3R	2093	DT	P-O3'-C3'	7.85	129.12	119.70
100	3N	7805	DT	O4'-C4'-C3'	-7.84	101.29	106.00
37	1l	35	DG	O4'-C1'-C2'	-7.83	99.63	105.90
84	2i	1038	DG	O4'-C1'-C2'	-7.81	99.65	105.90
100	3N	5364	DG	O4'-C1'-C2'	-7.81	99.65	105.90
75	2Z	1085	DG	O4'-C1'-C2'	-7.81	99.66	105.90
100	3N	5108	DA	O4'-C1'-C2'	-7.80	99.66	105.90
100	3N	7157	DG	O4'-C1'-C2'	-7.80	99.66	105.90
100	3N	5541	DT	O4'-C4'-C3'	-7.80	101.32	106.00
100	3N	8087	DT	O4'-C1'-C2'	-7.80	99.66	105.90
100	3N	7085	DA	O4'-C1'-C2'	-7.78	99.68	105.90
100	3N	5503	DG	O4'-C1'-C2'	-7.77	99.68	105.90
95	2t	2056	DT	O4'-C4'-C3'	-7.77	101.34	106.00
118	3R	2089	DG	O4'-C1'-C2'	-7.76	99.69	105.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
100	3N	3193	DT	O4'-C1'-C2'	-7.75	99.70	105.90
100	3N	4758	DC	P-O3'-C3'	7.75	129.00	119.70
58	2H	1075	DA	O4'-C1'-C2'	-7.75	99.70	105.90
22	1W	14	DG	O4'-C1'-C2'	-7.73	99.72	105.90
100	3N	4330	DA	O4'-C4'-C3'	-7.73	101.36	106.00
79	2d	1027	DG	O4'-C4'-C3'	-7.71	101.37	106.00
104	3D	2102	DC	O4'-C1'-N1	7.70	113.39	108.00
17	1R	47	DG	O4'-C1'-C2'	-7.70	99.74	105.90
100	3N	5493	DG	O4'-C4'-C3'	-7.70	101.38	106.00
104	3D	2102	DC	C1'-O4'-C4'	-7.70	102.40	110.10
28	1c	23	DA	O4'-C1'-C2'	-7.70	99.74	105.90
118	3R	2089	DG	O4'-C4'-C3'	-7.70	101.38	106.00
100	3N	7143	DG	O4'-C1'-C2'	-7.69	99.75	105.90
100	3N	7046	DG	O4'-C1'-C2'	-7.69	99.75	105.90
100	3N	3700	DC	O4'-C1'-C2'	-7.68	99.75	105.90
100	3N	7645	DG	O4'-C1'-C2'	-7.68	99.75	105.90
6	1F	31	DT	O4'-C4'-C3'	-7.67	101.40	106.00
54	2D	1052	DA	O4'-C4'-C3'	-7.67	101.40	106.00
100	3N	4470	DC	P-O3'-C3'	7.67	128.90	119.70
100	3N	3379	DC	O4'-C4'-C3'	-7.67	101.40	106.00
100	3N	6949	DG	O4'-C1'-C2'	-7.66	99.77	105.90
46	1u	1052	DG	O4'-C1'-C2'	-7.65	99.78	105.90
100	3N	4210	DG	O4'-C1'-C2'	-7.65	99.78	105.90
116	3P	2082	DG	O4'-C4'-C3'	-7.64	101.42	106.00
44	1s	1028	DG	O4'-C1'-C2'	-7.63	99.80	105.90
56	2F	1060	DG	O4'-C1'-C2'	-7.63	99.80	105.90
64	2O	1059	DG	P-O3'-C3'	7.63	128.85	119.70
100	3N	6761	DG	O4'-C1'-C2'	-7.62	99.80	105.90
100	3N	7748	DG	O4'-C1'-C2'	-7.62	99.80	105.90
100	3N	6692	DG	O4'-C1'-C2'	-7.61	99.82	105.90
6	1F	24	DA	O4'-C1'-C2'	-7.60	99.82	105.90
100	3N	5179	DC	O4'-C1'-C2'	-7.59	99.83	105.90
100	3N	7883	DT	O4'-C4'-C3'	-7.59	101.45	106.00
100	3N	6972	DA	O4'-C4'-C3'	-7.57	101.46	106.00
57	2G	1069	DG	O4'-C1'-C2'	-7.57	99.84	105.90
46	1u	1016	DG	O4'-C1'-C2'	-7.57	99.84	105.90
100	3N	7793	DT	O4'-C1'-C2'	-7.55	99.86	105.90
100	3N	7337	DT	O4'-C4'-C3'	-7.54	101.47	106.00
98	2w	2070	DC	P-O3'-C3'	7.54	128.75	119.70
100	3N	3882	DG	O4'-C1'-C2'	-7.53	99.88	105.90
8	1H	13	DA	N1-C6-N6	-7.51	114.09	118.60
55	2E	1075	DG	O4'-C1'-C2'	-7.51	99.89	105.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	1p	1018	DA	P-O3'-C3'	7.51	128.71	119.70
100	3N	4333	DA	P-O3'-C3'	7.50	128.69	119.70
100	3N	3570	DG	O4'-C1'-C2'	-7.50	99.90	105.90
100	3N	7278	DG	O4'-C4'-C3'	-7.49	101.50	104.50
68	2S	1017	DG	O4'-C1'-C2'	-7.48	99.91	105.90
42	1q	1025	DG	O4'-C1'-C2'	-7.48	99.92	105.90
111	3S	2081	DT	O4'-C4'-C3'	-7.48	101.51	104.50
100	3N	3512	DG	O4'-C1'-C2'	-7.46	99.93	105.90
100	3N	6751	DG	O4'-C1'-C2'	-7.46	99.93	105.90
41	1p	1034	DA	O4'-C1'-C2'	-7.46	99.93	105.90
100	3N	7890	DG	O4'-C1'-C2'	-7.46	99.94	105.90
115	3O	2080	DG	P-O3'-C3'	7.45	128.65	119.70
100	3N	4497	DG	O4'-C4'-C3'	-7.45	101.52	104.50
45	1t	1047	DG	O4'-C1'-C2'	-7.44	99.95	105.90
115	3O	2104	DG	O4'-C1'-C2'	-7.44	99.95	105.90
100	3N	4217	DG	P-O3'-C3'	7.43	128.62	119.70
100	3N	5356	DT	O4'-C1'-C2'	-7.43	99.95	105.90
115	3O	2106	DT	O4'-C1'-C2'	-7.42	99.96	105.90
36	1k	7	DG	O4'-C1'-C2'	-7.42	99.96	105.90
100	3N	7200	DG	O4'-C1'-C2'	-7.42	99.97	105.90
100	3N	8130	DG	O4'-C1'-C2'	-7.41	99.97	105.90
34	1i	1	DA	O4'-C1'-C2'	-7.41	99.97	105.90
4	1D	59	DG	O4'-C1'-C2'	-7.41	99.97	105.90
100	3N	5024	DG	O4'-C1'-C2'	-7.40	99.98	105.90
95	2t	2048	DG	O4'-C1'-C2'	-7.39	99.99	105.90
101	3A	2089	DG	O4'-C1'-C2'	-7.39	99.99	105.90
57	2G	1066	DG	O4'-C1'-C2'	-7.38	99.99	105.90
9	1I	41	DG	O4'-C1'-C2'	-7.38	99.99	105.90
100	3N	6637	DA	O4'-C1'-C2'	-7.38	99.99	105.90
100	3N	8039	DA	O4'-C1'-C2'	-7.38	99.99	105.90
100	3N	6591	DC	P-O3'-C3'	7.38	128.56	119.70
38	1m	1019	DA	O4'-C1'-C2'	-7.36	100.02	105.90
100	3N	7378	DG	O4'-C1'-C2'	-7.35	100.02	105.90
33	1h	9	DG	O4'-C1'-C2'	-7.34	100.02	105.90
100	3N	3335	DA	O4'-C1'-C2'	-7.34	100.03	105.90
100	3N	3882	DG	P-O3'-C3'	7.33	128.50	119.70
100	3N	3438	DA	P-O3'-C3'	7.33	128.50	119.70
46	1u	1028	DG	O4'-C1'-C2'	-7.33	100.04	105.90
100	3N	4985	DC	P-O3'-C3'	7.32	128.48	119.70
100	3N	5060	DG	O4'-C1'-C2'	-7.32	100.05	105.90
100	3N	5497	DG	O4'-C1'-C2'	-7.32	100.05	105.90
15	1P	6	DG	C1'-O4'-C4'	-7.32	102.78	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
100	3N	8399	DA	O4'-C1'-C2'	-7.31	100.05	105.90
87	2l	1032	DG	P-O3'-C3'	7.30	128.47	119.70
100	3N	5038	DG	O4'-C1'-C2'	-7.30	100.06	105.90
100	3N	7944	DG	O4'-C1'-C2'	-7.30	100.06	105.90
87	2l	1034	DC	P-O3'-C3'	7.30	128.46	119.70
51	2A	1076	DG	O4'-C1'-C2'	-7.30	100.06	105.90
93	2r	2054	DG	O4'-C1'-C2'	-7.28	100.07	105.90
110	3J	2066	DG	O4'-C1'-C2'	-7.28	100.07	105.90
100	3N	7036	DG	O4'-C1'-C2'	-7.28	100.08	105.90
87	2l	1018	DA	P-O3'-C3'	7.27	128.43	119.70
100	3N	3567	DT	P-O3'-C3'	7.27	128.43	119.70
100	3N	8174	DT	O4'-C1'-C2'	-7.26	100.09	105.90
6	1F	6	DG	O4'-C1'-C2'	-7.26	100.09	105.90
26	1a	25	DG	O4'-C1'-C2'	-7.26	100.09	105.90
100	3N	6956	DG	O4'-C1'-C2'	-7.26	100.09	105.90
100	3N	4818	DA	O4'-C1'-C2'	-7.25	100.10	105.90
100	3N	5452	DA	P-O3'-C3'	7.25	128.41	119.70
100	3N	4889	DG	O4'-C1'-C2'	-7.25	100.10	105.90
100	3N	4290	DG	C1'-O4'-C4'	-7.24	102.86	110.10
100	3N	4463	DG	O4'-C1'-C2'	-7.24	100.11	105.90
28	1c	26	DA	P-O3'-C3'	7.23	128.38	119.70
100	3N	4012	DC	P-O3'-C3'	7.22	128.37	119.70
100	3N	6809	DG	O4'-C1'-C2'	-7.21	100.13	105.90
31	1f	4	DG	O4'-C1'-C2'	-7.21	100.13	105.90
36	1k	15	DG	O4'-C1'-C2'	-7.21	100.13	105.90
104	3D	2089	DG	O4'-C1'-C2'	-7.21	100.13	105.90
100	3N	6615	DA	O4'-C1'-C2'	-7.21	100.14	105.90
100	3N	6892	DG	O4'-C1'-C2'	-7.19	100.14	105.90
100	3N	5048	DG	O4'-C1'-C2'	-7.19	100.15	105.90
100	3N	8239	DA	O4'-C1'-C2'	-7.19	100.15	105.90
114	3M	2080	DG	P-O3'-C3'	7.19	128.32	119.70
15	1P	25	DT	O4'-C1'-C2'	-7.18	100.16	105.90
100	3N	7772	DA	O4'-C1'-C2'	-7.17	100.17	105.90
67	2R	1063	DT	O4'-C1'-C2'	-7.17	100.17	105.90
100	3N	5337	DG	O4'-C1'-C2'	-7.16	100.17	105.90
11	1K	15	DG	O4'-C1'-C2'	-7.16	100.17	105.90
100	3N	7596	DG	O4'-C1'-C2'	-7.15	100.18	105.90
100	3N	3546	DG	O4'-C1'-C2'	-7.13	100.20	105.90
100	3N	8023	DA	O4'-C1'-C2'	-7.13	100.20	105.90
95	2t	2075	DG	O4'-C1'-C2'	-7.13	100.20	105.90
100	3N	8432	DG	O4'-C1'-C2'	-7.12	100.21	105.90
100	3N	7049	DG	O4'-C1'-C2'	-7.12	100.21	105.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
97	2v	2042	DG	O4'-C1'-C2'	-7.11	100.21	105.90
100	3N	6574	DC	O4'-C4'-C3'	-7.11	101.66	104.50
93	2r	2051	DG	O4'-C1'-C2'	-7.10	100.22	105.90
100	3N	5287	DG	O4'-C1'-C2'	-7.10	100.22	105.90
115	3O	2080	DG	O4'-C1'-C2'	-7.10	100.22	105.90
4	1D	6	DG	O4'-C1'-C2'	-7.09	100.22	105.90
64	2O	1062	DT	C1'-O4'-C4'	-7.09	103.01	110.10
100	3N	3528	DG	O4'-C4'-C3'	-7.09	101.66	104.50
100	3N	7022	DA	O4'-C1'-C2'	-7.07	100.24	105.90
76	2a	1067	DT	P-O3'-C3'	7.07	128.19	119.70
100	3N	4115	DG	O4'-C1'-C2'	-7.07	100.25	105.90
100	3N	8205	DG	O4'-C1'-C2'	-7.07	100.25	105.90
100	3N	7473	DG	O4'-C1'-C2'	-7.05	100.26	105.90
43	1r	1016	DA	O4'-C1'-C2'	-7.05	100.26	105.90
98	2w	2093	DA	O4'-C1'-C2'	-7.05	100.26	105.90
113	3L	2092	DG	O4'-C1'-C2'	-7.05	100.26	105.90
100	3N	5145	DA	O4'-C1'-C2'	-7.04	100.27	105.90
118	3R	2080	DG	O4'-C1'-C2'	-7.03	100.28	105.90
100	3N	7822	DG	O4'-C1'-C2'	-7.03	100.28	105.90
118	3R	2099	DG	O4'-C1'-C2'	-7.03	100.28	105.90
4	1D	5	DT	P-O3'-C3'	7.01	128.11	119.70
84	2i	1064	DA	O4'-C1'-C2'	-7.00	100.30	105.90
50	2N	1053	DA	C1'-O4'-C4'	-7.00	103.10	110.10
100	3N	5396	DT	O4'-C1'-C2'	-7.00	100.30	105.90
100	3N	4222	DT	O4'-C1'-C2'	-6.99	100.31	105.90
65	2P	1067	DG	P-O3'-C3'	6.99	128.08	119.70
100	3N	8360	DC	P-O3'-C3'	6.98	128.08	119.70
100	3N	6834	DG	O4'-C1'-C2'	-6.98	100.32	105.90
100	3N	3248	DA	O4'-C1'-C2'	-6.98	100.32	105.90
100	3N	3193	DT	O4'-C4'-C3'	-6.97	101.71	104.50
100	3N	4170	DT	O4'-C4'-C3'	-6.97	101.71	104.50
100	3N	4061	DA	O4'-C1'-C2'	-6.96	100.33	105.90
79	2d	1027	DG	C1'-O4'-C4'	-6.96	103.14	110.10
100	3N	4652	DA	P-O3'-C3'	6.96	128.05	119.70
17	1R	48	DG	O4'-C1'-C2'	-6.95	100.34	105.90
100	3N	4331	DA	O4'-C1'-C2'	-6.95	100.34	105.90
100	3N	7240	DG	O4'-C1'-C2'	-6.95	100.34	105.90
102	3B	2116	DA	O4'-C1'-C2'	-6.95	100.34	105.90
100	3N	7211	DT	C4'-C3'-C2'	-6.95	96.85	103.10
100	3N	5364	DG	O4'-C1'-N9	6.95	112.86	108.00
100	3N	7710	DA	P-O3'-C3'	6.94	128.03	119.70
62	2L	1033	DG	C1'-O4'-C4'	-6.94	103.16	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
61	2K	1020	DA	O4'-C1'-C2'	-6.92	100.36	105.90
100	3N	7809	DG	C1'-O4'-C4'	-6.92	103.18	110.10
100	3N	8458	DG	O4'-C1'-C2'	-6.92	100.36	105.90
100	3N	7432	DG	O4'-C1'-C2'	-6.92	100.36	105.90
100	3N	3851	DA	O4'-C1'-C2'	-6.91	100.37	105.90
100	3N	7929	DG	O4'-C1'-C2'	-6.91	100.37	105.90
11	1K	13	DG	P-O3'-C3'	6.91	127.99	119.70
100	3N	3429	DA	O4'-C1'-C2'	-6.89	100.39	105.90
100	3N	4764	DA	O4'-C1'-C2'	-6.89	100.39	105.90
40	1o	1012	DG	O4'-C1'-C2'	-6.88	100.39	105.90
100	3N	6782	DC	P-O3'-C3'	6.88	127.95	119.70
100	3N	8270	DA	O4'-C1'-C2'	-6.87	100.41	105.90
39	1n	1059	DG	P-O3'-C3'	6.86	127.94	119.70
100	3N	4773	DG	O4'-C1'-C2'	-6.86	100.41	105.90
100	3N	6965	DG	O4'-C1'-C2'	-6.86	100.41	105.90
100	3N	7539	DG	O4'-C1'-C2'	-6.85	100.42	105.90
27	1b	27	DC	P-O3'-C3'	6.84	127.91	119.70
38	1m	1025	DG	O4'-C1'-C2'	-6.84	100.43	105.90
6	1F	9	DA	O4'-C1'-C2'	-6.84	100.43	105.90
100	3N	5196	DT	P-O3'-C3'	6.84	127.90	119.70
15	1P	6	DG	O4'-C4'-C3'	-6.83	101.77	104.50
100	3N	8138	DT	O4'-C1'-C2'	-6.83	100.43	105.90
6	1F	11	DG	O4'-C1'-C2'	-6.83	100.44	105.90
100	3N	3107	DG	O4'-C1'-C2'	-6.83	100.44	105.90
15	1P	31	DC	O4'-C4'-C3'	-6.82	101.77	104.50
100	3N	7029	DA	O4'-C1'-C2'	-6.81	100.45	105.90
70	2U	1066	DG	O4'-C1'-C2'	-6.79	100.46	105.90
46	1u	1039	DG	P-O3'-C3'	6.79	127.85	119.70
92	2q	2088	DG	C1'-O4'-C4'	-6.79	103.31	110.10
100	3N	3882	DG	C1'-O4'-C4'	-6.79	103.31	110.10
35	1j	18	DA	O4'-C1'-C2'	-6.78	100.47	105.90
17	1R	6	DG	O4'-C1'-C2'	-6.78	100.48	105.90
49	1x	1013	DG	O4'-C1'-C2'	-6.78	100.48	105.90
100	3N	4788	DG	O4'-C1'-C2'	-6.78	100.48	105.90
100	3N	7478	DT	P-O3'-C3'	6.78	127.83	119.70
1	1A	4	DG	O4'-C1'-C2'	-6.77	100.48	105.90
100	3N	5379	DC	O4'-C4'-C3'	-6.77	101.79	104.50
13	1M	1	DC	C1'-O4'-C4'	-6.77	103.33	110.10
76	2a	1086	DG	O4'-C1'-C2'	-6.77	100.49	105.90
100	3N	6812	DT	O4'-C4'-C3'	-6.77	101.79	104.50
36	1k	38	DG	O4'-C1'-C2'	-6.76	100.49	105.90
68	2S	1017	DG	O4'-C4'-C3'	-6.76	101.79	104.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
107	3G	2072	DA	O4'-C1'-C2'	-6.76	100.49	105.90
100	3N	4330	DA	C4'-C3'-C2'	-6.76	97.02	103.10
100	3N	6709	DG	O4'-C1'-C2'	-6.76	100.49	105.90
109	3I	2108	DT	O4'-C1'-C2'	-6.76	100.50	105.90
95	2t	2054	DC	O4'-C1'-C2'	-6.75	100.50	105.90
100	3N	5544	DG	O4'-C1'-C2'	-6.75	100.50	105.90
100	3N	4436	DA	O4'-C4'-C3'	-6.75	101.80	104.50
100	3N	7398	DA	P-O3'-C3'	6.75	127.80	119.70
31	1f	21	DA	O4'-C1'-C2'	-6.74	100.51	105.90
100	3N	6878	DG	P-O3'-C3'	6.74	127.79	119.70
100	3N	5108	DA	O4'-C4'-C3'	-6.74	101.81	104.50
108	3H	2103	DG	O4'-C4'-C3'	-6.74	101.81	104.50
114	3M	2096	DG	O4'-C1'-C2'	-6.73	100.51	105.90
9	1I	10	DG	O4'-C1'-C2'	-6.73	100.52	105.90
40	1o	1032	DA	O4'-C1'-C2'	-6.73	100.52	105.90
49	1x	1020	DG	O4'-C1'-C2'	-6.73	100.52	105.90
2	1B	54	DA	P-O3'-C3'	6.72	127.77	119.70
100	3N	7157	DG	P-O3'-C3'	6.72	127.77	119.70
54	2D	1052	DA	C1'-O4'-C4'	-6.72	103.38	110.10
100	3N	5191	DG	O4'-C4'-C3'	-6.72	101.81	104.50
5	1E	27	DC	P-O3'-C3'	6.71	127.76	119.70
100	3N	7304	DT	O4'-C1'-C2'	-6.71	100.53	105.90
100	3N	8214	DG	O4'-C1'-C2'	-6.71	100.53	105.90
33	1h	38	DG	O4'-C1'-C2'	-6.71	100.53	105.90
105	3E	2091	DA	O4'-C4'-C3'	-6.71	101.82	104.50
100	3N	4283	DA	O4'-C4'-C3'	-6.71	101.82	104.50
64	2O	1051	DA	O4'-C1'-C2'	-6.70	100.54	105.90
100	3N	4244	DA	O4'-C1'-C2'	-6.69	100.55	105.90
100	3N	5292	DA	O4'-C1'-C2'	-6.69	100.55	105.90
100	3N	7972	DG	O4'-C1'-C2'	-6.68	100.55	105.90
100	3N	7320	DG	O4'-C1'-C2'	-6.67	100.56	105.90
3	1C	10	DT	P-O3'-C3'	6.67	127.70	119.70
53	2C	1074	DT	O4'-C1'-C2'	-6.65	100.58	105.90
100	3N	3905	DC	P-O3'-C3'	6.65	127.68	119.70
100	3N	4917	DT	O4'-C4'-C3'	-6.65	101.84	104.50
100	3N	6893	DA	P-O3'-C3'	6.65	127.68	119.70
100	3N	4701	DA	O4'-C4'-C3'	-6.65	101.84	104.50
66	2Q	1071	DG	O4'-C1'-C2'	-6.65	100.58	105.90
18	1S	9	DT	O4'-C1'-N1	6.64	112.65	108.00
100	3N	3463	DC	P-O3'-C3'	6.64	127.67	119.70
60	2J	1060	DG	O4'-C1'-C2'	-6.64	100.59	105.90
100	3N	7635	DA	O4'-C4'-C3'	-6.64	101.84	104.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
100	3N	5471	DA	O4'-C1'-C2'	-6.63	100.59	105.90
100	3N	7164	DA	N1-C6-N6	-6.63	114.62	118.60
109	3I	2115	DA	P-O3'-C3'	6.63	127.66	119.70
100	3N	7164	DA	O4'-C1'-C2'	-6.63	100.60	105.90
100	3N	7480	DC	O4'-C1'-C2'	-6.63	100.60	105.90
100	3N	4614	DG	O4'-C1'-C2'	-6.62	100.60	105.90
100	3N	7216	DA	O4'-C1'-C2'	-6.62	100.60	105.90
96	2u	2086	DT	O4'-C4'-C3'	-6.62	101.85	104.50
100	3N	8166	DA	O4'-C1'-C2'	-6.62	100.61	105.90
83	2h	1102	DA	O4'-C1'-C2'	-6.61	100.61	105.90
100	3N	3216	DT	O4'-C4'-C3'	-6.61	101.86	104.50
100	3N	6908	DC	O4'-C1'-C2'	-6.61	100.61	105.90
100	3N	8046	DG	O4'-C1'-C2'	-6.61	100.61	105.90
100	3N	8071	DC	O4'-C4'-C3'	-6.61	101.86	104.50
100	3N	7911	DG	C1'-O4'-C4'	-6.61	103.49	110.10
41	1p	1036	DT	O4'-C1'-C2'	-6.59	100.63	105.90
73	2X	1067	DA	O4'-C1'-C2'	-6.59	100.63	105.90
100	3N	5410	DA	C1'-O4'-C4'	-6.59	103.51	110.10
100	3N	8112	DG	P-O3'-C3'	6.58	127.60	119.70
2	1B	39	DT	P-O3'-C3'	6.58	127.59	119.70
100	3N	3216	DT	C4'-C3'-C2'	-6.57	97.19	103.10
100	3N	4131	DT	O4'-C1'-C2'	-6.57	100.64	105.90
100	3N	4603	DT	C1'-O4'-C4'	-6.57	103.53	110.10
100	3N	4011	DG	O4'-C1'-C2'	-6.57	100.65	105.90
100	3N	5101	DA	O4'-C1'-C2'	-6.57	100.65	105.90
100	3N	8057	DG	O4'-C1'-C2'	-6.57	100.65	105.90
100	3N	5207	DG	O4'-C1'-C2'	-6.56	100.65	105.90
98	2w	2089	DA	O4'-C1'-C2'	-6.56	100.65	105.90
100	3N	4436	DA	O4'-C1'-C2'	-6.56	100.65	105.90
100	3N	3452	DG	O4'-C1'-C2'	-6.56	100.65	105.90
64	2O	1059	DG	O4'-C1'-N9	6.56	112.59	108.00
10	1J	6	DG	O4'-C1'-C2'	-6.56	100.66	105.90
55	2E	1055	DT	O4'-C4'-C3'	-6.55	101.88	104.50
100	3N	4226	DT	O4'-C4'-C3'	-6.55	101.88	104.50
100	3N	4403	DA	O4'-C1'-C2'	-6.54	100.67	105.90
5	1E	11	DA	O4'-C1'-C2'	-6.54	100.67	105.90
37	1l	7	DG	P-O3'-C3'	6.54	127.55	119.70
100	3N	3331	DA	P-O3'-C3'	6.54	127.55	119.70
100	3N	5211	DA	P-O3'-C3'	6.54	127.54	119.70
54	2D	1061	DT	O4'-C1'-C2'	-6.53	100.67	105.90
65	2P	1059	DG	P-O3'-C3'	6.53	127.54	119.70
100	3N	5237	DT	O4'-C4'-C3'	-6.53	101.89	104.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
100	3N	3881	DG	O4'-C1'-C2'	-6.53	100.68	105.90
29	1d	26	DG	O4'-C1'-C2'	-6.52	100.68	105.90
64	2O	1062	DT	O4'-C4'-C3'	-6.52	101.89	104.50
100	3N	6972	DA	C4'-C3'-C2'	-6.52	97.23	103.10
39	1n	1019	DG	O4'-C1'-N9	6.51	112.56	108.00
52	2B	1049	DC	O4'-C1'-C2'	-6.51	100.69	105.90
100	3N	3907	DA	O4'-C1'-C2'	-6.50	100.70	105.90
100	3N	4556	DT	P-O3'-C3'	6.50	127.51	119.70
100	3N	3287	DG	O4'-C1'-C2'	-6.50	100.70	105.90
57	2G	1066	DG	O4'-C4'-C3'	-6.50	101.90	104.50
32	1g	8	DG	O4'-C1'-C2'	-6.50	100.70	105.90
100	3N	7261	DA	O4'-C1'-C2'	-6.49	100.70	105.90
114	3M	2081	DG	P-O3'-C3'	6.49	127.49	119.70
100	3N	4859	DG	O4'-C1'-C2'	-6.49	100.71	105.90
15	1P	6	DG	O4'-C1'-C2'	-6.49	100.71	105.90
100	3N	3113	DG	O4'-C1'-C2'	-6.48	100.71	105.90
100	3N	8382	DG	O4'-C1'-C2'	-6.48	100.71	105.90
108	3H	2132	DG	O4'-C1'-C2'	-6.48	100.72	105.90
100	3N	8288	DT	O4'-C1'-C2'	-6.48	100.72	105.90
100	3N	5541	DT	O4'-C1'-C2'	-6.48	100.72	105.90
100	3N	8313	DT	C1'-O4'-C4'	-6.48	103.62	110.10
100	3N	3778	DG	O4'-C1'-C2'	-6.47	100.72	105.90
100	3N	4217	DG	O4'-C1'-C2'	-6.47	100.72	105.90
100	3N	7631	DG	O4'-C1'-C2'	-6.47	100.72	105.90
17	1R	34	DA	P-O3'-C3'	6.46	127.46	119.70
91	2p	2061	DG	C1'-O4'-C4'	-6.46	103.64	110.10
100	3N	7601	DG	O4'-C1'-C2'	-6.46	100.73	105.90
100	3N	3436	DG	O4'-C1'-C2'	-6.46	100.74	105.90
66	2Q	1071	DG	C1'-O4'-C4'	-6.45	103.65	110.10
72	2W	1083	DA	O4'-C1'-C2'	-6.45	100.74	105.90
100	3N	8255	DA	O4'-C1'-C2'	-6.45	100.74	105.90
42	1q	1047	DG	O4'-C1'-C2'	-6.45	100.74	105.90
44	1s	1028	DG	O4'-C4'-C3'	-6.45	101.92	104.50
61	2K	1034	DG	O4'-C1'-C2'	-6.44	100.75	105.90
100	3N	5013	DG	O4'-C1'-C2'	-6.44	100.75	105.90
100	3N	3343	DG	O4'-C1'-C2'	-6.44	100.75	105.90
100	3N	7559	DT	O4'-C1'-C2'	-6.44	100.75	105.90
100	3N	4092	DG	O4'-C1'-C2'	-6.43	100.75	105.90
100	3N	5349	DC	O4'-C1'-C2'	-6.43	100.76	105.90
100	3N	6676	DG	O4'-C1'-C2'	-6.42	100.77	105.90
100	3N	8082	DC	P-O3'-C3'	6.42	127.40	119.70
109	3I	2088	DC	C1'-O4'-C4'	-6.42	103.69	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	1x	1022	DG	O4'-C1'-C2'	-6.41	100.77	105.90
34	1i	14	DC	O4'-C1'-C2'	-6.41	100.77	105.90
79	2d	1076	DG	O4'-C1'-C2'	-6.41	100.78	105.90
48	1w	1035	DG	O4'-C1'-C2'	-6.39	100.79	105.90
67	2R	1065	DT	O4'-C4'-C3'	-6.38	101.95	104.50
100	3N	4654	DC	O4'-C1'-C2'	-6.38	100.79	105.90
100	3N	7559	DT	P-O3'-C3'	6.38	127.36	119.70
108	3H	2139	DC	O4'-C1'-C2'	-6.38	100.80	105.90
100	3N	7772	DA	O4'-C4'-C3'	-6.37	101.95	104.50
100	3N	4821	DA	N1-C6-N6	-6.37	114.78	118.60
34	1i	14	DC	O4'-C4'-C3'	-6.36	101.95	104.50
100	3N	7645	DG	O4'-C4'-C3'	-6.36	101.96	104.50
100	3N	6768	DG	O4'-C1'-C2'	-6.36	100.81	105.90
100	3N	8172	DG	O4'-C1'-C2'	-6.35	100.82	105.90
100	3N	7925	DG	O4'-C1'-C2'	-6.35	100.82	105.90
103	3C	2105	DA	O4'-C1'-C2'	-6.35	100.82	105.90
100	3N	5077	DG	O4'-C1'-C2'	-6.34	100.83	105.90
27	1b	17	DA	O4'-C1'-C2'	-6.33	100.84	105.90
100	3N	3670	DG	O4'-C1'-C2'	-6.33	100.84	105.90
100	3N	8149	DC	P-O3'-C3'	6.33	127.29	119.70
1	1A	27	DG	P-O3'-C3'	6.32	127.29	119.70
100	3N	3265	DG	O4'-C1'-C2'	-6.32	100.84	105.90
100	3N	4878	DA	O4'-C1'-C2'	-6.30	100.86	105.90
100	3N	7000	DG	O4'-C1'-C2'	-6.30	100.86	105.90
100	3N	5115	DG	C1'-O4'-C4'	-6.30	103.80	110.10
110	3J	2048	DC	P-O3'-C3'	-6.30	112.14	119.70
7	1G	8	DA	O4'-C1'-C2'	-6.30	100.86	105.90
4	1D	43	DG	O4'-C1'-C2'	-6.29	100.86	105.90
38	1m	1019	DA	C1'-O4'-C4'	-6.29	103.81	110.10
51	2A	1071	DG	O4'-C1'-C2'	-6.29	100.87	105.90
100	3N	7407	DG	O4'-C1'-C2'	-6.29	100.87	105.90
1	1A	8	DG	C5-C6-O6	-6.28	124.83	128.60
89	2n	2079	DG	O4'-C1'-C2'	-6.28	100.88	105.90
100	3N	8332	DG	C1'-O4'-C4'	-6.27	103.83	110.10
100	3N	4734	DG	O4'-C1'-C2'	-6.27	100.88	105.90
2	1B	39	DT	O4'-C1'-C2'	-6.27	100.89	105.90
79	2d	1063	DG	O4'-C1'-C2'	-6.27	100.89	105.90
100	3N	7777	DG	O4'-C1'-C2'	-6.27	100.89	105.90
87	2l	1032	DG	O4'-C1'-C2'	-6.27	100.89	105.90
15	1P	12	DG	O4'-C1'-C2'	-6.26	100.89	105.90
56	2F	1046	DA	O4'-C1'-C2'	-6.26	100.89	105.90
100	3N	7134	DC	P-O3'-C3'	6.26	127.21	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
100	3N	7805	DT	C1'-O4'-C4'	-6.26	103.84	110.10
100	3N	7337	DT	O4'-C1'-C2'	-6.26	100.89	105.90
100	3N	3248	DA	O4'-C4'-C3'	-6.25	102.00	104.50
46	1u	1031	DA	O4'-C1'-C2'	-6.25	100.90	105.90
81	2f	1059	DG	O4'-C1'-C2'	-6.25	100.90	105.90
100	3N	3589	DG	O4'-C4'-C3'	-6.25	102.00	104.50
100	3N	7809	DG	O4'-C1'-C2'	-6.25	100.90	105.90
82	2g	1082	DG	O4'-C1'-C2'	-6.24	100.91	105.90
100	3N	8435	DG	O4'-C1'-C2'	-6.24	100.91	105.90
93	2r	2056	DC	O4'-C1'-C2'	-6.24	100.91	105.90
36	1k	7	DG	O4'-C4'-C3'	-6.23	102.01	104.50
100	3N	6982	DA	O4'-C1'-C2'	-6.23	100.91	105.90
41	1p	1018	DA	N1-C6-N6	-6.23	114.86	118.60
96	2u	2064	DA	C1'-O4'-C4'	-6.23	103.87	110.10
100	3N	4629	DG	O4'-C1'-C2'	-6.23	100.92	105.90
114	3M	2078	DG	O4'-C1'-C2'	-6.23	100.92	105.90
100	3N	4649	DT	O4'-C1'-C2'	-6.22	100.92	105.90
100	3N	4226	DT	C4'-C3'-C2'	-6.22	97.50	103.10
100	3N	4032	DA	P-O3'-C3'	6.22	127.16	119.70
102	3B	2111	DG	O4'-C1'-C2'	-6.22	100.93	105.90
48	1w	1027	DC	O4'-C1'-C2'	-6.21	100.93	105.90
100	3N	8397	DG	O4'-C1'-C2'	-6.21	100.93	105.90
85	2j	1046	DA	O4'-C1'-C2'	-6.21	100.93	105.90
100	3N	5478	DG	O4'-C1'-C2'	-6.20	100.94	105.90
100	3N	7768	DG	C1'-O4'-C4'	-6.20	103.91	110.10
92	2q	2088	DG	O4'-C4'-C3'	-6.19	102.03	104.50
31	1f	34	DG	O4'-C1'-C2'	-6.19	100.95	105.90
100	3N	4523	DA	O4'-C1'-C2'	-6.19	100.95	105.90
59	2l	1025	DA	C1'-O4'-C4'	-6.18	103.92	110.10
100	3N	3952	DG	O4'-C1'-C2'	-6.18	100.96	105.90
100	3N	4927	DG	P-O3'-C3'	6.18	127.11	119.70
100	3N	6977	DG	O4'-C1'-C2'	-6.18	100.96	105.90
108	3H	2099	DG	O4'-C1'-C2'	-6.18	100.96	105.90
100	3N	4042	DG	O4'-C1'-C2'	-6.18	100.96	105.90
95	2t	2077	DG	O4'-C1'-C2'	-6.17	100.96	105.90
100	3N	3526	DG	O4'-C1'-C2'	-6.17	100.96	105.90
2	1B	46	DG	O4'-C1'-C2'	-6.17	100.97	105.90
32	1g	14	DG	O4'-C1'-C2'	-6.16	100.97	105.90
48	1w	1025	DG	P-O3'-C3'	6.16	127.09	119.70
17	1R	39	DG	O4'-C1'-C2'	-6.15	100.98	105.90
100	3N	7067	DA	P-O3'-C3'	6.15	127.08	119.70
48	1w	1036	DC	C2-N1-C1'	6.15	125.56	118.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
100	3N	7915	DG	C1'-O4'-C4'	-6.14	103.95	110.10
100	3N	8449	DA	O4'-C1'-C2'	-6.14	100.99	105.90
13	1M	25	DG	P-O3'-C3'	6.13	127.06	119.70
76	2a	1086	DG	C1'-O4'-C4'	-6.13	103.97	110.10
93	2r	2054	DG	C1'-O4'-C4'	-6.13	103.97	110.10
100	3N	5450	DA	O4'-C1'-C2'	-6.12	101.00	105.90
100	3N	5389	DA	O4'-C1'-C2'	-6.12	101.00	105.90
100	3N	6626	DG	O4'-C1'-C2'	-6.12	101.00	105.90
105	3E	2084	DA	N1-C6-N6	-6.12	114.93	118.60
100	3N	6971	DG	O4'-C1'-C2'	-6.11	101.01	105.90
100	3N	7848	DC	P-O3'-C3'	6.11	127.04	119.70
34	1i	18	DA	O4'-C1'-C2'	-6.11	101.01	105.90
77	2b	1082	DG	O4'-C1'-C2'	-6.11	101.01	105.90
86	2k	1060	DG	O4'-C1'-C2'	-6.11	101.01	105.90
18	1S	36	DC	P-O3'-C3'	6.11	127.03	119.70
43	1r	1008	DG	O4'-C1'-C2'	-6.11	101.02	105.90
100	3N	8354	DT	O4'-C1'-C2'	-6.11	101.02	105.90
118	3R	2095	DG	O4'-C1'-C2'	-6.10	101.02	105.90
8	1H	13	DA	O4'-C1'-C2'	-6.10	101.02	105.90
100	3N	4489	DG	O4'-C1'-C2'	-6.10	101.02	105.90
100	3N	7607	DG	O4'-C1'-C2'	-6.10	101.02	105.90
109	3I	2099	DG	O4'-C1'-C2'	-6.09	101.03	105.90
100	3N	4202	DA	O4'-C1'-C2'	-6.09	101.03	105.90
100	3N	3193	DT	C1'-O4'-C4'	-6.09	104.01	110.10
100	3N	4380	DG	O4'-C1'-C2'	-6.09	101.03	105.90
34	1i	30	DG	O4'-C1'-C2'	-6.08	101.03	105.90
100	3N	3981	DC	P-O3'-C3'	6.08	127.00	119.70
100	3N	3818	DT	O4'-C1'-C2'	-6.08	101.04	105.90
100	3N	4841	DG	O4'-C1'-C2'	-6.08	101.04	105.90
100	3N	7920	DT	O4'-C1'-C2'	-6.08	101.04	105.90
100	3N	4444	DA	O4'-C1'-C2'	-6.07	101.04	105.90
18	1S	13	DG	O4'-C1'-C2'	-6.07	101.04	105.90
110	3J	2041	DA	C1'-O4'-C4'	-6.07	104.03	110.10
48	1w	1025	DG	O4'-C1'-C2'	-6.07	101.04	105.90
73	2X	1069	DG	P-O3'-C3'	6.07	126.98	119.70
100	3N	7767	DG	O4'-C1'-C2'	-6.07	101.05	105.90
9	1I	10	DG	C1'-O4'-C4'	-6.07	104.03	110.10
100	3N	7398	DA	O4'-C1'-C2'	-6.06	101.05	105.90
100	3N	3269	DC	O4'-C1'-C2'	-6.06	101.05	105.90
42	1q	1052	DC	P-O3'-C3'	6.05	126.97	119.70
100	3N	4652	DA	O4'-C1'-C2'	-6.05	101.06	105.90
16	1Q	17	DG	O4'-C1'-C2'	-6.05	101.06	105.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
22	1W	14	DG	P-O3'-C3'	6.05	126.96	119.70
100	3N	5493	DG	C1'-O4'-C4'	-6.05	104.05	110.10
2	1B	13	DG	O4'-C1'-C2'	-6.05	101.06	105.90
19	1T	1	DC	C1'-O4'-C4'	-6.05	104.05	110.10
9	1I	10	DG	P-O3'-C3'	6.04	126.95	119.70
94	2s	2072	DA	P-O3'-C3'	6.04	126.95	119.70
100	3N	4313	DA	O4'-C1'-C2'	-6.04	101.07	105.90
100	3N	3200	DG	O4'-C1'-C2'	-6.04	101.07	105.90
100	3N	4776	DT	O4'-C1'-C2'	-6.03	101.07	105.90
100	3N	6574	DC	C4'-C3'-C2'	-6.03	97.67	103.10
77	2b	1041	DT	C1'-O4'-C4'	-6.03	104.07	110.10
100	3N	7224	DG	O4'-C1'-C2'	-6.03	101.08	105.90
100	3N	7598	DG	O4'-C1'-C2'	-6.03	101.08	105.90
100	3N	8133	DG	O4'-C1'-C2'	-6.03	101.08	105.90
70	2U	1062	DA	C4'-C3'-C2'	-6.03	97.67	103.10
105	3E	2084	DA	C1'-O4'-C4'	-6.03	104.07	110.10
100	3N	5326	DG	O4'-C1'-C2'	-6.03	101.08	105.90
83	2h	1065	DA	C1'-O4'-C4'	-6.03	104.08	110.10
100	3N	5283	DG	O4'-C1'-C2'	-6.03	101.08	105.90
102	3B	2109	DG	O4'-C1'-C2'	-6.02	101.08	105.90
103	3C	2093	DG	O4'-C1'-C2'	-6.02	101.08	105.90
76	2a	1083	DC	P-O3'-C3'	6.02	126.92	119.70
94	2s	2063	DA	P-O3'-C3'	6.01	126.92	119.70
100	3N	3198	DC	C2-N1-C1'	6.01	125.41	118.80
105	3E	2115	DG	O4'-C1'-C2'	-6.01	101.09	105.90
35	1j	22	DG	O4'-C1'-C2'	-6.01	101.09	105.90
100	3N	3488	DC	P-O3'-C3'	6.01	126.91	119.70
69	2T	1041	DG	C1'-O4'-C4'	-6.01	104.09	110.10
42	1q	1008	DG	C1'-O4'-C4'	-6.00	104.10	110.10
2	1B	23	DG	P-O3'-C3'	6.00	126.90	119.70
100	3N	7431	DG	O4'-C1'-C2'	-6.00	101.10	105.90
100	3N	4987	DG	P-O3'-C3'	5.99	126.89	119.70
23	1X	4	DG	O4'-C1'-C2'	-5.99	101.11	105.90
100	3N	4608	DA	O4'-C1'-C2'	-5.99	101.11	105.90
100	3N	5021	DC	P-O3'-C3'	5.99	126.88	119.70
100	3N	7686	DA	O4'-C1'-C2'	-5.98	101.12	105.90
100	3N	3878	DA	P-O3'-C3'	5.98	126.87	119.70
44	1s	1039	DA	O4'-C1'-C2'	-5.97	101.12	105.90
27	1b	6	DG	C1'-O4'-C4'	-5.97	104.13	110.10
100	3N	7233	DG	O4'-C1'-C2'	-5.97	101.12	105.90
100	3N	7542	DG	O4'-C1'-C2'	-5.97	101.12	105.90
100	3N	5534	DG	O4'-C1'-C2'	-5.97	101.13	105.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
37	1l	35	DG	O4'-C4'-C3'	-5.97	102.11	104.50
100	3N	4321	DG	O4'-C1'-C2'	-5.96	101.13	105.90
100	3N	5364	DG	C1'-O4'-C4'	-5.96	104.14	110.10
109	3I	2122	DG	O4'-C1'-C2'	-5.96	101.13	105.90
100	3N	7519	DA	O4'-C1'-C2'	-5.96	101.14	105.90
60	2J	1068	DA	O4'-C4'-C3'	-5.95	102.12	104.50
100	3N	7216	DA	N1-C6-N6	-5.94	115.03	118.60
100	3N	8178	DG	O4'-C1'-C2'	-5.94	101.15	105.90
100	3N	6589	DA	O4'-C1'-C2'	-5.94	101.15	105.90
14	1O	32	DA	O4'-C1'-C2'	-5.93	101.16	105.90
100	3N	3450	DG	O4'-C1'-C2'	-5.93	101.16	105.90
100	3N	7731	DG	O4'-C1'-C2'	-5.93	101.16	105.90
18	1S	10	DT	O4'-C1'-C2'	-5.92	101.16	105.90
22	1W	23	DC	O4'-C1'-C2'	-5.92	101.16	105.90
100	3N	6772	DG	O4'-C1'-C2'	-5.92	101.16	105.90
117	3Q	2089	DA	C1'-O4'-C4'	-5.92	104.18	110.10
86	2k	1074	DG	O4'-C1'-C2'	-5.92	101.16	105.90
100	3N	5485	DT	P-O3'-C3'	5.92	126.81	119.70
15	1P	31	DC	C4'-C3'-C2'	-5.92	97.77	103.10
33	1h	14	DA	O4'-C1'-C2'	-5.92	101.17	105.90
100	3N	5377	DA	O4'-C4'-C3'	-5.92	102.13	104.50
6	1F	7	DG	C1'-O4'-C4'	-5.91	104.19	110.10
100	3N	7067	DA	O4'-C1'-C2'	-5.91	101.17	105.90
100	3N	3528	DG	C1'-O4'-C4'	-5.91	104.19	110.10
50	2N	1073	DG	O4'-C1'-C2'	-5.91	101.17	105.90
17	1R	34	DA	O4'-C1'-C2'	-5.91	101.17	105.90
100	3N	4018	DG	O4'-C1'-C2'	-5.91	101.17	105.90
57	2G	1066	DG	C1'-O4'-C4'	-5.90	104.20	110.10
100	3N	3603	DG	C1'-O4'-C4'	-5.90	104.20	110.10
18	1S	9	DT	O4'-C1'-C2'	-5.90	101.18	105.90
100	3N	3443	DA	O4'-C1'-C2'	-5.90	101.18	105.90
100	3N	4551	DG	O4'-C1'-C2'	-5.89	101.19	105.90
100	3N	4293	DA	O4'-C1'-C2'	-5.89	101.19	105.90
100	3N	7875	DG	P-O3'-C3'	5.89	126.76	119.70
100	3N	3882	DG	O4'-C1'-N9	5.88	112.12	108.00
100	3N	3892	DG	O4'-C1'-C2'	-5.88	101.19	105.90
68	2S	1041	DG	O4'-C1'-C2'	-5.88	101.19	105.90
28	1c	26	DA	O4'-C1'-C2'	-5.88	101.20	105.90
50	2N	1069	DG	O4'-C1'-C2'	-5.88	101.20	105.90
100	3N	5515	DG	O4'-C1'-C2'	-5.88	101.20	105.90
100	3N	7484	DA	O4'-C1'-C2'	-5.87	101.20	105.90
108	3H	2092	DG	O4'-C1'-C2'	-5.87	101.21	105.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
108	3H	2105	DC	O4'-C1'-C2'	-5.87	101.21	105.90
18	1S	11	DT	O4'-C1'-C2'	-5.86	101.21	105.90
100	3N	4179	DG	O4'-C1'-C2'	-5.86	101.21	105.90
100	3N	8160	DG	O4'-C1'-C2'	-5.86	101.21	105.90
22	1W	23	DC	P-O3'-C3'	5.86	126.73	119.70
42	1q	1025	DG	O4'-C4'-C3'	-5.86	102.16	104.50
93	2r	2054	DG	O4'-C1'-N9	5.86	112.10	108.00
100	3N	5111	DA	O4'-C1'-C2'	-5.86	101.21	105.90
100	3N	6837	DT	C1'-O4'-C4'	-5.86	104.24	110.10
100	3N	8123	DT	O4'-C1'-C2'	-5.86	101.21	105.90
6	1F	31	DT	C4'-C3'-C2'	-5.86	97.83	103.10
100	3N	8281	DG	O4'-C1'-C2'	-5.86	101.22	105.90
87	2l	1029	DG	O4'-C1'-C2'	-5.85	101.22	105.90
1	1A	42	DG	O4'-C1'-C2'	-5.85	101.22	105.90
100	3N	3335	DA	P-O3'-C3'	5.85	126.72	119.70
100	3N	7425	DG	P-O3'-C3'	5.85	126.72	119.70
100	3N	7887	DG	O4'-C1'-C2'	-5.85	101.22	105.90
45	1t	1030	DC	P-O3'-C3'	5.85	126.72	119.70
21	1V	20	DG	O4'-C1'-C2'	-5.85	101.22	105.90
100	3N	4452	DG	C1'-O4'-C4'	-5.85	104.25	110.10
100	3N	8245	DG	O4'-C1'-C2'	-5.85	101.22	105.90
100	3N	3756	DC	P-O3'-C3'	5.84	126.71	119.70
100	3N	5331	DA	O4'-C1'-C2'	-5.84	101.22	105.90
100	3N	4375	DC	O4'-C1'-C2'	-5.84	101.23	105.90
100	3N	4939	DG	O4'-C4'-C3'	-5.84	102.16	104.50
100	3N	8121	DG	O4'-C1'-C2'	-5.84	101.23	105.90
21	1V	1	DC	C1'-O4'-C4'	-5.84	104.26	110.10
100	3N	3104	DG	O4'-C1'-C2'	-5.84	101.23	105.90
100	3N	5508	DA	O4'-C1'-C2'	-5.83	101.23	105.90
115	3O	2106	DT	O4'-C4'-C3'	-5.83	102.17	104.50
100	3N	8445	DT	O4'-C1'-C2'	-5.83	101.24	105.90
60	2J	1049	DC	C2-N1-C1'	5.83	125.21	118.80
100	3N	7557	DG	O4'-C1'-C2'	-5.83	101.24	105.90
100	3N	3969	DG	O4'-C1'-C2'	-5.82	101.24	105.90
67	2R	1075	DC	P-O3'-C3'	5.82	126.69	119.70
100	3N	8458	DG	O4'-C4'-C3'	-5.82	102.17	104.50
31	1f	21	DA	C1'-O4'-C4'	-5.82	104.28	110.10
98	2w	2071	DC	O4'-C1'-N1	5.82	112.07	108.00
100	3N	7476	DG	O4'-C1'-C2'	-5.82	101.25	105.90
100	3N	4092	DG	O4'-C1'-N9	5.82	112.07	108.00
100	3N	7244	DA	O4'-C1'-C2'	-5.81	101.25	105.90
100	3N	7793	DT	C1'-O4'-C4'	-5.81	104.29	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
100	3N	7052	DA	C1'-O4'-C4'	-5.81	104.29	110.10
100	3N	3659	DG	O4'-C4'-C3'	-5.81	102.18	104.50
100	3N	7846	DA	P-O3'-C3'	5.81	126.67	119.70
100	3N	3570	DG	C1'-O4'-C4'	-5.80	104.30	110.10
100	3N	8130	DG	P-O3'-C3'	5.80	126.67	119.70
115	3O	2073	DG	O4'-C1'-C2'	-5.80	101.26	105.90
76	2a	1063	DT	C1'-O4'-C4'	-5.80	104.30	110.10
100	3N	7921	DC	C2-N1-C1'	5.80	125.18	118.80
100	3N	4708	DC	O4'-C1'-C2'	-5.80	101.26	105.90
100	3N	3335	DA	C1'-O4'-C4'	-5.79	104.31	110.10
100	3N	5462	DG	O4'-C1'-C2'	-5.79	101.27	105.90
100	3N	3287	DG	P-O3'-C3'	5.79	126.65	119.70
83	2h	1070	DT	O4'-C1'-C2'	-5.79	101.27	105.90
93	2r	2043	DG	O4'-C1'-C2'	-5.79	101.27	105.90
100	3N	7386	DA	O4'-C1'-C2'	-5.79	101.27	105.90
100	3N	8208	DG	O4'-C1'-C2'	-5.78	101.27	105.90
100	3N	5455	DA	C4'-C3'-C2'	-5.78	97.90	103.10
100	3N	3402	DG	O4'-C1'-C2'	-5.78	101.28	105.90
27	1b	23	DG	O4'-C1'-C2'	-5.78	101.28	105.90
100	3N	7840	DC	P-O3'-C3'	5.78	126.63	119.70
100	3N	7850	DG	O4'-C1'-C2'	-5.77	101.28	105.90
100	3N	3327	DG	C1'-O4'-C4'	-5.77	104.33	110.10
100	3N	5382	DC	P-O3'-C3'	5.77	126.62	119.70
102	3B	2091	DG	O4'-C1'-C2'	-5.76	101.29	105.90
78	2c	1050	DA	O4'-C1'-C2'	-5.76	101.29	105.90
55	2E	1073	DG	O4'-C1'-C2'	-5.76	101.29	105.90
84	2i	1058	DC	O4'-C1'-C2'	-5.76	101.30	105.90
100	3N	4157	DG	O4'-C1'-C2'	-5.76	101.29	105.90
100	3N	8029	DC	O4'-C1'-C2'	-5.76	101.30	105.90
100	3N	4081	DA	O4'-C4'-C3'	-5.75	102.20	104.50
100	3N	3223	DG	C1'-O4'-C4'	-5.75	104.35	110.10
8	1H	20	DT	O4'-C1'-C2'	-5.75	101.30	105.90
68	2S	1044	DG	O4'-C1'-C2'	-5.75	101.30	105.90
100	3N	4830	DT	O4'-C1'-C2'	-5.74	101.31	105.90
100	3N	6938	DG	O4'-C1'-C2'	-5.74	101.31	105.90
95	2t	2056	DT	C1'-O4'-C4'	-5.74	104.36	110.10
100	3N	5521	DG	O4'-C1'-C2'	-5.74	101.31	105.90
20	1U	6	DA	O4'-C1'-C2'	-5.74	101.31	105.90
100	3N	6597	DT	O4'-C1'-C2'	-5.74	101.31	105.90
100	3N	3139	DA	O4'-C1'-C2'	-5.74	101.31	105.90
100	3N	3913	DA	O4'-C1'-C2'	-5.74	101.31	105.90
50	2N	1075	DT	C4'-C3'-C2'	-5.73	97.94	103.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1A	29	DA	O4'-C1'-C2'	-5.73	101.32	105.90
8	1H	42	DG	O4'-C1'-C2'	-5.73	101.31	105.90
1	1A	13	DA	P-O3'-C3'	5.73	126.58	119.70
100	3N	4685	DA	O4'-C1'-C2'	-5.73	101.32	105.90
100	3N	4512	DG	O4'-C1'-C2'	-5.72	101.32	105.90
105	3E	2094	DG	O4'-C1'-C2'	-5.72	101.32	105.90
100	3N	3180	DG	O4'-C1'-C2'	-5.72	101.32	105.90
100	3N	4968	DA	O4'-C4'-C3'	-5.72	102.21	104.50
31	1f	6	DA	O4'-C1'-C2'	-5.72	101.32	105.90
95	2t	2062	DG	C5-C6-O6	-5.72	125.17	128.60
100	3N	3258	DG	O4'-C1'-C2'	-5.72	101.32	105.90
100	3N	4082	DA	C1'-O4'-C4'	-5.72	104.38	110.10
100	3N	4654	DC	P-O3'-C3'	5.72	126.56	119.70
100	3N	4781	DA	P-O3'-C3'	5.72	126.56	119.70
100	3N	4792	DA	P-O3'-C3'	5.72	126.56	119.70
118	3R	2089	DG	C1'-O4'-C4'	-5.72	104.38	110.10
65	2P	1053	DC	C4'-C3'-C2'	-5.72	97.95	103.10
53	2C	1072	DG	O4'-C1'-C2'	-5.71	101.33	105.90
21	1V	5	DG	O4'-C1'-C2'	-5.71	101.33	105.90
35	1j	18	DA	P-O3'-C3'	5.71	126.55	119.70
90	2o	2066	DA	P-O3'-C3'	5.71	126.56	119.70
35	1j	18	DA	C1'-O4'-C4'	-5.71	104.39	110.10
81	2f	1066	DA	O4'-C1'-C2'	-5.71	101.33	105.90
100	3N	5055	DG	P-O3'-C3'	5.71	126.55	119.70
25	1Z	14	DT	C1'-O4'-C4'	-5.71	104.39	110.10
100	3N	4725	DG	C1'-O4'-C4'	-5.71	104.39	110.10
11	1K	31	DC	C1'-O4'-C4'	-5.70	104.40	110.10
100	3N	3898	DG	P-O3'-C3'	5.70	126.55	119.70
100	3N	4806	DA	O4'-C1'-C2'	-5.70	101.34	105.90
100	3N	5175	DG	C1'-O4'-C4'	-5.70	104.40	110.10
37	1l	35	DG	C1'-O4'-C4'	-5.70	104.40	110.10
100	3N	6660	DA	O4'-C1'-C2'	-5.70	101.34	105.90
100	3N	4492	DA	O4'-C1'-C2'	-5.69	101.35	105.90
114	3M	2106	DA	N1-C6-N6	-5.69	115.18	118.60
41	1p	1042	DG	C4'-C3'-C2'	-5.69	97.98	103.10
100	3N	7060	DC	O4'-C1'-C2'	-5.69	101.35	105.90
100	3N	5450	DA	P-O3'-C3'	5.68	126.52	119.70
100	3N	8239	DA	C1'-O4'-C4'	-5.68	104.42	110.10
100	3N	5379	DC	O4'-C1'-C2'	-5.68	101.36	105.90
64	2O	1061	DA	P-O3'-C3'	5.68	126.51	119.70
100	3N	7452	DG	P-O3'-C3'	5.68	126.51	119.70
36	1k	23	DA	O4'-C1'-C2'	-5.67	101.36	105.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
100	3N	4037	DT	P-O3'-C3'	5.67	126.50	119.70
100	3N	4683	DG	O4'-C1'-C2'	-5.67	101.36	105.90
88	2m	2064	DG	P-O3'-C3'	5.67	126.50	119.70
100	3N	3816	DG	O4'-C1'-C2'	-5.67	101.36	105.90
100	3N	5504	DC	P-O3'-C3'	5.67	126.50	119.70
100	3N	7078	DG	O4'-C1'-C2'	-5.67	101.36	105.90
115	3O	2106	DT	C1'-O4'-C4'	-5.67	104.43	110.10
4	1D	6	DG	C1'-O4'-C4'	-5.67	104.44	110.10
100	3N	3343	DG	P-O3'-C3'	5.66	126.50	119.70
72	2W	1064	DA	O4'-C1'-C2'	-5.66	101.37	105.90
100	3N	8301	DG	O4'-C1'-C2'	-5.66	101.37	105.90
100	3N	5260	DG	O4'-C1'-C2'	-5.65	101.38	105.90
109	3I	2101	DG	O4'-C1'-C2'	-5.65	101.38	105.90
100	3N	8358	DG	O4'-C1'-C2'	-5.65	101.38	105.90
100	3N	3761	DA	O4'-C1'-C2'	-5.65	101.38	105.90
100	3N	3516	DG	P-O3'-C3'	5.65	126.48	119.70
39	1n	1019	DG	O4'-C1'-C2'	-5.65	101.38	105.90
100	3N	7429	DG	O4'-C1'-C2'	-5.64	101.38	105.90
100	3N	3447	DA	O4'-C1'-C2'	-5.64	101.39	105.90
100	3N	7230	DG	P-O3'-C3'	5.64	126.47	119.70
100	3N	7550	DT	P-O3'-C3'	5.64	126.47	119.70
68	2S	1017	DG	C5-C6-O6	-5.64	125.22	128.60
8	1H	1	DA	C1'-O4'-C4'	-5.64	104.46	110.10
100	3N	4081	DA	C4'-C3'-C2'	-5.64	98.03	103.10
93	2r	2056	DC	O4'-C1'-N1	5.63	111.94	108.00
100	3N	7352	DA	O4'-C1'-C2'	-5.63	101.39	105.90
100	3N	7720	DA	P-O3'-C3'	5.63	126.46	119.70
1	1A	8	DG	N1-C6-O6	5.63	123.28	119.90
62	2L	1048	DT	P-O3'-C3'	5.63	126.46	119.70
100	3N	5287	DG	O4'-C4'-C3'	-5.63	102.25	104.50
100	3N	8115	DA	O4'-C1'-C2'	-5.63	101.39	105.90
100	3N	7029	DA	P-O3'-C3'	5.63	126.46	119.70
100	3N	5280	DG	C1'-O4'-C4'	-5.63	104.47	110.10
100	3N	3804	DG	O4'-C1'-C2'	-5.62	101.40	105.90
100	3N	4644	DG	O4'-C1'-C2'	-5.62	101.40	105.90
68	2S	1055	DG	O4'-C1'-C2'	-5.62	101.41	105.90
100	3N	6602	DG	O4'-C1'-C2'	-5.61	101.41	105.90
75	2Z	1058	DA	O4'-C1'-C2'	-5.61	101.41	105.90
99	2x	2043	DG	O4'-C1'-C2'	-5.61	101.41	105.90
100	3N	5108	DA	C1'-O4'-C4'	-5.61	104.49	110.10
100	3N	5265	DT	P-O3'-C3'	5.61	126.43	119.70
100	3N	7809	DG	O4'-C1'-N9	5.61	111.92	108.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
106	3F	2099	DA	O4'-C1'-C2'	-5.61	101.41	105.90
24	1Y	24	DG	O4'-C1'-C2'	-5.61	101.42	105.90
2	1B	28	DG	O4'-C1'-C2'	-5.60	101.42	105.90
82	2g	1058	DG	O4'-C1'-C2'	-5.60	101.42	105.90
100	3N	5377	DA	C1'-O4'-C4'	-5.60	104.50	110.10
109	3I	2088	DC	O4'-C1'-C2'	-5.60	101.42	105.90
11	1K	1	DT	C4'-C3'-C2'	-5.60	98.06	103.10
100	3N	7717	DA	O4'-C1'-C2'	-5.60	101.42	105.90
23	1X	6	DA	O4'-C1'-C2'	-5.59	101.42	105.90
20	1U	18	DG	C5-C6-O6	-5.59	125.24	128.60
46	1u	1034	DG	O4'-C1'-C2'	-5.59	101.43	105.90
68	2S	1017	DG	C1'-O4'-C4'	-5.59	104.51	110.10
4	1D	6	DG	O4'-C4'-C3'	-5.59	102.26	104.50
98	2w	2093	DA	O4'-C4'-C3'	-5.59	102.27	104.50
100	3N	3197	DG	O4'-C1'-C2'	-5.59	101.43	105.90
100	3N	7981	DG	C1'-O4'-C4'	-5.59	104.51	110.10
53	2C	1080	DT	O4'-C1'-C2'	-5.58	101.43	105.90
57	2G	1059	DG	O4'-C1'-C2'	-5.58	101.43	105.90
61	2K	1034	DG	P-O3'-C3'	5.58	126.40	119.70
100	3N	5077	DG	C1'-O4'-C4'	-5.58	104.52	110.10
79	2d	1073	DG	O4'-C1'-C2'	-5.58	101.43	105.90
100	3N	7383	DG	O4'-C1'-C2'	-5.58	101.43	105.90
100	3N	4329	DG	O4'-C1'-C2'	-5.58	101.43	105.90
20	1U	17	DC	N3-C4-C5	-5.58	119.67	121.90
67	2R	1065	DT	C1'-O4'-C4'	-5.58	104.52	110.10
100	3N	8288	DT	O4'-C4'-C3'	-5.58	102.27	104.50
32	1g	14	DG	O4'-C1'-N9	5.58	111.90	108.00
100	3N	4915	DG	O4'-C1'-C2'	-5.58	101.44	105.90
100	3N	5111	DA	P-O3'-C3'	5.58	126.39	119.70
110	3J	2066	DG	C1'-O4'-C4'	-5.57	104.53	110.10
67	2R	1059	DG	P-O3'-C3'	5.57	126.38	119.70
111	3S	2106	DG	C1'-O4'-C4'	-5.56	104.54	110.10
68	2S	1037	DA	O4'-C1'-C2'	-5.56	101.45	105.90
100	3N	4554	DA	O4'-C1'-C2'	-5.56	101.45	105.90
100	3N	7452	DG	O4'-C1'-C2'	-5.56	101.45	105.90
105	3E	2130	DG	O4'-C1'-C2'	-5.56	101.45	105.90
6	1F	41	DA	N1-C6-N6	-5.56	115.27	118.60
10	1J	8	DG	O4'-C1'-C2'	-5.56	101.45	105.90
65	2P	1077	DG	O4'-C1'-C2'	-5.56	101.45	105.90
15	1P	12	DG	C1'-O4'-C4'	-5.55	104.55	110.10
80	2e	1055	DA	O4'-C1'-C2'	-5.55	101.46	105.90
100	3N	3603	DG	O4'-C4'-C3'	-5.55	102.28	104.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
81	2f	1075	DA	O4'-C1'-C2'	-5.55	101.46	105.90
1	1A	7	DG	O4'-C1'-C2'	-5.55	101.46	105.90
3	1C	10	DT	O4'-C1'-C2'	-5.55	101.46	105.90
100	3N	3694	DG	O4'-C1'-C2'	-5.55	101.46	105.90
16	1Q	8	DA	O4'-C1'-C2'	-5.55	101.46	105.90
100	3N	7012	DG	O4'-C1'-C2'	-5.54	101.47	105.90
100	3N	7550	DT	O4'-C1'-C2'	-5.54	101.47	105.90
79	2d	1062	DC	P-O3'-C3'	5.54	126.35	119.70
100	3N	6959	DG	O4'-C1'-C2'	-5.54	101.47	105.90
25	1Z	12	DG	O4'-C1'-C2'	-5.54	101.47	105.90
76	2a	1043	DA	O4'-C1'-C2'	-5.54	101.47	105.90
100	3N	7845	DG	O4'-C1'-C2'	-5.54	101.47	105.90
45	1t	1034	DG	O4'-C1'-C2'	-5.54	101.47	105.90
100	3N	4362	DG	O4'-C1'-C2'	-5.53	101.47	105.90
100	3N	3516	DG	O4'-C1'-C2'	-5.53	101.48	105.90
100	3N	4587	DG	O4'-C1'-C2'	-5.53	101.48	105.90
100	3N	7850	DG	P-O3'-C3'	5.53	126.33	119.70
100	3N	4080	DC	O4'-C1'-C2'	-5.52	101.48	105.90
100	3N	4107	DA	O4'-C4'-C3'	-5.52	102.29	104.50
104	3D	2117	DA	N1-C6-N6	-5.52	115.29	118.60
73	2X	1062	DG	P-O3'-C3'	5.52	126.32	119.70
100	3N	5564	DG	O4'-C1'-C2'	-5.52	101.48	105.90
105	3E	2108	DA	C1'-O4'-C4'	-5.52	104.58	110.10
100	3N	5175	DG	O4'-C4'-C3'	-5.52	102.29	104.50
100	3N	5179	DC	C1'-O4'-C4'	-5.52	104.58	110.10
100	3N	3466	DA	P-O3'-C3'	5.51	126.32	119.70
37	1l	14	DA	P-O3'-C3'	5.51	126.31	119.70
100	3N	8085	DG	O4'-C1'-C2'	-5.51	101.49	105.90
14	1O	21	DA	O4'-C1'-C2'	-5.51	101.49	105.90
100	3N	6678	DC	O4'-C1'-C2'	-5.51	101.49	105.90
103	3C	2078	DG	O4'-C1'-C2'	-5.51	101.49	105.90
77	2b	1096	DA	O4'-C1'-C2'	-5.51	101.49	105.90
100	3N	3785	DG	O4'-C1'-C2'	-5.51	101.49	105.90
62	2L	1033	DG	O4'-C4'-C3'	-5.51	102.30	104.50
100	3N	3578	DG	O4'-C1'-C2'	-5.51	101.49	105.90
100	3N	6595	DC	P-O3'-C3'	5.51	126.31	119.70
100	3N	8408	DG	O4'-C1'-C2'	-5.50	101.50	105.90
28	1c	38	DG	O4'-C1'-C2'	-5.50	101.50	105.90
100	3N	5541	DT	C1'-O4'-C4'	-5.50	104.60	110.10
16	1Q	30	DA	O4'-C1'-C2'	-5.50	101.50	105.90
100	3N	5483	DG	O4'-C1'-C2'	-5.50	101.50	105.90
100	3N	8106	DG	O4'-C1'-C2'	-5.50	101.50	105.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
100	3N	3898	DG	O4'-C1'-C2'	-5.49	101.51	105.90
100	3N	7934	DT	O4'-C1'-C2'	-5.49	101.51	105.90
106	3F	2101	DT	C1'-O4'-C4'	-5.49	104.61	110.10
108	3H	2143	DG	O4'-C1'-C2'	-5.49	101.51	105.90
109	3I	2120	DG	O4'-C1'-C2'	-5.49	101.51	105.90
100	3N	3356	DA	P-O3'-C3'	5.49	126.28	119.70
36	1k	39	DT	P-O3'-C3'	5.48	126.28	119.70
83	2h	1070	DT	P-O3'-C3'	5.48	126.28	119.70
96	2u	2086	DT	O4'-C1'-C2'	-5.48	101.51	105.90
100	3N	4917	DT	C4'-C3'-C2'	-5.48	98.17	103.10
114	3M	2080	DG	O4'-C1'-C2'	-5.48	101.51	105.90
104	3D	2104	DG	O4'-C1'-C2'	-5.48	101.52	105.90
100	3N	5402	DA	O4'-C1'-C2'	-5.48	101.52	105.90
100	3N	7975	DG	C1'-O4'-C4'	-5.48	104.62	110.10
65	2P	1067	DG	O4'-C1'-C2'	-5.48	101.52	105.90
100	3N	5237	DT	O4'-C1'-C2'	-5.48	101.52	105.90
66	2Q	1081	DA	O4'-C1'-C2'	-5.47	101.52	105.90
100	3N	7920	DT	P-O3'-C3'	5.47	126.27	119.70
100	3N	8450	DG	C1'-O4'-C4'	-5.47	104.63	110.10
78	2c	1061	DG	C4-N9-C1'	5.47	133.61	126.50
94	2s	2055	DA	O4'-C1'-C2'	-5.47	101.52	105.90
106	3F	2119	DT	O4'-C1'-C2'	-5.47	101.53	105.90
53	2C	1061	DA	O4'-C1'-C2'	-5.46	101.53	105.90
18	1S	17	DA	P-O3'-C3'	5.46	126.25	119.70
59	2I	1025	DA	O4'-C1'-C2'	-5.46	101.53	105.90
100	3N	5331	DA	P-O3'-C3'	5.46	126.25	119.70
100	3N	7120	DT	P-O3'-C3'	5.46	126.25	119.70
100	3N	7805	DT	O4'-C1'-C2'	-5.46	101.53	105.90
100	3N	7367	DC	P-O3'-C3'	5.45	126.24	119.70
104	3D	2102	DC	O4'-C1'-C2'	-5.45	101.54	105.90
8	1H	7	DT	P-O3'-C3'	5.45	126.24	119.70
100	3N	7645	DG	C1'-O4'-C4'	-5.45	104.65	110.10
15	1P	35	DG	O4'-C1'-C2'	-5.45	101.54	105.90
92	2q	2064	DA	P-O3'-C3'	5.45	126.24	119.70
100	3N	4360	DC	C2-N1-C1'	5.45	124.79	118.80
103	3C	2108	DG	O4'-C1'-C2'	-5.45	101.54	105.90
27	1b	6	DG	O4'-C1'-C2'	-5.44	101.55	105.90
55	2E	1075	DG	O4'-C4'-C3'	-5.44	102.32	104.50
100	3N	4762	DG	O4'-C1'-C2'	-5.44	101.55	105.90
100	3N	3816	DG	P-O3'-C3'	5.44	126.22	119.70
100	3N	4541	DG	O4'-C1'-C2'	-5.43	101.55	105.90
100	3N	7365	DG	P-O3'-C3'	5.43	126.22	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
45	1t	1047	DG	C1'-O4'-C4'	-5.43	104.67	110.10
84	2i	1042	DG	O4'-C1'-C2'	-5.43	101.55	105.90
100	3N	7995	DG	O4'-C1'-C2'	-5.43	101.55	105.90
100	3N	6579	DG	O4'-C1'-C2'	-5.43	101.56	105.90
100	3N	8043	DG	O4'-C1'-C2'	-5.43	101.56	105.90
106	3F	2138	DA	O4'-C1'-C2'	-5.43	101.56	105.90
98	2w	2071	DC	O4'-C1'-C2'	-5.42	101.56	105.90
100	3N	4791	DG	O4'-C1'-C2'	-5.42	101.57	105.90
100	3N	7526	DT	C1'-O4'-C4'	-5.42	104.68	110.10
100	3N	4575	DG	O4'-C1'-C2'	-5.42	101.57	105.90
62	2L	1041	DT	O4'-C1'-C2'	-5.41	101.57	105.90
98	2w	2057	DG	C1'-O4'-C4'	-5.41	104.69	110.10
100	3N	4956	DG	O4'-C1'-C2'	-5.41	101.57	105.90
100	3N	8009	DG	O4'-C1'-C2'	-5.41	101.57	105.90
100	3N	5154	DG	O4'-C1'-C2'	-5.41	101.57	105.90
74	2Y	1034	DG	C1'-O4'-C4'	-5.41	104.69	110.10
40	1o	1049	DG	O4'-C1'-C2'	-5.41	101.58	105.90
98	2w	2059	DG	O4'-C1'-C2'	-5.41	101.58	105.90
100	3N	4233	DG	C1'-O4'-C4'	-5.41	104.69	110.10
100	3N	6723	DA	O4'-C1'-C2'	-5.41	101.58	105.90
11	1K	15	DG	C1'-O4'-C4'	-5.40	104.70	110.10
100	3N	6852	DG	O4'-C1'-C2'	-5.40	101.58	105.90
31	1f	6	DA	P-O3'-C3'	5.40	126.18	119.70
46	1u	1042	DG	O4'-C1'-C2'	-5.40	101.58	105.90
75	2Z	1058	DA	P-O3'-C3'	5.40	126.18	119.70
8	1H	27	DG	O4'-C1'-C2'	-5.40	101.58	105.90
70	2U	1032	DG	O4'-C1'-C2'	-5.40	101.58	105.90
100	3N	4545	DA	O4'-C1'-C2'	-5.40	101.58	105.90
100	3N	7454	DG	O4'-C1'-C2'	-5.40	101.58	105.90
100	3N	3862	DG	O4'-C1'-C2'	-5.40	101.58	105.90
81	2f	1056	DT	P-O3'-C3'	5.39	126.17	119.70
100	3N	5176	DC	P-O3'-C3'	5.39	126.17	119.70
100	3N	8082	DC	O4'-C1'-C2'	-5.39	101.58	105.90
100	3N	3146	DA	O4'-C1'-C2'	-5.39	101.58	105.90
100	3N	7608	DC	P-O3'-C3'	5.39	126.17	119.70
6	1F	11	DG	P-O3'-C3'	5.39	126.17	119.70
68	2S	1017	DG	N1-C6-O6	5.39	123.13	119.90
105	3E	2091	DA	C1'-O4'-C4'	-5.39	104.71	110.10
55	2E	1048	DT	C1'-O4'-C4'	-5.39	104.71	110.10
100	3N	5283	DG	P-O3'-C3'	5.39	126.17	119.70
100	3N	7085	DA	O4'-C4'-C3'	-5.39	102.34	104.50
104	3D	2086	DG	C1'-O4'-C4'	-5.39	104.71	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	1M	17	DG	O4'-C1'-C2'	-5.38	101.59	105.90
80	2e	1073	DG	O4'-C1'-C2'	-5.38	101.59	105.90
100	3N	4299	DT	O4'-C1'-C2'	-5.38	101.59	105.90
44	1s	1042	DC	C2-N1-C1'	5.38	124.72	118.80
114	3M	2075	DG	C1'-O4'-C4'	-5.38	104.72	110.10
75	2Z	1080	DG	O4'-C1'-C2'	-5.38	101.60	105.90
42	1q	1040	DT	O4'-C4'-C3'	-5.38	102.35	104.50
100	3N	4833	DG	O4'-C1'-C2'	-5.38	101.60	105.90
100	3N	5358	DA	O4'-C1'-C2'	-5.38	101.60	105.90
5	1E	44	DG	O4'-C1'-C2'	-5.38	101.60	105.90
4	1D	14	DA	P-O3'-C3'	5.37	126.14	119.70
65	2P	1069	DC	P-O3'-C3'	5.37	126.14	119.70
100	3N	7635	DA	C1'-O4'-C4'	-5.37	104.73	110.10
13	1M	8	DC	P-O3'-C3'	5.37	126.14	119.70
74	2Y	1050	DC	O4'-C1'-C2'	-5.37	101.61	105.90
76	2a	1040	DA	O4'-C1'-C2'	-5.37	101.61	105.90
100	3N	3745	DG	C1'-O4'-C4'	-5.37	104.73	110.10
42	1q	1040	DT	C4'-C3'-C2'	-5.37	98.27	103.10
48	1w	1035	DG	P-O3'-C3'	5.37	126.14	119.70
100	3N	3979	DT	P-O3'-C3'	5.37	126.14	119.70
33	1h	18	DT	P-O3'-C3'	5.36	126.14	119.70
58	2H	1067	DA	O4'-C1'-C2'	-5.36	101.61	105.90
100	3N	7196	DA	P-O3'-C3'	5.36	126.14	119.70
100	3N	6929	DG	O4'-C1'-C2'	-5.36	101.61	105.90
17	1R	47	DG	C5-C6-O6	-5.36	125.38	128.60
20	1U	18	DG	N1-C6-O6	5.36	123.12	119.90
100	3N	7278	DG	C1'-O4'-C4'	-5.36	104.74	110.10
40	1o	1026	DC	P-O3'-C3'	-5.36	113.27	119.70
100	3N	7443	DG	P-O3'-C3'	5.36	126.13	119.70
27	1b	25	DA	P-O3'-C3'	5.35	126.12	119.70
110	3J	2049	DC	C6-N1-C2	-5.35	118.16	120.30
73	2X	1045	DG	O4'-C1'-C2'	-5.35	101.62	105.90
100	3N	3509	DG	C1'-O4'-C4'	-5.35	104.75	110.10
100	3N	4932	DA	O4'-C1'-C2'	-5.35	101.62	105.90
100	3N	4313	DA	P-O3'-C3'	5.35	126.11	119.70
100	3N	4927	DG	O4'-C1'-C2'	-5.35	101.62	105.90
51	2A	1081	DG	O4'-C1'-C2'	-5.34	101.62	105.90
100	3N	4692	DG	P-O3'-C3'	5.34	126.11	119.70
4	1D	21	DA	O4'-C1'-C2'	-5.34	101.63	105.90
58	2H	1077	DC	P-O3'-C3'	5.34	126.11	119.70
100	3N	4796	DA	O4'-C1'-C2'	-5.34	101.63	105.90
100	3N	5002	DA	O4'-C1'-C2'	-5.34	101.63	105.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
100	3N	6670	DG	O4'-C1'-C2'	-5.34	101.63	105.90
51	2A	1076	DG	O4'-C4'-C3'	-5.34	102.36	104.50
100	3N	6876	DA	O4'-C1'-C2'	-5.34	101.63	105.90
100	3N	5409	DA	O4'-C1'-C2'	-5.34	101.63	105.90
100	3N	7362	DG	O4'-C1'-C2'	-5.34	101.63	105.90
77	2b	1048	DT	O4'-C1'-C2'	-5.33	101.63	105.90
55	2E	1057	DA	O4'-C1'-C2'	-5.33	101.63	105.90
22	1W	33	DG	O4'-C1'-C2'	-5.33	101.63	105.90
46	1u	1039	DG	O4'-C1'-C2'	-5.33	101.64	105.90
100	3N	7443	DG	O4'-C1'-C2'	-5.33	101.64	105.90
100	3N	7639	DG	O4'-C1'-C2'	-5.33	101.64	105.90
100	3N	3168	DG	O4'-C1'-C2'	-5.33	101.64	105.90
100	3N	4813	DA	O4'-C1'-C2'	-5.33	101.64	105.90
100	3N	7302	DG	P-O3'-C3'	5.33	126.09	119.70
100	3N	8037	DG	C5-C6-O6	-5.33	125.41	128.60
41	1p	1034	DA	C1'-O4'-C4'	-5.32	104.78	110.10
100	3N	3184	DT	O4'-C4'-C3'	-5.32	102.37	104.50
100	3N	3788	DG	O4'-C1'-C2'	-5.32	101.64	105.90
100	3N	3606	DG	O4'-C1'-C2'	-5.32	101.65	105.90
95	2t	2056	DT	O4'-C1'-N1	5.32	111.72	108.00
8	1H	15	DC	C1'-O4'-C4'	-5.31	104.79	110.10
100	3N	3091	DG	O4'-C1'-C2'	-5.31	101.65	105.90
115	3O	2095	DG	P-O3'-C3'	5.31	126.07	119.70
72	2W	1086	DA	O4'-C1'-C2'	-5.31	101.65	105.90
92	2q	2073	DA	O4'-C1'-C2'	-5.31	101.65	105.90
100	3N	3184	DT	C4'-C3'-C2'	-5.31	98.33	103.10
46	1u	1049	DG	C5-C6-O6	-5.30	125.42	128.60
92	2q	2073	DA	P-O3'-C3'	5.30	126.06	119.70
100	3N	8270	DA	C1'-O4'-C4'	-5.30	104.80	110.10
6	1F	21	DC	O4'-C1'-C2'	-5.30	101.66	105.90
44	1s	1028	DG	C1'-O4'-C4'	-5.30	104.80	110.10
100	3N	4410	DG	O4'-C1'-C2'	-5.30	101.66	105.90
100	3N	6618	DG	O4'-C1'-C2'	-5.30	101.66	105.90
87	2l	1016	DT	O4'-C1'-C2'	-5.30	101.66	105.90
115	3O	2097	DA	P-O3'-C3'	5.30	126.06	119.70
11	1K	12	DG	P-O3'-C3'	5.29	126.05	119.70
30	1e	3	DT	P-O3'-C3'	5.29	126.05	119.70
42	1q	1009	DT	P-O3'-C3'	5.29	126.05	119.70
51	2A	1060	DA	P-O3'-C3'	5.29	126.05	119.70
102	3B	2121	DC	P-O3'-C3'	5.29	126.05	119.70
115	3O	2073	DG	C1'-O4'-C4'	-5.29	104.81	110.10
100	3N	7714	DA	O4'-C1'-C2'	-5.29	101.67	105.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
32	1g	47	DA	P-O3'-C3'	5.29	126.05	119.70
81	2f	1049	DT	C1'-O4'-C4'	-5.29	104.81	110.10
100	3N	4939	DG	C1'-O4'-C4'	-5.29	104.81	110.10
105	3E	2108	DA	O4'-C4'-C3'	-5.29	102.39	104.50
100	3N	4244	DA	C1'-O4'-C4'	-5.29	104.81	110.10
100	3N	6787	DG	P-O3'-C3'	5.29	126.04	119.70
100	3N	7403	DG	O4'-C1'-C2'	-5.29	101.67	105.90
33	1h	18	DT	O4'-C1'-C2'	-5.28	101.67	105.90
100	3N	4517	DA	O4'-C1'-C2'	-5.28	101.67	105.90
100	3N	6651	DG	O4'-C1'-C2'	-5.28	101.67	105.90
100	3N	5042	DA	O4'-C1'-C2'	-5.28	101.68	105.90
100	3N	7856	DA	P-O3'-C3'	5.28	126.03	119.70
46	1u	1046	DG	C1'-O4'-C4'	-5.28	104.82	110.10
67	2R	1043	DA	O4'-C1'-C2'	-5.28	101.68	105.90
100	3N	7230	DG	O4'-C1'-C2'	-5.27	101.68	105.90
100	3N	3083	DG	O4'-C1'-C2'	-5.27	101.68	105.90
100	3N	3974	DG	C1'-O4'-C4'	-5.27	104.83	110.10
100	3N	4528	DC	C2-N1-C1'	5.27	124.60	118.80
37	1l	7	DG	O4'-C1'-C2'	-5.27	101.68	105.90
49	1x	1016	DA	N1-C6-N6	-5.27	115.44	118.60
88	2m	2042	DA	P-O3'-C3'	5.27	126.02	119.70
100	3N	3570	DG	O4'-C4'-C3'	-5.27	102.39	104.50
100	3N	7681	DC	O4'-C1'-C2'	-5.27	101.68	105.90
100	3N	8071	DC	C1'-O4'-C4'	-5.27	104.83	110.10
26	1a	31	DA	O4'-C1'-C2'	-5.27	101.69	105.90
100	3N	3379	DC	O4'-C1'-C2'	-5.27	101.69	105.90
100	3N	5431	DA	O4'-C1'-C2'	-5.27	101.69	105.90
100	3N	3762	DG	O4'-C1'-C2'	-5.26	101.69	105.90
100	3N	6692	DG	C1'-O4'-C4'	-5.26	104.84	110.10
100	3N	4620	DA	N1-C6-N6	-5.26	115.44	118.60
14	1O	6	DC	P-O3'-C3'	5.26	126.01	119.70
100	3N	3552	DA	O4'-C1'-C2'	-5.26	101.69	105.90
100	3N	3827	DG	O4'-C4'-C3'	-5.26	102.40	104.50
41	1p	1020	DT	O4'-C1'-C2'	-5.26	101.69	105.90
100	3N	3307	DG	O4'-C1'-C2'	-5.26	101.70	105.90
100	3N	3994	DA	C1'-O4'-C4'	-5.25	104.85	110.10
100	3N	6642	DG	P-O3'-C3'	5.25	126.00	119.70
17	1R	18	DG	O4'-C1'-C2'	-5.25	101.70	105.90
100	3N	5534	DG	C1'-O4'-C4'	-5.25	104.85	110.10
100	3N	7940	DG	O4'-C1'-C2'	-5.25	101.70	105.90
12	1L	4	DC	P-O3'-C3'	5.25	126.00	119.70
21	1V	9	DA	O4'-C1'-C2'	-5.25	101.70	105.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
25	1Z	21	DA	P-O3'-C3'	5.25	126.00	119.70
32	1g	35	DA	O4'-C1'-C2'	-5.25	101.70	105.90
100	3N	7748	DG	O4'-C4'-C3'	-5.25	102.40	104.50
16	1Q	36	DG	O4'-C1'-C2'	-5.24	101.71	105.90
37	1l	6	DG	O4'-C1'-C2'	-5.24	101.71	105.90
100	3N	3218	DA	P-O3'-C3'	5.24	125.99	119.70
100	3N	5358	DA	P-O3'-C3'	5.24	125.98	119.70
102	3B	2113	DG	N1-C6-O6	5.24	123.04	119.90
46	1u	1052	DG	O4'-C4'-C3'	-5.24	102.41	104.50
100	3N	5122	DT	O4'-C1'-C2'	-5.24	101.71	105.90
100	3N	5392	DA	C1'-O4'-C4'	-5.24	104.86	110.10
100	3N	6692	DG	O4'-C4'-C3'	-5.24	102.41	104.50
100	3N	7719	DC	O4'-C1'-C2'	-5.24	101.71	105.90
106	3F	2107	DG	O4'-C1'-C2'	-5.24	101.71	105.90
100	3N	3913	DA	O4'-C1'-N9	5.23	111.66	108.00
100	3N	4299	DT	C1'-O4'-C4'	-5.23	104.87	110.10
100	3N	6761	DG	O4'-C4'-C3'	-5.22	102.41	104.50
100	3N	8392	DT	O4'-C1'-C2'	-5.22	101.72	105.90
108	3H	2132	DG	O4'-C1'-N9	5.22	111.66	108.00
100	3N	5452	DA	O4'-C1'-C2'	-5.22	101.72	105.90
4	1D	17	DT	P-O3'-C3'	5.22	125.96	119.70
100	3N	3514	DG	O4'-C1'-C2'	-5.22	101.72	105.90
100	3N	3594	DT	P-O3'-C3'	5.22	125.96	119.70
100	3N	8348	DA	O4'-C1'-C2'	-5.22	101.72	105.90
2	1B	9	DG	O4'-C1'-C2'	-5.22	101.73	105.90
100	3N	6686	DG	P-O3'-C3'	5.22	125.96	119.70
100	3N	7331	DG	O4'-C1'-C2'	-5.22	101.73	105.90
102	3B	2113	DG	C5-C6-O6	-5.22	125.47	128.60
58	2H	1074	DC	C1'-O4'-C4'	-5.21	104.89	110.10
100	3N	5106	DG	O4'-C1'-C2'	-5.21	101.73	105.90
100	3N	7817	DA	O4'-C1'-C2'	-5.21	101.73	105.90
33	1h	27	DA	O4'-C1'-C2'	-5.21	101.73	105.90
20	1U	17	DC	O4'-C1'-C2'	-5.21	101.74	105.90
71	2V	1048	DA	O4'-C1'-C2'	-5.21	101.73	105.90
100	3N	3279	DG	P-O3'-C3'	5.21	125.95	119.70
100	3N	3512	DG	O4'-C4'-C3'	-5.21	102.42	104.50
100	3N	7688	DT	P-O3'-C3'	5.21	125.95	119.70
100	3N	6648	DT	P-O3'-C3'	5.21	125.95	119.70
24	1Y	20	DG	O4'-C1'-C2'	-5.20	101.74	105.90
95	2t	2062	DG	N1-C6-O6	5.20	123.02	119.90
100	3N	4158	DG	P-O3'-C3'	5.20	125.94	119.70
2	1B	48	DT	P-O3'-C3'	5.20	125.94	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	1e	12	DA	P-O3'-C3'	5.20	125.94	119.70
112	3K	2058	DC	P-O3'-C3'	5.20	125.94	119.70
100	3N	4701	DA	C1'-O4'-C4'	-5.20	104.91	110.10
100	3N	4755	DA	O4'-C1'-C2'	-5.19	101.75	105.90
100	3N	6611	DG	C1'-O4'-C4'	-5.19	104.91	110.10
17	1R	24	DC	O4'-C1'-C2'	-5.19	101.75	105.90
102	3B	2105	DA	O4'-C1'-C2'	-5.19	101.75	105.90
90	2o	2059	DG	O4'-C1'-C2'	-5.18	101.75	105.90
100	3N	3098	DG	O4'-C1'-C2'	-5.18	101.75	105.90
100	3N	3500	DG	O4'-C1'-C2'	-5.18	101.75	105.90
7	1G	8	DA	C1'-O4'-C4'	-5.18	104.92	110.10
80	2e	1076	DA	P-O3'-C3'	5.18	125.92	119.70
68	2S	1048	DA	P-O3'-C3'	5.18	125.91	119.70
5	1E	1	DA	C1'-O4'-C4'	-5.17	104.93	110.10
11	1K	17	DG	O4'-C1'-C2'	-5.17	101.76	105.90
22	1W	11	DG	O4'-C1'-C2'	-5.17	101.76	105.90
71	2V	1050	DT	O4'-C1'-C2'	-5.17	101.76	105.90
100	3N	7132	DC	P-O3'-C3'	5.17	125.91	119.70
42	1q	1008	DG	O4'-C4'-C3'	-5.17	102.43	104.50
98	2w	2093	DA	C1'-O4'-C4'	-5.17	104.93	110.10
21	1V	5	DG	P-O3'-C3'	5.17	125.90	119.70
73	2X	1038	DA	O4'-C1'-C2'	-5.17	101.77	105.90
100	3N	5519	DG	O4'-C1'-C2'	-5.17	101.77	105.90
100	3N	7514	DG	O4'-C1'-C2'	-5.17	101.77	105.90
3	1C	1	DA	O4'-C4'-C3'	-5.17	102.43	104.50
100	3N	7539	DG	P-O3'-C3'	5.17	125.90	119.70
10	1J	19	DA	O4'-C1'-C2'	-5.16	101.77	105.90
100	3N	4525	DG	O4'-C1'-C2'	-5.16	101.77	105.90
100	3N	4760	DC	O4'-C1'-C2'	-5.16	101.77	105.90
45	1t	1022	DA	O4'-C1'-C2'	-5.16	101.77	105.90
100	3N	5263	DG	O4'-C1'-C2'	-5.16	101.77	105.90
25	1Z	14	DT	O4'-C1'-C2'	-5.16	101.77	105.90
100	3N	4244	DA	P-O3'-C3'	5.16	125.89	119.70
100	3N	6591	DC	O4'-C1'-C2'	-5.16	101.77	105.90
104	3D	2127	DA	O4'-C1'-C2'	-5.16	101.77	105.90
64	2O	1059	DG	O4'-C4'-C3'	-5.15	102.44	104.50
76	2a	1077	DA	O4'-C1'-C2'	-5.15	101.78	105.90
80	2e	1068	DT	O4'-C1'-C2'	-5.15	101.78	105.90
100	3N	4045	DG	P-O3'-C3'	5.15	125.88	119.70
100	3N	3500	DG	P-O3'-C3'	5.14	125.87	119.70
15	1P	13	DC	O4'-C1'-N1	5.14	111.60	108.00
56	2F	1041	DG	O4'-C1'-C2'	-5.14	101.79	105.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
100	3N	3582	DG	O4'-C1'-C2'	-5.14	101.79	105.90
100	3N	4290	DG	O4'-C1'-C2'	-5.14	101.79	105.90
113	3L	2082	DG	O4'-C1'-C2'	-5.14	101.79	105.90
100	3N	3810	DA	O4'-C1'-C2'	-5.13	101.79	105.90
100	3N	4884	DG	O4'-C1'-C2'	-5.13	101.80	105.90
100	3N	7143	DG	C1'-O4'-C4'	-5.13	104.97	110.10
100	3N	3512	DG	C1'-O4'-C4'	-5.13	104.97	110.10
2	1B	6	DG	O4'-C1'-C2'	-5.13	101.80	105.90
36	1k	7	DG	C1'-O4'-C4'	-5.13	104.97	110.10
100	3N	3488	DC	O4'-C1'-C2'	-5.13	101.80	105.90
100	3N	3344	DC	C2-N1-C1'	5.12	124.44	118.80
100	3N	4471	DC	C2-N1-C1'	5.12	124.44	118.80
100	3N	6676	DG	P-O3'-C3'	5.12	125.85	119.70
43	1r	1033	DA	O4'-C1'-C2'	-5.12	101.80	105.90
116	3P	2082	DG	C5-C6-O6	-5.12	125.53	128.60
91	2p	2055	DT	P-O3'-C3'	5.12	125.84	119.70
100	3N	7911	DG	O4'-C1'-C2'	-5.12	101.81	105.90
46	1u	1028	DG	O4'-C4'-C3'	-5.11	102.45	104.50
100	3N	4250	DA	O4'-C1'-C2'	-5.11	101.81	105.90
100	3N	4596	DA	O4'-C1'-C2'	-5.11	101.81	105.90
100	3N	7676	DG	O4'-C1'-C2'	-5.11	101.81	105.90
1	1A	7	DG	P-O3'-C3'	5.11	125.83	119.70
77	2b	1096	DA	C1'-O4'-C4'	-5.11	104.99	110.10
51	2A	1072	DA	P-O3'-C3'	5.11	125.83	119.70
63	2M	1064	DG	O4'-C1'-C2'	-5.11	101.81	105.90
72	2W	1068	DT	O4'-C1'-C2'	-5.11	101.81	105.90
115	3O	2073	DG	O4'-C1'-N9	5.11	111.58	108.00
82	2g	1073	DT	C1'-O4'-C4'	-5.11	105.00	110.10
100	3N	6860	DG	O4'-C1'-C2'	-5.11	101.82	105.90
100	3N	5101	DA	P-O3'-C3'	5.10	125.82	119.70
100	3N	6822	DT	O4'-C1'-C2'	-5.10	101.82	105.90
100	3N	3123	DA	O4'-C4'-C3'	-5.10	102.46	104.50
100	3N	4333	DA	O4'-C1'-C2'	-5.10	101.82	105.90
100	3N	6936	DT	P-O3'-C3'	5.10	125.82	119.70
71	2V	1042	DT	O4'-C1'-C2'	-5.10	101.82	105.90
71	2V	1055	DG	O4'-C1'-C2'	-5.10	101.82	105.90
96	2u	2075	DG	O4'-C1'-C2'	-5.10	101.82	105.90
100	3N	3910	DT	P-O3'-C3'	5.10	125.82	119.70
100	3N	5048	DG	C1'-O4'-C4'	-5.10	105.00	110.10
58	2H	1079	DG	O4'-C1'-C2'	-5.10	101.82	105.90
100	3N	7752	DG	C5-C6-O6	-5.10	125.54	128.60
32	1g	14	DG	P-O3'-C3'	5.09	125.81	119.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
100	3N	5287	DG	C1'-O4'-C4'	-5.09	105.00	110.10
77	2b	1082	DG	P-O3'-C3'	5.09	125.81	119.70
92	2q	2088	DG	O4'-C1'-N9	5.09	111.56	108.00
77	2b	1058	DT	P-O3'-C3'	5.09	125.81	119.70
80	2e	1058	DG	O4'-C1'-C2'	-5.09	101.83	105.90
100	3N	4873	DT	O4'-C1'-C2'	-5.09	101.83	105.90
100	3N	8425	DG	O4'-C4'-C3'	-5.09	102.47	104.50
100	3N	7929	DG	P-O3'-C3'	5.08	125.80	119.70
101	3A	2122	DG	P-O3'-C3'	5.08	125.80	119.70
100	3N	7981	DG	O4'-C4'-C3'	-5.08	102.47	104.50
100	3N	7281	DT	C4'-C3'-C2'	-5.08	98.53	103.10
51	2A	1074	DG	O4'-C4'-C3'	-5.08	102.47	104.50
70	2U	1077	DG	P-O3'-C3'	5.08	125.79	119.70
100	3N	5271	DT	P-O3'-C3'	5.08	125.79	119.70
68	2S	1070	DA	O4'-C1'-C2'	-5.07	101.84	105.90
71	2V	1042	DT	P-O3'-C3'	5.07	125.79	119.70
18	1S	22	DA	O4'-C1'-C2'	-5.07	101.84	105.90
100	3N	7367	DC	O4'-C1'-C2'	-5.07	101.84	105.90
100	3N	3538	DT	O4'-C1'-C2'	-5.07	101.85	105.90
100	3N	7833	DG	O4'-C1'-C2'	-5.07	101.84	105.90
101	3A	2106	DG	N1-C6-O6	5.07	122.94	119.90
100	3N	7046	DG	O4'-C4'-C3'	-5.07	102.47	104.50
105	3E	2105	DG	O4'-C1'-C2'	-5.07	101.85	105.90
100	3N	5510	DT	P-O3'-C3'	5.06	125.77	119.70
100	3N	4603	DT	O4'-C1'-C2'	-5.06	101.85	105.90
74	2Y	1051	DC	P-O5'-C5'	5.05	128.99	120.90
9	1I	16	DC	O4'-C1'-C2'	-5.05	101.86	105.90
78	2c	1061	DG	C8-N9-C1'	-5.05	120.44	127.00
86	2k	1079	DT	P-O3'-C3'	5.05	125.76	119.70
100	3N	3287	DG	C1'-O4'-C4'	-5.04	105.06	110.10
54	2D	1061	DT	C1'-O4'-C4'	-5.04	105.06	110.10
100	3N	3659	DG	C1'-O4'-C4'	-5.04	105.06	110.10
100	3N	4416	DA	O4'-C1'-C2'	-5.04	101.86	105.90
69	2T	1041	DG	C5-C6-O6	-5.04	125.58	128.60
101	3A	2106	DG	C5-C6-O6	-5.04	125.58	128.60
27	1b	9	DG	O4'-C1'-C2'	-5.04	101.87	105.90
100	3N	3685	DA	O4'-C1'-C2'	-5.04	101.87	105.90
100	3N	7033	DG	O4'-C1'-C2'	-5.04	101.87	105.90
17	1R	40	DG	P-O3'-C3'	5.03	125.74	119.70
69	2T	1041	DG	O4'-C1'-C2'	-5.03	101.87	105.90
100	3N	8217	DG	O4'-C1'-C2'	-5.03	101.87	105.90
100	3N	4668	DG	O4'-C1'-C2'	-5.03	101.87	105.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
100	3N	8046	DG	C1'-O4'-C4'	-5.03	105.07	110.10
100	3N	4436	DA	C1'-O4'-C4'	-5.03	105.07	110.10
44	1s	1016	DA	C1'-O4'-C4'	-5.03	105.07	110.10
100	3N	5198	DT	O4'-C1'-C2'	-5.03	101.88	105.90
100	3N	6774	DT	P-O3'-C3'	5.03	125.73	119.70
103	3C	2097	DC	O4'-C1'-N1	5.03	111.52	108.00
100	3N	3357	DC	C2-N1-C1'	5.03	124.33	118.80
100	3N	3955	DC	P-O3'-C3'	5.03	125.73	119.70
100	3N	4308	DA	O4'-C1'-C2'	-5.03	101.88	105.90
83	2h	1065	DA	O4'-C1'-C2'	-5.02	101.88	105.90
100	3N	4082	DA	N1-C6-N6	-5.02	115.59	118.60
100	3N	3603	DG	O4'-C1'-N9	5.02	111.52	108.00
3	1C	1	DA	C1'-O4'-C4'	-5.02	105.08	110.10
100	3N	7107	DG	O4'-C1'-C2'	-5.02	101.88	105.90
79	2d	1046	DT	P-O3'-C3'	5.02	125.72	119.70
100	3N	6694	DA	O4'-C1'-C2'	-5.02	101.89	105.90
100	3N	4452	DG	O4'-C1'-C2'	-5.02	101.89	105.90
103	3C	2100	DA	P-O3'-C3'	5.02	125.72	119.70
41	1p	1029	DG	O4'-C1'-C2'	-5.01	101.89	105.90
100	3N	3343	DG	O4'-C1'-N9	5.01	111.51	108.00
100	3N	3206	DG	O4'-C1'-C2'	-5.01	101.89	105.90
100	3N	5229	DG	O4'-C1'-C2'	-5.01	101.89	105.90
100	3N	8110	DC	P-O3'-C3'	5.01	125.71	119.70
49	1x	1023	DT	P-O3'-C3'	5.01	125.71	119.70
55	2E	1075	DG	C1'-O4'-C4'	-5.00	105.10	110.10
56	2F	1049	DA	O4'-C1'-C2'	-5.00	101.90	105.90
12	1L	2	DG	P-O3'-C3'	5.00	125.70	119.70
80	2e	1049	DA	O4'-C1'-C2'	-5.00	101.90	105.90
100	3N	7625	DG	C1'-O4'-C4'	-5.00	105.10	110.10

There are no chirality outliers.

All (390) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	1A	40	DT	Sidechain
1	1A	49	DA	Sidechain
2	1B	10	DG	Sidechain
2	1B	11	DA	Sidechain
2	1B	14	DT	Sidechain
2	1B	16	DA	Sidechain
2	1B	3	DG	Sidechain
2	1B	4	DG	Sidechain

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Mol	Chain	Res	Type	Group
2	1B	6	DG	Sidechain
2	1B	7	DG	Sidechain
2	1B	9	DG	Sidechain
4	1D	10	DG	Sidechain
4	1D	16	DT	Sidechain
4	1D	3	DG	Sidechain
4	1D	48	DA	Sidechain
4	1D	9	DG	Sidechain
5	1E	12	DG	Sidechain
5	1E	27	DC	Sidechain
5	1E	35	DT	Sidechain
6	1F	28	DA	Sidechain
6	1F	3	DG	Sidechain
6	1F	46	DG	Sidechain
6	1F	6	DG	Sidechain
6	1F	8	DA	Sidechain
7	1G	9	DG	Sidechain
8	1H	13	DA	Sidechain
8	1H	14	DC	Sidechain
8	1H	40	DT	Sidechain
8	1H	48	DG	Sidechain
9	1I	10	DG	Sidechain
9	1I	12	DG	Sidechain
9	1I	13	DG	Sidechain
9	1I	15	DG	Sidechain
9	1I	6	DG	Sidechain
9	1I	7	DG	Sidechain
10	1J	24	DA	Sidechain
11	1K	12	DG	Sidechain
11	1K	15	DG	Sidechain
11	1K	3	DG	Sidechain
11	1K	4	DG	Sidechain
11	1K	46	DG	Sidechain
11	1K	6	DG	Sidechain
11	1K	7	DG	Sidechain
11	1K	9	DG	Sidechain
12	1L	8	DA	Sidechain
13	1M	25	DG	Sidechain
14	1O	1	DA	Sidechain
14	1O	10	DA	Sidechain
14	1O	33	DT	Sidechain
14	1O	7	DA	Sidechain

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Mol	Chain	Res	Type	Group
14	1O	8	DC	Sidechain
15	1P	10	DG	Sidechain
15	1P	12	DG	Sidechain
15	1P	13	DC	Sidechain
15	1P	3	DG	Sidechain
15	1P	4	DG	Sidechain
15	1P	41	DA	Sidechain
15	1P	45	DA	Sidechain
15	1P	46	DG	Sidechain
15	1P	9	DG	Sidechain
16	1Q	28	DA	Sidechain
17	1R	23	DG	Sidechain
17	1R	46	DC	Sidechain
17	1R	48	DG	Sidechain
18	1S	17	DA	Sidechain
18	1S	32	DA	Sidechain
20	1U	17	DC	Sidechain
22	1W	7	DT	Sidechain
23	1X	10	DT	Sidechain
23	1X	25	DT	Sidechain
23	1X	40	DG	Sidechain
23	1X	48	DG	Sidechain
25	1Z	14	DT	Sidechain
26	1a	12	DA	Sidechain
26	1a	17	DT	Sidechain
26	1a	46	DA	Sidechain
26	1a	47	DG	Sidechain
27	1b	16	DT	Sidechain
27	1b	4	DT	Sidechain
29	1d	24	DC	Sidechain
31	1f	1	DC	Sidechain
32	1g	14	DG	Sidechain
33	1h	2	DA	Sidechain
33	1h	23	DG	Sidechain
33	1h	48	DA	Sidechain
34	1i	32	DC	Sidechain
35	1j	17	DC	Sidechain
36	1k	16	DC	Sidechain
36	1k	5	DG	Sidechain
36	1k	9	DA	Sidechain
37	1l	1	DT	Sidechain
37	1l	16	DG	Sidechain

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Mol	Chain	Res	Type	Group
39	1n	1050	DC	Sidechain
40	1o	1024	DC	Sidechain
40	1o	1042	DC	Sidechain
41	1p	1043	DG	Sidechain
41	1p	1050	DA	Sidechain
42	1q	1008	DG	Sidechain
42	1q	1023	DC	Sidechain
42	1q	1040	DT	Sidechain
44	1s	1021	DC	Sidechain
44	1s	1031	DT	Sidechain
44	1s	1041	DT	Sidechain
46	1u	1063	DG	Sidechain
47	1v	1030	DT	Sidechain
48	1w	1021	DG	Sidechain
48	1w	1025	DG	Sidechain
48	1w	1028	DT	Sidechain
48	1w	1036	DC	Sidechain
52	2B	1032	DC	Sidechain
52	2B	1055	DA	Sidechain
52	2B	1058	DG	Sidechain
52	2B	1064	DT	Sidechain
53	2C	1080	DT	Sidechain
54	2D	1061	DT	Sidechain
56	2F	1025	DT	Sidechain
56	2F	1041	DG	Sidechain
56	2F	1042	DG	Sidechain
56	2F	1046	DA	Sidechain
56	2F	1052	DT	Sidechain
57	2G	1065	DC	Sidechain
57	2G	1072	DA	Sidechain
58	2H	1072	DA	Sidechain
60	2J	1073	DG	Sidechain
50	2N	1075	DT	Sidechain
50	2N	1076	DT	Sidechain
64	2O	1059	DG	Sidechain
64	2O	1061	DA	Sidechain
64	2O	1065	DA	Sidechain
65	2P	1054	DC	Sidechain
65	2P	1056	DA	Sidechain
65	2P	1064	DA	Sidechain
66	2Q	1057	DT	Sidechain
66	2Q	1081	DA	Sidechain

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Mol	Chain	Res	Type	Group
67	2R	1046	DT	Sidechain
67	2R	1061	DC	Sidechain
68	2S	1020	DG	Sidechain
68	2S	1024	DA	Sidechain
70	2U	1039	DG	Sidechain
71	2V	1067	DG	Sidechain
72	2W	1056	DA	Sidechain
72	2W	1063	DT	Sidechain
73	2X	1033	DT	Sidechain
74	2Y	1050	DC	Sidechain
75	2Z	1065	DT	Sidechain
77	2b	1058	DT	Sidechain
77	2b	1087	DA	Sidechain
77	2b	1095	DA	Sidechain
78	2c	1061	DG	Sidechain
78	2c	1069	DT	Sidechain
79	2d	1062	DC	Sidechain
80	2e	1068	DT	Sidechain
82	2g	1066	DA	Sidechain
83	2h	1057	DG	Sidechain
83	2h	1070	DT	Sidechain
83	2h	1080	DG	Sidechain
83	2h	1102	DA	Sidechain
84	2i	1039	DT	Sidechain
84	2i	1056	DA	Sidechain
84	2i	1063	DA	Sidechain
85	2j	1048	DG	Sidechain
85	2j	1049	DT	Sidechain
87	2l	1018	DA	Sidechain
87	2l	1033	DG	Sidechain
88	2m	2074	DA	Sidechain
89	2n	2081	DT	Sidechain
90	2o	2067	DT	Sidechain
91	2p	2060	DA	Sidechain
92	2q	2063	DG	Sidechain
92	2q	2071	DC	Sidechain
92	2q	2086	DA	Sidechain
92	2q	2087	DA	Sidechain
93	2r	2054	DG	Sidechain
93	2r	2055	DC	Sidechain
95	2t	2070	DA	Sidechain
96	2u	2087	DG	Sidechain

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Mol	Chain	Res	Type	Group
97	2v	2056	DG	Sidechain
97	2v	2062	DT	Sidechain
98	2w	2088	DA	Sidechain
98	2w	2091	DA	Sidechain
98	2w	2099	DG	Sidechain
101	3A	2117	DA	Sidechain
101	3A	2120	DG	Sidechain
102	3B	2109	DG	Sidechain
103	3C	2098	DC	Sidechain
103	3C	2104	DG	Sidechain
104	3D	2087	DT	Sidechain
104	3D	2102	DC	Sidechain
104	3D	2117	DA	Sidechain
106	3F	2102	DT	Sidechain
106	3F	2107	DG	Sidechain
106	3F	2119	DT	Sidechain
106	3F	2142	DA	Sidechain
107	3G	2075	DA	Sidechain
108	3H	2102	DT	Sidechain
108	3H	2107	DT	Sidechain
108	3H	2129	DC	Sidechain
108	3H	2132	DG	Sidechain
108	3H	2136	DA	Sidechain
109	3I	2114	DA	Sidechain
109	3I	2115	DA	Sidechain
110	3J	2049	DC	Sidechain
110	3J	2054	DA	Sidechain
112	3K	2049	DG	Sidechain
112	3K	2050	DA	Sidechain
112	3K	2064	DG	Sidechain
114	3M	2072	DT	Sidechain
114	3M	2088	DA	Sidechain
100	3N	3083	DG	Sidechain
100	3N	3085	DT	Sidechain
100	3N	3086	DT	Sidechain
100	3N	3106	DA	Sidechain
100	3N	3108	DT	Sidechain
100	3N	3140	DA	Sidechain
100	3N	3158	DA	Sidechain
100	3N	3182	DT	Sidechain
100	3N	3184	DT	Sidechain
100	3N	3216	DT	Sidechain

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Mol	Chain	Res	Type	Group
100	3N	3279	DG	Sidechain
100	3N	3312	DT	Sidechain
100	3N	3335	DA	Sidechain
100	3N	3343	DG	Sidechain
100	3N	3441	DG	Sidechain
100	3N	3462	DA	Sidechain
100	3N	3475	DC	Sidechain
100	3N	3506	DT	Sidechain
100	3N	3528	DG	Sidechain
100	3N	3539	DT	Sidechain
100	3N	3594	DT	Sidechain
100	3N	3595	DC	Sidechain
100	3N	3626	DT	Sidechain
100	3N	3681	DA	Sidechain
100	3N	3683	DT	Sidechain
100	3N	3684	DT	Sidechain
100	3N	3723	DT	Sidechain
100	3N	3727	DA	Sidechain
100	3N	3729	DC	Sidechain
100	3N	3734	DA	Sidechain
100	3N	3763	DT	Sidechain
100	3N	3812	DA	Sidechain
100	3N	3815	DC	Sidechain
100	3N	3818	DT	Sidechain
100	3N	3824	DA	Sidechain
100	3N	3876	DA	Sidechain
100	3N	3882	DG	Sidechain
100	3N	3884	DA	Sidechain
100	3N	3903	DG	Sidechain
100	3N	3914	DC	Sidechain
100	3N	3924	DC	Sidechain
100	3N	3964	DA	Sidechain
100	3N	3978	DT	Sidechain
100	3N	4001	DA	Sidechain
100	3N	4003	DG	Sidechain
100	3N	4012	DC	Sidechain
100	3N	4016	DA	Sidechain
100	3N	4037	DT	Sidechain
100	3N	4050	DT	Sidechain
100	3N	4081	DA	Sidechain
100	3N	4103	DC	Sidechain
100	3N	4106	DA	Sidechain

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Mol	Chain	Res	Type	Group
100	3N	4132	DT	Sidechain
100	3N	4203	DG	Sidechain
100	3N	4211	DA	Sidechain
100	3N	4226	DT	Sidechain
100	3N	4256	DT	Sidechain
100	3N	4259	DC	Sidechain
100	3N	4300	DC	Sidechain
100	3N	4333	DA	Sidechain
100	3N	4387	DT	Sidechain
100	3N	4404	DG	Sidechain
100	3N	4464	DG	Sidechain
100	3N	4467	DT	Sidechain
100	3N	4469	DT	Sidechain
100	3N	4514	DT	Sidechain
100	3N	4523	DA	Sidechain
100	3N	4528	DC	Sidechain
100	3N	4631	DT	Sidechain
100	3N	4646	DA	Sidechain
100	3N	4649	DT	Sidechain
100	3N	4723	DG	Sidechain
100	3N	4736	DT	Sidechain
100	3N	4757	DA	Sidechain
100	3N	4776	DT	Sidechain
100	3N	4805	DT	Sidechain
100	3N	4815	DT	Sidechain
100	3N	4843	DC	Sidechain
100	3N	4867	DA	Sidechain
100	3N	4897	DT	Sidechain
100	3N	4916	DC	Sidechain
100	3N	5014	DG	Sidechain
100	3N	5055	DG	Sidechain
100	3N	5081	DT	Sidechain
100	3N	5108	DA	Sidechain
100	3N	5122	DT	Sidechain
100	3N	5144	DT	Sidechain
100	3N	5145	DA	Sidechain
100	3N	5179	DC	Sidechain
100	3N	5243	DG	Sidechain
100	3N	5269	DT	Sidechain
100	3N	5281	DT	Sidechain
100	3N	5364	DG	Sidechain
100	3N	5377	DA	Sidechain

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Mol	Chain	Res	Type	Group
100	3N	5403	DG	Sidechain
100	3N	5426	DT	Sidechain
100	3N	5435	DA	Sidechain
100	3N	5442	DT	Sidechain
100	3N	5472	DC	Sidechain
100	3N	5493	DG	Sidechain
100	3N	5565	DT	Sidechain
100	3N	6625	DT	Sidechain
100	3N	6644	DT	Sidechain
100	3N	6646	DA	Sidechain
100	3N	6654	DT	Sidechain
100	3N	6725	DT	Sidechain
100	3N	6727	DT	Sidechain
100	3N	6774	DT	Sidechain
100	3N	6781	DG	Sidechain
100	3N	6812	DT	Sidechain
100	3N	6829	DT	Sidechain
100	3N	6834	DG	Sidechain
100	3N	6838	DG	Sidechain
100	3N	6844	DT	Sidechain
100	3N	6845	DT	Sidechain
100	3N	6899	DT	Sidechain
100	3N	6908	DC	Sidechain
100	3N	6931	DT	Sidechain
100	3N	6932	DA	Sidechain
100	3N	6991	DT	Sidechain
100	3N	7005	DC	Sidechain
100	3N	7019	DT	Sidechain
100	3N	7038	DC	Sidechain
100	3N	7142	DA	Sidechain
100	3N	7190	DT	Sidechain
100	3N	7195	DT	Sidechain
100	3N	7211	DT	Sidechain
100	3N	7270	DT	Sidechain
100	3N	7284	DA	Sidechain
100	3N	7285	DA	Sidechain
100	3N	7335	DA	Sidechain
100	3N	7337	DT	Sidechain
100	3N	7358	DT	Sidechain
100	3N	7391	DG	Sidechain
100	3N	7408	DC	Sidechain
100	3N	7443	DG	Sidechain

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Mol	Chain	Res	Type	Group
100	3N	7445	DC	Sidechain
100	3N	7459	DG	Sidechain
100	3N	7567	DA	Sidechain
100	3N	7635	DA	Sidechain
100	3N	7673	DT	Sidechain
100	3N	7690	DA	Sidechain
100	3N	7703	DC	Sidechain
100	3N	7722	DT	Sidechain
100	3N	7727	DT	Sidechain
100	3N	7751	DT	Sidechain
100	3N	7767	DG	Sidechain
100	3N	7777	DG	Sidechain
100	3N	7778	DA	Sidechain
100	3N	7784	DC	Sidechain
100	3N	7893	DT	Sidechain
100	3N	7931	DC	Sidechain
100	3N	7934	DT	Sidechain
100	3N	7944	DG	Sidechain
100	3N	8024	DG	Sidechain
100	3N	8027	DG	Sidechain
100	3N	8030	DT	Sidechain
100	3N	8055	DG	Sidechain
100	3N	8071	DC	Sidechain
100	3N	8079	DA	Sidechain
100	3N	8085	DG	Sidechain
100	3N	8087	DT	Sidechain
100	3N	8112	DG	Sidechain
100	3N	8116	DT	Sidechain
100	3N	8123	DT	Sidechain
100	3N	8127	DA	Sidechain
100	3N	8130	DG	Sidechain
100	3N	8208	DG	Sidechain
100	3N	8231	DA	Sidechain
100	3N	8246	DT	Sidechain
100	3N	8301	DG	Sidechain
100	3N	8306	DT	Sidechain
100	3N	8313	DT	Sidechain
100	3N	8318	DA	Sidechain
100	3N	8361	DT	Sidechain
100	3N	8383	DC	Sidechain
115	3O	2106	DT	Sidechain
117	3Q	2099	DA	Sidechain

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Mol	Chain	Res	Type	Group
117	3Q	2101	DT	Sidechain
117	3Q	2109	DG	Sidechain
117	3Q	2110	DA	Sidechain
111	3S	2107	DT	Sidechain

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1A	1082	0	587	0	0
2	1B	1137	0	619	0	0
3	1C	327	0	180	0	0
4	1D	1220	0	669	0	0
5	1E	1052	0	574	1	0
6	1F	950	0	521	1	0
7	1G	321	0	183	1	0
8	1H	970	0	541	0	0
9	1I	971	0	531	1	0
10	1J	492	0	276	0	0
11	1K	945	0	519	0	0
12	1L	333	0	179	0	0
13	1M	645	0	358	0	0
14	1O	808	0	448	1	0
15	1P	948	0	518	0	0
16	1Q	752	0	413	0	0
17	1R	976	0	539	0	0
18	1S	763	0	419	1	0
19	1T	318	0	181	0	0
20	1U	826	0	448	0	0
21	1V	521	0	298	0	0
22	1W	830	0	454	0	0
23	1X	983	0	538	1	0
24	1Y	544	0	308	0	0
25	1Z	531	0	294	0	0
26	1a	965	0	533	0	0
27	1b	665	0	361	0	0
28	1c	820	0	455	0	0
29	1d	826	0	452	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	1e	524	0	294	0	0
31	1f	804	0	453	0	0
32	1g	982	0	539	0	0
33	1h	993	0	542	0	0
34	1i	986	0	544	0	0
35	1j	659	0	360	0	0
36	1k	827	0	456	0	0
37	1l	980	0	545	0	0
38	1m	328	0	183	0	0
39	1n	1148	0	631	0	0
40	1o	821	0	450	0	0
41	1p	816	0	449	0	0
42	1q	981	0	541	0	0
43	1r	654	0	359	0	0
44	1s	649	0	363	0	0
45	1t	651	0	361	0	0
46	1u	982	0	544	0	0
47	1v	319	0	181	0	0
48	1w	808	0	452	0	0
49	1x	329	0	180	0	0
50	2N	736	0	409	0	0
51	2A	665	0	359	1	0
52	2B	975	0	538	1	0
53	2C	527	0	301	0	0
54	2D	652	0	362	0	0
55	2E	816	0	455	0	0
56	2F	988	0	545	0	0
57	2G	820	0	455	0	0
58	2H	807	0	452	0	0
59	2I	328	0	183	0	0
60	2J	599	0	327	0	0
61	2K	495	0	270	1	0
62	2L	653	0	363	0	0
63	2M	488	0	270	0	0
64	2O	532	0	297	2	0
65	2P	822	0	448	0	0
66	2Q	818	0	453	0	0
67	2R	822	0	453	0	0
68	2S	1192	0	650	0	0
69	2T	494	0	272	0	0
70	2U	1059	0	589	0	0
71	2V	815	0	457	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
72	2W	987	0	543	0	0
73	2X	974	0	539	0	0
74	2Y	656	0	360	0	0
75	2Z	818	0	456	0	0
76	2a	1179	0	656	0	0
77	2b	1149	0	633	0	0
78	2c	914	0	511	0	0
79	2d	1075	0	580	0	0
80	2e	766	0	421	0	0
81	2f	976	0	540	0	0
82	2g	972	0	538	0	0
83	2h	1156	0	631	0	0
84	2i	661	0	359	0	0
85	2j	326	0	183	0	0
86	2k	652	0	361	0	0
87	2l	980	0	537	0	0
88	2m	984	0	543	0	0
89	2n	325	0	184	0	0
90	2o	653	0	366	0	0
91	2p	656	0	362	0	0
92	2q	805	0	454	0	0
93	2r	485	0	272	0	0
94	2s	655	0	358	0	0
95	2t	824	0	448	0	0
96	2u	652	0	361	0	0
97	2v	651	0	367	0	0
98	2w	974	0	526	0	0
99	2x	320	0	180	0	0
100	3N	88890	0	49198	32	0
101	3A	841	0	447	0	0
102	3B	818	0	449	1	0
103	3C	982	0	541	0	0
104	3D	999	0	541	0	0
105	3E	991	0	536	0	0
106	3F	1131	0	635	0	0
107	3G	326	0	183	0	0
108	3H	1142	0	632	0	0
109	3I	736	0	405	0	0
110	3J	714	0	395	0	0
111	3S	655	0	363	0	0
112	3K	988	0	537	1	0
113	3L	760	0	414	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
114	3M	1129	0	620	0	0
115	3O	985	0	541	1	0
116	3P	785	0	430	0	0
117	3Q	539	0	290	0	0
118	3R	666	0	363	0	0
All	All	180167	0	99520	45	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 0.

All (45) 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)
100:3N:3913:DA:H2''	100:3N:3914:DC:C6	2.46	0.50
18:1S:8:DT:H1'	64:2O:1060:DC:C5	2.48	0.49
61:2K:1023:DG:H2'	61:2K:1024:DC:C5	2.48	0.48
102:3B:2120:DG:H2'	102:3B:2121:DC:C6	2.49	0.47
100:3N:3568:DA:H2'	100:3N:3569:DC:C6	2.49	0.47
100:3N:6882:DA:H2'	100:3N:6883:DC:C6	2.50	0.47
100:3N:6741:DA:H2'	100:3N:6742:DC:C6	2.50	0.47
100:3N:3595:DC:H2'	100:3N:3596:DC:C6	2.50	0.47
23:1X:10:DT:H2'	23:1X:11:DC:C6	2.50	0.46
100:3N:3728:DG:H2'	100:3N:3729:DC:C5	2.50	0.46
100:3N:3357:DC:H2''	100:3N:3358:DC:C6	2.51	0.46
112:3K:2057:DC:H2'	112:3K:2058:DC:C6	2.51	0.45
6:1F:22:DA:H2''	6:1F:23:DC:C6	4.21	0.45
100:3N:3280:DC:H2'	100:3N:3281:DC:C6	2.52	0.45
5:1E:38:DA:H2''	5:1E:39:DC:C6	2.51	0.45
100:3N:4102:DA:H2'	100:3N:4103:DC:C5	2.51	0.45
100:3N:7532:DC:H2'	100:3N:7533:DC:C6	2.52	0.45
100:3N:7665:DA:H2'	100:3N:7666:DC:C6	2.52	0.45
51:2A:1061:DA:H2'	51:2A:1062:DC:C6	2.52	0.44
100:3N:7212:DT:H2''	100:3N:7213:DC:C6	2.53	0.44
100:3N:4715:DG:H2'	100:3N:4716:DC:C6	2.52	0.43
100:3N:8116:DT:H2''	100:3N:8117:DC:C6	2.53	0.43
100:3N:3305:DT:H2''	100:3N:3306:DT:C6	2.53	0.43
64:2O:1059:DG:H21	100:3N:5132:DA:H62	1.66	0.43
100:3N:6885:DT:H2''	100:3N:6886:DC:C6	2.54	0.43
100:3N:3980:DA:H2'	100:3N:3981:DC:C6	2.54	0.43
100:3N:6973:DT:H2''	100:3N:6974:DC:C6	2.55	0.42
7:1G:9:DG:H2'	7:1G:10:DC:C5	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
100:3N:3336:DC:H2'	100:3N:3337:DC:C6	2.55	0.42
100:3N:6917:DT:H2''	100:3N:6918:DC:C6	2.55	0.42
100:3N:7426:DG:H2''	100:3N:7427:DT:C6	2.55	0.42
100:3N:4059:DT:H2''	100:3N:4060:DT:C6	2.55	0.41
100:3N:4562:DG:H3'	100:3N:4563:DC:C5'	2.50	0.41
100:3N:3336:DC:H2'	100:3N:3337:DC:C5	2.55	0.41
100:3N:7218:DT:H2''	100:3N:7219:DC:C5	2.54	0.41
9:1I:21:DA:H2'	9:1I:22:DC:C6	2.55	0.41
100:3N:3917:DA:H2''	100:3N:3918:DC:C6	2.56	0.41
52:2B:1030:DA:H2'	52:2B:1031:DC:C6	2.56	0.41
14:1O:2:DC:H2''	14:1O:3:DC:C6	2.57	0.40
100:3N:7503:DA:H2'	100:3N:7504:DC:C6	2.56	0.40
100:3N:8111:DT:H2'	100:3N:8112:DG:C8	2.57	0.40
115:3O:2115:DC:H2''	115:3O:2116:DC:C6	2.56	0.40
100:3N:4970:DT:H2''	100:3N:4971:DC:C5	2.56	0.40
100:3N:4246:DT:H2''	100:3N:4247:DC:C6	2.56	0.40
100:3N:7133:DT:H2'	100:3N:7134:DC:C6	2.56	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein molecules in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein molecules in this entry.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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.

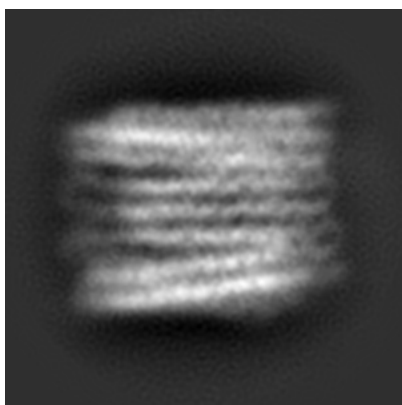
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-7304. These allow visual inspection of the internal detail of the map and identification of artifacts.

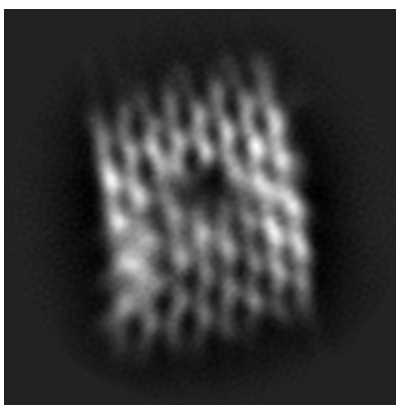
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

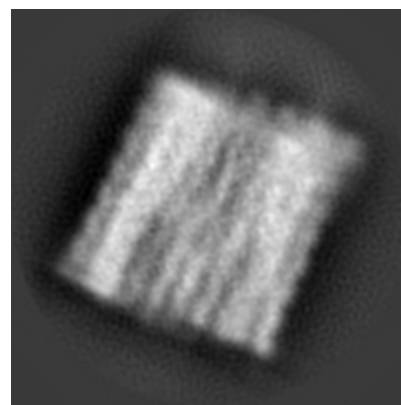
6.1.1 Primary map



X



Y



Z

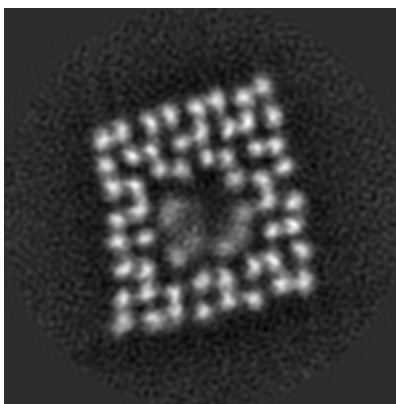
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

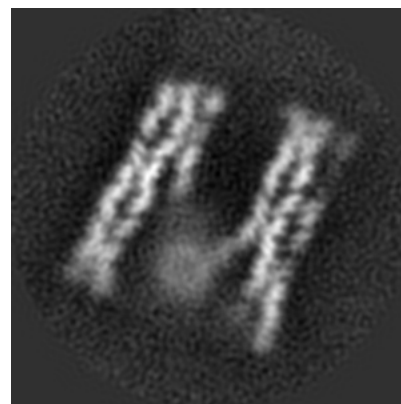
6.2.1 Primary map



X Index: 300



Y Index: 300

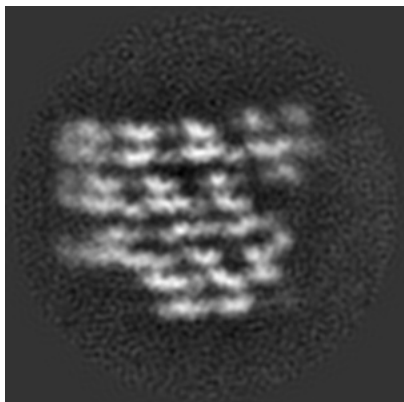


Z Index: 300

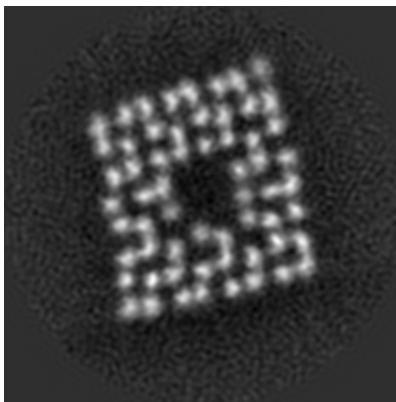
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

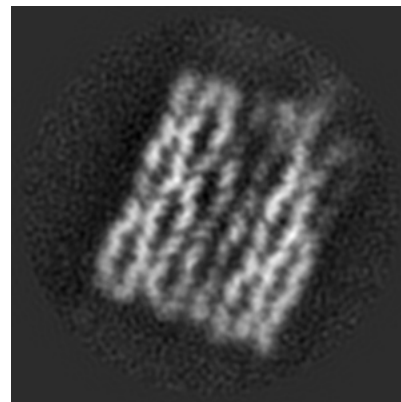
6.3.1 Primary map



X Index: 389



Y Index: 340

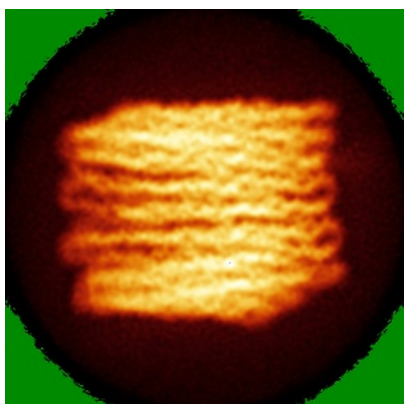


Z Index: 408

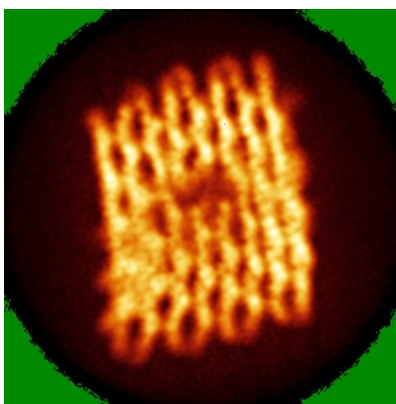
The images above show the largest variance slices of the map in three orthogonal directions.

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

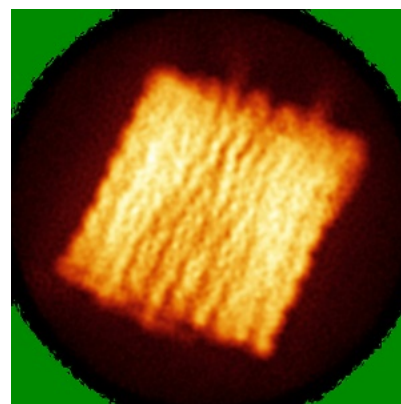
6.4.1 Primary map



X



Y

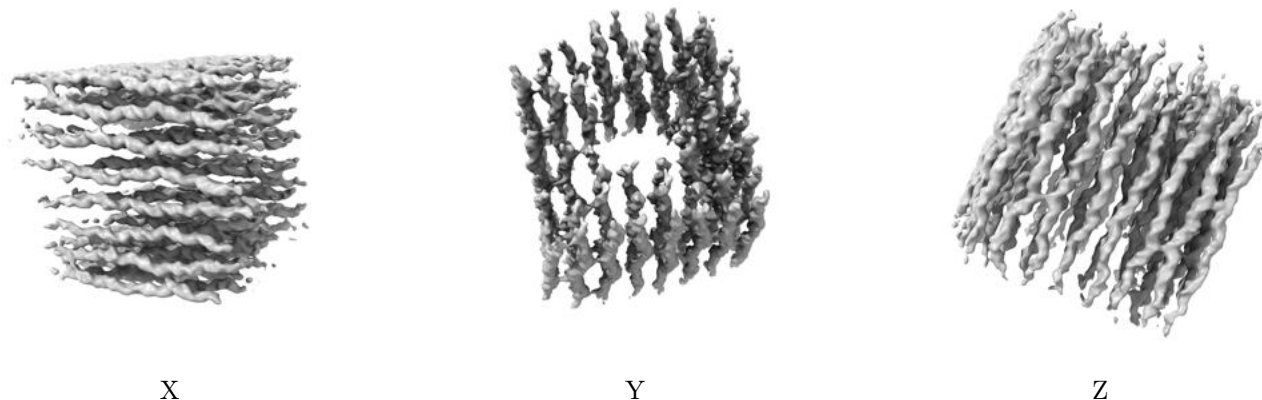


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.003. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

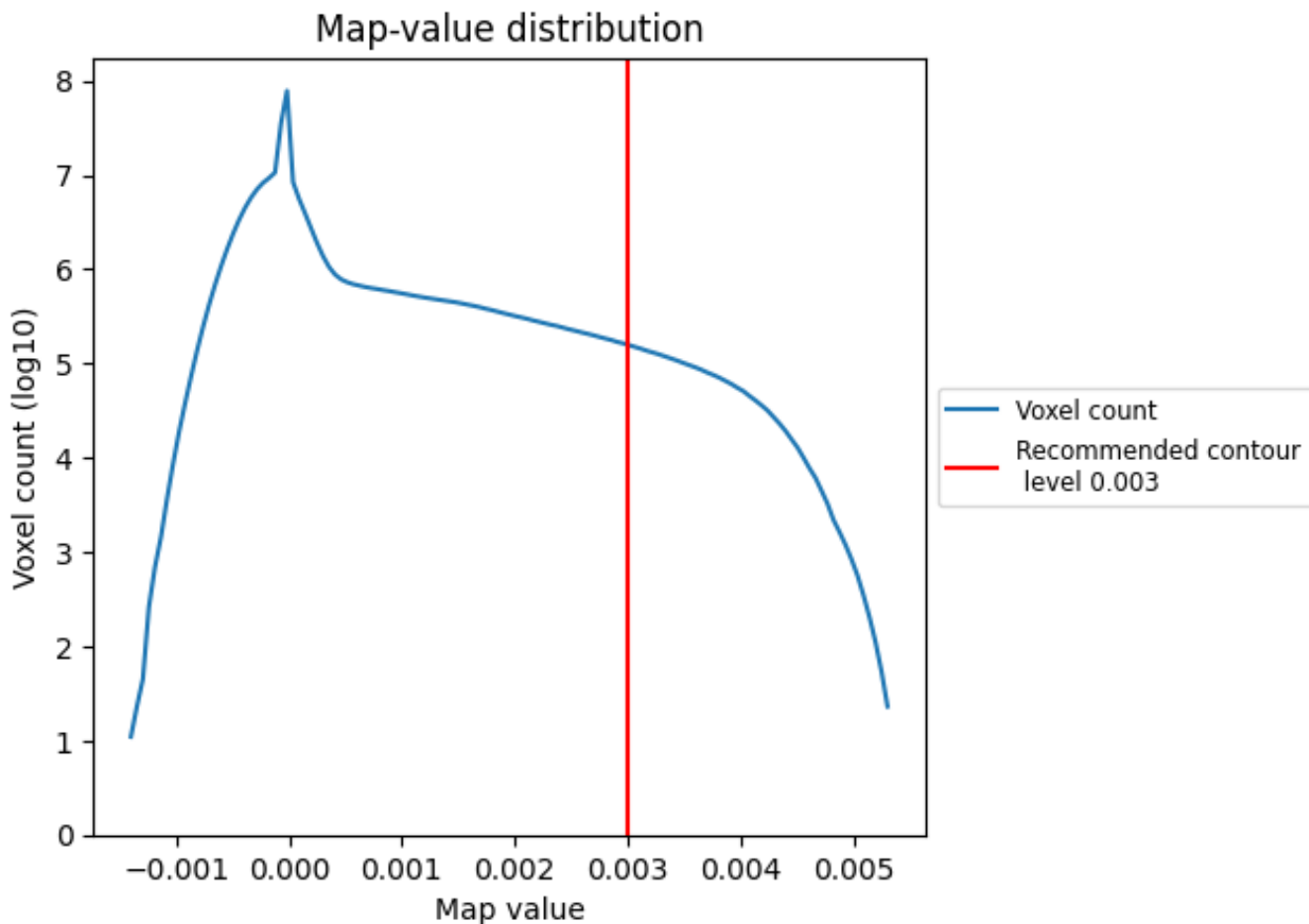
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

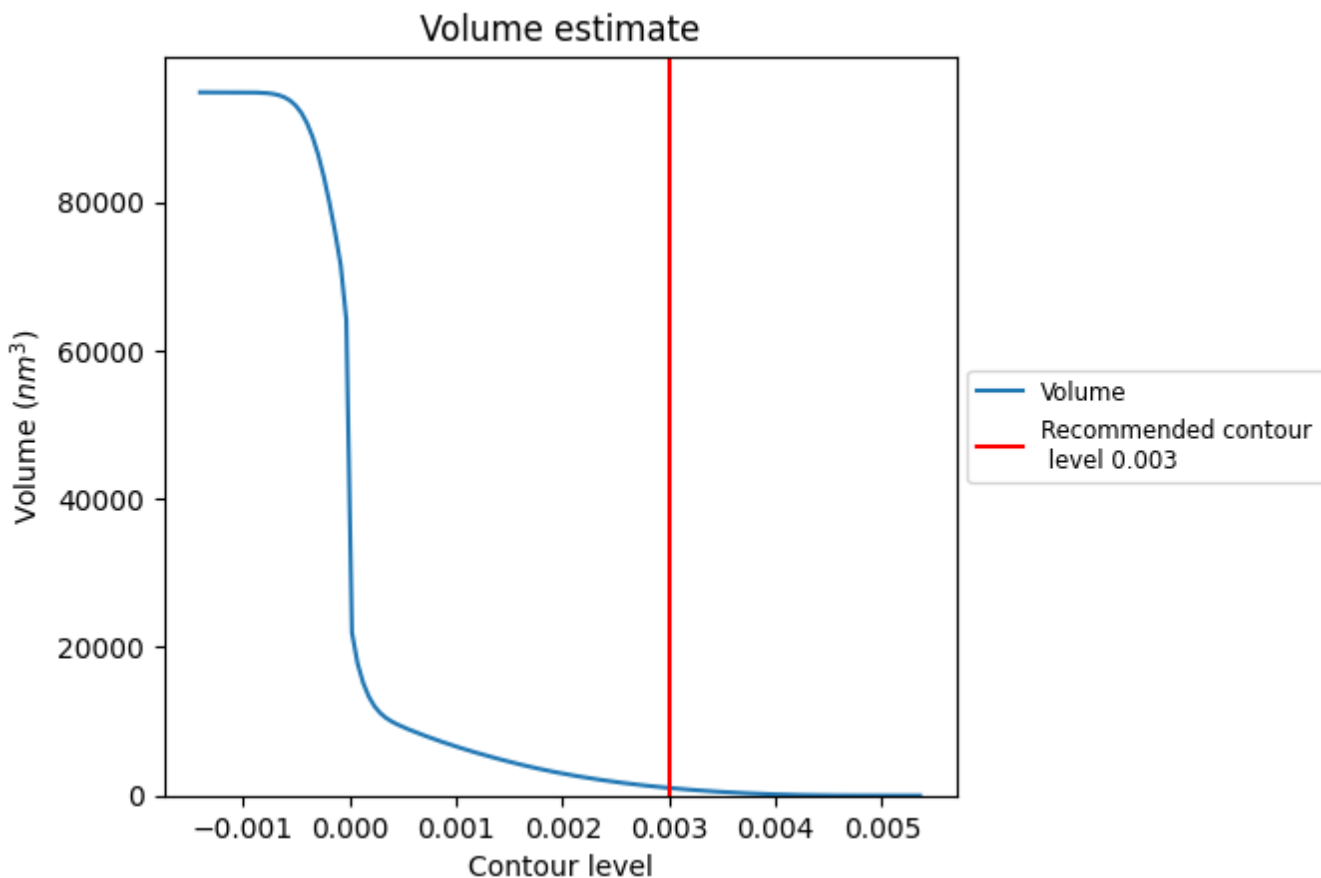
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

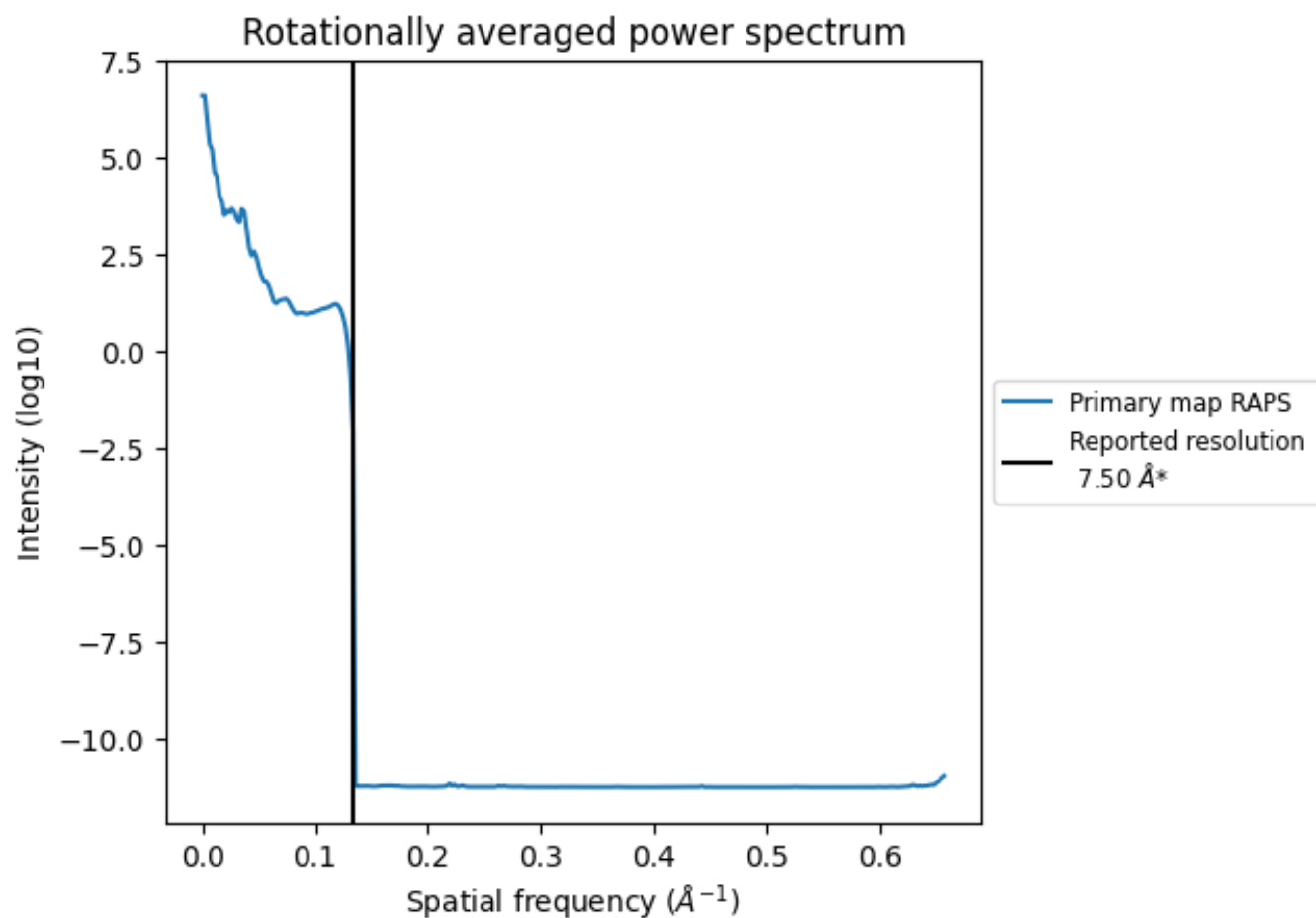
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1031 nm³; this corresponds to an approximate mass of 931 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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.133 Å⁻¹

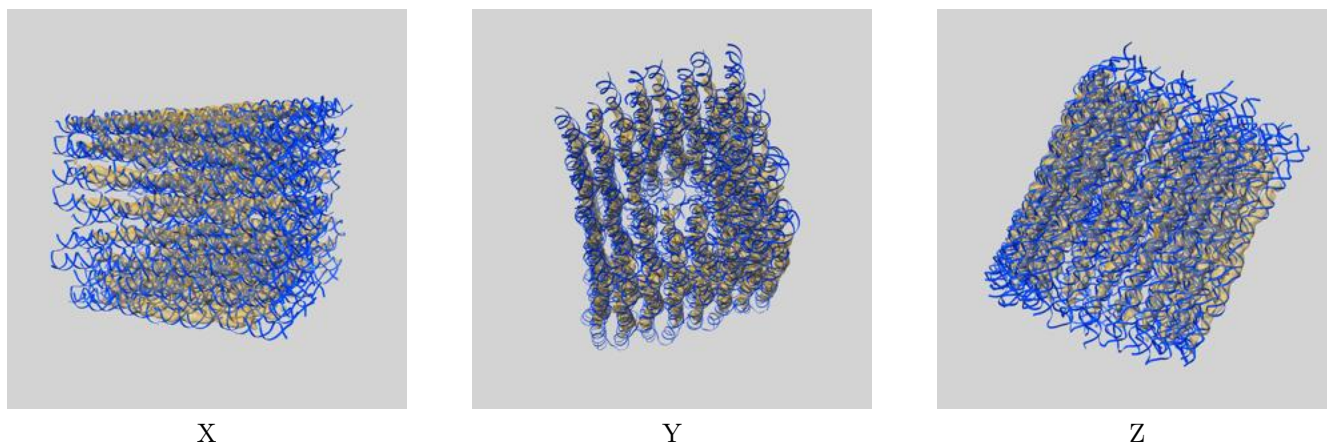
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

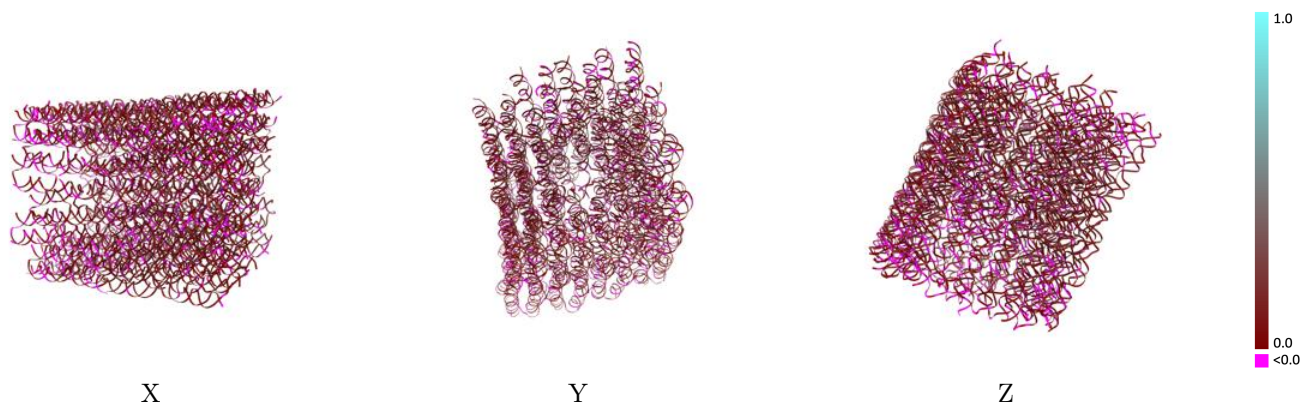
This section contains information regarding the fit between EMDB map EMD-7304 and PDB model 6BY7. Per-residue inclusion information can be found in section 3 on page 26.

9.1 Map-model overlay [i](#)



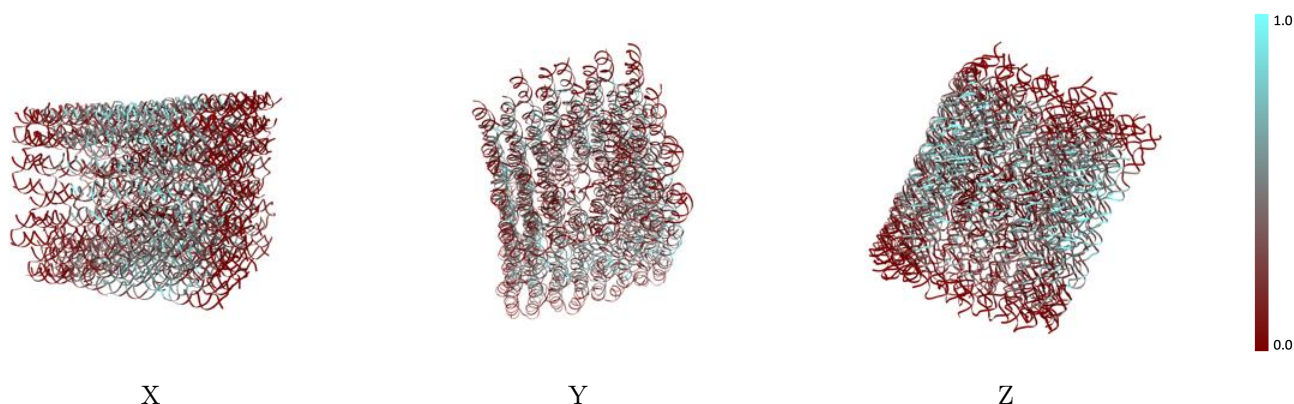
The images above show the 3D surface view of the map at the recommended contour level 0.003 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



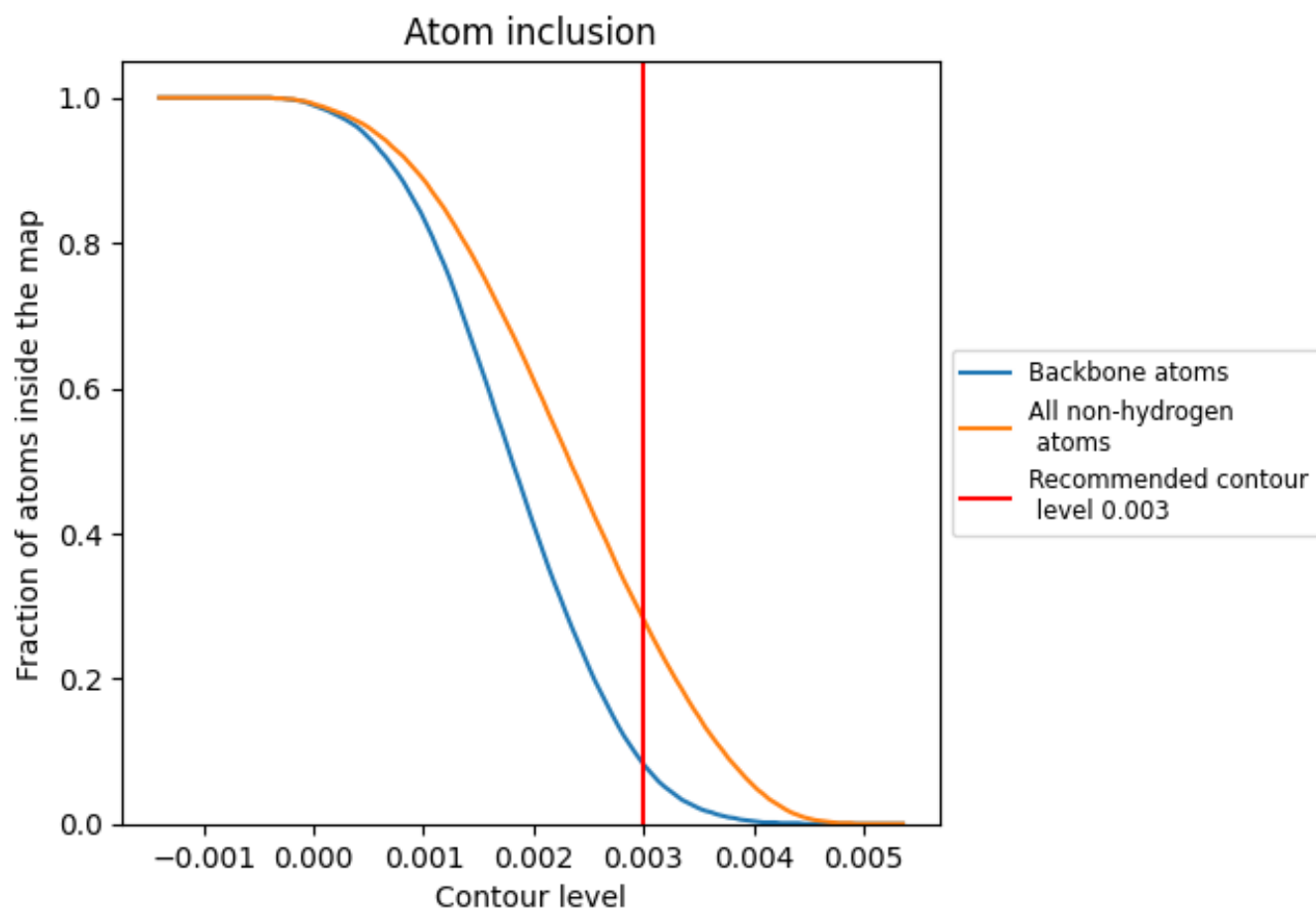
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.003).

9.4 Atom inclusion [i](#)



At the recommended contour level, 8% of all backbone atoms, 28% 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 (0.003) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.2810	0.0890
1A	0.4310	0.1180
1B	0.2710	0.0740
1C	0.0090	0.0780
1D	0.2440	0.0490
1E	0.2150	0.1140
1F	0.0000	0.0400
1G	0.1310	0.1220
1H	0.3330	0.1020
1I	0.1670	0.0980
1J	0.4170	0.1090
1K	0.0060	0.0470
1L	0.0000	0.0590
1M	0.4420	0.0990
1O	0.3720	0.0990
1P	0.0000	-0.0000
1Q	0.1900	0.1280
1R	0.3400	0.0950
1S	0.2880	0.0950
1T	0.0000	0.0930
1U	0.4590	0.0920
1V	0.0190	0.0310
1W	0.2050	0.0910
1X	0.3410	0.1020
1Y	0.1410	0.0670
1Z	0.0000	0.0670
1a	0.1320	0.0190
1b	0.4160	0.0830
1c	0.4730	0.1360
1d	0.2360	0.0650
1e	0.0000	0.0700
1f	0.4650	0.1250
1g	0.4400	0.1200
1h	0.4660	0.1120
1i	0.0270	0.0570























































































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Chain	Atom inclusion	Q-score
1j	0.3660	0.1510
1k	0.4220	0.0920
1l	0.0000	0.0510
1m	0.0150	0.0160
1n	0.4120	0.1210
1o	0.1020	0.0550
1p	0.3240	0.1090
1q	0.0650	0.0510
1r	0.4910	0.1130
1s	0.2310	0.0940
1t	0.4460	0.0900
1u	0.0370	0.0790
1v	0.0060	0.0500
1w	0.4860	0.1150
1x	0.0270	0.0500
2A	0.1130	0.0550
2B	0.3330	0.1370
2C	0.1330	0.0840
2D	0.4220	0.0860
2E	0.4060	0.0880
2F	0.4860	0.0980
2G	0.2410	0.0520
2H	0.0320	0.0470
2I	0.0000	0.0590
2J	0.1800	0.1170
2K	0.5330	0.1140
2L	0.2740	0.0640
2M	0.1070	0.0640
2N	0.3650	0.0790
2O	0.1090	0.0950
2P	0.4960	0.1150
2Q	0.4020	0.1040
2R	0.3980	0.0720
2S	0.1370	0.0570
2T	0.0470	0.0780
2U	0.4040	0.1100
2V	0.5040	0.1000
2W	0.4220	0.1050
2X	0.4410	0.1060
2Y	0.5840	0.1150
2Z	0.4140	0.1130
2a	0.1150	0.0650

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Chain	Atom inclusion	Q-score
2b	 0.5060	 0.1260
2c	 0.1120	 0.0940
2d	 0.4400	 0.1170
2e	 0.0870	 0.0930
2f	 0.4360	 0.1190
2g	 0.3300	 0.0640
2h	 0.4520	 0.0990
2i	 0.3190	 0.1180
2j	 0.0000	 0.0590
2k	 0.3600	 0.1290
2l	 0.4580	 0.1040
2m	 0.2300	 0.0840
2n	 0.0000	 0.0420
2o	 0.1590	 0.1100
2p	 0.4670	 0.1170
2q	 0.3700	 0.0680
2r	 0.2310	 0.1120
2s	 0.3540	 0.0890
2t	 0.0010	 0.0280
2u	 0.2620	 0.1180
2v	 0.4100	 0.0770
2w	 0.2390	 0.0630
2x	 0.0000	 0.0770
3A	 0.1330	 0.1130
3B	 0.4440	 0.1230
3C	 0.4110	 0.0930
3D	 0.4550	 0.1100
3E	 0.3490	 0.0990
3F	 0.5350	 0.1310
3G	 0.0030	 0.0640
3H	 0.2690	 0.1010
3I	 0.4480	 0.1130
3J	 0.0270	 0.0240
3K	 0.3320	 0.0900
3L	 0.2530	 0.0910
3M	 0.2930	 0.0720
3N	 0.2820	 0.0900
3O	 0.2050	 0.0530
3P	 0.0200	 0.0660
3Q	 0.0760	 0.0580
3R	 0.5480	 0.1200
3S	 0.2170	 0.0700