



Full wwPDB EM Validation Report ⓘ

Mar 10, 2026 – 05:58 PM UTC

PDB ID : 6BY7 / pdb_00006by7
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.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

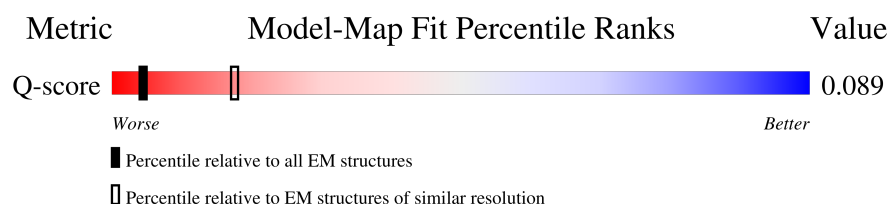
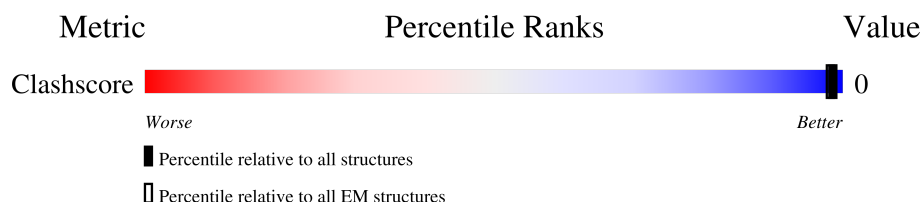
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

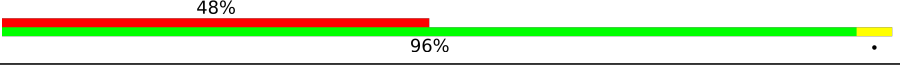
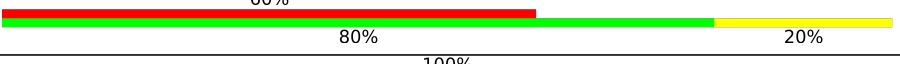
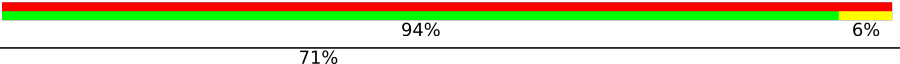
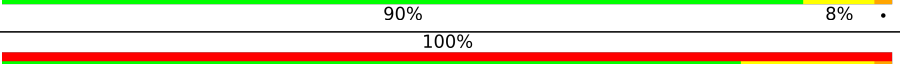
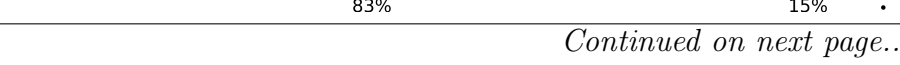
The reported resolution of this entry is 7.50 Å.

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)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Q-score	-	25397	436 (7.00 - 8.00)

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	

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Mol	Chain	Length	Quality of chain
7	1G	16	88% 81% 12% 6%
8	1H	48	56% 92% 8%
9	1I	47	83% 81% 19%
10	1J	24	58% 96% .
11	1K	46	100% 74% 24% .
12	1L	16	100% 94% 6%
13	1M	32	50% 94% 6%
14	1O	40	58% 82% 18%
15	1P	46	100% 80% 15% .
16	1Q	37	78% 95% 5%
17	1R	48	58% 90% 10%
18	1S	37	65% 89% 11%
19	1T	16	100% 100%
20	1U	40	38% 95% . .
21	1V	26	100% 100%
22	1W	40	80% 98% .
23	1X	48	56% 90% 8% .
24	1Y	27	85% 96% .
25	1Z	26	100% 96% .
26	1a	47	85% 87% 13%
27	1b	32	41% 84% 12% .
28	1c	40	32% 95% 5%
29	1d	40	75% 95% 5%
30	1e	26	100% 92% 8%
31	1f	40	38% 85% 15%

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Mol	Chain	Length	Quality of chain
32	1g	48	44% 98% .
33	1h	48	31% 94% 6%
34	1i	48	98% 92% 8%
35	1j	32	53% 97% .
36	1k	40	48% 92% 8%
37	1l	48	100% 96% .
38	1m	16	100% 94% 6%
39	1n	56	36% 93% 5% .
40	1o	40	95% 88% 12%
41	1p	40	65% 90% 10%
42	1q	48	94% 94% 6%
43	1r	32	34% 94% 6%
44	1s	32	69% 88% 12%
45	1t	32	47% 97% .
46	1u	48	100% 83% 17%
47	1v	16	100% 94% 6%
48	1w	40	40% 88% 12%
49	1x	16	94% 100%
50	2N	36	47% 92% 6% .
51	2A	32	94% 91% 6% .
52	2B	48	65% 83% 12% .
53	2C	26	88% 92% 8%
54	2D	32	50% 97% .
55	2E	40	50% 98% .
56	2F	48	42% 90% 10%

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Mol	Chain	Length	Quality of chain
57	2G	40	78% 92% 8%
58	2H	40	98% 98% .
59	2I	16	100% 100%
60	2J	29	83% 93% 7%
61	2K	24	38% 92% .
62	2L	32	69% 100%
63	2M	24	92% 100%
64	2O	26	88% 81% 12% .
65	2P	40	35% 85% 15%
66	2Q	40	58% 92% 8%
67	2R	40	42% 92% 8%
68	2S	58	86% 91% 9%
69	2T	24	96% 100%
70	2U	52	48% 98% .
71	2V	40	40% 98% .
72	2W	48	46% 96% .
73	2X	48	40% 96% .
74	2Y	32	16% 94% 6%
75	2Z	40	58% 92% 8%
76	2a	58	83% 97% .
77	2b	56	32% 91% 9%
78	2c	45	84% 96% .
79	2d	52	35% 94% 6%
80	2e	37	97% 97% .
81	2f	48	48% 100%

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Mol	Chain	Length	Quality of chain
82	2g	48	60% 94% 6%
83	2h	56	34% 93% 7%
84	2i	32	47% 91% 9%
85	2j	16	100% 81% 19%
86	2k	32	44% 100%
87	2l	48	40% 92% 6% .
88	2m	48	81% 98% .
89	2n	16	100% 88% 12%
90	2o	32	88% 97% .
91	2p	32	44% 94% 6%
92	2q	40	55% 90% 10%
93	2r	24	71% 88% 8% .
94	2s	32	56% 100%
95	2t	40	100% 88% 12%
96	2u	32	72% 94% 6%
97	2v	32	50% 84% 16%
98	2w	47	74% 77% 21% .
99	2x	16	100% 100%
100	3N	4346	66% 92% 7% .
101	3A	40	82% 95% 5%
102	3B	40	42% 92% 8%
103	3C	48	46% 94% 6%
104	3D	48	46% 92% 8%
105	3E	48	54% 96% .
106	3F	56	32% 91% 9%

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Mol	Chain	Length	Quality of chain
107	3G	16	100% 94% 6%
108	3H	56	71% 86% 14%
109	3I	36	42% 94% 6%
110	3J	35	100% 89% 11%
111	3S	32	78% 94% 6%
112	3K	48	63% 90% 10%
113	3L	37	65% 97% .
114	3M	55	65% 89% 11%
115	3O	48	75% 92% 8%
116	3P	38	100% 100%
117	3Q	26	88% 85% 12% .
118	3R	32	22% 94% 6%

2 Entry composition

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
1	1A	52	Total	C	N	O	P	0	0
			1082	516	213	302	51		

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

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

- 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
3	1C	16	Total	C	N	O	P	0	0
			327	156	66	90	15		

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

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

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

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

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

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

- 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
7	1G	16	Total	C	N	O	P	0	0
			321	155	55	96	15		

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

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

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

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

- 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
10	1J	24	Total	C	N	O	P	0	0
			492	238	86	145	23		

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

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

- 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
12	1L	16	Total	C	N	O	P	0	0
			333	158	73	87	15		

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

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

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

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

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

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

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

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

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

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

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

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

- 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
19	1T	16	Total	C	N	O	P	0	0
			318	153	57	93	15		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

- 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
34	1i	48	Total	C	N	O	P	0	0
			986	473	184	282	47		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
35	1j	32	Total	C	N	O	P	0	0
			659	314	130	184	31		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
36	1k	40	Total	C	N	O	P	0	0
			827	397	152	239	39		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
37	1l	48	Total	C	N	O	P	0	0
			980	470	175	288	47		

- 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
38	1m	16	Total	C	N	O	P	0	0
			328	157	59	97	15		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
39	1n	56	Total	C	N	O	P	0	0
			1148	548	217	328	55		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	1o	40	Total	C	N	O	P	0	0
			821	390	156	236	39		

- 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
48	1w	40	Total	C	N	O	P	0	0
			808	387	144	238	39		

- 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
49	1x	16	Total	C	N	O	P	0	0
			329	156	66	92	15		

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

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

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

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

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

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

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

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

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

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

- 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
62	2L	32	Total	C	N	O	P	0	0
			653	314	121	187	31		

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

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

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

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

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

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

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

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

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

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

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

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

- 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
76	2a	58	Total	C	N	O	P	0	0
			1179	566	214	342	57		

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

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

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

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

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

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

- 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
80	2e	37	Total	C	N	O	P	0	0
			766	367	143	220	36		

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

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

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

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

- 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
104	3D	48	Total	C	N	O	P	0	0
			999	473	193	286	47		

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

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

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

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

- 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
107	3G	16	Total	C	N	O	P	0	0
			326	157	59	95	15		

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

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

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

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

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

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

- 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		

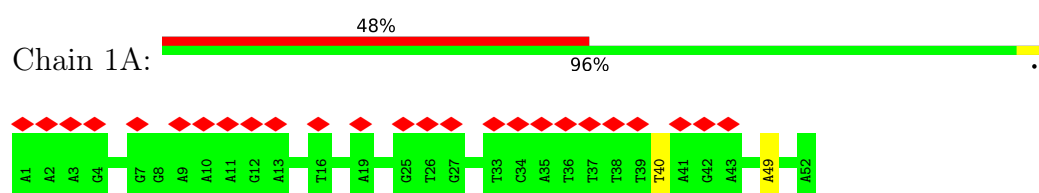
- Molecule 118 is a DNA chain called DNA (32-MER).

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

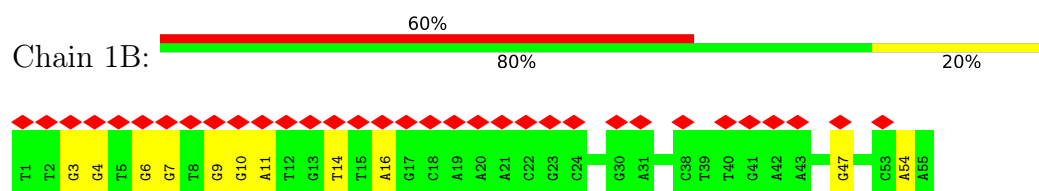
3 Residue-property plots [i](#)

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.

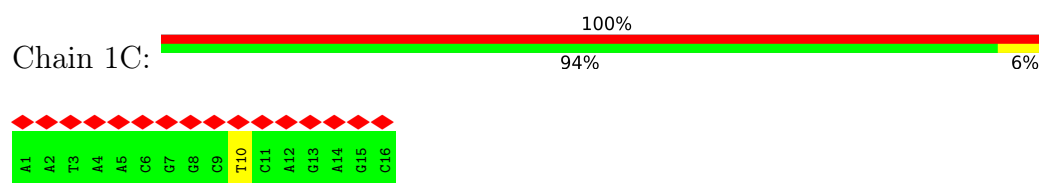
- Molecule 1: DNA (52-MER)



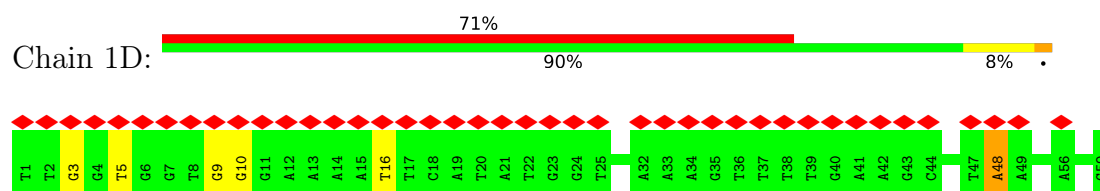
- Molecule 2: DNA (55-MER)



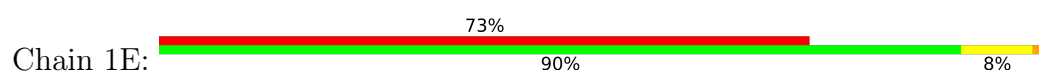
- Molecule 3: DNA (5'-D(*AP*AP*TP*AP*AP*CP*GP*GP*CP*TP*CP*AP*GP*AP*GP*C)-3')



- Molecule 4: DNA (59-MER)

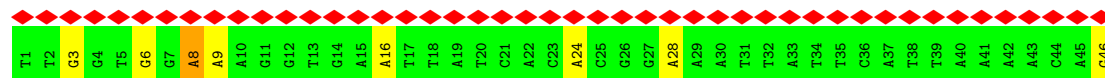
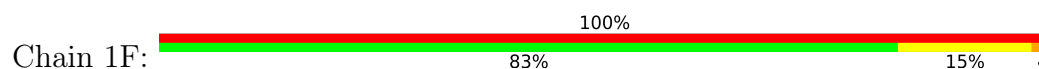


- Molecule 5: DNA (51-MER)

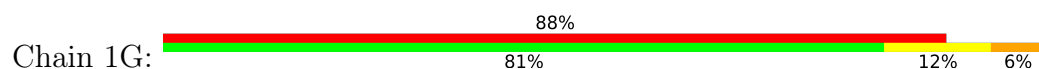




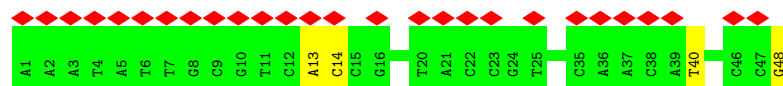
• Molecule 6: DNA (46-MER)



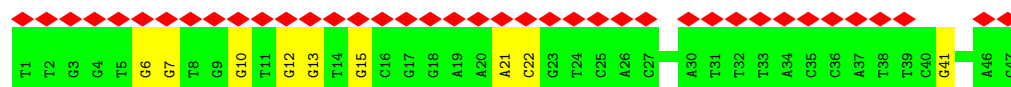
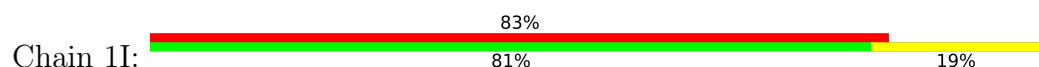
• Molecule 7: DNA (5'-D(*TP*CP*AP*AP*CP*CP*GP*AP*GP*CP*TP*TP*GP*CP*TP*T)-3')



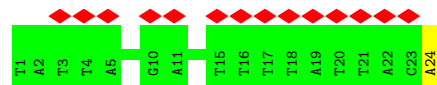
• Molecule 8: DNA (48-MER)



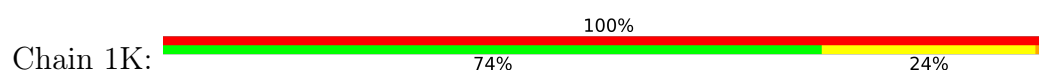
• Molecule 9: DNA (47-MER)



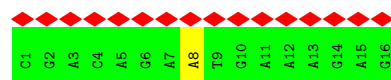
• Molecule 10: DNA (5'-D(*TP*AP*TP*TP*AP*GP*CP*GP*AP*GP*AP*TP*GP*GP*TP*TP*TP*TP*AP*TP*TP*AP*CP*A)-3')



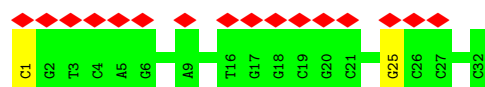
• Molecule 11: DNA (46-MER)



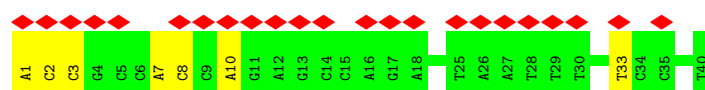
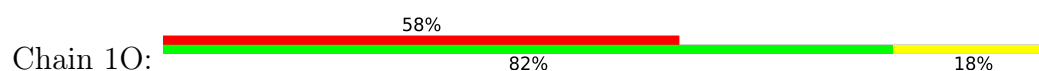
- Molecule 12: DNA (5'-D(*CP*GP*AP*CP*AP*GP*AP*AP*TP*GP*AP*AP*AP*GP*AP*G)-3')



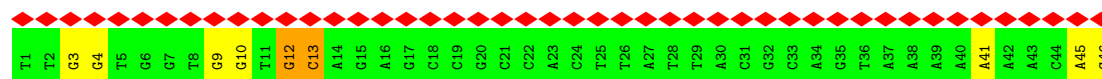
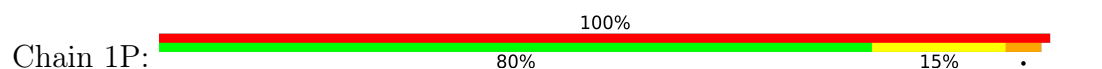
- Molecule 13: DNA (32-MER)



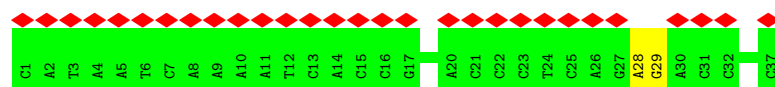
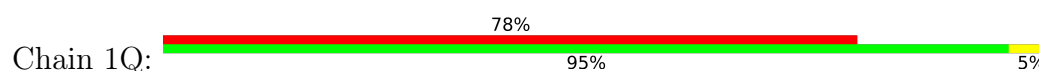
- Molecule 14: DNA (40-MER)



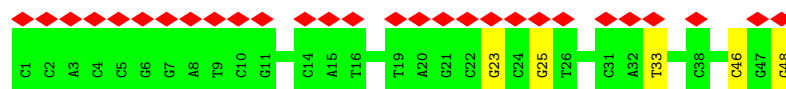
- Molecule 15: DNA (46-MER)



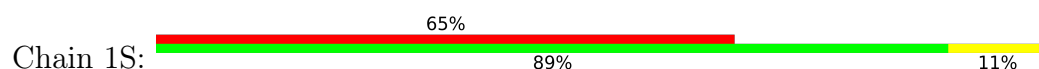
- Molecule 16: DNA (37-MER)

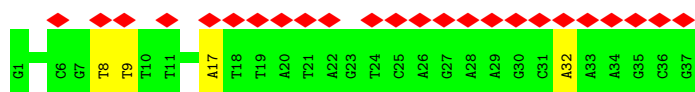


- Molecule 17: DNA (48-MER)

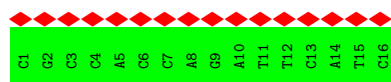


- Molecule 18: DNA (37-MER)

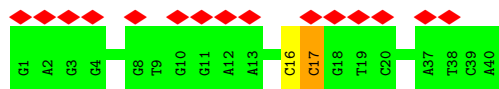
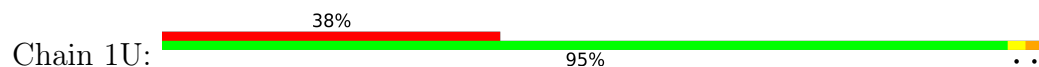




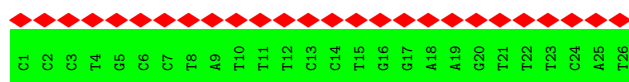
- Molecule 19: DNA (5'-D(*CP*GP*CP*CP*AP*CP*CP*AP*GP*AP*TP*TP*CP*AP*TP*C)-3')



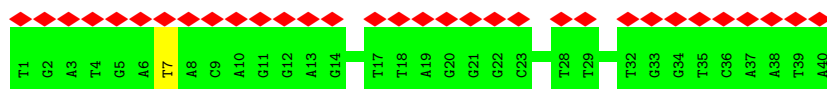
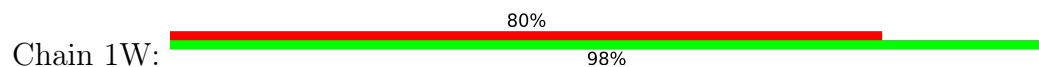
- Molecule 20: DNA (40-MER)



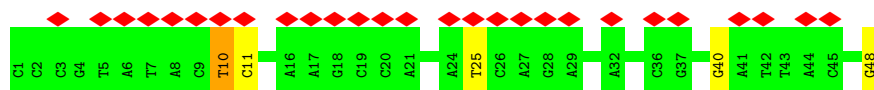
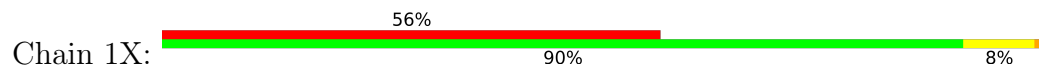
- Molecule 21: DNA (26-MER)



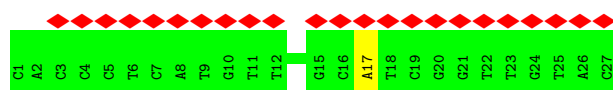
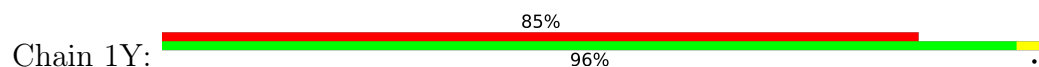
- Molecule 22: DNA (40-MER)



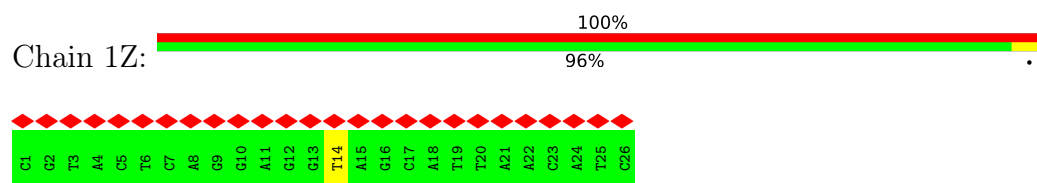
- Molecule 23: DNA (48-MER)



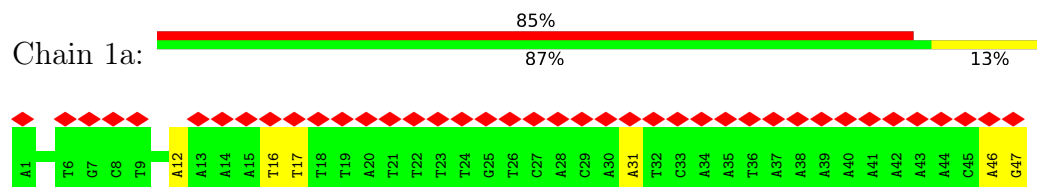
- Molecule 24: DNA (27-MER)



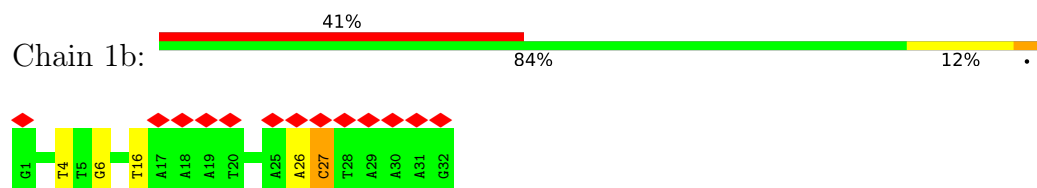
- Molecule 25: DNA (26-MER)



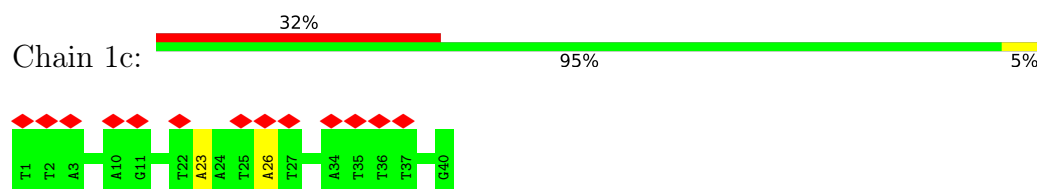
- Molecule 26: DNA (47-MER)



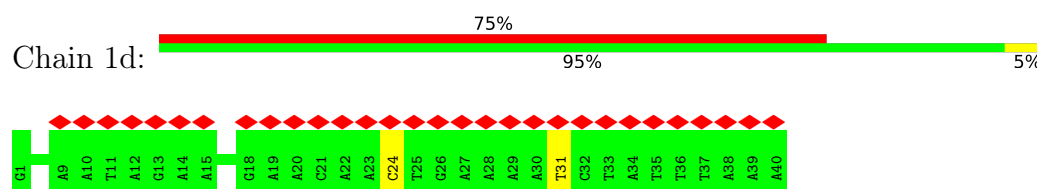
- Molecule 27: DNA (32-MER)



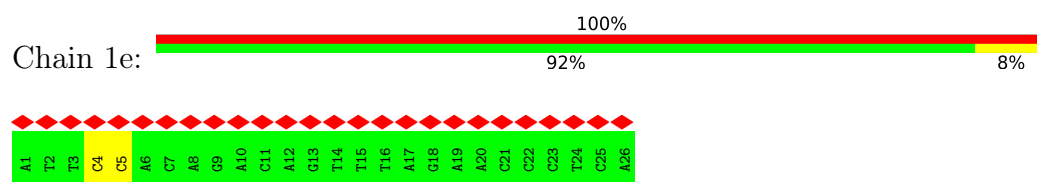
- Molecule 28: DNA (40-MER)



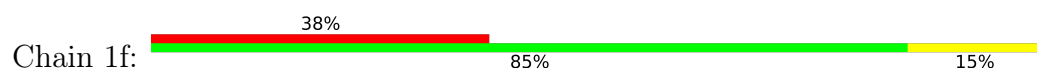
- Molecule 29: DNA (40-MER)



- Molecule 30: DNA (26-MER)

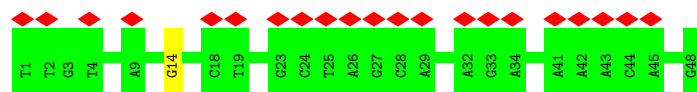
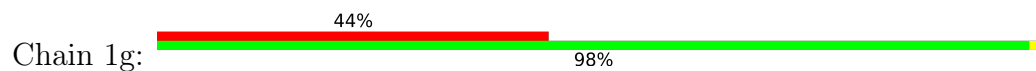


- Molecule 31: DNA (40-MER)

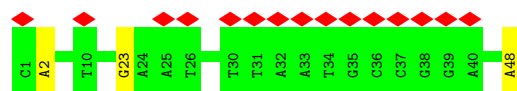




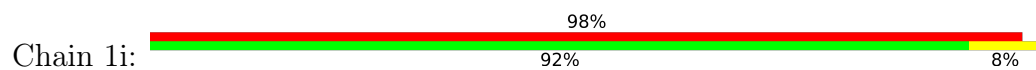
- Molecule 32: DNA (48-MER)



- Molecule 33: DNA (48-MER)



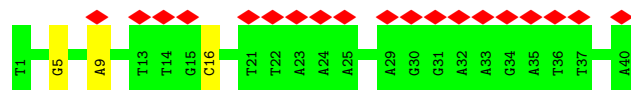
- Molecule 34: DNA (48-MER)



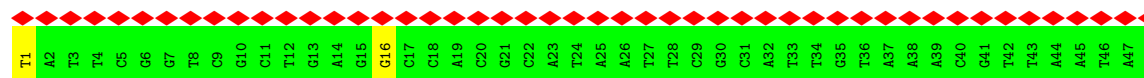
- Molecule 35: DNA (32-MER)



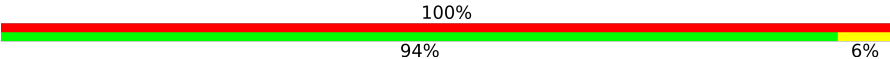
- Molecule 36: DNA (40-MER)

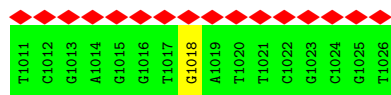


- Molecule 37: DNA (48-MER)

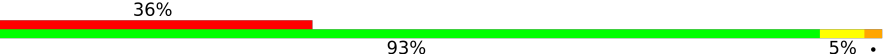


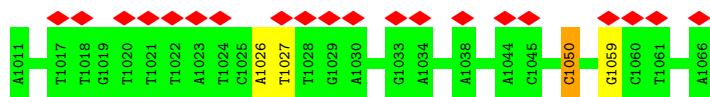
- Molecule 38: DNA (5'-D(P*TP*CP*GP*AP*GP*GP*TP*GP*AP*TP*TP*CP*GP*CP*GP*T)-3')

Chain 1m: 

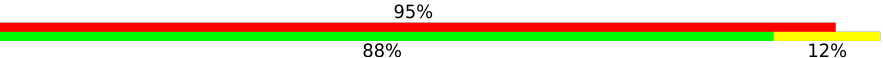


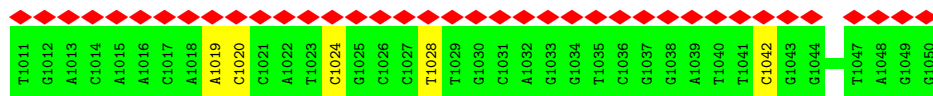
- Molecule 39: DNA (56-MER)

Chain 1n: 



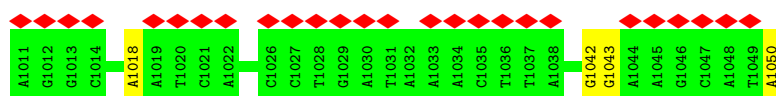
- Molecule 40: DNA (40-MER)

Chain 1o: 

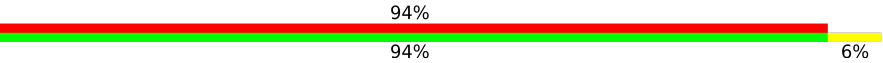


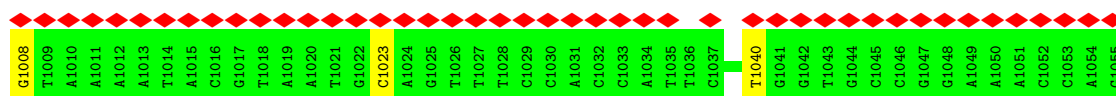
- Molecule 41: DNA (40-MER)

Chain 1p: 

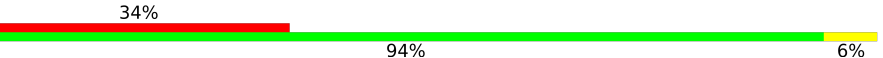


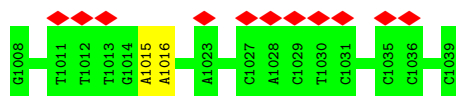
- Molecule 42: DNA (48-MER)

Chain 1q: 

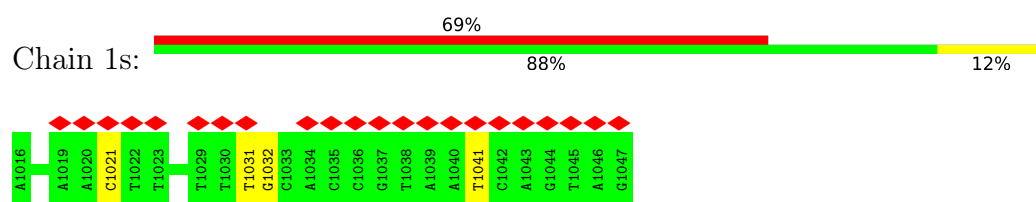


- Molecule 43: DNA (32-MER)

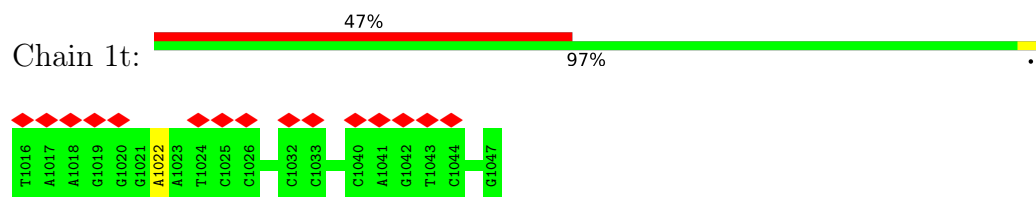
Chain 1r: 



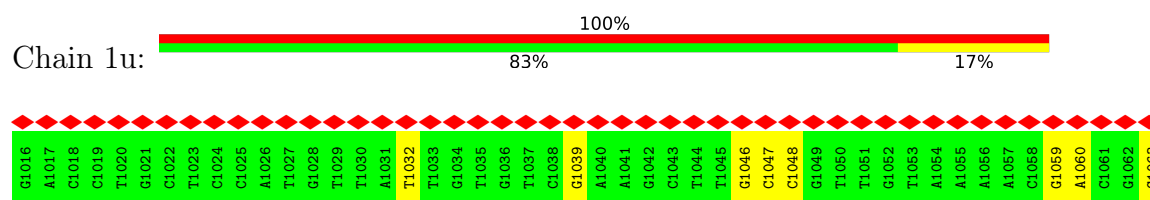
- Molecule 44: DNA (32-MER)



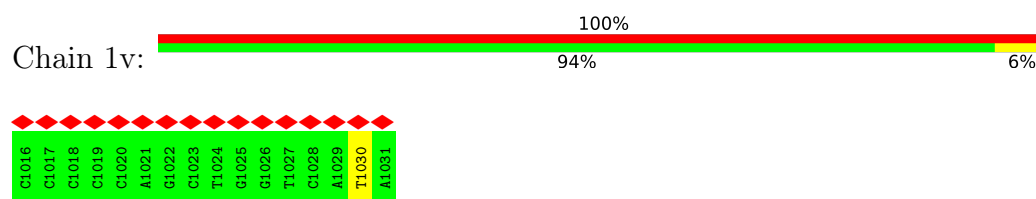
- Molecule 45: DNA (32-MER)



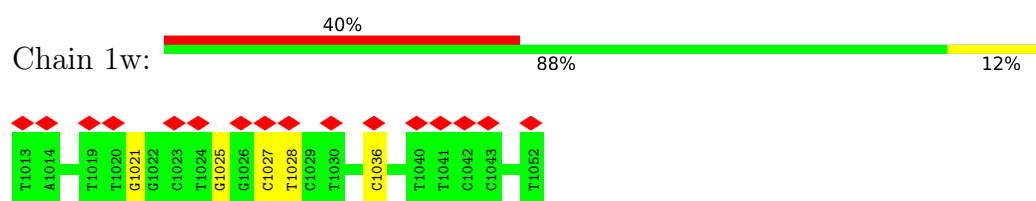
- Molecule 46: DNA (48-MER)



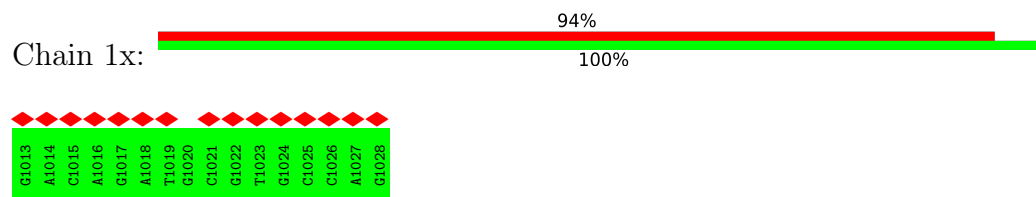
- Molecule 47: DNA (5'-D(P*CP*CP*CP*CP*CP*AP*GP*CP*TP*GP*GP*TP*CP*AP*TP*A)-3')



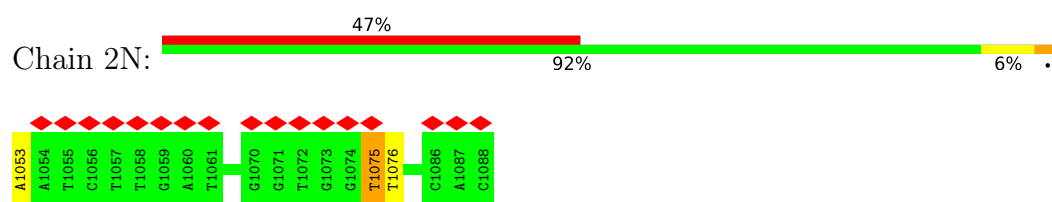
- Molecule 48: DNA (40-MER)



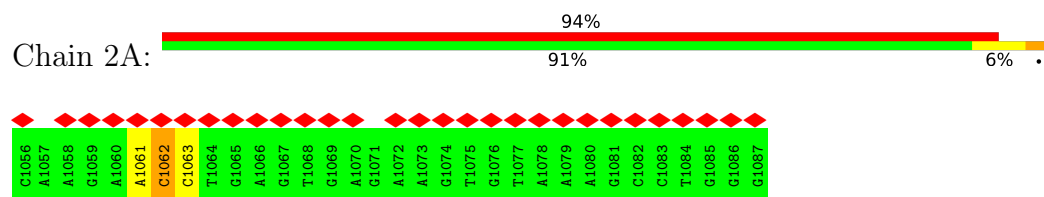
- Molecule 49: DNA (5'-D(P*GP*AP*CP*AP*GP*AP*TP*GP*CP*GP*TP*GP*CP*CP*AP*G)-3')



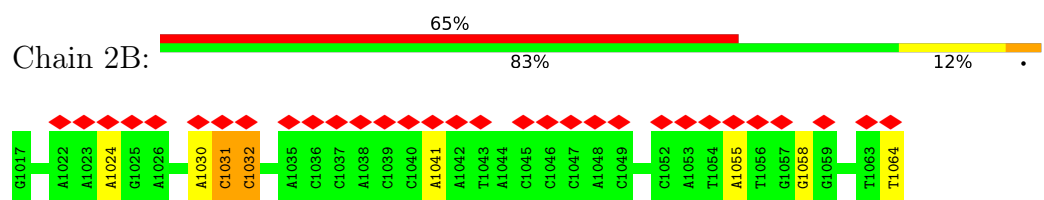
- Molecule 50: DNA (48-MER)



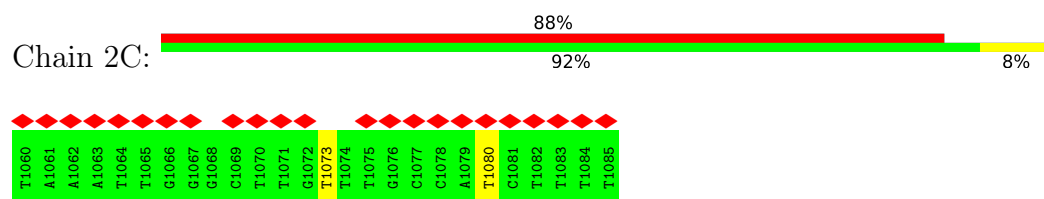
- Molecule 51: DNA (40-MER)



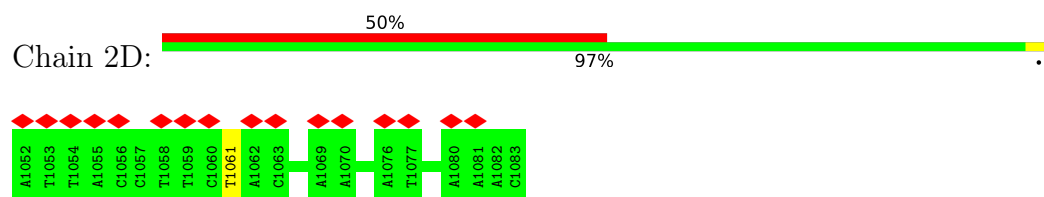
- Molecule 52: DNA (48-MER)



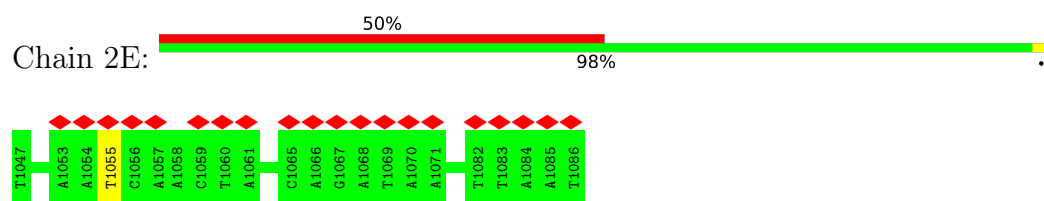
- Molecule 53: DNA (40-MER)



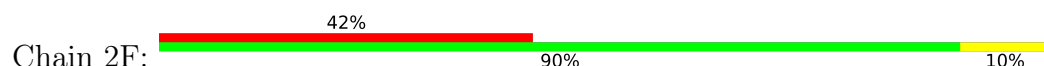
- Molecule 54: DNA (29-MER)

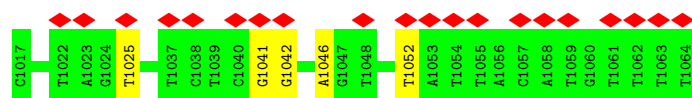


- Molecule 55: DNA (5'-D(P*CP*AP*TP*AP*AP*CP*GP*CP*AP*TP*AP*AP*AP*AP*CP*GP*AP*GP*GP*AP*GP*GP*TP*T)-3')

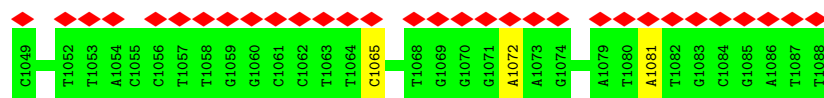
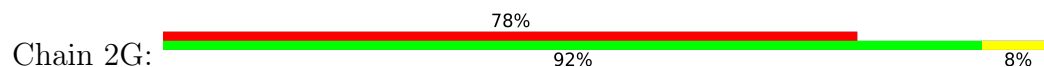


- Molecule 56: DNA (32-MER)

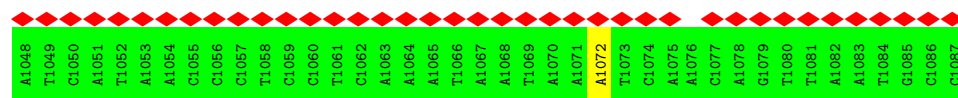




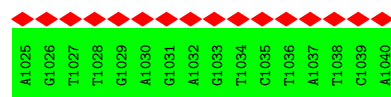
• Molecule 57: DNA (26-MER)



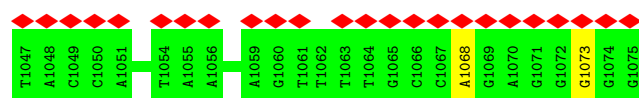
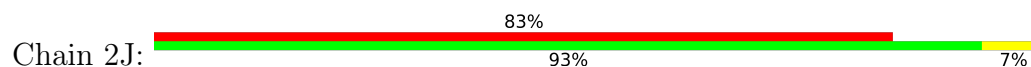
• Molecule 58: DNA (40-MER)



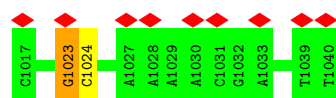
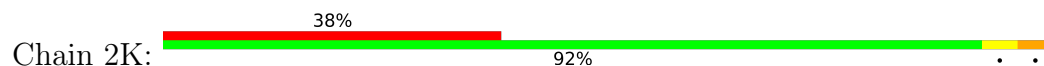
• Molecule 59: DNA (40-MER)



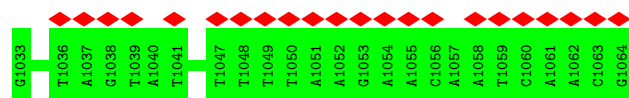
• Molecule 60: DNA (58-MER)



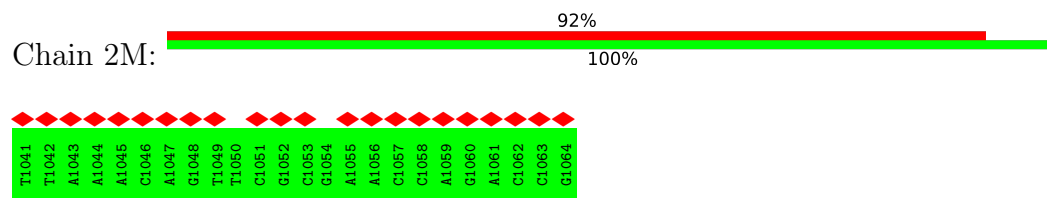
• Molecule 61: DNA (52-MER)



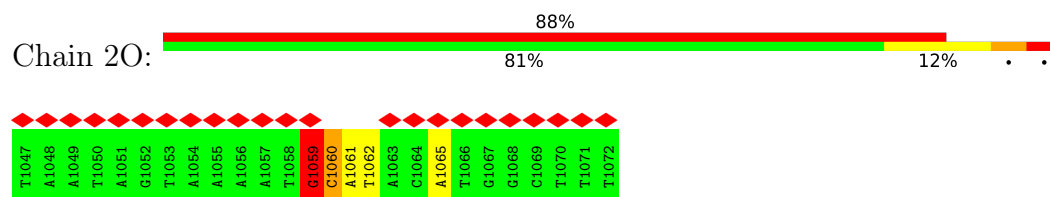
• Molecule 62: DNA (40-MER)



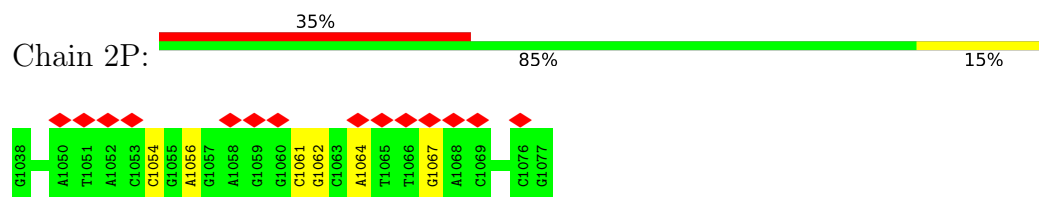
- Molecule 63: DNA (48-MER)



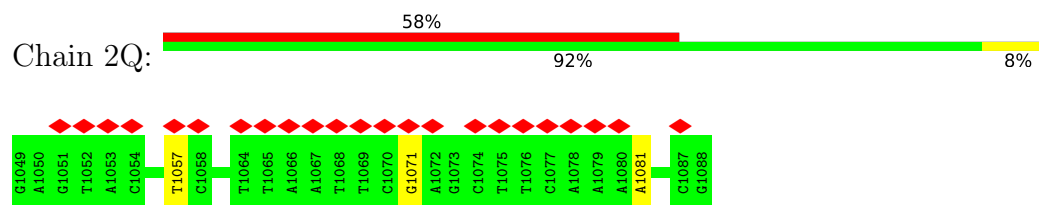
- Molecule 64: DNA (48-MER)



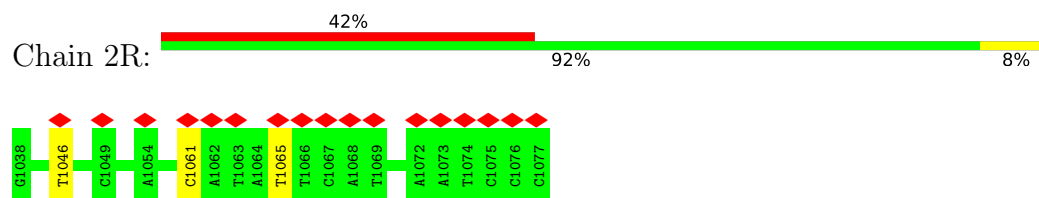
- Molecule 65: DNA (32-MER)



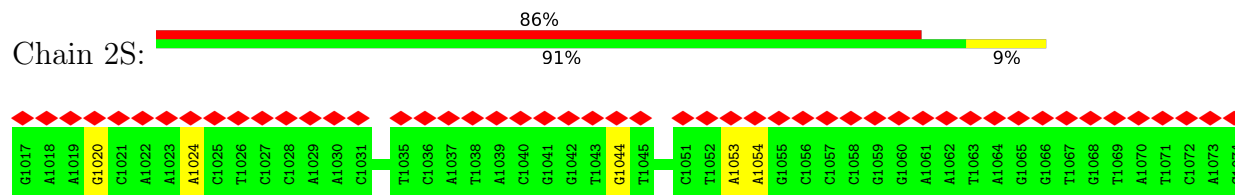
- Molecule 66: DNA (58-MER)



- Molecule 67: DNA (56-MER)

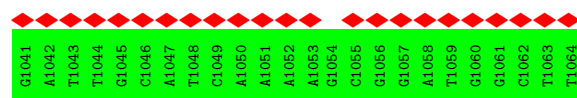


- Molecule 68: DNA (52-MER)

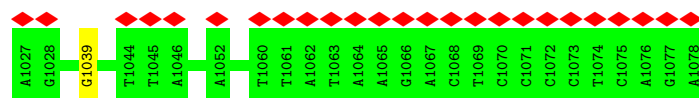


- Molecule 69: DNA (37-MER)

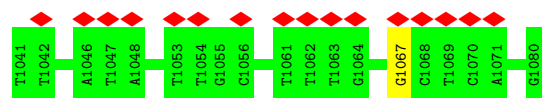




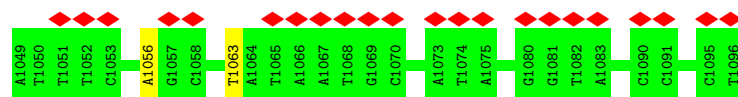
• Molecule 70: DNA (48-MER)



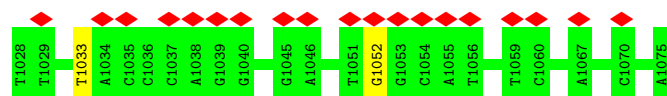
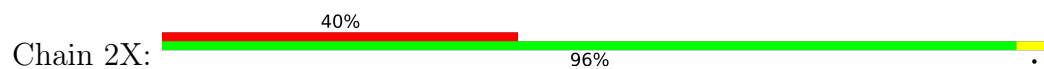
• Molecule 71: DNA (48-MER)



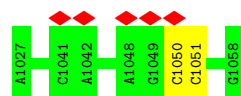
• Molecule 72: DNA (32-MER)



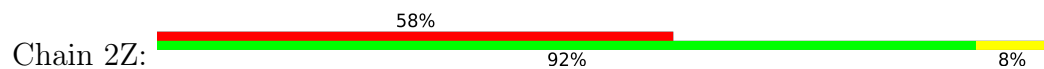
• Molecule 73: DNA (32-MER)



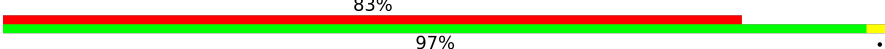
• Molecule 74: DNA (48-MER)

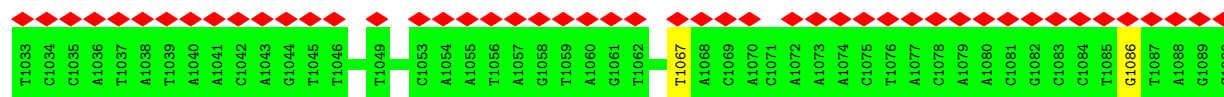


• Molecule 75: DNA (48-MER)

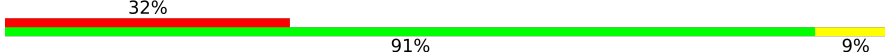


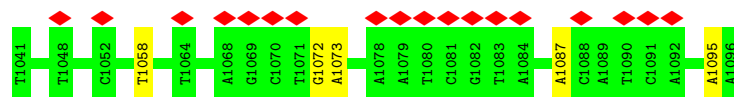
- Molecule 76: DNA (5'-D(P*TP*TP*TP*GP*TP*TP*AP*AP*AP*AP*CP*CP*GP*AP*TP*A)-3')

Chain 2a: 

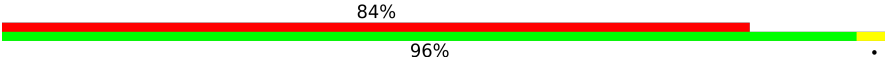


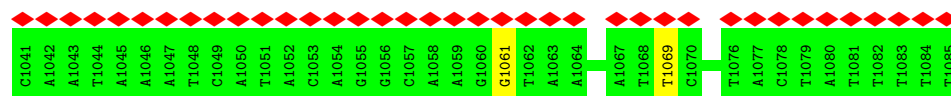
- Molecule 77: DNA (32-MER)

Chain 2b: 

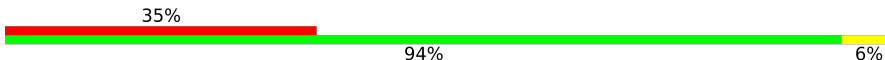


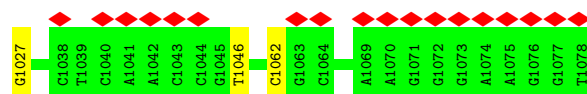
- Molecule 78: DNA (32-MER)

Chain 2c: 

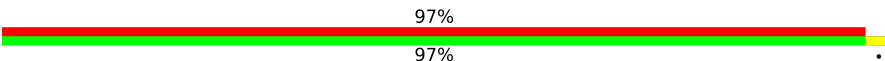


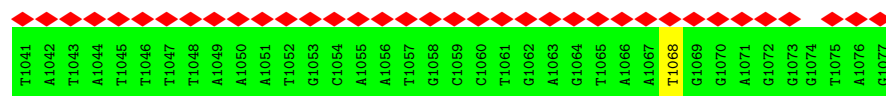
- Molecule 79: DNA (40-MER)

Chain 2d: 



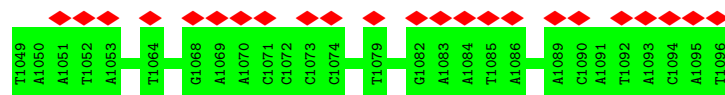
- Molecule 80: DNA (5'-D(P*CP*TP*GP*GP*CP*CP*TP*TP*CP*CP*TP*GP*TP*AP*GP*CP*CP*AP*AP*AP*AP*TP*A)-3')

Chain 2e: 



- Molecule 81: DNA (32-MER)

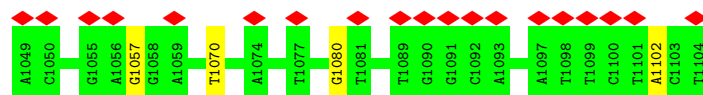
Chain 2f: 



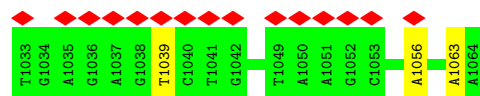
- Molecule 82: DNA (40-MER)



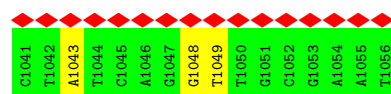
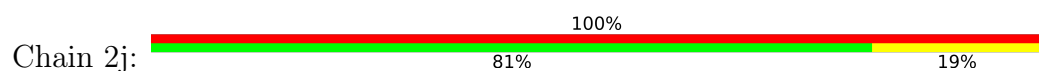
- Molecule 83: DNA (32-MER)



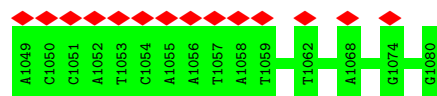
- Molecule 84: DNA (32-MER)



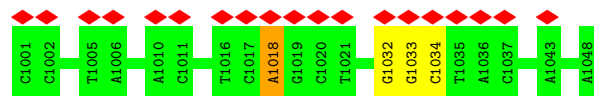
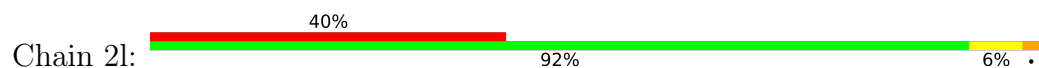
- Molecule 85: DNA (47-MER)



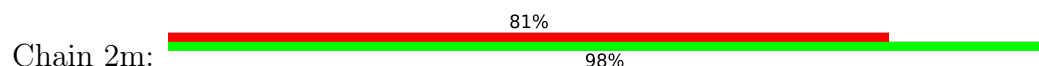
- Molecule 86: DNA (5'-D(P*CP*CP*AP*GP*TP*GP*CP*CP*AP*AP*AP*TP*CP*CP*GP*C)-3')

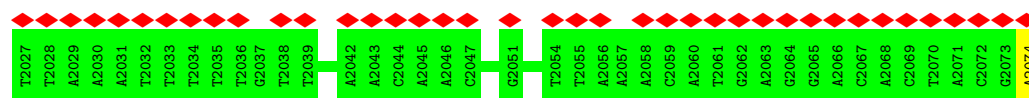


- Molecule 87: DNA (40-MER)

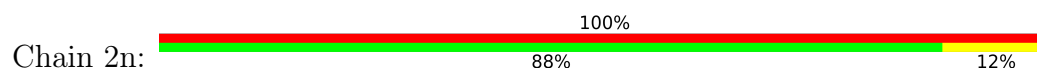


- Molecule 88: DNA (48-MER)

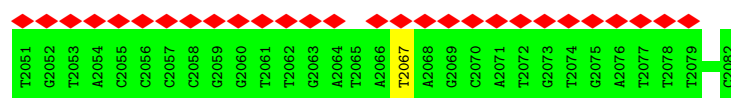
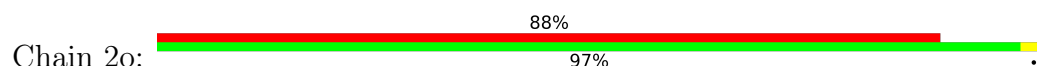




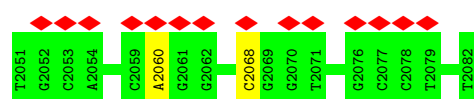
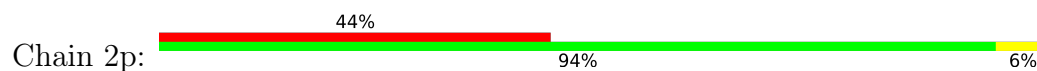
• Molecule 89: DNA (48-MER)



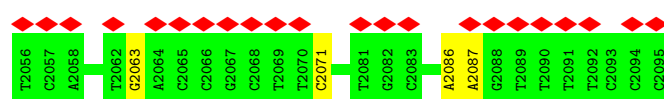
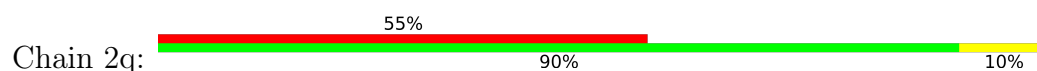
• Molecule 90: DNA (48-MER)



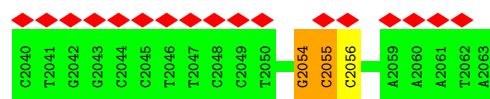
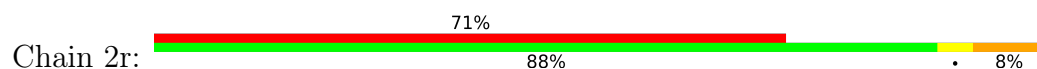
• Molecule 91: DNA (56-MER)



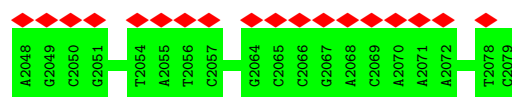
• Molecule 92: DNA (56-MER)

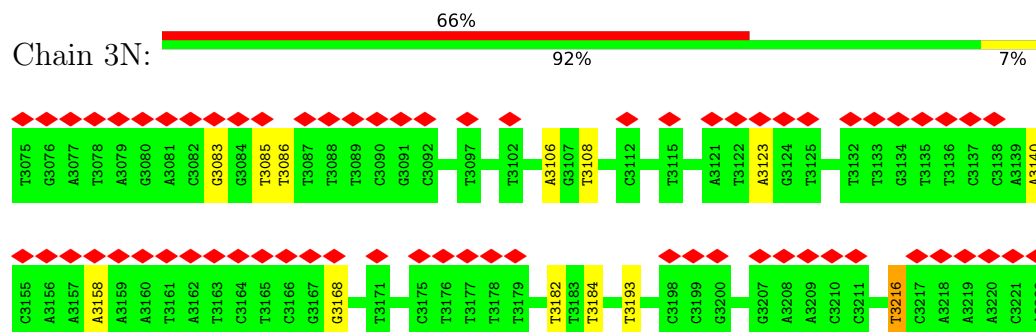


• Molecule 93: DNA (32-MER)



• Molecule 94: DNA (48-MER)



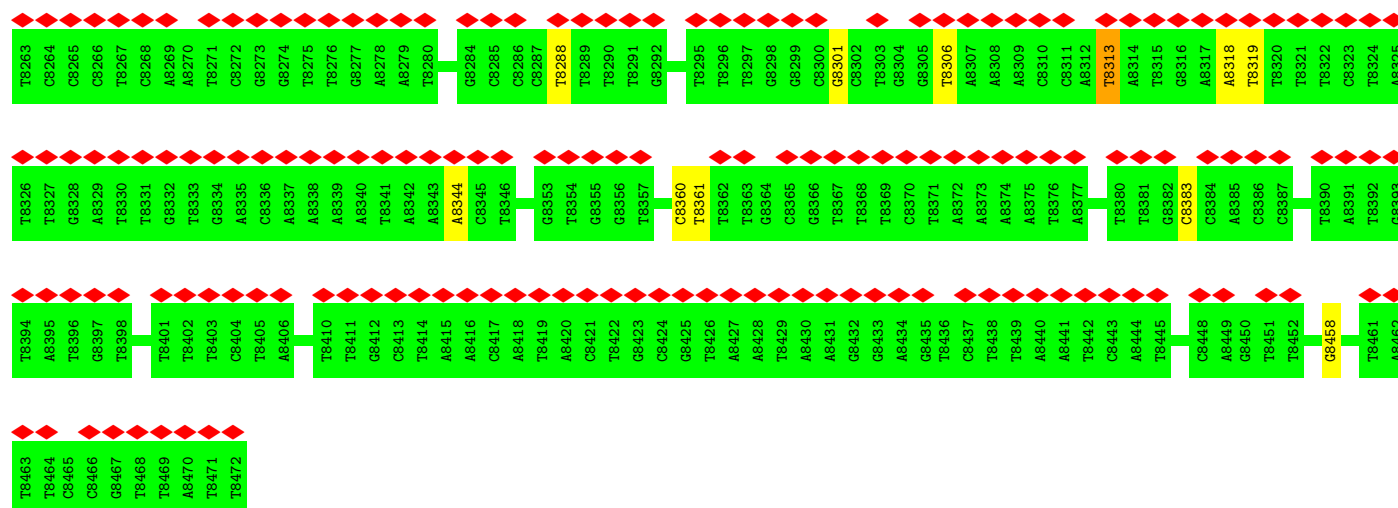


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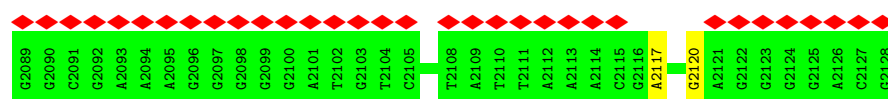
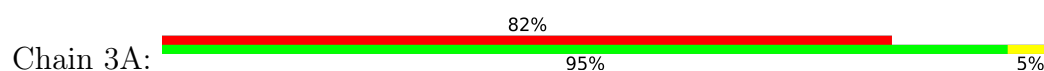
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T6885	C6886	G6892	A6893	A6894	A6895	T6899	T6906	C6907	C6908	T6917	C6918	C6924	T6927	T6928	G6929	C6930	T6931	A6932	C6933	C6934	C6935	T6936	C6937	G6938	T6939	T6940	C6941	C6942	G6943	A6944	T6945	G6946	C6947	T6948	G6949	T6950	C6957	T6958	G6959	C6960	A6963	T6967	G6968	T6973	C6974	G6977	C6978	A6979										
T6824	T6825	T6826	C6827	C6828	T6829	T6832	A6833	G6834	G6835	T6836	T6837	G6838	G6839	T6840	G6841	C6842	C6843	T6844	T6845	C6846	G6847	T6848	A6849	G6850	T6851	G6852	G6853	C6854	A6855	T6856	T6857	A6858	C6859	G6860	T6861	A6862	T6863	T6864	T6865	T6866	A6867	C6868	C6869	C6870	G6871	T6872	T6873	T6874	A6875	A6876	T6877	G6878	C6879	A6880	A6881	A6882	C6883	T6884
A6736	T6737	G6738	A6739	T6740	C6741	C6742	A6743	A6744	A6745	C6746	T6748	C6757	T6758	T6759	T6760	C6765	G6766	C6767	G6768	C6769	T6770	T6771	T6774	A6775	T6776	A6777	A6778	T6779	C6780	G6781	C6782	T6783	G6784	G6785	G6786	G6787	G6788	G6797	A6798	G6799	T6802	T6803	T6804	T6805	T6812	T6813	C6814	T6815	T6816	T6817	T6818	C6823						
T6661	T6664	T6665	G6666	T6673	G6674	C6675	C6684	C6685	G6686	G6687	C6688	T6689	A6690	A6691	G6692	T6693	A6694	A6695	C6696	A6697	T6698	G6699	G6700	A6701	G6702	C6703	A6704	G6705	G6706	T6707	C6708	G6709	C6710	G6711	G6712	A6713	T6714	T6715	T6716	C6717	G6718	A6719	G6720	A6721	C6722	A6723	A6724	T6725	T6726	T6727	A6728	G6732	G6733	C6734	G6735			
A5567	A5568	A5573	C6574	T6575	C6576	T6577	T6578	C6591	G6594	C6595	C6596	T6597	A6598	T6599	C6604	T6605	G6606	G6607	T6608	C6616	C6617	G6618	T6619	T6620	C6621	A6622	T6625	G6626	T6627	C6628	C6629	T6630	C6631	T6632	T6633	T6634	C6635	A6636	A6637	T6641	G6642	G6643	T6644	G6645	A6646	G6652	T6653	T6654	C6655	C6656								
G5486	G5493	T5494	C5495	A5496	G5497	G5498	C5505	T5506	T5507	A5508	A5512	C5513	T5514	G5515	A5516	A5517	T5518	G5519	T5526	T5527	T5528	A5529	C5529	T5530	T5531	T5536	G5537	A5538	T5539	T5540	T5541	G5542	G5543	G5544	T5545	A5546	A5547	T5548	G5549	A5550	A5551	T5552	A5553	T5554	C5555	C5556	G5557	G5558	C5561	T5562	T5563	G5564	T5565	C5566				
T5408	A5409	A5419	A5420	G5421	G5422	T5426	C5430	A5431	A5432	T5433	G5434	A5435	A5440	G5441	T5442	T5443	A5444	A5445	A5446	A5451	A5452	C5453	C5454	A5455	T5456	C5457	A5460	A5461	G5462	C5463	C5464	C5465	A5466	A5467	T5468	T5469	T5470	C5471	C5472	T5473	A5474	C5475	T5476	C5477	G5478	T5479	T5480	C5481	T5482	G5483	C5484	T5485						
C5341	G5342	T5343	T5344	A5345	G5346	T5347	T5348	C5349	T5353	T5354	A5355	T5356	T5357	A5358	A5359	C5360	G5364	A5365	T5366	T5367	T5368	T5369	T5370	C5371	T5372	T5373	C5374	C5375	C5376	A5377	A5378	C5379	G5380	T5381	C5382	C5383	T5384	G5385	A5386	C5387	T5388	A5389	A5390	A5391	A5392	T5393	A5394	A5395	T5396	G5397	A5398	G5399	C5400	C5401	G5403			
C5276	A5276	T5277	T5278	A5279	G5280	T5281	T5282	G5283	A5284	A5285	T5286	G5287	T5288	G5289	G5290	T5291	A5292	T5293	T5294	C5295	C5296	T5297	A5298	A5299	A5300	T5301	C5302	T5303	C5304	A5305	A5306	C5307	T5308	G5309	A5310	T5311	G5312	A5313	A5314	T5315	C5316	T5317	T5318	T5319	C5320	T5321	A5322	C5323	C5324	T5325	G5326	T5327	T5333	G5334	T5335	T5336	G5337	T5338

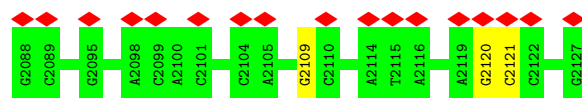
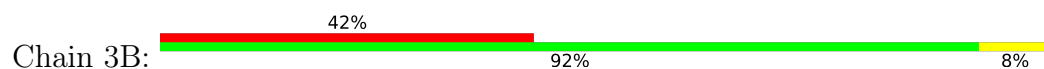




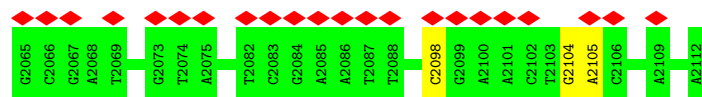
• Molecule 101: DNA (40-MER)



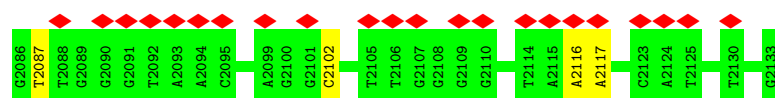
• Molecule 102: DNA (40-MER)



• Molecule 103: DNA (48-MER)

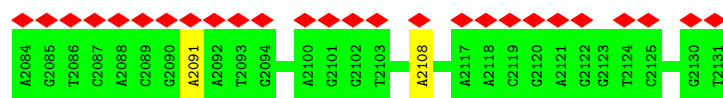


• Molecule 104: DNA (48-MER)

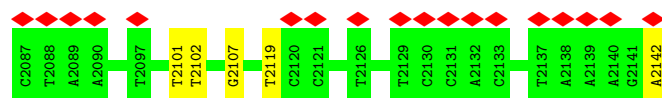


• Molecule 105: DNA (48-MER)

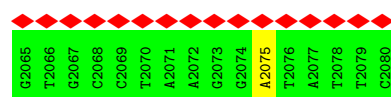




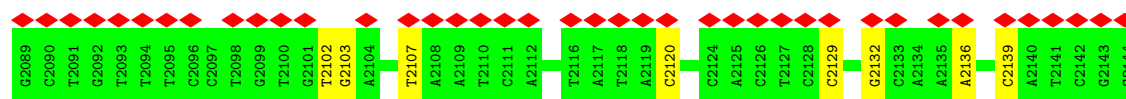
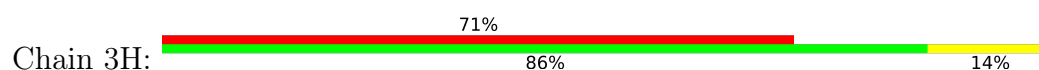
• Molecule 106: DNA (56-MER)



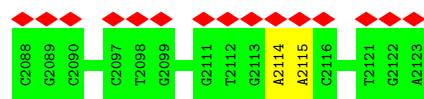
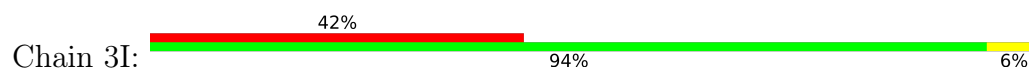
• Molecule 107: DNA (5'-D(*GP*TP*GP*CP*CP*TP*AP*AP*GP*GP*AP*TP*AP*TP*TP*C)-3')



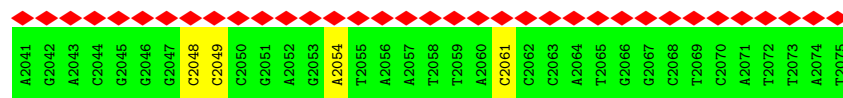
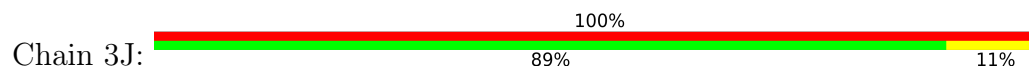
• Molecule 108: DNA (56-MER)



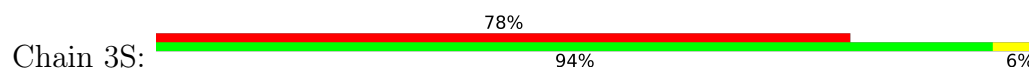
• Molecule 109: DNA (36-MER)

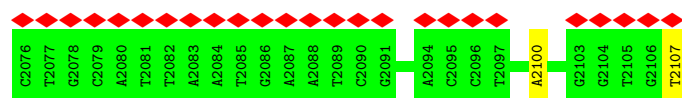


• Molecule 110: DNA (35-MER)

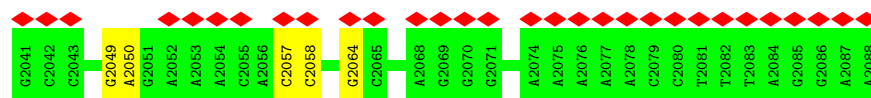
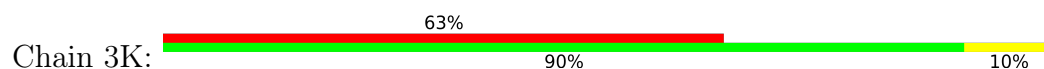


• Molecule 111: DNA (32-MER)

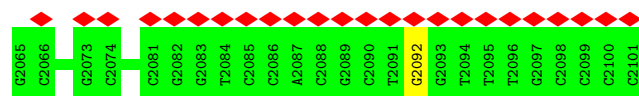




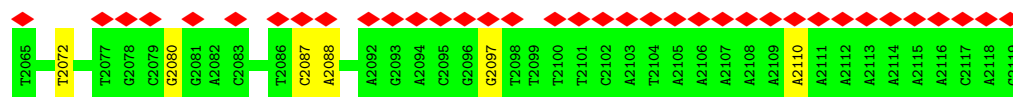
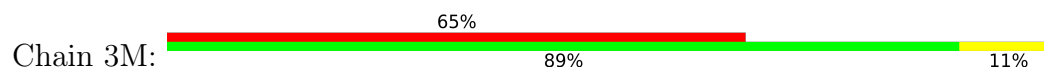
• Molecule 112: DNA (48-MER)



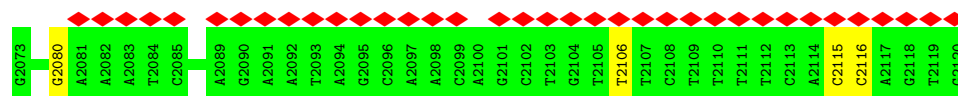
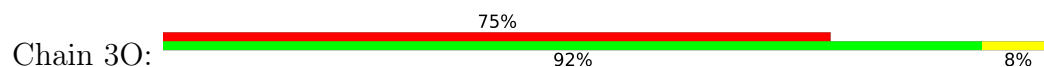
• Molecule 113: DNA (37-MER)



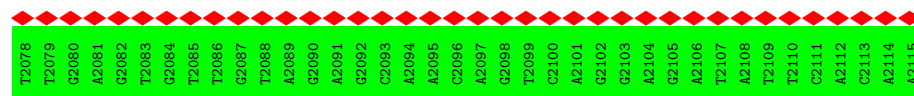
• Molecule 114: DNA (55-MER)



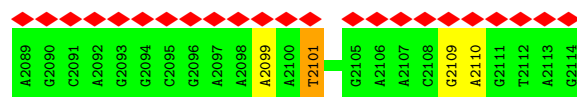
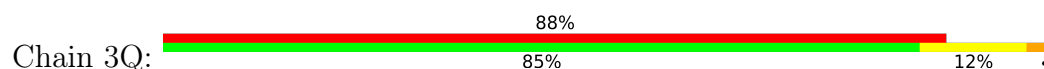
• Molecule 115: DNA (48-MER)



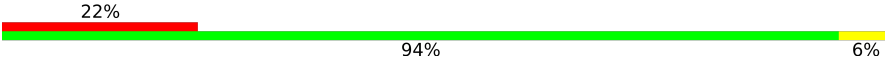
• Molecule 116: DNA (38-MER)

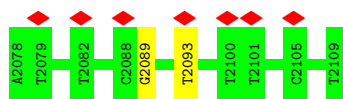


• Molecule 117: DNA (26-MER)



- Molecule 118: DNA (32-MER)

Chain 3R: 



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 ⓘ

5.1 Standard geometry ⓘ

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	0.65	0/1220	0.91	0/1885
2	1B	0.68	0/1279	0.94	2/1975 (0.1%)
3	1C	0.66	0/368	0.94	1/566 (0.2%)
4	1D	0.65	0/1372	0.89	2/2119 (0.1%)
5	1E	0.65	0/1185	0.86	1/1828 (0.1%)
6	1F	0.67	0/1069	1.08	4/1650 (0.2%)
7	1G	0.64	0/358	1.00	1/550 (0.2%)
8	1H	0.65	0/1087	0.93	0/1671
9	1I	0.69	0/1091	0.98	1/1685 (0.1%)
10	1J	0.64	0/551	0.91	0/850
11	1K	0.69	0/1061	1.06	5/1637 (0.3%)
12	1L	0.65	0/377	0.88	0/581
13	1M	0.67	0/722	0.93	1/1110 (0.1%)
14	1O	0.66	0/907	0.91	0/1394
15	1P	0.66	0/1066	0.97	2/1645 (0.1%)
16	1Q	0.64	0/846	0.90	1/1301 (0.1%)
17	1R	0.68	0/1094	0.99	2/1685 (0.1%)
18	1S	0.67	0/858	0.98	1/1324 (0.1%)
19	1T	0.63	0/355	0.92	0/544
20	1U	0.65	0/932	1.02	3/1437 (0.2%)
21	1V	0.64	0/580	0.92	0/892
22	1W	0.65	0/934	0.89	0/1443
23	1X	0.66	0/1106	0.91	0/1704
24	1Y	0.65	0/607	0.92	1/934 (0.1%)
25	1Z	0.64	0/596	0.91	0/918
26	1a	0.63	0/1086	0.94	2/1674 (0.1%)
27	1b	0.65	0/750	0.95	2/1158 (0.2%)
28	1c	0.64	0/921	0.90	2/1420 (0.1%)
29	1d	0.64	0/931	0.92	1/1436 (0.1%)
30	1e	0.64	0/587	0.88	0/902
31	1f	0.67	0/899	0.99	3/1382 (0.2%)
32	1g	0.66	0/1105	0.90	0/1702
33	1h	0.65	0/1118	0.89	0/1726
34	1i	0.65	0/1108	0.91	1/1709 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	1j	0.65	0/742	0.88	0/1144
36	1k	0.64	0/929	0.92	0/1435
37	1l	0.65	0/1098	0.91	0/1693
38	1m	0.67	0/367	1.02	1/566 (0.2%)
39	1n	0.66	0/1290	0.95	4/1989 (0.2%)
40	1o	0.67	0/922	0.96	1/1422 (0.1%)
41	1p	0.66	0/917	0.98	2/1412 (0.1%)
42	1q	0.65	0/1101	0.88	0/1697
43	1r	0.66	0/734	0.95	2/1131 (0.2%)
44	1s	0.65	0/727	1.01	1/1119 (0.1%)
45	1t	0.67	0/729	0.96	1/1123 (0.1%)
46	1u	0.67	0/1100	0.99	5/1697 (0.3%)
47	1v	0.66	0/356	0.84	0/546
48	1w	0.66	0/904	1.02	1/1391 (0.1%)
49	1x	0.68	0/370	0.96	0/570
50	2N	0.65	0/825	0.94	2/1272 (0.2%)
51	2A	0.67	0/750	0.98	2/1158 (0.2%)
52	2B	0.68	0/1095	0.99	4/1685 (0.2%)
53	2C	0.65	0/587	0.97	1/905 (0.1%)
54	2D	0.64	0/733	0.92	0/1128
55	2E	0.64	0/915	0.93	1/1410 (0.1%)
56	2F	0.65	0/1109	0.86	0/1712
57	2G	0.65	0/919	0.92	1/1418 (0.1%)
58	2H	0.64	0/905	0.92	0/1391
59	2I	0.61	0/368	0.87	0/567
60	2J	0.66	0/674	0.93	1/1040 (0.1%)
61	2K	0.65	0/558	0.90	1/860 (0.1%)
62	2L	0.65	0/733	0.92	0/1129
63	2M	0.64	0/548	0.85	0/843
64	2O	0.69	0/597	1.15	4/920 (0.4%)
65	2P	0.65	0/925	1.12	7/1426 (0.5%)
66	2Q	0.64	0/918	0.92	1/1415 (0.1%)
67	2R	0.65	0/924	0.94	1/1425 (0.1%)
68	2S	0.66	0/1341	1.03	7/2068 (0.3%)
69	2T	0.63	0/555	0.86	0/856
70	2U	0.65	0/1187	0.90	0/1829
71	2V	0.65	0/912	0.92	0/1406
72	2W	0.64	0/1109	0.86	0/1711
73	2X	0.67	0/1091	0.93	1/1680 (0.1%)
74	2Y	0.66	0/737	0.92	1/1136 (0.1%)
75	2Z	0.65	0/917	0.96	2/1414 (0.1%)
76	2a	0.64	0/1322	0.94	2/2036 (0.1%)
77	2b	0.66	0/1290	1.11	6/1990 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	2c	0.63	0/1025	0.88	0/1578
79	2d	0.66	0/1212	0.91	3/1870 (0.2%)
80	2e	0.63	0/861	0.86	0/1330
81	2f	0.65	0/1096	0.91	0/1687
82	2g	0.66	0/1091	0.94	2/1678 (0.1%)
83	2h	0.65	0/1301	0.89	0/2008
84	2i	0.66	0/746	0.89	0/1150
85	2j	0.66	0/365	0.86	0/562
86	2k	0.65	0/732	0.89	0/1127
87	2l	0.65	0/1102	0.89	3/1697 (0.2%)
88	2m	0.64	0/1106	0.89	0/1705
89	2n	0.66	0/364	0.99	1/560 (0.2%)
90	2o	0.64	0/730	0.90	0/1126
91	2p	0.66	0/735	0.95	1/1134 (0.1%)
92	2q	0.66	0/898	0.94	0/1382
93	2r	0.67	0/543	1.10	3/835 (0.4%)
94	2s	0.67	0/737	0.92	0/1135
95	2t	0.67	0/928	1.05	5/1431 (0.3%)
96	2u	0.66	0/731	0.94	1/1126 (0.1%)
97	2v	0.67	0/726	1.03	3/1120 (0.3%)
98	2w	0.66	0/1101	0.99	5/1698 (0.3%)
99	2x	0.63	0/358	0.87	0/549
100	3N	0.66	0/99584	0.95	130/153695 (0.1%)
101	3A	0.66	0/950	0.85	0/1470
102	3B	0.66	0/919	0.89	0/1416
103	3C	0.66	0/1103	0.94	1/1700 (0.1%)
104	3D	0.67	0/1124	0.92	1/1738 (0.1%)
105	3E	0.67	0/1116	0.96	2/1722 (0.1%)
106	3F	0.64	0/1265	0.94	1/1947 (0.1%)
107	3G	0.65	0/365	0.91	0/562
108	3H	0.67	0/1281	0.98	3/1974 (0.2%)
109	3I	0.66	0/826	0.96	0/1273
110	3J	0.67	0/801	0.96	2/1234 (0.2%)
111	3S	0.64	0/735	0.95	1/1133 (0.1%)
112	3K	0.66	0/1113	0.85	0/1716
113	3L	0.66	0/853	0.90	1/1316 (0.1%)
114	3M	0.66	0/1269	0.98	4/1957 (0.2%)
115	3O	0.64	0/1108	0.90	1/1708 (0.1%)
116	3P	0.64	0/883	0.84	0/1363
117	3Q	0.65	0/609	0.90	1/939 (0.1%)
118	3R	0.66	0/749	0.98	2/1158 (0.2%)
All	All	0.66	0/202097	0.94	279/311711 (0.1%)

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

There are no bond length outliers.

All (279) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
77	2b	1072	DG	O3'-P-O5'	19.62	133.44	104.00
65	2P	1061	DC	O3'-P-O5'	16.24	128.36	104.00
20	1U	17	DC	C6-N1-C1'	-14.30	98.25	119.70
68	2S	1053	DA	O3'-P-O5'	13.97	124.95	104.00
29	1d	31	DT	P-O3'-C3'	12.62	139.13	120.20
100	3N	4563	DC	P-O3'-C3'	12.37	138.75	120.20
100	3N	8344	DA	P-O3'-C3'	12.35	138.72	120.20
100	3N	7738	DC	P-O3'-C3'	12.32	138.69	120.20
48	1w	1027	DC	P-O3'-C3'	12.14	138.42	120.20
100	3N	7785	DG	P-O3'-C3'	12.14	138.41	120.20
51	2A	1063	DC	P-O3'-C3'	11.99	138.19	120.20
100	3N	7981	DG	P-O3'-C3'	11.94	138.12	120.20
39	1n	1027	DT	P-O3'-C3'	11.91	138.06	120.20
44	1s	1032	DG	P-O3'-C3'	11.74	137.80	120.20
95	2t	2062	DG	P-O3'-C3'	11.70	137.75	120.20
100	3N	4708	DC	P-O3'-C3'	11.68	137.71	120.20
20	1U	17	DC	C6-N1-C2	-11.43	103.45	120.60
111	3S	2100	DA	P-O3'-C3'	11.41	137.31	120.20
64	2O	1060	DC	P-O3'-C3'	11.34	137.20	120.20
93	2r	2056	DC	P-O3'-C3'	11.31	137.17	120.20
100	3N	3461	DC	P-O3'-C3'	11.31	137.17	120.20
26	1a	31	DA	P-O3'-C3'	11.28	137.13	120.20
100	3N	6829	DT	P-O3'-C3'	11.21	137.02	120.20
100	3N	7325	DC	P-O3'-C3'	11.20	136.99	120.20
100	3N	5124	DC	P-O3'-C3'	11.19	136.99	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	1F	16	DA	P-O3'-C3'	11.14	136.92	120.20
100	3N	3746	DA	P-O3'-C3'	11.11	136.87	120.20
100	3N	4375	DC	P-O3'-C3'	11.11	136.87	120.20
100	3N	3459	DC	P-O3'-C3'	11.08	136.81	120.20
100	3N	5292	DA	P-O3'-C3'	11.06	136.79	120.20
100	3N	7022	DA	P-O3'-C3'	11.05	136.77	120.20
98	2w	2089	DA	P-O3'-C3'	11.02	136.73	120.20
100	3N	7793	DT	P-O3'-C3'	10.95	136.63	120.20
100	3N	8319	DT	P-O3'-C3'	10.93	136.60	120.20
100	3N	4139	DT	P-O3'-C3'	10.92	136.59	120.20
100	3N	3957	DC	P-O3'-C3'	10.88	136.53	120.20
68	2S	1044	DG	P-O3'-C3'	10.83	136.44	120.20
100	3N	8172	DG	P-O3'-C3'	10.83	136.44	120.20
64	2O	1062	DT	P-O3'-C3'	10.82	136.43	120.20
100	3N	3923	DC	P-O3'-C3'	10.81	136.41	120.20
73	2X	1052	DG	P-O3'-C3'	10.76	136.35	120.20
114	3M	2110	DA	P-O3'-C3'	10.73	136.30	120.20
43	1r	1016	DA	P-O3'-C3'	10.72	136.27	120.20
100	3N	7060	DC	P-O3'-C3'	10.68	136.22	120.20
100	3N	8087	DT	P-O3'-C3'	10.68	136.21	120.20
100	3N	4356	DG	P-O3'-C3'	10.65	136.18	120.20
67	2R	1065	DT	P-O3'-C3'	10.63	136.15	120.20
52	2B	1041	DA	P-O3'-C3'	10.62	136.13	120.20
100	3N	3827	DG	P-O3'-C3'	10.58	136.07	120.20
95	2t	2054	DC	P-O3'-C3'	10.57	136.06	120.20
100	3N	3193	DT	P-O3'-C3'	10.55	136.03	120.20
100	3N	5269	DT	P-O3'-C3'	10.55	136.02	120.20
100	3N	7005	DC	P-O3'-C3'	10.52	135.99	120.20
100	3N	7696	DC	P-O3'-C3'	10.51	135.97	120.20
100	3N	3528	DG	P-O3'-C3'	10.50	135.94	120.20
9	1I	41	DG	P-O3'-C3'	10.48	135.92	120.20
100	3N	4865	DA	P-O3'-C3'	10.48	135.92	120.20
100	3N	6931	DT	P-O3'-C3'	10.42	135.83	120.20
100	3N	3570	DG	P-O3'-C3'	10.37	135.75	120.20
93	2r	2055	DC	P-O3'-C3'	10.36	135.75	120.20
100	3N	3700	DC	P-O3'-C3'	10.29	135.63	120.20
100	3N	7062	DC	P-O3'-C3'	10.29	135.63	120.20
100	3N	7778	DA	P-O3'-C3'	10.28	135.62	120.20
100	3N	7777	DG	P-O3'-C3'	10.27	135.60	120.20
89	2n	2075	DA	P-O3'-C3'	10.25	135.57	120.20
100	3N	7533	DC	P-O3'-C3'	10.25	135.57	120.20
110	3J	2061	DC	P-O3'-C3'	10.24	135.56	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
113	3L	2092	DG	P-O3'-C3'	10.21	135.51	120.20
100	3N	5377	DA	P-O3'-C3'	10.15	135.42	120.20
11	1K	15	DG	P-O3'-C3'	10.13	135.40	120.20
100	3N	7645	DG	P-O3'-C3'	10.11	135.37	120.20
98	2w	2093	DA	P-O3'-C3'	10.10	135.35	120.20
100	3N	3370	DC	P-O3'-C3'	10.10	135.34	120.20
18	1S	9	DT	P-O3'-C3'	10.08	135.32	120.20
68	2S	1053	DA	OP2-P-O3'	-10.08	77.75	108.00
20	1U	16	DC	P-O3'-C3'	10.08	135.32	120.20
100	3N	4283	DA	P-O3'-C3'	10.04	135.27	120.20
100	3N	7278	DG	P-O3'-C3'	10.04	135.26	120.20
100	3N	4726	DA	P-O3'-C3'	9.99	135.18	120.20
100	3N	6709	DG	P-O3'-C3'	9.93	135.09	120.20
11	1K	20	DA	P-O3'-C3'	9.89	135.04	120.20
77	2b	1073	DA	O5'-P-OP1	-9.89	79.33	109.00
100	3N	4633	DG	P-O3'-C3'	9.88	135.02	120.20
100	3N	3659	DG	P-O3'-C3'	9.83	134.95	120.20
100	3N	4968	DA	P-O3'-C3'	9.78	134.87	120.20
97	2v	2046	DA	P-O3'-C3'	9.77	134.85	120.20
6	1F	24	DA	P-O3'-C3'	9.77	134.85	120.20
100	3N	8039	DA	P-O3'-C3'	9.75	134.83	120.20
45	1t	1022	DA	P-O3'-C3'	9.65	134.68	120.20
114	3M	2087	DC	P-O3'-C3'	9.65	134.67	120.20
100	3N	4701	DA	P-O3'-C3'	9.57	134.56	120.20
11	1K	38	DA	P-O3'-C3'	9.57	134.56	120.20
15	1P	13	DC	P-O3'-C3'	9.55	134.53	120.20
100	3N	7635	DA	P-O3'-C3'	9.54	134.51	120.20
100	3N	6698	DT	P-O3'-C3'	9.53	134.50	120.20
100	3N	5191	DG	P-O3'-C3'	9.48	134.43	120.20
100	3N	5493	DG	P-O3'-C3'	9.45	134.37	120.20
97	2v	2039	DC	P-O3'-C3'	9.45	134.37	120.20
100	3N	3673	DG	P-O3'-C3'	9.43	134.34	120.20
100	3N	3875	DC	P-O3'-C3'	9.40	134.30	120.20
105	3E	2108	DA	P-O3'-C3'	9.40	134.30	120.20
11	1K	10	DG	P-O3'-C3'	9.39	134.29	120.20
100	3N	6934	DC	P-O3'-C3'	9.38	134.28	120.20
40	1o	1028	DT	P-O3'-C3'	9.35	134.23	120.20
100	3N	3994	DA	P-O3'-C3'	9.35	134.22	120.20
15	1P	12	DG	P-O3'-C3'	9.35	134.22	120.20
52	2B	1031	DC	P-O3'-C3'	9.34	134.21	120.20
100	3N	7944	DG	P-O3'-C3'	9.34	134.20	120.20
68	2S	1053	DA	OP1-P-O3'	-9.31	80.07	108.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
65	2P	1062	DG	O5'-P-OP1	-9.30	81.09	109.00
100	3N	7180	DT	P-O3'-C3'	9.30	134.15	120.20
100	3N	4818	DA	P-O3'-C3'	9.30	134.15	120.20
108	3H	2139	DC	P-O3'-C3'	9.28	134.12	120.20
27	1b	6	DG	P-O3'-C3'	9.27	134.11	120.20
76	2a	1086	DG	P-O3'-C3'	9.26	134.08	120.20
100	3N	4939	DG	P-O3'-C3'	9.23	134.05	120.20
100	3N	3248	DA	P-O3'-C3'	9.22	134.03	120.20
100	3N	3589	DG	P-O3'-C3'	9.15	133.93	120.20
79	2d	1027	DG	P-O3'-C3'	9.10	133.85	120.20
68	2S	1054	DA	O5'-P-OP1	-9.10	81.72	109.00
100	3N	8071	DC	P-O3'-C3'	9.10	133.84	120.20
100	3N	8288	DT	P-O3'-C3'	9.09	133.83	120.20
100	3N	4210	DG	P-O3'-C3'	9.09	133.83	120.20
100	3N	6637	DA	P-O3'-C3'	9.05	133.77	120.20
100	3N	5237	DT	P-O3'-C3'	9.03	133.74	120.20
118	3R	2089	DG	P-O3'-C3'	8.98	133.67	120.20
6	1F	9	DA	P-O3'-C3'	8.97	133.66	120.20
65	2P	1061	DC	OP2-P-O3'	-8.97	81.09	108.00
100	3N	3123	DA	P-O3'-C3'	8.96	133.63	120.20
117	3Q	2101	DT	P-O3'-C3'	8.89	133.54	120.20
100	3N	4972	DT	P-O3'-C3'	8.87	133.51	120.20
100	3N	3216	DT	P-O3'-C3'	8.87	133.50	120.20
100	3N	8458	DG	P-O3'-C3'	8.86	133.49	120.20
100	3N	5131	DA	P-O3'-C3'	8.79	133.38	120.20
100	3N	3379	DC	P-O3'-C3'	8.77	133.36	120.20
100	3N	6924	DC	P-O3'-C3'	8.74	133.31	120.20
65	2P	1061	DC	OP1-P-O3'	-8.73	81.82	108.00
100	3N	8313	DT	P-O3'-C3'	8.73	133.29	120.20
60	2J	1068	DA	P-O3'-C3'	8.70	133.25	120.20
100	3N	7085	DA	P-O3'-C3'	8.69	133.24	120.20
77	2b	1073	DA	O5'-P-OP2	-8.67	81.99	108.00
100	3N	3418	DG	P-O3'-C3'	8.66	133.20	120.20
6	1F	8	DA	P-O3'-C3'	8.64	133.16	120.20
100	3N	4452	DG	P-O3'-C3'	8.63	133.15	120.20
77	2b	1072	DG	OP1-P-O3'	-8.61	82.18	108.00
96	2u	2086	DT	P-O3'-C3'	8.56	133.04	120.20
65	2P	1062	DG	O5'-P-OP2	-8.56	82.33	108.00
34	1i	14	DC	P-O3'-C3'	8.48	132.92	120.20
100	3N	4092	DG	P-O3'-C3'	8.45	132.87	120.20
100	3N	7809	DG	P-O3'-C3'	8.44	132.87	120.20
100	3N	5379	DC	P-O3'-C3'	8.42	132.83	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
100	3N	7805	DT	P-O3'-C3'	8.40	132.80	120.20
100	3N	7052	DA	P-O3'-C3'	8.32	132.68	120.20
66	2Q	1071	DG	P-O3'-C3'	8.30	132.65	120.20
77	2b	1072	DG	OP2-P-O3'	-8.28	83.17	108.00
46	1u	1046	DG	P-O3'-C3'	8.24	132.56	120.20
41	1p	1042	DG	P-O3'-C3'	8.22	132.53	120.20
82	2g	1082	DG	P-O3'-C3'	8.19	132.49	120.20
31	1f	21	DA	P-O3'-C3'	8.17	132.45	120.20
39	1n	1050	DC	P-O3'-C3'	8.17	132.45	120.20
100	3N	6990	DT	P-O3'-C3'	8.12	132.39	120.20
100	3N	7725	DA	P-O3'-C3'	8.08	132.31	120.20
100	3N	4663	DA	P-O3'-C3'	8.04	132.25	120.20
28	1c	23	DA	P-O3'-C3'	8.01	132.21	120.20
100	3N	7166	DC	P-O3'-C3'	7.97	132.16	120.20
52	2B	1024	DA	P-O3'-C3'	7.89	132.04	120.20
100	3N	4917	DT	P-O3'-C3'	7.83	131.94	120.20
82	2g	1080	DT	P-O3'-C3'	7.74	131.81	120.20
100	3N	7211	DT	P-O3'-C3'	7.73	131.80	120.20
100	3N	7911	DG	P-O3'-C3'	7.71	131.76	120.20
106	3F	2101	DT	P-O3'-C3'	7.66	131.69	120.20
95	2t	2055	DG	P-O3'-C3'	7.64	131.67	120.20
13	1M	1	DC	P-O3'-C3'	7.59	131.59	120.20
68	2S	1054	DA	O5'-P-OP2	-7.59	85.24	108.00
108	3H	2120	DC	P-O3'-C3'	7.58	131.57	120.20
46	1u	1047	DC	P-O3'-C3'	7.58	131.56	120.20
97	2v	2038	DG	P-O3'-C3'	7.54	131.51	120.20
52	2B	1032	DC	P-O3'-C3'	7.48	131.42	120.20
103	3C	2105	DA	P-O3'-C3'	7.47	131.40	120.20
98	2w	2084	DC	P-O3'-C3'	7.45	131.38	120.20
100	3N	5268	DG	P-O3'-C3'	7.44	131.36	120.20
7	1G	8	DA	P-O3'-C3'	7.41	131.31	120.20
95	2t	2071	DT	P-O3'-C3'	7.39	131.29	120.20
26	1a	16	DT	P-O3'-C3'	7.36	131.24	120.20
108	3H	2103	DG	P-O3'-C3'	7.29	131.13	120.20
100	3N	5077	DG	P-O3'-C3'	7.24	131.05	120.20
38	1m	1018	DG	P-O3'-C3'	7.22	131.04	120.20
100	3N	5108	DA	P-O3'-C3'	7.22	131.03	120.20
39	1n	1026	DA	P-O3'-C3'	7.13	130.90	120.20
100	3N	6828	DG	P-O3'-C3'	7.08	130.82	120.20
51	2A	1062	DC	P-O3'-C3'	7.07	130.81	120.20
50	2N	1075	DT	P-O3'-C3'	7.05	130.78	120.20
46	1u	1032	DT	P-O3'-C3'	7.03	130.75	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
68	2S	1054	DA	OP1-P-OP2	7.00	141.00	120.00
16	1Q	29	DG	P-O3'-C3'	6.98	130.67	120.20
17	1R	33	DT	P-O3'-C3'	6.97	130.65	120.20
75	2Z	1063	DT	P-O3'-C3'	6.97	130.65	120.20
43	1r	1015	DA	P-O3'-C3'	6.96	130.64	120.20
100	3N	7337	DT	P-O3'-C3'	6.92	130.58	120.20
100	3N	5145	DA	P-O3'-C3'	6.91	130.56	120.20
65	2P	1062	DG	OP1-P-OP2	6.90	140.71	120.00
46	1u	1048	DC	P-O3'-C3'	6.87	130.50	120.20
104	3D	2116	DA	P-O3'-C3'	6.81	130.42	120.20
100	3N	8046	DG	P-O3'-C3'	6.75	130.32	120.20
75	2Z	1064	DT	P-O3'-C3'	6.67	130.21	120.20
105	3E	2091	DA	P-O3'-C3'	6.59	130.08	120.20
100	3N	6837	DT	P-O3'-C3'	6.50	129.94	120.20
93	2r	2054	DG	P-O3'-C3'	6.48	129.92	120.20
100	3N	7784	DC	P-O3'-C3'	6.48	129.92	120.20
100	3N	6908	DC	P-O3'-C3'	6.46	129.88	120.20
17	1R	25	DG	P-O3'-C3'	6.44	129.87	120.20
31	1f	14	DC	P-O3'-C3'	6.26	129.60	120.20
100	3N	3168	DG	P-O3'-C3'	6.24	129.56	120.20
114	3M	2097	DG	P-O3'-C3'	6.22	129.53	120.20
98	2w	2069	DA	P-O3'-C3'	6.19	129.49	120.20
2	1B	47	DG	P-O3'-C3'	6.10	129.35	120.20
24	1Y	17	DA	P-O3'-C3'	6.05	129.27	120.20
100	3N	5471	DA	P-O3'-C3'	6.04	129.25	120.20
74	2Y	1051	DC	P-O5'-C5'	5.99	128.99	120.00
118	3R	2093	DT	P-O3'-C3'	5.95	129.12	120.20
100	3N	4758	DC	P-O3'-C3'	5.87	129.00	120.20
100	3N	4470	DC	P-O3'-C3'	5.80	128.90	120.20
64	2O	1059	DG	P-O3'-C3'	5.77	128.85	120.20
100	3N	3683	DT	O4'-C1'-C2'	-5.76	97.75	106.40
98	2w	2070	DC	P-O3'-C3'	5.70	128.75	120.20
41	1p	1018	DA	P-O3'-C3'	5.67	128.71	120.20
100	3N	4333	DA	P-O3'-C3'	5.66	128.69	120.20
115	3O	2080	DG	P-O3'-C3'	5.63	128.65	120.20
77	2b	1073	DA	OP1-P-OP2	5.63	136.89	120.00
100	3N	4217	DG	P-O3'-C3'	5.61	128.62	120.20
100	3N	6591	DC	P-O3'-C3'	5.57	128.56	120.20
64	2O	1060	DC	O5'-C5'-C4'	5.54	119.12	110.80
100	3N	3882	DG	P-O3'-C3'	5.53	128.50	120.20
100	3N	3438	DA	P-O3'-C3'	5.53	128.50	120.20
100	3N	4985	DC	P-O3'-C3'	5.52	128.48	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
87	2l	1032	DG	P-O3'-C3'	5.51	128.47	120.20
87	2l	1034	DC	P-O3'-C3'	5.51	128.46	120.20
87	2l	1018	DA	P-O3'-C3'	5.49	128.43	120.20
100	3N	3567	DT	P-O3'-C3'	5.49	128.43	120.20
91	2p	2068	DC	P-O5'-C5'	5.48	128.22	120.00
100	3N	5452	DA	P-O3'-C3'	5.47	128.41	120.20
28	1c	26	DA	P-O3'-C3'	5.45	128.38	120.20
100	3N	4012	DC	P-O3'-C3'	5.45	128.37	120.20
4	1D	48	DA	P-O5'-C5'	5.42	128.13	120.00
114	3M	2080	DG	P-O3'-C3'	5.42	128.32	120.20
61	2K	1023	DG	P-O5'-C5'	5.40	128.09	120.00
110	3J	2048	DC	P-O3'-C3'	-5.37	112.14	120.20
76	2a	1067	DT	P-O3'-C3'	5.32	128.19	120.20
100	3N	7839	DT	P-O5'-C5'	5.30	127.95	120.00
55	2E	1055	DT	O4'-C1'-C2'	-5.29	98.47	106.40
4	1D	5	DT	P-O3'-C3'	5.27	128.11	120.20
65	2P	1067	DG	P-O3'-C3'	5.25	128.08	120.20
100	3N	8360	DC	P-O3'-C3'	5.25	128.08	120.20
100	3N	4652	DA	P-O3'-C3'	5.23	128.05	120.20
53	2C	1073	DT	P-O5'-C5'	5.23	127.84	120.00
100	3N	7710	DA	P-O3'-C3'	5.22	128.03	120.20
11	1K	13	DG	P-O3'-C3'	5.19	127.99	120.20
95	2t	2055	DG	C4'-C3'-O3'	5.19	117.78	110.00
100	3N	6782	DC	P-O3'-C3'	5.17	127.95	120.20
100	3N	7981	DG	O4'-C1'-C2'	-5.17	98.65	106.40
39	1n	1059	DG	P-O3'-C3'	5.16	127.94	120.20
27	1b	27	DC	P-O3'-C3'	5.14	127.91	120.20
57	2G	1081	DA	P-O5'-C5'	5.14	127.71	120.00
100	3N	5196	DT	P-O3'-C3'	5.13	127.90	120.20
100	3N	3528	DG	O4'-C1'-C2'	-5.11	98.73	106.40
31	1f	9	DG	P-O5'-C5'	5.11	127.66	120.00
46	1u	1039	DG	P-O3'-C3'	5.10	127.85	120.20
100	3N	6933	DC	P-O5'-C5'	5.09	127.64	120.00
100	3N	7478	DT	P-O3'-C3'	5.09	127.83	120.20
50	2N	1053	DA	O5'-C5'-C4'	5.08	118.41	110.80
79	2d	1046	DT	C4'-C3'-O3'	5.07	117.61	110.00
100	3N	7398	DA	P-O3'-C3'	5.06	127.80	120.20
100	3N	6878	DG	P-O3'-C3'	5.06	127.79	120.20
2	1B	54	DA	P-O3'-C3'	5.04	127.77	120.20
100	3N	7157	DG	P-O3'-C3'	5.04	127.77	120.20
5	1E	27	DC	P-O3'-C3'	5.04	127.76	120.20
100	3N	5175	DG	O4'-C1'-C2'	-5.02	98.87	106.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
79	2d	1027	DG	O4'-C1'-C2'	-5.02	98.87	106.40
3	1C	10	DT	P-O3'-C3'	5.00	127.70	120.20

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
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

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Mol	Chain	Res	Type	Group
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
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

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Mol	Chain	Res	Type	Group
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
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

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Mol	Chain	Res	Type	Group
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
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

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Mol	Chain	Res	Type	Group
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
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

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Mol	Chain	Res	Type	Group
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
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

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Mol	Chain	Res	Type	Group
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
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

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Mol	Chain	Res	Type	Group
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
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

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Mol	Chain	Res	Type	Group
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
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

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Mol	Chain	Res	Type	Group
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
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

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	0	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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	1	0
28	1c	820	0	455	0	0
29	1d	826	0	452	0	0
30	1e	524	0	294	1	0
31	1f	804	0	453	1	0
32	1g	982	0	539	0	0
33	1h	993	0	542	0	0
34	1i	986	0	544	1	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	1	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	1	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

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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
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	1	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	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
99	2x	320	0	180	0	0
100	3N	88890	0	49198	33	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
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	53	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 (53) 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
40:1o:1019:DA:H2'	40:1o:1020:DC:C6	2.48	0.49
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
27:1b:26:DA:H2'	27:1b:27:DC:C6	2.50	0.47
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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
112:3K:2057:DC:H2'	112:3K:2058:DC:C6	2.51	0.45
31:1f:22:DA:H2''	31:1f:23:DC:C6	2.52	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
34:1i:25:DT:H2'	34:1i:26:DC:C5	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
46:1u:1059:DG:H2''	46:1u:1060:DA:C8	2.55	0.42
7:1G:9:DG:H2'	7:1G:10:DC:C5	2.54	0.42
98:2w:2087:DA:H2''	98:2w:2088:DA:C8	2.54	0.42
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
85:2j:1043:DA:C2	100:3N:4265:DA:C2	3.07	0.41
30:1e:4:DC:H2'	30:1e:5:DC:C5	2.56	0.41
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
98:2w:2096:DA:H2'	98:2w:2097:DC:C6	2.55	0.40
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 oligosaccharides 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.

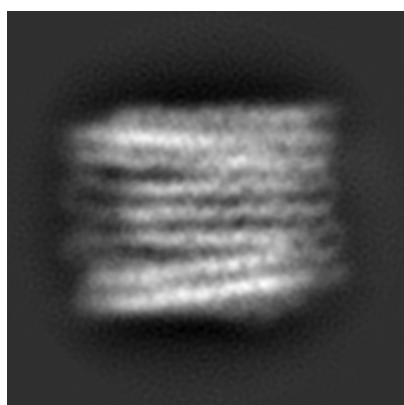
6 Map visualisation [i](#)

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.

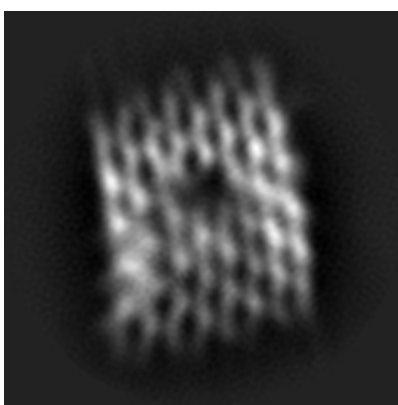
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

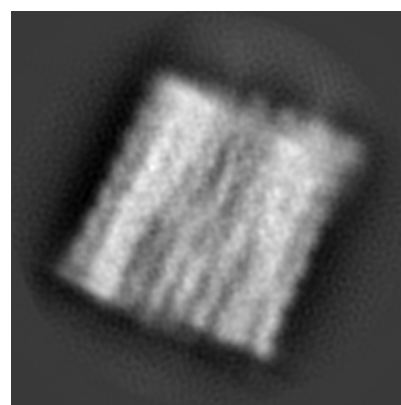
6.1.1 Primary map



X



Y



Z

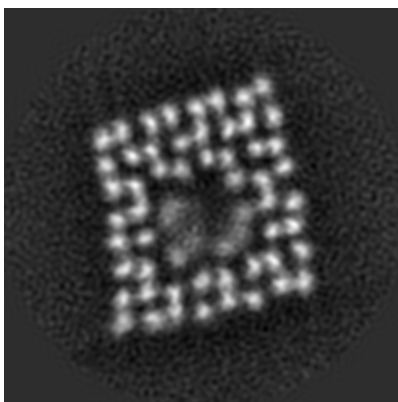
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

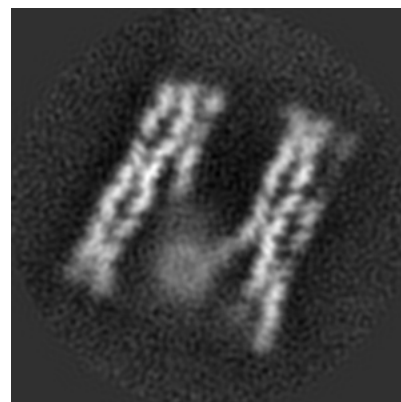
6.2.1 Primary map



X Index: 300



Y Index: 300

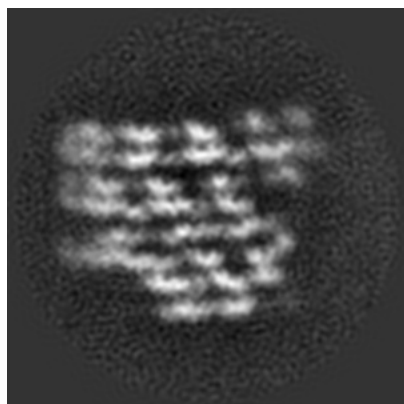


Z Index: 300

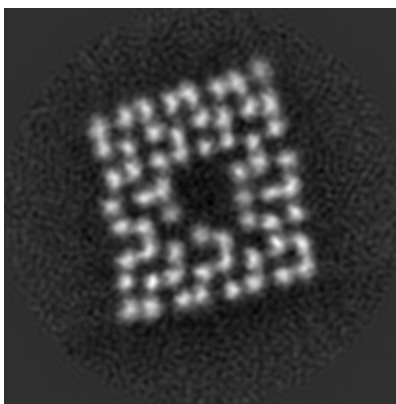
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

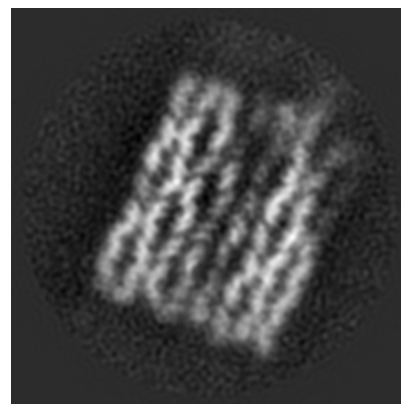
6.3.1 Primary map



X Index: 389



Y Index: 340

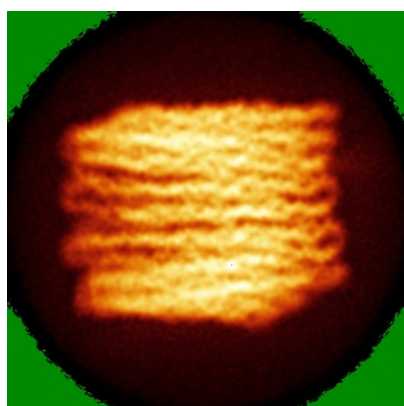


Z Index: 408

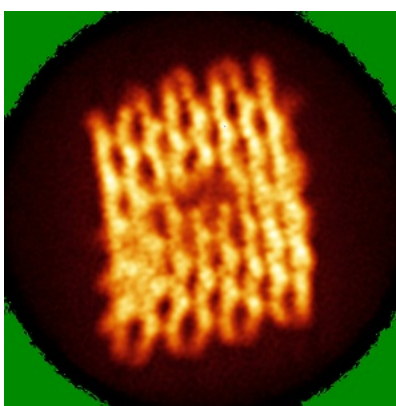
The images above show the largest variance slices of the map in three orthogonal directions.

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

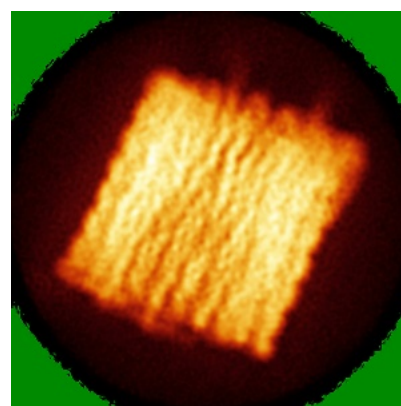
6.4.1 Primary map



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

This section was not generated.

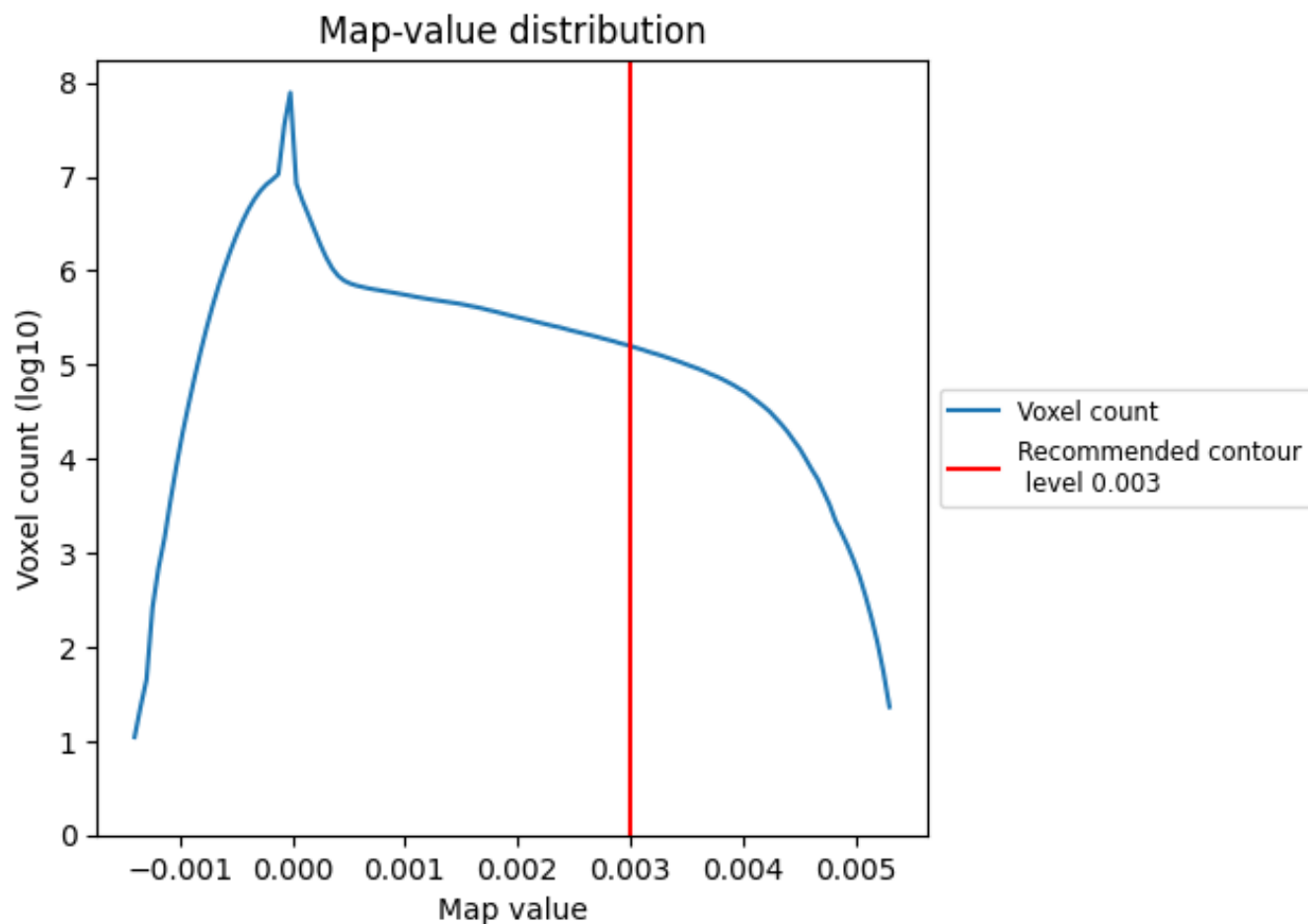
6.6 Mask visualisation

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

7 Map analysis [i](#)

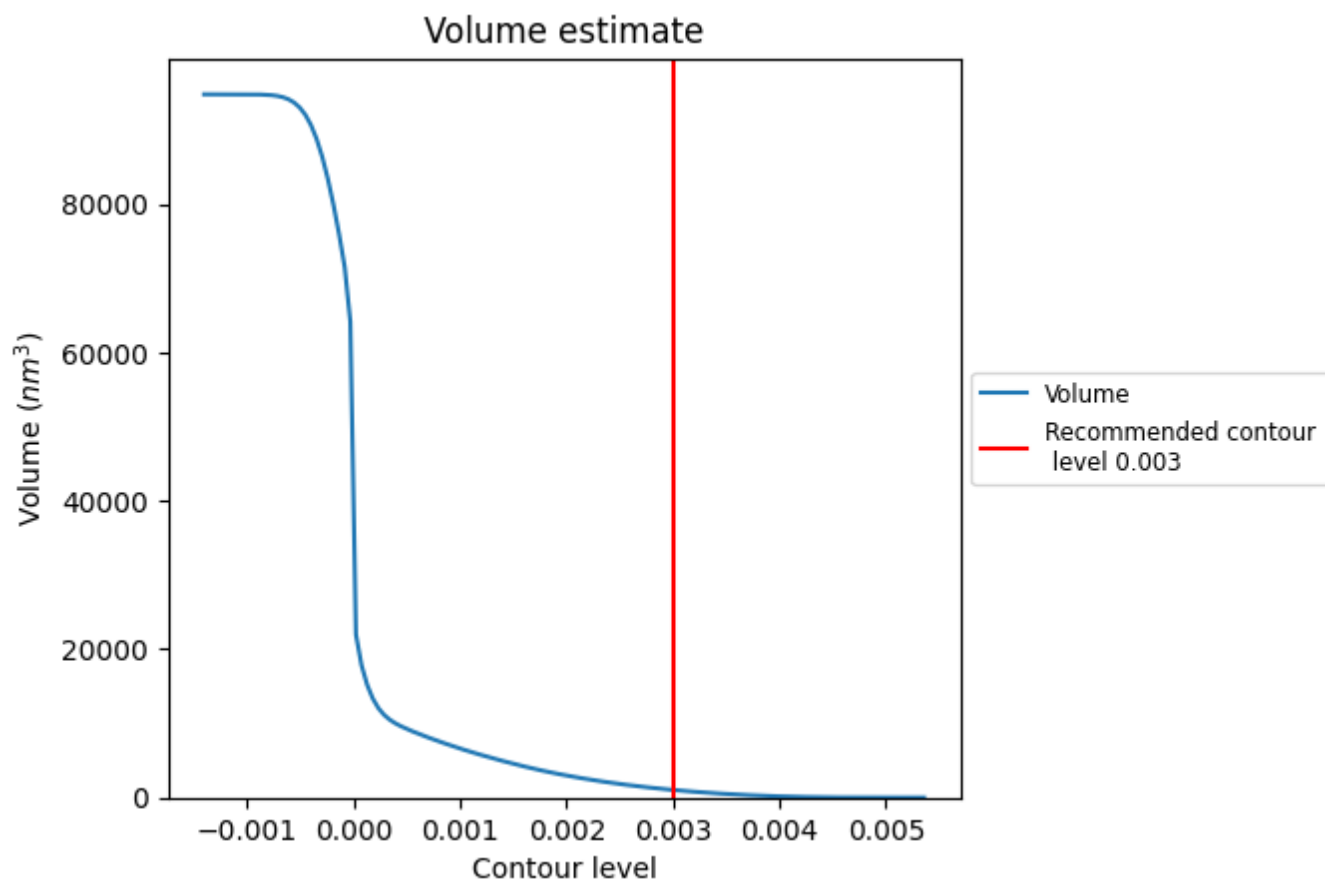
This section contains the results of statistical analysis of the map.

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.

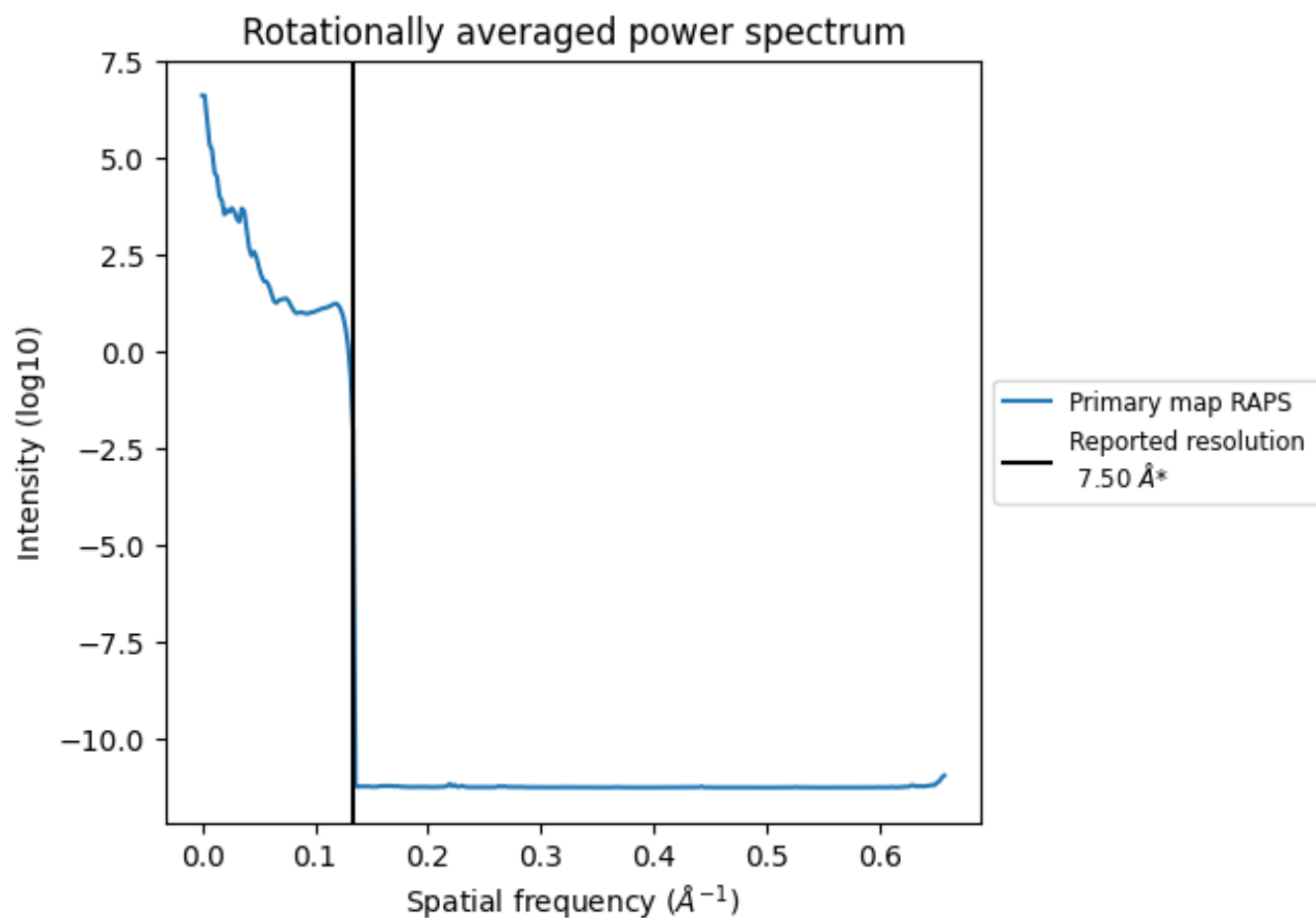
7.2 Volume estimate [i](#)



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 ⓘ



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

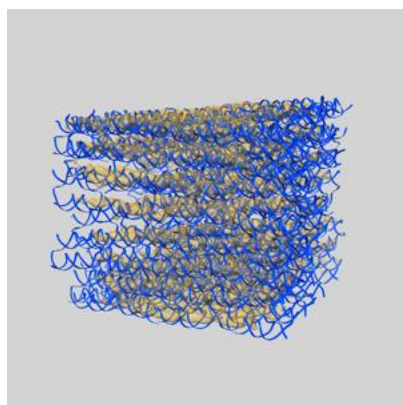
8 Fourier-Shell correlation ⓘ

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

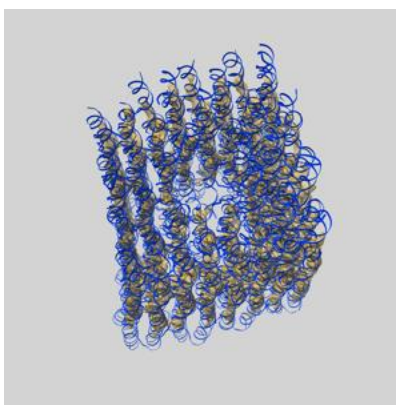
9 Map-model fit [i](#)

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](#).

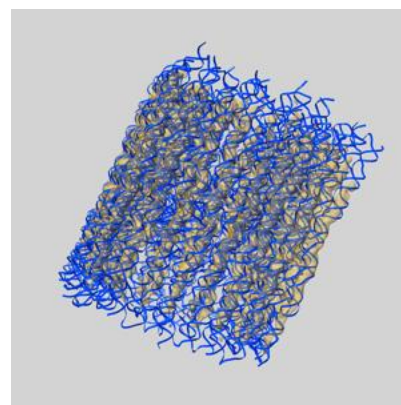
9.1 Map-model overlay [i](#)



X



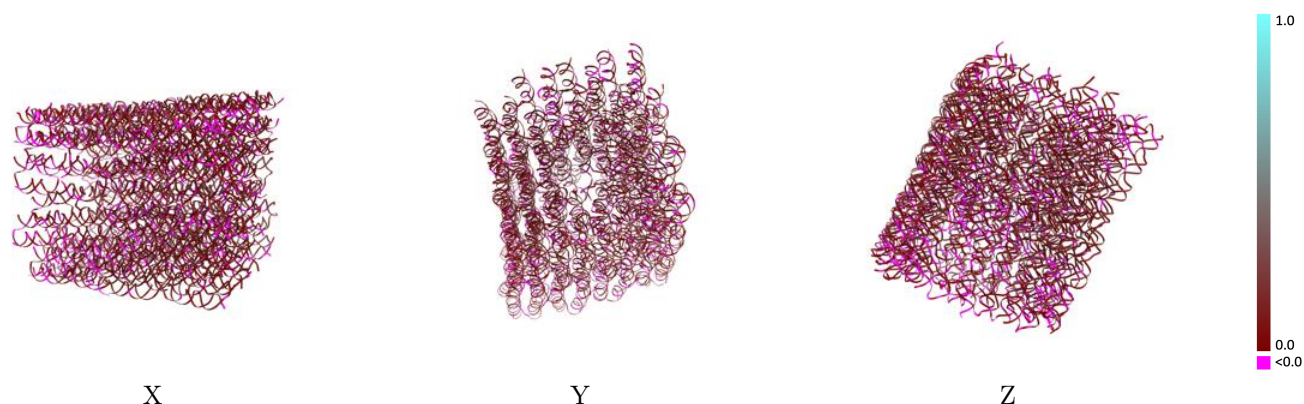
Y



Z

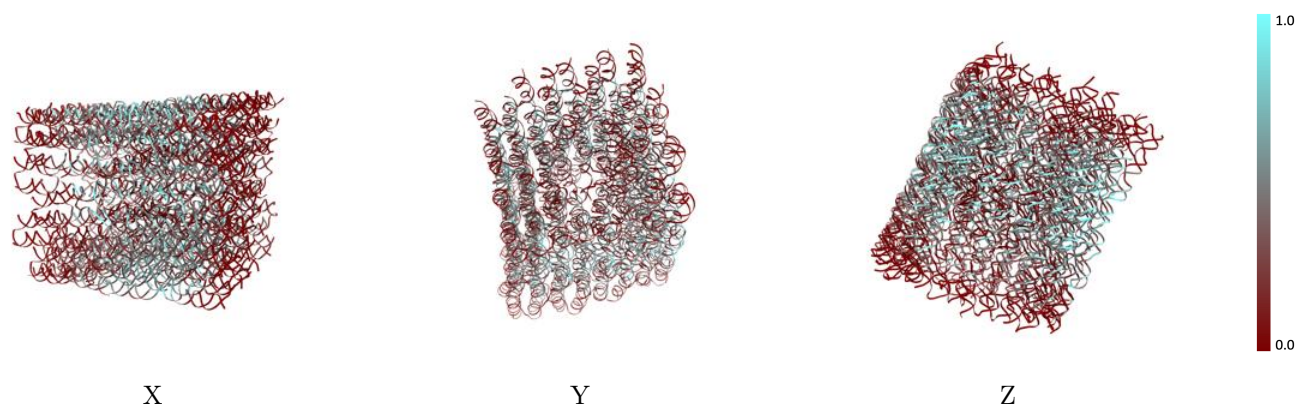
The images above show the 3D surface view of the map at the recommended contour level 0.003 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



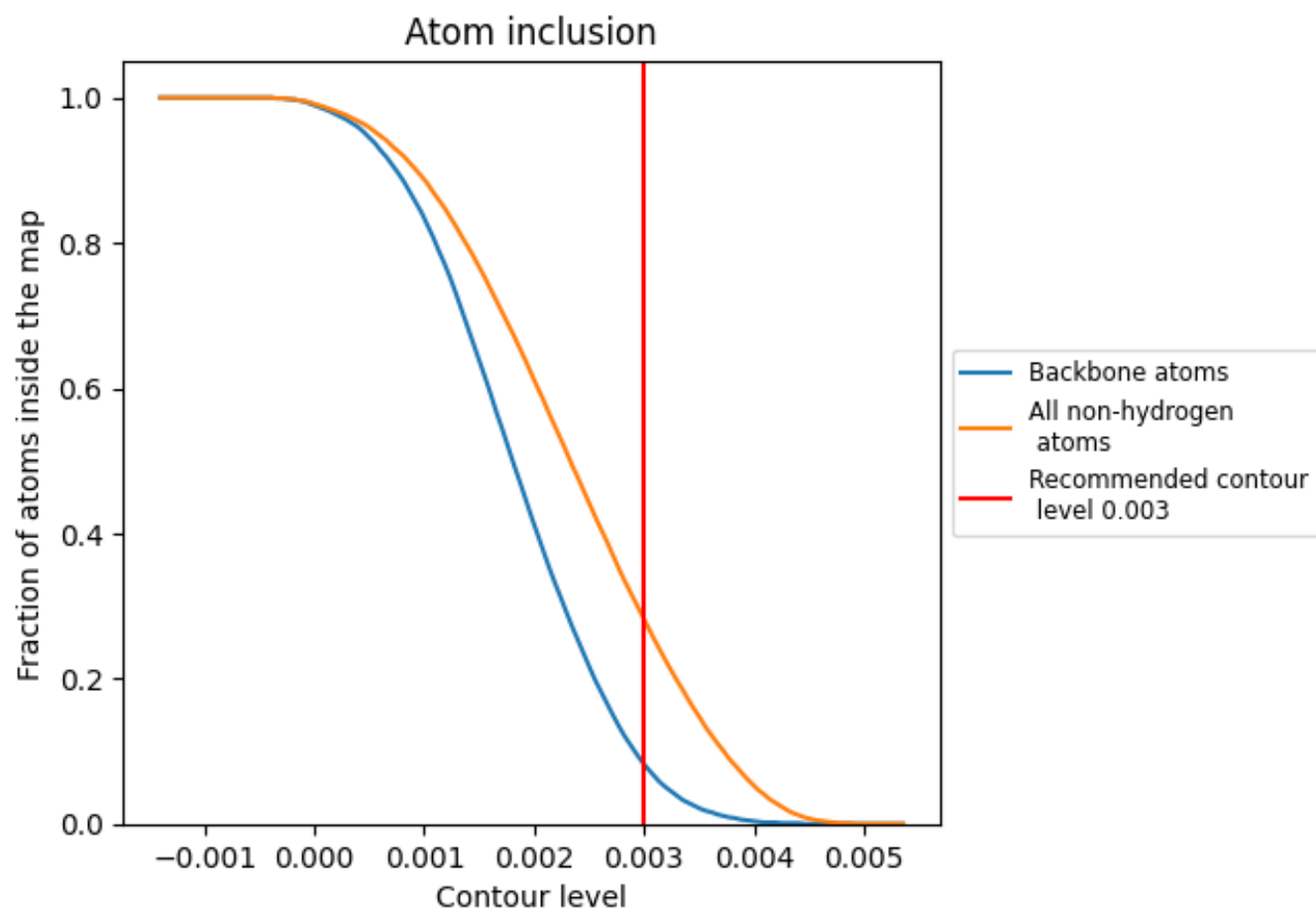
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.003).

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