



wwPDB EM Validation Summary Report ⓘ

Nov 19, 2022 – 11:28 pm GMT

PDB ID : 4V5X
EMDB ID : EMD-2210
Title : The cryo-EM structure of a 3D DNA-origami object
Authors : Bai, X.C.; Martin, T.G.; Scheres, S.H.W.; Dietz, H.
Deposited on : 2012-10-09
Resolution : 11.50 Å(reported)

This is a wwPDB EM Validation Summary 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.dev43
MolProbity : 4.02b-467
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2


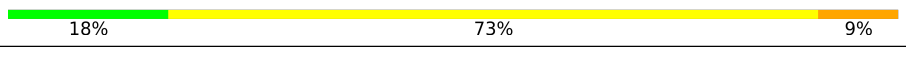
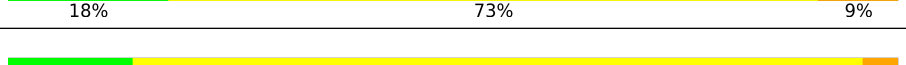
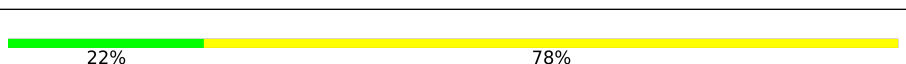
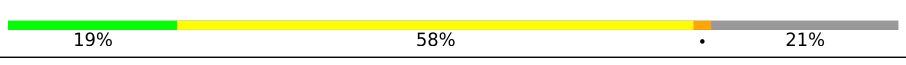
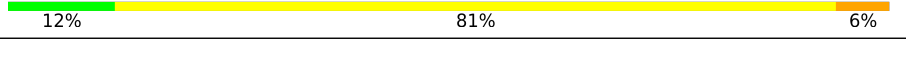
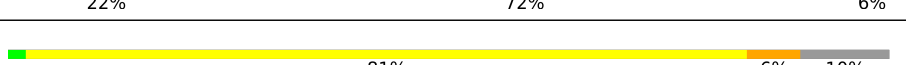
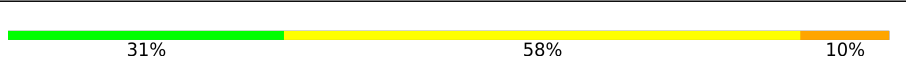
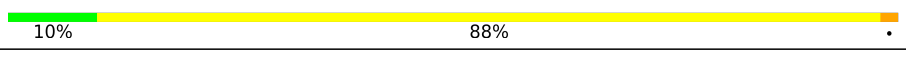
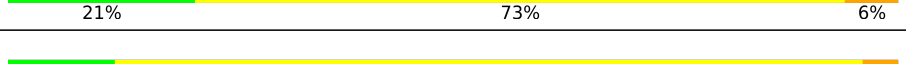
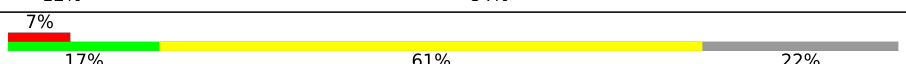
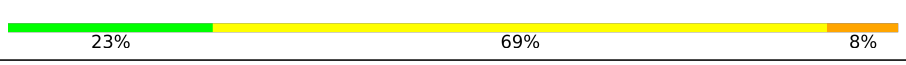
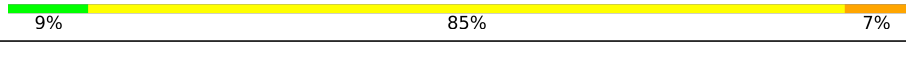
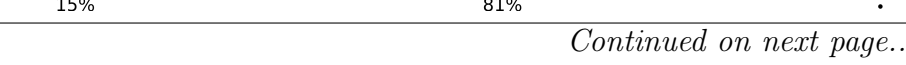


1 Overall quality at a glance

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

The reported resolution of this entry is 11.50 Å.

There are no overall percentile quality scores available for this entry.

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	AA	7249	 29% 66% 6%
2	A0	55	 18% 73% 9%
3	A1	44	 18% 73% 9%
4	A2	50	 14% 82% .
5	A3	40	 22% 78%
6	A4	48	 19% 58% . 21%
7	A5	48	 12% 81% 6%
8	A6	50	 22% 72% 6%
9	A7	48	 . 81% 6% 10%
10	A8	48	 31% 58% 10%
11	AB	40	 10% 88% .
12	AC	48	 21% 73% 6%
13	AD	50	 12% 84% .
14	AE	46	 7% 17% 61% 22%
15	AF	48	 23% 69% 8%
16	AG	46	 9% 85% 7%
17	AH	48	15% 81% .

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Mol	Chain	Length	Quality of chain
18	AI	48	17% 79%
19	AJ	52	25% 67% 8%
20	AK	60	25% 65% 10%
21	AL	48	29% 63% 8%
22	AM	50	28% 70%
23	AN	48	15% 79% 6%
24	AO	48	25% 69% 6%
25	AP	40	15% 82%
26	AQ	57	11% 79% 11%
27	AR	63	14% 59% 24%
28	AS	64	8% 47% 6% 39%
29	AT	48	17% 75% 8%
30	AU	48	12% 81% 6%
31	AV	52	21% 69% 10%
32	AW	50	18% 24% 46% 30%
33	AX	48	15% 83%
34	AY	42	24% 5% 62% 10% 24%
35	AZ	54	11% 81% 7%
36	Ab	45	24% 71%
37	Ac	70	17% 59% 21%
38	Ad	48	25% 73%
39	Af	48	15% 83%
40	Ag	48	23% 75%
41	Ah	44	30% 64% 7%
42	Ai	46	9% 67% 22%

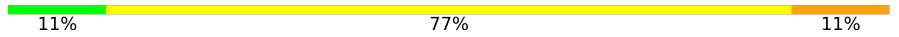
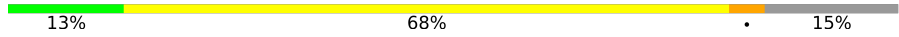

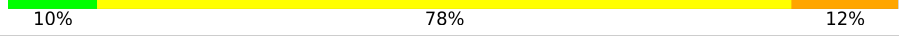
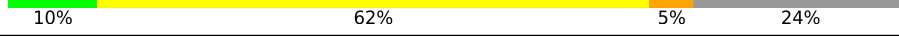
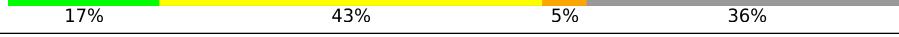
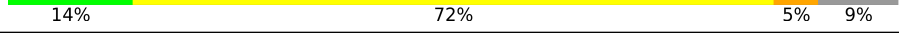

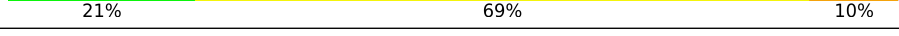
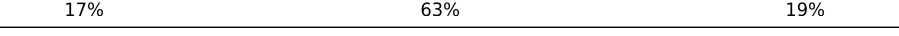
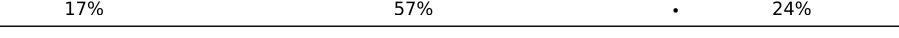
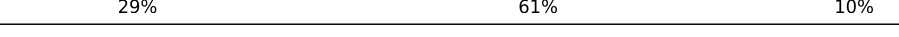

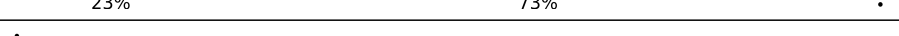


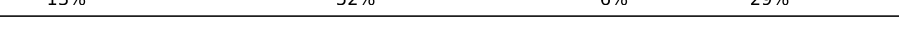
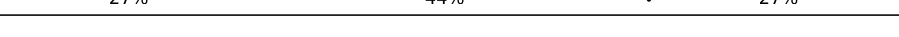
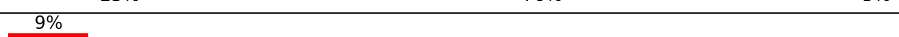




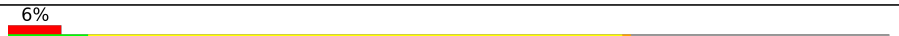

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Mol	Chain	Length	Quality of chain
43	Aj	62	16% 76% 8%
44	Ak	46	11% 74% 15%
45	Al	48	29% 63% 8%
46	Am	48	15% 83% .
47	An	48	25% 67% 8%
48	Ao	36	8% 89% .
49	As	48	33% 63% .
50	Au	48	27% 73%
51	Av	48	15% 63% 12% 10%
52	Aw	48	31% 65% .
53	Ax	52	21% 65% . 10%
54	Ay	38	11% 61% . 26%
55	Az	51	14% 51% 6% 29%
56	B0	48	19% 69% 12%
57	B1	59	15% 58% . 25%
58	B2	36	6% 89% 6%
59	B3	48	19% 79% .
60	B4	48	8% 50% 10% 31%
61	B5	40	18% 78% 5%
62	B6	50	8% 74% 8% 10%
63	B7	44	34% 57% 9%
64	B8	40	15% 68% 18%
65	B9	55	18% 51% . 27%
66	BB	48	17% 79% .
67	BC	44	23% 64% . 11%

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Mol	Chain	Length	Quality of chain
68	BD	35	
69	BE	68	
70	BF	40	
71	BG	49	
72	BH	42	
73	BI	42	
74	BJ	58	
75	BK	44	
76	BL	48	
77	BM	52	
78	BN	63	
79	BO	49	
80	BP	66	
81	BQ	48	
82	BR	64	
83	BS	48	
84	BT	52	
85	BU	55	
86	BV	44	
87	BW	53	
88	BX	48	
89	BY	48	
90	BZ	66	
91	Ba	48	
92	Bb	68	

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Mol	Chain	Length	Quality of chain
93	Bc	50	
94	Bd	56	
95	Be	48	
96	Bf	48	
97	Bg	47	
98	Bh	48	
99	Bi	67	
100	Bj	45	
101	Bk	67	
102	Bl	48	
103	Bm	48	
104	Bn	67	
105	Bo	67	
106	Bp	48	
107	Bq	58	
108	Br	51	
109	Bs	54	
110	C0	41	
111	C1	51	
112	C2	56	
113	C3	48	
114	C4	71	
115	C5	62	
116	C6	48	
117	C7	52	

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Mol	Chain	Length	Quality of chain
118	C8	44	27% 66% 7%
119	CB	54	33% 61% 6%
120	CC	47	21% 72% 6%
121	CD	48	19% 75% 6%
122	CE	40	18% 78% 5%
123	CF	40	22% 75% .
124	CG	44	25% 66% 9%
125	CH	48	29% 63% 8%
126	CI	44	18% 73% 9%
127	CJ	59	15% 58% 7% 20%
128	CK	48	17% 75% 8%
129	CL	48	25% 67% 8%
130	CM	54	9% 26% 63% 28%
131	CN	41	7% 22% 76% .
132	CO	48	31% 54% 15%
133	CP	56	20% 73% 7%
134	CQ	38	16% 55% . 26%
135	CR	48	27% 73%
136	CS	48	19% 54% 6% 21%
137	CT	48	15% 79% 6%
138	CU	32	19% 78% .
139	CV	53	32% 62% 6%
140	CW	38	18% 47% 8% 26%
141	CX	47	21% 72% 6%
142	CY	43	19% 81%

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Mol	Chain	Length	Quality of chain
143	CZ	48	15% 77% 8%
144	Cb	44	27% 68% 5%
145	Cc	62	11% 65% 8% 16%
146	Cd	42	36% 57% 7%
147	Ce	52	19% 71% 10%
148	Cf	48	6% 15% 63% 21%
149	Cg	46	11% 59% 9% 22%
150	Ch	47	21% 74% 5%
151	Ck	29	10% 28% 72%
152	Cp	48	21% 73% 6%
153	Cq	40	22% 65% 12%
154	Cr	46	9% 65% 22%
155	Cs	49	18% 65% 16%
156	Ct	44	27% 73%
157	Cu	60	18% 78% 4%
158	Cv	46	26% 57% 7% 11%
159	Cw	54	19% 72% 9%
160	Cx	46	13% 57% 9% 22%
161	Cy	66	23% 59% 15%
162	Cz	48	8% 81% 10%

2 Entry composition [i](#)

There are 162 unique types of molecules in this entry. The entry contains 294953 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 SCAFFOLD STRAND,SCAFFOLD STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	AA	7249	147963	70960	25928	43933	7142	0	0

- Molecule 2 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	A0	55	1116	543	222	303	48	0	0

- Molecule 3 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	A1	44	884	433	167	247	37	0	0

- Molecule 4 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	A2	50	1019	494	214	267	44	0	0

- Molecule 5 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
5	A3	40	796	390	144	228	34	0	0

- Molecule 6 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
6	A4	38	780	377	151	216	36	0	0

- Molecule 7 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A5	48	Total	C	N	O	P	0	0
			971	469	194	265	43		

- Molecule 8 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A6	50	Total	C	N	O	P	0	0
			1016	493	194	284	45		

- Molecule 9 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	A7	43	Total	C	N	O	P	0	0
			863	412	176	236	39		

- Molecule 10 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	A8	48	Total	C	N	O	P	0	0
			976	476	181	277	42		

- Molecule 11 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AB	40	Total	C	N	O	P	0	0
			799	382	152	228	37		

- Molecule 12 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AC	48	Total	C	N	O	P	0	0
			993	475	200	274	44		

- Molecule 13 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AD	50	Total	C	N	O	P	0	0
			1018	485	202	284	47		

- Molecule 14 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AE	36	Total	C	N	O	P	0	0
			734	354	135	211	34		

- Molecule 15 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AF	48	Total	C	N	O	P	0	0
			969	467	169	287	46		

- Molecule 16 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AG	46	Total	C	N	O	P	0	0
			939	447	192	257	43		

- Molecule 17 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AH	48	Total	C	N	O	P	0	0
			964	463	179	277	45		

- Molecule 18 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AI	48	Total	C	N	O	P	0	0
			967	470	193	263	41		

- Molecule 19 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AJ	52	Total	C	N	O	P	0	0
			1059	512	202	297	48		

- Molecule 20 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AK	60	Total	C	N	O	P	0	0
			1202	588	219	344	51		

- Molecule 21 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AL	48	Total	C	N	O	P	0	0
			971	470	169	287	45		

- Molecule 22 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AM	50	Total	C	N	O	P	0	0
			993	486	177	287	43		

- Molecule 23 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AN	48	Total	C	N	O	P	0	0
			968	465	183	276	44		

- Molecule 24 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AO	48	Total	C	N	O	P	0	0
			962	466	173	279	44		

- Molecule 25 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AP	40	Total	C	N	O	P	0	0
			802	388	149	229	36		

- Molecule 26 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AQ	57	Total	C	N	O	P	0	0
			1160	556	233	321	50		

- Molecule 27 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AR	48	Total	C	N	O	P	0	0
			975	470	187	274	44		

- Molecule 28 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AS	39	Total	C	N	O	P	0	0
			794	383	169	208	34		

- Molecule 29 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AT	48	Total	C	N	O	P	0	0
			973	470	190	271	42		

- Molecule 30 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AU	48	Total	C	N	O	P	0	0
			967	470	193	263	41		

- Molecule 31 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AV	52	Total	C	N	O	P	0	0
			1051	510	201	294	46		

- Molecule 32 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	AW	35	Total	C	N	O	P	0	0
			701	342	120	206	33		

- Molecule 33 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	AX	48	Total	C	N	O	P	0	0
			959	465	186	266	42		

- Molecule 34 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	AY	32	Total	C	N	O	P	0	0
			645	309	126	181	29		

- Molecule 35 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	AZ	54	Total	C	N	O	P	0	0
			1082	524	208	303	47		

- Molecule 36 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Ab	45	Total	C	N	O	P	0	0
			907	440	169	258	40		

- Molecule 37 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Ac	55	Total	C	N	O	P	0	0
			1115	542	220	305	48		

- Molecule 38 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Ad	48	Total	C	N	O	P	0	0
			958	468	171	277	42		

- Molecule 39 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Af	48	Total	C	N	O	P	0	0
			964	468	192	262	42		

- Molecule 40 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Ag	48	Total	C	N	O	P	0	0
			979	470	187	278	44		

- Molecule 41 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Ah	44	Total	C	N	O	P	0	0
			872	427	149	257	39		

- Molecule 42 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Ai	36	Total	C	N	O	P	0	0
			722	348	141	201	32		

- Molecule 43 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Aj	62	Total	C	N	O	P	0	0
			1257	610	248	344	55		

- Molecule 44 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Ak	46	Total	C	N	O	P	0	0
			946	454	197	255	40		

- Molecule 45 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Al	48	Total	C	N	O	P	0	0
			949	467	163	278	41		

- Molecule 46 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Am	48	Total	C	N	O	P	0	0
			963	466	182	273	42		

- Molecule 47 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	An	48	Total	C	N	O	P	0	0
			972	469	179	280	44		

- Molecule 48 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Ao	36	Total	C	N	O	P	0	0
			724	349	140	204	31		

- Molecule 49 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	As	48	Total	C	N	O	P	0	0
			971	476	172	281	42		

- Molecule 50 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Au	48	Total	C	N	O	P	0	0
			963	468	168	283	44		

- Molecule 51 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Av	43	Total	C	N	O	P	0	0
			869	419	172	240	38		

- Molecule 52 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Aw	48	Total	C	N	O	P	0	0
			960	470	172	276	42		

- Molecule 53 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	Ax	47	Total	C	N	O	P	0	0
			953	460	176	274	43		

- Molecule 54 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	Ay	28	Total	C	N	O	P	0	0
			568	275	112	156	25		

- Molecule 55 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	Az	36	Total	C	N	O	P	0	0
			737	355	146	204	32		

- Molecule 56 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	B0	48	Total	C	N	O	P	0	0
			977	467	184	282	44		

- Molecule 57 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	B1	44	Total	C	N	O	P	0	0
			900	434	181	245	40		

- Molecule 58 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	B2	36	Total	C	N	O	P	0	0
			734	350	148	203	33		

- Molecule 59 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	B3	48	Total	C	N	O	P	0	0
			976	469	182	280	45		

- Molecule 60 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	B4	33	Total	C	N	O	P	0	0
			664	320	130	184	30		

- Molecule 61 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	B5	40	Total	C	N	O	P	0	0
			816	392	160	227	37		

- Molecule 62 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	B6	45	Total	C	N	O	P	0	0
			929	443	187	256	43		

- Molecule 63 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	B7	44	Total	C	N	O	P	0	0
			892	432	153	266	41		

- Molecule 64 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	B8	33	Total	C	N	O	P	0	0
			653	315	120	187	31		

- Molecule 65 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	B9	40	Total	C	N	O	P	0	0
			810	393	150	231	36		

- Molecule 66 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	BB	48	Total	C	N	O	P	0	0
			982	469	191	276	46		

- Molecule 67 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	BC	39	Total	C	N	O	P	0	0
			798	385	152	224	37		

- Molecule 68 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	BD	35	Total	C	N	O	P	0	0
			727	344	151	199	33		

- Molecule 69 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	BE	58	Total	C	N	O	P	0	0
			1183	569	229	331	54		

- Molecule 70 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	BF	40	Total	C	N	O	P	0	0
			810	395	142	236	37		

- Molecule 71 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	BG	49	Total	C	N	O	P	0	0
			1007	481	203	277	46		

- Molecule 72 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	BH	32	Total	C	N	O	P	0	0
			644	312	123	180	29		

- Molecule 73 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	BI	27	Total	C	N	O	P	0	0
			544	265	98	156	25		

- Molecule 74 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	BJ	53	Total	C	N	O	P	0	0
			1076	517	200	310	49		

- Molecule 75 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	BK	44	Total	C	N	O	P	0	0
			894	433	176	245	40		

- Molecule 76 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	BL	48	Total	C	N	O	P	0	0
			966	467	172	283	44		

- Molecule 77 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	BM	42	Total	C	N	O	P	0	0
			855	413	160	243	39		

- Molecule 78 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	BN	48	Total	C	N	O	P	0	0
			970	468	177	280	45		

- Molecule 79 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	BO	49	Total	C	N	O	P	0	0
			984	477	168	293	46		

- Molecule 80 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	BP	41	Total	C	N	O	P	0	0
			824	399	147	240	38		

- Molecule 81 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	BQ	48	Total	C	N	O	P	0	0
			971	467	175	283	46		

- Molecule 82 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	BR	36	Total	C	N	O	P	0	0
			733	356	139	206	32		

- Molecule 83 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	BS	48	Total	C	N	O	P	0	0
			967	465	177	281	44		

- Molecule 84 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	BT	37	Total	C	N	O	P	0	0
			753	361	137	220	35		

- Molecule 85 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	BU	40	Total	C	N	O	P	0	0
			813	395	145	237	36		

- Molecule 86 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	BV	44	Total	C	N	O	P	0	0
			895	430	161	261	43		

- Molecule 87 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	BW	43	Total	C	N	O	P	0	0
			874	421	158	254	41		

- Molecule 88 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
88	BX	48	Total	C	N	O	P	0	0
			991	478	191	278	44		

- Molecule 89 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
89	BY	43	Total	C	N	O	P	0	0
			871	421	161	249	40		

- Molecule 90 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
90	BZ	43	Total	C	N	O	P	0	0
			870	419	166	245	40		

- Molecule 91 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
91	Ba	48	Total	C	N	O	P	0	0
			972	469	173	286	44		

- Molecule 92 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
92	Bb	48	Total	C	N	O	P	0	0
			974	466	191	273	44		

- Molecule 93 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
93	Bc	50	Total	C	N	O	P	0	0
			1015	487	185	297	46		

- Molecule 94 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
94	Bd	41	Total	C	N	O	P	0	0
			836	400	155	242	39		

- Molecule 95 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
95	Be	48	Total	C	N	O	P	0	0
			978	468	183	282	45		

- Molecule 96 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
96	Bf	48	Total	C	N	O	P	0	0
			981	468	192	277	44		

- Molecule 97 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
97	Bg	32	Total	C	N	O	P	0	0
			646	312	120	185	29		

- Molecule 98 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
98	Bh	38	Total	C	N	O	P	0	0
			784	375	147	226	36		

- Molecule 99 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
99	Bi	62	Total	C	N	O	P	0	0
			1255	604	233	360	58		

- Molecule 100 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
100	Bj	45	Total	C	N	O	P	0	0
			907	436	170	259	42		

- Molecule 101 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
101	Bk	47	Total	C	N	O	P	0	0
			964	461	193	266	44		

- Molecule 102 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
102	Bl	48	Total	C	N	O	P	0	0
			986	468	201	272	45		

- Molecule 103 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
103	Bm	48	Total	C	N	O	P	0	0
			964	466	176	278	44		

- Molecule 104 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
104	Bn	47	Total	C	N	O	P	0	0
			975	461	190	279	45		

- Molecule 105 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
105	Bo	57	Total	C	N	O	P	0	0
			1154	553	215	333	53		

- Molecule 106 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
106	Bp	48	Total	C	N	O	P	0	0
			985	468	198	274	45		

- Molecule 107 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
107	Bq	38	Total	C	N	O	P	0	0
			784	377	154	219	34		

- Molecule 108 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
108	Br	36	Total	C	N	O	P	0	0
			732	352	131	216	33		

- Molecule 109 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
109	Bs	39	Total	C	N	O	P	0	0
			800	380	166	218	36		

- Molecule 110 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
110	C0	31	Total	C	N	O	P	0	0
			632	303	120	180	29		

- Molecule 111 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
111	C1	36	Total	C	N	O	P	0	0
			732	354	147	198	33		

- Molecule 112 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
112	C2	56	Total	C	N	O	P	0	0
			1125	549	207	319	50		

- Molecule 113 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
113	C3	48	Total	C	N	O	P	0	0
			962	466	179	273	44		

- Molecule 114 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
114	C4	56	Total	C	N	O	P	0	0
			1133	548	208	325	52		

- Molecule 115 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
115	C5	62	Total	C	N	O	P	0	0
			1275	610	245	361	59		

- Molecule 116 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
116	C6	48	Total	C	N	O	P	0	0
			977	472	191	271	43		

- Molecule 117 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
117	C7	52	Total	C	N	O	P	0	0
			1056	515	184	309	48		

- Molecule 118 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
118	C8	44	Total	C	N	O	P	0	0
			892	433	164	256	39		

- Molecule 119 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
119	CB	54	Total	C	N	O	P	0	0
			1088	528	189	321	50		

- Molecule 120 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
120	CC	47	Total	C	N	O	P	0	0
			963	462	186	271	44		

- Molecule 121 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
121	CD	48	Total	C	N	O	P	0	0
			984	473	193	274	44		

- Molecule 122 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
122	CE	40	Total	C	N	O	P	0	0
			816	395	160	225	36		

- Molecule 123 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
123	CF	40	Total	C	N	O	P	0	0
			811	393	150	232	36		

- Molecule 124 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
124	CG	44	Total	C	N	O	P	0	0
			904	433	167	263	41		

- Molecule 125 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
125	CH	48	Total	C	N	O	P	0	0
			987	474	183	285	45		

- Molecule 126 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
126	CI	44	Total	C	N	O	P	0	0
			889	430	170	250	39		

- Molecule 127 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
127	CJ	47	Total	C	N	O	P	0	0
			946	459	183	262	42		

- Molecule 128 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
128	CK	48	Total	C	N	O	P	0	0
			981	473	196	269	43		

- Molecule 129 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
129	CL	48	Total	C	N	O	P	0	0
			967	472	179	274	42		

- Molecule 130 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
130	CM	39	Total	C	N	O	P	0	0
			801	383	163	218	37		

- Molecule 131 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
131	CN	41	Total	C	N	O	P	0	0
			848	406	164	238	40		

- Molecule 132 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
132	CO	48	Total	C	N	O	P	0	0
			975	474	180	278	43		

- Molecule 133 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
133	CP	56	Total	C	N	O	P	0	0
			1140	546	213	327	54		

- Molecule 134 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
134	CQ	28	Total	C	N	O	P	0	0
			557	273	105	155	24		

- Molecule 135 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
135	CR	48	Total	C	N	O	P	0	0
			969	469	170	284	46		

- Molecule 136 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
136	CS	38	Total	C	N	O	P	0	0
			773	374	145	219	35		

- Molecule 137 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
137	CT	48	Total	C	N	O	P	0	0
			982	474	189	276	43		

- Molecule 138 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
138	CU	32	Total	C	N	O	P	0	0
			648	312	123	182	31		

- Molecule 139 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
139	CV	53	Total	C	N	O	P	0	0
			1067	520	188	311	48		

- Molecule 140 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
140	CW	28	Total	C	N	O	P	0	0
			564	276	99	165	24		

- Molecule 141 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
141	CX	47	Total	C	N	O	P	0	0
			944	455	175	272	42		

- Molecule 142 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
142	CY	43	Total	C	N	O	P	0	0
			870	422	175	234	39		

- Molecule 143 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
143	CZ	48	Total	C	N	O	P	0	0
			987	474	201	267	45		

- Molecule 144 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
144	Cb	44	Total	C	N	O	P	0	0
			891	435	171	247	38		

- Molecule 145 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
145	Cc	52	Total	C	N	O	P	0	0
			1048	508	200	294	46		

- Molecule 146 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
146	Cd	42	Total	C	N	O	P	0	0
			859	417	159	243	40		

- Molecule 147 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
147	Ce	52	Total	C	N	O	P	0	0
			1049	509	199	295	46		

- Molecule 148 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
148	Cf	38	Total	C	N	O	P	0	0
			768	373	152	210	33		

- Molecule 149 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
149	Cg	36	Total	C	N	O	P	0	0
			735	354	150	199	32		

- Molecule 150 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
150	Ch	47	Total	C	N	O	P	0	0
			938	453	174	269	42		

- Molecule 151 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
151	Ck	29	Total	C	N	O	P	0	0
			585	284	100	174	27		

- Molecule 152 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
152	Cp	48	Total	C	N	O	P	0	0
			976	471	189	273	43		

- Molecule 153 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
153	Cq	40	Total	C	N	O	P	0	0
			827	395	157	236	39		

- Molecule 154 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
154	Cr	36	Total	C	N	O	P	0	0
			727	350	145	200	32		

- Molecule 155 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
155	Cs	49	Total	C	N	O	P	0	0
			1012	486	204	277	45		

- Molecule 156 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
156	Ct	44	Total	C	N	O	P	0	0
			886	432	159	255	40		

- Molecule 157 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
157	Cu	60	Total	C	N	O	P	0	0
			1216	589	239	334	54		

- Molecule 158 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
158	Cv	41	Total	C	N	O	P	0	0
			823	402	141	243	37		

- Molecule 159 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
159	Cw	54	Total	C	N	O	P	0	0
			1098	528	213	308	49		

- Molecule 160 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
160	Cx	36	Total	C	N	O	P	0	0
			730	353	145	200	32		

- Molecule 161 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
161	Cy	56	1145	554	223	318	50	0	0

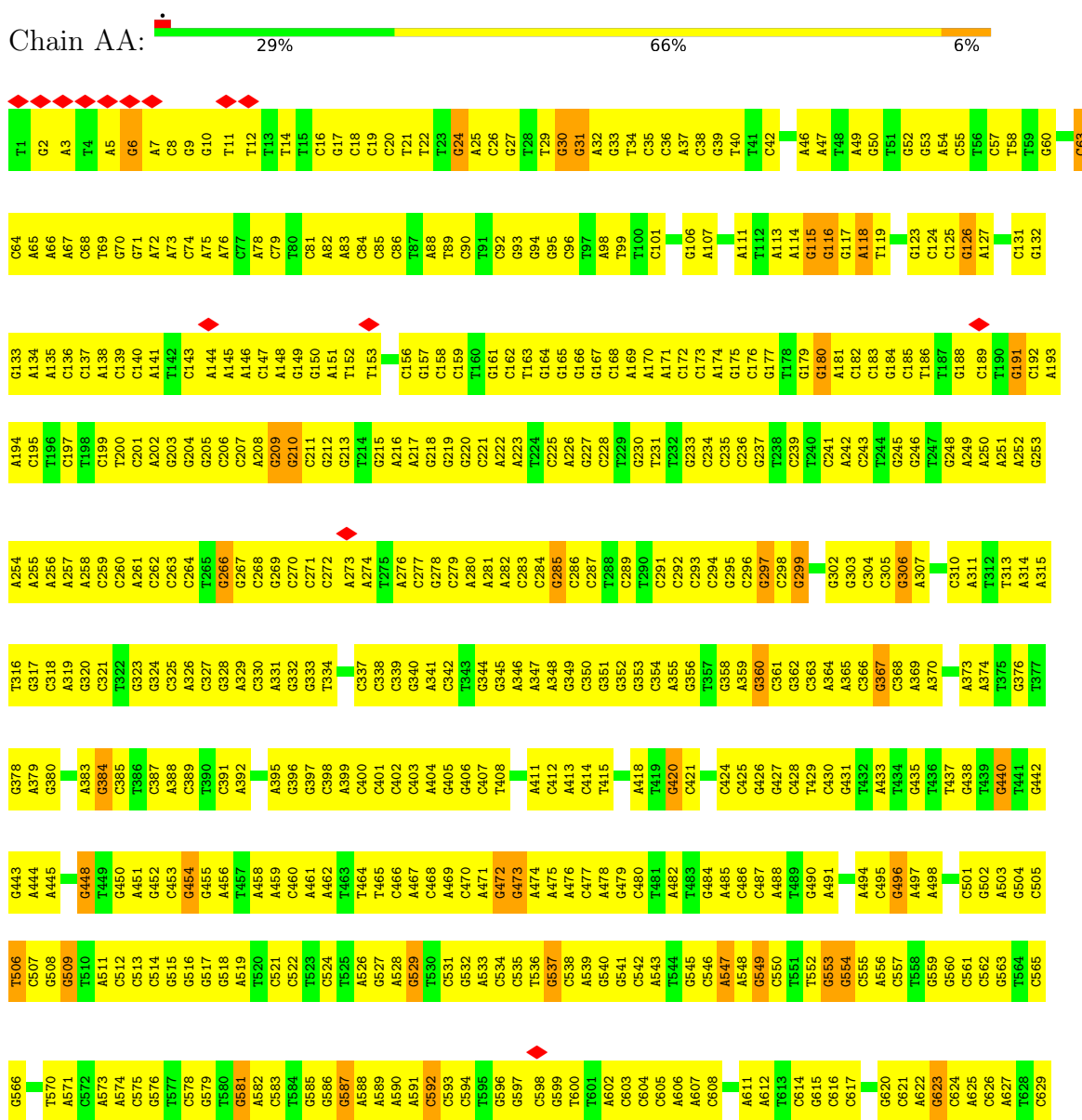
- Molecule 162 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
162	Cz	48	970	465	195	266	44	0	0

3 Residue-property plots

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

- Molecule 1: SCAFFOLD STRAND,SCAFFOLD STRAND



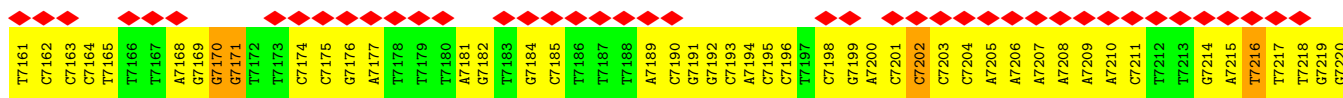
G1488	C1489	T1490	T1491	T1492	G1493	C1494	T1495	G1497	T1498	T1499	T1500	A1501	A1502	A1506	G1509	G1510	A1511	T1512	G1513	T1514	T1515	A1516	A1517	T1518	G1520	T1521	A1522	C1523	T1524	A1525	C1526	T1527	A1528	A1531	T1532	T1533	A1534	G1535	A1537	G1540	A1541	T1542	G1543	T1544	C1544	C1545	C1546	C1547	T1548	T1549	A1480	A1481	T1482	T1483	C1484	G1488	T1552	C1553																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																											
T1346	A1347	T1348	A1349	T1350	T1351	A1352	G1353	G1354	G1355	T1358	T1359	A1360	A1361	A1362	A1363	A1364	A1370	T1371	C1372	C1373	G1376	C1377	G1378	G1381	A1382	A1383	A1384	T1385	A1386	A1387	A1388	G1389	G1390	C1391	C1394	T1395	C1396	C1397	C1398	C1400	A1401	A1402	A1403	A1404	G1405	T1406	A1407	T1408	T1409	A1410	C1411	A1412	G1413	G1414	G1415	C1417	C1418	C1419	T1420	T1421	T1422	T1423	T1426	G1429	G1430	T1431	A1432	C1433	A1434	A1435	C1436	A1437	G1438	A1439	A1443	G1444	C1445	A1449	T1450	G1451	C1452	T1453	C1454	T1455	G1456	A1457	G1458	G1459	C1460	A1464	G1467	C1468	A1471	A1472	T1475	T1476	G1477	C1478	T1479	A1480	A1481	T1482	T1483	C1484	G1488	T1552	C1553																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																										
T1277	G1278	T1279	A1280	T1281	G1282	T1283	C1284	T1285	C1286	G1287	G1288	G1289	C1290	C1291	C1295	T1296	C1297	G1306	A1307	T1308	T1309	C1310	A1314	C1315	C1316	T1317	A1318	C1319	A1320	C1321	A1322	T1323	T1324	A1325	C1326	T1327	C1328	A1329	G1330	G1331	C1332	A1333	G1336	T1337	A1338	T1339	A1342	A1343	A1344	A1345	T1277	T1278	T1279	T1280	T1281	T1282	T1283	T1284	T1285	T1286	T1287	T1288	T1289	T1290	T1291	T1292	T1293	T1294	T1295	T1296	T1297	T1298	T1299	T1300	T1301	T1302	T1303	T1304	T1305	T1306	T1307	T1308	T1309	T1310	T1311	T1312	T1313	T1314	T1315	T1316	T1317	T1318	T1319	T1320	T1321	T1322	T1323	T1324	T1325	T1326	T1327	T1328	T1329	T1330	T1331	T1332	T1333	T1334	T1335	T1336	T1337	T1338	T1339	T1340	T1341	T1342	T1343	T1344	T1345	T1346	T1347	T1348	T1349	T1350	T1351	T1352	T1353	T1354	T1355	T1356	T1357	T1358	T1359	T1360	T1361	T1362	T1363	T1364	T1365	T1366	T1367	T1368	T1369	T1370	T1371	T1372	T1373	T1374	T1375	T1376	T1377	T1378	T1379	T1380	T1381	T1382	T1383	T1384	T1385	T1386	T1387	T1388	T1389	T1390	T1391	T1392	T1393	T1394	T1395	T1396	T1397	T1398	T1399	T1400	T1401	T1402	T1403	T1404	T1405	T1406	T1407	T1408	T1409	T1410	T1411	T1412	T1413	T1414	T1415	T1416	T1417	T1418	T1419	T1420	T1421	T1422	T1423	T1424	T1425	T1426	T1427	T1428	T1429	T1430	T1431	T1432	T1433	T1434	T1435	T1436	T1437	T1438	T1439	T1440	T1441	T1442	T1443	T1444	T1445	T1446	T1447	T1448	T1449	T1450	T1451	T1452	T1453	T1454	T1455	T1456	T1457	T1458	T1459	T1460	T1461	T1462	T1463	T1464	T1465	T1466	T1467	T1468	T1469	T1470	T1471	T1472	T1473	T1474	T1475	T1476	T1477	T1478	T1479	T1480	T1481	T1482	T1483	T1484	T1485	T1486	T1487	T1488	T1489	T1490	T1491	T1492	T1493	T1494	T1495	T1496	T1497	T1498	T1499	T1500	T1501	T1502	T1503	T1504	T1505	T1506	T1507	T1508	T1509	T1510	T1511	T1512	T1513	T1514	T1515	T1516	T1517	T1518	T1519	T1520	T1521	T1522	T1523	T1524	T1525	T1526	T1527	T1528	T1529	T1530	T1531	T1532	T1533	T1534	T1535	T1536	T1537	T1538	T1539	T1540	T1541	T1542	T1543	T1544	T1545	T1546	T1547	T1548	T1549	T1550	T1551	T1552	T1553	T1554	T1555	T1556	T1557	T1558	T1559	T1560	T1561	T1562	T1563	T1564	T1565	T1566	T1567	T1568	T1569	T1570	T1571	T1572	T1573	T1574	T1575	T1576	T1577	T1578	T1579	T1580	T1581	T1582	T1583	T1584	T1585	T1586	T1587	T1588	T1589	T1590	T1591	T1592	T1593	T1594	T1595	T1596	T1597	T1598	T1599	T1600	T1601	T1602	T1603	T1604	T1605	T1606	T1607	T1608	T1609	T1610	T1611	T1612	T1613	T1614	T1615	T1616	T1617	T1618	T1619	T1620	T1621	T1622	T1623	T1624	T1625	T1626	T1627	T1628	T1629	T1630	T1631	T1632	T1633	T1634	T1635	T1636	T1637	T1638	T1639	T1640	T1641	T1642	T1643	T1644	T1645	T1646	T1647	T1648	T1649	T1650	T1651	T1652	T1653	T1654	T1655	T1656	T1657	T1658	T1659	T1660	T1661	T1662	T1663	T1664	T1665	T1666	T1667	T1668	T1669	T1670	T1671	T1672	T1673	T1674	T1675	T1676	T1677	T1678	T1679	T1680	T1681	T1682	T1683	T1684	T1685	T1686	T1687	T1688	T1689	T1690	T1691	T1692	T1693	T1694	T1695	T1696	T1697	T1698	T1699	T1700	T1701	T1702	T1703	T1704	T1705	T1706	T1707	T1708	T1709	T1710	T1711	T1712	T1713	T1714	T1715	T1716	T1717	T1718	T1719	T1720	T1721	T1722	T1723	T1724	T1725	T1726	T1727	T1728	T1729	T1730	T1731	T1732	T1733	T1734	T1735	T1736	T1737	T1738	T1739	T1740	T1741	T1742	T1743	T1744	T1745	T1746	T1747	T1748	T1749	T1750	T1751	T1752	T1753	T1754	T1755	T1756	T1757	T1758	T1759	T1760	T1761	T1762	T1763	T1764	T1765	T1766	T1767	T1768	T1769	T1770	T1771	T1772	T1773	T1774	T1775	T1776	T1777	T1778	T1779	T1780	T1781	T1782	T1783	T1784	T1785	T1786	T1787	T1788	T1789	T1790	T1791	T1792	T1793	T1794	T1795	T1796	T1797	T1798	T1799	T1800	T1801	T1802	T1803	T1804	T1805	T1806	T1807	T1808	T1809	T1810	T1811	T1812	T1813	T1814	T1815	T1816	T1817	T1818	T1819	T1820	T1821	T1822	T1823	T1824	T1825	T1826	T1827	T1828	T1829	T1830	T1831	T1832	T1833	T1834	T1835	T1836	T1837	T1838	T1839	T1840	T1841	T1842	T1843	T1844	T1845	T1846	T1847	T1848	T1849	T1850	T1851	T1852	T1853	T1854	T1855	T1856	T1857	T1858	T1859	T1860	T1861	T1862	T1863	T1864	T1865	T1866	T1867	T1868	T1869	T1870	T1871	T1872	T1873	T1874	T1875	T1876	T1877	T1878	T1879	T1880	T1881	T1882	T1883	T1884	T1885	T1886	T1887	T1888	T1889	T1890	T1891	T1892	T1893	T1894	T1895	T1896	T1897	T1898	T1899	T1900	T1901	T1902	T1903	T1904	T1905	T1906	T1907	T1908	T1909	T1910	T1911	T1912	T1913	T1914	T1915	T1916	T1917	T1918	T1919	T1920	T1921	T1922	T1923	T1924	T1925	T1926	T1927	T1928	T1929	T1930	T1931	T1932	T1933	T1934	T1935	T1936	T1937	T1938	T1939	T1940	T1941	T1942	T1943	T1944	T1945	T1946	T1947	T1948	T1949	T1950	T1951	T1952	T1953	T1954	T1955	T1956	T1957	T1958	T1959	T1960	T1961	T1962	T1963	T1964	T1965	T1966	T1967	T1968	T1969	T1970	T1971	T1972	T1973	T1974	T1975	T1976	T1977	T1978	T1979	T1980	T1981	T1982	T1983	T1984	T1985	T1986	T1987	T1988	T1989	T1990	T1991	T1992	T1993	T1994	T1995	T1996	T1997	T1998	T1999	T2000	T2001	T2002	T2003	T2004	T2005	T2006	T2007	T2008	T2009	T2010	T2011	T2012	T2013	T2014	T2015	T2016	T2017	T2018	T2019	T2020	T2021	T2022	T2023	T2024	T2025	T2026	T2027	T2028	T2029	T2030	T2031	T2032	T2033	T2034	T2035	T2036	T2037	T2038	T2039	T2040	T2041	T2042	T2043	T2044	T2045	T2046	T2047	T2048	T2049	T2050	T2051	T2052	T2053	T2054	T2055	T2056	T2057	T2058	T2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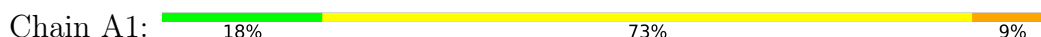
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A6249	T6318	T6390	C6455	A6524	C6588	T6589	G6721	A6787	C6853	A6915	A6977	T7038	T7102
G6250	G6319	G6391	T6456	T6525	T6591	T6654	A6788	A6788	T6854	A6916	C6978	G7039	T7103
G6253	A6320	C6393	G6457	G6526	T6591	C6656	C6723	T6789	T6854	T6917	G6979	G7040	T7104
A6256	C6322	T6394	T6458	G6527	G6592	A6657	G6725	A6790	G6857	C6918	C6981	G7042	C7105
G6257	C6323	G6395	G6460	C6528	G6595	C6661	T6726	A6793	G6858	C6920	C6982	C7106	C7106
T6258	A6324	T6396	G6461	A6530	G6596	A6662	A6727	T6794	G6859	G6924	T6983	T7044	T7107
G6259	A6325	G6397	T6462	G6461	C6597	A6663	T6728	T6795	C6860	A6924	C6984	T7045	T7108
C6260	G6326	T6398	G6463	C6533	G6598	A6664	A6730	A6796	C6862	A6925	T6986	A7046	T7109
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A6267	A6331	C6405	C6471	A6538	T6603	T6669	G6736	A6802	T6802	G6929	A6991	C7051	T7116
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C6302	T6366	G6437	G6505	G6571	A6636	C6699	C6770	T6834	A6836	C6960	G7026	C7083	T7141
G6303	C6368	A6439	G6505	T6572	T6637	C6706	C6770	T6835	A6836	C6961	A7026	G7084	T7142
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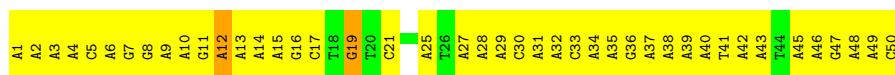
• Molecule 2: STAPLE STRAND



• Molecule 3: STAPLE STRAND



• Molecule 4: STAPLE STRAND



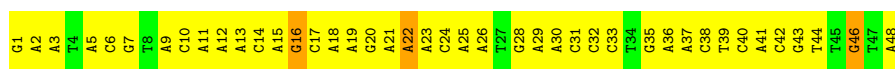
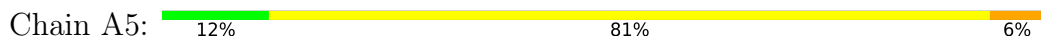
• Molecule 5: STAPLE STRAND



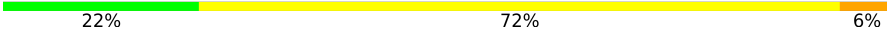
• Molecule 6: STAPLE STRAND



• Molecule 7: STAPLE STRAND

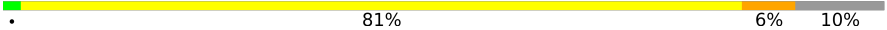


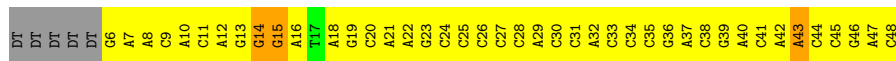
• Molecule 8: STAPLE STRAND

Chain A6:  22% 72% 6%



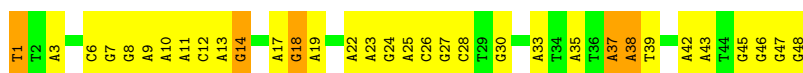
- Molecule 9: STAPLE STRAND

Chain A7:  81% 6% 10%




- Molecule 10: STAPLE STRAND

Chain A8:  31% 58% 10%



- Molecule 11: STAPLE STRAND

Chain AB:  10% 88%



- Molecule 12: STAPLE STRAND

Chain AC:  21% 73% 6%



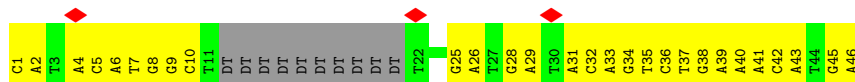
- Molecule 13: STAPLE STRAND

Chain AD:  12% 84%



- Molecule 14: STAPLE STRAND

Chain AE:  7% 17% 61% 22%



- Molecule 15: STAPLE STRAND

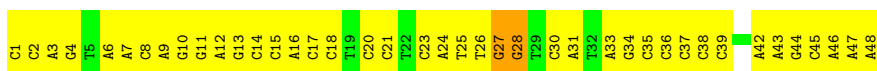
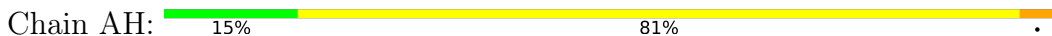
Chain AF:  23% 69% 8%



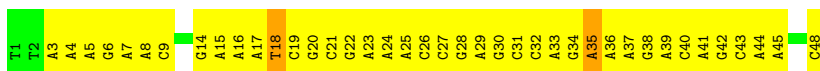
• Molecule 16: STAPLE STRAND



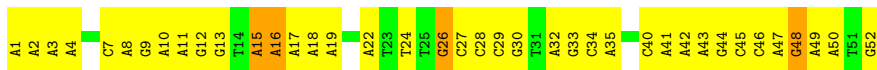
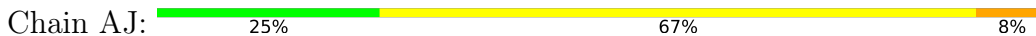
• Molecule 17: STAPLE STRAND



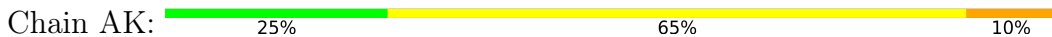
• Molecule 18: STAPLE STRAND



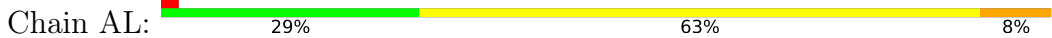
• Molecule 19: STAPLE STRAND



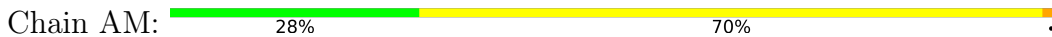
• Molecule 20: STAPLE STRAND

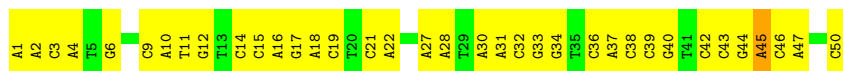


• Molecule 21: STAPLE STRAND

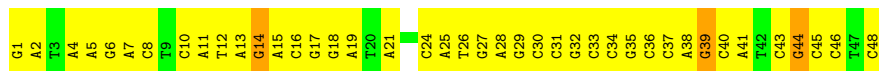


• Molecule 22: STAPLE STRAND

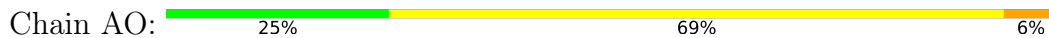




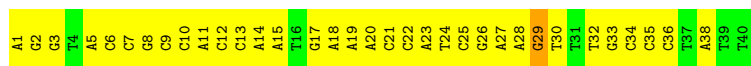
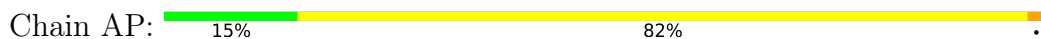
• Molecule 23: STAPLE STRAND



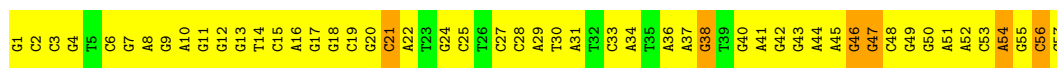
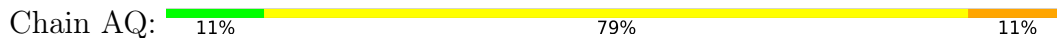
• Molecule 24: STAPLE STRAND



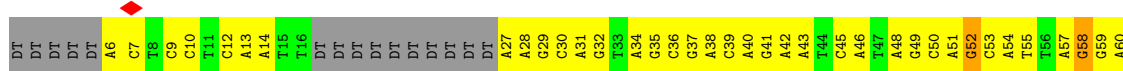
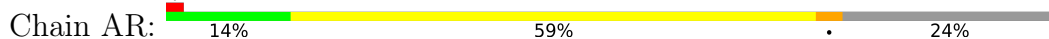
• Molecule 25: STAPLE STRAND



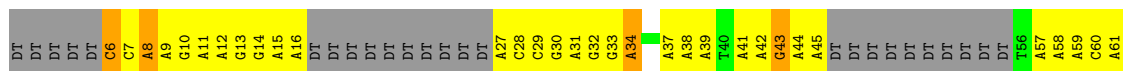
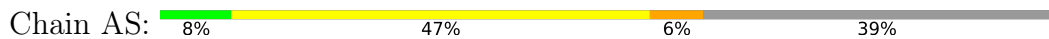
• Molecule 26: STAPLE STRAND



• Molecule 27: STAPLE STRAND



• Molecule 28: STAPLE STRAND



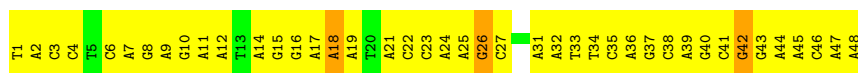
• Molecule 29: STAPLE STRAND

Chain AT: 17% 75% 8%



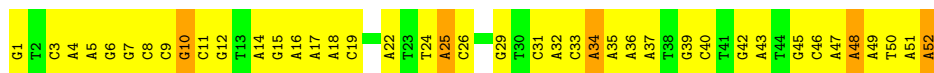
• Molecule 30: STAPLE STRAND

Chain AU: 12% 81% 6%



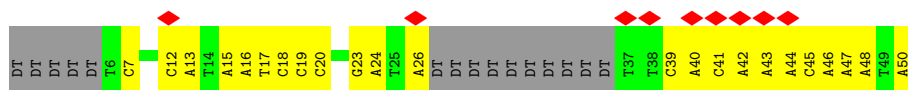
• Molecule 31: STAPLE STRAND

Chain AV: 21% 69% 10%



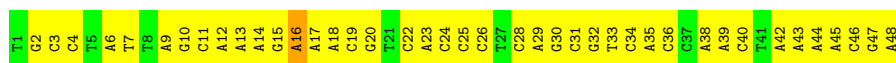
• Molecule 32: STAPLE STRAND

Chain AW: 18% 24% 46% 30%



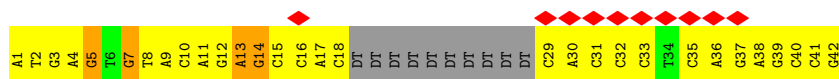
• Molecule 33: STAPLE STRAND

Chain AX: 15% 83%



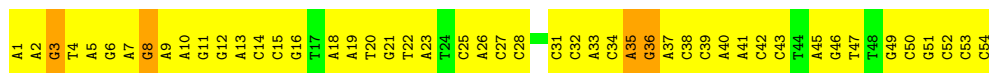
• Molecule 34: STAPLE STRAND

Chain AY: 5% 24% 62% 10% 24%



• Molecule 35: STAPLE STRAND

Chain AZ: 11% 81% 7%

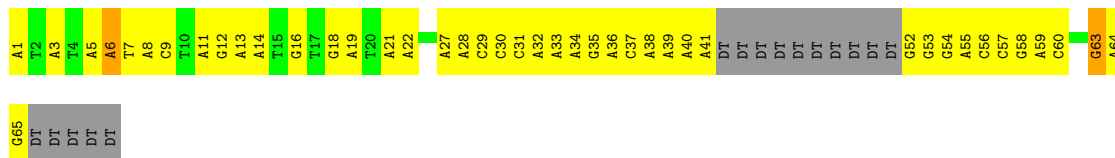


• Molecule 36: STAPLE STRAND

Chain Ab: 24% 71%



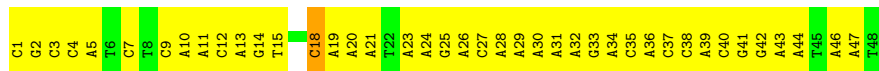
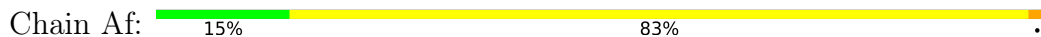
• Molecule 37: STAPLE STRAND



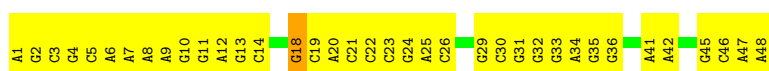
• Molecule 38: STAPLE STRAND



• Molecule 39: STAPLE STRAND



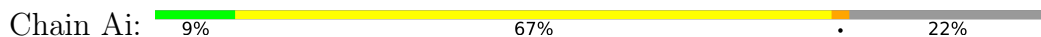
• Molecule 40: STAPLE STRAND



• Molecule 41: STAPLE STRAND

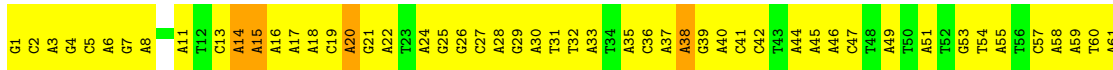


• Molecule 42: STAPLE STRAND



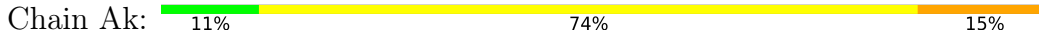
• Molecule 43: STAPLE STRAND





662

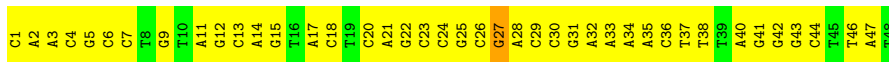
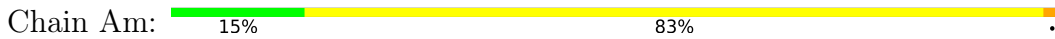
• Molecule 44: STAPLE STRAND



• Molecule 45: STAPLE STRAND



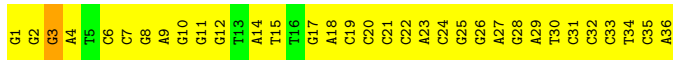
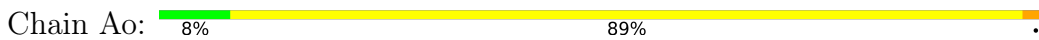
• Molecule 46: STAPLE STRAND



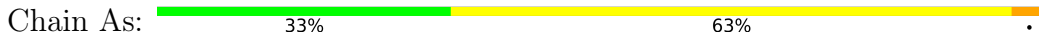
• Molecule 47: STAPLE STRAND



• Molecule 48: STAPLE STRAND



• Molecule 49: STAPLE STRAND



• Molecule 50: STAPLE STRAND

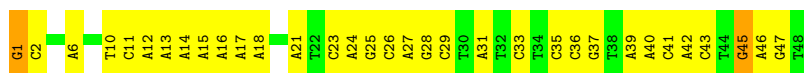
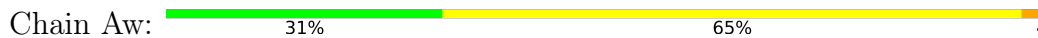




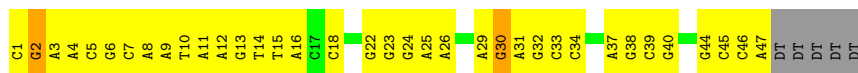
• Molecule 51: STAPLE STRAND



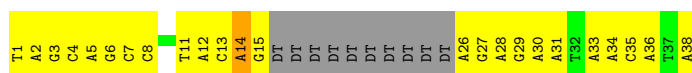
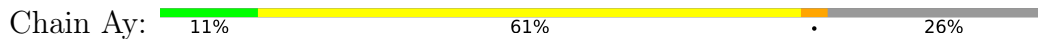
• Molecule 52: STAPLE STRAND



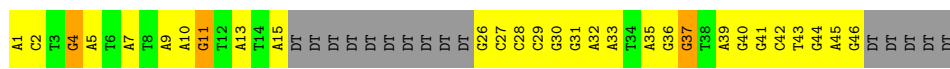
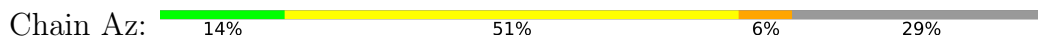
• Molecule 53: STAPLE STRAND



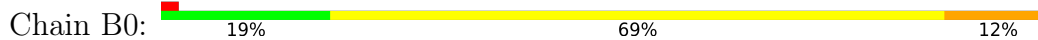
• Molecule 54: STAPLE STRAND



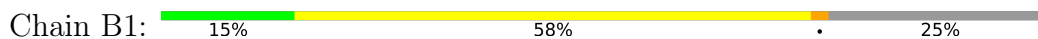
• Molecule 55: STAPLE STRAND

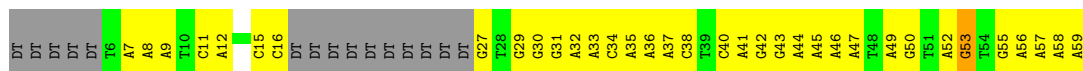


• Molecule 56: STAPLE STRAND

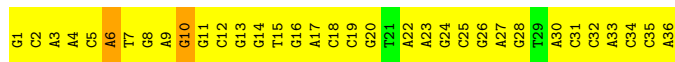


• Molecule 57: STAPLE STRAND

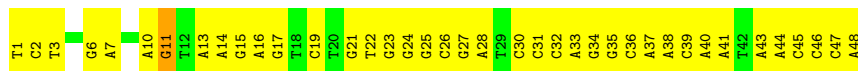
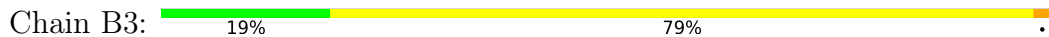




• Molecule 58: STAPLE STRAND



• Molecule 59: STAPLE STRAND



• Molecule 60: STAPLE STRAND



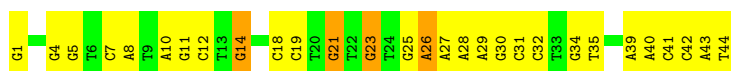
• Molecule 61: STAPLE STRAND



• Molecule 62: STAPLE STRAND



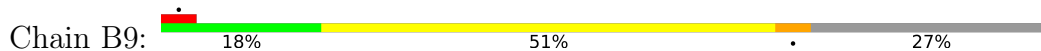
• Molecule 63: STAPLE STRAND



• Molecule 64: STAPLE STRAND



● Molecule 65: STAPLE STRAND



● Molecule 66: STAPLE STRAND



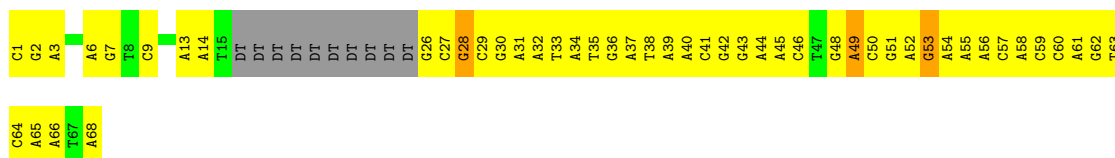
● Molecule 67: STAPLE STRAND



● Molecule 68: STAPLE STRAND



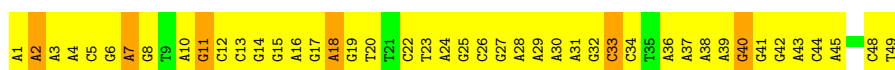
● Molecule 69: STAPLE STRAND



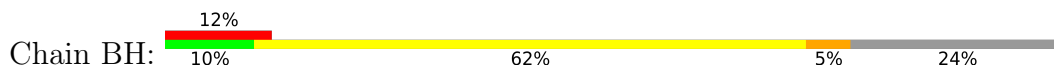
● Molecule 70: STAPLE STRAND



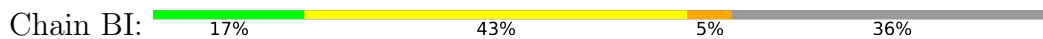
● Molecule 71: STAPLE STRAND



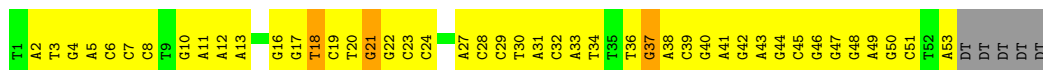
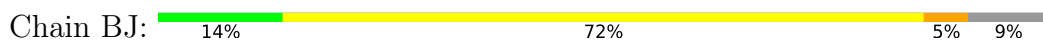
● Molecule 72: STAPLE STRAND



• Molecule 73: STAPLE STRAND



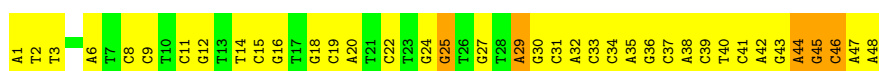
• Molecule 74: STAPLE STRAND



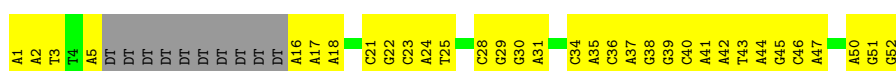
• Molecule 75: STAPLE STRAND



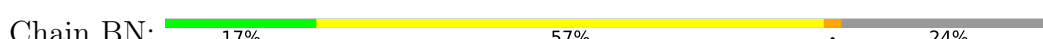
• Molecule 76: STAPLE STRAND



• Molecule 77: STAPLE STRAND

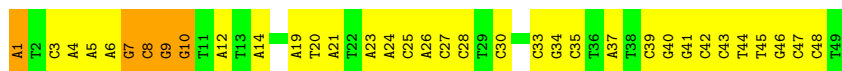


• Molecule 78: STAPLE STRAND

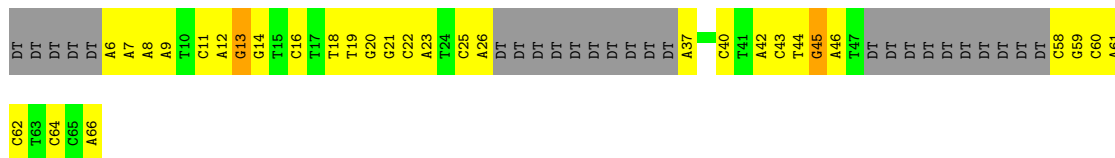
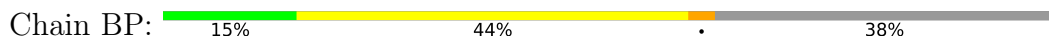


• Molecule 79: STAPLE STRAND

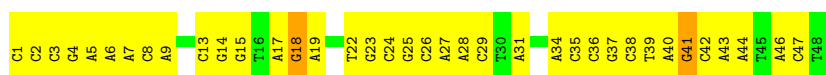




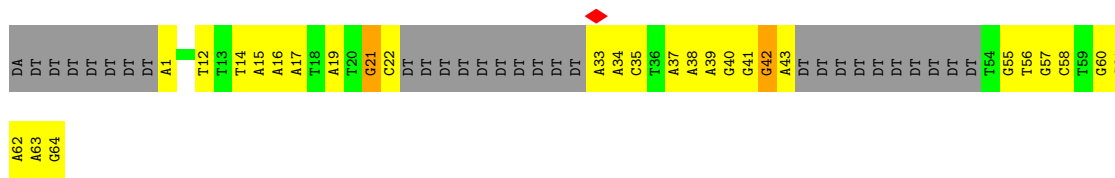
• Molecule 80: STAPLE STRAND



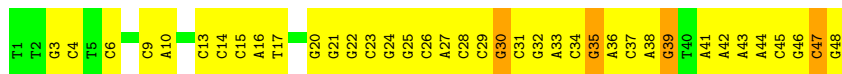
• Molecule 81: STAPLE STRAND



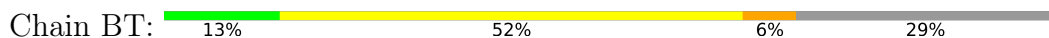
• Molecule 82: STAPLE STRAND



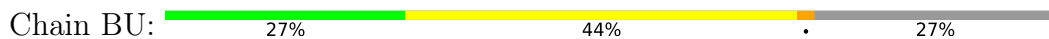
• Molecule 83: STAPLE STRAND



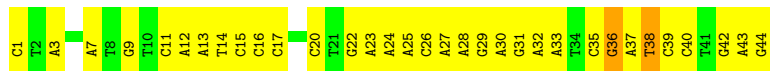
• Molecule 84: STAPLE STRAND



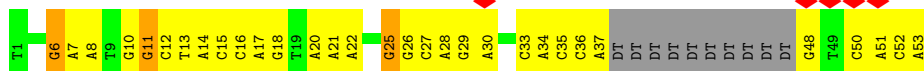
• Molecule 85: STAPLE STRAND



• Molecule 86: STAPLE STRAND



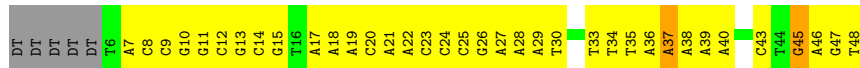
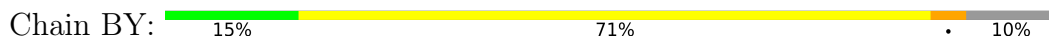
• Molecule 87: STAPLE STRAND



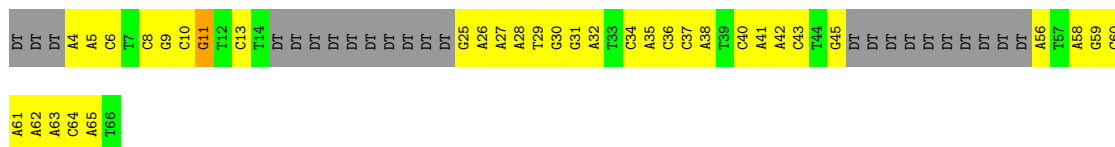
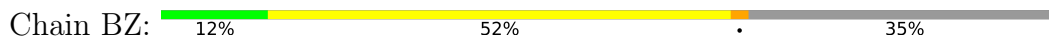
• Molecule 88: STAPLE STRAND



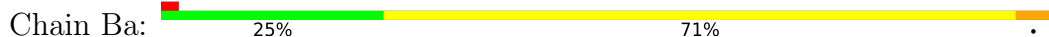
• Molecule 89: STAPLE STRAND



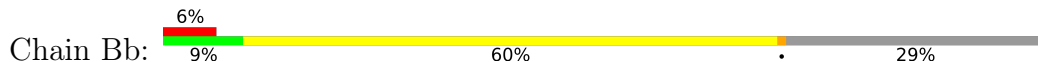
• Molecule 90: STAPLE STRAND

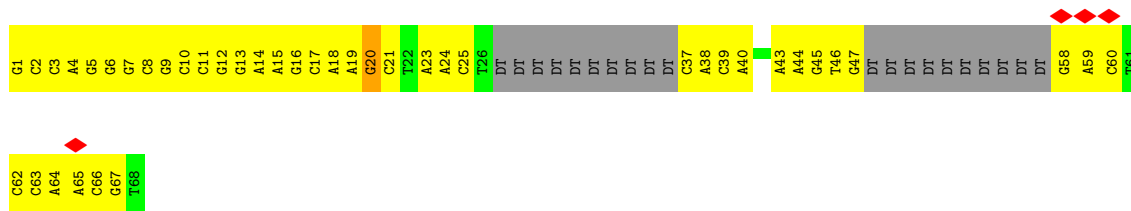


• Molecule 91: STAPLE STRAND

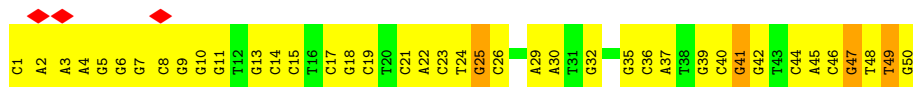


• Molecule 92: STAPLE STRAND





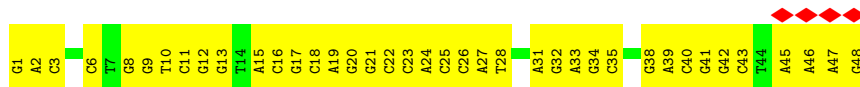
● Molecule 93: STAPLE STRAND



● Molecule 94: STAPLE STRAND



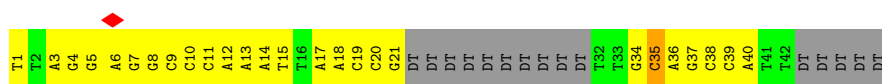
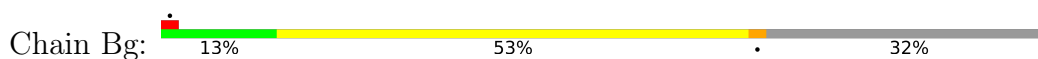
● Molecule 95: STAPLE STRAND



● Molecule 96: STAPLE STRAND



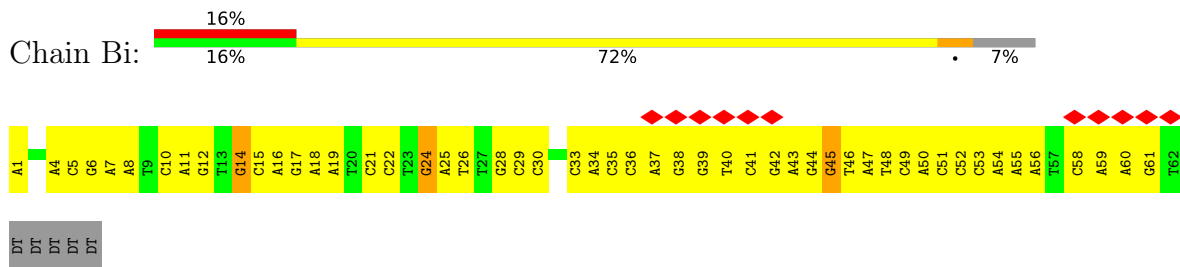
● Molecule 97: STAPLE STRAND



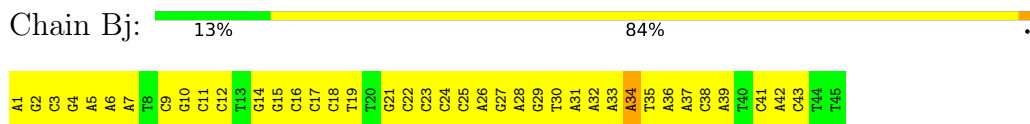
● Molecule 98: STAPLE STRAND



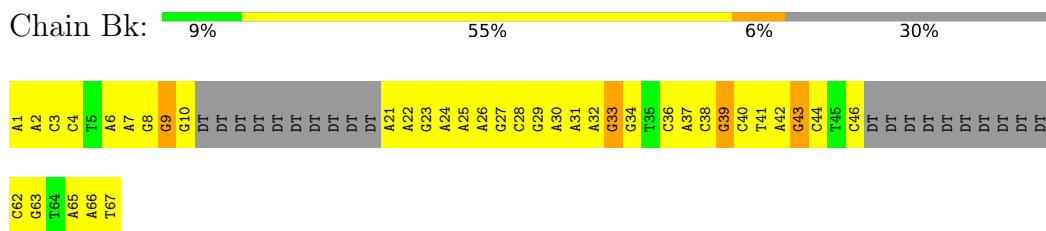
• Molecule 99: STAPLE STRAND



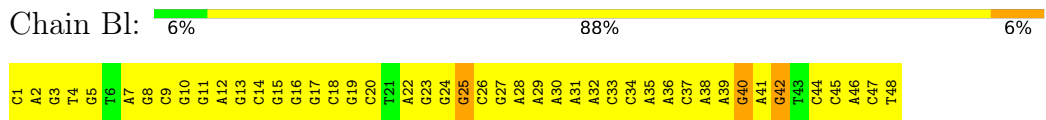
• Molecule 100: STAPLE STRAND



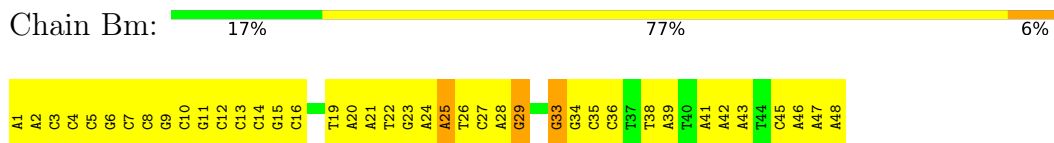
• Molecule 101: STAPLE STRAND



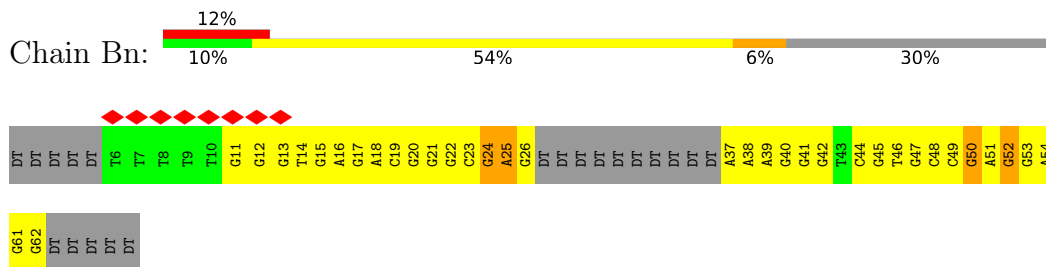
• Molecule 102: STAPLE STRAND



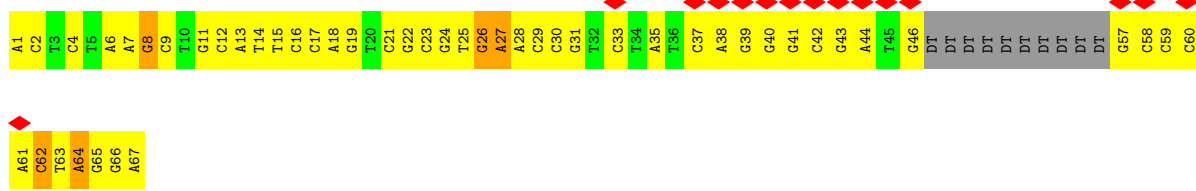
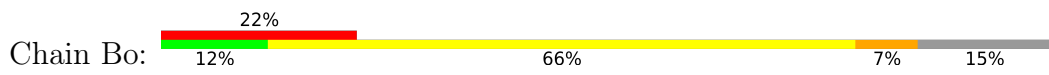
• Molecule 103: STAPLE STRAND



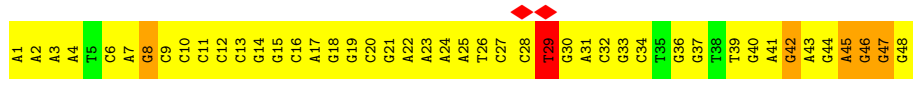
• Molecule 104: STAPLE STRAND



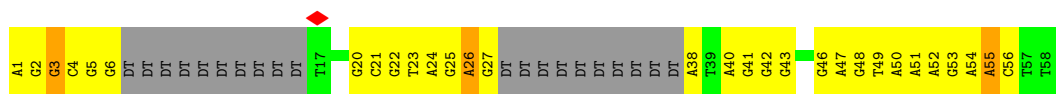
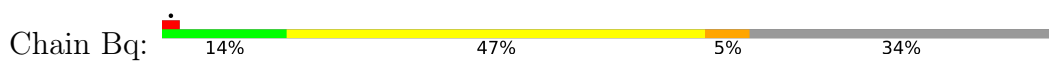
• Molecule 105: STAPLE STRAND



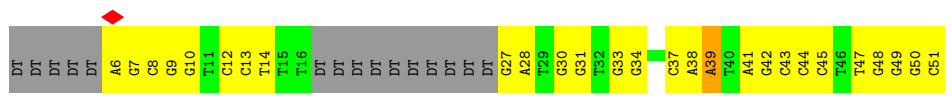
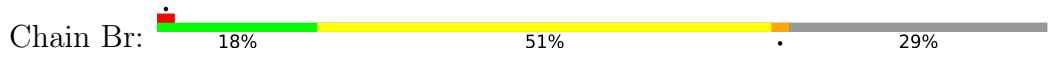
• Molecule 106: STAPLE STRAND



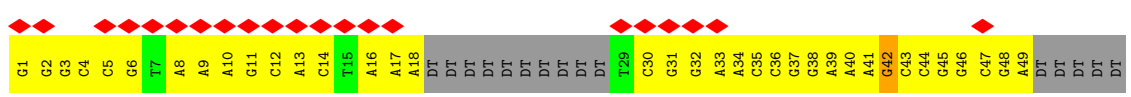
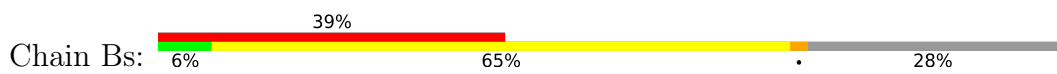
• Molecule 107: STAPLE STRAND



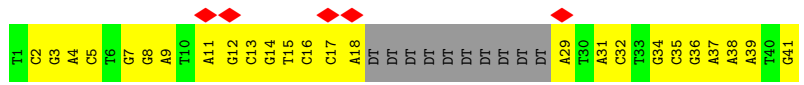
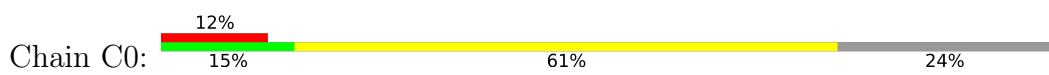
• Molecule 108: STAPLE STRAND



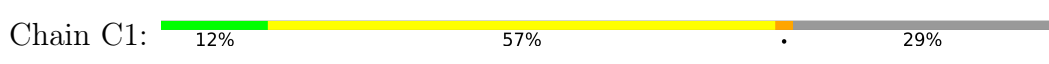
• Molecule 109: STAPLE STRAND

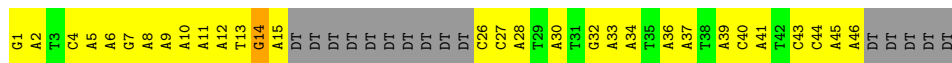


• Molecule 110: STAPLE STRAND



• Molecule 111: STAPLE STRAND





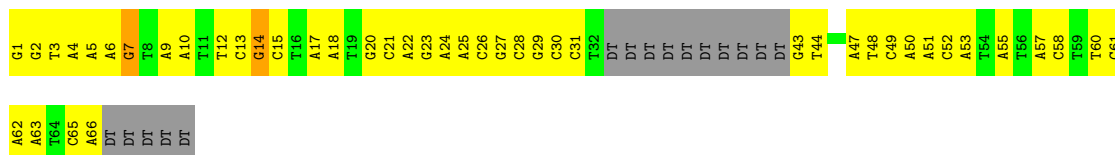
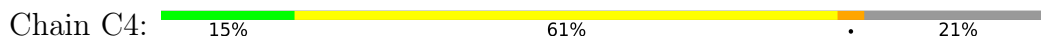
• Molecule 112: STAPLE STRAND



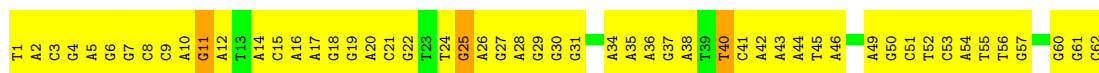
• Molecule 113: STAPLE STRAND



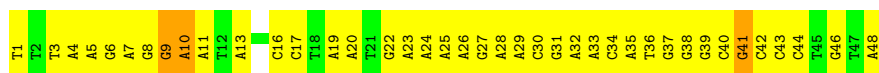
• Molecule 114: STAPLE STRAND



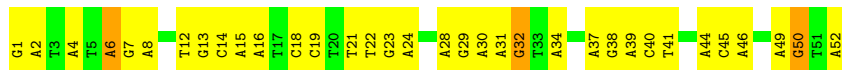
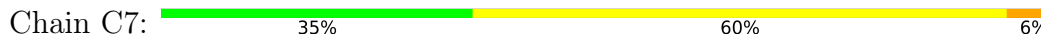
• Molecule 115: STAPLE STRAND



• Molecule 116: STAPLE STRAND



• Molecule 117: STAPLE STRAND



• Molecule 118: STAPLE STRAND

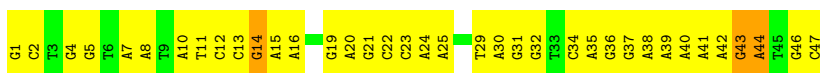
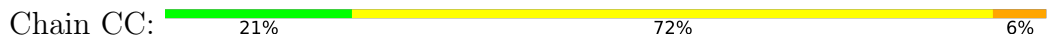




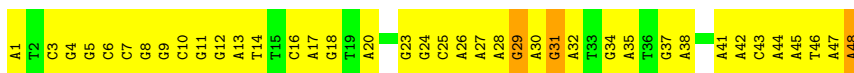
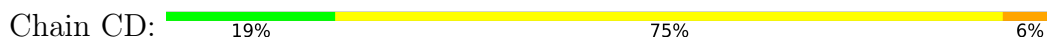
- Molecule 119: STAPLE STRAND



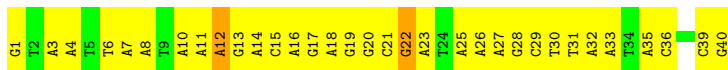
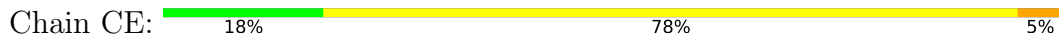
- Molecule 120: STAPLE STRAND



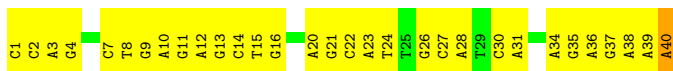
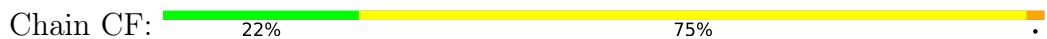
- Molecule 121: STAPLE STRAND



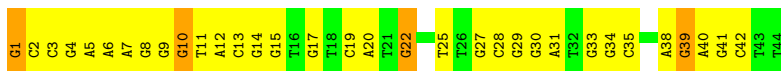
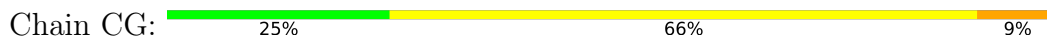
- Molecule 122: STAPLE STRAND



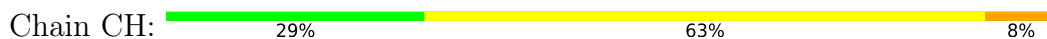
- Molecule 123: STAPLE STRAND



- Molecule 124: STAPLE STRAND



- Molecule 125: STAPLE STRAND

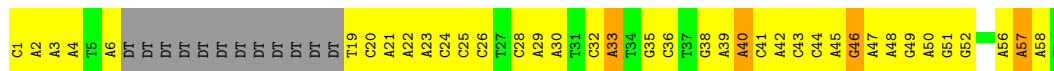
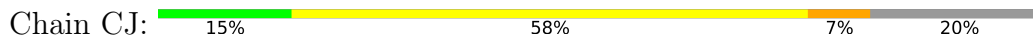




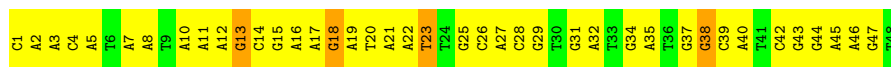
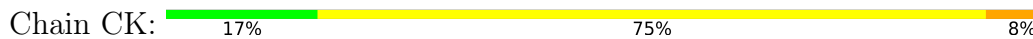
• Molecule 126: STAPLE STRAND



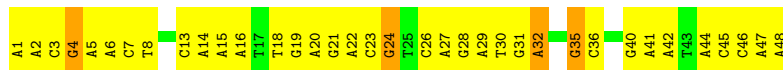
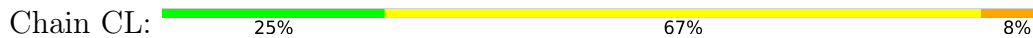
• Molecule 127: STAPLE STRAND



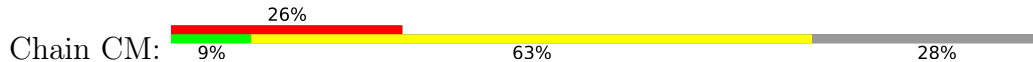
• Molecule 128: STAPLE STRAND



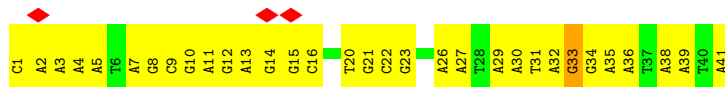
• Molecule 129: STAPLE STRAND



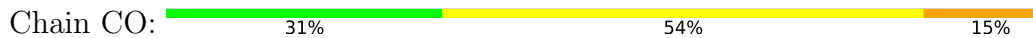
• Molecule 130: STAPLE STRAND



• Molecule 131: STAPLE STRAND



• Molecule 132: STAPLE STRAND

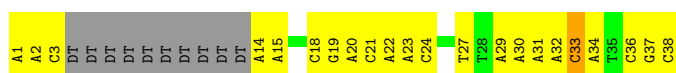
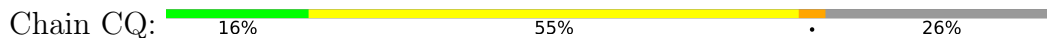




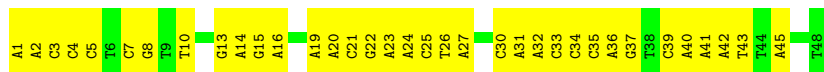
• Molecule 133: STAPLE STRAND



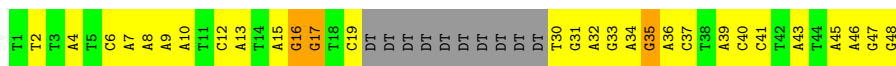
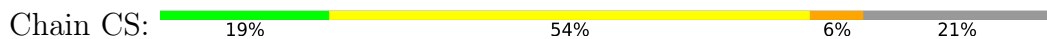
• Molecule 134: STAPLE STRAND



• Molecule 135: STAPLE STRAND



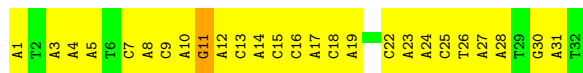
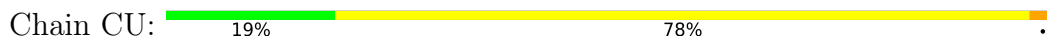
• Molecule 136: STAPLE STRAND



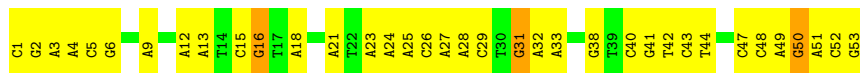
• Molecule 137: STAPLE STRAND



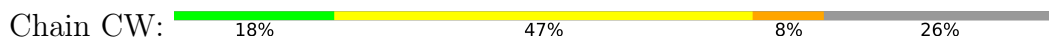
• Molecule 138: STAPLE STRAND



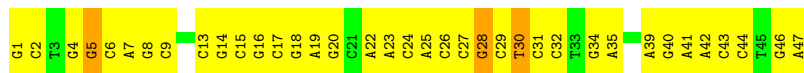
• Molecule 139: STAPLE STRAND



• Molecule 140: STAPLE STRAND



• Molecule 141: STAPLE STRAND



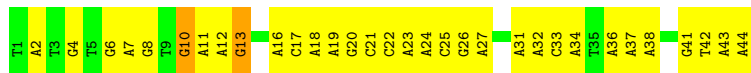
• Molecule 142: STAPLE STRAND



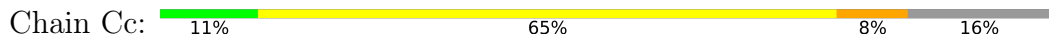
• Molecule 143: STAPLE STRAND



• Molecule 144: STAPLE STRAND

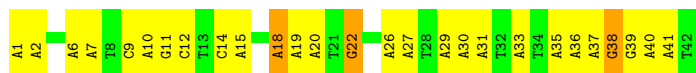


• Molecule 145: STAPLE STRAND

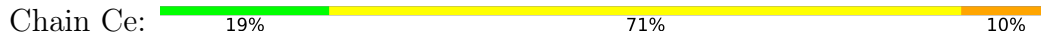


G62

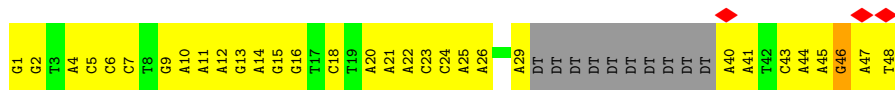
• Molecule 146: STAPLE STRAND



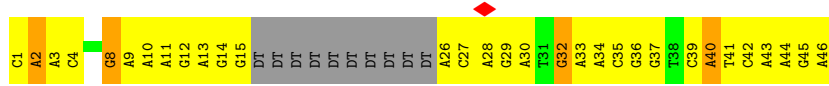
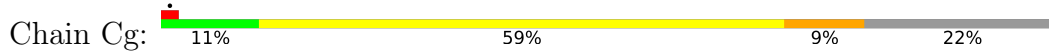
• Molecule 147: STAPLE STRAND



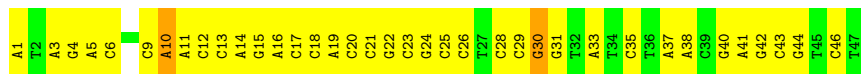
• Molecule 148: STAPLE STRAND



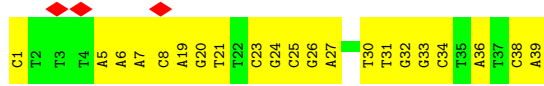
• Molecule 149: STAPLE STRAND



• Molecule 150: STAPLE STRAND



• Molecule 151: STAPLE STRAND



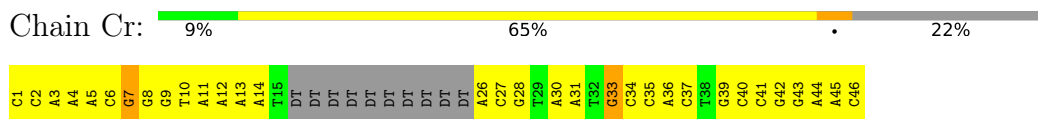
• Molecule 152: STAPLE STRAND



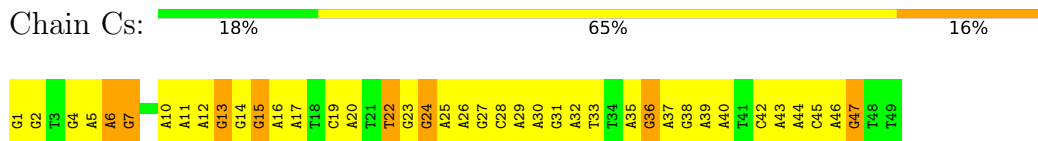
• Molecule 153: STAPLE STRAND



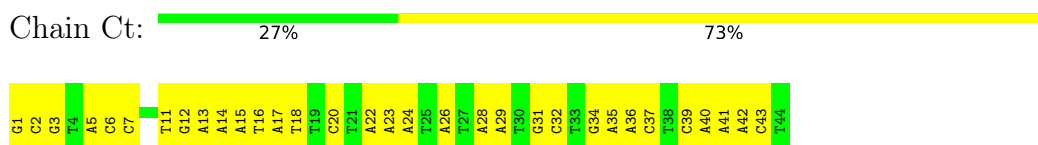
• Molecule 154: STAPLE STRAND



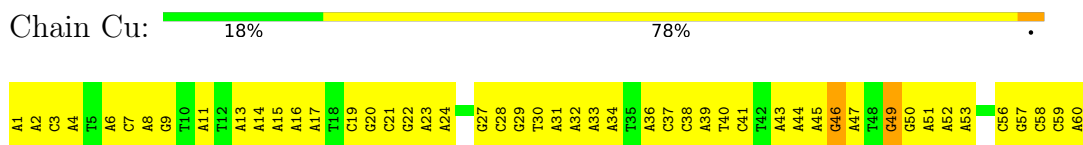
• Molecule 155: STAPLE STRAND



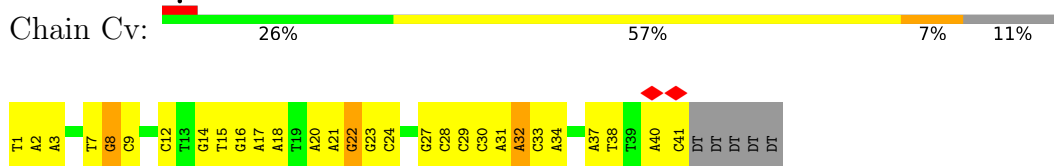
• Molecule 156: STAPLE STRAND



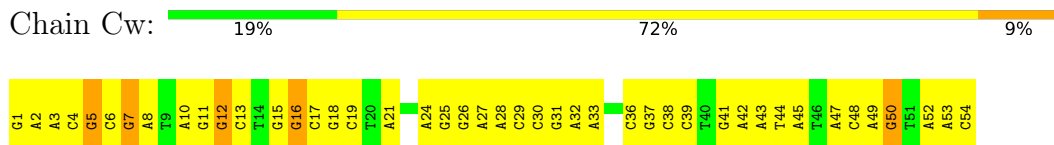
• Molecule 157: STAPLE STRAND



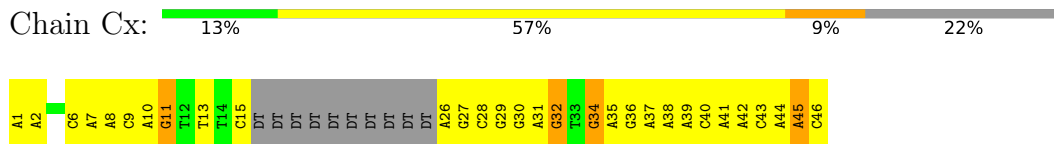
• Molecule 158: STAPLE STRAND



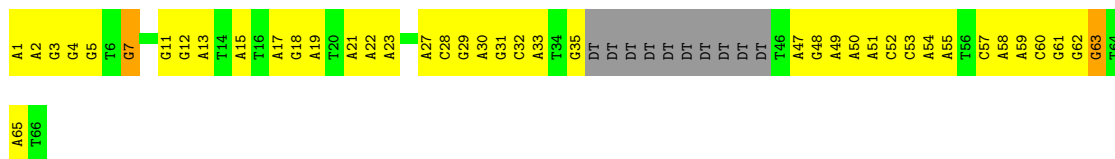
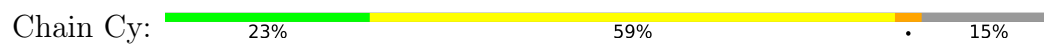
• Molecule 159: STAPLE STRAND



• Molecule 160: STAPLE STRAND



• Molecule 161: STAPLE STRAND



• Molecule 162: STAPLE STRAND



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	28502	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	WIENER FILTER (RELION)	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	10	Depositor
Minimum defocus (nm)	890	Depositor
Maximum defocus (nm)	4460	Depositor
Magnification	39436	Depositor
Image detector	FEI FALCON I (4k x 4k)	Depositor
Maximum map value	0.509	Depositor
Minimum map value	-0.314	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.032	Depositor
Recommended contour level	0.1	Depositor
Map size (\AA)	610.6, 610.6, 610.6	wwPDB
Map dimensions	172, 172, 172	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	3.55, 3.55, 3.55	Depositor

5 Model quality i

5.1 Standard geometry i

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	AA	1.62	60/165646 (0.0%)	2.35	13564/255486 (5.3%)
2	A0	1.60	1/1254 (0.1%)	2.59	132/1923 (6.9%)
3	A1	1.63	0/989	2.63	120/1514 (7.9%)
4	A2	1.68	0/1149	2.81	162/1762 (9.2%)
5	A3	1.61	0/888	2.61	93/1358 (6.8%)
6	A4	1.60	0/878	2.53	87/1352 (6.4%)
7	A5	1.63	0/1091	2.61	121/1673 (7.2%)
8	A6	1.60	1/1140 (0.1%)	2.51	114/1751 (6.5%)
9	A7	1.67	0/969	2.69	121/1484 (8.2%)
10	A8	1.61	1/1093 (0.1%)	2.47	99/1679 (5.9%)
11	AB	1.62	0/894	2.41	87/1370 (6.4%)
12	AC	1.65	0/1118	2.52	112/1723 (6.5%)
13	AD	1.65	0/1144	2.55	123/1759 (7.0%)
14	AE	1.61	0/823	2.38	76/1267 (6.0%)
15	AF	1.60	0/1082	2.32	88/1662 (5.3%)
16	AG	1.66	0/1057	2.57	118/1625 (7.3%)
17	AH	1.62	1/1079 (0.1%)	2.42	108/1656 (6.5%)
18	AI	1.67	1/1085 (0.1%)	2.65	129/1661 (7.8%)
19	AJ	1.60	0/1189	2.52	111/1828 (6.1%)
20	AK	1.58	3/1342 (0.2%)	2.44	127/2055 (6.2%)
21	AL	1.59	0/1085	2.33	85/1669 (5.1%)
22	AM	1.53	0/1107	2.30	94/1693 (5.6%)
23	AN	1.62	0/1084	2.46	107/1664 (6.4%)
24	AO	1.61	0/1075	2.43	106/1649 (6.4%)
25	AP	1.60	2/897 (0.2%)	2.40	82/1375 (6.0%)
26	AQ	1.69	1/1302 (0.1%)	2.64	151/1999 (7.6%)
27	AR	1.62	0/1094	2.47	105/1681 (6.2%)
28	AS	1.69	0/895	2.73	121/1372 (8.8%)
29	AT	1.64	1/1091 (0.1%)	2.50	119/1674 (7.1%)
30	AU	1.63	1/1085 (0.1%)	2.64	123/1661 (7.4%)
31	AV	1.58	3/1178 (0.3%)	2.45	116/1807 (6.4%)
32	AW	1.60	0/783	2.42	70/1202 (5.8%)
33	AX	1.64	1/1074 (0.1%)	2.57	111/1643 (6.8%)
34	AY	1.68	0/723	2.61	86/1109 (7.8%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	AZ	1.64	0/1211	2.48	123/1854 (6.6%)
36	Ab	1.60	0/1015	2.42	94/1557 (6.0%)
37	Ac	1.62	0/1252	2.57	137/1920 (7.1%)
38	Ad	1.55	0/1069	2.35	92/1637 (5.6%)
39	Af	1.64	0/1082	2.62	128/1656 (7.7%)
40	Ag	1.65	1/1098 (0.1%)	2.48	115/1689 (6.8%)
41	Ah	1.54	1/971 (0.1%)	2.31	76/1486 (5.1%)
42	Ai	1.65	0/809	2.55	99/1239 (8.0%)
43	Aj	1.64	0/1412	2.66	147/2166 (6.8%)
44	Ak	1.70	2/1065 (0.2%)	2.69	119/1637 (7.3%)
45	Al	1.55	1/1056 (0.1%)	2.37	96/1614 (5.9%)
46	Am	1.62	1/1077 (0.1%)	2.49	114/1650 (6.9%)
47	An	1.59	0/1088	2.34	93/1672 (5.6%)
48	Ao	1.64	1/810 (0.1%)	2.45	67/1241 (5.4%)
49	As	1.58	1/1085 (0.1%)	2.35	87/1666 (5.2%)
50	Au	1.56	0/1075	2.32	87/1650 (5.3%)
51	Av	1.61	0/975	2.47	100/1495 (6.7%)
52	Aw	1.59	0/1072	2.47	99/1642 (6.0%)
53	Ax	1.60	1/1067 (0.1%)	2.35	98/1640 (6.0%)
54	Ay	1.63	0/638	2.48	67/979 (6.8%)
55	Az	1.64	0/828	2.47	83/1273 (6.5%)
56	B0	1.61	2/1094 (0.2%)	2.33	99/1683 (5.9%)
57	B1	1.62	0/1013	2.52	106/1557 (6.8%)
58	B2	1.69	1/825 (0.1%)	2.62	91/1268 (7.2%)
59	B3	1.57	0/1094	2.36	99/1683 (5.9%)
60	B4	1.62	0/745	2.57	87/1142 (7.6%)
61	B5	1.61	0/917	2.49	93/1410 (6.6%)
62	B6	1.66	1/1047 (0.1%)	2.57	110/1614 (6.8%)
63	B7	1.59	1/996 (0.1%)	2.27	73/1533 (4.8%)
64	B8	1.56	0/730	2.41	68/1117 (6.1%)
65	B9	1.61	0/907	2.47	92/1393 (6.6%)
66	BB	1.63	0/1104	2.47	107/1700 (6.3%)
67	BC	1.59	0/897	2.48	86/1381 (6.2%)
68	BD	1.66	0/820	2.57	87/1265 (6.9%)
69	BE	1.62	0/1329	2.46	132/2044 (6.5%)
70	BF	1.56	0/906	2.34	67/1393 (4.8%)
71	BG	1.65	0/1134	2.65	127/1746 (7.3%)
72	BH	1.63	0/722	2.52	79/1107 (7.1%)
73	BI	1.56	0/609	2.41	57/935 (6.1%)
74	BJ	1.63	0/1205	2.40	110/1853 (5.9%)
75	BK	1.63	2/1005 (0.2%)	2.66	104/1543 (6.7%)
76	BL	1.60	0/1079	2.38	94/1657 (5.7%)
77	BM	1.60	1/959 (0.1%)	2.39	90/1475 (6.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	BN	1.62	0/1086	2.45	112/1669 (6.7%)
79	BO	1.57	1/1098 (0.1%)	2.34	97/1687 (5.7%)
80	BP	1.56	0/921	2.33	78/1414 (5.5%)
81	BQ	1.60	0/1087	2.41	100/1672 (6.0%)
82	BR	1.58	0/822	2.38	71/1263 (5.6%)
83	BS	1.59	0/1081	2.37	95/1660 (5.7%)
84	BT	1.63	0/843	2.32	68/1298 (5.2%)
85	BU	1.61	2/909 (0.2%)	2.32	69/1398 (4.9%)
86	BV	1.60	0/1003	2.42	97/1545 (6.3%)
87	BW	1.59	0/979	2.32	87/1507 (5.8%)
88	BX	1.61	0/1114	2.46	101/1717 (5.9%)
89	BY	1.60	0/976	2.42	89/1500 (5.9%)
90	BZ	1.61	0/976	2.44	98/1499 (6.5%)
91	Ba	1.61	0/1086	2.35	91/1670 (5.4%)
92	Bb	1.68	1/1093 (0.1%)	2.53	122/1679 (7.3%)
93	Bc	1.60	0/1135	2.31	93/1746 (5.3%)
94	Bd	1.62	0/937	2.34	81/1443 (5.6%)
95	Be	1.62	0/1096	2.39	96/1687 (5.7%)
96	Bf	1.69	0/1101	2.54	115/1694 (6.8%)
97	Bg	1.60	1/723 (0.1%)	2.37	67/1110 (6.0%)
98	Bh	1.63	0/880	2.33	78/1358 (5.7%)
99	Bi	1.63	1/1406 (0.1%)	2.47	142/2161 (6.6%)
100	Bj	1.60	0/1016	2.46	107/1560 (6.9%)
101	Bk	1.63	0/1085	2.53	120/1670 (7.2%)
102	Bl	1.67	0/1110	2.55	113/1709 (6.6%)
103	Bm	1.60	0/1078	2.40	101/1654 (6.1%)
104	Bn	1.67	0/1096	2.38	95/1693 (5.6%)
105	Bo	1.63	0/1292	2.37	117/1986 (5.9%)
106	Bp	1.67	1/1108 (0.1%)	2.59	118/1706 (6.9%)
107	Bq	1.64	0/881	2.43	88/1357 (6.5%)
108	Br	1.62	0/818	2.31	71/1259 (5.6%)
109	Bs	1.66	1/901 (0.1%)	2.51	93/1386 (6.7%)
110	C0	1.63	0/709	2.41	65/1091 (6.0%)
111	C1	1.58	0/824	2.57	98/1265 (7.7%)
112	C2	1.57	0/1259	2.39	110/1930 (5.7%)
113	C3	1.58	0/1077	2.44	99/1651 (6.0%)
114	C4	1.56	0/1269	2.39	122/1950 (6.3%)
115	C5	1.62	0/1433	2.43	130/2209 (5.9%)
116	C6	1.61	0/1097	2.58	116/1685 (6.9%)
117	C7	1.57	1/1181 (0.1%)	2.35	94/1817 (5.2%)
118	C8	1.61	1/998 (0.1%)	2.37	85/1533 (5.5%)
119	CB	1.55	2/1215 (0.2%)	2.26	93/1867 (5.0%)
120	CC	1.62	0/1082	2.50	97/1666 (5.8%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
121	CD	1.65	2/1106 (0.2%)	2.52	107/1702 (6.3%)
122	CE	1.61	0/917	2.61	89/1409 (6.3%)
123	CF	1.59	0/908	2.44	81/1395 (5.8%)
124	CG	1.62	0/1013	2.35	84/1562 (5.4%)
125	CH	1.59	0/1107	2.37	99/1707 (5.8%)
126	CI	1.61	0/996	2.45	97/1528 (6.3%)
127	CJ	1.61	0/1061	2.53	113/1626 (6.9%)
128	CK	1.63	0/1103	2.55	111/1695 (6.5%)
129	CL	1.59	0/1082	2.49	108/1659 (6.5%)
130	CM	1.65	0/903	2.62	104/1390 (7.5%)
131	CN	1.62	0/955	2.48	89/1474 (6.0%)
132	CO	1.60	1/1092 (0.1%)	2.46	105/1678 (6.3%)
133	CP	1.60	0/1279	2.41	123/1969 (6.2%)
134	CQ	1.65	0/623	2.53	68/952 (7.1%)
135	CR	1.56	0/1084	2.36	98/1667 (5.9%)
136	CS	1.60	0/867	2.43	75/1333 (5.6%)
137	CT	1.61	0/1102	2.48	110/1695 (6.5%)
138	CU	1.61	0/728	2.57	81/1119 (7.2%)
139	CV	1.59	0/1192	2.38	95/1830 (5.2%)
140	CW	1.62	0/629	2.35	60/965 (6.2%)
141	CX	1.61	1/1055 (0.1%)	2.36	90/1618 (5.6%)
142	CY	1.60	0/979	2.67	122/1501 (8.1%)
143	CZ	1.62	0/1113	2.58	125/1713 (7.3%)
144	Cb	1.60	3/999 (0.3%)	2.62	112/1532 (7.3%)
145	Cc	1.62	0/1174	2.45	122/1800 (6.8%)
146	Cd	1.58	0/965	2.48	92/1486 (6.2%)
147	Ce	1.60	1/1175 (0.1%)	2.48	124/1802 (6.9%)
148	Cf	1.60	0/862	2.50	86/1321 (6.5%)
149	Cg	1.64	0/827	2.53	88/1270 (6.9%)
150	Ch	1.62	0/1048	2.47	106/1605 (6.6%)
151	Ck	1.56	0/653	2.24	53/1004 (5.3%)
152	Cp	1.62	0/1095	2.48	106/1682 (6.3%)
153	Cq	1.62	0/930	2.46	84/1436 (5.8%)
154	Cr	1.64	1/816 (0.1%)	2.61	101/1251 (8.1%)
155	Cs	1.63	0/1140	2.59	110/1756 (6.3%)
156	Ct	1.58	1/991 (0.1%)	2.39	90/1521 (5.9%)
157	Cu	1.59	1/1366 (0.1%)	2.50	145/2096 (6.9%)
158	Cv	1.57	0/918	2.33	77/1409 (5.5%)
159	Cw	1.64	0/1232	2.53	133/1893 (7.0%)
160	Cx	1.66	0/820	2.63	94/1258 (7.5%)
161	Cy	1.60	0/1286	2.48	119/1977 (6.0%)
162	Cz	1.63	0/1090	2.57	123/1672 (7.4%)
All	All	1.62	117/330437 (0.0%)	2.41	29725/508627 (5.8%)

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	AA	40	448
2	A0	0	6
3	A1	1	4
4	A2	0	2
6	A4	0	2
7	A5	0	4
8	A6	0	4
9	A7	0	3
10	A8	0	5
11	AB	0	1
12	AC	0	3
13	AD	0	2
15	AF	1	4
16	AG	0	3
17	AH	1	2
18	AI	1	2
19	AJ	0	4
20	AK	0	8
21	AL	0	4
22	AM	0	1
23	AN	1	3
24	AO	2	3
25	AP	0	1
26	AQ	2	6
27	AR	0	2
28	AS	0	4
29	AT	1	4
30	AU	1	4
31	AV	1	5
33	AX	0	3
34	AY	1	4
35	AZ	2	4
36	Ab	2	2
37	Ac	0	2
38	Ad	0	2
39	Af	0	1
40	Ag	0	1
41	Ah	1	3
42	Ai	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
43	Aj	1	5
44	Ak	0	7
45	Al	1	4
46	Am	0	2
47	An	1	4
48	Ao	1	2
49	As	0	3
50	Au	1	0
51	Av	0	6
52	Aw	1	2
53	Ax	0	2
54	Ay	0	1
55	Az	0	3
56	B0	0	6
57	B1	0	1
58	B2	0	2
59	B3	1	1
60	B4	1	5
61	B5	1	2
62	B6	1	5
63	B7	0	5
65	B9	1	3
66	BB	1	3
67	BC	0	1
68	BD	0	4
69	BE	0	3
70	BF	1	2
71	BG	0	7
72	BH	0	2
73	BI	0	2
74	BJ	3	2
75	BK	0	1
76	BL	1	5
77	BM	0	1
78	BN	0	1
79	BO	0	6
80	BP	0	2
81	BQ	1	2
82	BR	0	3
83	BS	0	5
84	BT	0	3
85	BU	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
86	BV	2	1
87	BW	1	3
88	BX	0	7
89	BY	1	2
90	BZ	0	1
91	Ba	0	3
92	Bb	0	2
93	Bc	1	4
94	Bd	1	0
95	Be	1	0
96	Bf	1	4
97	Bg	1	1
98	Bh	0	2
99	Bi	0	3
100	Bj	0	1
101	Bk	0	4
102	Bl	0	3
103	Bm	1	3
104	Bn	0	5
105	Bo	1	5
106	Bp	2	7
107	Bq	0	3
108	Br	0	1
109	Bs	0	1
111	C1	0	1
112	C2	1	2
113	C3	1	4
114	C4	0	2
115	C5	3	3
116	C6	0	3
117	C7	0	4
118	C8	0	3
119	CB	0	3
120	CC	2	3
121	CD	2	3
122	CE	1	2
123	CF	0	2
124	CG	0	4
125	CH	0	4
126	CI	1	4
127	CJ	0	5
128	CK	1	5

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Mol	Chain	#Chirality outliers	#Planarity outliers
129	CL	1	5
131	CN	0	1
132	CO	1	7
133	CP	0	5
134	CQ	0	1
135	CR	2	0
136	CS	0	4
137	CT	2	5
138	CU	0	1
139	CV	0	3
140	CW	4	2
141	CX	0	3
142	CY	1	0
143	CZ	0	4
144	Cb	1	2
145	Cc	1	5
146	Cd	0	3
147	Ce	4	4
148	Cf	0	1
149	Cg	0	4
150	Ch	0	2
152	Cp	0	3
153	Cq	0	5
154	Cr	0	2
155	Cs	1	8
156	Ct	1	0
157	Cu	1	2
158	Cv	0	3
159	Cw	0	5
160	Cx	0	4
161	Cy	0	2
162	Cz	0	6
All	All	121	919

The worst 5 of 117 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AA	3933	DA	O3'-P	-78.44	0.67	1.61
1	AA	437	DT	O3'-P	-54.86	0.95	1.61
1	AA	186	DT	O3'-P	-51.03	0.99	1.61
1	AA	4125	DG	O3'-P	41.42	2.10	1.61
1	AA	955	DG	O3'-P	38.46	2.07	1.61

The worst 5 of 29725 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	378	DG	P-O3'-C3'	-68.56	37.43	119.70
1	AA	35	DC	P-O3'-C3'	-58.73	49.22	119.70
1	AA	511	DA	P-O3'-C3'	-52.67	56.49	119.70
1	AA	35	DC	O3'-P-O5'	-46.83	15.02	104.00
1	AA	378	DG	O3'-P-O5'	-45.16	18.19	104.00

5 of 121 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	AA	89	DT	C3'
1	AA	186	DT	C3'
1	AA	437	DT	C3'
1	AA	506	DT	C3'
1	AA	826	DT	C3'

5 of 919 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	24	DG	Sidechain
1	AA	30	DG	Sidechain
1	AA	31	DG	Sidechain
1	AA	6	DG	Sidechain
1	AA	63	DC	Sidechain

5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein molecules in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein molecules in this entry.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	AA	23
15	AF	1

The worst 5 of 24 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	AA	2465:DT	O3'	2466:DT	P	5.78
1	AA	6158:DC	O3'	6159:DA	P	3.30
1	AA	62:DT	O3'	63:DC	P	3.28
1	AA	590:DA	O3'	591:DA	P	3.28
1	AA	4430:DT	O3'	4431:DT	P	3.28

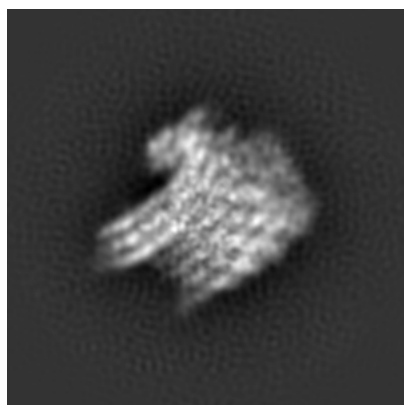
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2210. These allow visual inspection of the internal detail of the map and identification of artifacts.

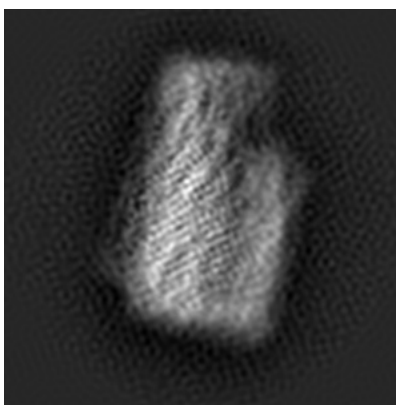
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

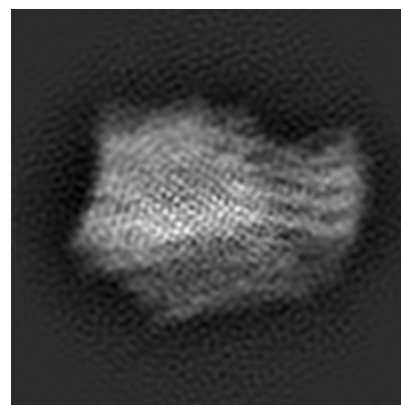
6.1.1 Primary map



X



Y

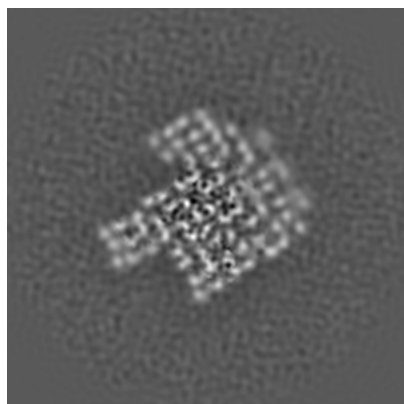


Z

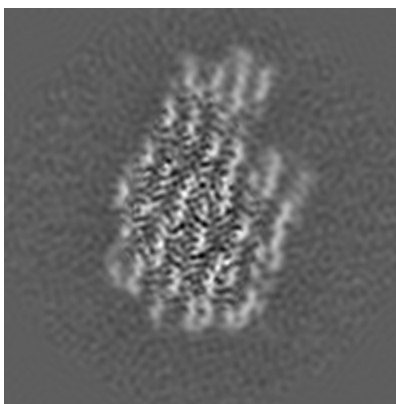
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

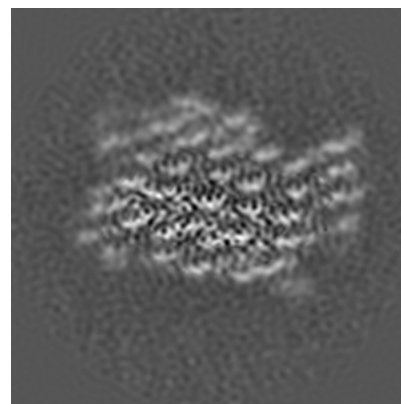
6.2.1 Primary map



X Index: 86



Y Index: 86

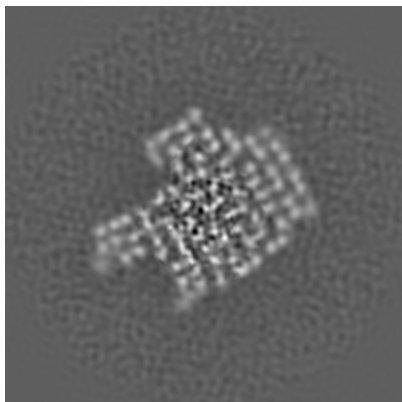


Z Index: 86

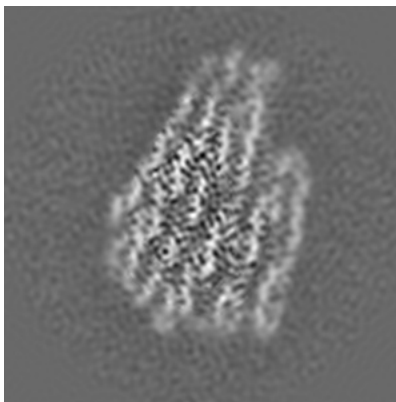
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

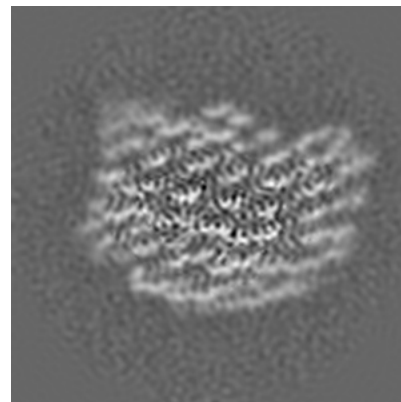
6.3.1 Primary map



X Index: 71



Y Index: 82

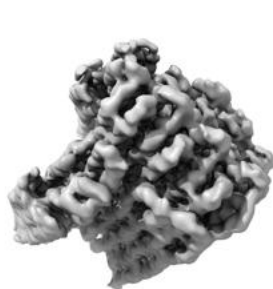


Z Index: 78

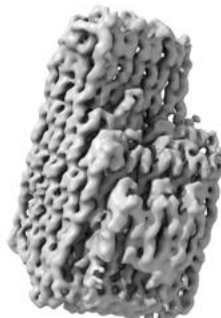
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views [i](#)

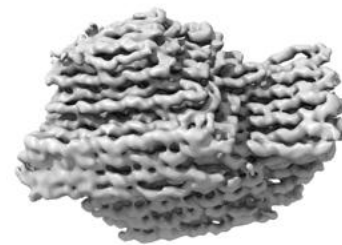
6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

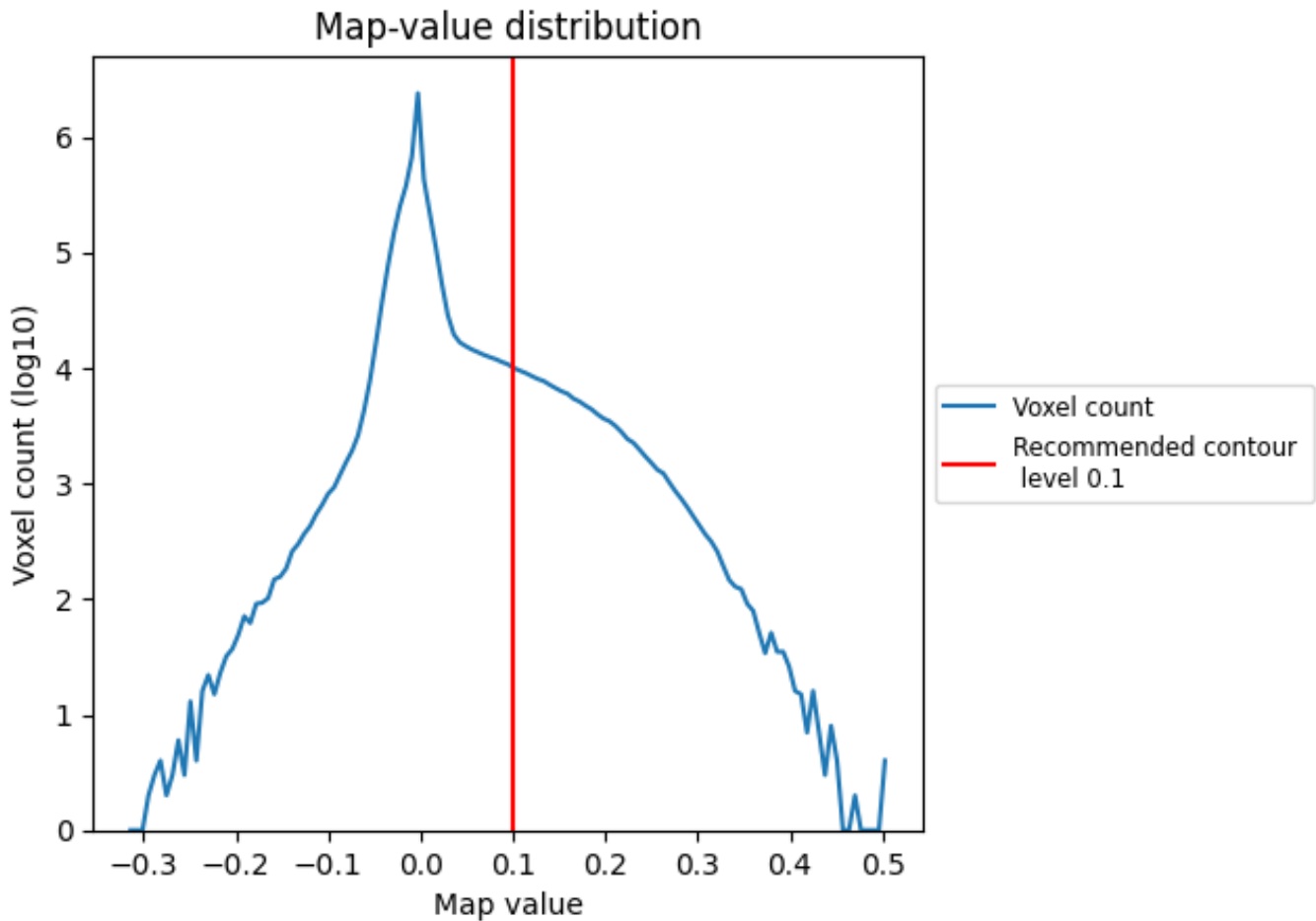
6.5 Mask visualisation

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

7 Map analysis [i](#)

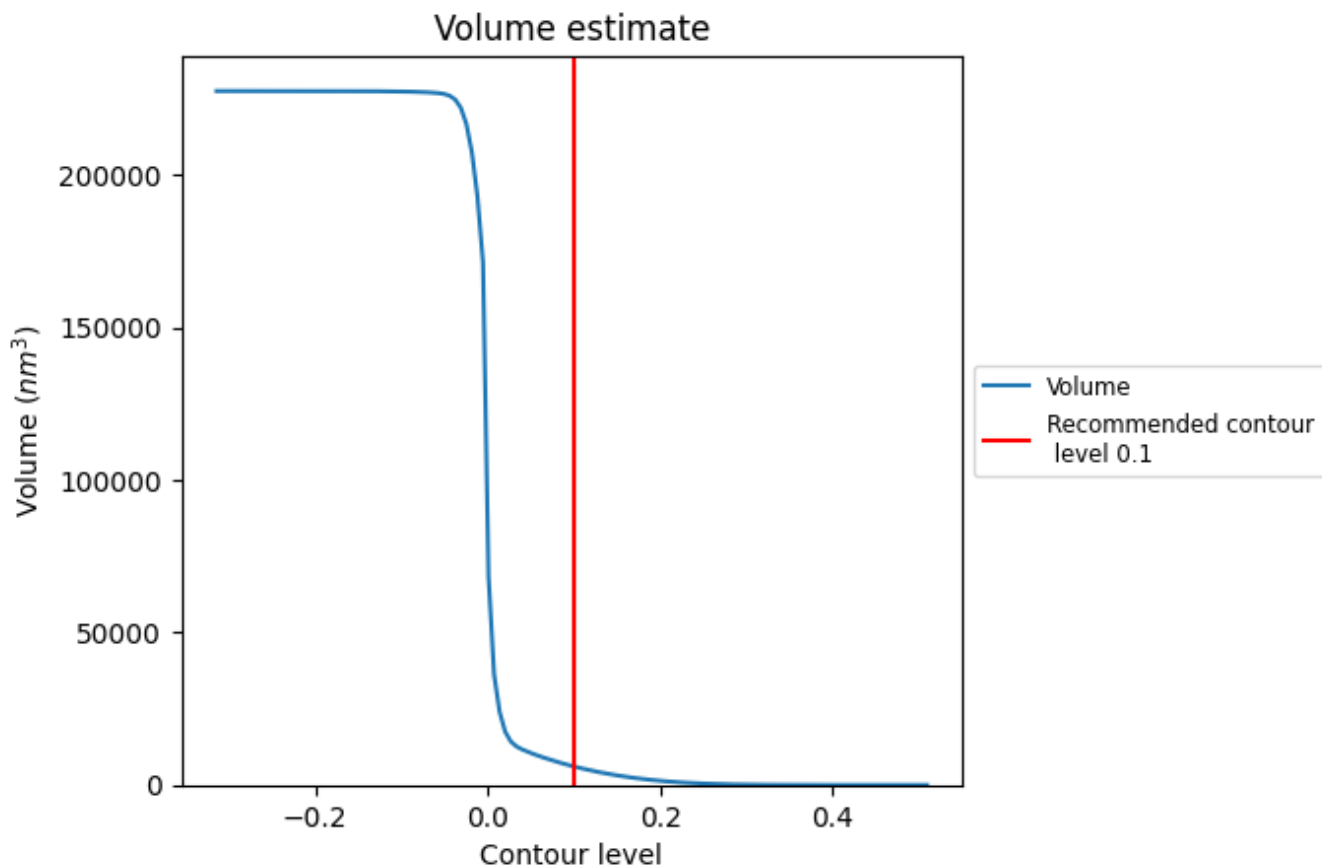
This section contains the results of statistical analysis of the map.

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.

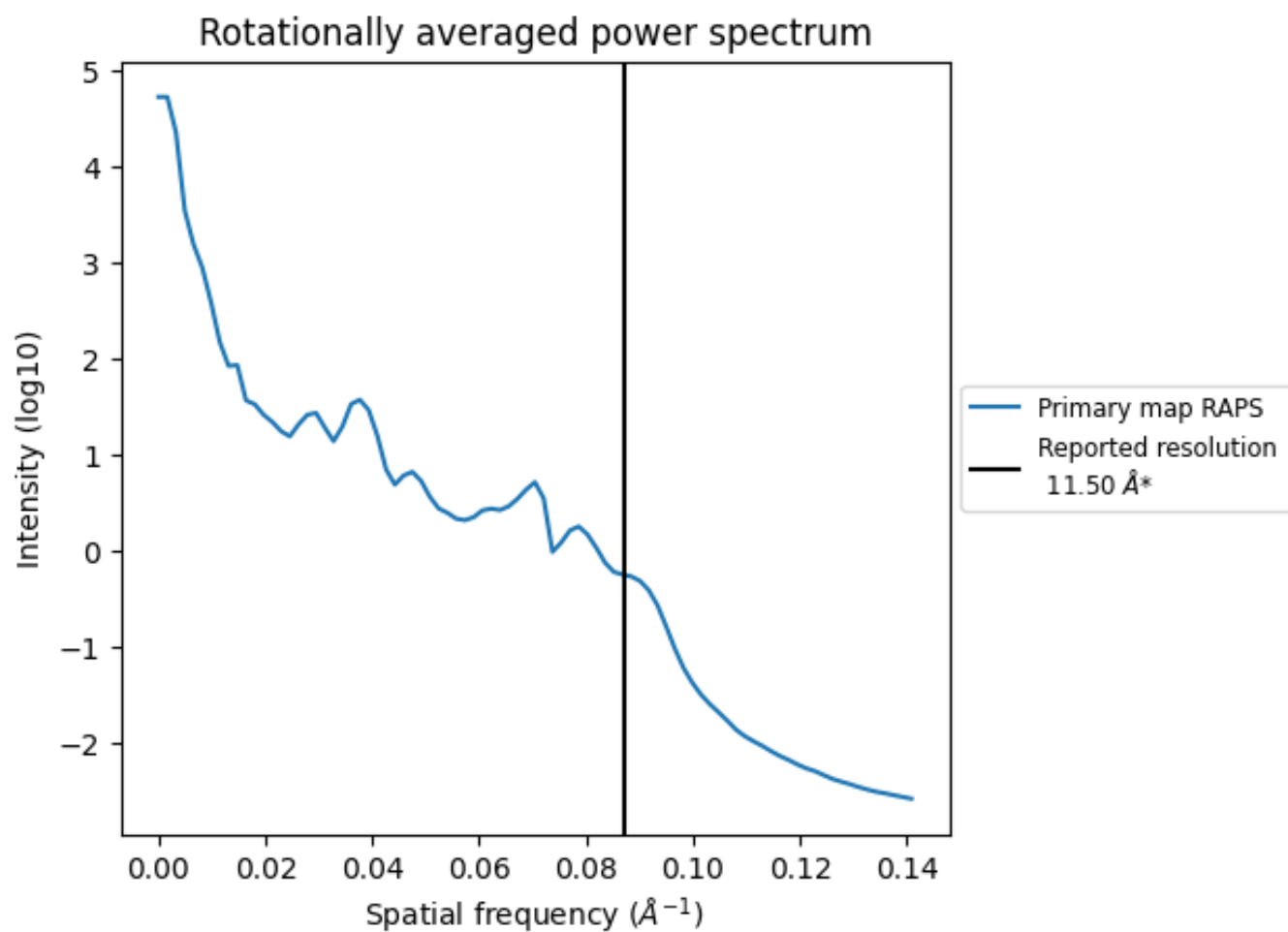
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 6064 nm^3 ; this corresponds to an approximate mass of 5477 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum [i](#)



*Reported resolution corresponds to spatial frequency of 0.087 Å⁻¹

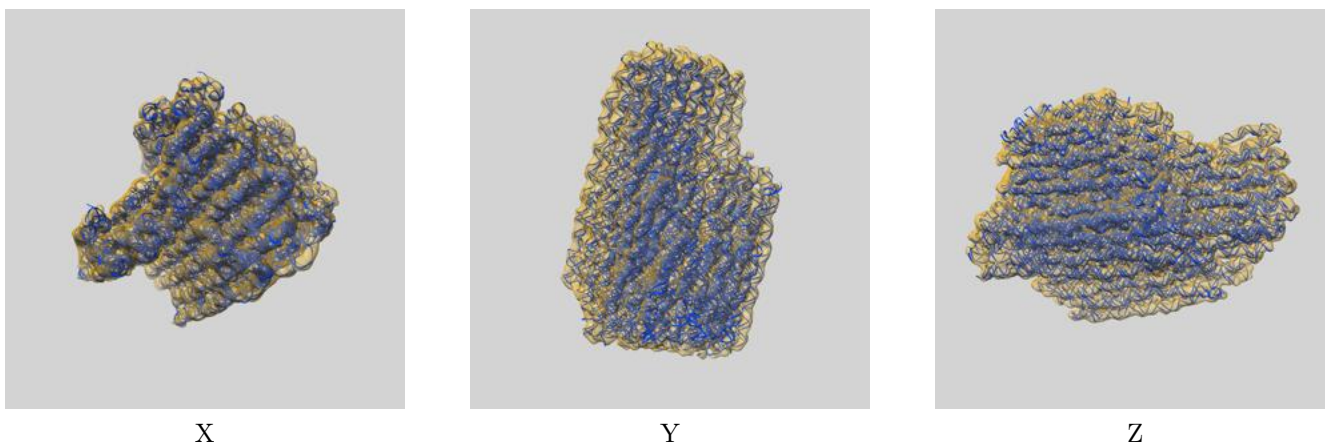
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

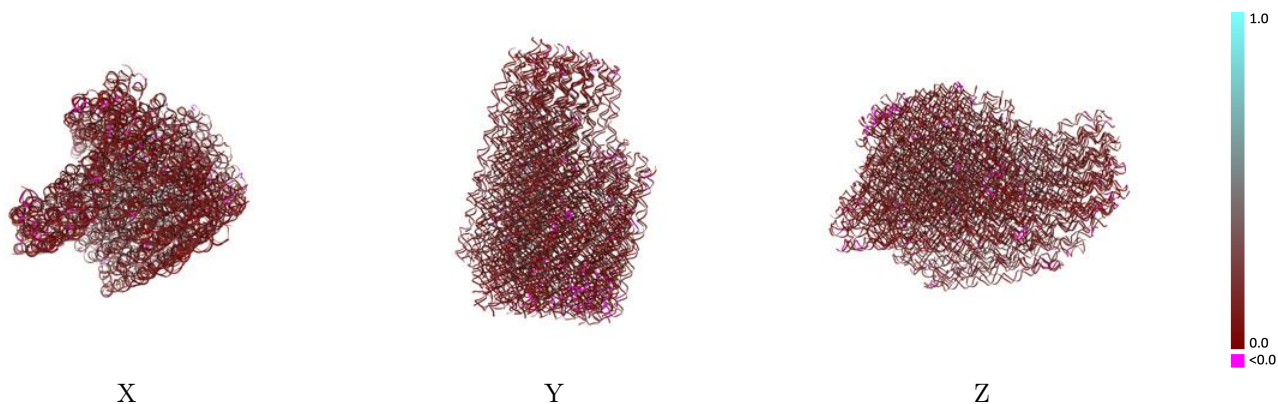
This section contains information regarding the fit between EMDB map EMD-2210 and PDB model 4V5X. Per-residue inclusion information can be found in section 3 on page 33.

9.1 Map-model overlay [i](#)



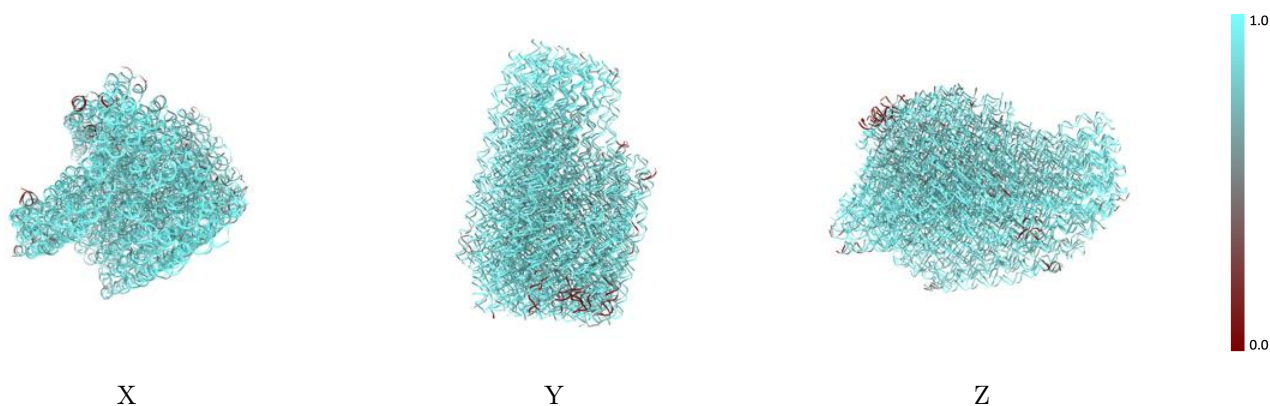
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



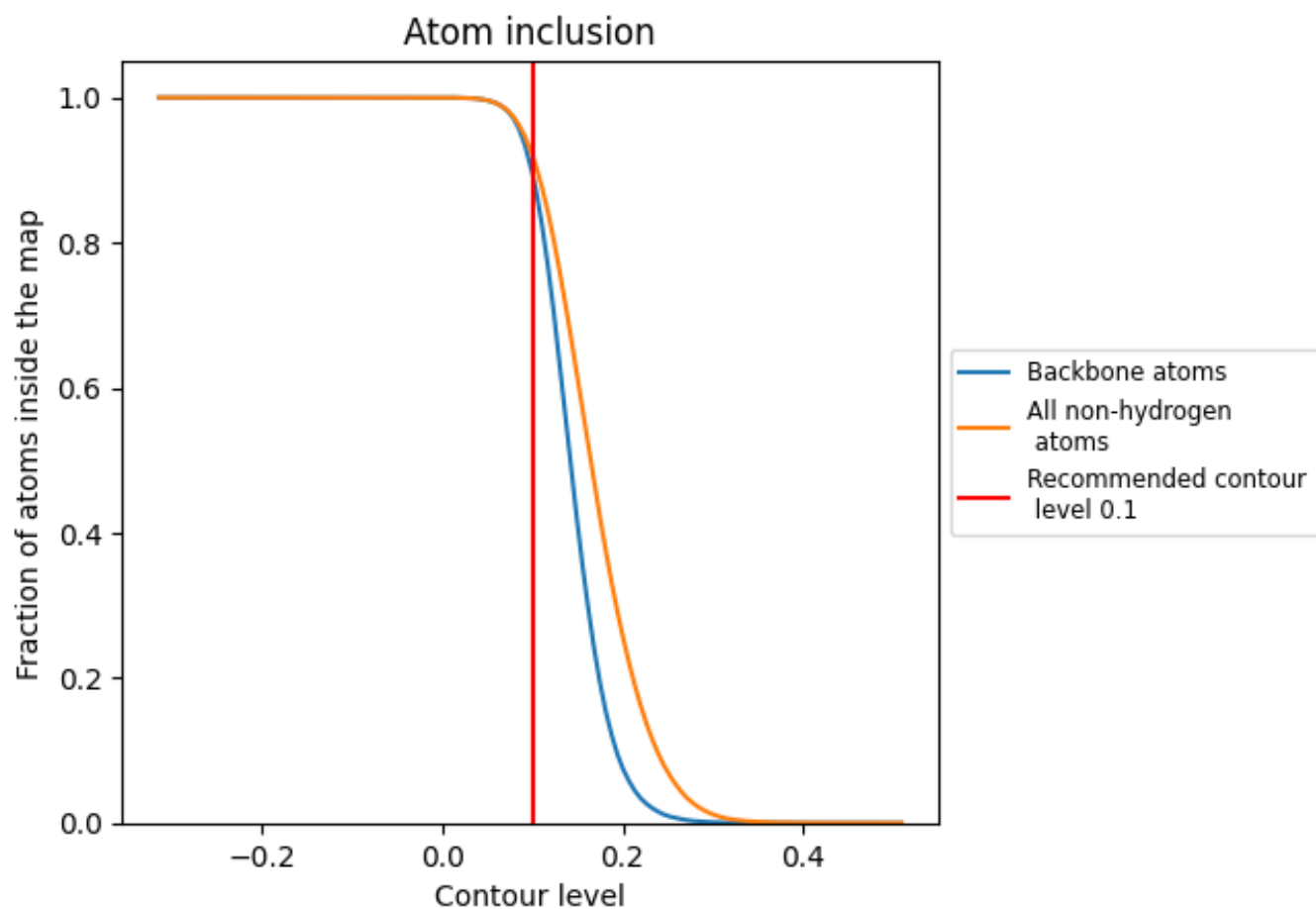
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 92% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9200	 0.1390
A0	 0.9749	 0.1650
A1	 0.9729	 0.1160
A2	 0.9500	 0.1680
A3	 0.9812	 0.1910
A4	 0.9167	 0.1090
A5	 0.9784	 0.1690
A6	 0.9754	 0.1390
A7	 0.9571	 0.1600
A8	 0.9529	 0.1710
AA	 0.9191	 0.1390
AB	 0.9249	 0.1300
AC	 0.9849	 0.1360
AD	 0.9538	 0.1260
AE	 0.7834	 0.1020
AF	 0.9587	 0.1230
AG	 0.9606	 0.1300
AH	 0.9637	 0.1260
AI	 0.9607	 0.1770
AJ	 0.9651	 0.1350
AK	 0.9825	 0.1950
AL	 0.8991	 0.1240
AM	 0.9678	 0.1610
AN	 0.9649	 0.1490
AO	 0.9595	 0.1310
AP	 0.9813	 0.1650
AQ	 0.9629	 0.1460
AR	 0.8964	 0.0980
AS	 0.9685	 0.1320
AT	 0.9548	 0.1490
AU	 0.9700	 0.1810
AV	 0.9743	 0.1680
AW	 0.6690	 0.0820
AX	 0.9781	 0.1860
AY	 0.6636	 0.1140























































































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Chain	Atom inclusion	Q-score
AZ	 0.9510	 0.1310
Ab	 0.9746	 0.1520
Ac	 0.9471	 0.1410
Ad	 0.9530	 0.1720
Af	 0.9616	 0.1480
Ag	 0.9622	 0.1400
Ah	 0.9472	 0.1490
Ai	 0.9335	 0.1140
Aj	 0.9610	 0.1830
Ak	 0.9556	 0.1720
Al	 0.9315	 0.1720
Am	 0.9325	 0.1580
An	 0.9537	 0.1620
Ao	 0.9489	 0.1940
As	 0.9701	 0.1700
Au	 0.9896	 0.1540
Av	 0.9655	 0.1540
Aw	 0.9563	 0.1800
Ax	 0.9412	 0.1190
Ay	 0.7588	 0.0960
Az	 0.9308	 0.1090
B0	 0.9427	 0.1420
B1	 0.9522	 0.1370
B2	 0.9441	 0.1720
B3	 0.9477	 0.1590
B4	 0.8389	 0.1140
B5	 0.8946	 0.1190
B6	 0.9214	 0.1270
B7	 0.9496	 0.1290
B8	 0.8652	 0.1230
B9	 0.9012	 0.1080
BB	 0.9633	 0.1340
BC	 0.9624	 0.1410
BD	 0.9532	 0.1370
BE	 0.8994	 0.1040
BF	 0.9494	 0.1520
BG	 0.9364	 0.1280
BH	 0.7640	 0.1060
BI	 0.9210	 0.1220
BJ	 0.9201	 0.1400
BK	 0.9508	 0.1780
BL	 0.9420	 0.1700





















































































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Chain	Atom inclusion	Q-score
BM	 0.9591	 0.1590
BN	 0.9175	 0.1100
BO	 0.9472	 0.1490
BP	 0.9369	 0.1130
BQ	 0.9526	 0.1370
BR	 0.8608	 0.1210
BS	 0.9452	 0.1840
BT	 0.9389	 0.1130
BU	 0.9311	 0.1250
BV	 0.9151	 0.0910
BW	 0.7952	 0.1120
BX	 0.9576	 0.1220
BY	 0.9506	 0.1340
BZ	 0.8977	 0.1250
Ba	 0.9012	 0.1480
Bb	 0.7875	 0.1130
Bc	 0.8591	 0.1350
Bd	 0.9151	 0.1250
Be	 0.8793	 0.1320
Bf	 0.9399	 0.1310
Bg	 0.8421	 0.1060
Bh	 0.9005	 0.1280
Bi	 0.7514	 0.0910
Bj	 0.9603	 0.1380
Bk	 0.8797	 0.1160
Bl	 0.8580	 0.1270
Bm	 0.9232	 0.1150
Bn	 0.7087	 0.1140
Bo	 0.6551	 0.0850
Bp	 0.8619	 0.1140
Bq	 0.8890	 0.1020
Br	 0.8374	 0.1200
Bs	 0.3912	 0.0700
C0	 0.7611	 0.1340
C1	 0.9399	 0.1270
C2	 0.9440	 0.1860
C3	 0.9688	 0.1520
C4	 0.8914	 0.1190
C5	 0.9529	 0.1460
C6	 0.8813	 0.1630
C7	 0.9413	 0.1270
C8	 0.9608	 0.1770





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Chain	Atom inclusion	Q-score
CB	 0.9494	 0.1510
CC	 0.9699	 0.1600
CD	 0.9675	 0.1690
CE	 0.9191	 0.1720
CF	 0.9346	 0.1850
CG	 0.9679	 0.1290
CH	 0.9574	 0.1620
CI	 0.9798	 0.1260
CJ	 0.9249	 0.1290
CK	 0.9501	 0.2000
CL	 0.9659	 0.1410
CM	 0.5356	 0.0950
CN	 0.7983	 0.1110
CO	 0.9487	 0.1820
CP	 0.9412	 0.1300
CQ	 0.9031	 0.1200
CR	 0.9598	 0.1340
CS	 0.9288	 0.1260
CT	 0.9532	 0.1990
CU	 0.9383	 0.1320
CV	 0.9719	 0.1260
CW	 0.9681	 0.1130
CX	 0.9417	 0.1630
CY	 0.9471	 0.1500
CZ	 0.8997	 0.1370
Cb	 0.9203	 0.1760
Cc	 0.9456	 0.1060
Cd	 0.9325	 0.1100
Ce	 0.9514	 0.1410
Cf	 0.8711	 0.1170
Cg	 0.9020	 0.1130
Ch	 0.9627	 0.1550
Ck	 0.8068	 0.1020
Cp	 0.9580	 0.1620
Cq	 0.9214	 0.1390
Cr	 0.9395	 0.1120
Cs	 0.9585	 0.1400
Ct	 0.9221	 0.1240
Cu	 0.9424	 0.1600
Cv	 0.9162	 0.1130
Cw	 0.9536	 0.1240
Cx	 0.9110	 0.1090

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Chain	Atom inclusion	Q-score
Cy	 0.9616	 0.1480
Cz	 0.9412	 0.1430