



## wwPDB EM Validation Summary Report ⓘ

Mar 21, 2026 – 07:02 PM UTC

PDB ID : 7ARV / pdb\_00007arv  
EMDB ID : EMD-11379  
Title : TwistTower\_native-twist  
Authors : Kube, M.; Kohler, F.; Feigl, E.; Nagel-Yuksel, B.; Willner, E.M.; Funke, J.J.; Gerling, T.; Stommer, P.; Honemann, M.N.; Martin, T.G.; Scheres, S.H.W.; Dietz, H.  
Deposited on : 2020-10-26  
Resolution : 7.40 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](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

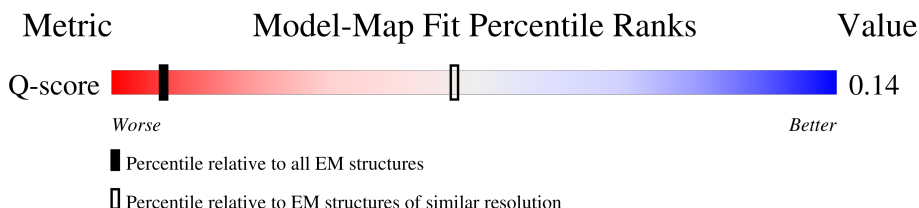
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*



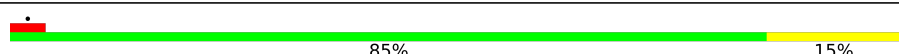
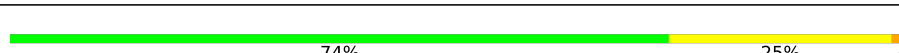
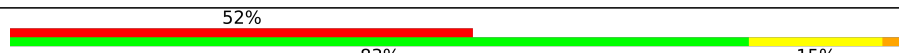
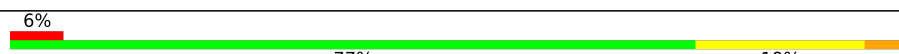


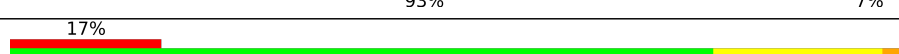

The reported resolution of this entry is 7.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Q-score	25397	412 ( 6.90 - 7.90 )

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  $\geq 3$ , 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	8064	 82% 17% .
2	AB	29	 100%
3	AC	48	 85% 15%
4	AD	53	 74% 25% .
5	AE	60	 83% 15% .
6	AF	48	 77% 19% .
7	AG	48	 79% 17% .
8	AH	60	 93% 7%
9	AI	42	 79% 19% .
10	AJ	60	 90% 10%

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Mol	Chain	Length	Quality of chain
11	AK	32	81% 19%
12	AL	40	72% 25%
13	AM	48	88% 12%
14	AN	32	88% 12%
15	AO	48	92% 8%
16	AP	40	85% 15%
17	AQ	45	84% 16%
18	AR	48	92% 8%
19	AS	48	79% 21%
20	AT	45	82% 16%
21	AU	48	79% 21%
22	AV	40	88% 12%
23	AW	58	83% 16%
24	AX	60	88% 10%
25	AY	32	81% 19%
26	AZ	48	81% 19%
27	Aa	40	90% 10%
28	Ab	48	75% 23%
29	Ac	40	70% 30%
30	Ad	53	85% 15%
31	Ae	40	75% 20% 5%
32	Af	32	78% 22%
33	Ag	58	88% 12%
34	Ah	60	82% 17%
35	Ai	48	83% 17%

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Mol	Chain	Length	Quality of chain
36	Aj	48	83% 17%
37	Ak	32	88% 9%
38	Al	48	85% 15%
39	Am	58	81% 19%
40	An	60	87% 13%
41	Ao	57	81% 19%
42	Ap	60	80% 20%
43	Aq	48	83% 17%
44	Ar	37	78% 19%
45	As	40	92% 8%
46	At	44	82% 18%
47	Au	40	82% 18%
48	Av	40	85% 15%
49	Aw	56	88% 12%
50	Ax	40	72% 28%
51	Ay	48	85% 12%
52	Az	45	84% 16%
53	A0	32	72% 25%
54	A1	48	81% 19%
55	A2	48	75% 23%
56	A3	56	79% 20%
57	A4	45	82% 18%
58	A5	48	88% 10%
59	A6	32	78% 22%
60	A7	32	84% 16%







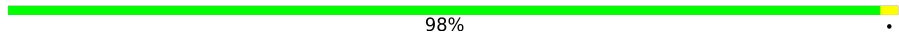






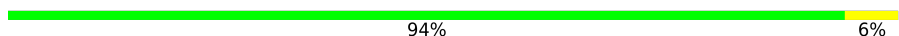


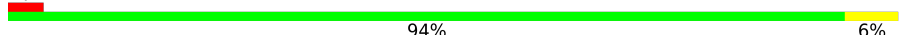








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Mol	Chain	Length	Quality of chain
61	A8	32	91% 9%
62	A9	48	81% 19%
63	BA	45	84% 16%
64	BB	32	72% 25% .
65	BC	45	9% 87% 13%
66	BD	57	5% 88% 12%
67	BE	57	28% 79% 19% .
68	BF	45	7% 76% 24%
69	BG	40	78% 20% .
70	BH	57	7% 74% 25% .
71	BI	57	26% 75% 25%
72	BJ	45	87% 13% .
73	BK	32	91% 9% .
74	BL	56	91% 9%
75	BM	32	91% 9%
76	BN	40	82% 18%
77	BO	48	77% 23%
78	BP	58	78% 22%
79	BQ	57	21% 81% 19%
80	BR	48	90% 10%
81	BS	48	81% 17% .
82	BT	48	90% 10%
83	BU	48	88% 10% .
84	BV	58	9% 83% 17%
85	BW	60	15% 75% 22% .



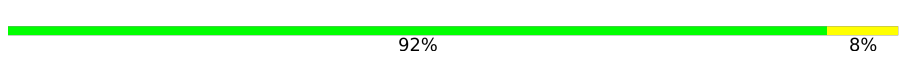



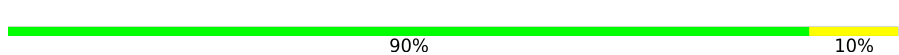





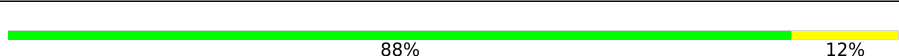
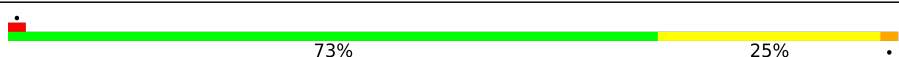
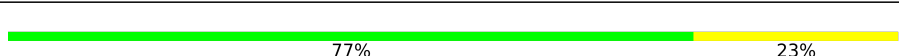

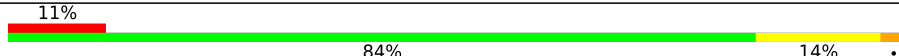

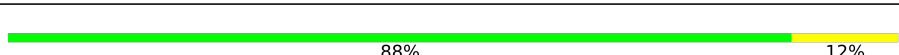
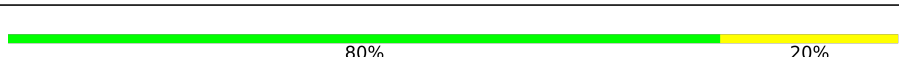
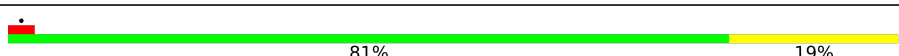



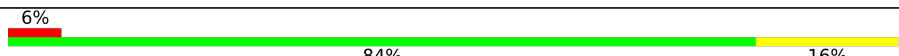
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Mol	Chain	Length	Quality of chain
86	BX	32	 88% 9%
87	BY	40	 75% 20% 5%
88	BZ	40	 78% 22%
89	Ba	48	 75% 23%
90	Bb	48	 71% 27%
91	Bc	32	 88% 12%
92	Bd	48	 98%
93	Be	48	 88% 10%
94	Bf	48	 88% 12%
95	Bg	40	 62% 35%
96	Bh	56	 80% 20%
97	Bi	40	 72% 22% 5%
98	Bj	32	 81% 16%
99	Bk	32	 94% 6%
100	Bl	48	 83% 17%
101	Bm	56	 84% 12%
102	Bn	48	 94% 6%
103	Bo	48	 90% 10%
104	Bp	40	 90% 10%
105	Bq	48	 85% 15%
106	Br	48	 85% 15%
107	Bs	32	 91% 9%
108	Bt	40	 85% 15%
109	Bu	40	 92% 8%
110	Bv	40	 85% 15%

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Mol	Chain	Length	Quality of chain
111	Bw	60	 82% 18%
112	Bx	45	 9% 80% 20%
113	By	40	 92% 8%
114	Bz	32	 84% 16%
115	B0	60	 5% 80% 20%
116	B1	60	 30% 80% 18%
117	B2	40	 90% 10%
118	B3	32	 84% 16%
119	B4	32	 88% 12%
120	B5	60	 7% 87% 13%
121	B6	53	 8% 79% 21%
122	B7	48	 88% 12%
123	B8	32	 88% 12%
124	B9	48	 73% 25%
125	CA	48	 77% 23%
126	CB	60	 17% 80% 18%
127	CC	37	 11% 84% 14%
128	CD	57	 72% 77% 23%
129	CE	32	 88% 12%
130	CF	40	 80% 20%
131	CG	32	 81% 19%
132	CH	53	 6% 75% 25%
133	CI	32	 84% 16%
134	CJ	57	 67% 81% 16%
135	CK	32	 6% 84% 16%

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Mol	Chain	Length	Quality of chain
136	CL	40	80% 20%
137	CM	32	81% 19%
138	CN	56	21% 88% 11%
139	CO	48	81% 17%
140	CP	48	77% 19%
141	CQ	57	9% 79% 21%
142	CR	60	52% 77% 23%
143	CS	48	83% 17%
144	CT	56	93%
145	CU	37	86% 14%
146	CV	32	91% 9%
147	CW	32	88% 12%
148	CX	57	86% 14%
149	CY	60	47% 83% 15%
150	CZ	48	85% 15%
151	Ca	48	90% 10%
152	Cb	40	72% 28%
153	Cc	32	9% 78% 22%
154	Cd	40	78% 18% 5%
155	Ce	40	82% 15%
156	Cf	32	81% 16%
157	Cg	40	92% 8%
158	Ch	40	85% 12%
159	Ci	48	88% 12%
160	Cj	40	82% 18%




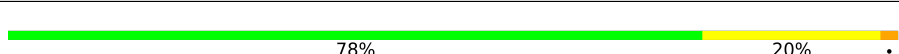

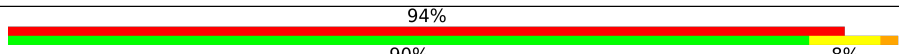

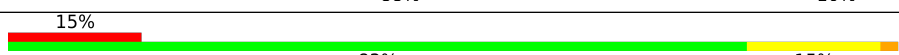
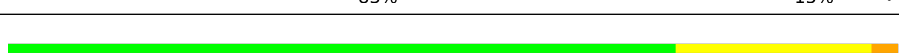
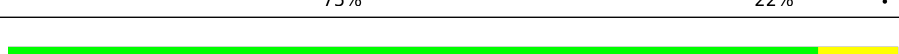
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Mol	Chain	Length	Quality of chain
161	Ck	48	85% 15%
162	Cl	40	82% 18%
163	Cm	48	71% 27%
164	Cn	40	15% 80% 20%
165	Co	40	8% 78% 22%
166	Cp	37	19% 78% 19%
167	Cq	37	19% 89% 11%
168	Cr	40	82% 15%
169	Cs	40	85% 15%
170	Ct	45	71% 27%
171	Cu	37	22% 81% 19%
172	Cv	40	72% 28%
173	Cw	40	90% 8%
174	Cx	32	81% 16%
175	Cy	32	84% 16%
176	Cz	32	100% 91% 9%
177	C0	57	7% 77% 23%
178	C1	57	100% 74% 25%
179	C2	32	81% 19%
180	C3	48	77% 23%
181	C4	48	88% 12%
182	C5	48	85% 15%
183	C6	48	83% 17%
184	C7	40	82% 15%
185	C8	48	81% 19%

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Mol	Chain	Length	Quality of chain
186	C9	57	 82% 18%
187	DA	45	 11% 76% 24%
188	DB	32	 84% 16%
189	DC	40	 78% 20% .
190	DD	45	 100% 69% 31%
191	DE	48	 94% 90% 8% .
192	DF	40	 28% 88% 10% .
193	DG	48	 15% 83% 15% .
194	DH	32	 75% 22% .
195	DI	32	 91% 9%

## 2 Entry composition [i](#)

There are 195 unique types of molecules in this entry. The entry contains 342569 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.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	AA	8064	164972	78873	29001	49035	8063	0	0

- Molecule 2 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	AB	29	582	282	90	182	28	0	0

- Molecule 3 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	AC	48	984	469	182	286	47	0	0

- Molecule 4 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
4	AD	53	1094	523	206	313	52	0	0

- Molecule 5 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
5	AE	60	1217	585	201	372	59	0	0

- Molecule 6 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
6	AF	48	982	469	179	287	47	0	0

- Molecule 7 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AG	48	Total	C	N	O	P	0	0
			991	470	193	281	47		

- Molecule 8 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AH	60	Total	C	N	O	P	0	0
			1224	593	196	376	59		

- Molecule 9 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AI	42	Total	C	N	O	P	0	0
			851	413	139	258	41		

- Molecule 10 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AJ	60	Total	C	N	O	P	0	0
			1218	593	193	373	59		

- Molecule 11 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AK	32	Total	C	N	O	P	0	0
			658	316	122	189	31		

- Molecule 12 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AL	40	Total	C	N	O	P	0	0
			815	393	138	245	39		

- Molecule 13 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AM	48	Total	C	N	O	P	0	0
			988	474	186	281	47		

- Molecule 14 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AN	32	Total	C	N	O	P	0	0
			662	317	130	184	31		

- Molecule 15 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AO	48	Total	C	N	O	P	0	0
			978	470	181	280	47		

- Molecule 16 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AP	40	Total	C	N	O	P	0	0
			817	390	159	229	39		

- Molecule 17 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AQ	45	Total	C	N	O	P	0	0
			914	443	151	276	44		

- Molecule 18 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AR	48	Total	C	N	O	P	0	0
			986	474	183	282	47		

- Molecule 19 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AS	48	Total	C	N	O	P	0	0
			988	471	192	278	47		

- Molecule 20 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AT	45	Total	C	N	O	P	0	0
			928	443	166	275	44		

- Molecule 21 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AU	48	Total	C	N	O	P	0	0
			977	467	178	285	47		

- Molecule 22 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AV	40	Total	C	N	O	P	0	0
			817	387	165	226	39		

- Molecule 23 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AW	58	Total	C	N	O	P	0	0
			1155	556	185	357	57		

- Molecule 24 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AX	60	Total	C	N	O	P	0	0
			1225	590	214	362	59		

- Molecule 25 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AY	32	Total	C	N	O	P	0	0
			659	314	124	190	31		

- Molecule 26 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AZ	48	Total	C	N	O	P	0	0
			990	472	191	280	47		

- Molecule 27 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Aa	40	Total	C	N	O	P	0	0
			823	396	147	241	39		

- Molecule 28 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Ab	48	Total	C	N	O	P	0	0
			986	468	189	282	47		

- Molecule 29 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Ac	40	Total	C	N	O	P	0	0
			812	390	150	233	39		

- Molecule 30 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Ad	53	Total	C	N	O	P	0	0
			1091	522	204	313	52		

- Molecule 31 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Ae	40	Total	C	N	O	P	0	0
			830	392	163	236	39		

- Molecule 32 is a DNA chain called STAPLE STRAND.

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

- Molecule 33 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Ag	58	Total	C	N	O	P	0	0
			1173	571	185	360	57		

- Molecule 34 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Ah	60	Total	C	N	O	P	0	0
			1233	594	216	364	59		

- Molecule 35 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Ai	48	Total	C	N	O	P	0	0
			979	467	172	293	47		

- Molecule 36 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Aj	48	Total	C	N	O	P	0	0
			969	466	170	286	47		

- Molecule 37 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Ak	32	Total	C	N	O	P	0	0
			652	312	123	186	31		

- Molecule 38 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Al	48	Total	C	N	O	P	0	0
			982	471	183	281	47		

- Molecule 39 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Am	58	Total	C	N	O	P	0	0
			1175	569	187	362	57		

- Molecule 40 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	An	60	Total	C	N	O	P	0	0
			1231	594	210	368	59		

- Molecule 41 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Ao	57	Total	C	N	O	P	0	0
			1167	563	199	349	56		

- Molecule 42 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
42	Ap	60	1217	590	187	381	59	0	0

- Molecule 43 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
43	Aq	48	985	468	183	287	47	0	0

- Molecule 44 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
44	Ar	37	752	361	137	218	36	0	0

- Molecule 45 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
45	As	40	817	396	138	244	39	0	0

- Molecule 46 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
46	At	44	899	432	168	256	43	0	0

- Molecule 47 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
47	Au	40	818	391	158	230	39	0	0

- Molecule 48 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
48	Av	40	814	387	153	235	39	0	0

- Molecule 49 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Aw	56	Total	C	N	O	P	0	0
			1137	545	199	338	55		

- Molecule 50 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Ax	40	Total	C	N	O	P	0	0
			815	393	141	242	39		

- Molecule 51 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Ay	48	Total	C	N	O	P	0	0
			990	471	195	277	47		

- Molecule 52 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Az	45	Total	C	N	O	P	0	0
			900	432	156	268	44		

- Molecule 53 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	A0	32	Total	C	N	O	P	0	0
			641	308	109	193	31		

- Molecule 54 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	A1	48	Total	C	N	O	P	0	0
			992	472	191	282	47		

- Molecule 55 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	A2	48	Total	C	N	O	P	0	0
			966	458	175	286	47		

- Molecule 56 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	A3	56	Total	C	N	O	P	0	0
			1151	546	222	328	55		

- Molecule 57 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	A4	45	Total	C	N	O	P	0	0
			931	445	170	272	44		

- Molecule 58 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	A5	48	Total	C	N	O	P	0	0
			991	471	192	281	47		

- Molecule 59 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	A6	32	Total	C	N	O	P	0	0
			655	313	119	192	31		

- Molecule 60 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	A7	32	Total	C	N	O	P	0	0
			643	307	122	183	31		

- Molecule 61 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	A8	32	Total	C	N	O	P	0	0
			658	312	129	186	31		

- Molecule 62 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	A9	48	Total	C	N	O	P	0	0
			988	468	195	278	47		

- Molecule 63 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
63	BA	45	918	439	176	259	44	0	0

- Molecule 64 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
64	BB	32	659	311	133	184	31	0	0

- Molecule 65 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
65	BC	45	910	438	153	275	44	0	0

- Molecule 66 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
66	BD	57	1156	561	183	356	56	0	0

- Molecule 67 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
67	BE	57	1155	559	191	349	56	0	0

- Molecule 68 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
68	BF	45	911	436	158	273	44	0	0

- Molecule 69 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
69	BG	40	807	387	147	234	39	0	0

- Molecule 70 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	BH	57	Total	C	N	O	P	0	0
			1156	564	177	359	56		

- Molecule 71 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	BI	57	Total	C	N	O	P	0	0
			1156	564	189	347	56		

- Molecule 72 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	BJ	45	Total	C	N	O	P	0	0
			918	443	157	274	44		

- Molecule 73 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	BK	32	Total	C	N	O	P	0	0
			655	313	119	192	31		

- Molecule 74 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	BL	56	Total	C	N	O	P	0	0
			1142	548	199	340	55		

- Molecule 75 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	BM	32	Total	C	N	O	P	0	0
			650	312	126	181	31		

- Molecule 76 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	BN	40	Total	C	N	O	P	0	0
			832	394	173	226	39		

- Molecule 77 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	BO	48	Total	C	N	O	P	0	0
			974	464	181	282	47		

- Molecule 78 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	BP	58	Total	C	N	O	P	0	0
			1175	569	196	353	57		

- Molecule 79 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	BQ	57	Total	C	N	O	P	0	0
			1147	558	183	350	56		

- Molecule 80 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	BR	48	Total	C	N	O	P	0	0
			995	475	191	282	47		

- Molecule 81 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	BS	48	Total	C	N	O	P	0	0
			975	470	169	289	47		

- Molecule 82 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	BT	48	Total	C	N	O	P	0	0
			973	465	174	287	47		

- Molecule 83 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	BU	48	Total	C	N	O	P	0	0
			981	466	182	286	47		

- Molecule 84 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	BV	58	Total	C	N	O	P	0	0
			1186	573	201	355	57		

- Molecule 85 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	BW	60	Total	C	N	O	P	0	0
			1213	586	191	377	59		

- Molecule 86 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	BX	32	Total	C	N	O	P	0	0
			657	311	127	188	31		

- Molecule 87 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	BY	40	Total	C	N	O	P	0	0
			831	392	160	240	39		

- Molecule 88 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
88	BZ	40	Total	C	N	O	P	0	0
			818	388	155	236	39		

- Molecule 89 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
89	Ba	48	Total	C	N	O	P	0	0
			1002	476	205	274	47		

- Molecule 90 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
90	Bb	48	Total	C	N	O	P	0	0
			971	464	175	285	47		

- Molecule 91 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
91	Bc	32	Total	C	N	O	P	0	0
			658	313	131	183	31		

- Molecule 92 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
92	Bd	48	Total	C	N	O	P	0	0
			992	473	202	270	47		

- Molecule 93 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
93	Be	48	Total	C	N	O	P	0	0
			976	469	176	284	47		

- Molecule 94 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
94	Bf	48	Total	C	N	O	P	0	0
			986	470	190	279	47		

- Molecule 95 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
95	Bg	40	Total	C	N	O	P	0	0
			812	389	142	242	39		

- Molecule 96 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
96	Bh	56	Total	C	N	O	P	0	0
			1157	552	222	328	55		

- Molecule 97 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
97	Bi	40	Total	C	N	O	P	0	0
			805	390	132	244	39		

- Molecule 98 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
98	Bj	32	Total	C	N	O	P	0	0
			653	313	125	184	31		

- Molecule 99 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
99	Bk	32	Total	C	N	O	P	0	0
			660	316	125	188	31		

- Molecule 100 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
100	Bl	48	Total	C	N	O	P	0	0
			974	463	176	288	47		

- Molecule 101 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
101	Bm	56	Total	C	N	O	P	0	0
			1148	548	205	340	55		

- Molecule 102 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
102	Bn	48	Total	C	N	O	P	0	0
			971	466	173	285	47		

- Molecule 103 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
103	Bo	48	Total	C	N	O	P	0	0
			994	471	201	275	47		

- Molecule 104 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
104	Bp	40	Total	C	N	O	P	0	0
			822	393	153	237	39		

- Molecule 105 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
105	Bq	48	Total	C	N	O	P	0	0
			986	470	169	300	47		

- Molecule 106 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
106	Br	48	Total	C	N	O	P	0	0
			992	471	189	285	47		

- Molecule 107 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
107	Bs	32	Total	C	N	O	P	0	0
			653	312	129	181	31		

- Molecule 108 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
108	Bt	40	Total	C	N	O	P	0	0
			823	391	158	235	39		

- Molecule 109 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
109	Bu	40	Total	C	N	O	P	0	0
			819	391	158	231	39		

- Molecule 110 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
110	Bv	40	Total	C	N	O	P	0	0
			812	388	149	236	39		

- Molecule 111 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
111	Bw	60	Total	C	N	O	P	0	0
			1216	592	194	371	59		

- Molecule 112 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
112	Bx	45	Total	C	N	O	P	0	0
			919	439	167	269	44		

- Molecule 113 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
113	By	40	Total	C	N	O	P	0	0
			823	389	169	226	39		

- Molecule 114 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
114	Bz	32	Total	C	N	O	P	0	0
			654	316	116	191	31		

- Molecule 115 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
115	B0	60	Total	C	N	O	P	0	0
			1210	590	187	374	59		

- Molecule 116 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
116	B1	60	Total	C	N	O	P	0	0
			1213	589	188	377	59		

- Molecule 117 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
117	B2	40	Total	C	N	O	P	0	0
			823	393	162	229	39		

- Molecule 118 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
118	B3	32	Total	C	N	O	P	0	0
			664	314	136	183	31		

- Molecule 119 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
119	B4	32	Total	C	N	O	P	0	0
			663	314	130	188	31		

- Molecule 120 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
120	B5	60	Total	C	N	O	P	0	0
			1223	590	214	360	59		

- Molecule 121 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
121	B6	53	Total	C	N	O	P	0	0
			1077	516	195	314	52		

- Molecule 122 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
122	B7	48	Total	C	N	O	P	0	0
			982	468	192	275	47		

- Molecule 123 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
123	B8	32	Total	C	N	O	P	0	0
			658	313	131	183	31		

- Molecule 124 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
124	B9	48	Total	C	N	O	P	0	0
			975	464	181	283	47		

- Molecule 125 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
125	CA	48	Total	C	N	O	P	0	0
			977	465	177	288	47		

- Molecule 126 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
126	CB	60	1223	592	212	360	59	0	0

- Molecule 127 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
127	CC	37	754	361	134	223	36	0	0

- Molecule 128 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
128	CD	57	1160	566	178	360	56	0	0

- Molecule 129 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
129	CE	32	667	313	134	189	31	0	0

- Molecule 130 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
130	CF	40	822	393	159	231	39	0	0

- Molecule 131 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
131	CG	32	658	315	123	189	31	0	0

- Molecule 132 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
132	CH	53	1087	521	205	309	52	0	0

- Molecule 133 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
133	CI	32	Total	C	N	O	P	0	0
			646	314	109	192	31		

- Molecule 134 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
134	CJ	57	Total	C	N	O	P	0	0
			1159	564	186	353	56		

- Molecule 135 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
135	CK	32	Total	C	N	O	P	0	0
			650	313	119	187	31		

- Molecule 136 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
136	CL	40	Total	C	N	O	P	0	0
			819	390	162	228	39		

- Molecule 137 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
137	CM	32	Total	C	N	O	P	0	0
			664	316	134	183	31		

- Molecule 138 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
138	CN	56	Total	C	N	O	P	0	0
			1153	553	218	327	55		

- Molecule 139 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
139	CO	48	Total	C	N	O	P	0	0
			979	467	190	275	47		

- Molecule 140 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
140	CP	48	Total	C	N	O	P	0	0
			992	473	181	291	47		

- Molecule 141 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
141	CQ	57	Total	C	N	O	P	0	0
			1162	564	189	353	56		

- Molecule 142 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
142	CR	60	Total	C	N	O	P	0	0
			1225	594	204	368	59		

- Molecule 143 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
143	CS	48	Total	C	N	O	P	0	0
			968	468	159	294	47		

- Molecule 144 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
144	CT	56	Total	C	N	O	P	0	0
			1158	554	220	329	55		

- Molecule 145 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
145	CU	37	Total	C	N	O	P	0	0
			759	364	146	213	36		

- Molecule 146 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
146	CV	32	Total	C	N	O	P	0	0
			656	314	124	187	31		

- Molecule 147 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
147	CW	32	Total	C	N	O	P	0	0
			652	314	121	186	31		

- Molecule 148 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
148	CX	57	Total	C	N	O	P	0	0
			1159	564	180	359	56		

- Molecule 149 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
149	CY	60	Total	C	N	O	P	0	0
			1211	593	187	372	59		

- Molecule 150 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
150	CZ	48	Total	C	N	O	P	0	0
			981	472	173	289	47		

- Molecule 151 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
151	Ca	48	Total	C	N	O	P	0	0
			984	473	193	271	47		

- Molecule 152 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
152	Cb	40	Total	C	N	O	P	0	0
			821	392	160	230	39		

- Molecule 153 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
153	Cc	32	Total	C	N	O	P	0	0
			655	314	121	189	31		

- Molecule 154 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
154	Cd	40	831	393	174	225	39	0	0

- Molecule 155 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
155	Ce	40	829	397	155	238	39	0	0

- Molecule 156 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
156	Cf	32	657	316	116	194	31	0	0

- Molecule 157 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
157	Cg	40	817	393	153	232	39	0	0

- Molecule 158 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
158	Ch	40	817	394	149	235	39	0	0

- Molecule 159 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
159	Ci	48	971	466	176	282	47	0	0

- Molecule 160 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
160	Cj	40	817	391	152	235	39	0	0

- Molecule 161 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
161	Ck	48	Total	C	N	O	P	0	0
			985	474	171	293	47		

- Molecule 162 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
162	Cl	40	Total	C	N	O	P	0	0
			821	393	159	230	39		

- Molecule 163 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
163	Cm	48	Total	C	N	O	P	0	0
			980	471	174	288	47		

- Molecule 164 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
164	Cn	40	Total	C	N	O	P	0	0
			819	393	150	237	39		

- Molecule 165 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
165	Co	40	Total	C	N	O	P	0	0
			811	388	152	232	39		

- Molecule 166 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
166	Cp	37	Total	C	N	O	P	0	0
			752	361	137	218	36		

- Molecule 167 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
167	Cq	37	Total	C	N	O	P	0	0
			754	360	144	214	36		

- Molecule 168 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
168	Cr	40	832	396	159	238	39	0	0

- Molecule 169 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
169	Cs	40	822	393	159	231	39	0	0

- Molecule 170 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
170	Ct	45	920	443	163	270	44	0	0

- Molecule 171 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
171	Cu	37	757	366	138	217	36	0	0

- Molecule 172 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
172	Cv	40	810	390	138	243	39	0	0

- Molecule 173 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
173	Cw	40	825	391	161	234	39	0	0

- Molecule 174 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
174	Cx	32	652	310	128	183	31	0	0

- Molecule 175 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
175	Cy	32	652	309	129	183	31	0	0

- Molecule 176 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
176	Cz	32	667	316	131	189	31	0	0

- Molecule 177 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
177	C0	57	1148	554	190	348	56	0	0

- Molecule 178 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
178	C1	57	1166	566	187	357	56	0	0

- Molecule 179 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
179	C2	32	657	315	123	188	31	0	0

- Molecule 180 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
180	C3	48	979	466	188	278	47	0	0

- Molecule 181 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
181	C4	48	977	470	178	282	47	0	0

- Molecule 182 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
182	C5	48	976	470	169	290	47	0	0

- Molecule 183 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
183	C6	48	997	473	196	281	47	0	0

- Molecule 184 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
184	C7	40	803	388	134	242	39	0	0

- Molecule 185 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
185	C8	48	991	472	194	278	47	0	0

- Molecule 186 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
186	C9	57	1158	563	187	352	56	0	0

- Molecule 187 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
187	DA	45	917	440	163	270	44	0	0

- Molecule 188 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
188	DB	32	646	310	119	186	31	0	0

- Molecule 189 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
189	DC	40	Total	C	N	O	P	0	0
			832	395	178	220	39		

- Molecule 190 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
190	DD	45	Total	C	N	O	P	0	0
			910	435	159	272	44		

- Molecule 191 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
191	DE	48	Total	C	N	O	P	0	0
			982	471	180	284	47		

- Molecule 192 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
192	DF	40	Total	C	N	O	P	0	0
			817	389	154	235	39		

- Molecule 193 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
193	DG	48	Total	C	N	O	P	0	0
			990	471	186	286	47		

- Molecule 194 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
194	DH	32	Total	C	N	O	P	0	0
			654	312	132	179	31		

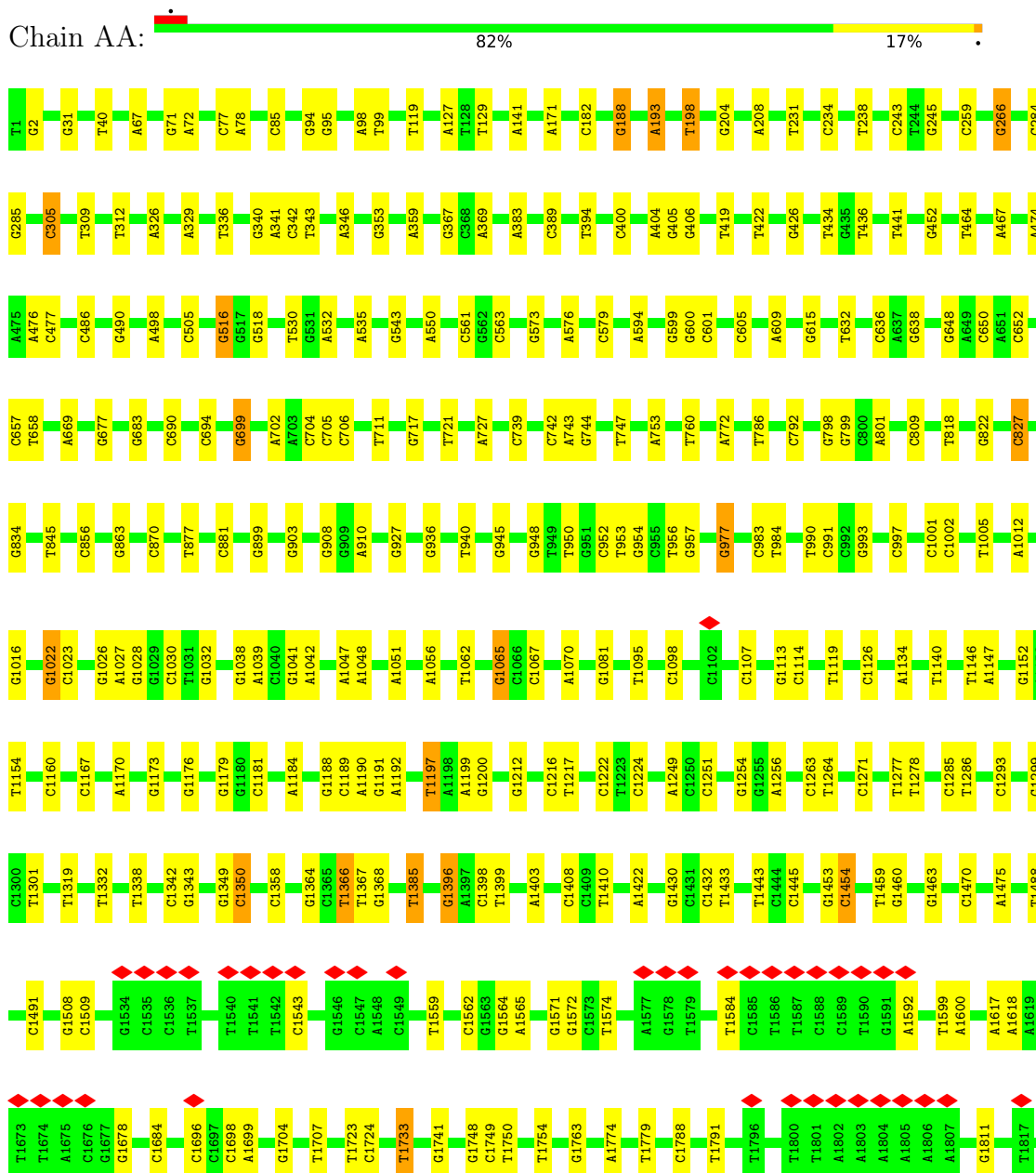
- Molecule 195 is a DNA chain called STAPLE STRAND.

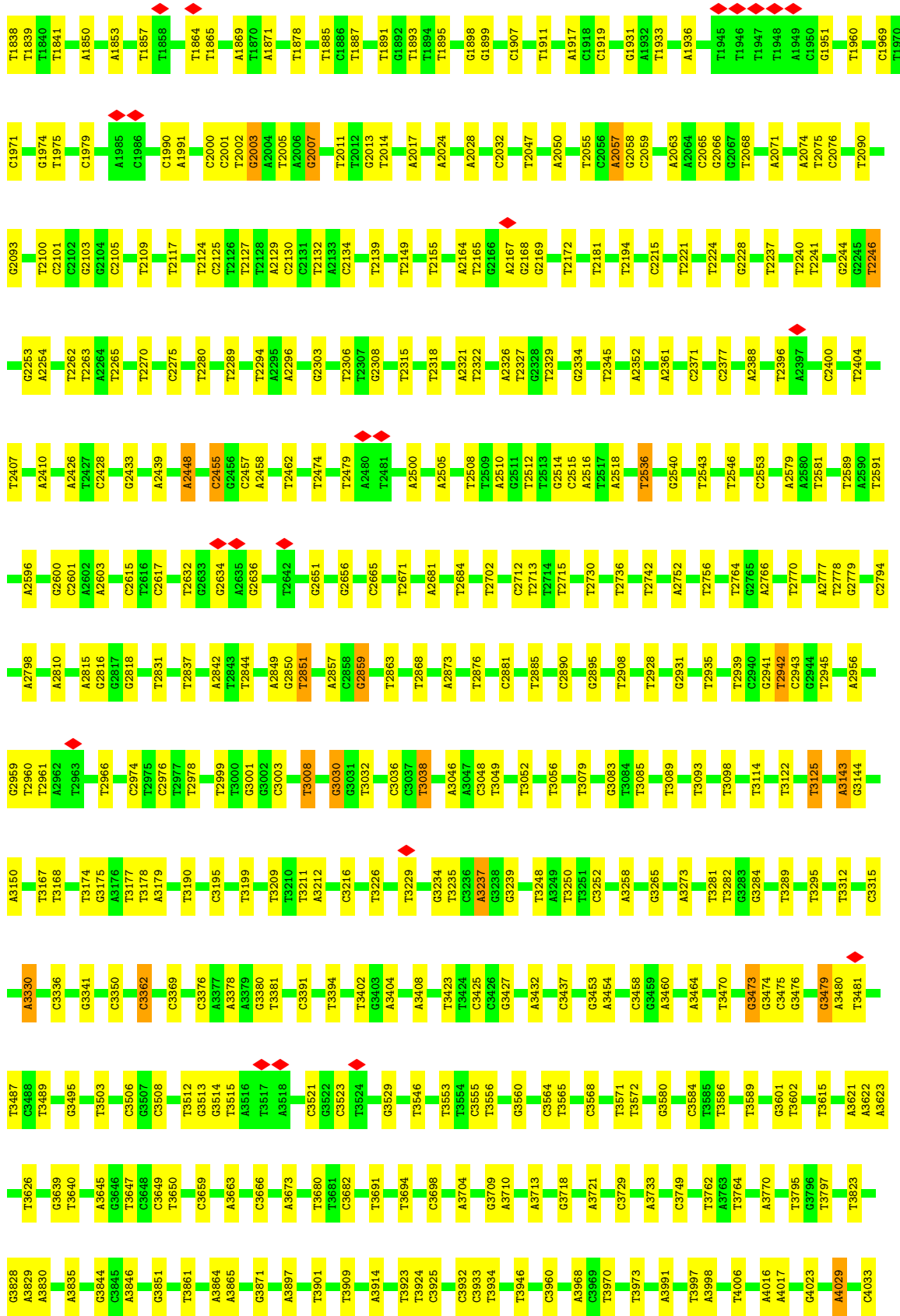
Mol	Chain	Residues	Atoms					AltConf	Trace
195	DI	32	Total	C	N	O	P	0	0
			653	314	118	190	31		

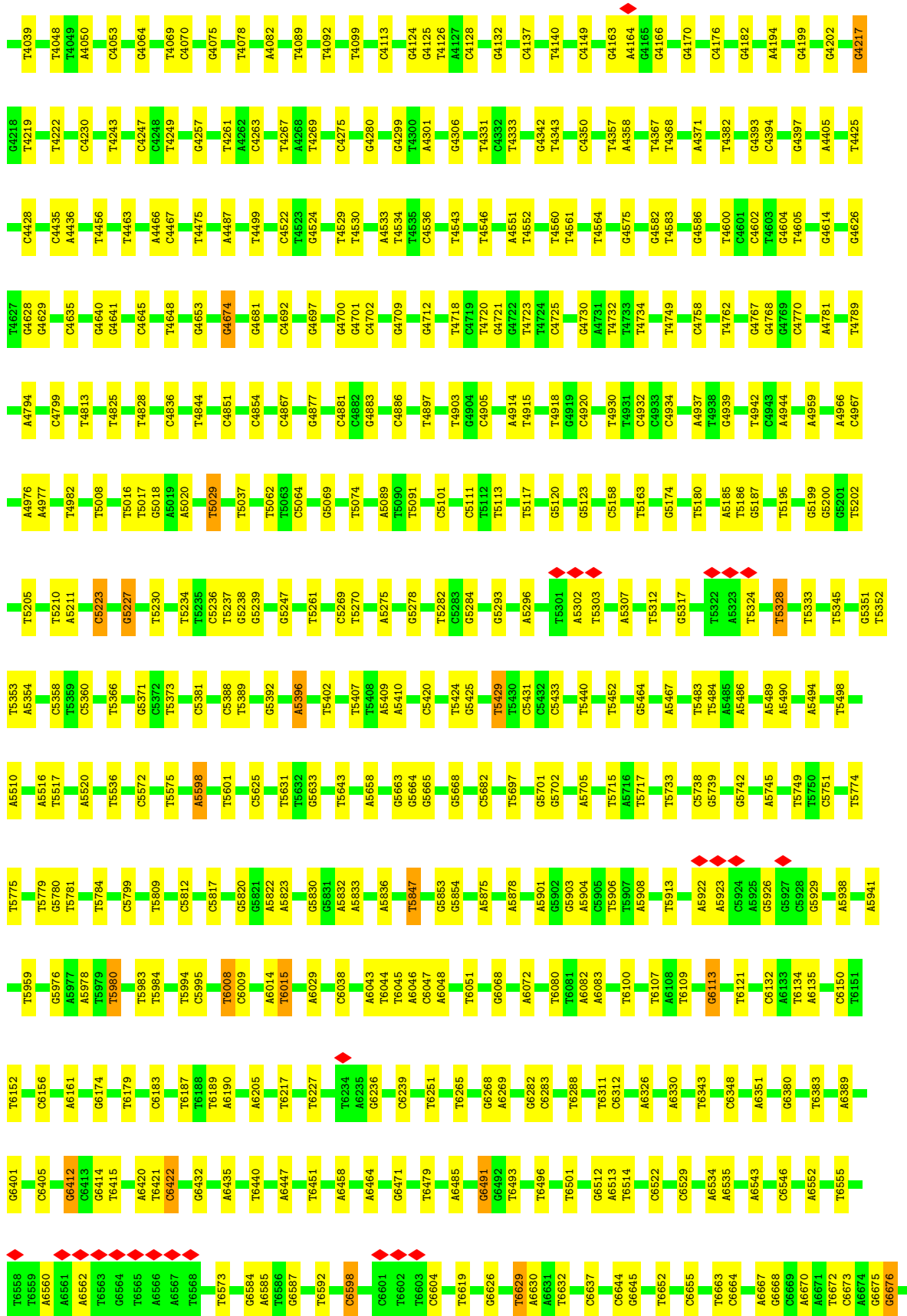
### 3 Residue-property plots

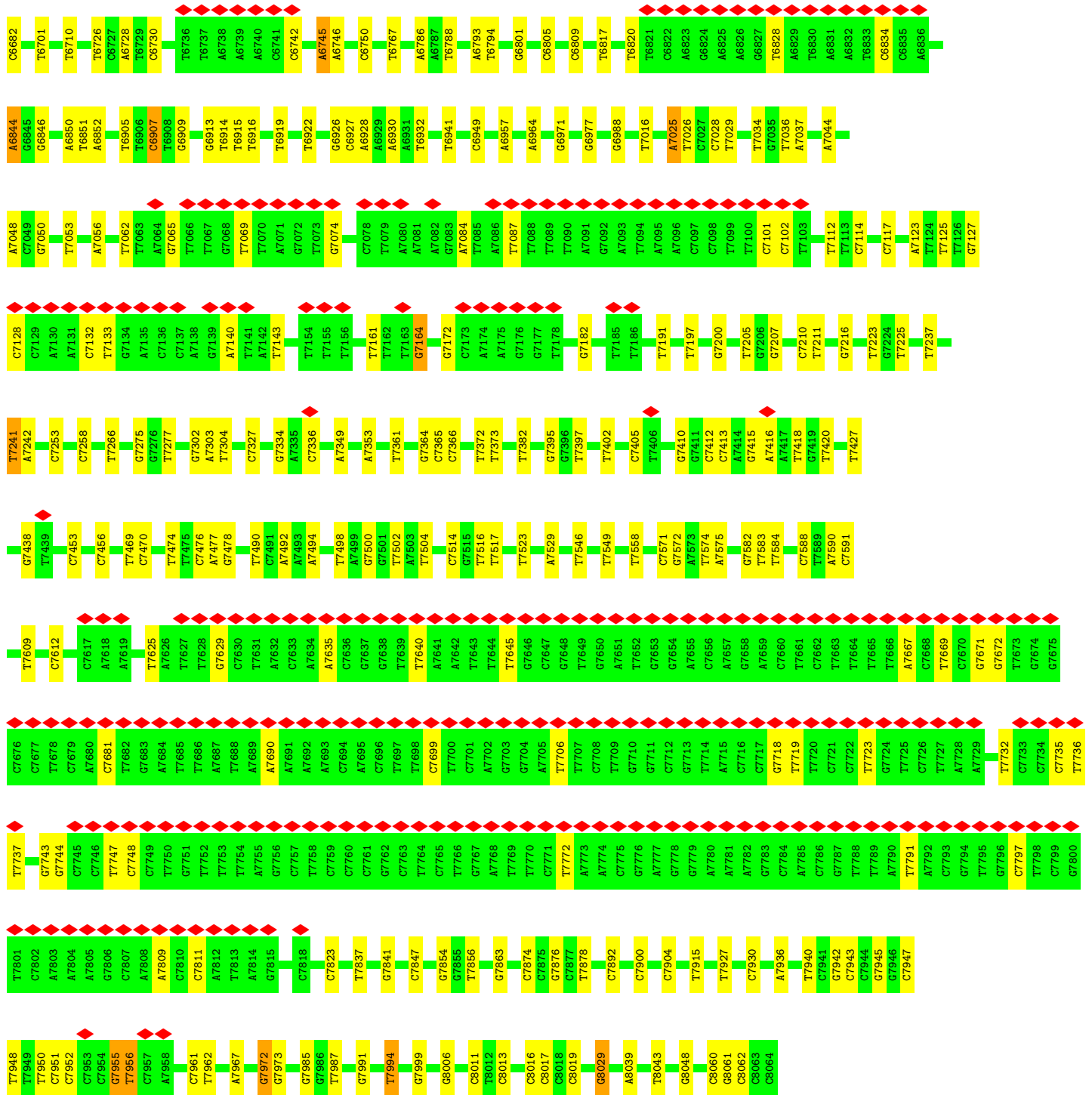
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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

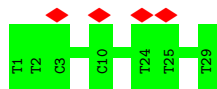




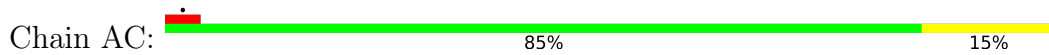




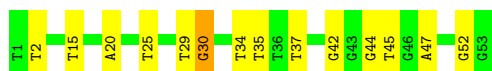
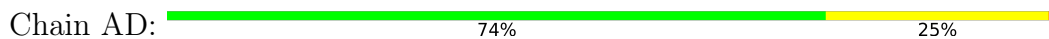
- Molecule 2: STAPLE STRAND



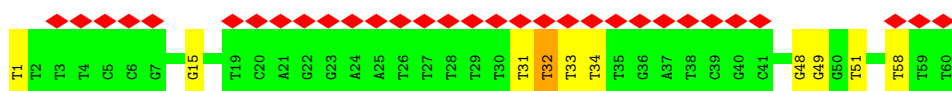
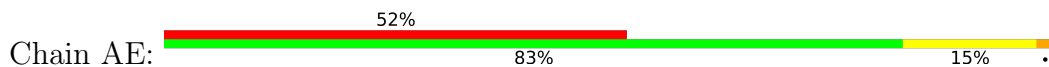
- Molecule 3: STAPLE STRAND



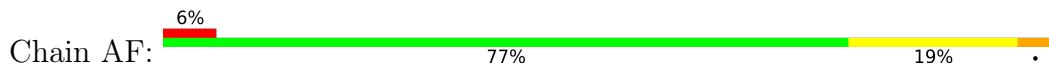
• Molecule 4: STAPLE STRAND



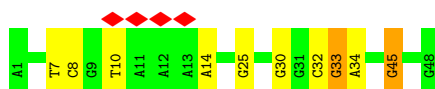
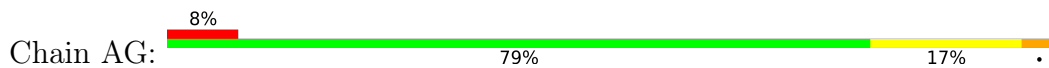
• Molecule 5: STAPLE STRAND



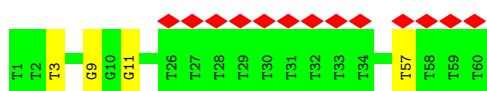
• Molecule 6: STAPLE STRAND



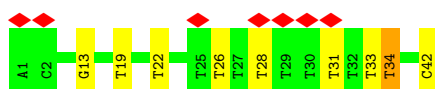
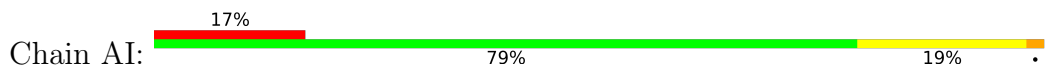
• Molecule 7: STAPLE STRAND



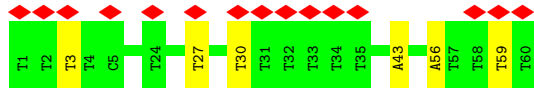
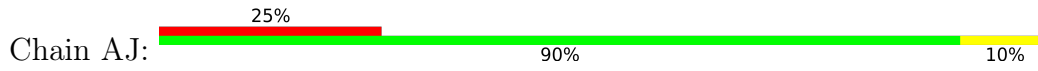
• Molecule 8: STAPLE STRAND



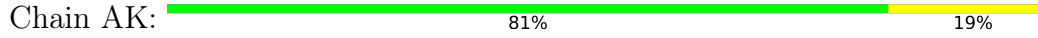
• Molecule 9: STAPLE STRAND



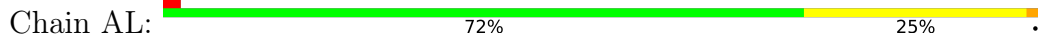
• Molecule 10: STAPLE STRAND



• Molecule 11: STAPLE STRAND



• Molecule 12: STAPLE STRAND



• Molecule 13: STAPLE STRAND



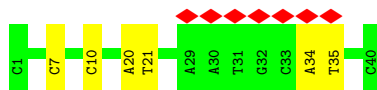
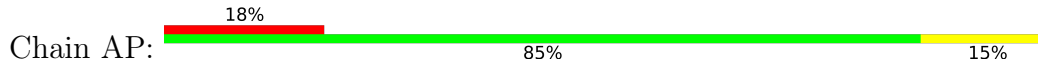
• Molecule 14: STAPLE STRAND



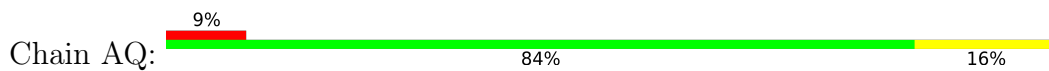
• Molecule 15: STAPLE STRAND



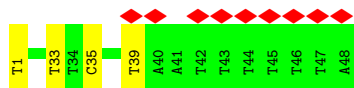
• Molecule 16: STAPLE STRAND



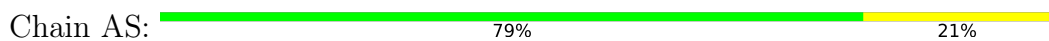
• Molecule 17: STAPLE STRAND



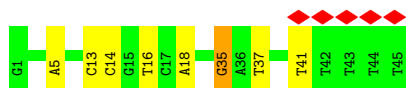
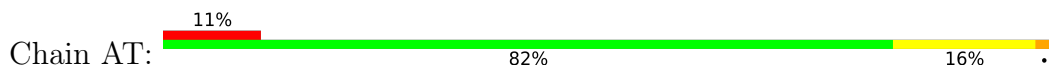
• Molecule 18: STAPLE STRAND



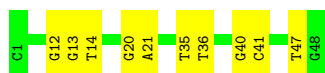
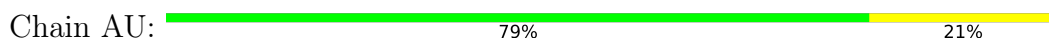
• Molecule 19: STAPLE STRAND



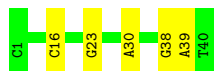
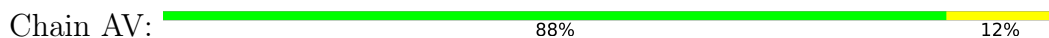
• Molecule 20: STAPLE STRAND



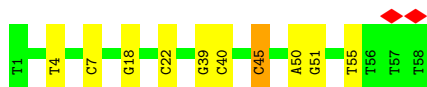
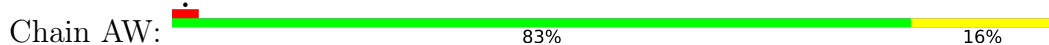
• Molecule 21: STAPLE STRAND



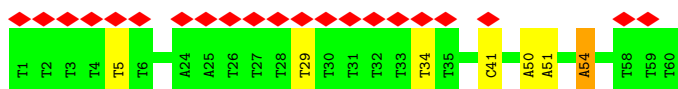
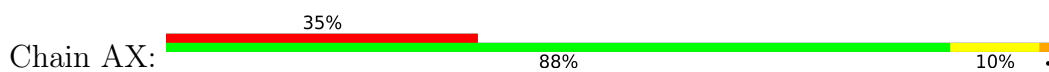
• Molecule 22: STAPLE STRAND



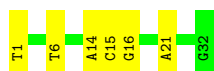
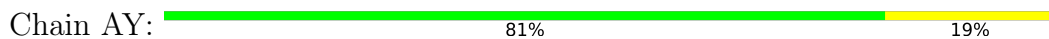
• Molecule 23: STAPLE STRAND



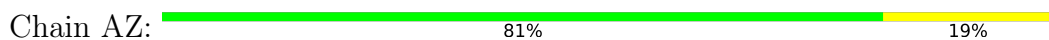
• Molecule 24: STAPLE STRAND



- Molecule 25: STAPLE STRAND



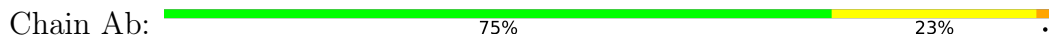
- Molecule 26: STAPLE STRAND



- Molecule 27: STAPLE STRAND



- Molecule 28: STAPLE STRAND



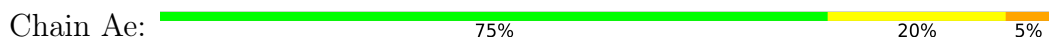
- Molecule 29: STAPLE STRAND



- Molecule 30: STAPLE STRAND

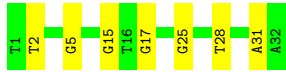
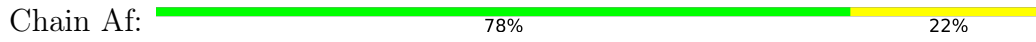


- Molecule 31: STAPLE STRAND

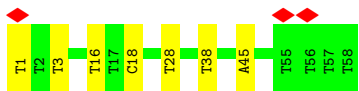
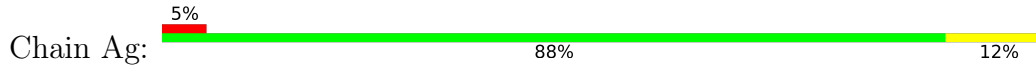




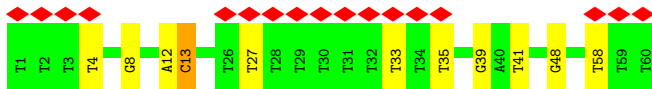
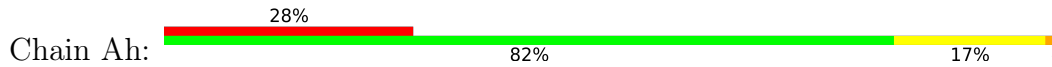
- Molecule 32: STAPLE STRAND



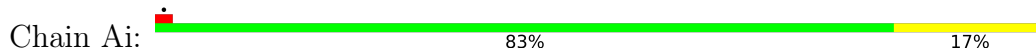
- Molecule 33: STAPLE STRAND



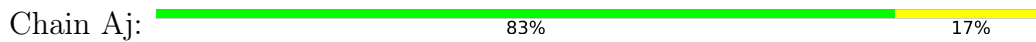
- Molecule 34: STAPLE STRAND



- Molecule 35: STAPLE STRAND



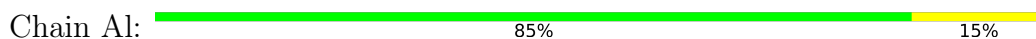
- Molecule 36: STAPLE STRAND



- Molecule 37: STAPLE STRAND

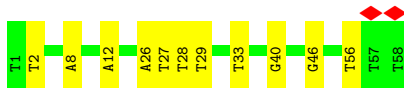
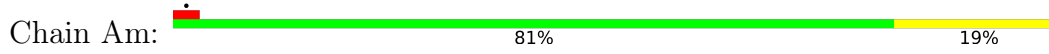


- Molecule 38: STAPLE STRAND

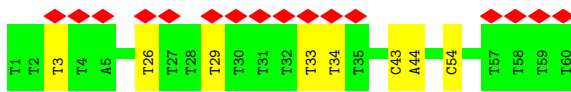
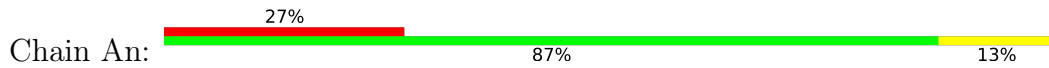




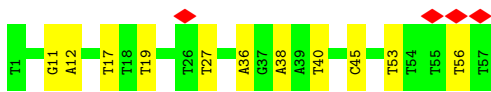
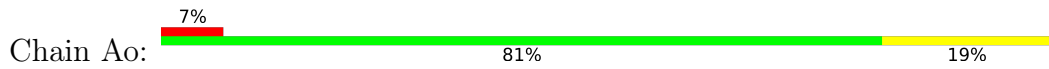
• Molecule 39: STAPLE STRAND



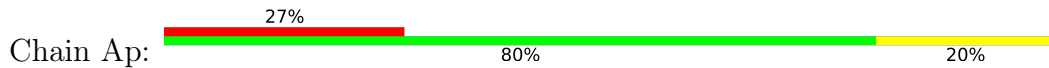
• Molecule 40: STAPLE STRAND



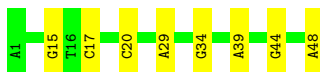
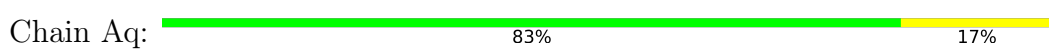
• Molecule 41: STAPLE STRAND



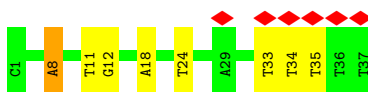
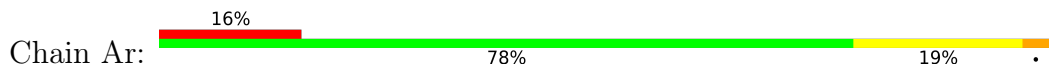
• Molecule 42: STAPLE STRAND



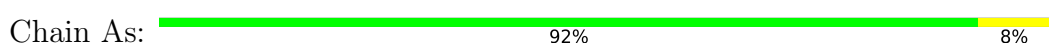
• Molecule 43: STAPLE STRAND



• Molecule 44: STAPLE STRAND

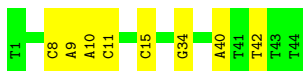
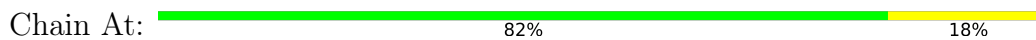


• Molecule 45: STAPLE STRAND

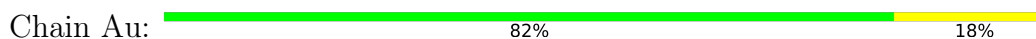




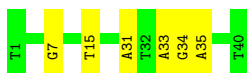
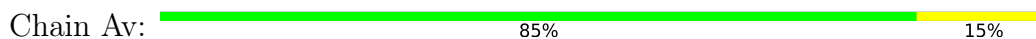
- Molecule 46: STAPLE STRAND



- Molecule 47: STAPLE STRAND



- Molecule 48: STAPLE STRAND



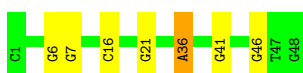
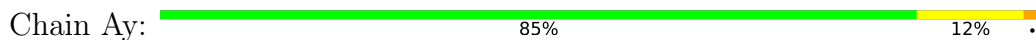
- Molecule 49: STAPLE STRAND



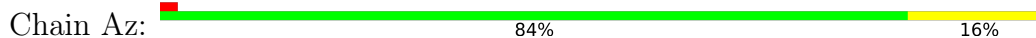
- Molecule 50: STAPLE STRAND

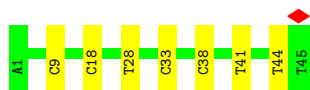


- Molecule 51: STAPLE STRAND



- Molecule 52: STAPLE STRAND

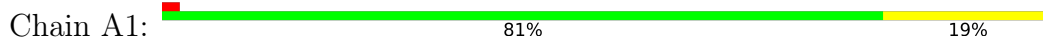




• Molecule 53: STAPLE STRAND



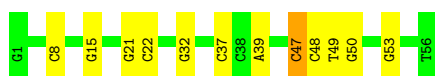
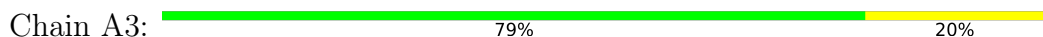
• Molecule 54: STAPLE STRAND



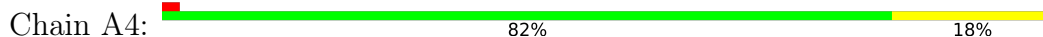
• Molecule 55: STAPLE STRAND



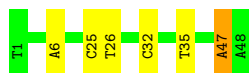
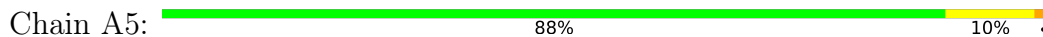
• Molecule 56: STAPLE STRAND



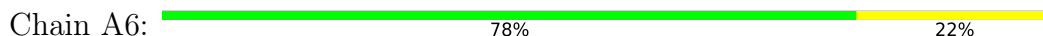
• Molecule 57: STAPLE STRAND



• Molecule 58: STAPLE STRAND

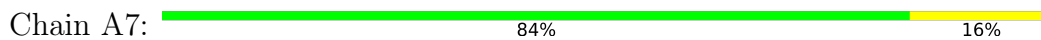


• Molecule 59: STAPLE STRAND





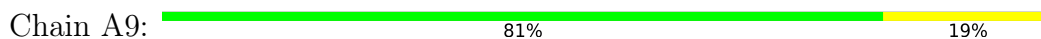
- Molecule 60: STAPLE STRAND



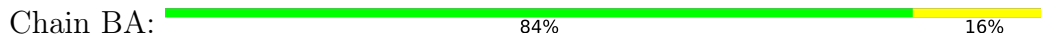
- Molecule 61: STAPLE STRAND



- Molecule 62: STAPLE STRAND



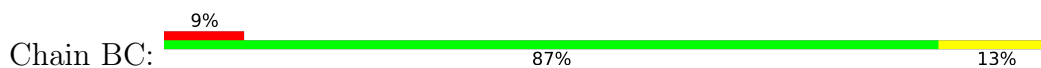
- Molecule 63: STAPLE STRAND



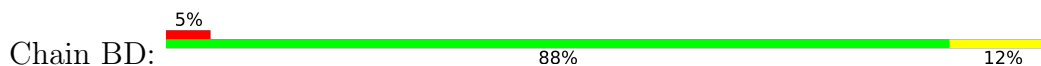
- Molecule 64: STAPLE STRAND

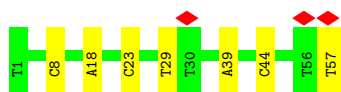


- Molecule 65: STAPLE STRAND

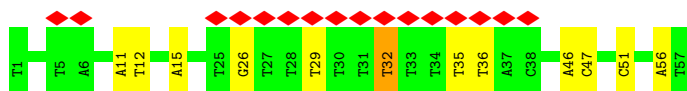
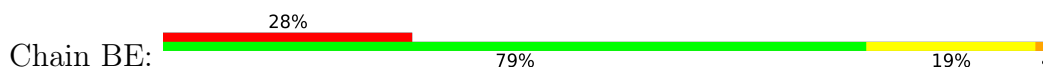


- Molecule 66: STAPLE STRAND

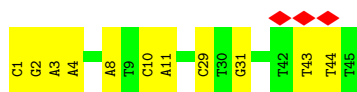
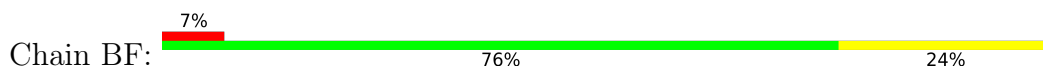




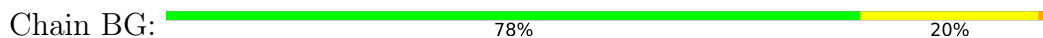
• Molecule 67: STAPLE STRAND



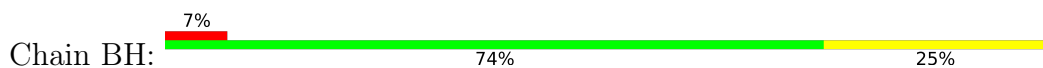
• Molecule 68: STAPLE STRAND



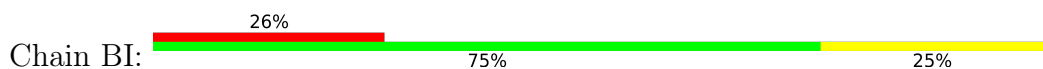
• Molecule 69: STAPLE STRAND



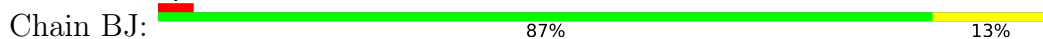
• Molecule 70: STAPLE STRAND



• Molecule 71: STAPLE STRAND

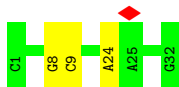


• Molecule 72: STAPLE STRAND

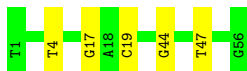


• Molecule 73: STAPLE STRAND





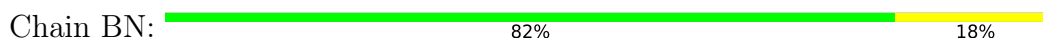
- Molecule 74: STAPLE STRAND



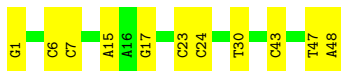
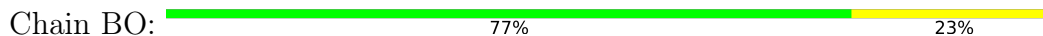
- Molecule 75: STAPLE STRAND



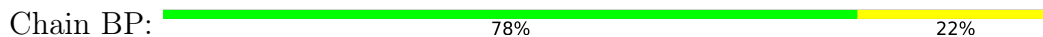
- Molecule 76: STAPLE STRAND



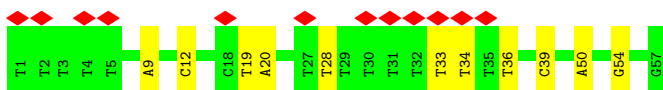
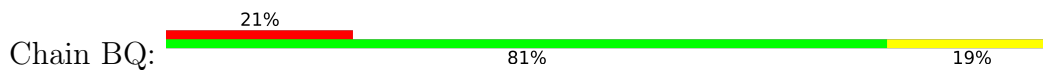
- Molecule 77: STAPLE STRAND



- Molecule 78: STAPLE STRAND



- Molecule 79: STAPLE STRAND

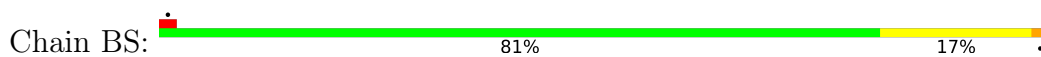


- Molecule 80: STAPLE STRAND

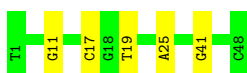




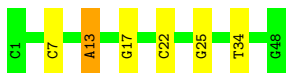
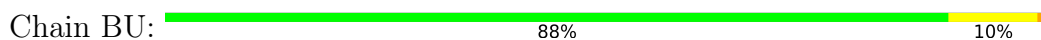
- Molecule 81: STAPLE STRAND



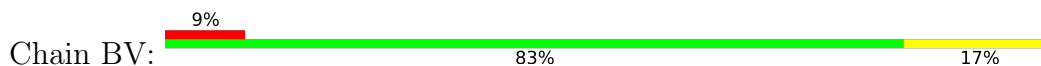
- Molecule 82: STAPLE STRAND



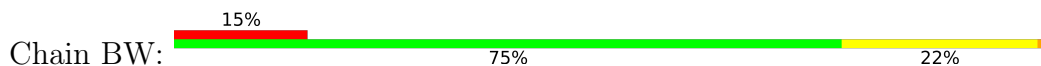
- Molecule 83: STAPLE STRAND



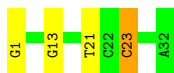
- Molecule 84: STAPLE STRAND



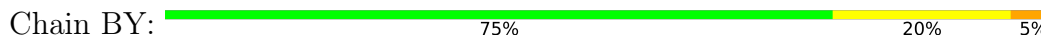
- Molecule 85: STAPLE STRAND



- Molecule 86: STAPLE STRAND

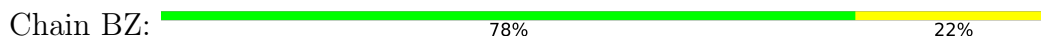


- Molecule 87: STAPLE STRAND

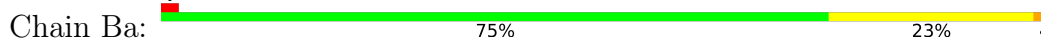




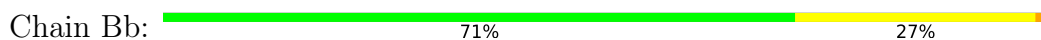
- Molecule 88: STAPLE STRAND



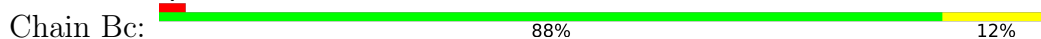
- Molecule 89: STAPLE STRAND



- Molecule 90: STAPLE STRAND



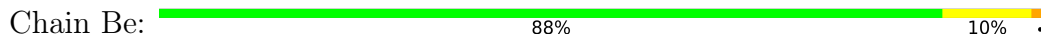
- Molecule 91: STAPLE STRAND



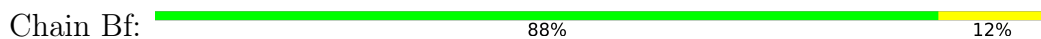
- Molecule 92: STAPLE STRAND



- Molecule 93: STAPLE STRAND



- Molecule 94: STAPLE STRAND

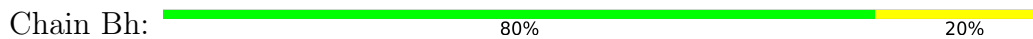




- Molecule 95: STAPLE STRAND



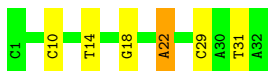
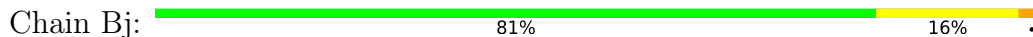
- Molecule 96: STAPLE STRAND



- Molecule 97: STAPLE STRAND



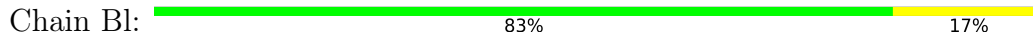
- Molecule 98: STAPLE STRAND



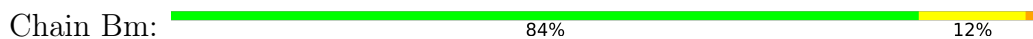
- Molecule 99: STAPLE STRAND



- Molecule 100: STAPLE STRAND

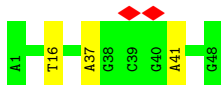


- Molecule 101: STAPLE STRAND





- Molecule 102: STAPLE STRAND



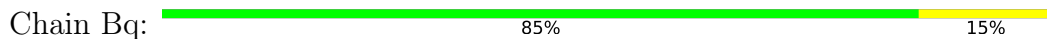
- Molecule 103: STAPLE STRAND



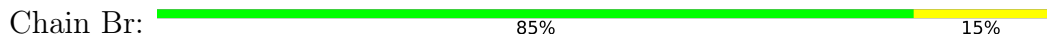
- Molecule 104: STAPLE STRAND



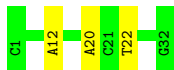
- Molecule 105: STAPLE STRAND



- Molecule 106: STAPLE STRAND



- Molecule 107: STAPLE STRAND



- Molecule 108: STAPLE STRAND

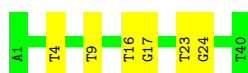
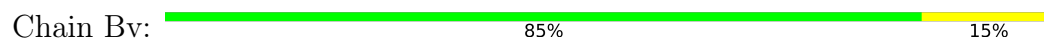




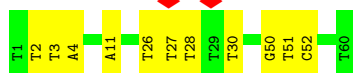
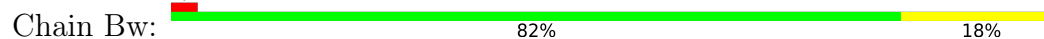
- Molecule 109: STAPLE STRAND



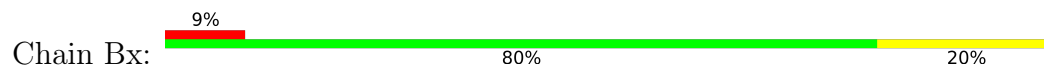
- Molecule 110: STAPLE STRAND



- Molecule 111: STAPLE STRAND



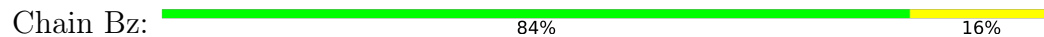
- Molecule 112: STAPLE STRAND



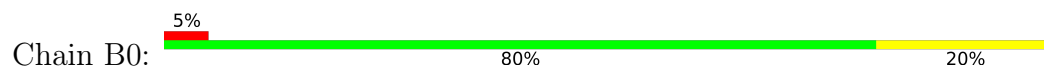
- Molecule 113: STAPLE STRAND

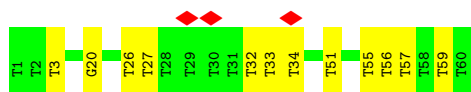


- Molecule 114: STAPLE STRAND

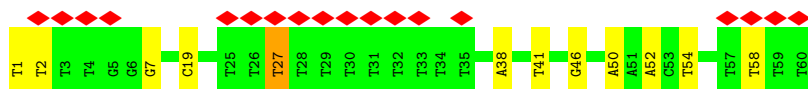
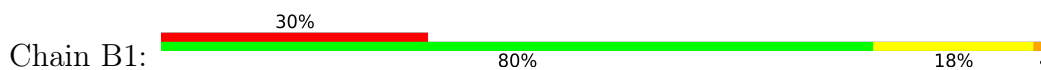


- Molecule 115: STAPLE STRAND





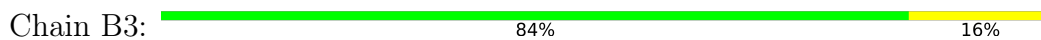
- Molecule 116: STAPLE STRAND



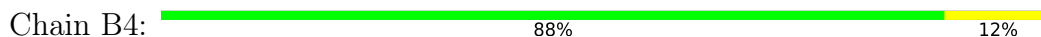
- Molecule 117: STAPLE STRAND



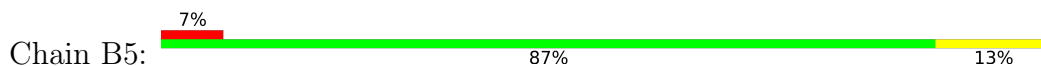
- Molecule 118: STAPLE STRAND



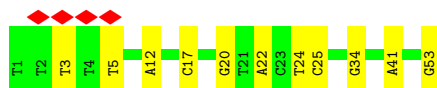
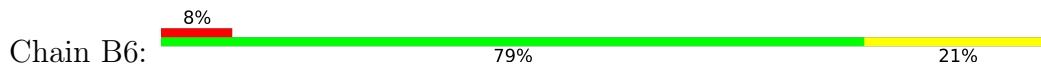
- Molecule 119: STAPLE STRAND



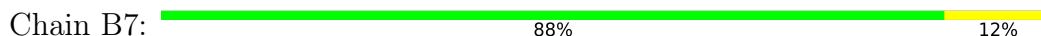
- Molecule 120: STAPLE STRAND



- Molecule 121: STAPLE STRAND



- Molecule 122: STAPLE STRAND

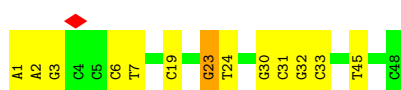
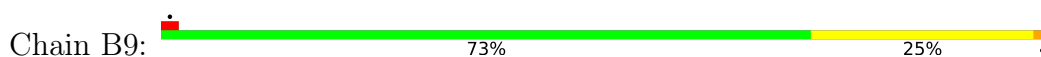




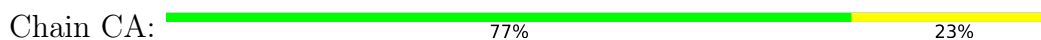
- Molecule 123: STAPLE STRAND



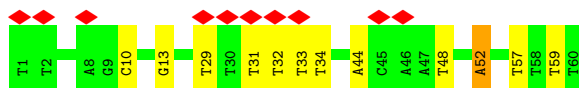
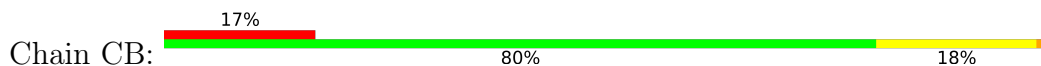
- Molecule 124: STAPLE STRAND



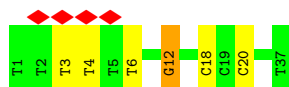
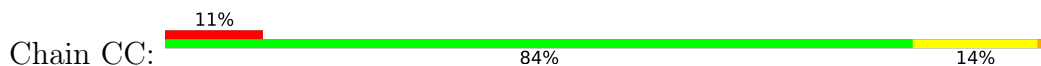
- Molecule 125: STAPLE STRAND



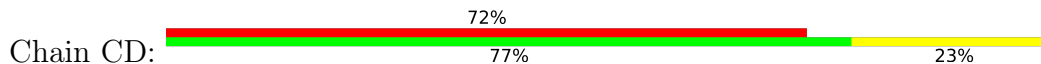
- Molecule 126: STAPLE STRAND



- Molecule 127: STAPLE STRAND



- Molecule 128: STAPLE STRAND

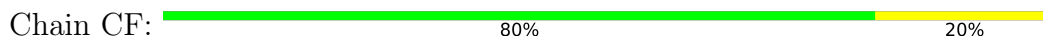


- Molecule 129: STAPLE STRAND

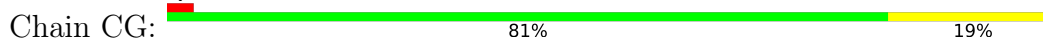




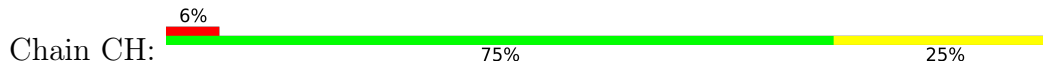
• Molecule 130: STAPLE STRAND



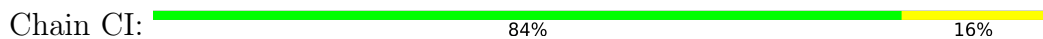
• Molecule 131: STAPLE STRAND



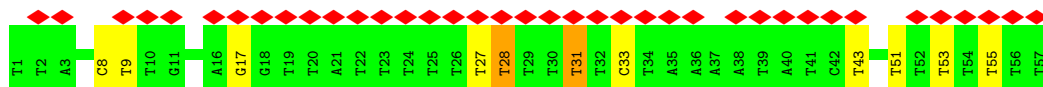
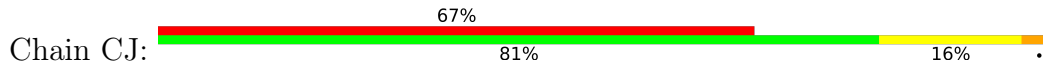
• Molecule 132: STAPLE STRAND



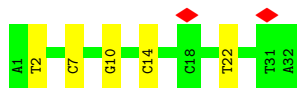
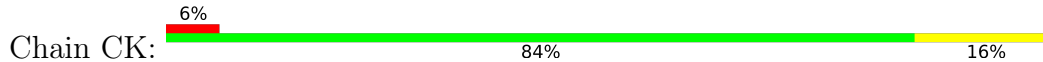
• Molecule 133: STAPLE STRAND



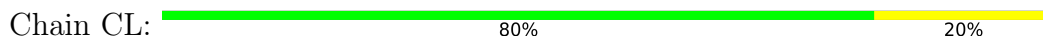
• Molecule 134: STAPLE STRAND



• Molecule 135: STAPLE STRAND

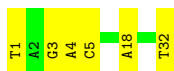
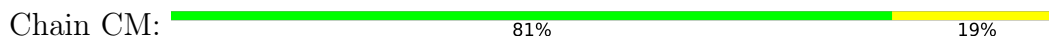


• Molecule 136: STAPLE STRAND

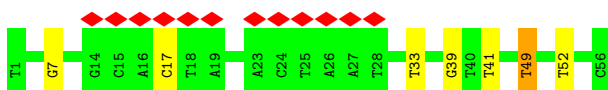
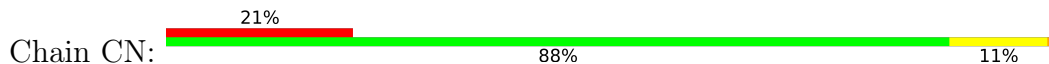




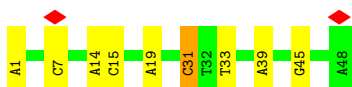
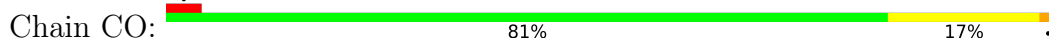
- Molecule 137: STAPLE STRAND



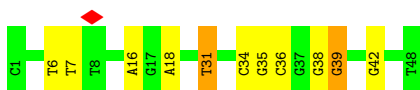
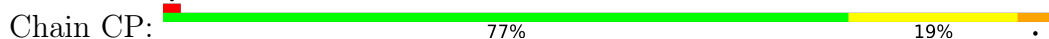
- Molecule 138: STAPLE STRAND



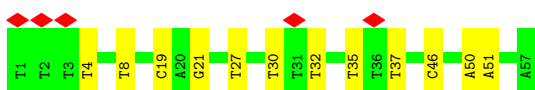
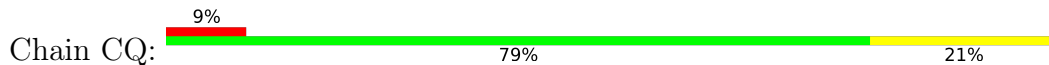
- Molecule 139: STAPLE STRAND



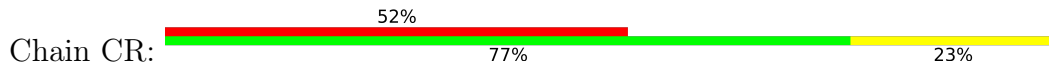
- Molecule 140: STAPLE STRAND



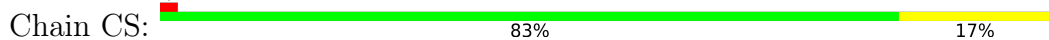
- Molecule 141: STAPLE STRAND



- Molecule 142: STAPLE STRAND

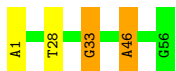


- Molecule 143: STAPLE STRAND

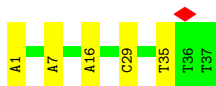




- Molecule 144: STAPLE STRAND



- Molecule 145: STAPLE STRAND



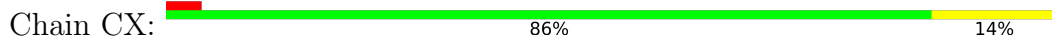
- Molecule 146: STAPLE STRAND



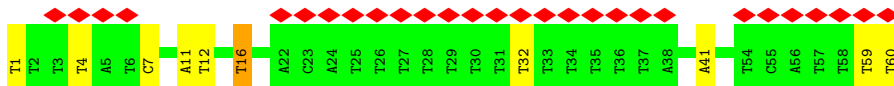
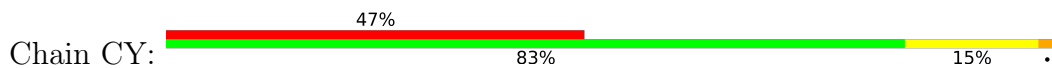
- Molecule 147: STAPLE STRAND



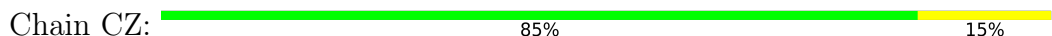
- Molecule 148: STAPLE STRAND



- Molecule 149: STAPLE STRAND



- Molecule 150: STAPLE STRAND





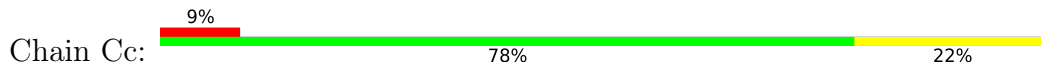
- Molecule 151: STAPLE STRAND



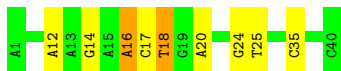
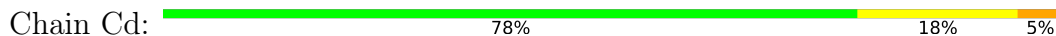
- Molecule 152: STAPLE STRAND



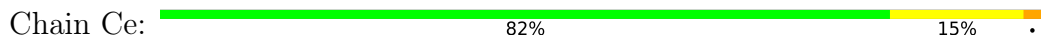
- Molecule 153: STAPLE STRAND



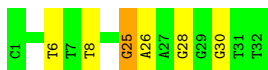
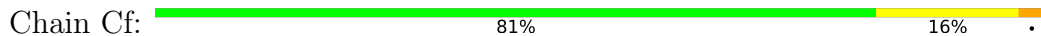
- Molecule 154: STAPLE STRAND



- Molecule 155: STAPLE STRAND



- Molecule 156: STAPLE STRAND

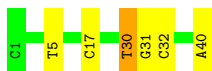
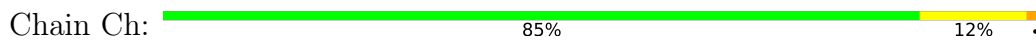


- Molecule 157: STAPLE STRAND

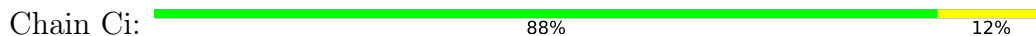




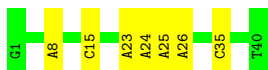
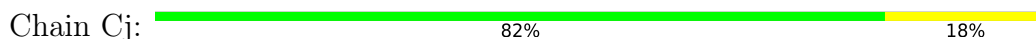
- Molecule 158: STAPLE STRAND



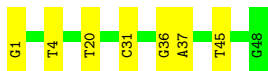
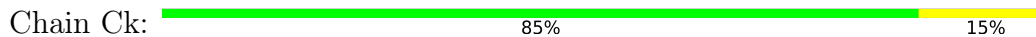
- Molecule 159: STAPLE STRAND



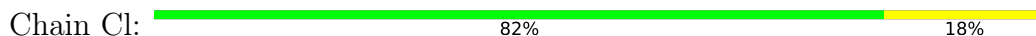
- Molecule 160: STAPLE STRAND



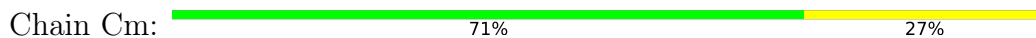
- Molecule 161: STAPLE STRAND



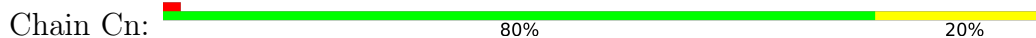
- Molecule 162: STAPLE STRAND



- Molecule 163: STAPLE STRAND

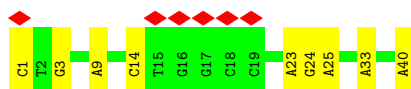
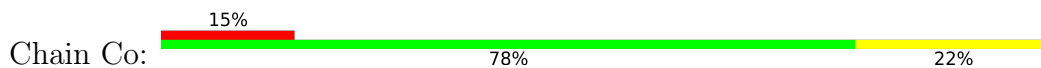


- Molecule 164: STAPLE STRAND

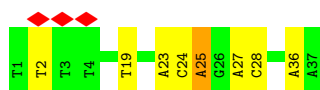
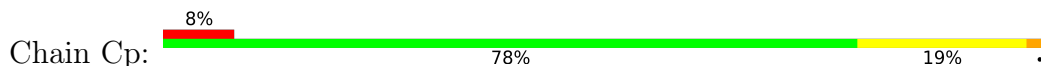




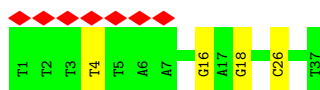
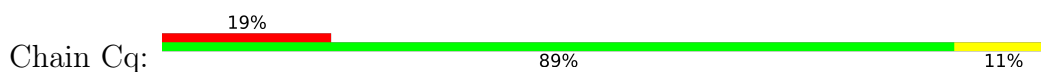
- Molecule 165: STAPLE STRAND



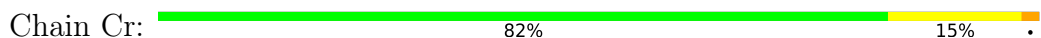
- Molecule 166: STAPLE STRAND



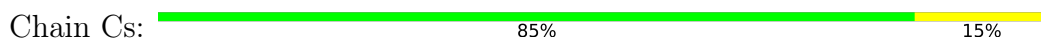
- Molecule 167: STAPLE STRAND



- Molecule 168: STAPLE STRAND



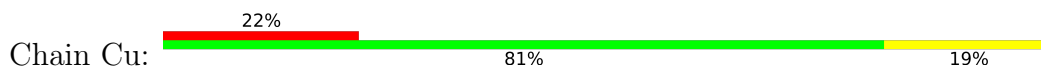
- Molecule 169: STAPLE STRAND

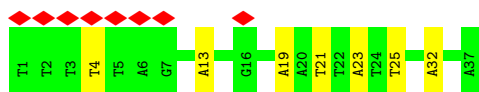


- Molecule 170: STAPLE STRAND



- Molecule 171: STAPLE STRAND





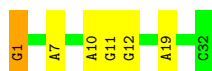
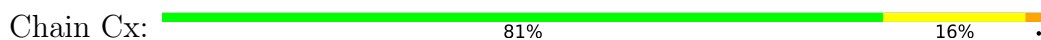
- Molecule 172: STAPLE STRAND



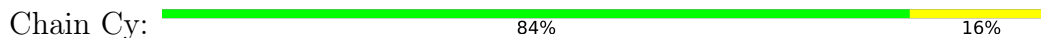
- Molecule 173: STAPLE STRAND



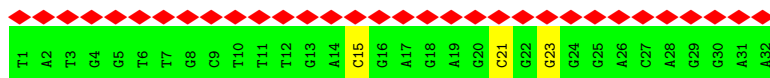
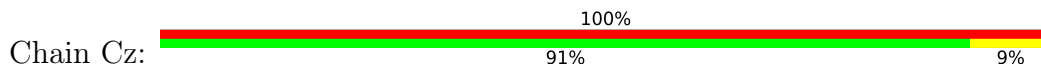
- Molecule 174: STAPLE STRAND



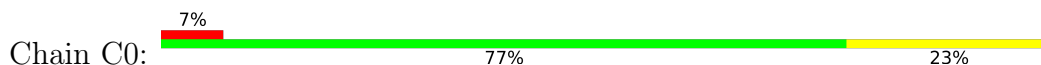
- Molecule 175: STAPLE STRAND



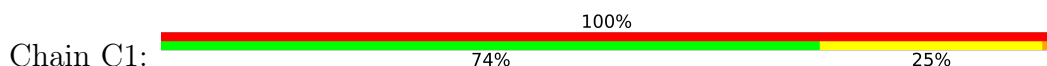
- Molecule 176: STAPLE STRAND



- Molecule 177: STAPLE STRAND

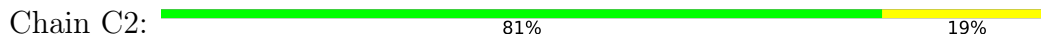


- Molecule 178: STAPLE STRAND

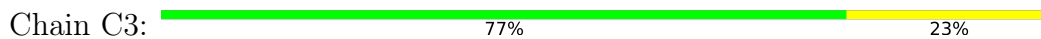




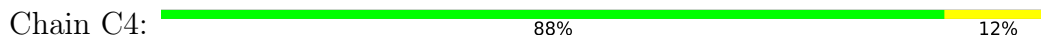
- Molecule 179: STAPLE STRAND



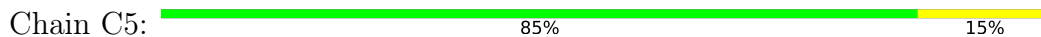
- Molecule 180: STAPLE STRAND



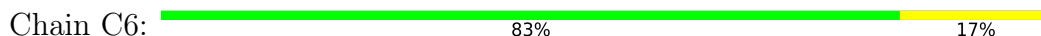
- Molecule 181: STAPLE STRAND



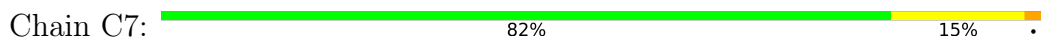
- Molecule 182: STAPLE STRAND



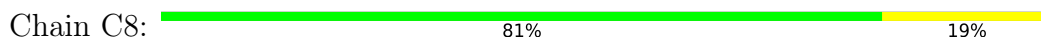
- Molecule 183: STAPLE STRAND



- Molecule 184: STAPLE STRAND

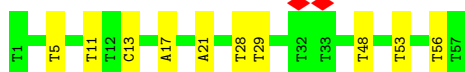
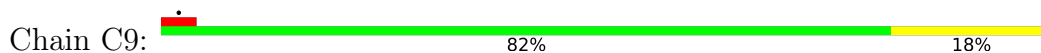


- Molecule 185: STAPLE STRAND

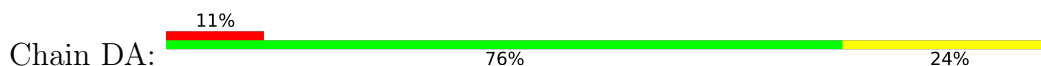




- Molecule 186: STAPLE STRAND



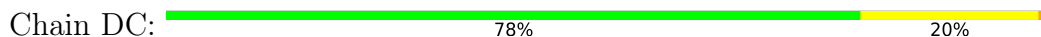
- Molecule 187: STAPLE STRAND



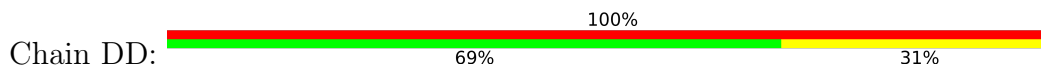
- Molecule 188: STAPLE STRAND



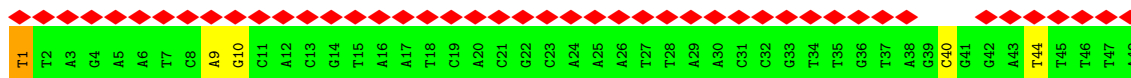
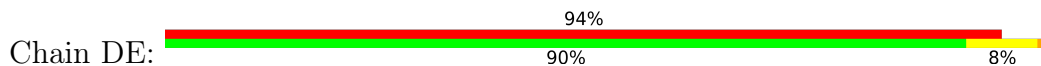
- Molecule 189: STAPLE STRAND



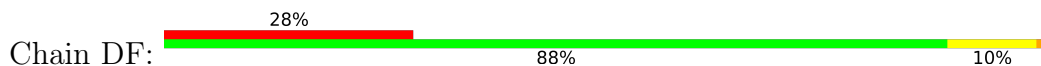
- Molecule 190: STAPLE STRAND

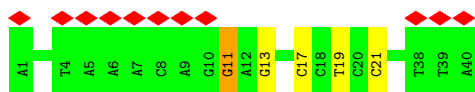


- Molecule 191: STAPLE STRAND

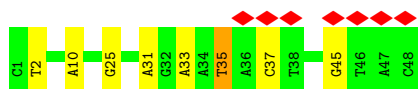
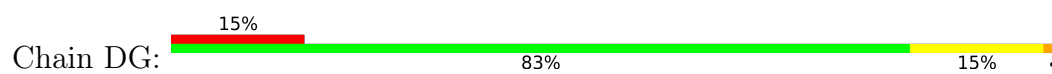


- Molecule 192: STAPLE STRAND

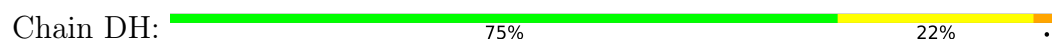




- Molecule 193: STAPLE STRAND



- Molecule 194: STAPLE STRAND



- Molecule 195: STAPLE STRAND



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	509812	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	55	Depositor
Minimum defocus (nm)	260.5	Depositor
Maximum defocus (nm)	3692	Depositor
Magnification	47000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.401	Depositor
Minimum map value	-0.217	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.051	Depositor
Map size (Å)	644.96, 644.96, 644.96	wwPDB
Map dimensions	464, 464, 464	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3900001, 1.3900001, 1.3900001	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	0.70	0/184801	1.00	363/285260 (0.1%)
2	AB	0.68	0/647	0.92	0/996
3	AC	0.71	0/1104	1.03	4/1703 (0.2%)
4	AD	0.69	0/1230	1.01	3/1899 (0.2%)
5	AE	0.69	0/1358	1.04	6/2094 (0.3%)
6	AF	0.71	0/1101	1.02	4/1698 (0.2%)
7	AG	0.72	0/1115	1.01	5/1721 (0.3%)
8	AH	0.68	0/1366	0.94	0/2109
9	AI	0.69	0/950	1.04	3/1464 (0.2%)
10	AJ	0.66	0/1359	0.96	1/2096 (0.0%)
11	AK	0.69	0/739	0.94	1/1140 (0.1%)
12	AL	0.67	0/911	0.99	2/1405 (0.1%)
13	AM	0.68	0/1111	0.95	0/1714
14	AN	0.70	0/746	1.03	1/1151 (0.1%)
15	AO	0.68	0/1098	0.94	0/1691
16	AP	0.69	0/919	0.92	1/1415 (0.1%)
17	AQ	0.67	0/1021	1.02	3/1574 (0.2%)
18	AR	0.69	0/1108	0.97	1/1709 (0.1%)
19	AS	0.70	0/1112	0.89	0/1715
20	AT	0.69	0/1040	1.01	3/1607 (0.2%)
21	AU	0.70	0/1095	1.01	2/1687 (0.1%)
22	AV	0.70	0/920	0.96	1/1416 (0.1%)
23	AW	0.70	0/1285	1.03	7/1975 (0.4%)
24	AX	0.68	0/1372	0.98	3/2116 (0.1%)
25	AY	0.69	0/740	0.91	1/1142 (0.1%)
26	AZ	0.70	0/1114	0.98	2/1719 (0.1%)
27	Aa	0.67	0/923	0.90	1/1425 (0.1%)
28	Ab	0.70	0/1108	0.97	3/1709 (0.2%)
29	Ac	0.70	0/911	0.96	0/1402
30	Ad	0.67	0/1226	0.94	1/1892 (0.1%)
31	Ae	0.70	0/934	1.04	5/1443 (0.3%)
32	Af	0.71	0/749	0.92	1/1158 (0.1%)
33	Ag	0.67	0/1308	0.98	0/2016
34	Ah	0.67	0/1382	0.98	2/2134 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	Ai	0.71	0/1095	0.94	1/1689 (0.1%)
36	Aj	0.69	0/1084	1.01	3/1668 (0.2%)
37	Ak	0.69	0/732	0.97	1/1127 (0.1%)
38	Al	0.67	0/1103	0.95	1/1700 (0.1%)
39	Am	0.69	0/1310	0.98	1/2020 (0.0%)
40	An	0.67	0/1378	0.94	1/2128 (0.0%)
41	Ao	0.68	0/1306	0.96	1/2016 (0.0%)
42	Ap	0.69	0/1355	1.02	4/2091 (0.2%)
43	Aq	0.71	0/1105	0.93	0/1705
44	Ar	0.68	0/843	0.92	1/1298 (0.1%)
45	As	0.67	0/914	1.02	1/1410 (0.1%)
46	At	0.67	0/1010	0.93	1/1556 (0.1%)
47	Au	0.69	0/920	0.98	0/1417
48	Av	0.71	0/913	1.03	3/1406 (0.2%)
49	Aw	0.69	0/1272	1.02	1/1960 (0.1%)
50	Ax	0.68	0/912	1.03	2/1406 (0.1%)
51	Ay	0.70	0/1115	0.99	4/1720 (0.2%)
52	Az	0.69	0/1005	0.96	2/1544 (0.1%)
53	A0	0.72	0/715	1.12	5/1099 (0.5%)
54	A1	0.70	0/1116	1.00	1/1723 (0.1%)
55	A2	0.72	0/1080	1.02	2/1661 (0.1%)
56	A3	0.72	0/1294	1.01	4/1996 (0.2%)
57	A4	0.69	0/1045	0.93	2/1615 (0.1%)
58	A5	0.71	0/1115	0.95	2/1721 (0.1%)
59	A6	0.71	0/734	0.93	0/1132
60	A7	0.71	0/721	0.98	3/1107 (0.3%)
61	A8	0.70	0/740	0.89	0/1141
62	A9	0.71	0/1112	1.00	3/1715 (0.2%)
63	BA	0.69	0/1032	0.92	1/1589 (0.1%)
64	BB	0.69	0/742	0.96	1/1144 (0.1%)
65	BC	0.70	0/1016	0.97	0/1565
66	BD	0.69	0/1289	1.05	3/1988 (0.2%)
67	BE	0.69	0/1290	1.00	3/1988 (0.2%)
68	BF	0.69	0/1018	1.01	4/1568 (0.3%)
69	BG	0.71	0/904	1.00	1/1390 (0.1%)
70	BH	0.66	0/1288	0.94	2/1987 (0.1%)
71	BI	0.68	0/1292	0.99	2/1991 (0.1%)
72	BJ	0.68	0/1027	0.97	1/1584 (0.1%)
73	BK	0.70	0/734	0.97	0/1132
74	BL	0.69	0/1278	1.02	1/1971 (0.1%)
75	BM	0.67	0/731	0.89	0/1124
76	BN	0.69	0/940	0.90	0/1451
77	BO	0.71	0/1092	1.01	4/1681 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
78	BP	0.68	0/1313	1.00	4/2023 (0.2%)
79	BQ	0.67	0/1279	0.99	2/1969 (0.1%)
80	BR	0.69	0/1120	0.93	1/1730 (0.1%)
81	BS	0.68	0/1091	1.02	4/1681 (0.2%)
82	BT	0.70	0/1089	0.98	0/1677
83	BU	0.71	0/1100	0.98	3/1696 (0.2%)
84	BV	0.68	0/1327	0.98	3/2048 (0.1%)
85	BW	0.69	0/1351	1.08	5/2083 (0.2%)
86	BX	0.71	0/738	1.01	1/1138 (0.1%)
87	BY	0.72	0/934	1.00	3/1444 (0.2%)
88	BZ	0.70	0/918	1.01	2/1415 (0.1%)
89	Ba	0.69	0/1132	0.95	4/1749 (0.2%)
90	Bb	0.73	0/1087	1.14	4/1673 (0.2%)
91	Bc	0.68	0/741	0.94	1/1142 (0.1%)
92	Bd	0.69	0/1120	0.96	0/1727
93	Be	0.70	0/1094	1.04	3/1685 (0.2%)
94	Bf	0.68	0/1109	0.96	1/1710 (0.1%)
95	Bg	0.72	0/908	1.12	4/1399 (0.3%)
96	Bh	0.69	0/1302	0.96	1/2010 (0.0%)
97	Bi	0.69	0/898	1.07	5/1382 (0.4%)
98	Bj	0.70	0/734	1.08	4/1130 (0.4%)
99	Bk	0.66	0/742	0.92	0/1145
100	Bl	0.70	0/1090	1.00	2/1679 (0.1%)
101	Bm	0.71	0/1286	1.08	4/1985 (0.2%)
102	Bn	0.69	0/1087	0.98	0/1673
103	Bo	0.70	0/1121	0.92	0/1730
104	Bp	0.70	0/923	0.99	0/1424
105	Bq	0.73	0/1102	1.02	3/1703 (0.2%)
106	Br	0.71	0/1115	0.98	2/1722 (0.1%)
107	Bs	0.71	0/735	0.92	0/1131
108	Bt	0.69	0/925	0.97	1/1427 (0.1%)
109	Bu	0.70	0/921	0.95	0/1419
110	Bv	0.71	0/910	1.01	0/1401
111	Bw	0.67	0/1357	0.98	2/2092 (0.1%)
112	Bx	0.70	0/1030	0.99	3/1588 (0.2%)
113	By	0.70	0/928	0.93	1/1430 (0.1%)
114	Bz	0.67	0/733	0.96	0/1130
115	B0	0.68	0/1348	1.05	5/2077 (0.2%)
116	B1	0.70	0/1351	0.97	2/2083 (0.1%)
117	B2	0.69	0/927	0.94	0/1429
118	B3	0.69	0/749	0.85	0/1156
119	B4	0.69	0/746	0.97	1/1152 (0.1%)
120	B5	0.68	0/1370	0.94	0/2112

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
121	B6	0.69	0/1207	0.98	0/1859
122	B7	0.69	0/1105	0.99	2/1702 (0.1%)
123	B8	0.69	0/741	0.90	0/1142
124	B9	0.71	0/1093	1.04	5/1683 (0.3%)
125	CA	0.69	0/1094	0.99	1/1686 (0.1%)
126	CB	0.67	0/1370	0.93	2/2112 (0.1%)
127	CC	0.72	0/844	1.03	3/1301 (0.2%)
128	CD	0.66	0/1293	0.99	4/1996 (0.2%)
129	CE	0.71	0/751	1.02	2/1161 (0.2%)
130	CF	0.69	0/925	1.02	1/1426 (0.1%)
131	CG	0.70	0/739	0.95	0/1140
132	CH	0.70	0/1222	0.98	1/1884 (0.1%)
133	CI	0.69	0/722	1.03	2/1111 (0.2%)
134	CJ	0.66	0/1294	1.03	6/1996 (0.3%)
135	CK	0.68	0/729	1.01	1/1122 (0.1%)
136	CL	0.70	0/922	1.04	2/1420 (0.1%)
137	CM	0.68	0/749	0.88	1/1156 (0.1%)
138	CN	0.69	0/1297	0.94	1/2001 (0.0%)
139	CO	0.70	0/1101	0.98	2/1695 (0.1%)
140	CP	0.71	0/1113	1.03	3/1720 (0.2%)
141	CQ	0.69	0/1298	1.02	2/2003 (0.1%)
142	CR	0.67	0/1370	0.96	1/2114 (0.0%)
143	CS	0.69	0/1080	0.97	0/1663
144	CT	0.69	0/1303	0.97	2/2012 (0.1%)
145	CU	0.67	0/854	0.96	1/1316 (0.1%)
146	CV	0.69	0/737	0.98	0/1136
147	CW	0.68	0/732	0.93	0/1127
148	CX	0.67	0/1292	1.03	3/1994 (0.2%)
149	CY	0.67	0/1350	0.98	2/2080 (0.1%)
150	CZ	0.70	0/1099	0.99	1/1695 (0.1%)
151	Ca	0.68	0/1109	0.96	0/1708
152	Cb	0.70	0/924	0.99	1/1424 (0.1%)
153	Cc	0.70	0/735	0.99	1/1133 (0.1%)
154	Cd	0.70	0/939	1.06	4/1449 (0.3%)
155	Ce	0.67	0/932	0.95	3/1440 (0.2%)
156	Cf	0.71	0/736	0.99	1/1136 (0.1%)
157	Cg	0.69	0/918	0.99	1/1414 (0.1%)
158	Ch	0.66	0/917	1.01	1/1413 (0.1%)
159	Ci	0.68	0/1088	0.98	0/1674
160	Cj	0.69	0/917	1.00	2/1413 (0.1%)
161	Ck	0.70	0/1103	1.00	2/1703 (0.1%)
162	Cl	0.67	0/924	0.93	1/1424 (0.1%)
163	Cm	0.71	0/1098	1.05	4/1693 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
164	Cn	0.70	0/919	1.03	1/1417 (0.1%)
165	Co	0.69	0/910	1.01	2/1400 (0.1%)
166	Cp	0.69	0/843	0.97	1/1298 (0.1%)
167	Cq	0.70	0/847	0.99	2/1304 (0.2%)
168	Cr	0.71	0/936	0.99	1/1447 (0.1%)
169	Cs	0.69	0/925	0.95	0/1426
170	Ct	0.68	0/1031	1.00	3/1590 (0.2%)
171	Cu	0.69	0/850	1.04	2/1310 (0.2%)
172	Cv	0.69	0/905	1.00	2/1394 (0.1%)
173	Cw	0.71	0/928	0.97	1/1432 (0.1%)
174	Cx	0.70	0/733	0.97	1/1128 (0.1%)
175	Cy	0.72	0/733	0.99	2/1128 (0.2%)
176	Cz	0.68	0/751	0.84	0/1161
177	C0	0.71	0/1281	1.05	5/1972 (0.3%)
178	C1	0.67	0/1302	0.99	4/2011 (0.2%)
179	C2	0.68	0/738	0.99	1/1138 (0.1%)
180	C3	0.70	0/1100	0.96	2/1694 (0.1%)
181	C4	0.68	0/1096	0.95	0/1688
182	C5	0.68	0/1092	1.02	2/1683 (0.1%)
183	C6	0.72	0/1123	0.97	2/1735 (0.1%)
184	C7	0.69	0/896	1.07	4/1378 (0.3%)
185	C8	0.70	0/1116	1.01	2/1722 (0.1%)
186	C9	0.68	0/1293	0.98	2/1994 (0.1%)
187	DA	0.70	0/1027	1.01	0/1583
188	DB	0.70	0/724	0.98	2/1113 (0.2%)
189	DC	0.69	0/942	1.00	4/1453 (0.3%)
190	DD	0.69	0/1017	0.99	3/1566 (0.2%)
191	DE	0.67	0/1102	0.95	2/1699 (0.1%)
192	DF	0.69	0/917	0.94	2/1413 (0.1%)
193	DG	0.68	0/1112	0.93	1/1717 (0.1%)
194	DH	0.70	0/737	1.00	3/1134 (0.3%)
195	DI	0.68	0/732	0.95	0/1128
All	All	0.69	0/383925	0.99	715/592251 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AA	1	1140
3	AC	0	3

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Mol	Chain	#Chirality outliers	#Planarity outliers
4	AD	0	12
5	AE	0	6
6	AF	0	9
7	AG	0	7
8	AH	0	4
9	AI	0	8
10	AJ	0	5
11	AK	0	5
12	AL	0	11
13	AM	0	6
14	AN	0	3
15	AO	0	4
16	AP	0	5
17	AQ	0	5
18	AR	0	3
19	AS	0	10
20	AT	0	6
21	AU	0	8
22	AV	0	4
23	AW	0	7
24	AX	0	5
25	AY	0	5
26	AZ	0	7
27	Aa	0	3
28	Ab	0	10
29	Ac	0	12
30	Ad	0	7
31	Ae	0	8
32	Af	0	6
33	Ag	0	7
34	Ah	0	10
35	Ai	0	7
36	Aj	0	5
37	Ak	0	4
38	Al	0	6
39	Am	0	10
40	An	0	7
41	Ao	0	10
42	Ap	0	8
43	Aq	0	8
44	Ar	0	8
45	As	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
46	At	0	7
47	Au	0	7
48	Av	0	3
49	Aw	0	6
50	Ax	0	9
51	Ay	0	4
52	Az	0	5
53	A0	0	5
54	A1	0	8
55	A2	0	11
56	A3	0	9
57	A4	0	6
58	A5	0	5
59	A6	0	7
60	A7	0	2
61	A8	0	3
62	A9	0	6
63	BA	0	6
64	BB	0	9
65	BC	0	6
66	BD	0	4
67	BE	0	10
68	BF	0	7
69	BG	0	9
70	BH	0	14
71	BI	0	12
72	BJ	0	5
73	BK	0	3
74	BL	0	4
75	BM	0	3
76	BN	0	7
77	BO	0	7
78	BP	0	10
79	BQ	0	9
80	BR	0	4
81	BS	0	6
82	BT	0	5
83	BU	0	4
84	BV	0	7
85	BW	0	12
86	BX	0	4
87	BY	0	9

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Mol	Chain	#Chirality outliers	#Planarity outliers
88	BZ	0	7
89	Ba	0	9
90	Bb	0	11
91	Bc	0	3
92	Bd	0	1
93	Be	0	4
94	Bf	0	5
95	Bg	0	12
96	Bh	0	10
97	Bi	0	8
98	Bj	0	4
99	Bk	0	2
100	Bl	0	6
101	Bm	0	7
102	Bn	0	3
103	Bo	0	5
104	Bp	0	4
105	Bq	0	4
106	Br	0	5
107	Bs	0	3
108	Bt	0	5
109	Bu	0	3
110	Bv	0	6
111	Bw	0	9
112	Bx	0	6
113	By	0	2
114	Bz	0	5
115	B0	0	7
116	B1	0	11
117	B2	0	4
118	B3	0	5
119	B4	0	3
120	B5	0	8
121	B6	0	11
122	B7	0	4
123	B8	0	4
124	B9	0	9
125	CA	0	10
126	CB	0	11
127	CC	0	4
128	CD	0	9
129	CE	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
130	CF	0	7
131	CG	0	6
132	CH	0	12
133	CI	0	3
134	CJ	0	7
135	CK	0	4
136	CL	0	6
137	CM	0	5
138	CN	0	7
139	CO	0	8
140	CP	0	11
141	CQ	0	10
142	CR	0	13
143	CS	0	8
144	CT	0	4
145	CU	0	4
146	CV	0	3
147	CW	0	4
148	CX	0	6
149	CY	0	9
150	CZ	0	6
151	Ca	0	5
152	Cb	0	10
153	Cc	0	6
154	Cd	0	8
155	Ce	0	5
156	Cf	0	6
157	Cg	0	2
158	Ch	0	6
159	Ci	0	6
160	Cj	0	5
161	Ck	0	5
162	Cl	0	6
163	Cm	0	11
164	Cn	0	7
165	Co	0	7
166	Cp	0	8
167	Cq	0	2
168	Cr	0	7
169	Cs	0	6
170	Ct	0	11
171	Cu	0	5

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Mol	Chain	#Chirality outliers	#Planarity outliers
172	Cv	0	9
173	Cw	0	4
174	Cx	0	6
175	Cy	0	3
176	Cz	0	3
177	C0	0	8
178	C1	0	13
179	C2	0	5
180	C3	0	10
181	C4	0	6
182	C5	0	5
183	C6	0	6
184	C7	0	5
185	C8	0	7
186	C9	0	8
187	DA	0	11
188	DB	0	4
189	DC	0	6
190	DD	0	11
191	DE	0	4
192	DF	0	4
193	DG	0	8
194	DH	0	6
195	DI	0	3
All	All	1	2388

There are no bond length outliers.

The worst 5 of 715 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	601	DC	P-O3'-C3'	14.73	142.30	120.20
1	AA	4222	DT	P-O3'-C3'	14.11	141.36	120.20
84	BV	39	DA	P-O3'-C3'	11.71	137.76	120.20
1	AA	486	DC	P-O3'-C3'	11.71	137.76	120.20
1	AA	6047	DC	P-O3'-C3'	11.61	137.62	120.20

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	AA	1863	DA	C3'

5 of 2388 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	31	DG	Sidechain
1	AA	40	DT	Sidechain
1	AA	67	DA	Sidechain
1	AA	71	DG	Sidechain
1	AA	78	DA	Sidechain

## 5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	164972	0	91301	0	0
2	AB	582	0	334	0	0
3	AC	984	0	542	0	0
4	AD	1094	0	600	0	0
5	AE	1217	0	685	0	0
6	AF	982	0	543	0	0
7	AG	991	0	539	0	0
8	AH	1224	0	692	0	0
9	AI	851	0	483	0	0
10	AJ	1218	0	693	0	0
11	AK	658	0	364	0	0
12	AL	815	0	458	0	0
13	AM	988	0	544	0	0
14	AN	662	0	362	0	0
15	AO	978	0	543	0	0
16	AP	817	0	449	0	0
17	AQ	914	0	517	0	0
18	AR	986	0	545	0	0
19	AS	988	0	540	0	0
20	AT	928	0	512	0	0
21	AU	977	0	542	0	0
22	AV	817	0	445	0	0
23	AW	1155	0	659	0	0
24	AX	1225	0	684	0	0
25	AY	659	0	362	0	0
26	AZ	990	0	541	0	0
27	Aa	823	0	457	0	0
28	Ab	986	0	539	0	0
29	Ac	812	0	452	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	Ad	1091	0	600	0	0
31	Ae	830	0	449	0	0
32	Af	666	0	363	0	0
33	Ag	1173	0	669	0	0
34	Ah	1233	0	686	0	0
35	Ai	979	0	544	0	0
36	Aj	969	0	544	0	0
37	Ak	652	0	361	0	0
38	Al	982	0	543	0	0
39	Am	1175	0	667	0	0
40	An	1231	0	688	0	0
41	Ao	1167	0	653	0	0
42	Ap	1217	0	693	0	0
43	Aq	985	0	541	0	0
44	Ar	752	0	419	0	0
45	As	817	0	460	0	0
46	At	899	0	498	0	0
47	Au	818	0	450	0	0
48	Av	814	0	449	0	0
49	Aw	1137	0	635	0	0
50	Ax	815	0	457	0	0
51	Ay	990	0	539	0	0
52	Az	900	0	508	0	0
53	A0	641	0	363	0	0
54	A1	992	0	541	0	0
55	A2	966	0	537	0	0
56	A3	1151	0	628	0	0
57	A4	931	0	512	0	0
58	A5	991	0	540	0	0
59	A6	655	0	363	0	0
60	A7	643	0	358	0	0
61	A8	658	0	359	0	0
62	A9	988	0	537	0	0
63	BA	918	0	506	0	0
64	BB	659	0	357	0	0
65	BC	910	0	513	0	0
66	BD	1156	0	657	0	0
67	BE	1155	0	653	0	0
68	BF	911	0	510	0	0
69	BG	807	0	451	0	0
70	BH	1156	0	661	0	0
71	BI	1156	0	657	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
72	BJ	918	0	515	0	0
73	BK	655	0	363	0	0
74	BL	1142	0	637	0	0
75	BM	650	0	360	0	0
76	BN	832	0	447	0	0
77	BO	974	0	539	0	0
78	BP	1175	0	664	0	0
79	BQ	1147	0	655	0	0
80	BR	995	0	543	0	0
81	BS	975	0	547	0	0
82	BT	973	0	542	0	0
83	BU	981	0	540	0	0
84	BV	1186	0	665	0	0
85	BW	1213	0	689	0	0
86	BX	657	0	359	0	0
87	BY	831	0	450	0	0
88	BZ	818	0	449	0	0
89	Ba	1002	0	539	0	0
90	Bb	971	0	541	0	0
91	Bc	658	0	359	0	0
92	Bd	992	0	538	0	0
93	Be	976	0	544	0	0
94	Bf	986	0	540	0	0
95	Bg	812	0	454	0	0
96	Bh	1157	0	632	0	0
97	Bi	805	0	458	0	0
98	Bj	653	0	361	0	0
99	Bk	660	0	363	0	0
100	Bl	974	0	540	0	0
101	Bm	1148	0	635	0	0
102	Bn	971	0	543	0	0
103	Bo	994	0	537	0	0
104	Bp	822	0	453	0	0
105	Bq	986	0	547	0	0
106	Br	992	0	541	0	0
107	Bs	653	0	359	0	0
108	Bt	823	0	450	0	0
109	Bu	819	0	450	0	0
110	Bv	812	0	451	0	0
111	Bw	1216	0	692	0	0
112	Bx	919	0	509	0	0
113	By	823	0	445	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
114	Bz	654	0	366	0	0
115	B0	1210	0	693	0	0
116	B1	1213	0	692	0	0
117	B2	823	0	450	0	0
118	B3	664	0	358	0	0
119	B4	663	0	360	0	0
120	B5	1223	0	684	0	0
121	B6	1077	0	599	0	0
122	B7	982	0	538	0	0
123	B8	658	0	359	0	0
124	B9	975	0	539	0	0
125	CA	977	0	541	0	0
126	CB	1223	0	686	0	0
127	CC	754	0	420	0	0
128	CD	1160	0	662	0	0
129	CE	667	0	358	0	0
130	CF	822	0	451	0	0
131	CG	658	0	363	0	0
132	CH	1087	0	599	0	0
133	CI	646	0	367	0	0
134	CJ	1159	0	658	0	0
135	CK	650	0	363	0	0
136	CL	819	0	448	0	0
137	CM	664	0	360	0	0
138	CN	1153	0	634	0	0
139	CO	979	0	538	0	0
140	CP	992	0	545	0	0
141	CQ	1162	0	657	0	0
142	CR	1225	0	690	0	0
143	CS	968	0	549	0	0
144	CT	1158	0	634	0	0
145	CU	759	0	418	0	0
146	CV	656	0	362	0	0
147	CW	652	0	363	0	0
148	CX	1159	0	660	0	0
149	CY	1211	0	695	0	0
150	CZ	981	0	547	0	0
151	Ca	984	0	541	0	0
152	Cb	821	0	450	0	0
153	Cc	655	0	363	0	0
154	Cd	831	0	446	0	0
155	Ce	829	0	455	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
156	Cf	657	0	366	0	0
157	Cg	817	0	453	0	0
158	Ch	817	0	455	0	0
159	Ci	971	0	542	0	0
160	Cj	817	0	452	0	0
161	Ck	985	0	549	0	0
162	Cl	821	0	451	0	0
163	Cm	980	0	546	0	0
164	Cn	819	0	454	0	0
165	Co	811	0	450	0	0
166	Cp	752	0	419	0	0
167	Cq	754	0	416	0	0
168	Cr	832	0	453	0	0
169	Cs	822	0	451	0	0
170	Ct	920	0	513	0	0
171	Cu	757	0	422	0	0
172	Cv	810	0	456	0	0
173	Cw	825	0	449	0	0
174	Cx	652	0	358	0	0
175	Cy	652	0	357	0	0
176	Cz	667	0	361	0	0
177	C0	1148	0	650	0	0
178	C1	1166	0	659	0	0
179	C2	657	0	363	0	0
180	C3	979	0	538	0	0
181	C4	977	0	544	0	0
182	C5	976	0	547	0	0
183	C6	997	0	540	0	0
184	C7	803	0	456	0	0
185	C8	991	0	540	0	0
186	C9	1158	0	657	0	0
187	DA	917	0	511	0	0
188	DB	646	0	361	0	0
189	DC	832	0	446	0	0
190	DD	910	0	509	0	0
191	DE	982	0	544	0	0
192	DF	817	0	450	0	0
193	DG	990	0	542	0	0
194	DH	654	0	358	0	0
195	DI	653	0	364	0	0
All	All	342569	0	189904	0	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including

hydrogen atoms). Clashscore could not be calculated for this entry.

There are no clashes within the asymmetric unit.

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

There are no protein molecules in this entry.

### 5.3.2 Protein sidechains [i](#)

There are no protein molecules in this entry.

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

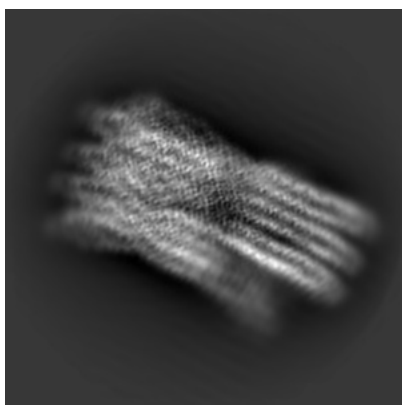
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11379. These allow visual inspection of the internal detail of the map and identification of artifacts.

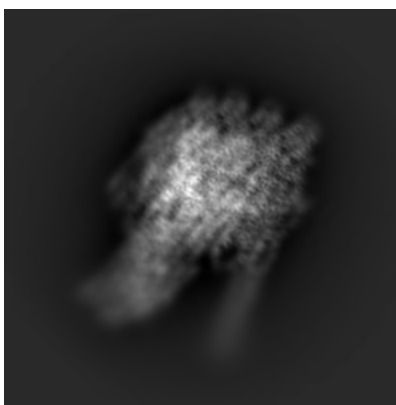
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

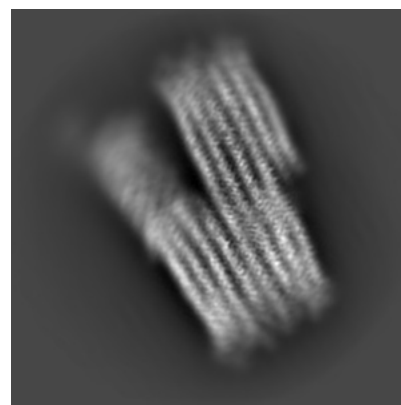
#### 6.1.1 Primary map



X



Y

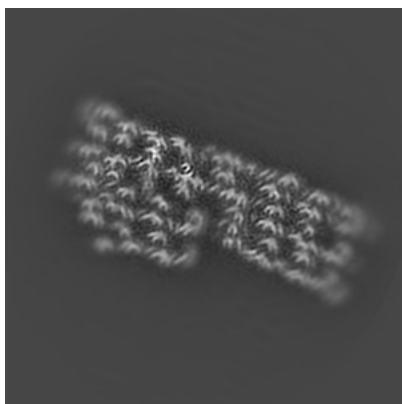


Z

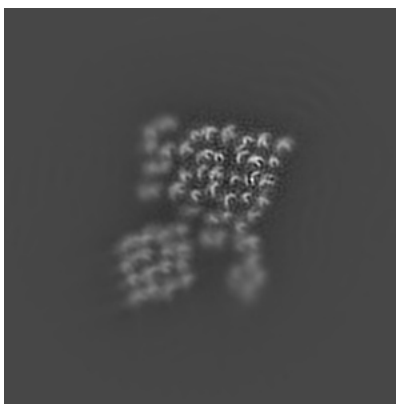
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

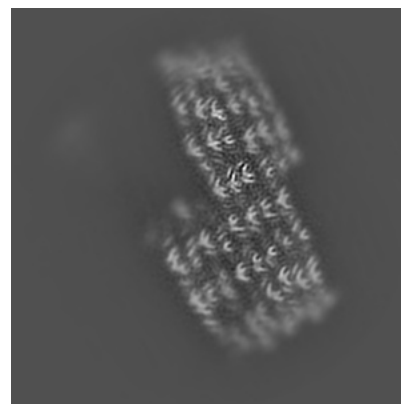
#### 6.2.1 Primary map



X Index: 232



Y Index: 232

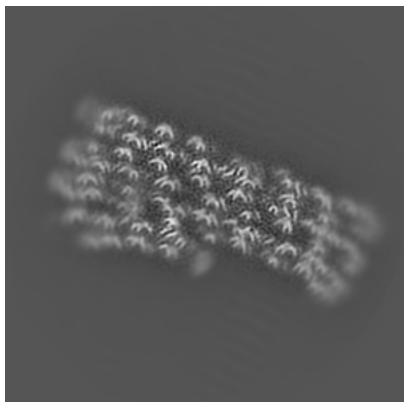


Z Index: 232

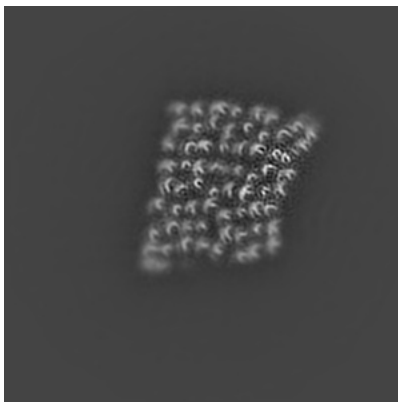
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

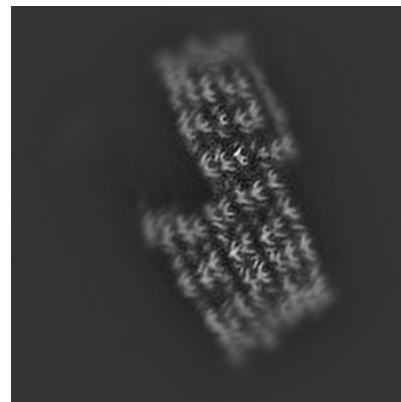
### 6.3.1 Primary map



X Index: 247



Y Index: 179

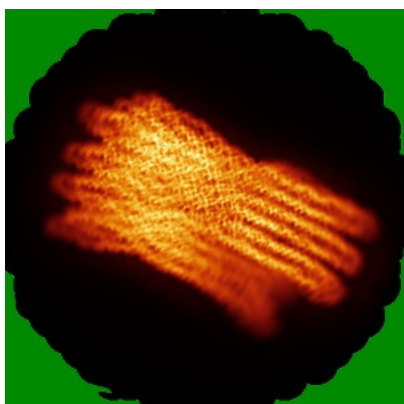


Z Index: 222

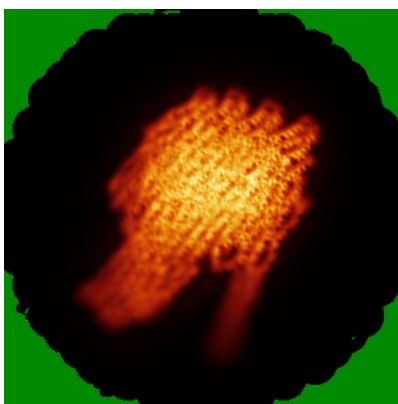
The images above show the largest variance slices of the map in three orthogonal directions.

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

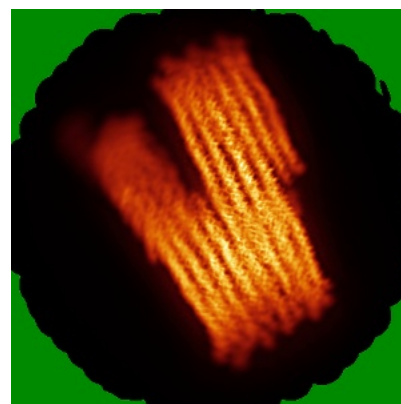
### 6.4.1 Primary map



X



Y

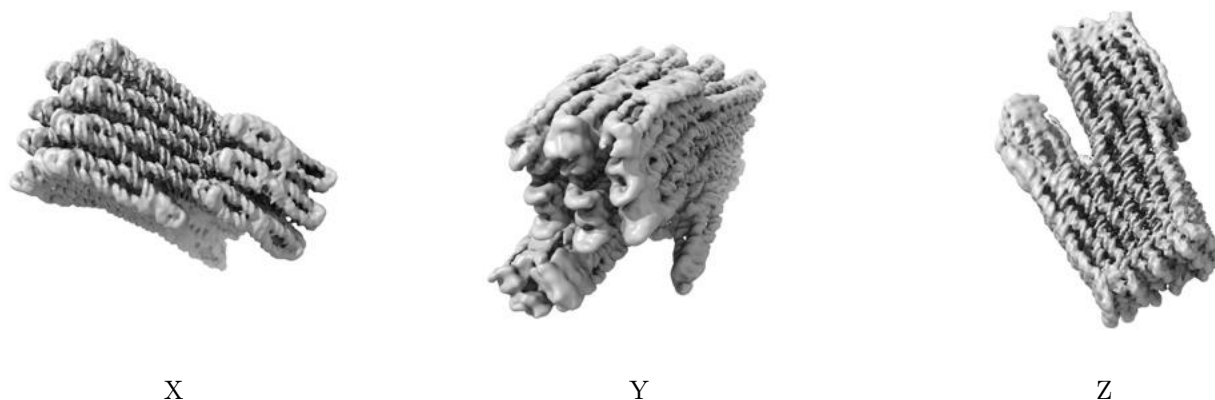


Z

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

## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.051. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

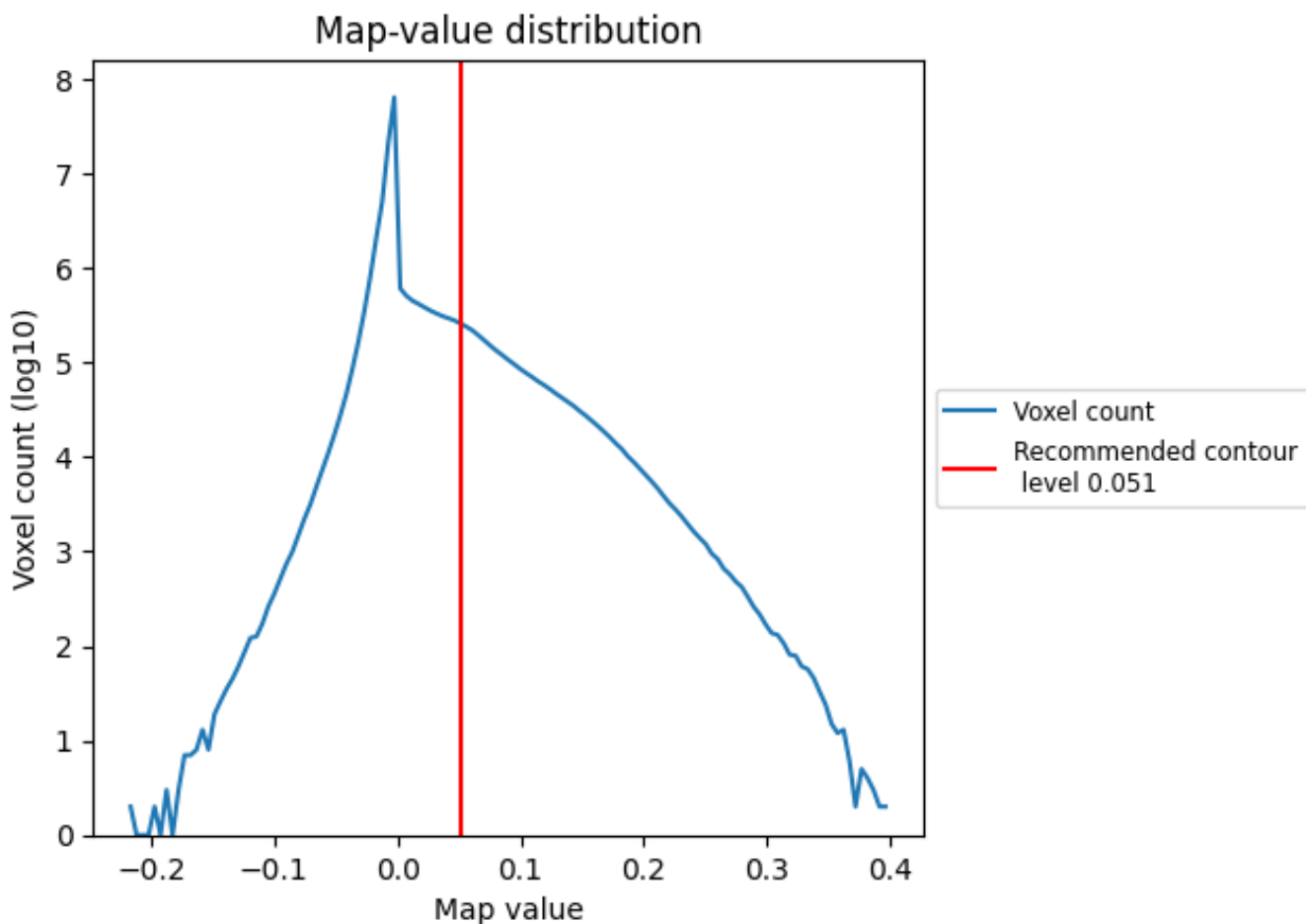
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

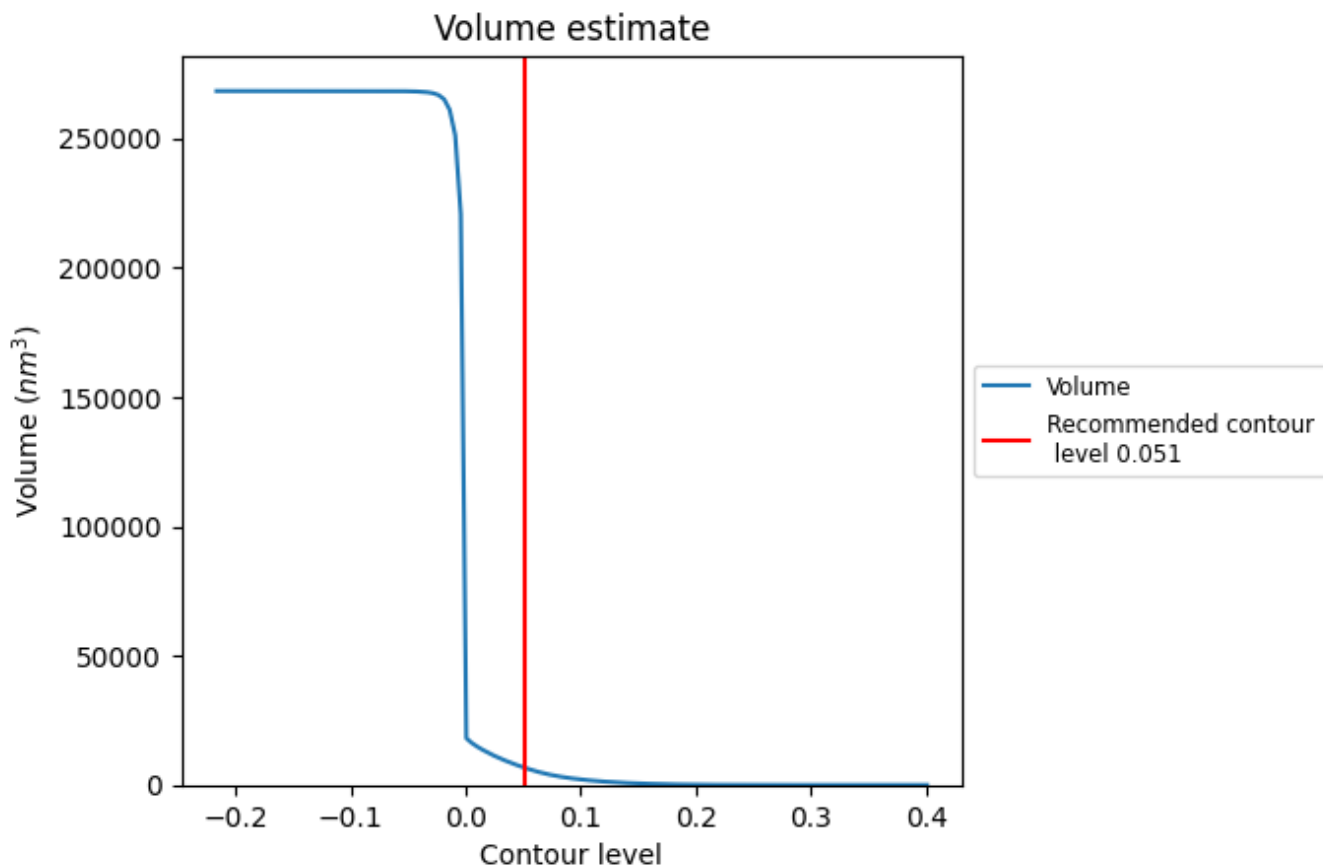
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



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

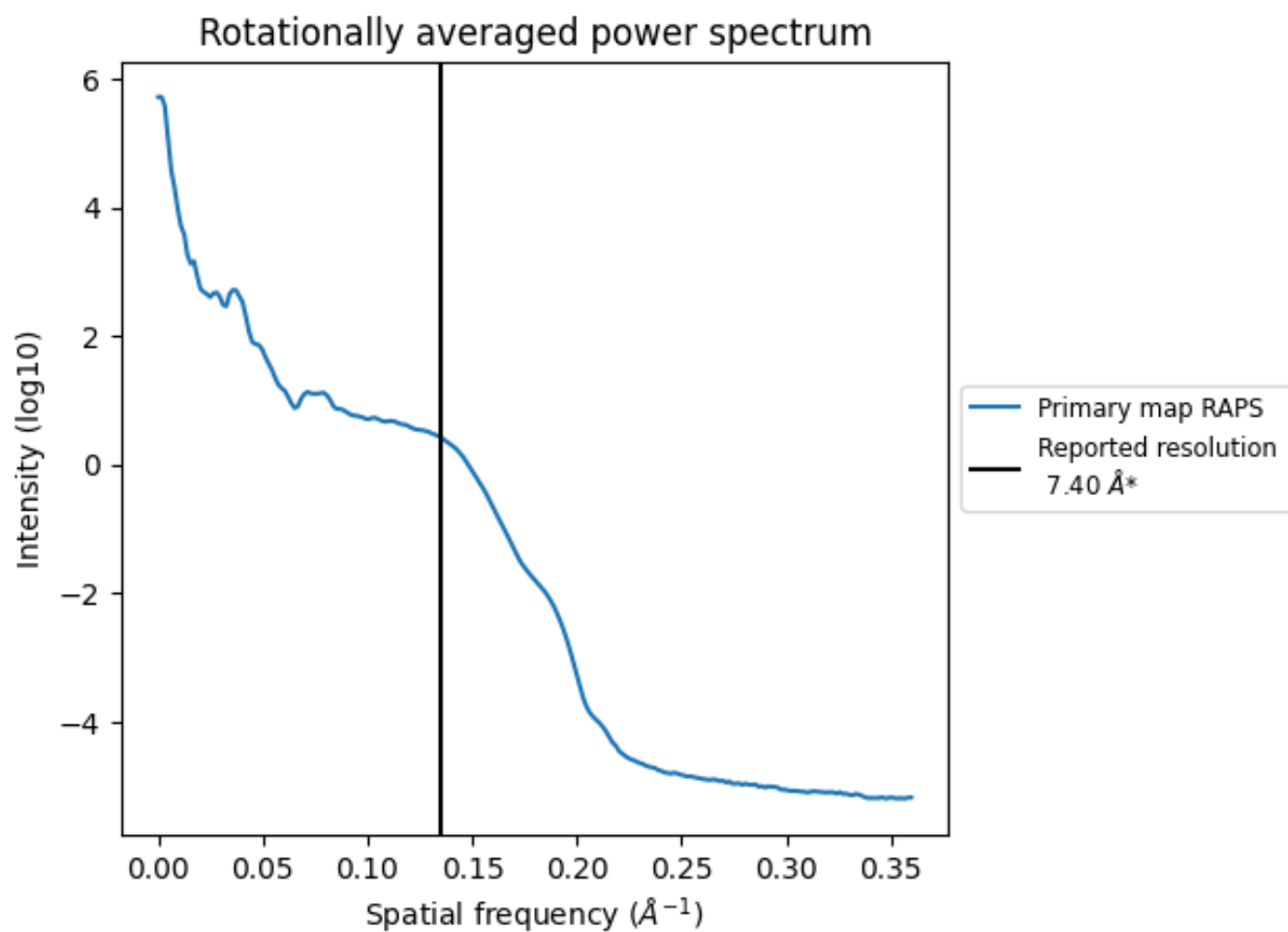
## 7.2 Volume estimate [\(i\)](#)



The volume at the recommended contour level is 6695 nm<sup>3</sup>; this corresponds to an approximate mass of 6048 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](#)

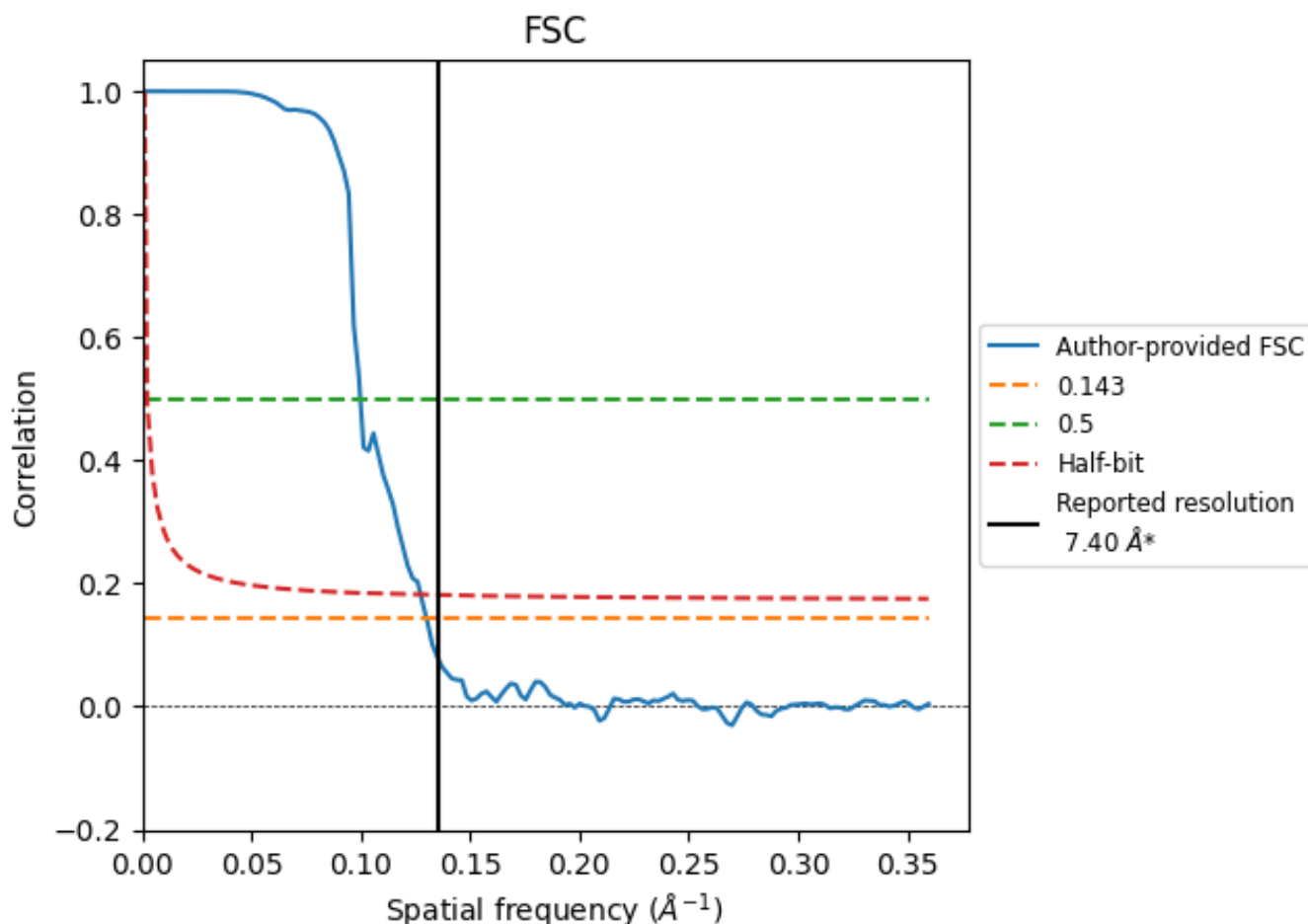


\*Reported resolution corresponds to spatial frequency of 0.135 Å<sup>-1</sup>

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.135 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

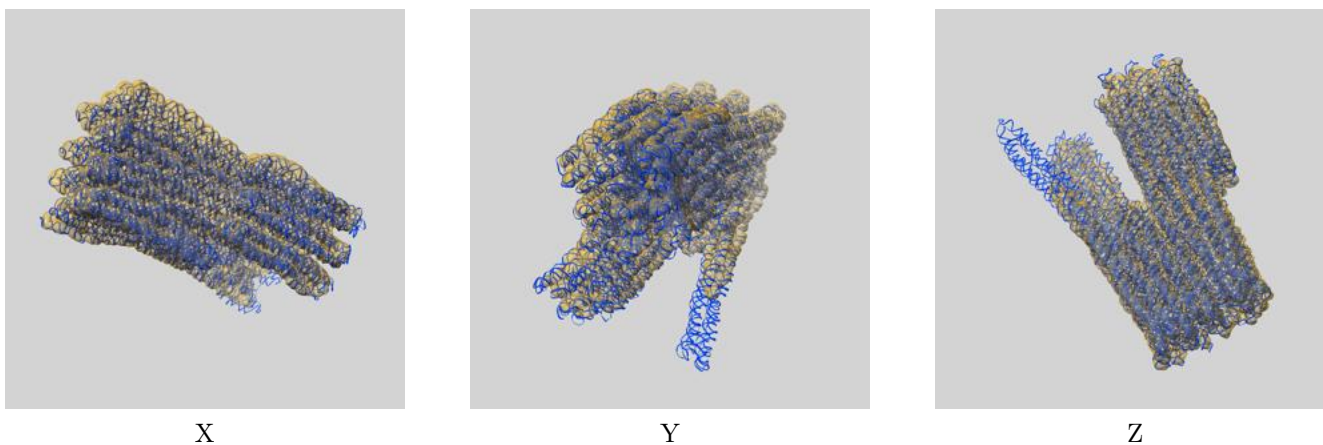
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.40	-	-
Author-provided FSC curve	7.69	10.03	7.86
Unmasked-calculated*	-	-	-

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

## 9 Map-model fit [i](#)

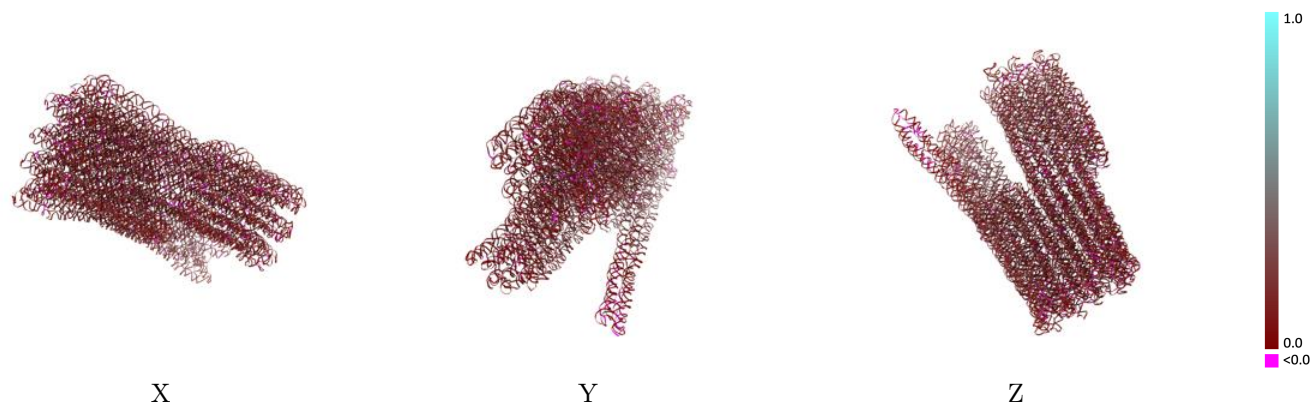
This section contains information regarding the fit between EMDB map EMD-11379 and PDB model 7ARV. Per-residue inclusion information can be found in section 3 on page 39.

### 9.1 Map-model overlay [i](#)



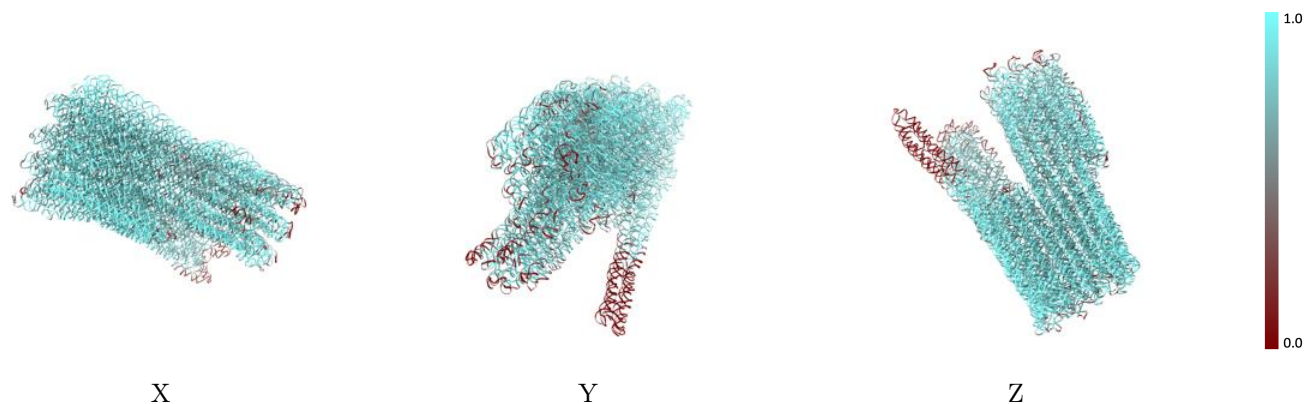
The images above show the 3D surface view of the map at the recommended contour level 0.051 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



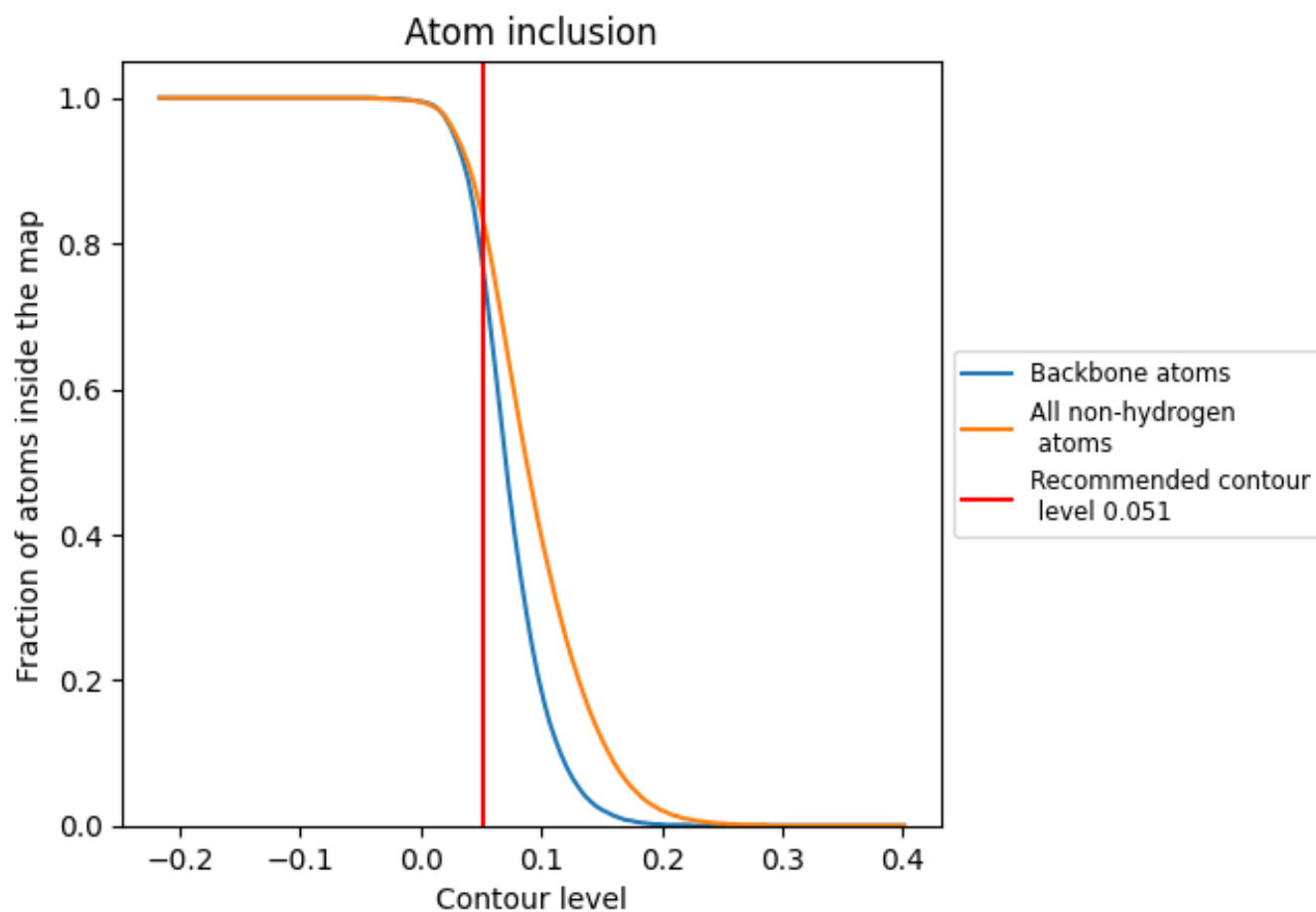
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.051).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 84% 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 (0.051) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8380	 0.1400
A0	 0.8550	 0.1250
A1	 0.8420	 0.1350
A2	 0.7910	 0.1050
A3	 0.8770	 0.1380
A4	 0.9080	 0.1430
A5	 0.9220	 0.1410
A6	 0.8290	 0.1290
A7	 0.9240	 0.1500
A8	 0.8970	 0.1500
A9	 0.8890	 0.1580
AA	 0.8580	 0.1440
AB	 0.6410	 0.1130
AC	 0.8480	 0.1330
AD	 0.9130	 0.1160
AE	 0.4170	 0.0720
AF	 0.8500	 0.1350
AG	 0.8520	 0.1320
AH	 0.6680	 0.0900
AI	 0.7320	 0.1060
AJ	 0.6590	 0.0950
AK	 0.9010	 0.1330
AL	 0.8860	 0.1230
AM	 0.9240	 0.1490
AN	 0.8910	 0.1610
AO	 0.8930	 0.1330
AP	 0.7480	 0.1310
AQ	 0.8080	 0.1340
AR	 0.7150	 0.1330
AS	 0.7970	 0.1190
AT	 0.8100	 0.1200
AU	 0.9000	 0.1440
AV	 0.8870	 0.1470
AW	 0.8930	 0.1000
AX	 0.5530	 0.0770























































































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Chain	Atom inclusion	Q-score
AY	 0.8760	 0.1660
AZ	 0.9360	 0.1560
Aa	 0.8720	 0.1230
Ab	 0.9070	 0.1490
Ac	 0.8570	 0.1400
Ad	 0.9040	 0.1360
Ae	 0.9190	 0.1140
Af	 0.8860	 0.1400
Ag	 0.8720	 0.1170
Ah	 0.6580	 0.1130
Ai	 0.8100	 0.1550
Aj	 0.8730	 0.1360
Ak	 0.8860	 0.1490
Al	 0.9040	 0.1500
Am	 0.8710	 0.1120
An	 0.6820	 0.1130
Ao	 0.8590	 0.1130
Ap	 0.6560	 0.1070
Aq	 0.9250	 0.1520
Ar	 0.7370	 0.1160
As	 0.9110	 0.1510
At	 0.9330	 0.1460
Au	 0.8860	 0.1290
Av	 0.8980	 0.1450
Aw	 0.8290	 0.1380
Ax	 0.8750	 0.1450
Ay	 0.9010	 0.1530
Az	 0.8720	 0.1260
B0	 0.7980	 0.1190
B1	 0.6210	 0.1200
B2	 0.8810	 0.1560
B3	 0.8790	 0.1700
B4	 0.8750	 0.1730
B5	 0.8070	 0.1210
B6	 0.8220	 0.1520
B7	 0.9160	 0.1540
B8	 0.9010	 0.1820
B9	 0.9190	 0.1720
BA	 0.9480	 0.1560
BB	 0.9130	 0.1510
BC	 0.8650	 0.1270
BD	 0.8980	 0.1340





















































































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Chain	Atom inclusion	Q-score
BE	 0.6850	 0.1030
BF	 0.8210	 0.1210
BG	 0.8910	 0.1630
BH	 0.7980	 0.1220
BI	 0.7050	 0.1170
BJ	 0.8130	 0.1590
BK	 0.8380	 0.1540
BL	 0.9190	 0.1460
BM	 0.8550	 0.1250
BN	 0.8930	 0.1460
BO	 0.8740	 0.1470
BP	 0.8540	 0.1230
BQ	 0.6820	 0.1040
BR	 0.8590	 0.1320
BS	 0.8860	 0.1560
BT	 0.9170	 0.1510
BU	 0.8910	 0.1610
BV	 0.8380	 0.1220
BW	 0.7240	 0.1110
BX	 0.9210	 0.1620
BY	 0.9250	 0.1430
BZ	 0.9310	 0.1660
Ba	 0.8800	 0.1400
Bb	 0.8580	 0.1450
Bc	 0.8130	 0.1300
Bd	 0.8590	 0.1450
Be	 0.8320	 0.1450
Bf	 0.8510	 0.1520
Bg	 0.9190	 0.1720
Bh	 0.9170	 0.1450
Bi	 0.9220	 0.1330
Bj	 0.8210	 0.1380
Bk	 0.9380	 0.1790
Bl	 0.8880	 0.1470
Bm	 0.9480	 0.1570
Bn	 0.9050	 0.1410
Bo	 0.9350	 0.1550
Bp	 0.8710	 0.1410
Bq	 0.8340	 0.1290
Br	 0.8700	 0.1520
Bs	 0.8550	 0.1590
Bt	 0.9470	 0.1650







































































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Chain	Atom inclusion	Q-score
Bu	 0.8960	 0.1400
Bv	 0.8650	 0.1460
Bw	 0.8650	 0.1180
Bx	 0.8460	 0.1460
By	 0.8970	 0.1590
Bz	 0.8320	 0.1490
C0	 0.8320	 0.1070
C1	 0.0000	 0.0300
C2	 0.9350	 0.1800
C3	 0.9200	 0.1710
C4	 0.9230	 0.1580
C5	 0.9580	 0.1710
C6	 0.9090	 0.1650
C7	 0.8780	 0.1600
C8	 0.8820	 0.1660
C9	 0.8650	 0.1280
CA	 0.8620	 0.1670
CB	 0.6570	 0.1090
CC	 0.8320	 0.1460
CD	 0.2470	 0.0510
CE	 0.9250	 0.1660
CF	 0.9150	 0.1600
CG	 0.8040	 0.1370
CH	 0.8970	 0.1760
CI	 0.9230	 0.1710
CJ	 0.3240	 0.0600
CK	 0.8480	 0.1330
CL	 0.8840	 0.1640
CM	 0.9280	 0.1890
CN	 0.6500	 0.1250
CO	 0.8460	 0.1480
CP	 0.8510	 0.1460
CQ	 0.8120	 0.1190
CR	 0.4620	 0.0650
CS	 0.8410	 0.1460
CT	 0.8560	 0.1630
CU	 0.9000	 0.1630
CV	 0.8800	 0.1640
CW	 0.9480	 0.1740
CX	 0.7900	 0.1210
CY	 0.5070	 0.0830
CZ	 0.8880	 0.1460

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Chain	Atom inclusion	Q-score
Ca	 0.9060	 0.1390
Cb	 0.9390	 0.1670
Cc	 0.7940	 0.1270
Cd	 0.9410	 0.1670
Ce	 0.8950	 0.1500
Cf	 0.8920	 0.1430
Cg	 0.9360	 0.1670
Ch	 0.9400	 0.1680
Ci	 0.9230	 0.1670
Cj	 0.9580	 0.1670
Ck	 0.9360	 0.1530
Cl	 0.9440	 0.1540
Cm	 0.9080	 0.1700
Cn	 0.8860	 0.1650
Co	 0.7450	 0.1320
Cp	 0.8380	 0.1520
Cq	 0.7240	 0.1270
Cr	 0.9150	 0.1890
Cs	 0.8640	 0.1220
Ct	 0.9170	 0.1710
Cu	 0.6530	 0.1260
Cv	 0.9490	 0.1760
Cw	 0.8900	 0.1620
Cx	 0.8850	 0.1560
Cy	 0.8740	 0.1580
Cz	 0.0000	 0.0480
DA	 0.8440	 0.1520
DB	 0.9520	 0.1760
DC	 0.8800	 0.1530
DD	 0.0000	 0.0360
DE	 0.0610	 0.0430
DF	 0.6080	 0.1130
DG	 0.7360	 0.1190
DH	 0.9390	 0.1710
DI	 0.9590	 0.1760