wwPDB EM Validation Summary Report (i)

Dec 18, 2022 – 08:49 pm GMT

PDB ID	:	7ARV
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*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.3

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 7.40 Å.

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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	• 69% 28% •
2	AB	29	14% 86% 14%
3	AC	48	• 75% 23% •
4	AD	53	62% 36% •
5	AE	60	52% 77% 20% •
6	AF	48	6% 71% 19% 10%
7	AG	48	8% 69% 25% 6%
8	AH	60	22% 85% 13% •
9	AI	42	17% 76% 21% •
10	AJ	60	25% 82% 17% •
11	AK	32	75% 19% 6%
12	AL	40	• 58% 35% 8%
13	AM	48	71% 27% •
14	AN	32	66% 34%
15	AO	48	73% 27%
16	AP	40	18% 70% 30%
17	AQ	45	9% 73% 24% •

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
18	AR	48	19% 77% 23%
19	AS	48	69% 29% •
20	AT	45	11% 69% 27% •
21	AU	48	67% 31% •
22	AV	40	62% 38%
23	AW	58	• 74% 19% 7%
24	AX	60	35% 83% 13% •
25	AY	32	72% 28%
26	AZ	48	71% 27% •
27	Aa	40	85% 15%
28	Ab	48	69% 25% 6%
29	Ac	40	60% 38% •
30	Ad	53	74% 23% •
31	Ae	40	62% 28% 10%
32	Af	32	66% 31% •
33	Ag	58	5% 76% 22% •
34	Ah	60	28% 73% 22% 5%
35	Ai	48	• 75% 21% •
36	Aj	48	69% 31%
37	Ak	32	72% 19% 9%
38	Al	48	73% 25% •
39	Am	58	• 74% 24% •
40	An	60	27% 82% 17% •
41	Ao	57	7% 75% 23% •
42	Ap	60	27% 68% 27% 5%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
43	Aq	48	69% 27% •
44	Ar	37	16% 76% 16% 8%
45	As	40	82% 15% •
46	At	44	75% 25%
47	Au	40	68% 32%
48	Av	40	68% 32%
49	Aw	56	71% 29%
50	Ax	40	55% 45%
51	Ay	48	73% 23% •
52	Az	45	• 82% 18%
53	A0	32	66% 25% 9%
54	A1	48	• 65% 33% •
55	A2	48	• 69% 19% 12%
56	A3	56	62% 27% 11%
57	A4	45	• 73% 24% •
58	A5	48	71% 27% •
59	A6	32	66% 31% •
60	A7	32	75% 22% •
61	A8	32	78% 22%
62	A9	48	67% 33%
63	BA	45	80% 18% •
64	BB	32	62% 25% 12%
65	BC	45	9% 73% 27%
66	BD	57	5% 75% 23% •
67	BE	57	28% 74% 19% 7%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
68	BF	45	7% 67% 33%
69	BG	40	65% 28% 8%
70	BH	57	7% 74% 25% •
71	BI	57	26% 70% 26% •
72	BJ	45	• 71% 29%
73	BK	32	• 72% 28%
74	BL	56	71% 29%
75	BM	32	84% 16%
76	BN	40	68% 32%
77	BO	48	63% 35% •
78	BP	58	69% 28% •
79	BQ	57	21% 72% 26% •
80	BR	48	81% 19%
81	BS	48	• 77% 15% 8%
82	BT	48	71% 25% •
83	BU	48	77% 21% •
84	BV	58	9% 81% 19%
85	BW	60	15% 68% 28% •
86	BX	32	72% 22% 6%
87	BY	40	62% 32% 5%
88	BZ	40	60% 38% •
89	Ba	48	• 71% 21% 8%
90	Bb	48	52% 40% 8%
91	Bc	32	• 75% 22% •
92	Bd	48	75% 25%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
93	Be	48	73% 23% •
94	Bf	48	73% 25% •
95	Bg	40	50% 42% 8%
96	Bh	56	68% 29% •
97	Bi	40	70% 20% 10%
98	Bj	32	62% 34% •
99	Bk	32	75% 25%
100	Bl	48	73% 25% •
101	Bm	56	77% 20% •
102	Bn	48	• 77% 19% •
103	Bo	48	73% 25% •
104	Bp	40	75% 22% •
105	Bq	48	67% 33%
106	Br	48	69% 31%
107	Bs	32	75% 25%
108	Bt	40	68% 30% •
109	Bu	40	72% 28%
110	Bv	40	68% 28% 5%
111	Bw	60	• 77% 17% 7%
112	Bx	45	9% 73% 24% •
113	By	40	72% 28%
114	Bz	32	75% 25%
115	B0	60	5% 72% 28%
116	B1	60	30% 78% 17% 5%
117	B2	40	65% 30% 5%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
118	B3	32	75% 25%
119	B4	32	69% 25% 6%
120	B5	60	7% 73% 25% •
121	B6	53	8% 66% 32% •
122	B7	48	75% 25%
123	B8	32	81% 19%
124	B9	48	• 63% 31% 6%
125	CA	48	67% 31% •
126	CB	60	17% 73% 25% •
127	CC	37	11% 76% 19% 5%
128	CD	57	72% 74% 26%
129	CE	32	66% 31% •
130	CF	40	60% 38% •
131	CG	32	• 69% 28% •
132	CH	53	6% 60% 38% •
133	CI	32	75% 25%
134	CJ	57	67% 67% 28% 5%
135	CK	32	6% 69% 31%
136	CL	40	68% 30% •
137	CM	32	75% 22% •
138	CN	56	21% 80% 14% 5%
139	CO	48	• 69% 27% •
140	CP	48	• 63% 31% 6%
141	CQ	57	9% 65% 33% •
142	CR	60	52% 70% 30%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
143	CS	48	69% 29%
144	CT	56	75% 21%
145	CU	37	78% 22%
146	CV	32	75% 19% 6%
147	CW	32	62% 38%
148	CX	57	74% 25%
149	CY	60	47% 80% 18%
150	CZ	48	67% 31%
151	Ca	48	71% 27%
152	Cb	40	60% 38%
153	Cc	32	9% 59% 41%
154	Cd	40	62% 25% 12%
155	Ce	40	70% 25% 5%
156	Cf	32	69% 28%
157	Cg	40	70% 30%
158	Ch	40	68% 25% 8%
159	Ci	48	69% 31%
160	Cj	40	70% 30%
161	Ck	48	71% 29%
162	Cl	40	72% 25%
163	Cm	48	58% 40%
164	Cn	40	52% 48%
165	Co	40	15% 65% 30% 5%
166	Cp	37	8% 70% 27%
167	Cq	37	19% 86% 11%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
168	Cr	40	68% 25% 8%
169	Cs	40	68% 32%
170	Ct	45	69% 24% 7%
171	Cu	37	22% 59% 41%
172	Cv	40	65% 30% 5%
173	Cw	40	70% 30%
174	Cx	32	66% 28% 6%
175	Cy	32	69% 31%
176	Cz	32	100% 88% 12%
177	C0	57	7% 68% 30%
178	C1	57	100% 67% 30%
179	C2	32	72% 22% 6%
180	C3	48	63% 35%
181	C4	48	71% 23% 6%
182	C5	48	73% 25%
183	C6	48	67% 31%
184	C7	40	68% 30%
185	C8	48	65% 33%
186	C9	57	81% 16%
187	DA	45	11% 62% 31% 7%
188	DB	32	72% 25%
189	DC	40	60% 38%
190	DD	45	100% 71% 22% 7%
191	DE	48	94% 77% 21%
192	DF	40	28% 75% 22%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
193	DG	48	15% 73% 25%
194	DH	32	69% 25% 6%
195	DI	32	72% 28%

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
			Total	C	N	O	P		
7	AG	48	991	470	193	281	47	0	0

- Molecule 8 is a DNA chain called STAPLE STRAND.

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

- Molecule 9 is a DNA chain called STAPLE STRAND.

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

- Molecule 10 is a DNA chain called STAPLE STRAND.

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

- Molecule 11 is a DNA chain called STAPLE STRAND.

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

- Molecule 12 is a DNA chain called STAPLE STRAND.

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

- Molecule 13 is a DNA chain called STAPLE STRAND.

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

- Molecule 14 is a DNA chain called STAPLE STRAND.

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

- Molecule 15 is a DNA chain called STAPLE STRAND.

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

- Molecule 16 is a DNA chain called STAPLE STRAND.

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

- Molecule 17 is a DNA chain called STAPLE STRAND.

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

- Molecule 18 is a DNA chain called STAPLE STRAND.

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

- Molecule 19 is a DNA chain called STAPLE STRAND.

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

- Molecule 20 is a DNA chain called STAPLE STRAND.

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

- Molecule 21 is a DNA chain called STAPLE STRAND.

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

- Molecule 22 is a DNA chain called STAPLE STRAND.

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

- Molecule 23 is a DNA chain called STAPLE STRAND.

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

- Molecule 24 is a DNA chain called STAPLE STRAND.

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

- Molecule 25 is a DNA chain called STAPLE STRAND.

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

- Molecule 26 is a DNA chain called STAPLE STRAND.

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

- Molecule 27 is a DNA chain called STAPLE STRAND.

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

- Molecule 28 is a DNA chain called STAPLE STRAND.

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

- Molecule 29 is a DNA chain called STAPLE STRAND.

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

- Molecule 30 is a DNA chain called STAPLE STRAND.

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

- Molecule 31 is a DNA chain called STAPLE STRAND.

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

- Molecule 32 is a DNA chain called STAPLE STRAND.

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

- Molecule 33 is a DNA chain called STAPLE STRAND.

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

- Molecule 34 is a DNA chain called STAPLE STRAND.

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

- Molecule 35 is a DNA chain called STAPLE STRAND.

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

- Molecule 36 is a DNA chain called STAPLE STRAND.

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

- Molecule 37 is a DNA chain called STAPLE STRAND.

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

- Molecule 38 is a DNA chain called STAPLE STRAND.

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

- Molecule 39 is a DNA chain called STAPLE STRAND.

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

- Molecule 40 is a DNA chain called STAPLE STRAND.

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

- Molecule 41 is a DNA chain called STAPLE STRAND.

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

- 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
			Total	C	N	O	P		
49	Aw	56	1137	545	199	338	55	0	0

- Molecule 50 is a DNA chain called STAPLE STRAND.

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

- Molecule 51 is a DNA chain called STAPLE STRAND.

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

- Molecule 52 is a DNA chain called STAPLE STRAND.

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

- Molecule 53 is a DNA chain called STAPLE STRAND.

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

- Molecule 54 is a DNA chain called STAPLE STRAND.

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

- Molecule 55 is a DNA chain called STAPLE STRAND.

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

- Molecule 56 is a DNA chain called STAPLE STRAND.

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

- Molecule 57 is a DNA chain called STAPLE STRAND.

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

- Molecule 58 is a DNA chain called STAPLE STRAND.

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

- Molecule 59 is a DNA chain called STAPLE STRAND.

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

- Molecule 60 is a DNA chain called STAPLE STRAND.

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

- Molecule 61 is a DNA chain called STAPLE STRAND.

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

- Molecule 62 is a DNA chain called STAPLE STRAND.

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

- 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
			Total	C	N	O	P		
70	BH	57	1156	564	177	359	56	0	0

- Molecule 71 is a DNA chain called STAPLE STRAND.

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

- Molecule 72 is a DNA chain called STAPLE STRAND.

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

- Molecule 73 is a DNA chain called STAPLE STRAND.

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

- Molecule 74 is a DNA chain called STAPLE STRAND.

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

- Molecule 75 is a DNA chain called STAPLE STRAND.

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

- Molecule 76 is a DNA chain called STAPLE STRAND.

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

- Molecule 77 is a DNA chain called STAPLE STRAND.

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

- Molecule 78 is a DNA chain called STAPLE STRAND.

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

- Molecule 79 is a DNA chain called STAPLE STRAND.

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

- Molecule 80 is a DNA chain called STAPLE STRAND.

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

- Molecule 81 is a DNA chain called STAPLE STRAND.

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

- Molecule 82 is a DNA chain called STAPLE STRAND.

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

- Molecule 83 is a DNA chain called STAPLE STRAND.

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

- Molecule 84 is a DNA chain called STAPLE STRAND.

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

- Molecule 85 is a DNA chain called STAPLE STRAND.

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

- Molecule 86 is a DNA chain called STAPLE STRAND.

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

- Molecule 87 is a DNA chain called STAPLE STRAND.

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

- Molecule 88 is a DNA chain called STAPLE STRAND.

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

- Molecule 89 is a DNA chain called STAPLE STRAND.

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

- Molecule 90 is a DNA chain called STAPLE STRAND.

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

- Molecule 91 is a DNA chain called STAPLE STRAND.

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

- Molecule 92 is a DNA chain called STAPLE STRAND.

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

- Molecule 93 is a DNA chain called STAPLE STRAND.

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

- Molecule 94 is a DNA chain called STAPLE STRAND.

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

- Molecule 95 is a DNA chain called STAPLE STRAND.

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

- Molecule 96 is a DNA chain called STAPLE STRAND.

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

- Molecule 97 is a DNA chain called STAPLE STRAND.

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

- Molecule 98 is a DNA chain called STAPLE STRAND.

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

- Molecule 99 is a DNA chain called STAPLE STRAND.

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

- Molecule 100 is a DNA chain called STAPLE STRAND.

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

- Molecule 101 is a DNA chain called STAPLE STRAND.

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

- Molecule 102 is a DNA chain called STAPLE STRAND.

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

- Molecule 103 is a DNA chain called STAPLE STRAND.

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

- Molecule 104 is a DNA chain called STAPLE STRAND.

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

- Molecule 105 is a DNA chain called STAPLE STRAND.

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

- Molecule 106 is a DNA chain called STAPLE STRAND.

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

- Molecule 107 is a DNA chain called STAPLE STRAND.

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

- Molecule 108 is a DNA chain called STAPLE STRAND.

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

- Molecule 109 is a DNA chain called STAPLE STRAND.

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

- Molecule 110 is a DNA chain called STAPLE STRAND.

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

- Molecule 111 is a DNA chain called STAPLE STRAND.

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

- Molecule 112 is a DNA chain called STAPLE STRAND.

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

- Molecule 113 is a DNA chain called STAPLE STRAND.

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

- Molecule 114 is a DNA chain called STAPLE STRAND.

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

- Molecule 115 is a DNA chain called STAPLE STRAND.

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

- Molecule 116 is a DNA chain called STAPLE STRAND.

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

- Molecule 117 is a DNA chain called STAPLE STRAND.

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

- Molecule 118 is a DNA chain called STAPLE STRAND.

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

- Molecule 119 is a DNA chain called STAPLE STRAND.

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

- Molecule 120 is a DNA chain called STAPLE STRAND.

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

- Molecule 121 is a DNA chain called STAPLE STRAND.

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

- Molecule 122 is a DNA chain called STAPLE STRAND.

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

- Molecule 123 is a DNA chain called STAPLE STRAND.

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

- Molecule 124 is a DNA chain called STAPLE STRAND.

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

- Molecule 125 is a DNA chain called STAPLE STRAND.

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

- 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
			Total	C	N	O	P		
133	CI	32	646	314	109	192	31	0	0

- Molecule 134 is a DNA chain called STAPLE STRAND.

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

- Molecule 135 is a DNA chain called STAPLE STRAND.

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

- Molecule 136 is a DNA chain called STAPLE STRAND.

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

- Molecule 137 is a DNA chain called STAPLE STRAND.

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

- Molecule 138 is a DNA chain called STAPLE STRAND.

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

- Molecule 139 is a DNA chain called STAPLE STRAND.

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

- Molecule 140 is a DNA chain called STAPLE STRAND.

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

- Molecule 141 is a DNA chain called STAPLE STRAND.

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

- Molecule 142 is a DNA chain called STAPLE STRAND.

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

- Molecule 143 is a DNA chain called STAPLE STRAND.

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

- Molecule 144 is a DNA chain called STAPLE STRAND.

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

- Molecule 145 is a DNA chain called STAPLE STRAND.

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

- Molecule 146 is a DNA chain called STAPLE STRAND.

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

- Molecule 147 is a DNA chain called STAPLE STRAND.

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

- Molecule 148 is a DNA chain called STAPLE STRAND.

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

- Molecule 149 is a DNA chain called STAPLE STRAND.

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

- Molecule 150 is a DNA chain called STAPLE STRAND.

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

- Molecule 151 is a DNA chain called STAPLE STRAND.

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

- Molecule 152 is a DNA chain called STAPLE STRAND.

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

- Molecule 153 is a DNA chain called STAPLE STRAND.

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

- 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
			Total	C	N	O	P		
161	Ck	48	985	474	171	293	47	0	0

- Molecule 162 is a DNA chain called STAPLE STRAND.

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

- Molecule 163 is a DNA chain called STAPLE STRAND.

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

- Molecule 164 is a DNA chain called STAPLE STRAND.

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

- Molecule 165 is a DNA chain called STAPLE STRAND.

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

- Molecule 166 is a DNA chain called STAPLE STRAND.

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

- Molecule 167 is a DNA chain called STAPLE STRAND.

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

- 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
			Total	C	N	O	P		
189	DC	40	832	395	178	220	39	0	0

- Molecule 190 is a DNA chain called STAPLE STRAND.

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

- Molecule 191 is a DNA chain called STAPLE STRAND.

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

- Molecule 192 is a DNA chain called STAPLE STRAND.

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

- Molecule 193 is a DNA chain called STAPLE STRAND.

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

- Molecule 194 is a DNA chain called STAPLE STRAND.

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

- Molecule 195 is a DNA chain called STAPLE STRAND.

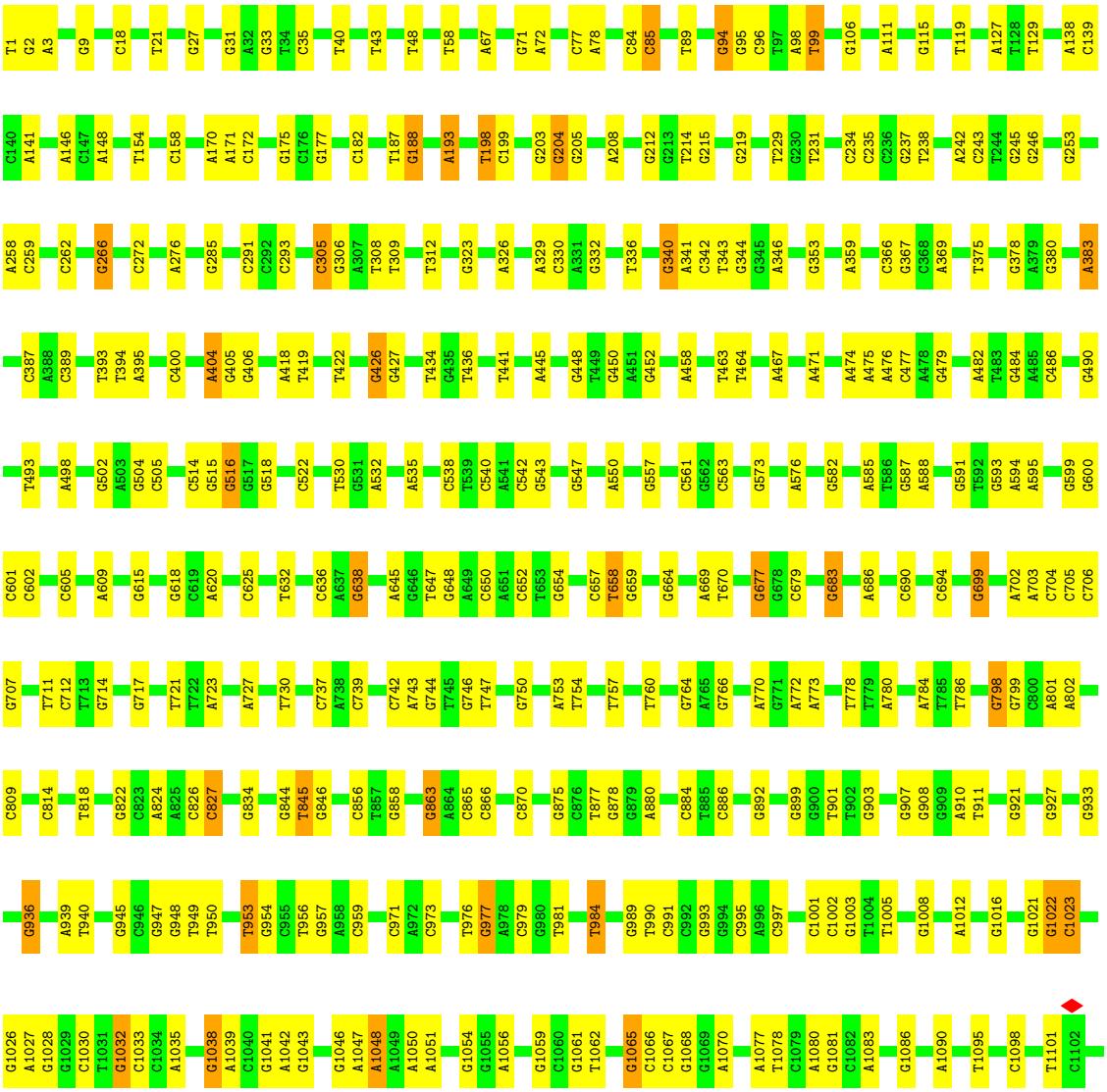
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
195	DI	32	653	314	118	190	31	0	0

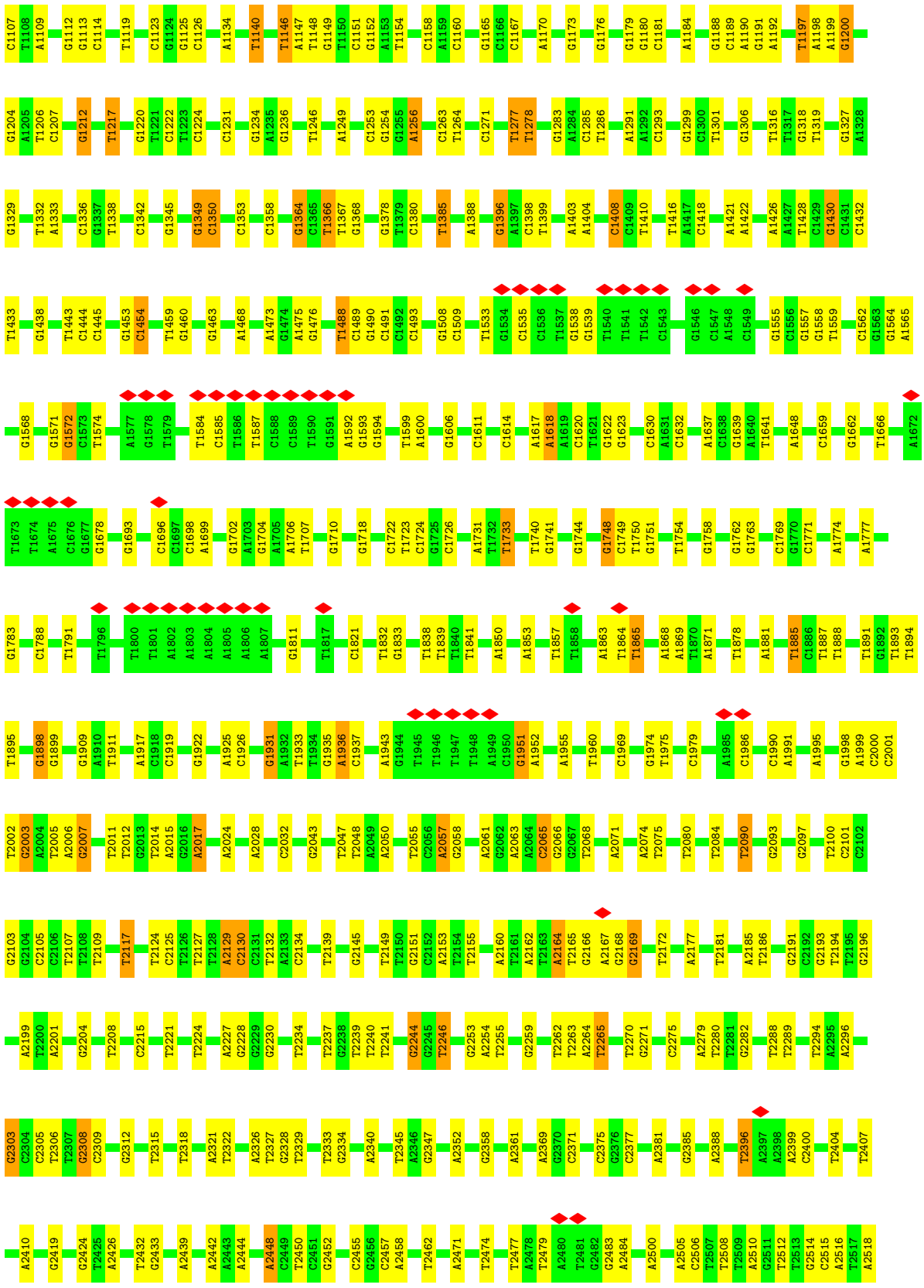
3 Residue-property plots (i)

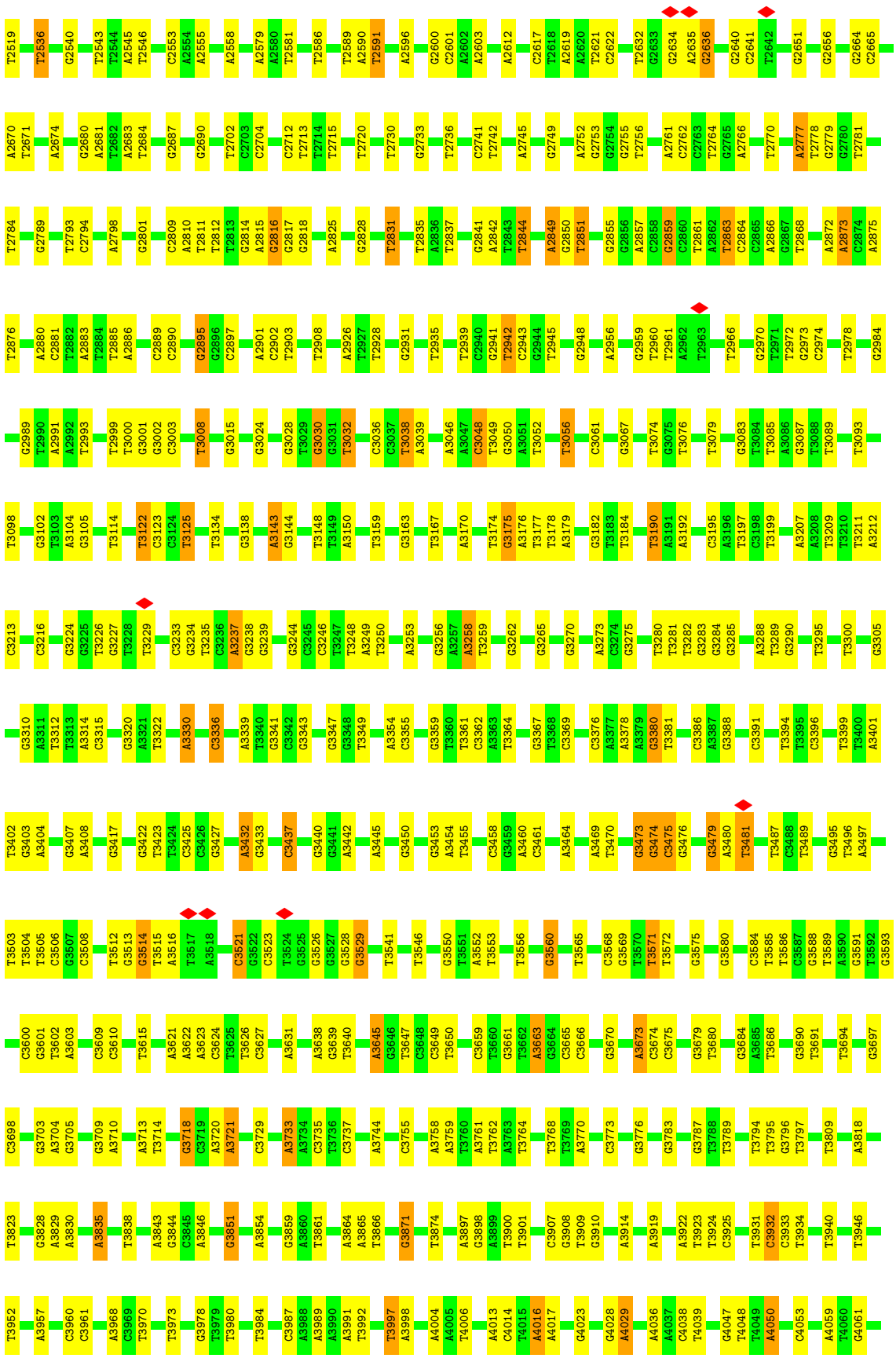
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

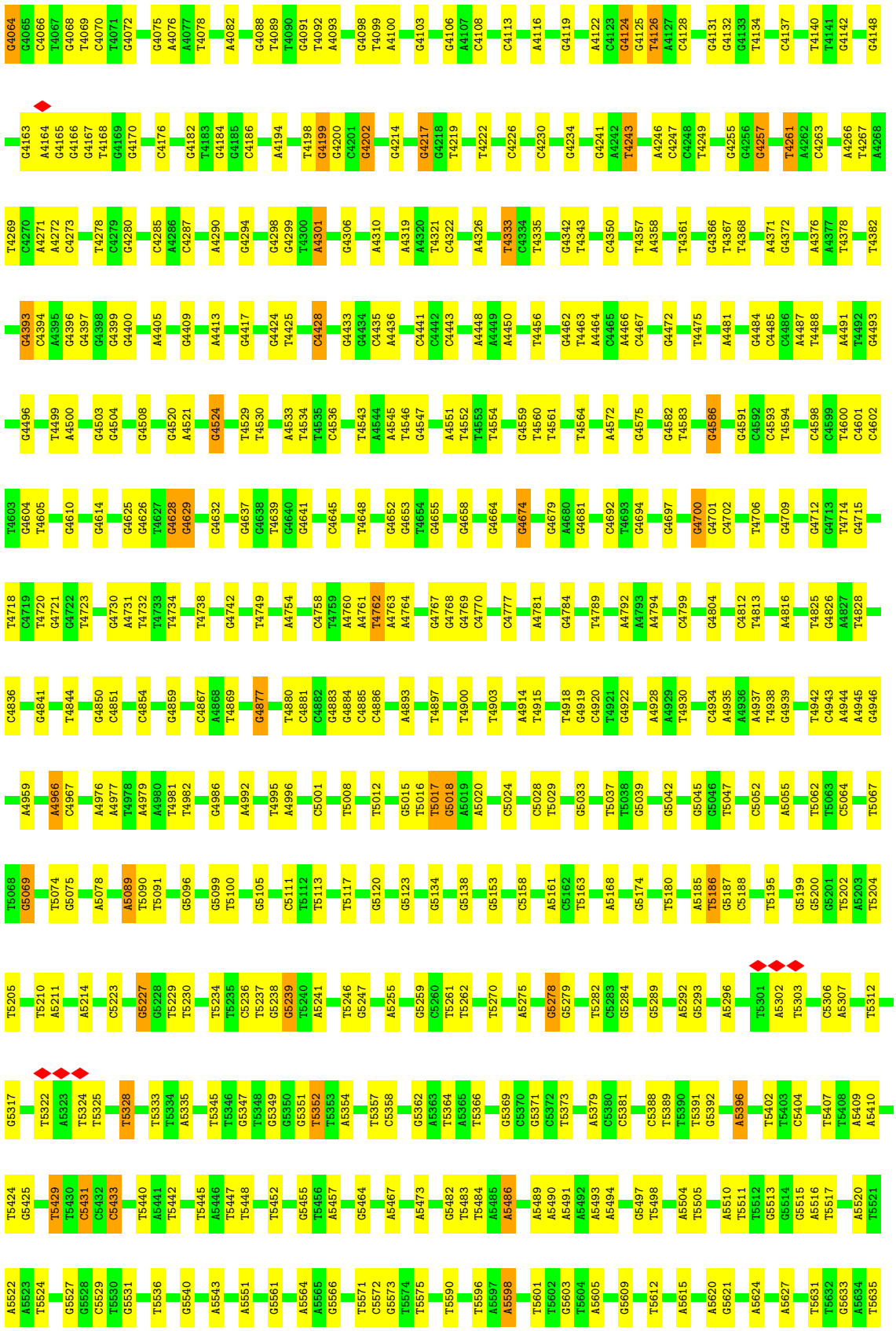
- Molecule 1: SCAFFOLD STRAND

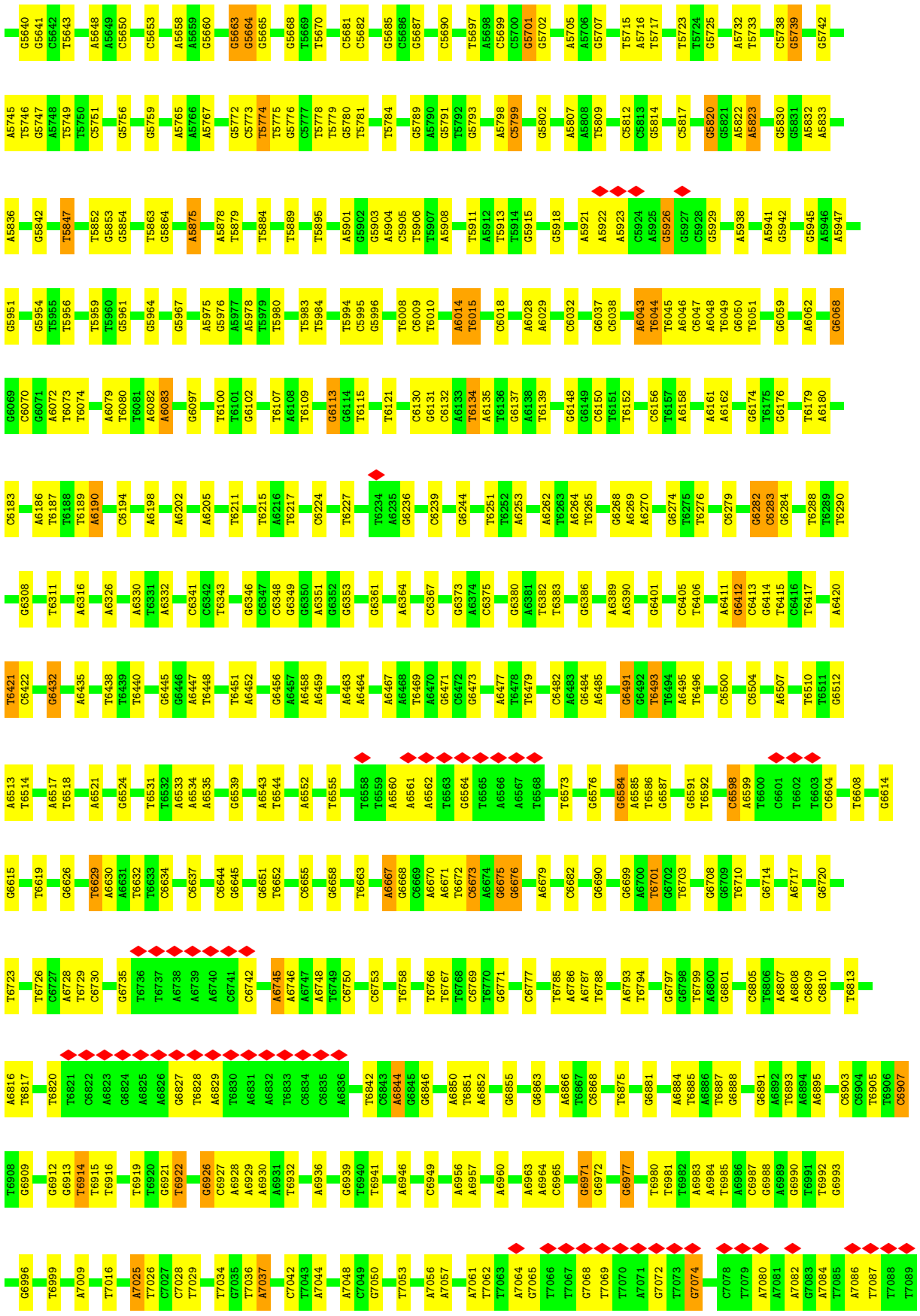
Chain AA:

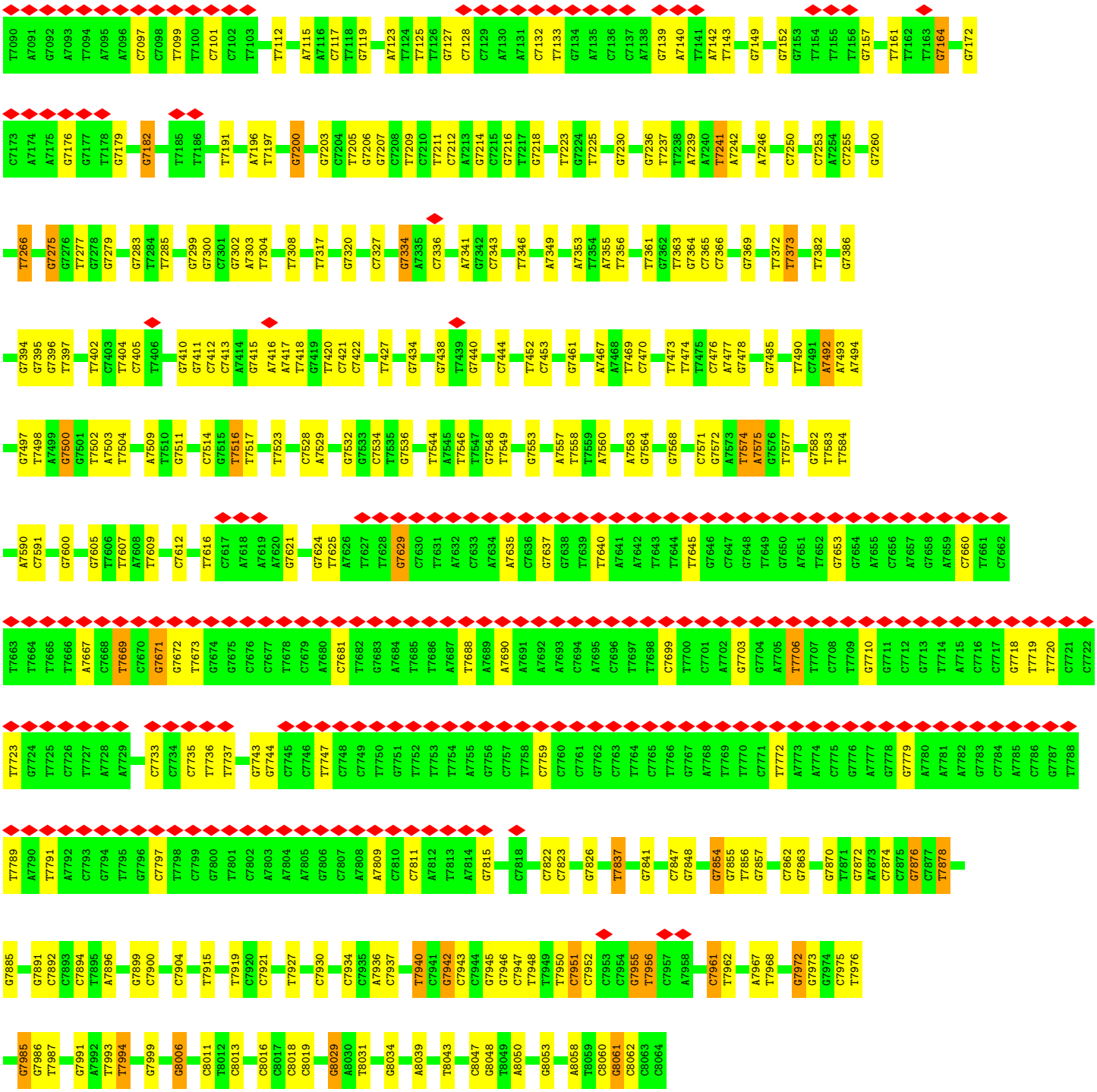



C1107 T1108 A1109 G1112 G1113 C1114 T1119 C1123 G1124 G1125 C1126 A1134 T1140 T1146 A1147 T1148 G1149 T1150 C1151 G1152 A1153 T1154 C1158 A1159 C1160 G1165 C1166 C1167 A1170 G1173 G1176 G1179 G1180 C1181 A1184 G1188 C1189 A1190 G1191 A1192 T1197 A1198 A1199 G1200
G1204 A1205 T1206 C1207 G1212 T1217 G1220 T1221 C1222 T1223 C1224 C1231 G1234 A1235 G1236 T1246 A1249 C1253 G1254 G1255 A1256 C1263 T1264 C1271 T1277 T1278 G1283 A1284 C1285 T1286 A1291 A1292 C1293 G1299 C1300 T1301 G1306 T1316 T1317 G1318 T1319 G1327 A1328
G1329 T1332 A1333 C1336 G1337 T1338 C1342 G1345 G1349 C1350 C1353 C1358 G1364 C1365 T1366 T1367 G1368 G1378 T1379 C1380 T1385 A1388 G1396 A1397 C1398 T1399 A1403 A1404 C1408 C1409 T1410 T1416 A1417 C1418 A1421 A1422 A1426 A1427 T1428 G1429 G1430 C1431 C1432
T1433 G1438 T1443 C1444 C1445 G1453 C1454 T1459 G1460 G1463 A1468 A1473 G1474 A1475 G1476 T1488 C1489 G1490 C1491 C1492 C1493 G1508 C1509 T1533 G1534 C1535 C1536 T1537 G1538 G1539 T1540 T1541 T1542 C1543 G1546 C1547 A1548 C1549 G1555 C1556 G1557 G1558 T1559 C1562 G1563 G1564 A1565
G1568 G1571 G1572 C1573 T1574 A1577 G1578 T1579 T1584 C1585 T1586 T1587 C1588 C1589 T1590 G1591 A1592 G1593 G1594 T1599 A1600 G1606 C1611 C1614 A1617 A1618 A1619 C1620 T1621 G1622 G1623 C1630 A1631 C1632 A1637 C1638 G1639 A1640 T1641 A1648 C1659 G1662 T1666 A1672
T1673 T1674 A1675 C1676 G1677 G1678 G1693 C1696 C1697 C1698 A1699 G1702 A1703 G1704 A1705 A1706 T1707 G1710 G1718 C1722 T1723 C1724 G1725 C1726 A1731 T1732 T1733 T1740 G1741 G1744 G1748 C1749 T1750 G1751 T1754 G1758 G1762 G1763 C1769 G1770 C1771 A1774 A1777
G1783 C1788 T1791 T1796 T1800 T1801 A1802 A1803 A1804 A1805 A1806 A1807 G1811 T1817 C1821 T1832 G1833 T1838 T1839 T1840 T1841 A1850 A1853 T1857 T1858 A1863 T1864 T1865 A1868 A1869 T1870 A1871 T1878 A1881 T1885 C1886 T1887 T1888 T1891 G1892 T1893 T1894
T1895 G1898 G1899 G1909 A1910 T1911 A1917 C1918 C1919 G1922 A1925 C1926 G1931 A1932 T1933 T1934 G1935 A1936 C1937 A1943 G1944 T1945 T1946 T1947 T1948 A1949 C1950 G1951 A1952 A1955 T1960 C1969 G1974 T1975 C1979 A1985 C1986 C1990 A1991 A1995 G1998 A1999 C2000 C2001
T2002 G2003 A2004 T2005 A2006 G2007 T2011 T2012 G2013 T2014 A2015 G2016 A2017 A2024 A2028 C2032 G2043 T2047 T2048 A2049 A2050 T2055 C2056 A2057 G2058 A2061 G2062 A2063 A2064 C2065 G2066 G2067 T2068 A2071 A2074 T2075 T2080 T2084 T2090 G2093 G2097 T2100 C2101 C2102
G2103 G2104 C2105 C2106 T2107 T2108 T2109 T2117 T2124 C2125 T2126 T2127 T2128 A2129 C2130 C2131 T2132 A2133 C2134 T2139 G2145 T2149 T2150 G2151 C2152 A2153 T2154 T2155 A2160 T2161 A2162 T2163 A2164 T2165 G2166 A2167 G2168 G2169 T2172 A2177 T2181 A2185 T2186 G2191 C2192 G2193 T2194 T2195 G2196
A2199 T2200 A2201 G2204 T2208 C2215 T2221 T2224 A2227 G2228 G2229 G2230 T2234 T2237 G2238 T2239 T2240 T2241 G2244 G2245 T2246 G2253 A2254 T2255 G2259 T2262 T2263 A2264 T2265 T2270 G2271 C2275 A2279 T2280 T2281 G2282 T2288 T2289 T2294 A2295 A2296
G2303 C2304 C2305 T2306 T2307 G2308 C2309 G2312 T2315 T2318 A2321 T2322 A2326 T2327 G2328 T2329 T2333 G2334 A2340 T2345 A2346 G2347 A2352 G2358 A2361 A2369 G2370 C2371 C2375 G2376 C2377 A2381 G2385 A2388 T2396 A2397 A2398 A2399 C2400 T2404 T2407
A2410 G2419 G2424 T2425 A2426 T2432 G2433 A2439 A2442 A2443 A2444 A2448 C2449 T2450 C2451 G2452 C2455 G2456 C2457 A2458 T2462 A2471 T2474 T2477 A2478 T2479 A2480 T2481 G2482 G2483 A2484 A2500 A2505 C2506 T2507 T2508 T2509 A2510 G2511 T2512 T2513 G2514 C2515 A2516 T2517 A2518


T2519 T2536 G2540 T2543 T2544 A2545 T2546 C2553 A2554 A2555 A2558 A2579 A2580 T2581 T2586 T2589 A2590 T2591 A2596 G2600 C2601 A2602 A2603 A2612 C2617 T2618 A2619 A2620 T2621 C2622 T2632 G2633 G2634 A2635 G2636 G2640 C2641 T2642 G2651 G2656 G2664 C2665
A2670 T2671 A2674 G2680 A2681 T2682 A2683 T2684 G2687 G2690 T2702 C2703 C2704 C2712 T2713 T2714 T2715 T2720 T2730 G2733 T2736 C2741 T2742 A2745 G2749 A2752 G2753 G2754 G2755 T2756 A2761 C2762 C2763 T2764 G2765 A2766 T2770 A2777 T2778 G2779 G2780 T2781
T2784 G2789 T2793 C2794 A2798 G2801 C2809 A2810 T2811 T2812 T2813 G2814 A2815 G2816 G2817 G2818 A2825 G2828 T2831 T2835 A2836 T2837 G2841 A2842 T2843 T2844 A2849 G2850 T2851 G2855 G2856 A2857 C2858 G2859 C2860 T2861 A2862 T2863 C2864 C2865 A2866 G2867 T2868 A2872 A2873 C2874 A2875
T2876 A2880 C2881 T2882 A2883 T2884 T2885 A2886 C2889 C2890 G2895 G2896 C2897 A2901 C2902 T2903 T2908 A2926 T2927 T2928 G2931 T2935 T2939 C2940 G2941 T2942 C2943 G2944 T2945 G2948 A2956 G2959 T2960 T2961 A2962 T2963 T2966 G2970 T2971 T2972 G2973 C2974 T2978 G2984
G2989 T2990 A2991 A2992 T2993 T2999 T3000 G3001 G3002 C3003 T3008 G3015 G3024 G3028 T3029 G3030 G3031 T3032 C3036 C3037 T3038 A3039 A3046 A3047 C3048 T3049 G3050 A3051 T3052 T3056 C3061 G3067 T3074 G3075 T3076 T3079 G3083 T3084 T3085 A3086 G3087 T3088 T3089 T3093
T3098 G3102 T3103 A3104 G3105 T3114 T3122 C3123 C3124 T3125 T3134 G3138 A3143 G3144 T3148 T3149 A3150 T3159 G3163 T3167 A3170 T3174 G3175 A3176 T3177 T3178 A3179 G3182 T3183 T3184 T3190 A3191 A3192 C3195 A3196 T3197 C3198 T3199 A3207 A3208 T3209 T3210 T3211 A3212
C3213 C3216 G3224 G3225 T3226 G3227 T3228 T3229 C3233 G3234 T3235 C3236 A3237 G3238 G3239 G3244 C3245 C3246 T3247 T3248 A3249 T3250 A3253 G3256 A3257 A3258 T3259 G3262 G3265 G3270 A3273 C3274 G3275 T3280 T3281 T3282 G3283 G3284 G3285 A3288 T3289 G3290 T3295 T3300 G3305
G3310 A3311 T3312 T3313 A3314 C3315 G3320 A3321 T3322 A3330 C3336 A3339 T3340 G3341 C3342 G3343 G3347 G3348 T3349 A3354 C3355 G3359 T3360 T3361 C3362 A3363 T3364 G3367 T3368 C3369 C3376 A3377 A3378 A3379 G3380 T3381 C3386 A3387 G3388 C3391 T3394 T3395 C3396 T3399 T3400 A3401
T3402 G3403 A3404 G3407 A3408 G3417 G3422 T3423 T3424 C3425 C3426 G3427 A3432 G3433 C3437 G3440 G3441 A3442 A3445 G3450 G3453 A3454 T3455 C3458 G3459 A3460 C3461 A3464 A3469 T3470 G3473 G3474 C3475 G3476 G3479 A3480 T3481 T3487 C3488 T3489 G3495 T3496 A3497
T3503 T3504 T3505 C3506 G3507 C3508 T3512 G3513 G3514 T3515 A3516 T3517 A3518 C3521 G3522 C3523 T3524 G3525 G3526 G3527 G3528 G3529 T3541 T3546 G3550 T3551 A3552 T3553 T3556 G3560 T3565 C3568 G3569 T3570 T3571 T3572 G3575 G3580 C3584 T3585 T3586 C3587 G3588 T3589 A3590 G3591 T3592 G3593
G3600 G3601 T3602 A3603 C3609 C3610 T3615 A3621 A3622 A3623 C3624 T3625 T3626 C3627 A3631 A3638 G3639 T3640 A3645 G3646 T3647 C3648 C3649 T3650 C3659 T3660 G3661 T3662 A3663 G3664 C3665 C3666 G3670 A3673 C3674 C3675 G3679 T3680 G3684 A3685 T3686 G3690 T3691 T3694 G3697
C3698 G3703 A3704 G3705 G3709 A3710 A3713 T3714 G3718 C3719 A3720 A3721 C3729 A3733 A3734 C3735 T3736 C3737 A3744 C3755 A3758 A3759 T3760 A3761 T3762 A3763 T3764 T3768 T3769 A3770 C3773 G3776 G3783 G3787 T3788 T3789 T3794 T3795 G3796 T3797 T3809 A3818
T3823 G3828 A3829 A3830 A3835 T3838 A3843 G3844 C3845 A3846 G3851 A3854 G3859 A3860 T3861 A3864 A3865 T3866 G3871 T3874 A3897 G3898 A3899 T3900 T3901 C3907 G3908 T3909 G3910 A3914 A3919 A3922 T3923 T3924 C3925 T3931 C3932 C3933 T3934 T3940 T3946
T3952 A3957 C3960 C3961 A3968 C3969 T3970 T3973 G3978 T3979 T3980 T3984 C3987 A3988 A3989 A3990 A3991 T3992 T3997 A3998 A4004 A4005 T4006 A4013 C4014 T4015 A4016 A4017 G4023 G4028 A4029 A4036 A4037 C4038 T4039 G4047 T4048 T4049 A4050 C4053 A4059 T4060 G4061

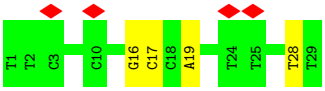

A5522 A5523 T5524 G5527 G5528 G5529 T5530 G5531 T5536 G5540 A5543 A5551 G5561 A5564 A5565 G5566 T5571 C5572 G5573 T5574 T5575 T5590 T5596 A5597 A5598 T5601 T5602 G5603 T5604 A5605 G5609 T5612 A5615 A5620 G5621 A5624 A5627 T5631 T5632 G5633 A5634 T5635
T5424 G5425 T5429 T5430 C5431 C5432 C5433 T5440 A5441 T5442 T5445 A5446 T5447 T5448 T5452 G5455 T5456 A5457 G5464 A5467 A5473 G5482 T5483 T5484 A5485 A5486 A5489 A5490 A5491 A5492 A5493 A5494 G5497 T5498 A5504 T5505 A5510 T5511 T5512 G5513 G5514 G5515 A5516 T5517 A5520 T5521
G5317 T5322 A5323 T5324 T5325 T5328 T5333 T5334 A5335 T5345 T5346 G5347 T5348 G5349 G5350 G5351 T5352 T5353 A5354 T5357 C5358 G5362 A5363 T5364 A5365 T5366 G5369 C5370 G5371 C5372 T5373 A5379 C5380 C5381 C5388 T5389 T5390 T5391 G5392 A5396 T5402 T5403 C5404 T5407 T5408 A5409 A5410
T5205 T5210 A5211 A5214 C5223 G5227 G5228 T5229 T5230 T5234 T5235 C5236 T5237 G5238 G5239 T5240 A5241 T5246 G5247 A5255 G5259 C5260 T5261 T5262 T5270 A5275 G5278 G5279 T5282 C5283 G5284 G5289 A5292 G5293 A5296 T5301 A5302 T5303 C5306 A5307 T5312
T5068 G5069 T5074 G5075 A5078 A5089 T5090 T5091 G5096 G5099 T5100 G5105 C5111 T5112 T5113 T5117 G5120 G5123 G5134 G5138 G5153 C5158 A5161 C5162 T5163 A5168 G5174 T5180 A5185 T5186 G5187 C5188 T5195 G5199 G5200 G5201 T5202 A5203 T5204
A4959 A4966 C4967 A4976 A4977 T4978 A4979 A4980 T4981 T4982 G4986 A4992 T4995 A4996 C5001 T5008 T5012 G5015 T5016 T5017 G5018 A5019 A5020 C5024 C5028 T5029 G5033 T5037 T5038 G5039 G5042 G5045 G5046 T5047 C5052 A5055 T5062 T5063 C5064 T5067
C4836 G4841 T4844 G4850 C4851 C4854 G4859 C4867 A4868 T4869 G4877 T4880 C4881 C4882 G4883 G4884 C4885 C4886 A4893 T4897 T4900 T4903 A4914 T4915 T4918 G4919 C4920 T4921 G4922 A4928 A4929 T4930 C4934 A4935 A4936 A4937 T4938 G4939 T4942 C4943 A4944 A4945 G4946
T4718 C4719 T4720 G4721 G4722 T4723 G4730 A4731 T4732 T4733 T4734 T4738 G4742 T4749 A4754 C4758 T4759 A4760 A4761 T4762 A4763 A4764 G4767 G4768 G4769 C4770 C4777 A4781 G4784 T4789 A4792 A4793 A4794 C4799 G4804 C4812 T4813 A4816 T4825 G4826 A4827 T4828
T4603 G4604 T4605 G4610 G4614 G4625 G4626 T4627 G4628 G4629 G4632 G4637 G4638 T4639 G4640 G4641 C4645 T4648 G4652 G4653 T4654 G4655 G4658 G4664 G4674 G4679 A4680 G4681 C4692 T4693 G4694 G4697 G4700 G4701 C4702 T4706 G4709 G4712 G4713 T4714 G4715
G4496 T4499 A4500 G4503 G4504 G4508 G4520 A4521 G4524 T4529 T4530 A4533 T4534 T4535 C4536 T4543 A4544 A4545 T4546 G4547 A4551 T4552 T4553 T4554 G4559 T4560 T4561 G4462 T4463 A4464 T4564 A4572 G4575 G4582 T4583 G4586 G4591 C4592 C4593 T4594 C4598 C4599 T4600 C4601 C4602
G4393 C4394 A4395 G4396 G4397 G4398 G4399 G4400 A4405 G4409 A4413 G4417 G4424 T4425 C4428 G4433 G4434 C4435 A4436 C4441 C4442 C4443 A4448 A4449 A4450 T4456 G4462 T4463 A4464 C4465 A4466 C4467 G4472 T4475 A4481 G4484 C4485 C4486 A4487 T4488 A4491 T4492 G4493
T4269 C4270 A4271 A4272 C4273 T4278 C4279 G4280 C4285 A4286 C4287 A4290 G4294 G4298 G4299 T4300 A4301 G4306 A4310 A4319 A4320 T4321 C4322 A4326 T4333 C4334 T4335 G4342 T4343 C4350 T4357 A4358 T4361 G4366 T4367 T4368 A4371 G4372 A4376 A4377 T4378 T4382
G4064 G4065 C4066 T4067 G4068 T4069 C4070 T4071 G4072 G4075 A4076 A4077 T4078 A4082 G4088 T4089 T4090 G4091 T4092 A4093 G4098 T4099 A4100 G4103 G4106 A4107 C4108 C4113 A4116 G4119 A4122 C4123 G4124 G4125 T4126 A4127 C4128 G4131 G4132 G4133 T4134 C4137 T4140 T4141 G4142 G4148
G4163 A4164 G4165 G4166 G4167 T4168 G4169 G4170 C4176 G4182 T4183 G4184 G4185 C4186 A4194 T4198 G4199 G4200 C4201 G4202 G4214 G4217 G4218 T4219 T4222 C4226 C4230 G4234 G4241 A4242 T4243 A4246 C4247 C4248 T4249 G4255 G4256 G4257 T4261 A4262 C4263 A4266 T4267 A4268


G5640 G5641 C5642 T5643 A5648 A5649 C5650 C5653 A5658 A5659 G5660 G5663 C5664 G5665 G5668 T5669 T5670 C5681 C5682 G5685 C5686 G5687 C5690 T5697 A5698 C5699 C5700 G5701 G5702 A5705 A5706 G5707 T5715 A5716 T5717 T5723 T5724 G5725 A5732 T5733 C5738 G5739 G5742
A5745 T5746 G5747 A5748 T5749 T5750 C5751 G5756 G5759 A5765 A5766 A5767 G5772 C5773 T5774 T5775 G5776 C5777 T5778 T5779 G5780 T5781 T5784 G5789 A5790 G5791 T5792 G5793 A5798 C5799 G5802 A5807 A5808 T5809 C5812 C5813 G5814 C5817 G5820 G5821 A5822 A5823 G5830 G5831 A5832 A5833
A5836 G5842 T5847 T5852 G5853 G5854 T5863 G5864 A5875 A5878 T5879 T5884 T5889 T5895 A5901 G5902 G5903 A5904 C5905 T5906 T5907 A5908 T5911 A5912 T5913 T5914 G5915 G5918 A5921 A5922 A5923 C5924 A5925 G5926 G5927 C5928 G5929 A5938 A5941 G5942 G5945 A5946 A5947
G5951 G5954 T5955 T5956 T5959 T5960 G5961 G5964 G5967 A5975 G5976 A5977 A5978 T5979 T5980 T5983 T5984 T5994 C5995 G5996 T6008 C6009 T6010 A6014 T6015 C6018 A6028 A6029 C6032 G6037 C6038 A6043 T6044 T6045 A6046 C6047 A6048 T6049 G6050 T6051 G6059 A6062 G6068
G6069 C6070 G6071 A6072 T6073 T6074 A6079 T6080 T6081 A6082 A6083 G6097 T6100 T6101 G6102 T6107 A6108 T6109 G6113 G6114 T6115 T6121 C6130 G6131 C6132 A6133 T6134 A6135 T6136 G6137 A6138 T6139 G6148 G6149 C6150 T6151 T6152 C6156 T6157 A6158 A6161 A6162 G6174 T6175 G6176 T6179 A6180
C6183 A6186 T6187 T6188 T6189 A6190 C6194 A6198 A6202 A6205 T6211 T6215 A6216 T6217 C6224 T6227 T6234 A6235 G6236 C6239 G6244 T6251 T6252 A6253 A6262 T6263 A6264 T6265 G6268 A6269 A6270 G6274 T6275 T6276 C6279 G6282 C6283 G6284 T6288 T6289 T6290
G6308 T6311 A6316 A6326 A6330 T6331 A6332 C6341 C6342 T6343 G6346 C6347 C6348 G6349 G6350 A6351 G6352 G6353 G6361 A6364 C6367 G6373 A6374 C6375 G6380 A6381 T6382 T6383 G6386 A6389 A6390 G6401 C6405 T6406 A6411 G6412 C6413 G6414 T6415 C6416 T6417 A6420
T6421 C6422 G6432 A6435 T6438 T6439 T6440 G6445 G6446 A6447 T6448 T6451 A6452 G6456 A6457 A6458 A6459 A6463 A6464 A6467 A6468 T6469 A6470 G6471 C6472 G6473 A6477 T6478 T6479 C6482 A6483 G6484 A6485 G6491 G6492 T6493 T6494 A6495 T6496 C6500 C6504 A6507 T6510 T6511 G6512
A6513 T6514 A6517 T6518 A6521 G6524 T6531 T6532 A6533 A6534 A6535 G6539 A6543 T6544 A6552 T6555 T6558 T6559 A6560 A6561 A6562 T6563 G6564 T6565 A6566 A6567 T6568 T6573 G6576 G6584 A6585 T6586 G6587 G6591 T6592 C6598 A6599 T6600 C6601 T6602 T6603 C6604 T6608 G6614
G6615 T6619 G6626 T6629 A6630 A6631 T6632 T6633 C6634 C6637 C6644 G6645 G6651 T6652 C6655 G6658 T6663 A6667 G6668 C6669 A6670 A6671 T6672 C6673 A6674 G6675 G6676 A6679 C6682 G6690 G6699 A6700 T6701 G6702 T6703 G6708 G6709 T6710 G6714 A6717 G6720
T6723 T6726 C6727 A6728 T6729 C6730 G6735 T6736 T6737 A6738 A6739 A6740 C6741 C6742 A6745 A6746 A6747 A6748 T6749 C6750 C6753 T6758 T6766 T6767 T6768 C6769 T6770 G6771 C6777 T6785 A6786 A6787 T6788 A6793 T6794 G6797 G6798 T6799 A6800 G6801 C6805 T6806 A6807 A6808 C6809 C6810 T6813
A6816 T6817 T6820 T6821 C6822 A6823 G6824 A6825 A6826 G6827 T6828 A6829 T6830 A6831 A6832 T6833 C6834 C6835 A6836 T6842 C6843 A6844 G6845 G6846 A6850 T6851 A6852 G6855 G6863 A6866 T6867 C6868 T6875 G6881 A6884 T6885 A6886 T6887 G6888 G6891 A6892 T6893 A6894 A6895 C6903 C6904 T6905 T6906 C6907
T6908 G6909 G6912 G6913 T6914 T6915 T6916 T6919 T6920 G6921 T6922 G6926 C6927 A6928 A6929 A6930 A6931 T6932 A6936 G6939 T6940 T6941 A6946 C6949 A6956 A6957 A6960 A6963 A6964 C6965 G6971 G6972 G6977 T6980 T6981 T6982 A6983 A6984 T6985 A6986 C6987 G6988 A6989 G6990 T6991 T6992 G6993
G6996 T6999 A7009 T7016 A7025 T7026 C7027 C7028 T7029 T7034 G7035 T7036 A7037 C7042 T7043 A7044 A7048 C7049 G7050 T7053 A7056 A7057 A7061 T7062 T7063 A7064 G7065 T7066 T7067 G7068 T7069 T7070 A7071 G7072 T7073 G7074 C7078 T7079 A7080 A7081 A7082 G7083 A7084 T7085 A7086 T7087 T7088 T7089



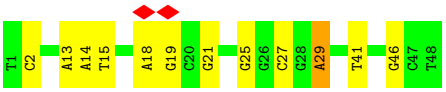
- Molecule 2: STAPLE STRAND

Chain AB:



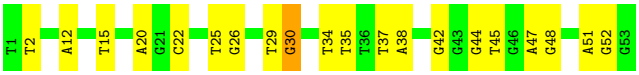
- Molecule 3: STAPLE STRAND

Chain AC:



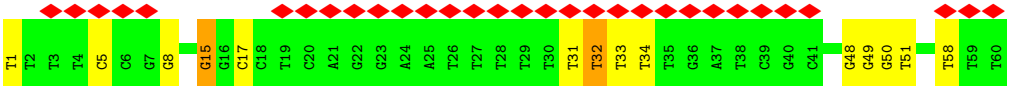
- Molecule 4: STAPLE STRAND

Chain AD:



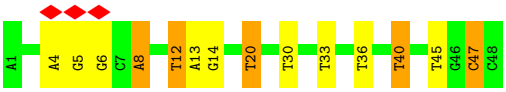
- Molecule 5: STAPLE STRAND

Chain AE:



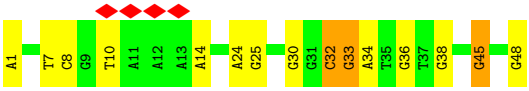
- Molecule 6: STAPLE STRAND

Chain AF:



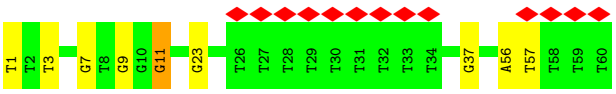
- Molecule 7: STAPLE STRAND

Chain AG:



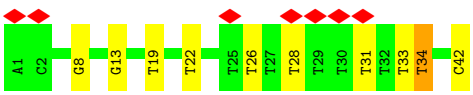
- Molecule 8: STAPLE STRAND

Chain AH:



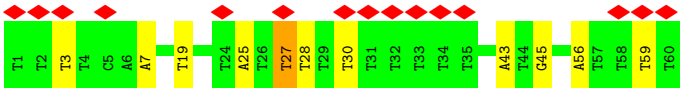
- Molecule 9: STAPLE STRAND

Chain AI:



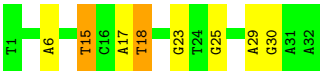
- Molecule 10: STAPLE STRAND

Chain AJ: 25% 82% 17%



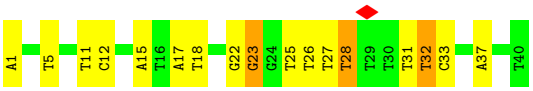
• Molecule 11: STAPLE STRAND

Chain AK: 75% 19% 6%



• Molecule 12: STAPLE STRAND

Chain AL: 58% 35% 8%

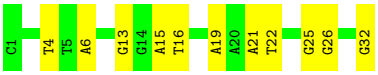


• Molecule 13: STAPLE STRAND

Chain AM: 71% 27%

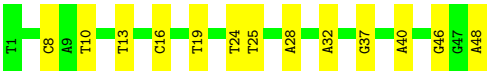
• Molecule 14: STAPLE STRAND

Chain AN: 66% 34%



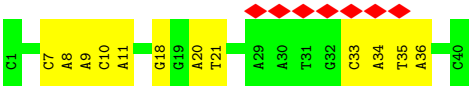
• Molecule 15: STAPLE STRAND

Chain AO: 73% 27%



• Molecule 16: STAPLE STRAND

Chain AP: 18% 70% 30%

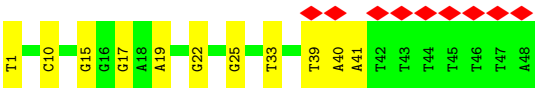


• Molecule 17: STAPLE STRAND

Chain AQ:

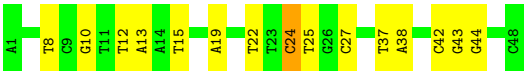
• Molecule 18: STAPLE STRAND

Chain AR:



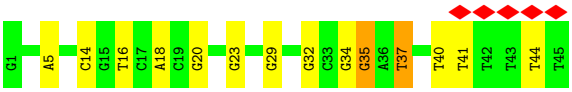
• Molecule 19: STAPLE STRAND

Chain AS:



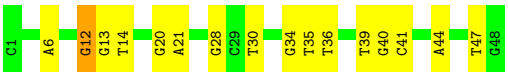
• Molecule 20: STAPLE STRAND

Chain AT:



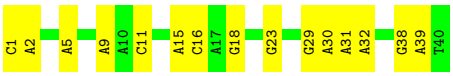
• Molecule 21: STAPLE STRAND

Chain AU:



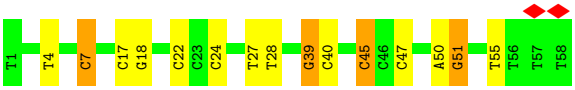
• Molecule 22: STAPLE STRAND

Chain AV:



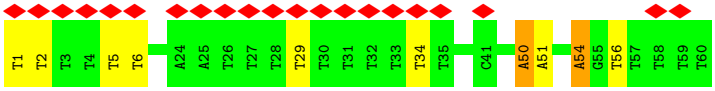
• Molecule 23: STAPLE STRAND

Chain AW:



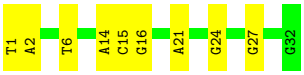
• Molecule 24: STAPLE STRAND

Chain AX: 35% 83% 13%



• Molecule 25: STAPLE STRAND

Chain AY: 72% 28%

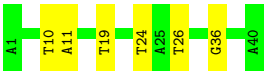


• Molecule 26: STAPLE STRAND

Chain AZ: 71% 27%

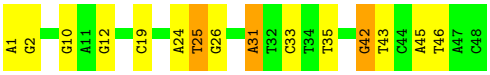
• Molecule 27: STAPLE STRAND

Chain Aa: 85% 15%



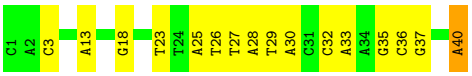
• Molecule 28: STAPLE STRAND

Chain Ab: 69% 25% 6%



• Molecule 29: STAPLE STRAND

Chain Ac: 60% 38%



• Molecule 30: STAPLE STRAND

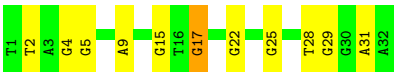
Chain Ad: 74% 23%

• Molecule 31: STAPLE STRAND

Chain Ae: 62% 28% 10%

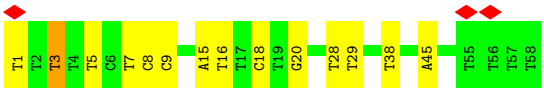
• Molecule 32: STAPLE STRAND

Chain Af:



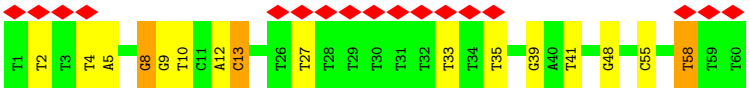
• Molecule 33: STAPLE STRAND

Chain Ag:



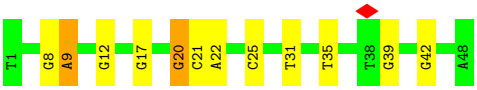
• Molecule 34: STAPLE STRAND

Chain Ah:



• Molecule 35: STAPLE STRAND

Chain Ai:



• Molecule 36: STAPLE STRAND

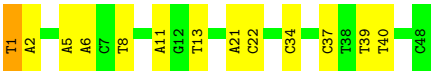
Chain Aj:

• Molecule 37: STAPLE STRAND

Chain Ak:

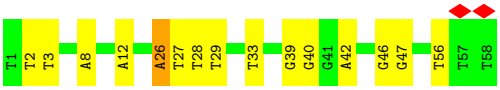
• Molecule 38: STAPLE STRAND

Chain Al:



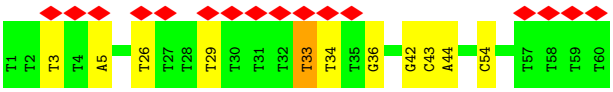
• Molecule 39: STAPLE STRAND

Chain Am:



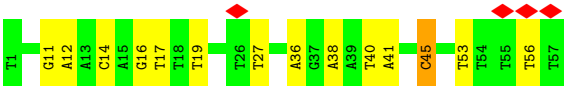
• Molecule 40: STAPLE STRAND

Chain An:



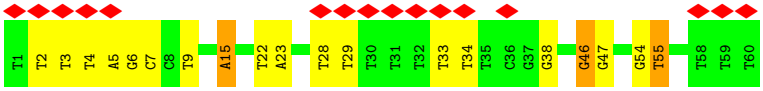
• Molecule 41: STAPLE STRAND

Chain Ao:



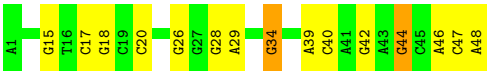
• Molecule 42: STAPLE STRAND

Chain Ap:



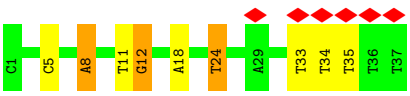
• Molecule 43: STAPLE STRAND

Chain Aq:



• Molecule 44: STAPLE STRAND

Chain Ar:



• Molecule 45: STAPLE STRAND

Chain As:

- Molecule 46: STAPLE STRAND

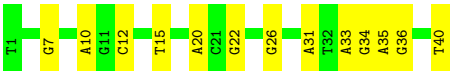
Chain At:

- Molecule 47: STAPLE STRAND

Chain Au:

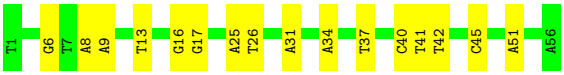
- Molecule 48: STAPLE STRAND

Chain Av:



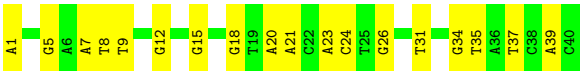
- Molecule 49: STAPLE STRAND

Chain Aw:



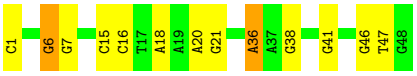
- Molecule 50: STAPLE STRAND

Chain Ax:



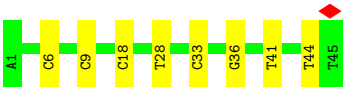
- Molecule 51: STAPLE STRAND

Chain Ay:



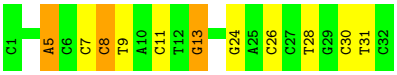
- Molecule 52: STAPLE STRAND

Chain Az:



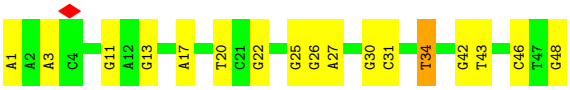
• Molecule 53: STAPLE STRAND

Chain A0:



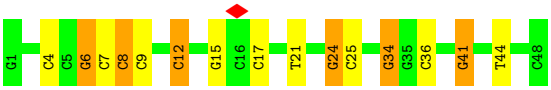
• Molecule 54: STAPLE STRAND

Chain A1:



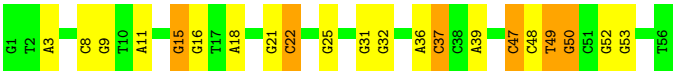
• Molecule 55: STAPLE STRAND

Chain A2:



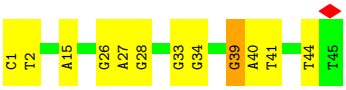
• Molecule 56: STAPLE STRAND

Chain A3:



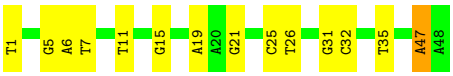
• Molecule 57: STAPLE STRAND

Chain A4:



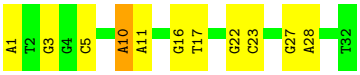
• Molecule 58: STAPLE STRAND

Chain A5:



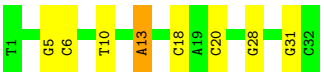
• Molecule 59: STAPLE STRAND

Chain A6:



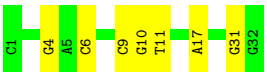
- Molecule 60: STAPLE STRAND

Chain A7:



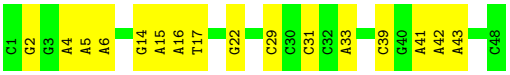
- Molecule 61: STAPLE STRAND

Chain A8:



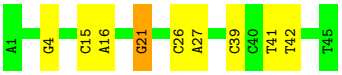
- Molecule 62: STAPLE STRAND

Chain A9:



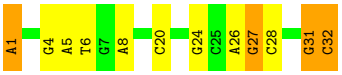
- Molecule 63: STAPLE STRAND

Chain BA:



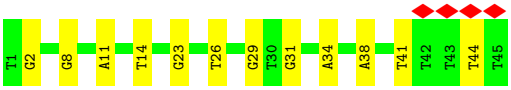
- Molecule 64: STAPLE STRAND

Chain BB:



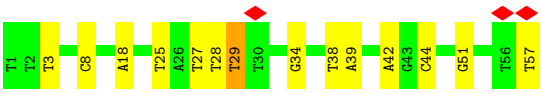
- Molecule 65: STAPLE STRAND

Chain BC:



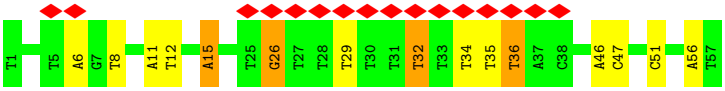
- Molecule 66: STAPLE STRAND

Chain BD:



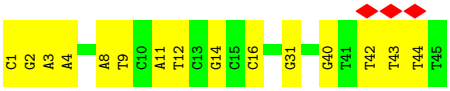
• Molecule 67: STAPLE STRAND

Chain BE:



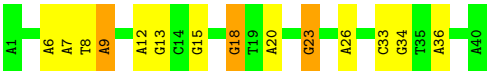
• Molecule 68: STAPLE STRAND

Chain BF:



• Molecule 69: STAPLE STRAND

Chain BG:

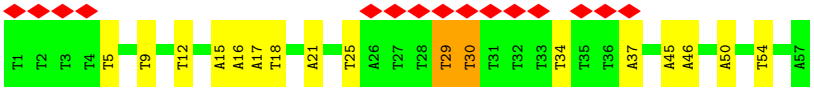


• Molecule 70: STAPLE STRAND

Chain BH:

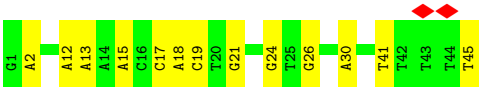
• Molecule 71: STAPLE STRAND

Chain BI:



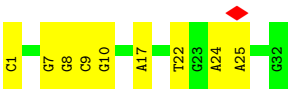
• Molecule 72: STAPLE STRAND

Chain BJ:



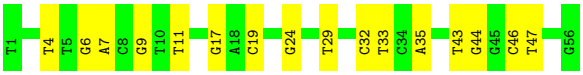
• Molecule 73: STAPLE STRAND

Chain BK:



• Molecule 74: STAPLE STRAND

Chain BL:

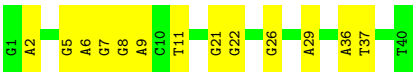


• Molecule 75: STAPLE STRAND

Chain BM:

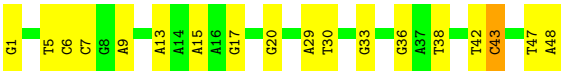
• Molecule 76: STAPLE STRAND

Chain BN:



• Molecule 77: STAPLE STRAND

Chain BO:

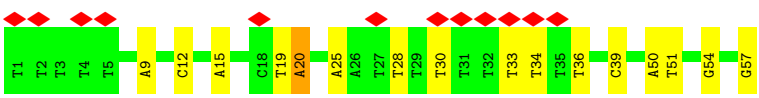


• Molecule 78: STAPLE STRAND

Chain BP:

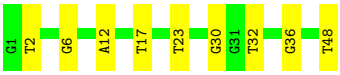
• Molecule 79: STAPLE STRAND

Chain BQ:



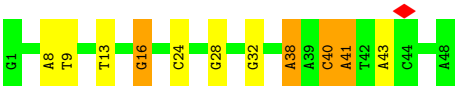
• Molecule 80: STAPLE STRAND

Chain BR:



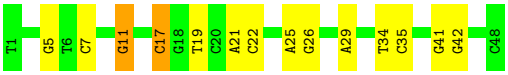
• Molecule 81: STAPLE STRAND

Chain BS:



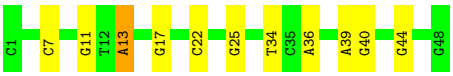
• Molecule 82: STAPLE STRAND

Chain BT:



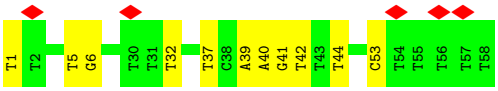
• Molecule 83: STAPLE STRAND

Chain BU:



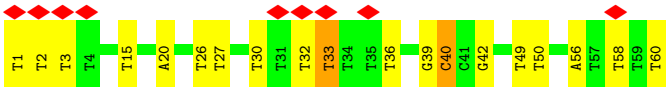
• Molecule 84: STAPLE STRAND

Chain BV:



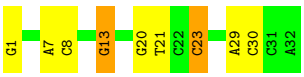
• Molecule 85: STAPLE STRAND

Chain BW:



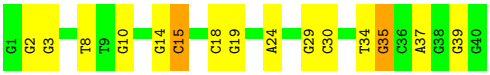
• Molecule 86: STAPLE STRAND

Chain BX:



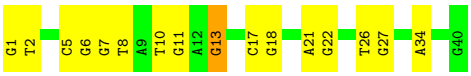
• Molecule 87: STAPLE STRAND

Chain BY:



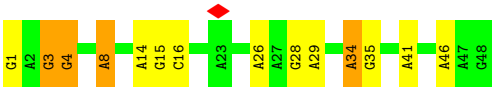
- Molecule 88: STAPLE STRAND

Chain BZ:



- Molecule 89: STAPLE STRAND

Chain Ba:

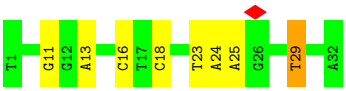


- Molecule 90: STAPLE STRAND

Chain Bb:

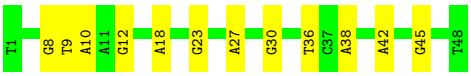
- Molecule 91: STAPLE STRAND

Chain Bc:



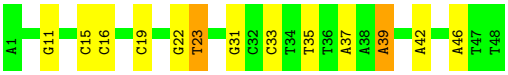
- Molecule 92: STAPLE STRAND

Chain Bd:



- Molecule 93: STAPLE STRAND

Chain Be:

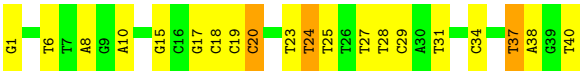


- Molecule 94: STAPLE STRAND

Chain Bf:

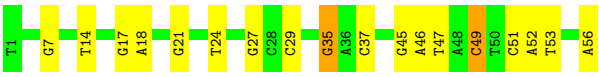
• Molecule 95: STAPLE STRAND

Chain Bg: 50% 42% 8%



• Molecule 96: STAPLE STRAND

Chain Bh: 68% 29%

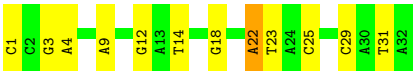


• Molecule 97: STAPLE STRAND

Chain Bi: 70% 20% 10%

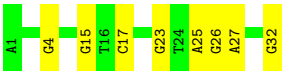
• Molecule 98: STAPLE STRAND

Chain Bj: 62% 34%



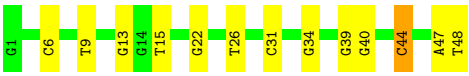
• Molecule 99: STAPLE STRAND

Chain Bk: 75% 25%



• Molecule 100: STAPLE STRAND

Chain Bl: 73% 25%

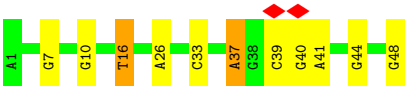


• Molecule 101: STAPLE STRAND

Chain Bm: 77% 20%

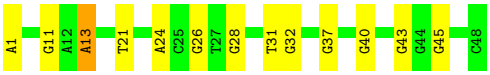
• Molecule 102: STAPLE STRAND

Chain Bn:



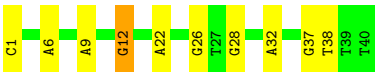
• Molecule 103: STAPLE STRAND

Chain Bo:



• Molecule 104: STAPLE STRAND

Chain Bp:

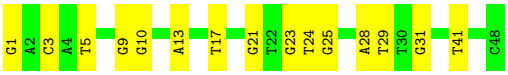


• Molecule 105: STAPLE STRAND

Chain Bq:

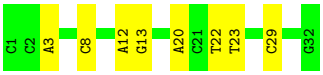
• Molecule 106: STAPLE STRAND

Chain Br:



• Molecule 107: STAPLE STRAND

Chain Bs:

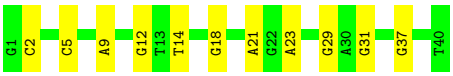


• Molecule 108: STAPLE STRAND

Chain Bt:

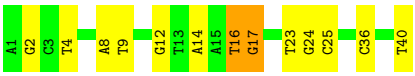
• Molecule 109: STAPLE STRAND

Chain Bu:



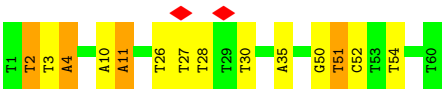
• Molecule 110: STAPLE STRAND

Chain Bv:



• Molecule 111: STAPLE STRAND

Chain Bw:

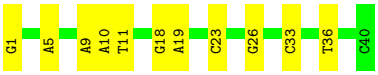


• Molecule 112: STAPLE STRAND

Chain Bx:

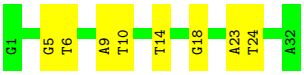
• Molecule 113: STAPLE STRAND

Chain By:



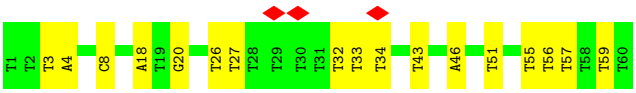
• Molecule 114: STAPLE STRAND

Chain Bz:



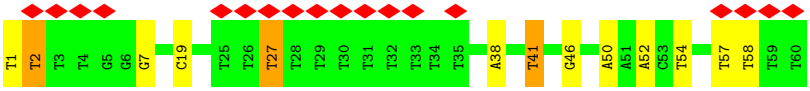
• Molecule 115: STAPLE STRAND

Chain B0:



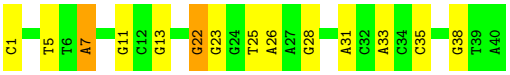
• Molecule 116: STAPLE STRAND

Chain B1:



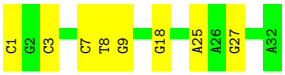
• Molecule 117: STAPLE STRAND

Chain B2:



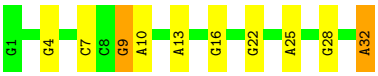
• Molecule 118: STAPLE STRAND

Chain B3:



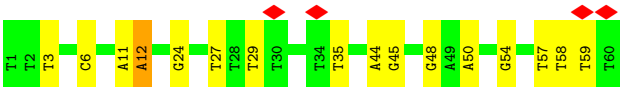
• Molecule 119: STAPLE STRAND

Chain B4:



• Molecule 120: STAPLE STRAND

Chain B5:

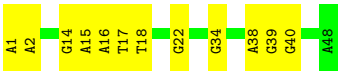


• Molecule 121: STAPLE STRAND

Chain B6:

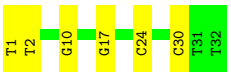
• Molecule 122: STAPLE STRAND

Chain B7:



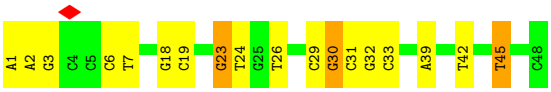
• Molecule 123: STAPLE STRAND

Chain B8:



• Molecule 124: STAPLE STRAND

Chain B9:

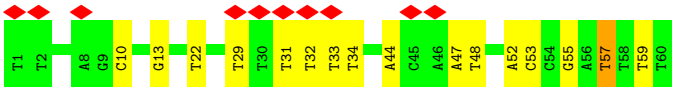


• Molecule 125: STAPLE STRAND

Chain CA:

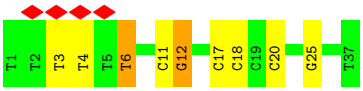
• Molecule 126: STAPLE STRAND

Chain CB:



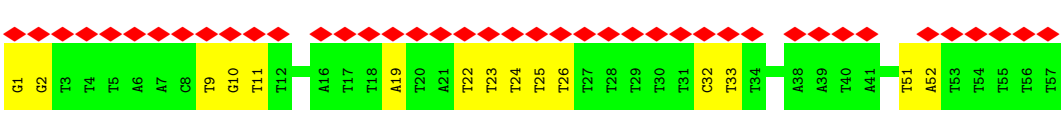
• Molecule 127: STAPLE STRAND

Chain CC:



• Molecule 128: STAPLE STRAND

Chain CD:

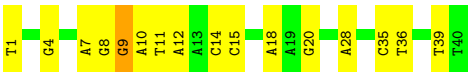


• Molecule 129: STAPLE STRAND

Chain CE:

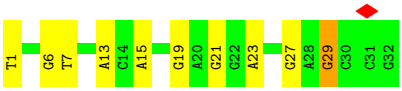
- Molecule 130: STAPLE STRAND

Chain CF:



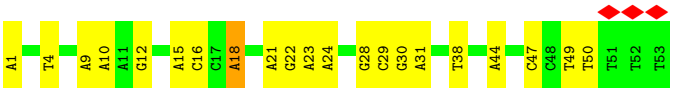
- Molecule 131: STAPLE STRAND

Chain CG:



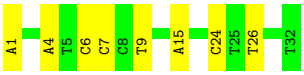
- Molecule 132: STAPLE STRAND

Chain CH:



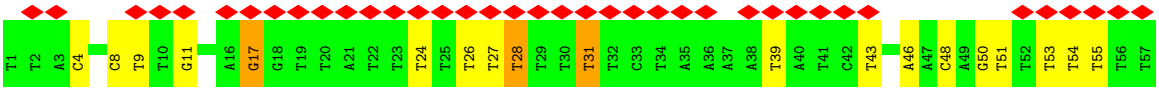
- Molecule 133: STAPLE STRAND

Chain CI:



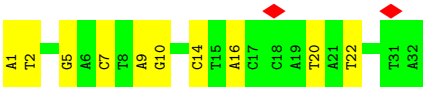
- Molecule 134: STAPLE STRAND

Chain CJ:



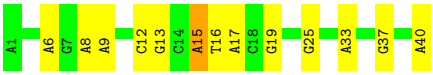
- Molecule 135: STAPLE STRAND

Chain CK:



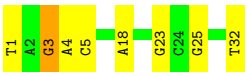
- Molecule 136: STAPLE STRAND

Chain CL:



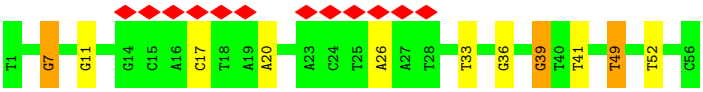
• Molecule 137: STAPLE STRAND

Chain CM:



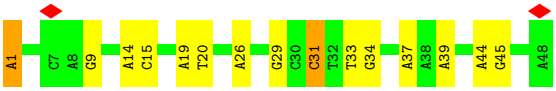
• Molecule 138: STAPLE STRAND

Chain CN:



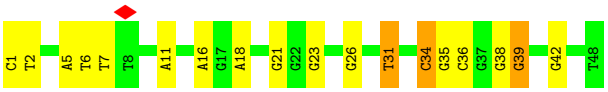
• Molecule 139: STAPLE STRAND

Chain CO:



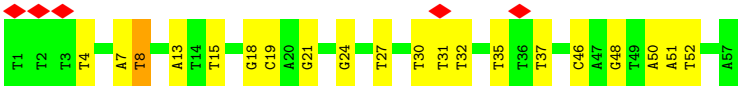
• Molecule 140: STAPLE STRAND

Chain CP:



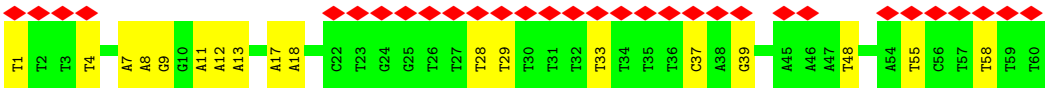
• Molecule 141: STAPLE STRAND

Chain CQ:



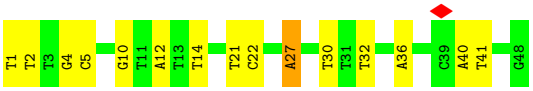
• Molecule 142: STAPLE STRAND

Chain CR:



• Molecule 143: STAPLE STRAND

Chain CS:

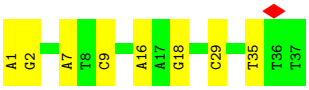


• Molecule 144: STAPLE STRAND

Chain CT: 75% 21%

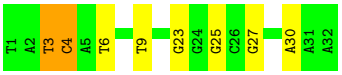
• Molecule 145: STAPLE STRAND

Chain CU: 78% 22%



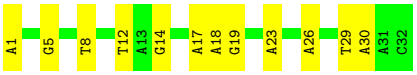
• Molecule 146: STAPLE STRAND

Chain CV: 75% 19% 6%



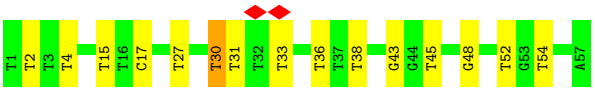
• Molecule 147: STAPLE STRAND

Chain CW: 62% 38%



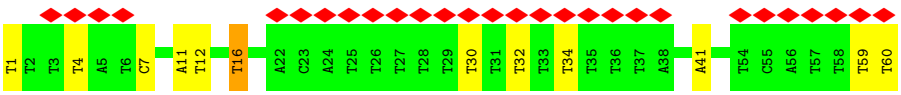
• Molecule 148: STAPLE STRAND

Chain CX: 74% 25%



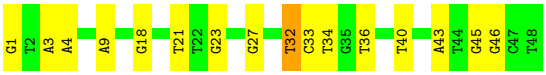
• Molecule 149: STAPLE STRAND

Chain CY: 47% 80% 18%



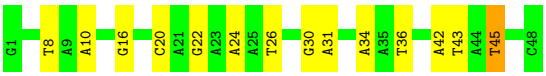
• Molecule 150: STAPLE STRAND

Chain CZ: 67% 31%



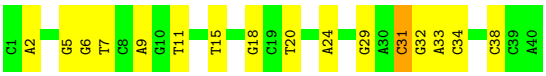
• Molecule 151: STAPLE STRAND

Chain Ca: 71% 27%



• Molecule 152: STAPLE STRAND

Chain Cb: 60% 38%

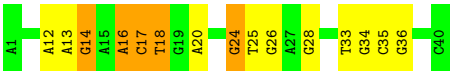


• Molecule 153: STAPLE STRAND

Chain Cc: 9% 59% 41%

• Molecule 154: STAPLE STRAND

Chain Cd: 62% 25% 12%

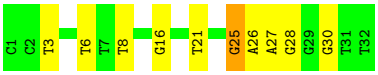


• Molecule 155: STAPLE STRAND

Chain Ce: 70% 25% 5%

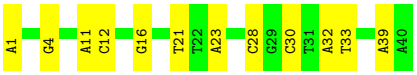
• Molecule 156: STAPLE STRAND

Chain Cf: 69% 28%



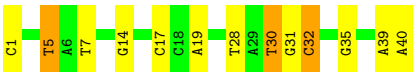
• Molecule 157: STAPLE STRAND

Chain Cg: 70% 30%



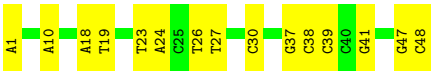
• Molecule 158: STAPLE STRAND

Chain Ch:



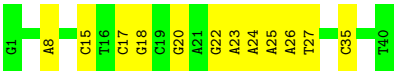
• Molecule 159: STAPLE STRAND

Chain Ci:



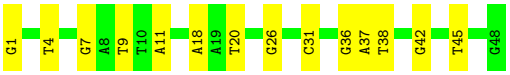
• Molecule 160: STAPLE STRAND

Chain Cj:



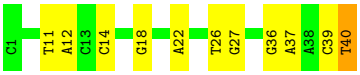
• Molecule 161: STAPLE STRAND

Chain Ck:



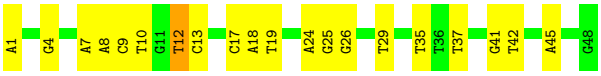
• Molecule 162: STAPLE STRAND

Chain Cl:



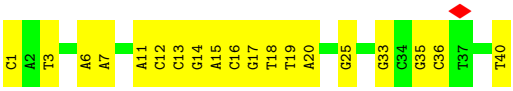
• Molecule 163: STAPLE STRAND

Chain Cm:



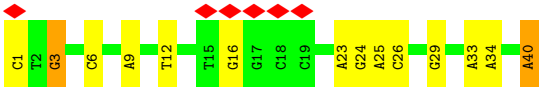
• Molecule 164: STAPLE STRAND

Chain Cn:



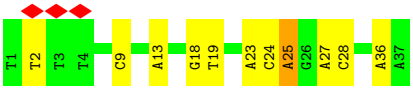
• Molecule 165: STAPLE STRAND

Chain Co:



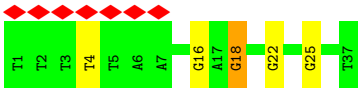
• Molecule 166: STAPLE STRAND

Chain Cp:



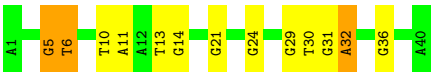
• Molecule 167: STAPLE STRAND

Chain Cq:



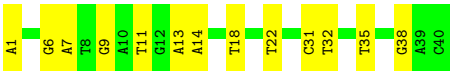
• Molecule 168: STAPLE STRAND

Chain Cr:



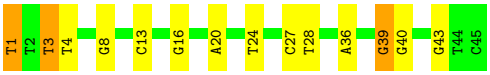
• Molecule 169: STAPLE STRAND

Chain Cs:



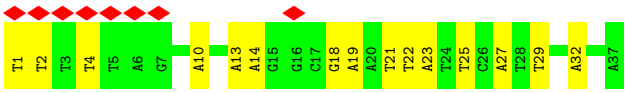
• Molecule 170: STAPLE STRAND

Chain Ct:



• Molecule 171: STAPLE STRAND

Chain Cu:



• Molecule 172: STAPLE STRAND

Chain Cv:

• Molecule 173: STAPLE STRAND

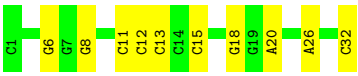
Chain Cw:

• Molecule 174: STAPLE STRAND

Chain Cx:

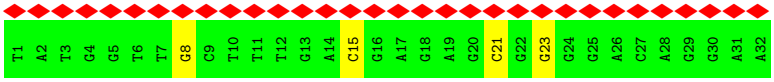
• Molecule 175: STAPLE STRAND

Chain Cy:



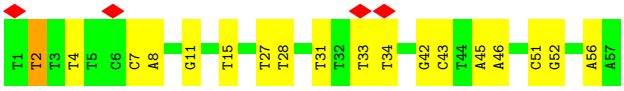
• Molecule 176: STAPLE STRAND

Chain Cz:



• Molecule 177: STAPLE STRAND

Chain C0:

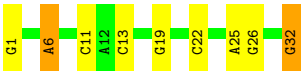


• Molecule 178: STAPLE STRAND

Chain C1:

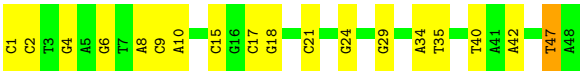
• Molecule 179: STAPLE STRAND

Chain C2:



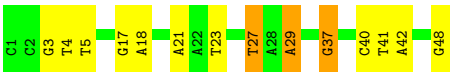
• Molecule 180: STAPLE STRAND

Chain C3:



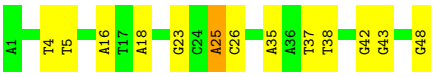
• Molecule 181: STAPLE STRAND

Chain C4:



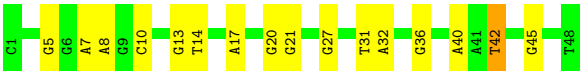
• Molecule 182: STAPLE STRAND

Chain C5:



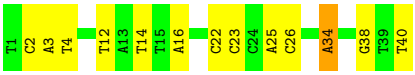
• Molecule 183: STAPLE STRAND

Chain C6:



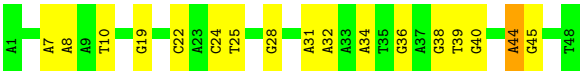
• Molecule 184: STAPLE STRAND

Chain C7:



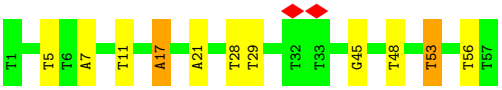
• Molecule 185: STAPLE STRAND

Chain C8:



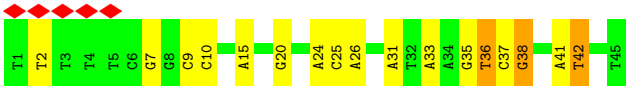
• Molecule 186: STAPLE STRAND

Chain C9:



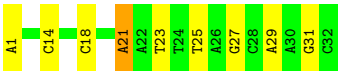
• Molecule 187: STAPLE STRAND

Chain DA:



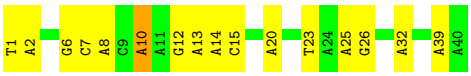
• Molecule 188: STAPLE STRAND

Chain DB:



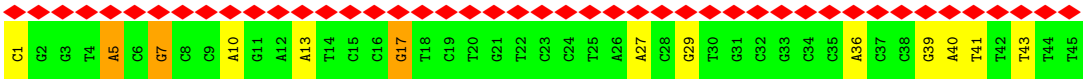
• Molecule 189: STAPLE STRAND

Chain DC:



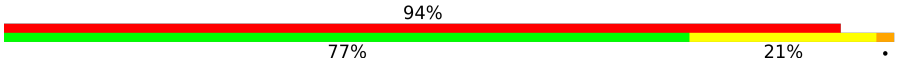
• Molecule 190: STAPLE STRAND

Chain DD:



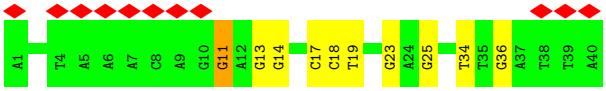
• Molecule 191: STAPLE STRAND

Chain DE:



• Molecule 192: STAPLE STRAND

Chain DF:

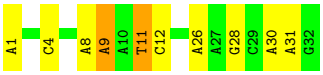


• Molecule 193: STAPLE STRAND

Chain DG:

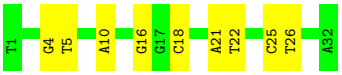
• Molecule 194: STAPLE STRAND

Chain DH:



• Molecule 195: STAPLE STRAND

Chain DI:



4 Experimental information (i)

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 ($e^-/Å^2$)	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	1.17	6/184801 (0.0%)	1.35	2299/285260 (0.8%)
2	AB	1.15	0/647	1.17	5/996 (0.5%)
3	AC	1.19	0/1104	1.35	14/1703 (0.8%)
4	AD	1.18	0/1230	1.39	17/1899 (0.9%)
5	AE	1.18	0/1358	1.39	15/2094 (0.7%)
6	AF	1.19	0/1101	1.41	18/1698 (1.1%)
7	AG	1.22	0/1115	1.37	16/1721 (0.9%)
8	AH	1.16	0/1366	1.22	10/2109 (0.5%)
9	AI	1.17	0/950	1.28	5/1464 (0.3%)
10	AJ	1.11	0/1359	1.21	9/2096 (0.4%)
11	AK	1.18	0/739	1.32	8/1140 (0.7%)
12	AL	1.14	0/911	1.35	13/1405 (0.9%)
13	AM	1.13	0/1111	1.29	9/1714 (0.5%)
14	AN	1.18	0/746	1.41	9/1151 (0.8%)
15	AO	1.12	0/1098	1.25	10/1691 (0.6%)
16	AP	1.18	0/919	1.27	8/1415 (0.6%)
17	AQ	1.13	0/1021	1.34	12/1574 (0.8%)
18	AR	1.20	1/1108 (0.1%)	1.29	9/1709 (0.5%)
19	AS	1.17	0/1112	1.24	7/1715 (0.4%)
20	AT	1.18	0/1040	1.35	14/1607 (0.9%)
21	AU	1.18	0/1095	1.34	9/1687 (0.5%)
22	AV	1.16	0/920	1.39	13/1416 (0.9%)
23	AW	1.16	0/1285	1.41	23/1975 (1.2%)
24	AX	1.15	0/1372	1.25	9/2116 (0.4%)
25	AY	1.18	0/740	1.22	5/1142 (0.4%)
26	AZ	1.17	0/1114	1.34	10/1719 (0.6%)
27	Aa	1.14	0/923	1.19	3/1425 (0.2%)
28	Ab	1.17	0/1108	1.32	14/1709 (0.8%)
29	Ac	1.20	1/911 (0.1%)	1.27	5/1402 (0.4%)
30	Ad	1.14	0/1226	1.29	16/1892 (0.8%)
31	Ae	1.20	0/934	1.51	19/1443 (1.3%)
32	Af	1.19	0/749	1.25	8/1158 (0.7%)
33	Ag	1.12	0/1308	1.24	11/2016 (0.5%)
34	Ah	1.14	0/1382	1.24	9/2134 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
35	Ai	1.20	0/1095	1.25	8/1689 (0.5%)
36	Aj	1.16	0/1084	1.34	10/1668 (0.6%)
37	Ak	1.15	0/732	1.33	10/1127 (0.9%)
38	Al	1.13	0/1103	1.25	11/1700 (0.6%)
39	Am	1.17	0/1310	1.23	9/2020 (0.4%)
40	An	1.14	0/1378	1.19	8/2128 (0.4%)
41	Ao	1.16	0/1306	1.22	7/2016 (0.3%)
42	Ap	1.17	0/1355	1.33	21/2091 (1.0%)
43	Aq	1.19	0/1105	1.31	10/1705 (0.6%)
44	Ar	1.15	0/843	1.20	6/1298 (0.5%)
45	As	1.13	0/914	1.33	11/1410 (0.8%)
46	At	1.13	0/1010	1.26	7/1556 (0.4%)
47	Au	1.15	0/920	1.39	9/1417 (0.6%)
48	Av	1.18	0/913	1.43	11/1406 (0.8%)
49	Aw	1.17	1/1272 (0.1%)	1.42	16/1960 (0.8%)
50	Ax	1.13	0/912	1.41	16/1406 (1.1%)
51	Ay	1.15	0/1115	1.35	17/1720 (1.0%)
52	Az	1.15	0/1005	1.24	3/1544 (0.2%)
53	A0	1.19	0/715	1.50	13/1099 (1.2%)
54	A1	1.18	0/1116	1.39	14/1723 (0.8%)
55	A2	1.20	1/1080 (0.1%)	1.44	21/1661 (1.3%)
56	A3	1.21	0/1294	1.43	24/1996 (1.2%)
57	A4	1.17	0/1045	1.26	10/1615 (0.6%)
58	A5	1.19	0/1115	1.35	14/1721 (0.8%)
59	A6	1.18	0/734	1.27	7/1132 (0.6%)
60	A7	1.17	0/721	1.33	8/1107 (0.7%)
61	A8	1.16	0/740	1.21	4/1141 (0.4%)
62	A9	1.20	0/1112	1.41	13/1715 (0.8%)
63	BA	1.14	0/1032	1.23	4/1589 (0.3%)
64	BB	1.18	0/742	1.35	8/1144 (0.7%)
65	BC	1.17	0/1016	1.26	9/1565 (0.6%)
66	BD	1.16	0/1289	1.38	15/1988 (0.8%)
67	BE	1.18	0/1290	1.31	13/1988 (0.7%)
68	BF	1.16	0/1018	1.36	14/1568 (0.9%)
69	BG	1.19	1/904 (0.1%)	1.41	14/1390 (1.0%)
70	BH	1.12	0/1288	1.16	2/1987 (0.1%)
71	BI	1.13	0/1292	1.27	10/1991 (0.5%)
72	BJ	1.15	0/1027	1.33	12/1584 (0.8%)
73	BK	1.19	0/734	1.36	8/1132 (0.7%)
74	BL	1.18	0/1278	1.36	17/1971 (0.9%)
75	BM	1.12	0/731	1.25	3/1124 (0.3%)
76	BN	1.17	0/940	1.29	7/1451 (0.5%)
77	BO	1.18	0/1092	1.43	16/1681 (1.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
78	BP	1.15	0/1313	1.28	11/2023 (0.5%)
79	BQ	1.13	0/1279	1.27	10/1969 (0.5%)
80	BR	1.15	0/1120	1.28	7/1730 (0.4%)
81	BS	1.16	0/1091	1.30	11/1681 (0.7%)
82	BT	1.17	0/1089	1.34	15/1677 (0.9%)
83	BU	1.16	0/1100	1.33	10/1696 (0.6%)
84	BV	1.15	0/1327	1.26	8/2048 (0.4%)
85	BW	1.17	0/1351	1.44	18/2083 (0.9%)
86	BX	1.21	0/738	1.35	7/1138 (0.6%)
87	BY	1.20	0/934	1.38	9/1444 (0.6%)
88	BZ	1.18	0/918	1.40	14/1415 (1.0%)
89	Ba	1.16	0/1132	1.32	14/1749 (0.8%)
90	Bb	1.23	0/1087	1.60	28/1673 (1.7%)
91	Bc	1.16	0/741	1.36	9/1142 (0.8%)
92	Bd	1.16	0/1120	1.36	15/1727 (0.9%)
93	Be	1.17	0/1094	1.41	16/1685 (0.9%)
94	Bf	1.15	0/1109	1.34	15/1710 (0.9%)
95	Bg	1.22	0/908	1.56	21/1399 (1.5%)
96	Bh	1.18	0/1302	1.31	16/2010 (0.8%)
97	Bi	1.14	0/898	1.39	11/1382 (0.8%)
98	Bj	1.20	0/734	1.56	13/1130 (1.2%)
99	Bk	1.12	0/742	1.35	11/1145 (1.0%)
100	Bl	1.18	0/1090	1.33	12/1679 (0.7%)
101	Bm	1.21	0/1286	1.46	15/1985 (0.8%)
102	Bn	1.17	1/1087 (0.1%)	1.36	14/1673 (0.8%)
103	Bo	1.18	0/1121	1.31	12/1730 (0.7%)
104	Bp	1.17	0/923	1.42	15/1424 (1.1%)
105	Bq	1.21	0/1102	1.35	14/1703 (0.8%)
106	Br	1.20	0/1115	1.39	15/1722 (0.9%)
107	Bs	1.16	0/735	1.28	5/1131 (0.4%)
108	Bt	1.18	0/925	1.39	14/1427 (1.0%)
109	Bu	1.16	0/921	1.31	9/1419 (0.6%)
110	Bv	1.20	0/910	1.38	11/1401 (0.8%)
111	Bw	1.13	0/1357	1.27	12/2092 (0.6%)
112	Bx	1.16	0/1030	1.35	14/1588 (0.9%)
113	By	1.18	0/928	1.36	11/1430 (0.8%)
114	Bz	1.15	0/733	1.20	3/1130 (0.3%)
115	B0	1.13	0/1348	1.30	12/2077 (0.6%)
116	B1	1.18	0/1351	1.22	5/2083 (0.2%)
117	B2	1.17	0/927	1.36	15/1429 (1.0%)
118	B3	1.17	0/749	1.19	4/1156 (0.3%)
119	B4	1.17	0/746	1.37	12/1152 (1.0%)
120	B5	1.14	0/1370	1.22	9/2112 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
121	B6	1.16	0/1207	1.31	10/1859 (0.5%)
122	B7	1.16	0/1105	1.42	15/1702 (0.9%)
123	B8	1.16	0/741	1.24	2/1142 (0.2%)
124	B9	1.18	0/1093	1.48	24/1683 (1.4%)
125	CA	1.15	0/1094	1.34	12/1686 (0.7%)
126	CB	1.13	0/1370	1.20	8/2112 (0.4%)
127	CC	1.19	0/844	1.34	7/1301 (0.5%)
128	CD	1.12	0/1293	1.27	9/1996 (0.5%)
129	CE	1.21	0/751	1.46	17/1161 (1.5%)
130	CF	1.17	0/925	1.40	12/1426 (0.8%)
131	CG	1.17	0/739	1.29	9/1140 (0.8%)
132	CH	1.16	0/1222	1.34	12/1884 (0.6%)
133	CI	1.15	0/722	1.32	5/1111 (0.5%)
134	CJ	1.12	0/1294	1.38	20/1996 (1.0%)
135	CK	1.13	0/729	1.40	11/1122 (1.0%)
136	CL	1.20	0/922	1.45	10/1420 (0.7%)
137	CM	1.16	0/749	1.23	6/1156 (0.5%)
138	CN	1.14	0/1297	1.25	10/2001 (0.5%)
139	CO	1.15	0/1101	1.37	10/1695 (0.6%)
140	CP	1.18	0/1113	1.40	15/1720 (0.9%)
141	CQ	1.16	1/1298 (0.1%)	1.31	14/2003 (0.7%)
142	CR	1.14	0/1370	1.20	5/2114 (0.2%)
143	CS	1.13	0/1080	1.28	9/1663 (0.5%)
144	CT	1.16	0/1303	1.34	17/2012 (0.8%)
145	CU	1.13	0/854	1.37	8/1316 (0.6%)
146	CV	1.17	0/737	1.34	9/1136 (0.8%)
147	CW	1.15	0/732	1.29	10/1127 (0.9%)
148	CX	1.14	0/1292	1.32	14/1994 (0.7%)
149	CY	1.13	0/1350	1.18	6/2080 (0.3%)
150	CZ	1.16	0/1099	1.37	16/1695 (0.9%)
151	Ca	1.13	0/1109	1.32	14/1708 (0.8%)
152	Cb	1.19	0/924	1.32	8/1424 (0.6%)
153	Cc	1.16	0/735	1.31	8/1133 (0.7%)
154	Cd	1.18	0/939	1.58	22/1449 (1.5%)
155	Ce	1.13	0/932	1.27	13/1440 (0.9%)
156	Cf	1.17	0/736	1.29	6/1136 (0.5%)
157	Cg	1.15	0/918	1.36	12/1414 (0.8%)
158	Ch	1.11	0/917	1.36	16/1413 (1.1%)
159	Ci	1.16	0/1088	1.33	12/1674 (0.7%)
160	Cj	1.15	0/917	1.36	9/1413 (0.6%)
161	Ck	1.17	0/1103	1.32	14/1703 (0.8%)
162	Cl	1.14	0/924	1.24	6/1424 (0.4%)
163	Cm	1.17	0/1098	1.36	12/1693 (0.7%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#|Z| >5	RMSZ	#|Z| >5
164	Cn	1.17	0/919	1.40	19/1417 (1.3%)
165	Co	1.15	0/910	1.44	15/1400 (1.1%)
166	Cp	1.15	0/843	1.34	6/1298 (0.5%)
167	Cq	1.15	0/847	1.35	6/1304 (0.5%)
168	Cr	1.18	0/936	1.37	11/1447 (0.8%)
169	Cs	1.15	0/925	1.32	10/1426 (0.7%)
170	Ct	1.15	0/1031	1.35	10/1590 (0.6%)
171	Cu	1.15	0/850	1.41	11/1310 (0.8%)
172	Cv	1.15	0/905	1.31	8/1394 (0.6%)
173	Cw	1.19	0/928	1.36	12/1432 (0.8%)
174	Cx	1.19	0/733	1.40	9/1128 (0.8%)
175	Cy	1.20	0/733	1.37	10/1128 (0.9%)
176	Cz	1.14	0/751	1.15	2/1161 (0.2%)
177	C0	1.18	1/1281 (0.1%)	1.41	17/1972 (0.9%)
178	C1	1.12	0/1302	1.23	9/2011 (0.4%)
179	C2	1.15	0/738	1.33	9/1138 (0.8%)
180	C3	1.17	0/1100	1.35	14/1694 (0.8%)
181	C4	1.14	0/1096	1.34	16/1688 (0.9%)
182	C5	1.14	0/1092	1.40	14/1683 (0.8%)
183	C6	1.20	0/1123	1.34	13/1735 (0.7%)
184	C7	1.13	0/896	1.40	11/1378 (0.8%)
185	C8	1.18	0/1116	1.39	16/1722 (0.9%)
186	C9	1.13	0/1293	1.21	7/1994 (0.4%)
187	DA	1.20	0/1027	1.35	12/1583 (0.8%)
188	DB	1.15	0/724	1.34	8/1113 (0.7%)
189	DC	1.17	0/942	1.43	13/1453 (0.9%)
190	DD	1.16	0/1017	1.31	9/1566 (0.6%)
191	DE	1.11	0/1102	1.26	13/1699 (0.8%)
192	DF	1.15	0/917	1.31	8/1413 (0.6%)
193	DG	1.13	0/1112	1.25	8/1717 (0.5%)
194	DH	1.17	0/737	1.40	8/1134 (0.7%)
195	DI	1.15	0/732	1.30	7/1128 (0.6%)
All	All	1.16	14/383925 (0.0%)	1.34	4478/592251 (0.8%)

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

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

Continued on next page...

Continued from previous page...

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

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	A2	8	DC	C5'-C4'	5.42	1.57	1.51
1	AA	2168	DG	C5'-C4'	5.39	1.57	1.51
18	AR	40	DA	N9-C4	5.34	1.41	1.37
1	AA	2816	DG	C2'-C1'	5.33	1.57	1.52
177	C0	4	DT	C5'-C4'	5.32	1.57	1.51

The worst 5 of 4478 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	AA	601	DC	P-O3'-C3'	18.83	142.30	119.70
1	AA	4222	DT	P-O3'-C3'	18.05	141.36	119.70
1	AA	486	DC	P-O3'-C3'	15.05	137.76	119.70
84	BV	39	DA	P-O3'-C3'	15.05	137.76	119.70

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	6047	DC	P-O3'-C3'	14.93	137.62	119.70

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

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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
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

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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
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

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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
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

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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
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

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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 monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

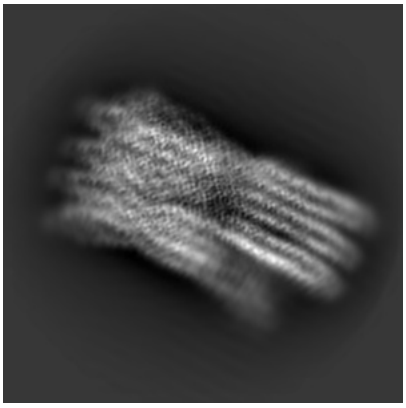
6 Map visualisation (i)

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

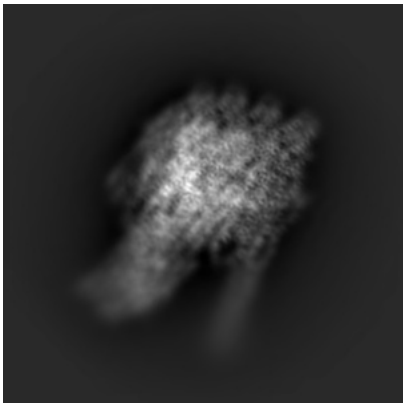
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

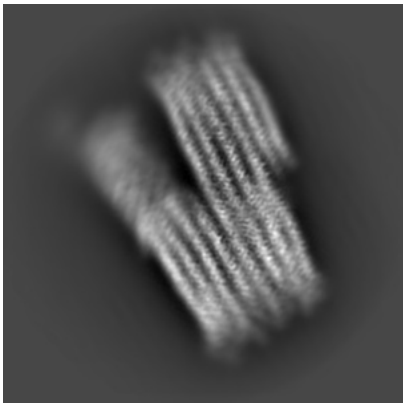
6.1.1 Primary map



X



Y

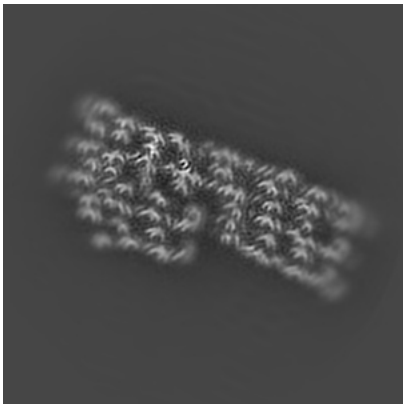


Z

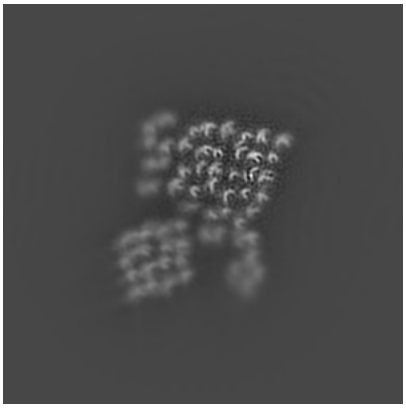
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

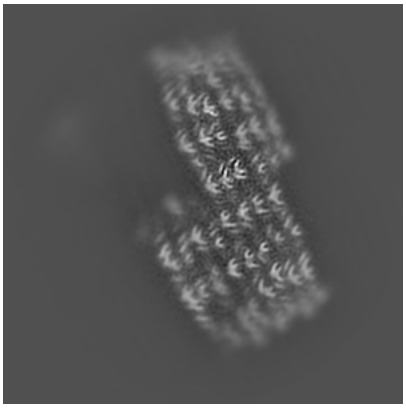
6.2.1 Primary map



X Index: 232



Y Index: 232

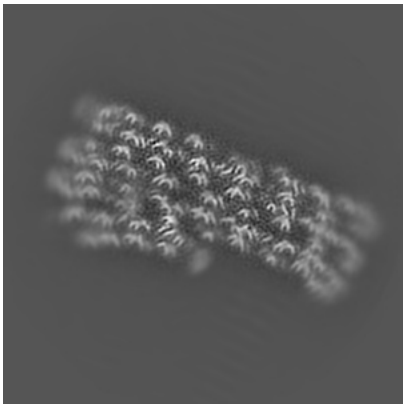


Z Index: 232

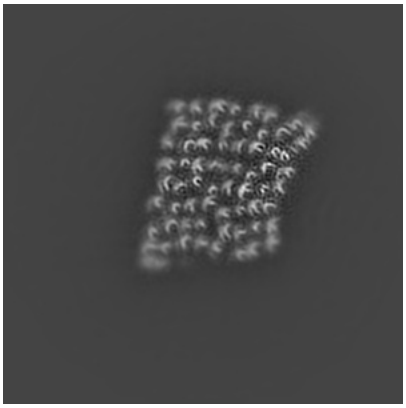
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

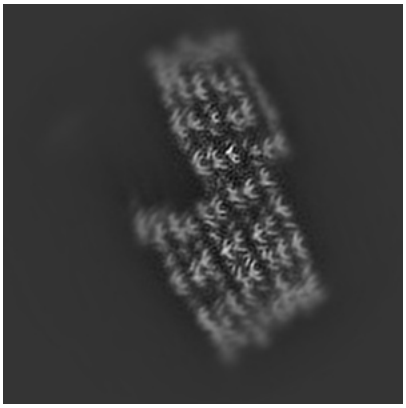
6.3.1 Primary map



X Index: 247



Y Index: 179

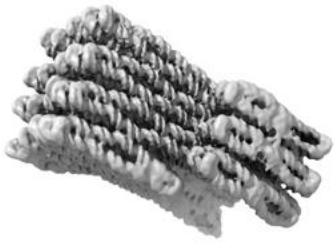


Z Index: 222

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

6.4 Orthogonal surface views (i)

6.4.1 Primary map



X

Y

Z

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

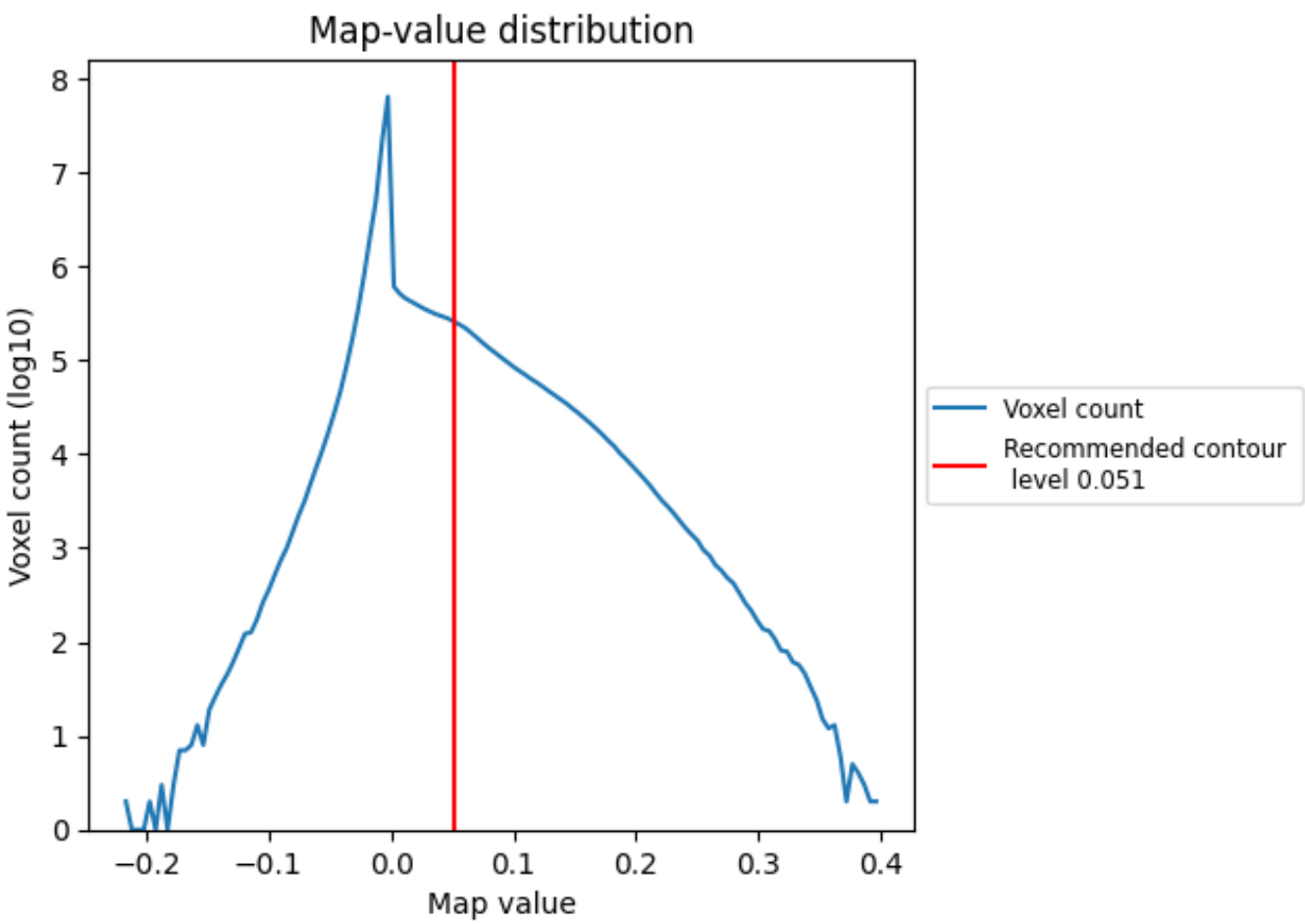
6.5 Mask visualisation (i)

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

7 Map analysis (i)

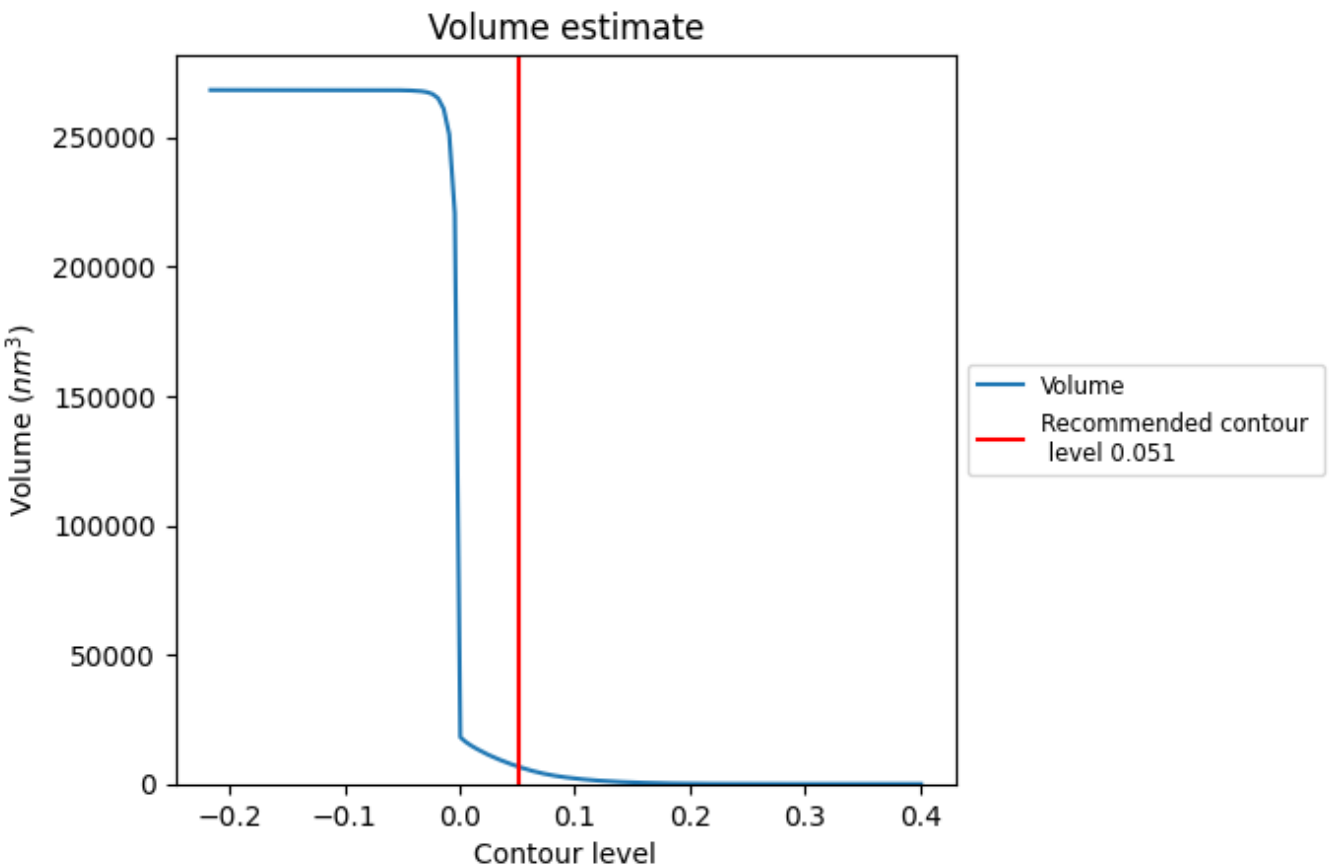
This section contains the results of statistical analysis of the map.

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.

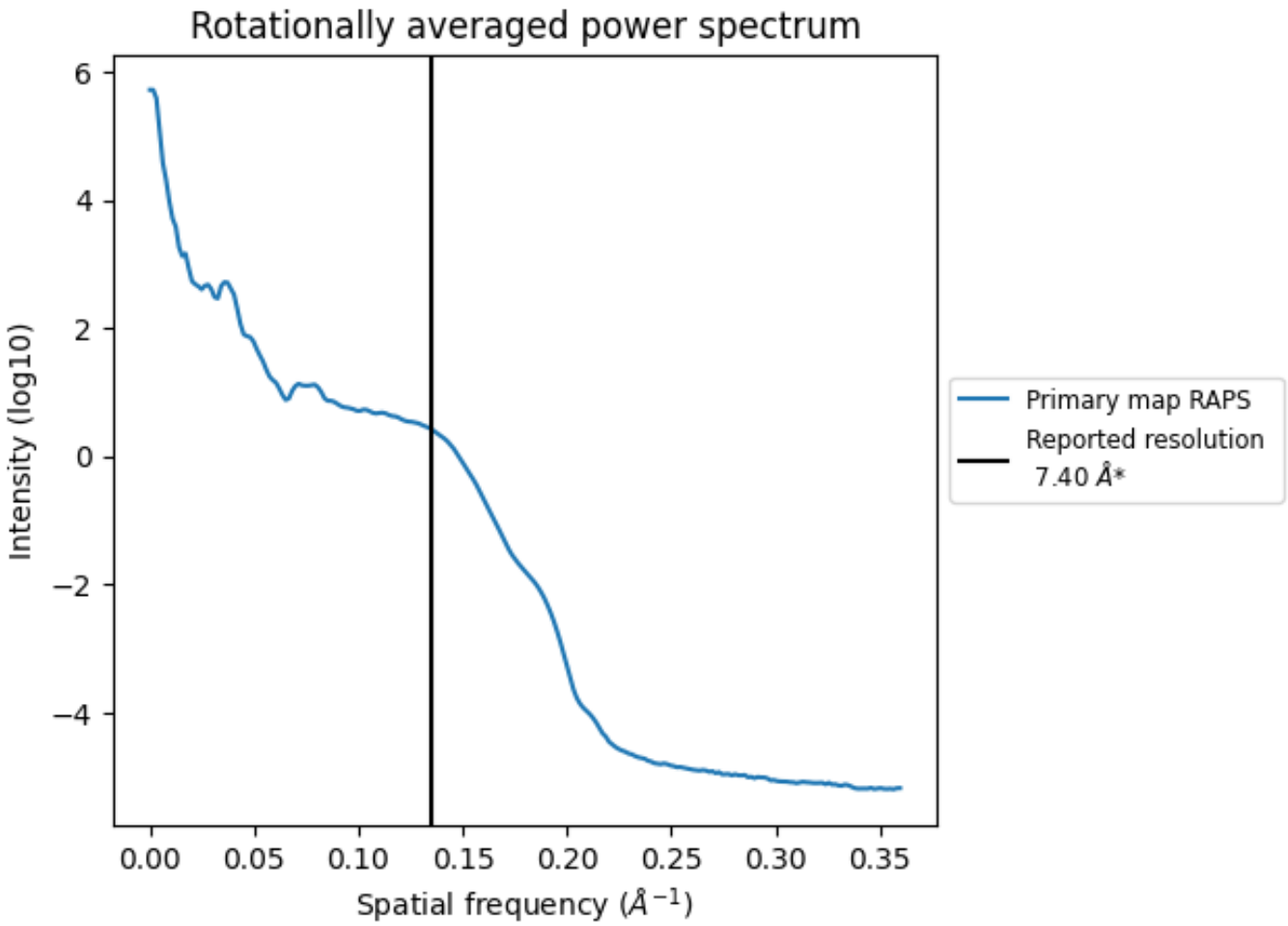
7.2 Volume estimate (i)



The volume at the recommended contour level is 6695 nm^3; 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)

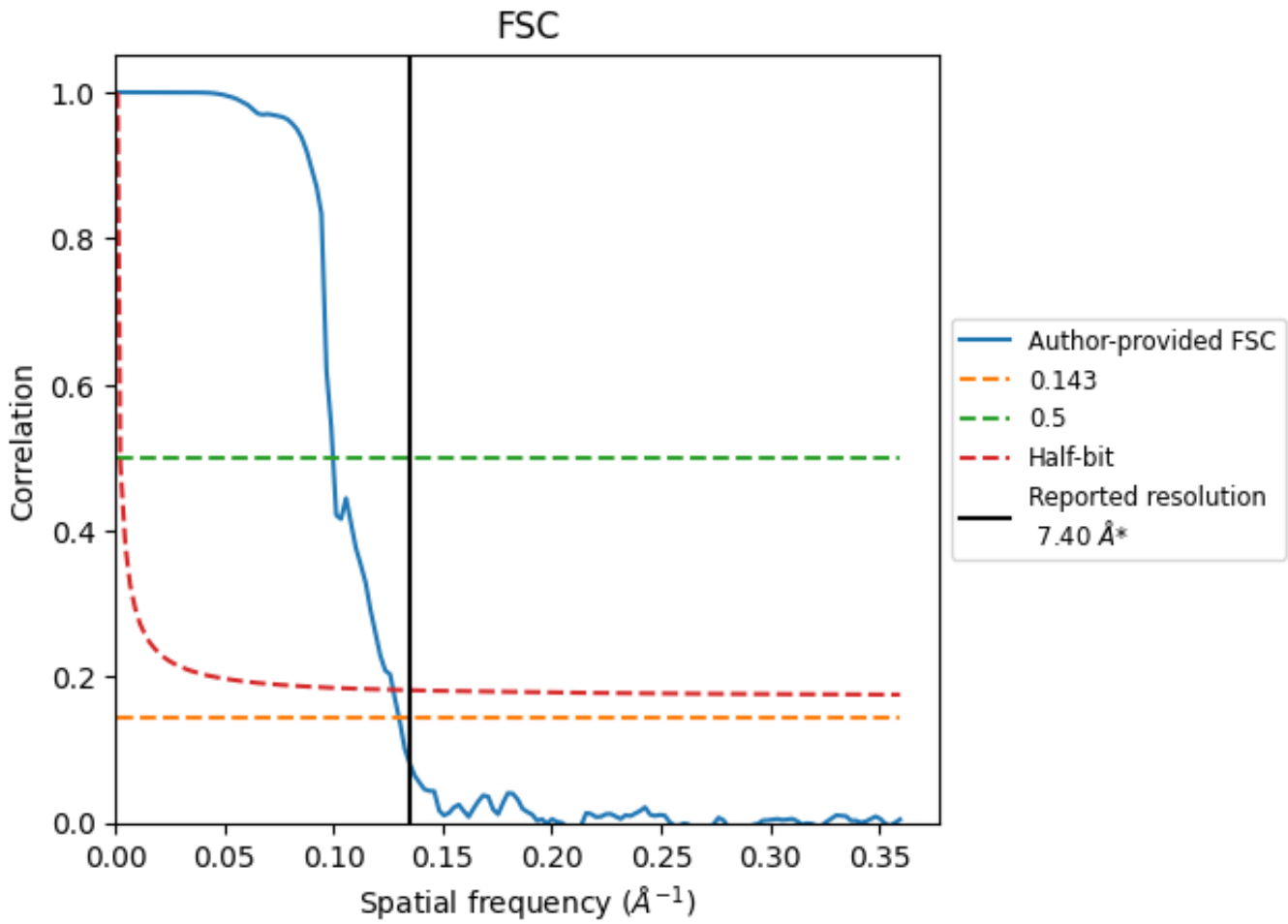


*Reported resolution corresponds to spatial frequency of 0.135 Å^{-1}

8 Fourier-Shell correlation (i)

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

8.1 FSC (i)



*Reported resolution corresponds to spatial frequency of 0.135 Å^{-1}

8.2 Resolution estimates (i)

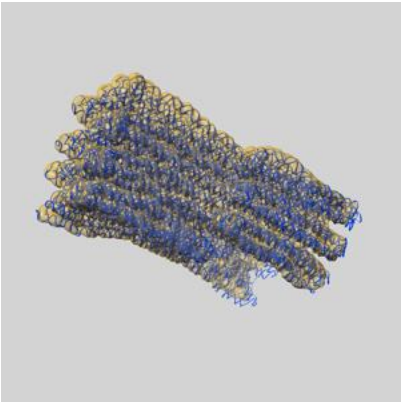
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.40	-	-
Author-provided FSC curve	7.69	10.03	7.86
Unmasked-calculated*	-	-	-

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

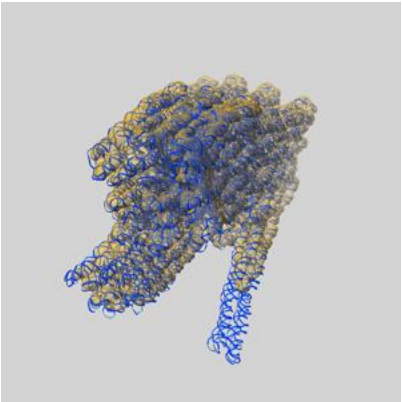
9 Map-model fit (i)

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.

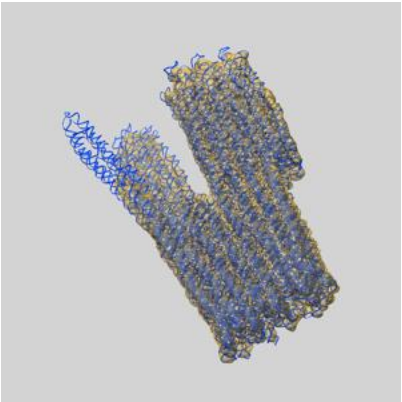
9.1 Map-model overlay (i)



X



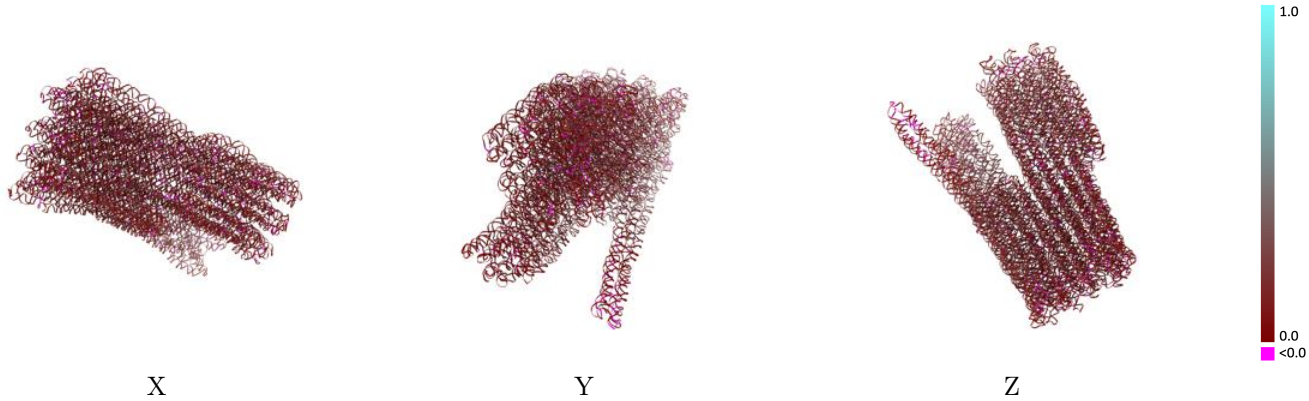
Y



Z

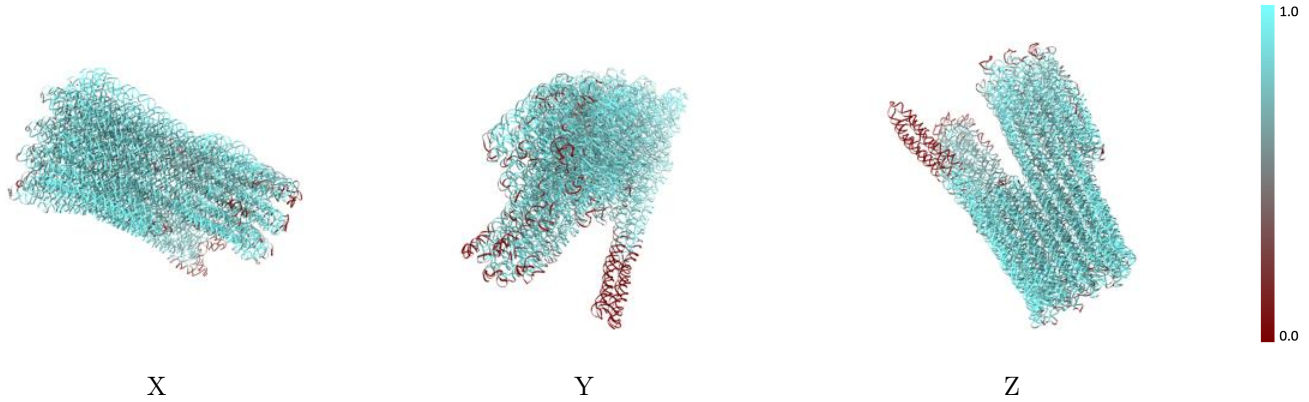
The images above show the 3D surface view of the map at the recommended contour level 0.051 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



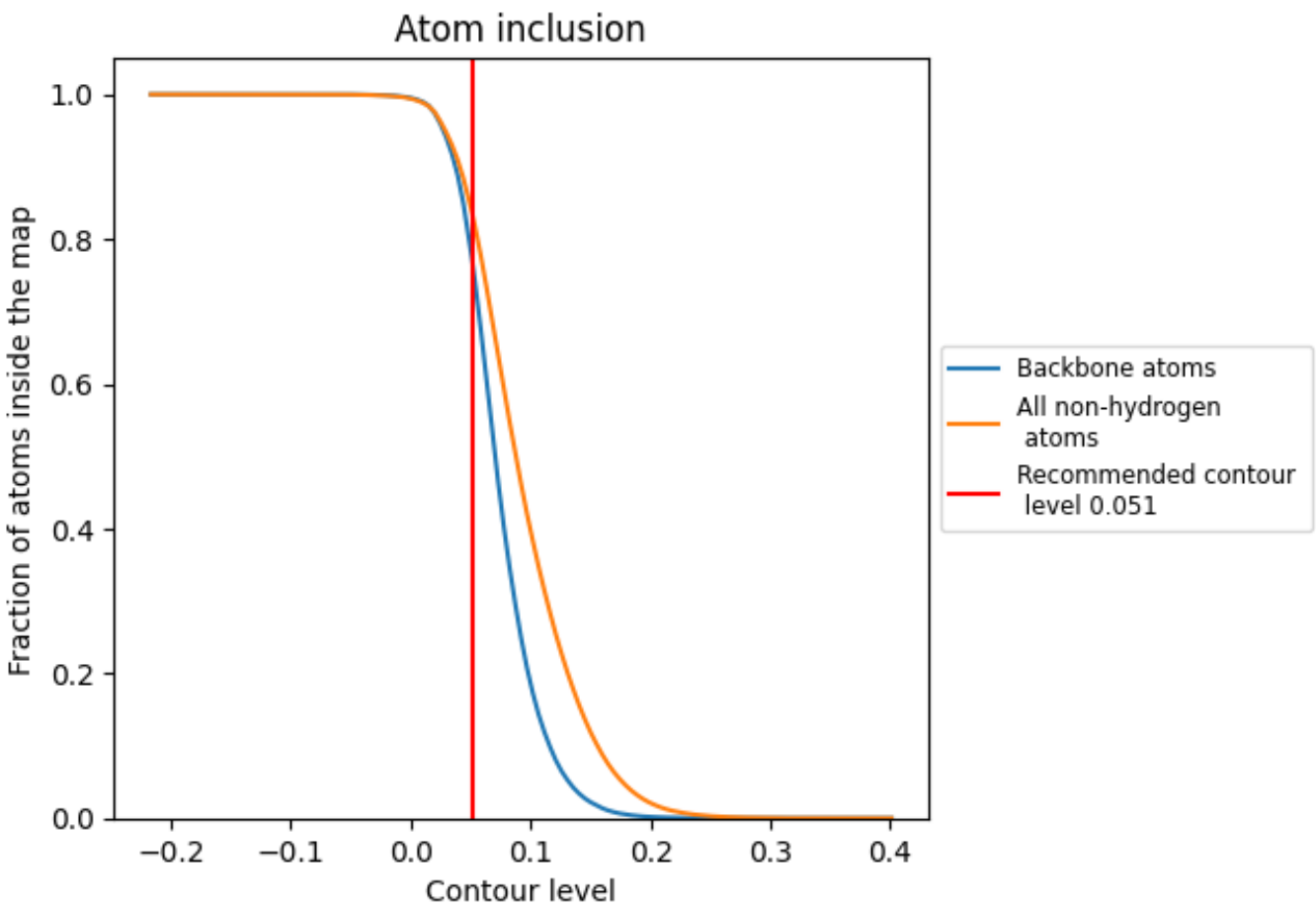
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 77% of all backbone atoms, 84% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

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	0.8382	0.1400
A0	0.8549	0.1250
A1	0.8417	0.1350
A2	0.7909	0.1050
A3	0.8775	0.1380
A4	0.9076	0.1430
A5	0.9223	0.1410
A6	0.8290	0.1290
A7	0.9238	0.1500
A8	0.8967	0.1500
A9	0.8887	0.1580
AA	0.8580	0.1440
AB	0.6409	0.1130
AC	0.8476	0.1330
AD	0.9132	0.1160
AE	0.4174	0.0720
AF	0.8503	0.1350
AG	0.8517	0.1320
AH	0.6683	0.0900
AI	0.7321	0.1060
AJ	0.6593	0.0950
AK	0.9012	0.1330
AL	0.8859	0.1230
AM	0.9241	0.1490
AN	0.8912	0.1610
AO	0.8926	0.1330
AP	0.7479	0.1310
AQ	0.8085	0.1340
AR	0.7150	0.1330
AS	0.7966	0.1190
AT	0.8103	0.1200
AU	0.8997	0.1440
AV	0.8874	0.1470
AW	0.8926	0.1000
AX	0.5535	0.0770

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
AY	0.8756	0.1660
AZ	0.9364	0.1560
Aa	0.8724	0.1230
Ab	0.9067	0.1490
Ac	0.8571	0.1400
Ad	0.9038	0.1360
Ae	0.9193	0.1140
Af	0.8859	0.1400
Ag	0.8721	0.1170
Ah	0.6577	0.1130
Ai	0.8100	0.1550
Aj	0.8731	0.1360
Ak	0.8865	0.1490
Al	0.9043	0.1500
Am	0.8706	0.1120
An	0.6824	0.1130
Ao	0.8586	0.1130
Ap	0.6565	0.1070
Aq	0.9249	0.1520
Ar	0.7367	0.1160
As	0.9106	0.1510
At	0.9333	0.1460
Au	0.8863	0.1290
Av	0.8980	0.1450
Aw	0.8294	0.1380
Ax	0.8748	0.1450
Ay	0.9010	0.1530
Az	0.8722	0.1260
B0	0.7983	0.1190
B1	0.6208	0.1200
B2	0.8809	0.1560
B3	0.8795	0.1700
B4	0.8748	0.1730
B5	0.8070	0.1210
B6	0.8217	0.1520
B7	0.9165	0.1540
B8	0.9012	0.1820
B9	0.9190	0.1720
BA	0.9477	0.1560
BB	0.9135	0.1510
BC	0.8648	0.1270
BD	0.8979	0.1340

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
BE	0.6848	0.1030
BF	0.8211	0.1210
BG	0.8910	0.1630
BH	0.7976	0.1220
BI	0.7050	0.1170
BJ	0.8126	0.1590
BK	0.8382	0.1540
BL	0.9186	0.1460
BM	0.8554	0.1250
BN	0.8930	0.1460
BO	0.8737	0.1470
BP	0.8536	0.1230
BQ	0.6818	0.1040
BR	0.8593	0.1320
BS	0.8862	0.1560
BT	0.9168	0.1510
BU	0.8909	0.1610
BV	0.8381	0.1220
BW	0.7238	0.1110
BX	0.9209	0.1620
BY	0.9254	0.1430
BZ	0.9315	0.1660
Ba	0.8802	0.1400
Bb	0.8579	0.1450
Bc	0.8131	0.1300
Bd	0.8589	0.1450
Be	0.8320	0.1450
Bf	0.8509	0.1520
Bg	0.9187	0.1720
Bh	0.9170	0.1450
Bi	0.9217	0.1330
Bj	0.8208	0.1380
Bk	0.9379	0.1790
Bl	0.8881	0.1470
Bm	0.9477	0.1570
Bn	0.9053	0.1410
Bo	0.9346	0.1550
Bp	0.8710	0.1410
Bq	0.8337	0.1290
Br	0.8700	0.1520
Bs	0.8545	0.1590
Bt	0.9465	0.1650

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Bu	0.8962	0.1400
Bv	0.8645	0.1460
Bw	0.8651	0.1180
Bx	0.8455	0.1460
By	0.8967	0.1590
Bz	0.8318	0.1490
C0	0.8319	0.1070
C1	0.0000	0.0300
C2	0.9346	0.1800
C3	0.9203	0.1710
C4	0.9232	0.1580
C5	0.9580	0.1710
C6	0.9087	0.1650
C7	0.8780	0.1600
C8	0.8819	0.1660
C9	0.8653	0.1280
CA	0.8618	0.1670
CB	0.6574	0.1090
CC	0.8316	0.1460
CD	0.2474	0.0510
CE	0.9250	0.1660
CF	0.9148	0.1600
CG	0.8040	0.1370
CH	0.8970	0.1760
CI	0.9226	0.1710
CJ	0.3236	0.0600
CK	0.8477	0.1330
CL	0.8840	0.1640
CM	0.9277	0.1890
CN	0.6505	0.1250
CO	0.8458	0.1480
CP	0.8508	0.1460
CQ	0.8124	0.1190
CR	0.4620	0.0650
CS	0.8409	0.1460
CT	0.8558	0.1630
CU	0.8999	0.1630
CV	0.8796	0.1640
CW	0.9479	0.1740
CX	0.7903	0.1210
CY	0.5070	0.0830
CZ	0.8879	0.1460

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Ca	0.9065	0.1390
Cb	0.9391	0.1670
Cc	0.7939	0.1270
Cd	0.9410	0.1670
Ce	0.8951	0.1500
Cf	0.8919	0.1430
Cg	0.9364	0.1670
Ch	0.9400	0.1680
Ci	0.9228	0.1670
Cj	0.9584	0.1670
Ck	0.9360	0.1530
Cl	0.9440	0.1540
Cm	0.9082	0.1700
Cn	0.8864	0.1650
Co	0.7448	0.1320
Cp	0.8378	0.1520
Cq	0.7241	0.1270
Cr	0.9147	0.1890
Cs	0.8637	0.1220
Ct	0.9174	0.1710
Cu	0.6526	0.1260
Cv	0.9494	0.1760
Cw	0.8897	0.1630
Cx	0.8850	0.1560
Cy	0.8742	0.1580
Cz	0.0000	0.0480
DA	0.8441	0.1520
DB	0.9520	0.1760
DC	0.8798	0.1530
DD	0.0000	0.0360
DE	0.0611	0.0430
DF	0.6083	0.1130
DG	0.7364	0.1190
DH	0.9388	0.1710
DI	0.9587	0.1760