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%

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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%

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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%

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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%

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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%

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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%

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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%

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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%

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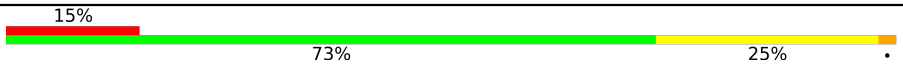
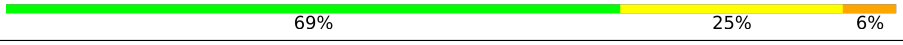
Mol	Chain	Length	Quality of chain
193	DG	48	
194	DH	32	
195	DI	32	

2 Entry composition (i)

There are 195 unique types of molecules in this entry. The entry contains 342569 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a DNA chain called SCAFFOLD STRAND.

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

- Molecule 2 is a DNA chain called STAPLE STRAND.

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

- Molecule 3 is a DNA chain called STAPLE STRAND.

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

- Molecule 4 is a DNA chain called STAPLE STRAND.

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

- Molecule 5 is a DNA chain called STAPLE STRAND.

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

- Molecule 6 is a DNA chain called STAPLE STRAND.

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

- Molecule 7 is a DNA chain called STAPLE STRAND.

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

- Molecule 8 is a DNA chain called STAPLE STRAND.

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

- Molecule 9 is a DNA chain called STAPLE STRAND.

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

- Molecule 10 is a DNA chain called STAPLE STRAND.

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

- Molecule 11 is a DNA chain called STAPLE STRAND.

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

- Molecule 12 is a DNA chain called STAPLE STRAND.

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

- Molecule 13 is a DNA chain called STAPLE STRAND.

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

- Molecule 14 is a DNA chain called STAPLE STRAND.

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

- Molecule 15 is a DNA chain called STAPLE STRAND.

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

- Molecule 16 is a DNA chain called STAPLE STRAND.

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

- Molecule 17 is a DNA chain called STAPLE STRAND.

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

- Molecule 18 is a DNA chain called STAPLE STRAND.

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

- Molecule 19 is a DNA chain called STAPLE STRAND.

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

- Molecule 20 is a DNA chain called STAPLE STRAND.

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

- Molecule 21 is a DNA chain called STAPLE STRAND.

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

- Molecule 22 is a DNA chain called STAPLE STRAND.

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

- Molecule 23 is a DNA chain called STAPLE STRAND.

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

- Molecule 24 is a DNA chain called STAPLE STRAND.

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

- Molecule 25 is a DNA chain called STAPLE STRAND.

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

- Molecule 26 is a DNA chain called STAPLE STRAND.

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

- Molecule 27 is a DNA chain called STAPLE STRAND.

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

- Molecule 28 is a DNA chain called STAPLE STRAND.

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

- Molecule 29 is a DNA chain called STAPLE STRAND.

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

- Molecule 30 is a DNA chain called STAPLE STRAND.

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

- Molecule 31 is a DNA chain called STAPLE STRAND.

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

- Molecule 32 is a DNA chain called STAPLE STRAND.

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

- Molecule 33 is a DNA chain called STAPLE STRAND.

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

- Molecule 34 is a DNA chain called STAPLE STRAND.

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

- Molecule 35 is a DNA chain called STAPLE STRAND.

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

- Molecule 36 is a DNA chain called STAPLE STRAND.

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

- Molecule 37 is a DNA chain called STAPLE STRAND.

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

- Molecule 38 is a DNA chain called STAPLE STRAND.

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

- Molecule 39 is a DNA chain called STAPLE STRAND.

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

- Molecule 40 is a DNA chain called STAPLE STRAND.

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

- Molecule 41 is a DNA chain called STAPLE STRAND.

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

- Molecule 42 is a DNA chain called STAPLE STRAND.

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

- Molecule 43 is a DNA chain called STAPLE STRAND.

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

- Molecule 44 is a DNA chain called STAPLE STRAND.

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

- Molecule 45 is a DNA chain called STAPLE STRAND.

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

- Molecule 46 is a DNA chain called STAPLE STRAND.

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

- Molecule 47 is a DNA chain called STAPLE STRAND.

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

- Molecule 48 is a DNA chain called STAPLE STRAND.

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

- Molecule 49 is a DNA chain called STAPLE STRAND.

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

- Molecule 50 is a DNA chain called STAPLE STRAND.

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

- Molecule 51 is a DNA chain called STAPLE STRAND.

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

- Molecule 52 is a DNA chain called STAPLE STRAND.

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

- Molecule 53 is a DNA chain called STAPLE STRAND.

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

- Molecule 54 is a DNA chain called STAPLE STRAND.

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

- Molecule 55 is a DNA chain called STAPLE STRAND.

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

- Molecule 56 is a DNA chain called STAPLE STRAND.

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

- Molecule 57 is a DNA chain called STAPLE STRAND.

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

- Molecule 58 is a DNA chain called STAPLE STRAND.

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

- Molecule 59 is a DNA chain called STAPLE STRAND.

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

- Molecule 60 is a DNA chain called STAPLE STRAND.

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

- Molecule 61 is a DNA chain called STAPLE STRAND.

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

- Molecule 62 is a DNA chain called STAPLE STRAND.

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

- Molecule 63 is a DNA chain called STAPLE STRAND.

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

- Molecule 64 is a DNA chain called STAPLE STRAND.

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

- Molecule 65 is a DNA chain called STAPLE STRAND.

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

- Molecule 66 is a DNA chain called STAPLE STRAND.

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

- Molecule 67 is a DNA chain called STAPLE STRAND.

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

- Molecule 68 is a DNA chain called STAPLE STRAND.

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

- Molecule 69 is a DNA chain called STAPLE STRAND.

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

- Molecule 70 is a DNA chain called STAPLE STRAND.

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

- Molecule 71 is a DNA chain called STAPLE STRAND.

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

- Molecule 72 is a DNA chain called STAPLE STRAND.

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

- Molecule 73 is a DNA chain called STAPLE STRAND.

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

- Molecule 74 is a DNA chain called STAPLE STRAND.

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

- Molecule 75 is a DNA chain called STAPLE STRAND.

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

- Molecule 76 is a DNA chain called STAPLE STRAND.

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

- Molecule 77 is a DNA chain called STAPLE STRAND.

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

- Molecule 78 is a DNA chain called STAPLE STRAND.

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

- Molecule 79 is a DNA chain called STAPLE STRAND.

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

- Molecule 80 is a DNA chain called STAPLE STRAND.

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

- Molecule 81 is a DNA chain called STAPLE STRAND.

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

- Molecule 82 is a DNA chain called STAPLE STRAND.

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

- Molecule 83 is a DNA chain called STAPLE STRAND.

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

- Molecule 84 is a DNA chain called STAPLE STRAND.

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

- Molecule 85 is a DNA chain called STAPLE STRAND.

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

- Molecule 86 is a DNA chain called STAPLE STRAND.

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

- Molecule 87 is a DNA chain called STAPLE STRAND.

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

- Molecule 88 is a DNA chain called STAPLE STRAND.

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

- Molecule 89 is a DNA chain called STAPLE STRAND.

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

- Molecule 90 is a DNA chain called STAPLE STRAND.

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

- Molecule 91 is a DNA chain called STAPLE STRAND.

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

- Molecule 92 is a DNA chain called STAPLE STRAND.

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

- Molecule 93 is a DNA chain called STAPLE STRAND.

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

- Molecule 94 is a DNA chain called STAPLE STRAND.

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

- Molecule 95 is a DNA chain called STAPLE STRAND.

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

- Molecule 96 is a DNA chain called STAPLE STRAND.

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

- Molecule 97 is a DNA chain called STAPLE STRAND.

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

- Molecule 98 is a DNA chain called STAPLE STRAND.

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

- Molecule 99 is a DNA chain called STAPLE STRAND.

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

- Molecule 100 is a DNA chain called STAPLE STRAND.

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

- Molecule 101 is a DNA chain called STAPLE STRAND.

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

- Molecule 102 is a DNA chain called STAPLE STRAND.

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

- Molecule 103 is a DNA chain called STAPLE STRAND.

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

- Molecule 104 is a DNA chain called STAPLE STRAND.

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

- Molecule 105 is a DNA chain called STAPLE STRAND.

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

- Molecule 106 is a DNA chain called STAPLE STRAND.

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

- Molecule 107 is a DNA chain called STAPLE STRAND.

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

- Molecule 108 is a DNA chain called STAPLE STRAND.

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

- Molecule 109 is a DNA chain called STAPLE STRAND.

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

- Molecule 110 is a DNA chain called STAPLE STRAND.

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

- Molecule 111 is a DNA chain called STAPLE STRAND.

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

- Molecule 112 is a DNA chain called STAPLE STRAND.

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

- Molecule 113 is a DNA chain called STAPLE STRAND.

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

- Molecule 114 is a DNA chain called STAPLE STRAND.

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

- Molecule 115 is a DNA chain called STAPLE STRAND.

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

- Molecule 116 is a DNA chain called STAPLE STRAND.

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

- Molecule 117 is a DNA chain called STAPLE STRAND.

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

- Molecule 118 is a DNA chain called STAPLE STRAND.

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

- Molecule 119 is a DNA chain called STAPLE STRAND.

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

- Molecule 120 is a DNA chain called STAPLE STRAND.

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

- Molecule 121 is a DNA chain called STAPLE STRAND.

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

- Molecule 122 is a DNA chain called STAPLE STRAND.

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

- Molecule 123 is a DNA chain called STAPLE STRAND.

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

- Molecule 124 is a DNA chain called STAPLE STRAND.

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

- Molecule 125 is a DNA chain called STAPLE STRAND.

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

- Molecule 126 is a DNA chain called STAPLE STRAND.

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

- Molecule 127 is a DNA chain called STAPLE STRAND.

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

- Molecule 128 is a DNA chain called STAPLE STRAND.

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

- Molecule 129 is a DNA chain called STAPLE STRAND.

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

- Molecule 130 is a DNA chain called STAPLE STRAND.

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

- Molecule 131 is a DNA chain called STAPLE STRAND.

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

- Molecule 132 is a DNA chain called STAPLE STRAND.

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

- Molecule 133 is a DNA chain called STAPLE STRAND.

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

- Molecule 134 is a DNA chain called STAPLE STRAND.

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

- Molecule 135 is a DNA chain called STAPLE STRAND.

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

- Molecule 136 is a DNA chain called STAPLE STRAND.

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

- Molecule 137 is a DNA chain called STAPLE STRAND.

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

- Molecule 138 is a DNA chain called STAPLE STRAND.

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

- Molecule 139 is a DNA chain called STAPLE STRAND.

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

- Molecule 140 is a DNA chain called STAPLE STRAND.

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

- Molecule 141 is a DNA chain called STAPLE STRAND.

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

- Molecule 142 is a DNA chain called STAPLE STRAND.

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

- Molecule 143 is a DNA chain called STAPLE STRAND.

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

- Molecule 144 is a DNA chain called STAPLE STRAND.

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

- Molecule 145 is a DNA chain called STAPLE STRAND.

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

- Molecule 146 is a DNA chain called STAPLE STRAND.

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

- Molecule 147 is a DNA chain called STAPLE STRAND.

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

- Molecule 148 is a DNA chain called STAPLE STRAND.

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

- Molecule 149 is a DNA chain called STAPLE STRAND.

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

- Molecule 150 is a DNA chain called STAPLE STRAND.

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

- Molecule 151 is a DNA chain called STAPLE STRAND.

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

- Molecule 152 is a DNA chain called STAPLE STRAND.

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

- Molecule 153 is a DNA chain called STAPLE STRAND.

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

- Molecule 154 is a DNA chain called STAPLE STRAND.

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

- Molecule 155 is a DNA chain called STAPLE STRAND.

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

- Molecule 156 is a DNA chain called STAPLE STRAND.

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

- Molecule 157 is a DNA chain called STAPLE STRAND.

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

- Molecule 158 is a DNA chain called STAPLE STRAND.

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

- Molecule 159 is a DNA chain called STAPLE STRAND.

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

- Molecule 160 is a DNA chain called STAPLE STRAND.

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

- Molecule 161 is a DNA chain called STAPLE STRAND.

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

- Molecule 162 is a DNA chain called STAPLE STRAND.

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

- Molecule 163 is a DNA chain called STAPLE STRAND.

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

- Molecule 164 is a DNA chain called STAPLE STRAND.

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

- Molecule 165 is a DNA chain called STAPLE STRAND.

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

- Molecule 166 is a DNA chain called STAPLE STRAND.

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

- Molecule 167 is a DNA chain called STAPLE STRAND.

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

- Molecule 168 is a DNA chain called STAPLE STRAND.

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

- Molecule 169 is a DNA chain called STAPLE STRAND.

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

- Molecule 170 is a DNA chain called STAPLE STRAND.

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

- Molecule 171 is a DNA chain called STAPLE STRAND.

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

- Molecule 172 is a DNA chain called STAPLE STRAND.

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

- Molecule 173 is a DNA chain called STAPLE STRAND.

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

- Molecule 174 is a DNA chain called STAPLE STRAND.

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

- Molecule 175 is a DNA chain called STAPLE STRAND.

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

- Molecule 176 is a DNA chain called STAPLE STRAND.

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

- Molecule 177 is a DNA chain called STAPLE STRAND.

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

- Molecule 178 is a DNA chain called STAPLE STRAND.

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

- Molecule 179 is a DNA chain called STAPLE STRAND.

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

- Molecule 180 is a DNA chain called STAPLE STRAND.

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

- Molecule 181 is a DNA chain called STAPLE STRAND.

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

- Molecule 182 is a DNA chain called STAPLE STRAND.

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

- Molecule 183 is a DNA chain called STAPLE STRAND.

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

- Molecule 184 is a DNA chain called STAPLE STRAND.

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

- Molecule 185 is a DNA chain called STAPLE STRAND.

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

- Molecule 186 is a DNA chain called STAPLE STRAND.

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

- Molecule 187 is a DNA chain called STAPLE STRAND.

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

- Molecule 188 is a DNA chain called STAPLE STRAND.

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

- Molecule 189 is a DNA chain called STAPLE STRAND.

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

- Molecule 190 is a DNA chain called STAPLE STRAND.

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

- Molecule 191 is a DNA chain called STAPLE STRAND.

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

- Molecule 192 is a DNA chain called STAPLE STRAND.

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

- Molecule 193 is a DNA chain called STAPLE STRAND.

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

- Molecule 194 is a DNA chain called STAPLE STRAND.

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

- Molecule 195 is a DNA chain called STAPLE STRAND.

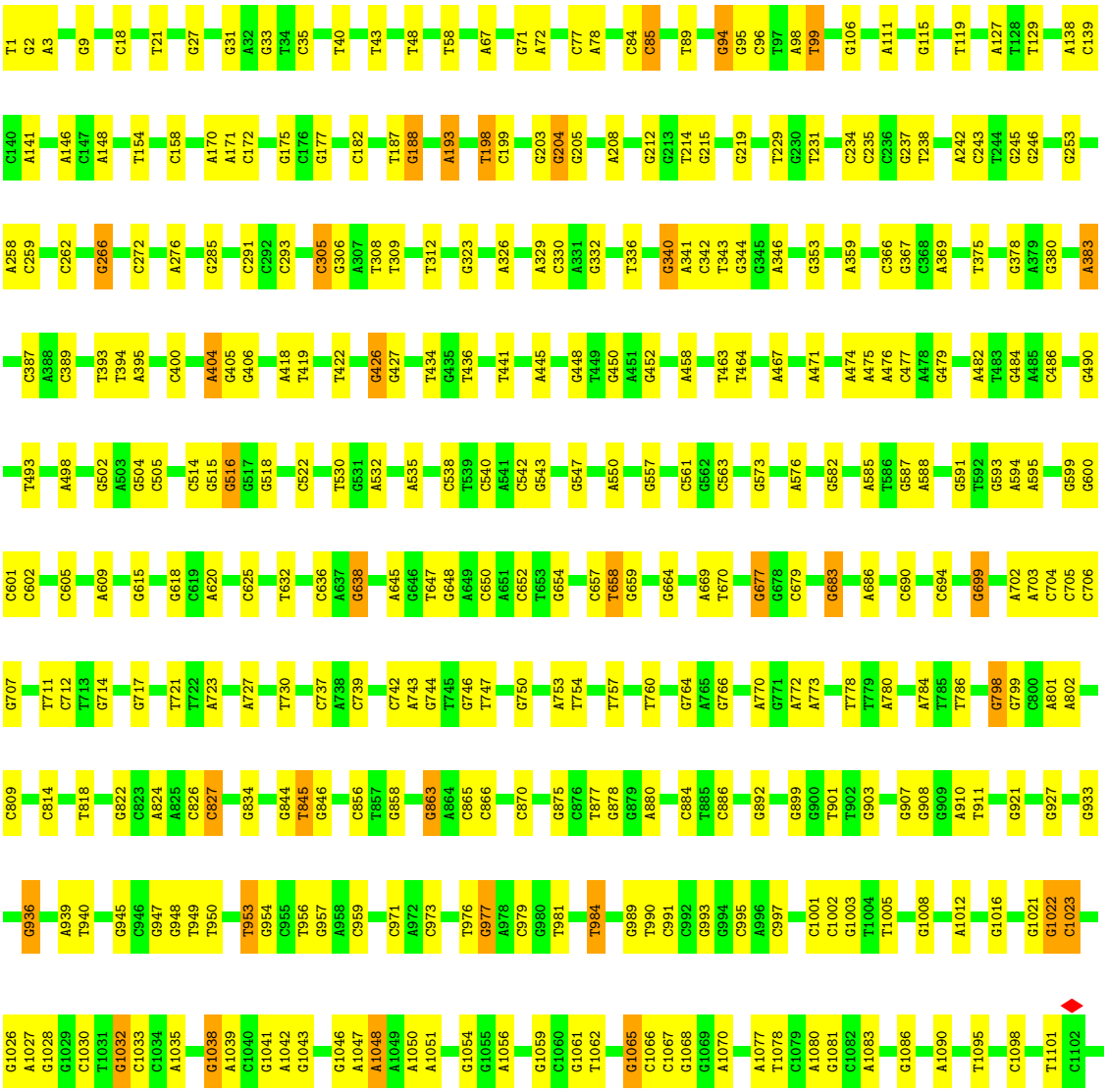
Mol	Chain	Residues	Atoms					AltConf	Trace
195	DI	32	Total 653	C 314	N 118	O 190	P 31	0	0

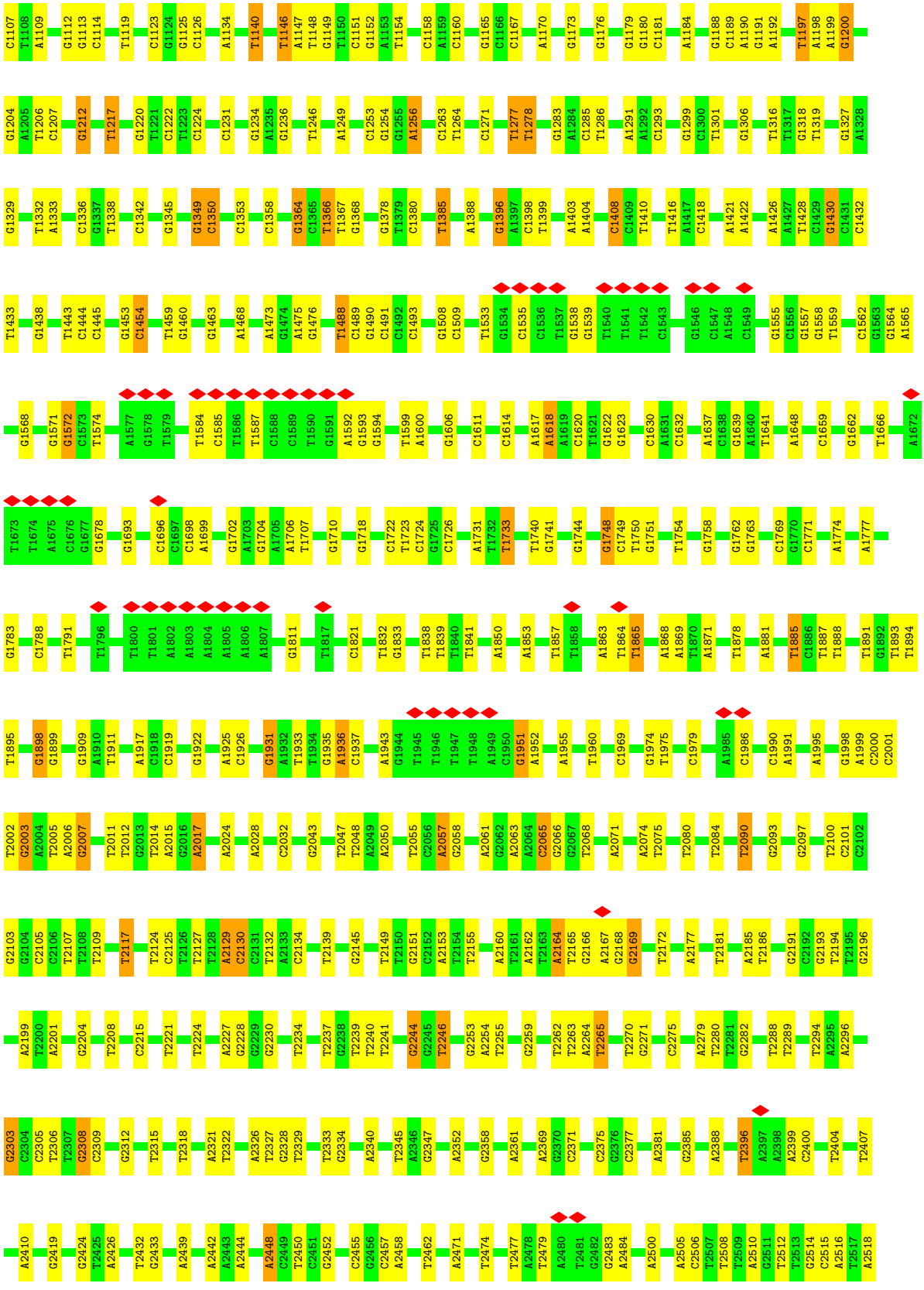
3 Residue-property plots (i)

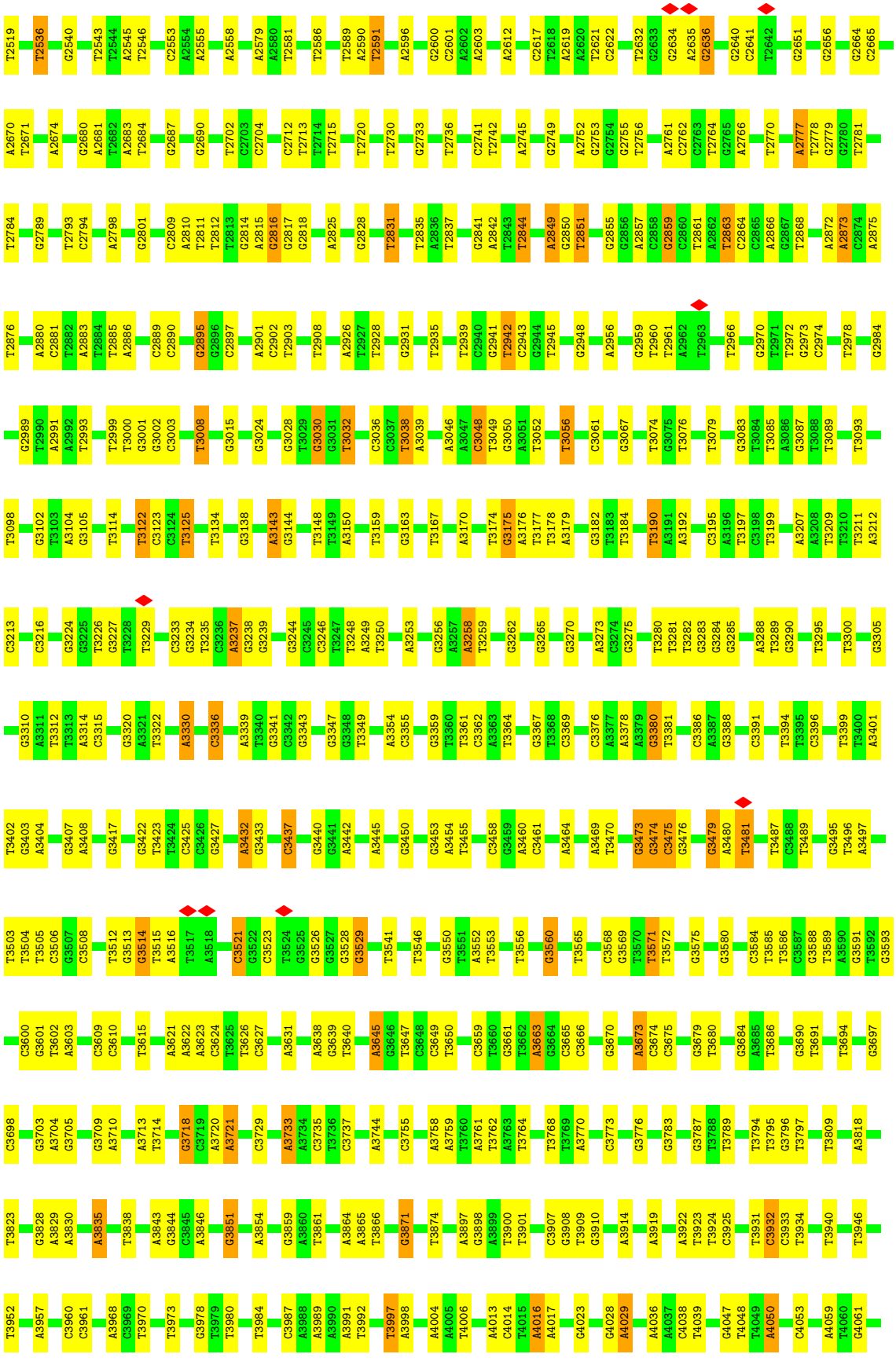
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

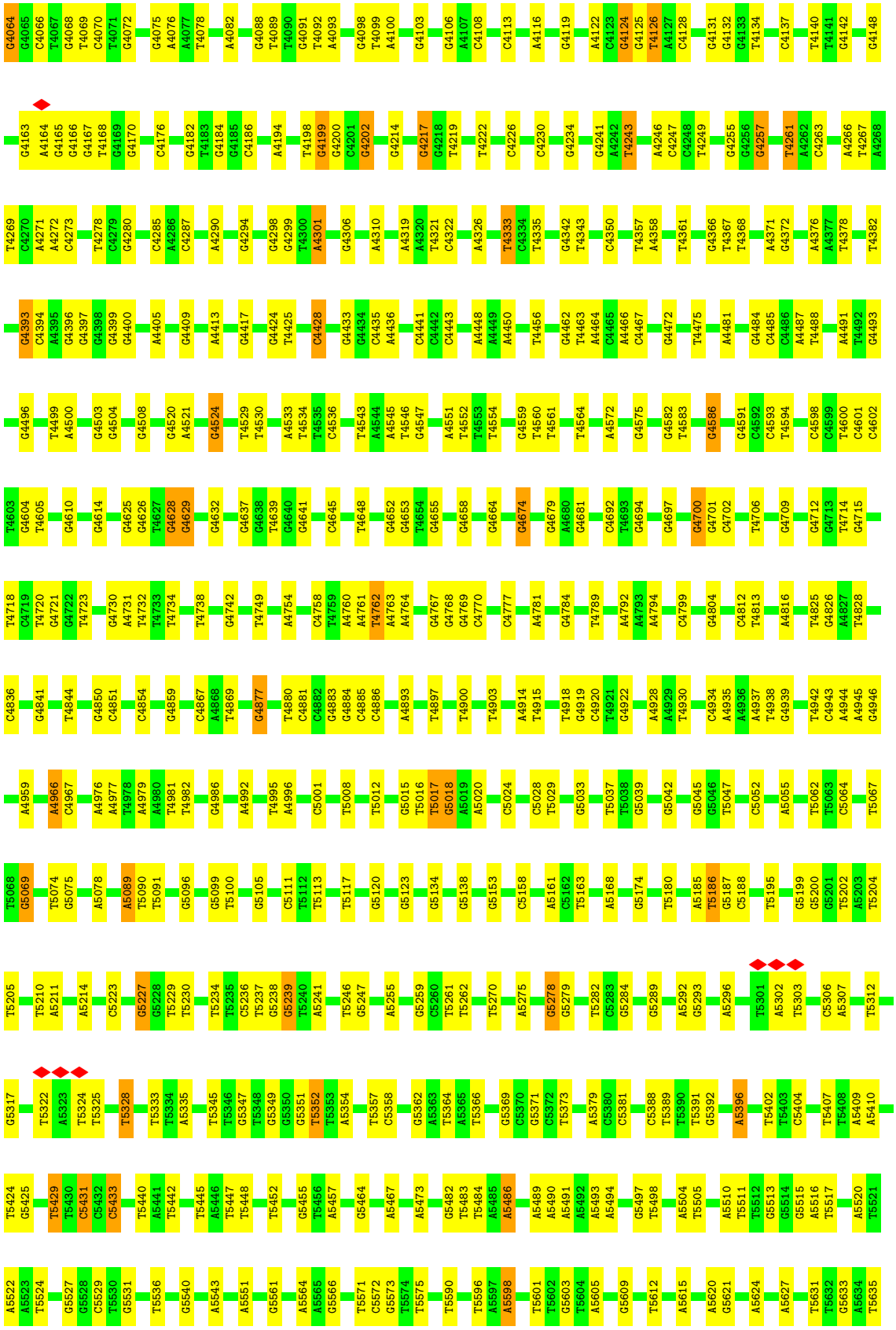
- Molecule 1: SCAFFOLD STRAND

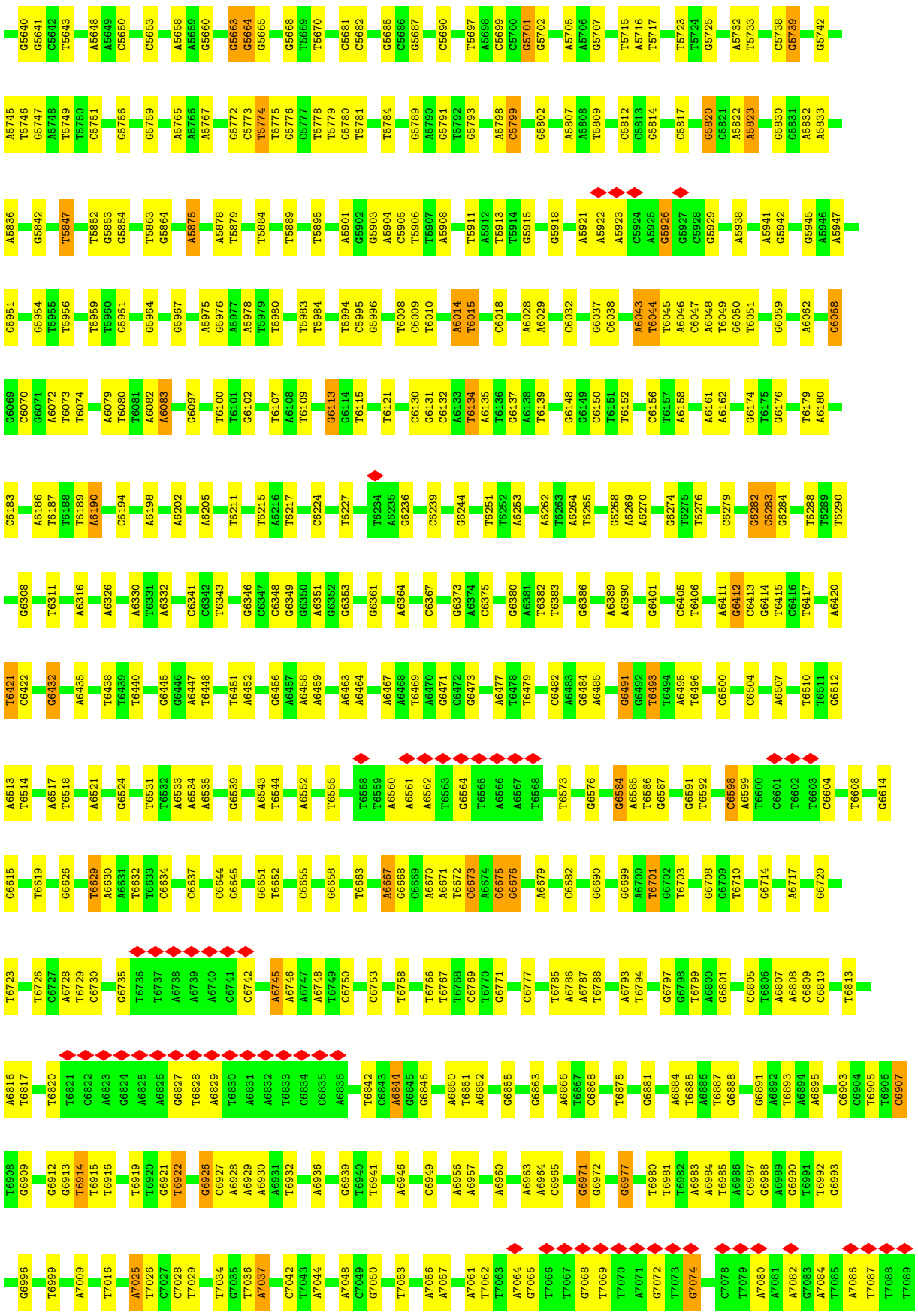
Chain AA:

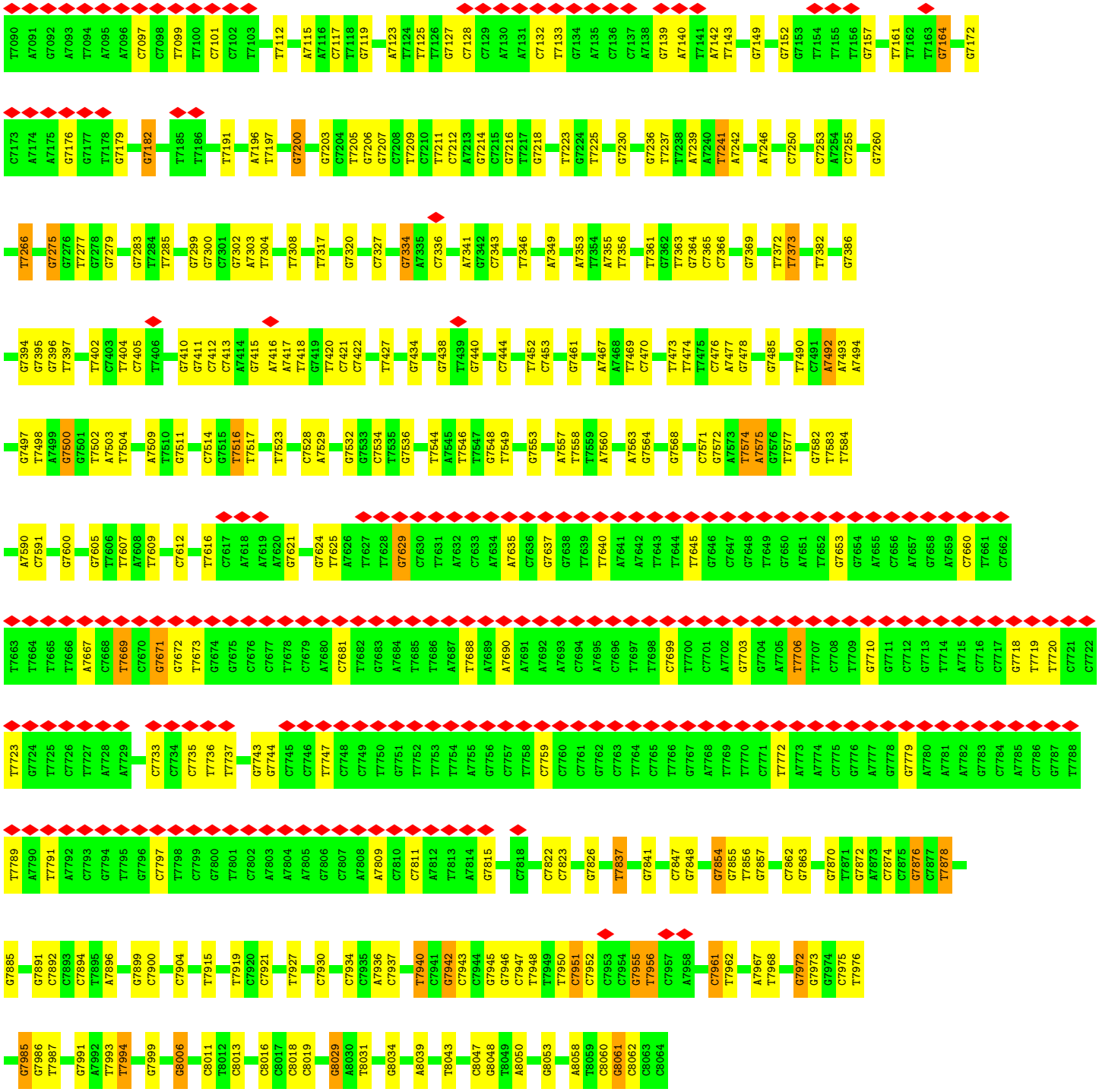



C1107 T1108 A1109 G1112 G1113 C1114 T1119 C1123 G1124 G1125 C1126 A1134 T1140 T1146 A1147 T1148 G1149 T1150 C1151 G1152 A1153 T1154 C1158 A1159 C1160 G1165 C1166 C1167 A1170 G1173 G1176 G1179 G1180 C1181 A1184 G1188 C1189 A1190 G1191 A1192 T1197 A1198 A1199 G1200
G1204 A1205 T1206 C1207 G1212 T1217 G1220 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 C1429 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 C2245 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 C2370 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



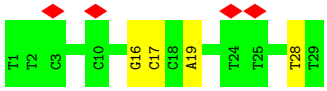






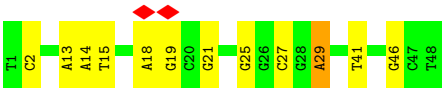
• Molecule 2: STAPLE STRAND

Chain AB:



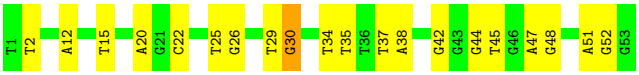
• Molecule 3: STAPLE STRAND

Chain AC:



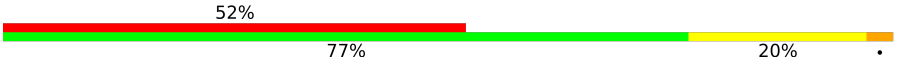
• Molecule 4: STAPLE STRAND

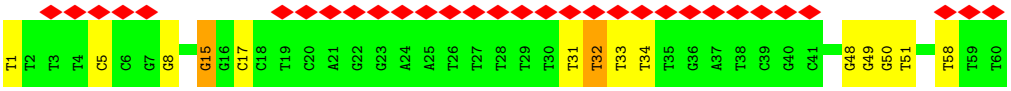
Chain AD:



• Molecule 5: STAPLE STRAND

Chain AE:



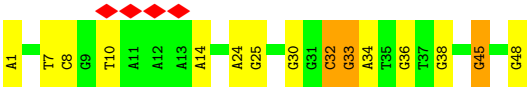


• Molecule 6: STAPLE STRAND

Chain AF:

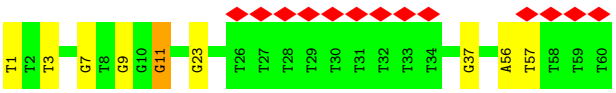
• Molecule 7: STAPLE STRAND

Chain AG:



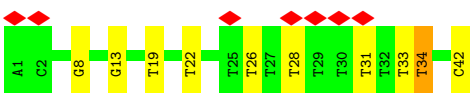
• Molecule 8: STAPLE STRAND

Chain AH:



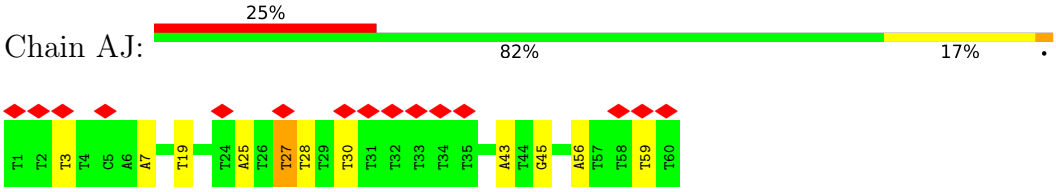
• Molecule 9: STAPLE STRAND

Chain AI:



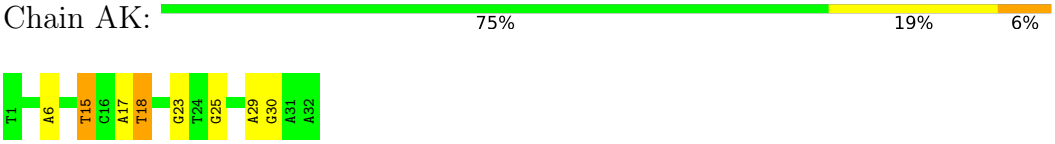
• Molecule 10: STAPLE STRAND

Chain AJ:



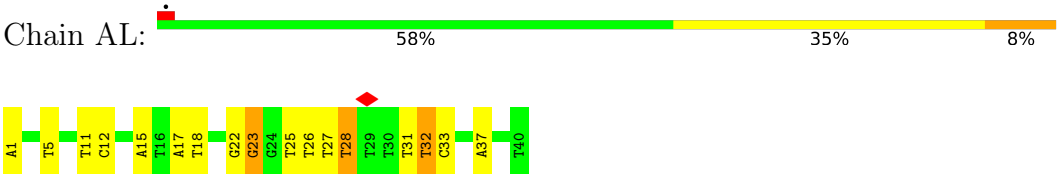
• Molecule 11: STAPLE STRAND

Chain AK:



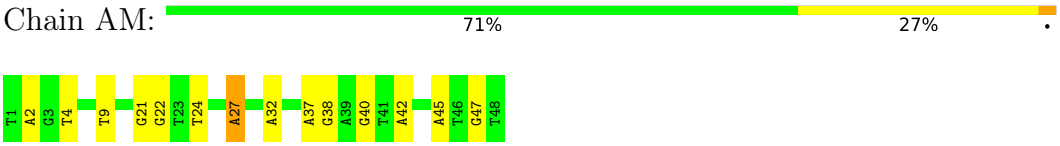
• Molecule 12: STAPLE STRAND

Chain AL:



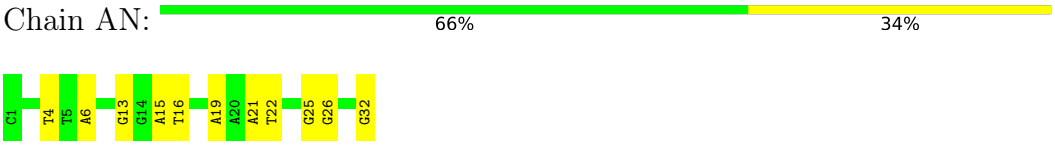
• Molecule 13: STAPLE STRAND

Chain AM:



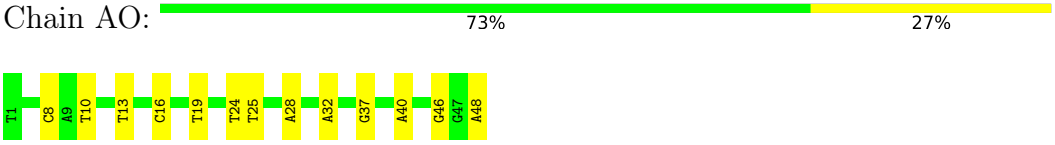
• Molecule 14: STAPLE STRAND

Chain AN:



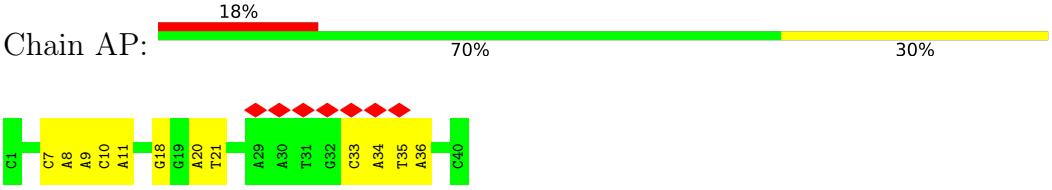
• Molecule 15: STAPLE STRAND

Chain AO:



• Molecule 16: STAPLE STRAND

Chain AP:

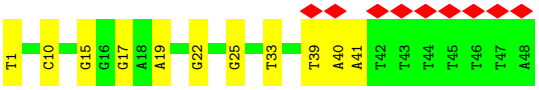


• Molecule 17: STAPLE STRAND

Chain AQ:

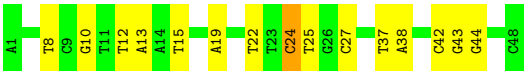
• Molecule 18: STAPLE STRAND

Chain AR:



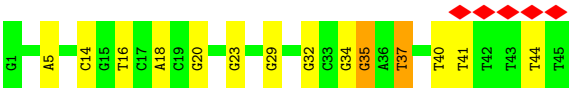
• Molecule 19: STAPLE STRAND

Chain AS:



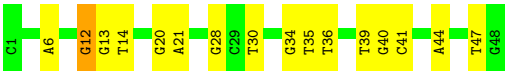
• Molecule 20: STAPLE STRAND

Chain AT:



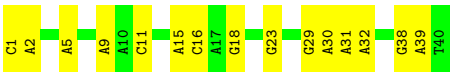
• Molecule 21: STAPLE STRAND

Chain AU:



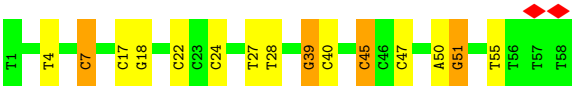
• Molecule 22: STAPLE STRAND

Chain AV:



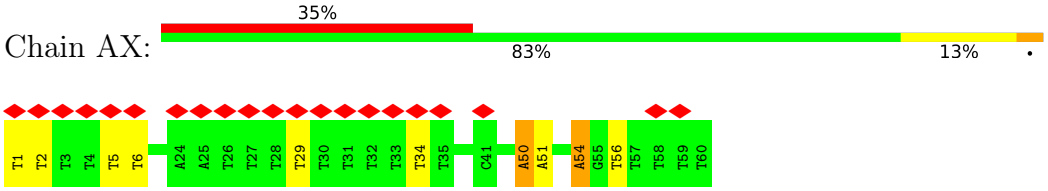
• Molecule 23: STAPLE STRAND

Chain AW:



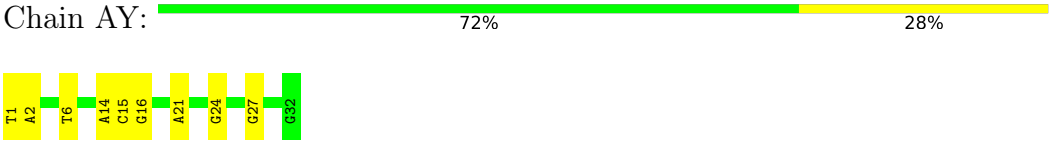
• Molecule 24: STAPLE STRAND

Chain AX:



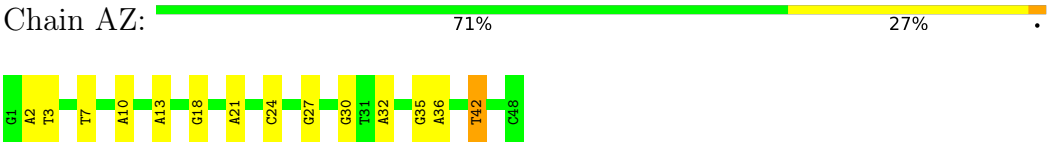
• Molecule 25: STAPLE STRAND

Chain AY:



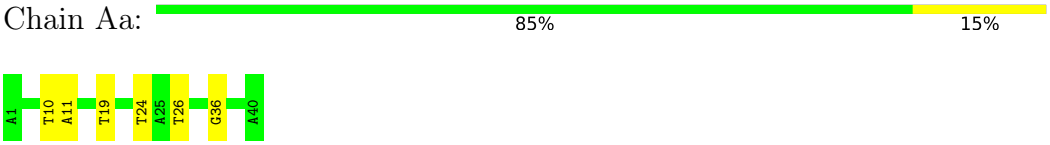
• Molecule 26: STAPLE STRAND

Chain AZ:



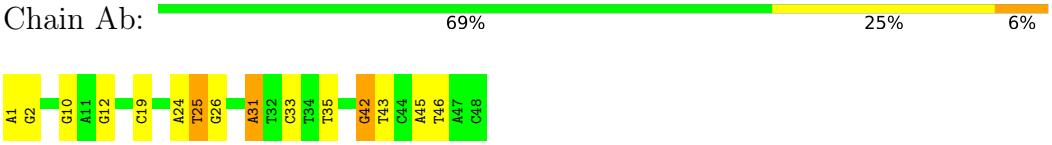
• Molecule 27: STAPLE STRAND

Chain Aa:



• Molecule 28: STAPLE STRAND

Chain Ab:

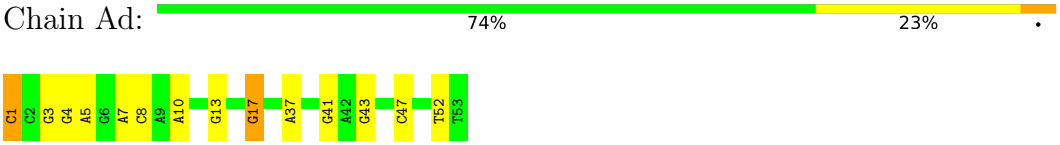


• Molecule 29: STAPLE STRAND

Chain Ac:

• Molecule 30: STAPLE STRAND

Chain Ad:

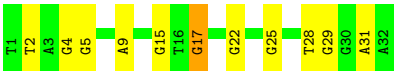


• Molecule 31: STAPLE STRAND

Chain Ae:

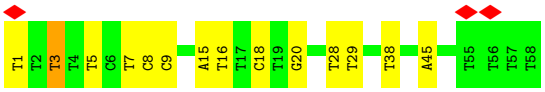
• Molecule 32: STAPLE STRAND

Chain Af:



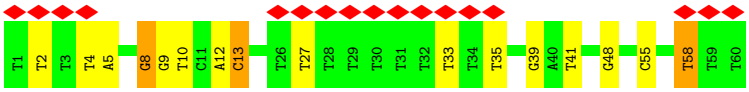
• Molecule 33: STAPLE STRAND

Chain Ag:



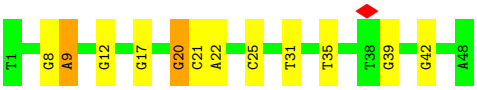
• Molecule 34: STAPLE STRAND

Chain Ah:



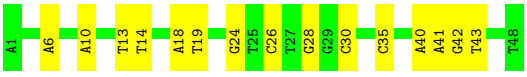
• Molecule 35: STAPLE STRAND

Chain Ai:



• Molecule 36: STAPLE STRAND

Chain Aj:

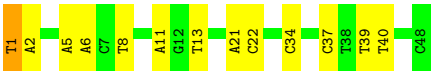


• Molecule 37: STAPLE STRAND

Chain Ak:

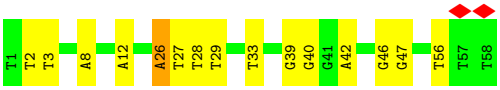
• Molecule 38: STAPLE STRAND

Chain Al:



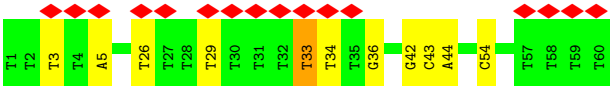
• Molecule 39: STAPLE STRAND

Chain Am:



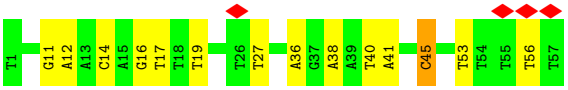
• Molecule 40: STAPLE STRAND

Chain An:



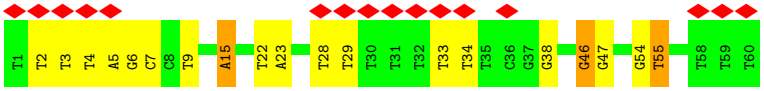
• Molecule 41: STAPLE STRAND

Chain Ao:



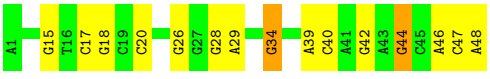
• Molecule 42: STAPLE STRAND

Chain Ap:



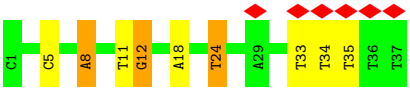
• Molecule 43: STAPLE STRAND

Chain Aq:



• Molecule 44: STAPLE STRAND

Chain Ar:



• Molecule 45: STAPLE STRAND

Chain As:

• Molecule 46: STAPLE STRAND

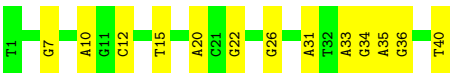
Chain At:

• Molecule 47: STAPLE STRAND

Chain Au:

• Molecule 48: STAPLE STRAND

Chain Av:

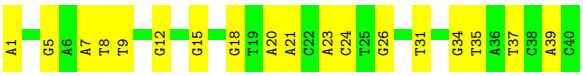


• Molecule 49: STAPLE STRAND

Chain Aw:

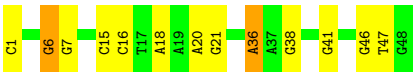
• Molecule 50: STAPLE STRAND

Chain Ax:



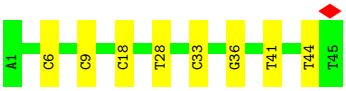
• Molecule 51: STAPLE STRAND

Chain Ay:



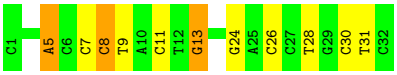
• Molecule 52: STAPLE STRAND

Chain Az:



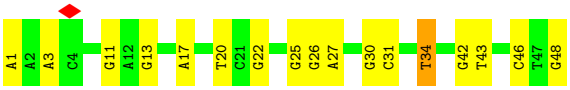
• Molecule 53: STAPLE STRAND

Chain A0:



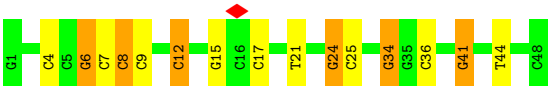
• Molecule 54: STAPLE STRAND

Chain A1:



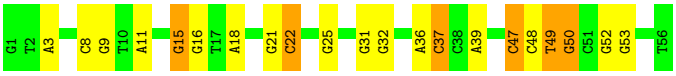
• Molecule 55: STAPLE STRAND

Chain A2:



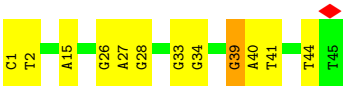
• Molecule 56: STAPLE STRAND

Chain A3:



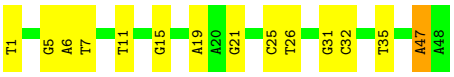
• Molecule 57: STAPLE STRAND

Chain A4:



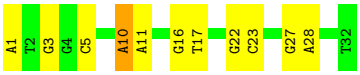
• Molecule 58: STAPLE STRAND

Chain A5:



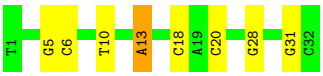
• Molecule 59: STAPLE STRAND

Chain A6:



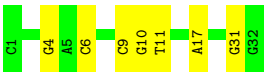
- Molecule 60: STAPLE STRAND

Chain A7:



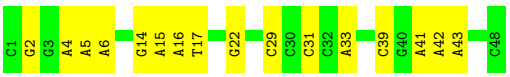
- Molecule 61: STAPLE STRAND

Chain A8:



- Molecule 62: STAPLE STRAND

Chain A9:

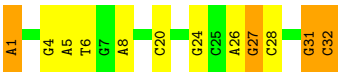


- Molecule 63: STAPLE STRAND

Chain BA:

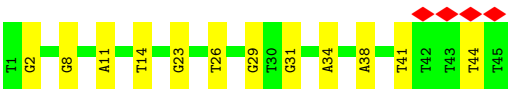
- Molecule 64: STAPLE STRAND

Chain BB:



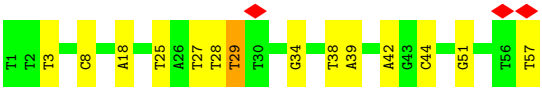
- Molecule 65: STAPLE STRAND

Chain BC:



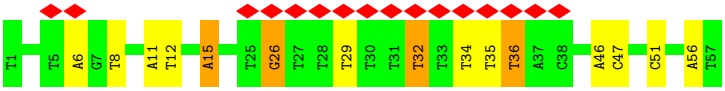
- Molecule 66: STAPLE STRAND

Chain BD:



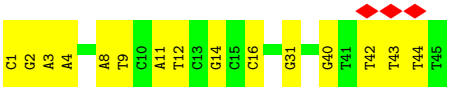
• Molecule 67: STAPLE STRAND

Chain BE:



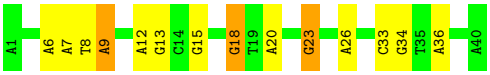
• Molecule 68: STAPLE STRAND

Chain BF:



• Molecule 69: STAPLE STRAND

Chain BG:

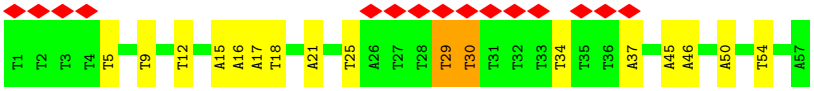


• Molecule 70: STAPLE STRAND

Chain BH:

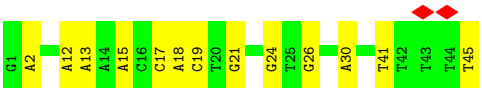
• Molecule 71: STAPLE STRAND

Chain BI:



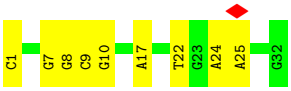
• Molecule 72: STAPLE STRAND

Chain BJ:



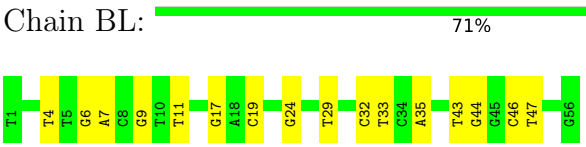
• Molecule 73: STAPLE STRAND

Chain BK:



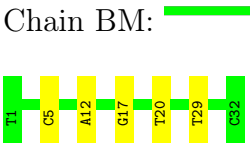
• Molecule 74: STAPLE STRAND

Chain BL:



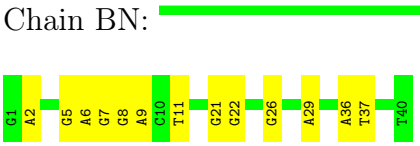
• Molecule 75: STAPLE STRAND

Chain BM:



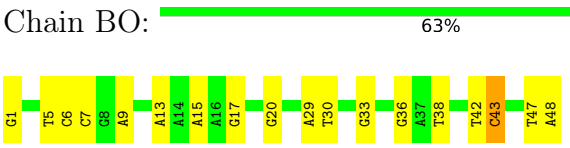
• Molecule 76: STAPLE STRAND

Chain BN:



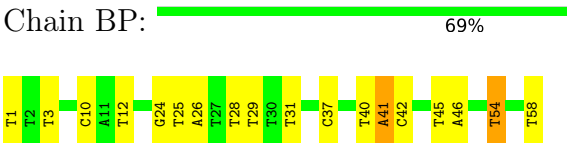
• Molecule 77: STAPLE STRAND

Chain BO:



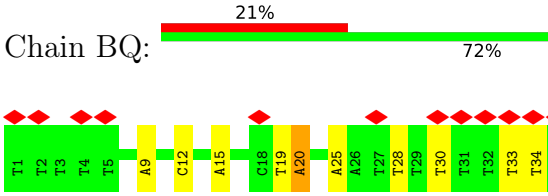
• Molecule 78: STAPLE STRAND

Chain BP:



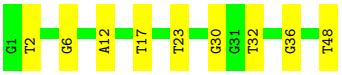
• Molecule 79: STAPLE STRAND

Chain BQ:



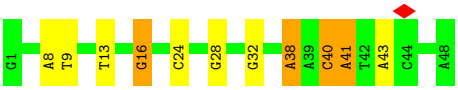
• Molecule 80: STAPLE STRAND

Chain BR:



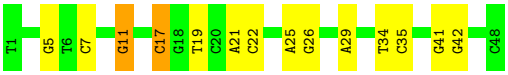
• Molecule 81: STAPLE STRAND

Chain BS:



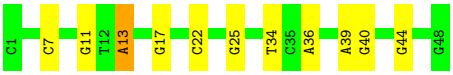
• Molecule 82: STAPLE STRAND

Chain BT:



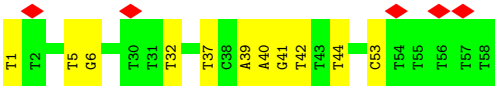
• Molecule 83: STAPLE STRAND

Chain BU:



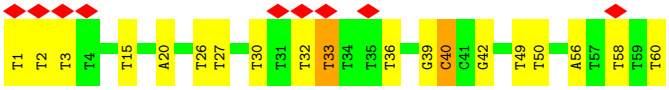
• Molecule 84: STAPLE STRAND

Chain BV:



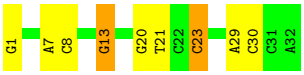
• Molecule 85: STAPLE STRAND

Chain BW:



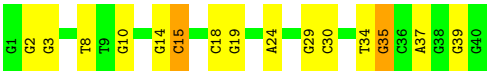
• Molecule 86: STAPLE STRAND

Chain BX:



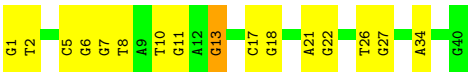
• Molecule 87: STAPLE STRAND

Chain BY:



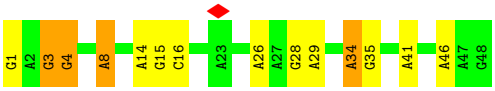
• Molecule 88: STAPLE STRAND

Chain BZ:



• Molecule 89: STAPLE STRAND

Chain Ba:

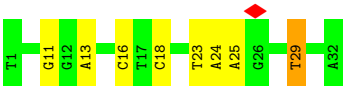


• Molecule 90: STAPLE STRAND

Chain Bb:

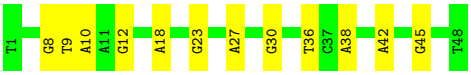
• Molecule 91: STAPLE STRAND

Chain Bc:



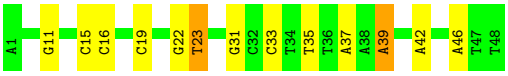
• Molecule 92: STAPLE STRAND

Chain Bd:



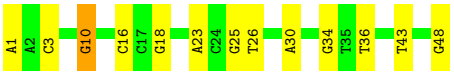
• Molecule 93: STAPLE STRAND

Chain Be:



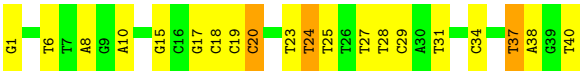
• Molecule 94: STAPLE STRAND

Chain Bf:



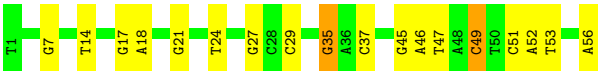
• Molecule 95: STAPLE STRAND

Chain Bg:



• Molecule 96: STAPLE STRAND

Chain Bh:

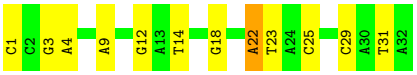


• Molecule 97: STAPLE STRAND

Chain Bi:

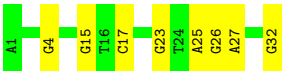
• Molecule 98: STAPLE STRAND

Chain Bj:



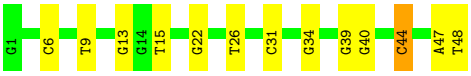
• Molecule 99: STAPLE STRAND

Chain Bk:



• Molecule 100: STAPLE STRAND

Chain Bl:

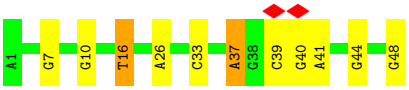


• Molecule 101: STAPLE STRAND

Chain Bm:

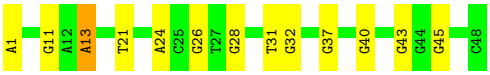
• Molecule 102: STAPLE STRAND

Chain Bn:



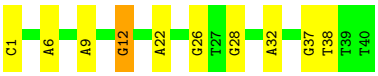
• Molecule 103: STAPLE STRAND

Chain Bo:



• Molecule 104: STAPLE STRAND

Chain Bp:

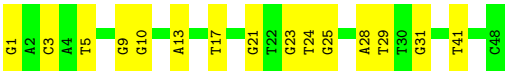


• Molecule 105: STAPLE STRAND

Chain Bq:

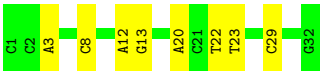
• Molecule 106: STAPLE STRAND

Chain Br:



• Molecule 107: STAPLE STRAND

Chain Bs:

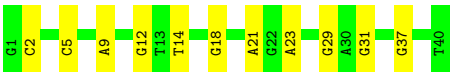


• Molecule 108: STAPLE STRAND

Chain Bt:

• Molecule 109: STAPLE STRAND

Chain Bu:

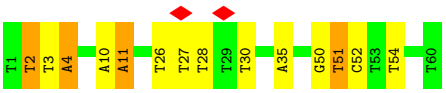


• Molecule 110: STAPLE STRAND

Chain Bv:

• Molecule 111: STAPLE STRAND

Chain Bw:

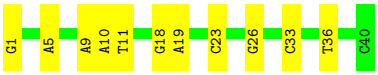


• Molecule 112: STAPLE STRAND

Chain Bx:

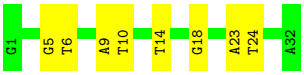
• Molecule 113: STAPLE STRAND

Chain By:



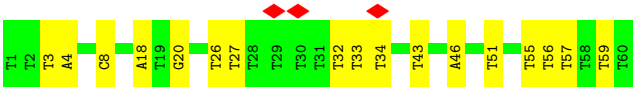
• Molecule 114: STAPLE STRAND

Chain Bz:



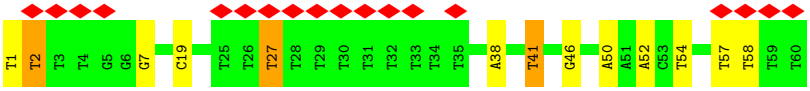
• Molecule 115: STAPLE STRAND

Chain B0:



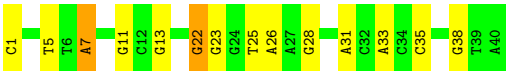
• Molecule 116: STAPLE STRAND

Chain B1:



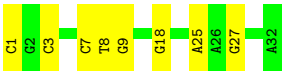
• Molecule 117: STAPLE STRAND

Chain B2:



• Molecule 118: STAPLE STRAND

Chain B3:

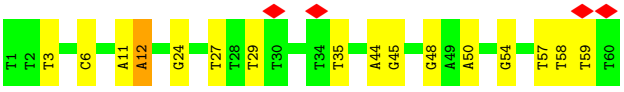


• Molecule 119: STAPLE STRAND

Chain B4:

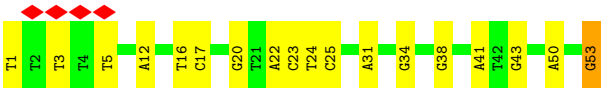
• Molecule 120: STAPLE STRAND

Chain B5:



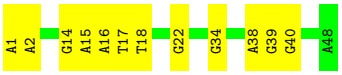
• Molecule 121: STAPLE STRAND

Chain B6:



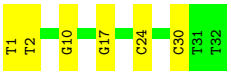
• Molecule 122: STAPLE STRAND

Chain B7:



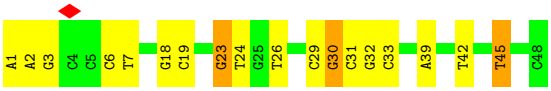
• Molecule 123: STAPLE STRAND

Chain B8:



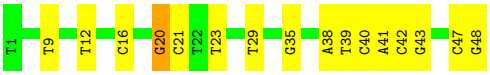
• Molecule 124: STAPLE STRAND

Chain B9:



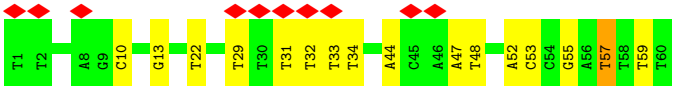
• Molecule 125: STAPLE STRAND

Chain CA:



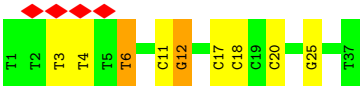
• Molecule 126: STAPLE STRAND

Chain CB:



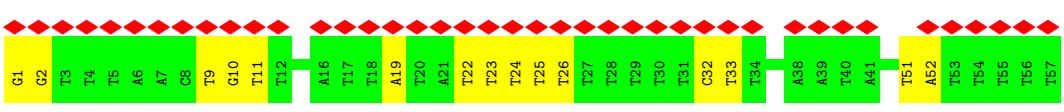
• Molecule 127: STAPLE STRAND

Chain CC:



• Molecule 128: STAPLE STRAND

Chain CD:

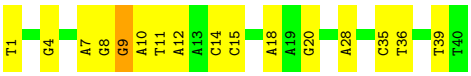


• Molecule 129: STAPLE STRAND

Chain CE:

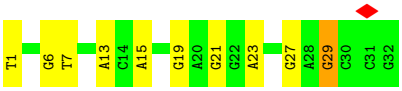
• Molecule 130: STAPLE STRAND

Chain CF:



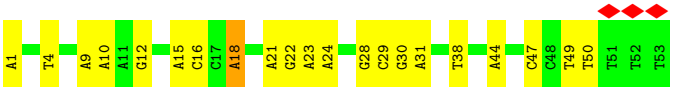
• Molecule 131: STAPLE STRAND

Chain CG:



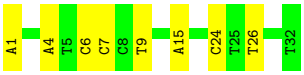
• Molecule 132: STAPLE STRAND

Chain CH:



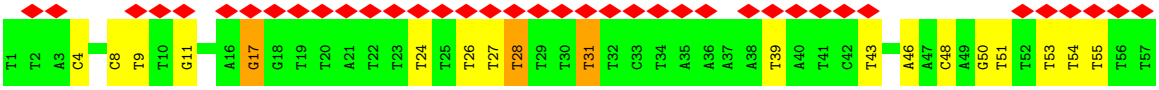
• Molecule 133: STAPLE STRAND

Chain CI:



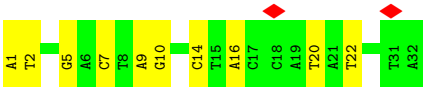
• Molecule 134: STAPLE STRAND

Chain CJ:



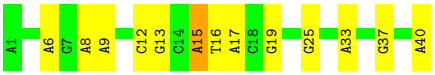
• Molecule 135: STAPLE STRAND

Chain CK:



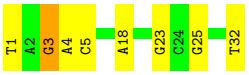
• Molecule 136: STAPLE STRAND

Chain CL:



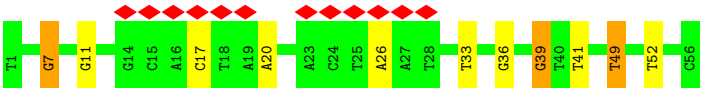
• Molecule 137: STAPLE STRAND

Chain CM:



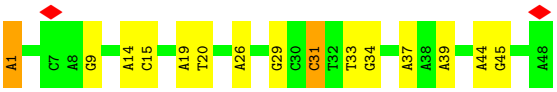
• Molecule 138: STAPLE STRAND

Chain CN:



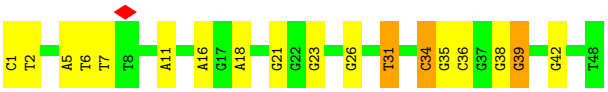
• Molecule 139: STAPLE STRAND

Chain CO:



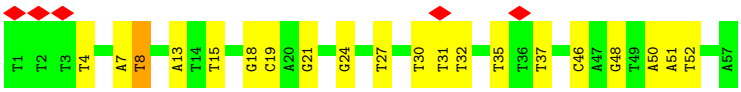
• Molecule 140: STAPLE STRAND

Chain CP:



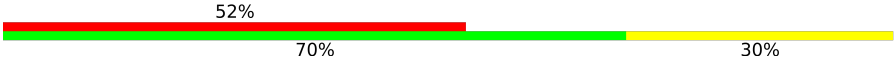
• Molecule 141: STAPLE STRAND

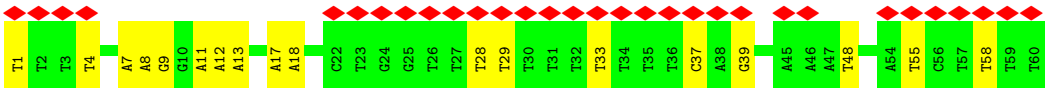
Chain CQ:



• Molecule 142: STAPLE STRAND

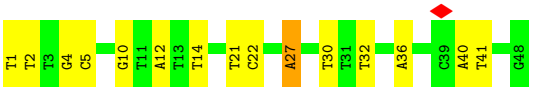
Chain CR:





• Molecule 143: STAPLE STRAND

Chain CS:

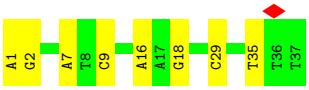


• Molecule 144: STAPLE STRAND

Chain CT:

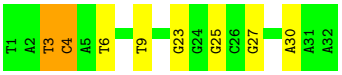
• Molecule 145: STAPLE STRAND

Chain CU:



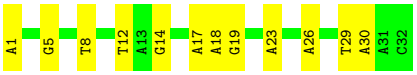
• Molecule 146: STAPLE STRAND

Chain CV:



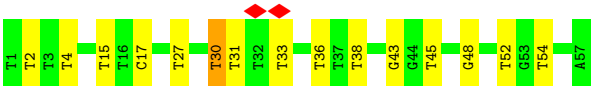
• Molecule 147: STAPLE STRAND

Chain CW:



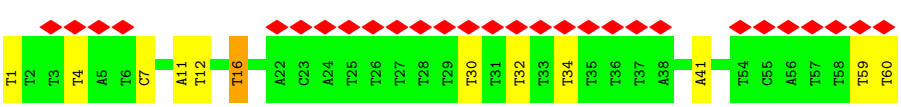
• Molecule 148: STAPLE STRAND

Chain CX:



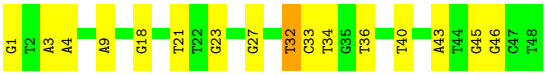
• Molecule 149: STAPLE STRAND

Chain CY:



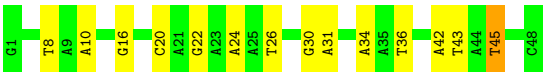
• Molecule 150: STAPLE STRAND

Chain CZ:



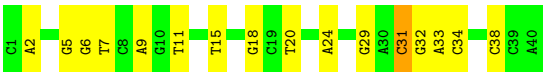
• Molecule 151: STAPLE STRAND

Chain Ca:



• Molecule 152: STAPLE STRAND

Chain Cb:



• Molecule 153: STAPLE STRAND

Chain Cc:

• Molecule 154: STAPLE STRAND

Chain Cd:

• Molecule 155: STAPLE STRAND

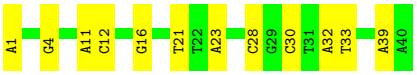
Chain Ce:

• Molecule 156: STAPLE STRAND

Chain Cf:

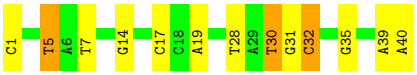
• Molecule 157: STAPLE STRAND

Chain Cg:



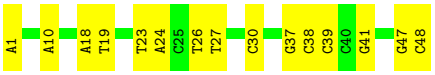
• Molecule 158: STAPLE STRAND

Chain Ch:



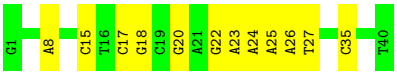
• Molecule 159: STAPLE STRAND

Chain Ci:



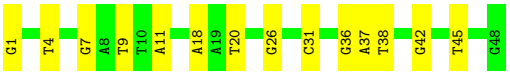
• Molecule 160: STAPLE STRAND

Chain Cj:



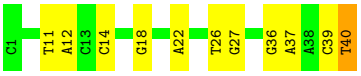
• Molecule 161: STAPLE STRAND

Chain Ck:



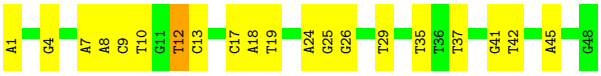
• Molecule 162: STAPLE STRAND

Chain Cl:



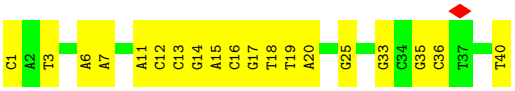
• Molecule 163: STAPLE STRAND

Chain Cm:

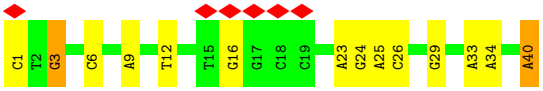


• Molecule 164: STAPLE STRAND

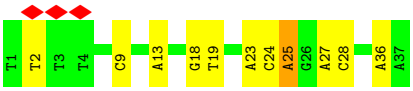
Chain Cn:



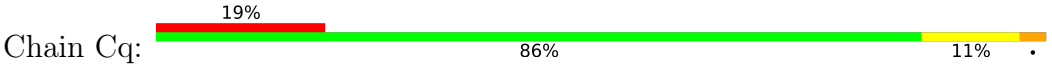
• Molecule 165: STAPLE STRAND

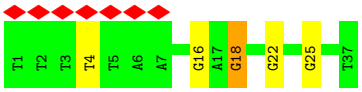


• Molecule 166: STAPLE STRAND

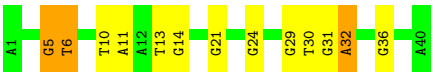


• Molecule 167: STAPLE STRAND





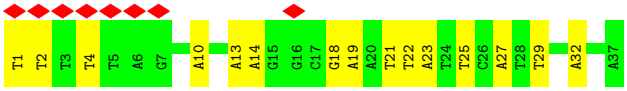
• Molecule 168: STAPLE STRAND



• Molecule 169: STAPLE STRAND

• Molecule 170: STAPLE STRAND

• Molecule 171: STAPLE STRAND



• Molecule 172: STAPLE STRAND

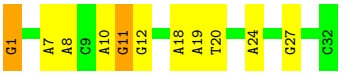
Chain Cv:

• Molecule 173: STAPLE STRAND

Chain Cw:

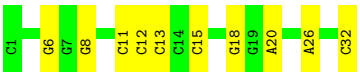
• Molecule 174: STAPLE STRAND

Chain Cx:



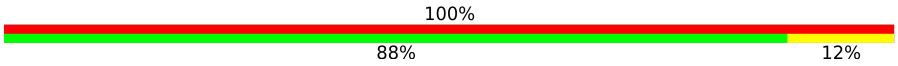
• Molecule 175: STAPLE STRAND

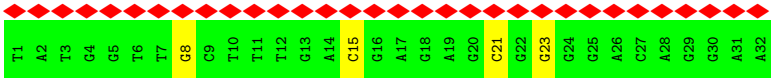
Chain Cy:



• Molecule 176: STAPLE STRAND

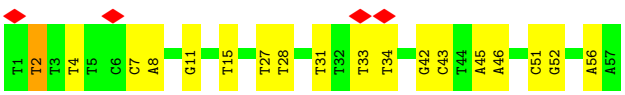
Chain Cz:





• Molecule 177: STAPLE STRAND

Chain C0:

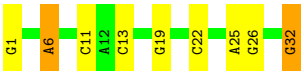


• Molecule 178: STAPLE STRAND

Chain C1:

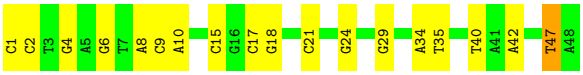
• Molecule 179: STAPLE STRAND

Chain C2:



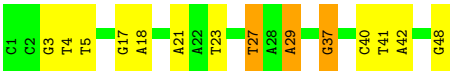
• Molecule 180: STAPLE STRAND

Chain C3:



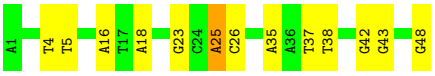
• Molecule 181: STAPLE STRAND

Chain C4:



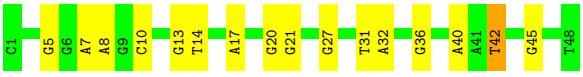
• Molecule 182: STAPLE STRAND

Chain C5:



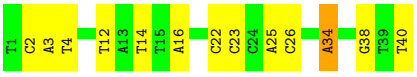
• Molecule 183: STAPLE STRAND

Chain C6:



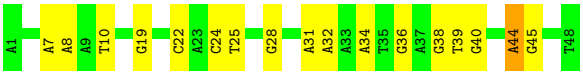
• Molecule 184: STAPLE STRAND

Chain C7:

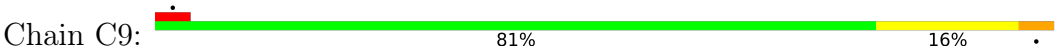


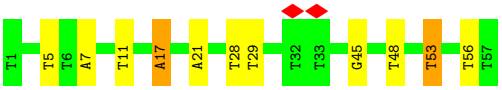
• Molecule 185: STAPLE STRAND

Chain C8:

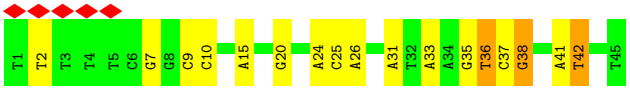


• Molecule 186: STAPLE STRAND

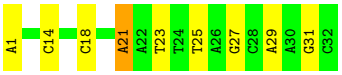




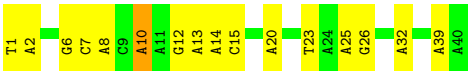
• Molecule 187: STAPLE STRAND



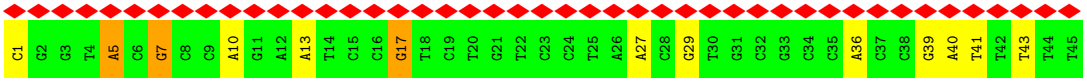
• Molecule 188: STAPLE STRAND



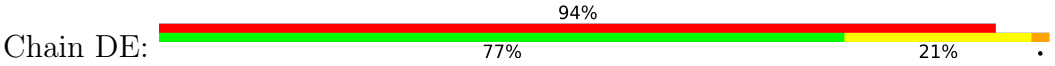
• Molecule 189: STAPLE STRAND

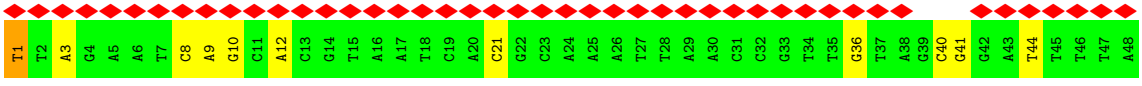


• Molecule 190: STAPLE STRAND

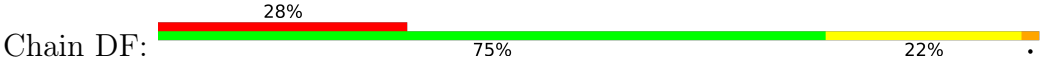


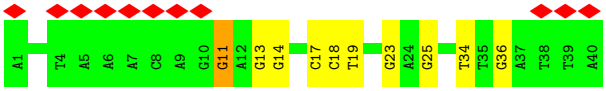
• Molecule 191: STAPLE STRAND



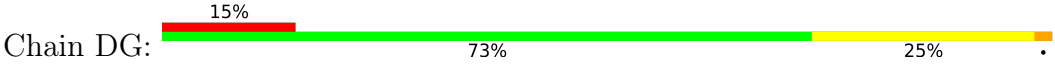


• Molecule 192: STAPLE STRAND

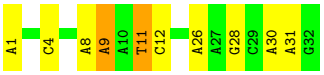




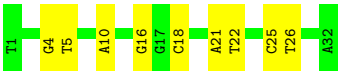
• Molecule 193: STAPLE STRAND



• Molecule 194: STAPLE STRAND



• Molecule 195: STAPLE STRAND



4 Experimental information (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

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

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

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

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

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

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

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
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

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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

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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

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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

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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

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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

5.3.1 Protein backbone

There are no protein molecules in this entry.

5.3.2 Protein sidechains

There are no protein molecules in this entry.

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

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.

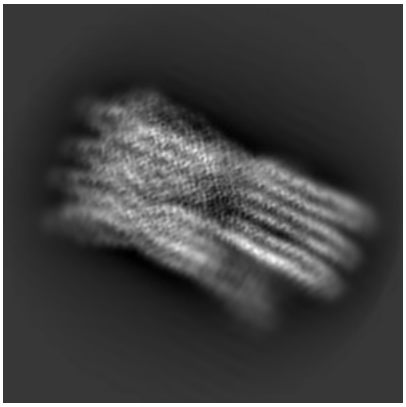
6 Map visualisation

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.

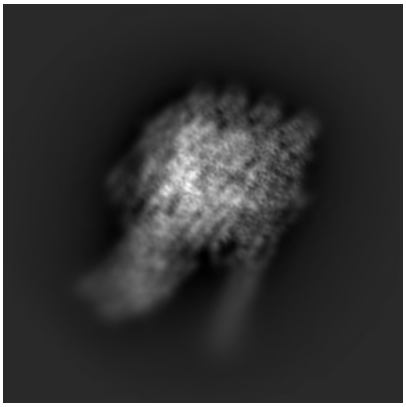
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

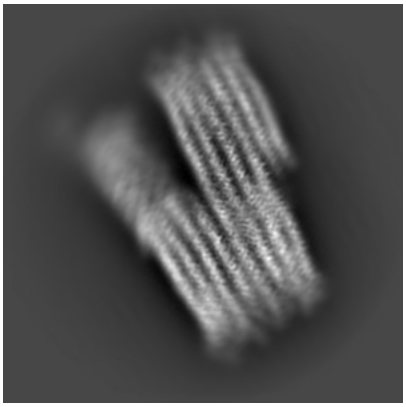
6.1.1 Primary map



X



Y

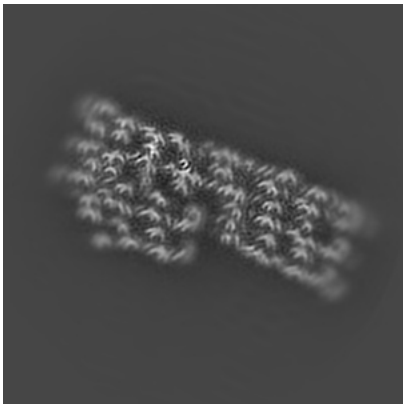


Z

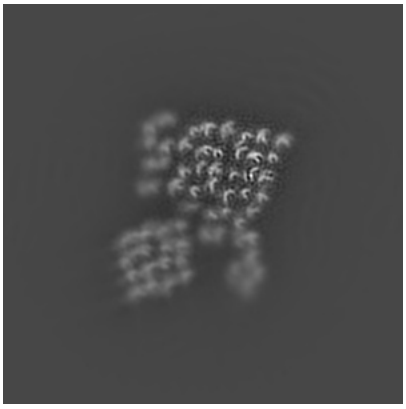
The images above show the map projected in three orthogonal directions.

6.2 Central slices

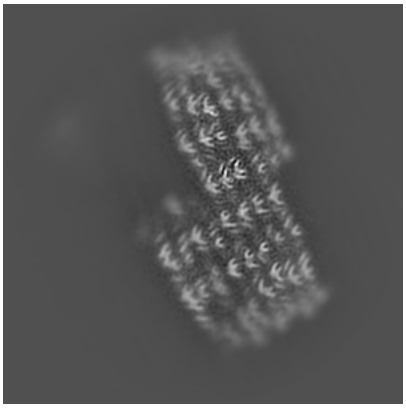
6.2.1 Primary map



X Index: 232



Y Index: 232

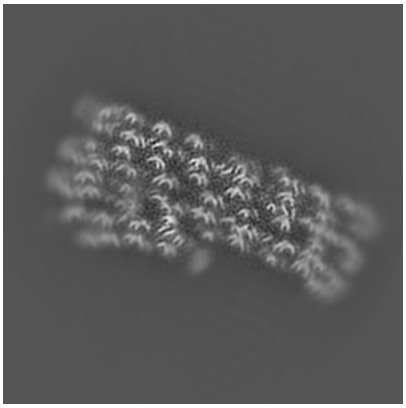


Z Index: 232

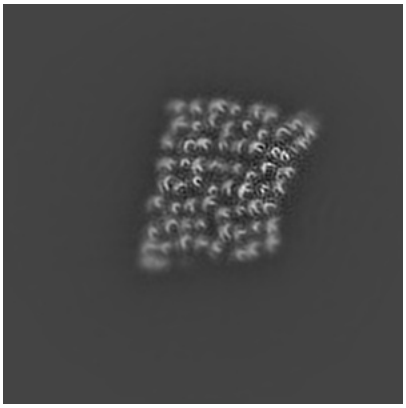
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

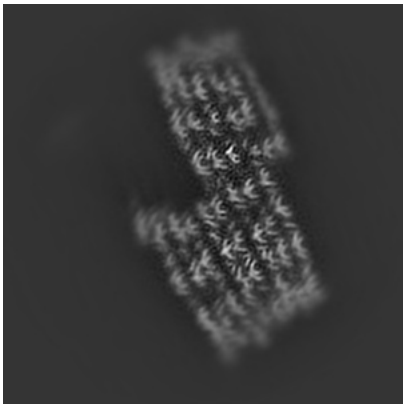
6.3.1 Primary map



X Index: 247



Y Index: 179

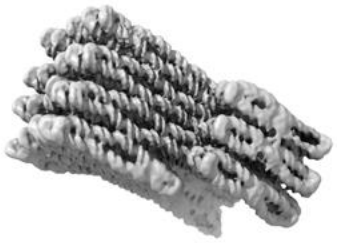


Z Index: 222

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.

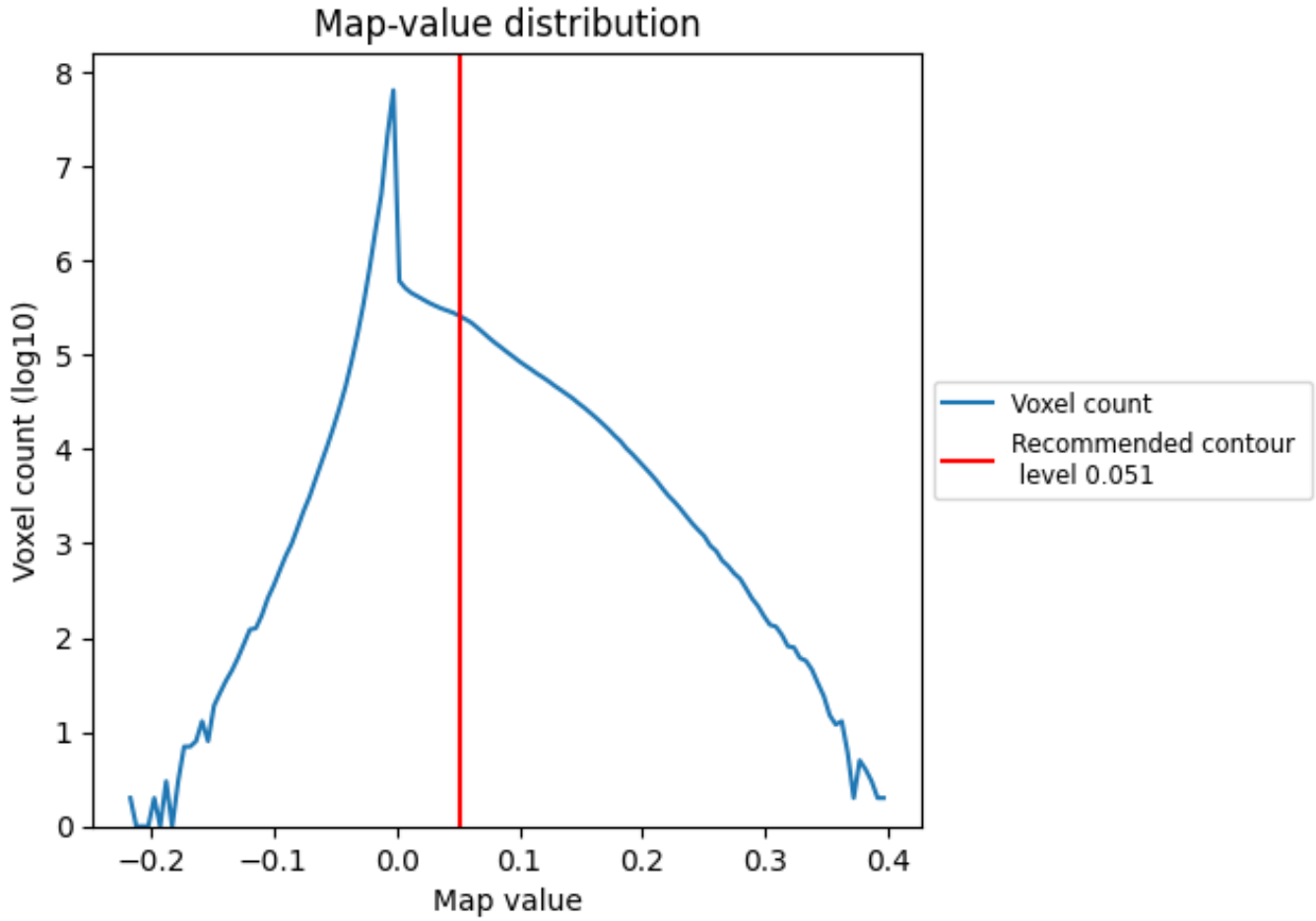
6.5 Mask visualisation (i)

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

7 Map analysis

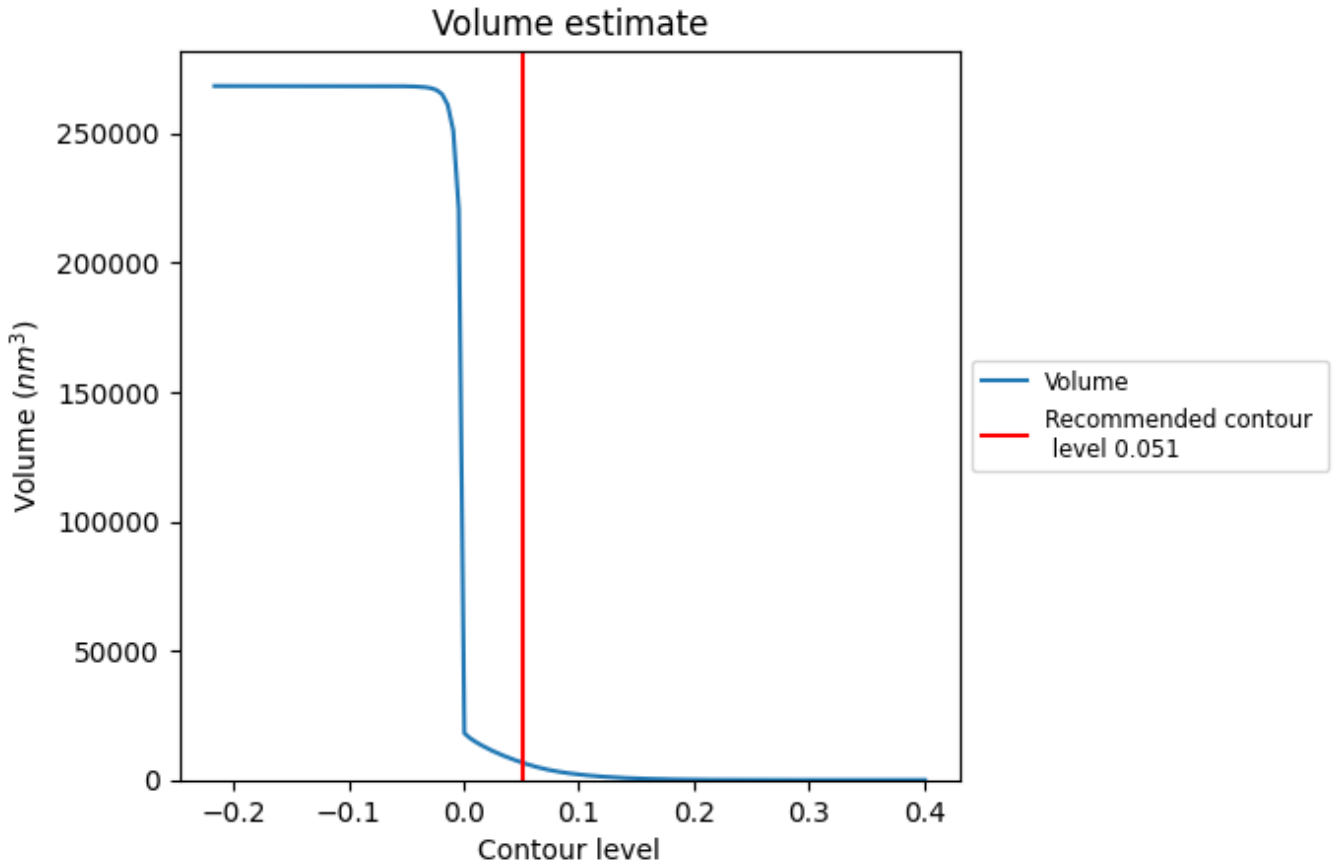
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

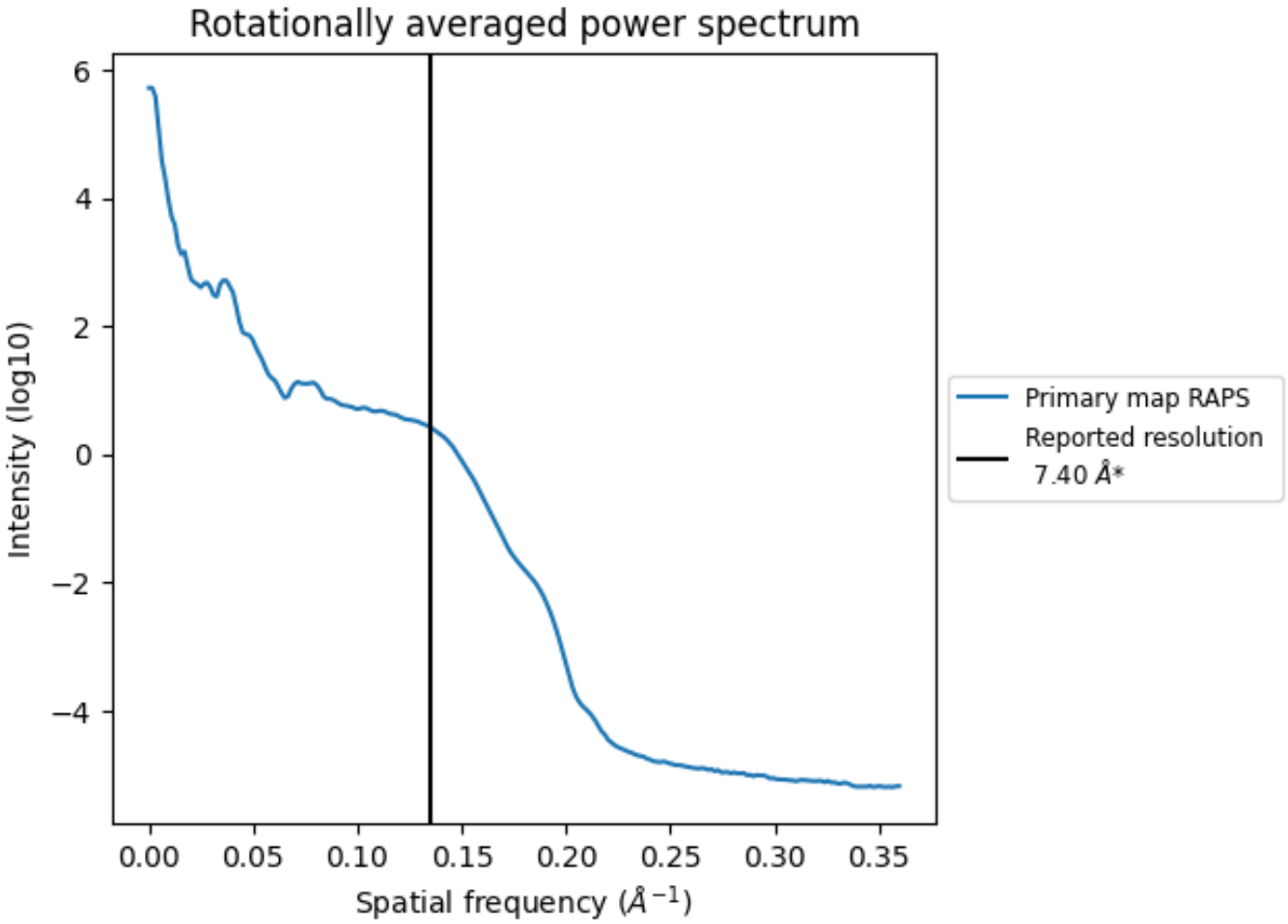
7.2 Volume estimate (i)



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)

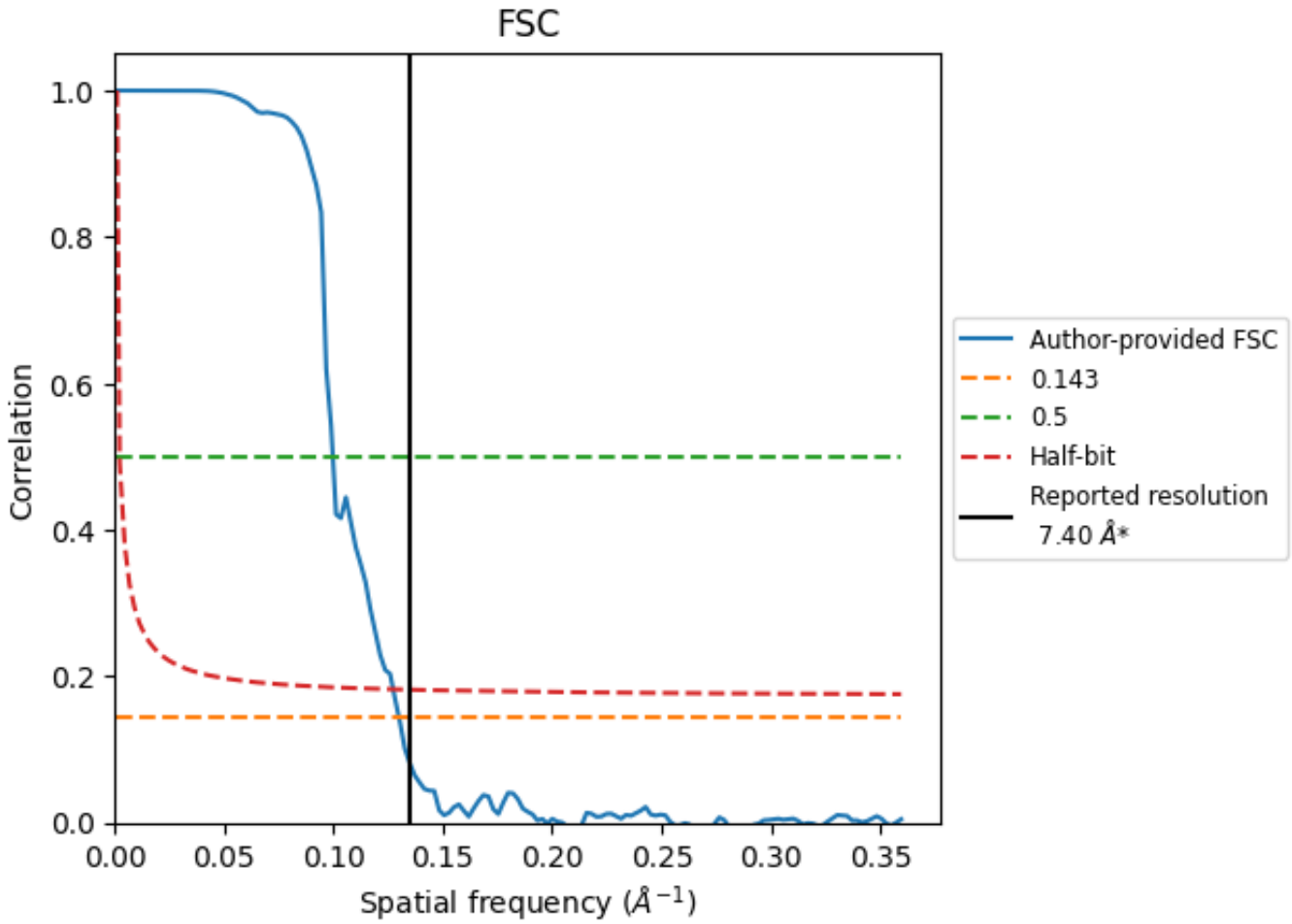


*Reported resolution corresponds to spatial frequency of 0.135 Å^{-1}

8 Fourier-Shell correlation

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



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

8.2 Resolution estimates (i)

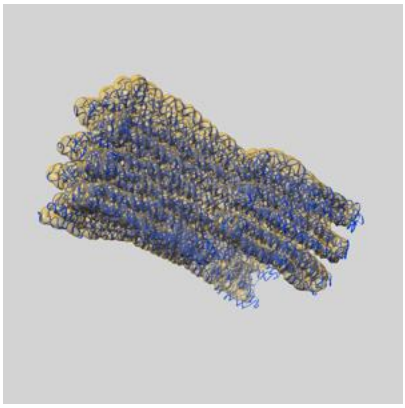
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.40	-	-
Author-provided FSC curve	7.69	10.03	7.86
Unmasked-calculated*	-	-	-

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

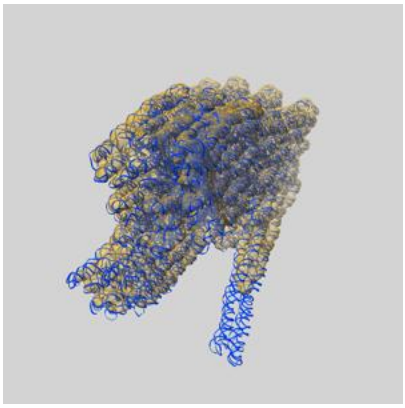
9 Map-model fit

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.

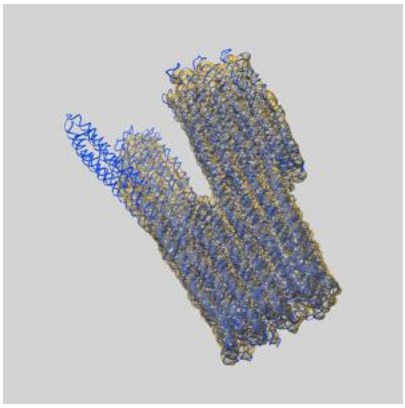
9.1 Map-model overlay



X



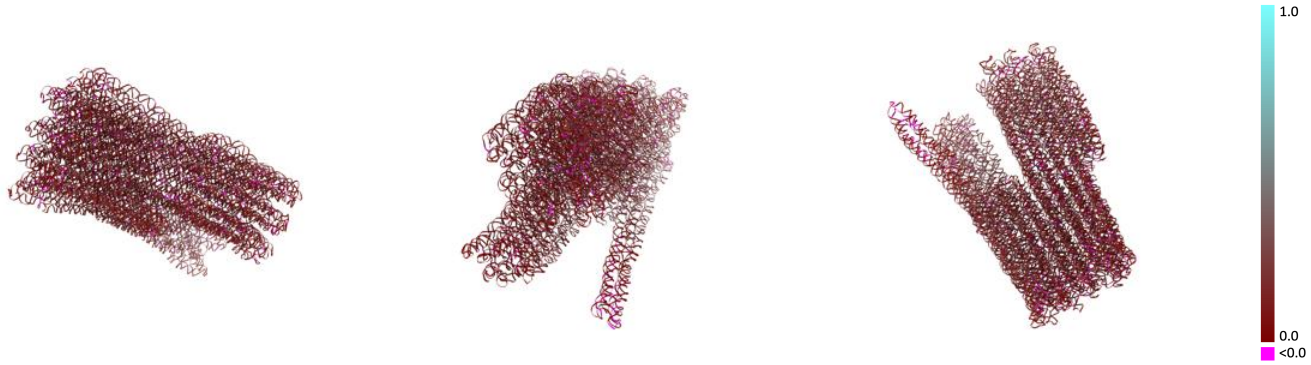
Y



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.

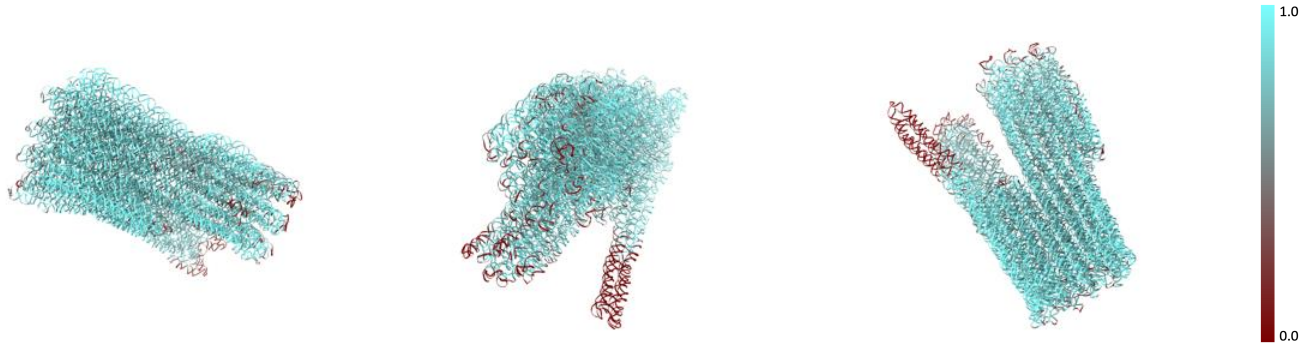
9.2 Q-score mapped to coordinate model



X Y Z

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.

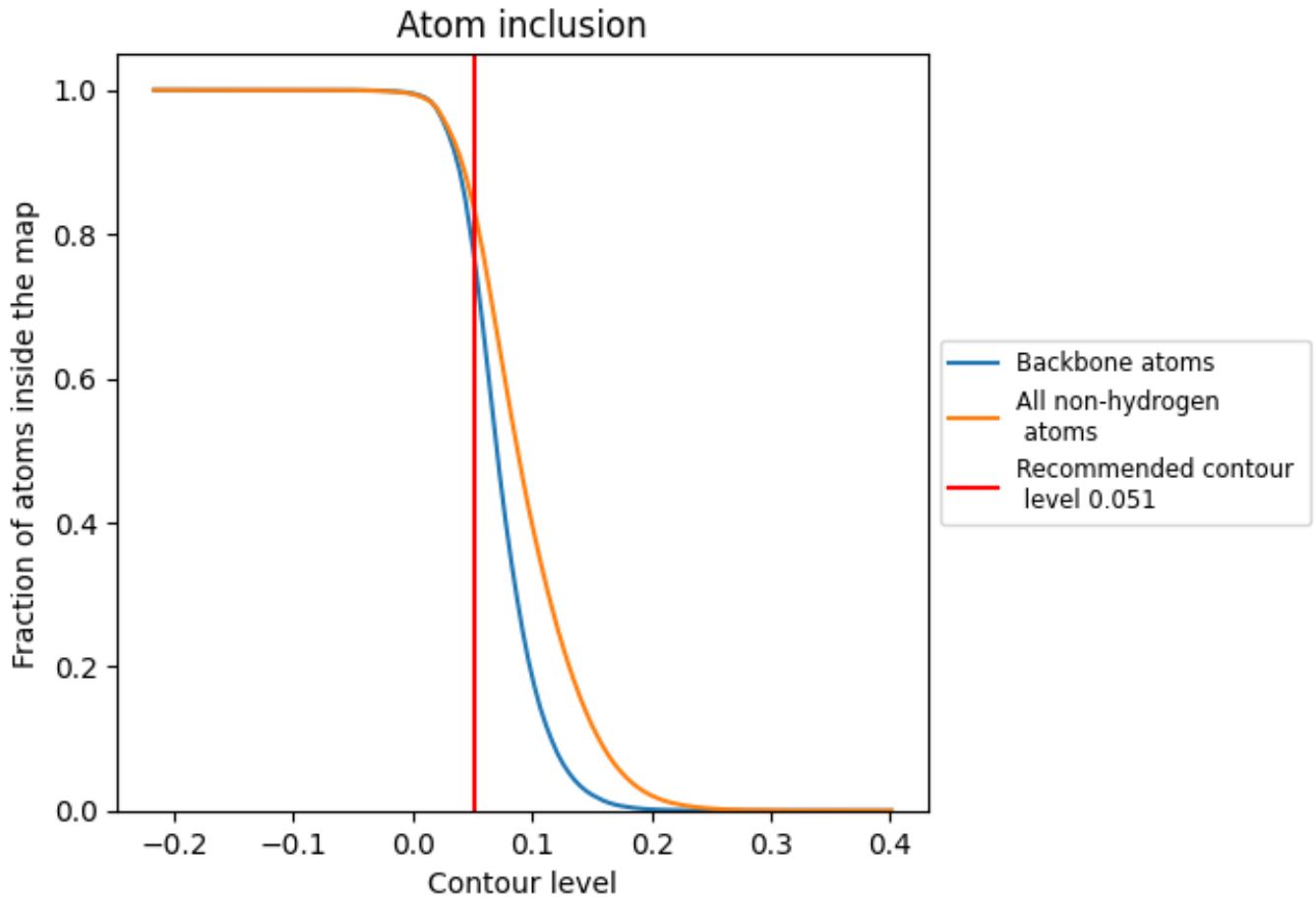
9.3 Atom inclusion mapped to coordinate model



X Y Z

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

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

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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

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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

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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

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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