



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 02:08 PM UTC

PDB ID : 7ARY / pdb_00007ary
EMDB ID : EMD-11378
Title : Twist-Tower_twist-corrected-variant
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 : 8.50 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

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

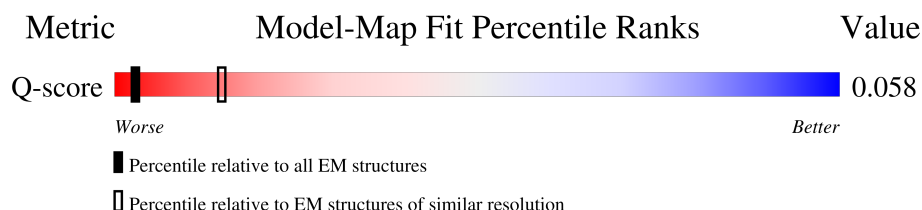
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

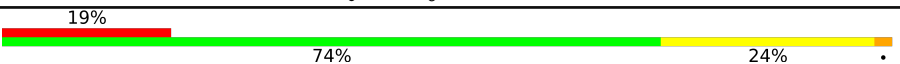
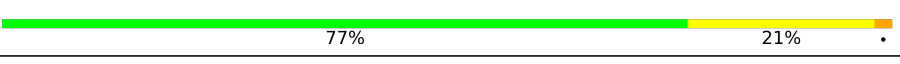
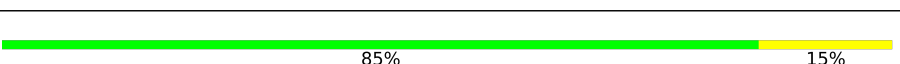
The reported resolution of this entry is 8.50 Å.

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



Metric	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Q-score	25397	328 (8.00 - 9.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	AA	8064	
2	AB	47	
3	AC	53	
4	AD	48	
5	AE	48	
6	AF	55	
7	AG	48	
8	AH	31	
9	AI	28	
10	AJ	48	

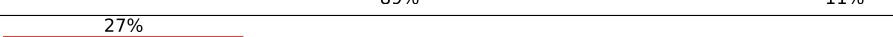
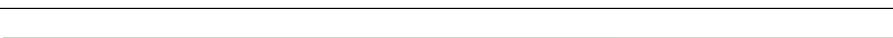
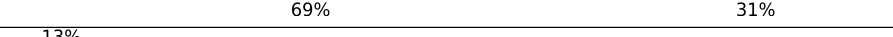
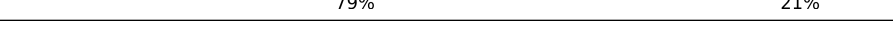
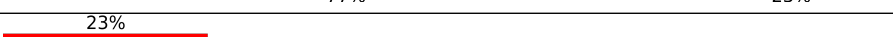
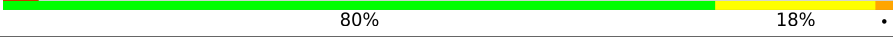
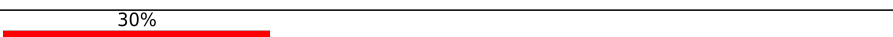
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Mol	Chain	Length	Quality of chain
11	AK	32	
12	AL	52	
13	AM	38	
14	AN	46	
15	AO	46	
16	AP	48	
17	AQ	48	
18	AR	46	
19	AS	50	
20	AT	47	
21	AU	40	
22	AV	45	
23	AW	48	
24	AX	37	
25	AY	47	
26	AZ	40	
27	Aa	53	
28	Ab	39	
29	Ac	31	
30	Ad	45	
31	Ae	52	
32	Af	46	
33	Ag	30	
34	Ah	39	
35	Ai	48	

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Mol	Chain	Length	Quality of chain
36	Aj	40	
37	Ak	38	
38	Al	56	
39	Am	38	
40	An	45	
41	Ao	46	
42	Ap	48	
43	Aq	32	
44	Ar	48	
45	As	48	
46	At	54	
47	Au	46	
48	Av	48	
49	Aw	48	
50	Ax	45	
51	Ay	31	
52	Az	30	
53	A0	32	
54	A1	48	
55	A2	46	
56	A3	30	
57	A4	45	
58	A5	45	
59	A6	48	
60	A7	48	

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Mol	Chain	Length	Quality of chain
61	A8	60	58% 77% 22%
62	A9	38	50% 82% 18%
63	BA	48	6% 81% 19%
64	BB	31	48% 74% 26%
65	BC	60	57% 88% 12%
66	BD	53	85% 15%
67	BE	32	84% 16%
68	BF	38	11% 74% 24%
69	BG	47	9% 64% 32%
70	BH	57	53% 82% 18%
71	BI	45	80% 20%
72	BJ	45	11% 78% 22%
73	BK	48	10% 69% 31%
74	BL	45	76% 24%
75	BM	48	25% 81% 17%
76	BN	30	40% 80% 13% 7%
77	BO	45	11% 71% 29%
78	BP	45	27% 69% 29%
79	BQ	45	27% 73% 27%
80	BR	38	21% 71% 26%
81	BS	48	19% 81% 19%
82	BT	52	13% 77% 21%
83	BU	39	5% 74% 23%
84	BV	32	31% 66% 34%
85	BW	31	81% 19%

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Mol	Chain	Length	Quality of chain
86	BX	45	
87	BY	52	
88	BZ	46	
89	Ba	46	
90	Bb	38	
91	Bc	45	
92	Bd	48	
93	Be	45	
94	Bf	38	
95	Bg	38	
96	Bh	40	
97	Bi	49	
98	Bj	48	
99	Bk	30	
100	Bl	40	
101	Bm	38	
102	Bn	43	
103	Bo	45	
104	Bp	47	
105	Bq	48	
106	Br	38	
107	Bs	30	
108	Bt	45	
109	Bu	49	
110	Bv	40	

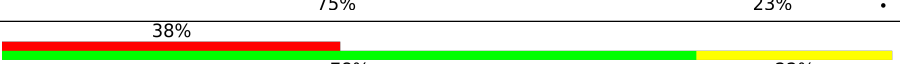
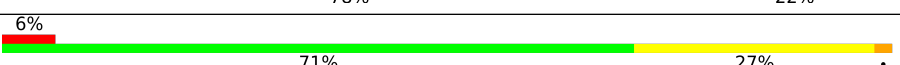
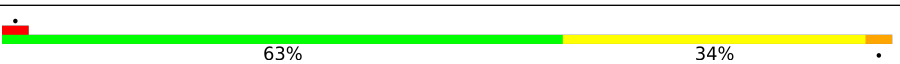
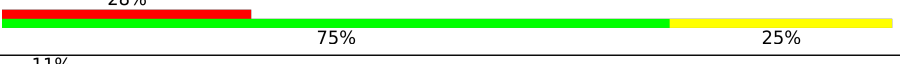
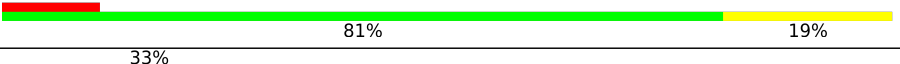
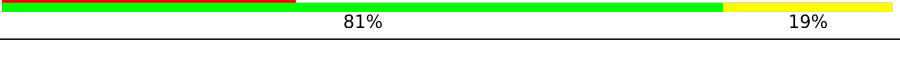
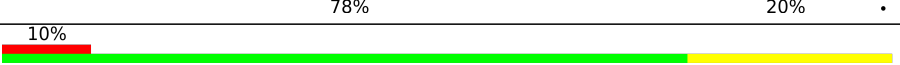
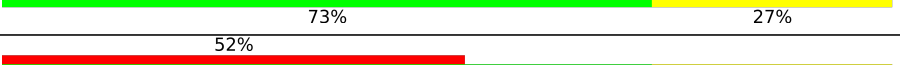
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Mol	Chain	Length	Quality of chain
111	Bw	37	
112	Bx	52	
113	By	30	
114	Bz	40	
115	B0	30	
116	B1	52	
117	B2	30	
118	B3	56	
119	B4	48	
120	B5	31	
121	B6	45	
122	B7	37	
123	B8	52	
124	B9	38	
125	CA	32	
126	CB	32	
127	CC	30	
128	CD	59	
129	CE	52	
130	CF	40	
131	CG	31	
132	CH	53	
133	CI	30	
134	CJ	49	
135	CK	56	

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Mol	Chain	Length	Quality of chain
136	CL	31	
137	CM	32	
138	CN	40	
139	CO	30	
140	CP	54	
141	CQ	48	
142	CR	45	
143	CS	48	
144	CT	38	
145	CU	30	
146	CV	32	
147	CW	47	
148	CX	48	
149	CY	48	
150	CZ	46	
151	Ca	39	
152	Cb	45	
153	Cc	30	
154	Cd	38	
155	Ce	30	
156	Cf	40	
157	Cg	38	
158	Ch	45	
159	Ci	48	
160	Cj	54	

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Mol	Chain	Length	Quality of chain
161	Ck	46	
162	Cl	45	
163	Cm	38	
164	Cn	45	
165	Co	37	
166	Cp	37	
167	Cq	36	
168	Cr	38	
169	Cs	39	
170	Ct	38	
171	Cu	36	
172	Cv	37	
173	Cw	31	
174	Cx	37	
175	Cy	45	
176	Cz	52	
177	C0	60	
178	C1	47	
179	C2	32	
180	C3	37	
181	C4	57	
182	C5	44	
183	C6	47	
184	C7	47	
185	C8	38	

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Mol	Chain	Length	Quality of chain
186	C9	37	
187	DA	60	
188	DB	43	
189	DC	46	
190	DD	38	
191	DE	46	
192	DF	31	

2 Entry composition [i](#)

There are 192 unique types of molecules in this entry. The entry contains 331913 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
1	AA	8064	Total	C	N	O	P	0	0
			164972	78873	29001	49035	8063		

- Molecule 2 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AB	47	Total	C	N	O	P	0	0
			972	463	191	272	46		

- Molecule 3 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AC	53	Total	C	N	O	P	0	0
			1091	520	212	307	52		

- Molecule 4 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AD	48	Total	C	N	O	P	0	0
			989	472	188	282	47		

- Molecule 5 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AE	48	Total	C	N	O	P	0	0
			971	465	171	288	47		

- Molecule 6 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AF	55	Total	C	N	O	P	0	0
			1131	540	216	321	54		

- Molecule 7 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AG	48	Total	C	N	O	P	0	0
			970	471	150	302	47		

- Molecule 8 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AH	31	Total	C	N	O	P	0	0
			636	307	116	183	30		

- Molecule 9 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AI	28	Total	C	N	O	P	0	0
			570	277	92	174	27		

- Molecule 10 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AJ	48	Total	C	N	O	P	0	0
			977	468	177	285	47		

- Molecule 11 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AK	32	Total	C	N	O	P	0	0
			657	312	123	191	31		

- Molecule 12 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AL	52	Total	C	N	O	P	0	0
			1065	511	188	315	51		

- Molecule 13 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AM	38	Total	C	N	O	P	0	0
			766	374	121	234	37		

- Molecule 14 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AN	46	Total	C	N	O	P	0	0
			946	453	174	274	45		

- Molecule 15 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AO	46	Total	C	N	O	P	0	0
			947	450	192	260	45		

- Molecule 16 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AP	48	Total	C	N	O	P	0	0
			982	470	175	290	47		

- Molecule 17 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AQ	48	Total	C	N	O	P	0	0
			972	473	157	295	47		

- Molecule 18 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AR	46	Total	C	N	O	P	0	0
			942	451	170	276	45		

- Molecule 19 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AS	50	Total	C	N	O	P	0	0
			1012	488	184	291	49		

- Molecule 20 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AT	47	Total	C	N	O	P	0	0
			959	458	184	271	46		

- Molecule 21 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AU	40	Total	C	N	O	P	0	0
			823	391	164	229	39		

- Molecule 22 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AV	45	Total	C	N	O	P	0	0
			918	445	149	280	44		

- Molecule 23 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AW	48	Total	C	N	O	P	0	0
			982	467	187	281	47		

- Molecule 24 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AX	37	Total	C	N	O	P	0	0
			763	360	156	211	36		

- Molecule 25 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AY	47	Total	C	N	O	P	0	0
			966	466	176	278	46		

- Molecule 26 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AZ	40	Total	C	N	O	P	0	0
			813	388	152	234	39		

- Molecule 27 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Aa	53	Total	C	N	O	P	0	0
			1086	519	204	311	52		

- Molecule 28 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Ab	39	Total	C	N	O	P	0	0
			798	383	145	232	38		

- Molecule 29 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Ac	31	Total	C	N	O	P	0	0
			624	300	108	186	30		

- Molecule 30 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Ad	45	Total	C	N	O	P	0	0
			927	443	187	253	44		

- Molecule 31 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Ae	52	Total	C	N	O	P	0	0
			1056	509	175	321	51		

- Molecule 32 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Af	46	Total	C	N	O	P	0	0
			936	449	169	273	45		

- Molecule 33 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Ag	30	Total	C	N	O	P	0	0
			616	296	109	182	29		

- Molecule 34 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Ah	39	Total	C	N	O	P	0	0
			801	380	157	226	38		

- Molecule 35 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Ai	48	Total	C	N	O	P	0	0
			981	475	158	301	47		

- Molecule 36 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Aj	40	Total	C	N	O	P	0	0
			820	392	163	226	39		

- Molecule 37 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Ak	38	Total	C	N	O	P	0	0
			775	371	145	222	37		

- Molecule 38 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Al	56	Total	C	N	O	P	0	0
			1136	546	207	328	55		

- Molecule 39 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Am	38	Total	C	N	O	P	0	0
			772	375	126	234	37		

- Molecule 40 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	An	45	Total	C	N	O	P	0	0
			912	435	168	265	44		

- Molecule 41 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Ao	46	Total	C	N	O	P	0	0
			942	450	180	267	45		

- Molecule 42 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Ap	48	Total	C	N	O	P	0	0
			974	470	166	291	47		

- Molecule 43 is a DNA chain called STAPLE STRAND.

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

- Molecule 44 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Ar	48	Total	C	N	O	P	0	0
			988	475	179	287	47		

- Molecule 45 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	As	48	Total	C	N	O	P	0	0
			991	471	204	269	47		

- Molecule 46 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	At	54	Total	C	N	O	P	0	0
			1105	528	210	314	53		

- Molecule 47 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Au	46	Total	C	N	O	P	0	0
			934	452	166	271	45		

- Molecule 48 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Av	48	Total	C	N	O	P	0	0
			985	473	187	278	47		

- Molecule 49 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Aw	48	Total	C	N	O	P	0	0
			964	466	155	296	47		

- Molecule 50 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Ax	45	Total	C	N	O	P	0	0
			917	439	179	255	44		

- Molecule 51 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	Ay	31	Total	C	N	O	P	0	0
			643	304	131	178	30		

- Molecule 52 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Az	30	Total	C	N	O	P	0	0
			613	293	118	173	29		

- 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
			647	308	124	184	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
			984	471	186	280	47		

- Molecule 55 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	A2	46	Total	C	N	O	P	0	0
			941	452	181	263	45		

- Molecule 56 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	A3	30	Total	C	N	O	P	0	0
			615	294	117	175	29		

- Molecule 57 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	A4	45	Total	C	N	O	P	0	0
			914	440	166	264	44		

- Molecule 58 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	A5	45	Total	C	N	O	P	0	0
			923	447	165	267	44		

- Molecule 59 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	A6	48	Total	C	N	O	P	0	0
			994	474	198	275	47		

- Molecule 60 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	A7	48	Total	C	N	O	P	0	0
			977	474	168	288	47		

- Molecule 61 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	A8	60	Total	C	N	O	P	0	0
			1206	582	192	373	59		

- Molecule 62 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	A9	38	Total	C	N	O	P	0	0
			778	371	151	219	37		

- Molecule 63 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	BA	48	Total	C	N	O	P	0	0
			980	469	188	276	47		

- Molecule 64 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	BB	31	Total	C	N	O	P	0	0
			637	303	129	175	30		

- Molecule 65 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	BC	60	Total	C	N	O	P	0	0
			1223	583	224	357	59		

- Molecule 66 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	BD	53	Total	C	N	O	P	0	0
			1088	521	211	304	52		

- Molecule 67 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	BE	32	Total	C	N	O	P	0	0
			648	312	120	185	31		

- Molecule 68 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	BF	38	Total	C	N	O	P	0	0
			779	373	155	214	37		

- Molecule 69 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	BG	47	Total	C	N	O	P	0	0
			959	462	162	289	46		

- Molecule 70 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	BH	57	Total	C	N	O	P	0	0
			1159	563	178	362	56		

- Molecule 71 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	BI	45	Total	C	N	O	P	0	0
			917	437	172	264	44		

- Molecule 72 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	BJ	45	Total	C	N	O	P	0	0
			927	442	179	262	44		

- Molecule 73 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	BK	48	Total	C	N	O	P	0	0
			981	470	178	286	47		

- Molecule 74 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	BL	45	Total	C	N	O	P	0	0
			918	441	165	268	44		

- Molecule 75 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	BM	48	Total	C	N	O	P	0	0
			990	475	188	280	47		

- Molecule 76 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	BN	30	Total	C	N	O	P	0	0
			618	296	118	175	29		

- Molecule 77 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	BO	45	Total	C	N	O	P	0	0
			914	438	165	267	44		

- Molecule 78 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	BP	45	Total	C	N	O	P	0	0
			920	440	178	258	44		

- Molecule 79 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	BQ	45	Total	C	N	O	P	0	0
			929	443	181	261	44		

- Molecule 80 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	BR	38	Total	C	N	O	P	0	0
			770	370	134	229	37		

- 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
			972	471	168	286	47		

- Molecule 82 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	BT	52	Total	C	N	O	P	0	0
			1070	507	213	299	51		

- Molecule 83 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	BU	39	Total	C	N	O	P	0	0
			784	375	138	233	38		

- Molecule 84 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	BV	32	Total	C	N	O	P	0	0
			646	311	109	195	31		

- Molecule 85 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	BW	31	Total	C	N	O	P	0	0
			624	297	117	180	30		

- Molecule 86 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	BX	45	Total	C	N	O	P	0	0
			913	438	168	263	44		

- Molecule 87 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	BY	52	Total	C	N	O	P	0	0
			1065	512	196	306	51		

- Molecule 88 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
88	BZ	46	Total	C	N	O	P	0	0
			957	453	189	270	45		

- Molecule 89 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
89	Ba	46	Total	C	N	O	P	0	0
			952	452	190	265	45		

- Molecule 90 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
90	Bb	38	Total	C	N	O	P	0	0
			791	376	161	217	37		

- Molecule 91 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
91	Bc	45	Total	C	N	O	P	0	0
			923	444	165	270	44		

- Molecule 92 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
92	Bd	48	Total	C	N	O	P	0	0
			985	473	190	275	47		

- Molecule 93 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
93	Be	45	Total	C	N	O	P	0	0
			908	432	174	258	44		

- Molecule 94 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
94	Bf	38	Total	C	N	O	P	0	0
			776	375	138	226	37		

- Molecule 95 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
95	Bg	38	Total	C	N	O	P	0	0
			783	373	149	224	37		

- Molecule 96 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
96	Bh	40	Total	C	N	O	P	0	0
			814	388	161	226	39		

- Molecule 97 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
97	Bi	49	Total	C	N	O	P	0	0
			993	483	159	303	48		

- Molecule 98 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
98	Bj	48	Total	C	N	O	P	0	0
			991	475	194	275	47		

- Molecule 99 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
99	Bk	30	Total	C	N	O	P	0	0
			620	296	124	171	29		

- Molecule 100 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
100	Bl	40	Total	C	N	O	P	0	0
			829	394	167	229	39		

- Molecule 101 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
101	Bm	38	Total	C	N	O	P	0	0
			773	370	149	217	37		

- Molecule 102 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
102	Bn	43	Total	C	N	O	P	0	0
			878	425	154	257	42		

- Molecule 103 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
103	Bo	45	Total	C	N	O	P	0	0
			914	445	149	276	44		

- Molecule 104 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
104	Bp	47	Total	C	N	O	P	0	0
			974	463	194	271	46		

- 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
			984	474	165	298	47		

- Molecule 106 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
106	Br	38	Total	C	N	O	P	0	0
			778	375	138	228	37		

- Molecule 107 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
107	Bs	30	Total	C	N	O	P	0	0
			609	296	100	184	29		

- Molecule 108 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
108	Bt	45	Total	C	N	O	P	0	0
			919	445	155	275	44		

- Molecule 109 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
109	Bu	49	Total	C	N	O	P	0	0
			1004	487	167	302	48		

- 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
			815	387	159	230	39		

- Molecule 111 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
111	Bw	37	Total	C	N	O	P	0	0
			752	365	136	215	36		

- Molecule 112 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
112	Bx	52	Total	C	N	O	P	0	0
			1059	516	168	324	51		

- Molecule 113 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
113	By	30	Total	C	N	O	P	0	0
			625	297	126	173	29		

- Molecule 114 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
114	Bz	40	Total	C	N	O	P	0	0
			821	393	162	227	39		

- Molecule 115 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
115	B0	30	Total	C	N	O	P	0	0
			613	296	112	176	29		

- Molecule 116 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
116	B1	52	Total	C	N	O	P	0	0
			1065	520	170	324	51		

- Molecule 117 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
117	B2	30	Total	C	N	O	P	0	0
			614	295	116	174	29		

- Molecule 118 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
118	B3	56	Total	C	N	O	P	0	0
			1143	545	214	329	55		

- Molecule 119 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
119	B4	48	Total	C	N	O	P	0	0
			988	468	195	278	47		

- Molecule 120 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
120	B5	31	Total	C	N	O	P	0	0
			632	308	106	188	30		

- Molecule 121 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
121	B6	45	Total	C	N	O	P	0	0
			929	444	171	270	44		

- Molecule 122 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
122	B7	37	Total	C	N	O	P	0	0
			761	362	145	218	36		

- Molecule 123 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
123	B8	52	Total	C	N	O	P	0	0
			1066	510	183	322	51		

- Molecule 124 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
124	B9	38	Total	C	N	O	P	0	0
			768	370	128	233	37		

- Molecule 125 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
125	CA	32	Total	C	N	O	P	0	0
			644	307	119	187	31		

- Molecule 126 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
126	CB	32	Total	C	N	O	P	0	0
			656	313	122	190	31		

- Molecule 127 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
127	CC	30	Total	C	N	O	P	0	0
			624	295	125	175	29		

- Molecule 128 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
128	CD	59	Total	C	N	O	P	0	0
			1200	576	204	362	58		

- Molecule 129 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
129	CE	52	Total	C	N	O	P	0	0
			1062	511	194	306	51		

- 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
			816	387	162	228	39		

- Molecule 131 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
131	CG	31	Total	C	N	O	P	0	0
			626	296	115	185	30		

- 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
			1098	522	204	320	52		

- Molecule 133 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
133	CI	30	Total	C	N	O	P	0	0
			614	293	115	177	29		

- Molecule 134 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
134	CJ	49	Total	C	N	O	P	0	0
			988	483	144	313	48		

- Molecule 135 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
135	CK	56	Total	C	N	O	P	0	0
			1138	548	181	354	55		

- Molecule 136 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
136	CL	31	Total	C	N	O	P	0	0
			640	304	122	184	30		

- Molecule 137 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
137	CM	32	Total	C	N	O	P	0	0
			653	311	127	184	31		

- Molecule 138 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
138	CN	40	Total	C	N	O	P	0	0
			827	394	164	230	39		

- Molecule 139 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
139	CO	30	Total	C	N	O	P	0	0
			607	291	108	179	29		

- Molecule 140 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
140	CP	54	Total	C	N	O	P	0	0
			1106	527	196	330	53		

- Molecule 141 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
141	CQ	48	Total	C	N	O	P	0	0
			976	465	180	284	47		

- Molecule 142 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
142	CR	45	Total	C	N	O	P	0	0
			923	442	167	270	44		

- Molecule 143 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
143	CS	48	Total	C	N	O	P	0	0
			983	466	185	285	47		

- Molecule 144 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
144	CT	38	Total	C	N	O	P	0	0
			769	366	144	222	37		

- Molecule 145 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
145	CU	30	Total	C	N	O	P	0	0
			619	294	123	173	29		

- Molecule 146 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
146	CV	32	Total	C	N	O	P	0	0
			652	309	126	186	31		

- Molecule 147 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
147	CW	47	Total	C	N	O	P	0	0
			970	462	183	279	46		

- Molecule 148 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
148	CX	48	Total	C	N	O	P	0	0
			974	472	158	297	47		

- Molecule 149 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
149	CY	48	Total	C	N	O	P	0	0
			995	468	201	279	47		

- Molecule 150 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
150	CZ	46	Total	C	N	O	P	0	0
			948	456	162	285	45		

- Molecule 151 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
151	Ca	39	Total	C	N	O	P	0	0
			798	380	157	223	38		

- Molecule 152 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
152	Cb	45	Total	C	N	O	P	0	0
			933	441	189	259	44		

- Molecule 153 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
153	Cc	30	Total	C	N	O	P	0	0
			616	293	112	182	29		

- Molecule 154 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
154	Cd	38	Total	C	N	O	P	0	0
			779	368	151	223	37		

- Molecule 155 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
155	Ce	30	Total	C	N	O	P	0	0
			603	288	105	181	29		

- Molecule 156 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
156	Cf	40	Total	C	N	O	P	0	0
			803	385	149	230	39		

- Molecule 157 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
157	Cg	38	Total	C	N	O	P	0	0
			779	371	145	226	37		

- Molecule 158 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
158	Ch	45	Total	C	N	O	P	0	0
			928	441	177	266	44		

- 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
			977	469	158	303	47		

- Molecule 160 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
160	Cj	54	Total	C	N	O	P	0	0
			1107	525	207	322	53		

- Molecule 161 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
161	Ck	46	Total	C	N	O	P	0	0
			948	451	185	267	45		

- Molecule 162 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
162	Cl	45	Total	C	N	O	P	0	0
			913	435	162	272	44		

- Molecule 163 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
163	Cm	38	Total	C	N	O	P	0	0
			765	369	123	236	37		

- Molecule 164 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
164	Cn	45	Total	C	N	O	P	0	0
			916	437	178	257	44		

- Molecule 165 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
165	Co	37	Total	C	N	O	P	0	0
			752	364	125	227	36		

- Molecule 166 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
166	Cp	37	Total	C	N	O	P	0	0
			752	358	134	224	36		

- Molecule 167 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
167	Cq	36	Total	C	N	O	P	0	0
			731	350	127	219	35		

- Molecule 168 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
168	Cr	38	Total	C	N	O	P	0	0
			778	371	142	228	37		

- Molecule 169 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
169	Cs	39	Total	C	N	O	P	0	0
			804	381	147	238	38		

- Molecule 170 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
170	Ct	38	Total	C	N	O	P	0	0
			781	371	157	216	37		

- Molecule 171 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
171	Cu	36	Total	C	N	O	P	0	0
			736	355	125	221	35		

- Molecule 172 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
172	Cv	37	Total	C	N	O	P	0	0
			748	360	123	229	36		

- Molecule 173 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
173	Cw	31	Total	C	N	O	P	0	0
			629	300	123	176	30		

- Molecule 174 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
174	Cx	37	Total	C	N	O	P	0	0
			761	364	152	209	36		

- Molecule 175 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
175	Cy	45	Total	C	N	O	P	0	0
			917	436	167	270	44		

- Molecule 176 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
176	Cz	52	Total	C	N	O	P	0	0
			1061	510	180	320	51		

- Molecule 177 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
177	C0	60	Total	C	N	O	P	0	0
			1215	590	190	376	59		

- Molecule 178 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
178	C1	47	Total	C	N	O	P	0	0
			964	461	178	279	46		

- Molecule 179 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
179	C2	32	Total	C	N	O	P	0	0
			660	316	125	188	31		

- Molecule 180 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
180	C3	37	Total	C	N	O	P	0	0
			757	360	141	220	36		

- Molecule 181 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
181	C4	57	Total	C	N	O	P	0	0
			1159	561	189	353	56		

- Molecule 182 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
182	C5	44	Total	C	N	O	P	0	0
			910	435	177	255	43		

- Molecule 183 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
183	C6	47	Total	C	N	O	P	0	0
			959	458	181	274	46		

- Molecule 184 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
184	C7	47	Total	C	N	O	P	0	0
			957	456	186	269	46		

- Molecule 185 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
185	C8	38	Total	C	N	O	P	0	0
			771	368	139	227	37		

- Molecule 186 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
186	C9	37	Total	C	N	O	P	0	0
			766	366	150	214	36		

- Molecule 187 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
187	DA	60	Total	C	N	O	P	0	0
			1225	589	221	356	59		

- Molecule 188 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
188	DB	43	Total	C	N	O	P	0	0
			876	418	155	261	42		

- Molecule 189 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
189	DC	46	Total	C	N	O	P	0	0
			952	453	195	259	45		

- Molecule 190 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
190	DD	38	Total	C	N	O	P	0	0
			775	369	144	225	37		

- Molecule 191 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
191	DE	46	Total	C	N	O	P	0	0
			940	446	181	268	45		

- Molecule 192 is a DNA chain called STAPLE STRAND.

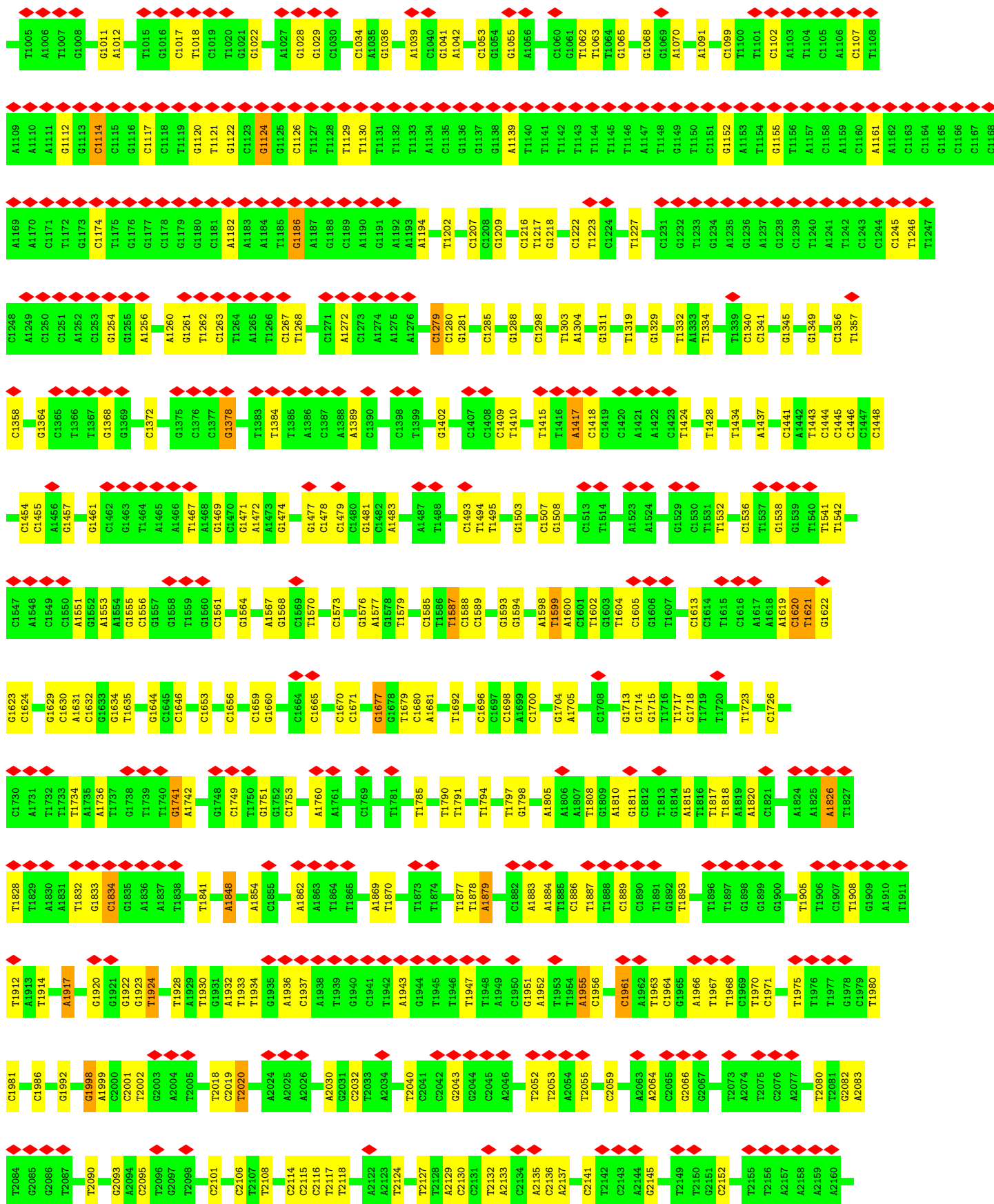
Mol	Chain	Residues	Atoms					AltConf	Trace
192	DF	31	Total	C	N	O	P	0	0
			638	304	125	179	30		

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.

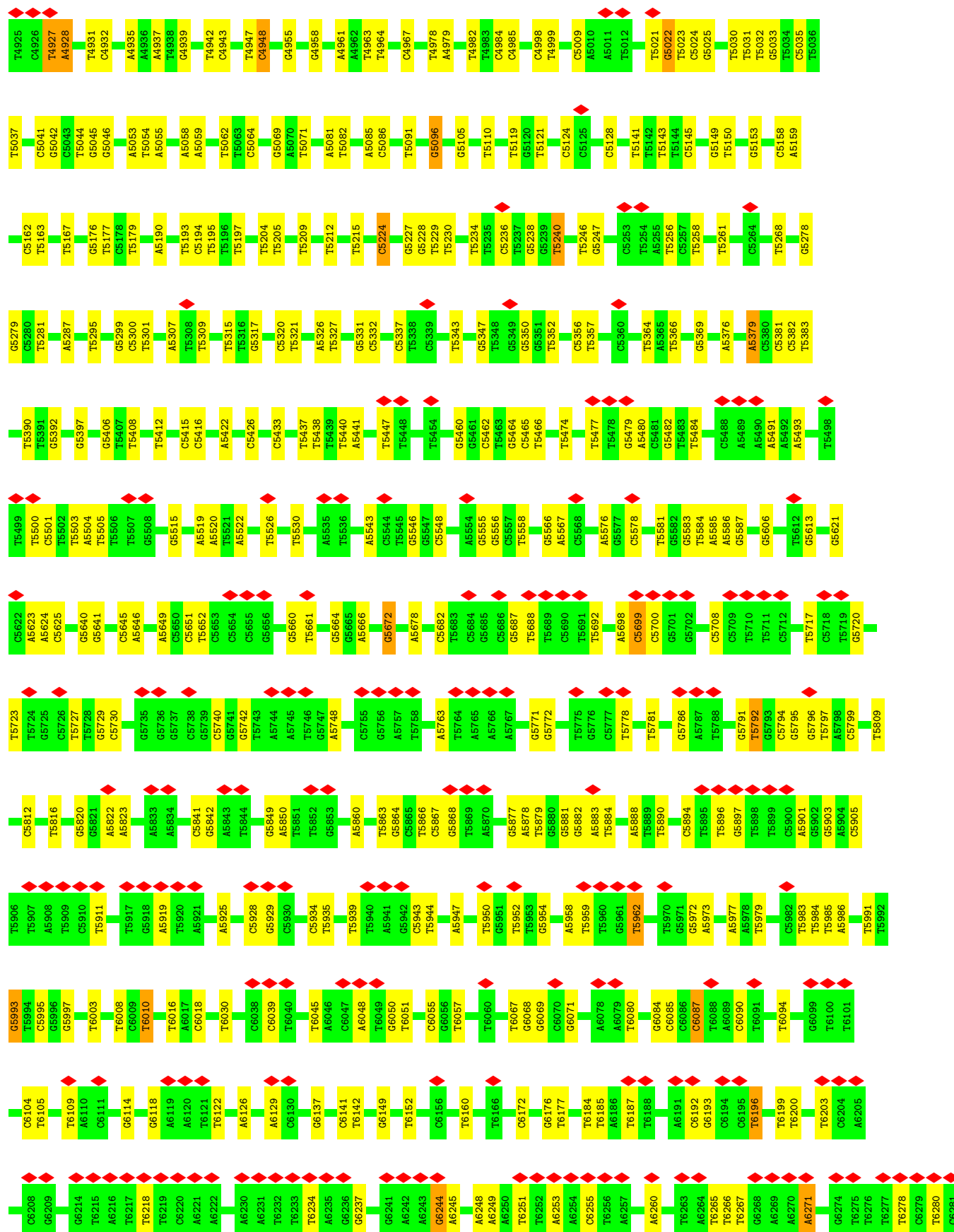
• Molecule 1: SCAFFOLD STRAND

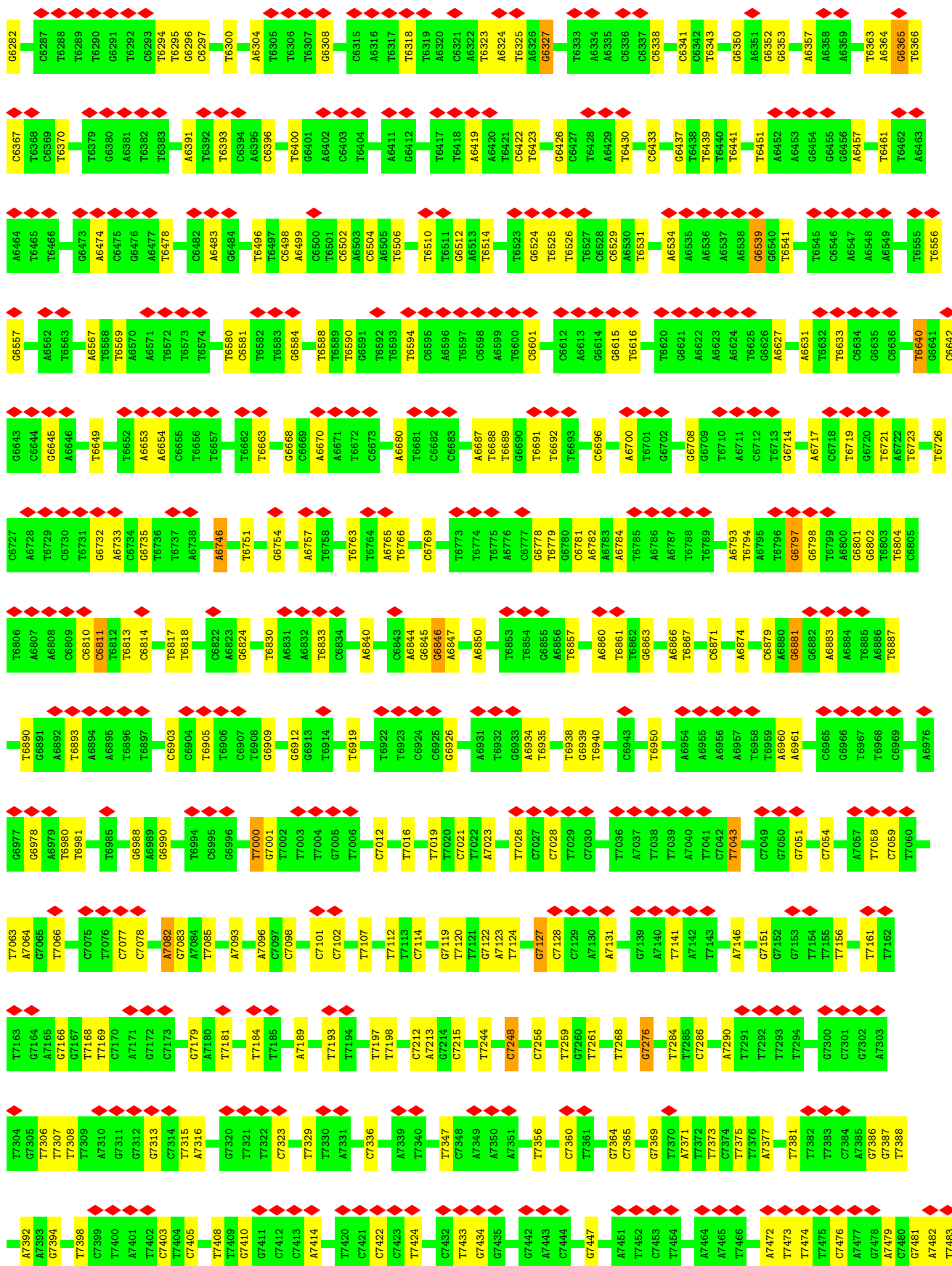


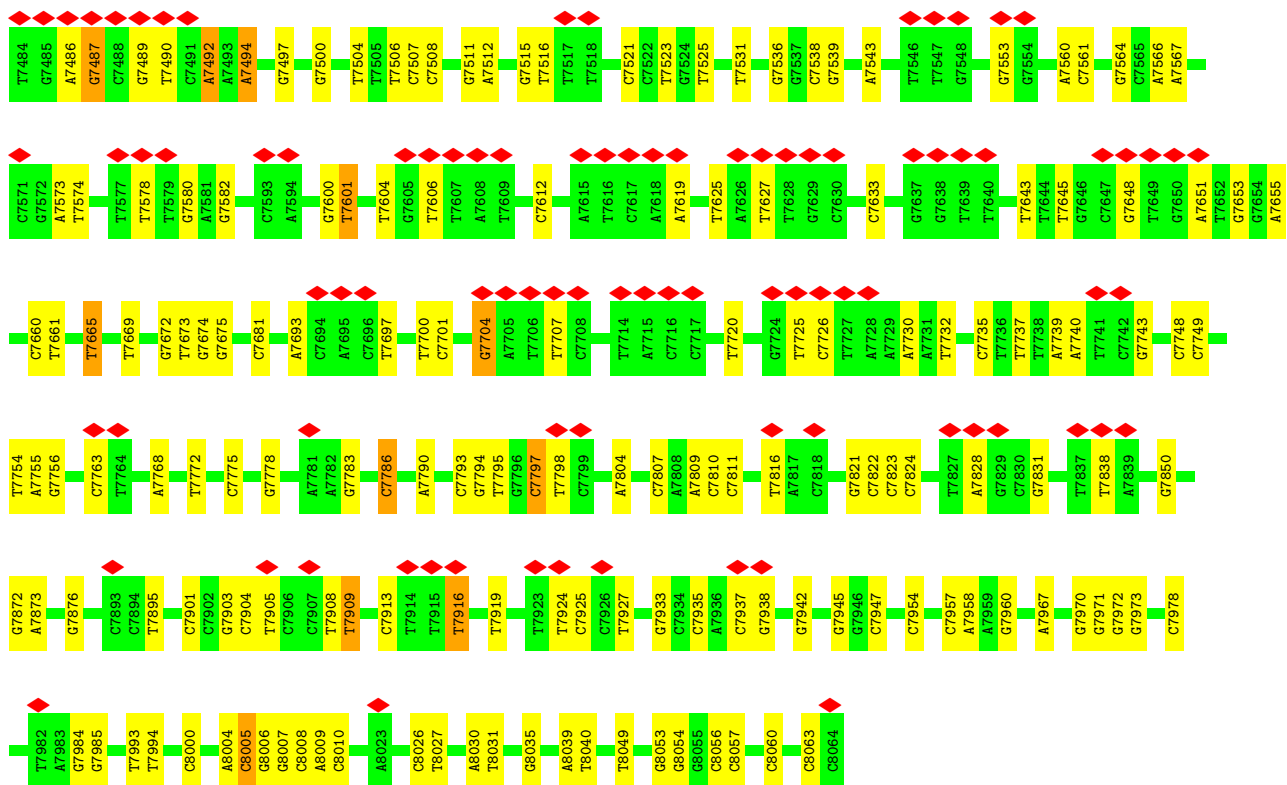




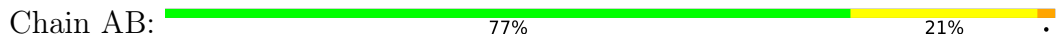
C4819	A4820	C4823	T4824	T4828	T4829	C4830	C4834	C4835	T4840	C4848	T4849	C4850	C4851	C4854	C4854	C4863	T4864	T4865	T4866	T4870	C4871	C4872	T4873	C4876	C4877	T4878	C4883	C4886	C4889	C4890	T4897	T4903	C4904	C4905	T4906	C4910	C4911	T4915	C4919	C4920	T4921	C4922												
T4723	G4727	G4728	T4729	C4730	C4731	T4732	T4733	T4734	T4735	G4736	A4737	T4738	T4741	G4742	A4743	A4744	G4747	G4750	C4751	C4752	A4753	A4754	A4755	C4756	C4757	C4758	T4759	A4760	A4761	G4767	G4768	C4769	C4770	T4771	T4772	T4773	G4774	A4775	C4776	C4777	G4778	C4785	C4786	A4792	G4798	T4805	A4814							
G4620	C4621	T4622	C4623	T4624	C4625	C4626	T4627	C4628	G4629	T4630	G4631	T4636	G4637	G4638	T4639	G4640	G4641	C4642	C4643	C4644	C4645	T4646	C4647	T4648	G4653	G4656	C4660	T4661	C4662	T4663	C4664	A4665	C4666	C4667	G4671	G4682	C4685	G4686	C4687	C4688	C4690	T4693	G4700	C4701	C4702	C4703	T4706	C4707						
A4519	C4520	T4528	T4529	C4530	C4531	C4540	T4541	T4542	T4546	G4550	T4557	G4563	T4564	G4565	T4570	C4571	A4572	C4573	C4574	C4577	A4578	A4579	C4588	C4591	T4594	C4598	C4599	T4600	C4601	C4602	T4603	C4604	T4605	C4606	A4607	A4608	T4609	G4610	C4611	T4612	C4613	G4614	C4615	G4616	G4617	C4618	G4619							
C4443	C4444	G4445	T4446	T4447	A4448	C4452	T4453	T4454	A4455	T4456	C4460	A4461	C4462	T4463	A4464	C4465	A4466	C4467	T4468	C4470	T4471	T4472	A4473	A4474	A4483	G4484	C4485	C4486	A4487	T4488	G4489	T4490	A4491	T4492	G4493	A4494	C4495	G4496	C4497	A4500	G4503	A4506	C4507	G4508	C4509	T4510	T4514	T4515	G4518					
C4332	T4333	C4334	A4338	C4339	C4340	A4341	C4342	T4343	C4344	A4347	T4357	A4358	C4359	T4360	T4361	T4362	C4363	T4368	T4369	C4370	A4371	A4376	A4377	T4378	C4379	A4380	C4381	T4382	G4386	C4389	T4390	A4402	T4403	T4404	G4409	T4410	T4411	A4415	C4418	A4421	T4425	G4433	C4434	C4437										
T4228	C4229	C4230	G4234	T4235	G4238	C4239	T4240	A4244	C4245	A4246	C4247	C4248	T4267	G4268	C4273	C4274	T4276	C4277	T4278	A4281	C4282	G4283	T4288	T4291	T4297	G4298	C4299	T4300	A4301	C4302	T4303	C4307	A4308	A4309	C4310	A4311	C4312	C4313	T4321	C4322	C4323	T4324	T4327											
C4149	T4150	A4151	T4152	C4153	C4154	C4155	T4156	C4157	A4158	A4159	A4160	A4161	T4162	C4163	A4164	C4165	C4166	C4167	T4168	C4169	G4170	T4171	C4172	C4173	C4174	T4175	C4176	T4177	C4178	A4179	C4180	A4181	C4182	T4183	C4184	C4185	C4186	C4187	C4188	T4189	G4193	C4202	G4203	T4204	G4211	C4212	T4213	G4214	C4215	C4216	C4221	T4222	A4223	A4224
T4049	A4050	C4051	G4052	C4053	T4054	A4055	C4056	C4057	T4058	A4059	T4060	G4061	A4062	C4063	G4064	C4065	C4066	T4067	G4068	T4069	C4070	T4071	T4078	G4079	C4080	T4081	T4082	C4083	T4089	T4092	A4093	G4094	T4097	G4104	A4111	A4112	C4113	T4114	C4115	A4116	G4119	T4120	T4121	C4122	C4123	G4124	T4130	G4131	G4132	C4145				
T3946	T3947	T3948	C3949	T3955	T3964	A3967	C3968	C3969	T3970	G3971	T3972	A3975	C3976	A3977	C3978	T3982	T3983	T3984	A3985	C3994	C3999	A4000	A4002	A4003	A4004	A4005	T4006	T4007	T4012	T4015	A4016	A4017	C4018	G4019	T4020	C4021	A4037	C4038	T4039	T4040	T4041	A4042	G4043	A4044	T4045	C4046	G4047	T4048						
C3820	T3821	G3828	A3829	C3830	C3834	C3848	A3852	T3861	T3866	C3871	C3882	A3883	C3884	C3885	C3886	T3887	C3896	A3899	T3902	C3908	T3909	G3910	A3913	A3916	T3917	A3918	T3919	T3920	T3921	A3922	T3923	T3924	A3928	A3929	T3930	T3931	C3932	C3933	T3936	T3942	C3945													
G3707	T3708	T3709	A3713	T3714	C3715	C3716	C3717	T3730	A3733	A3734	C3741	C3742	G3745	C3746	C3747	G3751	C3752	C3753	A3754	C3755	C3756	G3757	A3758	C3759	T3760	A3761	G3766	T3769	A3770	T3775	G3784	T3785	C3786	G3787	G3790	T3791	C3792	G3796	G3800	C3806	T3807	A3808	G3819											
C3582	C3583	C3587	G3593	C3594	C3595	A3596	C3600	T3607	C3610	A3616	A3621	T3625	T3629	C3630	A3631	T3640	A3645	C3646	T3647	C3648	C3649	T3650	C3651	A3652	T3660	A3663	T3668	C3671	T3672	A3673	T3686	C3687	C3688	C3689	T3693	T3694	T3695	G3700	C3701	T3702														



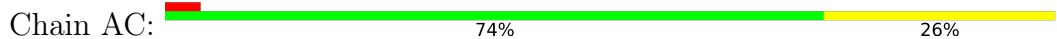




- Molecule 2: STAPLE STRAND



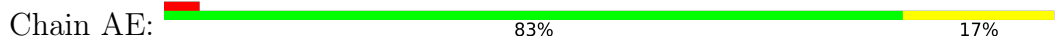
- Molecule 3: STAPLE STRAND



- Molecule 4: STAPLE STRAND



- Molecule 5: STAPLE STRAND





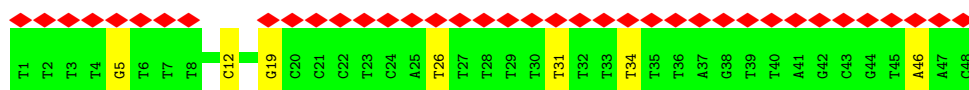
• Molecule 6: STAPLE STRAND

Chain AF: 67% 31% .



• Molecule 7: STAPLE STRAND

Chain AG: 79% 85% 15%



• Molecule 8: STAPLE STRAND

Chain AH: 77% 23%



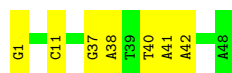
• Molecule 9: STAPLE STRAND

Chain AI: 75% 25%



• Molecule 10: STAPLE STRAND

Chain AJ: 85% 15%



• Molecule 11: STAPLE STRAND

Chain AK: 78% 22%



• Molecule 12: STAPLE STRAND

Chain AL: 27% 83% 17%



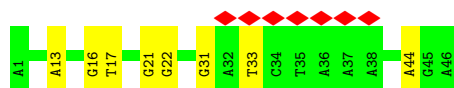
• Molecule 13: STAPLE STRAND

Chain AM: 95% 5%



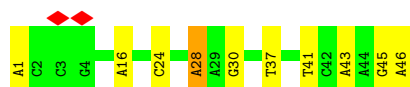
• Molecule 14: STAPLE STRAND

Chain AN: 15% 83% 17%



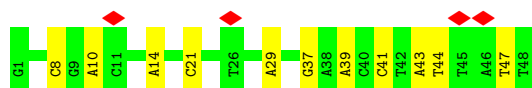
• Molecule 15: STAPLE STRAND

Chain AO: 78% 20% .



• Molecule 16: STAPLE STRAND

Chain AP: 8% 77% 23%



• Molecule 17: STAPLE STRAND

Chain AQ: 67% 79% 21%

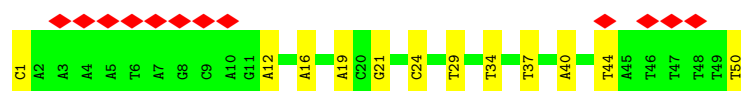
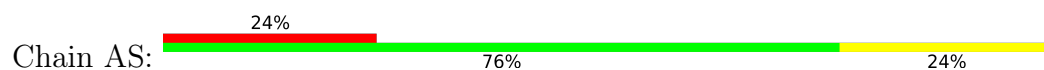


• Molecule 18: STAPLE STRAND

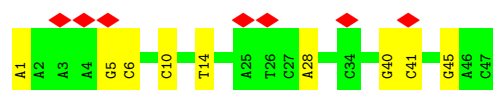
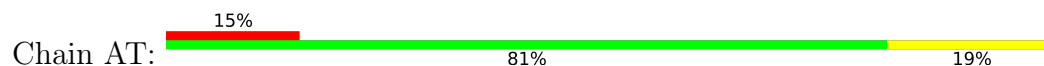
Chain AR: 9% 78% 20% .



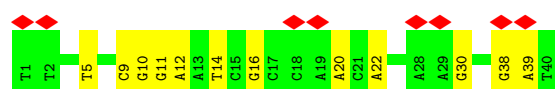
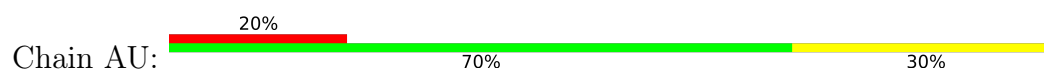
• Molecule 19: STAPLE STRAND



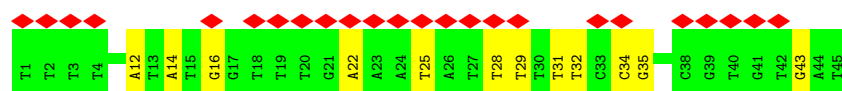
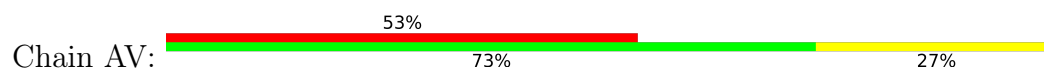
- Molecule 20: STAPLE STRAND



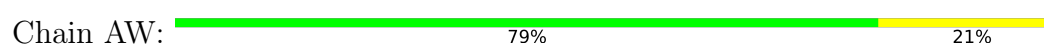
- Molecule 21: STAPLE STRAND



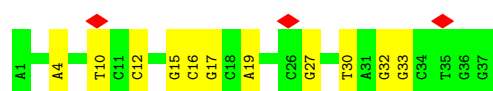
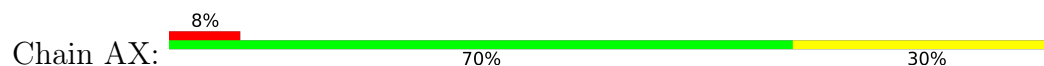
- Molecule 22: STAPLE STRAND



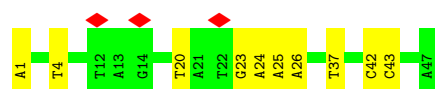
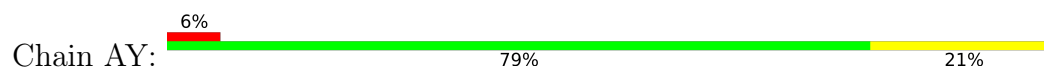
- Molecule 23: STAPLE STRAND



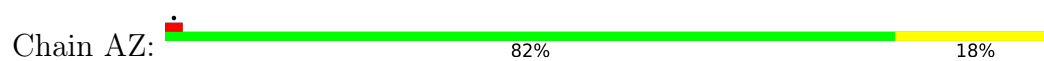
- Molecule 24: STAPLE STRAND



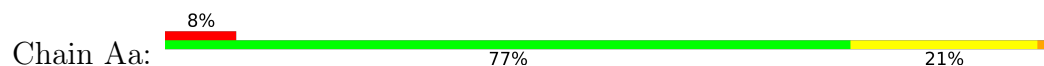
- Molecule 25: STAPLE STRAND



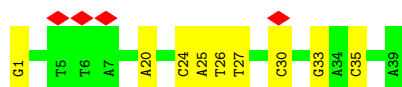
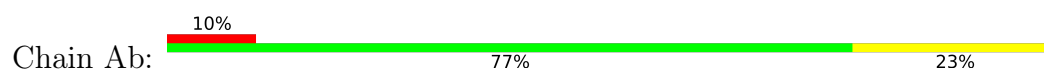
- Molecule 26: STAPLE STRAND



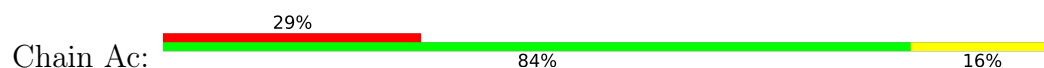
• Molecule 27: STAPLE STRAND



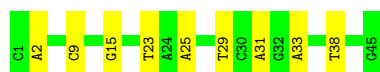
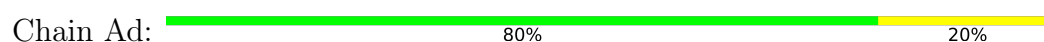
• Molecule 28: STAPLE STRAND



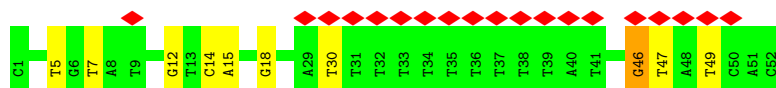
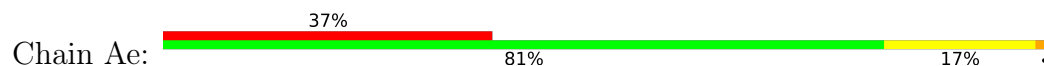
• Molecule 29: STAPLE STRAND



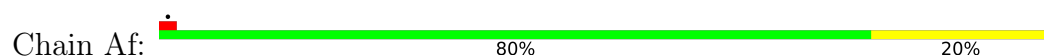
• Molecule 30: STAPLE STRAND



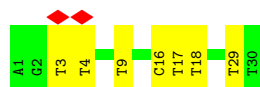
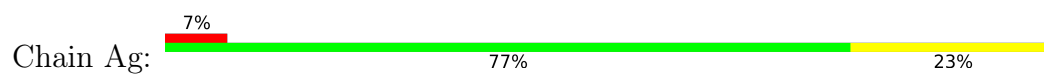
• Molecule 31: STAPLE STRAND



• Molecule 32: STAPLE STRAND



• Molecule 33: STAPLE STRAND



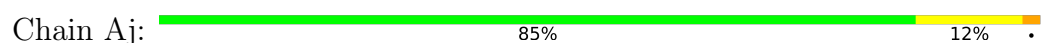
- Molecule 34: STAPLE STRAND



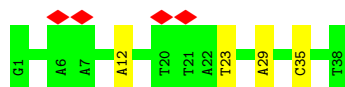
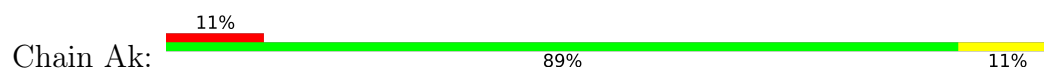
- Molecule 35: STAPLE STRAND



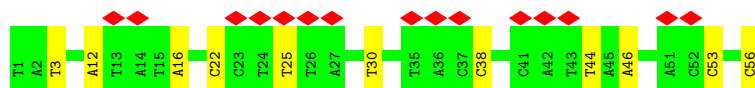
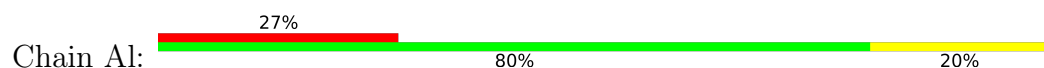
- Molecule 36: STAPLE STRAND



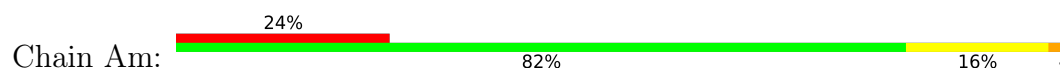
- Molecule 37: STAPLE STRAND



- Molecule 38: STAPLE STRAND



- Molecule 39: STAPLE STRAND



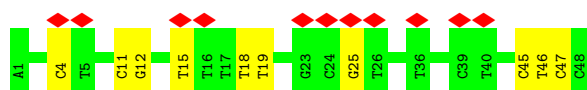
• Molecule 40: STAPLE STRAND

Chain An:  69% 31%

• Molecule 41: STAPLE STRAND

Chain Ao:  13% 83% 17%

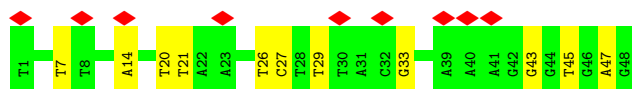
• Molecule 42: STAPLE STRAND

Chain Ap:  23% 79% 21%

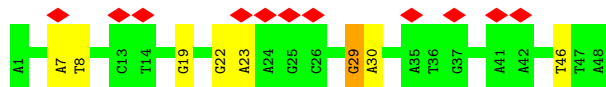
• Molecule 43: STAPLE STRAND

Chain Aq:  62% 38%

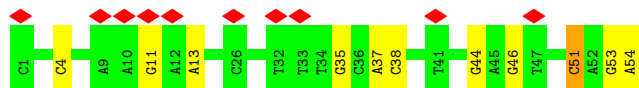
• Molecule 44: STAPLE STRAND

Chain Ar:  19% 77% 23%

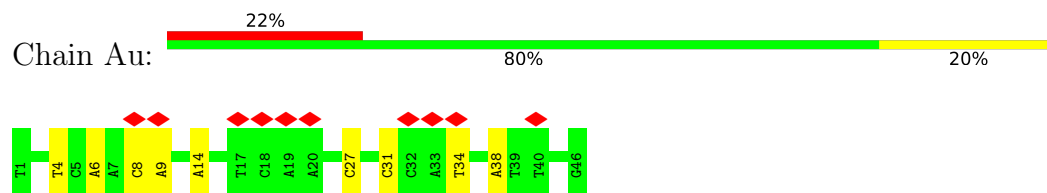
• Molecule 45: STAPLE STRAND

Chain As:  23% 83% 15%

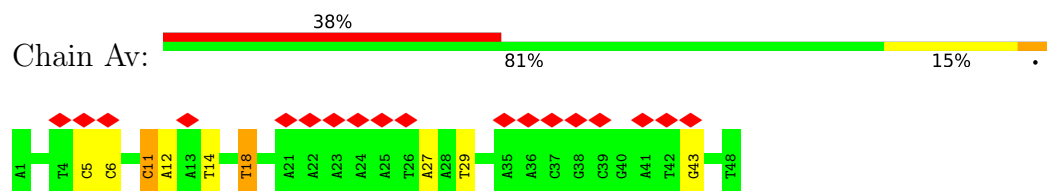
• Molecule 46: STAPLE STRAND

Chain At:  19% 80% 19%

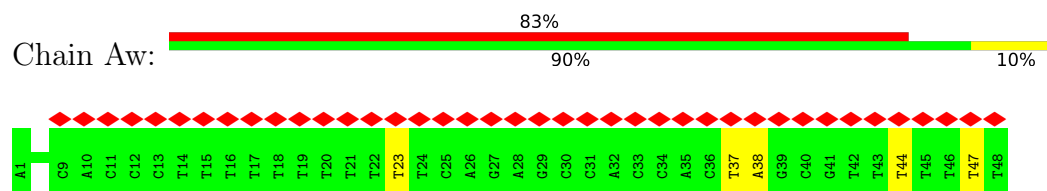
- Molecule 47: STAPLE STRAND



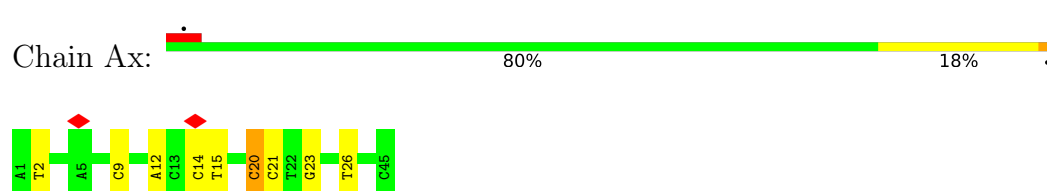
- Molecule 48: STAPLE STRAND



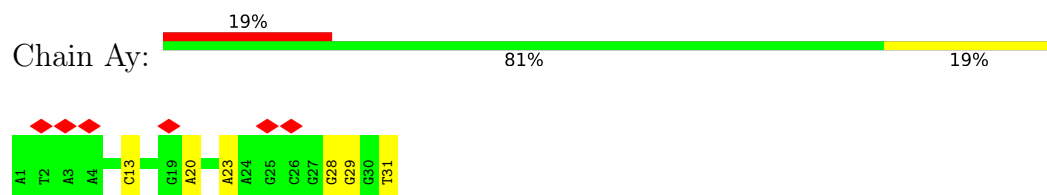
- Molecule 49: STAPLE STRAND



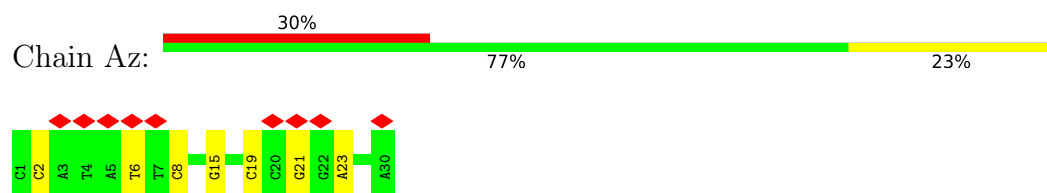
- Molecule 50: STAPLE STRAND



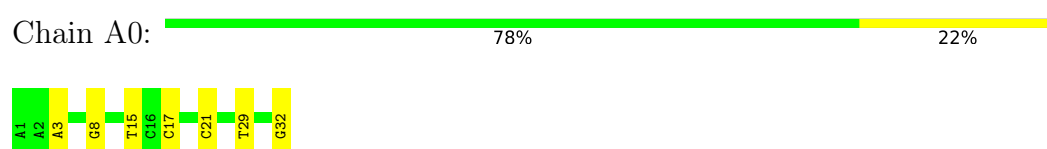
- Molecule 51: STAPLE STRAND



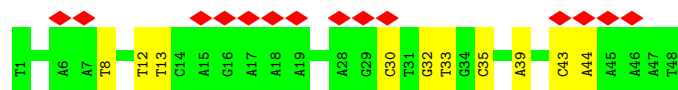
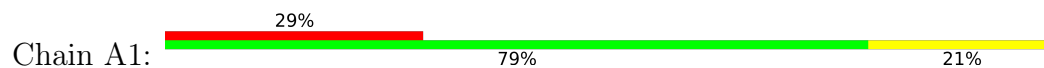
- Molecule 52: STAPLE STRAND



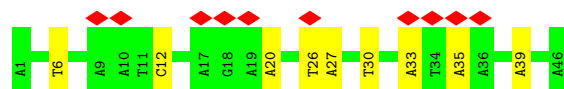
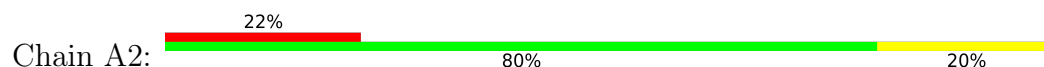
- Molecule 53: STAPLE STRAND



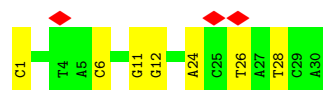
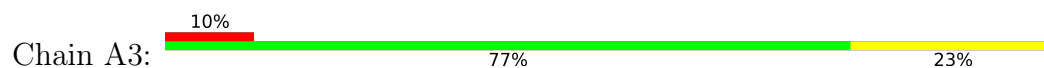
● Molecule 54: STAPLE STRAND



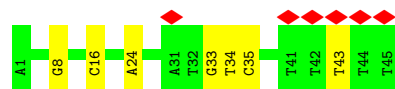
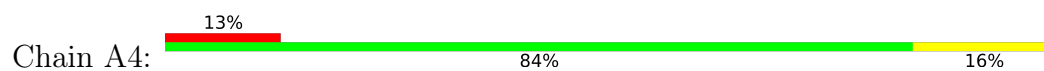
● Molecule 55: STAPLE STRAND



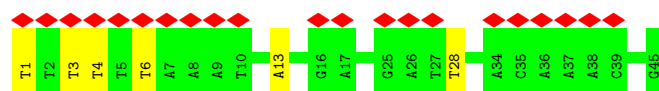
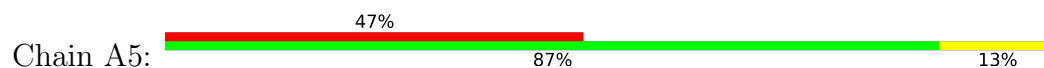
● Molecule 56: STAPLE STRAND



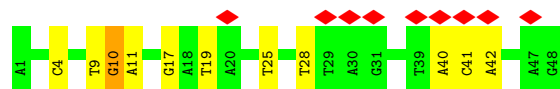
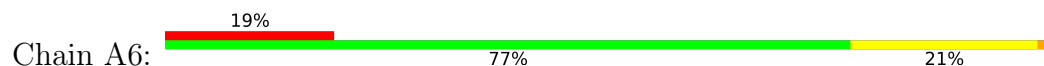
● Molecule 57: STAPLE STRAND



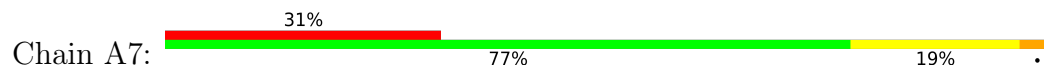
● Molecule 58: STAPLE STRAND

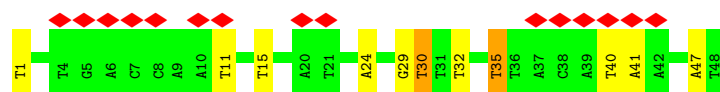


● Molecule 59: STAPLE STRAND

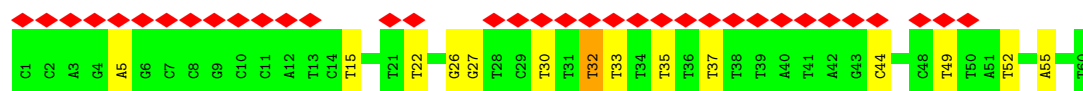


● Molecule 60: STAPLE STRAND

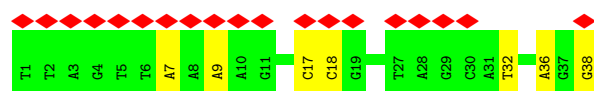
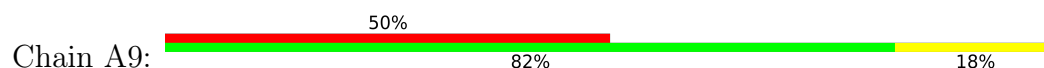




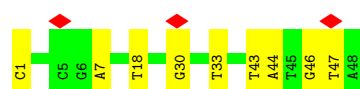
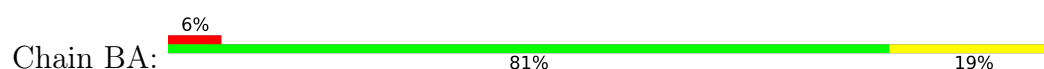
- Molecule 61: STAPLE STRAND



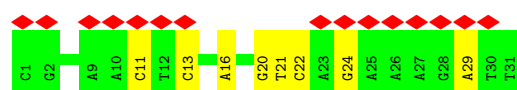
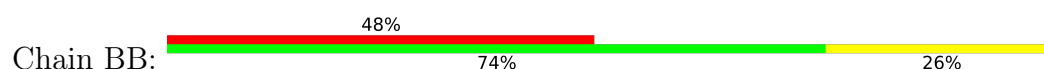
- Molecule 62: STAPLE STRAND



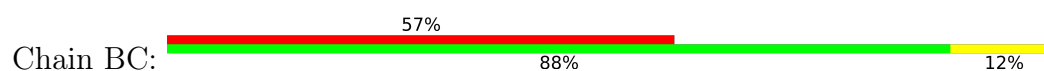
- Molecule 63: STAPLE STRAND



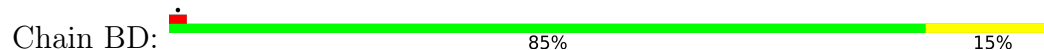
- Molecule 64: STAPLE STRAND



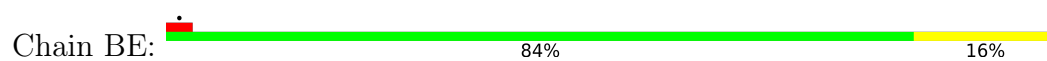
- Molecule 65: STAPLE STRAND



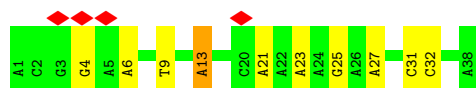
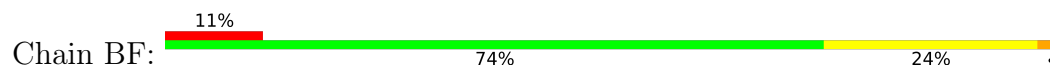
- Molecule 66: STAPLE STRAND



- Molecule 67: STAPLE STRAND



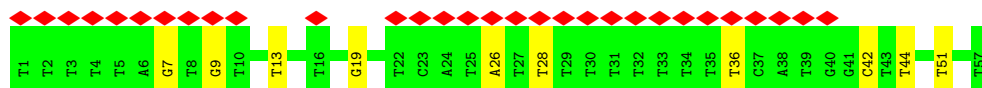
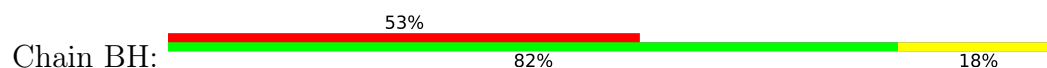
- Molecule 68: STAPLE STRAND



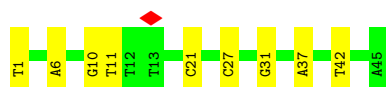
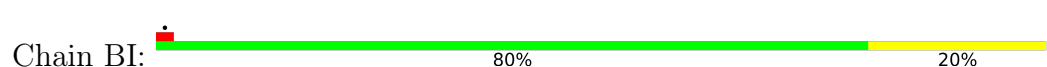
- Molecule 69: STAPLE STRAND



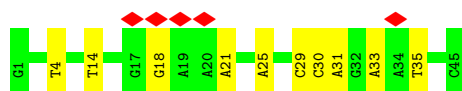
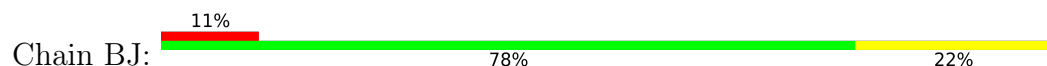
- Molecule 70: STAPLE STRAND



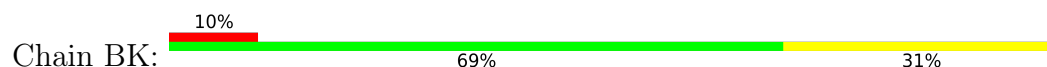
- Molecule 71: STAPLE STRAND



- Molecule 72: STAPLE STRAND



- Molecule 73: STAPLE STRAND



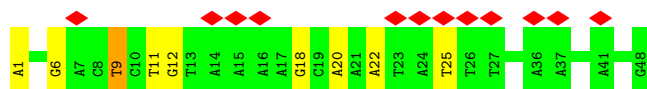
- Molecule 74: STAPLE STRAND

Chain BL:  76% 24%



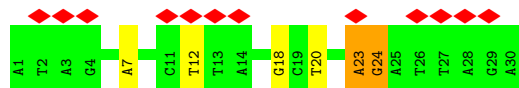
- Molecule 75: STAPLE STRAND

Chain BM:  25% 81% 17%



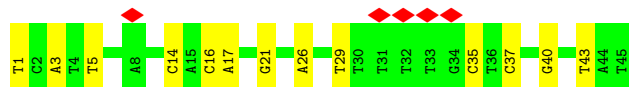
- Molecule 76: STAPLE STRAND

Chain BN:  40% 80% 13% 7%



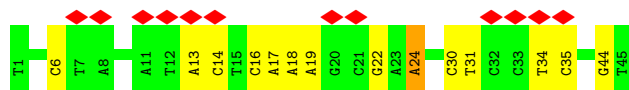
- Molecule 77: STAPLE STRAND

Chain BO:  11% 71% 29%



- Molecule 78: STAPLE STRAND

Chain BP:  27% 69% 29%



- Molecule 79: STAPLE STRAND

Chain BQ:  27% 73% 27%

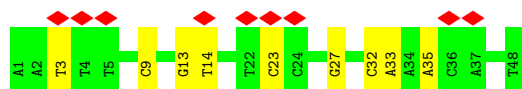
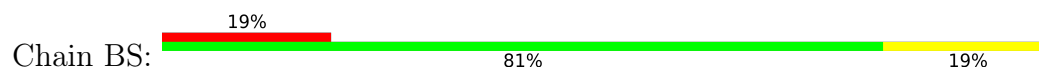


- Molecule 80: STAPLE STRAND

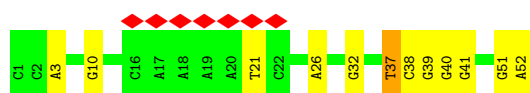
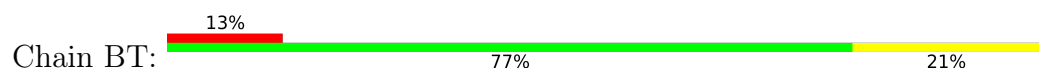
Chain BR:  21% 71% 26%



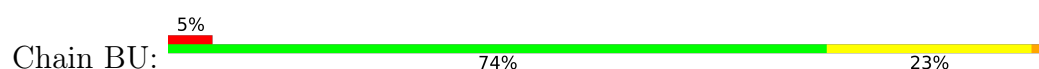
- Molecule 81: STAPLE STRAND



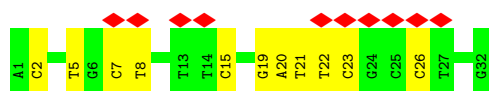
- Molecule 82: STAPLE STRAND



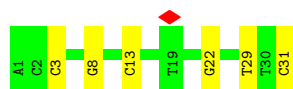
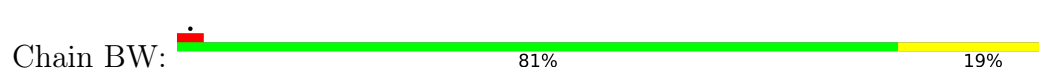
- Molecule 83: STAPLE STRAND



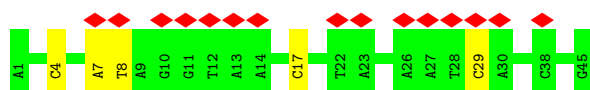
- Molecule 84: STAPLE STRAND



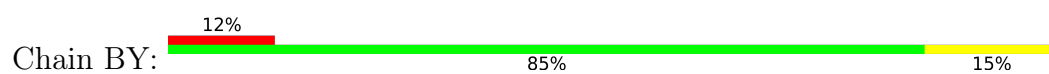
- Molecule 85: STAPLE STRAND



- Molecule 86: STAPLE STRAND



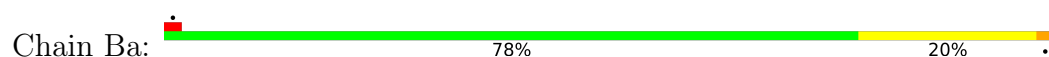
- Molecule 87: STAPLE STRAND



- Molecule 88: STAPLE STRAND



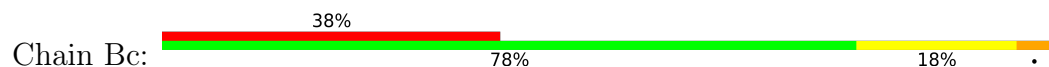
- Molecule 89: STAPLE STRAND



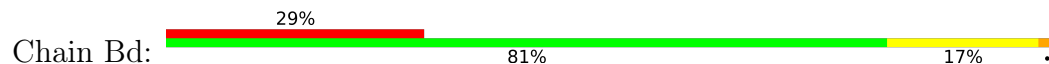
- Molecule 90: STAPLE STRAND



- Molecule 91: STAPLE STRAND



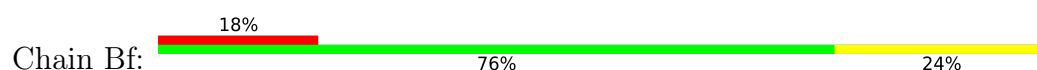
- Molecule 92: STAPLE STRAND



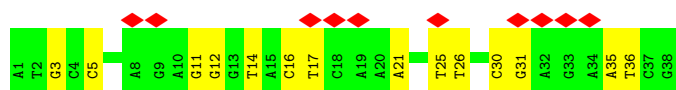
- Molecule 93: STAPLE STRAND



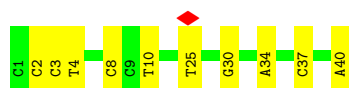
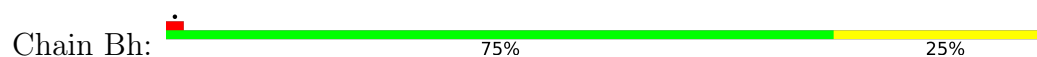
- Molecule 94: STAPLE STRAND



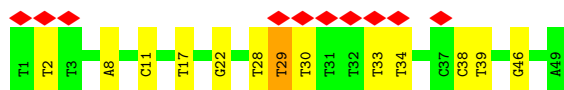
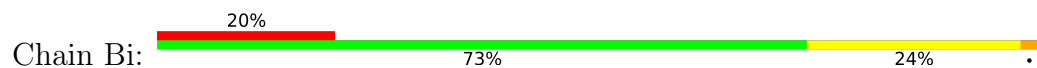
- Molecule 95: STAPLE STRAND



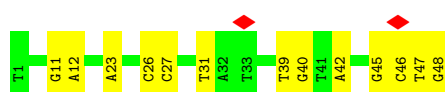
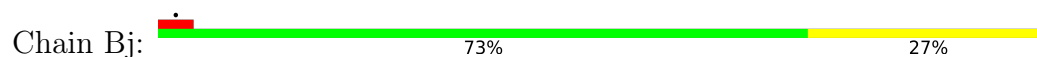
- Molecule 96: STAPLE STRAND



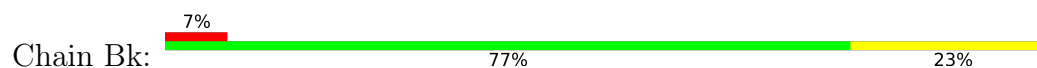
- Molecule 97: STAPLE STRAND



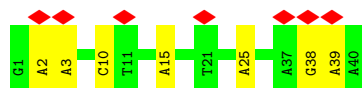
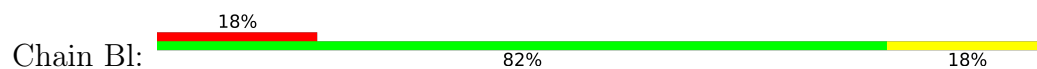
- Molecule 98: STAPLE STRAND



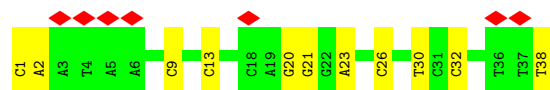
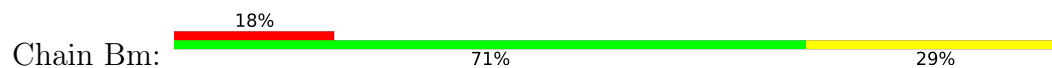
- Molecule 99: STAPLE STRAND



- Molecule 100: STAPLE STRAND



• Molecule 101: STAPLE STRAND



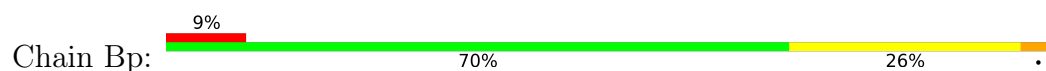
• Molecule 102: STAPLE STRAND



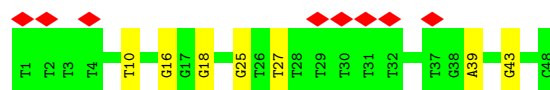
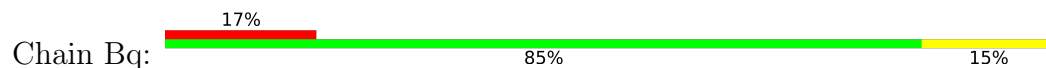
• Molecule 103: STAPLE STRAND



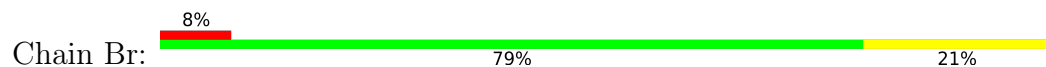
• Molecule 104: STAPLE STRAND



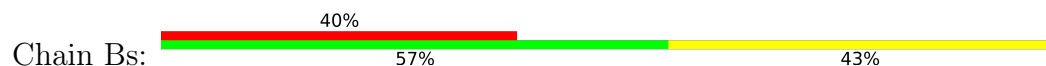
• Molecule 105: STAPLE STRAND

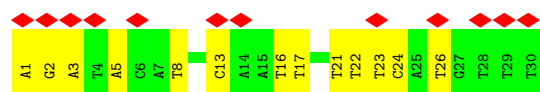


• Molecule 106: STAPLE STRAND

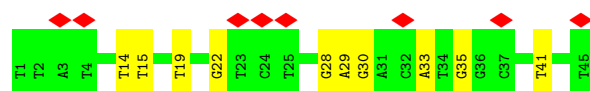
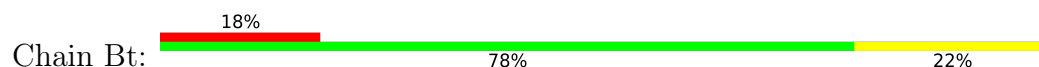


• Molecule 107: STAPLE STRAND

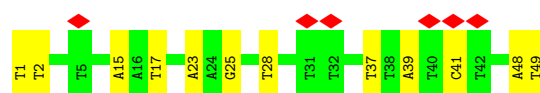
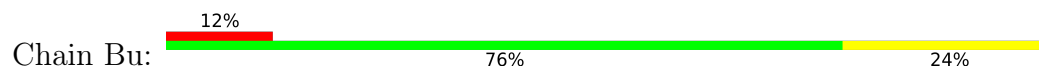




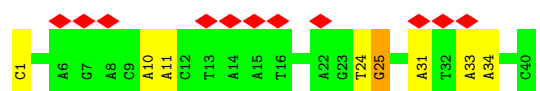
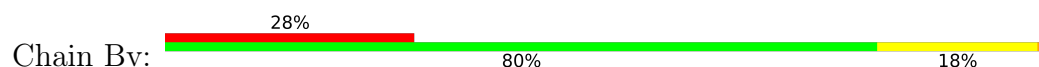
• Molecule 108: STAPLE STRAND



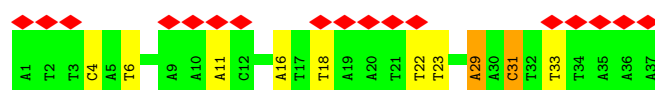
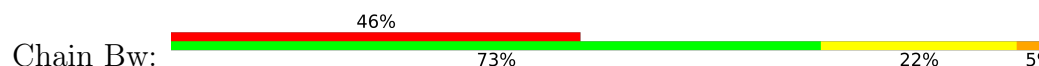
• Molecule 109: STAPLE STRAND



• Molecule 110: STAPLE STRAND



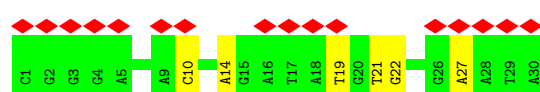
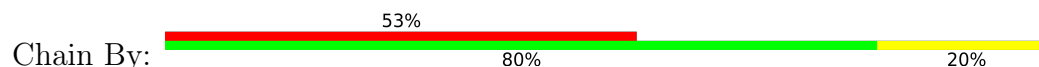
• Molecule 111: STAPLE STRAND



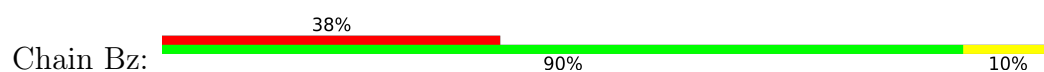
• Molecule 112: STAPLE STRAND



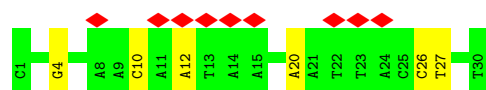
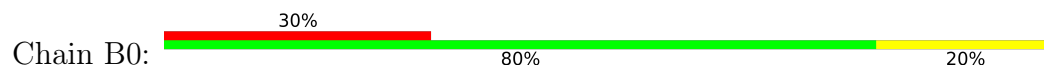
• Molecule 113: STAPLE STRAND



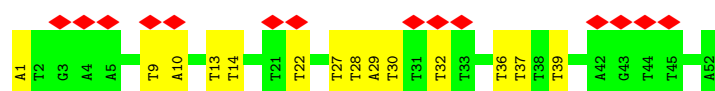
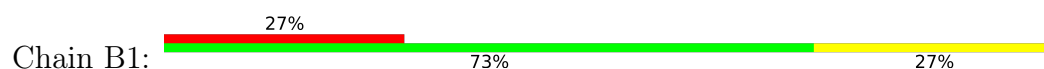
• Molecule 114: STAPLE STRAND



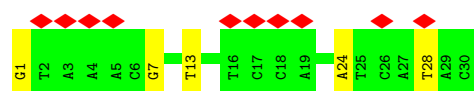
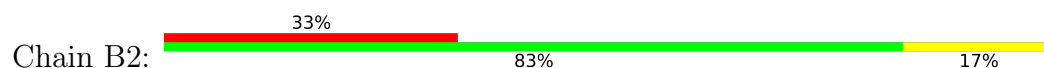
• Molecule 115: STAPLE STRAND



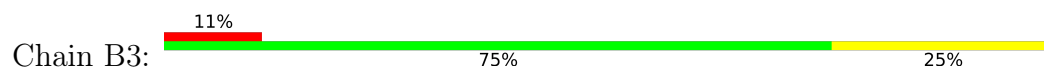
• Molecule 116: STAPLE STRAND



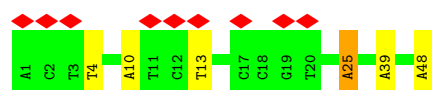
• Molecule 117: STAPLE STRAND



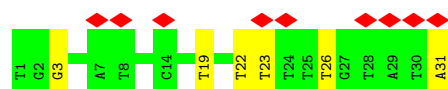
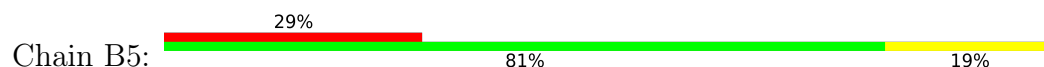
• Molecule 118: STAPLE STRAND



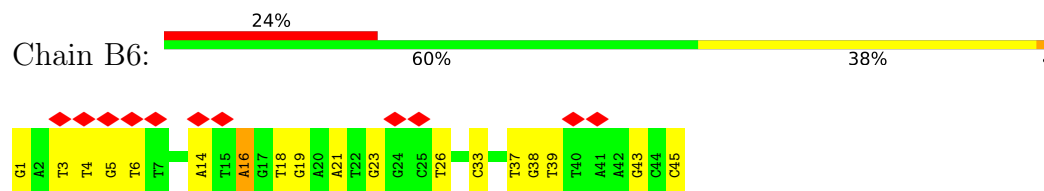
• Molecule 119: STAPLE STRAND



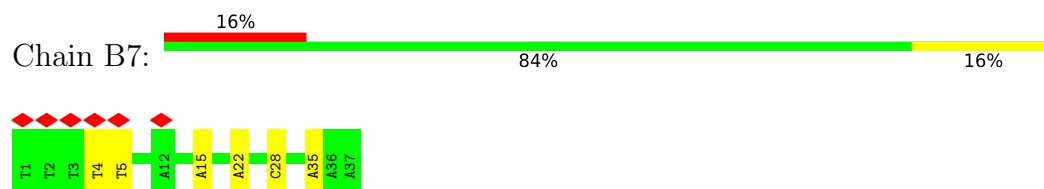
• Molecule 120: STAPLE STRAND



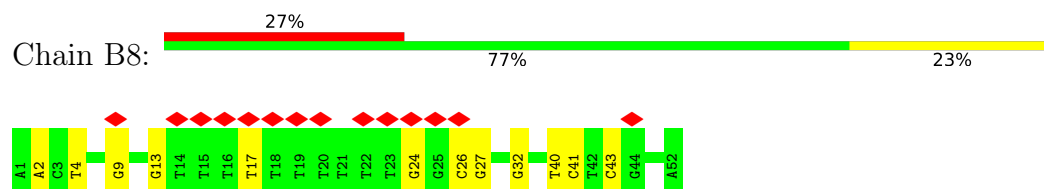
- Molecule 121: STAPLE STRAND



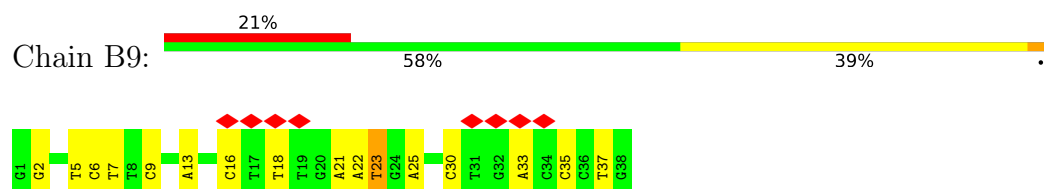
- Molecule 122: STAPLE STRAND



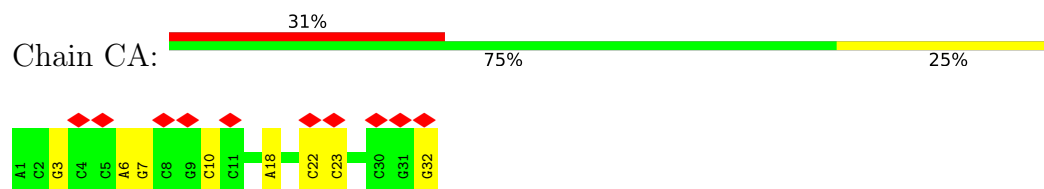
- Molecule 123: STAPLE STRAND



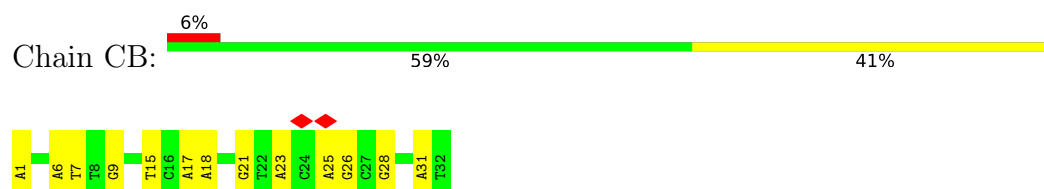
- Molecule 124: STAPLE STRAND



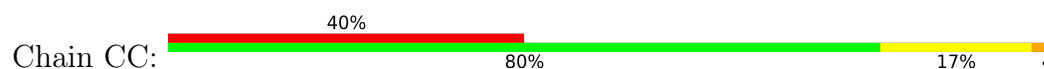
- Molecule 125: STAPLE STRAND

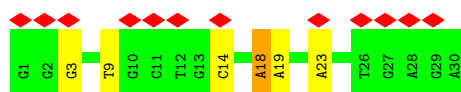


- Molecule 126: STAPLE STRAND

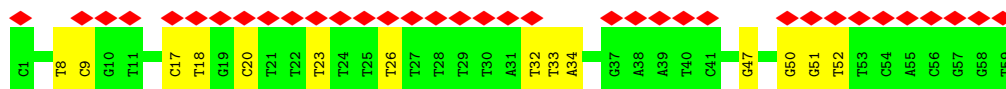
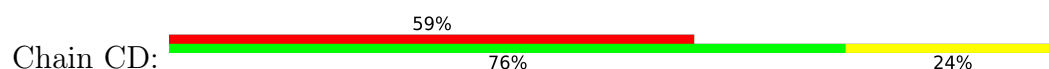


- Molecule 127: STAPLE STRAND

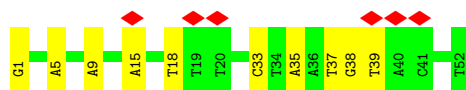
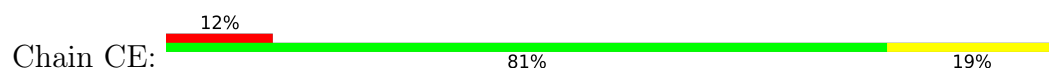




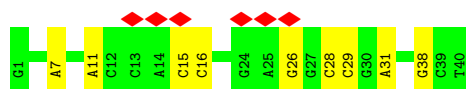
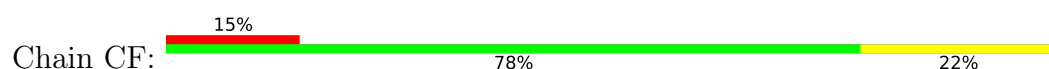
• Molecule 128: STAPLE STRAND



• Molecule 129: STAPLE STRAND



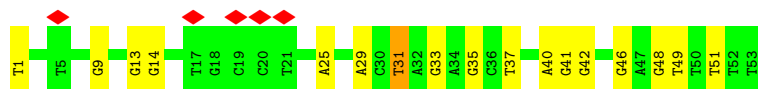
• Molecule 130: STAPLE STRAND



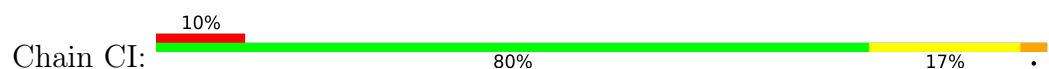
• Molecule 131: STAPLE STRAND



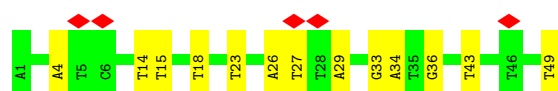
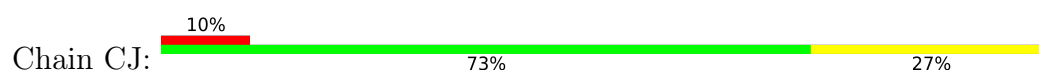
• Molecule 132: STAPLE STRAND



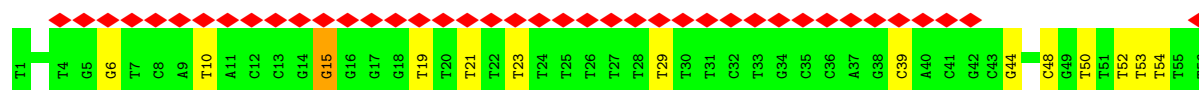
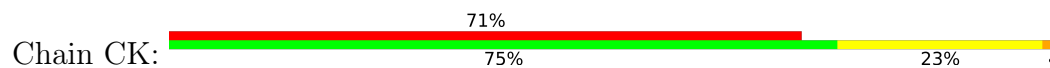
• Molecule 133: STAPLE STRAND



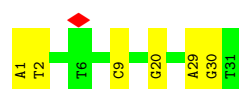
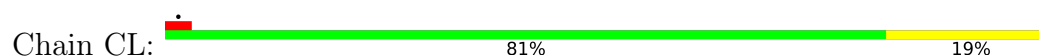
• Molecule 134: STAPLE STRAND



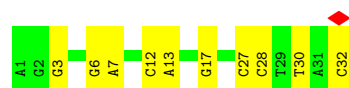
- Molecule 135: STAPLE STRAND



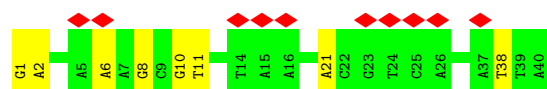
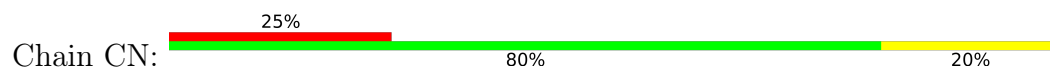
- Molecule 136: STAPLE STRAND



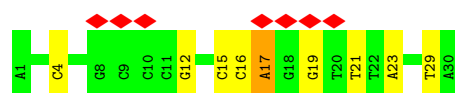
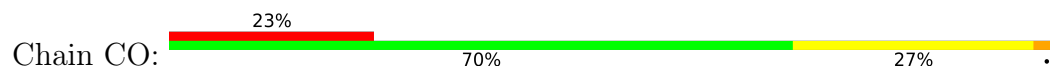
- Molecule 137: STAPLE STRAND



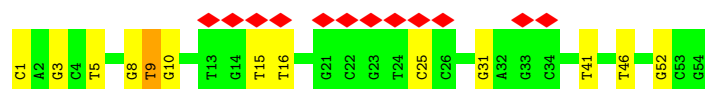
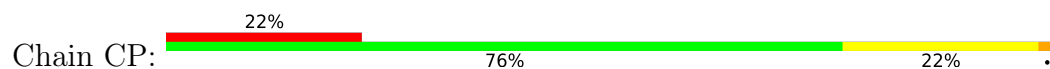
- Molecule 138: STAPLE STRAND



- Molecule 139: STAPLE STRAND



- Molecule 140: STAPLE STRAND



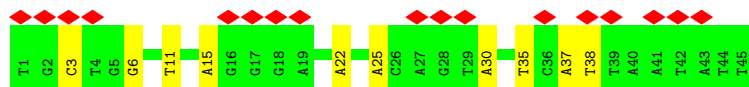
- Molecule 141: STAPLE STRAND

Chain CQ:  75% 23% .



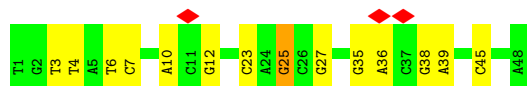
- Molecule 142: STAPLE STRAND

Chain CR:  38% 78% 22%



- Molecule 143: STAPLE STRAND

Chain CS:  6% 71% 27% .



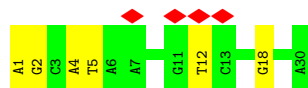
- Molecule 144: STAPLE STRAND

Chain CT:  63% 34% .



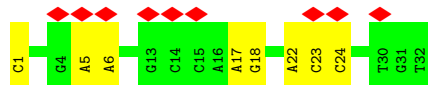
- Molecule 145: STAPLE STRAND

Chain CU:  13% 80% 20%



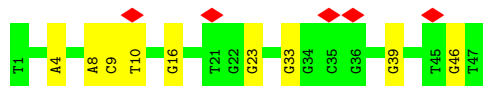
- Molecule 146: STAPLE STRAND

Chain CV:  28% 75% 25%

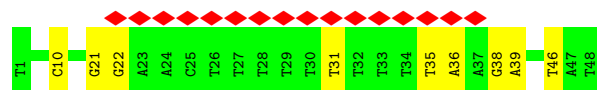
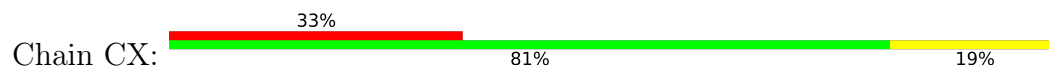


- Molecule 147: STAPLE STRAND

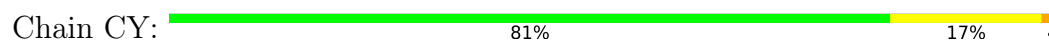
Chain CW:  11% 81% 19%



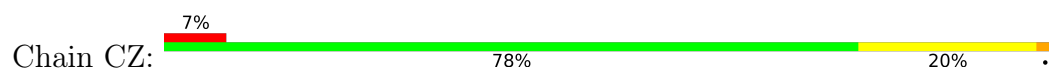
- Molecule 148: STAPLE STRAND



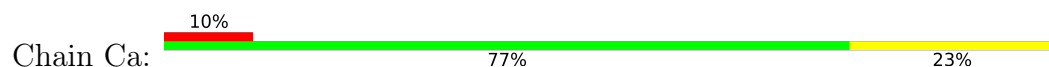
- Molecule 149: STAPLE STRAND



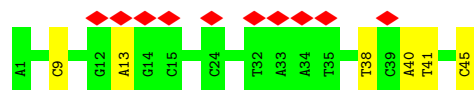
- Molecule 150: STAPLE STRAND



- Molecule 151: STAPLE STRAND



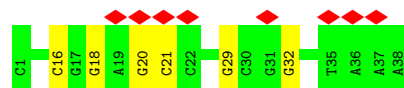
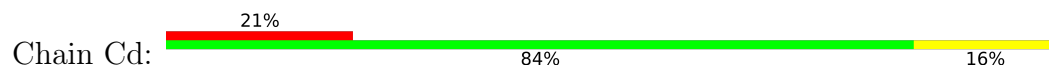
- Molecule 152: STAPLE STRAND



- Molecule 153: STAPLE STRAND



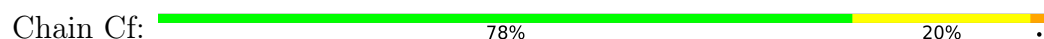
- Molecule 154: STAPLE STRAND



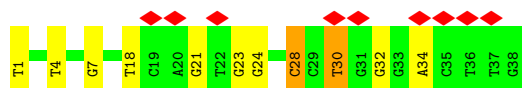
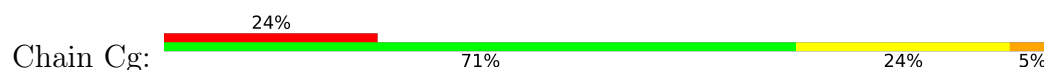
- Molecule 155: STAPLE STRAND



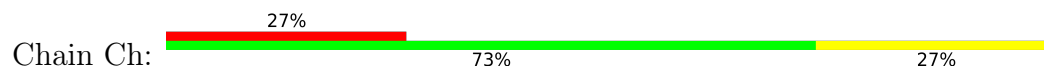
- Molecule 156: STAPLE STRAND



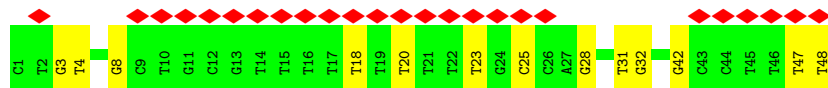
- Molecule 157: STAPLE STRAND



- Molecule 158: STAPLE STRAND



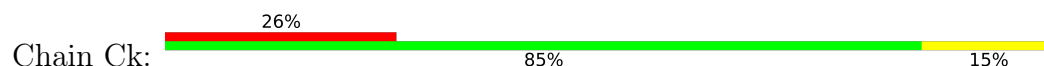
- Molecule 159: STAPLE STRAND



- Molecule 160: STAPLE STRAND



- Molecule 161: STAPLE STRAND

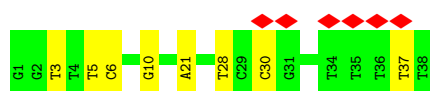
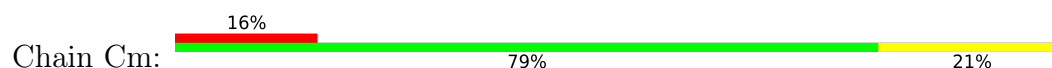




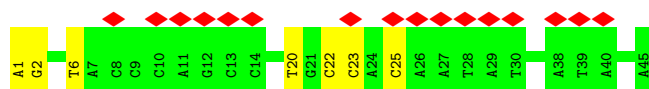
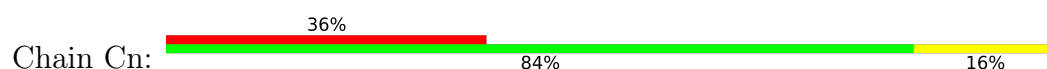
• Molecule 162: STAPLE STRAND



• Molecule 163: STAPLE STRAND



• Molecule 164: STAPLE STRAND



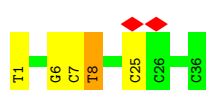
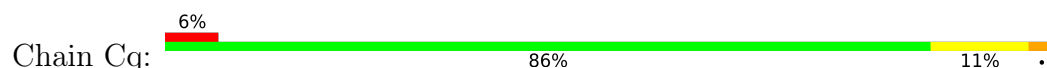
• Molecule 165: STAPLE STRAND



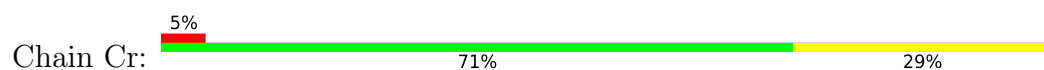
• Molecule 166: STAPLE STRAND



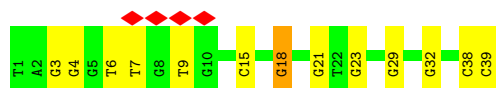
• Molecule 167: STAPLE STRAND



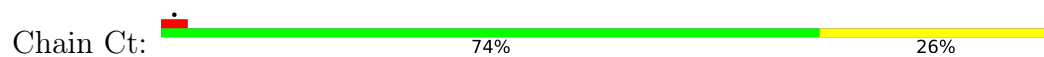
• Molecule 168: STAPLE STRAND



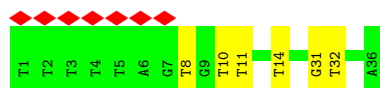
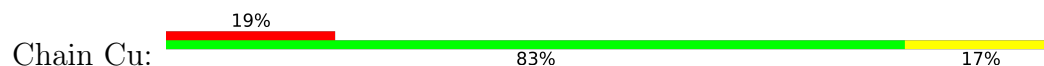
- Molecule 169: STAPLE STRAND



- Molecule 170: STAPLE STRAND



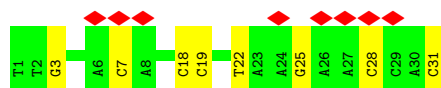
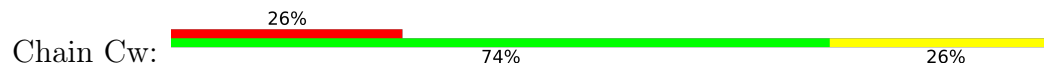
- Molecule 171: STAPLE STRAND



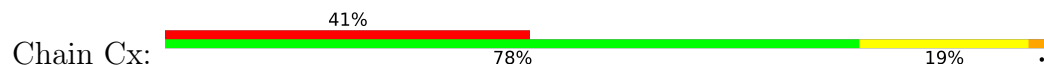
- Molecule 172: STAPLE STRAND



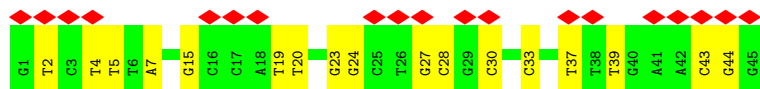
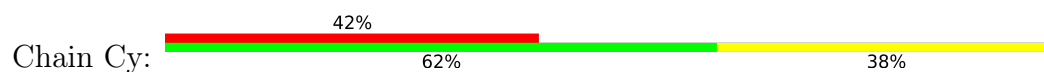
- Molecule 173: STAPLE STRAND



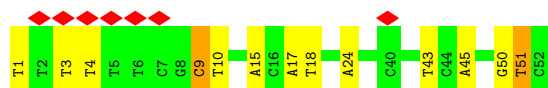
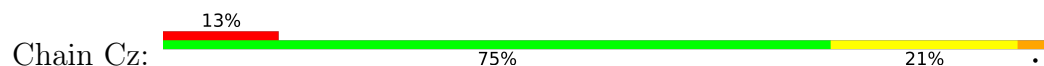
- Molecule 174: STAPLE STRAND



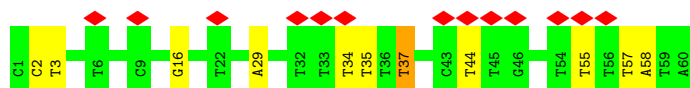
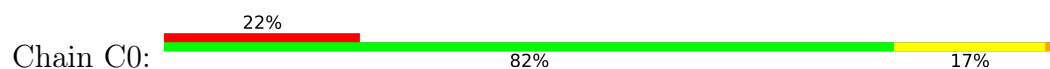
- Molecule 175: STAPLE STRAND



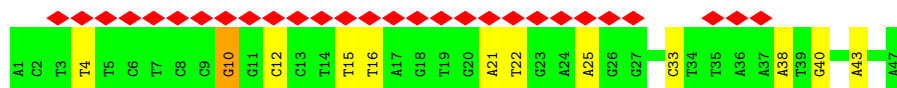
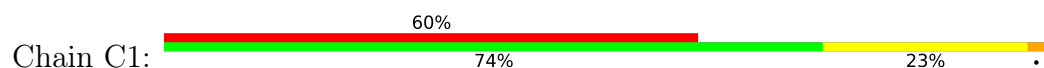
- Molecule 176: STAPLE STRAND



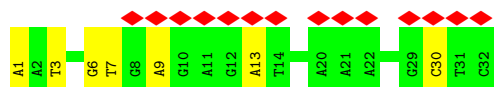
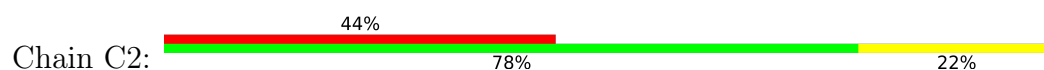
- Molecule 177: STAPLE STRAND



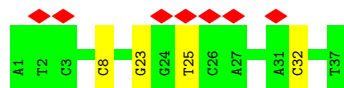
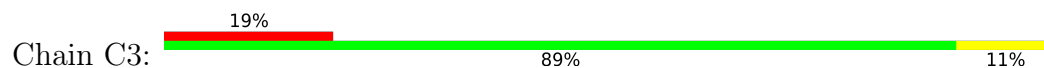
- Molecule 178: STAPLE STRAND



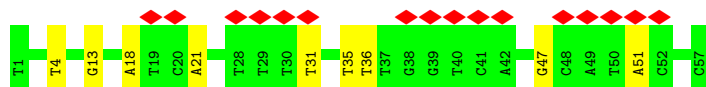
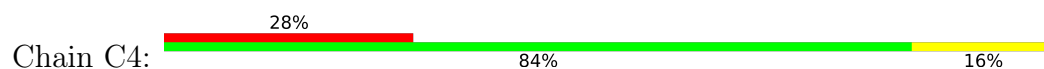
- Molecule 179: STAPLE STRAND



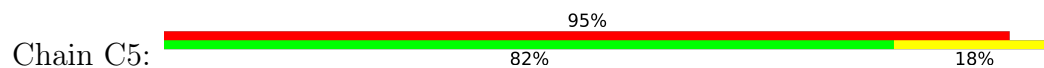
- Molecule 180: STAPLE STRAND



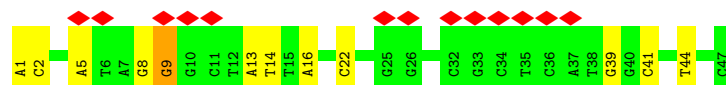
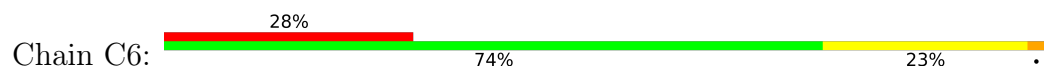
- Molecule 181: STAPLE STRAND



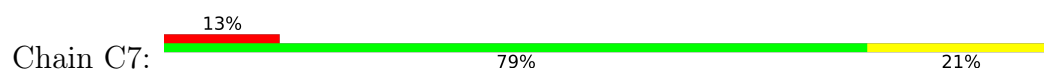
- Molecule 182: STAPLE STRAND



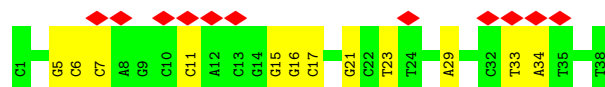
- Molecule 183: STAPLE STRAND



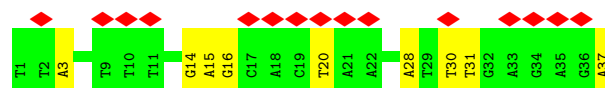
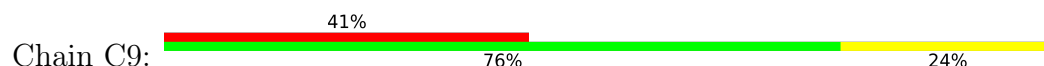
- Molecule 184: STAPLE STRAND



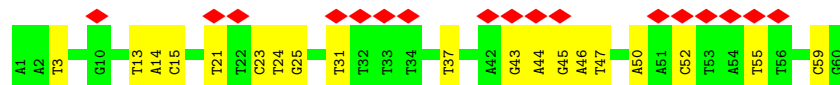
- Molecule 185: STAPLE STRAND



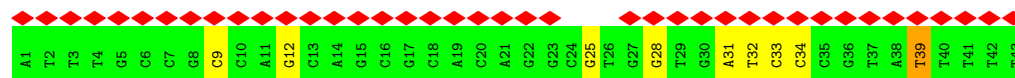
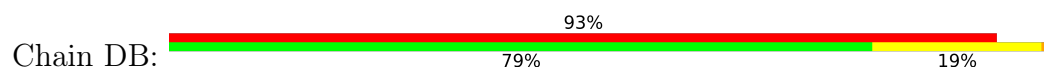
- Molecule 186: STAPLE STRAND



- Molecule 187: STAPLE STRAND

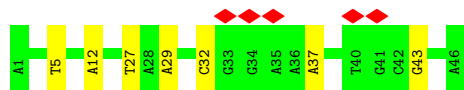


- Molecule 188: STAPLE STRAND



• Molecule 189: STAPLE STRAND

Chain DC:  11% 85% 15%



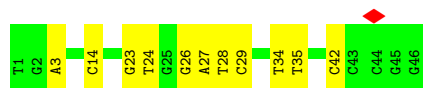
• Molecule 190: STAPLE STRAND

Chain DD:  76% 24%



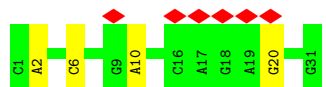
• Molecule 191: STAPLE STRAND

Chain DE:  76% 24%



• Molecule 192: STAPLE STRAND

Chain DF:  19% 87% 13%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	94834	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	51	Depositor
Minimum defocus (nm)	328.5	Depositor
Maximum defocus (nm)	2444.2	Depositor
Magnification	47000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.793	Depositor
Minimum map value	-0.309	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.037	Depositor
Recommended contour level	0.11	Depositor
Map size (Å)	639.39996, 639.39996, 639.39996	wwPDB
Map dimensions	230, 230, 230	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.7799997, 2.7799997, 2.7799997	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	AA	0.72	0/184801	1.03	423/285260 (0.1%)
2	AB	0.73	0/1095	1.02	2/1690 (0.1%)
3	AC	0.70	0/1228	0.97	1/1894 (0.1%)
4	AD	0.71	0/1112	0.99	4/1716 (0.2%)
5	AE	0.74	0/1086	1.03	3/1672 (0.2%)
6	AF	0.71	0/1272	0.98	2/1962 (0.1%)
7	AG	0.69	0/1080	1.04	2/1665 (0.1%)
8	AH	0.71	0/714	1.04	1/1101 (0.1%)
9	AI	0.70	0/636	1.05	1/981 (0.1%)
10	AJ	0.72	0/1095	0.98	0/1687
11	AK	0.75	0/737	1.09	4/1137 (0.4%)
12	AL	0.70	0/1193	1.03	4/1841 (0.2%)
13	AM	0.67	0/854	0.98	0/1315
14	AN	0.69	0/1062	0.92	0/1639
15	AO	0.71	0/1068	0.95	3/1646 (0.2%)
16	AP	0.72	0/1100	1.01	1/1697 (0.1%)
17	AQ	0.68	0/1085	0.99	3/1672 (0.2%)
18	AR	0.70	0/1056	0.97	1/1629 (0.1%)
19	AS	0.70	0/1135	0.93	0/1746
20	AT	0.73	0/1078	0.97	1/1660 (0.1%)
21	AU	0.73	0/927	0.91	0/1429
22	AV	0.72	0/1025	1.15	7/1582 (0.4%)
23	AW	0.72	0/1103	0.93	0/1700
24	AX	0.72	0/860	1.02	2/1326 (0.2%)
25	AY	0.71	0/1085	1.02	1/1674 (0.1%)
26	AZ	0.73	0/912	1.05	0/1404
27	Aa	0.72	0/1220	0.97	1/1881 (0.1%)
28	Ab	0.71	0/895	1.02	2/1380 (0.1%)
29	Ac	0.71	0/697	1.01	1/1072 (0.1%)
30	Ad	0.70	0/1046	1.01	1/1612 (0.1%)
31	Ae	0.70	0/1179	0.97	1/1818 (0.1%)
32	Af	0.74	0/1049	1.03	0/1616
33	Ag	0.74	0/690	1.00	1/1065 (0.1%)
34	Ah	0.72	0/901	1.02	2/1389 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	Ai	0.70	0/1095	0.99	3/1691 (0.2%)
36	Aj	0.71	0/924	1.03	2/1423 (0.1%)
37	Ak	0.70	0/870	1.05	2/1340 (0.1%)
38	Al	0.73	0/1274	1.02	2/1961 (0.1%)
39	Am	0.70	0/862	1.02	2/1329 (0.2%)
40	An	0.71	0/1022	1.00	2/1573 (0.1%)
41	Ao	0.70	0/1059	0.93	1/1632 (0.1%)
42	Ap	0.70	0/1089	1.08	4/1678 (0.2%)
43	Aq	0.72	0/746	0.99	1/1151 (0.1%)
44	Ar	0.73	0/1109	1.00	0/1712
45	As	0.71	0/1119	1.01	4/1725 (0.2%)
46	At	0.72	0/1242	1.01	2/1914 (0.1%)
47	Au	0.66	0/1047	0.96	2/1612 (0.1%)
48	Av	0.69	0/1108	1.02	3/1708 (0.2%)
49	Aw	0.71	0/1074	0.94	0/1653
50	Ax	0.71	0/1032	0.98	2/1588 (0.1%)
51	Ay	0.76	0/725	0.97	0/1119
52	Az	0.71	0/689	0.99	0/1061
53	A0	0.72	0/726	0.99	2/1116 (0.2%)
54	A1	0.73	0/1106	1.02	1/1705 (0.1%)
55	A2	0.69	0/1059	0.97	1/1631 (0.1%)
56	A3	0.74	0/691	0.97	1/1065 (0.1%)
57	A4	0.70	0/1025	0.98	0/1578
58	A5	0.66	0/1036	0.95	1/1598 (0.1%)
59	A6	0.73	0/1121	1.06	3/1730 (0.2%)
60	A7	0.68	0/1094	1.03	3/1686 (0.2%)
61	A8	0.71	0/1343	1.08	6/2068 (0.3%)
62	A9	0.73	0/875	0.99	0/1348
63	BA	0.71	0/1102	1.02	2/1697 (0.1%)
64	BB	0.74	0/718	1.01	1/1106 (0.1%)
65	BC	0.71	0/1371	0.97	1/2113 (0.0%)
66	BD	0.72	0/1225	0.96	1/1888 (0.1%)
67	BE	0.70	0/727	0.97	0/1118
68	BF	0.73	0/878	0.98	1/1352 (0.1%)
69	BG	0.73	0/1072	1.05	4/1654 (0.2%)
70	BH	0.69	0/1291	1.02	0/1993
71	BI	0.75	0/1029	0.95	0/1585
72	BJ	0.72	0/1043	0.97	1/1609 (0.1%)
73	BK	0.72	0/1100	0.97	2/1696 (0.1%)
74	BL	0.72	0/1029	1.04	3/1586 (0.2%)
75	BM	0.72	0/1114	0.98	1/1719 (0.1%)
76	BN	0.71	0/695	1.00	2/1072 (0.2%)
77	BO	0.75	0/1024	1.07	2/1577 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	BP	0.74	0/1035	1.03	3/1594 (0.2%)
79	BQ	0.71	0/1046	0.93	0/1614
80	BR	0.72	0/861	1.02	2/1326 (0.2%)
81	BS	0.65	0/1088	0.94	1/1675 (0.1%)
82	BT	0.73	0/1205	0.96	1/1858 (0.1%)
83	BU	0.74	0/876	1.11	4/1347 (0.3%)
84	BV	0.72	0/721	1.02	2/1110 (0.2%)
85	BW	0.70	0/699	0.96	1/1074 (0.1%)
86	BX	0.73	0/1024	0.99	3/1576 (0.2%)
87	BY	0.69	0/1196	0.99	2/1844 (0.1%)
88	BZ	0.71	0/1078	0.91	0/1666
89	Ba	0.72	0/1073	0.93	1/1656 (0.1%)
90	Bb	0.74	0/893	0.98	0/1379
91	Bc	0.75	0/1035	1.04	4/1597 (0.3%)
92	Bd	0.71	0/1109	0.98	2/1709 (0.1%)
93	Be	0.71	0/1019	1.00	3/1566 (0.2%)
94	Bf	0.71	0/870	0.99	0/1341
95	Bg	0.72	0/880	1.04	3/1358 (0.2%)
96	Bh	0.71	0/916	0.97	1/1409 (0.1%)
97	Bi	0.69	0/1108	1.09	3/1708 (0.2%)
98	Bj	0.73	0/1117	1.07	5/1723 (0.3%)
99	Bk	0.72	0/699	1.02	2/1078 (0.2%)
100	Bl	0.72	0/935	0.97	2/1443 (0.1%)
101	Bm	0.70	0/869	0.98	2/1337 (0.1%)
102	Bn	0.69	0/984	0.99	0/1517
103	Bo	0.71	0/1021	1.08	3/1574 (0.2%)
104	Bp	0.74	0/1098	1.14	6/1695 (0.4%)
105	Bq	0.70	0/1100	0.97	0/1699
106	Br	0.72	0/872	1.00	1/1345 (0.1%)
107	Bs	0.70	0/680	1.06	1/1048 (0.1%)
108	Bt	0.70	0/1028	1.03	2/1586 (0.1%)
109	Bu	0.69	0/1123	1.00	1/1734 (0.1%)
110	Bv	0.73	0/916	1.00	1/1410 (0.1%)
111	Bw	0.69	0/844	0.99	3/1299 (0.2%)
112	Bx	0.68	0/1182	0.98	0/1824
113	By	0.71	0/705	1.04	2/1089 (0.2%)
114	Bz	0.71	0/925	0.97	0/1425
115	B0	0.71	0/688	0.98	0/1060
116	B1	0.67	0/1190	1.01	1/1838 (0.1%)
117	B2	0.71	0/690	0.98	1/1063 (0.1%)
118	B3	0.71	0/1283	0.93	0/1977
119	B4	0.72	0/1112	0.96	2/1715 (0.1%)
120	B5	0.69	0/707	1.02	0/1090

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
121	B6	0.72	0/1043	1.02	2/1611 (0.1%)
122	B7	0.72	0/855	0.99	1/1319 (0.1%)
123	B8	0.73	0/1192	0.98	0/1841
124	B9	0.74	0/857	1.02	3/1320 (0.2%)
125	CA	0.73	0/721	1.03	3/1108 (0.3%)
126	CB	0.72	0/736	1.02	0/1135
127	CC	0.74	0/703	1.01	1/1086 (0.1%)
128	CD	0.74	0/1341	1.05	2/2068 (0.1%)
129	CE	0.71	0/1192	0.99	1/1837 (0.1%)
130	CF	0.73	0/918	0.98	2/1413 (0.1%)
131	CG	0.77	0/700	1.06	3/1077 (0.3%)
132	CH	0.73	0/1233	1.08	4/1906 (0.2%)
133	CI	0.73	0/689	1.08	3/1062 (0.3%)
134	CJ	0.70	0/1098	1.05	2/1693 (0.1%)
135	CK	0.72	0/1268	1.08	4/1957 (0.2%)
136	CL	0.71	0/719	1.01	2/1110 (0.2%)
137	CM	0.73	0/734	1.00	1/1130 (0.1%)
138	CN	0.72	0/932	0.97	0/1438
139	CO	0.71	0/679	1.01	3/1045 (0.3%)
140	CP	0.74	0/1238	1.02	2/1911 (0.1%)
141	CQ	0.73	0/1094	0.99	2/1685 (0.1%)
142	CR	0.72	0/1035	0.95	1/1597 (0.1%)
143	CS	0.73	0/1103	1.06	6/1701 (0.4%)
144	CT	0.73	0/862	1.08	4/1326 (0.3%)
145	CU	0.74	0/697	0.95	0/1075
146	CV	0.71	0/732	0.93	1/1127 (0.1%)
147	CW	0.71	0/1090	0.95	0/1683
148	CX	0.70	0/1087	1.04	1/1676 (0.1%)
149	CY	0.75	0/1121	0.99	1/1731 (0.1%)
150	CZ	0.71	0/1061	0.99	1/1640 (0.1%)
151	Ca	0.72	0/898	0.91	0/1383
152	Cb	0.73	0/1052	0.91	1/1624 (0.1%)
153	Cc	0.71	0/690	0.99	1/1065 (0.1%)
154	Cd	0.72	0/875	0.93	2/1349 (0.1%)
155	Ce	0.72	0/673	0.97	1/1035 (0.1%)
156	Cf	0.73	0/900	1.08	3/1382 (0.2%)
157	Cg	0.72	0/874	0.99	2/1348 (0.1%)
158	Ch	0.72	0/1043	0.95	1/1610 (0.1%)
159	Ci	0.73	0/1089	1.14	5/1681 (0.3%)
160	Cj	0.77	0/1242	1.05	5/1916 (0.3%)
161	Ck	0.72	0/1067	0.98	1/1646 (0.1%)
162	Cl	0.75	0/1021	1.07	4/1573 (0.3%)
163	Cm	0.72	0/852	1.06	1/1312 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
164	Cn	0.70	0/1030	0.94	0/1585
165	Co	0.70	0/840	1.12	3/1295 (0.2%)
166	Cp	0.75	0/841	1.03	3/1296 (0.2%)
167	Cq	0.74	0/817	1.03	2/1259 (0.2%)
168	Cr	0.74	0/872	1.02	0/1345
169	Cs	0.73	0/901	0.95	2/1392 (0.1%)
170	Ct	0.74	0/880	1.02	1/1356 (0.1%)
171	Cu	0.74	0/823	1.07	1/1270 (0.1%)
172	Cv	0.76	0/834	1.11	3/1285 (0.2%)
173	Cw	0.71	0/707	0.99	1/1087 (0.1%)
174	Cx	0.71	0/858	1.00	1/1322 (0.1%)
175	Cy	0.74	0/1027	0.98	1/1583 (0.1%)
176	Cz	0.72	0/1186	1.03	2/1830 (0.1%)
177	C0	0.68	0/1354	1.04	1/2088 (0.0%)
178	C1	0.70	0/1082	0.94	1/1669 (0.1%)
179	C2	0.71	0/742	1.01	2/1145 (0.2%)
180	C3	0.74	0/849	1.05	2/1309 (0.2%)
181	C4	0.70	0/1294	1.01	1/1996 (0.1%)
182	C5	0.70	0/1025	1.01	1/1582 (0.1%)
183	C6	0.72	0/1077	1.02	3/1659 (0.2%)
184	C7	0.71	0/1076	0.99	2/1656 (0.1%)
185	C8	0.70	0/863	0.95	3/1329 (0.2%)
186	C9	0.71	0/863	0.96	2/1332 (0.2%)
187	DA	0.70	0/1374	1.02	3/2118 (0.1%)
188	DB	0.73	0/980	1.00	5/1511 (0.3%)
189	DC	0.71	0/1075	0.93	1/1658 (0.1%)
190	DD	0.70	0/869	0.95	0/1339
191	DE	0.71	0/1056	0.97	1/1627 (0.1%)
192	DF	0.70	0/718	0.97	0/1107
All	All	0.72	0/372075	1.02	748/573956 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AA	26	1811
2	AB	0	10
3	AC	0	13
4	AD	0	12
5	AE	0	5

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

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Mol	Chain	#Chirality outliers	#Planarity outliers
48	Av	0	8
49	Aw	0	5
50	Ax	0	9
51	Ay	0	6
52	Az	0	7
53	A0	0	5
54	A1	0	9
55	A2	0	8
56	A3	0	6
57	A4	0	7
58	A5	0	5
59	A6	0	9
60	A7	0	10
61	A8	0	11
62	A9	0	7
63	BA	0	7
64	BB	0	7
65	BC	0	6
66	BD	0	7
67	BE	0	5
68	BF	0	10
69	BG	0	15
70	BH	0	10
71	BI	0	9
72	BJ	0	9
73	BK	0	13
74	BL	0	8
75	BM	0	9
76	BN	0	6
77	BO	0	11
78	BP	0	12
79	BQ	0	12
80	BR	0	10
81	BS	0	8
82	BT	0	12
83	BU	0	7
84	BV	0	9
85	BW	0	5
86	BX	0	2
87	BY	0	6
88	BZ	0	4
89	Ba	0	10

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Mol	Chain	#Chirality outliers	#Planarity outliers
90	Bb	0	16
91	Bc	0	8
92	Bd	0	8
93	Be	0	9
94	Bf	0	9
95	Bg	0	11
96	Bh	0	9
97	Bi	0	11
98	Bj	0	9
99	Bk	0	5
100	Bl	0	5
101	Bm	0	9
102	Bn	0	6
103	Bo	0	11
104	Bp	0	12
105	Bq	0	7
106	Br	0	7
107	Bs	0	12
108	Bt	0	8
109	Bu	0	11
110	Bv	0	8
111	Bw	0	9
112	Bx	0	17
113	By	0	4
114	Bz	0	4
115	B0	0	6
116	B1	0	13
117	B2	0	4
118	B3	0	14
119	B4	0	5
120	B5	0	6
121	B6	0	17
122	B7	0	5
123	B8	0	12
124	B9	0	14
125	CA	0	5
126	CB	0	13
127	CC	0	6
128	CD	0	12
129	CE	0	9
130	CF	0	7
131	CG	0	7

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Mol	Chain	#Chirality outliers	#Planarity outliers
132	CH	0	14
133	CI	0	4
134	CJ	0	11
135	CK	0	11
136	CL	0	4
137	CM	0	9
138	CN	0	8
139	CO	0	7
140	CP	0	12
141	CQ	0	11
142	CR	0	9
143	CS	0	11
144	CT	0	11
145	CU	0	6
146	CV	0	7
147	CW	0	9
148	CX	0	8
149	CY	0	9
150	CZ	0	10
151	Ca	0	9
152	Cb	0	5
153	Cc	0	14
154	Cd	0	4
155	Ce	0	10
156	Cf	0	7
157	Cg	0	11
158	Ch	0	11
159	Ci	0	8
160	Cj	0	18
161	Ck	0	6
162	Cl	0	11
163	Cm	0	7
164	Cn	0	7
165	Co	0	8
166	Cp	0	11
167	Cq	0	4
168	Cr	0	11
169	Cs	0	12
170	Ct	0	9
171	Cu	0	5
172	Cv	0	11
173	Cw	0	7

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Mol	Chain	#Chirality outliers	#Planarity outliers
174	Cx	0	8
175	Cy	0	16
176	Cz	0	13
177	C0	0	11
178	C1	0	12
179	C2	0	6
180	C3	0	2
181	C4	0	8
182	C5	0	7
183	C6	0	11
184	C7	0	8
185	C8	0	9
186	C9	0	7
187	DA	0	16
188	DB	0	5
189	DC	0	6
190	DD	0	9
191	DE	0	10
192	DF	0	4
All	All	26	3449

There are no bond length outliers.

The worst 5 of 748 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	1068	DG	P-O3'-C3'	12.57	139.06	120.20
1	AA	1599	DT	P-O3'-C3'	12.48	138.92	120.20
160	Cj	27	DG	P-O3'-C3'	11.94	138.10	120.20
1	AA	645	DA	P-O3'-C3'	11.64	137.65	120.20
1	AA	5153	DG	P-O3'-C3'	11.57	137.55	120.20

5 of 26 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	AA	1155	DG	C3'
1	AA	1417	DA	C3',C4'
1	AA	3394	DT	C3'
1	AA	3534	DA	C3',C4'
1	AA	3922	DA	C3',C4'

5 of 3449 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	1	DT	Sidechain
1	AA	10	DG	Sidechain
1	AA	14	DT	Sidechain
1	AA	18	DC	Sidechain
1	AA	3	DA	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	164972	0	91297	0	0
2	AB	972	0	529	0	0
3	AC	1091	0	596	0	0
4	AD	989	0	542	0	0
5	AE	971	0	543	0	0
6	AF	1131	0	620	0	0
7	AG	970	0	554	0	0
8	AH	636	0	354	0	0
9	AI	570	0	324	0	0
10	AJ	977	0	543	0	0
11	AK	657	0	361	0	0
12	AL	1065	0	592	0	0
13	AM	766	0	439	0	0
14	AN	946	0	522	0	0
15	AO	947	0	514	0	0
16	AP	982	0	545	0	0
17	AQ	972	0	553	0	0
18	AR	942	0	522	0	0
19	AS	1012	0	566	0	0
20	AT	959	0	528	0	0
21	AU	823	0	448	0	0
22	AV	918	0	519	0	0
23	AW	982	0	539	0	0
24	AX	763	0	412	0	0
25	AY	966	0	536	0	0
26	AZ	813	0	450	0	0
27	Aa	1086	0	598	0	0
28	Ab	798	0	443	0	0
29	Ac	624	0	352	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	Ad	927	0	505	0	0
31	Ae	1056	0	595	0	0
32	Af	936	0	521	0	0
33	Ag	616	0	343	0	0
34	Ah	801	0	437	0	0
35	Ai	981	0	554	0	0
36	Aj	820	0	449	0	0
37	Ak	775	0	429	0	0
38	Al	1136	0	633	0	0
39	Am	772	0	438	0	0
40	An	912	0	506	0	0
41	Ao	942	0	518	0	0
42	Ap	974	0	548	0	0
43	Aq	662	0	362	0	0
44	Ar	988	0	547	0	0
45	As	991	0	536	0	0
46	At	1105	0	608	0	0
47	Au	934	0	524	0	0
48	Av	985	0	543	0	0
49	Aw	964	0	549	0	0
50	Ax	917	0	505	0	0
51	Ay	643	0	347	0	0
52	Az	613	0	338	0	0
53	A0	647	0	358	0	0
54	A1	984	0	542	0	0
55	A2	941	0	519	0	0
56	A3	615	0	339	0	0
57	A4	914	0	510	0	0
58	A5	923	0	515	0	0
59	A6	994	0	540	0	0
60	A7	977	0	550	0	0
61	A8	1206	0	686	0	0
62	A9	778	0	427	0	0
63	BA	980	0	540	0	0
64	BB	637	0	347	0	0
65	BC	1223	0	676	0	0
66	BD	1088	0	597	0	0
67	BE	648	0	362	0	0
68	BF	779	0	427	0	0
69	BG	959	0	538	0	0
70	BH	1159	0	660	0	0
71	BI	917	0	506	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
72	BJ	927	0	507	0	0
73	BK	981	0	544	0	0
74	BL	918	0	511	0	0
75	BM	990	0	544	0	0
76	BN	618	0	340	0	0
77	BO	914	0	509	0	0
78	BP	920	0	506	0	0
79	BQ	929	0	507	0	0
80	BR	770	0	432	0	0
81	BS	972	0	548	0	0
82	BT	1070	0	581	0	0
83	BU	784	0	440	0	0
84	BV	646	0	365	0	0
85	BW	624	0	347	0	0
86	BX	913	0	508	0	0
87	BY	1065	0	590	0	0
88	BZ	957	0	517	0	0
89	Ba	952	0	516	0	0
90	Bb	791	0	427	0	0
91	Bc	923	0	513	0	0
92	Bd	985	0	542	0	0
93	Be	908	0	502	0	0
94	Bf	776	0	434	0	0
95	Bg	783	0	429	0	0
96	Bh	814	0	447	0	0
97	Bi	993	0	565	0	0
98	Bj	991	0	542	0	0
99	Bk	620	0	338	0	0
100	Bl	829	0	449	0	0
101	Bm	773	0	427	0	0
102	Bn	878	0	492	0	0
103	Bo	914	0	519	0	0
104	Bp	974	0	528	0	0
105	Bq	984	0	551	0	0
106	Br	778	0	434	0	0
107	Bs	609	0	346	0	0
108	Bt	919	0	517	0	0
109	Bu	1004	0	565	0	0
110	Bv	815	0	447	0	0
111	Bw	752	0	422	0	0
112	Bx	1059	0	602	0	0
113	By	625	0	338	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
114	Bz	821	0	450	0	0
115	B0	613	0	342	0	0
116	B1	1065	0	604	0	0
117	B2	614	0	340	0	0
118	B3	1143	0	630	0	0
119	B4	988	0	537	0	0
120	B5	632	0	358	0	0
121	B6	929	0	511	0	0
122	B7	761	0	417	0	0
123	B8	1066	0	593	0	0
124	B9	768	0	434	0	0
125	CA	644	0	359	0	0
126	CB	656	0	362	0	0
127	CC	624	0	337	0	0
128	CD	1200	0	672	0	0
129	CE	1062	0	590	0	0
130	CF	816	0	446	0	0
131	CG	626	0	347	0	0
132	CH	1098	0	600	0	0
133	CI	614	0	339	0	0
134	CJ	988	0	570	0	0
135	CK	1138	0	643	0	0
136	CL	640	0	350	0	0
137	CM	653	0	359	0	0
138	CN	827	0	450	0	0
139	CO	607	0	340	0	0
140	CP	1106	0	612	0	0
141	CQ	976	0	540	0	0
142	CR	923	0	511	0	0
143	CS	983	0	539	0	0
144	CT	769	0	426	0	0
145	CU	619	0	337	0	0
146	CV	652	0	358	0	0
147	CW	970	0	531	0	0
148	CX	974	0	552	0	0
149	CY	995	0	535	0	0
150	CZ	948	0	528	0	0
151	Ca	798	0	437	0	0
152	Cb	933	0	503	0	0
153	Cc	616	0	340	0	0
154	Cd	779	0	425	0	0
155	Ce	603	0	339	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
156	Cf	803	0	449	0	0
157	Cg	779	0	429	0	0
158	Ch	928	0	507	0	0
159	Ci	977	0	550	0	0
160	Cj	1107	0	607	0	0
161	Ck	948	0	517	0	0
162	Cl	913	0	508	0	0
163	Cm	765	0	435	0	0
164	Cn	916	0	504	0	0
165	Co	752	0	425	0	0
166	Cp	752	0	418	0	0
167	Cq	731	0	409	0	0
168	Cr	778	0	430	0	0
169	Cs	804	0	441	0	0
170	Ct	781	0	425	0	0
171	Cu	736	0	413	0	0
172	Cv	748	0	423	0	0
173	Cw	629	0	347	0	0
174	Cx	761	0	416	0	0
175	Cy	917	0	507	0	0
176	Cz	1061	0	594	0	0
177	C0	1215	0	692	0	0
178	C1	964	0	532	0	0
179	C2	660	0	363	0	0
180	C3	757	0	417	0	0
181	C4	1159	0	655	0	0
182	C5	910	0	497	0	0
183	C6	959	0	529	0	0
184	C7	957	0	526	0	0
185	C8	771	0	429	0	0
186	C9	766	0	418	0	0
187	DA	1225	0	681	0	0
188	DB	876	0	487	0	0
189	DC	952	0	515	0	0
190	DD	775	0	428	0	0
191	DE	940	0	515	0	0
192	DF	638	0	349	0	0
All	All	331913	0	183783	0	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). Clashscore could not be calculated for this entry.

There are no clashes within the asymmetric unit.

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein molecules in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein molecules in this entry.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

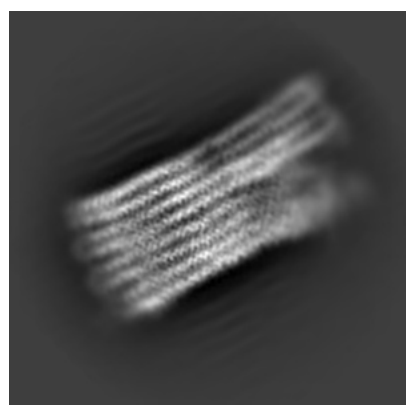
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11378. These allow visual inspection of the internal detail of the map and identification of artifacts.

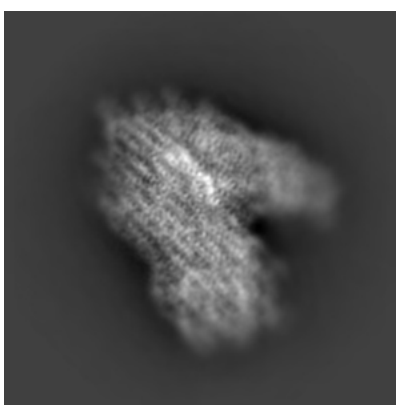
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

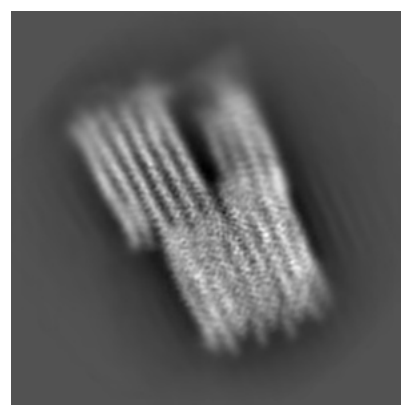
6.1.1 Primary map



X



Y



Z

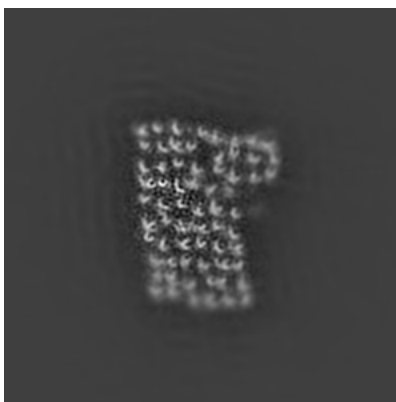
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

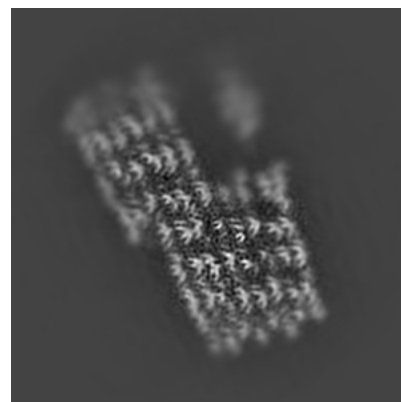
6.2.1 Primary map



X Index: 115



Y Index: 115



Z Index: 115

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

6.3 Largest variance slices [i](#)

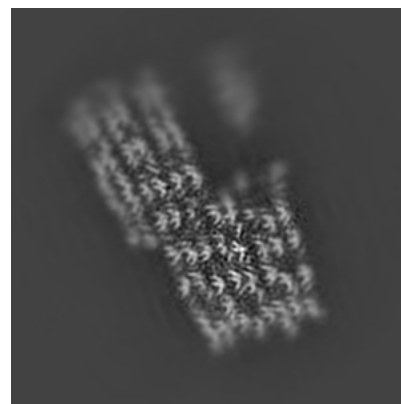
6.3.1 Primary map



X Index: 130



Y Index: 97

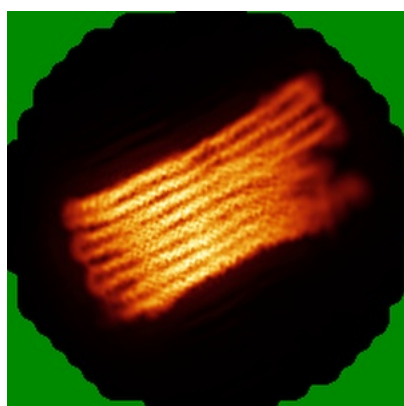


Z Index: 119

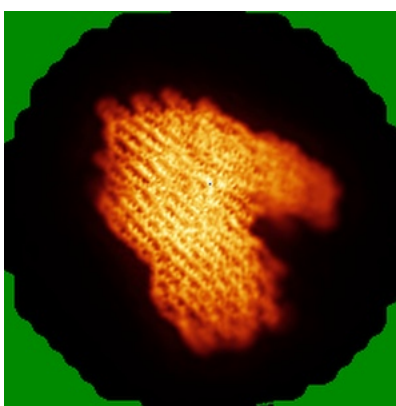
The images above show the largest variance slices of the map in three orthogonal directions.

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

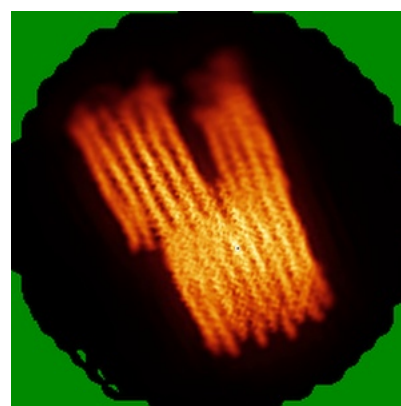
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views

This section was not generated.

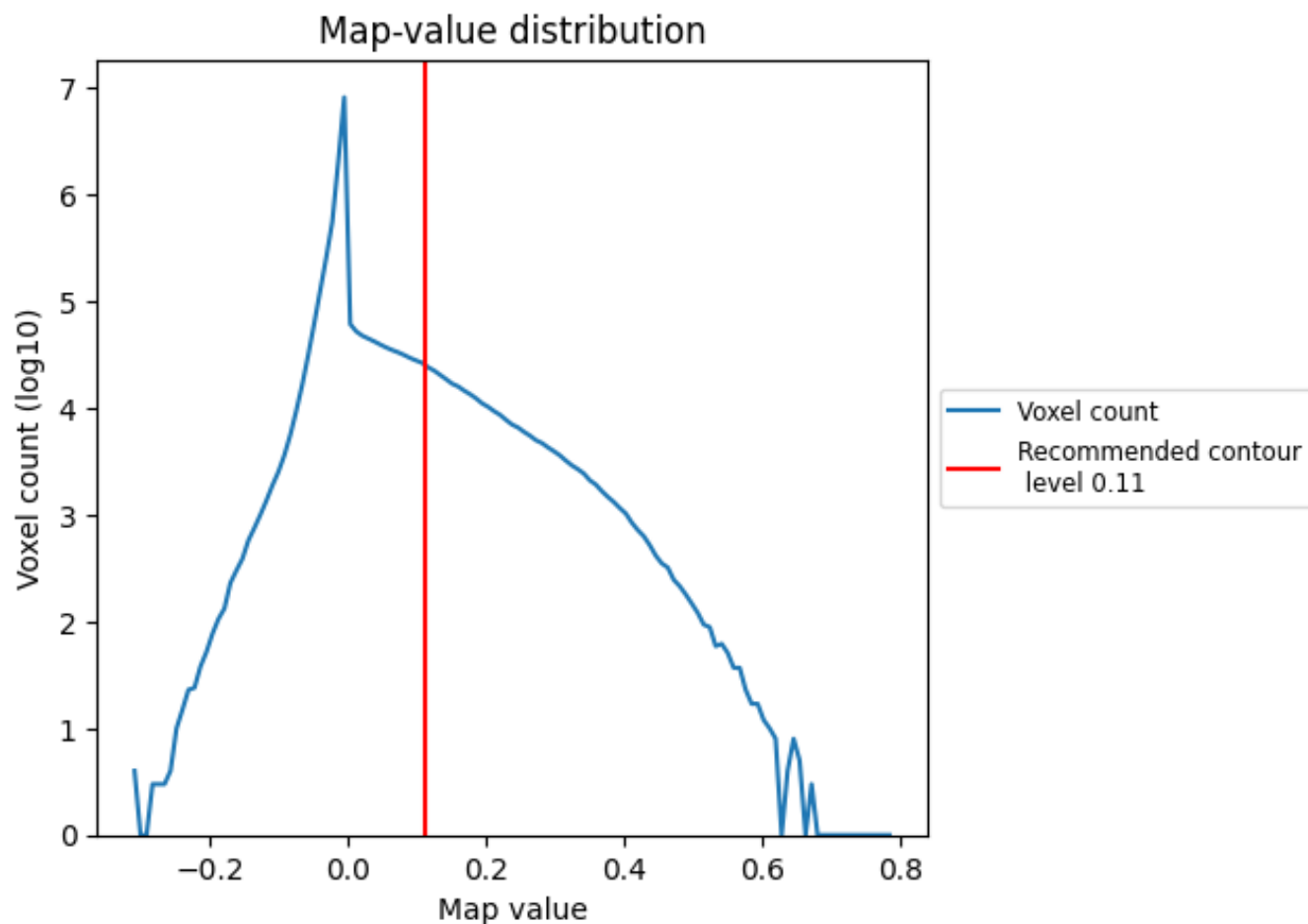
6.6 Mask visualisation

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

7 Map analysis [i](#)

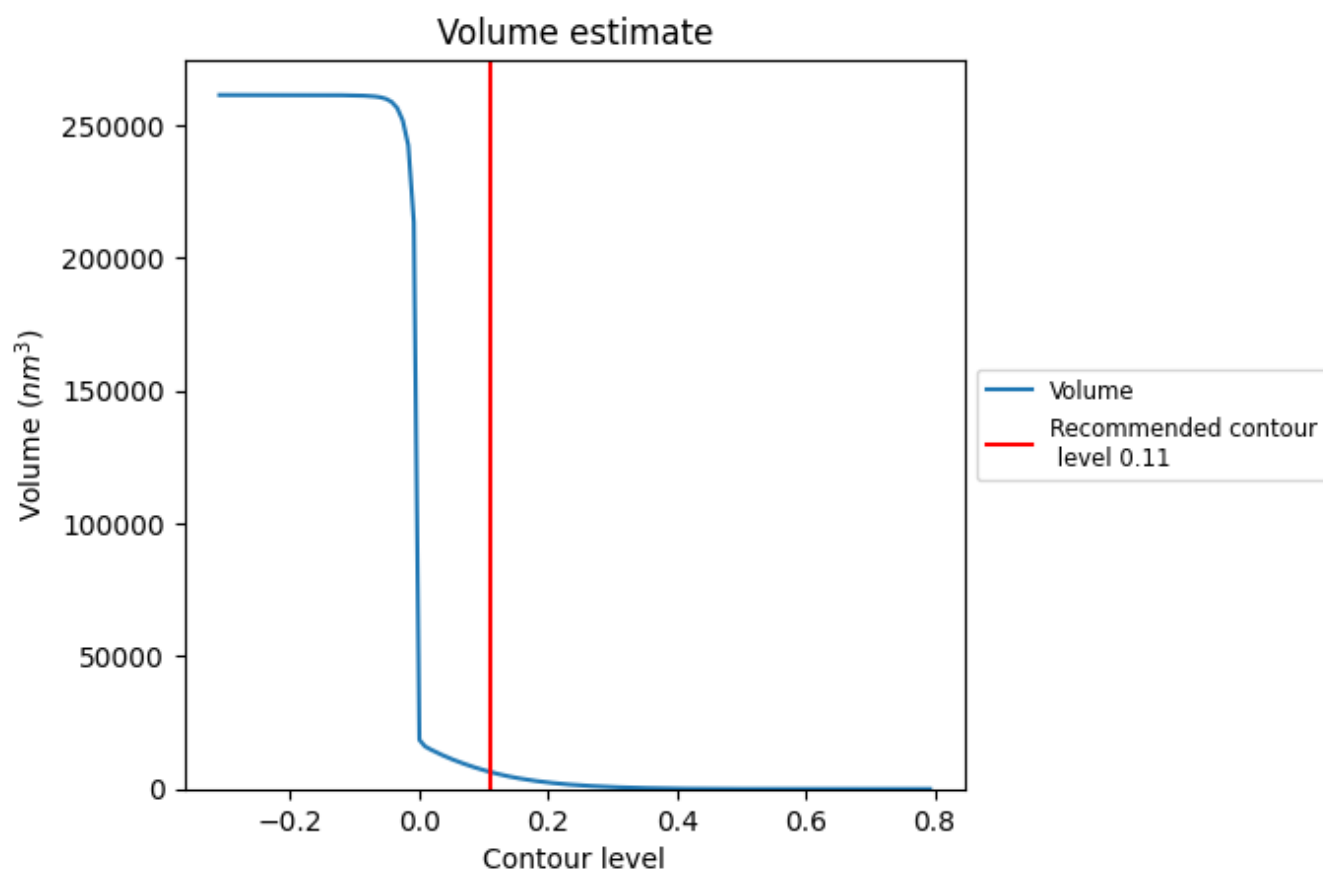
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

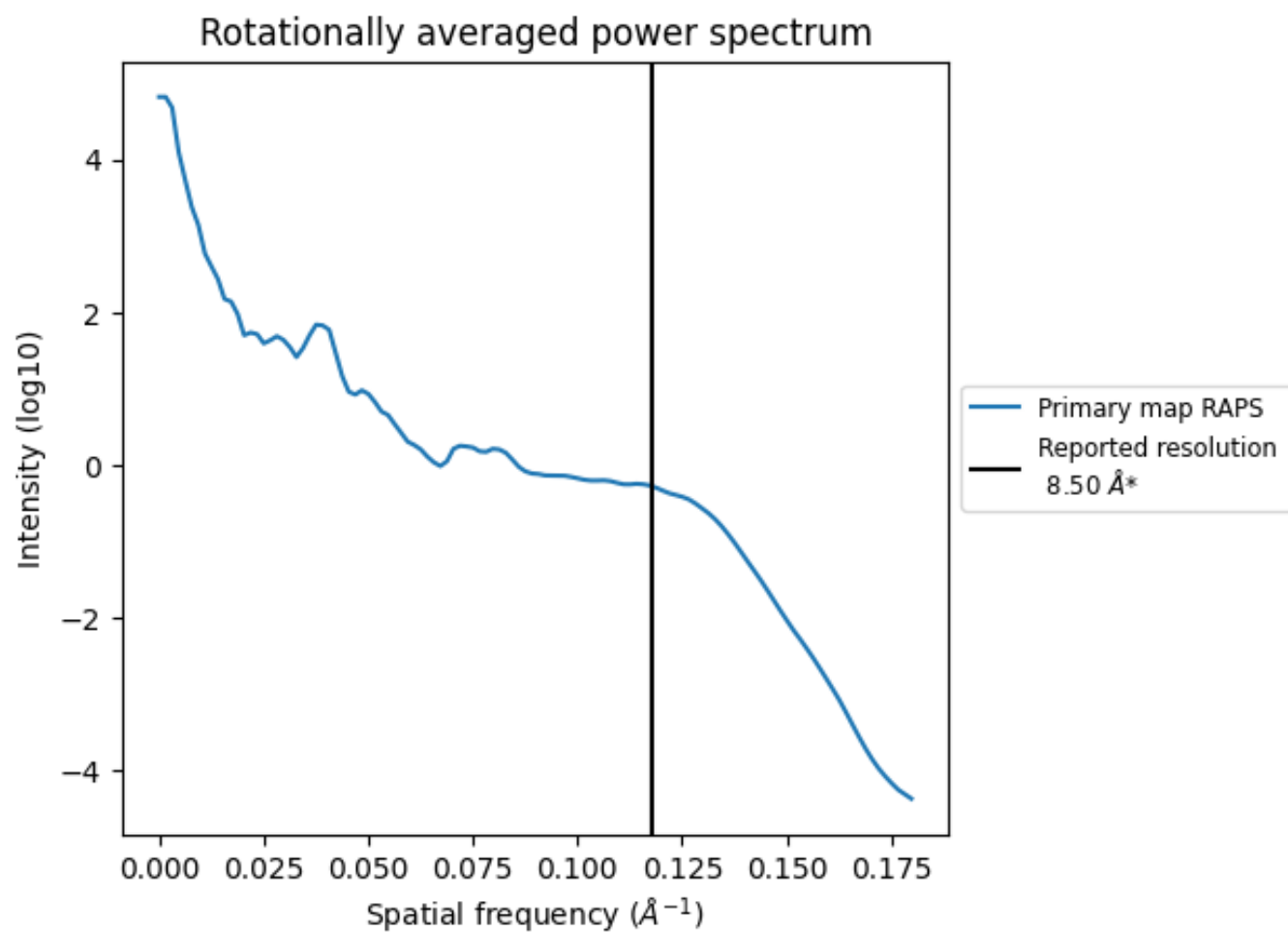
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 6439 nm^3 ; this corresponds to an approximate mass of 5817 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](#)

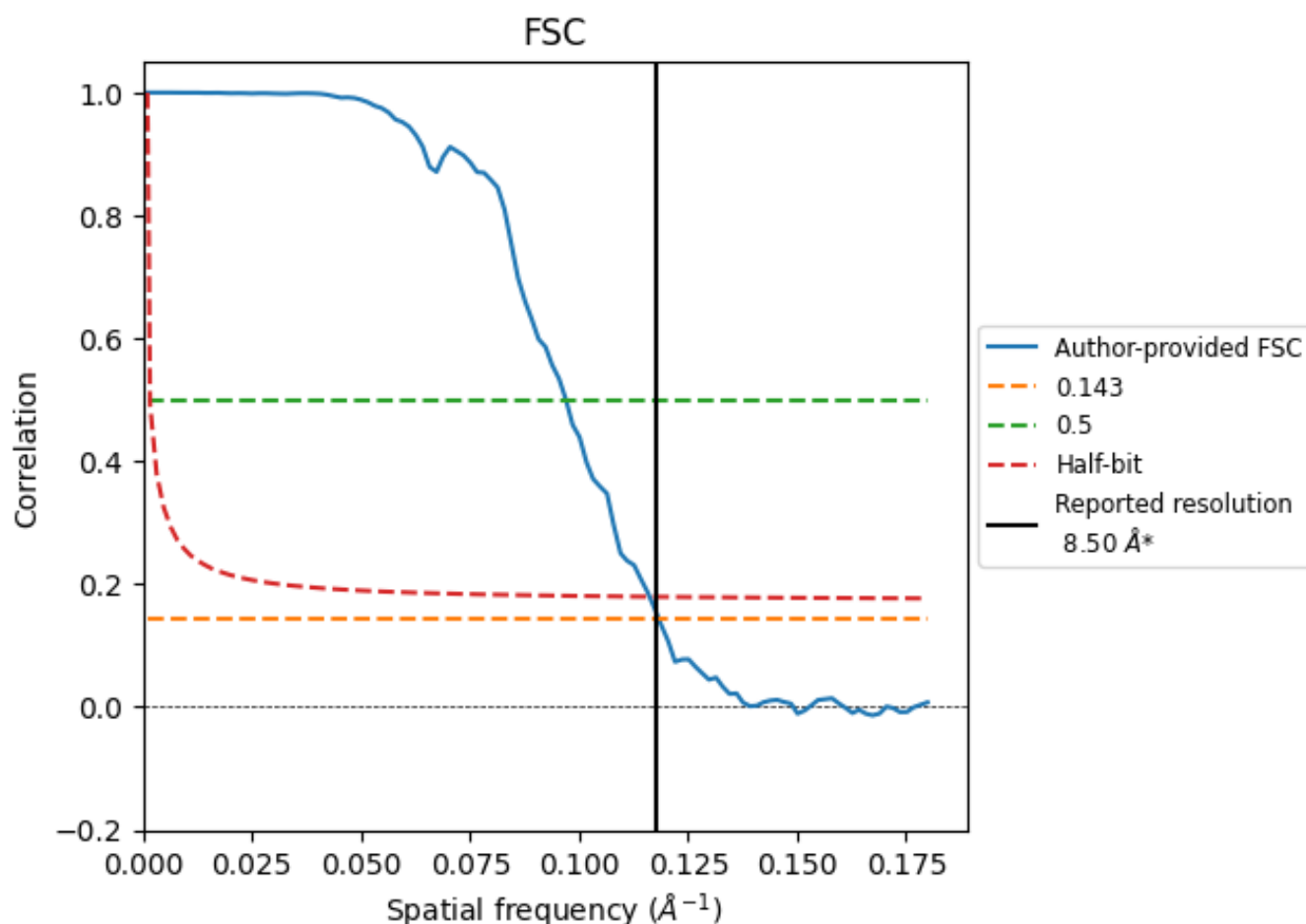


*Reported resolution corresponds to spatial frequency of 0.118 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.118 Å⁻¹

8.2 Resolution estimates [i](#)

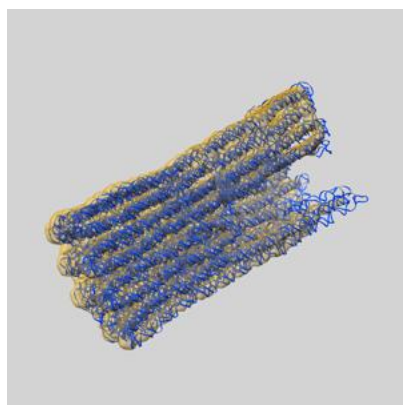
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	8.50	-	-
Author-provided FSC curve	8.45	10.32	8.61
Unmasked-calculated*	-	-	-

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

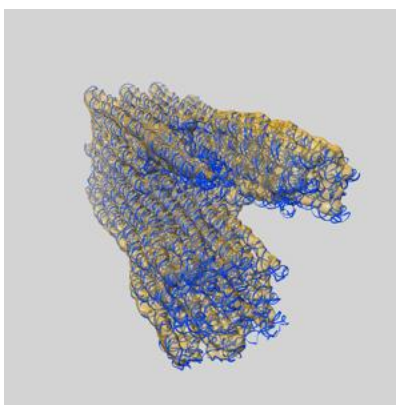
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11378 and PDB model 7ARY. Per-residue inclusion information can be found in section [3](#) on page [39](#).

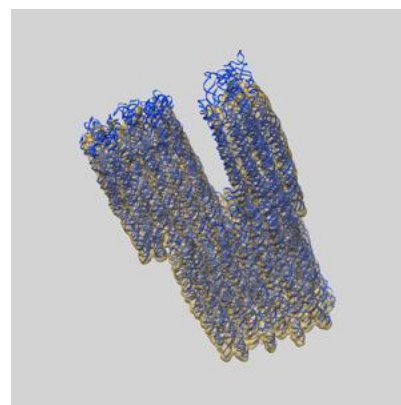
9.1 Map-model overlay [i](#)



X



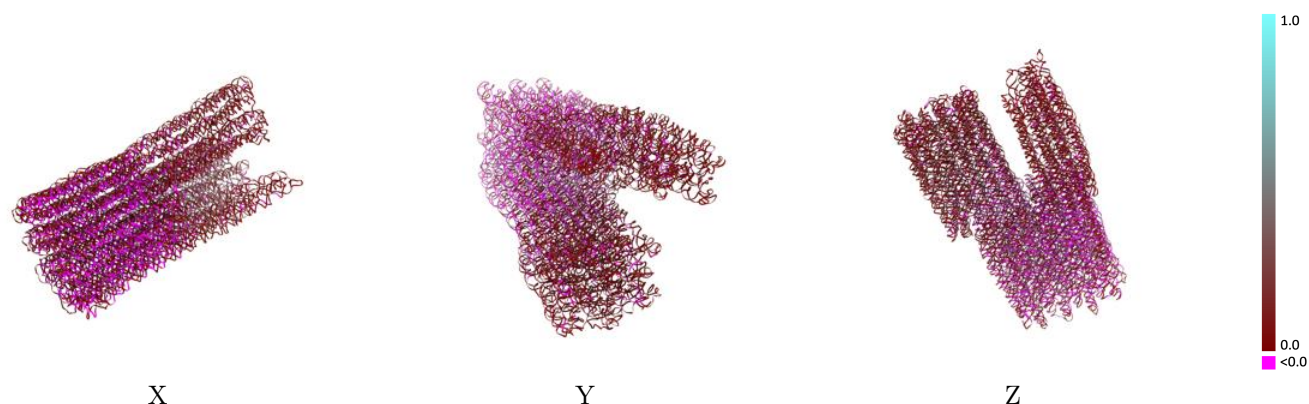
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.11 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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

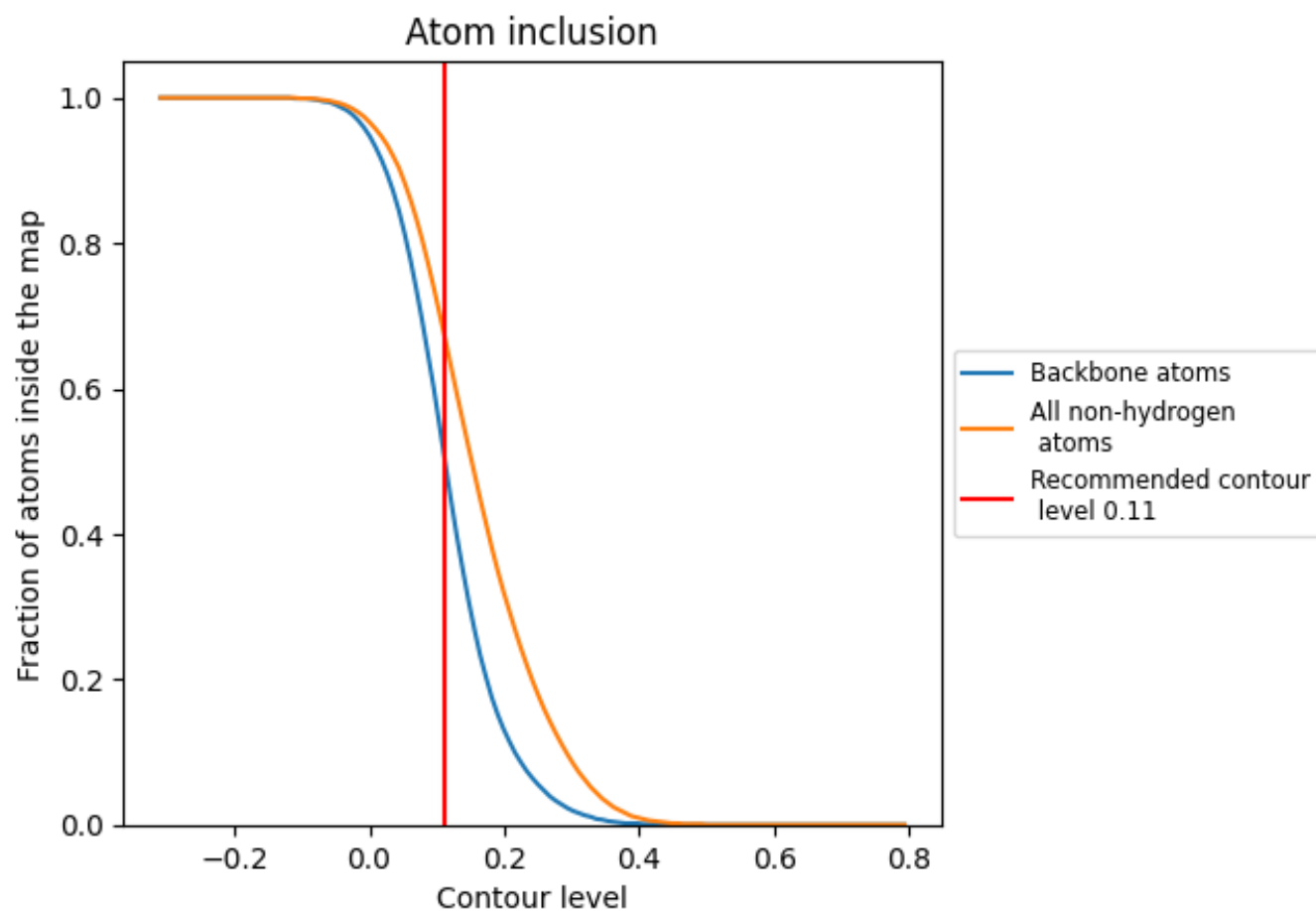


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion ⓘ



At the recommended contour level, 51% of all backbone atoms, 68% 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 (0.11) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.6780	 0.0580
A0	 0.8550	 0.1060
A1	 0.5980	 0.0140
A2	 0.7400	 0.0490
A3	 0.7590	 0.0710
A4	 0.6680	 0.0520
A5	 0.4760	 0.0360
A6	 0.6170	 -0.0000
A7	 0.6120	 0.0430
A8	 0.3730	 0.0680
A9	 0.4450	 0.0240
AA	 0.6840	 0.0600
AB	 0.8700	 0.1090
AC	 0.8140	 0.0630
AD	 0.8060	 0.1160
AE	 0.8550	 0.1230
AF	 0.8890	 0.1220
AG	 0.2020	 0.0360
AH	 0.9010	 0.1400
AI	 0.9650	 0.1160
AJ	 0.8650	 0.1110
AK	 0.8220	 0.1140
AL	 0.6630	 0.1040
AM	 0.8190	 0.1220
AN	 0.6670	 0.1010
AO	 0.8400	 0.1190
AP	 0.7230	 0.0610
AQ	 0.2900	 0.0590
AR	 0.7690	 0.1110
AS	 0.6650	 0.0970
AT	 0.6810	 0.0330
AU	 0.6570	 0.0050
AV	 0.4060	 0.0420
AW	 0.8460	 0.1020
AX	 0.7650	 0.0960



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Chain	Atom inclusion	Q-score
AY	 0.7920	 0.0770
AZ	 0.7720	 0.0930
Aa	 0.8570	 0.1100
Ab	 0.7470	 0.0480
Ac	 0.6440	 0.0640
Ad	 0.8450	 0.1220
Ae	 0.5220	 0.0940
Af	 0.8070	 0.1280
Ag	 0.8150	 0.0990
Ah	 0.7230	 0.0650
Ai	 0.3440	 0.0860
Aj	 0.8500	 0.0930
Ak	 0.7060	 0.0570
Al	 0.6080	 0.0240
Am	 0.6540	 0.0500
An	 0.8780	 0.1200
Ao	 0.7960	 0.0750
Ap	 0.7110	 0.0560
Aq	 0.7480	 0.0800
Ar	 0.6370	 0.0290
As	 0.6340	 0.0240
At	 0.6830	 0.0410
Au	 0.7260	 0.0430
Av	 0.6040	 0.0430
Aw	 0.1160	 0.0240
Ax	 0.8090	 0.1020
Ay	 0.6560	 0.0470
Az	 0.5660	 0.0260
B0	 0.6310	 0.0080
B1	 0.6580	 0.0520
B2	 0.5550	 -0.0010
B3	 0.6760	 0.0380
B4	 0.6680	 0.0010
B5	 0.5540	 0.0290
B6	 0.6440	 0.0150
B7	 0.6870	 0.0860
B8	 0.5610	 0.0620
B9	 0.5850	 -0.0160
BA	 0.6610	 0.0170
BB	 0.4650	 0.0220
BC	 0.3790	 0.0820
BD	 0.8560	 0.1140

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Chain	Atom inclusion	Q-score
BE	 0.7900	 0.0670
BF	 0.7750	 0.0750
BG	 0.6570	 0.0320
BH	 0.4030	 0.0890
BI	 0.7500	 0.0860
BJ	 0.7470	 0.0600
BK	 0.6900	 0.0400
BL	 0.8210	 0.1110
BM	 0.5830	 0.0170
BN	 0.5000	 -0.0140
BO	 0.7240	 0.0630
BP	 0.5730	 0.0050
BQ	 0.6020	 0.0110
BR	 0.7330	 0.0380
BS	 0.6750	 0.0550
BT	 0.7310	 0.1090
BU	 0.7250	 0.0500
BV	 0.5620	 0.0100
BW	 0.7550	 0.0920
BX	 0.6070	 0.0120
BY	 0.7170	 0.1210
BZ	 0.7810	 0.0910
Ba	 0.8440	 0.0950
Bb	 0.7140	 0.0280
Bc	 0.5620	 0.0030
Bd	 0.6420	 0.0350
Be	 0.8580	 0.1080
Bf	 0.6600	 0.0200
Bg	 0.6360	 0.0320
Bh	 0.7590	 0.0940
Bi	 0.7060	 0.1080
Bj	 0.7430	 0.0600
Bk	 0.8110	 0.1170
Bl	 0.6710	 0.0280
Bm	 0.7140	 0.0460
Bn	 0.7880	 0.0590
Bo	 0.7470	 0.0690
Bp	 0.7500	 0.0380
Bq	 0.6970	 0.0910
Br	 0.7350	 0.0600
Bs	 0.5160	 -0.0120
Bt	 0.7030	 0.0520

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Chain	Atom inclusion	Q-score
Bu	 0.7740	 0.0540
Bv	 0.6170	 0.0200
Bw	 0.5070	 -0.0270
Bx	 0.6070	 0.0450
By	 0.4670	 0.0030
Bz	 0.5250	 -0.0130
C0	 0.6630	 0.0450
C1	 0.3830	 0.0790
C2	 0.4500	 0.0660
C3	 0.6300	 -0.0260
C4	 0.6760	 0.0480
C5	 0.0360	 0.0450
C6	 0.5930	 -0.0190
C7	 0.7190	 0.0550
C8	 0.6710	 0.0330
C9	 0.5470	 0.0090
CA	 0.5500	 -0.0200
CB	 0.8340	 0.0750
CC	 0.5420	 -0.0490
CD	 0.3680	 0.0680
CE	 0.7230	 0.0340
CF	 0.6760	 0.0180
CG	 0.8070	 0.0820
CH	 0.7800	 0.0720
CI	 0.6380	 0.0110
CJ	 0.8120	 0.0470
CK	 0.2560	 0.0630
CL	 0.7870	 0.0990
CM	 0.7150	 0.0240
CN	 0.5940	 0.0070
CO	 0.6850	 0.0170
CP	 0.6960	 0.0910
CQ	 0.8160	 0.0860
CR	 0.5300	 -0.0420
CS	 0.7650	 0.0690
CT	 0.7700	 0.0710
CU	 0.6690	 -0.0130
CV	 0.6170	 -0.0110
CW	 0.7570	 0.0300
CX	 0.6180	 0.0940
CY	 0.8870	 0.1010
CZ	 0.8150	 0.0750

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Chain	Atom inclusion	Q-score
Ca	 0.7360	 0.0130
Cb	 0.6820	 0.0370
Cc	 0.8080	 0.1150
Cd	 0.6980	 0.0180
Ce	 0.8230	 0.0970
Cf	 0.8970	 0.1070
Cg	 0.6280	 0.0170
Ch	 0.6980	 0.0180
Ci	 0.4550	 0.0710
Cj	 0.7990	 0.0630
Ck	 0.6740	 0.0020
Cl	 0.8220	 0.0660
Cm	 0.7110	 0.0120
Cn	 0.6060	 -0.0180
Co	 0.5900	 -0.0170
Cp	 0.8510	 0.0740
Cq	 0.7990	 0.0680
Cr	 0.7930	 0.0530
Cs	 0.7900	 0.0800
Ct	 0.8410	 0.0970
Cu	 0.7470	 0.0940
Cv	 0.8540	 0.0820
Cw	 0.6150	 0.0080
Cx	 0.5300	 -0.0350
Cy	 0.5060	 -0.0220
Cz	 0.6930	 0.0410
DA	 0.6510	 0.0330
DB	 0.0430	 0.0530
DC	 0.7870	 0.0510
DD	 0.9080	 0.1270
DE	 0.8670	 0.1060
DF	 0.6630	 0.0020