wwPDB EM Validation Summary Report (i)

Nov 19, 2022 – 11:28 pm GMT

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

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

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

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

EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 11.50 Å.

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

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

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

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

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

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Mol	Chain	Length	Quality of chain
68	BD	35	11% 77% 11%
69	BE	68	13% 68% 15%
70	BF	40	35% 60% 5%
71	BG	49	10% 78% 12%
72	BH	42	12% 10% 62% 5% 24%
73	BI	42	17% 43% 5% 36%
74	BJ	58	14% 72% 5% 9%
75	BK	44	18% 80%
76	BL	48	21% 69% 10%
77	BM	52	17% 63% 19%
78	BN	63	17% 57% 24%
79	BO	49	29% 61% 10%
80	BP	66	15% 44% 38%
81	BQ	48	23% 73%
82	BR	64	12% 41% 44%
83	BS	48	21% 71% 8%
84	BT	52	13% 52% 6% 29%
85	BU	55	27% 44% 27%
86	BV	44	25% 70% 5%
87	BW	53	9% 23% 53% 6% 19%
88	BX	48	29% 56% 15%
89	BY	48	15% 71% 10%
90	BZ	66	12% 52% 35%
91	Ba	48	25% 71%
92	Bb	68	6% 9% 60% 29%

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Mol	Chain	Length	Quality of chain
93	Bc	50	6% 20% 72% 8%
94	Bd	56	16% 57% 27%
95	Be	48	8% 19% 81%
96	Bf	48	15% 77% 8%
97	Bg	47	13% 53% 32%
98	Bh	48	17% 58% 21%
99	Bi	67	16% 16% 72% 7%
100	Bj	45	13% 84%
101	Bk	67	9% 55% 6% 30%
102	Bl	48	6% 88% 6%
103	Bm	48	17% 77% 6%
104	Bn	67	12% 10% 54% 6% 30%
105	Bo	67	22% 12% 66% 7% 15%
106	Bp	48	6% 81% 10%
107	Bq	58	14% 47% 5% 34%
108	Br	51	18% 51% 29%
109	Bs	54	39% 6% 65% 28%
110	C0	41	12% 15% 61% 24%
111	C1	51	12% 57% 29%
112	C2	56	30% 66%
113	C3	48	21% 71% 8%
114	C4	71	15% 61% 21%
115	C5	62	15% 81% 5%
116	C6	48	17% 77% 6%
117	C7	52	35% 60% 6%

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

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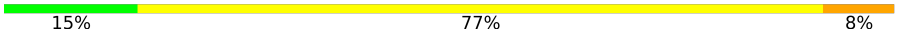
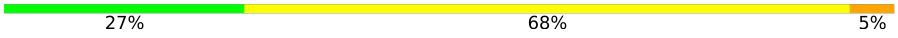
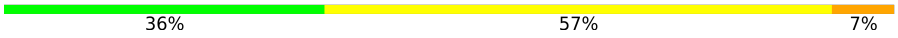
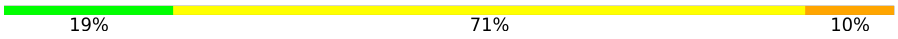
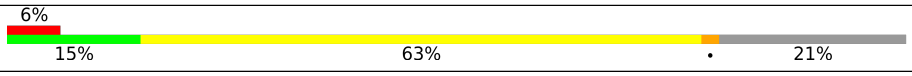
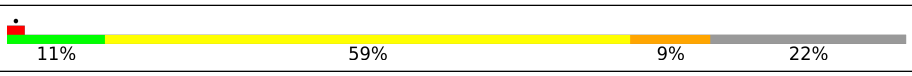
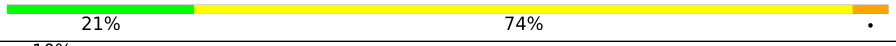
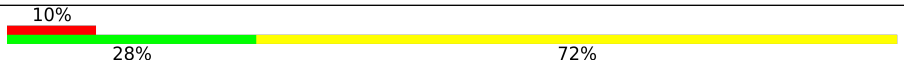
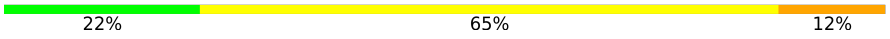
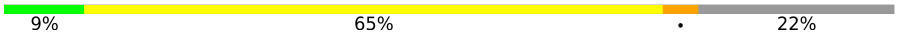
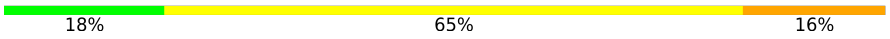
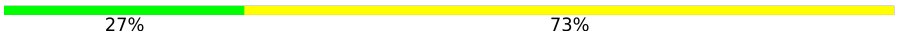
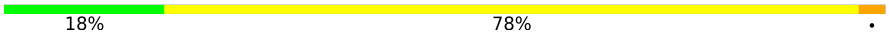
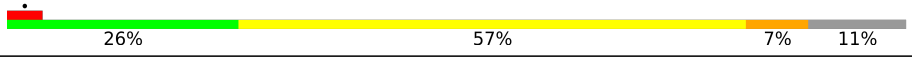
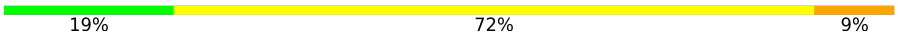
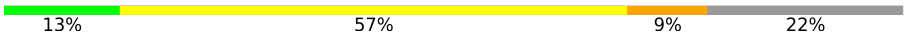
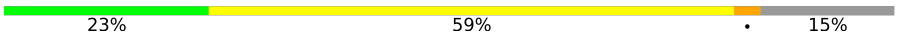
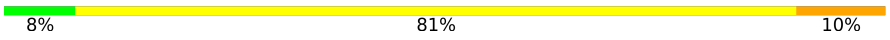
Mol	Chain	Length	Quality of chain
143	CZ	48	
144	Cb	44	
145	Cc	62	
146	Cd	42	
147	Ce	52	
148	Cf	48	
149	Cg	46	
150	Ch	47	
151	Ck	29	
152	Cp	48	
153	Cq	40	
154	Cr	46	
155	Cs	49	
156	Ct	44	
157	Cu	60	
158	Cv	46	
159	Cw	54	
160	Cx	46	
161	Cy	66	
162	Cz	48	

2 Entry composition (i)

There are 162 unique types of molecules in this entry. The entry contains 294953 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a DNA chain called SCAFFOLD STRAND,SCAFFOLD STRAND.

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

- Molecule 2 is a DNA chain called STAPLE STRAND.

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

- Molecule 3 is a DNA chain called STAPLE STRAND.

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

- Molecule 4 is a DNA chain called STAPLE STRAND.

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

- Molecule 5 is a DNA chain called STAPLE STRAND.

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

- Molecule 6 is a DNA chain called STAPLE STRAND.

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

- Molecule 7 is a DNA chain called STAPLE STRAND.

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

- Molecule 8 is a DNA chain called STAPLE STRAND.

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

- Molecule 9 is a DNA chain called STAPLE STRAND.

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

- Molecule 10 is a DNA chain called STAPLE STRAND.

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

- Molecule 11 is a DNA chain called STAPLE STRAND.

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

- Molecule 12 is a DNA chain called STAPLE STRAND.

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

- Molecule 13 is a DNA chain called STAPLE STRAND.

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

- Molecule 14 is a DNA chain called STAPLE STRAND.

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

- Molecule 15 is a DNA chain called STAPLE STRAND.

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

- Molecule 16 is a DNA chain called STAPLE STRAND.

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

- Molecule 17 is a DNA chain called STAPLE STRAND.

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

- Molecule 18 is a DNA chain called STAPLE STRAND.

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

- Molecule 19 is a DNA chain called STAPLE STRAND.

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

- Molecule 20 is a DNA chain called STAPLE STRAND.

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

- Molecule 21 is a DNA chain called STAPLE STRAND.

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

- Molecule 22 is a DNA chain called STAPLE STRAND.

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

- Molecule 23 is a DNA chain called STAPLE STRAND.

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

- Molecule 24 is a DNA chain called STAPLE STRAND.

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

- Molecule 25 is a DNA chain called STAPLE STRAND.

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

- Molecule 26 is a DNA chain called STAPLE STRAND.

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

- Molecule 27 is a DNA chain called STAPLE STRAND.

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

- Molecule 28 is a DNA chain called STAPLE STRAND.

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

- Molecule 29 is a DNA chain called STAPLE STRAND.

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

- Molecule 30 is a DNA chain called STAPLE STRAND.

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

- Molecule 31 is a DNA chain called STAPLE STRAND.

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

- Molecule 32 is a DNA chain called STAPLE STRAND.

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

- Molecule 33 is a DNA chain called STAPLE STRAND.

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

- Molecule 34 is a DNA chain called STAPLE STRAND.

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

- Molecule 35 is a DNA chain called STAPLE STRAND.

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

- Molecule 36 is a DNA chain called STAPLE STRAND.

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

- Molecule 37 is a DNA chain called STAPLE STRAND.

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

- Molecule 38 is a DNA chain called STAPLE STRAND.

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

- Molecule 39 is a DNA chain called STAPLE STRAND.

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

- Molecule 40 is a DNA chain called STAPLE STRAND.

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

- Molecule 41 is a DNA chain called STAPLE STRAND.

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

- Molecule 42 is a DNA chain called STAPLE STRAND.

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

- Molecule 43 is a DNA chain called STAPLE STRAND.

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

- Molecule 44 is a DNA chain called STAPLE STRAND.

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

- Molecule 45 is a DNA chain called STAPLE STRAND.

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

- Molecule 46 is a DNA chain called STAPLE STRAND.

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

- Molecule 47 is a DNA chain called STAPLE STRAND.

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

- Molecule 48 is a DNA chain called STAPLE STRAND.

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

- Molecule 49 is a DNA chain called STAPLE STRAND.

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

- Molecule 50 is a DNA chain called STAPLE STRAND.

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

- Molecule 51 is a DNA chain called STAPLE STRAND.

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

- Molecule 52 is a DNA chain called STAPLE STRAND.

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

- Molecule 53 is a DNA chain called STAPLE STRAND.

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

- Molecule 54 is a DNA chain called STAPLE STRAND.

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

- Molecule 55 is a DNA chain called STAPLE STRAND.

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

- Molecule 56 is a DNA chain called STAPLE STRAND.

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

- Molecule 57 is a DNA chain called STAPLE STRAND.

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

- Molecule 58 is a DNA chain called STAPLE STRAND.

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

- Molecule 59 is a DNA chain called STAPLE STRAND.

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

- Molecule 60 is a DNA chain called STAPLE STRAND.

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

- Molecule 61 is a DNA chain called STAPLE STRAND.

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

- Molecule 62 is a DNA chain called STAPLE STRAND.

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

- Molecule 63 is a DNA chain called STAPLE STRAND.

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

- Molecule 64 is a DNA chain called STAPLE STRAND.

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

- Molecule 65 is a DNA chain called STAPLE STRAND.

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

- Molecule 66 is a DNA chain called STAPLE STRAND.

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

- Molecule 67 is a DNA chain called STAPLE STRAND.

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

- Molecule 68 is a DNA chain called STAPLE STRAND.

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

- Molecule 69 is a DNA chain called STAPLE STRAND.

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

- Molecule 70 is a DNA chain called STAPLE STRAND.

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

- Molecule 71 is a DNA chain called STAPLE STRAND.

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

- Molecule 72 is a DNA chain called STAPLE STRAND.

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

- Molecule 73 is a DNA chain called STAPLE STRAND.

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

- Molecule 74 is a DNA chain called STAPLE STRAND.

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

- Molecule 75 is a DNA chain called STAPLE STRAND.

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

- Molecule 76 is a DNA chain called STAPLE STRAND.

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

- Molecule 77 is a DNA chain called STAPLE STRAND.

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

- Molecule 78 is a DNA chain called STAPLE STRAND.

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

- Molecule 79 is a DNA chain called STAPLE STRAND.

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

- Molecule 80 is a DNA chain called STAPLE STRAND.

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

- Molecule 81 is a DNA chain called STAPLE STRAND.

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

- Molecule 82 is a DNA chain called STAPLE STRAND.

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

- Molecule 83 is a DNA chain called STAPLE STRAND.

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

- Molecule 84 is a DNA chain called STAPLE STRAND.

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

- Molecule 85 is a DNA chain called STAPLE STRAND.

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

- Molecule 86 is a DNA chain called STAPLE STRAND.

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

- Molecule 87 is a DNA chain called STAPLE STRAND.

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

- Molecule 88 is a DNA chain called STAPLE STRAND.

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

- Molecule 89 is a DNA chain called STAPLE STRAND.

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

- Molecule 90 is a DNA chain called STAPLE STRAND.

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

- Molecule 91 is a DNA chain called STAPLE STRAND.

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

- Molecule 92 is a DNA chain called STAPLE STRAND.

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

- Molecule 93 is a DNA chain called STAPLE STRAND.

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

- Molecule 94 is a DNA chain called STAPLE STRAND.

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

- Molecule 95 is a DNA chain called STAPLE STRAND.

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

- Molecule 96 is a DNA chain called STAPLE STRAND.

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

- Molecule 97 is a DNA chain called STAPLE STRAND.

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

- Molecule 98 is a DNA chain called STAPLE STRAND.

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

- Molecule 99 is a DNA chain called STAPLE STRAND.

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

- Molecule 100 is a DNA chain called STAPLE STRAND.

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

- Molecule 101 is a DNA chain called STAPLE STRAND.

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

- Molecule 102 is a DNA chain called STAPLE STRAND.

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

- Molecule 103 is a DNA chain called STAPLE STRAND.

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

- Molecule 104 is a DNA chain called STAPLE STRAND.

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

- Molecule 105 is a DNA chain called STAPLE STRAND.

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

- Molecule 106 is a DNA chain called STAPLE STRAND.

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

- Molecule 107 is a DNA chain called STAPLE STRAND.

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

- Molecule 108 is a DNA chain called STAPLE STRAND.

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

- Molecule 109 is a DNA chain called STAPLE STRAND.

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

- Molecule 110 is a DNA chain called STAPLE STRAND.

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

- Molecule 111 is a DNA chain called STAPLE STRAND.

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

- Molecule 112 is a DNA chain called STAPLE STRAND.

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

- Molecule 113 is a DNA chain called STAPLE STRAND.

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

- Molecule 114 is a DNA chain called STAPLE STRAND.

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

- Molecule 115 is a DNA chain called STAPLE STRAND.

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

- Molecule 116 is a DNA chain called STAPLE STRAND.

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

- Molecule 117 is a DNA chain called STAPLE STRAND.

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

- Molecule 118 is a DNA chain called STAPLE STRAND.

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

- Molecule 119 is a DNA chain called STAPLE STRAND.

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

- Molecule 120 is a DNA chain called STAPLE STRAND.

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

- Molecule 121 is a DNA chain called STAPLE STRAND.

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

- Molecule 122 is a DNA chain called STAPLE STRAND.

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

- Molecule 123 is a DNA chain called STAPLE STRAND.

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

- Molecule 124 is a DNA chain called STAPLE STRAND.

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

- Molecule 125 is a DNA chain called STAPLE STRAND.

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

- Molecule 126 is a DNA chain called STAPLE STRAND.

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

- Molecule 127 is a DNA chain called STAPLE STRAND.

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

- Molecule 128 is a DNA chain called STAPLE STRAND.

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

- Molecule 129 is a DNA chain called STAPLE STRAND.

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

- Molecule 130 is a DNA chain called STAPLE STRAND.

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

- Molecule 131 is a DNA chain called STAPLE STRAND.

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

- Molecule 132 is a DNA chain called STAPLE STRAND.

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

- Molecule 133 is a DNA chain called STAPLE STRAND.

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

- Molecule 134 is a DNA chain called STAPLE STRAND.

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

- Molecule 135 is a DNA chain called STAPLE STRAND.

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

- Molecule 136 is a DNA chain called STAPLE STRAND.

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

- Molecule 137 is a DNA chain called STAPLE STRAND.

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

- Molecule 138 is a DNA chain called STAPLE STRAND.

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

- Molecule 139 is a DNA chain called STAPLE STRAND.

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

- Molecule 140 is a DNA chain called STAPLE STRAND.

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

- Molecule 141 is a DNA chain called STAPLE STRAND.

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

- Molecule 142 is a DNA chain called STAPLE STRAND.

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

- Molecule 143 is a DNA chain called STAPLE STRAND.

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

- Molecule 144 is a DNA chain called STAPLE STRAND.

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

- Molecule 145 is a DNA chain called STAPLE STRAND.

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

- Molecule 146 is a DNA chain called STAPLE STRAND.

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

- Molecule 147 is a DNA chain called STAPLE STRAND.

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

- Molecule 148 is a DNA chain called STAPLE STRAND.

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

- Molecule 149 is a DNA chain called STAPLE STRAND.

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

- Molecule 150 is a DNA chain called STAPLE STRAND.

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

- Molecule 151 is a DNA chain called STAPLE STRAND.

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

- Molecule 152 is a DNA chain called STAPLE STRAND.

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

- Molecule 153 is a DNA chain called STAPLE STRAND.

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

- Molecule 154 is a DNA chain called STAPLE STRAND.

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

- Molecule 155 is a DNA chain called STAPLE STRAND.

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

- Molecule 156 is a DNA chain called STAPLE STRAND.

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

- Molecule 157 is a DNA chain called STAPLE STRAND.

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

- Molecule 158 is a DNA chain called STAPLE STRAND.

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

- Molecule 159 is a DNA chain called STAPLE STRAND.

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

- Molecule 160 is a DNA chain called STAPLE STRAND.

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

- Molecule 161 is a DNA chain called STAPLE STRAND.

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

- Molecule 162 is a DNA chain called STAPLE STRAND.

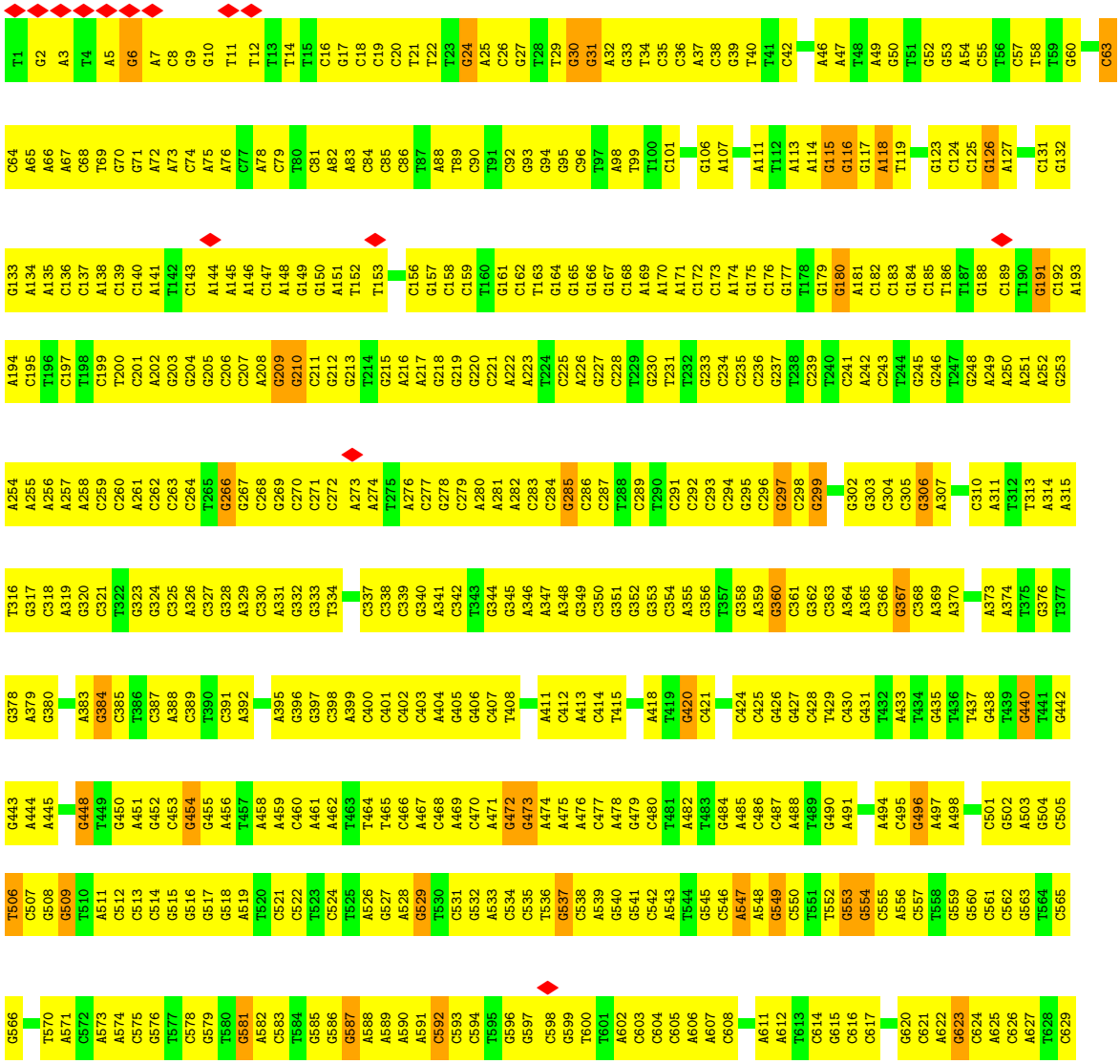
Mol	Chain	Residues	Atoms					AltConf	Trace
162	Cz	48	Total	C	N	O	P	0	0
			970	465	195	266	44		

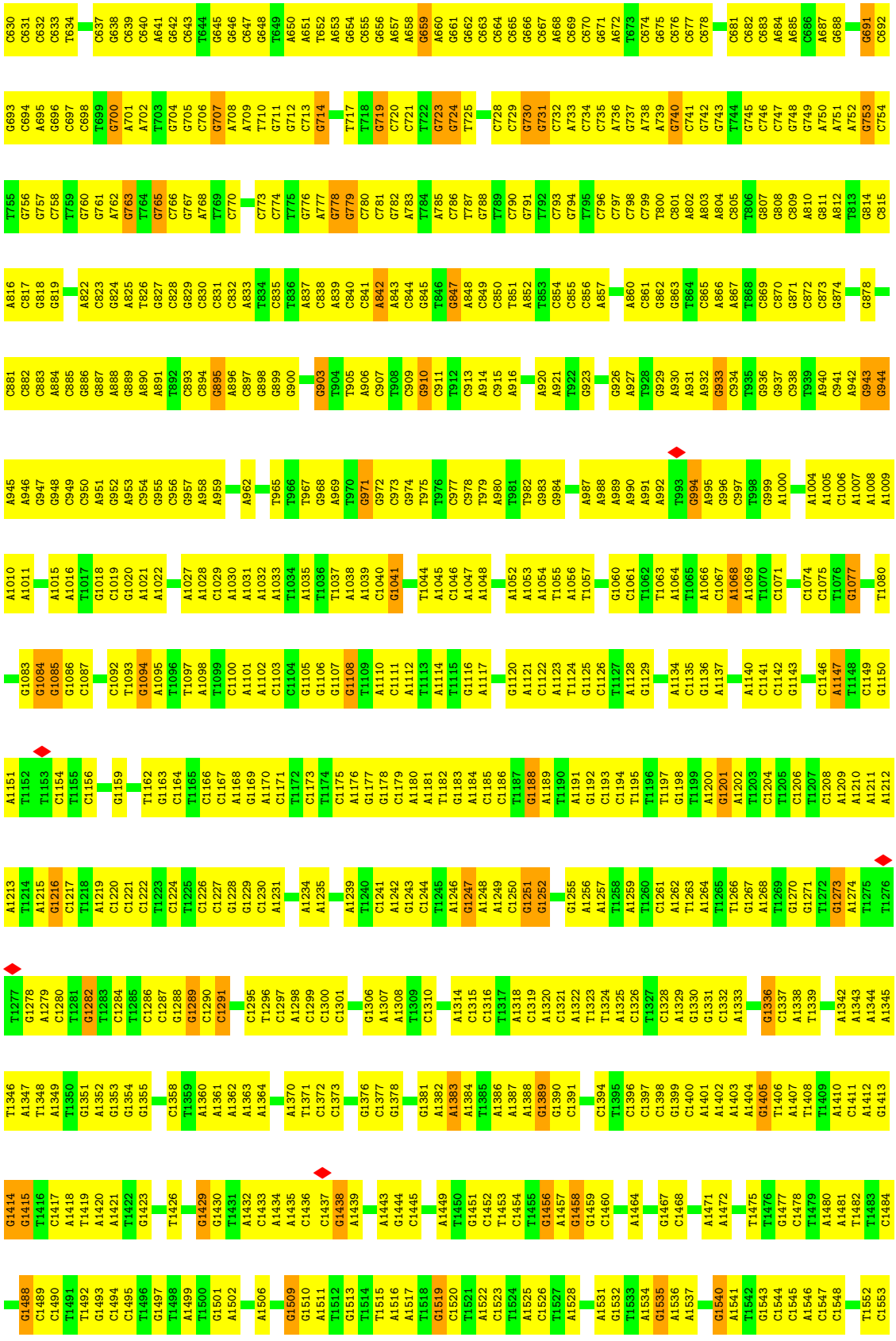
3 Residue-property plots (i)

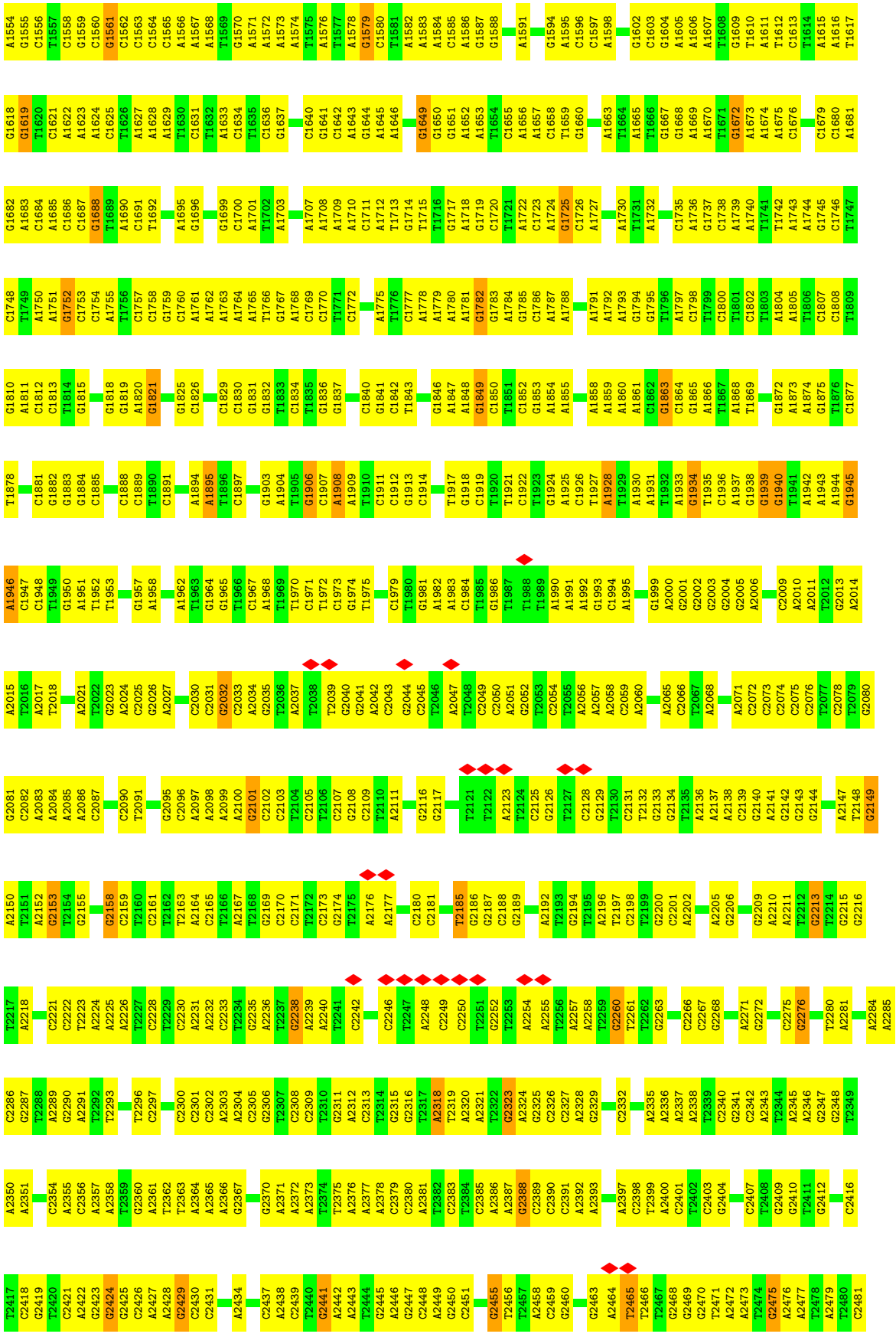
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

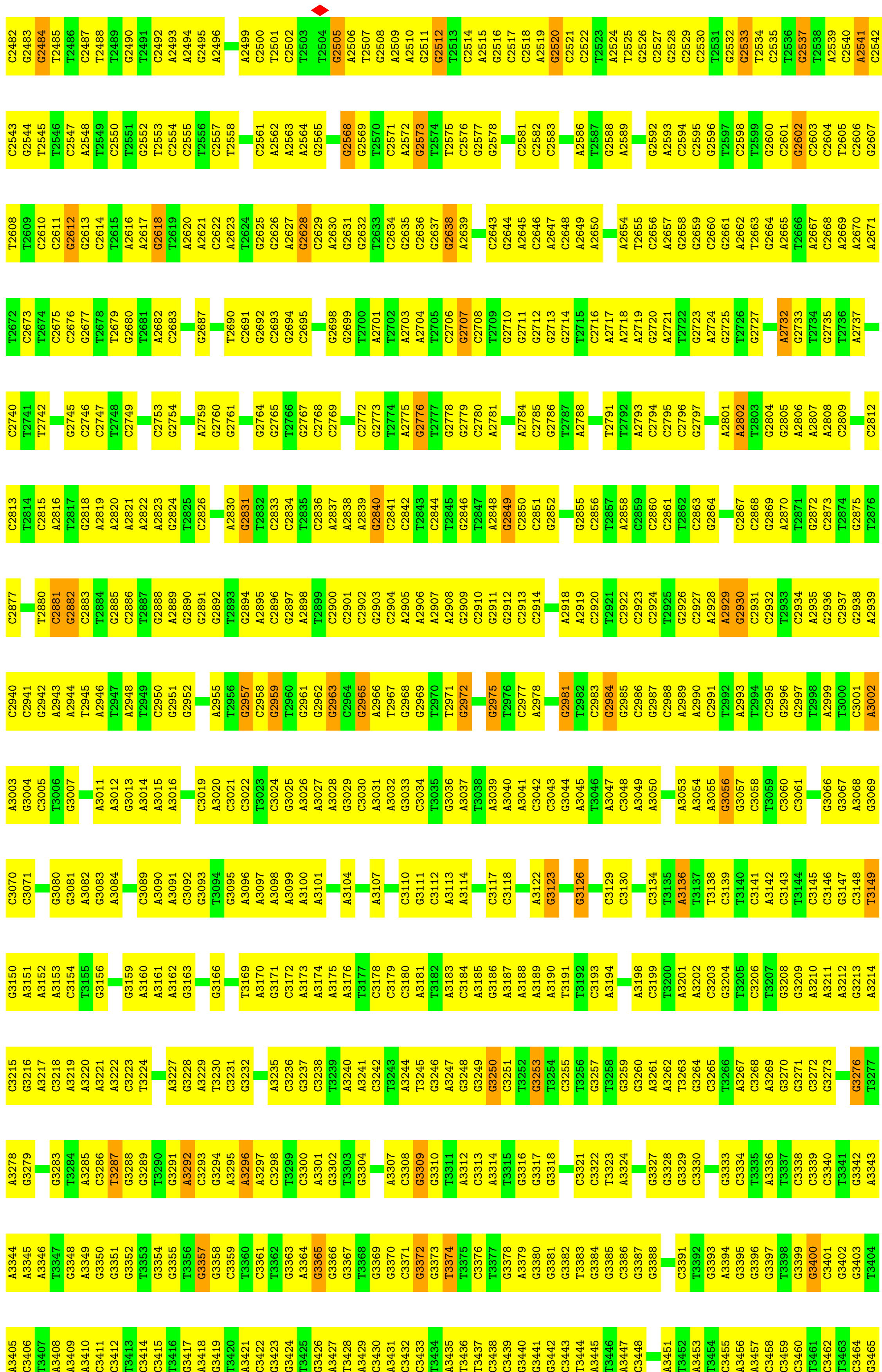
• Molecule 1: SCAFFOLD STRAND,SCAFFOLD STRAND

Chain AA:





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C2543 G2544 T2545 T2546 C2547 A2548 T2549 C2550 T2551 G2552 T2553 C2554 C2555 T2556 C2557 T2558 C2561 A2562 A2563 A2564 G2565 G2568 G2569 T2570 C2571 A2572 G2573 T2574 T2575 C2576 G2577 G2578 C2581 C2582 C2583 A2586 T2587 G2588 A2589 G2592 A2593 C2594 C2595 G2596 T2597 C2598 T2599 G2600 C2601 G2602 C2603 C2604 T2605 C2606 G2607
T2608 T2609 C2610 C2611 G2612 G2613 C2614 T2615 A2616 A2617 G2618 T2619 A2620 A2621 C2622 A2623 T2624 G2625 C2626 A2627 G2628 C2629 A2630 G2631 G2632 T2633 C2634 G2635 C2636 G2637 G2638 A2639 C2643 G2644 A2645 C2646 A2647 C2648 A2649 A2650 A2654 T2655 C2656 A2657 G2658 G2659 C2660 G2661 A2662 T2663 G2664 A2665 T2666 A2667 C2668 A2669 A2670 A2671
T2672 C2673 T2674 C2675 C2676 G2677 T2678 T2679 G2680 T2681 A2682 C2683 G2687 T2690 C2691 G2692 C2693 G2694 C2695 G2698 G2699 T2700 A2701 T2702 A2703 A2704 T2705 C2706 G2707 C2708 T2709 G2710 G2711 G2712 G2713 G2714 T2715 C2716 A2717 A2718 A2719 G2720 A2721 T2722 G2723 A2724 G2725 T2726 C2727 A2732 G2733 T2734 G2735 T2736 A2737
C2740 T2741 T2742 G2745 C2746 C2747 T2748 C2749 C2753 G2754 A2759 C2760 G2761 G2764 G2765 T2766 G2767 C2768 C2769 C2772 C2773 T2774 A2775 G2776 T2777 G2778 G2779 C2780 A2781 A2784 C2785 G2786 T2787 A2788 T2791 T2792 A2793 C2794 C2795 C2796 G2797 A2801 A2802 T2803 G2804 G2805 A2806 A2807 A2808 C2809 C2812
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C2940 C2941 G2942 A2943 A2944 T2945 A2946 T2947 A2948 T2949 C2950 G2951 G2952 A2955 T2956 G2957 C2958 G2959 T2960 G2961 G2962 G2963 C2964 G2965 A2966 T2967 G2968 G2969 T2970 T2971 G2972 G2975 T2976 C2977 A2978 G2981 T2982 C2983 G2984 G2985 C2986 G2987 C2988 A2989 A2990 C2991 T2992 A2993 T2994 C2995 G2996 G2997 T2998 A2999 T3000 C3001 A3002
A3003 G3004 C3005 T3006 G3007 A3011 A3012 G3013 A3014 A3015 A3016 C3019 A3020 C3021 C3022 T3023 C3024 G3025 A3026 A3027 A3028 G3029 C3030 A3031 A3032 G3033 C3034 T3035 G3036 A3037 T3038 A3039 A3040 A3041 C3042 G3043 G3044 A3045 T3046 A3047 C3048 A3049 A3050 A3053 A3054 A3055 G3056 G3057 C3058 T3059 C3060 C3061 G3066 G3067 A3068 G3069
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G3150 A3151 A3152 A3153 C3154 T3155 G3156 G3159 G3160 A3161 A3162 G3163 G3166 T3169 A3170 G3171 C3172 A3173 A3174 A3175 A3176 T3177 C3178 C3179 C3180 A3181 T3182 A3183 C3184 A3185 G3186 A3187 A3188 G3189 A3190 T3191 T3192 C3193 A3194 A3198 C3199 T3200 A3201 A3202 C3203 G3204 T3205 C3206 T3207 G3208 G3209 A3210 A3211 G3212 G3213 A3214
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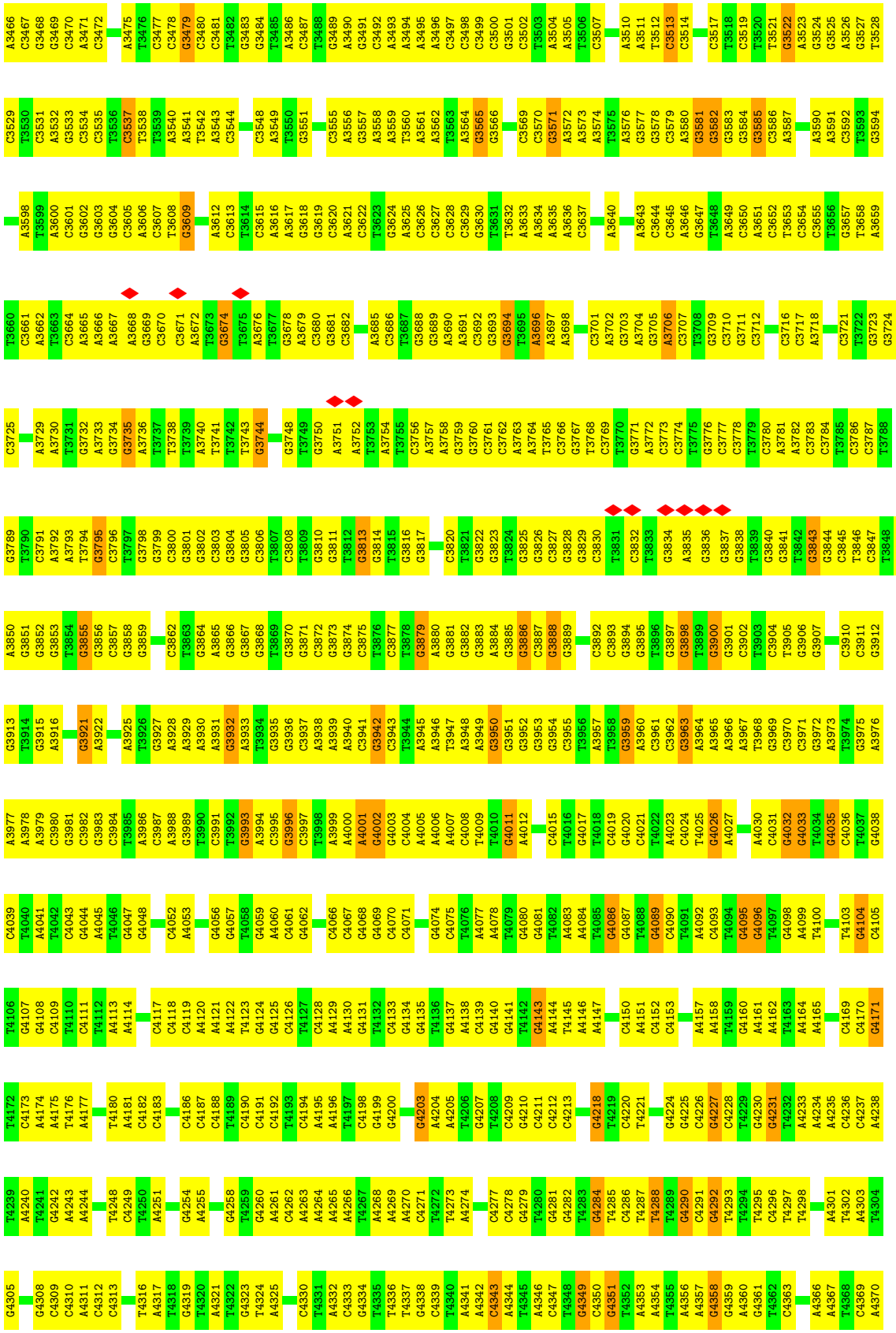
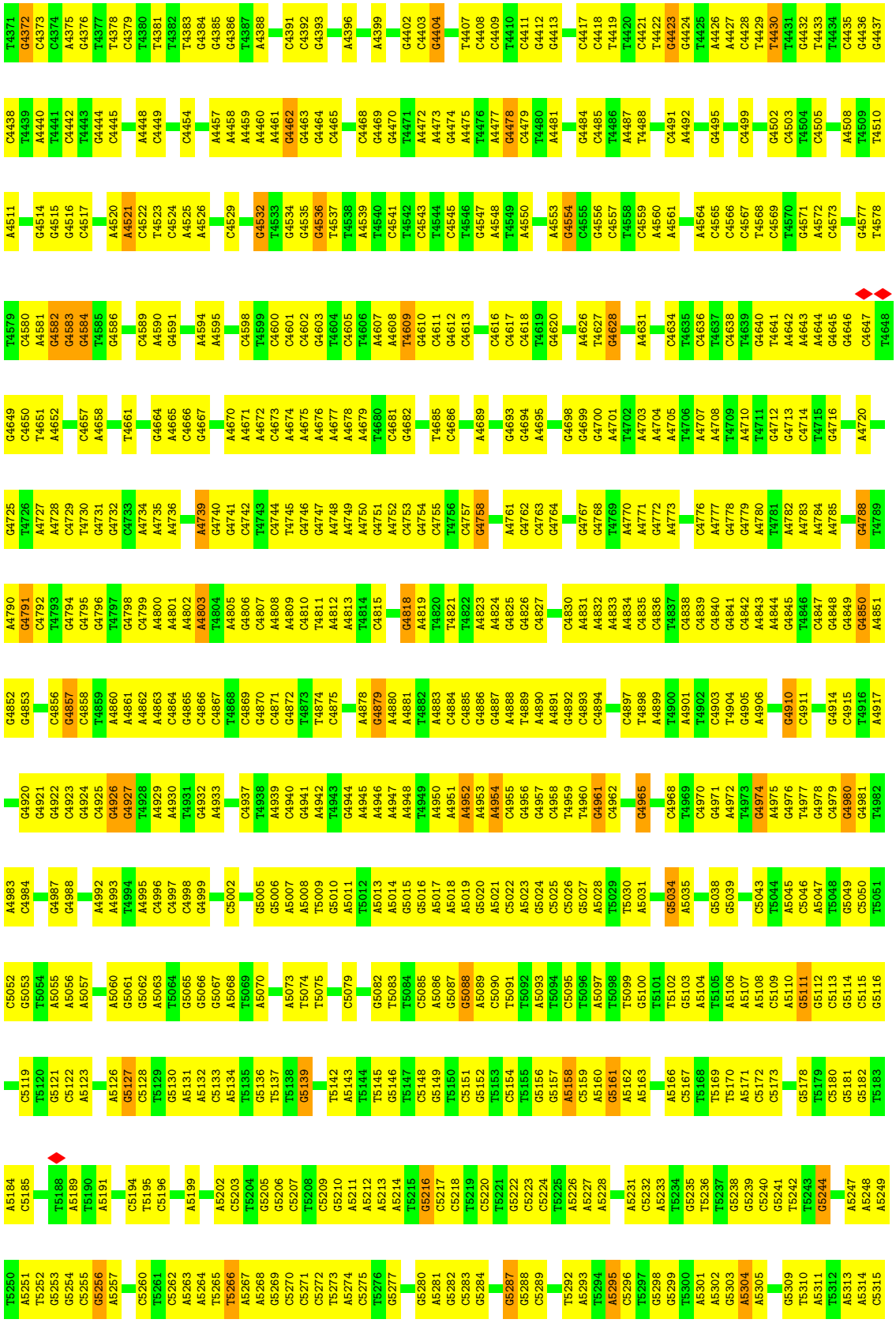
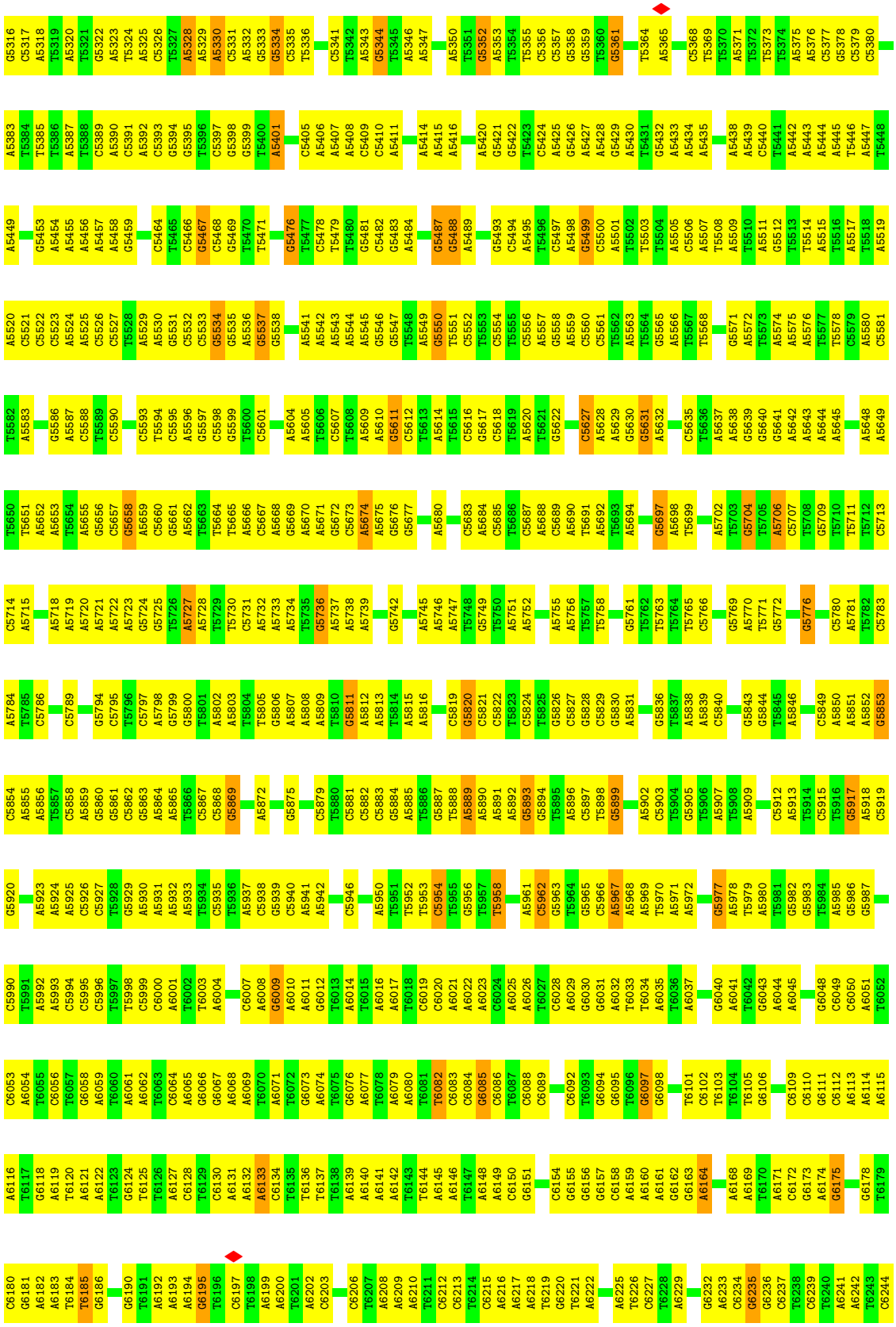
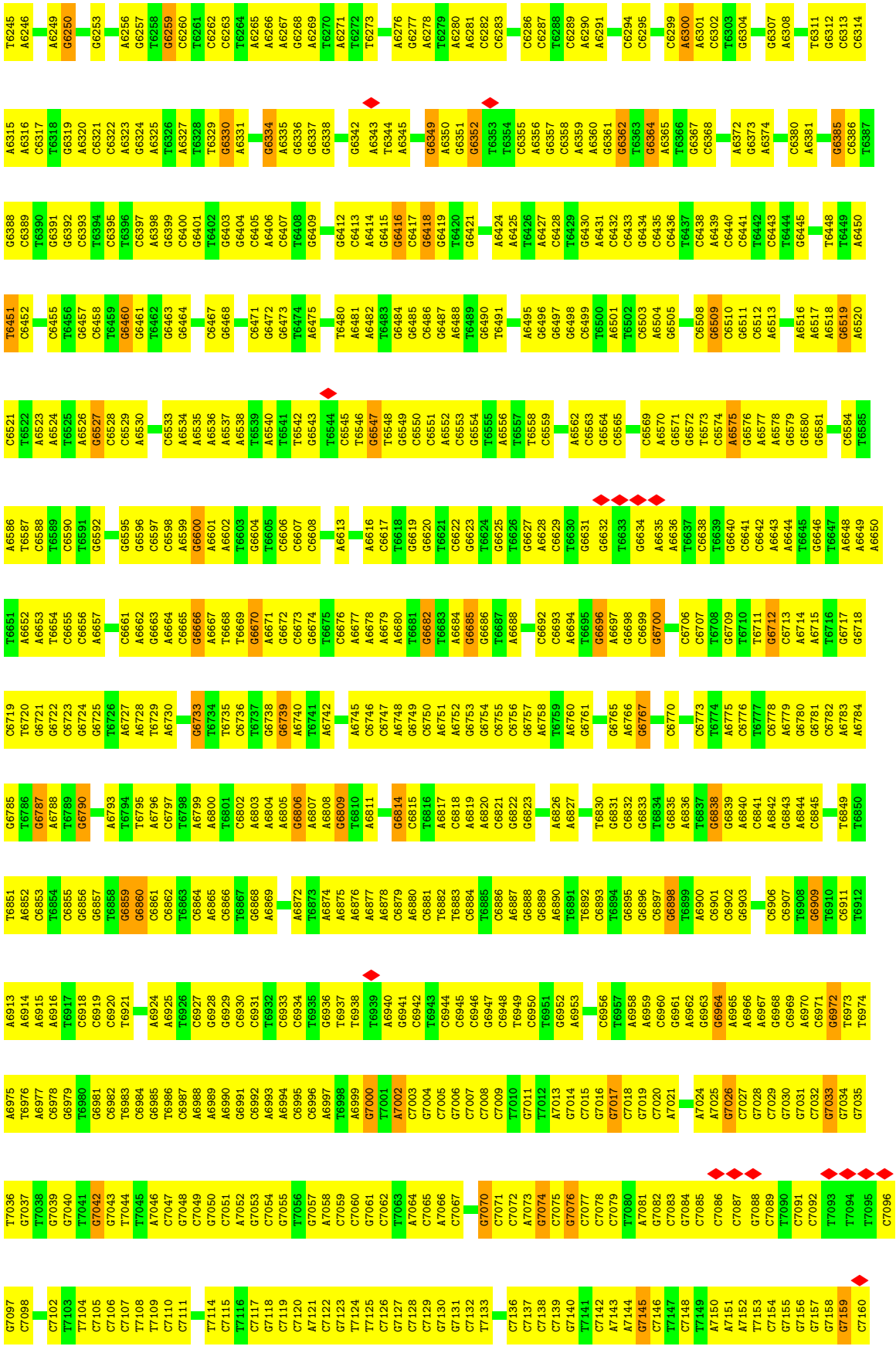
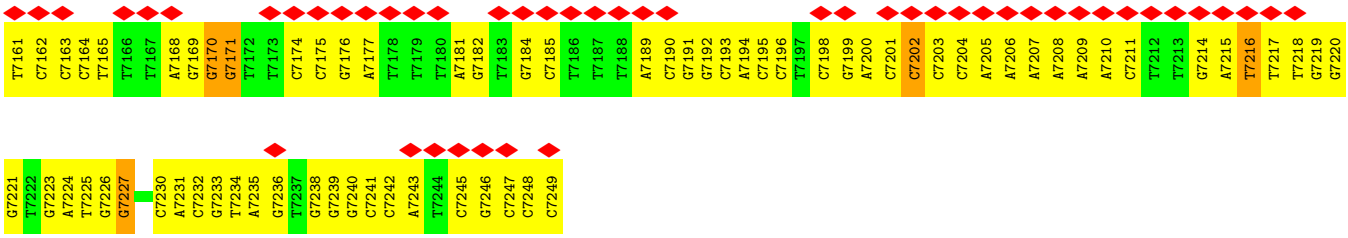
A3344 A3345 A3346 T3347 G3348 A3349 G3350 G3351 G3352 T3353 G3354 G3355 T3356 G3357 G3358 C3359 T3360 C3361 T3362 G3363 A3364 G3365 C3366 G3367 T3368 G3369 G3370 C3371 G3372 G3373 T3374 T3375 C3376 T3377 G3378 A3379 G3380 G3381 G3382 T3383 G3384 G3385 C3386 G3387 G3388 C3391 T3392 G3393 A3394 G3395 G3396 G3397 T3398 G3399 G3400 C3401 G3402 G3403 T3404
A3405 C3406 T3407 A3408 A3409 A3410 C3411 C3412 T3413 C3414 C3415 T3416 G3417 A3418 G3419 T3420 A3421 C3422 G3423 G3424 T3425 G3426 A3427 T3428 A3429 C3430 A3431 C3432 C3433 T3434 A3435 T3436 T3437 C3438 C3439 G3440 G3441 G3442 C3443 T3444 A3445 T3446 A3447 C3448 A3451 T3452 A3453 T3454 C3455 A3456 C3457 G3458 C3459 C3460 T3461 C3462 T3463 C3464 G3465





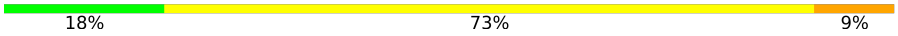






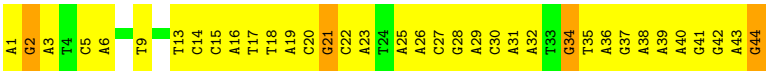
• Molecule 2: STAPLE STRAND

Chain A0:



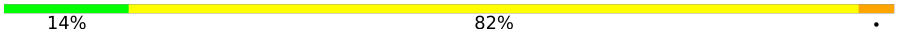
• Molecule 3: STAPLE STRAND

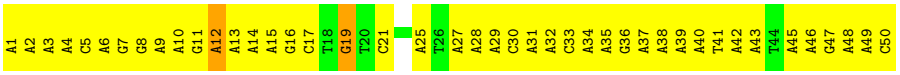
Chain A1:



• Molecule 4: STAPLE STRAND

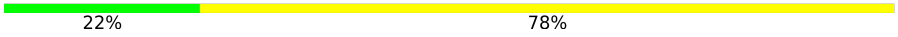
Chain A2:

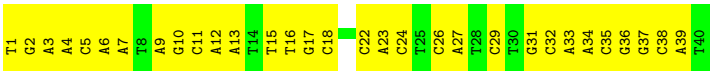




• Molecule 5: STAPLE STRAND

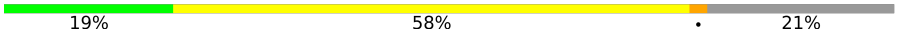
Chain A3:

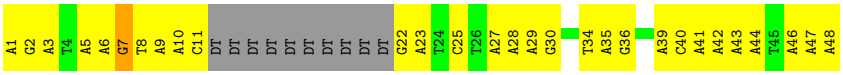




• Molecule 6: STAPLE STRAND

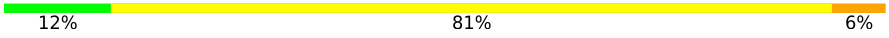
Chain A4:

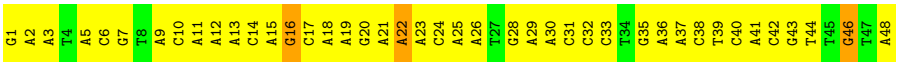




• Molecule 7: STAPLE STRAND

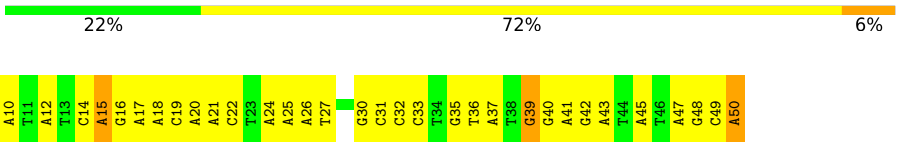
Chain A5:





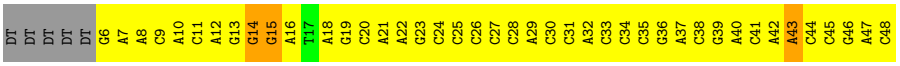
• Molecule 8: STAPLE STRAND

Chain A6:



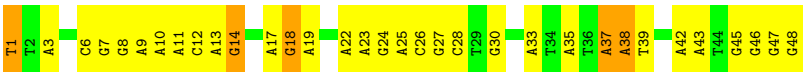
• Molecule 9: STAPLE STRAND

Chain A7:



• Molecule 10: STAPLE STRAND

Chain A8:

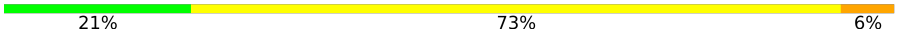


• Molecule 11: STAPLE STRAND

Chain AB:

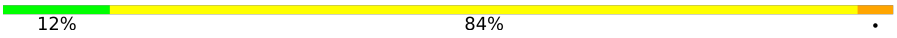
• Molecule 12: STAPLE STRAND

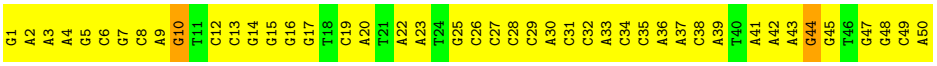
Chain AC:



• Molecule 13: STAPLE STRAND

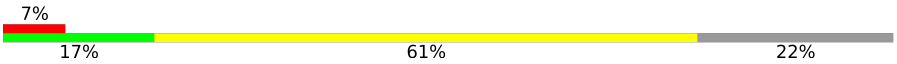
Chain AD:

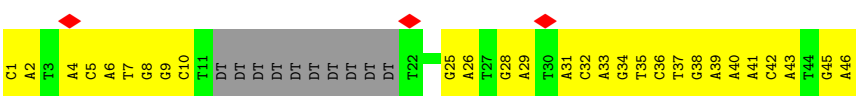




• Molecule 14: STAPLE STRAND

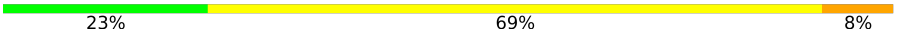
Chain AE:

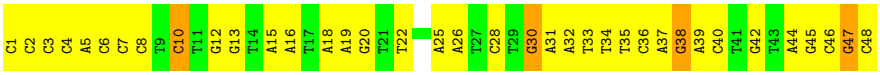




• Molecule 15: STAPLE STRAND

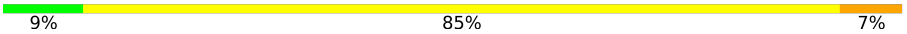
Chain AF:





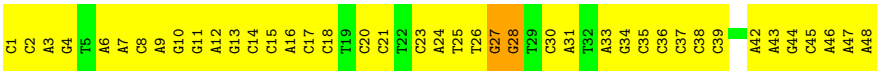
• Molecule 16: STAPLE STRAND

Chain AG:



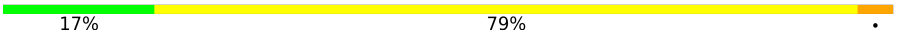
• Molecule 17: STAPLE STRAND

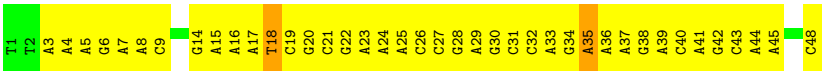
Chain AH:



• Molecule 18: STAPLE STRAND

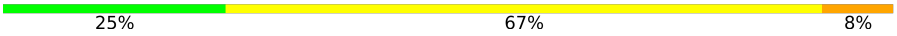
Chain AI:

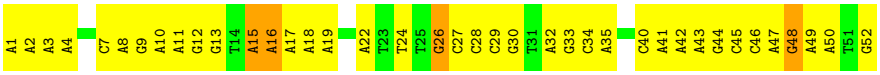




• Molecule 19: STAPLE STRAND

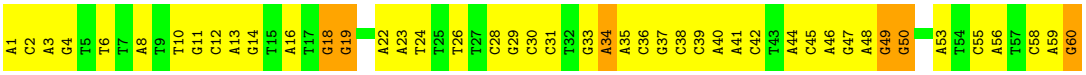
Chain AJ:





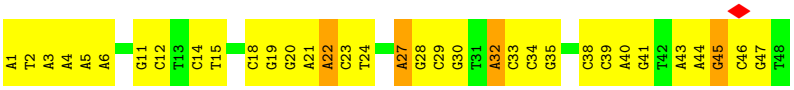
• Molecule 20: STAPLE STRAND

Chain AK:



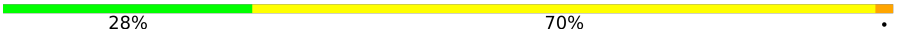
• Molecule 21: STAPLE STRAND

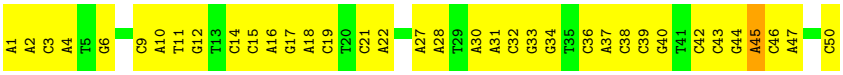
Chain AL:



• Molecule 22: STAPLE STRAND

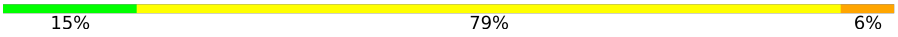
Chain AM:

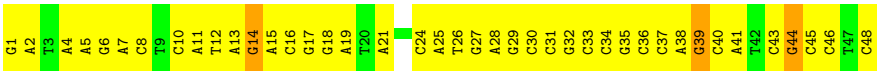




• Molecule 23: STAPLE STRAND

Chain AN:



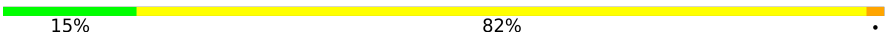


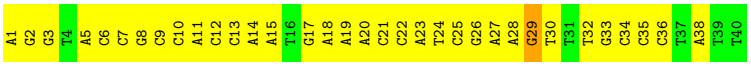
• Molecule 24: STAPLE STRAND

Chain AO:

• Molecule 25: STAPLE STRAND

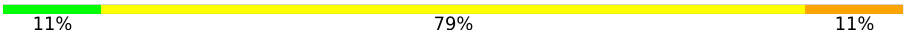
Chain AP:

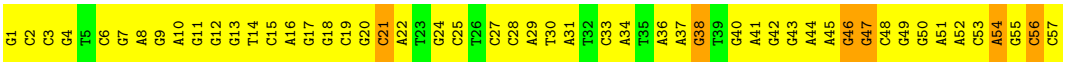




• Molecule 26: STAPLE STRAND

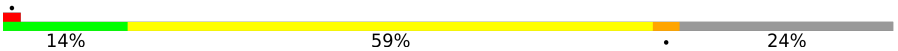
Chain AQ:

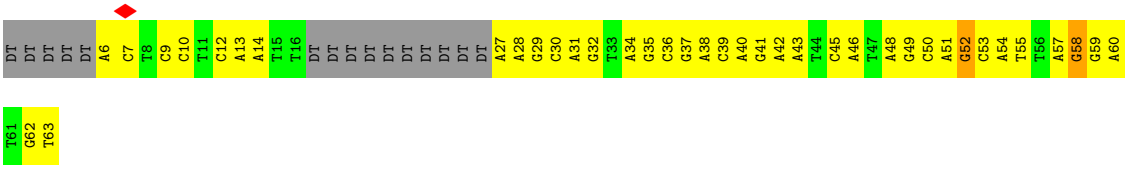




• Molecule 27: STAPLE STRAND

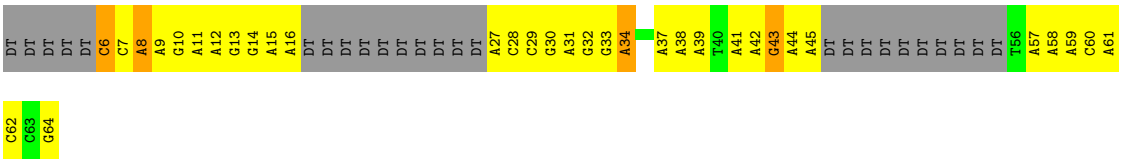
Chain AR:





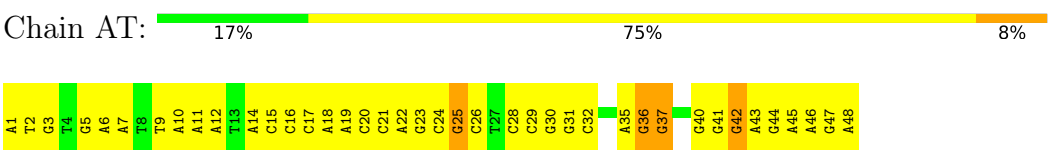
• Molecule 28: STAPLE STRAND

Chain AS:



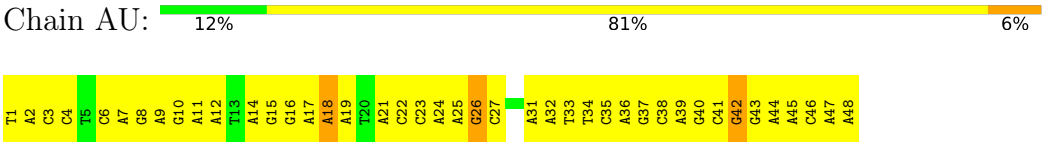
• Molecule 29: STAPLE STRAND

Chain AT:



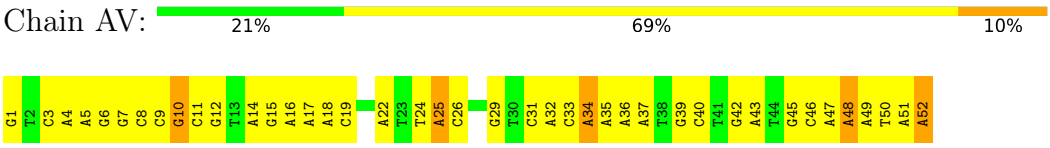
• Molecule 30: STAPLE STRAND

Chain AU:



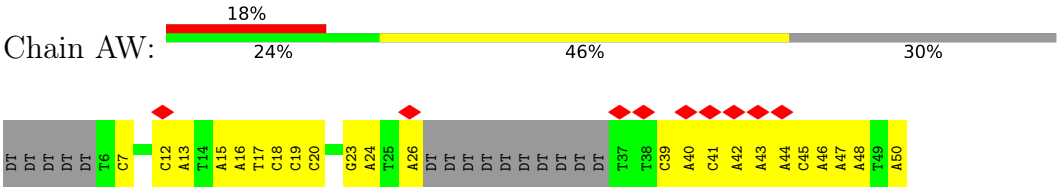
• Molecule 31: STAPLE STRAND

Chain AV:



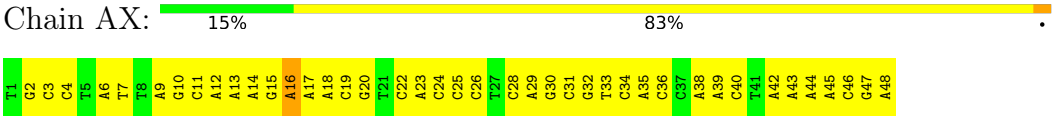
• Molecule 32: STAPLE STRAND

Chain AW:



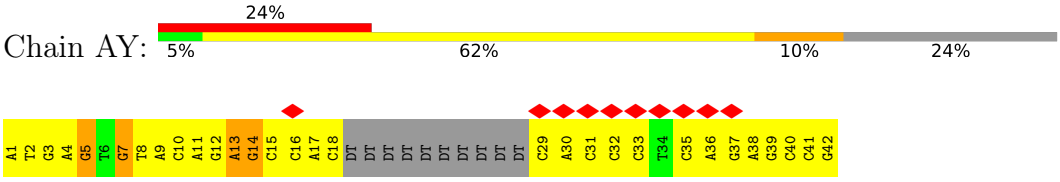
• Molecule 33: STAPLE STRAND

Chain AX:



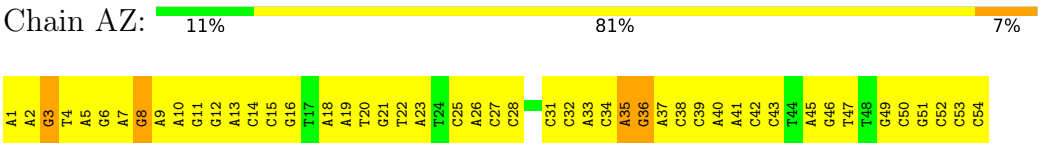
• Molecule 34: STAPLE STRAND

Chain AY:



• Molecule 35: STAPLE STRAND

Chain AZ:

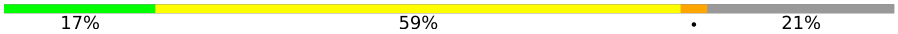


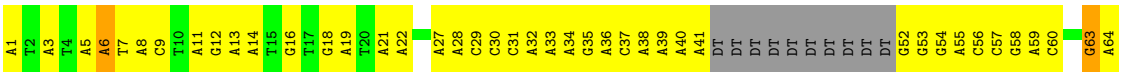
• Molecule 36: STAPLE STRAND

Chain Ab:

• Molecule 37: STAPLE STRAND

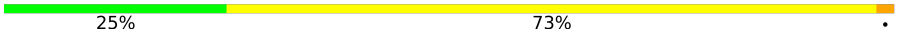
Chain Ac:





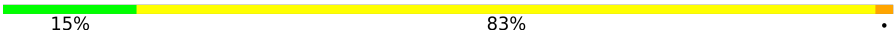
• Molecule 38: STAPLE STRAND

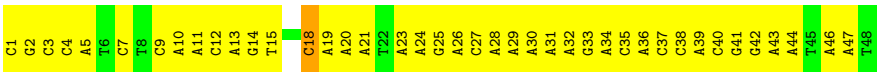
Chain Ad:



• Molecule 39: STAPLE STRAND

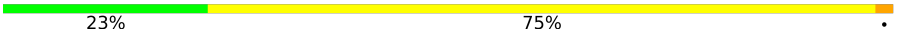
Chain Af:

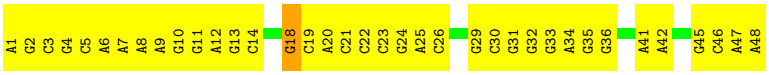




• Molecule 40: STAPLE STRAND

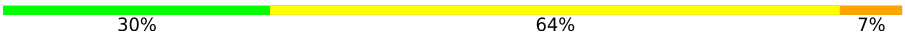
Chain Ag:





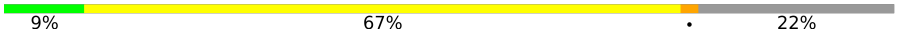
• Molecule 41: STAPLE STRAND

Chain Ah:



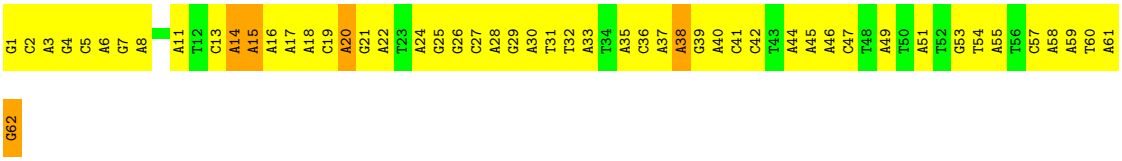
• Molecule 42: STAPLE STRAND

Chain Ai:



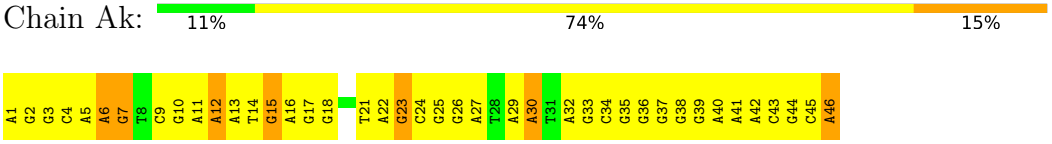
• Molecule 43: STAPLE STRAND

Chain Aj:



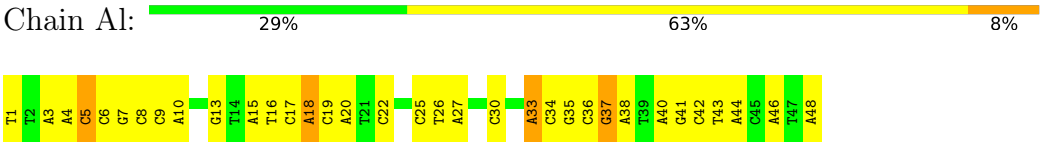
• Molecule 44: STAPLE STRAND

Chain Ak:



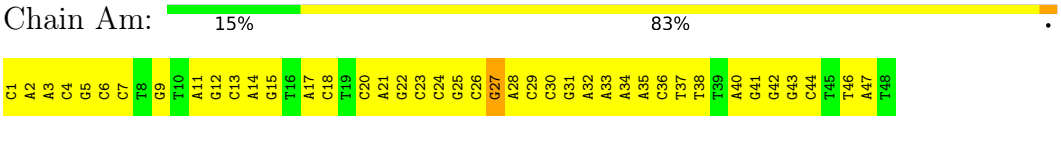
• Molecule 45: STAPLE STRAND

Chain Al:



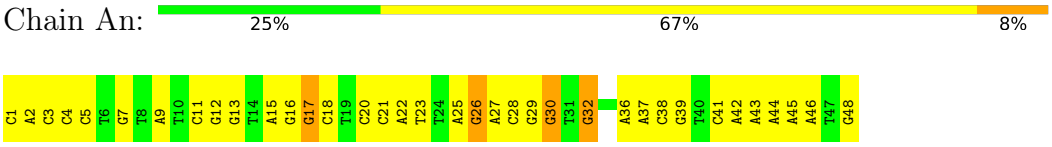
• Molecule 46: STAPLE STRAND

Chain Am:



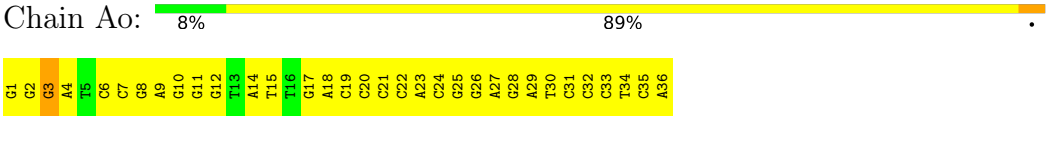
• Molecule 47: STAPLE STRAND

Chain An:



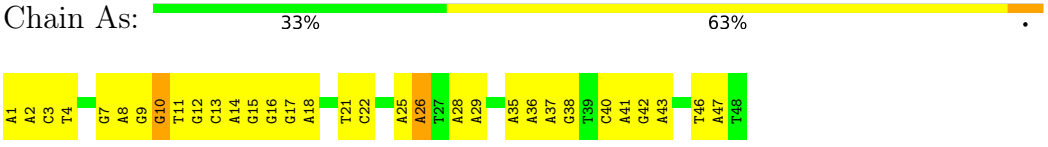
• Molecule 48: STAPLE STRAND

Chain Ao:



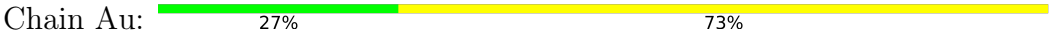
• Molecule 49: STAPLE STRAND

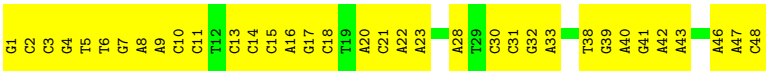
Chain As:



• Molecule 50: STAPLE STRAND

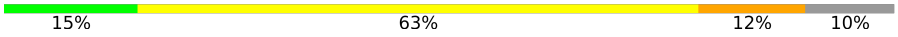
Chain Au:





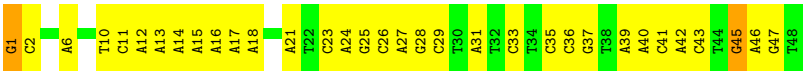
• Molecule 51: STAPLE STRAND

Chain Av:



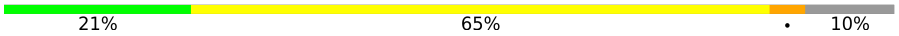
• Molecule 52: STAPLE STRAND

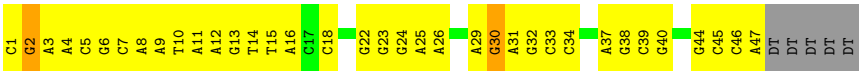
Chain Aw:



• Molecule 53: STAPLE STRAND

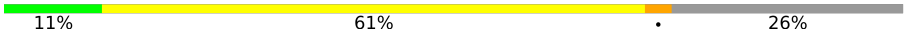
Chain Ax:

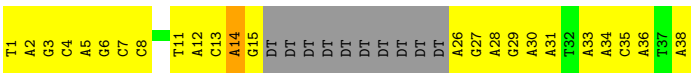




• Molecule 54: STAPLE STRAND

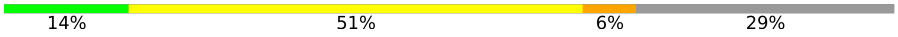
Chain Ay:





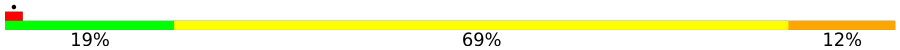
• Molecule 55: STAPLE STRAND

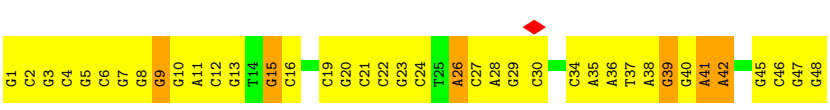
Chain Az:



• Molecule 56: STAPLE STRAND

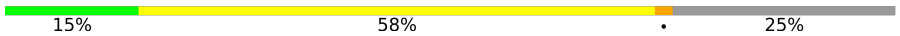
Chain B0:

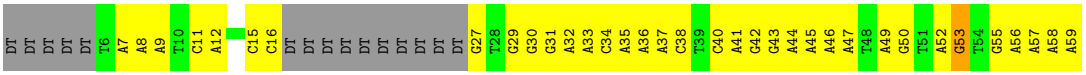




• Molecule 57: STAPLE STRAND

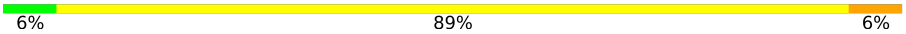
Chain B1:

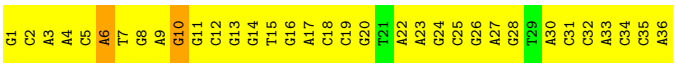




• Molecule 58: STAPLE STRAND

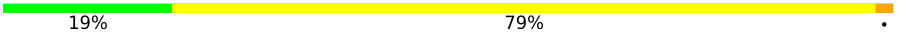
Chain B2:





• Molecule 59: STAPLE STRAND

Chain B3:

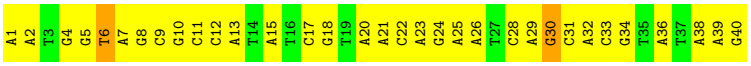


• Molecule 60: STAPLE STRAND

Chain B4:

• Molecule 61: STAPLE STRAND

Chain B5:

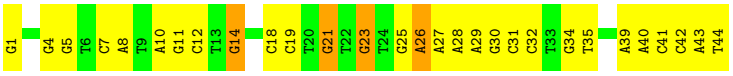


• Molecule 62: STAPLE STRAND

Chain B6:

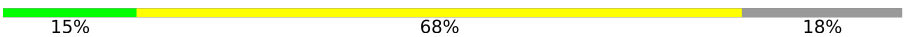
• Molecule 63: STAPLE STRAND

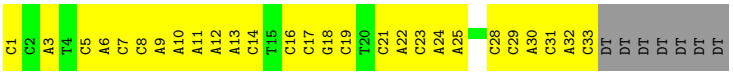
Chain B7:



• Molecule 64: STAPLE STRAND

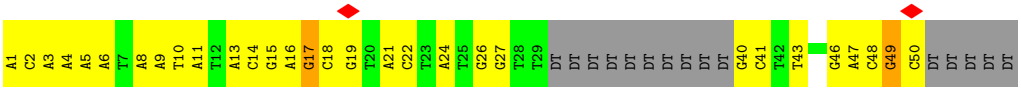
Chain B8:





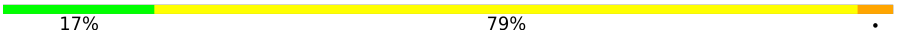
• Molecule 65: STAPLE STRAND

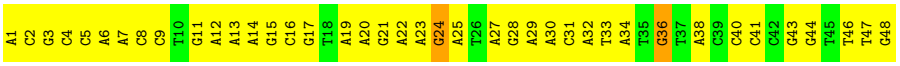
Chain B9:



• Molecule 66: STAPLE STRAND

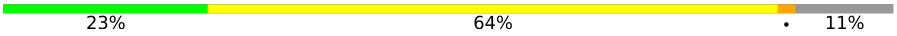
Chain BB:

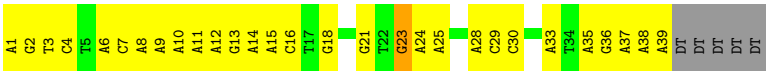




• Molecule 67: STAPLE STRAND

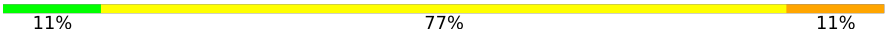
Chain BC:

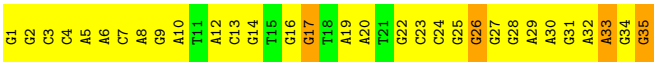




• Molecule 68: STAPLE STRAND

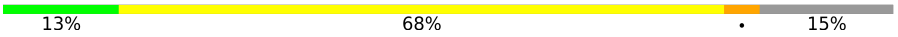
Chain BD:

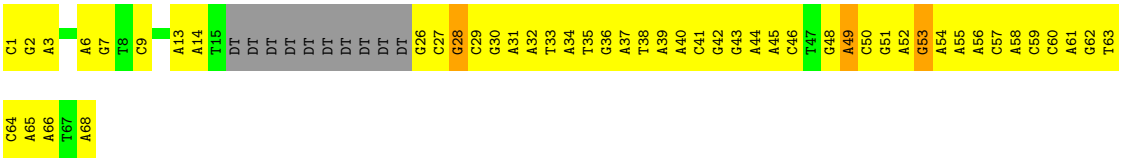




• Molecule 69: STAPLE STRAND

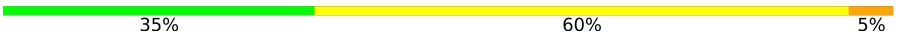
Chain BE:





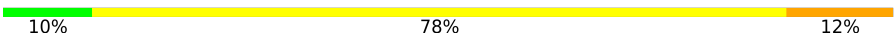
• Molecule 70: STAPLE STRAND

Chain BF:



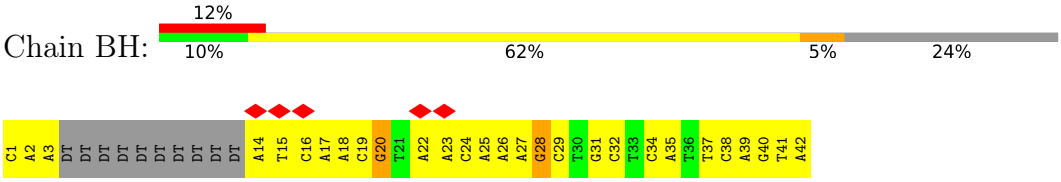
• Molecule 71: STAPLE STRAND

Chain BG:



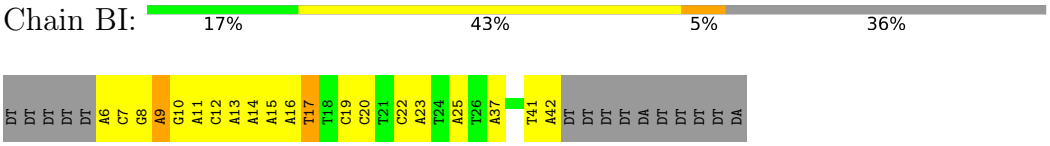
• Molecule 72: STAPLE STRAND

Chain BH:



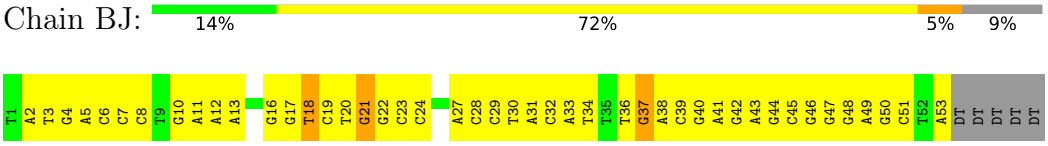
• Molecule 73: STAPLE STRAND

Chain BI:



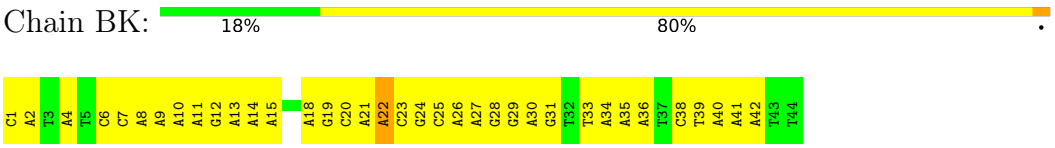
• Molecule 74: STAPLE STRAND

Chain BJ:



• Molecule 75: STAPLE STRAND

Chain BK:

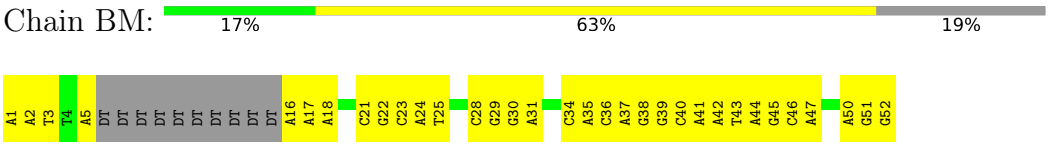


• Molecule 76: STAPLE STRAND

Chain BL:

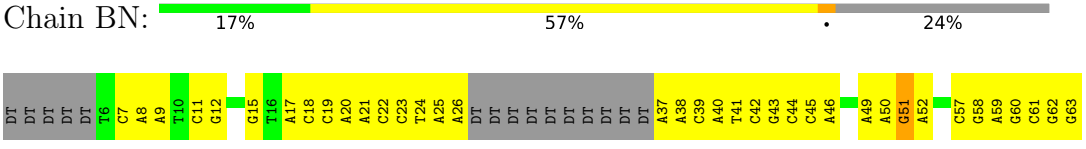
• Molecule 77: STAPLE STRAND

Chain BM:



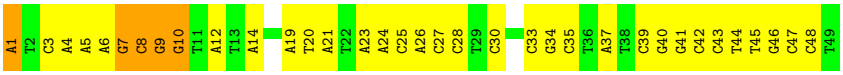
• Molecule 78: STAPLE STRAND

Chain BN:



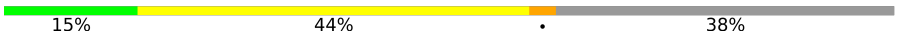
• Molecule 79: STAPLE STRAND

Chain BO:



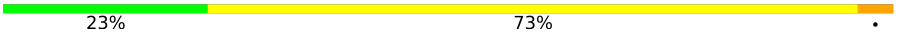
• Molecule 80: STAPLE STRAND

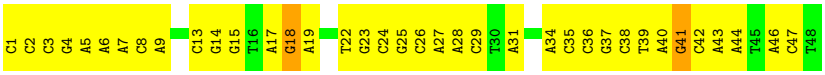
Chain BP:



• Molecule 81: STAPLE STRAND

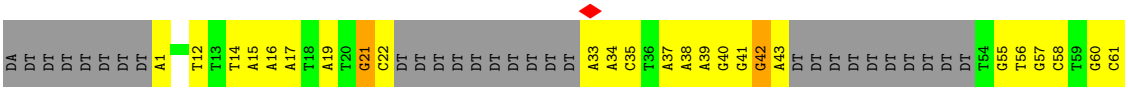
Chain BQ:





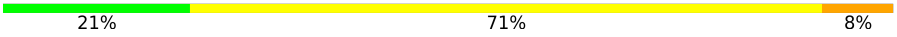
• Molecule 82: STAPLE STRAND

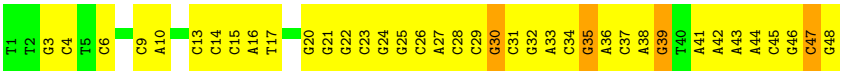
Chain BR:



• Molecule 83: STAPLE STRAND

Chain BS:



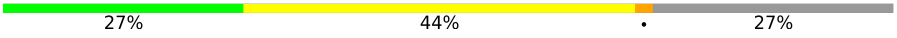


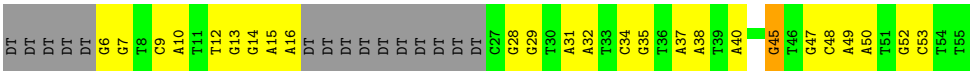
• Molecule 84: STAPLE STRAND

Chain BT:

• Molecule 85: STAPLE STRAND

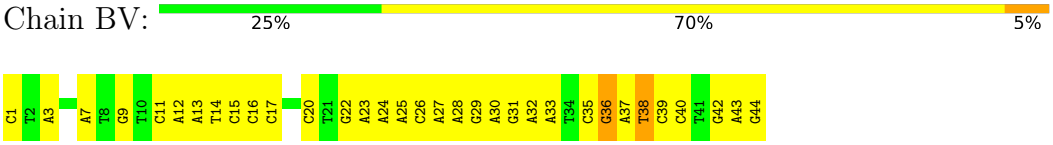
Chain BU:





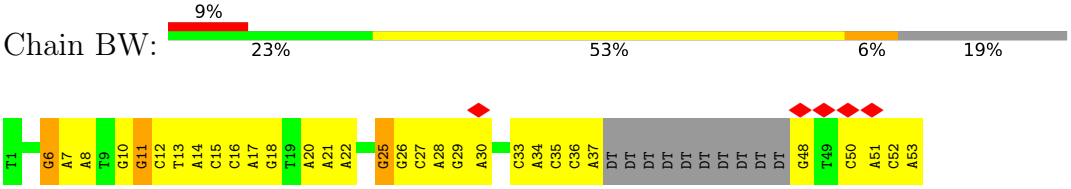
• Molecule 86: STAPLE STRAND

Chain BV:



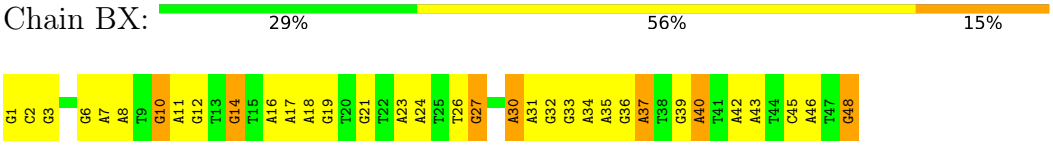
• Molecule 87: STAPLE STRAND

Chain BW:



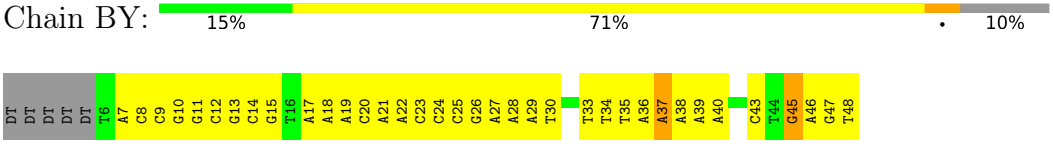
• Molecule 88: STAPLE STRAND

Chain BX:



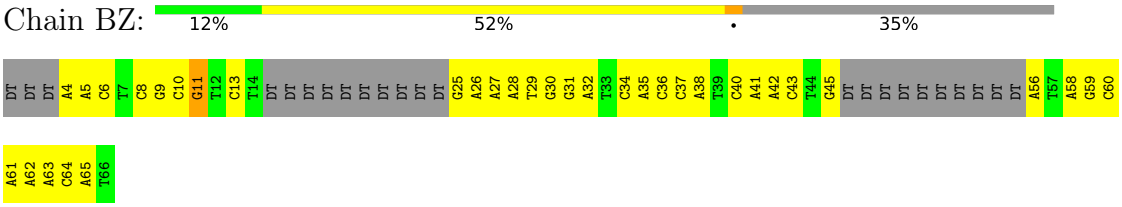
• Molecule 89: STAPLE STRAND

Chain BY:



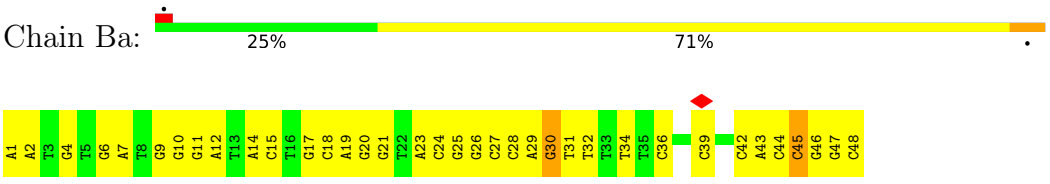
• Molecule 90: STAPLE STRAND

Chain BZ:



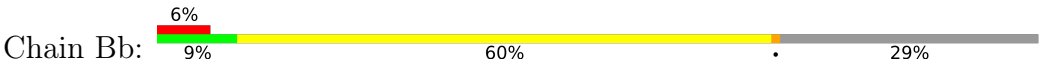
• Molecule 91: STAPLE STRAND

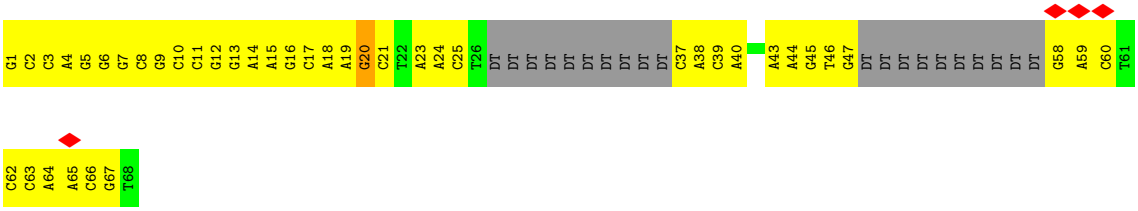
Chain Ba:



• Molecule 92: STAPLE STRAND

Chain Bb:



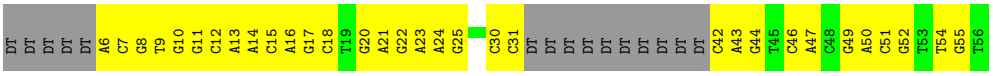


• Molecule 93: STAPLE STRAND

Chain Bc:

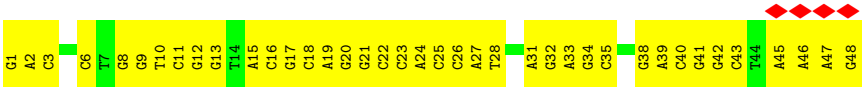
• Molecule 94: STAPLE STRAND

Chain Bd:



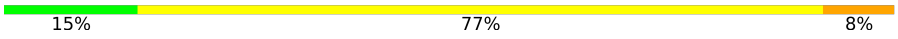
• Molecule 95: STAPLE STRAND

Chain Be:



• Molecule 96: STAPLE STRAND

Chain Bf:

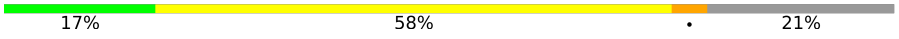


• Molecule 97: STAPLE STRAND

Chain Bg:

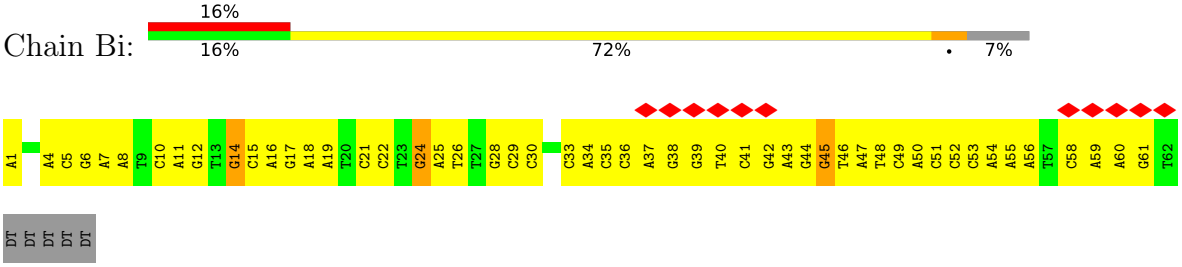
• Molecule 98: STAPLE STRAND

Chain Bh:



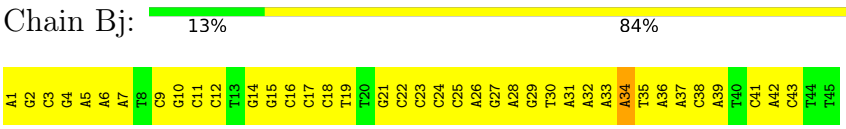
• Molecule 99: STAPLE STRAND

Chain Bi:



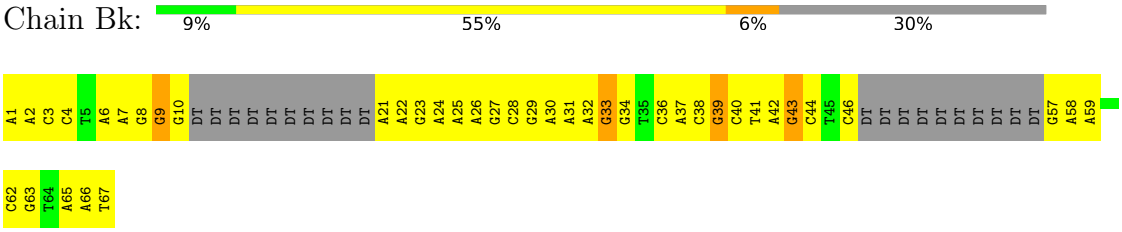
• Molecule 100: STAPLE STRAND

Chain Bj:



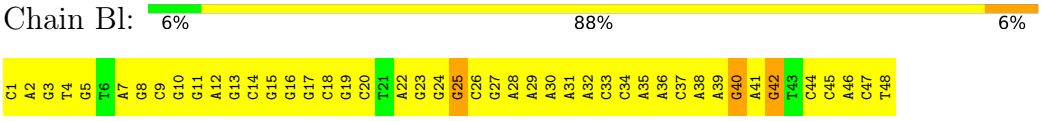
• Molecule 101: STAPLE STRAND

Chain Bk:



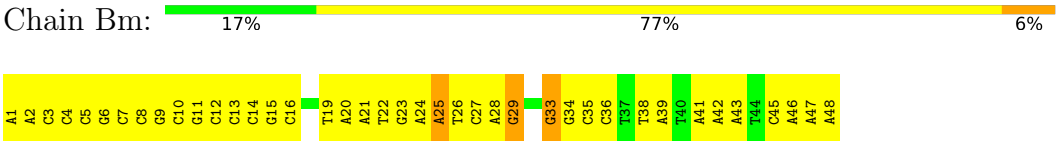
• Molecule 102: STAPLE STRAND

Chain Bl:



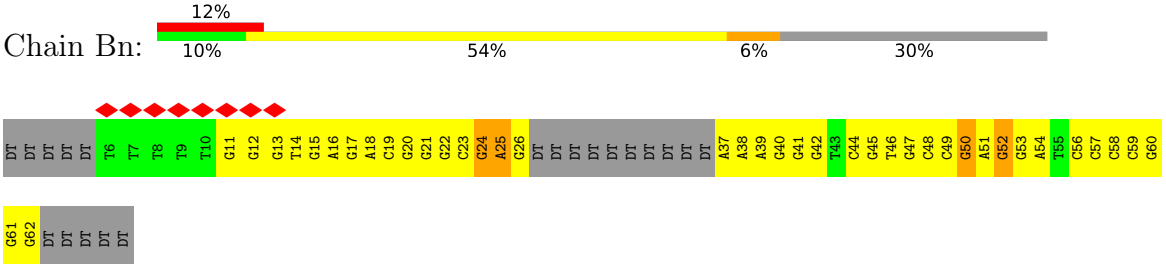
• Molecule 103: STAPLE STRAND

Chain Bm:



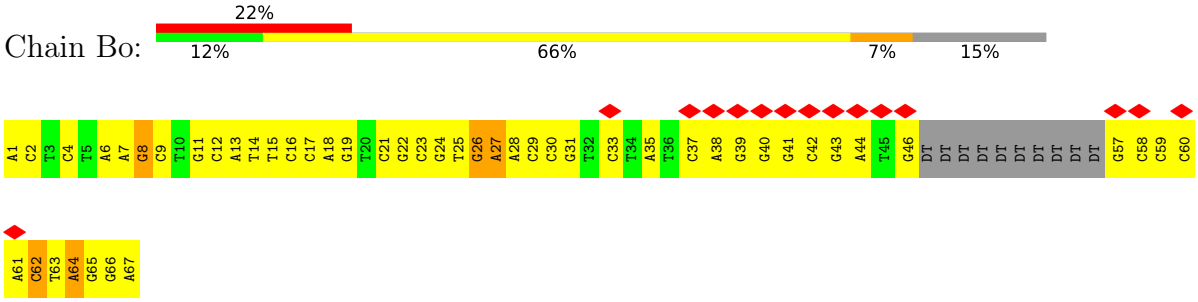
• Molecule 104: STAPLE STRAND

Chain Bn:



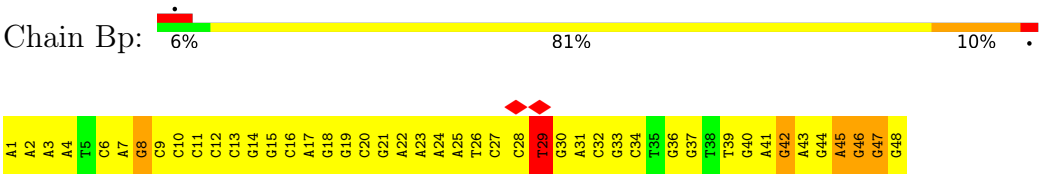
• Molecule 105: STAPLE STRAND

Chain Bo:



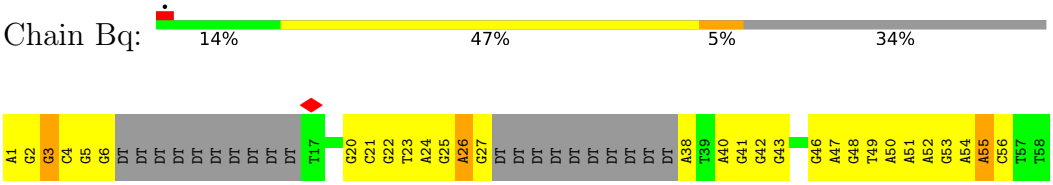
• Molecule 106: STAPLE STRAND

Chain Bp:



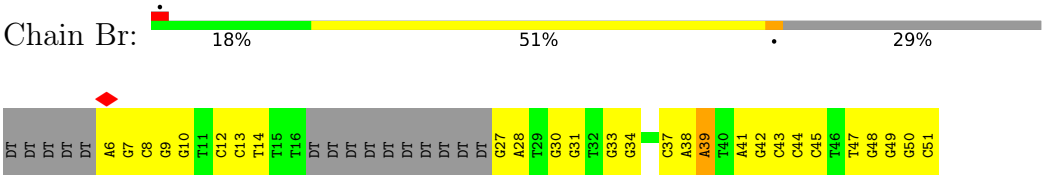
• Molecule 107: STAPLE STRAND

Chain Bq:



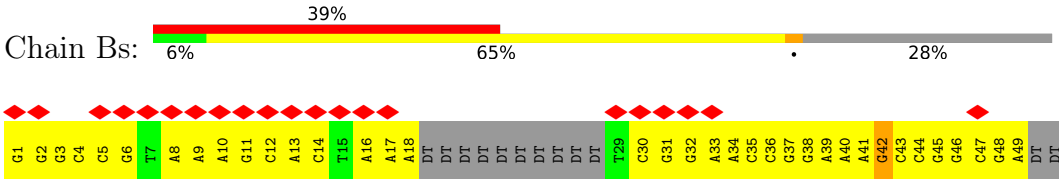
• Molecule 108: STAPLE STRAND

Chain Br:



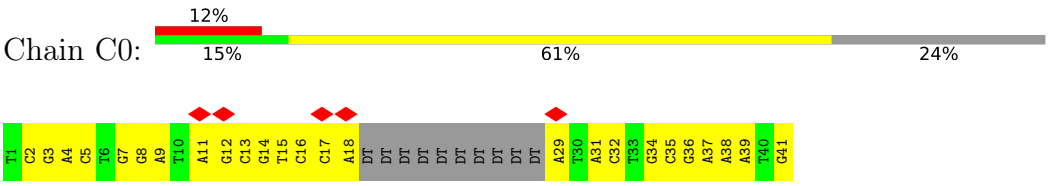
• Molecule 109: STAPLE STRAND

Chain Bs:



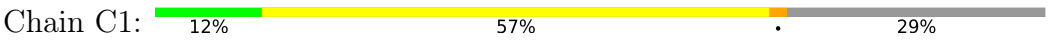
• Molecule 110: STAPLE STRAND

Chain C0:



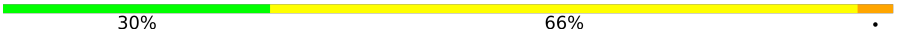
• Molecule 111: STAPLE STRAND

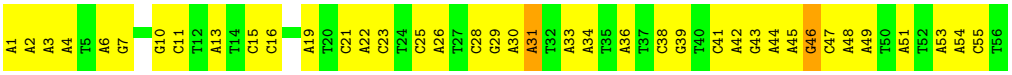
Chain C1:



• Molecule 112: STAPLE STRAND

Chain C2:



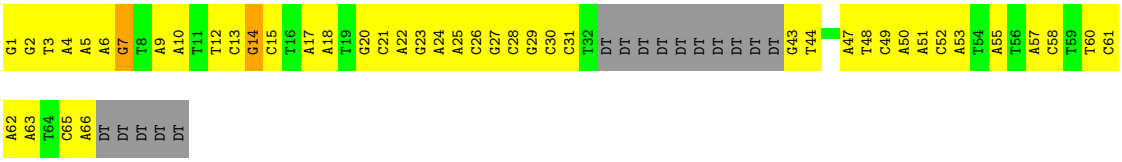


• Molecule 113: STAPLE STRAND

Chain C3:

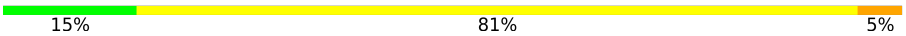
• Molecule 114: STAPLE STRAND

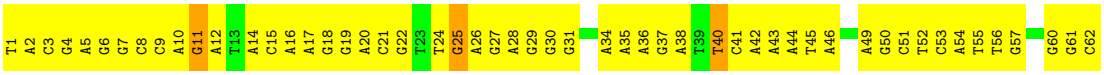
Chain C4:



• Molecule 115: STAPLE STRAND

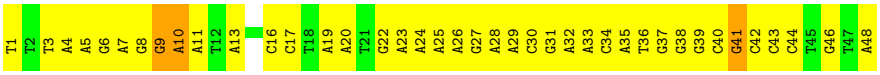
Chain C5:





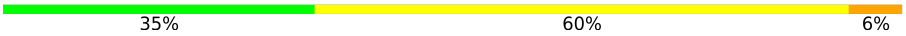
• Molecule 116: STAPLE STRAND

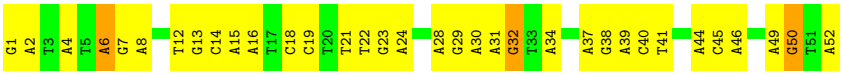
Chain C6:



• Molecule 117: STAPLE STRAND

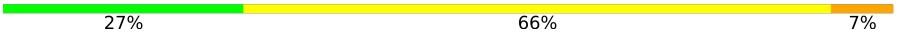
Chain C7:

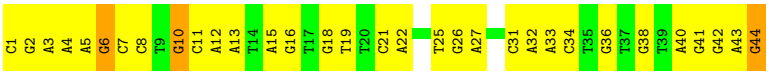




• Molecule 118: STAPLE STRAND

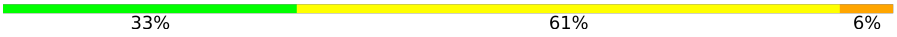
Chain C8:





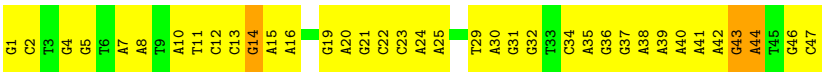
• Molecule 119: STAPLE STRAND

Chain CB:



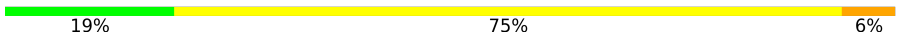
• Molecule 120: STAPLE STRAND

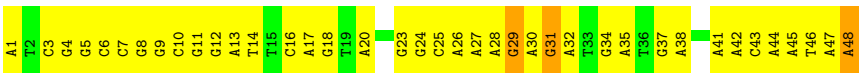
Chain CC:



• Molecule 121: STAPLE STRAND

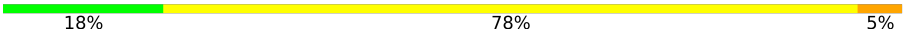
Chain CD:

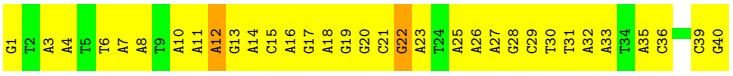




• Molecule 122: STAPLE STRAND

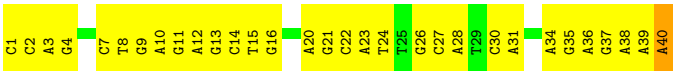
Chain CE:





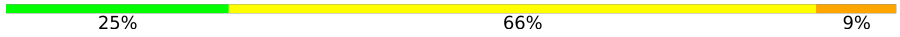
• Molecule 123: STAPLE STRAND

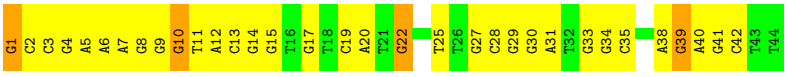
Chain CF:



• Molecule 124: STAPLE STRAND

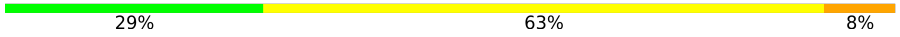
Chain CG:

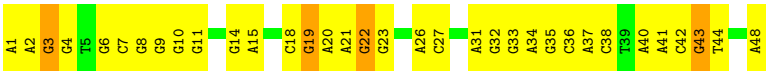




• Molecule 125: STAPLE STRAND

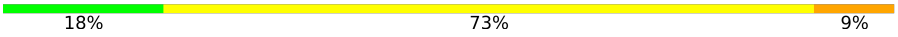
Chain CH:





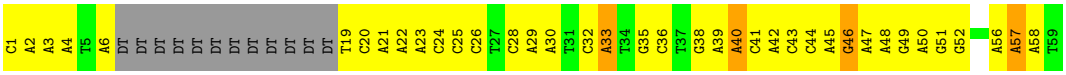
• Molecule 126: STAPLE STRAND

Chain CI:



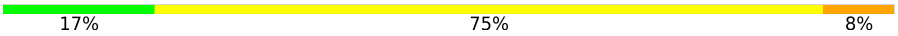
• Molecule 127: STAPLE STRAND

Chain CJ:



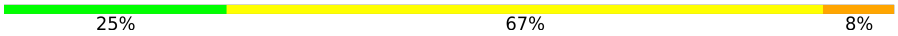
• Molecule 128: STAPLE STRAND

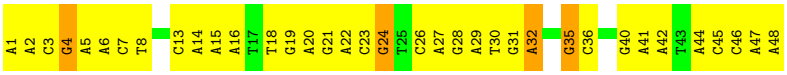
Chain CK:



• Molecule 129: STAPLE STRAND

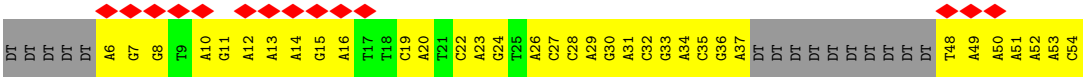
Chain CL:





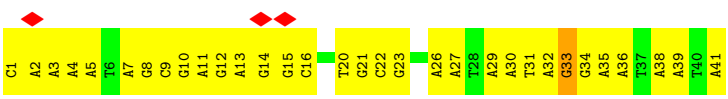
• Molecule 130: STAPLE STRAND

Chain CM:



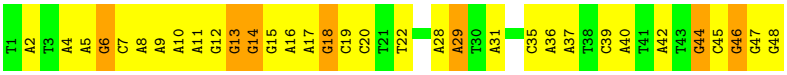
• Molecule 131: STAPLE STRAND

Chain CN:



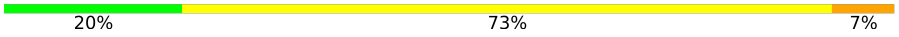
• Molecule 132: STAPLE STRAND

Chain CO:



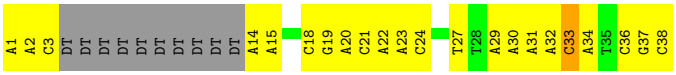
• Molecule 133: STAPLE STRAND

Chain CP:



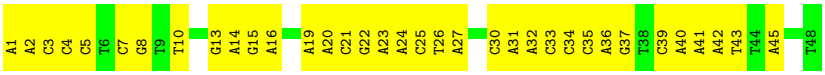
• Molecule 134: STAPLE STRAND

Chain CQ:



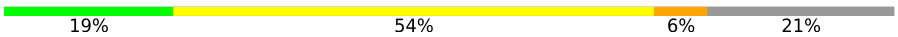
• Molecule 135: STAPLE STRAND

Chain CR:



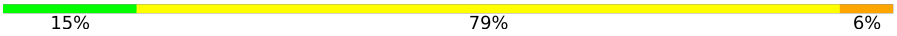
• Molecule 136: STAPLE STRAND

Chain CS:



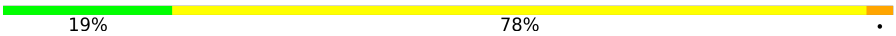
• Molecule 137: STAPLE STRAND

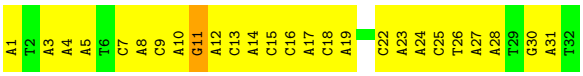
Chain CT:



• Molecule 138: STAPLE STRAND

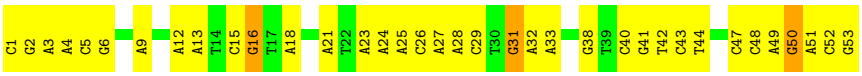
Chain CU:





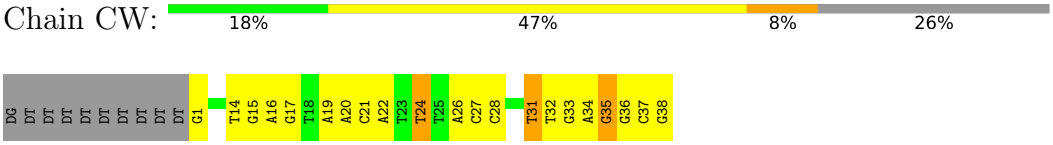
• Molecule 139: STAPLE STRAND

Chain CV:



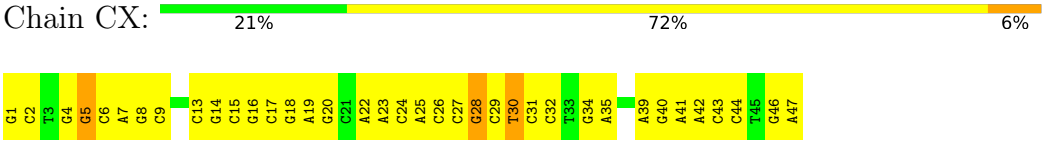
• Molecule 140: STAPLE STRAND

Chain CW:



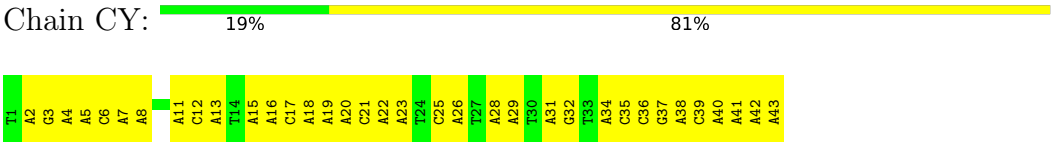
• Molecule 141: STAPLE STRAND

Chain CX:



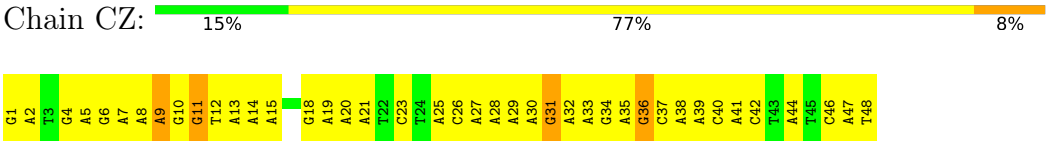
• Molecule 142: STAPLE STRAND

Chain CY:



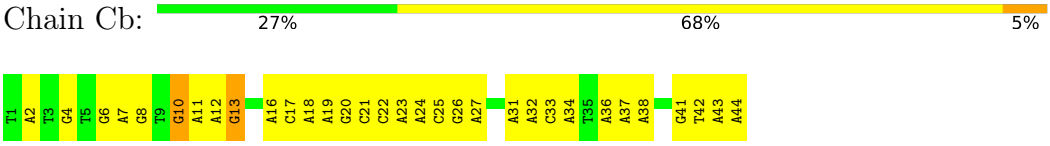
• Molecule 143: STAPLE STRAND

Chain CZ:



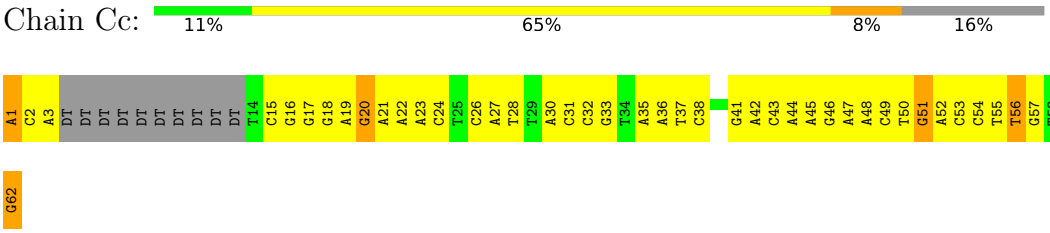
• Molecule 144: STAPLE STRAND

Chain Cb:



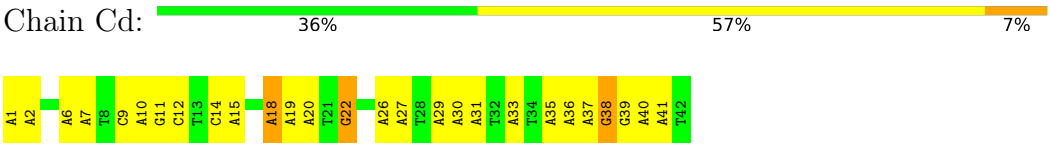
• Molecule 145: STAPLE STRAND

Chain Cc:



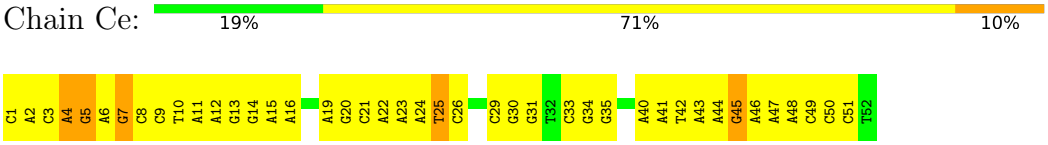
• Molecule 146: STAPLE STRAND

Chain Cd:



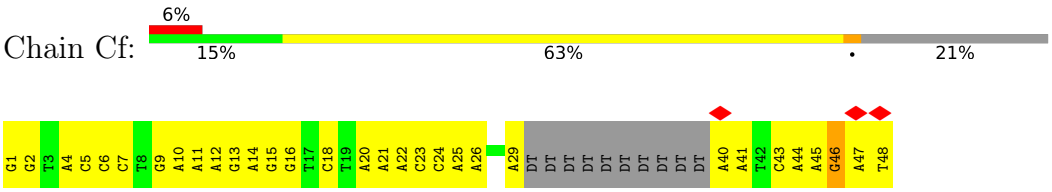
• Molecule 147: STAPLE STRAND

Chain Ce:



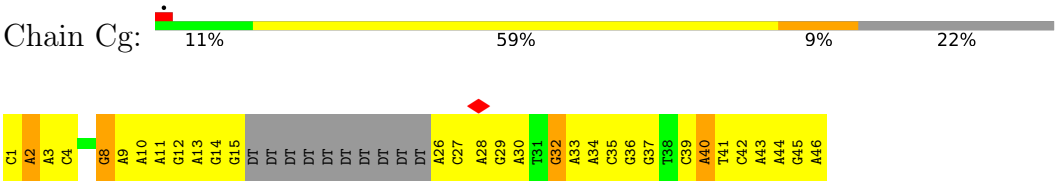
• Molecule 148: STAPLE STRAND

Chain Cf:



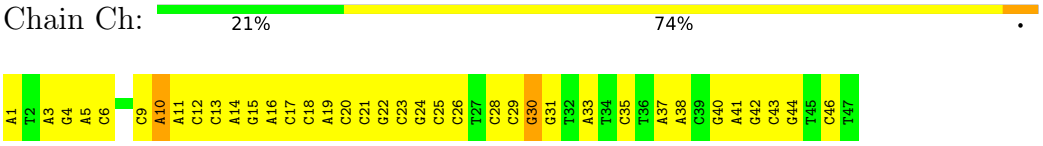
• Molecule 149: STAPLE STRAND

Chain Cg:



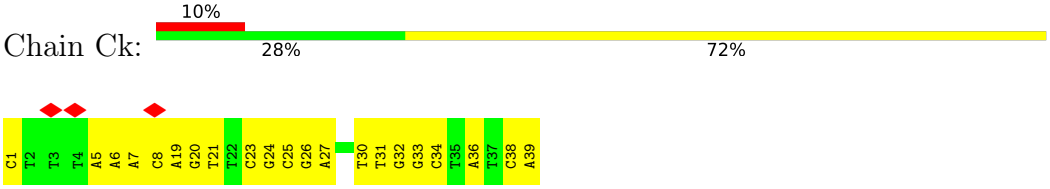
• Molecule 150: STAPLE STRAND

Chain Ch:



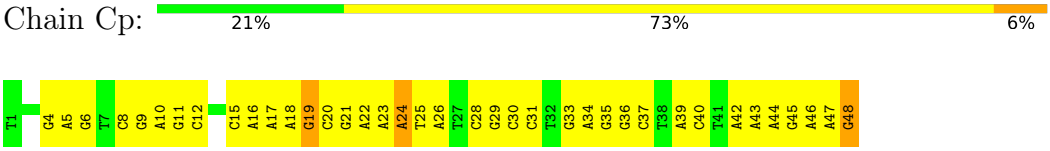
• Molecule 151: STAPLE STRAND

Chain Ck:



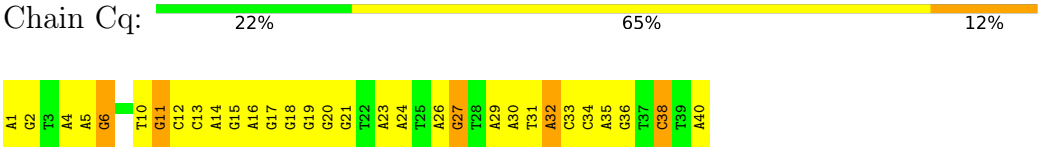
• Molecule 152: STAPLE STRAND

Chain Cp:



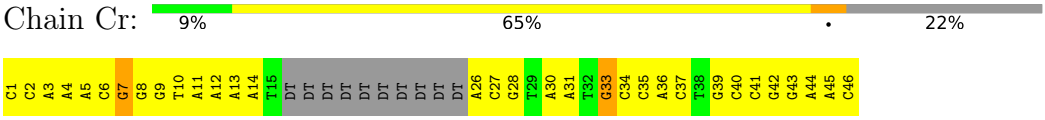
• Molecule 153: STAPLE STRAND

Chain Cq:



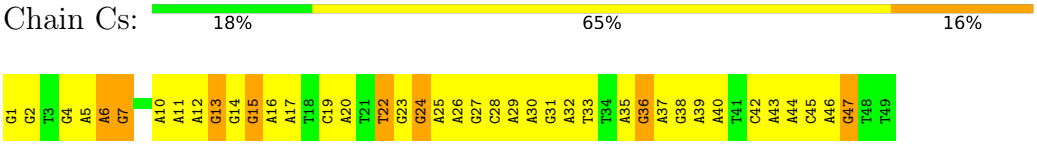
• Molecule 154: STAPLE STRAND

Chain Cr:



• Molecule 155: STAPLE STRAND

Chain Cs:

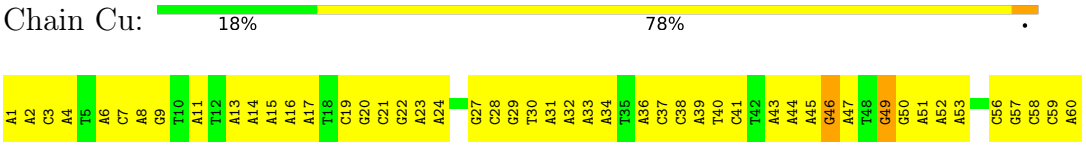


• Molecule 156: STAPLE STRAND

Chain Ct:

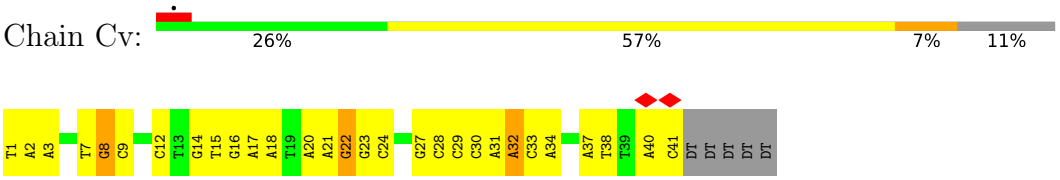
• Molecule 157: STAPLE STRAND

Chain Cu:



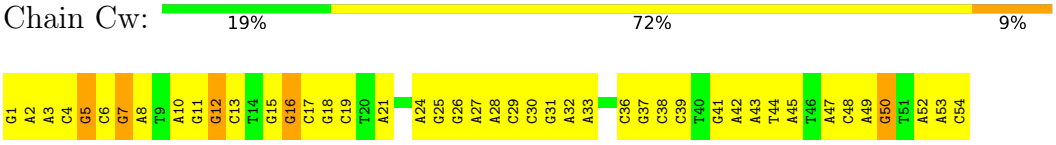
• Molecule 158: STAPLE STRAND

Chain Cv:



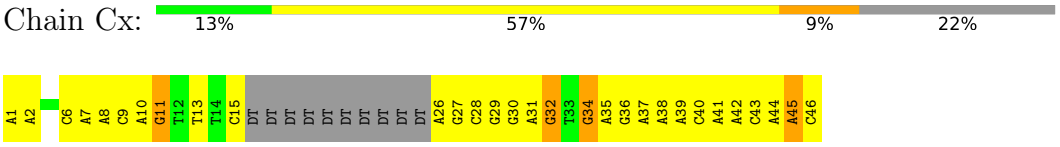
• Molecule 159: STAPLE STRAND

Chain Cw:



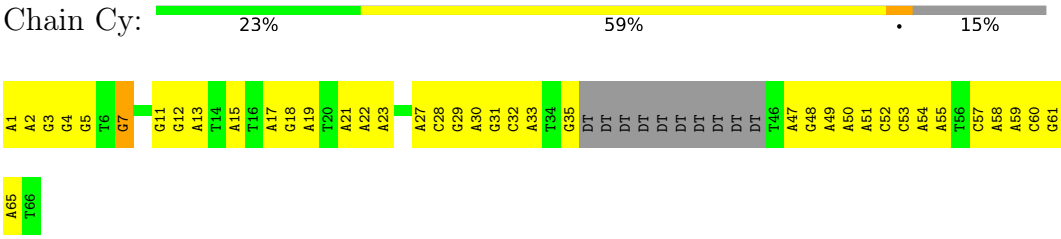
• Molecule 160: STAPLE STRAND

Chain Cx:



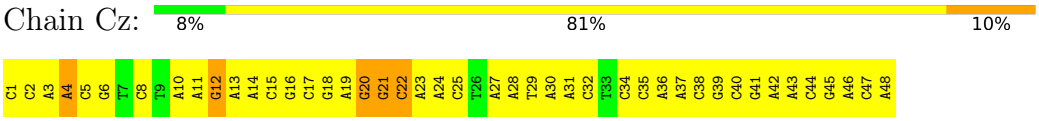
• Molecule 161: STAPLE STRAND

Chain Cy:



• Molecule 162: STAPLE STRAND

Chain Cz:



4 Experimental information (i)

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

5 Model quality (i)

5.1 Standard geometry (i)

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

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

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

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

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

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

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

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

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

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

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

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

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

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

5 of 121 chirality outliers are listed below:

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

5 of 919 planarity outliers are listed below:

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

5.2 Too-close contacts (i)

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

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

There are no protein molecules in this entry.

5.3.2 Protein sidechains (i)

There are no protein molecules in this entry.

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	AA	23
15	AF	1

The worst 5 of 24 chain breaks are listed below:

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

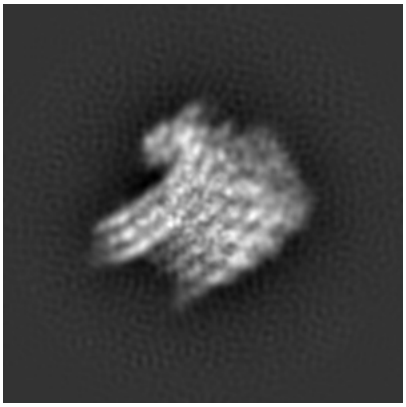
6 Map visualisation

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

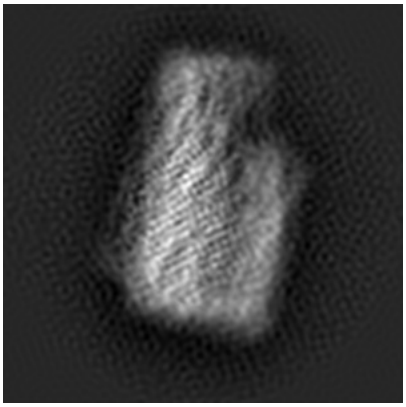
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

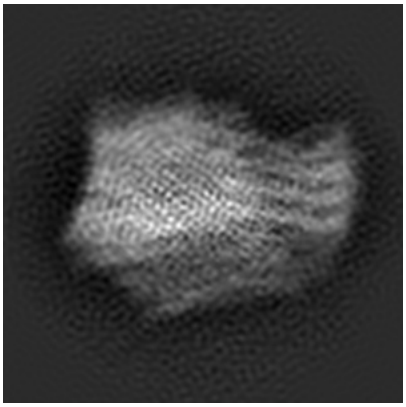
6.1.1 Primary map



X



Y

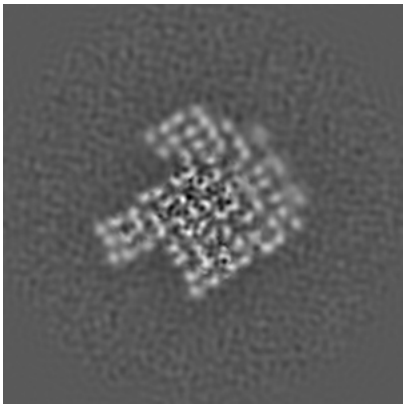


Z

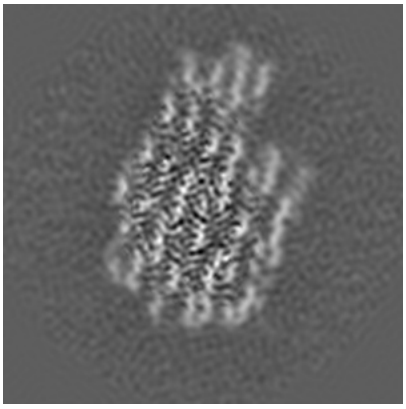
The images above show the map projected in three orthogonal directions.

6.2 Central slices

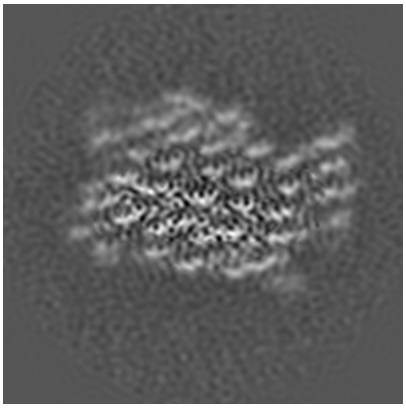
6.2.1 Primary map



X Index: 86



Y Index: 86

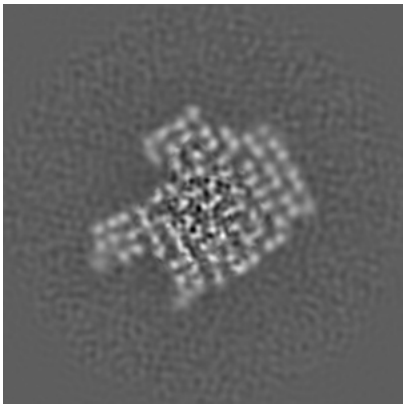


Z Index: 86

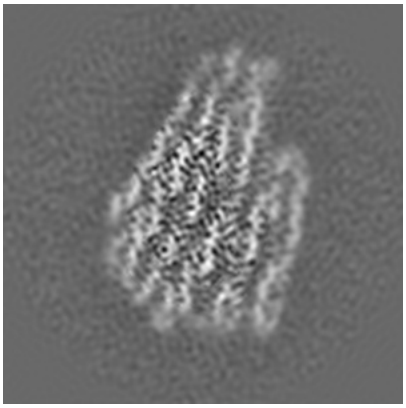
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

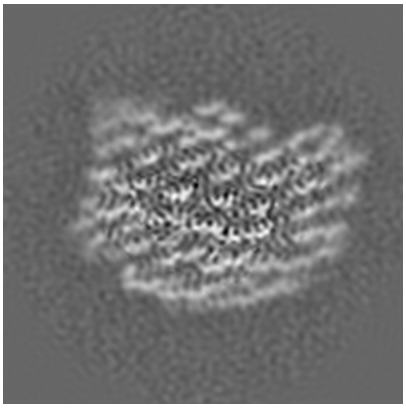
6.3.1 Primary map



X Index: 71



Y Index: 82

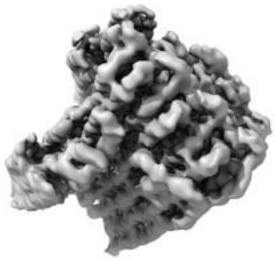


Z Index: 78

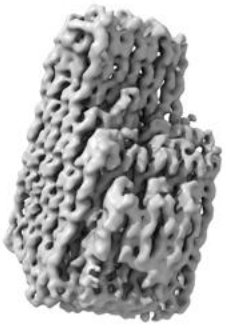
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views (i)

6.4.1 Primary map



X



Y

Z

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

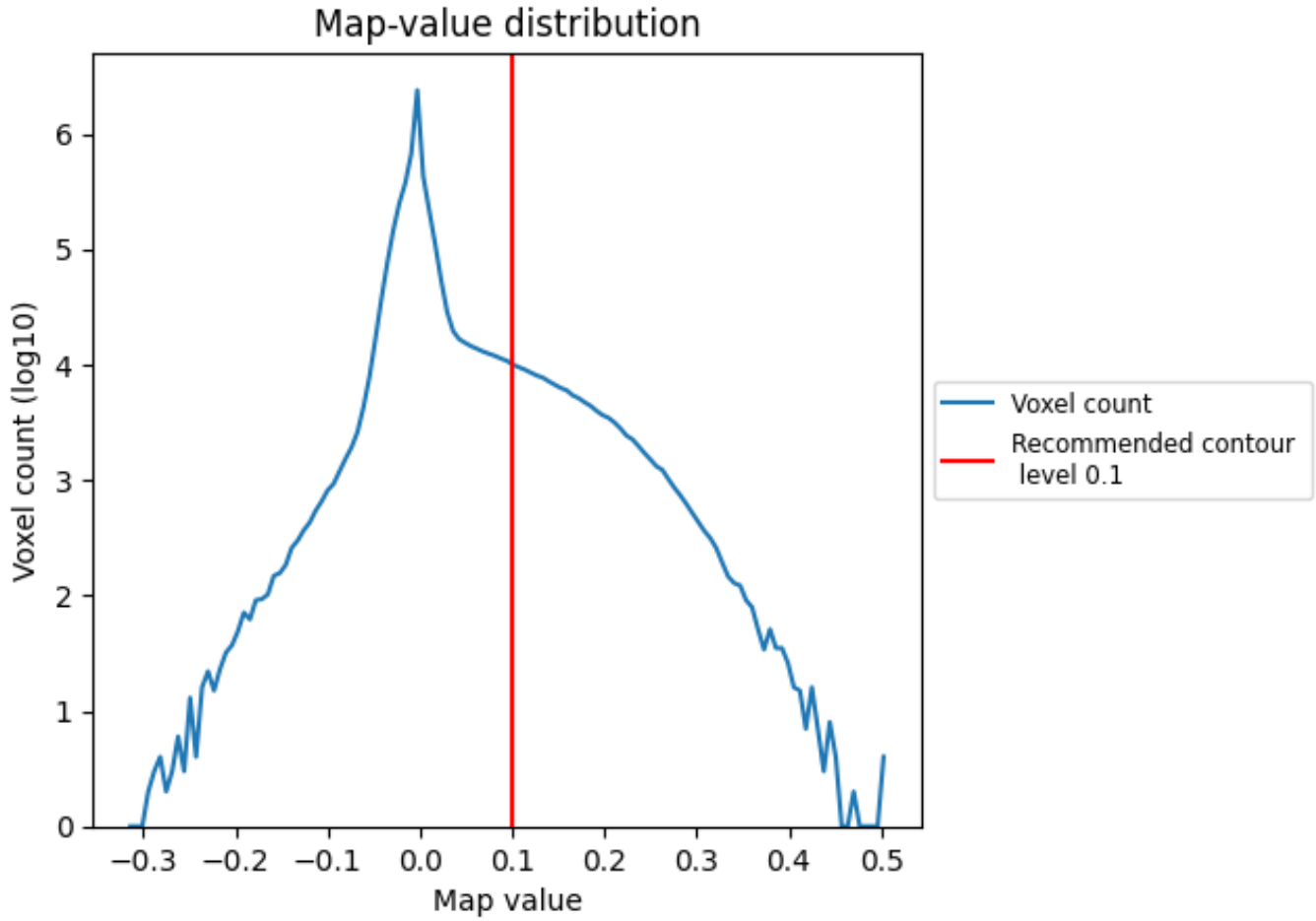
6.5 Mask visualisation (i)

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

7 Map analysis

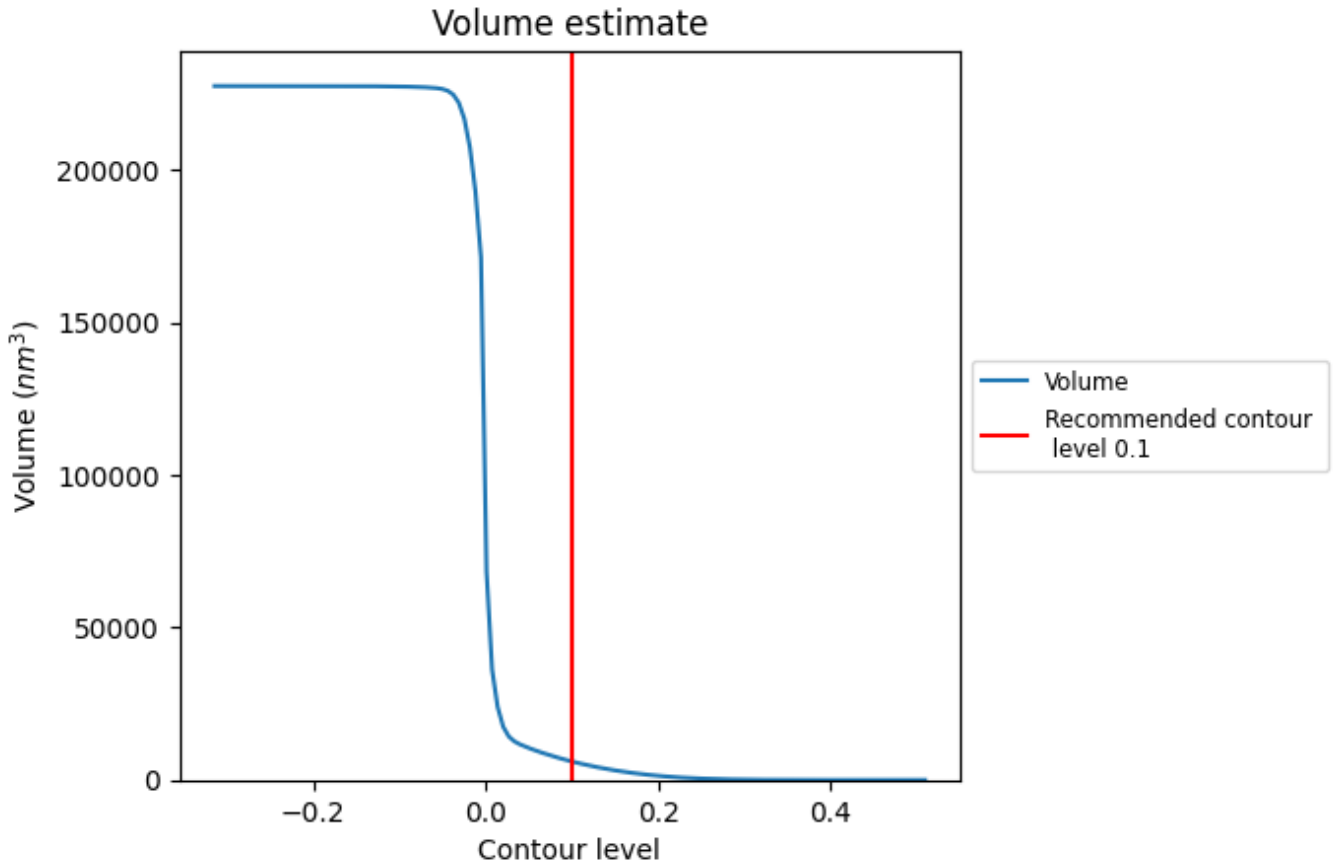
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

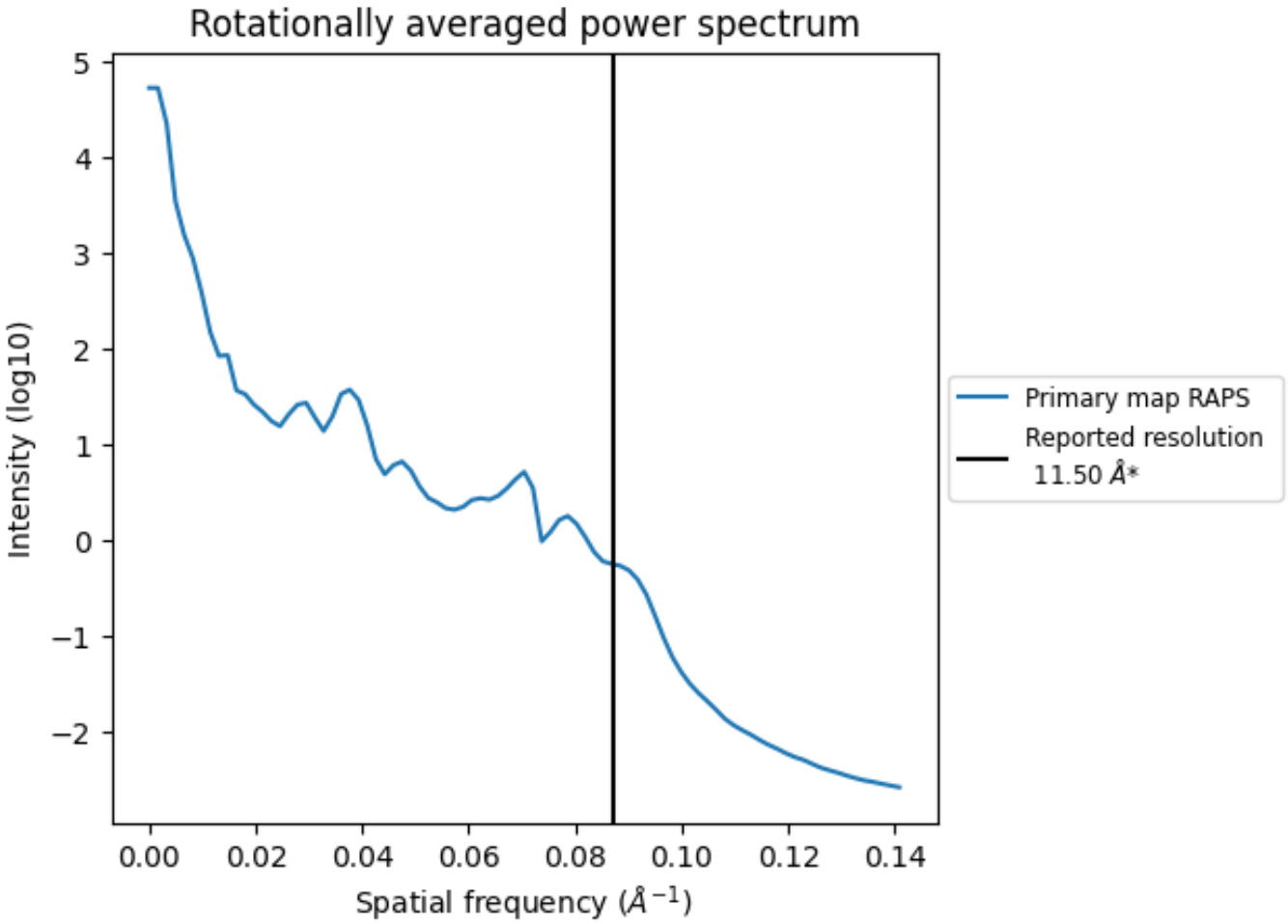
7.2 Volume estimate (i)



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

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

7.3 Rotationally averaged power spectrum (i)



*Reported resolution corresponds to spatial frequency of 0.087 Å^{-1}

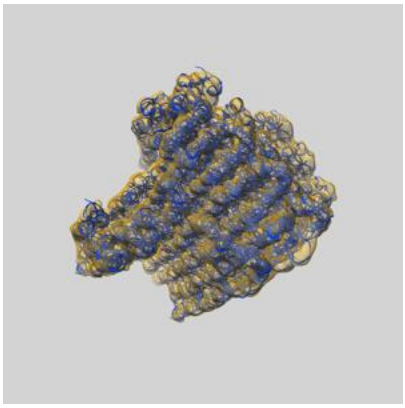
8 Fourier-Shell correlation (i)

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

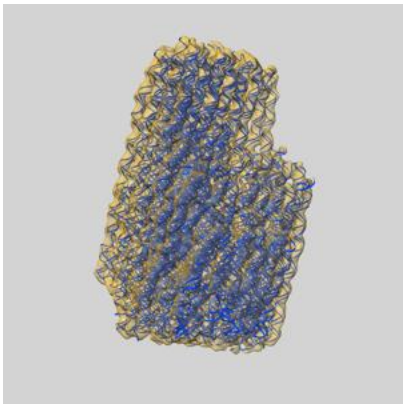
9 Map-model fit

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

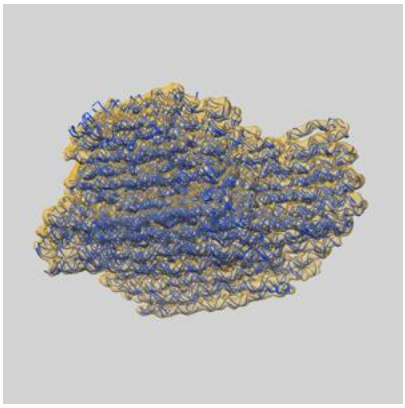
9.1 Map-model overlay



X



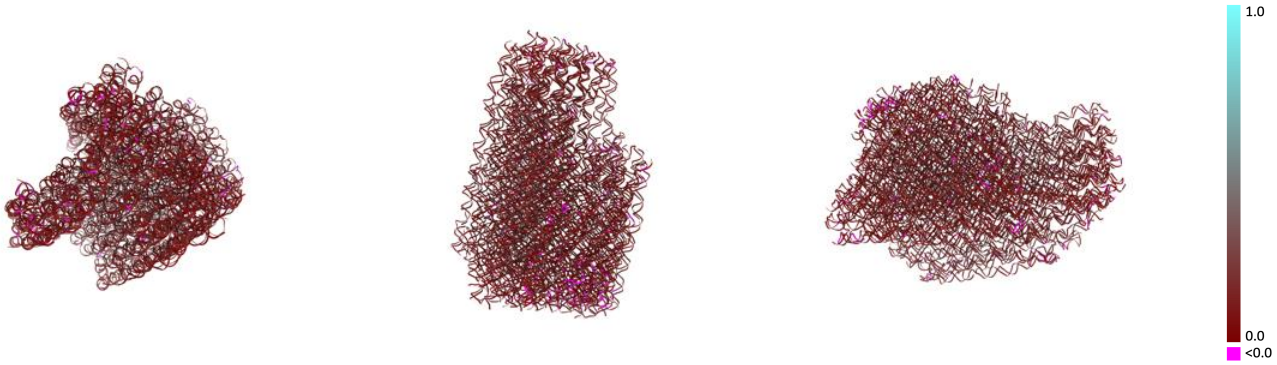
Y



Z

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

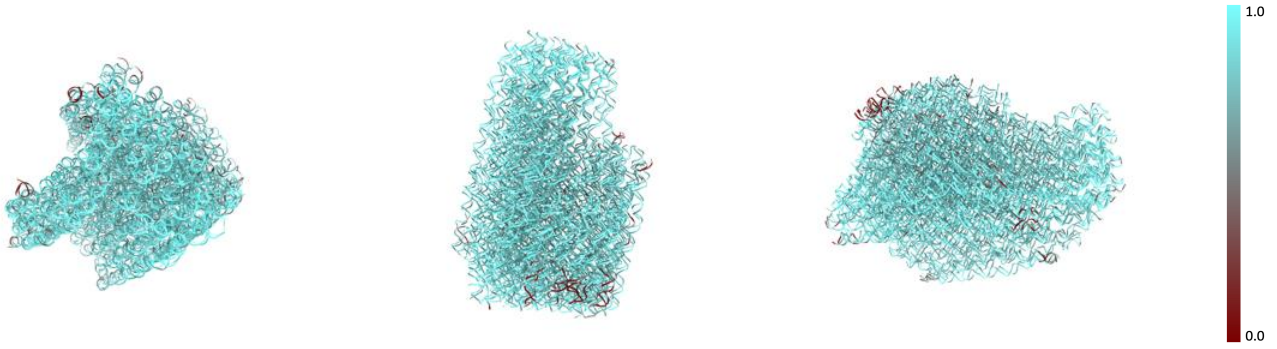
9.2 Q-score mapped to coordinate model



X Y Z

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

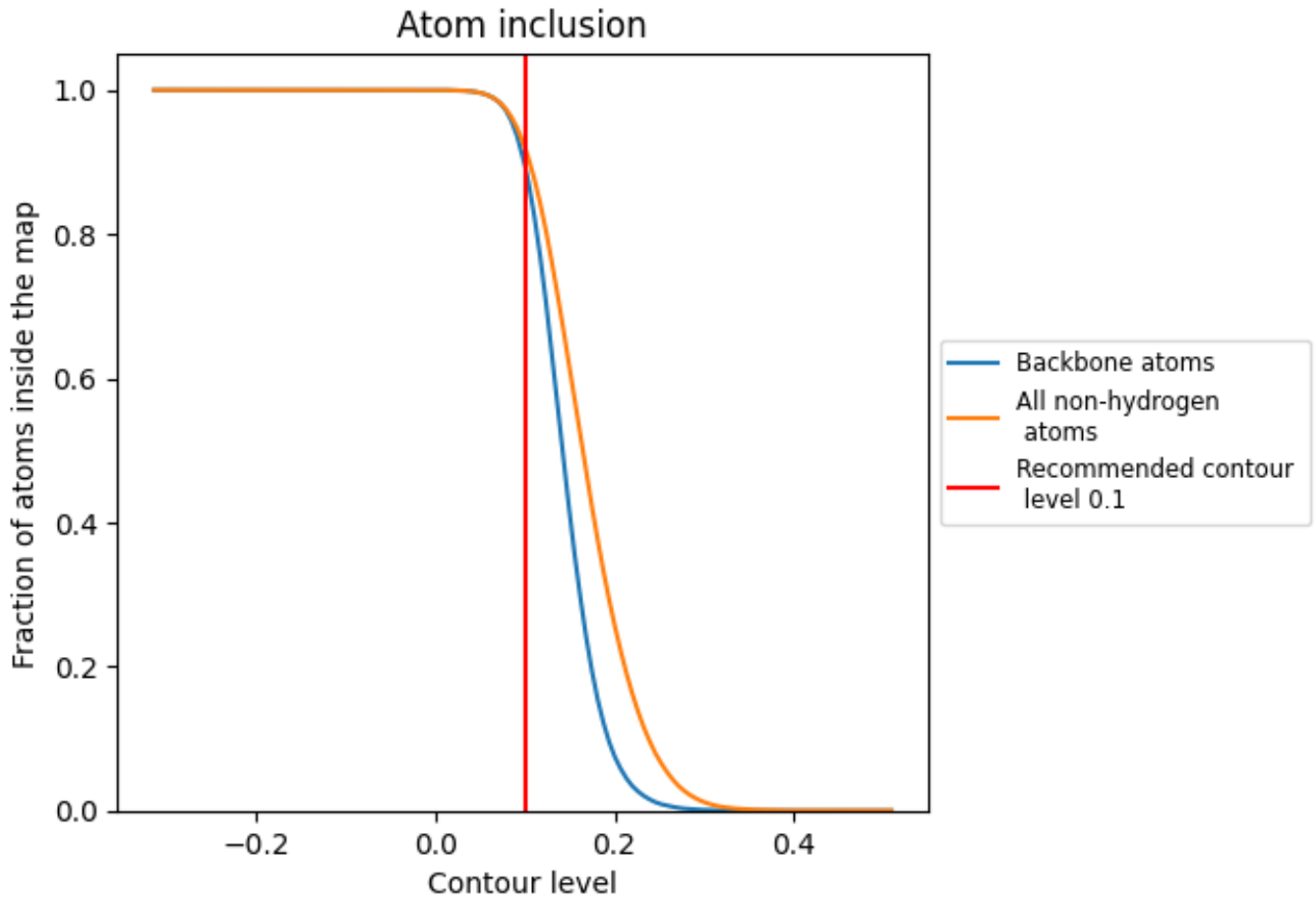
9.3 Atom inclusion mapped to coordinate model



X Y Z

The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.1).

9.4 Atom inclusion (i)



At the recommended contour level, 89% of all backbone atoms, 92% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (0.1) and Q-score for the entire model and for each chain.

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

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

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

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

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