



wwPDB EM Validation Summary Report ⓘ

Mar 21, 2026 – 06:38 PM UTC

PDB ID : 7ARE / pdb_00007are
EMDB ID : EMD-11881
Title : DNA origami pointer object v2
Authors : Thomas, M.; Feigl, E.; Kohler, F.; Kube, M.; Nagel-Yuksel, B.; Willner, E.M.; Funke, J.J.; Gerling, T.; Stommer, P.; Honemann, M.N.; Martin, T.G.; Scheres, S.H.W.; Dietz, H.
Deposited on : 2020-10-24
Resolution : 7.40 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

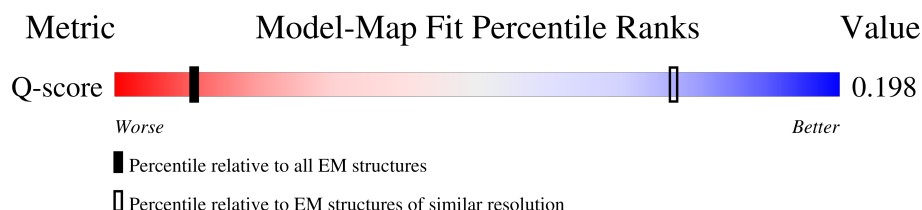
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

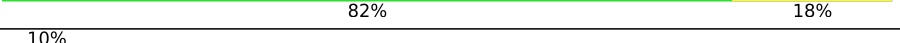
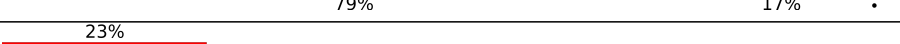
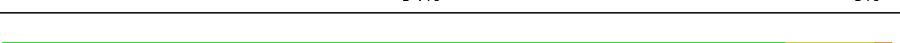
The reported resolution of this entry is 7.40 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	AA	7249	 81% 17% .
2	AB	40	 75% 25%
3	AC	31	 19% 81% 16% .
4	AD	40	 82% 18%
5	AE	48	 10% 79% 17% .
6	AF	31	 23% 94% 6%
7	AG	40	 88% 10% .
8	AH	31	 100% 84% 13% .
9	AI	45	 73% 82% 18%
10	AJ	40	 78% 20% .

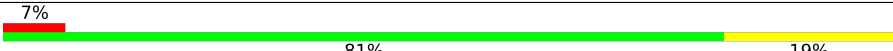
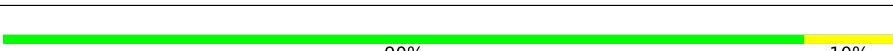
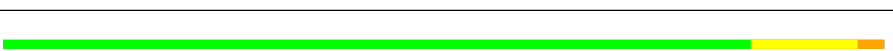
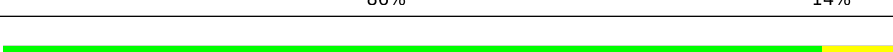
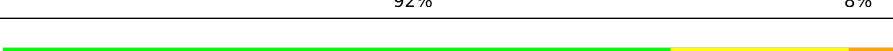
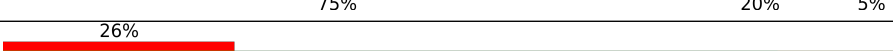
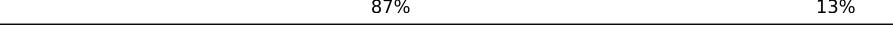
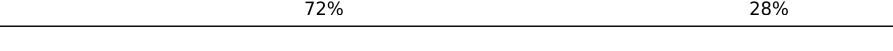
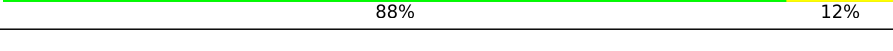
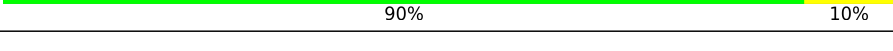
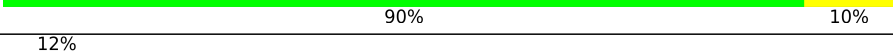
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Mol	Chain	Length	Quality of chain
11	AK	45	
12	AL	36	
13	AM	45	
14	AN	40	
15	AO	40	
16	AP	36	
17	AQ	45	
18	AR	34	
19	AS	36	
20	AT	34	
21	AU	34	
22	AV	34	
23	AW	32	
24	AX	42	
25	AY	40	
26	AZ	48	
27	Aa	40	
28	Ab	37	
29	Ac	50	
30	Ad	40	
31	Ae	37	
32	Af	48	
33	Ag	42	
34	Ah	37	
35	Ai	37	

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

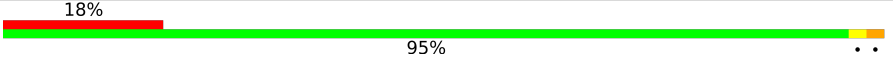
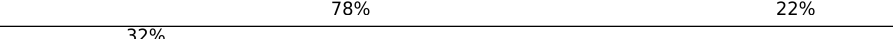
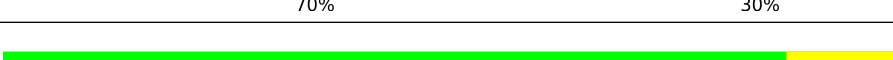
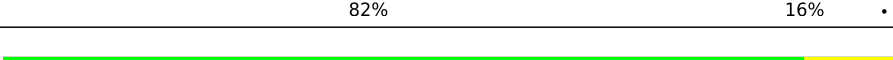
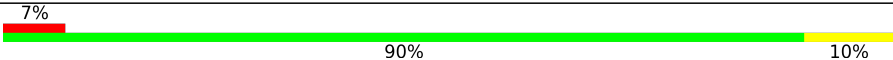
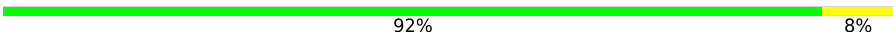
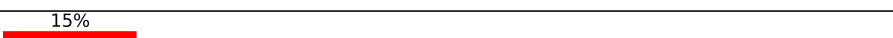
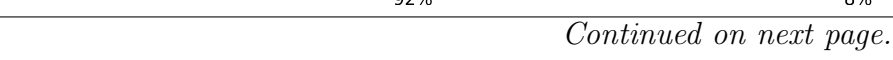
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Mol	Chain	Length	Quality of chain
61	A8	37	
62	A9	40	
63	BA	32	
64	BB	45	
65	BC	37	
66	BD	32	
67	BE	36	
68	BF	42	
69	BG	37	
70	BH	40	
71	BI	32	
72	BJ	40	
73	BK	32	
74	BL	37	
75	BM	32	
76	BN	32	
77	BO	40	
78	BP	48	
79	BQ	32	
80	BR	40	
81	BS	48	
82	BT	40	
83	BU	42	
84	BV	48	
85	BW	48	

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Mol	Chain	Length	Quality of chain
86	BX	40	
87	BY	40	
88	BZ	40	
89	Ba	40	
90	Bb	40	
91	Bc	32	
92	Bd	40	
93	Be	40	
94	Bf	44	
95	Bg	32	
96	Bh	40	
97	Bi	40	
98	Bj	49	
99	Bk	29	
100	Bl	42	
101	Bm	40	
102	Bn	40	
103	Bo	32	
104	Bp	40	
105	Bq	48	
106	Br	40	
107	Bs	31	
108	Bt	48	
109	Bu	40	
110	Bv	48	

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Mol	Chain	Length	Quality of chain
111	Bw	40	
112	Bx	40	
113	By	40	
114	Bz	40	
115	B0	40	
116	B1	42	
117	B2	31	
118	B3	40	
119	B4	48	
120	B5	50	
121	B6	31	
122	B7	29	
123	B8	40	
124	B9	40	
125	CA	40	
126	CB	34	
127	CC	40	
128	CD	40	
129	CE	34	
130	CF	32	
131	CG	40	
132	CH	40	
133	CI	40	
134	CJ	40	
135	CK	40	

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Mol	Chain	Length	Quality of chain
136	CL	44	
137	CM	37	
138	CN	40	
139	CO	40	
140	CP	48	
141	CQ	34	
142	CR	40	
143	CS	40	
144	CT	48	
145	CU	48	
146	CV	34	
147	CW	26	
148	CX	44	
149	CY	32	
150	CZ	26	
151	Ca	40	
152	Cb	34	
153	Cc	34	
154	Cd	40	
155	Ce	40	
156	Cf	40	
157	Cg	48	
158	Ch	48	
159	Ci	46	
160	Cj	48	

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Mol	Chain	Length	Quality of chain
161	Ck	44	23% 89% 11%
162	Cl	40	85% 15%
163	Cm	48	85% 15%
164	Cn	32	88% 12%
165	Co	44	34% 84% 16%
166	Cp	32	84% 16%
167	Cq	40	82% 18%
168	Cr	50	8% 76% 20%
169	Cs	40	85% 12%
170	Ct	40	80% 18%
171	Cu	40	85% 15%
172	Cv	40	90% 10%
173	Cw	42	93% 7%
174	Cx	50	74% 26%
175	Cy	42	19% 83% 17%
176	Cz	40	88% 12%
177	C0	48	81% 19%
178	C1	40	88% 12%
179	C2	40	92% 8%
180	C3	31	6% 81% 13% 6%
181	C4	40	88% 12%
182	C5	40	78% 20%
183	C6	45	7% 67% 31%
184	C7	34	35% 79% 21%
185	C8	48	85% 12%

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Mol	Chain	Length	Quality of chain
186	C9	48	 79% 19% .
187	DA	40	 82% 12% 5%
188	DB	48	 85% 12% .
189	DC	31	 55% 84% 16%
190	DD	40	 82% 18%
191	DE	50	 30% 90% 6% .
192	DF	50	 34% 82% 18%
193	DG	40	 90% 10%
194	DH	42	 31% 88% 12%
195	DI	37	 41% 76% 24%
196	DJ	48	 88% 8% .
197	DK	40	 85% 15%
198	DL	32	 72% 28%
199	DM	48	 88% 12%
200	DN	48	 83% 15% .
201	DO	24	 12% 75% 25%
202	DP	32	 91% 9%
203	DQ	40	 90% 10%

2 Entry composition

There are 203 unique types of molecules in this entry. The entry contains 311400 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a DNA chain called SCAFFOLD STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	7249	Total	C	N	O	P	0	0
			148273	70952	25939	44134	7248		

- Molecule 2 is a DNA chain called STAPLE STRAND.

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

- Molecule 3 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AC	31	Total	C	N	O	P	0	0
			630	306	105	189	30		

- Molecule 4 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AD	40	Total	C	N	O	P	0	0
			812	393	138	242	39		

- Molecule 5 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AE	48	Total	C	N	O	P	0	0
			978	469	173	289	47		

- Molecule 6 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AF	31	Total	C	N	O	P	0	0
			630	308	97	195	30		

- Molecule 7 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AG	40	Total	C	N	O	P	0	0
			814	393	138	244	39		

- Molecule 8 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AH	31	Total	C	N	O	P	0	0
			637	308	106	193	30		

- Molecule 9 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	AI	45	Total	C	N	O	P	0	0
			911	439	158	270	44		

- Molecule 10 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AJ	40	Total	C	N	O	P	0	0
			826	392	160	235	39		

- Molecule 11 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AK	45	Total	C	N	O	P	0	0
			909	443	142	280	44		

- Molecule 12 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AL	36	Total	C	N	O	P	0	0
			733	355	119	224	35		

- Molecule 13 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AM	45	Total	C	N	O	P	0	0
			925	445	167	269	44		

- Molecule 14 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	AN	40	Total	C	N	O	P	0	0
			819	394	149	237	39		

- Molecule 15 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AO	40	Total	C	N	O	P	0	0
			818	391	152	236	39		

- Molecule 16 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AP	36	Total	C	N	O	P	0	0
			736	355	131	215	35		

- Molecule 17 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AQ	45	Total	C	N	O	P	0	0
			912	440	157	271	44		

- Molecule 18 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AR	34	Total	C	N	O	P	0	0
			686	338	94	221	33		

- Molecule 19 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AS	36	Total	C	N	O	P	0	0
			734	360	114	225	35		

- Molecule 20 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	AT	34	Total	C	N	O	P	0	0
			699	340	119	207	33		

- Molecule 21 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	AU	34	Total	C	N	O	P	0	0
			679	336	90	220	33		

- Molecule 22 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	AV	34	Total	C	N	O	P	0	0
			698	336	126	203	33		

- Molecule 23 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AW	32	Total	C	N	O	P	0	0
			660	314	139	176	31		

- Molecule 24 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	AX	42	Total	C	N	O	P	0	0
			867	412	170	244	41		

- Molecule 25 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	AY	40	Total	C	N	O	P	0	0
			813	393	144	237	39		

- Molecule 26 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AZ	48	Total	C	N	O	P	0	0
			993	474	186	286	47		

- Molecule 27 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	Aa	40	Total	C	N	O	P	0	0
			815	392	142	242	39		

- Molecule 28 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Ab	37	Total	C	N	O	P	0	0
			747	367	107	237	36		

- Molecule 29 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	Ac	50	Total	C	N	O	P	0	0
			1033	494	193	297	49		

- Molecule 30 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	Ad	40	Total	C	N	O	P	0	0
			832	397	170	226	39		

- Molecule 31 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Ae	37	Total	C	N	O	P	0	0
			746	365	109	236	36		

- Molecule 32 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Af	48	Total	C	N	O	P	0	0
			981	469	188	277	47		

- Molecule 33 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Ag	42	Total	C	N	O	P	0	0
			871	415	179	236	41		

- Molecule 34 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Ah	37	Total	C	N	O	P	0	0
			746	364	119	227	36		

- Molecule 35 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Ai	37	Total	C	N	O	P	0	0
			756	365	130	225	36		

- Molecule 36 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Aj	31	Total	C	N	O	P	0	0
			641	310	110	191	30		

- Molecule 37 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Ak	40	Total	C	N	O	P	0	0
			816	392	148	237	39		

- Molecule 38 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Al	42	Total	C	N	O	P	0	0
			858	416	157	244	41		

- Molecule 39 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Am	40	Total	C	N	O	P	0	0
			809	390	138	242	39		

- Molecule 40 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	An	40	Total	C	N	O	P	0	0
			811	395	133	244	39		

- Molecule 41 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Ao	32	Total	C	N	O	P	0	0
			651	314	115	191	31		

- Molecule 42 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Ap	37	Total	C	N	O	P	0	0
			766	365	151	214	36		

- Molecule 43 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Aq	40	Total	C	N	O	P	0	0
			824	391	161	233	39		

- Molecule 44 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Ar	40	Total	C	N	O	P	0	0
			834	395	169	231	39		

- Molecule 45 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	As	31	Total	C	N	O	P	0	0
			619	302	94	193	30		

- Molecule 46 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	At	32	Total	C	N	O	P	0	0
			660	315	129	185	31		

- Molecule 47 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Au	32	Total	C	N	O	P	0	0
			665	314	142	178	31		

- Molecule 48 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Av	40	Total	C	N	O	P	0	0
			809	389	145	236	39		

- Molecule 49 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Aw	40	Total	C	N	O	P	0	0
			813	391	137	246	39		

- Molecule 50 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	Ax	32	Total	C	N	O	P	0	0
			655	315	123	186	31		

- Molecule 51 is a DNA chain called STAPLE STRAND.

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

- Molecule 52 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	Az	40	Total	C	N	O	P	0	0
			822	390	162	231	39		

- Molecule 53 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	A0	48	Total	C	N	O	P	0	0
			984	466	194	277	47		

- Molecule 54 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	A1	31	Total	C	N	O	P	0	0
			625	303	96	196	30		

- Molecule 55 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	A2	42	Total	C	N	O	P	0	0
			840	403	143	253	41		

- Molecule 56 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	A3	32	Total	C	N	O	P	0	0
			652	312	126	183	31		

- Molecule 57 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	A4	48	Total	C	N	O	P	0	0
			984	469	188	280	47		

- Molecule 58 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	A5	40	Total	C	N	O	P	0	0
			820	392	163	226	39		

- Molecule 59 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	A6	40	Total	C	N	O	P	0	0
			829	395	160	235	39		

- Molecule 60 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	A7	42	Total	C	N	O	P	0	0
			851	411	141	258	41		

- Molecule 61 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	A8	37	Total	C	N	O	P	0	0
			746	365	112	233	36		

- Molecule 62 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	A9	40	Total	C	N	O	P	0	0
			819	391	146	243	39		

- Molecule 63 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	BA	32	Total	C	N	O	P	0	0
			656	313	125	187	31		

- Molecule 64 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	BB	45	Total	C	N	O	P	0	0
			928	441	174	269	44		

- Molecule 65 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	BC	37	Total	C	N	O	P	0	0
			754	365	121	232	36		

- Molecule 66 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	BD	32	Total	C	N	O	P	0	0
			642	307	113	191	31		

- Molecule 67 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	BE	36	Total	C	N	O	P	0	0
			733	354	123	221	35		

- Molecule 68 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	BF	42	Total	C	N	O	P	0	0
			855	409	149	256	41		

- Molecule 69 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	BG	37	Total	C	N	O	P	0	0
			760	370	119	235	36		

- Molecule 70 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	BH	40	Total	C	N	O	P	0	0
			811	389	142	241	39		

- Molecule 71 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	BI	32	Total	C	N	O	P	0	0
			642	310	110	191	31		

- Molecule 72 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	BJ	40	Total	C	N	O	P	0	0
			814	391	146	238	39		

- Molecule 73 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	BK	32	Total	C	N	O	P	0	0
			654	315	120	188	31		

- Molecule 74 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	BL	37	Total	C	N	O	P	0	0
			751	361	128	226	36		

- Molecule 75 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	BM	32	Total	C	N	O	P	0	0
			660	315	120	194	31		

- Molecule 76 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	BN	32	Total	C	N	O	P	0	0
			656	313	119	193	31		

- Molecule 77 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	BO	40	Total	C	N	O	P	0	0
			819	390	153	237	39		

- Molecule 78 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	BP	48	Total	C	N	O	P	0	0
			969	462	180	280	47		

- Molecule 79 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	BQ	32	Total	C	N	O	P	0	0
			660	314	133	182	31		

- Molecule 80 is a DNA chain called STAPLE STRAND.

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

- Molecule 81 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	BS	48	Total	C	N	O	P	0	0
			984	473	181	283	47		

- Molecule 82 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	BT	40	Total	C	N	O	P	0	0
			817	390	156	232	39		

- Molecule 83 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	BU	42	Total	C	N	O	P	0	0
			852	410	148	253	41		

- Molecule 84 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	BV	48	Total	C	N	O	P	0	0
			988	473	178	290	47		

- Molecule 85 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	BW	48	Total	C	N	O	P	0	0
			960	472	128	313	47		

- Molecule 86 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	BX	40	Total	C	N	O	P	0	0
			805	391	134	241	39		

- Molecule 87 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
87	BY	40	Total	C	N	O	P	0	0
			806	390	132	245	39		

- Molecule 88 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
88	BZ	40	Total	C	N	O	P	0	0
			818	391	152	236	39		

- Molecule 89 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
89	Ba	40	Total	C	N	O	P	0	0
			804	384	147	234	39		

- Molecule 90 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
90	Bb	40	Total	C	N	O	P	0	0
			815	393	153	230	39		

- Molecule 91 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
91	Bc	32	Total	C	N	O	P	0	0
			656	312	129	184	31		

- Molecule 92 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
92	Bd	40	Total	C	N	O	P	0	0
			809	391	134	245	39		

- Molecule 93 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
93	Be	40	Total	C	N	O	P	0	0
			818	389	163	227	39		

- Molecule 94 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
94	Bf	44	Total	C	N	O	P	0	0
			900	435	144	278	43		

- Molecule 95 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
95	Bg	32	Total	C	N	O	P	0	0
			664	317	121	195	31		

- Molecule 96 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
96	Bh	40	Total	C	N	O	P	0	0
			835	392	175	229	39		

- Molecule 97 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
97	Bi	40	Total	C	N	O	P	0	0
			824	396	141	248	39		

- Molecule 98 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
98	Bj	49	Total	C	N	O	P	0	0
			997	480	162	307	48		

- Molecule 99 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
99	Bk	29	Total	C	N	O	P	0	0
			599	285	120	166	28		

- Molecule 100 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
100	Bl	42	Total	C	N	O	P	0	0
			859	410	154	254	41		

- Molecule 101 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
101	Bm	40	Total	C	N	O	P	0	0
			811	386	151	235	39		

- Molecule 102 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
102	Bn	40	Total	C	N	O	P	0	0
			817	387	159	232	39		

- Molecule 103 is a DNA chain called STAPLE STRAND.

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

- Molecule 104 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
104	Bp	40	Total	C	N	O	P	0	0
			806	387	141	239	39		

- Molecule 105 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
105	Bq	48	Total	C	N	O	P	0	0
			977	474	156	300	47		

- Molecule 106 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
106	Br	40	Total	C	N	O	P	0	0
			820	387	159	235	39		

- Molecule 107 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
107	Bs	31	Total	C	N	O	P	0	0
			629	305	103	191	30		

- Molecule 108 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
108	Bt	48	Total	C	N	O	P	0	0
			983	465	192	279	47		

- Molecule 109 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
109	Bu	40	Total	C	N	O	P	0	0
			807	386	154	228	39		

- Molecule 110 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
110	Bv	48	Total	C	N	O	P	0	0
			976	468	174	287	47		

- Molecule 111 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
111	Bw	40	Total	C	N	O	P	0	0
			824	396	153	236	39		

- Molecule 112 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
112	Bx	40	Total	C	N	O	P	0	0
			820	391	146	244	39		

- Molecule 113 is a DNA chain called STAPLE STRAND.

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

- Molecule 114 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
114	Bz	40	Total	C	N	O	P	0	0
			819	391	152	237	39		

- Molecule 115 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
115	B0	40	Total	C	N	O	P	0	0
			807	392	121	255	39		

- Molecule 116 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
116	B1	42	Total	C	N	O	P	0	0
			854	415	134	264	41		

- Molecule 117 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
117	B2	31	Total	C	N	O	P	0	0
			627	303	99	195	30		

- Molecule 118 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
118	B3	40	Total	C	N	O	P	0	0
			813	388	149	237	39		

- Molecule 119 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
119	B4	48	Total	C	N	O	P	0	0
			989	471	189	282	47		

- Molecule 120 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
120	B5	50	Total	C	N	O	P	0	0
			1023	490	179	305	49		

- Molecule 121 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
121	B6	31	Total	C	N	O	P	0	0
			634	308	106	190	30		

- Molecule 122 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
122	B7	29	Total	C	N	O	P	0	0
			589	287	97	177	28		

- Molecule 123 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
123	B8	40	Total	C	N	O	P	0	0
			819	390	159	231	39		

- Molecule 124 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
124	B9	40	Total	C	N	O	P	0	0
			828	392	160	237	39		

- Molecule 125 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
125	CA	40	Total	C	N	O	P	0	0
			808	385	149	235	39		

- Molecule 126 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
126	CB	34	Total	C	N	O	P	0	0
			699	333	132	201	33		

- Molecule 127 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
127	CC	40	Total	C	N	O	P	0	0
			814	393	141	241	39		

- Molecule 128 is a DNA chain called STAPLE STRAND.

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

- Molecule 129 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
129	CE	34	Total	C	N	O	P	0	0
			699	335	136	195	33		

- Molecule 130 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
130	CF	32	Total	C	N	O	P	0	0
			651	319	98	203	31		

- Molecule 131 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
131	CG	40	Total	C	N	O	P	0	0
			823	392	163	229	39		

- Molecule 132 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
132	CH	40	Total	C	N	O	P	0	0
			814	391	140	244	39		

- Molecule 133 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
133	CI	40	Total	C	N	O	P	0	0
			823	390	165	229	39		

- Molecule 134 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
134	CJ	40	Total	C	N	O	P	0	0
			815	391	152	233	39		

- Molecule 135 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
135	CK	40	Total	C	N	O	P	0	0
			823	394	167	223	39		

- Molecule 136 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
136	CL	44	Total	C	N	O	P	0	0
			893	429	156	265	43		

- Molecule 137 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
137	CM	37	Total	C	N	O	P	0	0
			746	361	122	227	36		

- Molecule 138 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
138	CN	40	Total	C	N	O	P	0	0
			808	392	130	247	39		

- Molecule 139 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
139	CO	40	Total	C	N	O	P	0	0
			805	385	137	244	39		

- Molecule 140 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
140	CP	48	Total	C	N	O	P	0	0
			987	472	197	271	47		

- Molecule 141 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
141	CQ	34	Total	C	N	O	P	0	0
			686	329	127	197	33		

- Molecule 142 is a DNA chain called STAPLE STRAND.

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

- Molecule 143 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
143	CS	40	Total	C	N	O	P	0	0
			808	389	145	235	39		

- Molecule 144 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
144	CT	48	Total	C	N	O	P	0	0
			965	468	159	291	47		

- Molecule 145 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
145	CU	48	Total	C	N	O	P	0	0
			980	469	182	282	47		

- Molecule 146 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
146	CV	34	Total	C	N	O	P	0	0
			691	336	111	211	33		

- Molecule 147 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
147	CW	26	Total	C	N	O	P	0	0
			535	257	100	153	25		

- Molecule 148 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
148	CX	44	Total	C	N	O	P	0	0
			902	434	163	262	43		

- Molecule 149 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
149	CY	32	Total	C	N	O	P	0	0
			670	316	143	180	31		

- Molecule 150 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
150	CZ	26	Total	C	N	O	P	0	0
			534	256	98	155	25		

- Molecule 151 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
151	Ca	40	Total	C	N	O	P	0	0
			824	393	162	230	39		

- Molecule 152 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
152	Cb	34	Total	C	N	O	P	0	0
			690	333	120	204	33		

- Molecule 153 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
153	Cc	34	Total	C	N	O	P	0	0
			693	335	124	201	33		

- Molecule 154 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
154	Cd	40	Total	C	N	O	P	0	0
			818	389	160	230	39		

- Molecule 155 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
155	Ce	40	Total	C	N	O	P	0	0
			822	396	153	234	39		

- Molecule 156 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
156	Cf	40	Total	C	N	O	P	0	0
			826	392	166	229	39		

- Molecule 157 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
157	Cg	48	Total	C	N	O	P	0	0
			991	470	196	278	47		

- Molecule 158 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
158	Ch	48	Total	C	N	O	P	0	0
			983	472	179	285	47		

- Molecule 159 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
159	Ci	46	Total	C	N	O	P	0	0
			942	454	164	279	45		

- Molecule 160 is a DNA chain called STAPLE STRAND.

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

- Molecule 161 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
161	Ck	44	Total	C	N	O	P	0	0
			899	437	151	268	43		

- Molecule 162 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
162	Cl	40	Total	C	N	O	P	0	0
			809	388	146	236	39		

- Molecule 163 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
163	Cm	48	Total	C	N	O	P	0	0
			990	472	197	274	47		

- Molecule 164 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
164	Cn	32	Total	C	N	O	P	0	0
			640	307	113	189	31		

- Molecule 165 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
165	Co	44	Total	C	N	O	P	0	0
			889	434	136	276	43		

- Molecule 166 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
166	Cp	32	Total	C	N	O	P	0	0
			664	319	125	189	31		

- Molecule 167 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
167	Cq	40	Total	C	N	O	P	0	0
			813	394	143	237	39		

- Molecule 168 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
168	Cr	50	Total	C	N	O	P	0	0
			1022	491	187	295	49		

- Molecule 169 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
169	Cs	40	Total	C	N	O	P	0	0
			812	392	145	236	39		

- Molecule 170 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
170	Ct	40	Total	C	N	O	P	0	0
			819	394	149	237	39		

- Molecule 171 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
171	Cu	40	Total	C	N	O	P	0	0
			819	392	160	228	39		

- Molecule 172 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
172	Cv	40	Total	C	N	O	P	0	0
			832	398	160	235	39		

- Molecule 173 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
173	Cw	42	Total	C	N	O	P	0	0
			856	413	148	254	41		

- Molecule 174 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
174	Cx	50	Total	C	N	O	P	0	0
			1019	488	181	301	49		

- Molecule 175 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
175	Cy	42	Total	C	N	O	P	0	0
			854	414	147	252	41		

- Molecule 176 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
176	Cz	40	Total	C	N	O	P	0	0
			818	391	152	236	39		

- Molecule 177 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
177	C0	48	Total	C	N	O	P	0	0
			990	474	186	283	47		

- Molecule 178 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
178	C1	40	Total	C	N	O	P	0	0
			830	393	165	233	39		

- Molecule 179 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
179	C2	40	Total	C	N	O	P	0	0
			824	393	156	236	39		

- Molecule 180 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
180	C3	31	Total	C	N	O	P	0	0
			626	307	89	200	30		

- Molecule 181 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
181	C4	40	Total	C	N	O	P	0	0
			824	393	159	233	39		

- Molecule 182 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
182	C5	40	Total	C	N	O	P	0	0
			826	394	155	238	39		

- Molecule 183 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
183	C6	45	Total	C	N	O	P	0	0
			910	442	143	281	44		

- Molecule 184 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
184	C7	34	Total	C	N	O	P	0	0
			684	337	92	222	33		

- Molecule 185 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
185	C8	48	Total	C	N	O	P	0	0
			980	468	189	276	47		

- Molecule 186 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
186	C9	48	Total	C	N	O	P	0	0
			984	467	199	271	47		

- Molecule 187 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
187	DA	40	Total	C	N	O	P	0	0
			814	388	152	235	39		

- Molecule 188 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
188	DB	48	Total	C	N	O	P	0	0
			975	469	173	286	47		

- Molecule 189 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
189	DC	31	Total	C	N	O	P	0	0
			632	309	96	197	30		

- Molecule 190 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
190	DD	40	Total	C	N	O	P	0	0
			821	397	143	242	39		

- Molecule 191 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
191	DE	50	Total	C	N	O	P	0	0
			1024	493	188	294	49		

- Molecule 192 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
192	DF	50	Total	C	N	O	P	0	0
			1024	495	186	294	49		

- Molecule 193 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
193	DG	40	Total	C	N	O	P	0	0
			821	393	156	233	39		

- Molecule 194 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
194	DH	42	Total	C	N	O	P	0	0
			850	411	150	248	41		

- Molecule 195 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
195	DI	37	Total	C	N	O	P	0	0
			747	362	124	225	36		

- Molecule 196 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
196	DJ	48	Total	C	N	O	P	0	0
			985	472	191	275	47		

- Molecule 197 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
197	DK	40	Total	C	N	O	P	0	0
			816	393	150	234	39		

- Molecule 198 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
198	DL	32	Total	C	N	O	P	0	0
			649	313	113	192	31		

- Molecule 199 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
199	DM	48	Total	C	N	O	P	0	0
			988	473	196	272	47		

- Molecule 200 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
200	DN	48	Total	C	N	O	P	0	0
			987	472	185	283	47		

- Molecule 201 is a DNA chain called STAPLE STRAND.

Mol	Chain	Residues	Atoms					AltConf	Trace
201	DO	24	Total	C	N	O	P	0	0
			481	239	64	155	23		

- Molecule 202 is a DNA chain called STAPLE STRAND.

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

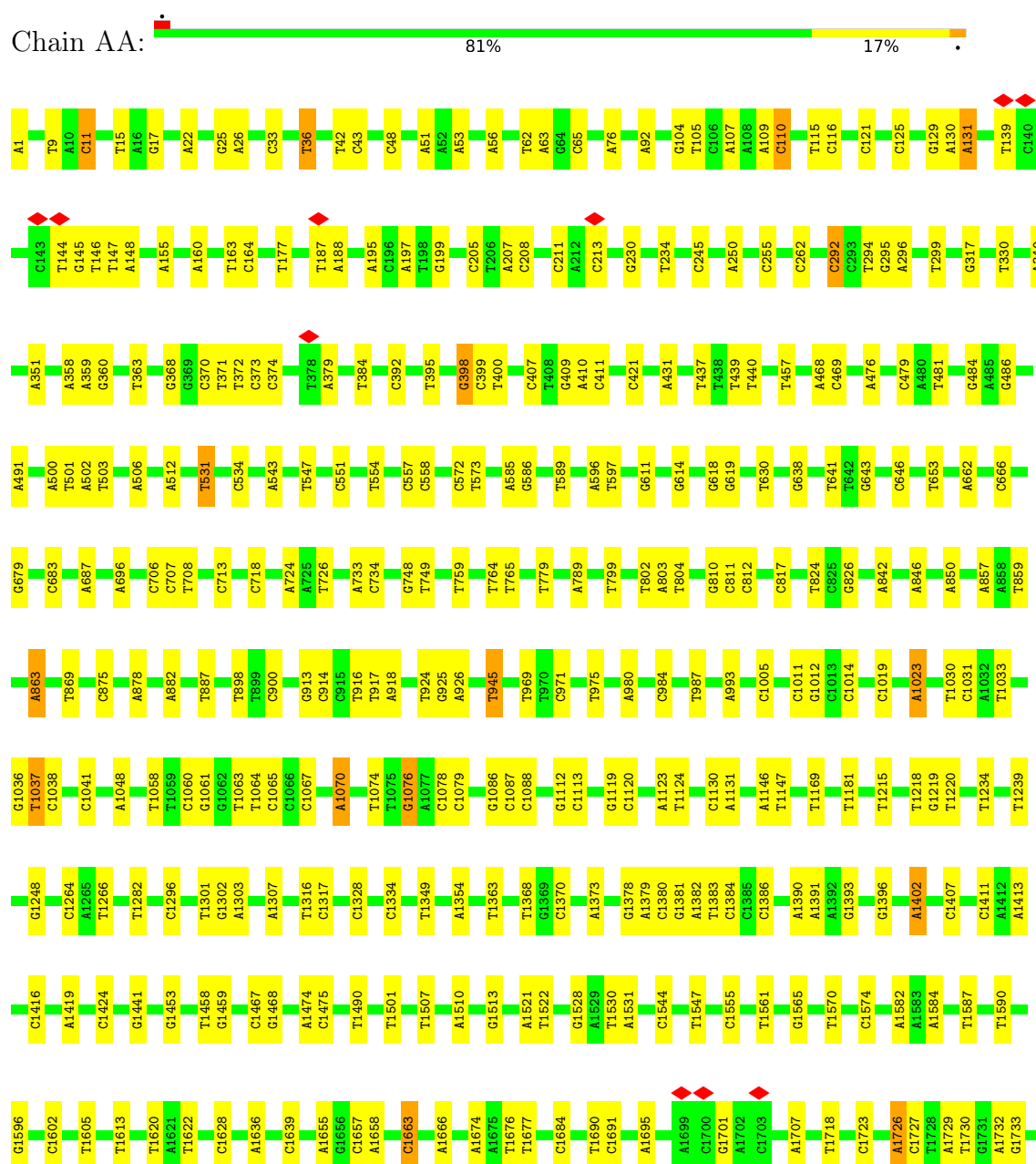
- Molecule 203 is a DNA chain called STAPLE STRAND.

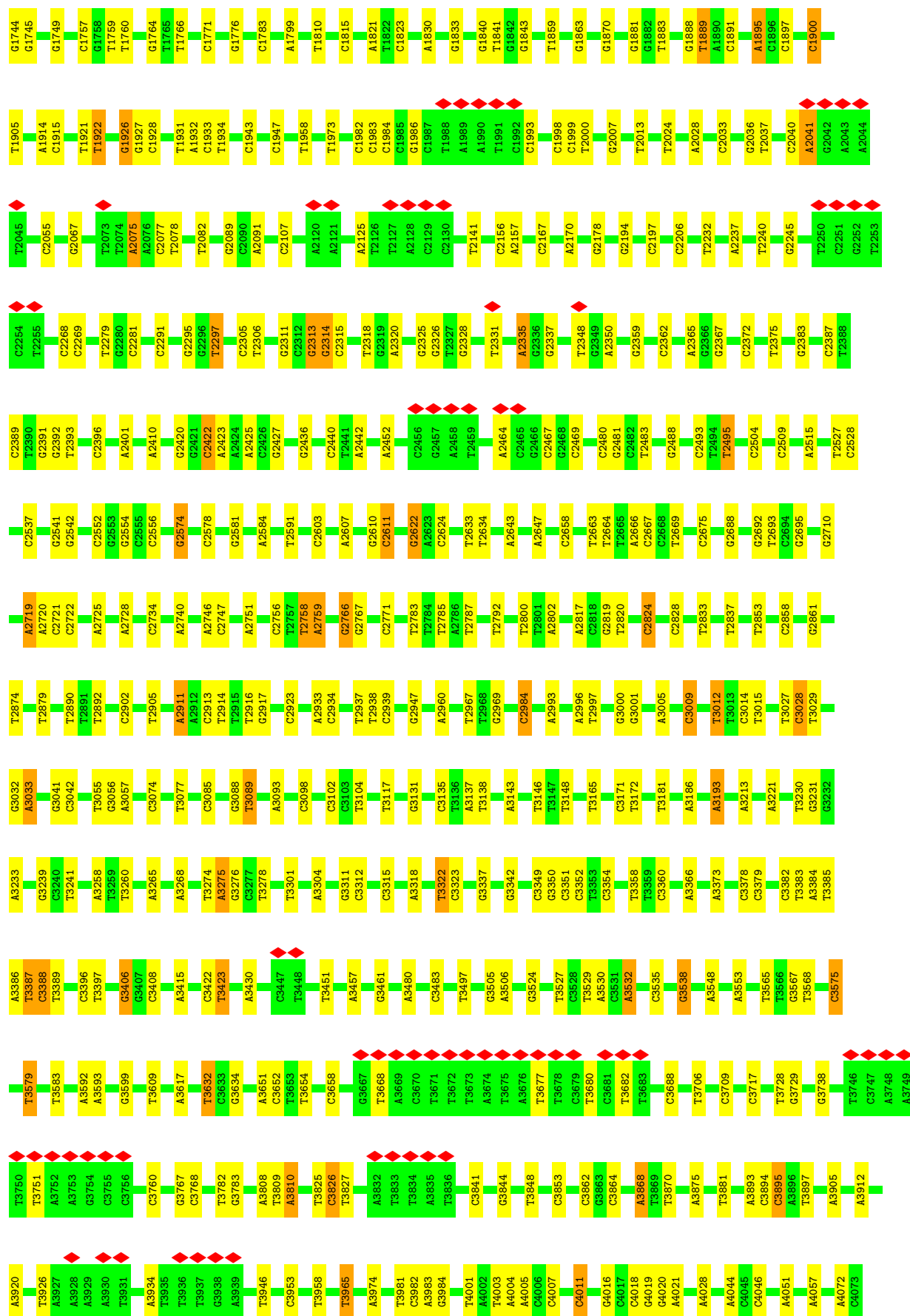
Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
203	DQ	40	826	392	163	232	39	0	0

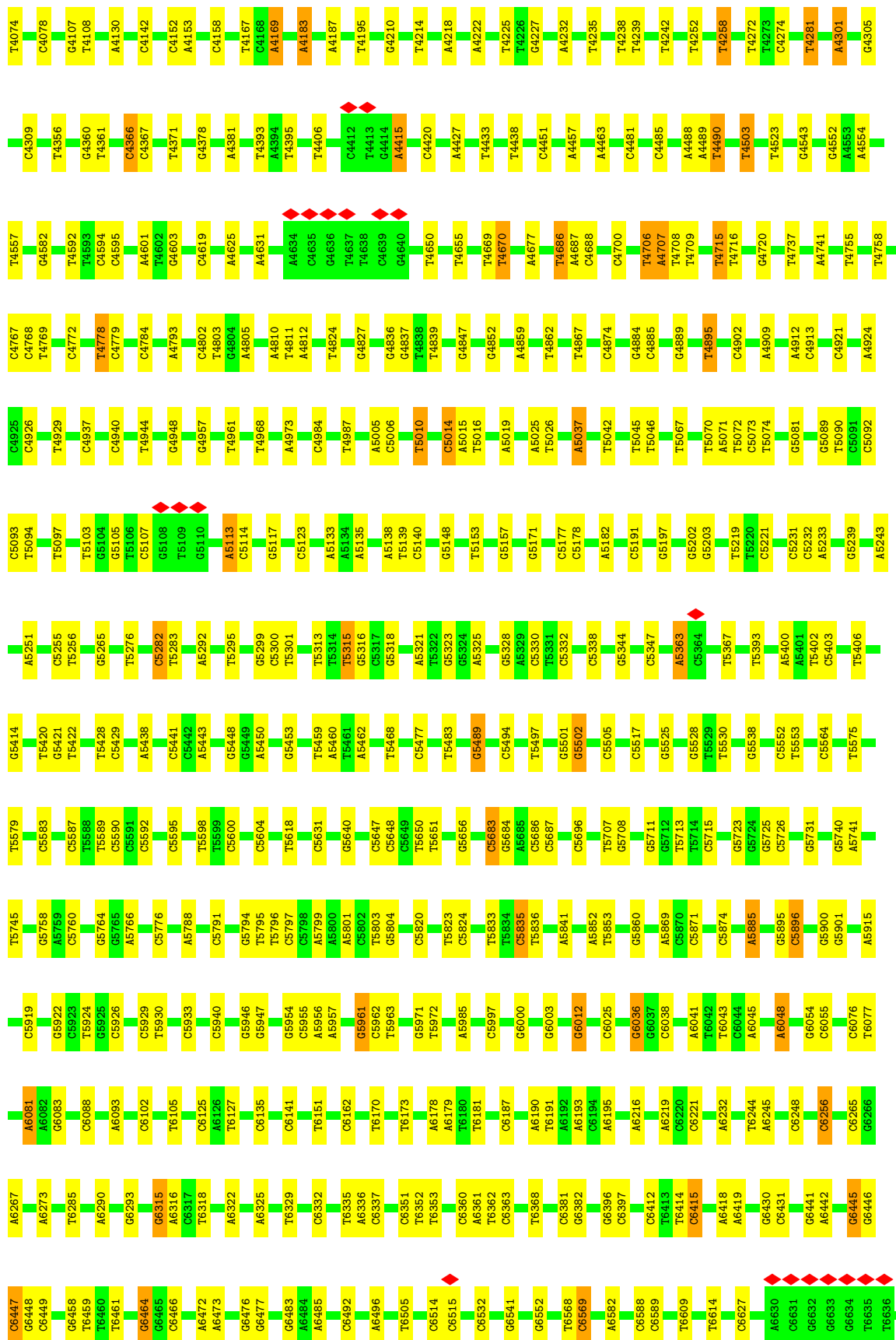
3 Residue-property plots

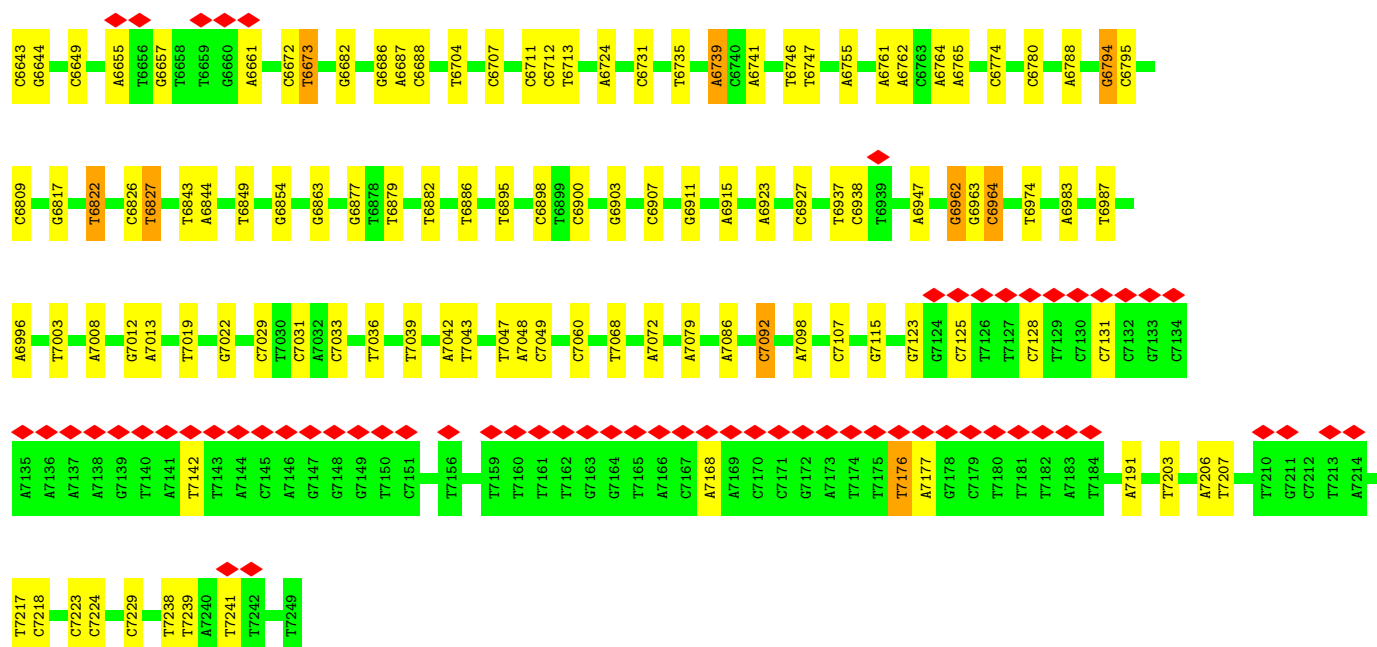
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: SCAFFOLD STRAND

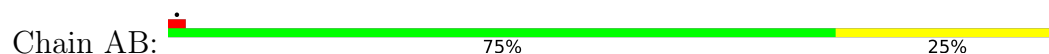




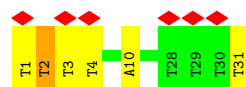
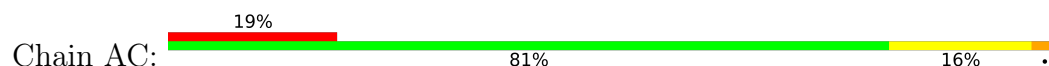




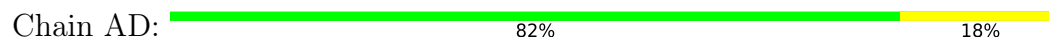
- Molecule 2: STAPLE STRAND



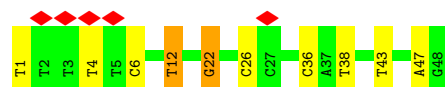
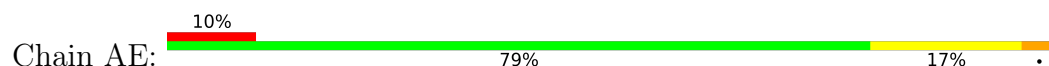
- Molecule 3: STAPLE STRAND



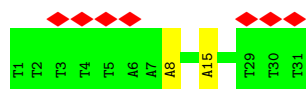
- Molecule 4: STAPLE STRAND



- Molecule 5: STAPLE STRAND



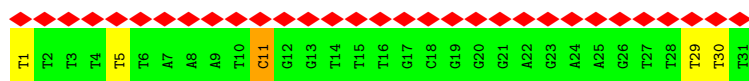
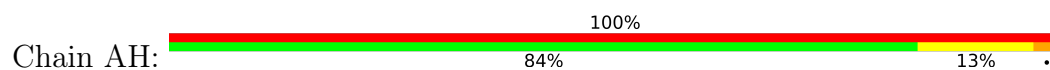
- Molecule 6: STAPLE STRAND



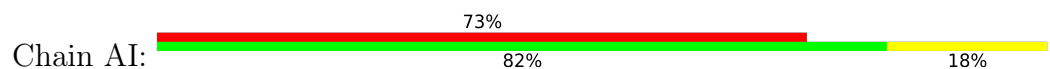
- Molecule 7: STAPLE STRAND



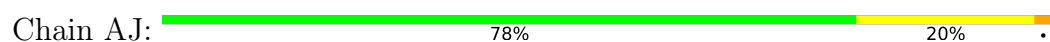
- Molecule 8: STAPLE STRAND



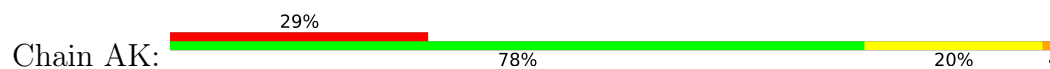
- Molecule 9: STAPLE STRAND



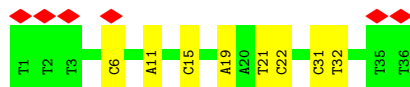
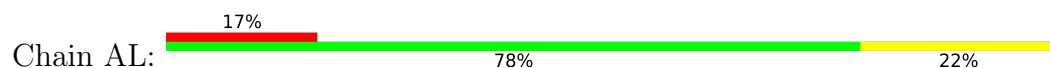
- Molecule 10: STAPLE STRAND



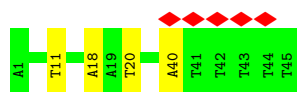
- Molecule 11: STAPLE STRAND



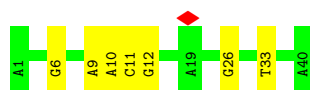
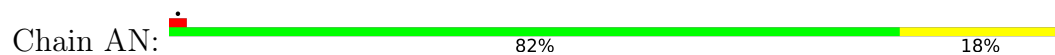
- Molecule 12: STAPLE STRAND



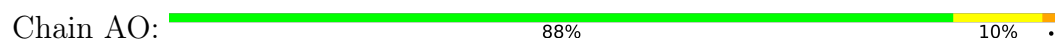
- Molecule 13: STAPLE STRAND



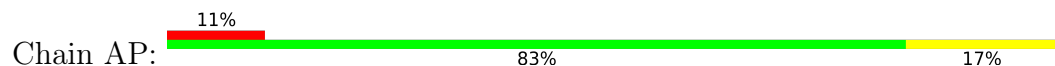
- Molecule 14: STAPLE STRAND



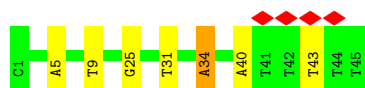
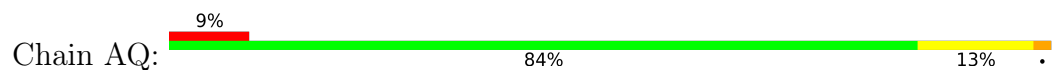
- Molecule 15: STAPLE STRAND



- Molecule 16: STAPLE STRAND



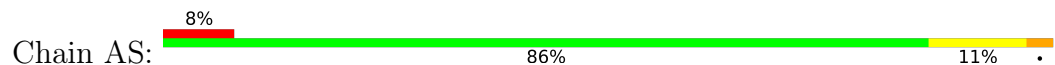
- Molecule 17: STAPLE STRAND



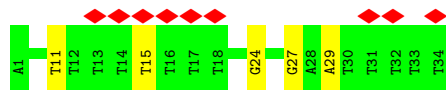
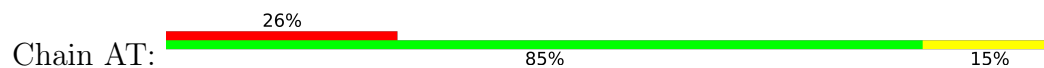
- Molecule 18: STAPLE STRAND



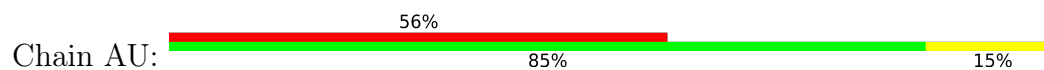
- Molecule 19: STAPLE STRAND



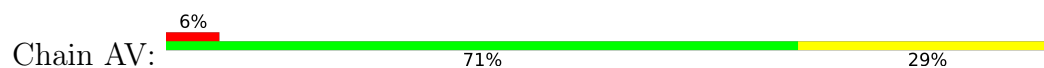
• Molecule 20: STAPLE STRAND



• Molecule 21: STAPLE STRAND



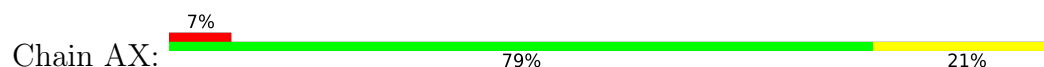
• Molecule 22: STAPLE STRAND



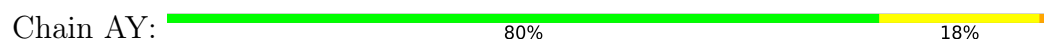
• Molecule 23: STAPLE STRAND



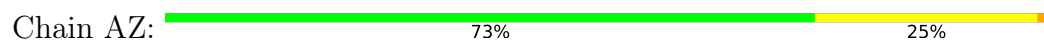
• Molecule 24: STAPLE STRAND



• Molecule 25: STAPLE STRAND



• Molecule 26: STAPLE STRAND



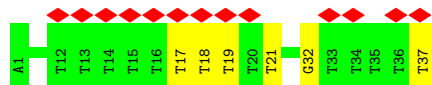
- Molecule 27: STAPLE STRAND

Chain Aa:  75% 22% .



- Molecule 28: STAPLE STRAND

Chain Ab:  35% 84% 16%



- Molecule 29: STAPLE STRAND

Chain Ac:  86% 12% .



- Molecule 30: STAPLE STRAND

Chain Ad:  82% 18%



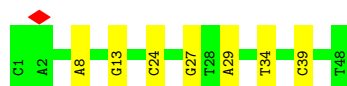
- Molecule 31: STAPLE STRAND

Chain Ae:  24% 84% 16%



- Molecule 32: STAPLE STRAND

Chain Af:  85% 15%

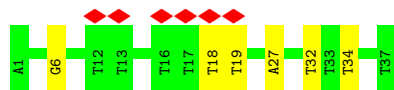
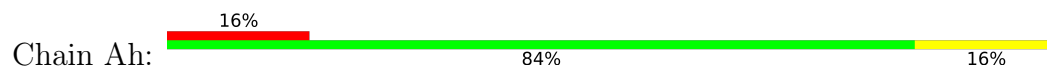


- Molecule 33: STAPLE STRAND

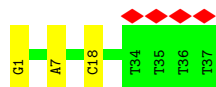
Chain Ag:  12% 83% 17%



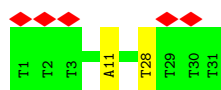
- Molecule 34: STAPLE STRAND



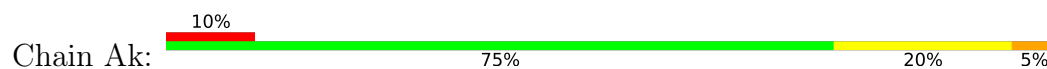
- Molecule 35: STAPLE STRAND



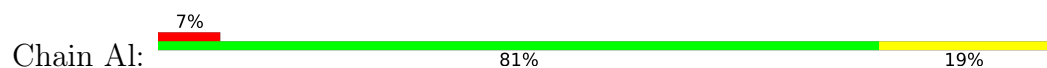
- Molecule 36: STAPLE STRAND



- Molecule 37: STAPLE STRAND



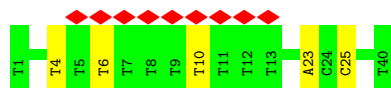
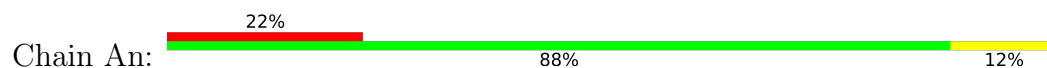
- Molecule 38: STAPLE STRAND



- Molecule 39: STAPLE STRAND



- Molecule 40: STAPLE STRAND



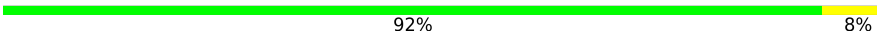
• Molecule 41: STAPLE STRAND

Chain Ao:  84% 12%

• Molecule 42: STAPLE STRAND

Chain Ap:  86% 14%

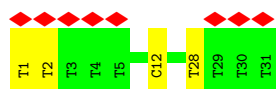
• Molecule 43: STAPLE STRAND

Chain Aq:  92% 8%

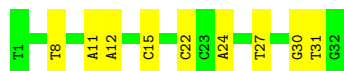
• Molecule 44: STAPLE STRAND

Chain Ar:  75% 20% 5%

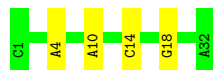
• Molecule 45: STAPLE STRAND

Chain As:  26% 87% 13%

• Molecule 46: STAPLE STRAND

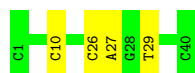
Chain At:  72% 28%

• Molecule 47: STAPLE STRAND

Chain Au:  88% 12%

• Molecule 48: STAPLE STRAND

Chain Av:  90% 10%



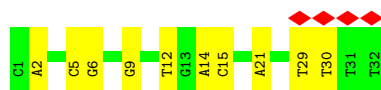
- Molecule 49: STAPLE STRAND

Chain Aw:  90% 10%



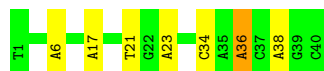
- Molecule 50: STAPLE STRAND

Chain Ax:  12% 69% 31%



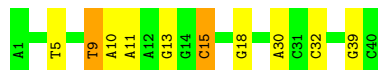
- Molecule 51: STAPLE STRAND

Chain Ay:  82% 15% .



- Molecule 52: STAPLE STRAND

Chain Az:  75% 20% 5%



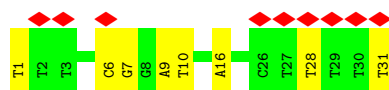
- Molecule 53: STAPLE STRAND

Chain A0:  85% 12% .

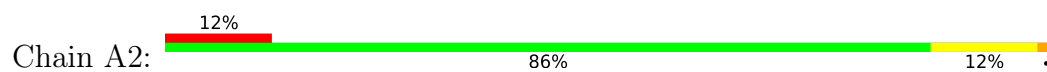


- Molecule 54: STAPLE STRAND

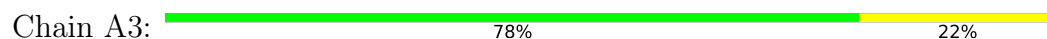
Chain A1:  29% 74% 26%



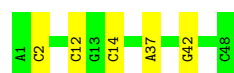
- Molecule 55: STAPLE STRAND



- Molecule 56: STAPLE STRAND



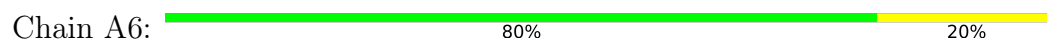
- Molecule 57: STAPLE STRAND



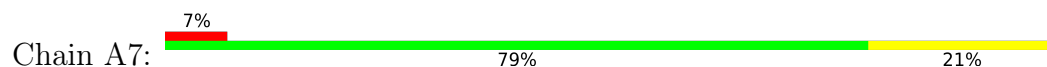
- Molecule 58: STAPLE STRAND



- Molecule 59: STAPLE STRAND



- Molecule 60: STAPLE STRAND



- Molecule 61: STAPLE STRAND

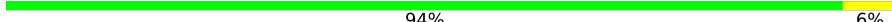


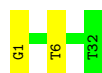
- Molecule 62: STAPLE STRAND

Chain A9:  88% 12%



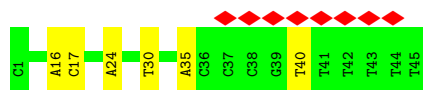
- Molecule 63: STAPLE STRAND

Chain BA:  94% 6%



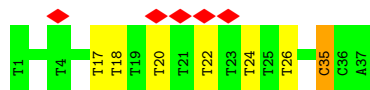
- Molecule 64: STAPLE STRAND

Chain BB:  18% 87% 13%



- Molecule 65: STAPLE STRAND

Chain BC:  14% 81% 16%



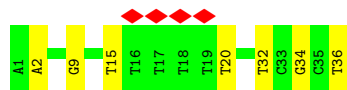
- Molecule 66: STAPLE STRAND

Chain BD:  78% 16% 6%



- Molecule 67: STAPLE STRAND

Chain BE:  11% 81% 19%

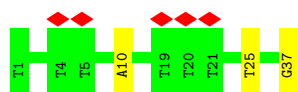
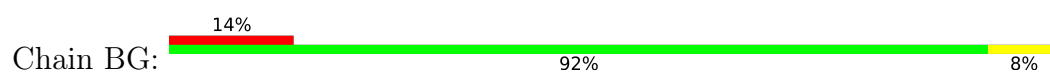


- Molecule 68: STAPLE STRAND

Chain BF:  7% 83% 17%



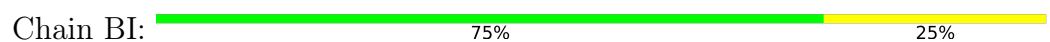
- Molecule 69: STAPLE STRAND



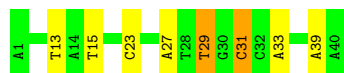
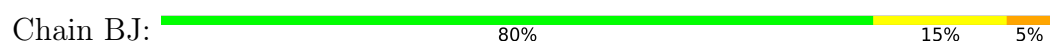
- Molecule 70: STAPLE STRAND



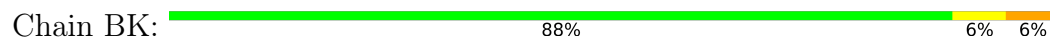
- Molecule 71: STAPLE STRAND



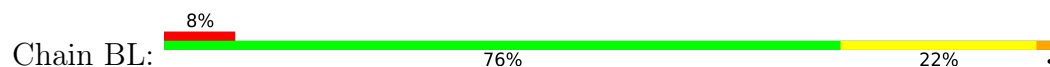
- Molecule 72: STAPLE STRAND



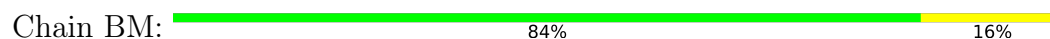
- Molecule 73: STAPLE STRAND



- Molecule 74: STAPLE STRAND

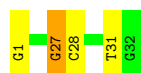


- Molecule 75: STAPLE STRAND



- Molecule 76: STAPLE STRAND

Chain BN:  88% 9%

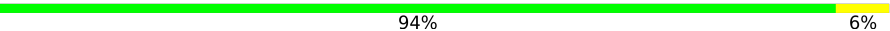


- Molecule 77: STAPLE STRAND

Chain BO:  92% 8%



- Molecule 78: STAPLE STRAND

Chain BP:  94% 6%



- Molecule 79: STAPLE STRAND

Chain BQ:  88% 12%



- Molecule 80: STAPLE STRAND

Chain BR:  82% 15%



- Molecule 81: STAPLE STRAND

Chain BS:  88% 12%



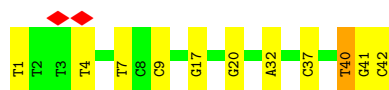
- Molecule 82: STAPLE STRAND

Chain BT:  78% 22%

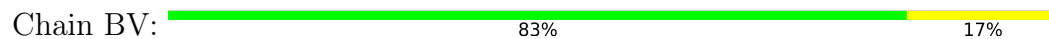


- Molecule 83: STAPLE STRAND

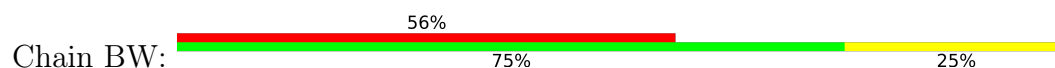
Chain BU:  5% 74% 24%



• Molecule 84: STAPLE STRAND



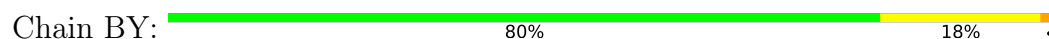
• Molecule 85: STAPLE STRAND



• Molecule 86: STAPLE STRAND



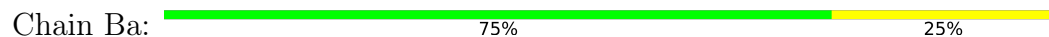
• Molecule 87: STAPLE STRAND



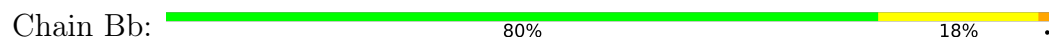
• Molecule 88: STAPLE STRAND



• Molecule 89: STAPLE STRAND

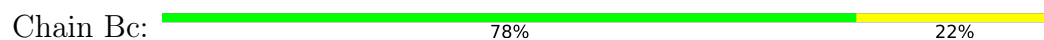


• Molecule 90: STAPLE STRAND

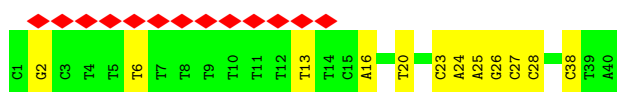




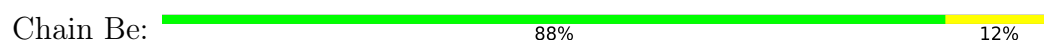
- Molecule 91: STAPLE STRAND



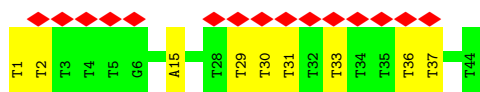
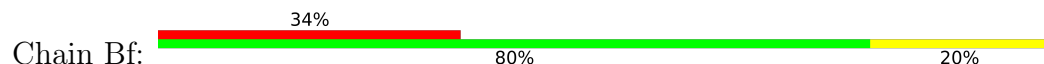
- Molecule 92: STAPLE STRAND



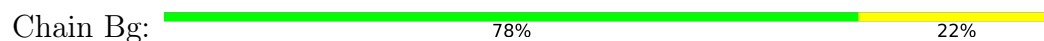
- Molecule 93: STAPLE STRAND



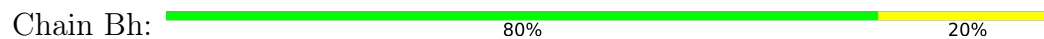
- Molecule 94: STAPLE STRAND



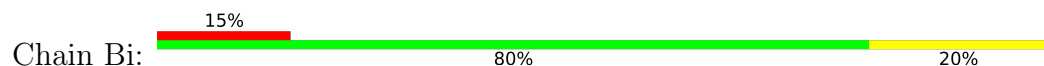
- Molecule 95: STAPLE STRAND



- Molecule 96: STAPLE STRAND

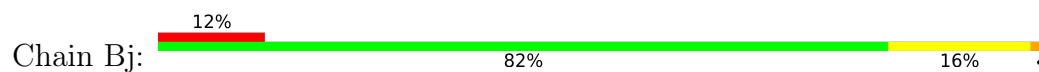


- Molecule 97: STAPLE STRAND

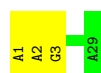




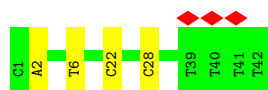
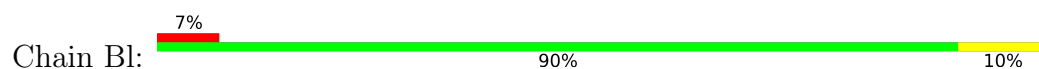
- Molecule 98: STAPLE STRAND



- Molecule 99: STAPLE STRAND



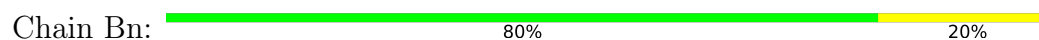
- Molecule 100: STAPLE STRAND



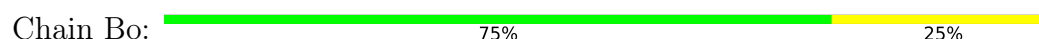
- Molecule 101: STAPLE STRAND



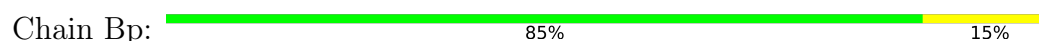
- Molecule 102: STAPLE STRAND



- Molecule 103: STAPLE STRAND

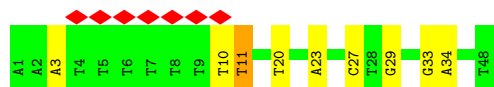
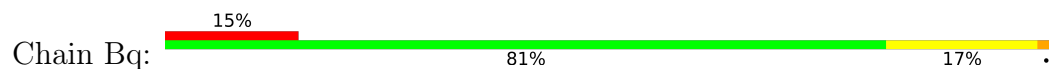


- Molecule 104: STAPLE STRAND





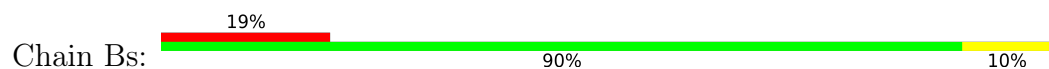
- Molecule 105: STAPLE STRAND



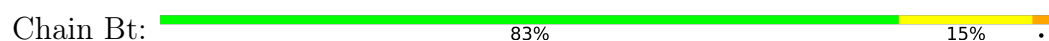
- Molecule 106: STAPLE STRAND



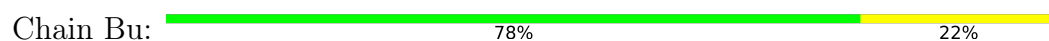
- Molecule 107: STAPLE STRAND



- Molecule 108: STAPLE STRAND



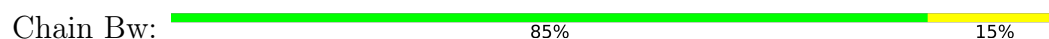
- Molecule 109: STAPLE STRAND



- Molecule 110: STAPLE STRAND



- Molecule 111: STAPLE STRAND

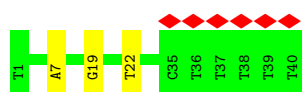
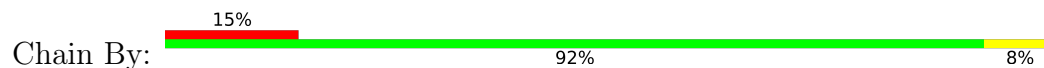




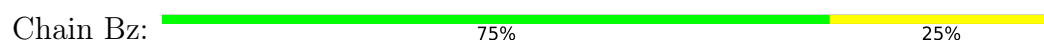
- Molecule 112: STAPLE STRAND



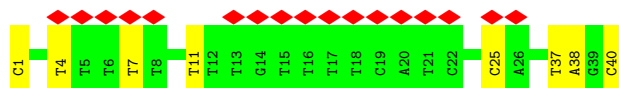
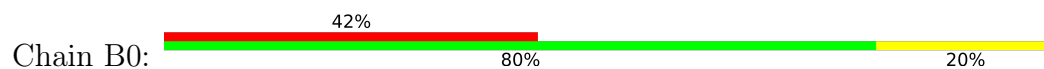
- Molecule 113: STAPLE STRAND



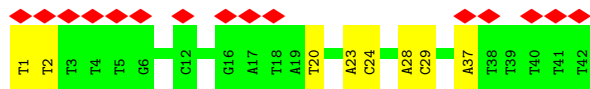
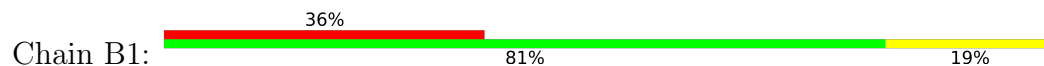
- Molecule 114: STAPLE STRAND



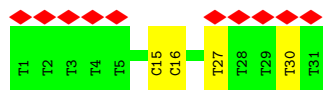
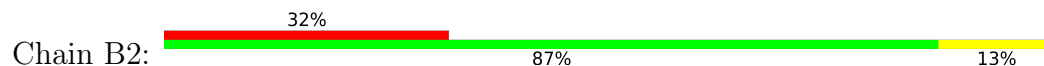
- Molecule 115: STAPLE STRAND



- Molecule 116: STAPLE STRAND



- Molecule 117: STAPLE STRAND

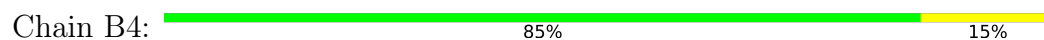


- Molecule 118: STAPLE STRAND





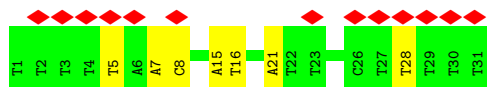
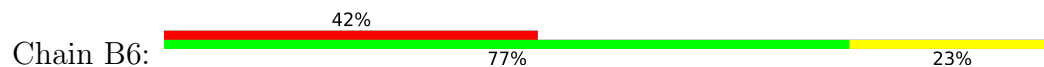
- Molecule 119: STAPLE STRAND



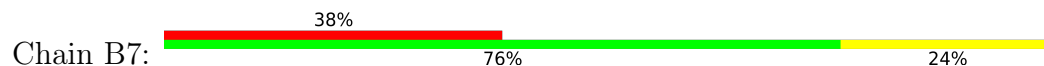
- Molecule 120: STAPLE STRAND



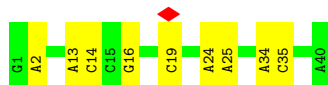
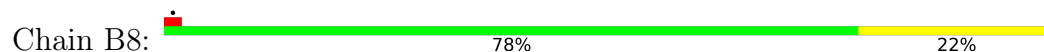
- Molecule 121: STAPLE STRAND



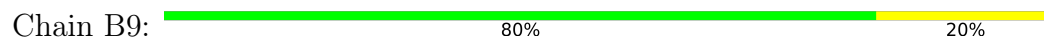
- Molecule 122: STAPLE STRAND



- Molecule 123: STAPLE STRAND



- Molecule 124: STAPLE STRAND

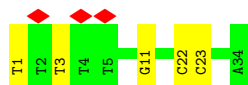
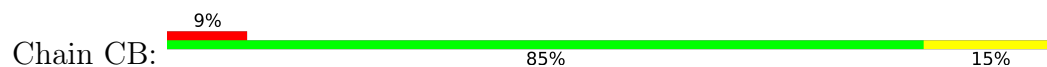


- Molecule 125: STAPLE STRAND





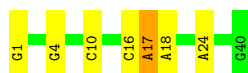
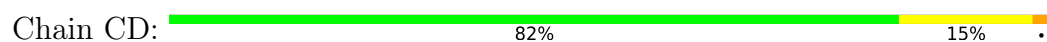
- Molecule 126: STAPLE STRAND



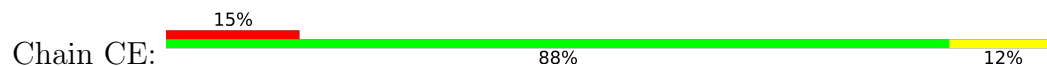
- Molecule 127: STAPLE STRAND



- Molecule 128: STAPLE STRAND



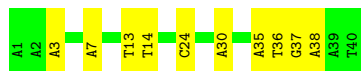
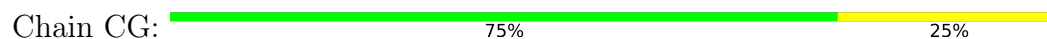
- Molecule 129: STAPLE STRAND



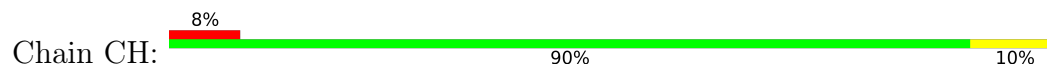
- Molecule 130: STAPLE STRAND

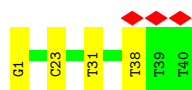


- Molecule 131: STAPLE STRAND



- Molecule 132: STAPLE STRAND





- Molecule 133: STAPLE STRAND

Chain CI: 90% 10%



- Molecule 134: STAPLE STRAND

Chain CJ: 78% 22%



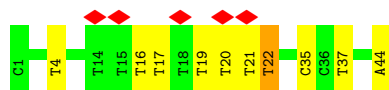
- Molecule 135: STAPLE STRAND

Chain CK: 78% 22%



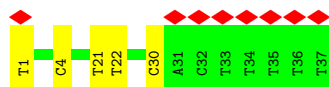
- Molecule 136: STAPLE STRAND

Chain CL: 11% 77% 20%



- Molecule 137: STAPLE STRAND

Chain CM: 22% 86% 14%



- Molecule 138: STAPLE STRAND

Chain CN: 88% 12%



- Molecule 139: STAPLE STRAND

Chain CO: 80% 18%



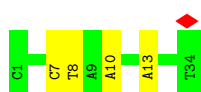
- Molecule 140: STAPLE STRAND

Chain CP: 83% 17%



- Molecule 141: STAPLE STRAND

Chain CQ: 88% 12%



- Molecule 142: STAPLE STRAND

Chain CR: 80% 20%



- Molecule 143: STAPLE STRAND

Chain CS: 85% 15%



- Molecule 144: STAPLE STRAND

Chain CT: 79% 21%



- Molecule 145: STAPLE STRAND

Chain CU: 85% 12%



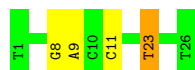
- Molecule 146: STAPLE STRAND

Chain CV: 29% 79% 21%



• Molecule 147: STAPLE STRAND

Chain CW: 85% 12% .



• Molecule 148: STAPLE STRAND

Chain CX: 23% 84% 16%



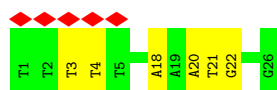
• Molecule 149: STAPLE STRAND

Chain CY: 81% 19%



• Molecule 150: STAPLE STRAND

Chain CZ: 19% 77% 23%



• Molecule 151: STAPLE STRAND

Chain Ca: 80% 15% 5%



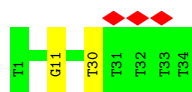
• Molecule 152: STAPLE STRAND

Chain Cb: 6% 85% 9% 6%



• Molecule 153: STAPLE STRAND

Chain Cc: 9% 94% 6%



• Molecule 154: STAPLE STRAND

Chain Cd: 75% 25%



• Molecule 155: STAPLE STRAND

Chain Ce: 80% 15% 5%



• Molecule 156: STAPLE STRAND

Chain Cf: 80% 20%



• Molecule 157: STAPLE STRAND

Chain Cg: 79% 17% .



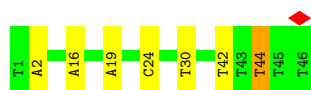
• Molecule 158: STAPLE STRAND

Chain Ch: 73% 27%



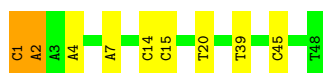
• Molecule 159: STAPLE STRAND

Chain Ci: 85% 13% .

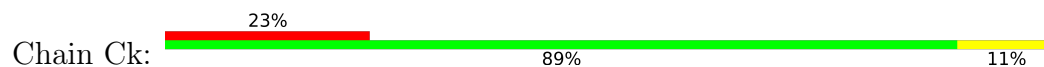


• Molecule 160: STAPLE STRAND

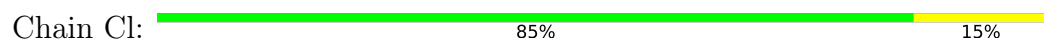
Chain Cj: 81% 15% .



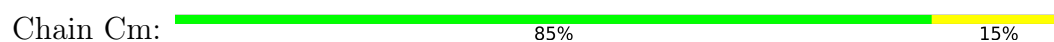
- Molecule 161: STAPLE STRAND



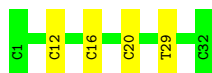
- Molecule 162: STAPLE STRAND



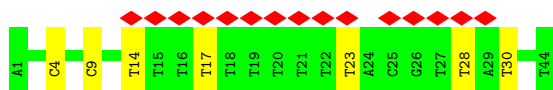
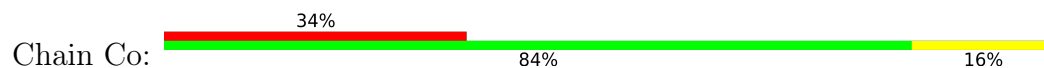
- Molecule 163: STAPLE STRAND



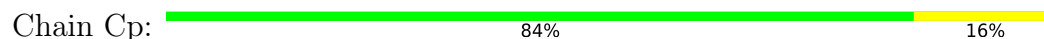
- Molecule 164: STAPLE STRAND



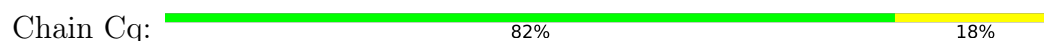
- Molecule 165: STAPLE STRAND



- Molecule 166: STAPLE STRAND

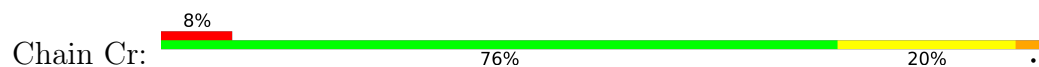


- Molecule 167: STAPLE STRAND

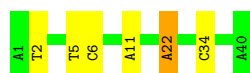
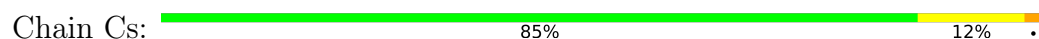




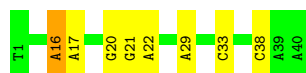
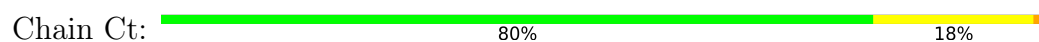
- Molecule 168: STAPLE STRAND



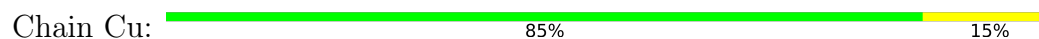
- Molecule 169: STAPLE STRAND



- Molecule 170: STAPLE STRAND



- Molecule 171: STAPLE STRAND



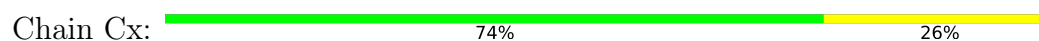
- Molecule 172: STAPLE STRAND



- Molecule 173: STAPLE STRAND

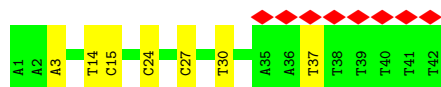
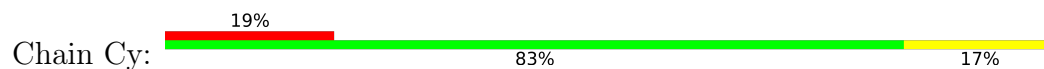


- Molecule 174: STAPLE STRAND





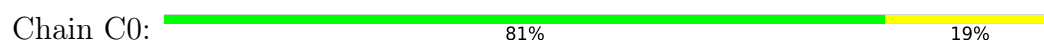
• Molecule 175: STAPLE STRAND



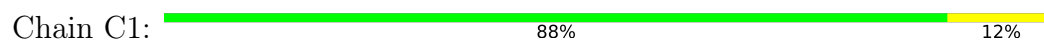
• Molecule 176: STAPLE STRAND



• Molecule 177: STAPLE STRAND



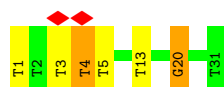
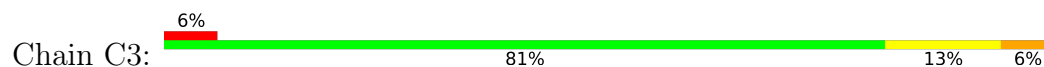
• Molecule 178: STAPLE STRAND



• Molecule 179: STAPLE STRAND



• Molecule 180: STAPLE STRAND



• Molecule 181: STAPLE STRAND





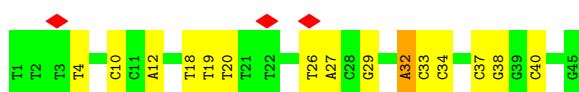
- Molecule 182: STAPLE STRAND

Chain C5: 78% 20% .



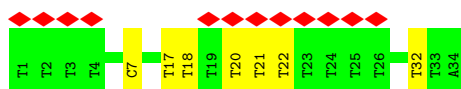
- Molecule 183: STAPLE STRAND

Chain C6: 7% 67% 31% .



- Molecule 184: STAPLE STRAND

Chain C7: 35% 79% 21% .



- Molecule 185: STAPLE STRAND

Chain C8: 85% 12% .



- Molecule 186: STAPLE STRAND

Chain C9: 79% 19% .



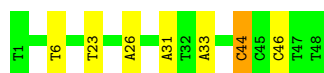
- Molecule 187: STAPLE STRAND

Chain DA: 82% 12% 5% .

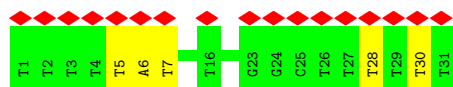
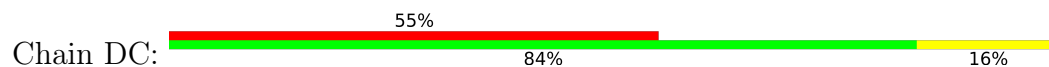


- Molecule 188: STAPLE STRAND

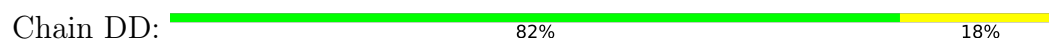
Chain DB: 85% 12% .



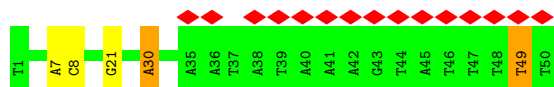
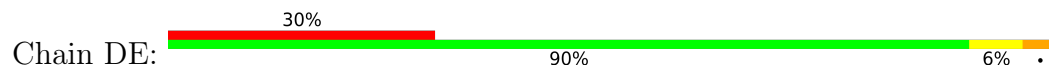
• Molecule 189: STAPLE STRAND



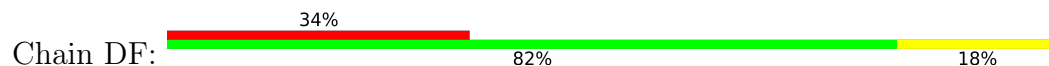
• Molecule 190: STAPLE STRAND



• Molecule 191: STAPLE STRAND



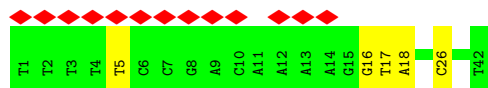
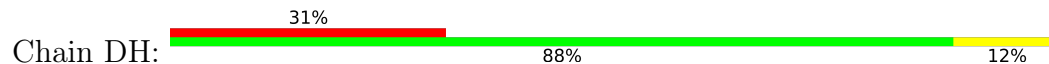
• Molecule 192: STAPLE STRAND



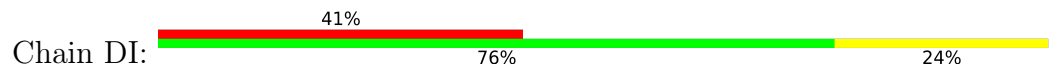
• Molecule 193: STAPLE STRAND

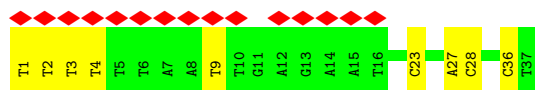


• Molecule 194: STAPLE STRAND

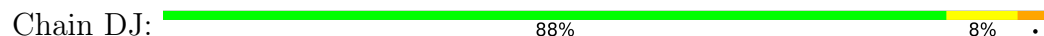


• Molecule 195: STAPLE STRAND

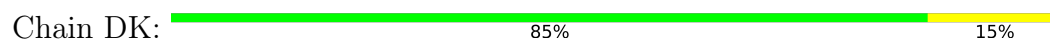




- Molecule 196: STAPLE STRAND



- Molecule 197: STAPLE STRAND



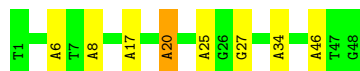
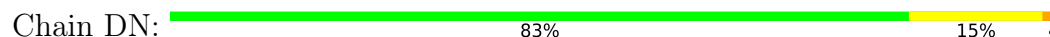
- Molecule 198: STAPLE STRAND



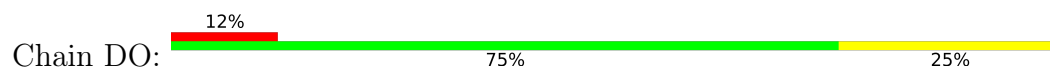
- Molecule 199: STAPLE STRAND



- Molecule 200: STAPLE STRAND



- Molecule 201: STAPLE STRAND



- Molecule 202: STAPLE STRAND





- Molecule 203: STAPLE STRAND



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	281527	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.627	Depositor
Minimum map value	-0.339	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.07	Depositor
Map size (Å)	671.61597, 671.61597, 671.61597	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.8655999, 1.8655999, 1.8655999	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	AA	0.70	0/166071	1.03	471/256351 (0.2%)
2	AB	0.67	0/919	0.99	1/1417 (0.1%)
3	AC	0.66	0/704	1.05	2/1085 (0.2%)
4	AD	0.68	0/908	1.03	0/1399
5	AE	0.70	0/1095	1.06	5/1688 (0.3%)
6	AF	0.63	0/702	0.92	0/1083
7	AG	0.69	0/910	1.04	2/1403 (0.1%)
8	AH	0.67	0/712	0.97	2/1100 (0.2%)
9	AI	0.68	0/1019	1.09	4/1569 (0.3%)
10	AJ	0.69	0/929	0.95	2/1434 (0.1%)
11	AK	0.70	0/1013	1.12	5/1561 (0.3%)
12	AL	0.67	0/818	0.97	2/1262 (0.2%)
13	AM	0.65	0/1038	0.93	1/1602 (0.1%)
14	AN	0.68	0/919	1.01	1/1417 (0.1%)
15	AO	0.69	0/918	1.00	1/1415 (0.1%)
16	AP	0.65	0/825	0.98	1/1272 (0.1%)
17	AQ	0.68	0/1020	1.01	2/1571 (0.1%)
18	AR	0.66	0/761	1.05	3/1174 (0.3%)
19	AS	0.62	0/819	0.95	1/1264 (0.1%)
20	AT	0.65	0/783	0.93	1/1209 (0.1%)
21	AU	0.66	0/752	1.04	2/1158 (0.2%)
22	AV	0.68	0/783	1.06	2/1208 (0.2%)
23	AW	0.69	0/746	0.88	1/1149 (0.1%)
24	AX	0.70	0/976	0.98	1/1506 (0.1%)
25	AY	0.67	0/911	1.09	4/1403 (0.3%)
26	AZ	0.68	0/1116	0.98	3/1724 (0.2%)
27	Aa	0.71	0/912	1.10	3/1406 (0.2%)
28	Ab	0.65	0/830	1.03	2/1280 (0.2%)
29	Ac	0.70	0/1161	1.01	2/1793 (0.1%)
30	Ad	0.70	0/940	1.00	1/1451 (0.1%)
31	Ae	0.66	0/829	1.02	0/1278
32	Af	0.67	0/1103	0.96	2/1699 (0.1%)
33	Ag	0.69	0/984	0.96	1/1518 (0.1%)
34	Ah	0.67	0/832	0.95	0/1281

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	Ai	0.66	0/846	0.97	1/1305 (0.1%)
36	Aj	0.68	0/718	0.98	0/1110
37	Ak	0.70	0/915	1.13	5/1410 (0.4%)
38	Al	0.66	0/964	0.98	1/1485 (0.1%)
39	Am	0.68	0/904	0.98	1/1392 (0.1%)
40	An	0.66	0/906	1.02	1/1396 (0.1%)
41	Ao	0.68	0/729	1.10	5/1123 (0.4%)
42	Ap	0.68	0/863	0.91	0/1332
43	Aq	0.72	0/927	1.01	2/1430 (0.1%)
44	Ar	0.71	0/941	1.10	5/1454 (0.3%)
45	As	0.67	0/688	1.01	1/1058 (0.1%)
46	At	0.73	0/743	1.02	1/1146 (0.1%)
47	Au	0.71	0/752	0.95	1/1160 (0.1%)
48	Av	0.69	0/906	1.06	2/1394 (0.1%)
49	Aw	0.71	0/908	1.05	1/1400 (0.1%)
50	Ax	0.68	0/736	1.10	6/1134 (0.5%)
51	Ay	0.71	0/927	1.08	1/1429 (0.1%)
52	Az	0.71	0/925	1.05	5/1426 (0.4%)
53	A0	0.68	0/1107	0.96	4/1706 (0.2%)
54	A1	0.67	0/695	0.98	0/1071
55	A2	0.67	0/937	1.03	5/1440 (0.3%)
56	A3	0.67	0/733	1.03	3/1128 (0.3%)
57	A4	0.68	0/1106	0.96	2/1705 (0.1%)
58	A5	0.70	0/924	1.08	6/1423 (0.4%)
59	A6	0.67	0/933	0.94	1/1441 (0.1%)
60	A7	0.67	0/950	1.03	3/1464 (0.2%)
61	A8	0.67	0/830	1.06	3/1279 (0.2%)
62	A9	0.70	0/917	1.02	2/1415 (0.1%)
63	BA	0.67	0/737	0.90	0/1136
64	BB	0.69	0/1042	0.96	0/1609
65	BC	0.67	0/841	1.07	4/1298 (0.3%)
66	BD	0.69	0/717	1.00	3/1102 (0.3%)
67	BE	0.69	0/819	0.98	1/1263 (0.1%)
68	BF	0.72	0/956	1.09	3/1474 (0.2%)
69	BG	0.68	0/848	0.99	0/1311
70	BH	0.70	0/907	0.98	2/1397 (0.1%)
71	BI	0.71	0/717	1.04	2/1102 (0.2%)
72	BJ	0.73	0/912	1.06	3/1405 (0.2%)
73	BK	0.71	0/734	1.14	4/1131 (0.4%)
74	BL	0.71	0/839	1.07	6/1293 (0.5%)
75	BM	0.72	0/740	1.04	1/1143 (0.1%)
76	BN	0.72	0/735	1.03	2/1134 (0.2%)
77	BO	0.70	0/919	1.00	2/1417 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	BP	0.70	0/1086	1.02	1/1670 (0.1%)
79	BQ	0.71	0/744	1.02	1/1147 (0.1%)
80	BR	0.67	0/911	1.02	3/1402 (0.2%)
81	BS	0.68	0/1105	1.02	4/1704 (0.2%)
82	BT	0.71	0/918	0.99	1/1414 (0.1%)
83	BU	0.68	0/953	1.08	4/1468 (0.3%)
84	BV	0.70	0/1108	1.04	2/1711 (0.1%)
85	BW	0.66	0/1063	1.05	2/1638 (0.1%)
86	BX	0.66	0/899	0.95	1/1383 (0.1%)
87	BY	0.69	0/899	1.04	2/1384 (0.1%)
88	BZ	0.69	0/918	1.02	3/1415 (0.2%)
89	Ba	0.72	0/900	1.05	4/1383 (0.3%)
90	Bb	0.67	0/916	0.98	2/1410 (0.1%)
91	Bc	0.70	0/738	0.99	2/1137 (0.2%)
92	Bd	0.66	0/903	0.95	2/1391 (0.1%)
93	Be	0.71	0/921	1.13	5/1418 (0.4%)
94	Bf	0.67	0/1004	0.94	0/1551
95	Bg	0.72	0/745	1.04	0/1152
96	Bh	0.76	0/943	1.04	1/1457 (0.1%)
97	Bi	0.67	0/922	0.99	1/1425 (0.1%)
98	Bj	0.69	0/1112	1.01	3/1716 (0.2%)
99	Bk	0.67	0/675	0.94	1/1041 (0.1%)
100	Bl	0.70	0/962	0.96	1/1484 (0.1%)
101	Bm	0.73	0/909	1.01	0/1399
102	Bn	0.73	0/918	1.04	1/1414 (0.1%)
103	Bo	0.72	0/735	1.02	1/1133 (0.1%)
104	Bp	0.68	0/901	0.93	0/1386
105	Bq	0.66	0/1090	1.00	2/1682 (0.1%)
106	Br	0.76	0/921	1.11	8/1420 (0.6%)
107	Bs	0.66	0/702	1.04	1/1082 (0.1%)
108	Bt	0.74	0/1105	1.04	3/1703 (0.2%)
109	Bu	0.69	0/906	1.04	5/1392 (0.4%)
110	Bv	0.69	0/1093	1.04	2/1684 (0.1%)
111	Bw	0.72	0/926	1.02	0/1429
112	Bx	0.72	0/918	1.01	1/1417 (0.1%)
113	By	0.67	0/905	0.93	0/1394
114	Bz	0.69	0/919	1.04	3/1417 (0.2%)
115	B0	0.69	0/897	1.07	2/1383 (0.1%)
116	B1	0.66	0/952	1.01	2/1469 (0.1%)
117	B2	0.69	0/698	1.03	3/1076 (0.3%)
118	B3	0.68	0/911	0.99	2/1403 (0.1%)
119	B4	0.66	0/1112	0.93	2/1716 (0.1%)
120	B5	0.68	0/1145	0.97	2/1767 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
121	B6	0.65	0/709	0.92	1/1094 (0.1%)
122	B7	0.62	0/658	0.93	1/1014 (0.1%)
123	B8	0.69	0/921	1.05	6/1419 (0.4%)
124	B9	0.75	0/931	1.06	1/1438 (0.1%)
125	CA	0.72	0/905	1.08	3/1392 (0.2%)
126	CB	0.70	0/785	1.02	3/1211 (0.2%)
127	CC	0.66	0/911	0.98	0/1404
128	CD	0.71	0/920	1.04	3/1416 (0.2%)
129	CE	0.66	0/787	0.92	1/1213 (0.1%)
130	CF	0.66	0/725	0.93	0/1119
131	CG	0.75	0/927	1.14	4/1429 (0.3%)
132	CH	0.68	0/910	0.93	0/1403
133	CI	0.71	0/927	1.00	0/1429
134	CJ	0.71	0/915	1.12	2/1409 (0.1%)
135	CK	0.67	0/929	0.92	1/1431 (0.1%)
136	CL	0.68	0/999	1.04	5/1539 (0.3%)
137	CM	0.65	0/832	0.92	1/1281 (0.1%)
138	CN	0.68	0/901	1.05	1/1388 (0.1%)
139	CO	0.74	0/898	1.07	2/1382 (0.1%)
140	CP	0.67	0/1113	0.95	2/1715 (0.1%)
141	CQ	0.67	0/769	0.96	0/1182
142	CR	0.70	0/924	1.08	2/1423 (0.1%)
143	CS	0.70	0/905	1.02	2/1392 (0.1%)
144	CT	0.68	0/1077	1.02	3/1657 (0.2%)
145	CU	0.71	0/1100	1.06	3/1695 (0.2%)
146	CV	0.66	0/771	0.99	1/1189 (0.1%)
147	CW	0.69	0/601	1.01	1/927 (0.1%)
148	CX	0.66	0/1012	0.91	1/1561 (0.1%)
149	CY	0.72	0/758	0.97	0/1171
150	CZ	0.69	0/599	1.06	1/924 (0.1%)
151	Ca	0.73	0/928	1.04	4/1431 (0.3%)
152	Cb	0.69	0/772	1.07	2/1189 (0.2%)
153	Cc	0.65	0/777	0.92	0/1197
154	Cd	0.73	0/920	1.10	4/1417 (0.3%)
155	Ce	0.70	0/924	1.08	4/1425 (0.3%)
156	Cf	0.77	0/931	1.08	2/1436 (0.1%)
157	Cg	0.71	0/1116	0.98	2/1722 (0.1%)
158	Ch	0.71	0/1103	1.04	3/1701 (0.2%)
159	Ci	0.67	0/1055	1.10	7/1628 (0.4%)
160	Cj	0.68	0/1100	0.98	2/1696 (0.1%)
161	Ck	0.65	0/1006	0.95	1/1552 (0.1%)
162	Cl	0.68	0/906	0.98	1/1394 (0.1%)
163	Cm	0.69	0/1116	0.95	0/1721

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
164	Cn	0.68	0/715	1.04	3/1098 (0.3%)
165	Co	0.65	0/990	0.93	1/1526 (0.1%)
166	Cp	0.69	0/747	0.93	1/1154 (0.1%)
167	Cq	0.69	0/911	1.04	1/1403 (0.1%)
168	Cr	0.70	0/1147	1.01	4/1768 (0.2%)
169	Cs	0.65	0/910	0.96	2/1401 (0.1%)
170	Ct	0.81	0/919	1.17	6/1417 (0.4%)
171	Cu	0.68	0/922	1.00	2/1420 (0.1%)
172	Cv	0.71	0/937	0.94	0/1448
173	Cw	0.68	0/958	1.04	1/1477 (0.1%)
174	Cx	0.70	0/1141	1.10	5/1759 (0.3%)
175	Cy	0.66	0/956	0.98	2/1473 (0.1%)
176	Cz	0.68	0/918	1.01	3/1415 (0.2%)
177	C0	0.68	0/1113	0.96	2/1718 (0.1%)
178	C1	0.74	0/935	0.99	0/1444
179	C2	0.69	0/926	0.99	0/1429
180	C3	0.66	0/695	1.11	4/1072 (0.4%)
181	C4	0.70	0/927	1.02	3/1430 (0.2%)
182	C5	0.69	0/928	0.94	2/1433 (0.1%)
183	C6	0.68	0/1014	1.12	7/1563 (0.4%)
184	C7	0.67	0/758	1.09	2/1169 (0.2%)
185	C8	0.67	0/1102	1.01	2/1697 (0.1%)
186	C9	0.69	0/1109	1.02	4/1708 (0.2%)
187	DA	0.68	0/913	1.01	3/1406 (0.2%)
188	DB	0.69	0/1092	0.97	2/1682 (0.1%)
189	DC	0.66	0/704	0.97	2/1087 (0.2%)
190	DD	0.71	0/920	1.02	1/1420 (0.1%)
191	DE	0.67	0/1150	0.98	3/1773 (0.2%)
192	DF	0.64	0/1150	0.89	0/1773
193	DG	0.66	0/923	0.91	1/1423 (0.1%)
194	DH	0.64	0/952	0.90	1/1465 (0.1%)
195	DI	0.68	0/834	1.01	3/1284 (0.2%)
196	DJ	0.64	0/1109	0.89	3/1709 (0.2%)
197	DK	0.67	0/916	0.96	1/1411 (0.1%)
198	DL	0.68	0/726	1.07	3/1118 (0.3%)
199	DM	0.66	0/1114	0.90	0/1717
200	DN	0.67	0/1109	0.95	2/1711 (0.1%)
201	DO	0.66	0/533	1.03	1/821 (0.1%)
202	DP	0.68	0/737	1.02	2/1134 (0.2%)
203	DQ	0.70	0/930	0.95	1/1435 (0.1%)
All	All	0.69	0/348922	1.02	887/538215 (0.2%)

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	11	1015
2	AB	0	9
3	AC	0	5
4	AD	0	7
5	AE	0	7
6	AF	0	2
7	AG	0	4
8	AH	0	4
9	AI	0	5
10	AJ	0	8
11	AK	0	6
12	AL	0	6
13	AM	0	3
14	AN	0	6
15	AO	0	5
16	AP	0	5
17	AQ	0	6
18	AR	0	7
19	AS	0	5
20	AT	0	4
21	AU	0	3
22	AV	0	8
23	AW	0	2
24	AX	0	8
25	AY	0	5
26	AZ	0	12
27	Aa	0	8
28	Ab	0	4
29	Ac	0	6
30	Ad	0	6
31	Ae	0	6
32	Af	0	5
33	Ag	0	6
34	Ah	0	6
35	Ai	0	2
36	Aj	0	2
37	Ak	0	8
38	Al	0	7
39	Am	0	3
40	An	0	4

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Mol	Chain	#Chirality outliers	#Planarity outliers
41	Ao	0	3
42	Ap	0	5
43	Aq	0	1
44	Ar	0	7
45	As	0	3
46	At	0	8
47	Au	0	3
48	Av	0	2
49	Aw	0	3
50	Ax	0	4
51	Ay	0	7
52	Az	0	7
53	A0	0	4
54	A1	0	8
55	A2	0	3
56	A3	0	4
57	A4	0	3
58	A5	0	10
59	A6	0	7
60	A7	0	6
61	A8	0	10
62	A9	0	4
63	BA	0	2
64	BB	0	6
65	BC	0	5
66	BD	0	6
67	BE	0	6
68	BF	0	4
69	BG	0	3
70	BH	0	3
71	BI	0	6
72	BJ	0	7
73	BK	0	2
74	BL	0	6
75	BM	0	4
76	BN	0	3
77	BO	0	1
78	BP	0	2
79	BQ	0	3
80	BR	0	5
81	BS	0	2
82	BT	0	8

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Mol	Chain	#Chirality outliers	#Planarity outliers
83	BU	0	8
84	BV	0	6
85	BW	0	10
86	BX	0	2
87	BY	0	7
88	BZ	0	3
89	Ba	0	6
90	Bb	0	7
91	Bc	0	5
92	Bd	0	10
93	Be	0	2
94	Bf	0	9
95	Bg	0	7
96	Bh	0	7
97	Bi	0	7
98	Bj	0	7
99	Bk	0	2
100	Bl	0	3
101	Bm	0	3
102	Bn	0	7
103	Bo	0	7
104	Bp	0	6
105	Bq	0	8
106	Br	0	10
107	Bs	0	2
108	Bt	0	6
109	Bu	0	5
110	Bv	0	2
111	Bw	0	6
112	Bx	0	2
113	By	0	3
114	Bz	0	7
115	B0	0	6
116	B1	0	6
117	B2	0	2
118	B3	0	3
119	B4	0	5
120	B5	0	4
121	B6	0	6
122	B7	0	6
123	B8	0	4
124	B9	0	7

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Mol	Chain	#Chirality outliers	#Planarity outliers
125	CA	0	9
126	CB	0	2
127	CC	0	5
128	CD	0	5
129	CE	0	3
130	CF	0	3
131	CG	0	6
132	CH	0	4
133	CI	0	4
134	CJ	0	7
135	CK	0	8
136	CL	0	6
137	CM	0	4
138	CN	0	4
139	CO	0	7
140	CP	0	6
141	CQ	0	4
142	CR	0	6
143	CS	0	4
144	CT	0	7
145	CU	0	6
146	CV	0	6
147	CW	0	4
148	CX	0	6
149	CY	0	6
150	CZ	0	5
151	Ca	0	6
152	Cb	0	5
153	Cc	0	2
154	Cd	0	6
155	Ce	0	6
156	Cf	0	6
157	Cg	0	10
158	Ch	0	11
159	Ci	0	4
160	Cj	0	9
161	Ck	0	4
162	Cl	0	5
163	Cm	0	7
164	Cn	0	1
165	Co	0	6
166	Cp	0	4

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Mol	Chain	#Chirality outliers	#Planarity outliers
167	Cq	0	6
168	Cr	0	10
169	Cs	0	5
170	Ct	0	5
171	Cu	0	4
172	Cv	0	4
173	Cw	0	2
174	Cx	0	9
175	Cy	0	5
176	Cz	0	2
177	C0	0	7
178	C1	0	5
179	C2	0	3
180	C3	0	4
181	C4	0	2
182	C5	0	8
183	C6	0	10
184	C7	0	5
185	C8	0	6
186	C9	0	7
187	DA	0	6
188	DB	0	6
189	DC	0	4
190	DD	0	6
191	DE	0	4
192	DF	0	9
193	DG	0	3
194	DH	0	4
195	DI	0	6
196	DJ	0	5
197	DK	0	5
198	DL	0	6
199	DM	0	6
200	DN	0	7
201	DO	0	5
202	DP	0	1
203	DQ	0	3
All	All	11	2081

There are no bond length outliers.

The worst 5 of 887 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
186	C9	34	DG	P-O3'-C3'	12.67	139.21	120.20
1	AA	3505	DG	P-O3'-C3'	12.33	138.69	120.20
198	DL	30	DC	P-O3'-C3'	12.31	138.67	120.20
97	Bi	12	DT	P-O3'-C3'	11.89	138.03	120.20
1	AA	3322	DT	P-O3'-C3'	11.85	137.98	120.20

5 of 11 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	AA	627	DG	C3'
1	AA	767	DT	C3'
1	AA	885	DA	C3'
1	AA	1025	DA	C3'
1	AA	1143	DG	C3'

5 of 2081 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	AA	1	DA	Sidechain
1	AA	11	DC	Sidechain
1	AA	17	DG	Sidechain
1	AA	22	DA	Sidechain
1	AA	9	DT	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	148273	0	82149	0	0
2	AB	819	0	454	0	0
3	AC	630	0	357	0	0
4	AD	812	0	458	0	0
5	AE	978	0	545	0	0
6	AF	630	0	361	0	0
7	AG	814	0	458	0	0
8	AH	637	0	358	0	0
9	AI	911	0	512	0	0
10	AJ	826	0	450	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	AK	909	0	520	0	0
12	AL	733	0	415	0	0
13	AM	925	0	513	0	0
14	AN	819	0	455	0	0
15	AO	818	0	452	0	0
16	AP	736	0	411	0	0
17	AQ	912	0	513	0	0
18	AR	686	0	400	0	0
19	AS	734	0	420	0	0
20	AT	699	0	393	0	0
21	AU	679	0	400	0	0
22	AV	698	0	388	0	0
23	AW	660	0	357	0	0
24	AX	867	0	472	0	0
25	AY	813	0	456	0	0
26	AZ	993	0	544	0	0
27	Aa	815	0	456	0	0
28	Ab	747	0	433	0	0
29	Ac	1033	0	567	0	0
30	Ad	832	0	450	0	0
31	Ae	746	0	431	0	0
32	Af	981	0	540	0	0
33	Ag	871	0	471	0	0
34	Ah	746	0	427	0	0
35	Ai	756	0	424	0	0
36	Aj	641	0	358	0	0
37	Ak	816	0	454	0	0
38	Al	858	0	479	0	0
39	Am	809	0	456	0	0
40	An	811	0	461	0	0
41	Ao	651	0	365	0	0
42	Ap	766	0	417	0	0
43	Aq	824	0	449	0	0
44	Ar	834	0	449	0	0
45	As	619	0	358	0	0
46	At	660	0	361	0	0
47	Au	665	0	356	0	0
48	Av	809	0	453	0	0
49	Aw	813	0	457	0	0
50	Ax	655	0	363	0	0
51	Ay	823	0	448	0	0
52	Az	822	0	448	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
53	A0	984	0	536	0	0
54	A1	625	0	358	0	0
55	A2	840	0	475	0	0
56	A3	652	0	360	0	0
57	A4	984	0	540	0	0
58	A5	820	0	449	0	0
59	A6	829	0	452	0	0
60	A7	851	0	481	0	0
61	A8	746	0	430	0	0
62	A9	819	0	454	0	0
63	BA	656	0	361	0	0
64	BB	928	0	508	0	0
65	BC	754	0	427	0	0
66	BD	642	0	361	0	0
67	BE	733	0	413	0	0
68	BF	855	0	477	0	0
69	BG	760	0	431	0	0
70	BH	811	0	454	0	0
71	BI	642	0	364	0	0
72	BJ	814	0	454	0	0
73	BK	654	0	364	0	0
74	BL	751	0	422	0	0
75	BM	660	0	364	0	0
76	BN	656	0	363	0	0
77	BO	819	0	451	0	0
78	BP	969	0	538	0	0
79	BQ	660	0	359	0	0
80	BR	812	0	452	0	0
81	BS	984	0	545	0	0
82	BT	817	0	450	0	0
83	BU	852	0	478	0	0
84	BV	988	0	546	0	0
85	BW	960	0	562	0	0
86	BX	805	0	458	0	0
87	BY	806	0	458	0	0
88	BZ	818	0	452	0	0
89	Ba	804	0	449	0	0
90	Bb	815	0	453	0	0
91	Bc	656	0	359	0	0
92	Bd	809	0	458	0	0
93	Be	818	0	447	0	0
94	Bf	900	0	508	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
95	Bg	664	0	365	0	0
96	Bh	835	0	445	0	0
97	Bi	824	0	459	0	0
98	Bj	997	0	562	0	0
99	Bk	599	0	326	0	0
100	Bl	859	0	476	0	0
101	Bm	811	0	449	0	0
102	Bn	817	0	447	0	0
103	Bo	655	0	363	0	0
104	Bp	806	0	453	0	0
105	Bq	977	0	554	0	0
106	Br	820	0	447	0	0
107	Bs	629	0	357	0	0
108	Bt	983	0	536	0	0
109	Bu	807	0	448	0	0
110	Bv	976	0	544	0	0
111	Bw	824	0	455	0	0
112	Bx	820	0	454	0	0
113	By	810	0	456	0	0
114	Bz	819	0	452	0	0
115	B0	807	0	463	0	0
116	B1	854	0	486	0	0
117	B2	627	0	357	0	0
118	B3	813	0	451	0	0
119	B4	989	0	541	0	0
120	B5	1023	0	569	0	0
121	B6	634	0	358	0	0
122	B7	589	0	335	0	0
123	B8	819	0	449	0	0
124	B9	828	0	450	0	0
125	CA	808	0	449	0	0
126	CB	699	0	384	0	0
127	CC	814	0	457	0	0
128	CD	817	0	445	0	0
129	CE	699	0	384	0	0
130	CF	651	0	374	0	0
131	CG	823	0	449	0	0
132	CH	814	0	456	0	0
133	CI	823	0	447	0	0
134	CJ	815	0	452	0	0
135	CK	823	0	449	0	0
136	CL	893	0	500	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
137	CM	746	0	424	0	0
138	CN	808	0	460	0	0
139	CO	805	0	453	0	0
140	CP	987	0	539	0	0
141	CQ	686	0	383	0	0
142	CR	820	0	449	0	0
143	CS	808	0	453	0	0
144	CT	965	0	549	0	0
145	CU	980	0	542	0	0
146	CV	691	0	393	0	0
147	CW	535	0	296	0	0
148	CX	902	0	501	0	0
149	CY	670	0	357	0	0
150	CZ	534	0	296	0	0
151	Ca	824	0	450	0	0
152	Cb	690	0	388	0	0
153	Cc	693	0	388	0	0
154	Cd	818	0	448	0	0
155	Ce	822	0	455	0	0
156	Cf	826	0	448	0	0
157	Cg	991	0	538	0	0
158	Ch	983	0	545	0	0
159	Ci	942	0	526	0	0
160	Cj	981	0	544	0	0
161	Ck	899	0	507	0	0
162	Cl	809	0	452	0	0
163	Cm	990	0	539	0	0
164	Cn	640	0	361	0	0
165	Co	889	0	510	0	0
166	Cp	664	0	365	0	0
167	Cq	813	0	457	0	0
168	Cr	1022	0	567	0	0
169	Cs	812	0	455	0	0
170	Ct	819	0	455	0	0
171	Cu	819	0	450	0	0
172	Cv	832	0	454	0	0
173	Cw	856	0	480	0	0
174	Cx	1019	0	567	0	0
175	Cy	854	0	481	0	0
176	Cz	818	0	452	0	0
177	C0	990	0	544	0	0
178	C1	830	0	449	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
179	C2	824	0	452	0	0
180	C3	626	0	363	0	0
181	C4	824	0	451	0	0
182	C5	826	0	453	0	0
183	C6	910	0	519	0	0
184	C7	684	0	400	0	0
185	C8	980	0	539	0	0
186	C9	984	0	535	0	0
187	DA	814	0	450	0	0
188	DB	975	0	545	0	0
189	DC	632	0	362	0	0
190	DD	821	0	459	0	0
191	DE	1024	0	568	0	0
192	DF	1024	0	570	0	0
193	DG	821	0	452	0	0
194	DH	850	0	478	0	0
195	DI	747	0	424	0	0
196	DJ	985	0	541	0	0
197	DK	816	0	454	0	0
198	DL	649	0	365	0	0
199	DM	988	0	540	0	0
200	DN	987	0	543	0	0
201	DO	481	0	284	0	0
202	DP	654	0	358	0	0
203	DQ	826	0	449	0	0
All	All	311400	0	172940	0	0

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

There are no clashes within the asymmetric unit.

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein molecules in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein molecules in this entry.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11881. These allow visual inspection of the internal detail of the map and identification of artifacts.

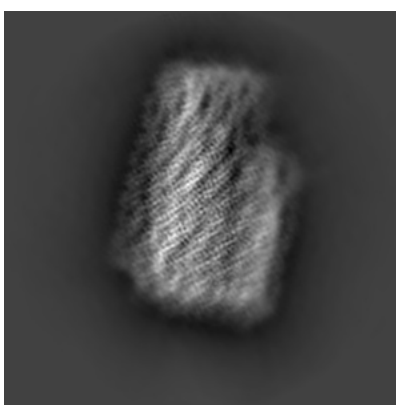
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

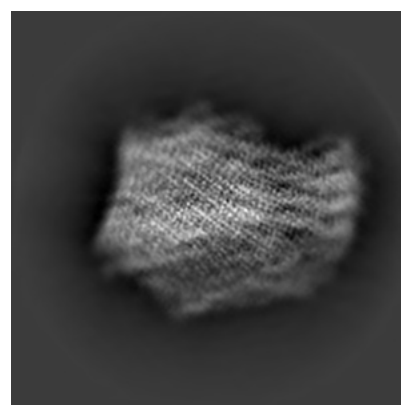
6.1.1 Primary map



X



Y

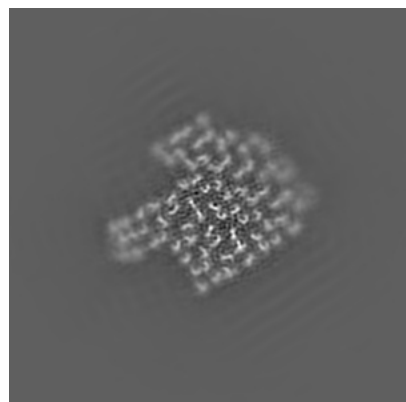


Z

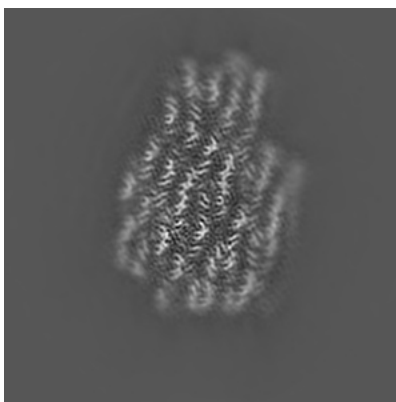
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

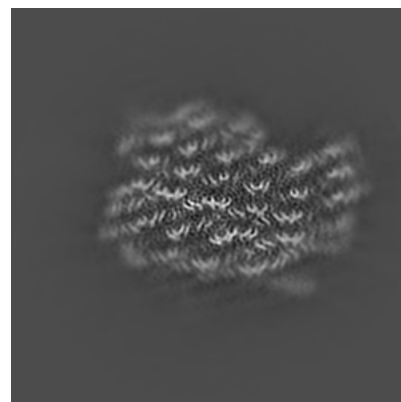
6.2.1 Primary map



X Index: 180



Y Index: 180

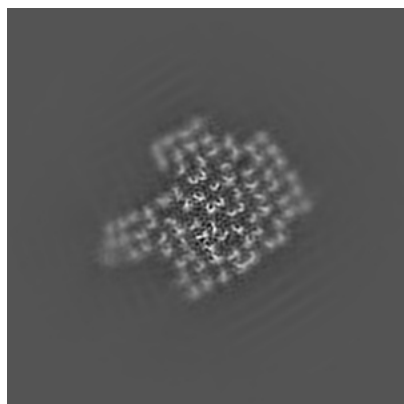


Z Index: 180

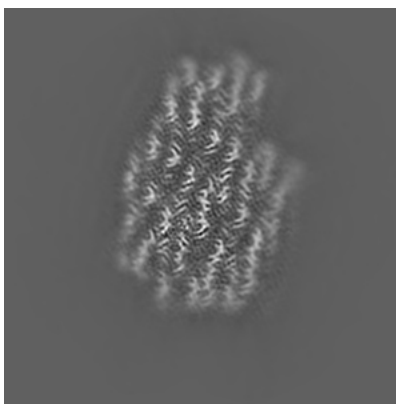
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

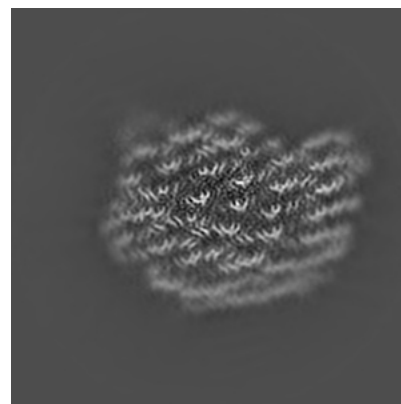
6.3.1 Primary map



X Index: 159



Y Index: 183

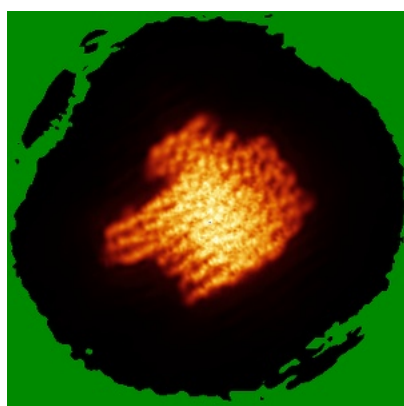


Z Index: 166

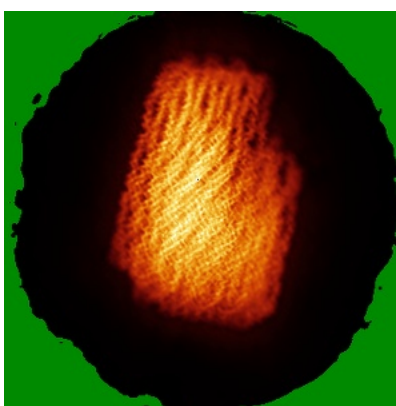
The images above show the largest variance slices of the map in three orthogonal directions.

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

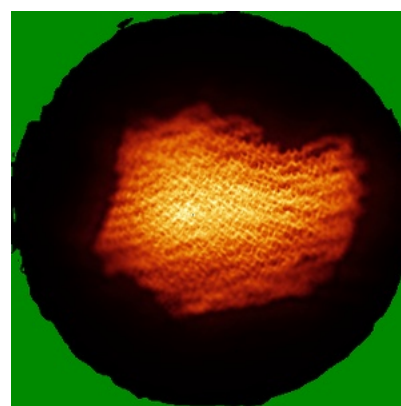
6.4.1 Primary map



X



Y

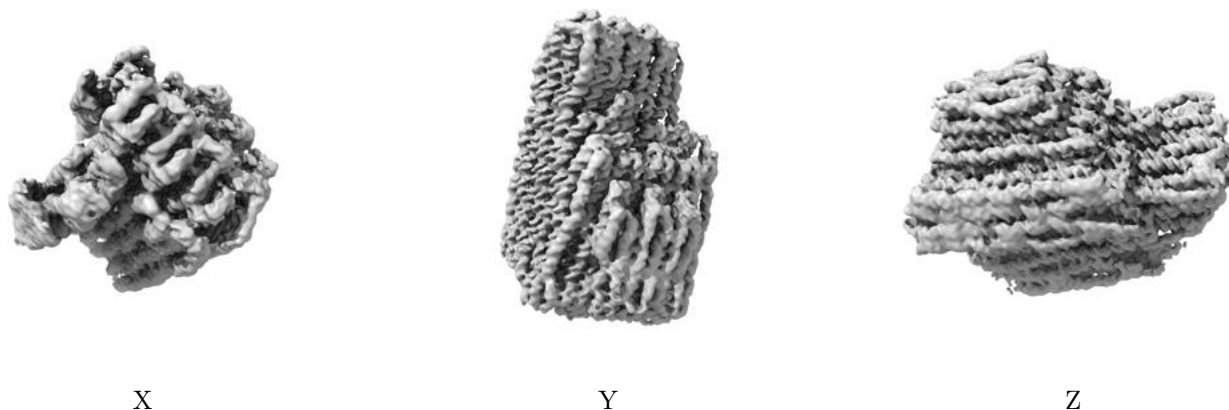


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.07. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

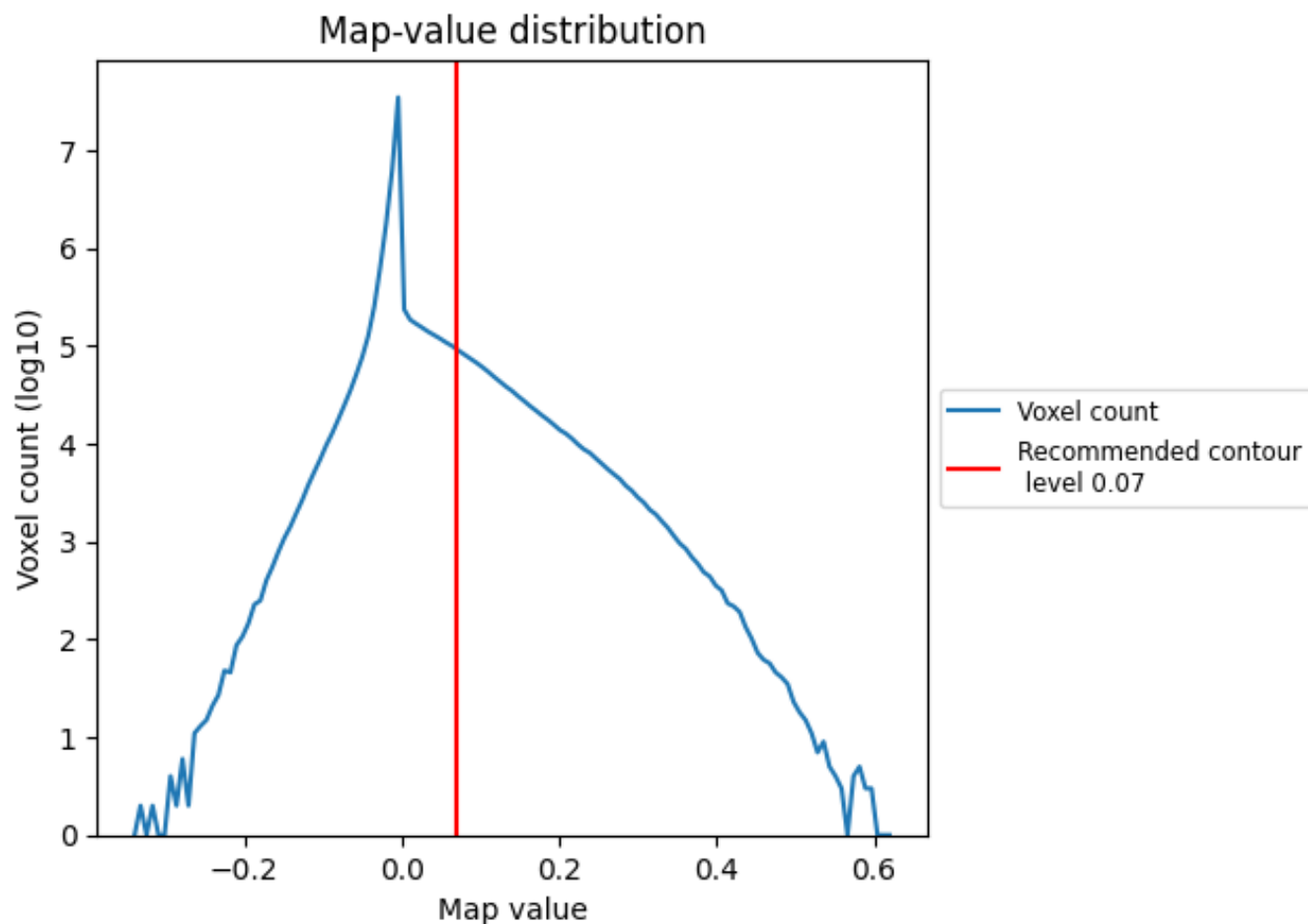
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

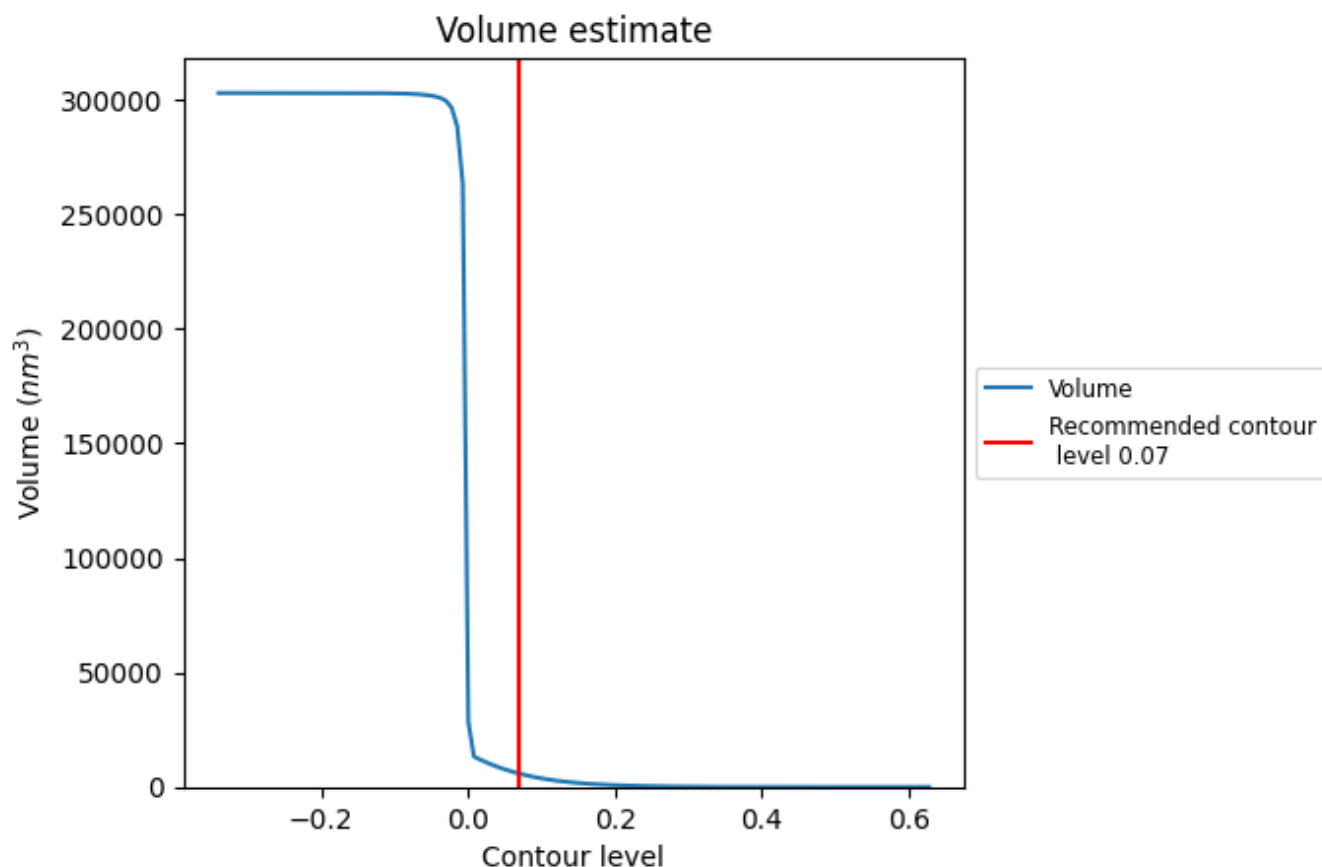
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

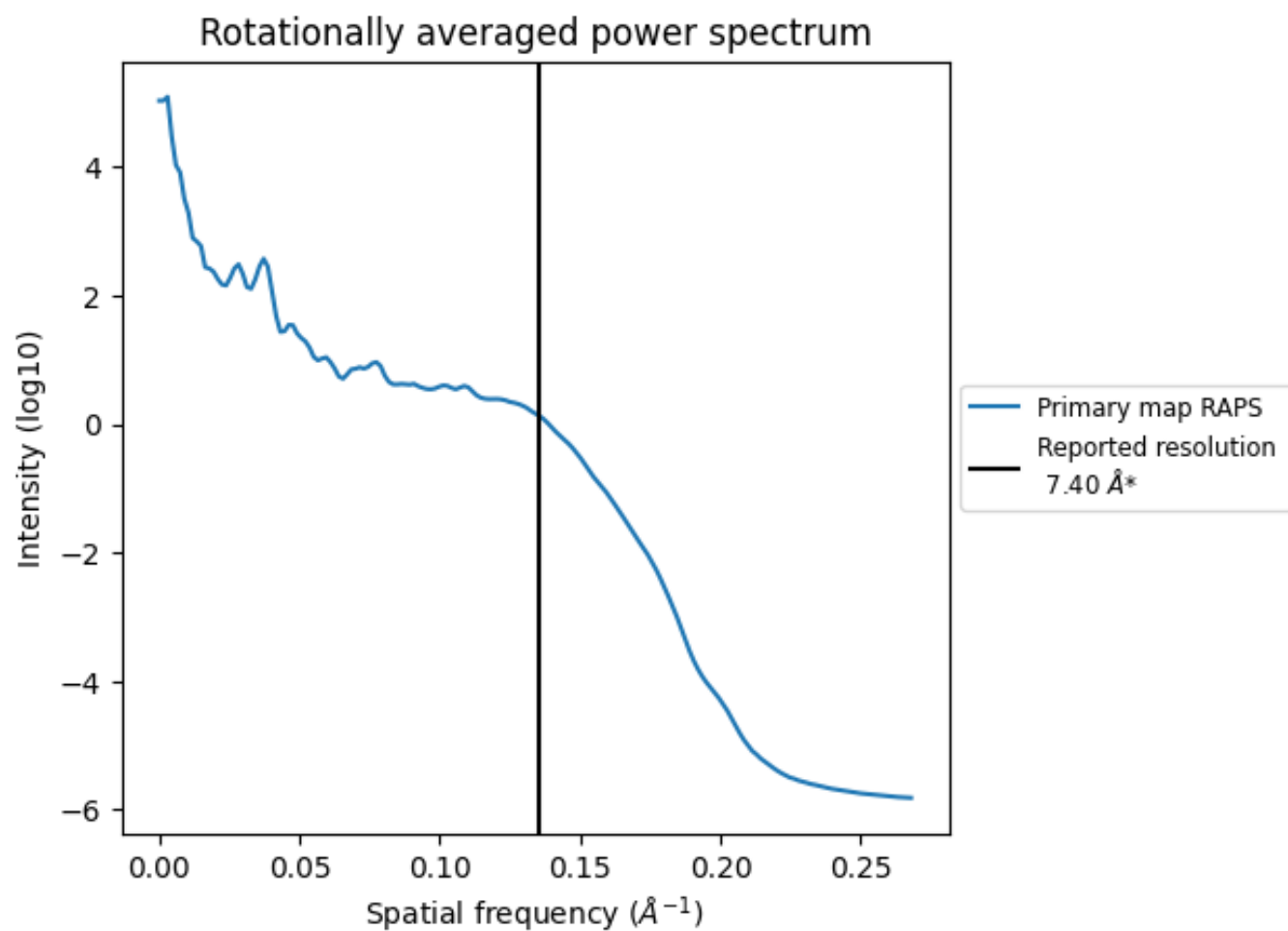
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5806 nm³; this corresponds to an approximate mass of 5245 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 ⓘ

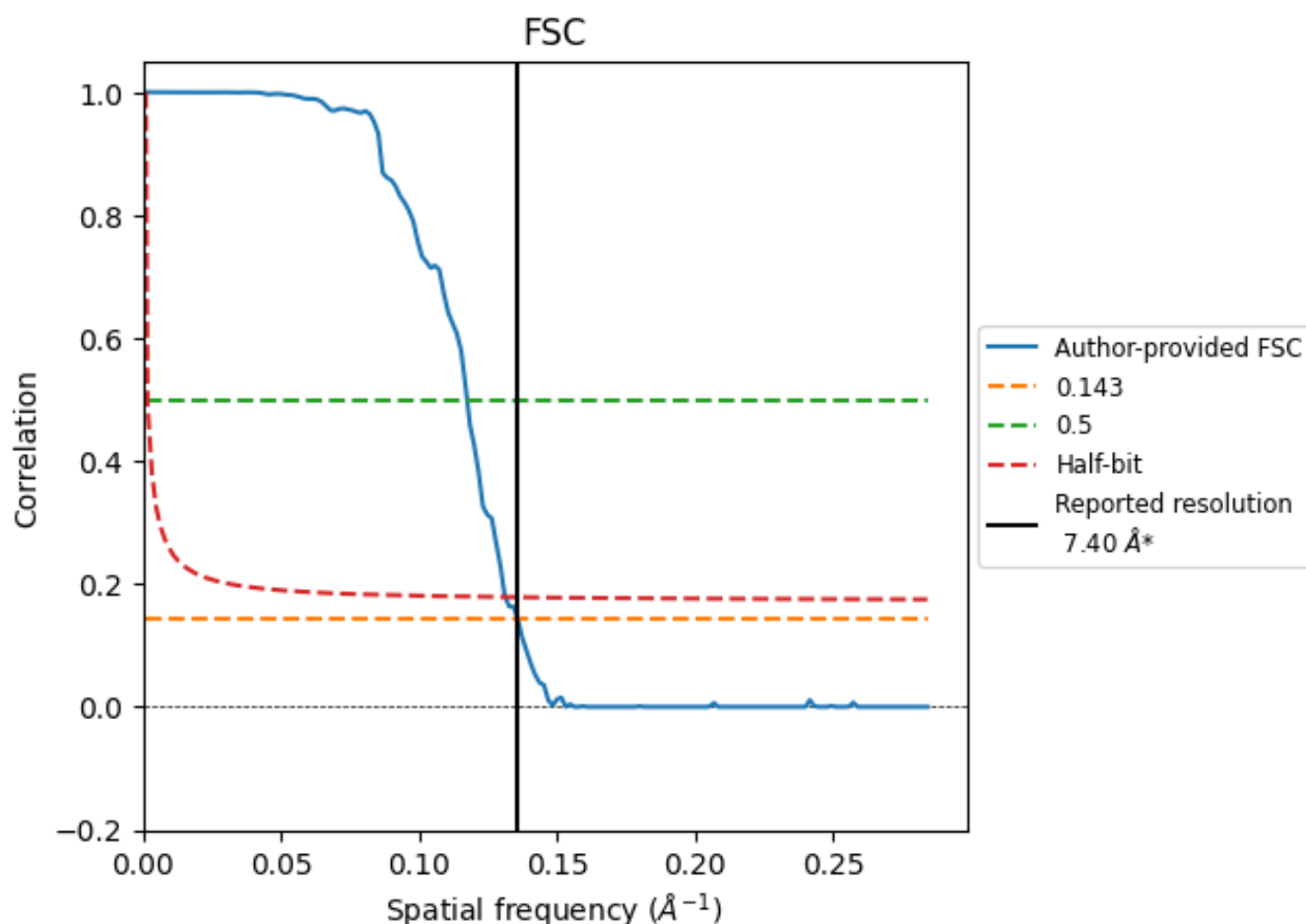


*Reported resolution corresponds to spatial frequency of 0.135 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.135 Å⁻¹

8.2 Resolution estimates [i](#)

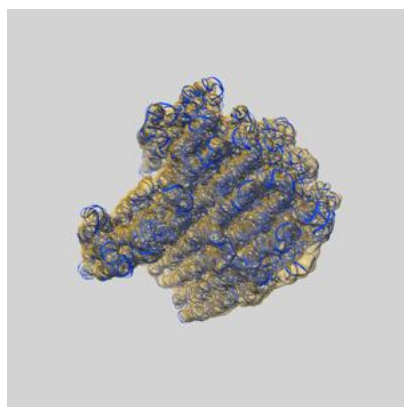
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.40	-	-
Author-provided FSC curve	7.37	8.53	7.62
Unmasked-calculated*	-	-	-

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

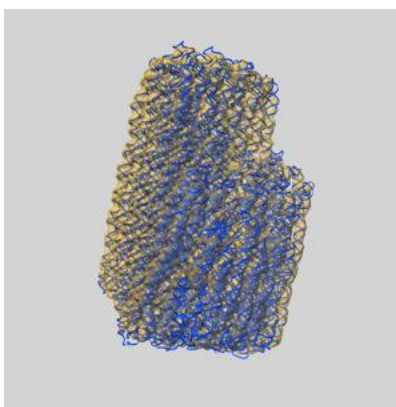
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11881 and PDB model 7ARE. Per-residue inclusion information can be found in section 3 on page 41.

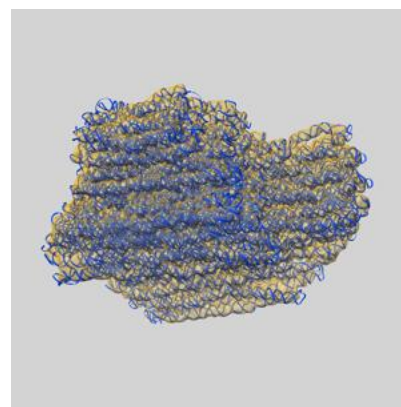
9.1 Map-model overlay [i](#)



X



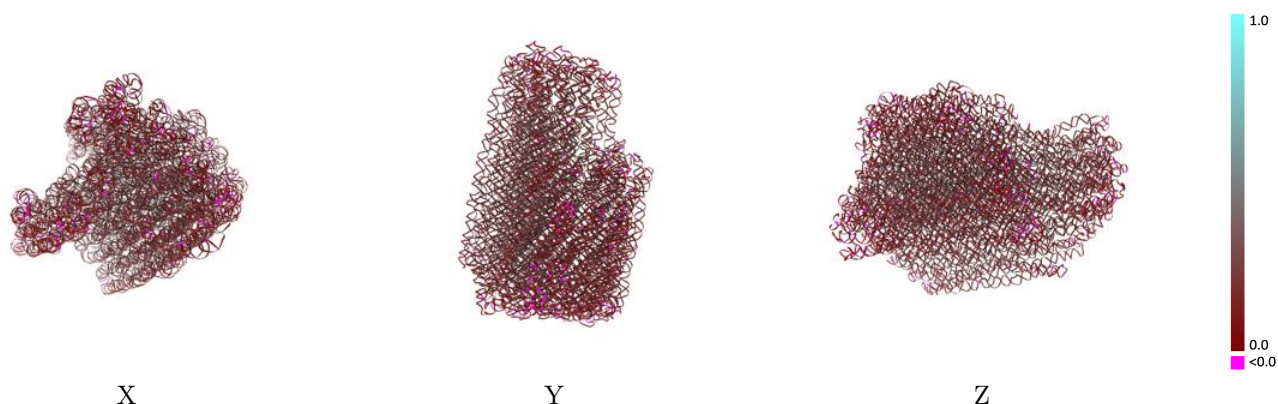
Y



Z

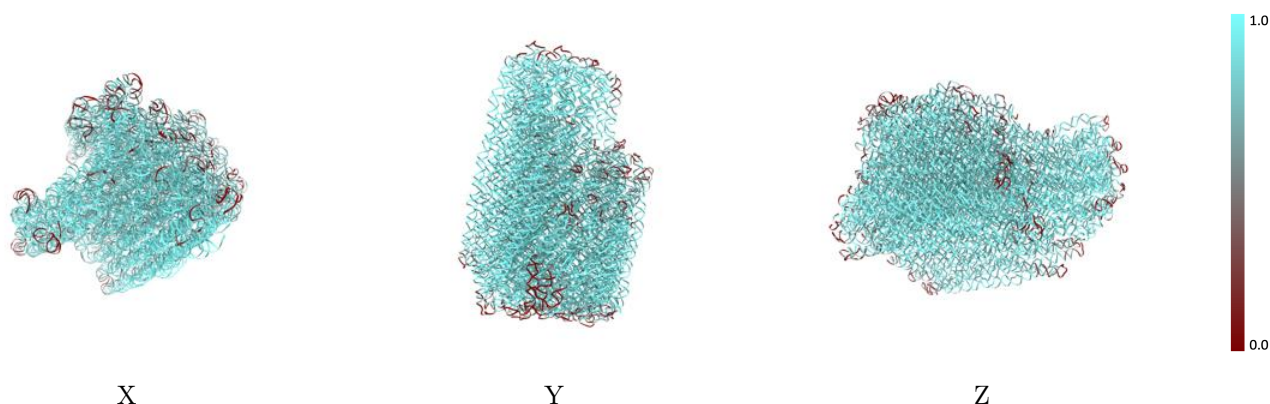
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



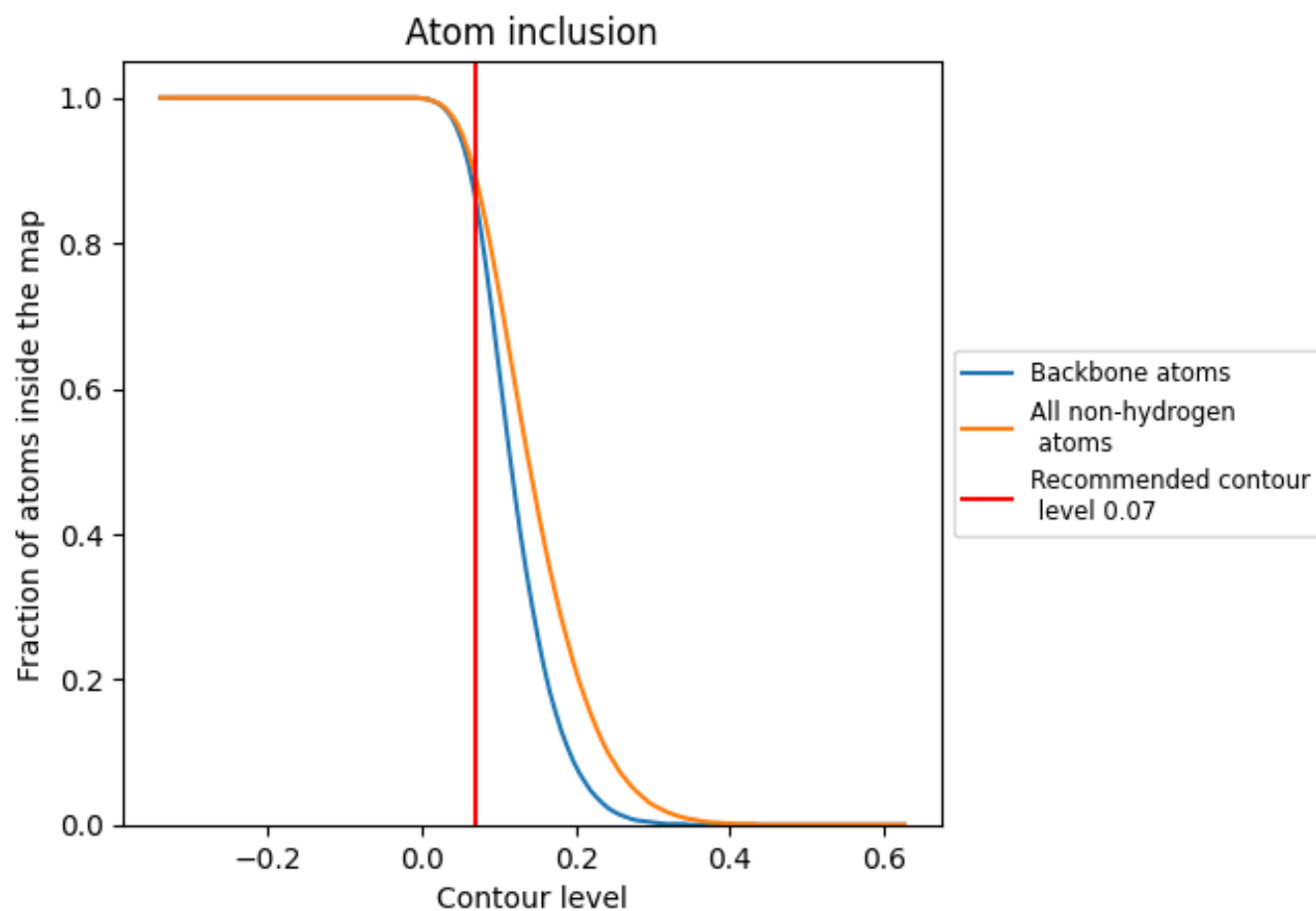
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.07).

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 89% 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 (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8910	 0.1980
A0	 0.9190	 0.1960
A1	 0.5940	 0.0920
A2	 0.7520	 0.1520
A3	 0.9060	 0.1560
A4	 0.9160	 0.1560
A5	 0.9720	 0.2420
A6	 0.9130	 0.1900
A7	 0.8440	 0.1610
A8	 0.7720	 0.1240
A9	 0.9230	 0.1560
AA	 0.9210	 0.2030
AB	 0.8620	 0.1570
AC	 0.6840	 0.1290
AD	 0.9160	 0.1530
AE	 0.8150	 0.1280
AF	 0.6560	 0.1290
AG	 0.9160	 0.1570
AH	 0.0000	 0.0460
AI	 0.2140	 0.0750
AJ	 0.9320	 0.2050
AK	 0.5560	 0.0930
AL	 0.7380	 0.1600
AM	 0.7630	 0.1420
AN	 0.8400	 0.1240
AO	 0.9220	 0.1960
AP	 0.7960	 0.1740
AQ	 0.7930	 0.1500
AR	 0.6300	 0.1220
AS	 0.7780	 0.1550
AT	 0.6170	 0.1250
AU	 0.4510	 0.0960
AV	 0.8870	 0.1870
AW	 0.9670	 0.2180
AX	 0.8820	 0.2160



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Chain	Atom inclusion	Q-score
AY	 0.9510	 0.1730
AZ	 0.9180	 0.1930
Aa	 0.9500	 0.2450
Ab	 0.6100	 0.1260
Ac	 0.9320	 0.2330
Ad	 0.9800	 0.2450
Ae	 0.6610	 0.1470
Af	 0.8820	 0.1890
Ag	 0.8570	 0.2250
Ah	 0.7010	 0.1400
Ai	 0.8450	 0.1610
Aj	 0.7910	 0.1750
Ak	 0.8460	 0.1900
Al	 0.8720	 0.1810
Am	 0.9890	 0.2500
An	 0.7080	 0.1530
Ao	 0.9690	 0.2330
Ap	 0.8990	 0.2210
Aq	 0.9750	 0.2350
Ar	 0.9640	 0.2320
As	 0.6590	 0.1090
At	 0.9560	 0.2490
Au	 0.9710	 0.2300
Av	 0.9680	 0.2080
Aw	 0.9770	 0.2520
Ax	 0.7590	 0.1420
Ay	 0.9700	 0.2720
Az	 0.9830	 0.2430
B0	 0.4770	 0.1020
B1	 0.5570	 0.0940
B2	 0.6010	 0.1050
B3	 0.8950	 0.1600
B4	 0.8830	 0.1420
B5	 0.6870	 0.1330
B6	 0.4760	 0.1040
B7	 0.5020	 0.1020
B8	 0.9100	 0.1470
B9	 0.9670	 0.2680
BA	 0.9540	 0.1720
BB	 0.6900	 0.1290
BC	 0.7450	 0.1530
BD	 0.9310	 0.1850

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Chain	Atom inclusion	Q-score
BE	 0.8240	 0.1700
BF	 0.8820	 0.2230
BG	 0.7700	 0.1460
BH	 0.9640	 0.2380
BI	 0.9750	 0.2720
BJ	 0.9680	 0.2810
BK	 0.9740	 0.2320
BL	 0.8320	 0.1970
BM	 0.9730	 0.2530
BN	 0.9740	 0.2540
BO	 0.9770	 0.2410
BP	 0.9410	 0.2310
BQ	 0.9350	 0.2250
BR	 0.9300	 0.2070
BS	 0.9620	 0.2160
BT	 0.9900	 0.2670
BU	 0.9390	 0.2120
BV	 0.9510	 0.2420
BW	 0.4030	 0.0950
BX	 0.7650	 0.1410
BY	 0.9630	 0.2430
BZ	 0.9840	 0.2290
Ba	 0.9600	 0.2460
Bb	 0.9580	 0.1810
Bc	 0.9850	 0.2380
Bd	 0.6390	 0.1370
Be	 0.9830	 0.2650
Bf	 0.5790	 0.1400
Bg	 0.9790	 0.2650
Bh	 0.9760	 0.2790
Bi	 0.8030	 0.1540
Bj	 0.8230	 0.1770
Bk	 0.9730	 0.2430
Bl	 0.8620	 0.2000
Bm	 0.9780	 0.2670
Bn	 0.9650	 0.2620
Bo	 0.9740	 0.2620
Bp	 0.9780	 0.2130
Bq	 0.7580	 0.1180
Br	 0.9630	 0.2490
Bs	 0.7500	 0.1680
Bt	 0.9860	 0.2570

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Chain	Atom inclusion	Q-score
Bu	 0.9770	 0.2370
Bv	 0.9530	 0.2200
Bw	 0.9790	 0.2690
Bx	 0.9830	 0.2520
By	 0.7840	 0.1700
Bz	 0.9500	 0.1920
C0	 0.9760	 0.2340
C1	 0.9770	 0.2680
C2	 0.9620	 0.2480
C3	 0.8310	 0.1230
C4	 0.9710	 0.2270
C5	 0.9490	 0.2210
C6	 0.8200	 0.1160
C7	 0.5250	 0.1180
C8	 0.9640	 0.2130
C9	 0.9820	 0.2490
CA	 0.9720	 0.2740
CB	 0.8710	 0.1730
CC	 0.9720	 0.2250
CD	 0.9740	 0.2050
CE	 0.8240	 0.1700
CF	 0.6050	 0.1390
CG	 0.9720	 0.2610
CH	 0.9020	 0.2150
CI	 0.9760	 0.2500
CJ	 0.9830	 0.2690
CK	 0.9790	 0.2470
CL	 0.7870	 0.1500
CM	 0.7430	 0.1730
CN	 0.9670	 0.2080
CO	 0.9740	 0.2610
CP	 0.9620	 0.2210
CQ	 0.8940	 0.1930
CR	 0.9760	 0.2610
CS	 0.9700	 0.2500
CT	 0.9740	 0.2330
CU	 0.9680	 0.2540
CV	 0.6190	 0.1500
CW	 0.8840	 0.1890
CX	 0.7420	 0.1620
CY	 0.9850	 0.2650
CZ	 0.7420	 0.1280

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Chain	Atom inclusion	Q-score
Ca	 0.9750	 0.2670
Cb	 0.9070	 0.1880
Cc	 0.8720	 0.1960
Cd	 0.9720	 0.2670
Ce	 0.9920	 0.2580
Cf	 0.9690	 0.2640
Cg	 0.9840	 0.2540
Ch	 0.9820	 0.2490
Ci	 0.9170	 0.2320
Cj	 0.9210	 0.1670
Ck	 0.7340	 0.1600
Cl	 0.9830	 0.2320
Cm	 0.9920	 0.2340
Cn	 0.9840	 0.2350
Co	 0.5400	 0.1460
Cp	 0.9850	 0.2130
Cq	 0.9850	 0.2420
Cr	 0.8910	 0.1880
Cs	 0.9610	 0.1930
Ct	 0.9510	 0.2260
Cu	 0.9770	 0.2440
Cv	 0.9660	 0.2680
Cw	 0.9080	 0.1640
Cx	 0.9330	 0.1880
Cy	 0.7800	 0.1480
Cz	 0.9440	 0.2080
DA	 0.9870	 0.2270
DB	 0.9800	 0.2270
DC	 0.4020	 0.0960
DD	 0.9710	 0.2170
DE	 0.6090	 0.1260
DF	 0.5840	 0.0990
DG	 0.9110	 0.1570
DH	 0.6510	 0.1240
DI	 0.5560	 0.1030
DJ	 0.9330	 0.1600
DK	 0.9500	 0.2080
DL	 0.9140	 0.1430
DM	 0.9410	 0.1510
DN	 0.9530	 0.1470
DO	 0.8460	 0.1570
DP	 0.9310	 0.1900

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Chain	Atom inclusion	Q-score
DQ	 0.9750	 0.2560