



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 03:23 PM UTC

PDB ID : 4V5X / pdb_00004v5x
EMDB ID : EMD-2210
Title : The cryo-EM structure of a 3D DNA-origami object
Authors : Bai, X.C.; Martin, T.G.; Scheres, S.H.W.; Dietz, H.
Deposited on : 2012-10-09
Resolution : 11.50 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ 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

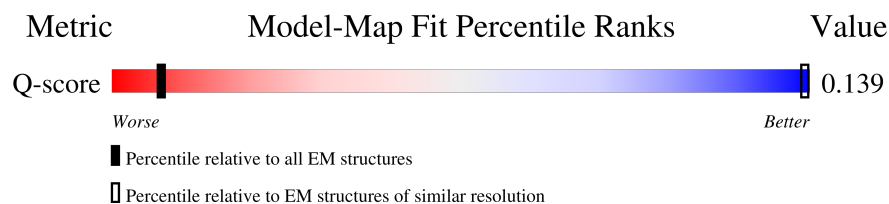
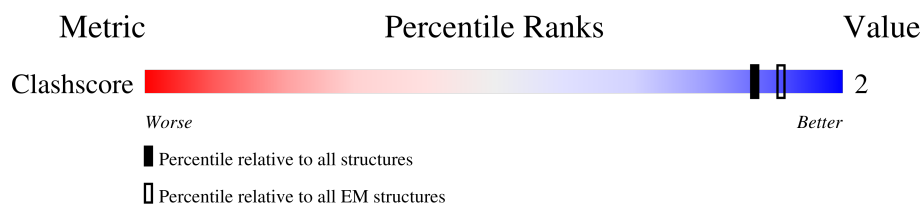
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 11.50 Å.

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



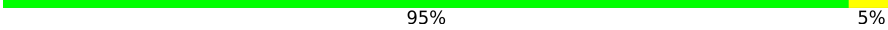
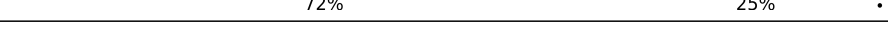
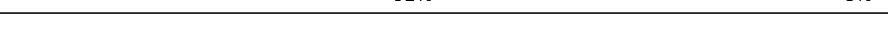
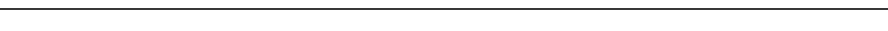
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Q-score	-	25397	117 (11.00 - 12.00)

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

Mol	Chain	Length	Quality of chain
1	AA	7249	 86% 13%
2	A0	55	 82% 16%
3	A1	44	 73% 20% 7%
4	A2	50	 76% 20%
5	A3	40	 65% 32%
6	A4	48	 67% 12% 21%

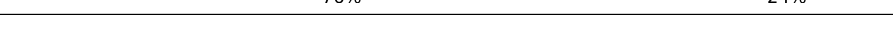
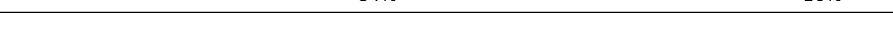
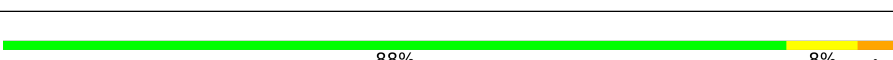
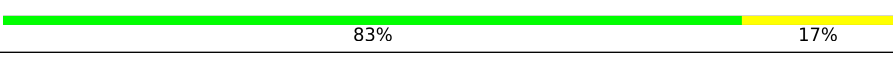
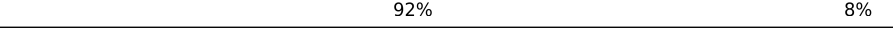
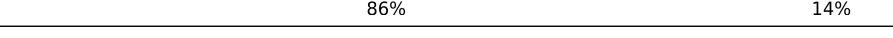
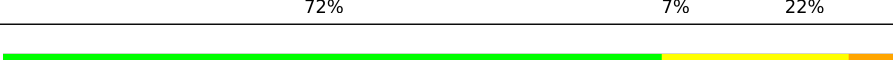
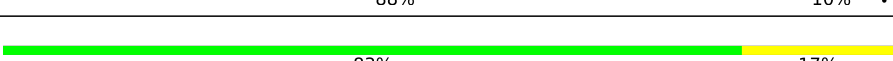
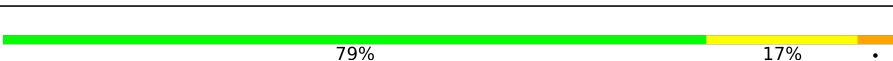
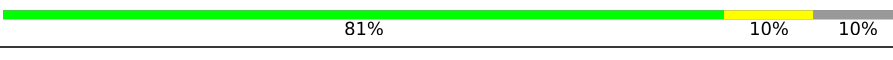
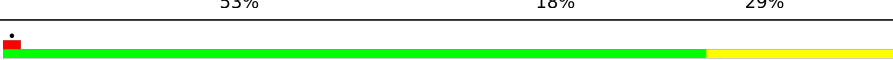
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Mol	Chain	Length	Quality of chain
7	A5	48	 83% 12% .
8	A6	50	 80% 18% .
9	A7	48	 77% 12% 10%
10	A8	48	 83% 12% .
11	AB	40	 95% 5%
12	AC	48	 85% 10% .
13	AD	50	 80% 18% .
14	AE	46	 7% 57% 22% 22%
15	AF	48	 83% 17%
16	AG	46	 78% 20% .
17	AH	48	 79% 19% .
18	AI	48	 90% 10%
19	AJ	52	 83% 13% .
20	AK	60	 72% 25% .
21	AL	48	 81% 17% .
22	AM	50	 86% 14%
23	AN	48	 81% 15% .
24	AO	48	 85% 12% .
25	AP	40	 92% 8%
26	AQ	57	 74% 21% 5%
27	AR	63	 70% 6% 24%
28	AS	64	 47% 14% 39%
29	AT	48	 81% 19%
30	AU	48	 77% 19% .
31	AV	52	 85% 12% .

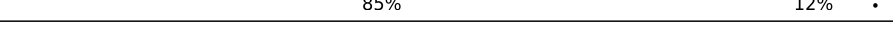
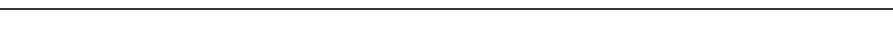
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Mol	Chain	Length	Quality of chain
32	AW	50	
33	AX	48	
34	AY	42	
35	AZ	54	
36	Ab	45	
37	Ac	70	
38	Ad	48	
39	Af	48	
40	Ag	48	
41	Ah	44	
42	Ai	46	
43	Aj	62	
44	Ak	46	
45	Al	48	
46	Am	48	
47	An	48	
48	Ao	36	
49	As	48	
50	Au	48	
51	Av	48	
52	Aw	48	
53	Ax	52	
54	Ay	38	
55	Az	51	
56	B0	48	

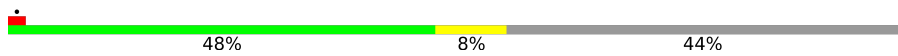
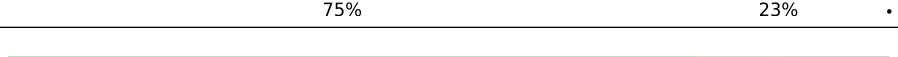
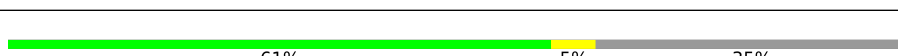
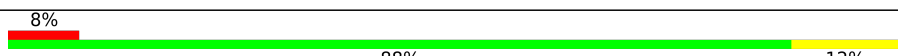
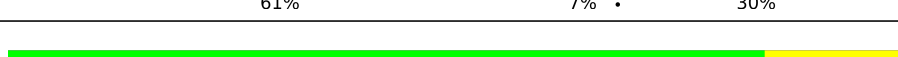
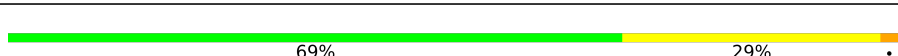
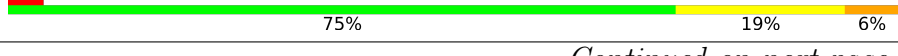
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Mol	Chain	Length	Quality of chain
57	B1	59	
58	B2	36	
59	B3	48	
60	B4	48	
61	B5	40	
62	B6	50	
63	B7	44	
64	B8	40	
65	B9	55	
66	BB	48	
67	BC	44	
68	BD	35	
69	BE	68	
70	BF	40	
71	BG	49	
72	BH	42	
73	BI	42	
74	BJ	58	
75	BK	44	
76	BL	48	
77	BM	52	
78	BN	63	
79	BO	49	
80	BP	66	
81	BQ	48	

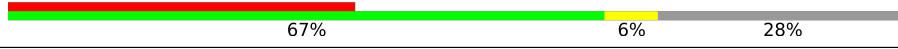
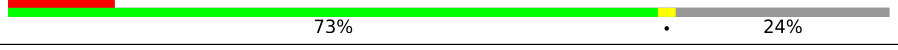
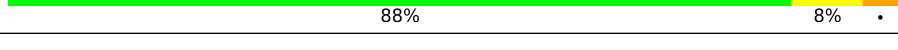
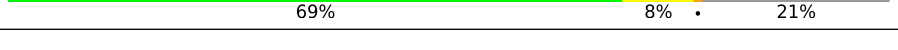
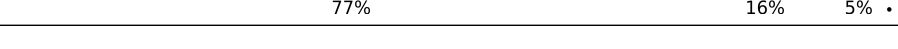
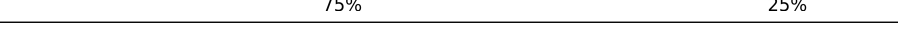
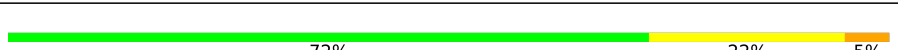
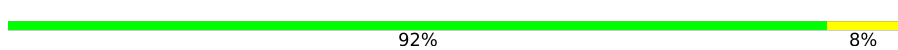
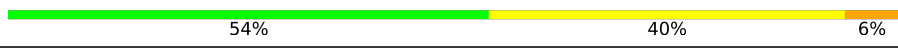
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Mol	Chain	Length	Quality of chain
82	BR	64	
83	BS	48	
84	BT	52	
85	BU	55	
86	BV	44	
87	BW	53	
88	BX	48	
89	BY	48	
90	BZ	66	
91	Ba	48	
92	Bb	68	
93	Bc	50	
94	Bd	56	
95	Be	48	
96	Bf	48	
97	Bg	47	
98	Bh	48	
99	Bi	67	
100	Bj	45	
101	Bk	67	
102	Bl	48	
103	Bm	48	
104	Bn	67	
105	Bo	67	
106	Bp	48	

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Mol	Chain	Length	Quality of chain
107	Bq	58	
108	Br	51	
109	Bs	54	
110	C0	41	
111	C1	51	
112	C2	56	
113	C3	48	
114	C4	71	
115	C5	62	
116	C6	48	
117	C7	52	
118	C8	44	
119	CB	54	
120	CC	47	
121	CD	48	
122	CE	40	
123	CF	40	
124	CG	44	
125	CH	48	
126	CI	44	
127	CJ	59	
128	CK	48	
129	CL	48	
130	CM	54	
131	CN	41	

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Mol	Chain	Length	Quality of chain
132	CO	48	
133	CP	56	
134	CQ	38	
135	CR	48	
136	CS	48	
137	CT	48	
138	CU	32	
139	CV	53	
140	CW	38	
141	CX	47	
142	CY	43	
143	CZ	48	
144	Cb	44	
145	Cc	62	
146	Cd	42	
147	Ce	52	
148	Cf	48	
149	Cg	46	
150	Ch	47	
151	Ck	29	
152	Cp	48	
153	Cq	40	
154	Cr	46	
155	Cs	49	
156	Ct	44	

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Mol	Chain	Length	Quality of chain
157	Cu	60	 88%7%5%
158	Cv	46	 76%13%11%
159	Cw	54	 72%26%
160	Cx	46	 59%20%22%
161	Cy	66	 74%11%15%
162	Cz	48	 77%23%

2 Entry composition

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

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

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

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

- Molecule 2 is a DNA chain called STAPLE STRAND.

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

- Molecule 3 is a DNA chain called STAPLE STRAND.

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

- Molecule 4 is a DNA chain called STAPLE STRAND.

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

- Molecule 5 is a DNA chain called STAPLE STRAND.

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

- Molecule 6 is a DNA chain called STAPLE STRAND.

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

- Molecule 7 is a DNA chain called STAPLE STRAND.

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

- Molecule 8 is a DNA chain called STAPLE STRAND.

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

- Molecule 9 is a DNA chain called STAPLE STRAND.

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

- Molecule 10 is a DNA chain called STAPLE STRAND.

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

- Molecule 11 is a DNA chain called STAPLE STRAND.

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

- Molecule 12 is a DNA chain called STAPLE STRAND.

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

- Molecule 13 is a DNA chain called STAPLE STRAND.

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

- Molecule 14 is a DNA chain called STAPLE STRAND.

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

- Molecule 15 is a DNA chain called STAPLE STRAND.

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

- Molecule 16 is a DNA chain called STAPLE STRAND.

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

- Molecule 17 is a DNA chain called STAPLE STRAND.

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

- Molecule 18 is a DNA chain called STAPLE STRAND.

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

- Molecule 19 is a DNA chain called STAPLE STRAND.

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

- Molecule 20 is a DNA chain called STAPLE STRAND.

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

- Molecule 21 is a DNA chain called STAPLE STRAND.

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

- Molecule 22 is a DNA chain called STAPLE STRAND.

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

- Molecule 23 is a DNA chain called STAPLE STRAND.

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

- Molecule 24 is a DNA chain called STAPLE STRAND.

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

- Molecule 25 is a DNA chain called STAPLE STRAND.

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

- Molecule 26 is a DNA chain called STAPLE STRAND.

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

- Molecule 27 is a DNA chain called STAPLE STRAND.

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

- Molecule 28 is a DNA chain called STAPLE STRAND.

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

- Molecule 29 is a DNA chain called STAPLE STRAND.

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

- Molecule 30 is a DNA chain called STAPLE STRAND.

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

- Molecule 31 is a DNA chain called STAPLE STRAND.

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

- Molecule 32 is a DNA chain called STAPLE STRAND.

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

- Molecule 33 is a DNA chain called STAPLE STRAND.

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

- Molecule 34 is a DNA chain called STAPLE STRAND.

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

- Molecule 35 is a DNA chain called STAPLE STRAND.

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

- Molecule 36 is a DNA chain called STAPLE STRAND.

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

- Molecule 37 is a DNA chain called STAPLE STRAND.

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

- Molecule 38 is a DNA chain called STAPLE STRAND.

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

- Molecule 39 is a DNA chain called STAPLE STRAND.

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

- Molecule 40 is a DNA chain called STAPLE STRAND.

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

- Molecule 41 is a DNA chain called STAPLE STRAND.

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

- Molecule 42 is a DNA chain called STAPLE STRAND.

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

- Molecule 43 is a DNA chain called STAPLE STRAND.

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

- Molecule 44 is a DNA chain called STAPLE STRAND.

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

- Molecule 45 is a DNA chain called STAPLE STRAND.

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

- Molecule 46 is a DNA chain called STAPLE STRAND.

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

- Molecule 47 is a DNA chain called STAPLE STRAND.

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

- Molecule 48 is a DNA chain called STAPLE STRAND.

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

- Molecule 49 is a DNA chain called STAPLE STRAND.

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

- Molecule 50 is a DNA chain called STAPLE STRAND.

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

- Molecule 51 is a DNA chain called STAPLE STRAND.

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

- Molecule 52 is a DNA chain called STAPLE STRAND.

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

- Molecule 53 is a DNA chain called STAPLE STRAND.

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

- Molecule 54 is a DNA chain called STAPLE STRAND.

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

- Molecule 55 is a DNA chain called STAPLE STRAND.

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

- Molecule 56 is a DNA chain called STAPLE STRAND.

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

- Molecule 57 is a DNA chain called STAPLE STRAND.

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

- Molecule 58 is a DNA chain called STAPLE STRAND.

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

- Molecule 59 is a DNA chain called STAPLE STRAND.

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

- Molecule 60 is a DNA chain called STAPLE STRAND.

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

- Molecule 61 is a DNA chain called STAPLE STRAND.

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

- Molecule 62 is a DNA chain called STAPLE STRAND.

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

- Molecule 63 is a DNA chain called STAPLE STRAND.

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

- Molecule 64 is a DNA chain called STAPLE STRAND.

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

- Molecule 65 is a DNA chain called STAPLE STRAND.

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

- Molecule 66 is a DNA chain called STAPLE STRAND.

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

- Molecule 67 is a DNA chain called STAPLE STRAND.

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

- Molecule 68 is a DNA chain called STAPLE STRAND.

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

- Molecule 69 is a DNA chain called STAPLE STRAND.

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

- Molecule 70 is a DNA chain called STAPLE STRAND.

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

- Molecule 71 is a DNA chain called STAPLE STRAND.

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

- Molecule 72 is a DNA chain called STAPLE STRAND.

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

- Molecule 73 is a DNA chain called STAPLE STRAND.

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

- Molecule 74 is a DNA chain called STAPLE STRAND.

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

- Molecule 75 is a DNA chain called STAPLE STRAND.

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

- Molecule 76 is a DNA chain called STAPLE STRAND.

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

- Molecule 77 is a DNA chain called STAPLE STRAND.

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

- Molecule 78 is a DNA chain called STAPLE STRAND.

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

- Molecule 79 is a DNA chain called STAPLE STRAND.

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

- Molecule 80 is a DNA chain called STAPLE STRAND.

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

- Molecule 81 is a DNA chain called STAPLE STRAND.

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

- Molecule 82 is a DNA chain called STAPLE STRAND.

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

- Molecule 83 is a DNA chain called STAPLE STRAND.

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

- Molecule 84 is a DNA chain called STAPLE STRAND.

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

- Molecule 85 is a DNA chain called STAPLE STRAND.

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

- Molecule 86 is a DNA chain called STAPLE STRAND.

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

- Molecule 87 is a DNA chain called STAPLE STRAND.

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

- Molecule 88 is a DNA chain called STAPLE STRAND.

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

- Molecule 89 is a DNA chain called STAPLE STRAND.

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

- Molecule 90 is a DNA chain called STAPLE STRAND.

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

- Molecule 91 is a DNA chain called STAPLE STRAND.

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

- Molecule 92 is a DNA chain called STAPLE STRAND.

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

- Molecule 93 is a DNA chain called STAPLE STRAND.

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

- Molecule 94 is a DNA chain called STAPLE STRAND.

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

- Molecule 95 is a DNA chain called STAPLE STRAND.

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

- Molecule 96 is a DNA chain called STAPLE STRAND.

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

- Molecule 97 is a DNA chain called STAPLE STRAND.

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

- Molecule 98 is a DNA chain called STAPLE STRAND.

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

- Molecule 99 is a DNA chain called STAPLE STRAND.

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

- Molecule 100 is a DNA chain called STAPLE STRAND.

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

- Molecule 101 is a DNA chain called STAPLE STRAND.

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

- Molecule 102 is a DNA chain called STAPLE STRAND.

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

- Molecule 103 is a DNA chain called STAPLE STRAND.

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

- Molecule 104 is a DNA chain called STAPLE STRAND.

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

- Molecule 105 is a DNA chain called STAPLE STRAND.

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

- Molecule 106 is a DNA chain called STAPLE STRAND.

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

- Molecule 107 is a DNA chain called STAPLE STRAND.

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

- Molecule 108 is a DNA chain called STAPLE STRAND.

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

- Molecule 109 is a DNA chain called STAPLE STRAND.

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

- Molecule 110 is a DNA chain called STAPLE STRAND.

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

- Molecule 111 is a DNA chain called STAPLE STRAND.

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

- Molecule 112 is a DNA chain called STAPLE STRAND.

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

- Molecule 113 is a DNA chain called STAPLE STRAND.

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

- Molecule 114 is a DNA chain called STAPLE STRAND.

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

- Molecule 115 is a DNA chain called STAPLE STRAND.

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

- Molecule 116 is a DNA chain called STAPLE STRAND.

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

- Molecule 117 is a DNA chain called STAPLE STRAND.

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

- Molecule 118 is a DNA chain called STAPLE STRAND.

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

- Molecule 119 is a DNA chain called STAPLE STRAND.

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

- Molecule 120 is a DNA chain called STAPLE STRAND.

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

- Molecule 121 is a DNA chain called STAPLE STRAND.

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

- Molecule 122 is a DNA chain called STAPLE STRAND.

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

- Molecule 123 is a DNA chain called STAPLE STRAND.

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

- Molecule 124 is a DNA chain called STAPLE STRAND.

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

- Molecule 125 is a DNA chain called STAPLE STRAND.

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

- Molecule 126 is a DNA chain called STAPLE STRAND.

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

- Molecule 127 is a DNA chain called STAPLE STRAND.

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

- Molecule 128 is a DNA chain called STAPLE STRAND.

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

- Molecule 129 is a DNA chain called STAPLE STRAND.

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

- Molecule 130 is a DNA chain called STAPLE STRAND.

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

- Molecule 131 is a DNA chain called STAPLE STRAND.

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

- Molecule 132 is a DNA chain called STAPLE STRAND.

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

- Molecule 133 is a DNA chain called STAPLE STRAND.

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

- Molecule 134 is a DNA chain called STAPLE STRAND.

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

- Molecule 135 is a DNA chain called STAPLE STRAND.

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

- Molecule 136 is a DNA chain called STAPLE STRAND.

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

- Molecule 137 is a DNA chain called STAPLE STRAND.

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

- Molecule 138 is a DNA chain called STAPLE STRAND.

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

- Molecule 139 is a DNA chain called STAPLE STRAND.

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

- Molecule 140 is a DNA chain called STAPLE STRAND.

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

- Molecule 141 is a DNA chain called STAPLE STRAND.

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

- Molecule 142 is a DNA chain called STAPLE STRAND.

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

- Molecule 143 is a DNA chain called STAPLE STRAND.

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

- Molecule 144 is a DNA chain called STAPLE STRAND.

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

- Molecule 145 is a DNA chain called STAPLE STRAND.

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

- Molecule 146 is a DNA chain called STAPLE STRAND.

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

- Molecule 147 is a DNA chain called STAPLE STRAND.

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

- Molecule 148 is a DNA chain called STAPLE STRAND.

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

- Molecule 149 is a DNA chain called STAPLE STRAND.

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

- Molecule 150 is a DNA chain called STAPLE STRAND.

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

- Molecule 151 is a DNA chain called STAPLE STRAND.

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

- Molecule 152 is a DNA chain called STAPLE STRAND.

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

- Molecule 153 is a DNA chain called STAPLE STRAND.

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

- Molecule 154 is a DNA chain called STAPLE STRAND.

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

- Molecule 155 is a DNA chain called STAPLE STRAND.

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

- Molecule 156 is a DNA chain called STAPLE STRAND.

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

- Molecule 157 is a DNA chain called STAPLE STRAND.

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

- Molecule 158 is a DNA chain called STAPLE STRAND.

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

- Molecule 159 is a DNA chain called STAPLE STRAND.

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

- Molecule 160 is a DNA chain called STAPLE STRAND.

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

- Molecule 161 is a DNA chain called STAPLE STRAND.

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

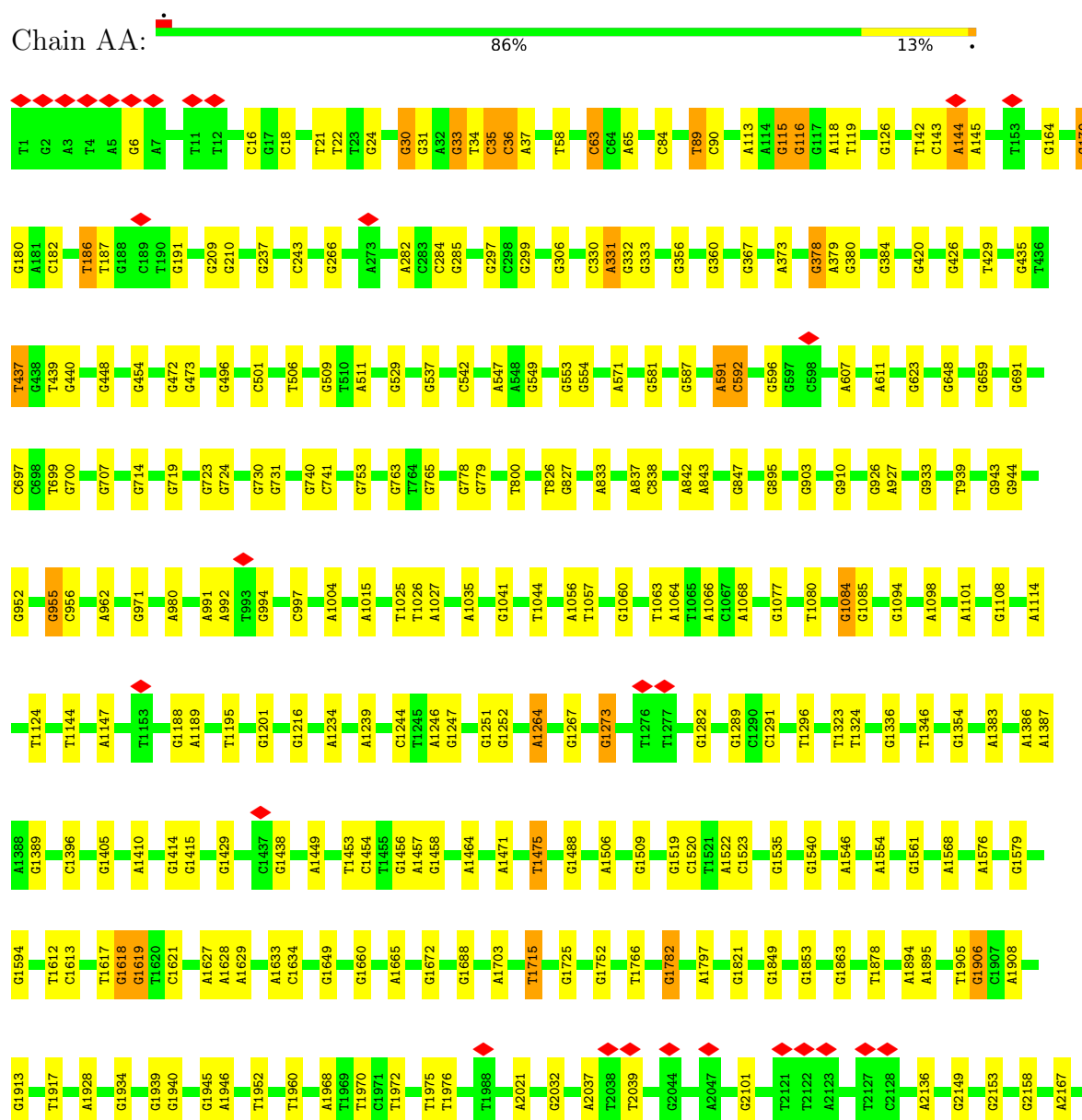
- Molecule 162 is a DNA chain called STAPLE STRAND.

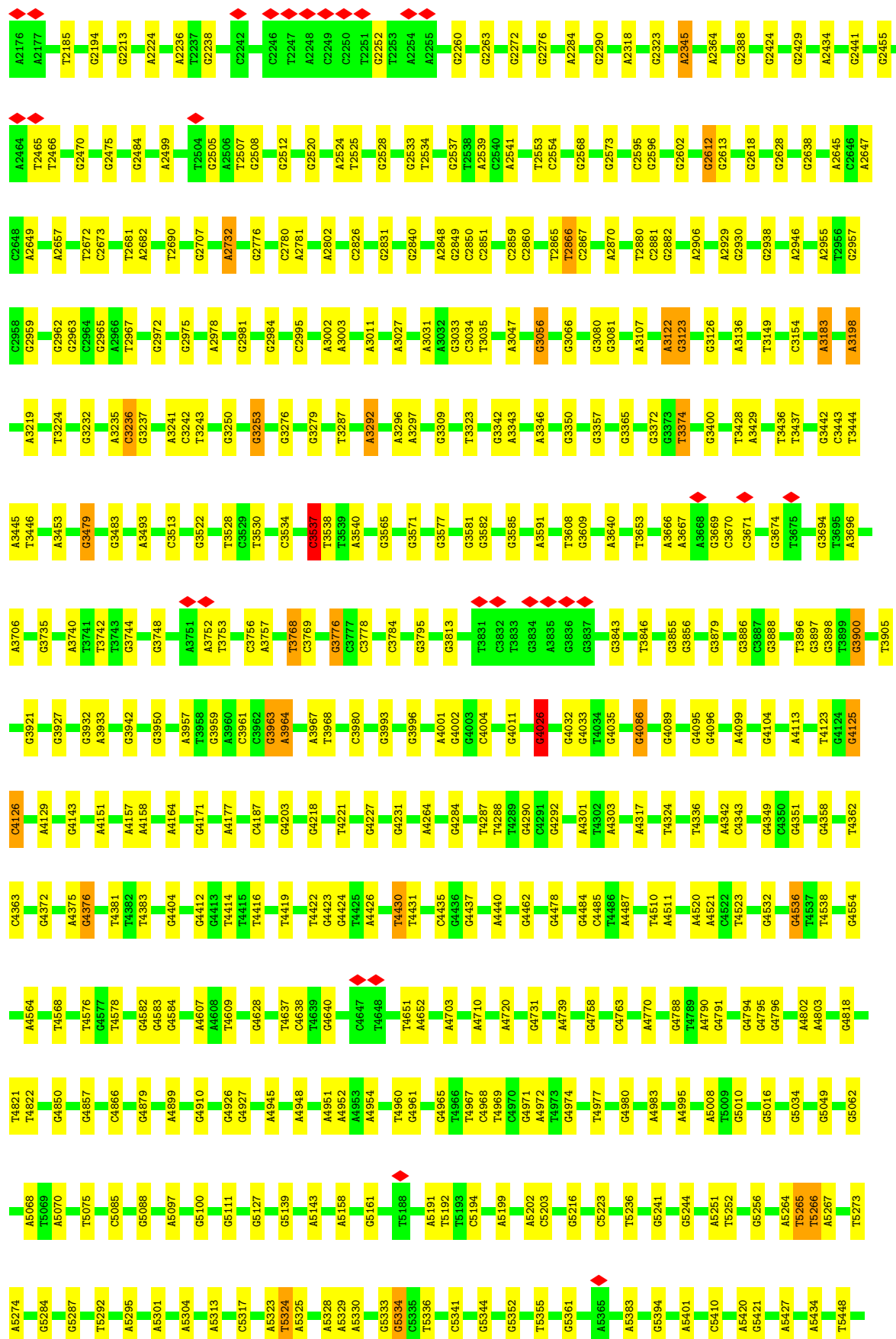
Mol	Chain	Residues	Atoms					AltConf	Trace
162	Cz	48	Total	C	N	O	P	0	0
			970	465	195	266	44		

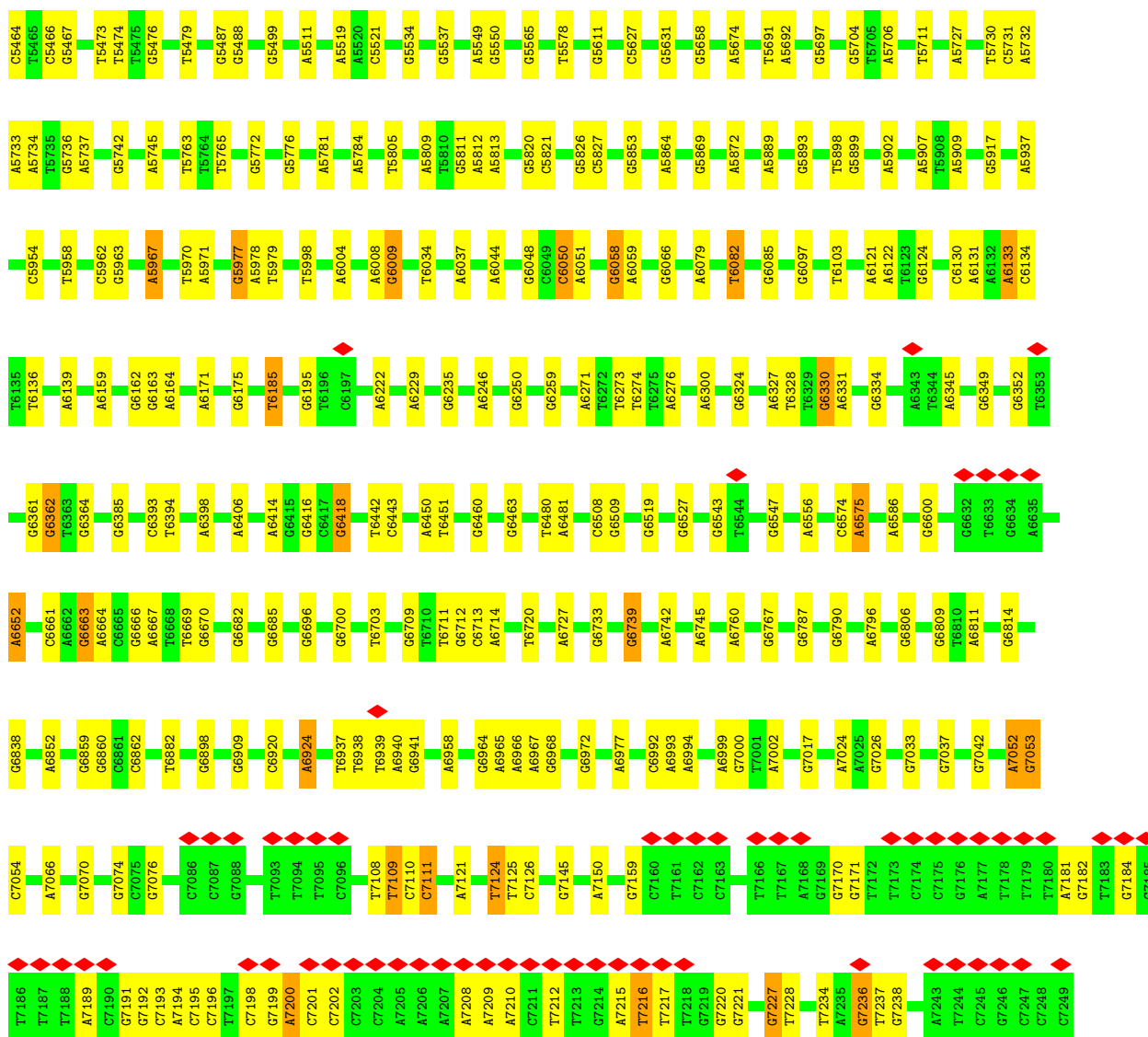
3 Residue-property plots

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

- Molecule 1: SCAFFOLD STRAND,SCAFFOLD STRAND







• Molecule 2: STAPLE STRAND

Chain A0: 82% 16% .



• Molecule 3: STAPLE STRAND

Chain A1: 73% 20% 7%



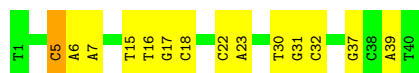
• Molecule 4: STAPLE STRAND

Chain A2: 76% 20% .



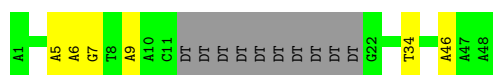
- Molecule 5: STAPLE STRAND

Chain A3: 65% 32% .



- Molecule 6: STAPLE STRAND

Chain A4: 67% 12% 21%



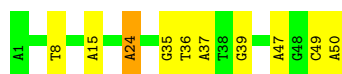
- Molecule 7: STAPLE STRAND

Chain A5: 83% 12% .



- Molecule 8: STAPLE STRAND

Chain A6: 80% 18% .



- Molecule 9: STAPLE STRAND

Chain A7: 77% 12% 10%



- Molecule 10: STAPLE STRAND

Chain A8: 83% 12% .



- Molecule 11: STAPLE STRAND

Chain AB: 95% 5%



- Molecule 12: STAPLE STRAND

Chain AC: 85% 10%



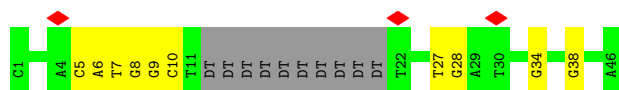
- Molecule 13: STAPLE STRAND

Chain AD: 80% 18%



- Molecule 14: STAPLE STRAND

Chain AE: 7% 57% 22% 22%



- Molecule 15: STAPLE STRAND

Chain AF: 83% 17%



- Molecule 16: STAPLE STRAND

Chain AG: 78% 20%



- Molecule 17: STAPLE STRAND

Chain AH: 79% 19%



- Molecule 18: STAPLE STRAND

Chain AI: 90% 10%



• Molecule 19: STAPLE STRAND

Chain AJ: 83% 13% .



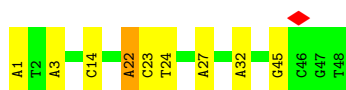
• Molecule 20: STAPLE STRAND

Chain AK: 72% 25% .



• Molecule 21: STAPLE STRAND

Chain AL: 81% 17% .



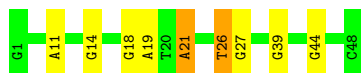
• Molecule 22: STAPLE STRAND

Chain AM: 86% 14%



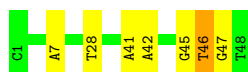
• Molecule 23: STAPLE STRAND

Chain AN: 81% 15% .



• Molecule 24: STAPLE STRAND

Chain AO: 85% 12% .



• Molecule 25: STAPLE STRAND

Chain AP: 92% 8%



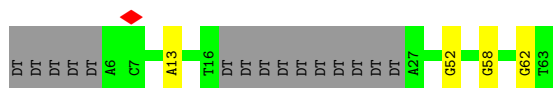
- Molecule 26: STAPLE STRAND

Chain AQ: 74% 21% 5%



- Molecule 27: STAPLE STRAND

Chain AR: 70% 6% 24%



- Molecule 28: STAPLE STRAND

Chain AS: 47% 14% 39%



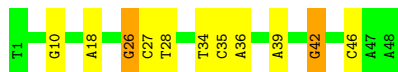
- Molecule 29: STAPLE STRAND

Chain AT: 81% 19%



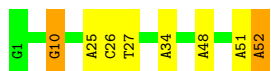
- Molecule 30: STAPLE STRAND

Chain AU: 77% 19%



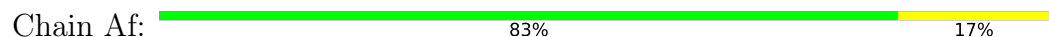
- Molecule 31: STAPLE STRAND

Chain AV: 85% 12%



- Molecule 32: STAPLE STRAND

Chain AW: 18% 62% 8% 30%

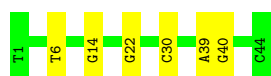
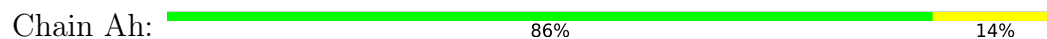




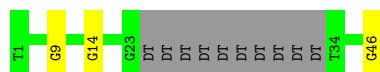
- Molecule 40: STAPLE STRAND



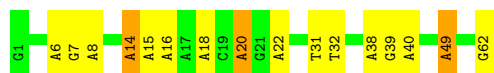
- Molecule 41: STAPLE STRAND



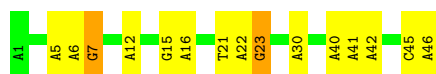
- Molecule 42: STAPLE STRAND



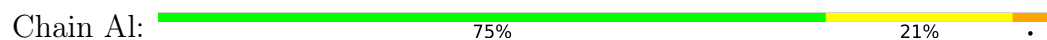
- Molecule 43: STAPLE STRAND



- Molecule 44: STAPLE STRAND



- Molecule 45: STAPLE STRAND



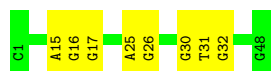
- Molecule 46: STAPLE STRAND





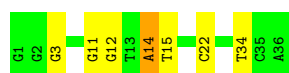
- Molecule 47: STAPLE STRAND

Chain An: 83% 17%



- Molecule 48: STAPLE STRAND

Chain Ao: 81% 17% .



- Molecule 49: STAPLE STRAND

Chain As: 79% 17% .



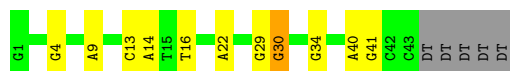
- Molecule 50: STAPLE STRAND

Chain Au: 85% 15%



- Molecule 51: STAPLE STRAND

Chain Av: 67% 21% . 10%



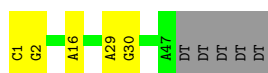
- Molecule 52: STAPLE STRAND

Chain Aw: 79% 17% .

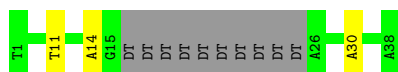


- Molecule 53: STAPLE STRAND

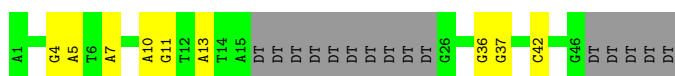
Chain Ax: 81% 10% 10%



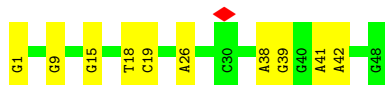
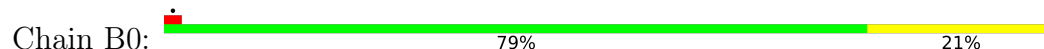
- Molecule 54: STAPLE STRAND



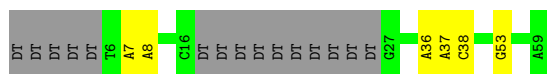
- Molecule 55: STAPLE STRAND



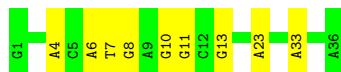
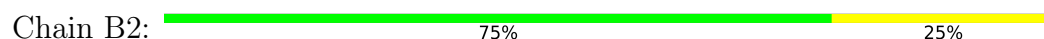
- Molecule 56: STAPLE STRAND



- Molecule 57: STAPLE STRAND



- Molecule 58: STAPLE STRAND



- Molecule 59: STAPLE STRAND



- Molecule 60: STAPLE STRAND





• Molecule 61: STAPLE STRAND

Chain B5: 85% 10% 5%



• Molecule 62: STAPLE STRAND

Chain B6: 76% 10% 10%



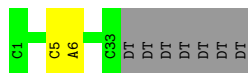
• Molecule 63: STAPLE STRAND

Chain B7: 82% 18%



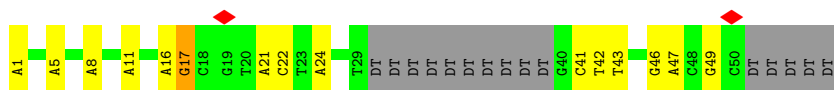
• Molecule 64: STAPLE STRAND

Chain B8: 78% 5% 18%



• Molecule 65: STAPLE STRAND

Chain B9: 45% 25% 27%



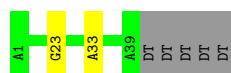
• Molecule 66: STAPLE STRAND

Chain BB: 85% 15%



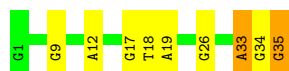
• Molecule 67: STAPLE STRAND

Chain BC: 84% 5% 11%



- Molecule 68: STAPLE STRAND

Chain BD: 74% 20% 6%



- Molecule 69: STAPLE STRAND

Chain BE: 71% 15% 15%



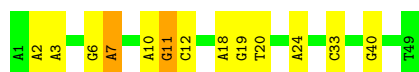
- Molecule 70: STAPLE STRAND

Chain BF: 85% 12% .



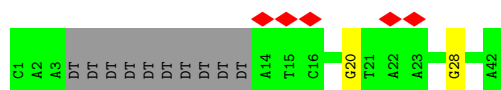
- Molecule 71: STAPLE STRAND

Chain BG: 73% 22% .



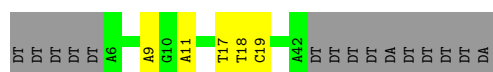
- Molecule 72: STAPLE STRAND

Chain BH: 12% 71% 5% 24%



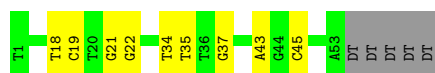
- Molecule 73: STAPLE STRAND

Chain BI: 52% 12% 36%

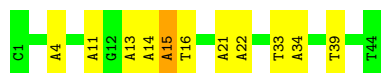
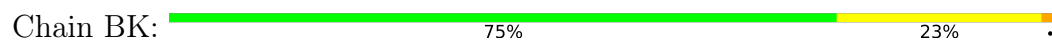


- Molecule 74: STAPLE STRAND

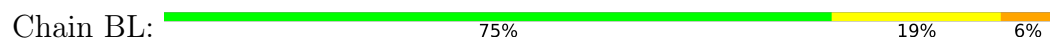
Chain BJ: 76% 16% 9%



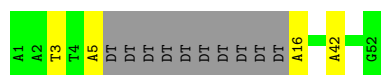
- Molecule 75: STAPLE STRAND



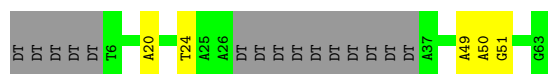
- Molecule 76: STAPLE STRAND



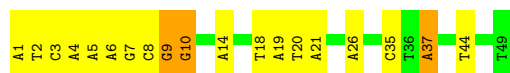
- Molecule 77: STAPLE STRAND



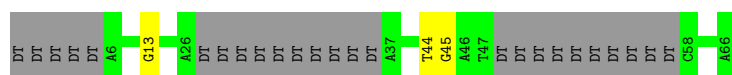
- Molecule 78: STAPLE STRAND



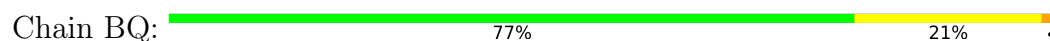
- Molecule 79: STAPLE STRAND



- Molecule 80: STAPLE STRAND

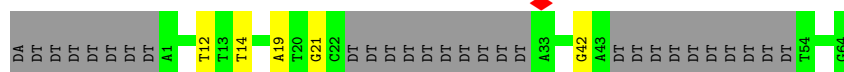


- Molecule 81: STAPLE STRAND





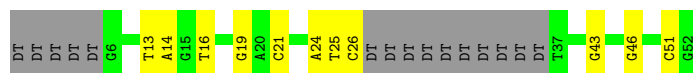
- Molecule 82: STAPLE STRAND



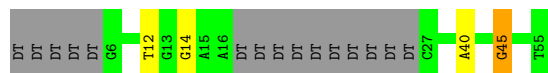
- Molecule 83: STAPLE STRAND



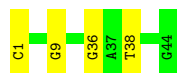
- Molecule 84: STAPLE STRAND



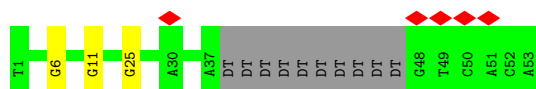
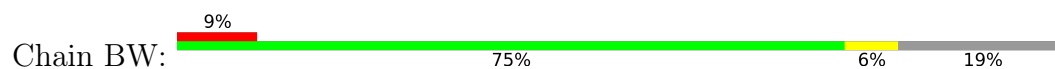
- Molecule 85: STAPLE STRAND



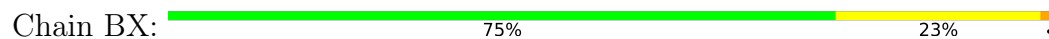
- Molecule 86: STAPLE STRAND



- Molecule 87: STAPLE STRAND

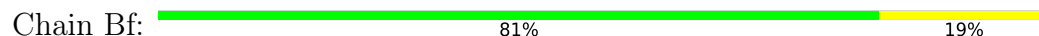


- Molecule 88: STAPLE STRAND

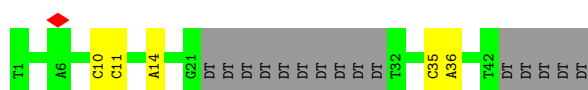




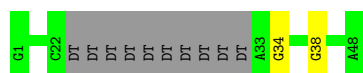
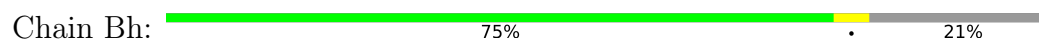
• Molecule 96: STAPLE STRAND



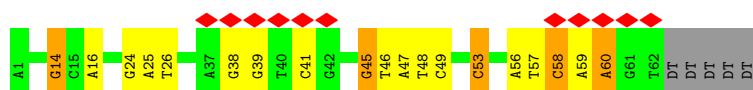
• Molecule 97: STAPLE STRAND



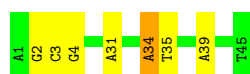
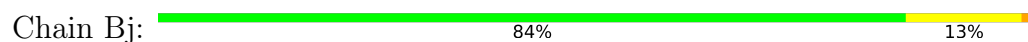
• Molecule 98: STAPLE STRAND



• Molecule 99: STAPLE STRAND



• Molecule 100: STAPLE STRAND

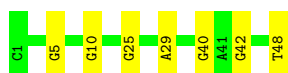


• Molecule 101: STAPLE STRAND

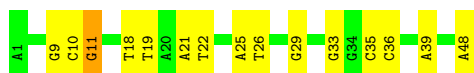


• Molecule 102: STAPLE STRAND

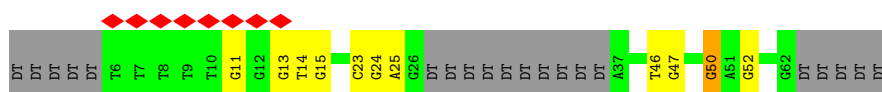




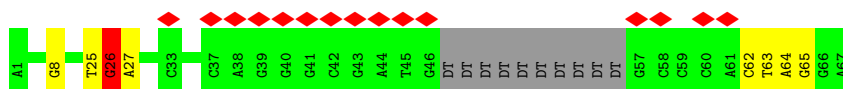
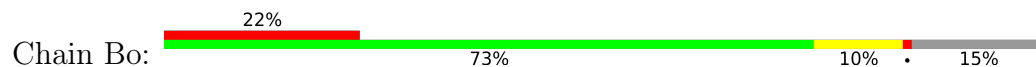
• Molecule 103: STAPLE STRAND



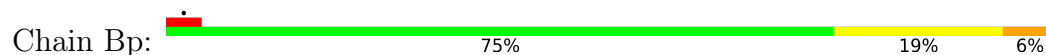
• Molecule 104: STAPLE STRAND



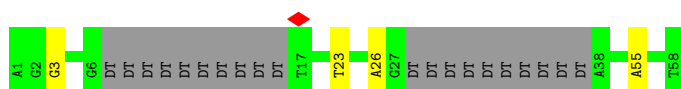
• Molecule 105: STAPLE STRAND



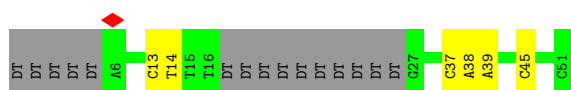
• Molecule 106: STAPLE STRAND



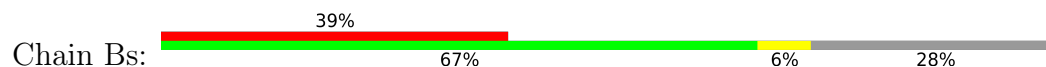
• Molecule 107: STAPLE STRAND

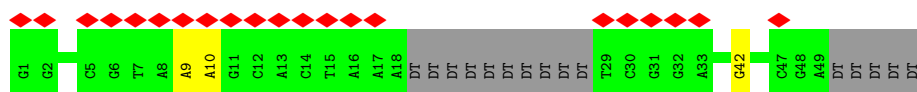


• Molecule 108: STAPLE STRAND

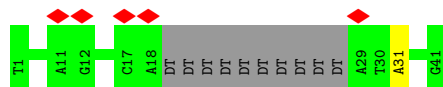
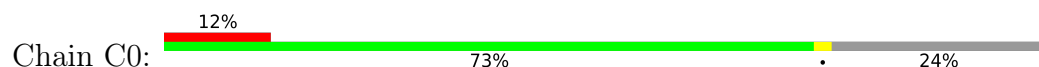


• Molecule 109: STAPLE STRAND

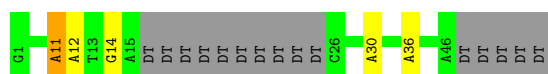




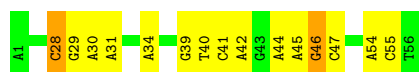
- Molecule 110: STAPLE STRAND



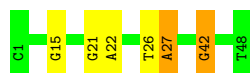
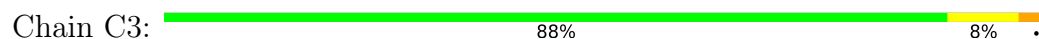
- Molecule 111: STAPLE STRAND



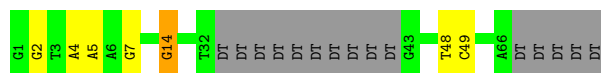
- Molecule 112: STAPLE STRAND



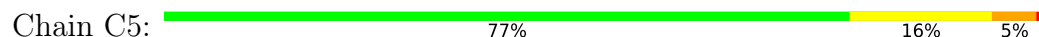
- Molecule 113: STAPLE STRAND



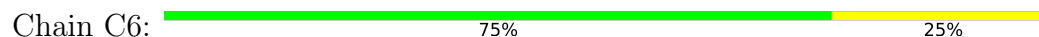
- Molecule 114: STAPLE STRAND

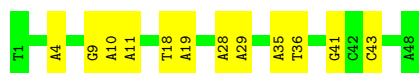


- Molecule 115: STAPLE STRAND



- Molecule 116: STAPLE STRAND





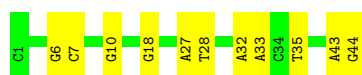
- Molecule 117: STAPLE STRAND

Chain C7: 83% 15%



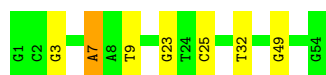
- Molecule 118: STAPLE STRAND

Chain C8: 75% 25%



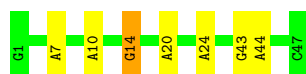
- Molecule 119: STAPLE STRAND

Chain CB: 87% 11%



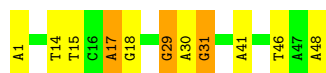
- Molecule 120: STAPLE STRAND

Chain CC: 85% 13%



- Molecule 121: STAPLE STRAND

Chain CD: 77% 17% 6%



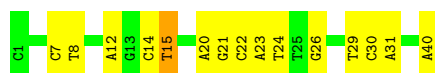
- Molecule 122: STAPLE STRAND

Chain CE: 72% 22% 5%



- Molecule 123: STAPLE STRAND

Chain CF: 62% 35%



- Molecule 124: STAPLE STRAND

Chain CG: 86% 11%



- Molecule 125: STAPLE STRAND

Chain CH: 92% 8%



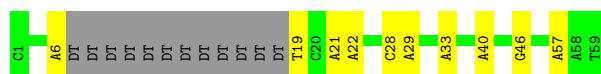
- Molecule 126: STAPLE STRAND

Chain CI: 68% 30%



- Molecule 127: STAPLE STRAND

Chain CJ: 63% 17% 20%



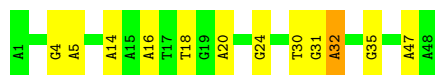
- Molecule 128: STAPLE STRAND

Chain CK: 54% 40% 6%



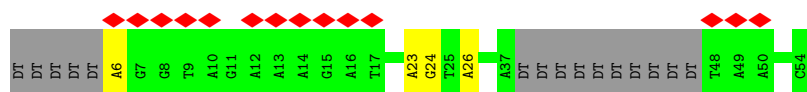
- Molecule 129: STAPLE STRAND

Chain CL: 75% 23%

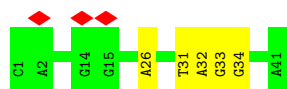


- Molecule 130: STAPLE STRAND

Chain CM: 26% 65% 7% 28%



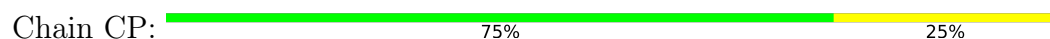
- Molecule 131: STAPLE STRAND



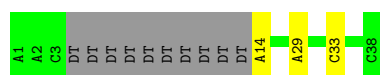
- Molecule 132: STAPLE STRAND



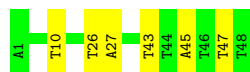
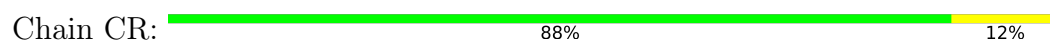
- Molecule 133: STAPLE STRAND



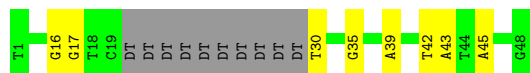
- Molecule 134: STAPLE STRAND



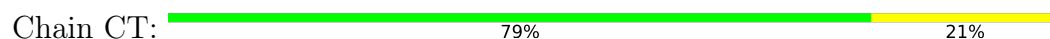
- Molecule 135: STAPLE STRAND



- Molecule 136: STAPLE STRAND



- Molecule 137: STAPLE STRAND





- Molecule 138: STAPLE STRAND

Chain CU: 84% 12% .



- Molecule 139: STAPLE STRAND

Chain CV: 87% 13%



- Molecule 140: STAPLE STRAND

Chain CW: 55% 16% . 26%



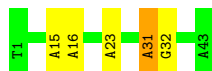
- Molecule 141: STAPLE STRAND

Chain CX: 83% 15% .



- Molecule 142: STAPLE STRAND

Chain CY: 88% 9% .



- Molecule 143: STAPLE STRAND

Chain CZ: 79% 17% .



- Molecule 144: STAPLE STRAND

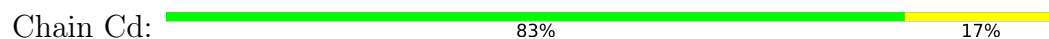
Chain Cb: 68% 32%



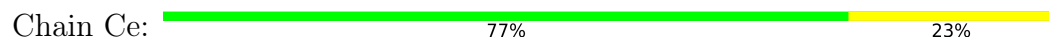
- Molecule 145: STAPLE STRAND



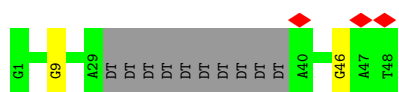
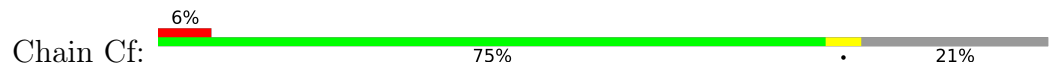
- Molecule 146: STAPLE STRAND



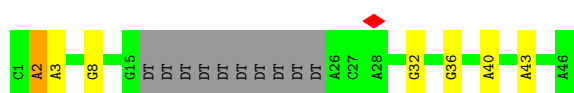
- Molecule 147: STAPLE STRAND



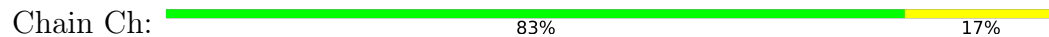
- Molecule 148: STAPLE STRAND



- Molecule 149: STAPLE STRAND

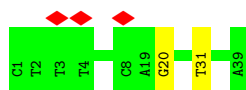


- Molecule 150: STAPLE STRAND



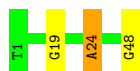
- Molecule 151: STAPLE STRAND





- Molecule 152: STAPLE STRAND

Chain Cp: 94% . .



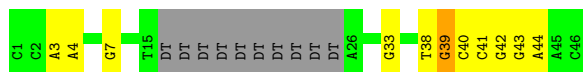
- Molecule 153: STAPLE STRAND

Chain Cq: 82% 15% .



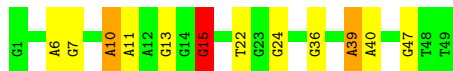
- Molecule 154: STAPLE STRAND

Chain Cr: 54% 22% . 22%



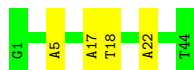
- Molecule 155: STAPLE STRAND

Chain Cs: 76% 18% . .



- Molecule 156: STAPLE STRAND

Chain Ct: 91% 9%



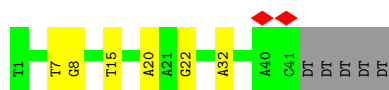
- Molecule 157: STAPLE STRAND

Chain Cu: 88% 7% 5%



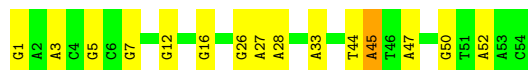
- Molecule 158: STAPLE STRAND

Chain Cv: 76% 13% 11%



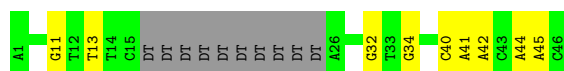
- Molecule 159: STAPLE STRAND

Chain Cw: 72% 26%



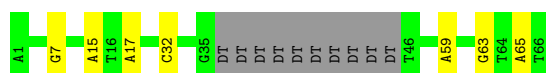
- Molecule 160: STAPLE STRAND

Chain Cx: 59% 20% 22%



- Molecule 161: STAPLE STRAND

Chain Cy: 74% 11% 15%



- Molecule 162: STAPLE STRAND

Chain Cz: 77% 23%



4 Experimental information

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	AA	0.82	18/165646 (0.0%)	1.35	372/255486 (0.1%)
2	A0	0.76	0/1254	1.38	3/1923 (0.2%)
3	A1	0.78	0/989	1.51	7/1514 (0.5%)
4	A2	0.80	0/1149	1.45	7/1762 (0.4%)
5	A3	0.78	0/888	1.52	8/1358 (0.6%)
6	A4	0.77	0/878	1.37	2/1352 (0.1%)
7	A5	0.77	0/1091	1.41	5/1673 (0.3%)
8	A6	0.76	0/1140	1.42	6/1751 (0.3%)
9	A7	0.80	0/969	1.39	2/1484 (0.1%)
10	A8	0.76	0/1093	1.33	3/1679 (0.2%)
11	AB	0.77	0/894	1.29	1/1370 (0.1%)
12	AC	0.77	0/1118	1.33	1/1723 (0.1%)
13	AD	0.79	0/1144	1.40	5/1759 (0.3%)
14	AE	0.77	0/823	1.32	2/1267 (0.2%)
15	AF	0.78	0/1082	1.31	2/1662 (0.1%)
16	AG	0.80	0/1057	1.36	5/1625 (0.3%)
17	AH	0.78	0/1079	1.35	3/1656 (0.2%)
18	AI	0.79	0/1085	1.40	3/1661 (0.2%)
19	AJ	0.77	0/1189	1.40	4/1828 (0.2%)
20	AK	0.74	0/1342	1.37	5/2055 (0.2%)
21	AL	0.77	0/1085	1.32	1/1669 (0.1%)
22	AM	0.73	0/1107	1.26	1/1693 (0.1%)
23	AN	0.79	0/1084	1.38	4/1664 (0.2%)
24	AO	0.78	0/1075	1.38	7/1649 (0.4%)
25	AP	0.76	0/897	1.32	1/1375 (0.1%)
26	AQ	0.81	0/1302	1.49	10/1999 (0.5%)
27	AR	0.77	0/1094	1.35	2/1681 (0.1%)
28	AS	0.81	0/895	1.42	5/1372 (0.4%)
29	AT	0.79	0/1091	1.35	2/1674 (0.1%)
30	AU	0.76	0/1085	1.36	5/1661 (0.3%)
31	AV	0.74	0/1178	1.32	0/1807
32	AW	0.79	0/783	1.40	3/1202 (0.2%)
33	AX	0.78	0/1074	1.41	7/1643 (0.4%)
34	AY	0.79	0/723	1.46	6/1109 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	AZ	0.78	0/1211	1.37	7/1854 (0.4%)
36	Ab	0.76	0/1015	1.36	2/1557 (0.1%)
37	Ac	0.77	0/1252	1.36	6/1920 (0.3%)
38	Ad	0.74	0/1069	1.31	4/1637 (0.2%)
39	Af	0.78	0/1082	1.41	5/1656 (0.3%)
40	Ag	0.79	0/1098	1.35	3/1689 (0.2%)
41	Ah	0.75	0/971	1.34	1/1486 (0.1%)
42	Ai	0.80	0/809	1.38	2/1239 (0.2%)
43	Aj	0.78	0/1412	1.45	13/2166 (0.6%)
44	Ak	0.79	0/1065	1.47	10/1637 (0.6%)
45	Al	0.75	0/1056	1.37	4/1614 (0.2%)
46	Am	0.76	0/1077	1.37	5/1650 (0.3%)
47	An	0.76	0/1088	1.28	1/1672 (0.1%)
48	Ao	0.77	0/810	1.35	2/1241 (0.2%)
49	As	0.75	0/1085	1.34	2/1666 (0.1%)
50	Au	0.77	0/1075	1.36	5/1650 (0.3%)
51	Av	0.76	0/975	1.28	1/1495 (0.1%)
52	Aw	0.77	0/1072	1.39	7/1642 (0.4%)
53	Ax	0.76	0/1067	1.30	1/1640 (0.1%)
54	Ay	0.77	0/638	1.31	2/979 (0.2%)
55	Az	0.78	0/828	1.36	5/1273 (0.4%)
56	B0	0.77	0/1094	1.30	1/1683 (0.1%)
57	B1	0.76	0/1013	1.31	1/1557 (0.1%)
58	B2	0.81	0/825	1.41	7/1268 (0.6%)
59	B3	0.76	0/1094	1.30	2/1683 (0.1%)
60	B4	0.78	0/745	1.38	2/1142 (0.2%)
61	B5	0.76	0/917	1.36	3/1410 (0.2%)
62	B6	0.78	0/1047	1.45	3/1614 (0.2%)
63	B7	0.77	0/996	1.33	2/1533 (0.1%)
64	B8	0.75	0/730	1.28	0/1117
65	B9	0.78	0/907	1.43	9/1393 (0.6%)
66	BB	0.78	0/1104	1.32	2/1700 (0.1%)
67	BC	0.76	0/897	1.33	0/1381
68	BD	0.77	0/820	1.37	2/1265 (0.2%)
69	BE	0.77	0/1329	1.34	3/2044 (0.1%)
70	BF	0.77	0/906	1.37	3/1393 (0.2%)
71	BG	0.79	0/1134	1.49	9/1746 (0.5%)
72	BH	0.78	0/722	1.36	0/1107
73	BI	0.76	0/609	1.34	3/935 (0.3%)
74	BJ	0.79	0/1205	1.36	4/1853 (0.2%)
75	BK	0.78	0/1005	1.48	9/1543 (0.6%)
76	BL	0.77	0/1079	1.38	7/1657 (0.4%)
77	BM	0.79	1/959 (0.1%)	1.27	0/1475

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	BN	0.80	0/1086	1.41	3/1669 (0.2%)
79	BO	0.76	0/1098	1.38	11/1687 (0.7%)
80	BP	0.77	0/921	1.31	1/1414 (0.1%)
81	BQ	0.78	0/1087	1.38	7/1672 (0.4%)
82	BR	0.74	0/822	1.29	1/1263 (0.1%)
83	BS	0.76	0/1081	1.30	4/1660 (0.2%)
84	BT	0.79	0/843	1.36	4/1298 (0.3%)
85	BU	0.79	0/909	1.34	4/1398 (0.3%)
86	BV	0.78	0/1003	1.35	2/1545 (0.1%)
87	BW	0.76	0/979	1.28	0/1507
88	BX	0.76	0/1114	1.34	1/1717 (0.1%)
89	BY	0.77	0/976	1.36	4/1500 (0.3%)
90	BZ	0.77	0/976	1.34	0/1499
91	Ba	0.78	0/1086	1.41	9/1670 (0.5%)
92	Bb	0.80	0/1093	1.40	5/1679 (0.3%)
93	Bc	0.76	0/1135	1.33	3/1746 (0.2%)
94	Bd	0.78	0/937	1.30	0/1443
95	Be	0.78	0/1096	1.33	3/1687 (0.2%)
96	Bf	0.81	0/1101	1.45	3/1694 (0.2%)
97	Bg	0.75	0/723	1.32	2/1110 (0.2%)
98	Bh	0.77	0/880	1.26	0/1358
99	Bi	0.77	0/1406	1.37	7/2161 (0.3%)
100	Bj	0.76	0/1016	1.37	3/1560 (0.2%)
101	Bk	0.77	0/1085	1.31	2/1670 (0.1%)
102	Bl	0.79	0/1110	1.35	3/1709 (0.2%)
103	Bm	0.77	0/1078	1.34	7/1654 (0.4%)
104	Bn	0.78	0/1096	1.29	4/1693 (0.2%)
105	Bo	0.77	0/1292	1.29	4/1986 (0.2%)
106	Bp	0.78	0/1108	1.38	6/1706 (0.4%)
107	Bq	0.76	0/881	1.29	1/1357 (0.1%)
108	Br	0.76	0/818	1.29	2/1259 (0.2%)
109	Bs	0.75	0/901	1.26	0/1386
110	C0	0.76	0/709	1.27	0/1091
111	C1	0.75	0/824	1.35	2/1265 (0.2%)
112	C2	0.74	0/1259	1.32	6/1930 (0.3%)
113	C3	0.76	0/1077	1.33	3/1651 (0.2%)
114	C4	0.76	0/1269	1.32	4/1950 (0.2%)
115	C5	0.78	0/1433	1.37	10/2209 (0.5%)
116	C6	0.75	0/1097	1.40	7/1685 (0.4%)
117	C7	0.76	0/1181	1.33	2/1817 (0.1%)
118	C8	0.78	0/998	1.36	6/1533 (0.4%)
119	CB	0.75	0/1215	1.29	2/1867 (0.1%)
120	CC	0.78	0/1082	1.39	3/1666 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
121	CD	0.79	0/1106	1.41	8/1702 (0.5%)
122	CE	0.75	0/917	1.46	7/1409 (0.5%)
123	CF	0.74	0/908	1.37	7/1395 (0.5%)
124	CG	0.77	0/1013	1.29	2/1562 (0.1%)
125	CH	0.76	0/1107	1.31	0/1707
126	CI	0.76	0/996	1.33	5/1528 (0.3%)
127	CJ	0.77	0/1061	1.38	3/1626 (0.2%)
128	CK	0.77	0/1103	1.38	8/1695 (0.5%)
129	CL	0.76	0/1082	1.39	3/1659 (0.2%)
130	CM	0.78	0/903	1.35	3/1390 (0.2%)
131	CN	0.78	0/955	1.38	2/1474 (0.1%)
132	CO	0.76	0/1092	1.40	5/1678 (0.3%)
133	CP	0.77	0/1279	1.35	7/1969 (0.4%)
134	CQ	0.78	0/623	1.37	1/952 (0.1%)
135	CR	0.76	0/1084	1.33	4/1667 (0.2%)
136	CS	0.78	0/867	1.37	0/1333
137	CT	0.76	0/1102	1.36	4/1695 (0.2%)
138	CU	0.78	0/728	1.45	3/1119 (0.3%)
139	CV	0.78	0/1192	1.35	3/1830 (0.2%)
140	CW	0.80	0/629	1.34	3/965 (0.3%)
141	CX	0.77	0/1055	1.31	8/1618 (0.5%)
142	CY	0.77	0/979	1.42	4/1501 (0.3%)
143	CZ	0.78	0/1113	1.40	4/1713 (0.2%)
144	Cb	0.75	0/999	1.43	6/1532 (0.4%)
145	Cc	0.77	0/1174	1.32	4/1800 (0.2%)
146	Cd	0.77	0/965	1.39	2/1486 (0.1%)
147	Ce	0.76	0/1175	1.41	8/1802 (0.4%)
148	Cf	0.75	0/862	1.35	0/1321
149	Cg	0.78	0/827	1.33	2/1270 (0.2%)
150	Ch	0.78	0/1048	1.39	6/1605 (0.4%)
151	Ck	0.76	0/653	1.28	2/1004 (0.2%)
152	Cp	0.76	0/1095	1.32	1/1682 (0.1%)
153	Cq	0.78	0/930	1.35	1/1436 (0.1%)
154	Cr	0.80	0/816	1.48	8/1251 (0.6%)
155	Cs	0.77	0/1140	1.40	3/1756 (0.2%)
156	Ct	0.76	0/991	1.33	1/1521 (0.1%)
157	Cu	0.75	0/1366	1.37	4/2096 (0.2%)
158	Cv	0.77	0/918	1.36	2/1409 (0.1%)
159	Cw	0.79	0/1232	1.38	8/1893 (0.4%)
160	Cx	0.79	0/820	1.46	6/1258 (0.5%)
161	Cy	0.76	0/1286	1.33	2/1977 (0.1%)
162	Cz	0.77	0/1090	1.37	3/1672 (0.2%)
All	All	0.80	19/330437 (0.0%)	1.35	974/508627 (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	40	448
2	A0	0	6
3	A1	1	4
4	A2	0	2
6	A4	0	2
7	A5	0	4
8	A6	0	4
9	A7	0	3
10	A8	0	5
11	AB	0	1
12	AC	0	3
13	AD	0	2
15	AF	1	4
16	AG	0	3
17	AH	1	2
18	AI	1	2
19	AJ	0	4
20	AK	0	8
21	AL	0	4
22	AM	0	1
23	AN	1	3
24	AO	2	3
25	AP	0	1
26	AQ	2	6
27	AR	0	2
28	AS	0	4
29	AT	1	4
30	AU	1	4
31	AV	1	5
33	AX	0	3
34	AY	1	4
35	AZ	2	4
36	Ab	2	2
37	Ac	0	2
38	Ad	0	2
39	Af	0	1
40	Ag	0	1
41	Ah	1	3
42	Ai	0	1

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

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

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

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	AA	3933	DA	O3'-P	-62.75	0.67	1.61
1	AA	437	DT	O3'-P	-43.89	0.95	1.61
1	AA	186	DT	O3'-P	-40.82	0.99	1.61
1	AA	4125	DG	O3'-P	33.14	2.10	1.61
1	AA	955	DG	O3'-P	30.77	2.07	1.61

The worst 5 of 974 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	35	DC	O3'-P-O5'	-59.32	15.02	104.00
1	AA	378	DG	O3'-P-O5'	-57.21	18.19	104.00
1	AA	378	DG	P-O3'-C3'	-55.18	37.43	120.20
1	AA	35	DC	P-O3'-C3'	-47.32	49.22	120.20
1	AA	511	DA	P-O3'-C3'	-42.47	56.49	120.20

5 of 121 chirality outliers are listed below:

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

5 of 919 planarity outliers are listed below:

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

5.2 Too-close contacts [i](#)

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	147963	0	82380	494	0
2	A0	1116	0	632	2	0
3	A1	884	0	511	23	0
4	A2	1019	0	570	6	0
5	A3	796	0	464	8	0
6	A4	780	0	433	2	0
7	A5	971	0	546	3	0
8	A6	1016	0	574	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	A7	863	0	482	1	0
10	A8	976	0	557	2	0
11	AB	799	0	450	0	0
12	AC	993	0	546	5	0
13	AD	1018	0	562	4	0
14	AE	734	0	411	28	0
15	AF	969	0	548	1	0
16	AG	939	0	516	3	0
17	AH	964	0	543	7	0
18	AI	967	0	551	2	0
19	AJ	1059	0	594	12	0
20	AK	1202	0	697	5	0
21	AL	971	0	551	10	0
22	AM	993	0	579	4	0
23	AN	968	0	545	9	0
24	AO	962	0	549	0	0
25	AP	802	0	457	1	0
26	AQ	1160	0	649	9	0
27	AR	975	0	547	0	0
28	AS	794	0	443	0	0
29	AT	973	0	550	4	0
30	AU	967	0	551	10	0
31	AV	1051	0	597	15	0
32	AW	701	0	402	1	0
33	AX	959	0	548	5	0
34	AY	645	0	362	0	0
35	AZ	1082	0	618	5	0
36	Ab	907	0	517	3	0
37	Ac	1115	0	632	39	0
38	Ad	958	0	555	2	0
39	Af	964	0	547	6	0
40	Ag	979	0	547	0	0
41	Ah	872	0	509	1	0
42	Ai	722	0	409	0	0
43	Aj	1257	0	710	2	0
44	Ak	946	0	525	3	0
45	Al	949	0	559	4	0
46	Am	963	0	550	1	0
47	An	972	0	549	2	0
48	Ao	724	0	412	4	0
49	As	971	0	560	5	0
50	Au	963	0	552	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
51	Av	869	0	490	5	0
52	Aw	960	0	556	2	0
53	Ax	953	0	538	2	0
54	Ay	568	0	320	0	0
55	Az	737	0	412	1	0
56	B0	977	0	545	2	0
57	B1	900	0	501	2	0
58	B2	734	0	406	0	0
59	B3	976	0	546	3	0
60	B4	664	0	374	2	0
61	B5	816	0	454	3	0
62	B6	929	0	507	1	0
63	B7	892	0	507	1	0
64	B8	653	0	372	1	0
65	B9	810	0	460	5	0
66	BB	982	0	541	2	0
67	BC	798	0	444	1	0
68	BD	727	0	393	11	0
69	BE	1183	0	659	3	0
70	BF	810	0	462	2	0
71	BG	1007	0	553	1	0
72	BH	644	0	365	0	0
73	BI	544	0	310	0	0
74	BJ	1076	0	604	2	0
75	BK	894	0	502	13	0
76	BL	966	0	550	5	0
77	BM	855	0	480	4	0
78	BN	970	0	547	2	0
79	BO	984	0	562	15	0
80	BP	824	0	469	0	0
81	BQ	971	0	545	4	0
82	BR	733	0	415	1	0
83	BS	967	0	547	24	0
84	BT	753	0	421	4	0
85	BU	813	0	463	0	0
86	BV	895	0	499	0	0
87	BW	874	0	490	0	0
88	BX	991	0	551	7	0
89	BY	871	0	491	1	0
90	BZ	870	0	488	2	0
91	Ba	972	0	551	5	0
92	Bb	974	0	543	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
93	Bc	1015	0	571	5	0
94	Bd	836	0	465	0	0
95	Be	978	0	545	4	0
96	Bf	981	0	543	10	0
97	Bg	646	0	366	2	0
98	Bh	784	0	433	0	0
99	Bi	1255	0	704	35	0
100	Bj	907	0	510	16	0
101	Bk	964	0	531	1	0
102	Bl	986	0	539	1	0
103	Bm	964	0	548	17	0
104	Bn	975	0	530	9	0
105	Bo	1154	0	647	1	0
106	Bp	985	0	540	2	0
107	Bq	784	0	434	0	0
108	Br	732	0	413	4	0
109	Bs	800	0	438	17	0
110	C0	632	0	352	1	0
111	C1	732	0	409	2	0
112	C2	1125	0	645	17	0
113	C3	962	0	547	1	0
114	C4	1133	0	640	1	0
115	C5	1275	0	703	16	0
116	C6	977	0	549	2	0
117	C7	1056	0	602	4	0
118	C8	892	0	508	1	0
119	CB	1088	0	621	3	0
120	CC	963	0	534	2	0
121	CD	984	0	547	2	0
122	CE	816	0	458	6	0
123	CF	811	0	460	10	0
124	CG	904	0	503	1	0
125	CH	987	0	549	0	0
126	CI	889	0	504	8	0
127	CJ	946	0	537	2	0
128	CK	981	0	548	7	0
129	CL	967	0	555	13	0
130	CM	801	0	439	1	0
131	CN	848	0	464	2	0
132	CO	975	0	554	10	0
133	CP	1140	0	633	5	0
134	CQ	557	0	323	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
135	CR	969	0	548	2	0
136	CS	773	0	435	6	0
137	CT	982	0	551	1	0
138	CU	648	0	361	2	0
139	CV	1067	0	612	1	0
140	CW	564	0	327	7	0
141	CX	944	0	537	0	0
142	CY	870	0	489	2	0
143	CZ	987	0	543	8	0
144	Cb	891	0	509	4	0
145	Cc	1048	0	595	4	0
146	Cd	859	0	481	2	0
147	Ce	1049	0	597	1	0
148	Cf	768	0	436	1	0
149	Cg	735	0	410	3	0
150	Ch	938	0	536	0	0
151	Ck	585	0	334	0	0
152	Cp	976	0	549	0	0
153	Cq	827	0	453	2	0
154	Cr	727	0	409	9	0
155	Cs	1012	0	558	3	0
156	Ct	886	0	507	3	0
157	Cu	1216	0	685	5	0
158	Cv	823	0	475	1	0
159	Cw	1098	0	615	4	0
160	Cx	730	0	411	0	0
161	Cy	1145	0	643	3	0
162	Cz	970	0	541	1	0
All	All	294953	0	165169	913	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

The worst 5 of 913 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A1:18:DT:C5'	3:A1:19:DA:H2''	1.16	1.61
1:AA:378:DG:H5''	1:AA:379:DA:C2'	1.33	1.57
3:A1:18:DT:H5''	3:A1:19:DA:C2'	1.32	1.57
37:Ac:22:DA:C2'	37:Ac:23:DT:H5''	1.29	1.55
1:AA:3666:DA:C5'	14:AE:7:DT:C7	1.81	1.54

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	AA	23
15	AF	1

The worst 5 of 24 chain breaks are listed below:

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

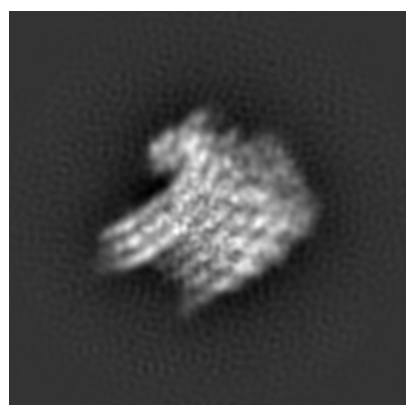
6 Map visualisation [i](#)

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

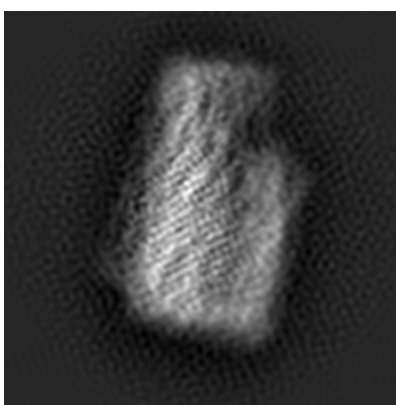
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

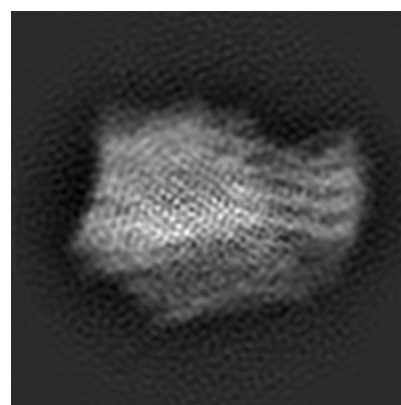
6.1.1 Primary map



X



Y

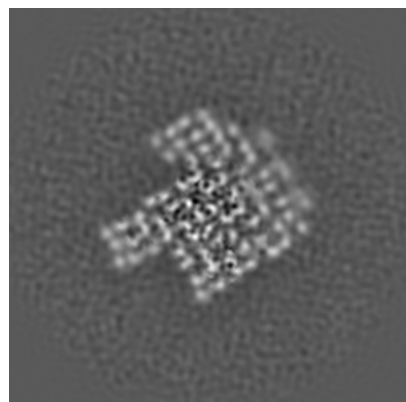


Z

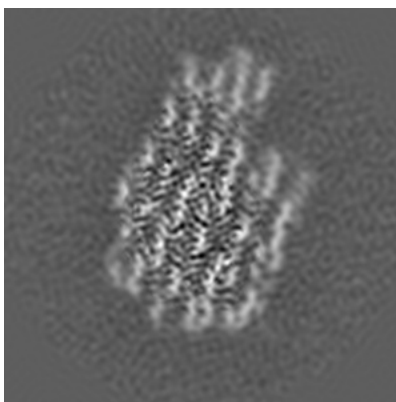
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

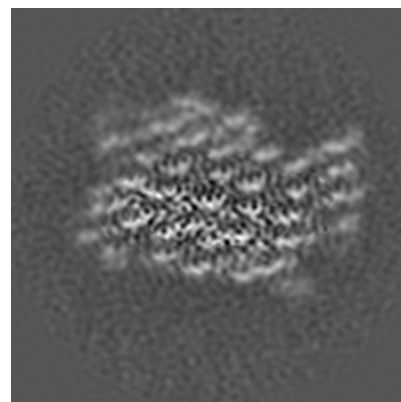
6.2.1 Primary map



X Index: 86



Y Index: 86

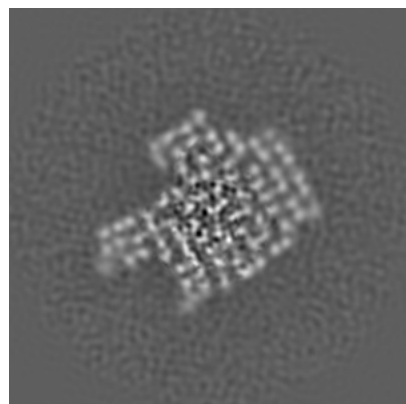


Z Index: 86

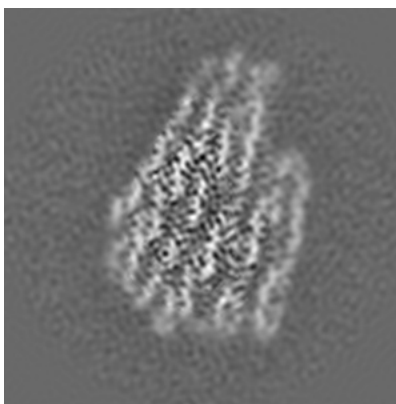
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

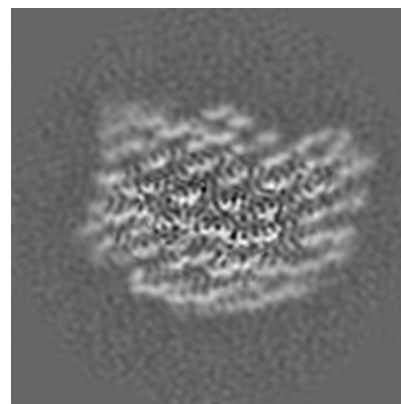
6.3.1 Primary map



X Index: 71



Y Index: 82

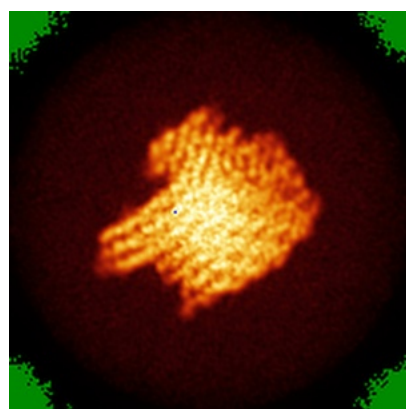


Z Index: 78

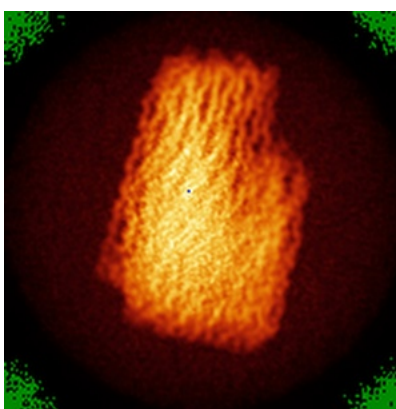
The images above show the largest variance slices of the map in three orthogonal directions.

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

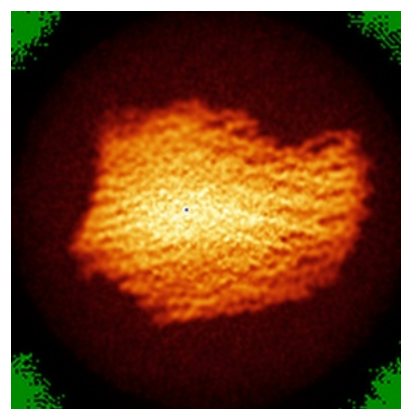
6.4.1 Primary map



X



Y

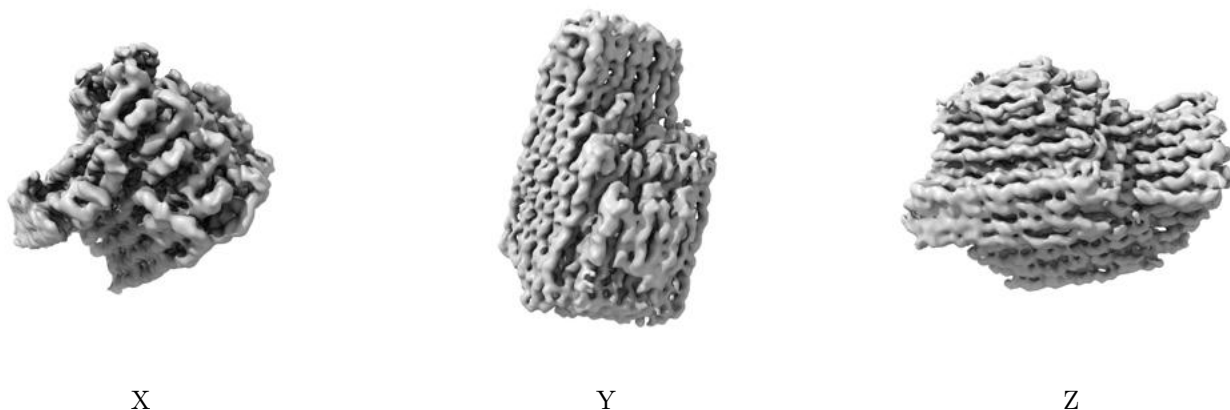


Z

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 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

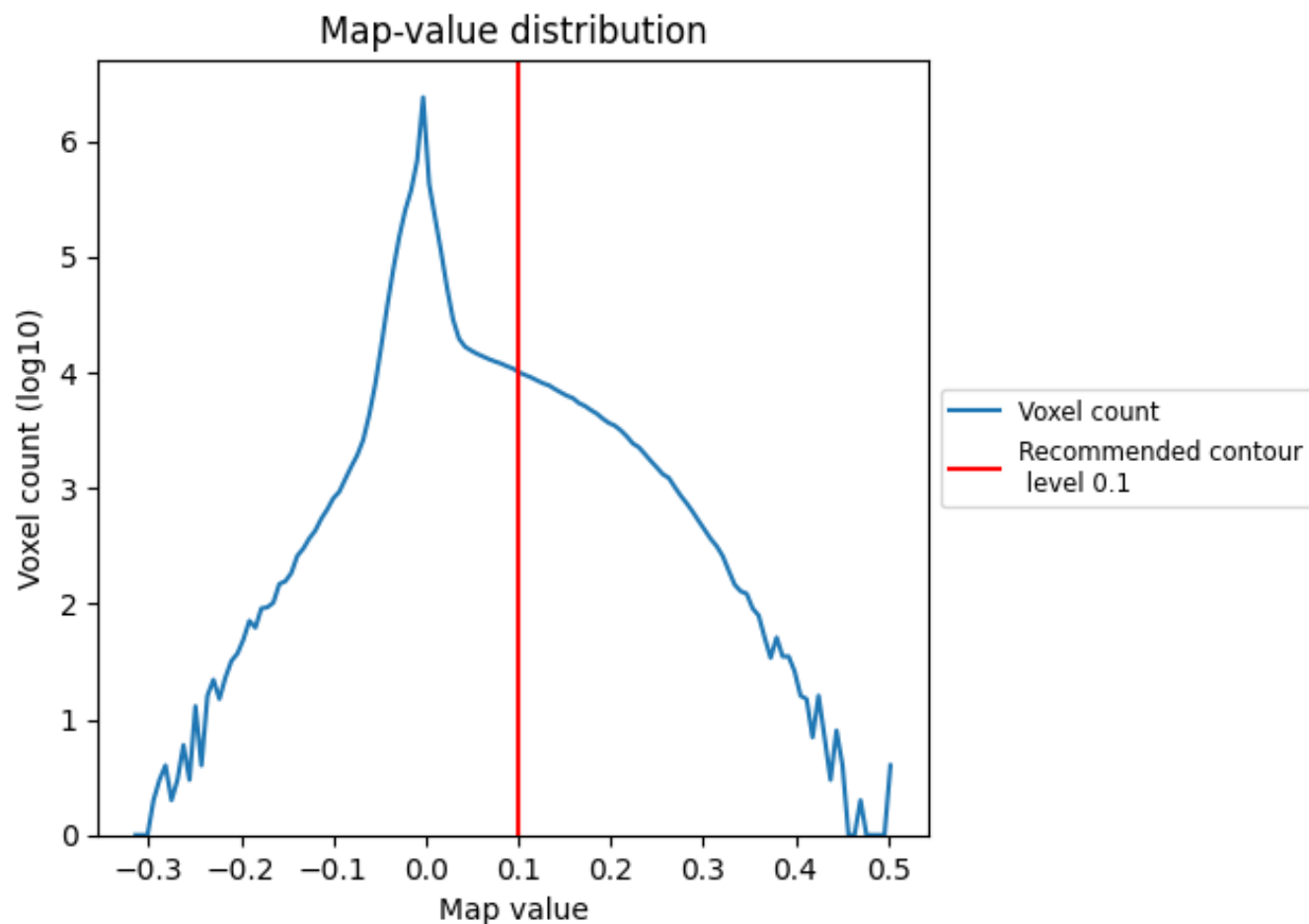
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

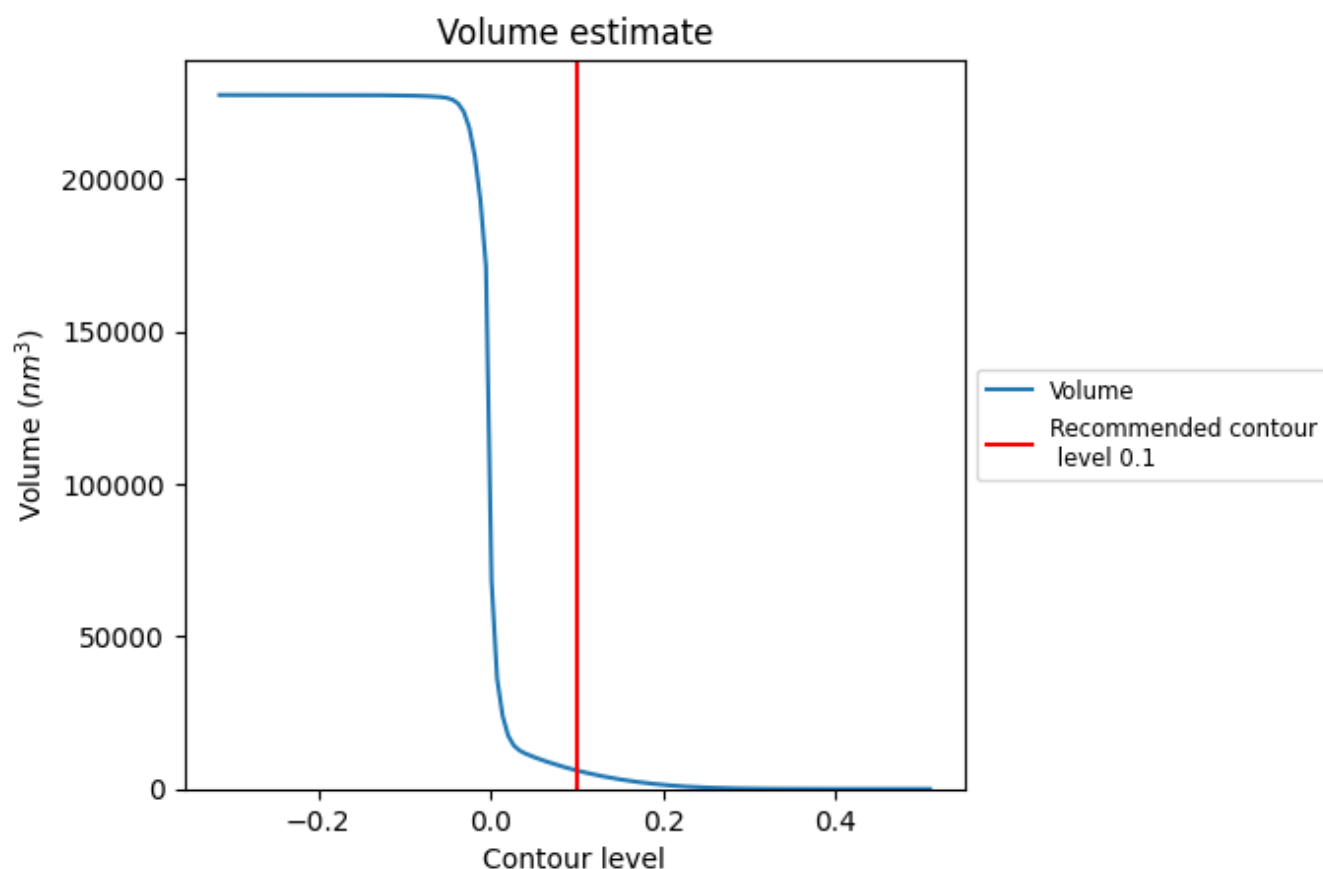
This section contains the results of statistical analysis of the map.

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.

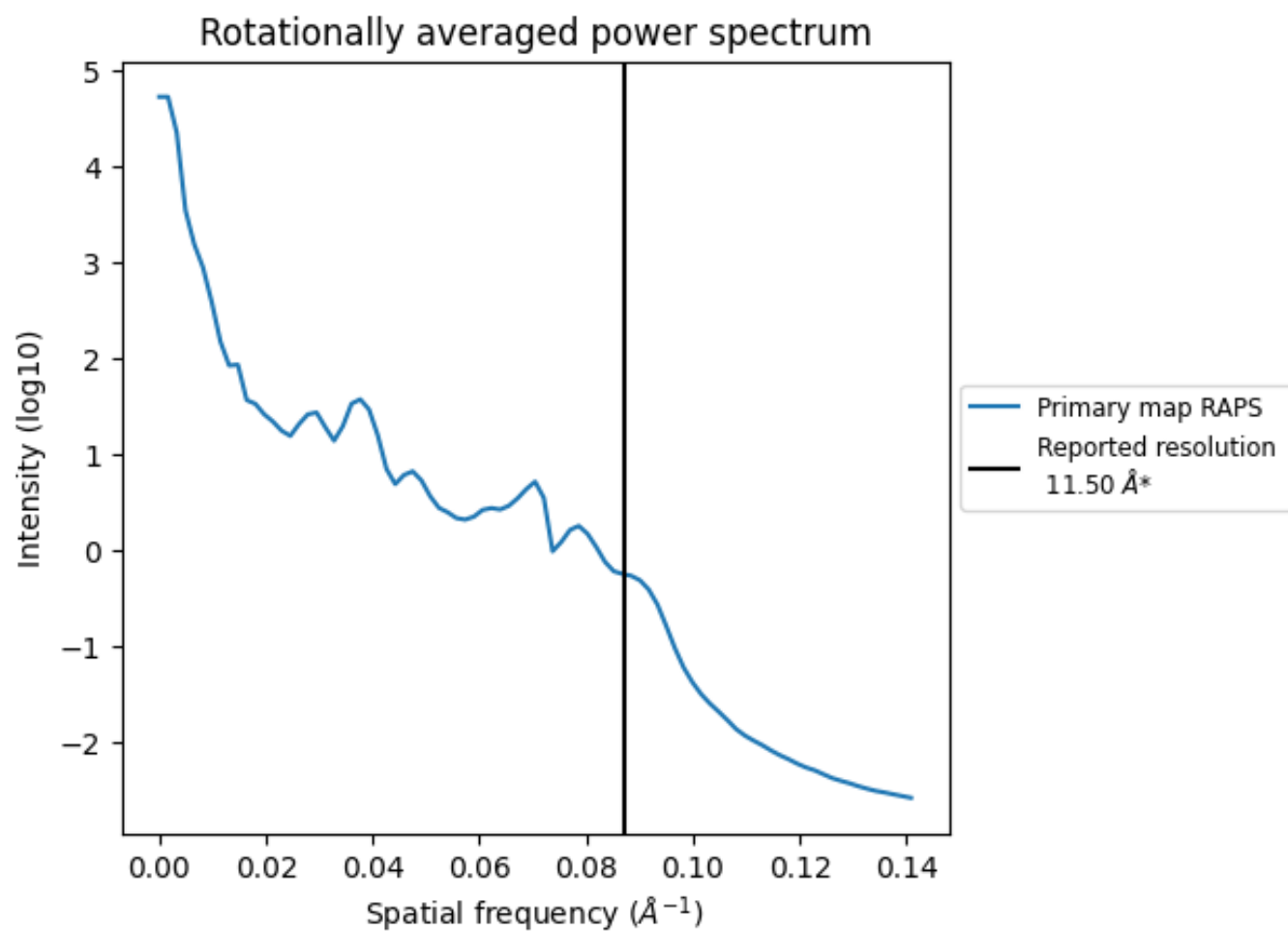
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 6064 nm³; this corresponds to an approximate mass of 5477 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.087 Å⁻¹

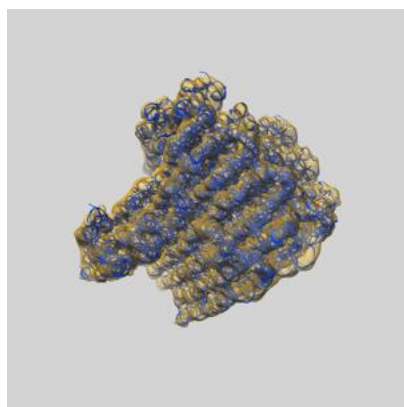
8 Fourier-Shell correlation

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

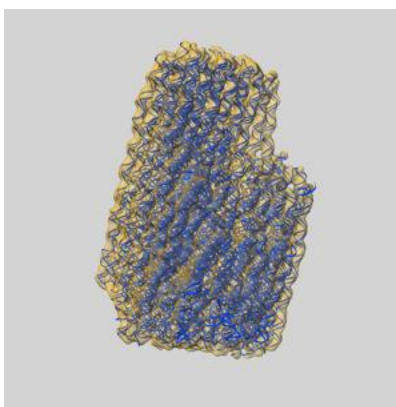
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-2210 and PDB model 4V5X. Per-residue inclusion information can be found in [section 3](#) on [page 34](#).

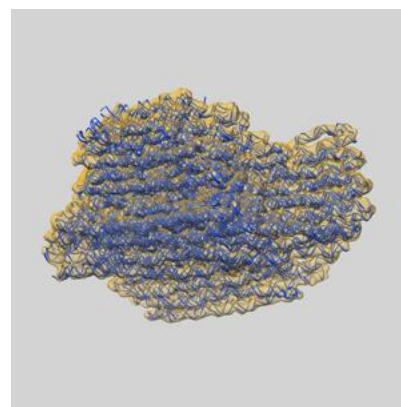
9.1 Map-model overlay [i](#)



X



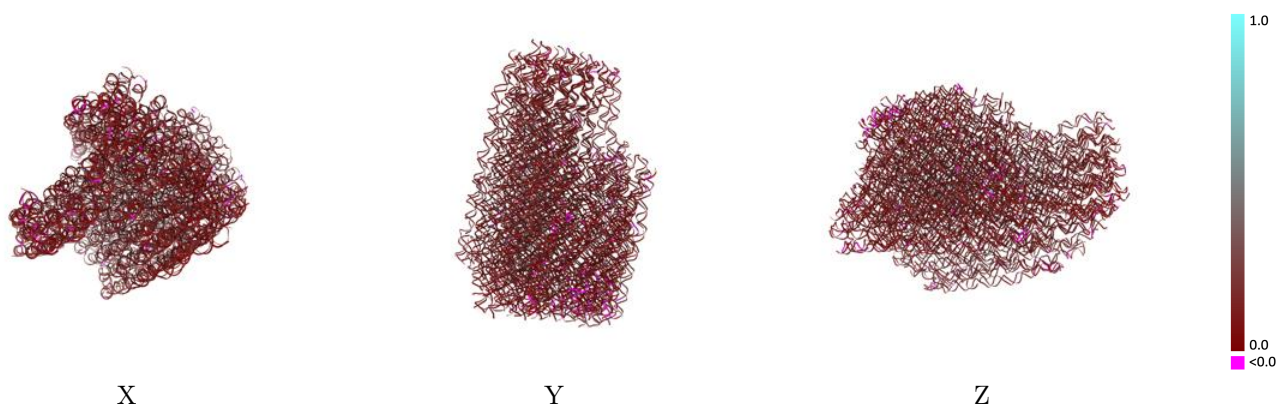
Y



Z

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

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

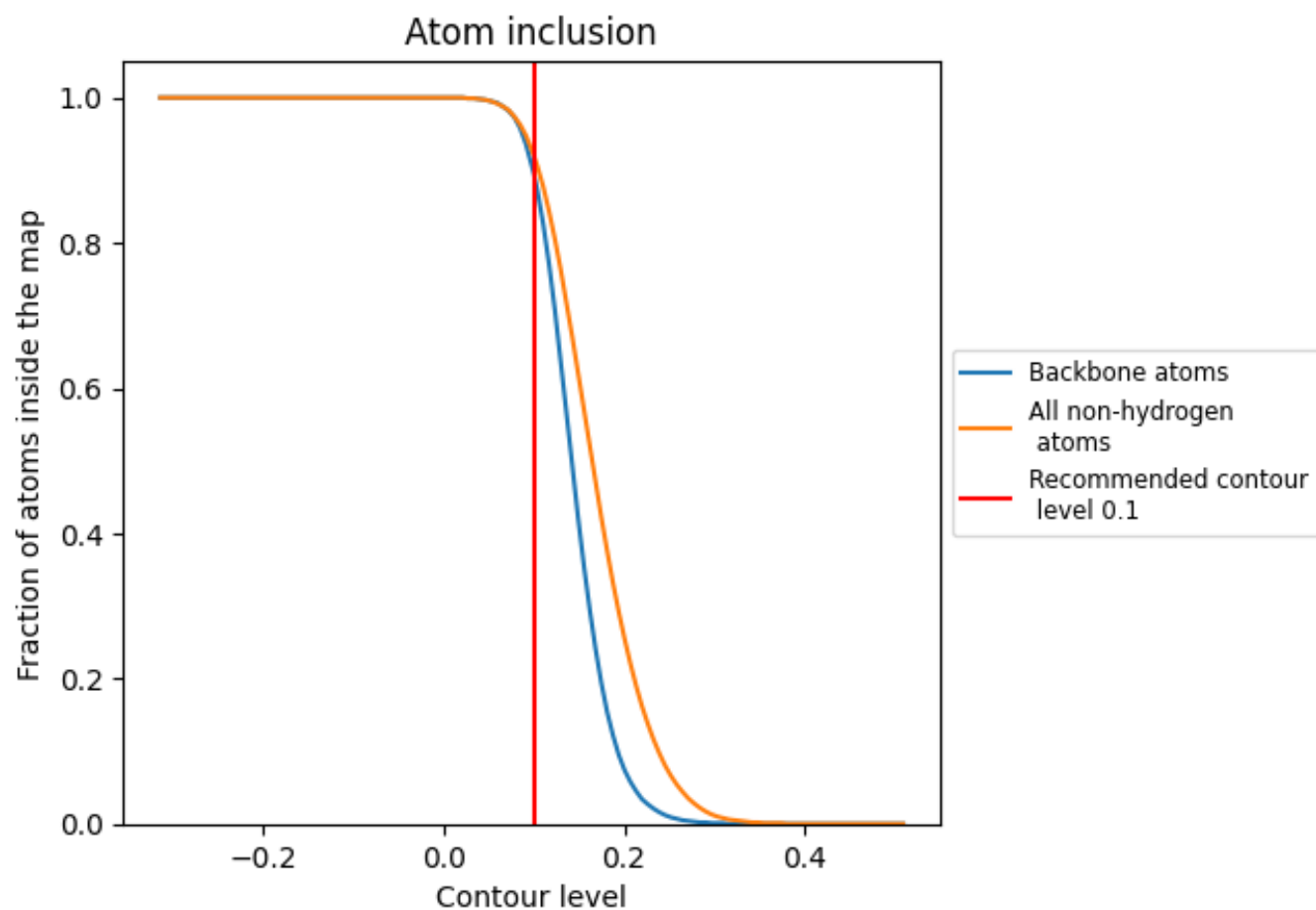


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 92% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

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

Chain	Atom inclusion	Q-score
All	 0.9200	 0.1390
A0	 0.9750	 0.1650
A1	 0.9730	 0.1160
A2	 0.9500	 0.1680
A3	 0.9810	 0.1910
A4	 0.9170	 0.1090
A5	 0.9780	 0.1690
A6	 0.9750	 0.1390
A7	 0.9570	 0.1600
A8	 0.9530	 0.1710
AA	 0.9190	 0.1390
AB	 0.9250	 0.1300
AC	 0.9850	 0.1360
AD	 0.9540	 0.1260
AE	 0.7830	 0.1020
AF	 0.9590	 0.1230
AG	 0.9610	 0.1300
AH	 0.9640	 0.1260
AI	 0.9610	 0.1770
AJ	 0.9650	 0.1350
AK	 0.9830	 0.1950
AL	 0.8990	 0.1240
AM	 0.9680	 0.1610
AN	 0.9650	 0.1490
AO	 0.9600	 0.1310
AP	 0.9810	 0.1650
AQ	 0.9630	 0.1460
AR	 0.8960	 0.0980
AS	 0.9690	 0.1330
AT	 0.9550	 0.1490
AU	 0.9700	 0.1810
AV	 0.9740	 0.1680
AW	 0.6690	 0.0820
AX	 0.9780	 0.1860
AY	 0.6640	 0.1140



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Chain	Atom inclusion	Q-score
AZ	 0.9510	 0.1310
Ab	 0.9750	 0.1520
Ac	 0.9470	 0.1410
Ad	 0.9530	 0.1720
Af	 0.9620	 0.1480
Ag	 0.9620	 0.1400
Ah	 0.9470	 0.1490
Ai	 0.9330	 0.1140
Aj	 0.9610	 0.1830
Ak	 0.9560	 0.1720
Al	 0.9310	 0.1720
Am	 0.9320	 0.1580
An	 0.9540	 0.1620
Ao	 0.9490	 0.1940
As	 0.9700	 0.1700
Au	 0.9900	 0.1540
Av	 0.9660	 0.1540
Aw	 0.9560	 0.1800
Ax	 0.9410	 0.1190
Ay	 0.7590	 0.0960
Az	 0.9310	 0.1090
B0	 0.9430	 0.1420
B1	 0.9520	 0.1370
B2	 0.9440	 0.1720
B3	 0.9480	 0.1590
B4	 0.8390	 0.1140
B5	 0.8950	 0.1190
B6	 0.9210	 0.1270
B7	 0.9500	 0.1290
B8	 0.8650	 0.1230
B9	 0.9010	 0.1080
BB	 0.9630	 0.1340
BC	 0.9620	 0.1410
BD	 0.9530	 0.1370
BE	 0.8990	 0.1040
BF	 0.9490	 0.1520
BG	 0.9360	 0.1280
BH	 0.7640	 0.1060
BI	 0.9210	 0.1220
BJ	 0.9200	 0.1400
BK	 0.9510	 0.1780
BL	 0.9420	 0.1700

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Chain	Atom inclusion	Q-score
BM	 0.9590	 0.1590
BN	 0.9170	 0.1100
BO	 0.9470	 0.1490
BP	 0.9370	 0.1130
BQ	 0.9530	 0.1370
BR	 0.8610	 0.1210
BS	 0.9450	 0.1840
BT	 0.9390	 0.1130
BU	 0.9310	 0.1250
BV	 0.9150	 0.0910
BW	 0.7950	 0.1120
BX	 0.9580	 0.1220
BY	 0.9510	 0.1340
BZ	 0.8980	 0.1250
Ba	 0.9010	 0.1480
Bb	 0.7870	 0.1130
Bc	 0.8590	 0.1350
Bd	 0.9150	 0.1250
Be	 0.8790	 0.1320
Bf	 0.9400	 0.1310
Bg	 0.8420	 0.1060
Bh	 0.9000	 0.1280
Bi	 0.7510	 0.0910
Bj	 0.9600	 0.1380
Bk	 0.8800	 0.1160
Bl	 0.8580	 0.1270
Bm	 0.9230	 0.1150
Bn	 0.7090	 0.1140
Bo	 0.6550	 0.0850
Bp	 0.8620	 0.1140
Bq	 0.8890	 0.1020
Br	 0.8370	 0.1200
Bs	 0.3910	 0.0700
C0	 0.7610	 0.1340
C1	 0.9400	 0.1270
C2	 0.9440	 0.1860
C3	 0.9690	 0.1520
C4	 0.8910	 0.1190
C5	 0.9530	 0.1460
C6	 0.8810	 0.1630
C7	 0.9410	 0.1270
C8	 0.9610	 0.1770

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Chain	Atom inclusion	Q-score
CB	 0.9490	 0.1510
CC	 0.9700	 0.1600
CD	 0.9680	 0.1690
CE	 0.9190	 0.1720
CF	 0.9350	 0.1850
CG	 0.9680	 0.1290
CH	 0.9570	 0.1620
CI	 0.9800	 0.1260
CJ	 0.9250	 0.1290
CK	 0.9500	 0.2000
CL	 0.9660	 0.1410
CM	 0.5360	 0.0950
CN	 0.7980	 0.1110
CO	 0.9490	 0.1820
CP	 0.9410	 0.1290
CQ	 0.9030	 0.1200
CR	 0.9600	 0.1340
CS	 0.9290	 0.1260
CT	 0.9530	 0.1990
CU	 0.9380	 0.1320
CV	 0.9720	 0.1260
CW	 0.9680	 0.1130
CX	 0.9420	 0.1630
CY	 0.9470	 0.1500
CZ	 0.9000	 0.1370
Cb	 0.9200	 0.1760
Cc	 0.9460	 0.1060
Cd	 0.9320	 0.1100
Ce	 0.9510	 0.1410
Cf	 0.8710	 0.1170
Cg	 0.9020	 0.1130
Ch	 0.9630	 0.1550
Ck	 0.8070	 0.1020
Cp	 0.9580	 0.1620
Cq	 0.9210	 0.1390
Cr	 0.9400	 0.1120
Cs	 0.9590	 0.1400
Ct	 0.9220	 0.1240
Cu	 0.9420	 0.1600
Cv	 0.9160	 0.1130
Cw	 0.9540	 0.1240
Cx	 0.9110	 0.1090

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Chain	Atom inclusion	Q-score
Cy	 0.9620	 0.1480
Cz	 0.9410	 0.1430