



Full wwPDB EM Validation Report ⓘ

Mar 21, 2026 – 07:06 PM UTC

PDB ID : 7ARV / pdb_00007arv
EMDB ID : EMD-11379
Title : TwistTower_native-twist
Authors : Kube, M.; Kohler, F.; Feigl, E.; Nagel-Yuksel, B.; Willner, E.M.; Funke, J.J.;
Gerling, T.; Stommer, P.; Honemann, M.N.; Martin, T.G.; Scheres, S.H.W.;
Dietz, H.
Deposited on : 2020-10-26
Resolution : 7.40 Å(reported)

This is a Full wwPDB EM Validation 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:

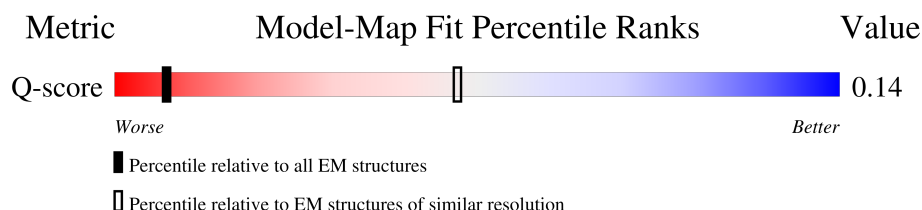
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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

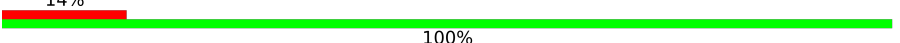
The reported resolution of this entry is 7.40 Å.

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.



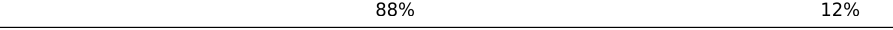
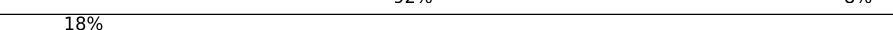
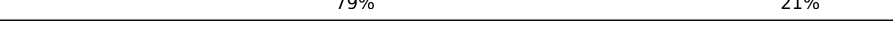
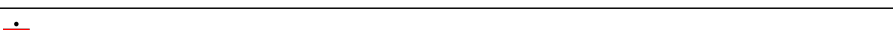
Metric	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Q-score	25397	412 (6.90 - 7.90)

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	8064	 14% 82% 17% .
2	AB	29	 100%
3	AC	48	 6% 85% 15% .
4	AD	53	 52% 74% 25% .
5	AE	60	 83% 15% .
6	AF	48	 6% 77% 19% .
7	AG	48	 8% 79% 17% .
8	AH	60	 22% 93% 7%
9	AI	42	 17% 79% 19% .
10	AJ	60	 25% 90% 10%

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Mol	Chain	Length	Quality of chain
11	AK	32	
12	AL	40	
13	AM	48	
14	AN	32	
15	AO	48	
16	AP	40	
17	AQ	45	
18	AR	48	
19	AS	48	
20	AT	45	
21	AU	48	
22	AV	40	
23	AW	58	
24	AX	60	
25	AY	32	
26	AZ	48	
27	Aa	40	
28	Ab	48	
29	Ac	40	
30	Ad	53	
31	Ae	40	
32	Af	32	
33	Ag	58	
34	Ah	60	
35	Ai	48	

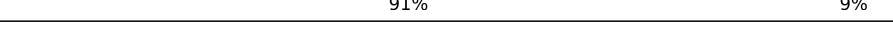
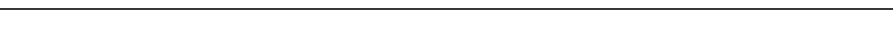
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Mol	Chain	Length	Quality of chain
36	Aj	48	 83% 17%
37	Ak	32	 88% 9% .
38	Al	48	 85% 15%
39	Am	58	 81% 19%
40	An	60	 27% 87% 13%
41	Ao	57	 7% 81% 19%
42	Ap	60	 27% 80% 20%
43	Aq	48	 83% 17%
44	Ar	37	 16% 78% 19% .
45	As	40	 92% 8%
46	At	44	 82% 18%
47	Au	40	 82% 18%
48	Av	40	 85% 15%
49	Aw	56	 88% 12%
50	Ax	40	 72% 28%
51	Ay	48	 85% 12% .
52	Az	45	 84% 16%
53	A0	32	 72% 25% .
54	A1	48	 81% 19%
55	A2	48	 75% 23% .
56	A3	56	 79% 20% .
57	A4	45	 82% 18%
58	A5	48	 88% 10% .
59	A6	32	 78% 22%
60	A7	32	 84% 16%

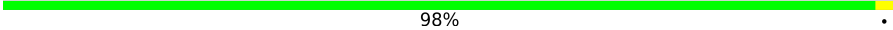
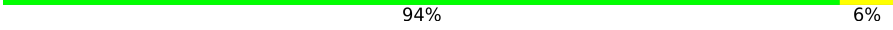
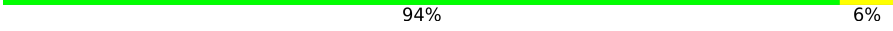
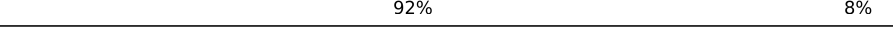
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Mol	Chain	Length	Quality of chain
61	A8	32	 91% 9%
62	A9	48	 81% 19%
63	BA	45	 84% 16%
64	BB	32	 72% 25% .
65	BC	45	 9% 87% 13%
66	BD	57	 5% 88% 12%
67	BE	57	 28% 79% 19% .
68	BF	45	 7% 76% 24%
69	BG	40	 78% 20% .
70	BH	57	 7% 74% 25% .
71	BI	57	 26% 75% 25%
72	BJ	45	 87% 13% .
73	BK	32	 91% 9% .
74	BL	56	 91% 9%
75	BM	32	 91% 9%
76	BN	40	 82% 18%
77	BO	48	 77% 23%
78	BP	58	 78% 22%
79	BQ	57	 21% 81% 19%
80	BR	48	 90% 10%
81	BS	48	 81% 17% .
82	BT	48	 90% 10%
83	BU	48	 88% 10% .
84	BV	58	 9% 83% 17%
85	BW	60	 15% 75% 22% .

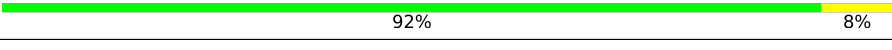
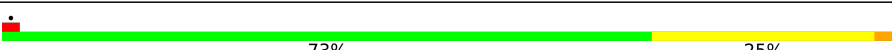
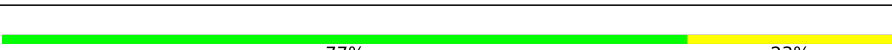
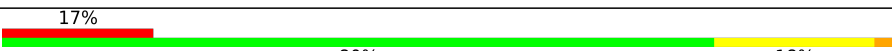
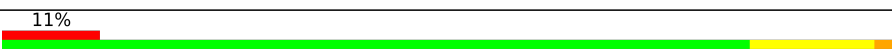
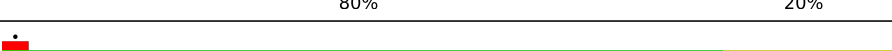
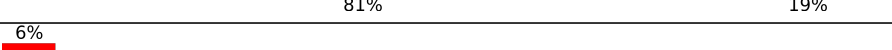
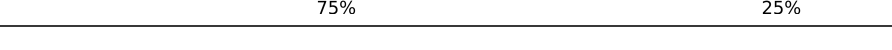
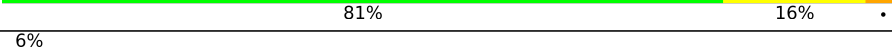
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Mol	Chain	Length	Quality of chain
86	BX	32	 88% 9%
87	BY	40	 75% 20% 5%
88	BZ	40	 78% 22%
89	Ba	48	 75% 23%
90	Bb	48	 71% 27%
91	Bc	32	 88% 12%
92	Bd	48	 98%
93	Be	48	 88% 10%
94	Bf	48	 88% 12%
95	Bg	40	 62% 35%
96	Bh	56	 80% 20%
97	Bi	40	 72% 22% 5%
98	Bj	32	 81% 16%
99	Bk	32	 94% 6%
100	Bl	48	 83% 17%
101	Bm	56	 84% 12%
102	Bn	48	 94% 6%
103	Bo	48	 90% 10%
104	Bp	40	 90% 10%
105	Bq	48	 85% 15%
106	Br	48	 85% 15%
107	Bs	32	 91% 9%
108	Bt	40	 85% 15%
109	Bu	40	 92% 8%
110	Bv	40	 85% 15%

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Mol	Chain	Length	Quality of chain
111	Bw	60	
112	Bx	45	
113	By	40	
114	Bz	32	
115	B0	60	
116	B1	60	
117	B2	40	
118	B3	32	
119	B4	32	
120	B5	60	
121	B6	53	
122	B7	48	
123	B8	32	
124	B9	48	
125	CA	48	
126	CB	60	
127	CC	37	
128	CD	57	
129	CE	32	
130	CF	40	
131	CG	32	
132	CH	53	
133	CI	32	
134	CJ	57	
135	CK	32	

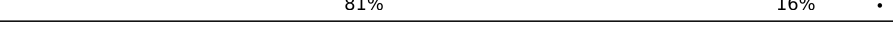
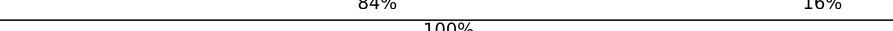
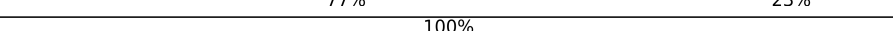
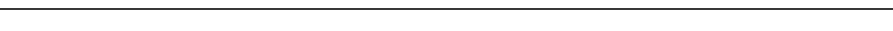
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Mol	Chain	Length	Quality of chain
136	CL	40	
137	CM	32	
138	CN	56	
139	CO	48	
140	CP	48	
141	CQ	57	
142	CR	60	
143	CS	48	
144	CT	56	
145	CU	37	
146	CV	32	
147	CW	32	
148	CX	57	
149	CY	60	
150	CZ	48	
151	Ca	48	
152	Cb	40	
153	Cc	32	
154	Cd	40	
155	Ce	40	
156	Cf	32	
157	Cg	40	
158	Ch	40	
159	Ci	48	
160	Cj	40	

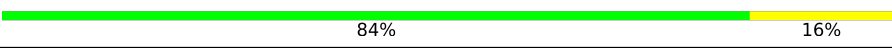
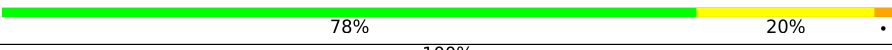
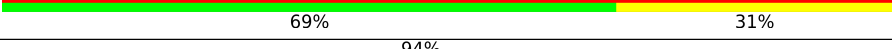
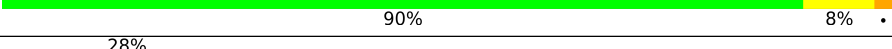
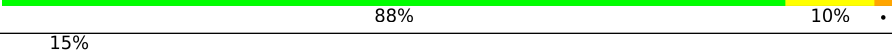
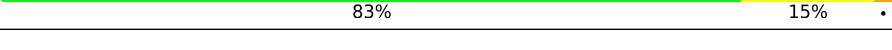
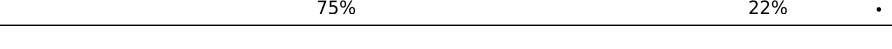
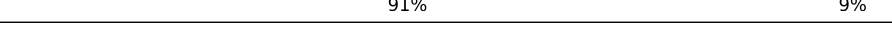
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Mol	Chain	Length	Quality of chain
161	Ck	48	
162	Cl	40	
163	Cm	48	
164	Cn	40	
165	Co	40	
166	Cp	37	
167	Cq	37	
168	Cr	40	
169	Cs	40	
170	Ct	45	
171	Cu	37	
172	Cv	40	
173	Cw	40	
174	Cx	32	
175	Cy	32	
176	Cz	32	
177	C0	57	
178	C1	57	
179	C2	32	
180	C3	48	
181	C4	48	
182	C5	48	
183	C6	48	
184	C7	40	
185	C8	48	

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Mol	Chain	Length	Quality of chain
186	C9	57	
187	DA	45	
188	DB	32	
189	DC	40	
190	DD	45	
191	DE	48	
192	DF	40	
193	DG	48	
194	DH	32	
195	DI	32	

2 Entry composition

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

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

- Molecule 1 is a DNA chain called SCAFFOLD STRAND.

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

- Molecule 2 is a DNA chain called STAPLE STRAND.

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

- Molecule 3 is a DNA chain called STAPLE STRAND.

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

- Molecule 4 is a DNA chain called STAPLE STRAND.

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

- Molecule 5 is a DNA chain called STAPLE STRAND.

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

- Molecule 6 is a DNA chain called STAPLE STRAND.

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

- Molecule 7 is a DNA chain called STAPLE STRAND.

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

- Molecule 8 is a DNA chain called STAPLE STRAND.

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

- Molecule 9 is a DNA chain called STAPLE STRAND.

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

- Molecule 10 is a DNA chain called STAPLE STRAND.

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

- Molecule 11 is a DNA chain called STAPLE STRAND.

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

- Molecule 12 is a DNA chain called STAPLE STRAND.

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

- Molecule 13 is a DNA chain called STAPLE STRAND.

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

- Molecule 14 is a DNA chain called STAPLE STRAND.

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

- Molecule 15 is a DNA chain called STAPLE STRAND.

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

- Molecule 16 is a DNA chain called STAPLE STRAND.

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

- 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
			914	443	151	276	44		

- Molecule 18 is a DNA chain called STAPLE STRAND.

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

- Molecule 19 is a DNA chain called STAPLE STRAND.

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

- Molecule 20 is a DNA chain called STAPLE STRAND.

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

- Molecule 21 is a DNA chain called STAPLE STRAND.

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

- Molecule 22 is a DNA chain called STAPLE STRAND.

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

- Molecule 23 is a DNA chain called STAPLE STRAND.

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

- Molecule 24 is a DNA chain called STAPLE STRAND.

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

- Molecule 25 is a DNA chain called STAPLE STRAND.

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

- 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
			990	472	191	280	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
			823	396	147	241	39		

- Molecule 28 is a DNA chain called STAPLE STRAND.

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

- Molecule 29 is a DNA chain called STAPLE STRAND.

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

- Molecule 30 is a DNA chain called STAPLE STRAND.

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

- Molecule 31 is a DNA chain called STAPLE STRAND.

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

- Molecule 32 is a DNA chain called STAPLE STRAND.

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

- Molecule 33 is a DNA chain called STAPLE STRAND.

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

- Molecule 34 is a DNA chain called STAPLE STRAND.

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

- Molecule 35 is a DNA chain called STAPLE STRAND.

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

- Molecule 36 is a DNA chain called STAPLE STRAND.

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

- Molecule 37 is a DNA chain called STAPLE STRAND.

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

- Molecule 38 is a DNA chain called STAPLE STRAND.

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

- Molecule 39 is a DNA chain called STAPLE STRAND.

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

- Molecule 40 is a DNA chain called STAPLE STRAND.

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

- Molecule 41 is a DNA chain called STAPLE STRAND.

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

- Molecule 42 is a DNA chain called STAPLE STRAND.

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

- Molecule 43 is a DNA chain called STAPLE STRAND.

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

- Molecule 44 is a DNA chain called STAPLE STRAND.

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

- Molecule 45 is a DNA chain called STAPLE STRAND.

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

- Molecule 46 is a DNA chain called STAPLE STRAND.

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

- Molecule 47 is a DNA chain called STAPLE STRAND.

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

- Molecule 48 is a DNA chain called STAPLE STRAND.

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

- Molecule 49 is a DNA chain called STAPLE STRAND.

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

- Molecule 50 is a DNA chain called STAPLE STRAND.

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

- Molecule 51 is a DNA chain called STAPLE STRAND.

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

- Molecule 52 is a DNA chain called STAPLE STRAND.

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

- Molecule 53 is a DNA chain called STAPLE STRAND.

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

- Molecule 54 is a DNA chain called STAPLE STRAND.

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

- Molecule 55 is a DNA chain called STAPLE STRAND.

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

- Molecule 56 is a DNA chain called STAPLE STRAND.

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

- Molecule 57 is a DNA chain called STAPLE STRAND.

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

- Molecule 58 is a DNA chain called STAPLE STRAND.

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

- Molecule 59 is a DNA chain called STAPLE STRAND.

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

- Molecule 60 is a DNA chain called STAPLE STRAND.

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

- Molecule 61 is a DNA chain called STAPLE STRAND.

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

- Molecule 62 is a DNA chain called STAPLE STRAND.

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

- Molecule 63 is a DNA chain called STAPLE STRAND.

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

- Molecule 64 is a DNA chain called STAPLE STRAND.

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

- Molecule 65 is a DNA chain called STAPLE STRAND.

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

- Molecule 66 is a DNA chain called STAPLE STRAND.

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

- Molecule 67 is a DNA chain called STAPLE STRAND.

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

- Molecule 68 is a DNA chain called STAPLE STRAND.

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

- Molecule 69 is a DNA chain called STAPLE STRAND.

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

- Molecule 70 is a DNA chain called STAPLE STRAND.

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

- Molecule 71 is a DNA chain called STAPLE STRAND.

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

- Molecule 72 is a DNA chain called STAPLE STRAND.

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

- 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
			655	313	119	192	31		

- Molecule 74 is a DNA chain called STAPLE STRAND.

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

- 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
			650	312	126	181	31		

- Molecule 76 is a DNA chain called STAPLE STRAND.

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

- Molecule 77 is a DNA chain called STAPLE STRAND.

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

- Molecule 78 is a DNA chain called STAPLE STRAND.

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

- Molecule 79 is a DNA chain called STAPLE STRAND.

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

- Molecule 80 is a DNA chain called STAPLE STRAND.

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

- Molecule 81 is a DNA chain called STAPLE STRAND.

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

- Molecule 82 is a DNA chain called STAPLE STRAND.

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

- Molecule 83 is a DNA chain called STAPLE STRAND.

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

- Molecule 84 is a DNA chain called STAPLE STRAND.

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

- Molecule 85 is a DNA chain called STAPLE STRAND.

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

- Molecule 86 is a DNA chain called STAPLE STRAND.

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

- Molecule 87 is a DNA chain called STAPLE STRAND.

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

- Molecule 88 is a DNA chain called STAPLE STRAND.

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

- Molecule 89 is a DNA chain called STAPLE STRAND.

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

- Molecule 90 is a DNA chain called STAPLE STRAND.

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

- Molecule 91 is a DNA chain called STAPLE STRAND.

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

- Molecule 92 is a DNA chain called STAPLE STRAND.

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

- Molecule 93 is a DNA chain called STAPLE STRAND.

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

- Molecule 94 is a DNA chain called STAPLE STRAND.

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

- Molecule 95 is a DNA chain called STAPLE STRAND.

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

- Molecule 96 is a DNA chain called STAPLE STRAND.

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

- 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
			805	390	132	244	39		

- Molecule 98 is a DNA chain called STAPLE STRAND.

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

- Molecule 99 is a DNA chain called STAPLE STRAND.

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

- Molecule 100 is a DNA chain called STAPLE STRAND.

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

- Molecule 101 is a DNA chain called STAPLE STRAND.

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

- Molecule 102 is a DNA chain called STAPLE STRAND.

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

- Molecule 103 is a DNA chain called STAPLE STRAND.

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

- Molecule 104 is a DNA chain called STAPLE STRAND.

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

- Molecule 105 is a DNA chain called STAPLE STRAND.

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

- Molecule 106 is a DNA chain called STAPLE STRAND.

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

- Molecule 107 is a DNA chain called STAPLE STRAND.

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

- Molecule 108 is a DNA chain called STAPLE STRAND.

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

- Molecule 109 is a DNA chain called STAPLE STRAND.

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

- Molecule 110 is a DNA chain called STAPLE STRAND.

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

- Molecule 111 is a DNA chain called STAPLE STRAND.

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

- Molecule 112 is a DNA chain called STAPLE STRAND.

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

- 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
			823	389	169	226	39		

- Molecule 114 is a DNA chain called STAPLE STRAND.

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

- Molecule 115 is a DNA chain called STAPLE STRAND.

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

- Molecule 116 is a DNA chain called STAPLE STRAND.

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

- Molecule 117 is a DNA chain called STAPLE STRAND.

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

- Molecule 118 is a DNA chain called STAPLE STRAND.

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

- Molecule 119 is a DNA chain called STAPLE STRAND.

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

- Molecule 120 is a DNA chain called STAPLE STRAND.

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

- Molecule 121 is a DNA chain called STAPLE STRAND.

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

- Molecule 122 is a DNA chain called STAPLE STRAND.

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

- Molecule 123 is a DNA chain called STAPLE STRAND.

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

- Molecule 124 is a DNA chain called STAPLE STRAND.

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

- Molecule 125 is a DNA chain called STAPLE STRAND.

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

- Molecule 126 is a DNA chain called STAPLE STRAND.

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

- Molecule 127 is a DNA chain called STAPLE STRAND.

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

- Molecule 128 is a DNA chain called STAPLE STRAND.

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

- Molecule 129 is a DNA chain called STAPLE STRAND.

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

- Molecule 130 is a DNA chain called STAPLE STRAND.

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

- Molecule 131 is a DNA chain called STAPLE STRAND.

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

- Molecule 132 is a DNA chain called STAPLE STRAND.

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

- Molecule 133 is a DNA chain called STAPLE STRAND.

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

- Molecule 134 is a DNA chain called STAPLE STRAND.

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

- Molecule 135 is a DNA chain called STAPLE STRAND.

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

- Molecule 136 is a DNA chain called STAPLE STRAND.

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

- Molecule 137 is a DNA chain called STAPLE STRAND.

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

- Molecule 138 is a DNA chain called STAPLE STRAND.

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

- Molecule 139 is a DNA chain called STAPLE STRAND.

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

- 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
			992	473	181	291	47		

- Molecule 141 is a DNA chain called STAPLE STRAND.

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

- Molecule 142 is a DNA chain called STAPLE STRAND.

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

- Molecule 143 is a DNA chain called STAPLE STRAND.

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

- Molecule 144 is a DNA chain called STAPLE STRAND.

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

- Molecule 145 is a DNA chain called STAPLE STRAND.

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

- Molecule 146 is a DNA chain called STAPLE STRAND.

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

- Molecule 147 is a DNA chain called STAPLE STRAND.

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

- Molecule 148 is a DNA chain called STAPLE STRAND.

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

- Molecule 149 is a DNA chain called STAPLE STRAND.

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

- Molecule 150 is a DNA chain called STAPLE STRAND.

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

- Molecule 151 is a DNA chain called STAPLE STRAND.

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

- Molecule 152 is a DNA chain called STAPLE STRAND.

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

- Molecule 153 is a DNA chain called STAPLE STRAND.

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

- Molecule 154 is a DNA chain called STAPLE STRAND.

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

- Molecule 155 is a DNA chain called STAPLE STRAND.

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

- Molecule 156 is a DNA chain called STAPLE STRAND.

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

- Molecule 157 is a DNA chain called STAPLE STRAND.

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

- Molecule 158 is a DNA chain called STAPLE STRAND.

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

- Molecule 159 is a DNA chain called STAPLE STRAND.

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

- Molecule 160 is a DNA chain called STAPLE STRAND.

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

- Molecule 161 is a DNA chain called STAPLE STRAND.

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

- 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
			821	393	159	230	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
			980	471	174	288	47		

- Molecule 164 is a DNA chain called STAPLE STRAND.

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

- Molecule 165 is a DNA chain called STAPLE STRAND.

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

- Molecule 166 is a DNA chain called STAPLE STRAND.

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

- Molecule 167 is a DNA chain called STAPLE STRAND.

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

- Molecule 168 is a DNA chain called STAPLE STRAND.

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

- 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
			822	393	159	231	39		

- Molecule 170 is a DNA chain called STAPLE STRAND.

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

- Molecule 171 is a DNA chain called STAPLE STRAND.

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

- 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
			810	390	138	243	39		

- Molecule 173 is a DNA chain called STAPLE STRAND.

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

- Molecule 174 is a DNA chain called STAPLE STRAND.

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

- Molecule 175 is a DNA chain called STAPLE STRAND.

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

- Molecule 176 is a DNA chain called STAPLE STRAND.

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

- Molecule 177 is a DNA chain called STAPLE STRAND.

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

- Molecule 178 is a DNA chain called STAPLE STRAND.

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

- Molecule 179 is a DNA chain called STAPLE STRAND.

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

- Molecule 180 is a DNA chain called STAPLE STRAND.

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

- Molecule 181 is a DNA chain called STAPLE STRAND.

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

- Molecule 182 is a DNA chain called STAPLE STRAND.

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

- Molecule 183 is a DNA chain called STAPLE STRAND.

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

- Molecule 184 is a DNA chain called STAPLE STRAND.

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

- 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
			991	472	194	278	47		

- Molecule 186 is a DNA chain called STAPLE STRAND.

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

- Molecule 187 is a DNA chain called STAPLE STRAND.

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

- Molecule 188 is a DNA chain called STAPLE STRAND.

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

- Molecule 189 is a DNA chain called STAPLE STRAND.

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

- Molecule 190 is a DNA chain called STAPLE STRAND.

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

- Molecule 191 is a DNA chain called STAPLE STRAND.

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

- Molecule 192 is a DNA chain called STAPLE STRAND.

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

- Molecule 193 is a DNA chain called STAPLE STRAND.

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

- Molecule 194 is a DNA chain called STAPLE STRAND.

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

- Molecule 195 is a DNA chain called STAPLE STRAND.

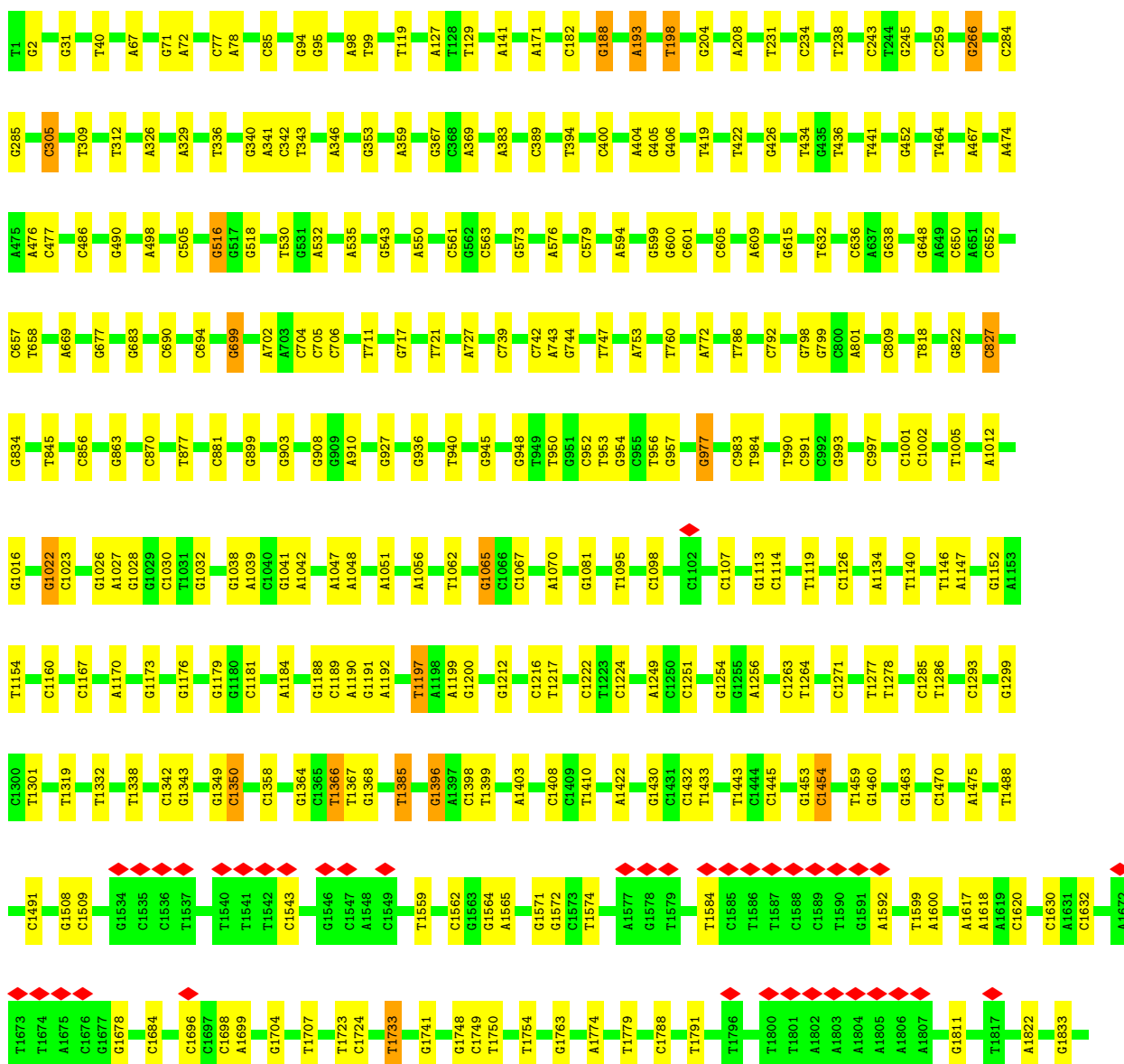
Mol	Chain	Residues	Atoms					AltConf	Trace
195	DI	32	Total	C	N	O	P	0	0
			653	314	118	190	31		

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.

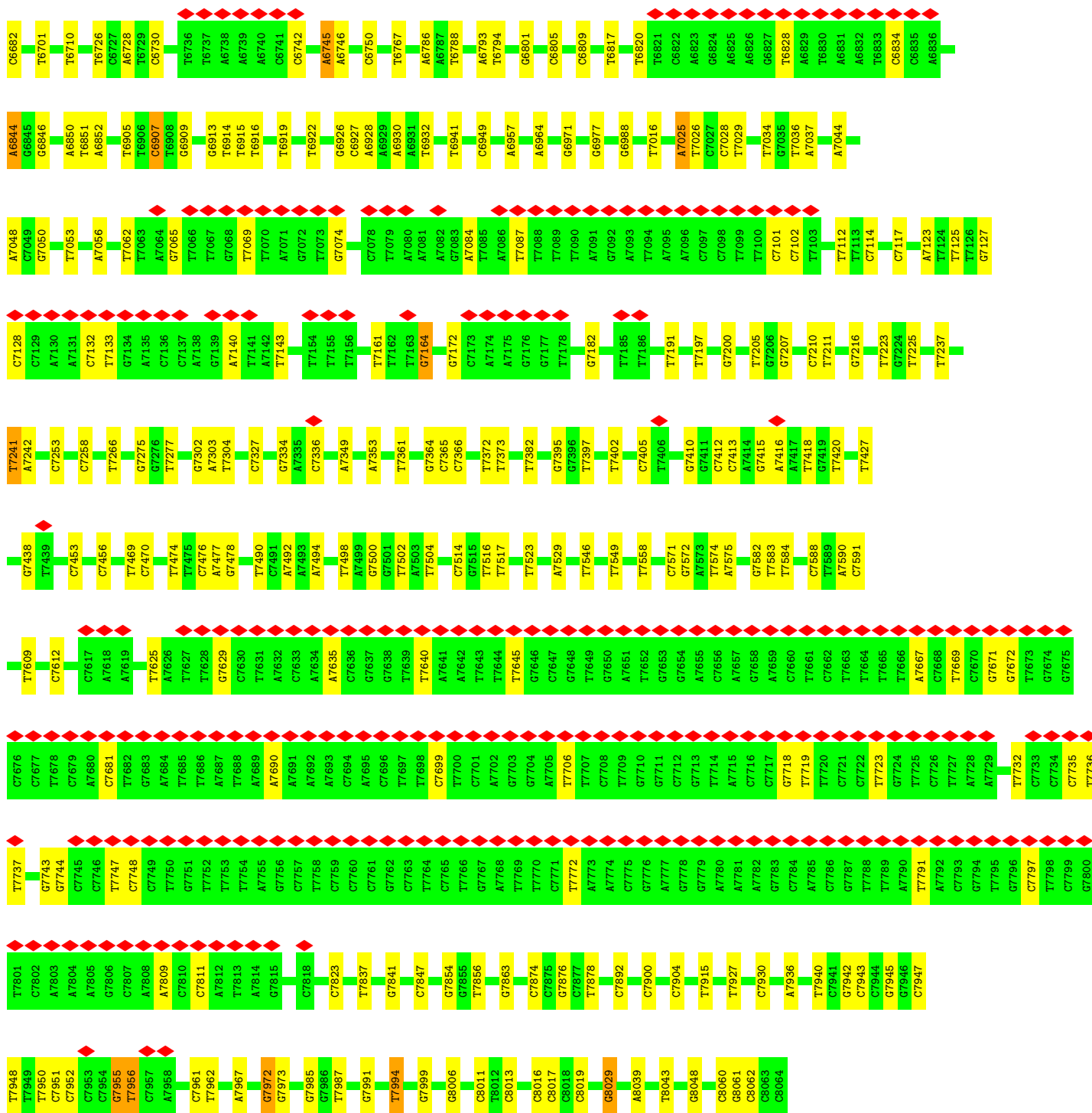
• Molecule 1: SCAFFOLD STRAND

Chain AA:  82% 17%

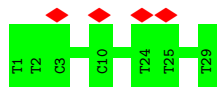


G3828	T3487	A3300	A3150	G2959	A2798	A2596	T2407	G2583	G2093	C1971	T1838
A3829	C3488	C3336	T3167	T2960	A2810	G2600	A2410	A2254	T2100	G1974	T1839
A3830	T3489	C3336	T3168	A2961	A2810	G2600	A2410	A2254	C2101	T1975	T1840
A3835	G3495	G3341	T3174	T2966	A2815	A2602	A2426	T2262	C2102	C1979	T1841
G3844	T3503	C3350	G3175	T2966	G2816	A2602	A2427	T2263	G2103	A1850	A1850
C3846	C3506	C3350	A3176	T2966	G2817	A2603	C2428	A2264	G2104	A1853	A1853
A3846	C3507	C3362	T3177	C2974	G2818	C2615	G2433	T2285	C2105	A1857	A1857
C3849	G3508	C3362	A3178	T2975	G2819	C2617	A2439	T2270	T2109	C1986	T1857
G3851	T3512	C3369	A3179	T2977	T2831	C2617	A2439	C2275	T2117	A1991	T1858
T3861	G3513	C3376	T3190	T2978	T2837	T2632	A2448	T2280	T2124	A1991	T1864
A3864	G3514	A3377	C3195	T2999	A2842	G2633	C2455	T2280	C2125	C2000	T1865
A3865	T3515	A3378	T3199	T3000	T2843	G2634	G2456	T2289	T2126	C2001	A1869
G3871	A3516	A3379	T3199	T3000	T2844	G2635	C2457	T2289	T2127	T2002	A1870
A3873	C3517	A3380	T3209	G3001	T2844	G2636	A2458	T2294	G2128	G2003	A1871
T3901	A3518	T3381	T3210	C3002	A2849	T2642	T2462	A2295	A2129	A2004	T1878
T3909	C3521	T3381	T3211	C3003	C2850	T2642	T2462	A2296	C2130	T2005	A1871
A3914	G3522	T3394	A3212	T3008	T2851	G2651	T2474	G2303	C2131	A2006	T1878
T3923	C3523	T3394	C3216	G3030	A2857	G2656	T2479	T2306	A2133	G2007	T1885
C3925	T3524	T3402	T3226	G3031	C2858	G2656	T2479	T2307	T2011	T2012	G1886
G3932	G3529	G3403	T3229	T3032	T2863	C2665	A2480	G2308	G2013	T2014	T1887
C3933	T3546	A3404	T3229	C3036	T2868	C2665	A2480	T2315	A2017	A2024	T1891
T3934	T3553	A3408	G3234	C3037	T2868	C2665	A2480	T2318	A2024	A2028	T1893
T3946	T3554	T3423	T3235	T3038	T2873	C2665	A2480	T2318	A2028	A2032	T1895
C3960	C3555	T3424	T3236	T3038	T2876	C2665	A2480	T2318	A2032	C2047	G1898
A3968	T3556	C3425	C3237	T3049	T2881	C2665	A2480	T2318	A2032	T2047	G1899
T3970	G3560	G3427	G3239	T3052	C2885	C2665	A2480	T2318	A2032	T2047	C1907
T3973	G3564	A3432	T3248	T3056	T2885	C2665	A2480	T2318	A2032	T2047	T1911
A3991	T3565	C3437	A3249	T3056	C2890	C2665	A2480	T2318	A2032	T2047	A1917
T3997	C3568	G3453	T3251	T3079	G2895	C2665	A2480	T2318	A2032	T2047	G1918
A3998	T3571	A3454	C3252	T3083	T2908	C2665	A2480	T2318	A2032	T2047	C1919
T4006	T3572	G3458	A3258	T3085	T2928	C2665	A2480	T2318	A2032	T2047	G1931
A4017	G3580	A3460	G3265	T3085	T2928	C2665	A2480	T2318	A2032	T2047	A1932
G4023	C3584	A3464	A3273	T3089	G2931	C2665	A2480	T2318	A2032	T2047	T1933
A4029	T3585	T3470	T3281	T3098	T2935	C2665	A2480	T2318	A2032	T2047	A1936
C4033	T3586	G3473	T3282	T3098	T2935	C2665	A2480	T2318	A2032	T2047	T1945
	T3589	C3474	G3284	T3114	T2939	C2665	A2480	T2318	A2032	T2047	T1946
	G3601	G3475	T3289	T3122	G2941	C2665	A2480	T2318	A2032	T2047	T1947
	T3602	G3476	T3295	T3125	T2942	C2665	A2480	T2318	A2032	T2047	T1948
	T3615	G3479	T3312	T3144	G2944	C2665	A2480	T2318	A2032	T2047	A1949
	A3621	A3480	T3312	T3144	G2944	C2665	A2480	T2318	A2032	T2047	C1950
	A3622	T3481	T3312	T3144	G2944	C2665	A2480	T2318	A2032	T2047	G1951
	A3623	T3481	T3312	T3144	G2944	C2665	A2480	T2318	A2032	T2047	T1960
			T3315	T3144	G2944	C2665	A2480	T2318	A2032	T2047	C1969
				T3144	G2944	C2665	A2480	T2318	A2032	T2047	T1970

T6558	G6401	T6182	T5959	T5775	A5510	T5383	T5205	A4976	A4794	T4627	C4428	G4218	T4039
T6559	C6405	C6156	G5976	T5779	A5516	A5394	T5210	A4977	A4799	G4628	C4435	T4219	T4048
A5560	A5978	A6161	A5977	G5780	T5517	C5358	A5211	T4982	C4799	G4629	A4436	T4222	T4049
A5561	C6413	G6174	A5978	T5781	A5520	C5360	C5223	T5008	T4813	C4635	T4456	C4230	A4050
T6563	T6414	G5979	T5979	T5784	T5536	T5386	G5227	T5016	T4825	G4640	T4463	T4243	C4053
G5564	T6415	T5980	T5980	C5799	C5572	G5372	G5236	T5017	T4828	G4641	T4467	C4247	C4064
T6565	A6420	C6183	T5983	T5809	C5575	C5372	T5230	G5018	T4836	C4645	A4466	C4248	T4069
A5566	T6421	T5984	T5984	T5809	T5575	T5373	T5234	A5019	C4836	T4648	C4467	T4249	C4070
A5567	C6422	C5812	T5994	C5812	A5598	C5381	T5235	A5020	T4844	G4653	T4475	G4257	
T6568	G6432	C5817	C5995	C5817	C5598	C5388	C5236	T5029	C4851	G4657	A4487	T4261	G4075
T6573	A6435	G5820	C6009	G5820	T5601	T5389	T5237	T5037	C4854	G4674	T4499	A4262	T4078
G5584	T6440	A5822	A6014	A5822	C5625	G5392	G5239	T5062	C4867	G4681	T4522	C4263	A4082
A5585	A6447	A5823	T6015	A5823	T5631	G5396	G5247	T5063	C4877	G4692	T4523	T4267	T4089
G5587	T6451	G5830	A6029	G5830	T5632	A5396	T5261	C5064	C4881	G4697	G4524	T4269	T4092
T6592	A6458	G5831	C6038	G5831	G5633	T5402	T5269	G5069	C4882	G4700	T4529	C4275	T4099
C5598	A6464	A5833	A6043	A5833	T5643	T5407	C5270	T5074	C4883	G4701	T4530	G4280	
C6601	T6471	A5836	T6044	A5836	A5658	A5409	A5275	A5089	C4886	G4709	A4533	G4299	C4113
T6602	T6479	T5847	A6046	T5847	C5663	A5410	G5278	T5091	C4897	G4712	T4534	A4301	C4124
T6603	T6485	G5853	A6048	G5853	C5665	C5420	T5282	C5101	T4897	G4718	T4543	G4306	T4126
C6604	T6619	G5854	T6051	G5854	G5668	T5424	G5283	C5111	T4903	G4719	T4546	C4331	C4128
T6619	G6626	A5875	G6068	A5875	C5682	G5425	G5293	T5112	G4904	T4720	T4552	T4333	C4132
G6626	T6493	A5878	A6072	A5878	T5697	C5431	A5296	T5113	A4914	G4722	A4551	T4333	C4137
T6629	T6496	A5901	A6072	A5901	G5701	C5433	T5301	T5117	T4918	G4723	T4560	G4342	T4140
A6630	T6501	G5902	T6080	G5902	G5702	C5433	A5302	G5120	G4919	G4730	T4561	T4343	C4149
A6631	T6501	G5903	T6081	G5903	A5705	T5440	T5303	G5123	C4920	G4731	T4564	C4350	
T6632	C6512	C5905	A6082	C5905	T5715	T5452	A5307	C5158	T4930	T4732	G4575	T4357	G4163
C6637	A6513	T5907	A6083	T5907	A5716	C5464	A5312	T5163	C4931	T4733	G4582	A4358	A4164
C6644	T6514	A5908	T6100	A5908	T5717	G5464	T5317	T5180	C4932	T4734	T4583	T4367	G4165
G6645	C6522	T5913	T6107	T5913	T5733	A5467	G5317	G5174	C4934	T4749	T4586	T4368	G4166
T6652	C6529	A5922	T6109	A5922	C5738	T5483	A5317	T5180	A4937	C4758	G4586	A4371	G4170
C6655	A6534	A5923	T6109	A5923	G5739	T5484	T5322	A5185	T4938	T4762	T4600	T4382	C4176
T6663	A6535	C5924	T6121	C5924	G5742	A5486	A5323	T5186	G4939	G4767	C4602	T4382	G4182
C6664	A6543	A5925	C6132	A5925	A5745	A5486	T5324	G5187	T4942	G4768	T4603	C4393	G4194
A6667	C6546	G5926	C6132	G5926	T5749	A5489	T5328	T5195	A4944	G4769	G4604	C4393	A4194
C6668	A6670	C5927	A6133	C5927	T5750	A5490	T5333	G5199	A4959	C4770	T4605	G4397	G4199
C6669	A6671	G5928	A6135	G5928	C5751	A5494	T5345	G5200	A4966	A4781	G4614	A4405	G4202
A6670	T6672	G5929	C6150	A5938	T5774	T5498	G5351	G5201	C4967	T4789	G4626	T4425	
A6671	G6674	A5938	T6151	A5938			T5352	T5202					G4217
T6672	G6675												
C6673	G6676												
A6674													
G6675													
G6676													



- Molecule 2: STAPLE STRAND



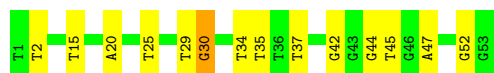
- Molecule 3: STAPLE STRAND

Chain AC:  85% 15%

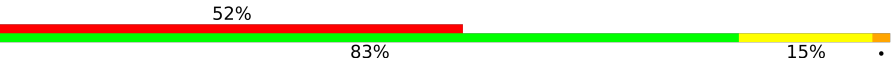


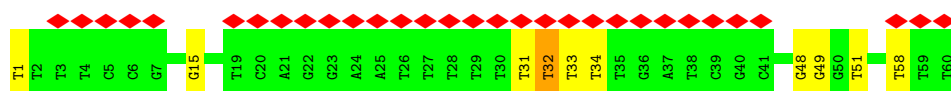
• Molecule 4: STAPLE STRAND

Chain AD:  74% 25%



• Molecule 5: STAPLE STRAND

Chain AE:  52% 83% 15%



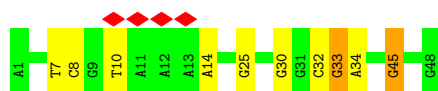
• Molecule 6: STAPLE STRAND

Chain AF:  6% 77% 19%

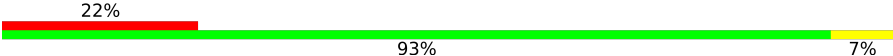


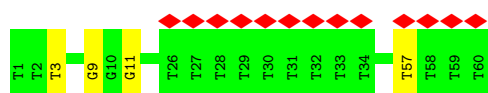
• Molecule 7: STAPLE STRAND

Chain AG:  8% 79% 17%



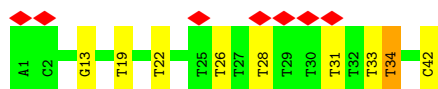
• Molecule 8: STAPLE STRAND

Chain AH:  22% 93% 7%

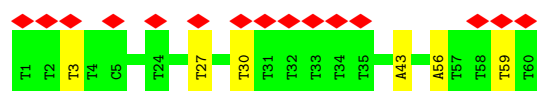


• Molecule 9: STAPLE STRAND

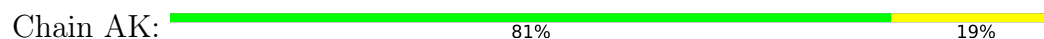
Chain AI:  17% 79% 19%



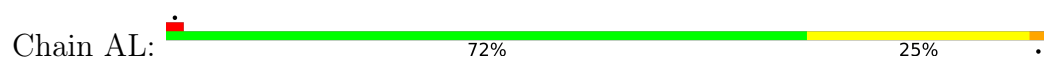
• Molecule 10: STAPLE STRAND



- Molecule 11: STAPLE STRAND



- Molecule 12: STAPLE STRAND



- Molecule 13: STAPLE STRAND



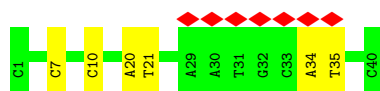
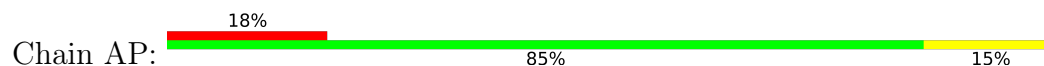
- Molecule 14: STAPLE STRAND



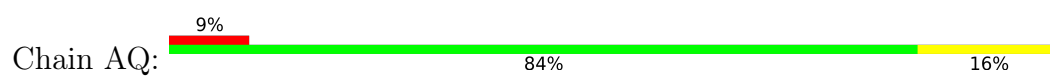
- Molecule 15: STAPLE STRAND



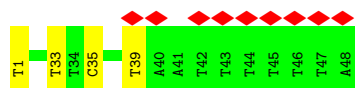
- Molecule 16: STAPLE STRAND



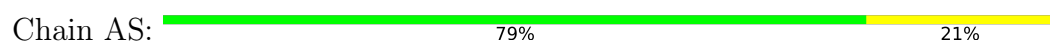
- Molecule 17: STAPLE STRAND



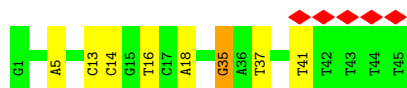
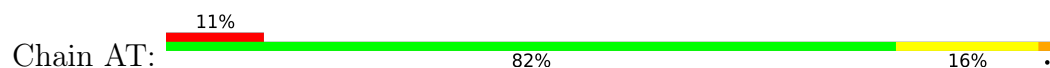
- Molecule 18: STAPLE STRAND



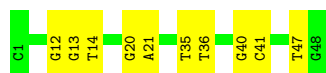
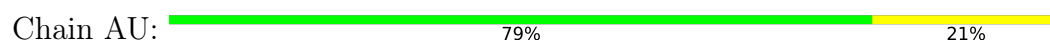
- Molecule 19: STAPLE STRAND



- Molecule 20: STAPLE STRAND



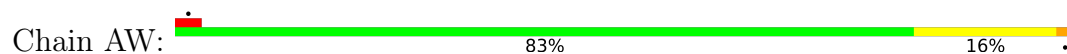
- Molecule 21: STAPLE STRAND



- Molecule 22: STAPLE STRAND



- Molecule 23: STAPLE STRAND



- Molecule 24: STAPLE STRAND

Chain AX: 



- Molecule 25: STAPLE STRAND

Chain AY: 



- Molecule 26: STAPLE STRAND

Chain AZ: 



- Molecule 27: STAPLE STRAND

Chain Aa: 



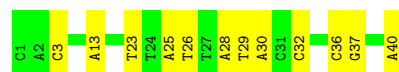
- Molecule 28: STAPLE STRAND

Chain Ab: 



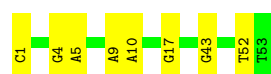
- Molecule 29: STAPLE STRAND

Chain Ac: 



- Molecule 30: STAPLE STRAND

Chain Ad: 

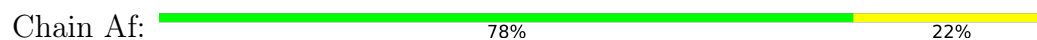


- Molecule 31: STAPLE STRAND

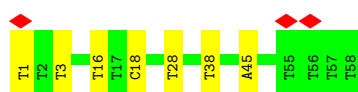
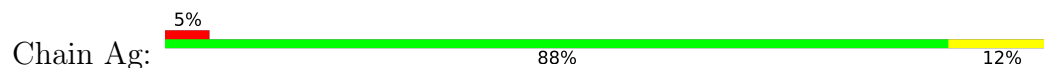
Chain Ae: 



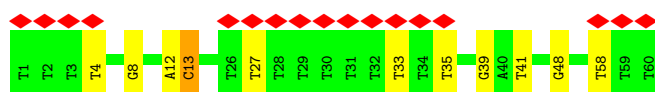
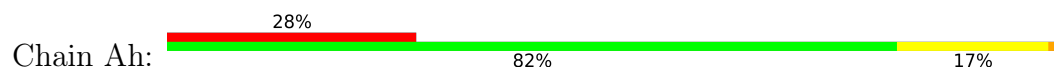
- Molecule 32: STAPLE STRAND



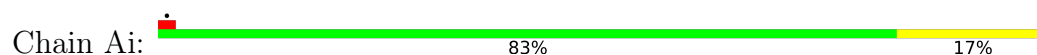
- Molecule 33: STAPLE STRAND



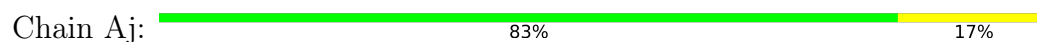
- Molecule 34: STAPLE STRAND



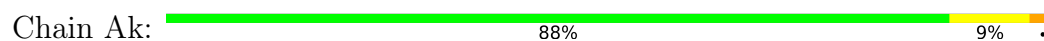
- Molecule 35: STAPLE STRAND



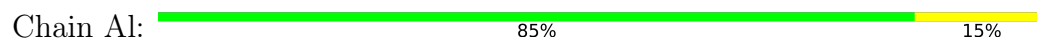
- Molecule 36: STAPLE STRAND



- Molecule 37: STAPLE STRAND

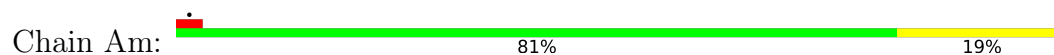


- Molecule 38: STAPLE STRAND

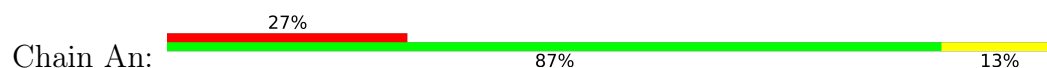




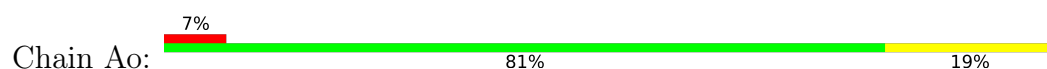
• Molecule 39: STAPLE STRAND



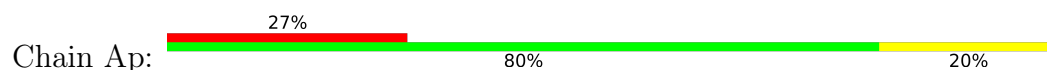
• Molecule 40: STAPLE STRAND



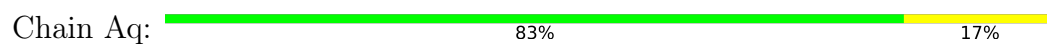
• Molecule 41: STAPLE STRAND



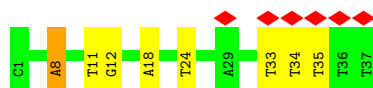
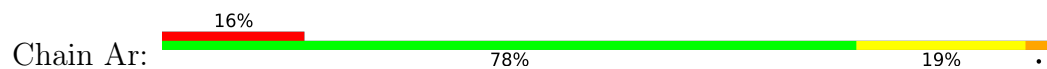
• Molecule 42: STAPLE STRAND



• Molecule 43: STAPLE STRAND



• Molecule 44: STAPLE STRAND

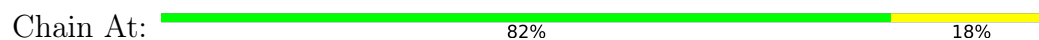


• Molecule 45: STAPLE STRAND

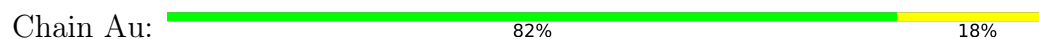




- Molecule 46: STAPLE STRAND



- Molecule 47: STAPLE STRAND



- Molecule 48: STAPLE STRAND



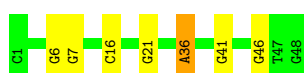
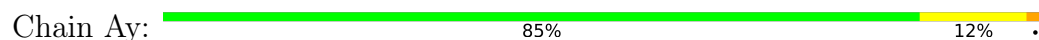
- Molecule 49: STAPLE STRAND



- Molecule 50: STAPLE STRAND

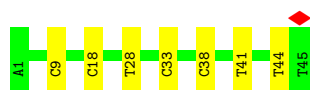


- Molecule 51: STAPLE STRAND



- Molecule 52: STAPLE STRAND





- Molecule 53: STAPLE STRAND

Chain A0: 72% 25% .



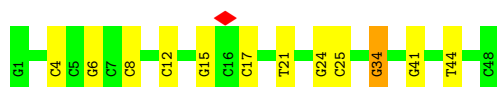
- Molecule 54: STAPLE STRAND

Chain A1: 81% 19% .



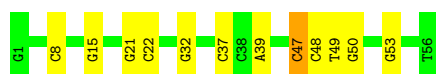
- Molecule 55: STAPLE STRAND

Chain A2: 75% 23% .



- Molecule 56: STAPLE STRAND

Chain A3: 79% 20% .



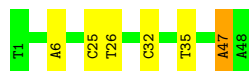
- Molecule 57: STAPLE STRAND

Chain A4: 82% 18% .



- Molecule 58: STAPLE STRAND

Chain A5: 88% 10% .

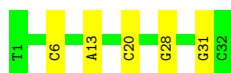
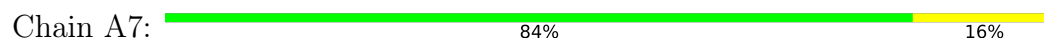


- Molecule 59: STAPLE STRAND

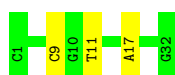
Chain A6: 78% 22%



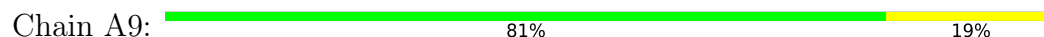
- Molecule 60: STAPLE STRAND



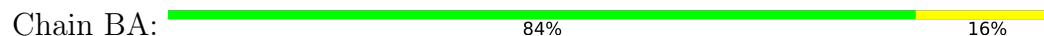
- Molecule 61: STAPLE STRAND



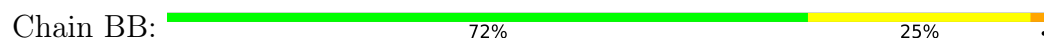
- Molecule 62: STAPLE STRAND



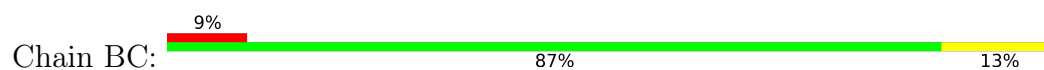
- Molecule 63: STAPLE STRAND



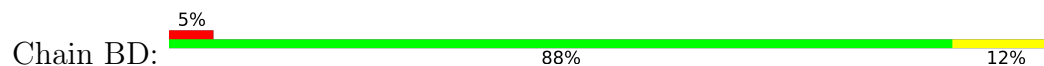
- Molecule 64: STAPLE STRAND



- Molecule 65: STAPLE STRAND

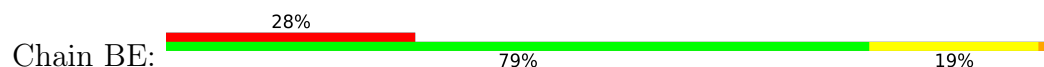


- Molecule 66: STAPLE STRAND

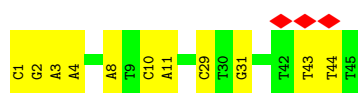
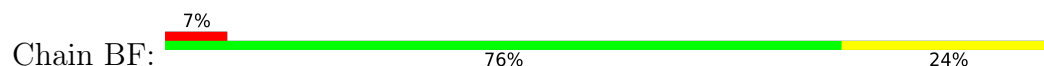




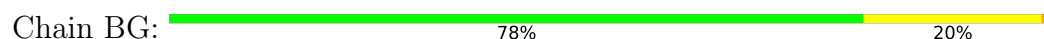
• Molecule 67: STAPLE STRAND



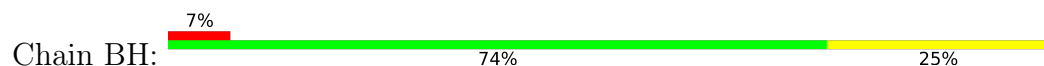
• Molecule 68: STAPLE STRAND



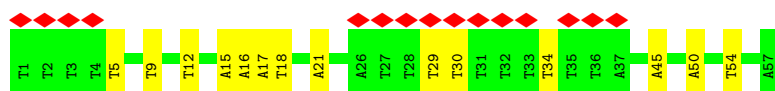
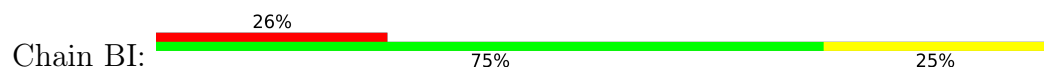
• Molecule 69: STAPLE STRAND



• Molecule 70: STAPLE STRAND



• Molecule 71: STAPLE STRAND

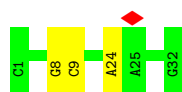


• Molecule 72: STAPLE STRAND



• Molecule 73: STAPLE STRAND





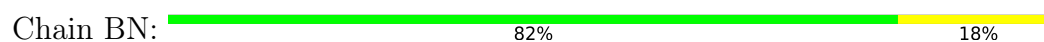
• Molecule 74: STAPLE STRAND



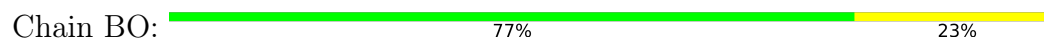
• Molecule 75: STAPLE STRAND



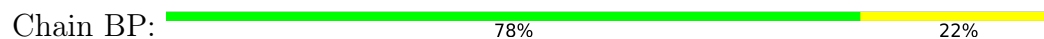
• Molecule 76: STAPLE STRAND



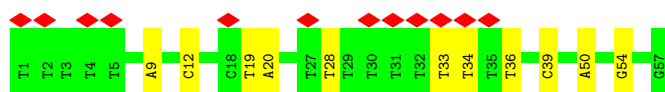
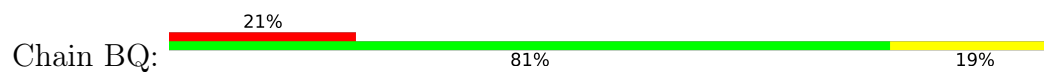
• Molecule 77: STAPLE STRAND



• Molecule 78: STAPLE STRAND



• Molecule 79: STAPLE STRAND

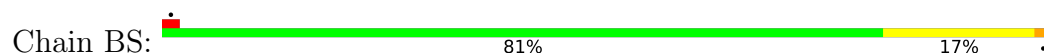


• Molecule 80: STAPLE STRAND





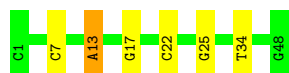
- Molecule 81: STAPLE STRAND



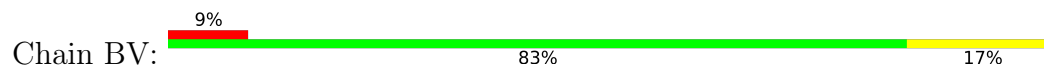
- Molecule 82: STAPLE STRAND



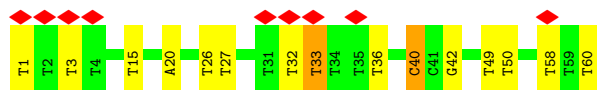
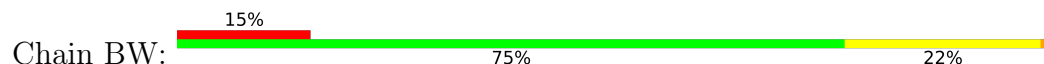
- Molecule 83: STAPLE STRAND



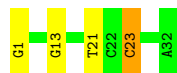
- Molecule 84: STAPLE STRAND



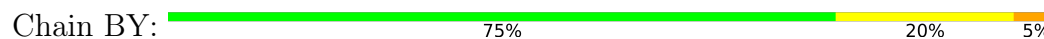
- Molecule 85: STAPLE STRAND



- Molecule 86: STAPLE STRAND



- Molecule 87: STAPLE STRAND





• Molecule 88: STAPLE STRAND

Chain BZ: 78% 22%



• Molecule 89: STAPLE STRAND

Chain Ba: 75% 23% .



• Molecule 90: STAPLE STRAND

Chain Bb: 71% 27% .



• Molecule 91: STAPLE STRAND

Chain Bc: 88% 12% .



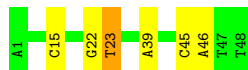
• Molecule 92: STAPLE STRAND

Chain Bd: 98% .



• Molecule 93: STAPLE STRAND

Chain Be: 88% 10% .



• Molecule 94: STAPLE STRAND

Chain Bf: 88% 12%



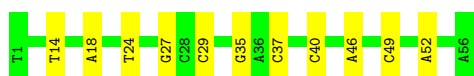
- Molecule 95: STAPLE STRAND

Chain Bg: 62% 35% .



- Molecule 96: STAPLE STRAND

Chain Bh: 80% 20%



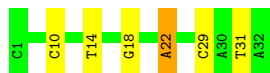
- Molecule 97: STAPLE STRAND

Chain Bi: 72% 22% 5%



- Molecule 98: STAPLE STRAND

Chain Bj: 81% 16% .



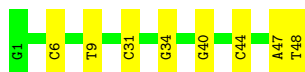
- Molecule 99: STAPLE STRAND

Chain Bk: 94% 6%



- Molecule 100: STAPLE STRAND

Chain Bl: 83% 17%

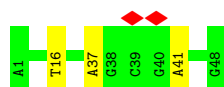


- Molecule 101: STAPLE STRAND

Chain Bm: 84% 12% .



- Molecule 102: STAPLE STRAND



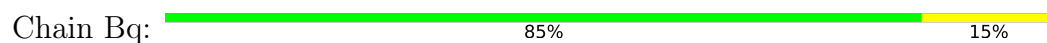
- Molecule 103: STAPLE STRAND



- Molecule 104: STAPLE STRAND



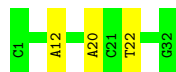
- Molecule 105: STAPLE STRAND



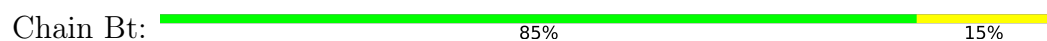
- Molecule 106: STAPLE STRAND



- Molecule 107: STAPLE STRAND



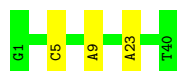
- Molecule 108: STAPLE STRAND





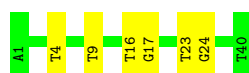
- Molecule 109: STAPLE STRAND

Chain Bu: 92% 8%



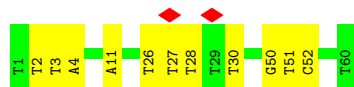
- Molecule 110: STAPLE STRAND

Chain Bv: 85% 15%



- Molecule 111: STAPLE STRAND

Chain Bw: 82% 18%



- Molecule 112: STAPLE STRAND

Chain Bx: 9% 80% 20%



- Molecule 113: STAPLE STRAND

Chain By: 92% 8%



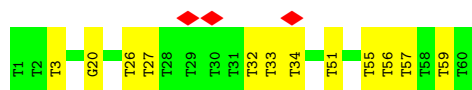
- Molecule 114: STAPLE STRAND

Chain Bz: 84% 16%

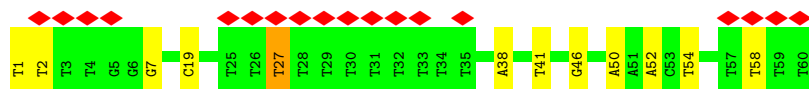
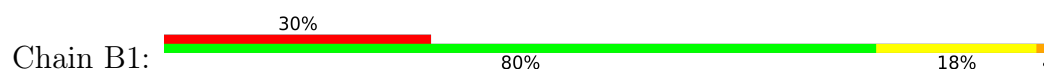


- Molecule 115: STAPLE STRAND

Chain B0: 5% 80% 20%



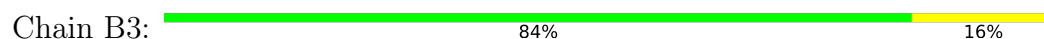
- Molecule 116: STAPLE STRAND



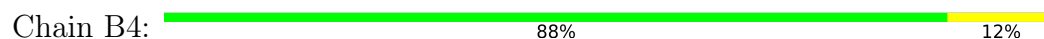
- Molecule 117: STAPLE STRAND



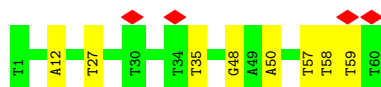
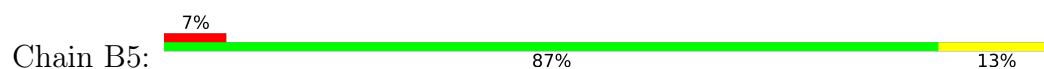
- Molecule 118: STAPLE STRAND



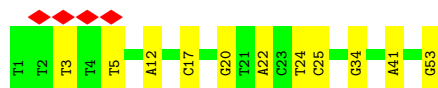
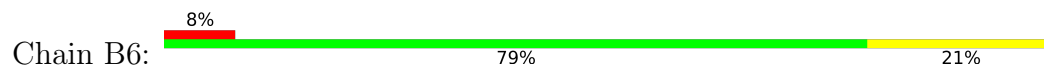
- Molecule 119: STAPLE STRAND



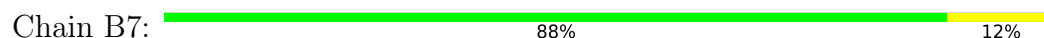
- Molecule 120: STAPLE STRAND



- Molecule 121: STAPLE STRAND

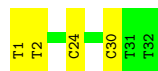
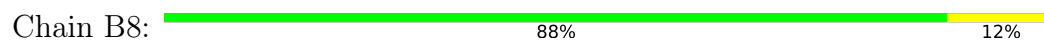


- Molecule 122: STAPLE STRAND

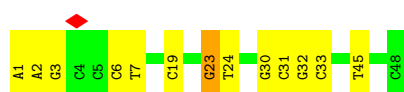
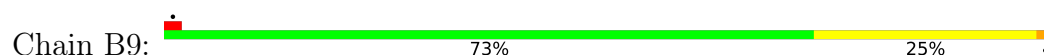




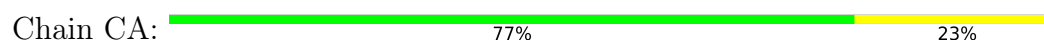
- Molecule 123: STAPLE STRAND



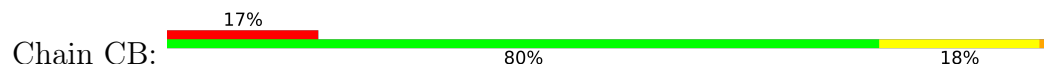
- Molecule 124: STAPLE STRAND



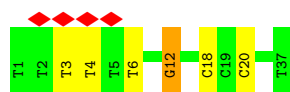
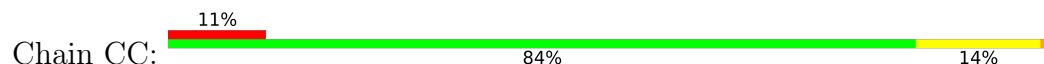
- Molecule 125: STAPLE STRAND



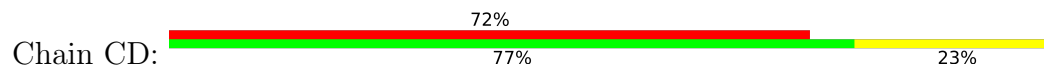
- Molecule 126: STAPLE STRAND



- Molecule 127: STAPLE STRAND



- Molecule 128: STAPLE STRAND

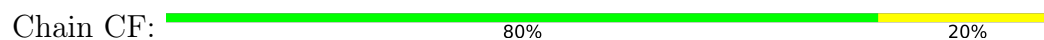


- Molecule 129: STAPLE STRAND

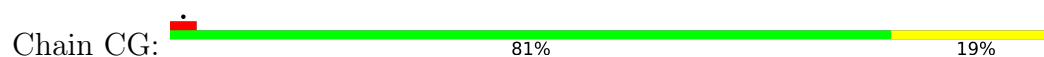




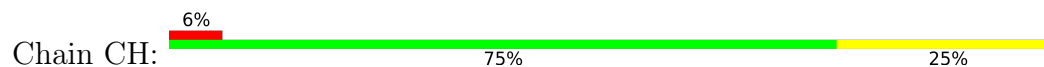
- Molecule 130: STAPLE STRAND



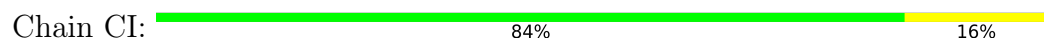
- Molecule 131: STAPLE STRAND



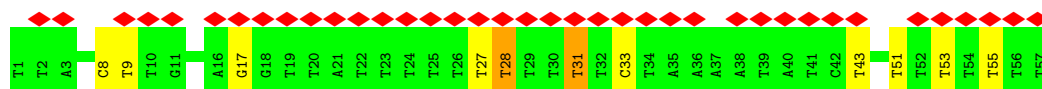
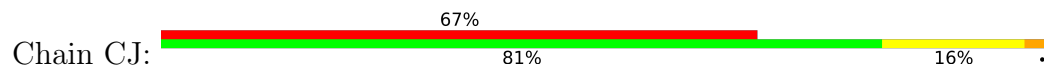
- Molecule 132: STAPLE STRAND



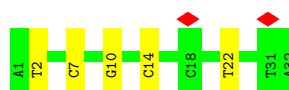
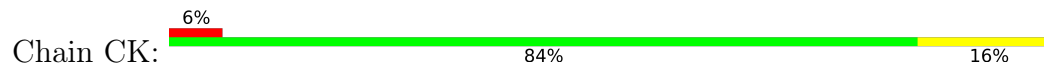
- Molecule 133: STAPLE STRAND



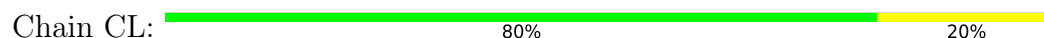
- Molecule 134: STAPLE STRAND



- Molecule 135: STAPLE STRAND

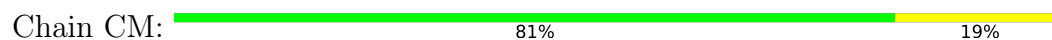


- Molecule 136: STAPLE STRAND

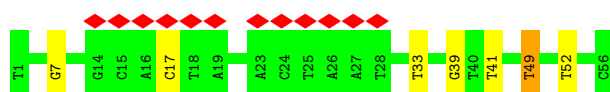




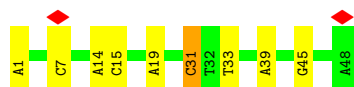
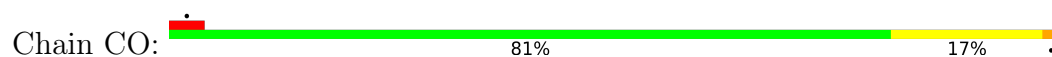
• Molecule 137: STAPLE STRAND



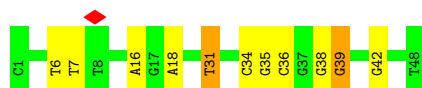
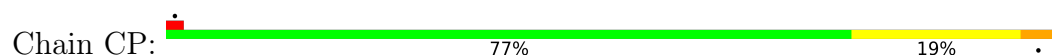
• Molecule 138: STAPLE STRAND



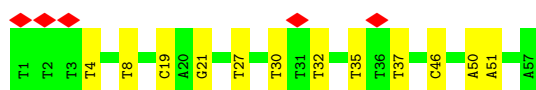
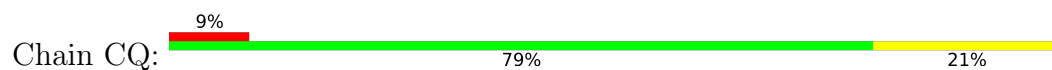
• Molecule 139: STAPLE STRAND



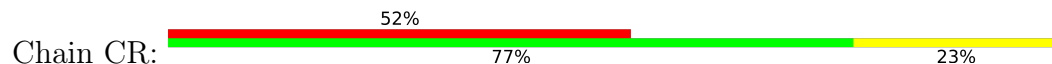
• Molecule 140: STAPLE STRAND



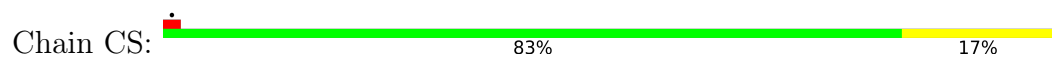
• Molecule 141: STAPLE STRAND



• Molecule 142: STAPLE STRAND



• Molecule 143: STAPLE STRAND





- Molecule 144: STAPLE STRAND

Chain CT: 93%



- Molecule 145: STAPLE STRAND

Chain CU: 86%



- Molecule 146: STAPLE STRAND

Chain CV: 91%



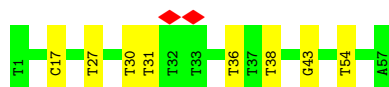
- Molecule 147: STAPLE STRAND

Chain CW: 88%



- Molecule 148: STAPLE STRAND

Chain CX: 86%



- Molecule 149: STAPLE STRAND

Chain CY: 47% 83% 15%



- Molecule 150: STAPLE STRAND

Chain CZ: 85%



- Molecule 151: STAPLE STRAND

Chain Ca: 90% 10%



- Molecule 152: STAPLE STRAND

Chain Cb: 72% 28%



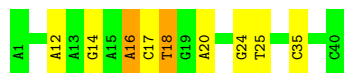
- Molecule 153: STAPLE STRAND

Chain Cc: 9% 78% 22%



- Molecule 154: STAPLE STRAND

Chain Cd: 78% 18% 5%



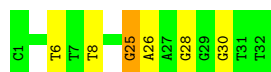
- Molecule 155: STAPLE STRAND

Chain Ce: 82% 15%



- Molecule 156: STAPLE STRAND

Chain Cf: 81% 16%



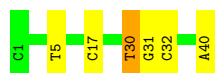
- Molecule 157: STAPLE STRAND

Chain Cg: 92% 8%



- Molecule 158: STAPLE STRAND

Chain Ch: 85% 12%



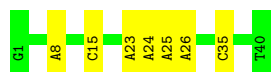
- Molecule 159: STAPLE STRAND

Chain Ci: 88% 12%



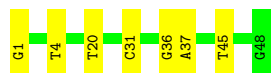
- Molecule 160: STAPLE STRAND

Chain Cj: 82% 18%



- Molecule 161: STAPLE STRAND

Chain Ck: 85% 15%



- Molecule 162: STAPLE STRAND

Chain Cl: 82% 18%



- Molecule 163: STAPLE STRAND

Chain Cm: 71% 27%

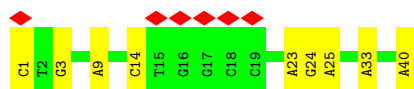
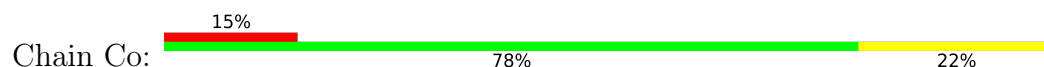


- Molecule 164: STAPLE STRAND

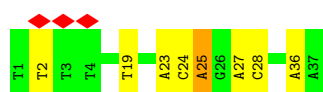
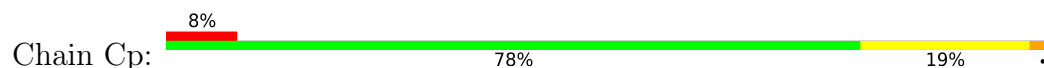
Chain Cn: 80% 20%



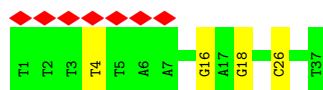
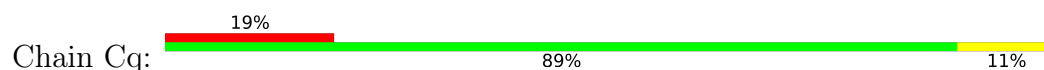
- Molecule 165: STAPLE STRAND



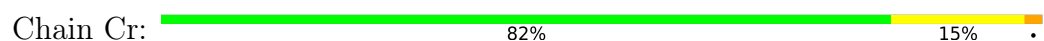
- Molecule 166: STAPLE STRAND



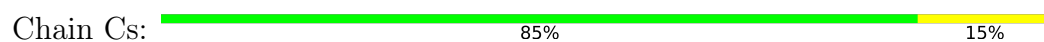
- Molecule 167: STAPLE STRAND



- Molecule 168: STAPLE STRAND



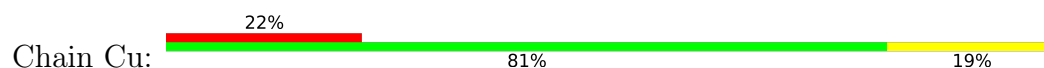
- Molecule 169: STAPLE STRAND

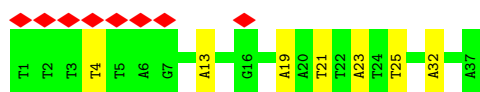


- Molecule 170: STAPLE STRAND



- Molecule 171: STAPLE STRAND





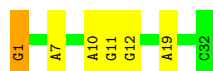
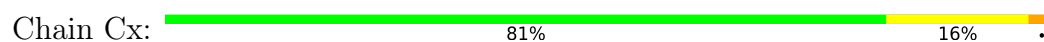
• Molecule 172: STAPLE STRAND



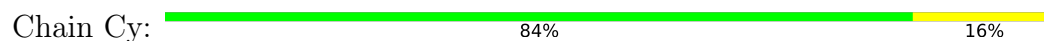
• Molecule 173: STAPLE STRAND



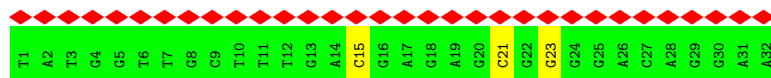
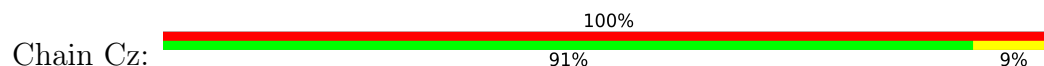
• Molecule 174: STAPLE STRAND



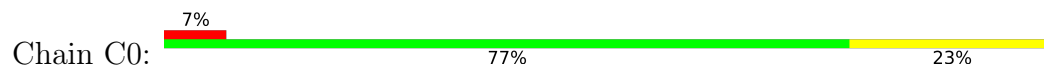
• Molecule 175: STAPLE STRAND



• Molecule 176: STAPLE STRAND



• Molecule 177: STAPLE STRAND

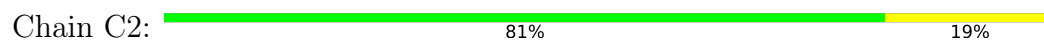


• Molecule 178: STAPLE STRAND

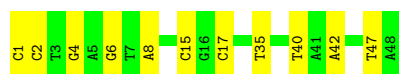
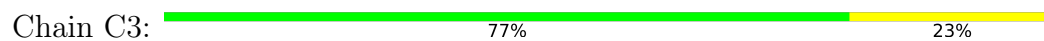




• Molecule 179: STAPLE STRAND



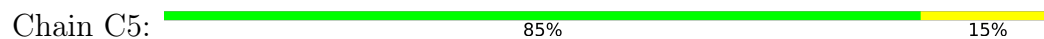
• Molecule 180: STAPLE STRAND



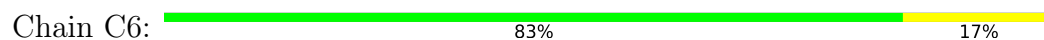
• Molecule 181: STAPLE STRAND



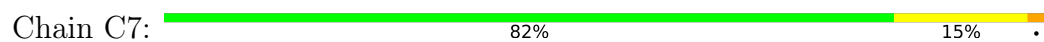
• Molecule 182: STAPLE STRAND



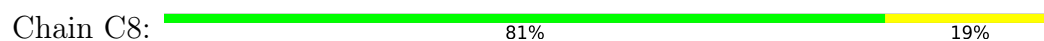
• Molecule 183: STAPLE STRAND



• Molecule 184: STAPLE STRAND

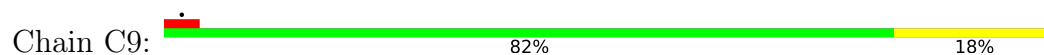


• Molecule 185: STAPLE STRAND

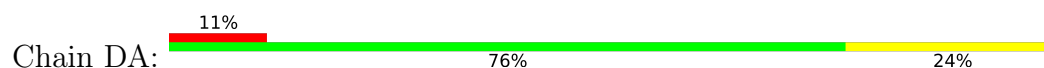




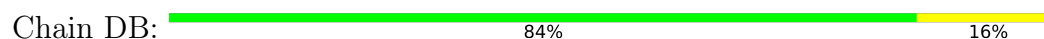
- Molecule 186: STAPLE STRAND



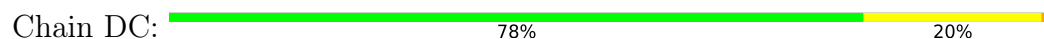
- Molecule 187: STAPLE STRAND



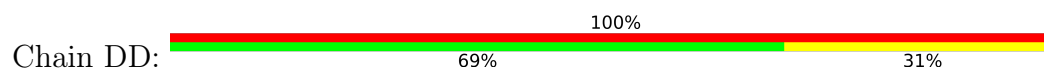
- Molecule 188: STAPLE STRAND



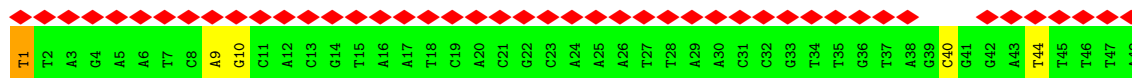
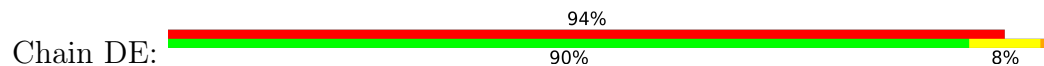
- Molecule 189: STAPLE STRAND



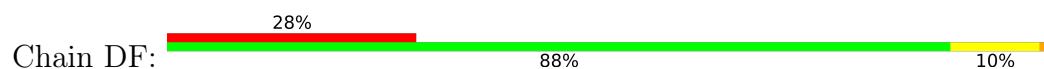
- Molecule 190: STAPLE STRAND

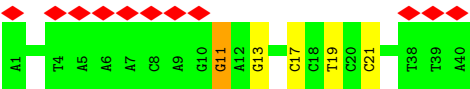


- Molecule 191: STAPLE STRAND

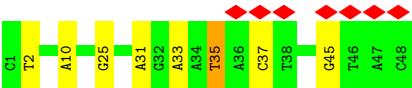
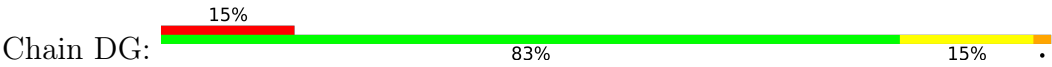


- Molecule 192: STAPLE STRAND

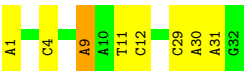
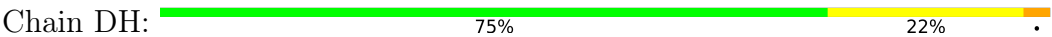




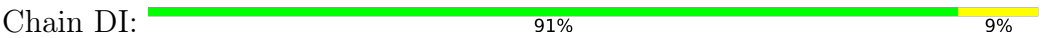
• Molecule 193: STAPLE STRAND



• Molecule 194: STAPLE STRAND



• Molecule 195: STAPLE STRAND



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	509812	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	55	Depositor
Minimum defocus (nm)	260.5	Depositor
Maximum defocus (nm)	3692	Depositor
Magnification	47000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.401	Depositor
Minimum map value	-0.217	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.051	Depositor
Map size ($\text{\AA}$)	644.96, 644.96, 644.96	wwPDB
Map dimensions	464, 464, 464	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.3900001, 1.3900001, 1.3900001	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	AA	0.70	0/184801	1.00	363/285260 (0.1%)
2	AB	0.68	0/647	0.92	0/996
3	AC	0.71	0/1104	1.03	4/1703 (0.2%)
4	AD	0.69	0/1230	1.01	3/1899 (0.2%)
5	AE	0.69	0/1358	1.04	6/2094 (0.3%)
6	AF	0.71	0/1101	1.02	4/1698 (0.2%)
7	AG	0.72	0/1115	1.01	5/1721 (0.3%)
8	AH	0.68	0/1366	0.94	0/2109
9	AI	0.69	0/950	1.04	3/1464 (0.2%)
10	AJ	0.66	0/1359	0.96	1/2096 (0.0%)
11	AK	0.69	0/739	0.94	1/1140 (0.1%)
12	AL	0.67	0/911	0.99	2/1405 (0.1%)
13	AM	0.68	0/1111	0.95	0/1714
14	AN	0.70	0/746	1.03	1/1151 (0.1%)
15	AO	0.68	0/1098	0.94	0/1691
16	AP	0.69	0/919	0.92	1/1415 (0.1%)
17	AQ	0.67	0/1021	1.02	3/1574 (0.2%)
18	AR	0.69	0/1108	0.97	1/1709 (0.1%)
19	AS	0.70	0/1112	0.89	0/1715
20	AT	0.69	0/1040	1.01	3/1607 (0.2%)
21	AU	0.70	0/1095	1.01	2/1687 (0.1%)
22	AV	0.70	0/920	0.96	1/1416 (0.1%)
23	AW	0.70	0/1285	1.03	7/1975 (0.4%)
24	AX	0.68	0/1372	0.98	3/2116 (0.1%)
25	AY	0.69	0/740	0.91	1/1142 (0.1%)
26	AZ	0.70	0/1114	0.98	2/1719 (0.1%)
27	Aa	0.67	0/923	0.90	1/1425 (0.1%)
28	Ab	0.70	0/1108	0.97	3/1709 (0.2%)
29	Ac	0.70	0/911	0.96	0/1402
30	Ad	0.67	0/1226	0.94	1/1892 (0.1%)
31	Ae	0.70	0/934	1.04	5/1443 (0.3%)
32	Af	0.71	0/749	0.92	1/1158 (0.1%)
33	Ag	0.67	0/1308	0.98	0/2016
34	Ah	0.67	0/1382	0.98	2/2134 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	Ai	0.71	0/1095	0.94	1/1689 (0.1%)
36	Aj	0.69	0/1084	1.01	3/1668 (0.2%)
37	Ak	0.69	0/732	0.97	1/1127 (0.1%)
38	Al	0.67	0/1103	0.95	1/1700 (0.1%)
39	Am	0.69	0/1310	0.98	1/2020 (0.0%)
40	An	0.67	0/1378	0.94	1/2128 (0.0%)
41	Ao	0.68	0/1306	0.96	1/2016 (0.0%)
42	Ap	0.69	0/1355	1.02	4/2091 (0.2%)
43	Aq	0.71	0/1105	0.93	0/1705
44	Ar	0.68	0/843	0.92	1/1298 (0.1%)
45	As	0.67	0/914	1.02	1/1410 (0.1%)
46	At	0.67	0/1010	0.93	1/1556 (0.1%)
47	Au	0.69	0/920	0.98	0/1417
48	Av	0.71	0/913	1.03	3/1406 (0.2%)
49	Aw	0.69	0/1272	1.02	1/1960 (0.1%)
50	Ax	0.68	0/912	1.03	2/1406 (0.1%)
51	Ay	0.70	0/1115	0.99	4/1720 (0.2%)
52	Az	0.69	0/1005	0.96	2/1544 (0.1%)
53	A0	0.72	0/715	1.12	5/1099 (0.5%)
54	A1	0.70	0/1116	1.00	1/1723 (0.1%)
55	A2	0.72	0/1080	1.02	2/1661 (0.1%)
56	A3	0.72	0/1294	1.01	4/1996 (0.2%)
57	A4	0.69	0/1045	0.93	2/1615 (0.1%)
58	A5	0.71	0/1115	0.95	2/1721 (0.1%)
59	A6	0.71	0/734	0.93	0/1132
60	A7	0.71	0/721	0.98	3/1107 (0.3%)
61	A8	0.70	0/740	0.89	0/1141
62	A9	0.71	0/1112	1.00	3/1715 (0.2%)
63	BA	0.69	0/1032	0.92	1/1589 (0.1%)
64	BB	0.69	0/742	0.96	1/1144 (0.1%)
65	BC	0.70	0/1016	0.97	0/1565
66	BD	0.69	0/1289	1.05	3/1988 (0.2%)
67	BE	0.69	0/1290	1.00	3/1988 (0.2%)
68	BF	0.69	0/1018	1.01	4/1568 (0.3%)
69	BG	0.71	0/904	1.00	1/1390 (0.1%)
70	BH	0.66	0/1288	0.94	2/1987 (0.1%)
71	BI	0.68	0/1292	0.99	2/1991 (0.1%)
72	BJ	0.68	0/1027	0.97	1/1584 (0.1%)
73	BK	0.70	0/734	0.97	0/1132
74	BL	0.69	0/1278	1.02	1/1971 (0.1%)
75	BM	0.67	0/731	0.89	0/1124
76	BN	0.69	0/940	0.90	0/1451
77	BO	0.71	0/1092	1.01	4/1681 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	BP	0.68	0/1313	1.00	4/2023 (0.2%)
79	BQ	0.67	0/1279	0.99	2/1969 (0.1%)
80	BR	0.69	0/1120	0.93	1/1730 (0.1%)
81	BS	0.68	0/1091	1.02	4/1681 (0.2%)
82	BT	0.70	0/1089	0.98	0/1677
83	BU	0.71	0/1100	0.98	3/1696 (0.2%)
84	BV	0.68	0/1327	0.98	3/2048 (0.1%)
85	BW	0.69	0/1351	1.08	5/2083 (0.2%)
86	BX	0.71	0/738	1.01	1/1138 (0.1%)
87	BY	0.72	0/934	1.00	3/1444 (0.2%)
88	BZ	0.70	0/918	1.01	2/1415 (0.1%)
89	Ba	0.69	0/1132	0.95	4/1749 (0.2%)
90	Bb	0.73	0/1087	1.14	4/1673 (0.2%)
91	Bc	0.68	0/741	0.94	1/1142 (0.1%)
92	Bd	0.69	0/1120	0.96	0/1727
93	Be	0.70	0/1094	1.04	3/1685 (0.2%)
94	Bf	0.68	0/1109	0.96	1/1710 (0.1%)
95	Bg	0.72	0/908	1.12	4/1399 (0.3%)
96	Bh	0.69	0/1302	0.96	1/2010 (0.0%)
97	Bi	0.69	0/898	1.07	5/1382 (0.4%)
98	Bj	0.70	0/734	1.08	4/1130 (0.4%)
99	Bk	0.66	0/742	0.92	0/1145
100	Bl	0.70	0/1090	1.00	2/1679 (0.1%)
101	Bm	0.71	0/1286	1.08	4/1985 (0.2%)
102	Bn	0.69	0/1087	0.98	0/1673
103	Bo	0.70	0/1121	0.92	0/1730
104	Bp	0.70	0/923	0.99	0/1424
105	Bq	0.73	0/1102	1.02	3/1703 (0.2%)
106	Br	0.71	0/1115	0.98	2/1722 (0.1%)
107	Bs	0.71	0/735	0.92	0/1131
108	Bt	0.69	0/925	0.97	1/1427 (0.1%)
109	Bu	0.70	0/921	0.95	0/1419
110	Bv	0.71	0/910	1.01	0/1401
111	Bw	0.67	0/1357	0.98	2/2092 (0.1%)
112	Bx	0.70	0/1030	0.99	3/1588 (0.2%)
113	By	0.70	0/928	0.93	1/1430 (0.1%)
114	Bz	0.67	0/733	0.96	0/1130
115	B0	0.68	0/1348	1.05	5/2077 (0.2%)
116	B1	0.70	0/1351	0.97	2/2083 (0.1%)
117	B2	0.69	0/927	0.94	0/1429
118	B3	0.69	0/749	0.85	0/1156
119	B4	0.69	0/746	0.97	1/1152 (0.1%)
120	B5	0.68	0/1370	0.94	0/2112

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
121	B6	0.69	0/1207	0.98	0/1859
122	B7	0.69	0/1105	0.99	2/1702 (0.1%)
123	B8	0.69	0/741	0.90	0/1142
124	B9	0.71	0/1093	1.04	5/1683 (0.3%)
125	CA	0.69	0/1094	0.99	1/1686 (0.1%)
126	CB	0.67	0/1370	0.93	2/2112 (0.1%)
127	CC	0.72	0/844	1.03	3/1301 (0.2%)
128	CD	0.66	0/1293	0.99	4/1996 (0.2%)
129	CE	0.71	0/751	1.02	2/1161 (0.2%)
130	CF	0.69	0/925	1.02	1/1426 (0.1%)
131	CG	0.70	0/739	0.95	0/1140
132	CH	0.70	0/1222	0.98	1/1884 (0.1%)
133	CI	0.69	0/722	1.03	2/1111 (0.2%)
134	CJ	0.66	0/1294	1.03	6/1996 (0.3%)
135	CK	0.68	0/729	1.01	1/1122 (0.1%)
136	CL	0.70	0/922	1.04	2/1420 (0.1%)
137	CM	0.68	0/749	0.88	1/1156 (0.1%)
138	CN	0.69	0/1297	0.94	1/2001 (0.0%)
139	CO	0.70	0/1101	0.98	2/1695 (0.1%)
140	CP	0.71	0/1113	1.03	3/1720 (0.2%)
141	CQ	0.69	0/1298	1.02	2/2003 (0.1%)
142	CR	0.67	0/1370	0.96	1/2114 (0.0%)
143	CS	0.69	0/1080	0.97	0/1663
144	CT	0.69	0/1303	0.97	2/2012 (0.1%)
145	CU	0.67	0/854	0.96	1/1316 (0.1%)
146	CV	0.69	0/737	0.98	0/1136
147	CW	0.68	0/732	0.93	0/1127
148	CX	0.67	0/1292	1.03	3/1994 (0.2%)
149	CY	0.67	0/1350	0.98	2/2080 (0.1%)
150	CZ	0.70	0/1099	0.99	1/1695 (0.1%)
151	Ca	0.68	0/1109	0.96	0/1708
152	Cb	0.70	0/924	0.99	1/1424 (0.1%)
153	Cc	0.70	0/735	0.99	1/1133 (0.1%)
154	Cd	0.70	0/939	1.06	4/1449 (0.3%)
155	Ce	0.67	0/932	0.95	3/1440 (0.2%)
156	Cf	0.71	0/736	0.99	1/1136 (0.1%)
157	Cg	0.69	0/918	0.99	1/1414 (0.1%)
158	Ch	0.66	0/917	1.01	1/1413 (0.1%)
159	Ci	0.68	0/1088	0.98	0/1674
160	Cj	0.69	0/917	1.00	2/1413 (0.1%)
161	Ck	0.70	0/1103	1.00	2/1703 (0.1%)
162	Cl	0.67	0/924	0.93	1/1424 (0.1%)
163	Cm	0.71	0/1098	1.05	4/1693 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
164	Cn	0.70	0/919	1.03	1/1417 (0.1%)
165	Co	0.69	0/910	1.01	2/1400 (0.1%)
166	Cp	0.69	0/843	0.97	1/1298 (0.1%)
167	Cq	0.70	0/847	0.99	2/1304 (0.2%)
168	Cr	0.71	0/936	0.99	1/1447 (0.1%)
169	Cs	0.69	0/925	0.95	0/1426
170	Ct	0.68	0/1031	1.00	3/1590 (0.2%)
171	Cu	0.69	0/850	1.04	2/1310 (0.2%)
172	Cv	0.69	0/905	1.00	2/1394 (0.1%)
173	Cw	0.71	0/928	0.97	1/1432 (0.1%)
174	Cx	0.70	0/733	0.97	1/1128 (0.1%)
175	Cy	0.72	0/733	0.99	2/1128 (0.2%)
176	Cz	0.68	0/751	0.84	0/1161
177	C0	0.71	0/1281	1.05	5/1972 (0.3%)
178	C1	0.67	0/1302	0.99	4/2011 (0.2%)
179	C2	0.68	0/738	0.99	1/1138 (0.1%)
180	C3	0.70	0/1100	0.96	2/1694 (0.1%)
181	C4	0.68	0/1096	0.95	0/1688
182	C5	0.68	0/1092	1.02	2/1683 (0.1%)
183	C6	0.72	0/1123	0.97	2/1735 (0.1%)
184	C7	0.69	0/896	1.07	4/1378 (0.3%)
185	C8	0.70	0/1116	1.01	2/1722 (0.1%)
186	C9	0.68	0/1293	0.98	2/1994 (0.1%)
187	DA	0.70	0/1027	1.01	0/1583
188	DB	0.70	0/724	0.98	2/1113 (0.2%)
189	DC	0.69	0/942	1.00	4/1453 (0.3%)
190	DD	0.69	0/1017	0.99	3/1566 (0.2%)
191	DE	0.67	0/1102	0.95	2/1699 (0.1%)
192	DF	0.69	0/917	0.94	2/1413 (0.1%)
193	DG	0.68	0/1112	0.93	1/1717 (0.1%)
194	DH	0.70	0/737	1.00	3/1134 (0.3%)
195	DI	0.68	0/732	0.95	0/1128
All	All	0.69	0/383925	0.99	715/592251 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	AA	1	1140
3	AC	0	3

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

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

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

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

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

There are no bond length outliers.

All (715) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	601	DC	P-O3'-C3'	14.73	142.30	120.20
1	AA	4222	DT	P-O3'-C3'	14.11	141.36	120.20
84	BV	39	DA	P-O3'-C3'	11.71	137.76	120.20
1	AA	486	DC	P-O3'-C3'	11.71	137.76	120.20
1	AA	6047	DC	P-O3'-C3'	11.61	137.62	120.20
115	B0	57	DT	P-O3'-C3'	11.53	137.50	120.20
1	AA	182	DC	P-O3'-C3'	11.53	137.49	120.20
1	AA	266	DG	P-O3'-C3'	11.48	137.42	120.20
1	AA	1491	DC	P-O3'-C3'	11.47	137.41	120.20
14	AN	25	DG	P-O3'-C3'	11.34	137.22	120.20
1	AA	5392	DG	P-O3'-C3'	11.34	137.21	120.20
1	AA	6562	DA	P-O3'-C3'	11.29	137.13	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	7336	DC	P-O3'-C3'	11.24	137.05	120.20
136	CL	12	DC	P-O3'-C3'	11.12	136.89	120.20
1	AA	2536	DT	P-O3'-C3'	10.94	136.61	120.20
1	AA	997	DC	P-O3'-C3'	10.93	136.59	120.20
1	AA	6629	DT	P-O3'-C3'	10.91	136.56	120.20
95	Bg	18	DC	P-O3'-C3'	10.84	136.46	120.20
90	Bb	9	DA	P-O3'-C3'	10.83	136.45	120.20
1	AA	6132	DC	P-O3'-C3'	10.83	136.44	120.20
1	AA	4217	DG	P-O3'-C3'	10.80	136.41	120.20
1	AA	636	DC	P-O3'-C3'	10.79	136.38	120.20
1	AA	2057	DA	P-O3'-C3'	10.73	136.30	120.20
87	BY	14	DG	P-O3'-C3'	10.72	136.28	120.20
1	AA	518	DG	P-O3'-C3'	10.71	136.26	120.20
5	AE	49	DG	P-O3'-C3'	10.69	136.24	120.20
1	AA	5665	DG	P-O3'-C3'	10.69	136.23	120.20
20	AT	18	DA	P-O3'-C3'	10.64	136.16	120.20
1	AA	3212	DA	P-O3'-C3'	10.57	136.05	120.20
53	A0	13	DG	P-O3'-C3'	10.54	136.00	120.20
1	AA	652	DC	P-O3'-C3'	10.53	136.00	120.20
3	AC	27	DC	P-O3'-C3'	10.50	135.94	120.20
1	AA	3143	DA	P-O3'-C3'	10.46	135.89	120.20
1	AA	1366	DT	P-O3'-C3'	10.44	135.85	120.20
101	Bm	31	DT	P-O3'-C3'	10.40	135.80	120.20
153	Cc	4	DC	P-O3'-C3'	10.40	135.80	120.20
177	C0	4	DT	P-O3'-C3'	10.35	135.72	120.20
50	Ax	18	DG	P-O3'-C3'	10.20	135.50	120.20
31	Ae	22	DA	P-O3'-C3'	10.20	135.49	120.20
105	Bq	10	DG	P-O3'-C3'	10.19	135.49	120.20
1	AA	2377	DC	P-O3'-C3'	10.17	135.46	120.20
101	Bm	23	DT	P-O3'-C3'	10.15	135.43	120.20
1	AA	6082	DA	P-O3'-C3'	10.11	135.36	120.20
26	AZ	24	DC	P-O3'-C3'	10.09	135.34	120.20
1	AA	3823	DT	P-O3'-C3'	10.08	135.32	120.20
1	AA	1067	DC	P-O3'-C3'	10.08	135.32	120.20
1	AA	4394	DC	P-O3'-C3'	10.03	135.24	120.20
1	AA	3515	DT	P-O3'-C3'	10.03	135.24	120.20
1	AA	6015	DT	P-O3'-C3'	10.01	135.21	120.20
160	Cj	15	DC	P-O3'-C3'	9.96	135.14	120.20
1	AA	1459	DT	P-O3'-C3'	9.95	135.13	120.20
4	AD	15	DT	P-O3'-C3'	9.95	135.13	120.20
1	AA	4718	DT	P-O3'-C3'	9.94	135.11	120.20
9	AI	22	DT	P-O3'-C3'	9.93	135.10	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	1396	DG	P-O3'-C3'	9.90	135.06	120.20
85	BW	42	DG	P-O3'-C3'	9.89	135.04	120.20
1	AA	5598	DA	P-O3'-C3'	9.86	134.99	120.20
1	AA	3623	DA	P-O3'-C3'	9.80	134.90	120.20
136	CL	6	DA	P-O3'-C3'	9.79	134.88	120.20
144	CT	33	DG	P-O3'-C3'	9.79	134.88	120.20
1	AA	3008	DT	P-O3'-C3'	9.77	134.85	120.20
48	Av	7	DG	P-O3'-C3'	9.76	134.84	120.20
1	AA	7736	DT	P-O3'-C3'	9.72	134.78	120.20
66	BD	8	DC	P-O3'-C3'	9.72	134.78	120.20
83	BU	17	DG	P-O3'-C3'	9.72	134.78	120.20
1	AA	5702	DG	P-O3'-C3'	9.71	134.76	120.20
1	AA	3865	DA	P-O3'-C3'	9.66	134.69	120.20
1	AA	3330	DA	P-O3'-C3'	9.65	134.67	120.20
1	AA	1098	DC	P-O3'-C3'	9.63	134.65	120.20
17	AQ	11	DT	P-O3'-C3'	9.63	134.64	120.20
74	BL	17	DG	P-O3'-C3'	9.62	134.63	120.20
1	AA	2505	DA	P-O3'-C3'	9.60	134.60	120.20
1	AA	98	DA	P-O3'-C3'	9.58	134.56	120.20
21	AU	47	DT	P-O3'-C3'	9.58	134.56	120.20
1	AA	5922	DA	P-O3'-C3'	9.56	134.54	120.20
84	BV	40	DA	P-O3'-C3'	9.53	134.50	120.20
1	AA	2011	DT	P-O3'-C3'	9.51	134.47	120.20
1	AA	650	DC	P-O3'-C3'	9.51	134.46	120.20
1	AA	1299	DG	P-O3'-C3'	9.49	134.44	120.20
1	AA	7302	DG	P-O3'-C3'	9.49	134.44	120.20
1	AA	4564	DT	P-O3'-C3'	9.49	134.43	120.20
122	B7	17	DT	P-O3'-C3'	9.47	134.41	120.20
1	AA	7438	DG	P-O3'-C3'	9.45	134.37	120.20
189	DC	10	DA	P-O3'-C3'	9.45	134.37	120.20
1	AA	7277	DT	P-O3'-C3'	9.39	134.28	120.20
1	AA	834	DG	P-O3'-C3'	9.38	134.26	120.20
1	AA	7303	DA	P-O3'-C3'	9.34	134.22	120.20
1	AA	4709	DG	P-O3'-C3'	9.33	134.19	120.20
184	C7	34	DA	P-O3'-C3'	9.30	134.15	120.20
148	CX	54	DT	P-O3'-C3'	9.29	134.13	120.20
182	C5	42	DG	P-O3'-C3'	9.24	134.06	120.20
1	AA	7571	DC	P-O3'-C3'	9.23	134.04	120.20
48	Av	31	DA	P-O3'-C3'	9.16	133.94	120.20
1	AA	6626	DG	P-O3'-C3'	9.13	133.90	120.20
97	Bi	31	DA	P-O3'-C3'	9.13	133.89	120.20
56	A3	47	DC	P-O3'-C3'	9.11	133.86	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
62	A9	41	DA	P-O3'-C3'	9.10	133.84	120.20
1	AA	530	DT	P-O3'-C3'	9.07	133.81	120.20
90	Bb	8	DA	P-O3'-C3'	9.07	133.80	120.20
154	Cd	18	DT	P-O3'-C3'	9.06	133.79	120.20
39	Am	40	DG	P-O3'-C3'	9.05	133.78	120.20
93	Be	15	DC	P-O3'-C3'	9.04	133.76	120.20
63	BA	42	DT	P-O3'-C3'	9.03	133.74	120.20
53	A0	11	DC	P-O3'-C3'	9.01	133.72	120.20
1	AA	6585	DA	P-O3'-C3'	9.01	133.71	120.20
72	BJ	17	DC	P-O3'-C3'	8.98	133.67	120.20
1	AA	2194	DT	P-O3'-C3'	8.97	133.66	120.20
1	AA	4048	DT	P-O3'-C3'	8.94	133.62	120.20
90	Bb	7	DA	P-O3'-C3'	8.94	133.61	120.20
1	AA	3079	DT	P-O3'-C3'	8.92	133.57	120.20
1	AA	2851	DT	P-O3'-C3'	8.86	133.49	120.20
164	Cn	36	DC	P-O3'-C3'	8.84	133.46	120.20
163	Cm	25	DG	P-O3'-C3'	8.84	133.45	120.20
85	BW	20	DA	P-O3'-C3'	8.83	133.45	120.20
1	AA	2779	DG	P-O3'-C3'	8.80	133.40	120.20
140	CP	39	DG	P-O3'-C3'	8.80	133.40	120.20
1	AA	4583	DT	P-O3'-C3'	8.79	133.39	120.20
1	AA	342	DC	P-O3'-C3'	8.79	133.38	120.20
67	BE	46	DA	P-O3'-C3'	8.78	133.36	120.20
1	AA	3046	DA	P-O3'-C3'	8.76	133.33	120.20
1	AA	1460	DG	P-O3'-C3'	8.75	133.33	120.20
183	C6	7	DA	P-O3'-C3'	8.73	133.30	120.20
9	AI	34	DT	P-O3'-C3'	8.73	133.29	120.20
1	AA	7523	DT	P-O3'-C3'	8.69	133.24	120.20
51	Ay	16	DC	P-O3'-C3'	8.67	133.21	120.20
1	AA	4851	DC	P-O3'-C3'	8.67	133.20	120.20
64	BB	31	DG	P-O3'-C3'	8.66	133.19	120.20
1	AA	705	DC	P-O3'-C3'	8.64	133.16	120.20
149	CY	16	DT	P-O3'-C3'	8.62	133.13	120.20
1	AA	1181	DC	P-O3'-C3'	8.61	133.11	120.20
1	AA	72	DA	P-O3'-C3'	8.60	133.10	120.20
1	AA	6927	DC	P-O3'-C3'	8.59	133.08	120.20
1	AA	2974	DC	P-O3'-C3'	8.58	133.07	120.20
1	AA	743	DA	P-O3'-C3'	8.56	133.04	120.20
1	AA	8016	DC	P-O3'-C3'	8.52	132.98	120.20
62	A9	39	DC	P-O3'-C3'	8.51	132.96	120.20
38	Al	22	DC	P-O3'-C3'	8.51	132.96	120.20
55	A2	25	DC	P-O3'-C3'	8.49	132.94	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	1197	DT	P-O3'-C3'	8.48	132.93	120.20
175	Cy	15	DC	P-O3'-C3'	8.48	132.92	120.20
1	AA	5402	DT	P-O3'-C3'	8.48	132.91	120.20
1	AA	516	DG	P-O3'-C3'	8.47	132.91	120.20
135	CK	10	DG	P-O3'-C3'	8.47	132.90	120.20
129	CE	17	DC	P-O3'-C3'	8.46	132.89	120.20
28	Ab	26	DG	P-O3'-C3'	8.44	132.86	120.20
178	C1	2	DT	P-O3'-C3'	8.44	132.86	120.20
1	AA	1190	DA	P-O3'-C3'	8.43	132.85	120.20
106	Br	9	DG	P-O3'-C3'	8.43	132.84	120.20
31	Ae	27	DA	P-O3'-C3'	8.41	132.81	120.20
1	AA	305	DC	P-O3'-C3'	8.38	132.77	120.20
7	AG	25	DG	P-O3'-C3'	8.38	132.77	120.20
86	BX	23	DC	P-O3'-C3'	8.37	132.75	120.20
78	BP	12	DT	P-O3'-C3'	8.35	132.73	120.20
1	AA	1979	DC	P-O3'-C3'	8.34	132.71	120.20
1	AA	6535	DA	P-O3'-C3'	8.33	132.69	120.20
93	Be	23	DT	P-O3'-C3'	8.32	132.69	120.20
1	AA	353	DG	P-O3'-C3'	8.32	132.68	120.20
24	AX	54	DA	P-O3'-C3'	8.31	132.67	120.20
1	AA	3391	DC	P-O3'-C3'	8.30	132.65	120.20
163	Cm	7	DA	P-O3'-C3'	8.29	132.64	120.20
124	B9	31	DC	P-O3'-C3'	8.29	132.63	120.20
1	AA	2007	DG	P-O3'-C3'	8.26	132.59	120.20
179	C2	26	DG	P-O3'-C3'	8.23	132.55	120.20
53	A0	7	DC	P-O3'-C3'	8.20	132.49	120.20
1	AA	5572	DC	P-O3'-C3'	8.19	132.48	120.20
1	AA	77	DC	P-O3'-C3'	8.16	132.45	120.20
1	AA	7412	DC	P-O3'-C3'	8.15	132.43	120.20
115	B0	55	DT	P-O3'-C3'	8.15	132.42	120.20
1	AA	3479	DG	P-O3'-C3'	8.14	132.41	120.20
189	DC	7	DC	P-O3'-C3'	8.10	132.35	120.20
85	BW	1	DT	P-O3'-C3'	8.09	132.33	120.20
1	AA	7945	DG	P-O3'-C3'	8.08	132.32	120.20
89	Ba	1	DG	P-O3'-C3'	8.07	132.31	120.20
100	Bl	34	DG	P-O3'-C3'	8.06	132.29	120.20
1	AA	4944	DA	P-O3'-C3'	8.03	132.24	120.20
1	AA	7955	DG	P-O3'-C3'	8.02	132.23	120.20
130	CF	15	DC	P-O3'-C3'	8.01	132.21	120.20
68	BF	31	DG	P-O3'-C3'	7.99	132.19	120.20
78	BP	42	DC	P-O3'-C3'	7.99	132.19	120.20
1	AA	1733	DT	P-O3'-C3'	7.99	132.18	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	4768	DG	P-O3'-C3'	7.98	132.18	120.20
1	AA	3489	DT	P-O3'-C3'	7.97	132.15	120.20
98	Bj	22	DA	P-O3'-C3'	7.96	132.14	120.20
1	AA	5396	DA	P-O3'-C3'	7.95	132.13	120.20
85	BW	40	DC	P-O3'-C3'	7.95	132.13	120.20
90	Bb	47	DG	P-O3'-C3'	7.93	132.10	120.20
170	Ct	3	DT	P-O3'-C3'	7.92	132.08	120.20
34	Ah	4	DT	P-O3'-C3'	7.91	132.07	120.20
101	Bm	7	DA	P-O3'-C3'	7.91	132.07	120.20
154	Cd	35	DC	P-O3'-C3'	7.91	132.06	120.20
1	AA	3476	DG	P-O3'-C3'	7.90	132.05	120.20
1	AA	6161	DA	P-O3'-C3'	7.89	132.03	120.20
1	AA	856	DC	P-O3'-C3'	7.88	132.03	120.20
1	AA	4604	DG	P-O3'-C3'	7.87	132.00	120.20
115	B0	32	DT	P-O3'-C3'	7.85	131.98	120.20
166	Cp	25	DA	P-O3'-C3'	7.85	131.97	120.20
71	BI	45	DA	P-O3'-C3'	7.83	131.94	120.20
101	Bm	17	DG	P-O3'-C3'	7.82	131.93	120.20
20	AT	35	DG	P-O3'-C3'	7.82	131.93	120.20
1	AA	4881	DC	P-O3'-C3'	7.81	131.92	120.20
1	AA	2215	DC	P-O3'-C3'	7.80	131.91	120.20
184	C7	23	DC	P-O3'-C3'	7.80	131.91	120.20
1	AA	7856	DT	P-O3'-C3'	7.80	131.90	120.20
177	C0	7	DC	P-O3'-C3'	7.80	131.90	120.20
1	AA	801	DA	P-O3'-C3'	7.79	131.88	120.20
1	AA	7572	DG	P-O3'-C3'	7.78	131.87	120.20
1	AA	2457	DC	P-O3'-C3'	7.78	131.87	120.20
4	AD	44	DG	P-O3'-C3'	7.76	131.85	120.20
134	CJ	27	DT	P-O3'-C3'	7.76	131.84	120.20
80	BR	23	DT	P-O3'-C3'	7.76	131.84	120.20
97	Bi	30	DC	P-O3'-C3'	7.74	131.81	120.20
1	AA	3968	DA	P-O3'-C3'	7.74	131.81	120.20
1	AA	5328	DT	P-O3'-C3'	7.73	131.79	120.20
128	CD	51	DT	P-O3'-C3'	7.73	131.80	120.20
1	AA	3195	DC	P-O3'-C3'	7.72	131.78	120.20
167	Cq	4	DT	P-O3'-C3'	7.72	131.78	120.20
1	AA	3178	DT	P-O3'-C3'	7.72	131.78	120.20
1	AA	7349	DA	P-O3'-C3'	7.71	131.77	120.20
100	Bl	31	DC	P-O3'-C3'	7.69	131.74	120.20
1	AA	3003	DC	P-O3'-C3'	7.68	131.72	120.20
1	AA	367	DG	P-O3'-C3'	7.67	131.71	120.20
60	A7	20	DC	P-O3'-C3'	7.67	131.71	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
185	C8	22	DC	P-O3'-C3'	7.66	131.69	120.20
1	AA	1126	DC	P-O3'-C3'	7.65	131.67	120.20
1	AA	1367	DT	P-O3'-C3'	7.64	131.67	120.20
16	AP	7	DC	P-O3'-C3'	7.64	131.67	120.20
1	AA	6745	DA	P-O3'-C3'	7.64	131.66	120.20
42	Ap	3	DT	P-O3'-C3'	7.64	131.66	120.20
188	DB	18	DC	P-O3'-C3'	7.64	131.66	120.20
1	AA	5185	DA	P-O3'-C3'	7.64	131.65	120.20
6	AF	20	DT	P-O3'-C3'	7.63	131.64	120.20
1	AA	2942	DT	P-O3'-C3'	7.62	131.63	120.20
1	AA	2296	DA	P-O3'-C3'	7.62	131.62	120.20
1	AA	3125	DT	P-O3'-C3'	7.62	131.62	120.20
1	AA	1887	DT	P-O3'-C3'	7.61	131.61	120.20
1	AA	2334	DG	P-O3'-C3'	7.60	131.60	120.20
1	AA	2941	DG	P-O3'-C3'	7.59	131.59	120.20
124	B9	1	DA	P-O3'-C3'	7.58	131.57	120.20
1	AA	8011	DC	P-O3'-C3'	7.56	131.54	120.20
1	AA	3933	DC	P-O3'-C3'	7.55	131.53	120.20
134	CJ	31	DT	P-O3'-C3'	7.53	131.49	120.20
87	BY	15	DC	P-O3'-C3'	7.52	131.48	120.20
3	AC	41	DT	P-O3'-C3'	7.51	131.47	120.20
1	AA	7476	DC	P-O3'-C3'	7.51	131.47	120.20
1	AA	1350	DC	P-O3'-C3'	7.50	131.44	120.20
1	AA	1114	DC	P-O3'-C3'	7.48	131.41	120.20
81	BS	24	DC	P-O5'-C5'	7.47	131.21	120.00
28	Ab	19	DC	P-O3'-C3'	7.46	131.39	120.20
134	CJ	28	DT	P-O3'-C3'	7.43	131.35	120.20
171	Cu	32	DA	P-O3'-C3'	7.43	131.35	120.20
186	C9	28	DT	P-O3'-C3'	7.42	131.32	120.20
7	AG	8	DC	P-O3'-C3'	7.40	131.31	120.20
1	AA	3038	DT	P-O3'-C3'	7.38	131.27	120.20
128	CD	24	DT	P-O3'-C3'	7.38	131.27	120.20
134	CJ	53	DT	P-O3'-C3'	7.38	131.26	120.20
184	C7	3	DA	P-O3'-C3'	7.37	131.26	120.20
1	AA	7405	DC	P-O3'-C3'	7.37	131.25	120.20
1	AA	7413	DC	P-O5'-C5'	7.36	131.04	120.00
1	AA	2999	DT	P-O3'-C3'	7.36	131.24	120.20
1	AA	2315	DT	P-O3'-C3'	7.36	131.24	120.20
1	AA	3568	DC	P-O3'-C3'	7.36	131.24	120.20
97	Bi	5	DC	P-O3'-C3'	7.35	131.23	120.20
23	AW	18	DG	P-O3'-C3'	7.34	131.21	120.20
105	Bq	45	DC	P-O3'-C3'	7.33	131.20	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	2155	DT	P-O3'-C3'	7.33	131.20	120.20
1	AA	2540	DG	P-O3'-C3'	7.33	131.20	120.20
1	AA	6189	DT	P-O3'-C3'	7.33	131.19	120.20
1	AA	5358	DC	P-O3'-C3'	7.30	131.16	120.20
81	BS	9	DT	P-O3'-C3'	7.30	131.15	120.20
88	BZ	27	DG	P-O3'-C3'	7.30	131.15	120.20
87	BY	35	DG	P-O3'-C3'	7.30	131.15	120.20
185	C8	24	DC	P-O3'-C3'	7.27	131.10	120.20
1	AA	4306	DG	P-O3'-C3'	7.26	131.09	120.20
1	AA	2600	DG	P-O3'-C3'	7.25	131.08	120.20
51	Ay	21	DG	P-O3'-C3'	7.24	131.06	120.20
83	BU	7	DC	P-O3'-C3'	7.23	131.05	120.20
194	DH	9	DA	P-O3'-C3'	7.22	131.03	120.20
1	AA	563	DC	P-O3'-C3'	7.22	131.03	120.20
17	AQ	4	DG	P-O3'-C3'	7.21	131.02	120.20
1	AA	690	DC	P-O3'-C3'	7.21	131.02	120.20
1	AA	1620	DC	P-O3'-C3'	7.20	131.00	120.20
67	BE	32	DT	P-O3'-C3'	7.20	131.00	120.20
1	AA	1969	DC	P-O3'-C3'	7.20	131.00	120.20
1	AA	3546	DT	P-O3'-C3'	7.20	131.00	120.20
1	AA	6805	DC	P-O5'-C5'	7.19	130.78	120.00
5	AE	32	DT	P-O3'-C3'	7.18	130.97	120.20
119	B4	7	DC	P-O3'-C3'	7.17	130.96	120.20
42	Ap	5	DA	P-O3'-C3'	7.16	130.94	120.20
10	AJ	56	DA	P-O3'-C3'	7.16	130.93	120.20
24	AX	29	DT	P-O3'-C3'	7.16	130.93	120.20
45	As	6	DT	P-O3'-C3'	7.16	130.94	120.20
1	AA	2581	DT	P-O3'-C3'	7.15	130.92	120.20
1	AA	5817	DC	P-O5'-C5'	7.13	130.69	120.00
79	BQ	33	DT	P-O3'-C3'	7.13	130.89	120.20
1	AA	3282	DT	P-O3'-C3'	7.12	130.88	120.20
170	Ct	40	DG	P-O3'-C3'	7.10	130.85	120.20
1	AA	3376	DC	P-O5'-C5'	7.10	130.65	120.00
1	AA	1630	DC	P-O3'-C3'	7.10	130.85	120.20
1	AA	5847	DT	P-O3'-C3'	7.10	130.84	120.20
127	CC	12	DG	P-O3'-C3'	7.09	130.84	120.20
1	AA	6107	DT	P-O3'-C3'	7.09	130.84	120.20
1	AA	3584	DC	P-O3'-C3'	7.08	130.83	120.20
126	CB	31	DT	P-O3'-C3'	7.08	130.82	120.20
1	AA	1113	DG	P-O3'-C3'	7.07	130.81	120.20
42	Ap	2	DT	P-O3'-C3'	7.06	130.80	120.20
148	CX	27	DT	P-O3'-C3'	7.05	130.78	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
95	Bg	37	DT	P-O3'-C3'	7.05	130.78	120.20
5	AE	58	DT	P-O3'-C3'	7.04	130.76	120.20
112	Bx	1	DT	P-O3'-C3'	7.04	130.76	120.20
1	AA	1878	DT	P-O3'-C3'	7.03	130.75	120.20
1	AA	6598	DC	P-O3'-C3'	7.03	130.75	120.20
1	AA	1562	DC	P-O3'-C3'	7.02	130.73	120.20
1	AA	5440	DT	P-O3'-C3'	7.02	130.72	120.20
1	AA	7930	DC	P-O5'-C5'	7.01	130.51	120.00
1	AA	7743	DG	P-O3'-C3'	7.01	130.71	120.20
66	BD	39	DA	P-O3'-C3'	7.00	130.70	120.20
1	AA	6183	DC	P-O5'-C5'	7.00	130.50	120.00
1	AA	799	DG	P-O3'-C3'	7.00	130.69	120.20
1	AA	2105	DC	P-O3'-C3'	7.00	130.69	120.20
89	Ba	4	DG	P-O3'-C3'	6.98	130.67	120.20
1	AA	1081	DG	P-O3'-C3'	6.97	130.66	120.20
51	Ay	36	DA	P-O3'-C3'	6.96	130.64	120.20
57	A4	34	DG	P-O3'-C3'	6.95	130.63	120.20
1	AA	4023	DG	P-O3'-C3'	6.95	130.63	120.20
1	AA	2960	DT	P-O3'-C3'	6.94	130.61	120.20
32	Af	2	DT	P-O3'-C3'	6.93	130.60	120.20
1	AA	3281	DT	P-O3'-C3'	6.93	130.59	120.20
190	DD	40	DA	P-O3'-C3'	6.93	130.59	120.20
1	AA	7494	DA	P-O3'-C3'	6.92	130.58	120.20
1	AA	1342	DC	P-O5'-C5'	6.90	130.34	120.00
78	BP	26	DA	P-O3'-C3'	6.88	130.52	120.20
1	AA	6957	DA	P-O3'-C3'	6.88	130.52	120.20
133	CI	9	DT	P-O3'-C3'	6.87	130.50	120.20
50	Ax	31	DT	P-O3'-C3'	6.84	130.47	120.20
154	Cd	16	DA	P-O3'-C3'	6.84	130.47	120.20
1	AA	5324	DT	P-O3'-C3'	6.84	130.46	120.20
70	BH	3	DT	P-O3'-C3'	6.84	130.46	120.20
1	AA	7892	DC	P-O5'-C5'	6.83	130.24	120.00
1	AA	2794	DC	P-O5'-C5'	6.82	130.23	120.00
124	B9	23	DG	P-O3'-C3'	6.82	130.43	120.20
1	AA	1398	DC	P-O3'-C3'	6.82	130.43	120.20
1	AA	3381	DT	P-O3'-C3'	6.81	130.41	120.20
54	A1	46	DC	P-O5'-C5'	6.80	130.21	120.00
1	AA	7237	DT	P-O3'-C3'	6.80	130.39	120.20
31	Ae	11	DC	P-O3'-C3'	6.79	130.39	120.20
83	BU	13	DA	P-O3'-C3'	6.79	130.39	120.20
124	B9	19	DC	P-O3'-C3'	6.79	130.39	120.20
91	Bc	23	DT	P-O3'-C3'	6.77	130.36	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	7164	DG	P-O3'-C3'	6.77	130.35	120.20
1	AA	4176	DC	P-O5'-C5'	6.75	130.13	120.00
95	Bg	29	DC	P-O3'-C3'	6.75	130.33	120.20
115	B0	26	DT	P-O3'-C3'	6.75	130.33	120.20
122	B7	22	DG	P-O3'-C3'	6.75	130.33	120.20
41	Ao	53	DT	P-O3'-C3'	6.75	130.32	120.20
1	AA	6604	DC	P-O5'-C5'	6.74	130.11	120.00
189	DC	32	DA	P-O3'-C3'	6.74	130.31	120.20
1	AA	827	DC	P-O3'-C3'	6.73	130.30	120.20
171	Cu	23	DA	P-O3'-C3'	6.73	130.29	120.20
3	AC	2	DC	P-O3'-C3'	6.72	130.28	120.20
138	CN	49	DT	P-O3'-C3'	6.71	130.27	120.20
141	CQ	37	DT	P-O3'-C3'	6.71	130.26	120.20
1	AA	4789	DT	P-O3'-C3'	6.70	130.25	120.20
58	A5	47	DA	P-O3'-C3'	6.70	130.25	120.20
1	AA	6383	DT	P-O3'-C3'	6.69	130.23	120.20
5	AE	51	DT	P-O3'-C3'	6.68	130.23	120.20
140	CP	31	DT	P-O3'-C3'	6.68	130.22	120.20
1	AA	7241	DT	P-O5'-C5'	6.66	129.98	120.00
79	BQ	39	DC	P-O5'-C5'	6.66	129.98	120.00
85	BW	33	DT	P-O3'-C3'	6.63	130.15	120.20
116	B1	27	DT	P-O3'-C3'	6.63	130.14	120.20
162	Cl	22	DA	P-O3'-C3'	6.63	130.14	120.20
1	AA	4499	DT	P-O3'-C3'	6.62	130.13	120.20
161	Ck	4	DT	P-O3'-C3'	6.61	130.12	120.20
1	AA	4886	DC	P-O3'-C3'	6.60	130.10	120.20
1	AA	657	DC	P-O3'-C3'	6.60	130.09	120.20
1	AA	5237	DT	P-O3'-C3'	6.60	130.09	120.20
1	AA	1454	DC	P-O3'-C3'	6.58	130.07	120.20
115	B0	59	DT	P-O3'-C3'	6.58	130.07	120.20
1	AA	6907	DC	P-O5'-C5'	6.58	129.87	120.00
1	AA	5429	DT	P-O3'-C3'	6.56	130.03	120.20
1	AA	7956	DT	P-O3'-C3'	6.54	130.02	120.20
1	AA	1453	DG	P-O3'-C3'	6.54	130.01	120.20
127	CC	20	DC	P-O3'-C3'	6.54	130.00	120.20
192	DF	11	DG	P-O3'-C3'	6.53	129.99	120.20
157	Cg	1	DA	P-O3'-C3'	6.51	129.97	120.20
168	Cr	6	DT	P-O3'-C3'	6.51	129.96	120.20
62	A9	31	DC	P-O3'-C3'	6.51	129.96	120.20
1	AA	3666	DC	P-O3'-C3'	6.50	129.96	120.20
1	AA	2	DG	P-O3'-C3'	6.49	129.94	120.20
1	AA	2306	DT	P-O3'-C3'	6.49	129.93	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	AW	45	DC	P-O3'-C3'	6.47	129.91	120.20
26	AZ	21	DA	P-O3'-C3'	6.46	129.89	120.20
1	AA	4602	DC	P-O3'-C3'	6.46	129.88	120.20
1	AA	3425	DC	P-O5'-C5'	6.43	129.64	120.00
188	DB	18	DC	P-O5'-C5'	6.42	129.63	120.00
36	Aj	26	DC	P-O5'-C5'	6.42	129.62	120.00
77	BO	7	DC	P-O3'-C3'	6.41	129.82	120.20
194	DH	1	DA	P-O3'-C3'	6.41	129.82	120.20
1	AA	1224	DC	P-O5'-C5'	6.41	129.61	120.00
68	BF	8	DA	P-O3'-C3'	6.40	129.80	120.20
60	A7	6	DC	P-O3'-C3'	6.39	129.79	120.20
6	AF	6	DG	P-O3'-C3'	6.39	129.78	120.20
144	CT	46	DA	P-O3'-C3'	6.39	129.79	120.20
21	AU	41	DC	P-O3'-C3'	6.37	129.76	120.20
111	Bw	27	DT	P-O3'-C3'	6.37	129.75	120.20
1	AA	2003	DG	P-O3'-C3'	6.35	129.73	120.20
1	AA	8011	DC	P-O5'-C5'	6.34	129.51	120.00
1	AA	7994	DT	P-O3'-C3'	6.34	129.71	120.20
1	AA	1385	DT	P-O3'-C3'	6.34	129.71	120.20
1	AA	4029	DA	P-O3'-C3'	6.34	129.70	120.20
46	At	11	DC	P-O3'-C3'	6.34	129.71	120.20
163	Cm	8	DA	P-O3'-C3'	6.33	129.69	120.20
23	AW	40	DC	P-O3'-C3'	6.32	129.67	120.20
44	Ar	8	DA	P-O3'-C3'	6.30	129.65	120.20
1	AA	7366	DC	P-O3'-C3'	6.29	129.63	120.20
1	AA	4881	DC	P-O5'-C5'	6.28	129.42	120.00
1	AA	2665	DC	P-O3'-C3'	6.28	129.62	120.20
1	AA	5227	DG	P-O3'-C3'	6.26	129.59	120.20
111	Bw	30	DT	P-O3'-C3'	6.24	129.57	120.20
56	A3	48	DC	P-O3'-C3'	6.24	129.56	120.20
25	AY	15	DC	P-O3'-C3'	6.22	129.53	120.20
1	AA	3216	DC	P-O5'-C5'	6.21	129.32	120.00
1	AA	8062	DC	P-O5'-C5'	6.20	129.31	120.00
1	AA	2617	DC	P-O5'-C5'	6.20	129.29	120.00
1	AA	2890	DC	P-O5'-C5'	6.19	129.28	120.00
52	Az	18	DC	P-O5'-C5'	6.18	129.28	120.00
6	AF	47	DC	P-O3'-C3'	6.17	129.46	120.20
34	Ah	13	DC	P-O3'-C3'	6.17	129.45	120.20
1	AA	3666	DC	P-O5'-C5'	6.17	129.25	120.00
1	AA	243	DC	P-O5'-C5'	6.16	129.25	120.00
95	Bg	23	DT	P-O3'-C3'	6.16	129.44	120.20
1	AA	1051	DA	P-O3'-C3'	6.16	129.43	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
178	C1	1	DT	P-O3'-C3'	6.15	129.43	120.20
1	AA	5111	DC	P-O5'-C5'	6.12	129.18	120.00
1	AA	188	DG	P-O5'-C5'	6.12	129.18	120.00
1	AA	7117	DC	P-O5'-C5'	6.10	129.16	120.00
155	Ce	7	DT	P-O3'-C3'	6.10	129.35	120.20
155	Ce	2	DG	P-O3'-C3'	6.07	129.31	120.20
1	AA	1022	DG	P-O3'-C3'	6.07	129.30	120.20
1	AA	954	DG	P-O3'-C3'	6.06	129.29	120.20
1	AA	6730	DC	P-O5'-C5'	6.05	129.07	120.00
94	Bf	16	DC	P-O5'-C5'	6.04	129.07	120.00
1	AA	3659	DC	P-O5'-C5'	6.04	129.06	120.00
1	AA	6644	DC	P-O3'-C3'	6.04	129.26	120.20
141	CQ	46	DC	P-O3'-C3'	6.01	129.22	120.20
172	Cv	6	DC	P-O5'-C5'	6.01	129.01	120.00
1	AA	6746	DA	P-O3'-C3'	5.97	129.16	120.20
1	AA	8029	DG	P-O5'-C5'	5.97	128.96	120.00
7	AG	34	DA	P-O3'-C3'	5.96	129.15	120.20
1	AA	8019	DC	P-O5'-C5'	5.95	128.92	120.00
1	AA	4635	DC	P-O5'-C5'	5.92	128.89	120.00
160	Cj	26	DA	P-O3'-C3'	5.92	129.09	120.20
158	Ch	30	DT	P-O3'-C3'	5.92	129.08	120.20
1	AA	4466	DA	P-O3'-C3'	5.91	129.07	120.20
1	AA	5751	DC	P-O5'-C5'	5.91	128.87	120.00
1	AA	983	DC	P-O5'-C5'	5.91	128.87	120.00
1	AA	4721	DG	P-O3'-C3'	5.90	129.05	120.20
129	CE	6	DT	P-O3'-C3'	5.89	129.04	120.20
4	AD	30	DG	P-O3'-C3'	5.89	129.03	120.20
1	AA	605	DC	P-O5'-C5'	5.88	128.83	120.00
1	AA	3237	DA	P-O3'-C3'	5.87	129.00	120.20
1	AA	2455	DC	P-O5'-C5'	5.84	128.77	120.00
193	DG	35	DT	P-O3'-C3'	5.84	128.96	120.20
1	AA	5029	DT	P-O5'-C5'	5.83	128.75	120.00
1	AA	952	DC	P-O5'-C5'	5.83	128.75	120.00
184	C7	23	DC	P-O5'-C5'	5.82	128.73	120.00
1	AA	7210	DC	P-O5'-C5'	5.80	128.70	120.00
1	AA	5223	DC	P-O5'-C5'	5.79	128.68	120.00
173	Cw	3	DC	P-O5'-C5'	5.79	128.68	120.00
1	AA	5353	DT	P-O5'-C5'	5.76	128.64	120.00
1	AA	3030	DG	P-O3'-C3'	5.75	128.83	120.20
52	Az	38	DC	P-O5'-C5'	5.74	128.62	120.00
1	AA	1779	DT	P-O5'-C5'	5.74	128.61	120.00
12	AL	28	DT	P-O3'-C3'	5.73	128.80	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	Aa	13	DC	P-O5'-C5'	5.73	128.60	120.00
89	Ba	16	DC	C2-N1-C1'	5.73	128.29	119.70
51	Ay	41	DG	P-O3'-C3'	5.72	128.78	120.20
56	A3	21	DG	P-O3'-C3'	5.72	128.78	120.20
154	Cd	18	DT	C1'-O4'-C4'	-5.72	101.12	109.70
81	BS	40	DC	P-O3'-C3'	5.71	128.77	120.20
1	AA	706	DC	P-O5'-C5'	5.70	128.56	120.00
1	AA	2426	DA	P-O3'-C3'	5.70	128.75	120.20
1	AA	4932	DC	P-O5'-C5'	5.70	128.55	120.00
1	AA	2013	DG	P-O5'-C5'	5.70	128.55	120.00
139	CO	31	DC	P-O3'-C3'	5.70	128.75	120.20
7	AG	33	DG	P-O3'-C3'	5.69	128.74	120.20
191	DE	10	DG	P-O3'-C3'	5.69	128.74	120.20
1	AA	579	DC	P-O5'-C5'	5.66	128.49	120.00
1	AA	1696	DC	P-O3'-C3'	5.66	128.69	120.20
77	BO	24	DC	P-O5'-C5'	5.66	128.49	120.00
1	AA	2076	DC	P-O5'-C5'	5.66	128.48	120.00
1	AA	6422	DC	P-O5'-C5'	5.65	128.48	120.00
1	AA	3709	DG	P-O5'-C5'	5.65	128.47	120.00
1	AA	6501	DT	P-O5'-C5'	5.64	128.47	120.00
1	AA	5901	DA	P-O3'-C3'	5.64	128.66	120.20
1	AA	2859	DG	P-O3'-C3'	5.64	128.66	120.20
1	AA	5101	DC	P-O5'-C5'	5.64	128.46	120.00
124	B9	24	DT	P-O3'-C3'	5.63	128.65	120.20
150	CZ	46	DG	P-O3'-C3'	5.63	128.65	120.20
97	Bi	13	DC	P-O5'-C5'	5.63	128.44	120.00
137	CM	5	DC	P-O3'-C3'	5.62	128.63	120.20
145	CU	1	DA	P-O3'-C3'	5.62	128.63	120.20
1	AA	198	DT	P-O3'-C3'	5.61	128.62	120.20
1	AA	1070	DA	P-O3'-C3'	5.61	128.61	120.20
53	A0	26	DC	P-O3'-C3'	5.61	128.61	120.20
70	BH	50	DC	P-O5'-C5'	5.61	128.41	120.00
1	AA	2976	DC	P-O5'-C5'	5.60	128.41	120.00
1	AA	2059	DC	P-O5'-C5'	5.60	128.39	120.00
155	Ce	15	DT	P-O3'-C3'	5.59	128.59	120.20
1	AA	193	DA	P-O3'-C3'	5.59	128.59	120.20
1	AA	3150	DA	P-O3'-C3'	5.59	128.58	120.20
1	AA	5738	DC	P-O3'-C3'	5.58	128.57	120.20
1	AA	4905	DC	P-O5'-C5'	5.58	128.36	120.00
1	AA	7874	DC	P-O3'-C3'	5.57	128.56	120.20
1	AA	3378	DA	P-O3'-C3'	5.57	128.55	120.20
1	AA	4674	DG	O4'-C4'-C3'	-5.57	97.05	105.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	881	DC	P-O5'-C5'	5.56	128.34	120.00
106	Br	1	DG	P-O3'-C3'	5.55	128.53	120.20
1	AA	6113	DG	P-O3'-C3'	5.55	128.53	120.20
128	CD	35	DC	P-O5'-C5'	5.55	128.32	120.00
1	AA	1065	DG	P-O3'-C3'	5.54	128.50	120.20
1	AA	4275	DC	P-O5'-C5'	5.52	128.28	120.00
98	Bj	10	DC	P-O5'-C5'	5.52	128.28	120.00
12	AL	28	DT	C1'-O4'-C4'	-5.52	101.42	109.70
1	AA	6239	DC	P-O5'-C5'	5.51	128.27	120.00
134	CJ	55	DT	O4'-C4'-C3'	-5.51	97.14	105.40
1	AA	4640	DG	P-O5'-C5'	5.50	128.25	120.00
1	AA	7748	DC	P-O5'-C5'	5.50	128.25	120.00
77	BO	23	DC	P-O5'-C5'	5.48	128.22	120.00
98	Bj	29	DC	P-O5'-C5'	5.47	128.21	120.00
1	AA	1343	DG	P-O5'-C5'	5.47	128.20	120.00
56	A3	53	DG	O4'-C1'-C2'	-5.47	98.20	106.40
156	Cf	25	DG	P-O3'-C3'	5.46	128.39	120.20
1	AA	6008	DT	P-O5'-C5'	5.46	128.19	120.00
1	AA	6844	DA	P-O3'-C3'	5.46	128.39	120.20
1	AA	6850	DA	P-O3'-C3'	5.46	128.38	120.20
35	Ai	15	DC	P-O5'-C5'	5.45	128.18	120.00
1	AA	7102	DC	P-O5'-C5'	5.45	128.18	120.00
133	CI	19	DA	P-O5'-C5'	5.45	128.17	120.00
182	C5	6	DC	P-O5'-C5'	5.44	128.16	120.00
81	BS	39	DA	P-O5'-C5'	5.44	128.16	120.00
1	AA	1822	DA	P-O5'-C5'	5.42	128.14	120.00
23	AW	4	DT	C2-N1-C1'	5.42	127.48	119.35
170	Ct	34	DC	P-O5'-C5'	5.42	128.13	120.00
1	AA	4522	DC	P-O5'-C5'	5.42	128.13	120.00
58	A5	26	DT	P-O3'-C3'	5.42	128.32	120.20
1	AA	1971	DC	P-O5'-C5'	5.41	128.12	120.00
1	AA	4070	DC	P-O3'-C3'	5.41	128.31	120.20
1	AA	8017	DC	P-O5'-C5'	5.40	128.10	120.00
1	AA	6412	DG	P-O3'-C3'	5.40	128.30	120.20
3	AC	19	DG	P-O3'-C3'	5.40	128.30	120.20
1	AA	3252	DC	P-O5'-C5'	5.38	128.07	120.00
31	Ae	27	DA	O4'-C1'-C2'	-5.37	98.34	106.40
77	BO	1	DG	O4'-C4'-C3'	-5.37	97.34	105.40
1	AA	3168	DT	P-O5'-C5'	5.37	128.06	120.00
1	AA	7258	DC	P-O5'-C5'	5.37	128.05	120.00
1	AA	1543	DC	P-O5'-C5'	5.37	128.05	120.00
7	AG	45	DG	P-O3'-C3'	5.37	128.25	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
126	CB	52	DA	P-O5'-C5'	5.36	128.04	120.00
1	AA	3362	DC	P-O5'-C5'	5.36	128.04	120.00
6	AF	46	DG	P-O5'-C5'	5.36	128.03	120.00
1	AA	7732	DT	P-O5'-C5'	5.35	128.02	120.00
1	AA	3046	DA	O4'-C1'-C2'	-5.34	98.38	106.40
1	AA	530	DT	O4'-C1'-C2'	-5.34	98.39	106.40
1	AA	1216	DC	P-O5'-C5'	5.34	128.00	120.00
1	AA	5360	DC	P-O5'-C5'	5.33	128.00	120.00
163	Cm	12	DT	P-O3'-C3'	5.33	128.20	120.20
180	C3	1	DC	C2-N1-C1'	5.33	127.69	119.70
127	CC	3	DT	P-O3'-C3'	5.33	128.19	120.20
48	Av	33	DA	O4'-C1'-C2'	-5.33	98.41	106.40
37	Ak	21	DC	P-O5'-C5'	5.32	127.98	120.00
1	AA	490	DG	P-O3'-C3'	5.32	128.18	120.20
140	CP	39	DG	O4'-C1'-C2'	-5.32	98.42	106.40
128	CD	26	DT	O4'-C1'-C2'	-5.31	98.43	106.40
194	DH	29	DC	P-O5'-C5'	5.31	127.97	120.00
1	AA	2428	DC	P-O5'-C5'	5.31	127.97	120.00
1	AA	7952	DC	P-O3'-C3'	5.31	128.16	120.20
149	CY	7	DC	P-O3'-C3'	5.31	128.16	120.20
1	AA	4048	DT	O4'-C1'-C2'	-5.30	98.44	106.40
1	AA	2074	DA	P-O3'-C3'	5.30	128.15	120.20
1	AA	7690	DA	P-O3'-C3'	5.29	128.13	120.20
55	A2	34	DG	P-O3'-C3'	5.28	128.13	120.20
1	AA	5064	DC	P-O5'-C5'	5.26	127.90	120.00
1	AA	6156	DC	P-O3'-C3'	5.26	128.10	120.20
1	AA	977	DG	P-O3'-C3'	5.26	128.09	120.20
40	An	54	DC	P-O3'-C3'	5.26	128.09	120.20
1	AA	739	DC	P-O3'-C3'	5.26	128.09	120.20
1	AA	3473	DG	P-O3'-C3'	5.25	128.08	120.20
1	AA	4331	DT	P-O5'-C5'	5.25	127.88	120.00
1	AA	6676	DG	P-O3'-C3'	5.24	128.07	120.20
66	BD	23	DC	P-O5'-C5'	5.24	127.86	120.00
1	AA	7128	DC	P-O3'-C3'	5.24	128.06	120.20
1	AA	284	DC	P-O5'-C5'	5.24	127.86	120.00
1	AA	3555	DC	P-O5'-C5'	5.23	127.85	120.00
11	AK	12	DC	P-O5'-C5'	5.23	127.85	120.00
178	C1	2	DT	C4'-C3'-O3'	5.23	117.85	110.00
1	AA	4149	DC	P-O5'-C5'	5.23	127.85	120.00
1	AA	2400	DC	O4'-C1'-C2'	-5.23	98.55	106.40
1	AA	5269	DC	P-O5'-C5'	5.23	127.85	120.00
1	AA	7991	DG	P-O3'-C3'	5.23	128.05	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	AW	4	DT	N1-C1'-C2'	5.23	121.34	113.50
142	CR	18	DA	P-O3'-C3'	5.23	128.04	120.20
174	Cx	1	DG	O4'-C4'-C3'	-5.22	97.56	105.40
1	AA	5187	DG	P-O3'-C3'	5.22	128.03	120.20
69	BG	9	DA	O4'-C1'-N9	5.22	116.23	108.40
93	Be	45	DC	P-O5'-C5'	5.22	127.83	120.00
1	AA	3216	DC	P-O3'-C3'	5.22	128.03	120.20
1	AA	2615	DC	P-O5'-C5'	5.22	127.83	120.00
1	AA	7469	DT	C1'-O4'-C4'	-5.22	101.88	109.70
161	Ck	36	DG	P-O3'-C3'	5.21	128.01	120.20
148	CX	54	DT	O4'-C1'-C2'	-5.21	98.59	106.40
18	AR	35	DC	P-O5'-C5'	5.20	127.80	120.00
88	BZ	32	DC	P-O5'-C5'	5.20	127.80	120.00
30	Ad	9	DA	P-O5'-C5'	5.20	127.80	120.00
97	Bi	21	DA	P-O5'-C5'	5.20	127.80	120.00
98	Bj	29	DC	P-O3'-C3'	5.20	127.99	120.20
1	AA	7744	DG	P-O3'-C3'	5.19	127.99	120.20
31	Ae	1	DC	O4'-C1'-C2'	-5.19	98.61	106.40
1	AA	5420	DC	P-O5'-C5'	5.18	127.77	120.00
177	C0	13	DC	P-O5'-C5'	5.18	127.77	120.00
1	AA	2764	DT	P-O3'-C3'	5.17	127.95	120.20
1	AA	3079	DT	O4'-C1'-C2'	-5.17	98.65	106.40
1	AA	3506	DC	O4'-C4'-C3'	-5.17	97.65	105.40
152	Cb	36	DA	P-O5'-C5'	5.17	127.75	120.00
178	C1	54	DC	P-O5'-C5'	5.17	127.75	120.00
1	AA	4128	DC	P-O3'-C3'	5.16	127.94	120.20
177	C0	52	DG	P-O3'-C3'	5.16	127.94	120.20
1	AA	1684	DC	P-O5'-C5'	5.16	127.74	120.00
1	AA	1470	DC	P-O5'-C5'	5.16	127.74	120.00
1	AA	7588	DC	P-O5'-C5'	5.16	127.74	120.00
23	AW	4	DT	O4'-C4'-C3'	-5.16	97.67	105.40
1	AA	4725	DC	P-O5'-C5'	5.16	127.73	120.00
1	AA	6664	DC	P-O5'-C5'	5.15	127.73	120.00
60	A7	31	DG	P-O3'-C3'	5.15	127.92	120.20
172	Cv	38	DC	P-O5'-C5'	5.15	127.72	120.00
1	AA	2246	DT	P-O3'-C3'	5.14	127.92	120.20
1	AA	6522	DC	P-O5'-C5'	5.14	127.72	120.00
36	Aj	16	DC	P-O5'-C5'	5.14	127.71	120.00
134	CJ	33	DC	P-O5'-C5'	5.14	127.71	120.00
183	C6	30	DC	P-O5'-C5'	5.14	127.70	120.00
49	Aw	10	DC	P-O5'-C5'	5.13	127.70	120.00
53	A0	20	DC	P-O5'-C5'	5.13	127.70	120.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
105	Bq	40	DC	P-O5'-C5'	5.13	127.70	120.00
190	DD	28	DC	P-O5'-C5'	5.13	127.70	120.00
57	A4	33	DG	O4'-C1'-C2'	-5.13	98.70	106.40
1	AA	4583	DT	O4'-C1'-C2'	-5.13	98.71	106.40
1	AA	5625	DC	P-O5'-C5'	5.12	127.68	120.00
1	AA	7114	DC	P-O5'-C5'	5.12	127.68	120.00
177	C0	41	DC	P-O5'-C5'	5.12	127.67	120.00
1	AA	4033	DC	P-O5'-C5'	5.11	127.67	120.00
1	AA	6312	DC	P-O5'-C5'	5.11	127.67	120.00
113	By	19	DA	P-O3'-C3'	5.11	127.87	120.20
78	BP	42	DC	P-O5'-C5'	5.11	127.66	120.00
1	AA	699	DG	P-O3'-C3'	5.09	127.84	120.20
191	DE	1	DT	O4'-C4'-C3'	-5.09	97.76	105.40
1	AA	6491	DG	P-O3'-C3'	5.09	127.83	120.20
112	Bx	26	DC	P-O5'-C5'	5.09	127.63	120.00
180	C3	1	DC	O4'-C4'-C3'	-5.09	97.77	105.40
5	AE	1	DT	O4'-C4'-C3'	-5.09	97.77	105.40
1	AA	1001	DC	O4'-C1'-C2'	-5.08	98.78	106.40
175	Cy	26	DA	P-O3'-C3'	5.08	127.83	120.20
1	AA	2448	DA	P-O3'-C3'	5.08	127.82	120.20
68	BF	10	DC	P-O5'-C5'	5.08	127.62	120.00
71	BI	50	DA	O4'-C1'-C2'	-5.08	98.78	106.40
1	AA	5123	DG	O4'-C4'-C3'	-5.08	97.78	105.40
84	BV	17	DC	P-O5'-C5'	5.08	127.62	120.00
189	DC	9	DC	P-O5'-C5'	5.08	127.61	120.00
190	DD	33	DG	P-O5'-C5'	5.07	127.61	120.00
1	AA	3350	DC	P-O5'-C5'	5.07	127.61	120.00
20	AT	13	DC	P-O5'-C5'	5.07	127.61	120.00
68	BF	29	DC	P-O5'-C5'	5.07	127.61	120.00
1	AA	899	DG	P-O3'-C3'	5.07	127.80	120.20
67	BE	35	DT	C4'-C3'-O3'	5.07	117.60	110.00
96	Bh	40	DC	P-O5'-C5'	5.07	127.60	120.00
5	AE	49	DG	C4'-C3'-O3'	5.06	117.60	110.00
186	C9	13	DC	P-O5'-C5'	5.06	127.59	120.00
24	AX	41	DC	P-O5'-C5'	5.06	127.59	120.00
9	AI	22	DT	O4'-C1'-C2'	-5.06	98.81	106.40
116	B1	38	DA	P-O3'-C3'	5.06	127.79	120.20
1	AA	7025	DA	C1'-O4'-C4'	-5.06	102.11	109.70
1	AA	1251	DC	P-O5'-C5'	5.06	127.58	120.00
1	AA	6529	DC	P-O5'-C5'	5.06	127.58	120.00
1	AA	2134	DC	P-O3'-C3'	5.05	127.78	120.20
36	Aj	5	DC	P-O5'-C5'	5.05	127.58	120.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	7456	DC	P-O5'-C5'	5.05	127.58	120.00
132	CH	8	DC	P-O5'-C5'	5.05	127.57	120.00
1	AA	3749	DC	P-O5'-C5'	5.05	127.57	120.00
125	CA	2	DC	P-O5'-C5'	5.05	127.57	120.00
1	AA	234	DC	P-O3'-C3'	5.04	127.77	120.20
1	AA	5980	DT	P-O5'-C5'	5.04	127.57	120.00
1	AA	6546	DC	P-O5'-C5'	5.04	127.56	120.00
1	AA	7395	DG	O4'-C1'-C2'	-5.04	98.84	106.40
112	Bx	7	DT	P-O3'-C3'	5.04	127.77	120.20
1	AA	6834	DC	P-O5'-C5'	5.04	127.56	120.00
22	AV	16	DC	P-O5'-C5'	5.04	127.56	120.00
165	Co	14	DC	P-O5'-C5'	5.04	127.56	120.00
167	Cq	26	DC	P-O5'-C5'	5.04	127.56	120.00
165	Co	1	DC	C2-N1-C1'	5.03	127.25	119.70
1	AA	2168	DG	C4'-C3'-O3'	5.03	117.54	110.00
1	AA	1723	DT	P-O5'-C5'	5.03	127.54	120.00
42	Ap	28	DT	O4'-C1'-C2'	-5.03	98.86	106.40
192	DF	21	DC	P-O5'-C5'	5.03	127.54	120.00
17	AQ	11	DT	O4'-C1'-C2'	-5.02	98.86	106.40
89	Ba	26	DA	P-O3'-C3'	5.02	127.74	120.20
1	AA	1907	DC	P-O5'-C5'	5.02	127.53	120.00
1	AA	3682	DC	P-O5'-C5'	5.02	127.53	120.00
1	AA	7972	DG	P-O3'-C3'	5.02	127.73	120.20
139	CO	7	DC	P-O5'-C5'	5.02	127.53	120.00
1	AA	4604	DG	O4'-C4'-C3'	-5.02	97.88	105.40
28	Ab	12	DG	P-O5'-C5'	5.02	127.53	120.00
1	AA	3564	DC	P-O5'-C5'	5.01	127.52	120.00
1	AA	792	DC	P-O5'-C5'	5.00	127.51	120.00
1	AA	7304	DT	C1'-O4'-C4'	-5.00	102.19	109.70
23	AW	4	DT	C6-N1-C1'	-5.00	111.84	119.35
108	Bt	1	DC	O4'-C1'-C2'	-5.00	98.90	106.40

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	AA	1863	DA	C3'

All (2388) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
53	A0	13	DG	Sidechain
53	A0	30	DC	Sidechain

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Mol	Chain	Res	Type	Group
53	A0	5	DA	Sidechain
53	A0	8	DC	Sidechain
53	A0	9	DT	Sidechain
54	A1	1	DA	Sidechain
54	A1	20	DT	Sidechain
54	A1	22	DG	Sidechain
54	A1	27	DA	Sidechain
54	A1	3	DA	Sidechain
54	A1	31	DC	Sidechain
54	A1	34	DT	Sidechain
54	A1	43	DT	Sidechain
55	A2	12	DC	Sidechain
55	A2	15	DG	Sidechain
55	A2	17	DC	Sidechain
55	A2	21	DT	Sidechain
55	A2	24	DG	Sidechain
55	A2	34	DG	Sidechain
55	A2	4	DC	Sidechain
55	A2	41	DG	Sidechain
55	A2	44	DT	Sidechain
55	A2	6	DG	Sidechain
55	A2	8	DC	Sidechain
56	A3	15	DG	Sidechain
56	A3	22	DC	Sidechain
56	A3	32	DG	Sidechain
56	A3	37	DC	Sidechain
56	A3	39	DA	Sidechain
56	A3	47	DC	Sidechain
56	A3	49	DT	Sidechain
56	A3	50	DG	Sidechain
56	A3	8	DC	Sidechain
57	A4	1	DC	Sidechain
57	A4	2	DT	Sidechain
57	A4	27	DA	Sidechain
57	A4	39	DG	Sidechain
57	A4	40	DA	Sidechain
57	A4	44	DT	Sidechain
58	A5	25	DC	Sidechain
58	A5	32	DC	Sidechain
58	A5	35	DT	Sidechain
58	A5	47	DA	Sidechain
58	A5	6	DA	Sidechain

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Mol	Chain	Res	Type	Group
59	A6	1	DA	Sidechain
59	A6	10	DA	Sidechain
59	A6	17	DT	Sidechain
59	A6	23	DC	Sidechain
59	A6	28	DA	Sidechain
59	A6	3	DG	Sidechain
59	A6	5	DC	Sidechain
60	A7	13	DA	Sidechain
60	A7	28	DG	Sidechain
61	A8	11	DT	Sidechain
61	A8	17	DA	Sidechain
61	A8	9	DC	Sidechain
62	A9	14	DG	Sidechain
62	A9	15	DA	Sidechain
62	A9	17	DT	Sidechain
62	A9	4	DA	Sidechain
62	A9	42	DA	Sidechain
62	A9	6	DA	Sidechain
1	AA	1002	DC	Sidechain
1	AA	1005	DT	Sidechain
1	AA	1012	DA	Sidechain
1	AA	1016	DG	Sidechain
1	AA	1022	DG	Sidechain
1	AA	1023	DC	Sidechain
1	AA	1026	DG	Sidechain
1	AA	1027	DA	Sidechain
1	AA	1028	DG	Sidechain
1	AA	1030	DC	Sidechain
1	AA	1032	DG	Sidechain
1	AA	1038	DG	Sidechain
1	AA	1039	DA	Sidechain
1	AA	1041	DG	Sidechain
1	AA	1042	DA	Sidechain
1	AA	1047	DA	Sidechain
1	AA	1048	DA	Sidechain
1	AA	1056	DA	Sidechain
1	AA	1062	DT	Sidechain
1	AA	1065	DG	Sidechain
1	AA	1095	DT	Sidechain
1	AA	1107	DC	Sidechain
1	AA	1119	DT	Sidechain
1	AA	1134	DA	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	1140	DT	Sidechain
1	AA	1146	DT	Sidechain
1	AA	1147	DA	Sidechain
1	AA	1152	DG	Sidechain
1	AA	1154	DT	Sidechain
1	AA	1160	DC	Sidechain
1	AA	1167	DC	Sidechain
1	AA	1170	DA	Sidechain
1	AA	1173	DG	Sidechain
1	AA	1176	DG	Sidechain
1	AA	1179	DG	Sidechain
1	AA	1184	DA	Sidechain
1	AA	1188	DG	Sidechain
1	AA	1189	DC	Sidechain
1	AA	119	DT	Sidechain
1	AA	1191	DG	Sidechain
1	AA	1192	DA	Sidechain
1	AA	1197	DT	Sidechain
1	AA	1199	DA	Sidechain
1	AA	1200	DG	Sidechain
1	AA	1212	DG	Sidechain
1	AA	1217	DT	Sidechain
1	AA	1222	DC	Sidechain
1	AA	1249	DA	Sidechain
1	AA	1254	DG	Sidechain
1	AA	1256	DA	Sidechain
1	AA	1263	DC	Sidechain
1	AA	1264	DT	Sidechain
1	AA	127	DA	Sidechain
1	AA	1271	DC	Sidechain
1	AA	1277	DT	Sidechain
1	AA	1278	DT	Sidechain
1	AA	1285	DC	Sidechain
1	AA	1286	DT	Sidechain
1	AA	129	DT	Sidechain
1	AA	1293	DC	Sidechain
1	AA	1301	DT	Sidechain
1	AA	1319	DT	Sidechain
1	AA	1332	DT	Sidechain
1	AA	1338	DT	Sidechain
1	AA	1349	DG	Sidechain
1	AA	1350	DC	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	1358	DC	Sidechain
1	AA	1364	DG	Sidechain
1	AA	1366	DT	Sidechain
1	AA	1368	DG	Sidechain
1	AA	1385	DT	Sidechain
1	AA	1396	DG	Sidechain
1	AA	1399	DT	Sidechain
1	AA	1403	DA	Sidechain
1	AA	1408	DC	Sidechain
1	AA	141	DA	Sidechain
1	AA	1410	DT	Sidechain
1	AA	1422	DA	Sidechain
1	AA	1430	DG	Sidechain
1	AA	1432	DC	Sidechain
1	AA	1433	DT	Sidechain
1	AA	1443	DT	Sidechain
1	AA	1445	DC	Sidechain
1	AA	1454	DC	Sidechain
1	AA	1463	DG	Sidechain
1	AA	1475	DA	Sidechain
1	AA	1488	DT	Sidechain
1	AA	1508	DG	Sidechain
1	AA	1509	DC	Sidechain
1	AA	1559	DT	Sidechain
1	AA	1564	DG	Sidechain
1	AA	1565	DA	Sidechain
1	AA	1571	DG	Sidechain
1	AA	1572	DG	Sidechain
1	AA	1574	DT	Sidechain
1	AA	1584	DT	Sidechain
1	AA	1592	DA	Sidechain
1	AA	1599	DT	Sidechain
1	AA	1600	DA	Sidechain
1	AA	1617	DA	Sidechain
1	AA	1618	DA	Sidechain
1	AA	1632	DC	Sidechain
1	AA	1678	DG	Sidechain
1	AA	1698	DC	Sidechain
1	AA	1699	DA	Sidechain
1	AA	1704	DG	Sidechain
1	AA	1707	DT	Sidechain
1	AA	171	DA	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	1724	DC	Sidechain
1	AA	1733	DT	Sidechain
1	AA	1741	DG	Sidechain
1	AA	1748	DG	Sidechain
1	AA	1749	DC	Sidechain
1	AA	1750	DT	Sidechain
1	AA	1754	DT	Sidechain
1	AA	1763	DG	Sidechain
1	AA	1774	DA	Sidechain
1	AA	1788	DC	Sidechain
1	AA	1791	DT	Sidechain
1	AA	1811	DG	Sidechain
1	AA	1833	DG	Sidechain
1	AA	1838	DT	Sidechain
1	AA	1839	DT	Sidechain
1	AA	1841	DT	Sidechain
1	AA	1850	DA	Sidechain
1	AA	1853	DA	Sidechain
1	AA	1857	DT	Sidechain
1	AA	1864	DT	Sidechain
1	AA	1865	DT	Sidechain
1	AA	1869	DA	Sidechain
1	AA	1871	DA	Sidechain
1	AA	188	DG	Sidechain
1	AA	1885	DT	Sidechain
1	AA	1891	DT	Sidechain
1	AA	1893	DT	Sidechain
1	AA	1895	DT	Sidechain
1	AA	1898	DG	Sidechain
1	AA	1899	DG	Sidechain
1	AA	1911	DT	Sidechain
1	AA	1917	DA	Sidechain
1	AA	1919	DC	Sidechain
1	AA	193	DA	Sidechain
1	AA	1931	DG	Sidechain
1	AA	1933	DT	Sidechain
1	AA	1936	DA	Sidechain
1	AA	1951	DG	Sidechain
1	AA	1960	DT	Sidechain
1	AA	1974	DG	Sidechain
1	AA	1975	DT	Sidechain
1	AA	198	DT	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	1990	DC	Sidechain
1	AA	1991	DA	Sidechain
1	AA	2000	DC	Sidechain
1	AA	2001	DC	Sidechain
1	AA	2002	DT	Sidechain
1	AA	2003	DG	Sidechain
1	AA	2005	DT	Sidechain
1	AA	2007	DG	Sidechain
1	AA	2014	DT	Sidechain
1	AA	2017	DA	Sidechain
1	AA	2024	DA	Sidechain
1	AA	2028	DA	Sidechain
1	AA	2032	DC	Sidechain
1	AA	204	DG	Sidechain
1	AA	2047	DT	Sidechain
1	AA	2050	DA	Sidechain
1	AA	2055	DT	Sidechain
1	AA	2057	DA	Sidechain
1	AA	2058	DG	Sidechain
1	AA	2063	DA	Sidechain
1	AA	2065	DC	Sidechain
1	AA	2066	DG	Sidechain
1	AA	2068	DT	Sidechain
1	AA	2071	DA	Sidechain
1	AA	2075	DT	Sidechain
1	AA	208	DA	Sidechain
1	AA	2090	DT	Sidechain
1	AA	2093	DG	Sidechain
1	AA	2100	DT	Sidechain
1	AA	2101	DC	Sidechain
1	AA	2103	DG	Sidechain
1	AA	2109	DT	Sidechain
1	AA	2117	DT	Sidechain
1	AA	2124	DT	Sidechain
1	AA	2125	DC	Sidechain
1	AA	2127	DT	Sidechain
1	AA	2129	DA	Sidechain
1	AA	2130	DC	Sidechain
1	AA	2132	DT	Sidechain
1	AA	2139	DT	Sidechain
1	AA	2149	DT	Sidechain
1	AA	2164	DA	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	2165	DT	Sidechain
1	AA	2167	DA	Sidechain
1	AA	2169	DG	Sidechain
1	AA	2172	DT	Sidechain
1	AA	2181	DT	Sidechain
1	AA	2221	DT	Sidechain
1	AA	2224	DT	Sidechain
1	AA	2228	DG	Sidechain
1	AA	2237	DT	Sidechain
1	AA	2240	DT	Sidechain
1	AA	2241	DT	Sidechain
1	AA	2244	DG	Sidechain
1	AA	2246	DT	Sidechain
1	AA	2253	DG	Sidechain
1	AA	2254	DA	Sidechain
1	AA	2262	DT	Sidechain
1	AA	2263	DT	Sidechain
1	AA	2265	DT	Sidechain
1	AA	2270	DT	Sidechain
1	AA	2275	DC	Sidechain
1	AA	2280	DT	Sidechain
1	AA	2289	DT	Sidechain
1	AA	2294	DT	Sidechain
1	AA	2303	DG	Sidechain
1	AA	2308	DG	Sidechain
1	AA	231	DT	Sidechain
1	AA	2318	DT	Sidechain
1	AA	2321	DA	Sidechain
1	AA	2322	DT	Sidechain
1	AA	2326	DA	Sidechain
1	AA	2327	DT	Sidechain
1	AA	2329	DT	Sidechain
1	AA	2345	DT	Sidechain
1	AA	2352	DA	Sidechain
1	AA	2361	DA	Sidechain
1	AA	2371	DC	Sidechain
1	AA	238	DT	Sidechain
1	AA	2388	DA	Sidechain
1	AA	2396	DT	Sidechain
1	AA	2404	DT	Sidechain
1	AA	2407	DT	Sidechain
1	AA	2410	DA	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	2433	DG	Sidechain
1	AA	2439	DA	Sidechain
1	AA	2448	DA	Sidechain
1	AA	245	DG	Sidechain
1	AA	2455	DC	Sidechain
1	AA	2458	DA	Sidechain
1	AA	2462	DT	Sidechain
1	AA	2474	DT	Sidechain
1	AA	2479	DT	Sidechain
1	AA	2500	DA	Sidechain
1	AA	2508	DT	Sidechain
1	AA	2510	DA	Sidechain
1	AA	2512	DT	Sidechain
1	AA	2514	DG	Sidechain
1	AA	2515	DC	Sidechain
1	AA	2516	DA	Sidechain
1	AA	2518	DA	Sidechain
1	AA	2536	DT	Sidechain
1	AA	2543	DT	Sidechain
1	AA	2546	DT	Sidechain
1	AA	2553	DC	Sidechain
1	AA	2579	DA	Sidechain
1	AA	2589	DT	Sidechain
1	AA	259	DC	Sidechain
1	AA	2591	DT	Sidechain
1	AA	2596	DA	Sidechain
1	AA	2601	DC	Sidechain
1	AA	2603	DA	Sidechain
1	AA	2632	DT	Sidechain
1	AA	2634	DG	Sidechain
1	AA	2636	DG	Sidechain
1	AA	2651	DG	Sidechain
1	AA	2656	DG	Sidechain
1	AA	266	DG	Sidechain
1	AA	2671	DT	Sidechain
1	AA	2681	DA	Sidechain
1	AA	2684	DT	Sidechain
1	AA	2702	DT	Sidechain
1	AA	2712	DC	Sidechain
1	AA	2713	DT	Sidechain
1	AA	2715	DT	Sidechain
1	AA	2730	DT	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	2736	DT	Sidechain
1	AA	2742	DT	Sidechain
1	AA	2752	DA	Sidechain
1	AA	2756	DT	Sidechain
1	AA	2766	DA	Sidechain
1	AA	2770	DT	Sidechain
1	AA	2777	DA	Sidechain
1	AA	2778	DT	Sidechain
1	AA	2798	DA	Sidechain
1	AA	2810	DA	Sidechain
1	AA	2815	DA	Sidechain
1	AA	2816	DG	Sidechain
1	AA	2818	DG	Sidechain
1	AA	2831	DT	Sidechain
1	AA	2837	DT	Sidechain
1	AA	2842	DA	Sidechain
1	AA	2844	DT	Sidechain
1	AA	2849	DA	Sidechain
1	AA	285	DG	Sidechain
1	AA	2850	DG	Sidechain
1	AA	2851	DT	Sidechain
1	AA	2857	DA	Sidechain
1	AA	2859	DG	Sidechain
1	AA	2863	DT	Sidechain
1	AA	2868	DT	Sidechain
1	AA	2873	DA	Sidechain
1	AA	2876	DT	Sidechain
1	AA	2881	DC	Sidechain
1	AA	2885	DT	Sidechain
1	AA	2895	DG	Sidechain
1	AA	2908	DT	Sidechain
1	AA	2928	DT	Sidechain
1	AA	2931	DG	Sidechain
1	AA	2935	DT	Sidechain
1	AA	2939	DT	Sidechain
1	AA	2942	DT	Sidechain
1	AA	2943	DC	Sidechain
1	AA	2945	DT	Sidechain
1	AA	2956	DA	Sidechain
1	AA	2959	DG	Sidechain
1	AA	2961	DT	Sidechain
1	AA	2966	DT	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	2978	DT	Sidechain
1	AA	3001	DG	Sidechain
1	AA	3008	DT	Sidechain
1	AA	3030	DG	Sidechain
1	AA	3032	DT	Sidechain
1	AA	3036	DC	Sidechain
1	AA	3038	DT	Sidechain
1	AA	3048	DC	Sidechain
1	AA	3049	DT	Sidechain
1	AA	305	DC	Sidechain
1	AA	3052	DT	Sidechain
1	AA	3056	DT	Sidechain
1	AA	3083	DG	Sidechain
1	AA	3085	DT	Sidechain
1	AA	3089	DT	Sidechain
1	AA	309	DT	Sidechain
1	AA	3093	DT	Sidechain
1	AA	3098	DT	Sidechain
1	AA	31	DG	Sidechain
1	AA	3114	DT	Sidechain
1	AA	312	DT	Sidechain
1	AA	3122	DT	Sidechain
1	AA	3125	DT	Sidechain
1	AA	3143	DA	Sidechain
1	AA	3144	DG	Sidechain
1	AA	3167	DT	Sidechain
1	AA	3174	DT	Sidechain
1	AA	3175	DG	Sidechain
1	AA	3177	DT	Sidechain
1	AA	3179	DA	Sidechain
1	AA	3190	DT	Sidechain
1	AA	3199	DT	Sidechain
1	AA	3209	DT	Sidechain
1	AA	3211	DT	Sidechain
1	AA	3226	DT	Sidechain
1	AA	3229	DT	Sidechain
1	AA	3234	DG	Sidechain
1	AA	3235	DT	Sidechain
1	AA	3237	DA	Sidechain
1	AA	3239	DG	Sidechain
1	AA	3248	DT	Sidechain
1	AA	3250	DT	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	3258	DA	Sidechain
1	AA	326	DA	Sidechain
1	AA	3265	DG	Sidechain
1	AA	3273	DA	Sidechain
1	AA	3284	DG	Sidechain
1	AA	3289	DT	Sidechain
1	AA	329	DA	Sidechain
1	AA	3295	DT	Sidechain
1	AA	3312	DT	Sidechain
1	AA	3315	DC	Sidechain
1	AA	3330	DA	Sidechain
1	AA	3336	DC	Sidechain
1	AA	3341	DG	Sidechain
1	AA	336	DT	Sidechain
1	AA	3362	DC	Sidechain
1	AA	3369	DC	Sidechain
1	AA	3380	DG	Sidechain
1	AA	3394	DT	Sidechain
1	AA	340	DG	Sidechain
1	AA	3402	DT	Sidechain
1	AA	3404	DA	Sidechain
1	AA	3408	DA	Sidechain
1	AA	341	DA	Sidechain
1	AA	3423	DT	Sidechain
1	AA	3427	DG	Sidechain
1	AA	343	DT	Sidechain
1	AA	3432	DA	Sidechain
1	AA	3437	DC	Sidechain
1	AA	3453	DG	Sidechain
1	AA	3454	DA	Sidechain
1	AA	3458	DC	Sidechain
1	AA	346	DA	Sidechain
1	AA	3460	DA	Sidechain
1	AA	3464	DA	Sidechain
1	AA	3470	DT	Sidechain
1	AA	3473	DG	Sidechain
1	AA	3474	DG	Sidechain
1	AA	3475	DC	Sidechain
1	AA	3479	DG	Sidechain
1	AA	3480	DA	Sidechain
1	AA	3481	DT	Sidechain
1	AA	3487	DT	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	3495	DG	Sidechain
1	AA	3503	DT	Sidechain
1	AA	3508	DC	Sidechain
1	AA	3512	DT	Sidechain
1	AA	3513	DG	Sidechain
1	AA	3514	DG	Sidechain
1	AA	3521	DC	Sidechain
1	AA	3523	DC	Sidechain
1	AA	3529	DG	Sidechain
1	AA	3553	DT	Sidechain
1	AA	3556	DT	Sidechain
1	AA	3560	DG	Sidechain
1	AA	3565	DT	Sidechain
1	AA	3571	DT	Sidechain
1	AA	3572	DT	Sidechain
1	AA	3580	DG	Sidechain
1	AA	3586	DT	Sidechain
1	AA	3589	DT	Sidechain
1	AA	359	DA	Sidechain
1	AA	3601	DG	Sidechain
1	AA	3602	DT	Sidechain
1	AA	3615	DT	Sidechain
1	AA	3621	DA	Sidechain
1	AA	3622	DA	Sidechain
1	AA	3626	DT	Sidechain
1	AA	3639	DG	Sidechain
1	AA	3640	DT	Sidechain
1	AA	3645	DA	Sidechain
1	AA	3647	DT	Sidechain
1	AA	3649	DC	Sidechain
1	AA	3650	DT	Sidechain
1	AA	3663	DA	Sidechain
1	AA	3673	DA	Sidechain
1	AA	3680	DT	Sidechain
1	AA	369	DA	Sidechain
1	AA	3691	DT	Sidechain
1	AA	3694	DT	Sidechain
1	AA	3698	DC	Sidechain
1	AA	3704	DA	Sidechain
1	AA	3710	DA	Sidechain
1	AA	3713	DA	Sidechain
1	AA	3718	DG	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	3721	DA	Sidechain
1	AA	3729	DC	Sidechain
1	AA	3733	DA	Sidechain
1	AA	3762	DT	Sidechain
1	AA	3764	DT	Sidechain
1	AA	3770	DA	Sidechain
1	AA	3795	DT	Sidechain
1	AA	3797	DT	Sidechain
1	AA	3828	DG	Sidechain
1	AA	3829	DA	Sidechain
1	AA	383	DA	Sidechain
1	AA	3830	DA	Sidechain
1	AA	3835	DA	Sidechain
1	AA	3844	DG	Sidechain
1	AA	3846	DA	Sidechain
1	AA	3851	DG	Sidechain
1	AA	3861	DT	Sidechain
1	AA	3864	DA	Sidechain
1	AA	3871	DG	Sidechain
1	AA	389	DC	Sidechain
1	AA	3897	DA	Sidechain
1	AA	3901	DT	Sidechain
1	AA	3909	DT	Sidechain
1	AA	3914	DA	Sidechain
1	AA	3923	DT	Sidechain
1	AA	3924	DT	Sidechain
1	AA	3925	DC	Sidechain
1	AA	3932	DC	Sidechain
1	AA	3934	DT	Sidechain
1	AA	394	DT	Sidechain
1	AA	3946	DT	Sidechain
1	AA	3960	DC	Sidechain
1	AA	3970	DT	Sidechain
1	AA	3973	DT	Sidechain
1	AA	3991	DA	Sidechain
1	AA	3997	DT	Sidechain
1	AA	3998	DA	Sidechain
1	AA	40	DT	Sidechain
1	AA	400	DC	Sidechain
1	AA	4006	DT	Sidechain
1	AA	4016	DA	Sidechain
1	AA	4017	DA	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	4029	DA	Sidechain
1	AA	4039	DT	Sidechain
1	AA	404	DA	Sidechain
1	AA	405	DG	Sidechain
1	AA	4050	DA	Sidechain
1	AA	4053	DC	Sidechain
1	AA	406	DG	Sidechain
1	AA	4064	DG	Sidechain
1	AA	4069	DT	Sidechain
1	AA	4075	DG	Sidechain
1	AA	4078	DT	Sidechain
1	AA	4082	DA	Sidechain
1	AA	4089	DT	Sidechain
1	AA	4092	DT	Sidechain
1	AA	4099	DT	Sidechain
1	AA	4113	DC	Sidechain
1	AA	4124	DG	Sidechain
1	AA	4125	DG	Sidechain
1	AA	4126	DT	Sidechain
1	AA	4132	DG	Sidechain
1	AA	4137	DC	Sidechain
1	AA	4140	DT	Sidechain
1	AA	4163	DG	Sidechain
1	AA	4164	DA	Sidechain
1	AA	4166	DG	Sidechain
1	AA	4170	DG	Sidechain
1	AA	4182	DG	Sidechain
1	AA	419	DT	Sidechain
1	AA	4194	DA	Sidechain
1	AA	4199	DG	Sidechain
1	AA	4202	DG	Sidechain
1	AA	4217	DG	Sidechain
1	AA	4219	DT	Sidechain
1	AA	422	DT	Sidechain
1	AA	4230	DC	Sidechain
1	AA	4243	DT	Sidechain
1	AA	4247	DC	Sidechain
1	AA	4249	DT	Sidechain
1	AA	4257	DG	Sidechain
1	AA	426	DG	Sidechain
1	AA	4261	DT	Sidechain
1	AA	4263	DC	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	4267	DT	Sidechain
1	AA	4269	DT	Sidechain
1	AA	4280	DG	Sidechain
1	AA	4299	DG	Sidechain
1	AA	4301	DA	Sidechain
1	AA	4333	DT	Sidechain
1	AA	434	DT	Sidechain
1	AA	4342	DG	Sidechain
1	AA	4343	DT	Sidechain
1	AA	4350	DC	Sidechain
1	AA	4357	DT	Sidechain
1	AA	4358	DA	Sidechain
1	AA	436	DT	Sidechain
1	AA	4367	DT	Sidechain
1	AA	4368	DT	Sidechain
1	AA	4371	DA	Sidechain
1	AA	4382	DT	Sidechain
1	AA	4393	DG	Sidechain
1	AA	4397	DG	Sidechain
1	AA	4405	DA	Sidechain
1	AA	441	DT	Sidechain
1	AA	4425	DT	Sidechain
1	AA	4428	DC	Sidechain
1	AA	4435	DC	Sidechain
1	AA	4436	DA	Sidechain
1	AA	4456	DT	Sidechain
1	AA	4463	DT	Sidechain
1	AA	4467	DC	Sidechain
1	AA	4475	DT	Sidechain
1	AA	4487	DA	Sidechain
1	AA	452	DG	Sidechain
1	AA	4524	DG	Sidechain
1	AA	4529	DT	Sidechain
1	AA	4530	DT	Sidechain
1	AA	4533	DA	Sidechain
1	AA	4534	DT	Sidechain
1	AA	4536	DC	Sidechain
1	AA	4543	DT	Sidechain
1	AA	4546	DT	Sidechain
1	AA	4551	DA	Sidechain
1	AA	4552	DT	Sidechain
1	AA	4560	DT	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	4561	DT	Sidechain
1	AA	4575	DG	Sidechain
1	AA	4582	DG	Sidechain
1	AA	4586	DG	Sidechain
1	AA	4600	DT	Sidechain
1	AA	4605	DT	Sidechain
1	AA	4614	DG	Sidechain
1	AA	4626	DG	Sidechain
1	AA	4628	DG	Sidechain
1	AA	4629	DG	Sidechain
1	AA	464	DT	Sidechain
1	AA	4641	DG	Sidechain
1	AA	4645	DC	Sidechain
1	AA	4648	DT	Sidechain
1	AA	4653	DG	Sidechain
1	AA	467	DA	Sidechain
1	AA	4674	DG	Sidechain
1	AA	4681	DG	Sidechain
1	AA	4692	DC	Sidechain
1	AA	4697	DG	Sidechain
1	AA	4700	DG	Sidechain
1	AA	4701	DG	Sidechain
1	AA	4702	DC	Sidechain
1	AA	4712	DG	Sidechain
1	AA	4720	DT	Sidechain
1	AA	4723	DT	Sidechain
1	AA	4730	DG	Sidechain
1	AA	4732	DT	Sidechain
1	AA	4734	DT	Sidechain
1	AA	474	DA	Sidechain
1	AA	4749	DT	Sidechain
1	AA	4758	DC	Sidechain
1	AA	476	DA	Sidechain
1	AA	4762	DT	Sidechain
1	AA	4767	DG	Sidechain
1	AA	477	DC	Sidechain
1	AA	4770	DC	Sidechain
1	AA	4781	DA	Sidechain
1	AA	4794	DA	Sidechain
1	AA	4799	DC	Sidechain
1	AA	4813	DT	Sidechain
1	AA	4825	DT	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	4828	DT	Sidechain
1	AA	4836	DC	Sidechain
1	AA	4844	DT	Sidechain
1	AA	4854	DC	Sidechain
1	AA	4867	DC	Sidechain
1	AA	4877	DG	Sidechain
1	AA	4883	DG	Sidechain
1	AA	4897	DT	Sidechain
1	AA	4903	DT	Sidechain
1	AA	4914	DA	Sidechain
1	AA	4915	DT	Sidechain
1	AA	4918	DT	Sidechain
1	AA	4920	DC	Sidechain
1	AA	4930	DT	Sidechain
1	AA	4934	DC	Sidechain
1	AA	4937	DA	Sidechain
1	AA	4939	DG	Sidechain
1	AA	4942	DT	Sidechain
1	AA	4959	DA	Sidechain
1	AA	4966	DA	Sidechain
1	AA	4967	DC	Sidechain
1	AA	4976	DA	Sidechain
1	AA	4977	DA	Sidechain
1	AA	498	DA	Sidechain
1	AA	4982	DT	Sidechain
1	AA	5008	DT	Sidechain
1	AA	5016	DT	Sidechain
1	AA	5017	DT	Sidechain
1	AA	5018	DG	Sidechain
1	AA	5020	DA	Sidechain
1	AA	5029	DT	Sidechain
1	AA	5037	DT	Sidechain
1	AA	505	DC	Sidechain
1	AA	5062	DT	Sidechain
1	AA	5069	DG	Sidechain
1	AA	5074	DT	Sidechain
1	AA	5089	DA	Sidechain
1	AA	5091	DT	Sidechain
1	AA	5113	DT	Sidechain
1	AA	5117	DT	Sidechain
1	AA	5120	DG	Sidechain
1	AA	5158	DC	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	516	DG	Sidechain
1	AA	5163	DT	Sidechain
1	AA	5174	DG	Sidechain
1	AA	5180	DT	Sidechain
1	AA	5186	DT	Sidechain
1	AA	5195	DT	Sidechain
1	AA	5199	DG	Sidechain
1	AA	5200	DG	Sidechain
1	AA	5202	DT	Sidechain
1	AA	5205	DT	Sidechain
1	AA	5210	DT	Sidechain
1	AA	5211	DA	Sidechain
1	AA	5223	DC	Sidechain
1	AA	5227	DG	Sidechain
1	AA	5230	DT	Sidechain
1	AA	5234	DT	Sidechain
1	AA	5236	DC	Sidechain
1	AA	5238	DG	Sidechain
1	AA	5239	DG	Sidechain
1	AA	5247	DG	Sidechain
1	AA	5261	DT	Sidechain
1	AA	5270	DT	Sidechain
1	AA	5275	DA	Sidechain
1	AA	5278	DG	Sidechain
1	AA	5282	DT	Sidechain
1	AA	5284	DG	Sidechain
1	AA	5293	DG	Sidechain
1	AA	5296	DA	Sidechain
1	AA	5302	DA	Sidechain
1	AA	5303	DT	Sidechain
1	AA	5307	DA	Sidechain
1	AA	5312	DT	Sidechain
1	AA	5317	DG	Sidechain
1	AA	532	DA	Sidechain
1	AA	5328	DT	Sidechain
1	AA	5333	DT	Sidechain
1	AA	5345	DT	Sidechain
1	AA	535	DA	Sidechain
1	AA	5351	DG	Sidechain
1	AA	5352	DT	Sidechain
1	AA	5354	DA	Sidechain
1	AA	5366	DT	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	5371	DG	Sidechain
1	AA	5373	DT	Sidechain
1	AA	5381	DC	Sidechain
1	AA	5388	DC	Sidechain
1	AA	5389	DT	Sidechain
1	AA	5396	DA	Sidechain
1	AA	5407	DT	Sidechain
1	AA	5409	DA	Sidechain
1	AA	5410	DA	Sidechain
1	AA	5424	DT	Sidechain
1	AA	5425	DG	Sidechain
1	AA	5429	DT	Sidechain
1	AA	543	DG	Sidechain
1	AA	5431	DC	Sidechain
1	AA	5433	DC	Sidechain
1	AA	5452	DT	Sidechain
1	AA	5464	DG	Sidechain
1	AA	5467	DA	Sidechain
1	AA	5483	DT	Sidechain
1	AA	5484	DT	Sidechain
1	AA	5486	DA	Sidechain
1	AA	5489	DA	Sidechain
1	AA	5490	DA	Sidechain
1	AA	5494	DA	Sidechain
1	AA	5498	DT	Sidechain
1	AA	550	DA	Sidechain
1	AA	5510	DA	Sidechain
1	AA	5516	DA	Sidechain
1	AA	5517	DT	Sidechain
1	AA	5520	DA	Sidechain
1	AA	5536	DT	Sidechain
1	AA	5575	DT	Sidechain
1	AA	5598	DA	Sidechain
1	AA	5601	DT	Sidechain
1	AA	561	DC	Sidechain
1	AA	5631	DT	Sidechain
1	AA	5633	DG	Sidechain
1	AA	5643	DT	Sidechain
1	AA	5658	DA	Sidechain
1	AA	5663	DG	Sidechain
1	AA	5664	DG	Sidechain
1	AA	5668	DG	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	5682	DC	Sidechain
1	AA	5697	DT	Sidechain
1	AA	5701	DG	Sidechain
1	AA	5705	DA	Sidechain
1	AA	5715	DT	Sidechain
1	AA	5717	DT	Sidechain
1	AA	573	DG	Sidechain
1	AA	5733	DT	Sidechain
1	AA	5739	DG	Sidechain
1	AA	5742	DG	Sidechain
1	AA	5745	DA	Sidechain
1	AA	5749	DT	Sidechain
1	AA	576	DA	Sidechain
1	AA	5774	DT	Sidechain
1	AA	5775	DT	Sidechain
1	AA	5779	DT	Sidechain
1	AA	5780	DG	Sidechain
1	AA	5781	DT	Sidechain
1	AA	5784	DT	Sidechain
1	AA	5799	DC	Sidechain
1	AA	5809	DT	Sidechain
1	AA	5812	DC	Sidechain
1	AA	5820	DG	Sidechain
1	AA	5822	DA	Sidechain
1	AA	5823	DA	Sidechain
1	AA	5830	DG	Sidechain
1	AA	5832	DA	Sidechain
1	AA	5833	DA	Sidechain
1	AA	5836	DA	Sidechain
1	AA	5847	DT	Sidechain
1	AA	5853	DG	Sidechain
1	AA	5854	DG	Sidechain
1	AA	5875	DA	Sidechain
1	AA	5878	DA	Sidechain
1	AA	5903	DG	Sidechain
1	AA	5904	DA	Sidechain
1	AA	5906	DT	Sidechain
1	AA	5908	DA	Sidechain
1	AA	5913	DT	Sidechain
1	AA	5923	DA	Sidechain
1	AA	5926	DG	Sidechain
1	AA	5929	DG	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	5938	DA	Sidechain
1	AA	594	DA	Sidechain
1	AA	5941	DA	Sidechain
1	AA	5959	DT	Sidechain
1	AA	5976	DG	Sidechain
1	AA	5978	DA	Sidechain
1	AA	5980	DT	Sidechain
1	AA	5983	DT	Sidechain
1	AA	5984	DT	Sidechain
1	AA	599	DG	Sidechain
1	AA	5994	DT	Sidechain
1	AA	5995	DC	Sidechain
1	AA	600	DG	Sidechain
1	AA	6008	DT	Sidechain
1	AA	6009	DC	Sidechain
1	AA	6014	DA	Sidechain
1	AA	6015	DT	Sidechain
1	AA	6029	DA	Sidechain
1	AA	6038	DC	Sidechain
1	AA	6043	DA	Sidechain
1	AA	6044	DT	Sidechain
1	AA	6045	DT	Sidechain
1	AA	6046	DA	Sidechain
1	AA	6048	DA	Sidechain
1	AA	6051	DT	Sidechain
1	AA	6068	DG	Sidechain
1	AA	6072	DA	Sidechain
1	AA	6080	DT	Sidechain
1	AA	6083	DA	Sidechain
1	AA	609	DA	Sidechain
1	AA	6100	DT	Sidechain
1	AA	6109	DT	Sidechain
1	AA	6113	DG	Sidechain
1	AA	6121	DT	Sidechain
1	AA	6134	DT	Sidechain
1	AA	6135	DA	Sidechain
1	AA	615	DG	Sidechain
1	AA	6150	DC	Sidechain
1	AA	6152	DT	Sidechain
1	AA	6174	DG	Sidechain
1	AA	6179	DT	Sidechain
1	AA	6187	DT	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	6190	DA	Sidechain
1	AA	6205	DA	Sidechain
1	AA	6217	DT	Sidechain
1	AA	6227	DT	Sidechain
1	AA	6236	DG	Sidechain
1	AA	6251	DT	Sidechain
1	AA	6265	DT	Sidechain
1	AA	6268	DG	Sidechain
1	AA	6269	DA	Sidechain
1	AA	6282	DG	Sidechain
1	AA	6283	DC	Sidechain
1	AA	6288	DT	Sidechain
1	AA	6311	DT	Sidechain
1	AA	632	DT	Sidechain
1	AA	6326	DA	Sidechain
1	AA	6330	DA	Sidechain
1	AA	6343	DT	Sidechain
1	AA	6348	DC	Sidechain
1	AA	6351	DA	Sidechain
1	AA	638	DG	Sidechain
1	AA	6380	DG	Sidechain
1	AA	6389	DA	Sidechain
1	AA	6401	DG	Sidechain
1	AA	6405	DC	Sidechain
1	AA	6412	DG	Sidechain
1	AA	6414	DG	Sidechain
1	AA	6415	DT	Sidechain
1	AA	6420	DA	Sidechain
1	AA	6421	DT	Sidechain
1	AA	6422	DC	Sidechain
1	AA	6432	DG	Sidechain
1	AA	6435	DA	Sidechain
1	AA	6440	DT	Sidechain
1	AA	6447	DA	Sidechain
1	AA	6451	DT	Sidechain
1	AA	6458	DA	Sidechain
1	AA	6464	DA	Sidechain
1	AA	6471	DG	Sidechain
1	AA	6479	DT	Sidechain
1	AA	648	DG	Sidechain
1	AA	6485	DA	Sidechain
1	AA	6491	DG	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	6493	DT	Sidechain
1	AA	6496	DT	Sidechain
1	AA	6512	DG	Sidechain
1	AA	6513	DA	Sidechain
1	AA	6514	DT	Sidechain
1	AA	6534	DA	Sidechain
1	AA	6543	DA	Sidechain
1	AA	6552	DA	Sidechain
1	AA	6555	DT	Sidechain
1	AA	6560	DA	Sidechain
1	AA	6573	DT	Sidechain
1	AA	658	DT	Sidechain
1	AA	6584	DG	Sidechain
1	AA	6587	DG	Sidechain
1	AA	6592	DT	Sidechain
1	AA	6598	DC	Sidechain
1	AA	6619	DT	Sidechain
1	AA	6629	DT	Sidechain
1	AA	6630	DA	Sidechain
1	AA	6632	DT	Sidechain
1	AA	6637	DC	Sidechain
1	AA	6645	DG	Sidechain
1	AA	6652	DT	Sidechain
1	AA	6655	DC	Sidechain
1	AA	6663	DT	Sidechain
1	AA	6667	DA	Sidechain
1	AA	6668	DG	Sidechain
1	AA	6670	DA	Sidechain
1	AA	6672	DT	Sidechain
1	AA	6673	DC	Sidechain
1	AA	6675	DG	Sidechain
1	AA	6676	DG	Sidechain
1	AA	6682	DC	Sidechain
1	AA	669	DA	Sidechain
1	AA	67	DA	Sidechain
1	AA	6701	DT	Sidechain
1	AA	6710	DT	Sidechain
1	AA	6726	DT	Sidechain
1	AA	6728	DA	Sidechain
1	AA	6742	DC	Sidechain
1	AA	6745	DA	Sidechain
1	AA	6750	DC	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	6767	DT	Sidechain
1	AA	677	DG	Sidechain
1	AA	6786	DA	Sidechain
1	AA	6788	DT	Sidechain
1	AA	6793	DA	Sidechain
1	AA	6794	DT	Sidechain
1	AA	6801	DG	Sidechain
1	AA	6809	DC	Sidechain
1	AA	6817	DT	Sidechain
1	AA	6820	DT	Sidechain
1	AA	6828	DT	Sidechain
1	AA	683	DG	Sidechain
1	AA	6844	DA	Sidechain
1	AA	6846	DG	Sidechain
1	AA	6851	DT	Sidechain
1	AA	6852	DA	Sidechain
1	AA	6905	DT	Sidechain
1	AA	6907	DC	Sidechain
1	AA	6909	DG	Sidechain
1	AA	6913	DG	Sidechain
1	AA	6914	DT	Sidechain
1	AA	6915	DT	Sidechain
1	AA	6916	DT	Sidechain
1	AA	6919	DT	Sidechain
1	AA	6922	DT	Sidechain
1	AA	6926	DG	Sidechain
1	AA	6928	DA	Sidechain
1	AA	6930	DA	Sidechain
1	AA	6932	DT	Sidechain
1	AA	694	DC	Sidechain
1	AA	6941	DT	Sidechain
1	AA	6949	DC	Sidechain
1	AA	6964	DA	Sidechain
1	AA	6971	DG	Sidechain
1	AA	6977	DG	Sidechain
1	AA	6988	DG	Sidechain
1	AA	699	DG	Sidechain
1	AA	7016	DT	Sidechain
1	AA	702	DA	Sidechain
1	AA	7025	DA	Sidechain
1	AA	7026	DT	Sidechain
1	AA	7028	DC	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	7029	DT	Sidechain
1	AA	7034	DT	Sidechain
1	AA	7036	DT	Sidechain
1	AA	7037	DA	Sidechain
1	AA	704	DC	Sidechain
1	AA	7044	DA	Sidechain
1	AA	7048	DA	Sidechain
1	AA	7050	DG	Sidechain
1	AA	7053	DT	Sidechain
1	AA	7056	DA	Sidechain
1	AA	7062	DT	Sidechain
1	AA	7065	DG	Sidechain
1	AA	7069	DT	Sidechain
1	AA	7074	DG	Sidechain
1	AA	7084	DA	Sidechain
1	AA	7087	DT	Sidechain
1	AA	71	DG	Sidechain
1	AA	7101	DC	Sidechain
1	AA	711	DT	Sidechain
1	AA	7112	DT	Sidechain
1	AA	7123	DA	Sidechain
1	AA	7125	DT	Sidechain
1	AA	7127	DG	Sidechain
1	AA	7132	DC	Sidechain
1	AA	7133	DT	Sidechain
1	AA	7140	DA	Sidechain
1	AA	7143	DT	Sidechain
1	AA	7161	DT	Sidechain
1	AA	7164	DG	Sidechain
1	AA	717	DG	Sidechain
1	AA	7172	DG	Sidechain
1	AA	7182	DG	Sidechain
1	AA	7191	DT	Sidechain
1	AA	7197	DT	Sidechain
1	AA	7200	DG	Sidechain
1	AA	7205	DT	Sidechain
1	AA	7207	DG	Sidechain
1	AA	721	DT	Sidechain
1	AA	7211	DT	Sidechain
1	AA	7216	DG	Sidechain
1	AA	7223	DT	Sidechain
1	AA	7225	DT	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	7241	DT	Sidechain
1	AA	7242	DA	Sidechain
1	AA	7253	DC	Sidechain
1	AA	7266	DT	Sidechain
1	AA	727	DA	Sidechain
1	AA	7275	DG	Sidechain
1	AA	7327	DC	Sidechain
1	AA	7334	DG	Sidechain
1	AA	7353	DA	Sidechain
1	AA	7361	DT	Sidechain
1	AA	7364	DG	Sidechain
1	AA	7365	DC	Sidechain
1	AA	7372	DT	Sidechain
1	AA	7373	DT	Sidechain
1	AA	7382	DT	Sidechain
1	AA	7397	DT	Sidechain
1	AA	7402	DT	Sidechain
1	AA	7410	DG	Sidechain
1	AA	7415	DG	Sidechain
1	AA	7416	DA	Sidechain
1	AA	7418	DT	Sidechain
1	AA	742	DC	Sidechain
1	AA	7420	DT	Sidechain
1	AA	7427	DT	Sidechain
1	AA	744	DG	Sidechain
1	AA	7453	DC	Sidechain
1	AA	747	DT	Sidechain
1	AA	7470	DC	Sidechain
1	AA	7474	DT	Sidechain
1	AA	7477	DA	Sidechain
1	AA	7478	DG	Sidechain
1	AA	7490	DT	Sidechain
1	AA	7492	DA	Sidechain
1	AA	7498	DT	Sidechain
1	AA	7500	DG	Sidechain
1	AA	7502	DT	Sidechain
1	AA	7504	DT	Sidechain
1	AA	7514	DC	Sidechain
1	AA	7516	DT	Sidechain
1	AA	7517	DT	Sidechain
1	AA	7529	DA	Sidechain
1	AA	753	DA	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	7546	DT	Sidechain
1	AA	7549	DT	Sidechain
1	AA	7558	DT	Sidechain
1	AA	7574	DT	Sidechain
1	AA	7575	DA	Sidechain
1	AA	7582	DG	Sidechain
1	AA	7583	DT	Sidechain
1	AA	7584	DT	Sidechain
1	AA	7590	DA	Sidechain
1	AA	7591	DC	Sidechain
1	AA	760	DT	Sidechain
1	AA	7609	DT	Sidechain
1	AA	7612	DC	Sidechain
1	AA	7625	DT	Sidechain
1	AA	7629	DG	Sidechain
1	AA	7635	DA	Sidechain
1	AA	7640	DT	Sidechain
1	AA	7645	DT	Sidechain
1	AA	7667	DA	Sidechain
1	AA	7669	DT	Sidechain
1	AA	7671	DG	Sidechain
1	AA	7672	DG	Sidechain
1	AA	7681	DC	Sidechain
1	AA	7699	DC	Sidechain
1	AA	7706	DT	Sidechain
1	AA	7718	DG	Sidechain
1	AA	7719	DT	Sidechain
1	AA	772	DA	Sidechain
1	AA	7723	DT	Sidechain
1	AA	7735	DC	Sidechain
1	AA	7737	DT	Sidechain
1	AA	7747	DT	Sidechain
1	AA	7772	DT	Sidechain
1	AA	7791	DT	Sidechain
1	AA	7797	DC	Sidechain
1	AA	78	DA	Sidechain
1	AA	7809	DA	Sidechain
1	AA	7811	DC	Sidechain
1	AA	7823	DC	Sidechain
1	AA	7837	DT	Sidechain
1	AA	7841	DG	Sidechain
1	AA	7847	DC	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	7854	DG	Sidechain
1	AA	786	DT	Sidechain
1	AA	7863	DG	Sidechain
1	AA	7876	DG	Sidechain
1	AA	7878	DT	Sidechain
1	AA	7900	DC	Sidechain
1	AA	7904	DC	Sidechain
1	AA	7915	DT	Sidechain
1	AA	7927	DT	Sidechain
1	AA	7936	DA	Sidechain
1	AA	7940	DT	Sidechain
1	AA	7942	DG	Sidechain
1	AA	7943	DC	Sidechain
1	AA	7947	DC	Sidechain
1	AA	7948	DT	Sidechain
1	AA	7950	DT	Sidechain
1	AA	7951	DC	Sidechain
1	AA	7955	DG	Sidechain
1	AA	7956	DT	Sidechain
1	AA	7961	DC	Sidechain
1	AA	7962	DT	Sidechain
1	AA	7967	DA	Sidechain
1	AA	7972	DG	Sidechain
1	AA	7973	DG	Sidechain
1	AA	798	DG	Sidechain
1	AA	7985	DG	Sidechain
1	AA	7987	DT	Sidechain
1	AA	7994	DT	Sidechain
1	AA	7999	DG	Sidechain
1	AA	8006	DG	Sidechain
1	AA	8013	DC	Sidechain
1	AA	8029	DG	Sidechain
1	AA	8039	DA	Sidechain
1	AA	8043	DT	Sidechain
1	AA	8048	DG	Sidechain
1	AA	8060	DC	Sidechain
1	AA	8061	DG	Sidechain
1	AA	809	DC	Sidechain
1	AA	818	DT	Sidechain
1	AA	822	DG	Sidechain
1	AA	827	DC	Sidechain
1	AA	845	DT	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	85	DC	Sidechain
1	AA	863	DG	Sidechain
1	AA	870	DC	Sidechain
1	AA	877	DT	Sidechain
1	AA	903	DG	Sidechain
1	AA	908	DG	Sidechain
1	AA	910	DA	Sidechain
1	AA	927	DG	Sidechain
1	AA	936	DG	Sidechain
1	AA	94	DG	Sidechain
1	AA	940	DT	Sidechain
1	AA	945	DG	Sidechain
1	AA	948	DG	Sidechain
1	AA	95	DG	Sidechain
1	AA	950	DT	Sidechain
1	AA	953	DT	Sidechain
1	AA	956	DT	Sidechain
1	AA	957	DG	Sidechain
1	AA	977	DG	Sidechain
1	AA	984	DT	Sidechain
1	AA	99	DT	Sidechain
1	AA	990	DT	Sidechain
1	AA	991	DC	Sidechain
1	AA	993	DG	Sidechain
3	AC	25	DG	Sidechain
3	AC	29	DA	Sidechain
3	AC	46	DG	Sidechain
4	AD	2	DT	Sidechain
4	AD	20	DA	Sidechain
4	AD	25	DT	Sidechain
4	AD	29	DT	Sidechain
4	AD	30	DG	Sidechain
4	AD	34	DT	Sidechain
4	AD	35	DT	Sidechain
4	AD	37	DT	Sidechain
4	AD	42	DG	Sidechain
4	AD	45	DT	Sidechain
4	AD	47	DA	Sidechain
4	AD	52	DG	Sidechain
5	AE	15	DG	Sidechain
5	AE	31	DT	Sidechain
5	AE	32	DT	Sidechain

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Mol	Chain	Res	Type	Group
5	AE	33	DT	Sidechain
5	AE	34	DT	Sidechain
5	AE	48	DG	Sidechain
6	AF	12	DT	Sidechain
6	AF	13	DA	Sidechain
6	AF	20	DT	Sidechain
6	AF	30	DT	Sidechain
6	AF	36	DT	Sidechain
6	AF	40	DT	Sidechain
6	AF	47	DC	Sidechain
6	AF	5	DG	Sidechain
6	AF	8	DA	Sidechain
7	AG	10	DT	Sidechain
7	AG	14	DA	Sidechain
7	AG	30	DG	Sidechain
7	AG	32	DC	Sidechain
7	AG	33	DG	Sidechain
7	AG	45	DG	Sidechain
7	AG	7	DT	Sidechain
8	AH	11	DG	Sidechain
8	AH	3	DT	Sidechain
8	AH	57	DT	Sidechain
8	AH	9	DG	Sidechain
9	AI	13	DG	Sidechain
9	AI	19	DT	Sidechain
9	AI	26	DT	Sidechain
9	AI	28	DT	Sidechain
9	AI	31	DT	Sidechain
9	AI	33	DT	Sidechain
9	AI	34	DT	Sidechain
9	AI	42	DC	Sidechain
10	AJ	27	DT	Sidechain
10	AJ	3	DT	Sidechain
10	AJ	30	DT	Sidechain
10	AJ	43	DA	Sidechain
10	AJ	59	DT	Sidechain
11	AK	15	DT	Sidechain
11	AK	18	DT	Sidechain
11	AK	25	DG	Sidechain
11	AK	30	DG	Sidechain
11	AK	6	DA	Sidechain
12	AL	12	DC	Sidechain

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Mol	Chain	Res	Type	Group
12	AL	17	DA	Sidechain
12	AL	22	DG	Sidechain
12	AL	23	DG	Sidechain
12	AL	25	DT	Sidechain
12	AL	27	DT	Sidechain
12	AL	28	DT	Sidechain
12	AL	31	DT	Sidechain
12	AL	32	DT	Sidechain
12	AL	37	DA	Sidechain
12	AL	5	DT	Sidechain
13	AM	2	DA	Sidechain
13	AM	22	DG	Sidechain
13	AM	27	DA	Sidechain
13	AM	32	DA	Sidechain
13	AM	38	DG	Sidechain
13	AM	40	DG	Sidechain
14	AN	15	DA	Sidechain
14	AN	22	DT	Sidechain
14	AN	4	DT	Sidechain
15	AO	19	DT	Sidechain
15	AO	25	DT	Sidechain
15	AO	28	DA	Sidechain
15	AO	48	DA	Sidechain
16	AP	10	DC	Sidechain
16	AP	20	DA	Sidechain
16	AP	21	DT	Sidechain
16	AP	34	DA	Sidechain
16	AP	35	DT	Sidechain
17	AQ	23	DT	Sidechain
17	AQ	24	DT	Sidechain
17	AQ	30	DT	Sidechain
17	AQ	40	DG	Sidechain
17	AQ	5	DC	Sidechain
18	AR	1	DT	Sidechain
18	AR	33	DT	Sidechain
18	AR	39	DT	Sidechain
19	AS	12	DT	Sidechain
19	AS	15	DT	Sidechain
19	AS	22	DT	Sidechain
19	AS	24	DC	Sidechain
19	AS	25	DT	Sidechain
19	AS	27	DC	Sidechain

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Mol	Chain	Res	Type	Group
19	AS	38	DA	Sidechain
19	AS	42	DC	Sidechain
19	AS	44	DG	Sidechain
19	AS	8	DT	Sidechain
20	AT	14	DC	Sidechain
20	AT	16	DT	Sidechain
20	AT	35	DG	Sidechain
20	AT	37	DT	Sidechain
20	AT	41	DT	Sidechain
20	AT	5	DA	Sidechain
21	AU	12	DG	Sidechain
21	AU	13	DG	Sidechain
21	AU	14	DT	Sidechain
21	AU	20	DG	Sidechain
21	AU	21	DA	Sidechain
21	AU	35	DT	Sidechain
21	AU	36	DT	Sidechain
21	AU	40	DG	Sidechain
22	AV	23	DG	Sidechain
22	AV	30	DA	Sidechain
22	AV	38	DG	Sidechain
22	AV	39	DA	Sidechain
23	AW	22	DC	Sidechain
23	AW	39	DG	Sidechain
23	AW	45	DC	Sidechain
23	AW	50	DA	Sidechain
23	AW	51	DG	Sidechain
23	AW	55	DT	Sidechain
23	AW	7	DC	Sidechain
24	AX	34	DT	Sidechain
24	AX	5	DT	Sidechain
24	AX	50	DA	Sidechain
24	AX	51	DA	Sidechain
24	AX	54	DA	Sidechain
25	AY	1	DT	Sidechain
25	AY	14	DA	Sidechain
25	AY	16	DG	Sidechain
25	AY	21	DA	Sidechain
25	AY	6	DT	Sidechain
26	AZ	13	DA	Sidechain
26	AZ	2	DA	Sidechain
26	AZ	27	DG	Sidechain

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Mol	Chain	Res	Type	Group
26	AZ	30	DG	Sidechain
26	AZ	36	DA	Sidechain
26	AZ	42	DT	Sidechain
26	AZ	7	DT	Sidechain
27	Aa	11	DA	Sidechain
27	Aa	19	DT	Sidechain
27	Aa	26	DT	Sidechain
28	Ab	12	DG	Sidechain
28	Ab	2	DG	Sidechain
28	Ab	24	DA	Sidechain
28	Ab	25	DT	Sidechain
28	Ab	31	DA	Sidechain
28	Ab	35	DT	Sidechain
28	Ab	42	DG	Sidechain
28	Ab	43	DT	Sidechain
28	Ab	45	DA	Sidechain
28	Ab	46	DT	Sidechain
29	Ac	13	DA	Sidechain
29	Ac	23	DT	Sidechain
29	Ac	25	DA	Sidechain
29	Ac	26	DT	Sidechain
29	Ac	28	DA	Sidechain
29	Ac	29	DT	Sidechain
29	Ac	3	DC	Sidechain
29	Ac	30	DA	Sidechain
29	Ac	32	DC	Sidechain
29	Ac	36	DC	Sidechain
29	Ac	37	DG	Sidechain
29	Ac	40	DA	Sidechain
30	Ad	1	DC	Sidechain
30	Ad	10	DA	Sidechain
30	Ad	17	DG	Sidechain
30	Ad	4	DG	Sidechain
30	Ad	43	DG	Sidechain
30	Ad	5	DA	Sidechain
30	Ad	52	DT	Sidechain
31	Ae	1	DC	Sidechain
31	Ae	10	DG	Sidechain
31	Ae	11	DC	Sidechain
31	Ae	14	DT	Sidechain
31	Ae	19	DG	Sidechain
31	Ae	33	DG	Sidechain

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Mol	Chain	Res	Type	Group
31	Ae	34	DG	Sidechain
31	Ae	4	DA	Sidechain
32	Af	15	DG	Sidechain
32	Af	17	DG	Sidechain
32	Af	25	DG	Sidechain
32	Af	28	DT	Sidechain
32	Af	31	DA	Sidechain
32	Af	5	DG	Sidechain
33	Ag	1	DT	Sidechain
33	Ag	16	DT	Sidechain
33	Ag	18	DC	Sidechain
33	Ag	28	DT	Sidechain
33	Ag	3	DT	Sidechain
33	Ag	38	DT	Sidechain
33	Ag	45	DA	Sidechain
34	Ah	12	DA	Sidechain
34	Ah	13	DC	Sidechain
34	Ah	27	DT	Sidechain
34	Ah	33	DT	Sidechain
34	Ah	35	DT	Sidechain
34	Ah	39	DG	Sidechain
34	Ah	41	DT	Sidechain
34	Ah	48	DG	Sidechain
34	Ah	58	DT	Sidechain
34	Ah	8	DG	Sidechain
35	Ai	20	DG	Sidechain
35	Ai	21	DC	Sidechain
35	Ai	25	DC	Sidechain
35	Ai	31	DT	Sidechain
35	Ai	35	DT	Sidechain
35	Ai	8	DG	Sidechain
35	Ai	9	DA	Sidechain
36	Aj	14	DT	Sidechain
36	Aj	19	DT	Sidechain
36	Aj	30	DC	Sidechain
36	Aj	40	DA	Sidechain
36	Aj	43	DT	Sidechain
37	Ak	17	DA	Sidechain
37	Ak	21	DC	Sidechain
37	Ak	3	DG	Sidechain
37	Ak	32	DG	Sidechain
38	Al	1	DT	Sidechain

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Mol	Chain	Res	Type	Group
38	Al	13	DT	Sidechain
38	Al	34	DC	Sidechain
38	Al	37	DC	Sidechain
38	Al	6	DA	Sidechain
38	Al	8	DT	Sidechain
39	Am	12	DA	Sidechain
39	Am	2	DT	Sidechain
39	Am	26	DA	Sidechain
39	Am	27	DT	Sidechain
39	Am	28	DT	Sidechain
39	Am	29	DT	Sidechain
39	Am	33	DT	Sidechain
39	Am	46	DG	Sidechain
39	Am	56	DT	Sidechain
39	Am	8	DA	Sidechain
40	An	26	DT	Sidechain
40	An	29	DT	Sidechain
40	An	3	DT	Sidechain
40	An	33	DT	Sidechain
40	An	34	DT	Sidechain
40	An	43	DC	Sidechain
40	An	44	DA	Sidechain
41	Ao	11	DG	Sidechain
41	Ao	12	DA	Sidechain
41	Ao	17	DT	Sidechain
41	Ao	19	DT	Sidechain
41	Ao	27	DT	Sidechain
41	Ao	36	DA	Sidechain
41	Ao	38	DA	Sidechain
41	Ao	40	DT	Sidechain
41	Ao	45	DC	Sidechain
41	Ao	56	DT	Sidechain
42	Ap	15	DA	Sidechain
42	Ap	22	DT	Sidechain
42	Ap	46	DG	Sidechain
42	Ap	47	DG	Sidechain
42	Ap	54	DG	Sidechain
42	Ap	55	DT	Sidechain
42	Ap	7	DC	Sidechain
42	Ap	9	DT	Sidechain
43	Aq	15	DG	Sidechain
43	Aq	17	DC	Sidechain

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Mol	Chain	Res	Type	Group
43	Aq	20	DC	Sidechain
43	Aq	29	DA	Sidechain
43	Aq	34	DG	Sidechain
43	Aq	39	DA	Sidechain
43	Aq	44	DG	Sidechain
43	Aq	48	DA	Sidechain
44	Ar	11	DT	Sidechain
44	Ar	12	DG	Sidechain
44	Ar	18	DA	Sidechain
44	Ar	24	DT	Sidechain
44	Ar	33	DT	Sidechain
44	Ar	34	DT	Sidechain
44	Ar	35	DT	Sidechain
44	Ar	8	DA	Sidechain
45	As	23	DT	Sidechain
45	As	32	DG	Sidechain
46	At	10	DA	Sidechain
46	At	15	DC	Sidechain
46	At	34	DG	Sidechain
46	At	40	DA	Sidechain
46	At	42	DT	Sidechain
46	At	8	DC	Sidechain
46	At	9	DA	Sidechain
47	Au	11	DA	Sidechain
47	Au	15	DG	Sidechain
47	Au	2	DC	Sidechain
47	Au	27	DC	Sidechain
47	Au	35	DT	Sidechain
47	Au	4	DT	Sidechain
47	Au	40	DC	Sidechain
48	Av	15	DT	Sidechain
48	Av	34	DG	Sidechain
48	Av	35	DA	Sidechain
49	Aw	13	DT	Sidechain
49	Aw	25	DA	Sidechain
49	Aw	31	DA	Sidechain
49	Aw	34	DA	Sidechain
49	Aw	37	DT	Sidechain
49	Aw	40	DC	Sidechain
50	Ax	1	DA	Sidechain
50	Ax	15	DG	Sidechain
50	Ax	21	DA	Sidechain

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Mol	Chain	Res	Type	Group
50	Ax	23	DA	Sidechain
50	Ax	24	DC	Sidechain
50	Ax	35	DT	Sidechain
50	Ax	37	DT	Sidechain
50	Ax	7	DA	Sidechain
50	Ax	8	DT	Sidechain
51	Ay	36	DA	Sidechain
51	Ay	46	DG	Sidechain
51	Ay	6	DG	Sidechain
51	Ay	7	DG	Sidechain
52	Az	28	DT	Sidechain
52	Az	33	DC	Sidechain
52	Az	41	DT	Sidechain
52	Az	44	DT	Sidechain
52	Az	9	DC	Sidechain
115	B0	20	DG	Sidechain
115	B0	27	DT	Sidechain
115	B0	3	DT	Sidechain
115	B0	33	DT	Sidechain
115	B0	34	DT	Sidechain
115	B0	51	DT	Sidechain
115	B0	56	DT	Sidechain
116	B1	1	DT	Sidechain
116	B1	19	DC	Sidechain
116	B1	2	DT	Sidechain
116	B1	27	DT	Sidechain
116	B1	41	DT	Sidechain
116	B1	46	DG	Sidechain
116	B1	50	DA	Sidechain
116	B1	52	DA	Sidechain
116	B1	54	DT	Sidechain
116	B1	58	DT	Sidechain
116	B1	7	DG	Sidechain
117	B2	22	DG	Sidechain
117	B2	33	DA	Sidechain
117	B2	5	DT	Sidechain
117	B2	7	DA	Sidechain
118	B3	25	DA	Sidechain
118	B3	3	DC	Sidechain
118	B3	7	DC	Sidechain
118	B3	8	DT	Sidechain
118	B3	9	DG	Sidechain

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Mol	Chain	Res	Type	Group
119	B4	22	DG	Sidechain
119	B4	32	DA	Sidechain
119	B4	9	DG	Sidechain
120	B5	12	DA	Sidechain
120	B5	27	DT	Sidechain
120	B5	35	DT	Sidechain
120	B5	48	DG	Sidechain
120	B5	50	DA	Sidechain
120	B5	57	DT	Sidechain
120	B5	58	DT	Sidechain
120	B5	59	DT	Sidechain
121	B6	12	DA	Sidechain
121	B6	17	DC	Sidechain
121	B6	20	DG	Sidechain
121	B6	22	DA	Sidechain
121	B6	24	DT	Sidechain
121	B6	25	DC	Sidechain
121	B6	3	DT	Sidechain
121	B6	34	DG	Sidechain
121	B6	41	DA	Sidechain
121	B6	5	DT	Sidechain
121	B6	53	DG	Sidechain
122	B7	14	DG	Sidechain
122	B7	15	DA	Sidechain
122	B7	39	DG	Sidechain
122	B7	40	DG	Sidechain
123	B8	1	DT	Sidechain
123	B8	2	DT	Sidechain
123	B8	24	DC	Sidechain
123	B8	30	DC	Sidechain
124	B9	2	DA	Sidechain
124	B9	23	DG	Sidechain
124	B9	3	DG	Sidechain
124	B9	30	DG	Sidechain
124	B9	32	DG	Sidechain
124	B9	33	DC	Sidechain
124	B9	45	DT	Sidechain
124	B9	6	DC	Sidechain
124	B9	7	DT	Sidechain
63	BA	15	DC	Sidechain
63	BA	21	DG	Sidechain
63	BA	26	DC	Sidechain

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Mol	Chain	Res	Type	Group
63	BA	27	DA	Sidechain
63	BA	39	DC	Sidechain
63	BA	41	DT	Sidechain
64	BB	1	DA	Sidechain
64	BB	24	DG	Sidechain
64	BB	27	DG	Sidechain
64	BB	28	DC	Sidechain
64	BB	31	DG	Sidechain
64	BB	32	DC	Sidechain
64	BB	5	DA	Sidechain
64	BB	6	DT	Sidechain
64	BB	8	DA	Sidechain
65	BC	14	DT	Sidechain
65	BC	23	DG	Sidechain
65	BC	26	DT	Sidechain
65	BC	38	DA	Sidechain
65	BC	41	DT	Sidechain
65	BC	44	DT	Sidechain
66	BD	18	DA	Sidechain
66	BD	29	DT	Sidechain
66	BD	44	DC	Sidechain
66	BD	57	DT	Sidechain
67	BE	11	DA	Sidechain
67	BE	12	DT	Sidechain
67	BE	15	DA	Sidechain
67	BE	26	DG	Sidechain
67	BE	29	DT	Sidechain
67	BE	32	DT	Sidechain
67	BE	36	DT	Sidechain
67	BE	47	DC	Sidechain
67	BE	51	DC	Sidechain
67	BE	56	DA	Sidechain
68	BF	1	DC	Sidechain
68	BF	11	DA	Sidechain
68	BF	2	DG	Sidechain
68	BF	3	DA	Sidechain
68	BF	4	DA	Sidechain
68	BF	43	DT	Sidechain
68	BF	44	DT	Sidechain
69	BG	13	DG	Sidechain
69	BG	15	DG	Sidechain
69	BG	18	DG	Sidechain

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Mol	Chain	Res	Type	Group
69	BG	23	DG	Sidechain
69	BG	34	DG	Sidechain
69	BG	6	DA	Sidechain
69	BG	7	DA	Sidechain
69	BG	8	DT	Sidechain
69	BG	9	DA	Sidechain
70	BH	15	DA	Sidechain
70	BH	16	DT	Sidechain
70	BH	3	DT	Sidechain
70	BH	31	DT	Sidechain
70	BH	35	DT	Sidechain
70	BH	37	DC	Sidechain
70	BH	39	DT	Sidechain
70	BH	4	DT	Sidechain
70	BH	42	DA	Sidechain
70	BH	47	DA	Sidechain
70	BH	48	DC	Sidechain
70	BH	52	DT	Sidechain
70	BH	54	DT	Sidechain
70	BH	6	DT	Sidechain
71	BI	12	DT	Sidechain
71	BI	15	DA	Sidechain
71	BI	16	DA	Sidechain
71	BI	17	DA	Sidechain
71	BI	18	DT	Sidechain
71	BI	21	DA	Sidechain
71	BI	29	DT	Sidechain
71	BI	30	DT	Sidechain
71	BI	34	DT	Sidechain
71	BI	5	DT	Sidechain
71	BI	54	DT	Sidechain
71	BI	9	DT	Sidechain
72	BJ	13	DA	Sidechain
72	BJ	18	DA	Sidechain
72	BJ	19	DC	Sidechain
72	BJ	2	DA	Sidechain
72	BJ	41	DT	Sidechain
73	BK	24	DA	Sidechain
73	BK	8	DG	Sidechain
73	BK	9	DC	Sidechain
74	BL	19	DC	Sidechain
74	BL	4	DT	Sidechain

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Mol	Chain	Res	Type	Group
74	BL	44	DG	Sidechain
74	BL	47	DT	Sidechain
75	BM	17	DG	Sidechain
75	BM	29	DT	Sidechain
75	BM	5	DC	Sidechain
76	BN	11	DT	Sidechain
76	BN	2	DA	Sidechain
76	BN	22	DG	Sidechain
76	BN	37	DT	Sidechain
76	BN	6	DA	Sidechain
76	BN	8	DG	Sidechain
76	BN	9	DA	Sidechain
77	BO	15	DA	Sidechain
77	BO	17	DG	Sidechain
77	BO	30	DT	Sidechain
77	BO	43	DC	Sidechain
77	BO	47	DT	Sidechain
77	BO	48	DA	Sidechain
77	BO	6	DC	Sidechain
78	BP	10	DC	Sidechain
78	BP	29	DT	Sidechain
78	BP	3	DT	Sidechain
78	BP	31	DT	Sidechain
78	BP	37	DC	Sidechain
78	BP	40	DT	Sidechain
78	BP	41	DA	Sidechain
78	BP	46	DA	Sidechain
78	BP	54	DT	Sidechain
78	BP	58	DT	Sidechain
79	BQ	12	DC	Sidechain
79	BQ	19	DT	Sidechain
79	BQ	20	DA	Sidechain
79	BQ	28	DT	Sidechain
79	BQ	34	DT	Sidechain
79	BQ	36	DT	Sidechain
79	BQ	50	DA	Sidechain
79	BQ	54	DG	Sidechain
79	BQ	9	DA	Sidechain
80	BR	17	DT	Sidechain
80	BR	2	DT	Sidechain
80	BR	32	DT	Sidechain
80	BR	48	DT	Sidechain

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Mol	Chain	Res	Type	Group
81	BS	13	DT	Sidechain
81	BS	16	DG	Sidechain
81	BS	38	DA	Sidechain
81	BS	40	DC	Sidechain
81	BS	41	DA	Sidechain
81	BS	43	DA	Sidechain
82	BT	11	DG	Sidechain
82	BT	17	DC	Sidechain
82	BT	19	DT	Sidechain
82	BT	25	DA	Sidechain
82	BT	41	DG	Sidechain
83	BU	13	DA	Sidechain
83	BU	22	DC	Sidechain
83	BU	25	DG	Sidechain
83	BU	34	DT	Sidechain
84	BV	32	DT	Sidechain
84	BV	37	DT	Sidechain
84	BV	42	DT	Sidechain
84	BV	44	DT	Sidechain
84	BV	5	DT	Sidechain
84	BV	53	DC	Sidechain
84	BV	6	DG	Sidechain
85	BW	15	DT	Sidechain
85	BW	26	DT	Sidechain
85	BW	27	DT	Sidechain
85	BW	3	DT	Sidechain
85	BW	32	DT	Sidechain
85	BW	33	DT	Sidechain
85	BW	36	DT	Sidechain
85	BW	40	DC	Sidechain
85	BW	49	DT	Sidechain
85	BW	50	DT	Sidechain
85	BW	58	DT	Sidechain
85	BW	60	DT	Sidechain
86	BX	1	DG	Sidechain
86	BX	13	DG	Sidechain
86	BX	21	DT	Sidechain
86	BX	23	DC	Sidechain
87	BY	15	DC	Sidechain
87	BY	19	DG	Sidechain
87	BY	24	DA	Sidechain
87	BY	3	DG	Sidechain

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Mol	Chain	Res	Type	Group
87	BY	30	DC	Sidechain
87	BY	34	DT	Sidechain
87	BY	35	DG	Sidechain
87	BY	39	DG	Sidechain
87	BY	8	DT	Sidechain
88	BZ	10	DT	Sidechain
88	BZ	13	DG	Sidechain
88	BZ	17	DC	Sidechain
88	BZ	2	DT	Sidechain
88	BZ	22	DG	Sidechain
88	BZ	5	DC	Sidechain
88	BZ	7	DG	Sidechain
89	Ba	15	DG	Sidechain
89	Ba	29	DA	Sidechain
89	Ba	3	DG	Sidechain
89	Ba	34	DA	Sidechain
89	Ba	35	DG	Sidechain
89	Ba	4	DG	Sidechain
89	Ba	41	DA	Sidechain
89	Ba	46	DA	Sidechain
89	Ba	8	DA	Sidechain
90	Bb	1	DG	Sidechain
90	Bb	10	DG	Sidechain
90	Bb	14	DT	Sidechain
90	Bb	2	DT	Sidechain
90	Bb	20	DA	Sidechain
90	Bb	21	DG	Sidechain
90	Bb	27	DA	Sidechain
90	Bb	37	DC	Sidechain
90	Bb	43	DG	Sidechain
90	Bb	48	DA	Sidechain
90	Bb	9	DA	Sidechain
91	Bc	13	DA	Sidechain
91	Bc	25	DA	Sidechain
91	Bc	29	DT	Sidechain
92	Bd	36	DT	Sidechain
93	Be	22	DG	Sidechain
93	Be	23	DT	Sidechain
93	Be	39	DA	Sidechain
93	Be	46	DA	Sidechain
94	Bf	1	DA	Sidechain
94	Bf	10	DG	Sidechain

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Mol	Chain	Res	Type	Group
94	Bf	23	DA	Sidechain
94	Bf	26	DT	Sidechain
94	Bf	3	DC	Sidechain
95	Bg	1	DG	Sidechain
95	Bg	10	DA	Sidechain
95	Bg	15	DG	Sidechain
95	Bg	20	DC	Sidechain
95	Bg	24	DT	Sidechain
95	Bg	27	DT	Sidechain
95	Bg	28	DT	Sidechain
95	Bg	31	DT	Sidechain
95	Bg	34	DC	Sidechain
95	Bg	37	DT	Sidechain
95	Bg	40	DT	Sidechain
95	Bg	6	DT	Sidechain
96	Bh	14	DT	Sidechain
96	Bh	18	DA	Sidechain
96	Bh	24	DT	Sidechain
96	Bh	27	DG	Sidechain
96	Bh	29	DC	Sidechain
96	Bh	35	DG	Sidechain
96	Bh	37	DC	Sidechain
96	Bh	46	DA	Sidechain
96	Bh	49	DC	Sidechain
96	Bh	52	DA	Sidechain
97	Bi	1	DG	Sidechain
97	Bi	22	DT	Sidechain
97	Bi	24	DT	Sidechain
97	Bi	3	DC	Sidechain
97	Bi	30	DC	Sidechain
97	Bi	31	DA	Sidechain
97	Bi	36	DA	Sidechain
97	Bi	37	DT	Sidechain
98	Bj	14	DT	Sidechain
98	Bj	18	DG	Sidechain
98	Bj	22	DA	Sidechain
98	Bj	31	DT	Sidechain
99	Bk	26	DG	Sidechain
99	Bk	27	DA	Sidechain
100	Bl	40	DG	Sidechain
100	Bl	44	DC	Sidechain
100	Bl	47	DA	Sidechain

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Mol	Chain	Res	Type	Group
100	Bl	48	DT	Sidechain
100	Bl	6	DC	Sidechain
100	Bl	9	DT	Sidechain
101	Bm	16	DA	Sidechain
101	Bm	17	DG	Sidechain
101	Bm	31	DT	Sidechain
101	Bm	42	DT	Sidechain
101	Bm	53	DA	Sidechain
101	Bm	8	DT	Sidechain
101	Bm	9	DG	Sidechain
102	Bn	16	DT	Sidechain
102	Bn	37	DA	Sidechain
102	Bn	41	DA	Sidechain
103	Bo	13	DA	Sidechain
103	Bo	21	DT	Sidechain
103	Bo	31	DT	Sidechain
103	Bo	40	DG	Sidechain
103	Bo	45	DG	Sidechain
104	Bp	12	DG	Sidechain
104	Bp	32	DA	Sidechain
104	Bp	38	DT	Sidechain
104	Bp	6	DA	Sidechain
105	Bq	1	DG	Sidechain
105	Bq	19	DT	Sidechain
105	Bq	42	DT	Sidechain
105	Bq	6	DT	Sidechain
106	Br	17	DT	Sidechain
106	Br	24	DT	Sidechain
106	Br	29	DT	Sidechain
106	Br	41	DT	Sidechain
106	Br	5	DT	Sidechain
107	Bs	12	DA	Sidechain
107	Bs	20	DA	Sidechain
107	Bs	22	DT	Sidechain
108	Bt	11	DG	Sidechain
108	Bt	21	DC	Sidechain
108	Bt	32	DT	Sidechain
108	Bt	38	DG	Sidechain
108	Bt	9	DG	Sidechain
109	Bu	23	DA	Sidechain
109	Bu	5	DC	Sidechain
109	Bu	9	DA	Sidechain

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Mol	Chain	Res	Type	Group
110	Bv	16	DT	Sidechain
110	Bv	17	DG	Sidechain
110	Bv	23	DT	Sidechain
110	Bv	24	DG	Sidechain
110	Bv	4	DT	Sidechain
110	Bv	9	DT	Sidechain
111	Bw	11	DA	Sidechain
111	Bw	2	DT	Sidechain
111	Bw	26	DT	Sidechain
111	Bw	28	DT	Sidechain
111	Bw	3	DT	Sidechain
111	Bw	4	DA	Sidechain
111	Bw	50	DG	Sidechain
111	Bw	51	DT	Sidechain
111	Bw	52	DC	Sidechain
112	Bx	15	DT	Sidechain
112	Bx	17	DT	Sidechain
112	Bx	20	DA	Sidechain
112	Bx	21	DG	Sidechain
112	Bx	29	DG	Sidechain
112	Bx	4	DT	Sidechain
113	By	10	DA	Sidechain
113	By	23	DC	Sidechain
114	Bz	10	DT	Sidechain
114	Bz	14	DT	Sidechain
114	Bz	24	DT	Sidechain
114	Bz	6	DT	Sidechain
114	Bz	9	DA	Sidechain
177	C0	11	DG	Sidechain
177	C0	2	DT	Sidechain
177	C0	27	DT	Sidechain
177	C0	28	DT	Sidechain
177	C0	33	DT	Sidechain
177	C0	34	DT	Sidechain
177	C0	42	DG	Sidechain
177	C0	43	DC	Sidechain
178	C1	1	DT	Sidechain
178	C1	13	DA	Sidechain
178	C1	14	DT	Sidechain
178	C1	24	DT	Sidechain
178	C1	28	DT	Sidechain
178	C1	29	DT	Sidechain

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Mol	Chain	Res	Type	Group
178	C1	3	DT	Sidechain
178	C1	34	DT	Sidechain
178	C1	36	DT	Sidechain
178	C1	4	DT	Sidechain
178	C1	5	DT	Sidechain
178	C1	56	DC	Sidechain
178	C1	6	DG	Sidechain
179	C2	1	DG	Sidechain
179	C2	13	DC	Sidechain
179	C2	25	DA	Sidechain
179	C2	32	DG	Sidechain
179	C2	6	DA	Sidechain
180	C3	15	DC	Sidechain
180	C3	17	DC	Sidechain
180	C3	2	DC	Sidechain
180	C3	35	DT	Sidechain
180	C3	4	DG	Sidechain
180	C3	40	DT	Sidechain
180	C3	42	DA	Sidechain
180	C3	47	DT	Sidechain
180	C3	6	DG	Sidechain
180	C3	8	DA	Sidechain
181	C4	18	DA	Sidechain
181	C4	27	DT	Sidechain
181	C4	29	DA	Sidechain
181	C4	37	DG	Sidechain
181	C4	4	DT	Sidechain
181	C4	40	DC	Sidechain
182	C5	16	DA	Sidechain
182	C5	25	DA	Sidechain
182	C5	38	DT	Sidechain
182	C5	4	DT	Sidechain
182	C5	5	DT	Sidechain
183	C6	14	DT	Sidechain
183	C6	17	DA	Sidechain
183	C6	21	DG	Sidechain
183	C6	27	DG	Sidechain
183	C6	31	DT	Sidechain
183	C6	42	DT	Sidechain
184	C7	12	DT	Sidechain
184	C7	14	DT	Sidechain
184	C7	2	DC	Sidechain

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Mol	Chain	Res	Type	Group
184	C7	34	DA	Sidechain
184	C7	4	DT	Sidechain
185	C8	19	DG	Sidechain
185	C8	31	DA	Sidechain
185	C8	39	DT	Sidechain
185	C8	40	DG	Sidechain
185	C8	44	DA	Sidechain
185	C8	45	DG	Sidechain
185	C8	7	DA	Sidechain
186	C9	11	DT	Sidechain
186	C9	17	DA	Sidechain
186	C9	21	DA	Sidechain
186	C9	29	DT	Sidechain
186	C9	48	DT	Sidechain
186	C9	5	DT	Sidechain
186	C9	53	DT	Sidechain
186	C9	56	DT	Sidechain
125	CA	12	DT	Sidechain
125	CA	16	DC	Sidechain
125	CA	20	DG	Sidechain
125	CA	21	DC	Sidechain
125	CA	29	DT	Sidechain
125	CA	35	DG	Sidechain
125	CA	42	DC	Sidechain
125	CA	43	DG	Sidechain
125	CA	48	DG	Sidechain
125	CA	9	DT	Sidechain
126	CB	10	DC	Sidechain
126	CB	13	DG	Sidechain
126	CB	29	DT	Sidechain
126	CB	32	DT	Sidechain
126	CB	33	DT	Sidechain
126	CB	34	DT	Sidechain
126	CB	44	DA	Sidechain
126	CB	48	DT	Sidechain
126	CB	52	DA	Sidechain
126	CB	57	DT	Sidechain
126	CB	59	DT	Sidechain
127	CC	12	DG	Sidechain
127	CC	18	DC	Sidechain
127	CC	4	DT	Sidechain
127	CC	6	DT	Sidechain

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Mol	Chain	Res	Type	Group
128	CD	11	DT	Sidechain
128	CD	2	DG	Sidechain
128	CD	22	DT	Sidechain
128	CD	23	DT	Sidechain
128	CD	25	DT	Sidechain
128	CD	32	DC	Sidechain
128	CD	33	DT	Sidechain
128	CD	52	DA	Sidechain
128	CD	9	DT	Sidechain
129	CE	24	DG	Sidechain
129	CE	4	DG	Sidechain
130	CF	10	DA	Sidechain
130	CF	12	DA	Sidechain
130	CF	36	DT	Sidechain
130	CF	39	DT	Sidechain
130	CF	7	DA	Sidechain
130	CF	8	DG	Sidechain
130	CF	9	DG	Sidechain
131	CG	15	DA	Sidechain
131	CG	23	DA	Sidechain
131	CG	27	DG	Sidechain
131	CG	29	DG	Sidechain
131	CG	6	DG	Sidechain
131	CG	7	DT	Sidechain
132	CH	1	DA	Sidechain
132	CH	16	DC	Sidechain
132	CH	18	DA	Sidechain
132	CH	22	DG	Sidechain
132	CH	23	DA	Sidechain
132	CH	29	DC	Sidechain
132	CH	31	DA	Sidechain
132	CH	38	DT	Sidechain
132	CH	44	DA	Sidechain
132	CH	49	DT	Sidechain
132	CH	50	DT	Sidechain
132	CH	9	DA	Sidechain
133	CI	1	DA	Sidechain
133	CI	15	DA	Sidechain
133	CI	4	DA	Sidechain
134	CJ	17	DG	Sidechain
134	CJ	28	DT	Sidechain
134	CJ	31	DT	Sidechain

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Mol	Chain	Res	Type	Group
134	CJ	43	DT	Sidechain
134	CJ	51	DT	Sidechain
134	CJ	8	DC	Sidechain
134	CJ	9	DT	Sidechain
135	CK	14	DC	Sidechain
135	CK	2	DT	Sidechain
135	CK	22	DT	Sidechain
135	CK	7	DC	Sidechain
136	CL	13	DG	Sidechain
136	CL	15	DA	Sidechain
136	CL	16	DT	Sidechain
136	CL	19	DG	Sidechain
136	CL	40	DA	Sidechain
136	CL	8	DA	Sidechain
137	CM	1	DT	Sidechain
137	CM	18	DA	Sidechain
137	CM	3	DG	Sidechain
137	CM	32	DT	Sidechain
137	CM	4	DA	Sidechain
138	CN	17	DC	Sidechain
138	CN	33	DT	Sidechain
138	CN	39	DG	Sidechain
138	CN	41	DT	Sidechain
138	CN	49	DT	Sidechain
138	CN	52	DT	Sidechain
138	CN	7	DG	Sidechain
139	CO	1	DA	Sidechain
139	CO	14	DA	Sidechain
139	CO	15	DC	Sidechain
139	CO	19	DA	Sidechain
139	CO	31	DC	Sidechain
139	CO	33	DT	Sidechain
139	CO	39	DA	Sidechain
139	CO	45	DG	Sidechain
140	CP	16	DA	Sidechain
140	CP	18	DA	Sidechain
140	CP	31	DT	Sidechain
140	CP	34	DC	Sidechain
140	CP	35	DG	Sidechain
140	CP	36	DC	Sidechain
140	CP	38	DG	Sidechain
140	CP	39	DG	Sidechain

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Mol	Chain	Res	Type	Group
140	CP	42	DG	Sidechain
140	CP	6	DT	Sidechain
140	CP	7	DT	Sidechain
141	CQ	19	DC	Sidechain
141	CQ	21	DG	Sidechain
141	CQ	27	DT	Sidechain
141	CQ	30	DT	Sidechain
141	CQ	32	DT	Sidechain
141	CQ	35	DT	Sidechain
141	CQ	4	DT	Sidechain
141	CQ	50	DA	Sidechain
141	CQ	51	DA	Sidechain
141	CQ	8	DT	Sidechain
142	CR	1	DT	Sidechain
142	CR	11	DA	Sidechain
142	CR	12	DA	Sidechain
142	CR	13	DA	Sidechain
142	CR	28	DT	Sidechain
142	CR	29	DT	Sidechain
142	CR	33	DT	Sidechain
142	CR	37	DC	Sidechain
142	CR	39	DG	Sidechain
142	CR	4	DT	Sidechain
142	CR	58	DT	Sidechain
142	CR	7	DA	Sidechain
142	CR	8	DA	Sidechain
143	CS	1	DT	Sidechain
143	CS	2	DT	Sidechain
143	CS	21	DT	Sidechain
143	CS	22	DC	Sidechain
143	CS	27	DA	Sidechain
143	CS	30	DT	Sidechain
143	CS	36	DA	Sidechain
143	CS	41	DT	Sidechain
144	CT	1	DA	Sidechain
144	CT	28	DT	Sidechain
144	CT	33	DG	Sidechain
144	CT	46	DA	Sidechain
145	CU	16	DA	Sidechain
145	CU	29	DC	Sidechain
145	CU	35	DT	Sidechain
145	CU	7	DA	Sidechain

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Mol	Chain	Res	Type	Group
146	CV	3	DT	Sidechain
146	CV	4	DC	Sidechain
146	CV	6	DT	Sidechain
147	CW	12	DT	Sidechain
147	CW	17	DA	Sidechain
147	CW	23	DA	Sidechain
147	CW	29	DT	Sidechain
148	CX	17	DC	Sidechain
148	CX	30	DT	Sidechain
148	CX	31	DT	Sidechain
148	CX	36	DT	Sidechain
148	CX	38	DT	Sidechain
148	CX	43	DG	Sidechain
149	CY	1	DT	Sidechain
149	CY	11	DA	Sidechain
149	CY	12	DT	Sidechain
149	CY	16	DT	Sidechain
149	CY	32	DT	Sidechain
149	CY	4	DT	Sidechain
149	CY	41	DA	Sidechain
149	CY	59	DT	Sidechain
149	CY	60	DT	Sidechain
150	CZ	21	DT	Sidechain
150	CZ	32	DT	Sidechain
150	CZ	33	DC	Sidechain
150	CZ	36	DT	Sidechain
150	CZ	4	DA	Sidechain
150	CZ	40	DT	Sidechain
151	Ca	31	DA	Sidechain
151	Ca	36	DT	Sidechain
151	Ca	42	DA	Sidechain
151	Ca	45	DT	Sidechain
151	Ca	8	DT	Sidechain
152	Cb	11	DT	Sidechain
152	Cb	15	DT	Sidechain
152	Cb	2	DA	Sidechain
152	Cb	20	DT	Sidechain
152	Cb	24	DA	Sidechain
152	Cb	31	DC	Sidechain
152	Cb	34	DC	Sidechain
152	Cb	6	DG	Sidechain
152	Cb	7	DT	Sidechain

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Mol	Chain	Res	Type	Group
152	Cb	9	DA	Sidechain
153	Cc	1	DT	Sidechain
153	Cc	10	DT	Sidechain
153	Cc	14	DA	Sidechain
153	Cc	19	DT	Sidechain
153	Cc	2	DC	Sidechain
153	Cc	22	DA	Sidechain
154	Cd	12	DA	Sidechain
154	Cd	14	DG	Sidechain
154	Cd	16	DA	Sidechain
154	Cd	17	DC	Sidechain
154	Cd	18	DT	Sidechain
154	Cd	20	DA	Sidechain
154	Cd	24	DG	Sidechain
154	Cd	25	DT	Sidechain
155	Ce	1	DT	Sidechain
155	Ce	12	DG	Sidechain
155	Ce	17	DG	Sidechain
155	Ce	29	DG	Sidechain
155	Ce	7	DT	Sidechain
156	Cf	25	DG	Sidechain
156	Cf	26	DA	Sidechain
156	Cf	28	DG	Sidechain
156	Cf	30	DG	Sidechain
156	Cf	6	DT	Sidechain
156	Cf	8	DT	Sidechain
157	Cg	21	DT	Sidechain
157	Cg	33	DT	Sidechain
158	Ch	17	DC	Sidechain
158	Ch	30	DT	Sidechain
158	Ch	31	DG	Sidechain
158	Ch	32	DC	Sidechain
158	Ch	40	DA	Sidechain
158	Ch	5	DT	Sidechain
159	Ci	19	DT	Sidechain
159	Ci	23	DT	Sidechain
159	Ci	26	DT	Sidechain
159	Ci	38	DC	Sidechain
159	Ci	47	DG	Sidechain
159	Ci	48	DC	Sidechain
160	Cj	23	DA	Sidechain
160	Cj	24	DA	Sidechain

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Mol	Chain	Res	Type	Group
160	Cj	25	DA	Sidechain
160	Cj	35	DC	Sidechain
160	Cj	8	DA	Sidechain
161	Ck	1	DG	Sidechain
161	Ck	20	DT	Sidechain
161	Ck	31	DC	Sidechain
161	Ck	37	DA	Sidechain
161	Ck	45	DT	Sidechain
162	Cl	11	DT	Sidechain
162	Cl	12	DA	Sidechain
162	Cl	14	DC	Sidechain
162	Cl	36	DG	Sidechain
162	Cl	37	DA	Sidechain
162	Cl	40	DT	Sidechain
163	Cm	1	DA	Sidechain
163	Cm	12	DT	Sidechain
163	Cm	13	DC	Sidechain
163	Cm	19	DT	Sidechain
163	Cm	24	DA	Sidechain
163	Cm	29	DT	Sidechain
163	Cm	35	DT	Sidechain
163	Cm	37	DT	Sidechain
163	Cm	42	DT	Sidechain
163	Cm	45	DA	Sidechain
163	Cm	9	DC	Sidechain
164	Cn	11	DA	Sidechain
164	Cn	12	DC	Sidechain
164	Cn	13	DC	Sidechain
164	Cn	16	DC	Sidechain
164	Cn	19	DT	Sidechain
164	Cn	25	DG	Sidechain
164	Cn	40	DT	Sidechain
165	Co	23	DA	Sidechain
165	Co	24	DG	Sidechain
165	Co	25	DA	Sidechain
165	Co	3	DG	Sidechain
165	Co	33	DA	Sidechain
165	Co	40	DA	Sidechain
165	Co	9	DA	Sidechain
166	Cp	19	DT	Sidechain
166	Cp	2	DT	Sidechain
166	Cp	23	DA	Sidechain

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Mol	Chain	Res	Type	Group
166	Cp	24	DC	Sidechain
166	Cp	25	DA	Sidechain
166	Cp	27	DA	Sidechain
166	Cp	28	DC	Sidechain
166	Cp	36	DA	Sidechain
167	Cq	16	DG	Sidechain
167	Cq	18	DG	Sidechain
168	Cr	10	DT	Sidechain
168	Cr	14	DG	Sidechain
168	Cr	24	DG	Sidechain
168	Cr	30	DT	Sidechain
168	Cr	32	DA	Sidechain
168	Cr	5	DG	Sidechain
168	Cr	6	DT	Sidechain
169	Cs	1	DA	Sidechain
169	Cs	13	DA	Sidechain
169	Cs	22	DT	Sidechain
169	Cs	31	DC	Sidechain
169	Cs	32	DT	Sidechain
169	Cs	7	DA	Sidechain
170	Ct	1	DT	Sidechain
170	Ct	16	DG	Sidechain
170	Ct	20	DA	Sidechain
170	Ct	24	DT	Sidechain
170	Ct	27	DC	Sidechain
170	Ct	28	DT	Sidechain
170	Ct	3	DT	Sidechain
170	Ct	36	DA	Sidechain
170	Ct	39	DG	Sidechain
170	Ct	4	DT	Sidechain
170	Ct	43	DG	Sidechain
171	Cu	13	DA	Sidechain
171	Cu	19	DA	Sidechain
171	Cu	21	DT	Sidechain
171	Cu	25	DT	Sidechain
171	Cu	4	DT	Sidechain
172	Cv	1	DT	Sidechain
172	Cv	14	DA	Sidechain
172	Cv	15	DT	Sidechain
172	Cv	19	DC	Sidechain
172	Cv	20	DC	Sidechain
172	Cv	23	DA	Sidechain

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Mol	Chain	Res	Type	Group
172	Cv	26	DA	Sidechain
172	Cv	37	DT	Sidechain
172	Cv	7	DC	Sidechain
173	Cw	2	DT	Sidechain
173	Cw	20	DG	Sidechain
173	Cw	25	DA	Sidechain
173	Cw	3	DC	Sidechain
174	Cx	1	DG	Sidechain
174	Cx	10	DA	Sidechain
174	Cx	11	DG	Sidechain
174	Cx	12	DG	Sidechain
174	Cx	19	DA	Sidechain
174	Cx	7	DA	Sidechain
175	Cy	20	DA	Sidechain
175	Cy	32	DC	Sidechain
175	Cy	8	DG	Sidechain
176	Cz	15	DC	Sidechain
176	Cz	21	DC	Sidechain
176	Cz	23	DG	Sidechain
187	DA	10	DC	Sidechain
187	DA	15	DA	Sidechain
187	DA	2	DT	Sidechain
187	DA	24	DA	Sidechain
187	DA	26	DA	Sidechain
187	DA	31	DA	Sidechain
187	DA	36	DT	Sidechain
187	DA	37	DC	Sidechain
187	DA	38	DG	Sidechain
187	DA	42	DT	Sidechain
187	DA	7	DG	Sidechain
188	DB	1	DA	Sidechain
188	DB	21	DA	Sidechain
188	DB	29	DA	Sidechain
188	DB	31	DG	Sidechain
189	DC	1	DT	Sidechain
189	DC	10	DA	Sidechain
189	DC	13	DA	Sidechain
189	DC	15	DC	Sidechain
189	DC	2	DA	Sidechain
189	DC	8	DA	Sidechain
190	DD	1	DC	Sidechain
190	DD	10	DA	Sidechain

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Mol	Chain	Res	Type	Group
190	DD	13	DA	Sidechain
190	DD	17	DG	Sidechain
190	DD	27	DA	Sidechain
190	DD	29	DG	Sidechain
190	DD	36	DA	Sidechain
190	DD	41	DT	Sidechain
190	DD	43	DT	Sidechain
190	DD	5	DA	Sidechain
190	DD	7	DG	Sidechain
191	DE	1	DT	Sidechain
191	DE	40	DC	Sidechain
191	DE	44	DT	Sidechain
191	DE	9	DA	Sidechain
192	DF	11	DG	Sidechain
192	DF	13	DG	Sidechain
192	DF	17	DC	Sidechain
192	DF	19	DT	Sidechain
193	DG	10	DA	Sidechain
193	DG	2	DT	Sidechain
193	DG	25	DG	Sidechain
193	DG	31	DA	Sidechain
193	DG	33	DA	Sidechain
193	DG	35	DT	Sidechain
193	DG	37	DC	Sidechain
193	DG	45	DG	Sidechain
194	DH	11	DT	Sidechain
194	DH	12	DC	Sidechain
194	DH	30	DA	Sidechain
194	DH	31	DA	Sidechain
194	DH	4	DC	Sidechain
194	DH	9	DA	Sidechain
195	DI	18	DC	Sidechain
195	DI	25	DC	Sidechain
195	DI	5	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	164972	0	91301	0	0
2	AB	582	0	334	0	0
3	AC	984	0	542	0	0
4	AD	1094	0	600	0	0
5	AE	1217	0	685	0	0
6	AF	982	0	543	0	0
7	AG	991	0	539	0	0
8	AH	1224	0	692	0	0
9	AI	851	0	483	0	0
10	AJ	1218	0	693	0	0
11	AK	658	0	364	0	0
12	AL	815	0	458	0	0
13	AM	988	0	544	0	0
14	AN	662	0	362	0	0
15	AO	978	0	543	0	0
16	AP	817	0	449	0	0
17	AQ	914	0	517	0	0
18	AR	986	0	545	0	0
19	AS	988	0	540	0	0
20	AT	928	0	512	0	0
21	AU	977	0	542	0	0
22	AV	817	0	445	0	0
23	AW	1155	0	659	0	0
24	AX	1225	0	684	0	0
25	AY	659	0	362	0	0
26	AZ	990	0	541	0	0
27	Aa	823	0	457	0	0
28	Ab	986	0	539	0	0
29	Ac	812	0	452	0	0
30	Ad	1091	0	600	0	0
31	Ae	830	0	449	0	0
32	Af	666	0	363	0	0
33	Ag	1173	0	669	0	0
34	Ah	1233	0	686	0	0
35	Ai	979	0	544	0	0
36	Aj	969	0	544	0	0
37	Ak	652	0	361	0	0
38	Al	982	0	543	0	0
39	Am	1175	0	667	0	0
40	An	1231	0	688	0	0
41	Ao	1167	0	653	0	0
42	Ap	1217	0	693	0	0
43	Aq	985	0	541	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	Ar	752	0	419	0	0
45	As	817	0	460	0	0
46	At	899	0	498	0	0
47	Au	818	0	450	0	0
48	Av	814	0	449	0	0
49	Aw	1137	0	635	0	0
50	Ax	815	0	457	0	0
51	Ay	990	0	539	0	0
52	Az	900	0	508	0	0
53	A0	641	0	363	0	0
54	A1	992	0	541	0	0
55	A2	966	0	537	0	0
56	A3	1151	0	628	0	0
57	A4	931	0	512	0	0
58	A5	991	0	540	0	0
59	A6	655	0	363	0	0
60	A7	643	0	358	0	0
61	A8	658	0	359	0	0
62	A9	988	0	537	0	0
63	BA	918	0	506	0	0
64	BB	659	0	357	0	0
65	BC	910	0	513	0	0
66	BD	1156	0	657	0	0
67	BE	1155	0	653	0	0
68	BF	911	0	510	0	0
69	BG	807	0	451	0	0
70	BH	1156	0	661	0	0
71	BI	1156	0	657	0	0
72	BJ	918	0	515	0	0
73	BK	655	0	363	0	0
74	BL	1142	0	637	0	0
75	BM	650	0	360	0	0
76	BN	832	0	447	0	0
77	BO	974	0	539	0	0
78	BP	1175	0	664	0	0
79	BQ	1147	0	655	0	0
80	BR	995	0	543	0	0
81	BS	975	0	547	0	0
82	BT	973	0	542	0	0
83	BU	981	0	540	0	0
84	BV	1186	0	665	0	0
85	BW	1213	0	689	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
86	BX	657	0	359	0	0
87	BY	831	0	450	0	0
88	BZ	818	0	449	0	0
89	Ba	1002	0	539	0	0
90	Bb	971	0	541	0	0
91	Bc	658	0	359	0	0
92	Bd	992	0	538	0	0
93	Be	976	0	544	0	0
94	Bf	986	0	540	0	0
95	Bg	812	0	454	0	0
96	Bh	1157	0	632	0	0
97	Bi	805	0	458	0	0
98	Bj	653	0	361	0	0
99	Bk	660	0	363	0	0
100	Bl	974	0	540	0	0
101	Bm	1148	0	635	0	0
102	Bn	971	0	543	0	0
103	Bo	994	0	537	0	0
104	Bp	822	0	453	0	0
105	Bq	986	0	547	0	0
106	Br	992	0	541	0	0
107	Bs	653	0	359	0	0
108	Bt	823	0	450	0	0
109	Bu	819	0	450	0	0
110	Bv	812	0	451	0	0
111	Bw	1216	0	692	0	0
112	Bx	919	0	509	0	0
113	By	823	0	445	0	0
114	Bz	654	0	366	0	0
115	B0	1210	0	693	0	0
116	B1	1213	0	692	0	0
117	B2	823	0	450	0	0
118	B3	664	0	358	0	0
119	B4	663	0	360	0	0
120	B5	1223	0	684	0	0
121	B6	1077	0	599	0	0
122	B7	982	0	538	0	0
123	B8	658	0	359	0	0
124	B9	975	0	539	0	0
125	CA	977	0	541	0	0
126	CB	1223	0	686	0	0
127	CC	754	0	420	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
128	CD	1160	0	662	0	0
129	CE	667	0	358	0	0
130	CF	822	0	451	0	0
131	CG	658	0	363	0	0
132	CH	1087	0	599	0	0
133	CI	646	0	367	0	0
134	CJ	1159	0	658	0	0
135	CK	650	0	363	0	0
136	CL	819	0	448	0	0
137	CM	664	0	360	0	0
138	CN	1153	0	634	0	0
139	CO	979	0	538	0	0
140	CP	992	0	545	0	0
141	CQ	1162	0	657	0	0
142	CR	1225	0	690	0	0
143	CS	968	0	549	0	0
144	CT	1158	0	634	0	0
145	CU	759	0	418	0	0
146	CV	656	0	362	0	0
147	CW	652	0	363	0	0
148	CX	1159	0	660	0	0
149	CY	1211	0	695	0	0
150	CZ	981	0	547	0	0
151	Ca	984	0	541	0	0
152	Cb	821	0	450	0	0
153	Cc	655	0	363	0	0
154	Cd	831	0	446	0	0
155	Ce	829	0	455	0	0
156	Cf	657	0	366	0	0
157	Cg	817	0	453	0	0
158	Ch	817	0	455	0	0
159	Ci	971	0	542	0	0
160	Cj	817	0	452	0	0
161	Ck	985	0	549	0	0
162	Cl	821	0	451	0	0
163	Cm	980	0	546	0	0
164	Cn	819	0	454	0	0
165	Co	811	0	450	0	0
166	Cp	752	0	419	0	0
167	Cq	754	0	416	0	0
168	Cr	832	0	453	0	0
169	Cs	822	0	451	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
170	Ct	920	0	513	0	0
171	Cu	757	0	422	0	0
172	Cv	810	0	456	0	0
173	Cw	825	0	449	0	0
174	Cx	652	0	358	0	0
175	Cy	652	0	357	0	0
176	Cz	667	0	361	0	0
177	C0	1148	0	650	0	0
178	C1	1166	0	659	0	0
179	C2	657	0	363	0	0
180	C3	979	0	538	0	0
181	C4	977	0	544	0	0
182	C5	976	0	547	0	0
183	C6	997	0	540	0	0
184	C7	803	0	456	0	0
185	C8	991	0	540	0	0
186	C9	1158	0	657	0	0
187	DA	917	0	511	0	0
188	DB	646	0	361	0	0
189	DC	832	0	446	0	0
190	DD	910	0	509	0	0
191	DE	982	0	544	0	0
192	DF	817	0	450	0	0
193	DG	990	0	542	0	0
194	DH	654	0	358	0	0
195	DI	653	0	364	0	0
All	All	342569	0	189904	0	0

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

There are no clashes within the asymmetric unit.

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

There are no protein molecules in this entry.

5.3.2 Protein sidechains [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.

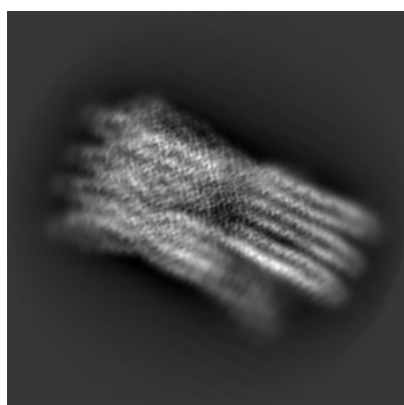
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11379. These allow visual inspection of the internal detail of the map and identification of artifacts.

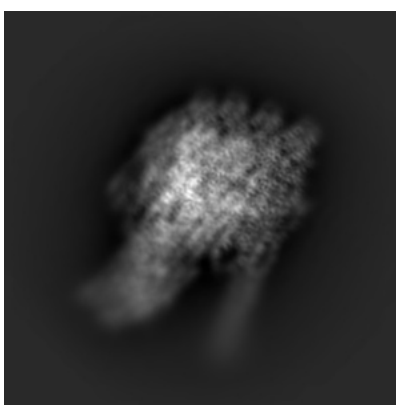
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

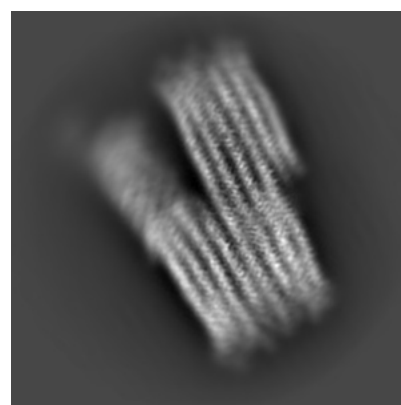
6.1.1 Primary map



X



Y

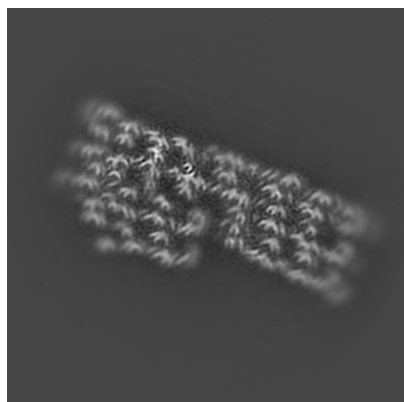


Z

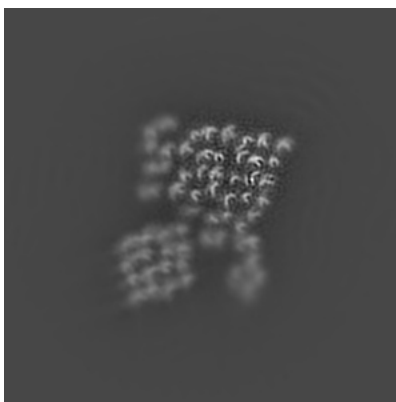
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

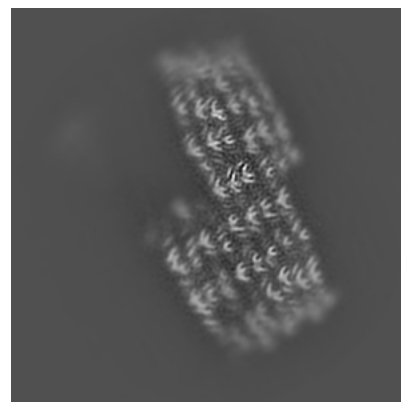
6.2.1 Primary map



X Index: 232



Y Index: 232

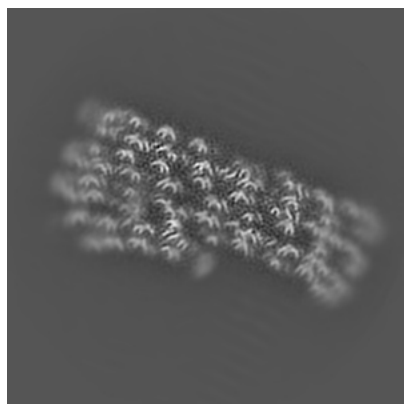


Z Index: 232

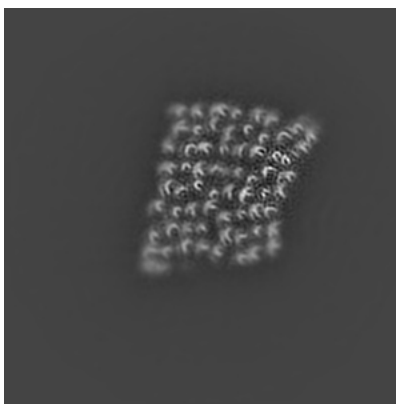
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

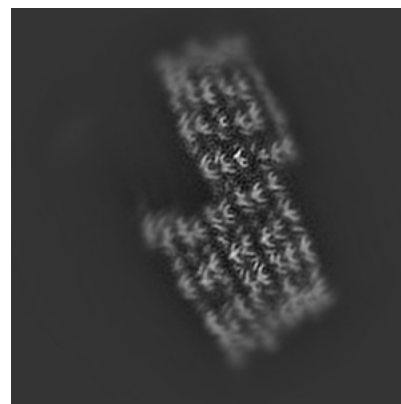
6.3.1 Primary map



X Index: 247



Y Index: 179

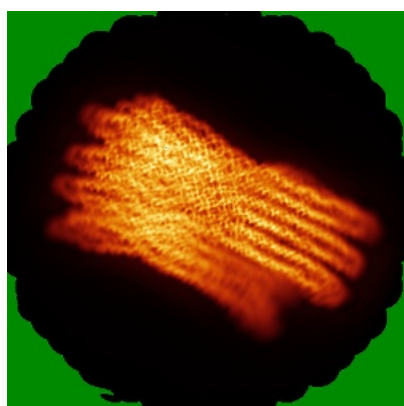


Z Index: 222

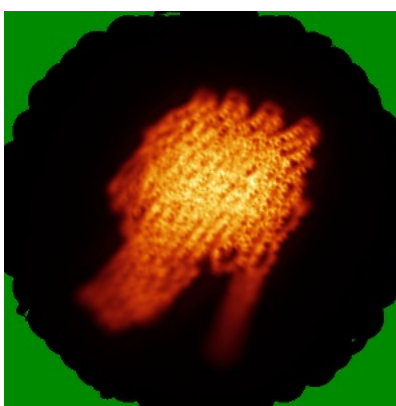
The images above show the largest variance slices of the map in three orthogonal directions.

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

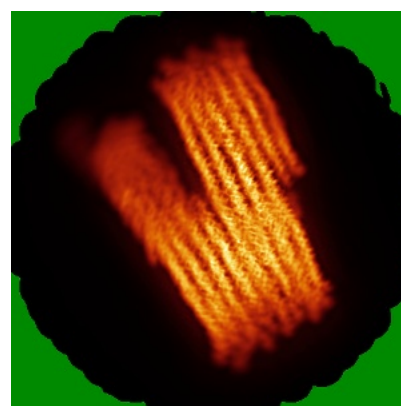
6.4.1 Primary map



X



Y

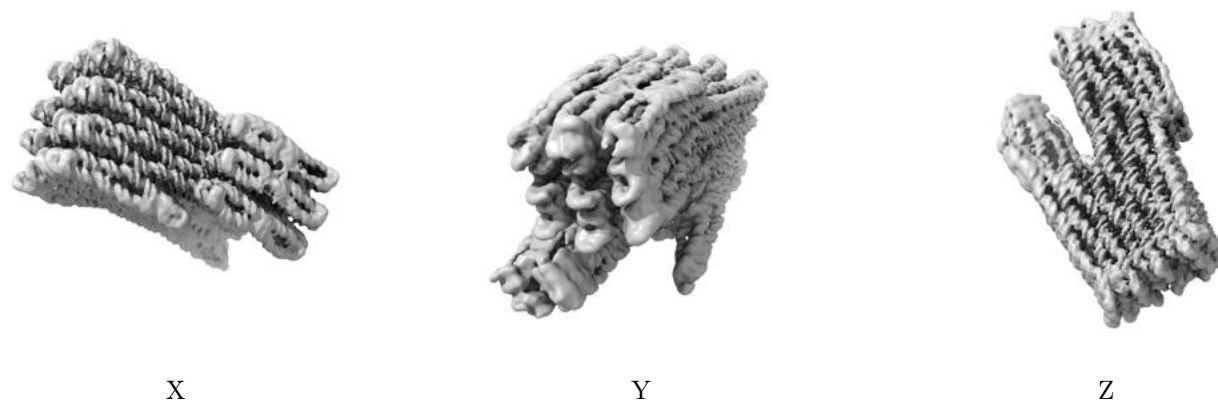


Z

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

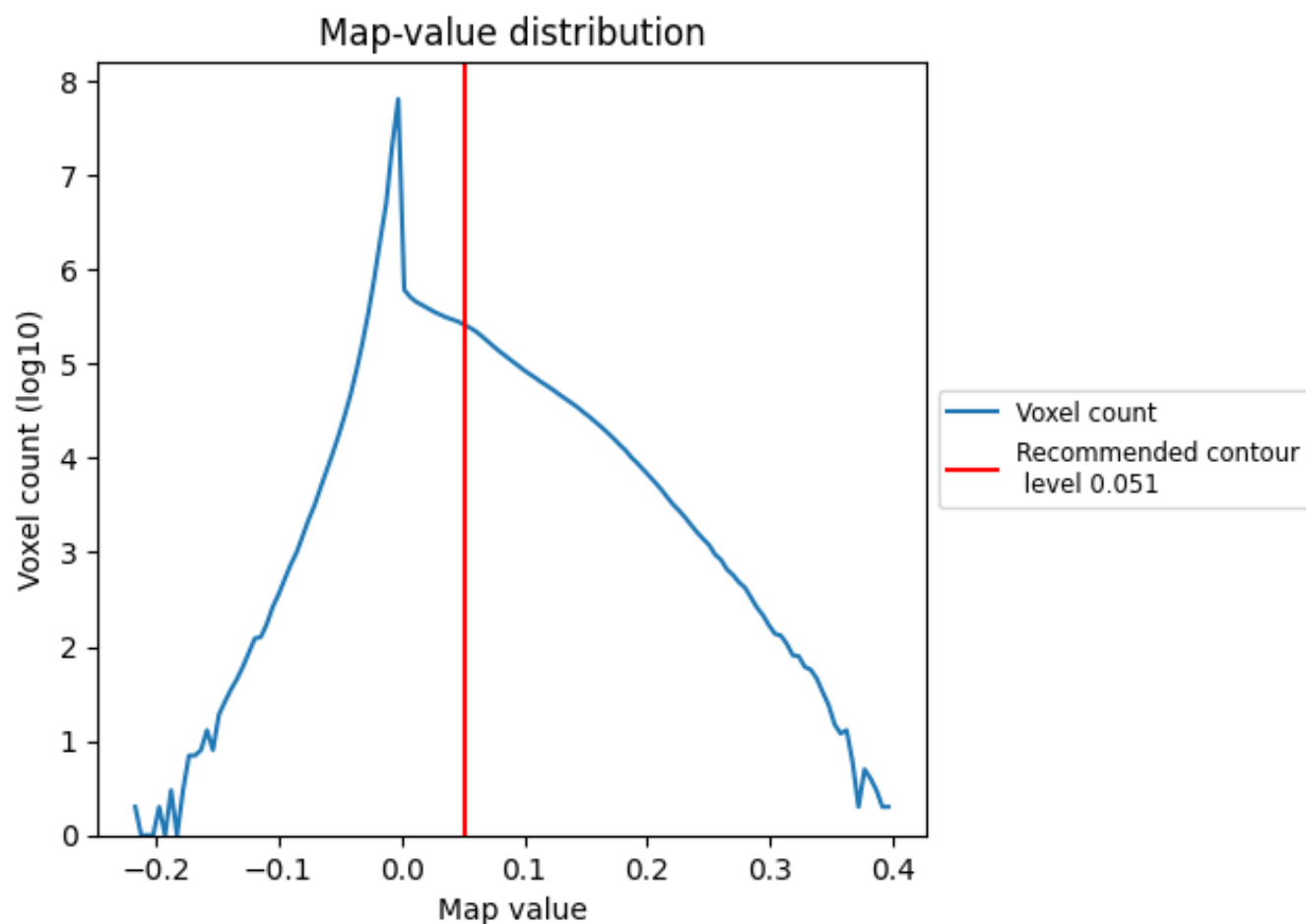
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

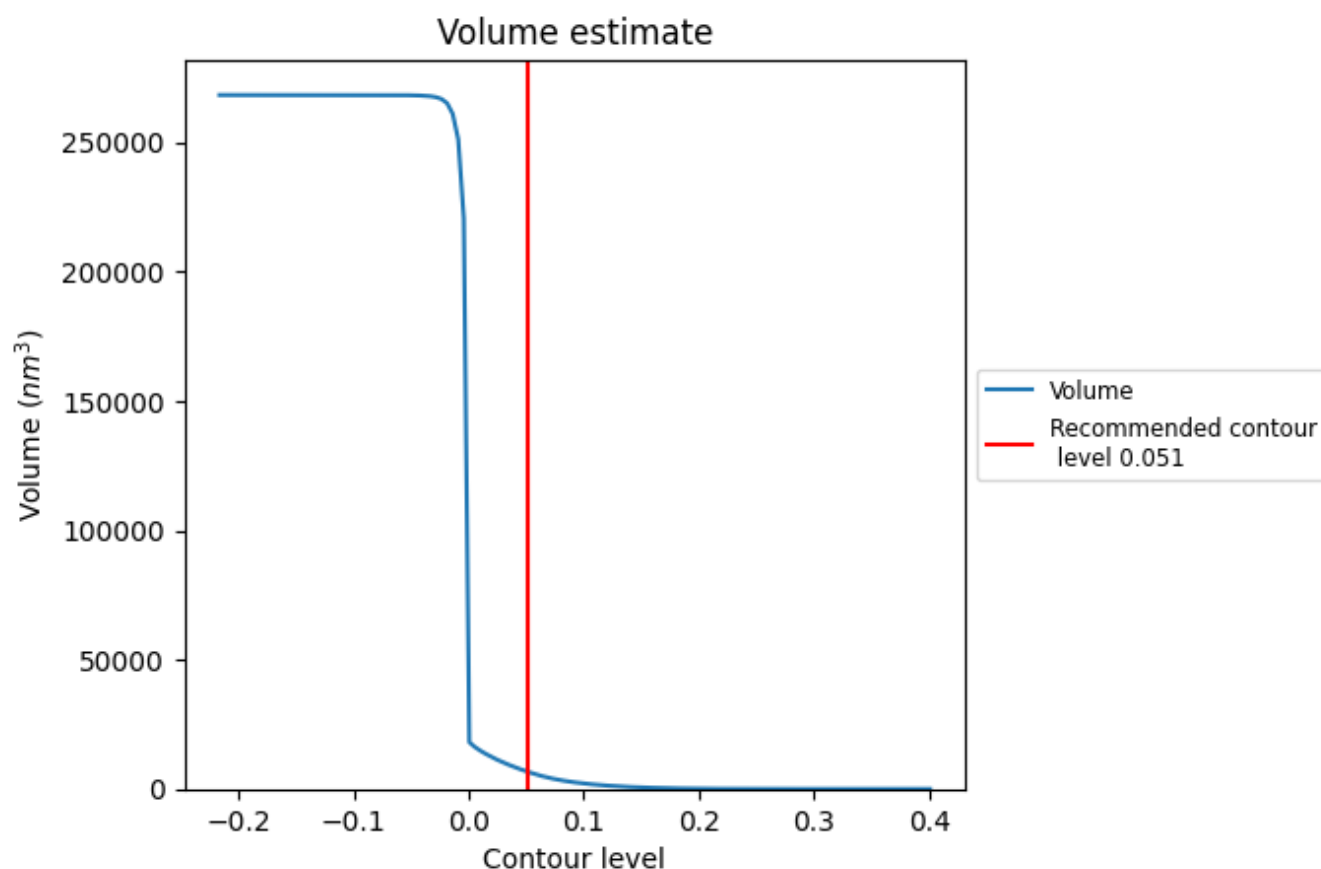
This section contains the results of statistical analysis of the map.

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.

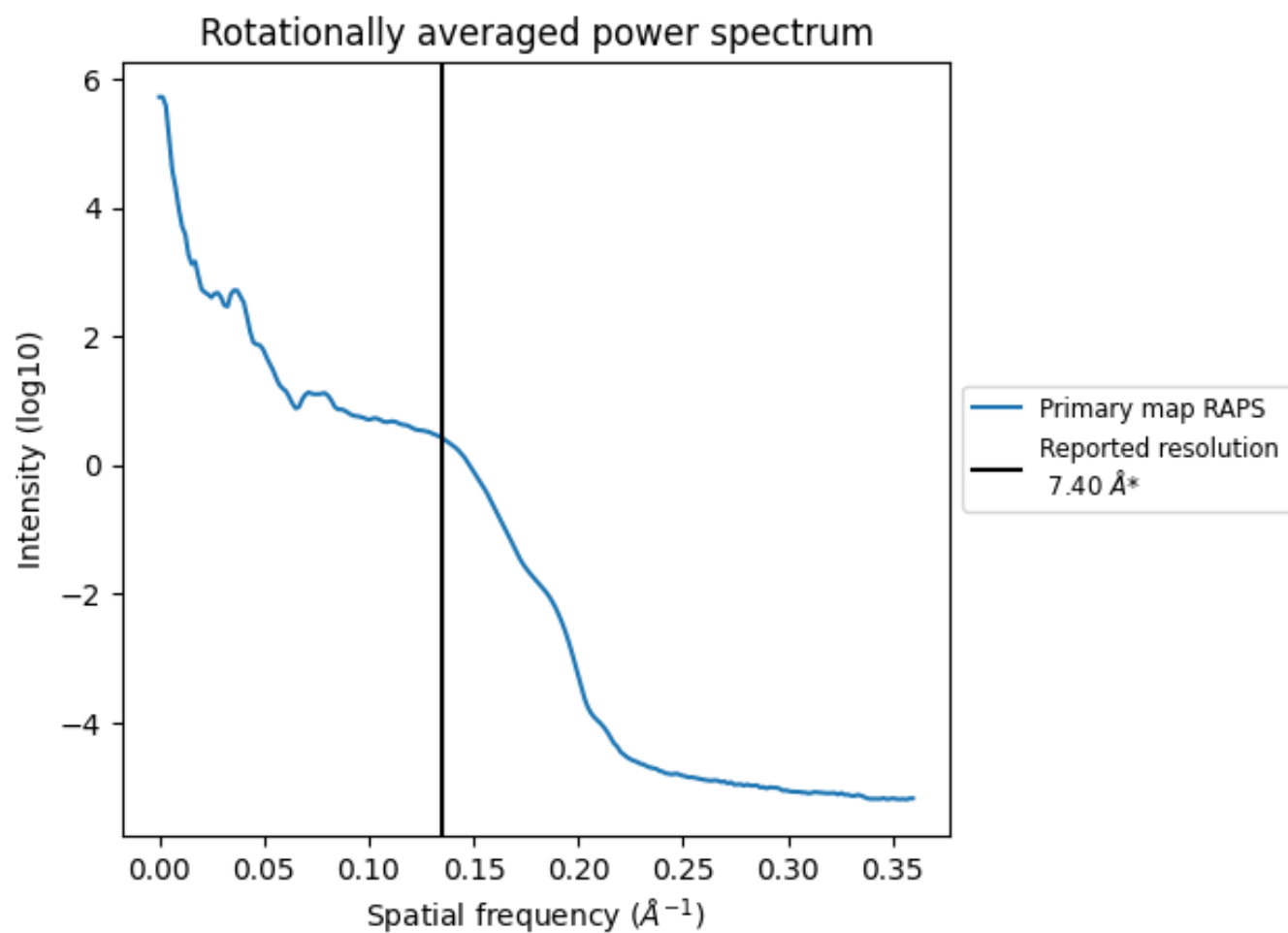
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 6695 nm³; this corresponds to an approximate mass of 6048 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

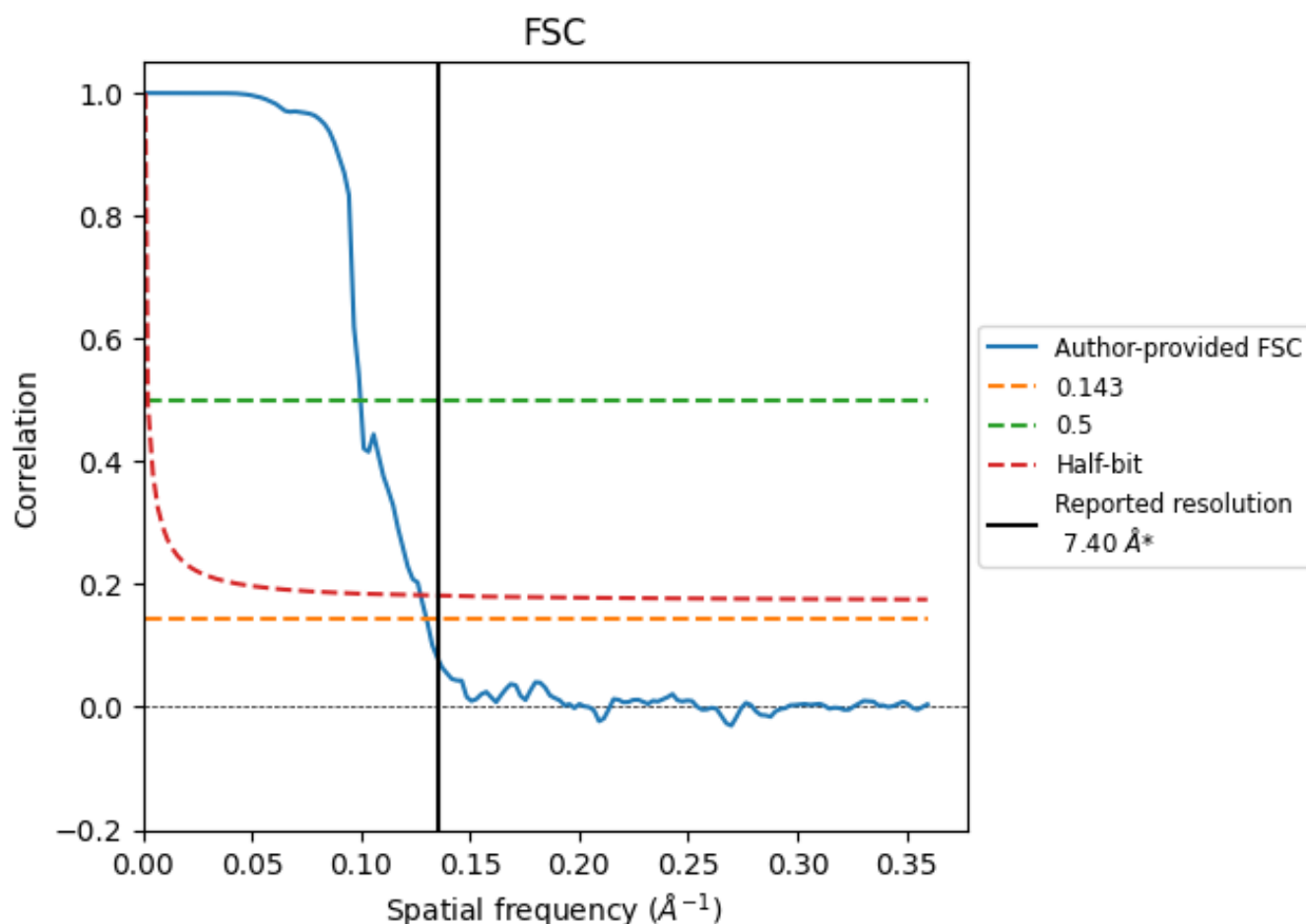


*Reported resolution corresponds to spatial frequency of 0.135 Å⁻¹

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](#)

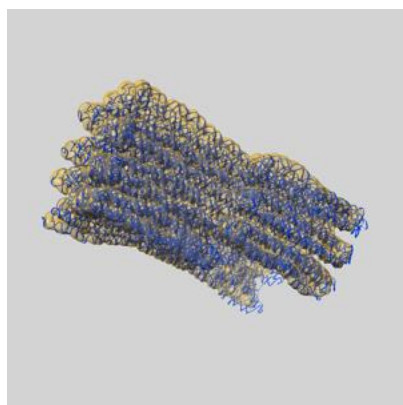
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.40	-	-
Author-provided FSC curve	7.69	10.03	7.86
Unmasked-calculated*	-	-	-

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

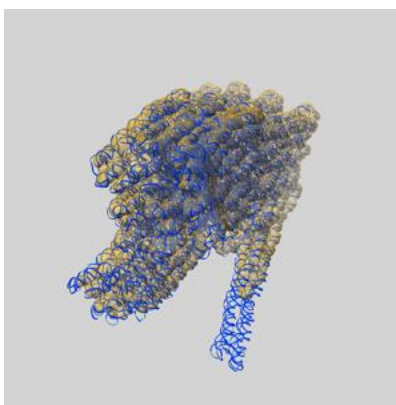
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11379 and PDB model 7ARV. Per-residue inclusion information can be found in section 3 on page 39.

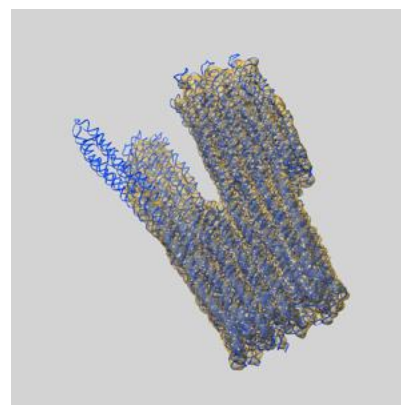
9.1 Map-model overlay [i](#)



X



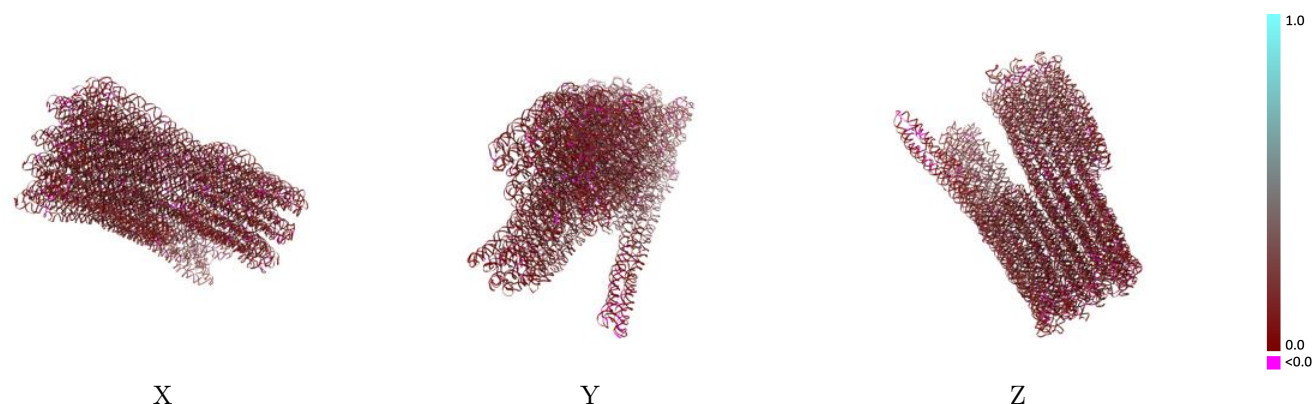
Y



Z

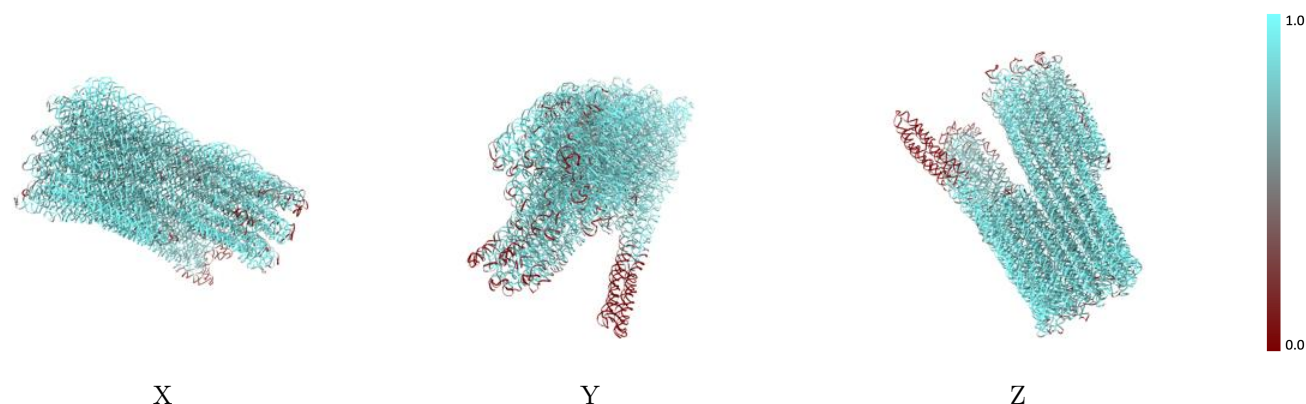
The images above show the 3D surface view of the map at the recommended contour level 0.051 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



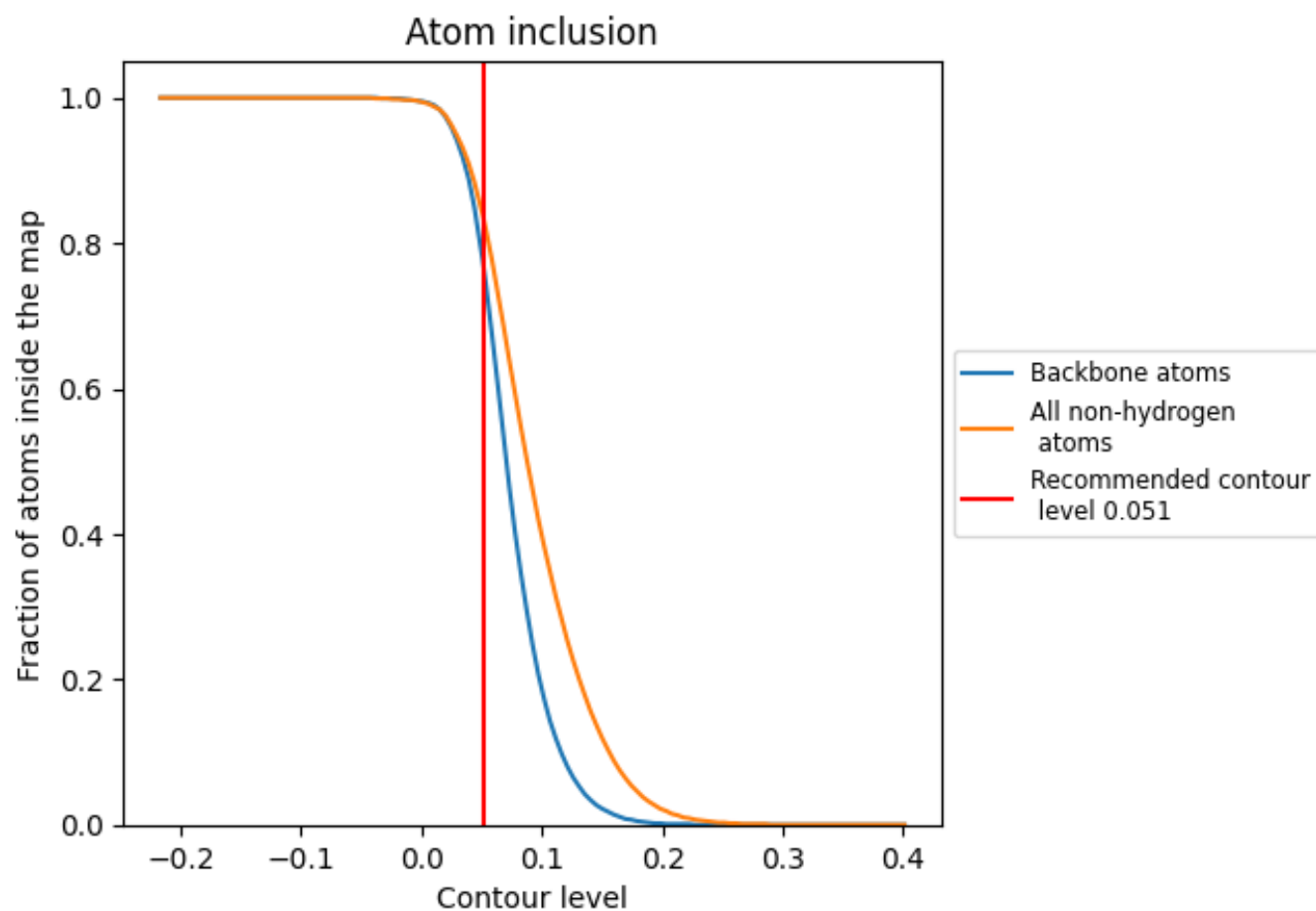
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.051).

9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 84% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.051) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8380	 0.1400
A0	 0.8550	 0.1250
A1	 0.8420	 0.1350
A2	 0.7910	 0.1050
A3	 0.8770	 0.1380
A4	 0.9080	 0.1430
A5	 0.9220	 0.1410
A6	 0.8290	 0.1290
A7	 0.9240	 0.1500
A8	 0.8970	 0.1500
A9	 0.8890	 0.1580
AA	 0.8580	 0.1440
AB	 0.6410	 0.1130
AC	 0.8480	 0.1330
AD	 0.9130	 0.1160
AE	 0.4170	 0.0720
AF	 0.8500	 0.1350
AG	 0.8520	 0.1320
AH	 0.6680	 0.0900
AI	 0.7320	 0.1060
AJ	 0.6590	 0.0950
AK	 0.9010	 0.1330
AL	 0.8860	 0.1230
AM	 0.9240	 0.1490
AN	 0.8910	 0.1610
AO	 0.8930	 0.1330
AP	 0.7480	 0.1310
AQ	 0.8080	 0.1340
AR	 0.7150	 0.1330
AS	 0.7970	 0.1190
AT	 0.8100	 0.1200
AU	 0.9000	 0.1440
AV	 0.8870	 0.1470
AW	 0.8930	 0.1000
AX	 0.5530	 0.0770



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Chain	Atom inclusion	Q-score
AY	 0.8760	 0.1660
AZ	 0.9360	 0.1560
Aa	 0.8720	 0.1230
Ab	 0.9070	 0.1490
Ac	 0.8570	 0.1400
Ad	 0.9040	 0.1360
Ae	 0.9190	 0.1140
Af	 0.8860	 0.1400
Ag	 0.8720	 0.1170
Ah	 0.6580	 0.1130
Ai	 0.8100	 0.1550
Aj	 0.8730	 0.1360
Ak	 0.8860	 0.1490
Al	 0.9040	 0.1500
Am	 0.8710	 0.1120
An	 0.6820	 0.1130
Ao	 0.8590	 0.1130
Ap	 0.6560	 0.1070
Aq	 0.9250	 0.1520
Ar	 0.7370	 0.1160
As	 0.9110	 0.1510
At	 0.9330	 0.1460
Au	 0.8860	 0.1290
Av	 0.8980	 0.1450
Aw	 0.8290	 0.1380
Ax	 0.8750	 0.1450
Ay	 0.9010	 0.1530
Az	 0.8720	 0.1260
B0	 0.7980	 0.1190
B1	 0.6210	 0.1200
B2	 0.8810	 0.1560
B3	 0.8790	 0.1700
B4	 0.8750	 0.1730
B5	 0.8070	 0.1210
B6	 0.8220	 0.1520
B7	 0.9160	 0.1540
B8	 0.9010	 0.1820
B9	 0.9190	 0.1720
BA	 0.9480	 0.1560
BB	 0.9130	 0.1510
BC	 0.8650	 0.1270
BD	 0.8980	 0.1340

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Chain	Atom inclusion	Q-score
BE	 0.6850	 0.1030
BF	 0.8210	 0.1210
BG	 0.8910	 0.1630
BH	 0.7980	 0.1220
BI	 0.7050	 0.1170
BJ	 0.8130	 0.1590
BK	 0.8380	 0.1540
BL	 0.9190	 0.1460
BM	 0.8550	 0.1250
BN	 0.8930	 0.1460
BO	 0.8740	 0.1470
BP	 0.8540	 0.1230
BQ	 0.6820	 0.1040
BR	 0.8590	 0.1320
BS	 0.8860	 0.1560
BT	 0.9170	 0.1510
BU	 0.8910	 0.1610
BV	 0.8380	 0.1220
BW	 0.7240	 0.1110
BX	 0.9210	 0.1620
BY	 0.9250	 0.1430
BZ	 0.9310	 0.1660
Ba	 0.8800	 0.1400
Bb	 0.8580	 0.1450
Bc	 0.8130	 0.1300
Bd	 0.8590	 0.1450
Be	 0.8320	 0.1450
Bf	 0.8510	 0.1520
Bg	 0.9190	 0.1720
Bh	 0.9170	 0.1450
Bi	 0.9220	 0.1330
Bj	 0.8210	 0.1380
Bk	 0.9380	 0.1790
Bl	 0.8880	 0.1470
Bm	 0.9480	 0.1570
Bn	 0.9050	 0.1410
Bo	 0.9350	 0.1550
Bp	 0.8710	 0.1410
Bq	 0.8340	 0.1290
Br	 0.8700	 0.1520
Bs	 0.8550	 0.1590
Bt	 0.9470	 0.1650

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Chain	Atom inclusion	Q-score
Bu	 0.8960	 0.1400
Bv	 0.8650	 0.1460
Bw	 0.8650	 0.1180
Bx	 0.8460	 0.1460
By	 0.8970	 0.1590
Bz	 0.8320	 0.1490
C0	 0.8320	 0.1070
C1	 0.0000	 0.0300
C2	 0.9350	 0.1800
C3	 0.9200	 0.1710
C4	 0.9230	 0.1580
C5	 0.9580	 0.1710
C6	 0.9090	 0.1650
C7	 0.8780	 0.1600
C8	 0.8820	 0.1660
C9	 0.8650	 0.1280
CA	 0.8620	 0.1670
CB	 0.6570	 0.1090
CC	 0.8320	 0.1460
CD	 0.2470	 0.0510
CE	 0.9250	 0.1660
CF	 0.9150	 0.1600
CG	 0.8040	 0.1370
CH	 0.8970	 0.1760
CI	 0.9230	 0.1710
CJ	 0.3240	 0.0600
CK	 0.8480	 0.1330
CL	 0.8840	 0.1640
CM	 0.9280	 0.1890
CN	 0.6500	 0.1250
CO	 0.8460	 0.1480
CP	 0.8510	 0.1460
CQ	 0.8120	 0.1190
CR	 0.4620	 0.0650
CS	 0.8410	 0.1460
CT	 0.8560	 0.1630
CU	 0.9000	 0.1630
CV	 0.8800	 0.1640
CW	 0.9480	 0.1740
CX	 0.7900	 0.1210
CY	 0.5070	 0.0830
CZ	 0.8880	 0.1460

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Chain	Atom inclusion	Q-score
Ca	 0.9060	 0.1390
Cb	 0.9390	 0.1670
Cc	 0.7940	 0.1270
Cd	 0.9410	 0.1670
Ce	 0.8950	 0.1500
Cf	 0.8920	 0.1430
Cg	 0.9360	 0.1670
Ch	 0.9400	 0.1680
Ci	 0.9230	 0.1670
Cj	 0.9580	 0.1670
Ck	 0.9360	 0.1530
Cl	 0.9440	 0.1540
Cm	 0.9080	 0.1700
Cn	 0.8860	 0.1650
Co	 0.7450	 0.1320
Cp	 0.8380	 0.1520
Cq	 0.7240	 0.1270
Cr	 0.9150	 0.1890
Cs	 0.8640	 0.1220
Ct	 0.9170	 0.1710
Cu	 0.6530	 0.1260
Cv	 0.9490	 0.1760
Cw	 0.8900	 0.1620
Cx	 0.8850	 0.1560
Cy	 0.8740	 0.1580
Cz	 0.0000	 0.0480
DA	 0.8440	 0.1520
DB	 0.9520	 0.1760
DC	 0.8800	 0.1530
DD	 0.0000	 0.0360
DE	 0.0610	 0.0430
DF	 0.6080	 0.1130
DG	 0.7360	 0.1190
DH	 0.9390	 0.1710
DI	 0.9590	 0.1760