



Full wwPDB EM Validation Report ⓘ

Mar 21, 2026 – 06:43 PM UTC

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

This is a 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:

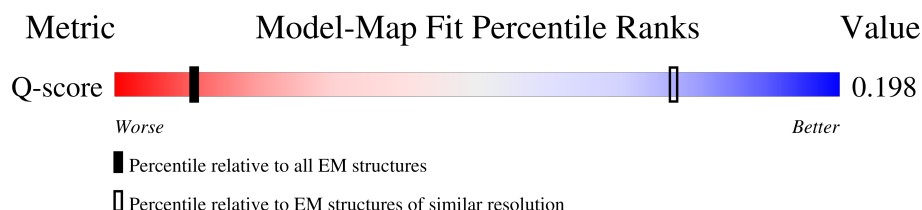
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

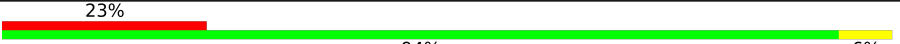
The reported resolution of this entry is 7.40 Å.

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	7249	 81% 17% .
2	AB	40	 75% 25% .
3	AC	31	 81% 16% .
4	AD	40	 82% 18% .
5	AE	48	 79% 17% .
6	AF	31	 94% 6% .
7	AG	40	 88% 10% .
8	AH	31	 84% 13% .
9	AI	45	 82% 18% .
10	AJ	40	 78% 20% .

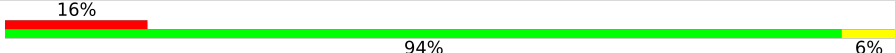
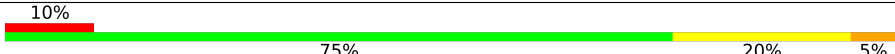
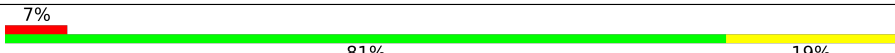
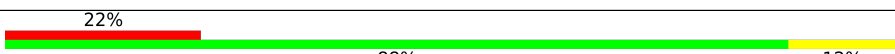
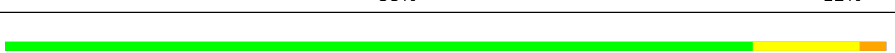
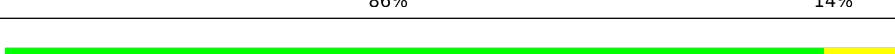
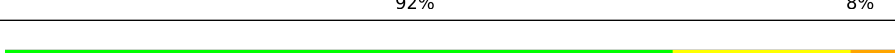
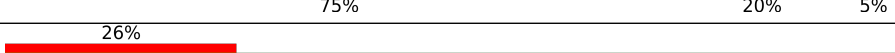
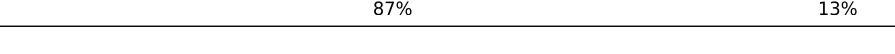
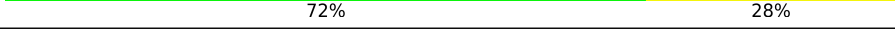
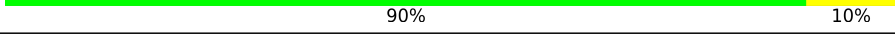
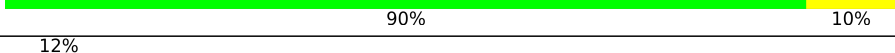
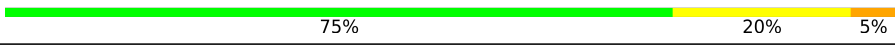
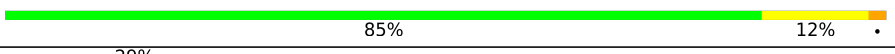
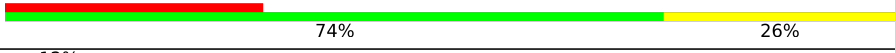
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Mol	Chain	Length	Quality of chain
11	AK	45	
12	AL	36	
13	AM	45	
14	AN	40	
15	AO	40	
16	AP	36	
17	AQ	45	
18	AR	34	
19	AS	36	
20	AT	34	
21	AU	34	
22	AV	34	
23	AW	32	
24	AX	42	
25	AY	40	
26	AZ	48	
27	Aa	40	
28	Ab	37	
29	Ac	50	
30	Ad	40	
31	Ae	37	
32	Af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

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

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

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

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

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

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Mol	Chain	Length	Quality of chain
161	Ck	44	
162	Cl	40	
163	Cm	48	
164	Cn	32	
165	Co	44	
166	Cp	32	
167	Cq	40	
168	Cr	50	
169	Cs	40	
170	Ct	40	
171	Cu	40	
172	Cv	40	
173	Cw	42	
174	Cx	50	
175	Cy	42	
176	Cz	40	
177	C0	48	
178	C1	40	
179	C2	40	
180	C3	31	
181	C4	40	
182	C5	40	
183	C6	45	
184	C7	34	
185	C8	48	

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

2 Entry composition

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

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

- Molecule 1 is a DNA chain called SCAFFOLD STRAND.

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

- Molecule 2 is a DNA chain called STAPLE STRAND.

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

- Molecule 3 is a DNA chain called STAPLE STRAND.

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

- Molecule 4 is a DNA chain called STAPLE STRAND.

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

- Molecule 5 is a DNA chain called STAPLE STRAND.

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

- Molecule 6 is a DNA chain called STAPLE STRAND.

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

- Molecule 7 is a DNA chain called STAPLE STRAND.

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

- Molecule 8 is a DNA chain called STAPLE STRAND.

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

- Molecule 9 is a DNA chain called STAPLE STRAND.

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

- Molecule 10 is a DNA chain called STAPLE STRAND.

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

- Molecule 11 is a DNA chain called STAPLE STRAND.

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

- Molecule 12 is a DNA chain called STAPLE STRAND.

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

- Molecule 13 is a DNA chain called STAPLE STRAND.

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

- Molecule 14 is a DNA chain called STAPLE STRAND.

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

- Molecule 15 is a DNA chain called STAPLE STRAND.

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

- Molecule 16 is a DNA chain called STAPLE STRAND.

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

- Molecule 17 is a DNA chain called STAPLE STRAND.

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

- Molecule 18 is a DNA chain called STAPLE STRAND.

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

- Molecule 19 is a DNA chain called STAPLE STRAND.

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

- Molecule 20 is a DNA chain called STAPLE STRAND.

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

- Molecule 21 is a DNA chain called STAPLE STRAND.

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

- Molecule 22 is a DNA chain called STAPLE STRAND.

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

- Molecule 23 is a DNA chain called STAPLE STRAND.

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

- Molecule 24 is a DNA chain called STAPLE STRAND.

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

- Molecule 25 is a DNA chain called STAPLE STRAND.

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

- Molecule 26 is a DNA chain called STAPLE STRAND.

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

- Molecule 27 is a DNA chain called STAPLE STRAND.

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

- Molecule 28 is a DNA chain called STAPLE STRAND.

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

- Molecule 29 is a DNA chain called STAPLE STRAND.

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

- Molecule 30 is a DNA chain called STAPLE STRAND.

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

- Molecule 31 is a DNA chain called STAPLE STRAND.

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

- Molecule 32 is a DNA chain called STAPLE STRAND.

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

- Molecule 33 is a DNA chain called STAPLE STRAND.

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

- Molecule 34 is a DNA chain called STAPLE STRAND.

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

- Molecule 35 is a DNA chain called STAPLE STRAND.

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

- Molecule 36 is a DNA chain called STAPLE STRAND.

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

- Molecule 37 is a DNA chain called STAPLE STRAND.

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

- Molecule 38 is a DNA chain called STAPLE STRAND.

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

- Molecule 39 is a DNA chain called STAPLE STRAND.

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

- Molecule 40 is a DNA chain called STAPLE STRAND.

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

- Molecule 41 is a DNA chain called STAPLE STRAND.

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

- Molecule 42 is a DNA chain called STAPLE STRAND.

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

- Molecule 43 is a DNA chain called STAPLE STRAND.

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

- Molecule 44 is a DNA chain called STAPLE STRAND.

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

- Molecule 45 is a DNA chain called STAPLE STRAND.

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

- Molecule 46 is a DNA chain called STAPLE STRAND.

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

- Molecule 47 is a DNA chain called STAPLE STRAND.

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

- Molecule 48 is a DNA chain called STAPLE STRAND.

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

- Molecule 49 is a DNA chain called STAPLE STRAND.

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

- Molecule 50 is a DNA chain called STAPLE STRAND.

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

- Molecule 51 is a DNA chain called STAPLE STRAND.

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

- Molecule 52 is a DNA chain called STAPLE STRAND.

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

- Molecule 53 is a DNA chain called STAPLE STRAND.

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

- Molecule 54 is a DNA chain called STAPLE STRAND.

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

- Molecule 55 is a DNA chain called STAPLE STRAND.

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

- Molecule 56 is a DNA chain called STAPLE STRAND.

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

- Molecule 57 is a DNA chain called STAPLE STRAND.

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

- Molecule 58 is a DNA chain called STAPLE STRAND.

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

- Molecule 59 is a DNA chain called STAPLE STRAND.

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

- Molecule 60 is a DNA chain called STAPLE STRAND.

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

- Molecule 61 is a DNA chain called STAPLE STRAND.

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

- Molecule 62 is a DNA chain called STAPLE STRAND.

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

- Molecule 63 is a DNA chain called STAPLE STRAND.

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

- Molecule 64 is a DNA chain called STAPLE STRAND.

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

- Molecule 65 is a DNA chain called STAPLE STRAND.

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

- Molecule 66 is a DNA chain called STAPLE STRAND.

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

- Molecule 67 is a DNA chain called STAPLE STRAND.

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

- Molecule 68 is a DNA chain called STAPLE STRAND.

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

- Molecule 69 is a DNA chain called STAPLE STRAND.

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

- Molecule 70 is a DNA chain called STAPLE STRAND.

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

- Molecule 71 is a DNA chain called STAPLE STRAND.

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

- Molecule 72 is a DNA chain called STAPLE STRAND.

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

- Molecule 73 is a DNA chain called STAPLE STRAND.

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

- Molecule 74 is a DNA chain called STAPLE STRAND.

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

- Molecule 75 is a DNA chain called STAPLE STRAND.

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

- Molecule 76 is a DNA chain called STAPLE STRAND.

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

- Molecule 77 is a DNA chain called STAPLE STRAND.

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

- Molecule 78 is a DNA chain called STAPLE STRAND.

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

- Molecule 79 is a DNA chain called STAPLE STRAND.

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

- Molecule 80 is a DNA chain called STAPLE STRAND.

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

- Molecule 81 is a DNA chain called STAPLE STRAND.

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

- Molecule 82 is a DNA chain called STAPLE STRAND.

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

- Molecule 83 is a DNA chain called STAPLE STRAND.

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

- Molecule 84 is a DNA chain called STAPLE STRAND.

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

- Molecule 85 is a DNA chain called STAPLE STRAND.

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

- Molecule 86 is a DNA chain called STAPLE STRAND.

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

- Molecule 87 is a DNA chain called STAPLE STRAND.

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

- Molecule 88 is a DNA chain called STAPLE STRAND.

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

- Molecule 89 is a DNA chain called STAPLE STRAND.

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

- Molecule 90 is a DNA chain called STAPLE STRAND.

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

- Molecule 91 is a DNA chain called STAPLE STRAND.

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

- Molecule 92 is a DNA chain called STAPLE STRAND.

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

- Molecule 93 is a DNA chain called STAPLE STRAND.

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

- Molecule 94 is a DNA chain called STAPLE STRAND.

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

- Molecule 95 is a DNA chain called STAPLE STRAND.

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

- Molecule 96 is a DNA chain called STAPLE STRAND.

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

- Molecule 97 is a DNA chain called STAPLE STRAND.

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

- Molecule 98 is a DNA chain called STAPLE STRAND.

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

- Molecule 99 is a DNA chain called STAPLE STRAND.

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

- Molecule 100 is a DNA chain called STAPLE STRAND.

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

- Molecule 101 is a DNA chain called STAPLE STRAND.

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

- Molecule 102 is a DNA chain called STAPLE STRAND.

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

- Molecule 103 is a DNA chain called STAPLE STRAND.

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

- Molecule 104 is a DNA chain called STAPLE STRAND.

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

- Molecule 105 is a DNA chain called STAPLE STRAND.

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

- Molecule 106 is a DNA chain called STAPLE STRAND.

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

- Molecule 107 is a DNA chain called STAPLE STRAND.

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

- Molecule 108 is a DNA chain called STAPLE STRAND.

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

- Molecule 109 is a DNA chain called STAPLE STRAND.

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

- Molecule 110 is a DNA chain called STAPLE STRAND.

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

- Molecule 111 is a DNA chain called STAPLE STRAND.

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

- Molecule 112 is a DNA chain called STAPLE STRAND.

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

- Molecule 113 is a DNA chain called STAPLE STRAND.

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

- Molecule 114 is a DNA chain called STAPLE STRAND.

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

- Molecule 115 is a DNA chain called STAPLE STRAND.

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

- Molecule 116 is a DNA chain called STAPLE STRAND.

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

- Molecule 117 is a DNA chain called STAPLE STRAND.

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

- Molecule 118 is a DNA chain called STAPLE STRAND.

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

- Molecule 119 is a DNA chain called STAPLE STRAND.

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

- Molecule 120 is a DNA chain called STAPLE STRAND.

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

- Molecule 121 is a DNA chain called STAPLE STRAND.

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

- Molecule 122 is a DNA chain called STAPLE STRAND.

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

- Molecule 123 is a DNA chain called STAPLE STRAND.

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

- Molecule 124 is a DNA chain called STAPLE STRAND.

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

- Molecule 125 is a DNA chain called STAPLE STRAND.

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

- Molecule 126 is a DNA chain called STAPLE STRAND.

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

- Molecule 127 is a DNA chain called STAPLE STRAND.

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

- Molecule 128 is a DNA chain called STAPLE STRAND.

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

- Molecule 129 is a DNA chain called STAPLE STRAND.

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

- Molecule 130 is a DNA chain called STAPLE STRAND.

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

- Molecule 131 is a DNA chain called STAPLE STRAND.

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

- Molecule 132 is a DNA chain called STAPLE STRAND.

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

- Molecule 133 is a DNA chain called STAPLE STRAND.

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

- Molecule 134 is a DNA chain called STAPLE STRAND.

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

- Molecule 135 is a DNA chain called STAPLE STRAND.

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

- Molecule 136 is a DNA chain called STAPLE STRAND.

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

- Molecule 137 is a DNA chain called STAPLE STRAND.

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

- Molecule 138 is a DNA chain called STAPLE STRAND.

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

- Molecule 139 is a DNA chain called STAPLE STRAND.

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

- Molecule 140 is a DNA chain called STAPLE STRAND.

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

- Molecule 141 is a DNA chain called STAPLE STRAND.

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

- Molecule 142 is a DNA chain called STAPLE STRAND.

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

- Molecule 143 is a DNA chain called STAPLE STRAND.

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

- Molecule 144 is a DNA chain called STAPLE STRAND.

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

- Molecule 145 is a DNA chain called STAPLE STRAND.

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

- Molecule 146 is a DNA chain called STAPLE STRAND.

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

- Molecule 147 is a DNA chain called STAPLE STRAND.

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

- Molecule 148 is a DNA chain called STAPLE STRAND.

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

- Molecule 149 is a DNA chain called STAPLE STRAND.

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

- Molecule 150 is a DNA chain called STAPLE STRAND.

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

- Molecule 151 is a DNA chain called STAPLE STRAND.

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

- Molecule 152 is a DNA chain called STAPLE STRAND.

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

- Molecule 153 is a DNA chain called STAPLE STRAND.

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

- Molecule 154 is a DNA chain called STAPLE STRAND.

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

- Molecule 155 is a DNA chain called STAPLE STRAND.

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

- Molecule 156 is a DNA chain called STAPLE STRAND.

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

- Molecule 157 is a DNA chain called STAPLE STRAND.

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

- Molecule 158 is a DNA chain called STAPLE STRAND.

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

- Molecule 159 is a DNA chain called STAPLE STRAND.

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

- Molecule 160 is a DNA chain called STAPLE STRAND.

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

- Molecule 161 is a DNA chain called STAPLE STRAND.

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

- Molecule 162 is a DNA chain called STAPLE STRAND.

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

- Molecule 163 is a DNA chain called STAPLE STRAND.

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

- Molecule 164 is a DNA chain called STAPLE STRAND.

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

- Molecule 165 is a DNA chain called STAPLE STRAND.

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

- Molecule 166 is a DNA chain called STAPLE STRAND.

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

- Molecule 167 is a DNA chain called STAPLE STRAND.

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

- Molecule 168 is a DNA chain called STAPLE STRAND.

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

- Molecule 169 is a DNA chain called STAPLE STRAND.

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

- Molecule 170 is a DNA chain called STAPLE STRAND.

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

- Molecule 171 is a DNA chain called STAPLE STRAND.

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

- Molecule 172 is a DNA chain called STAPLE STRAND.

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

- Molecule 173 is a DNA chain called STAPLE STRAND.

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

- Molecule 174 is a DNA chain called STAPLE STRAND.

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

- Molecule 175 is a DNA chain called STAPLE STRAND.

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

- Molecule 176 is a DNA chain called STAPLE STRAND.

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

- Molecule 177 is a DNA chain called STAPLE STRAND.

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

- Molecule 178 is a DNA chain called STAPLE STRAND.

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

- Molecule 179 is a DNA chain called STAPLE STRAND.

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

- Molecule 180 is a DNA chain called STAPLE STRAND.

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

- Molecule 181 is a DNA chain called STAPLE STRAND.

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

- Molecule 182 is a DNA chain called STAPLE STRAND.

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

- Molecule 183 is a DNA chain called STAPLE STRAND.

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

- Molecule 184 is a DNA chain called STAPLE STRAND.

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

- Molecule 185 is a DNA chain called STAPLE STRAND.

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

- Molecule 186 is a DNA chain called STAPLE STRAND.

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

- Molecule 187 is a DNA chain called STAPLE STRAND.

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

- Molecule 188 is a DNA chain called STAPLE STRAND.

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

- Molecule 189 is a DNA chain called STAPLE STRAND.

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

- Molecule 190 is a DNA chain called STAPLE STRAND.

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

- Molecule 191 is a DNA chain called STAPLE STRAND.

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

- Molecule 192 is a DNA chain called STAPLE STRAND.

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

- Molecule 193 is a DNA chain called STAPLE STRAND.

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

- Molecule 194 is a DNA chain called STAPLE STRAND.

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

- Molecule 195 is a DNA chain called STAPLE STRAND.

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

- Molecule 196 is a DNA chain called STAPLE STRAND.

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

- Molecule 197 is a DNA chain called STAPLE STRAND.

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

- Molecule 198 is a DNA chain called STAPLE STRAND.

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

- Molecule 199 is a DNA chain called STAPLE STRAND.

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

- Molecule 200 is a DNA chain called STAPLE STRAND.

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

- Molecule 201 is a DNA chain called STAPLE STRAND.

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

- Molecule 202 is a DNA chain called STAPLE STRAND.

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

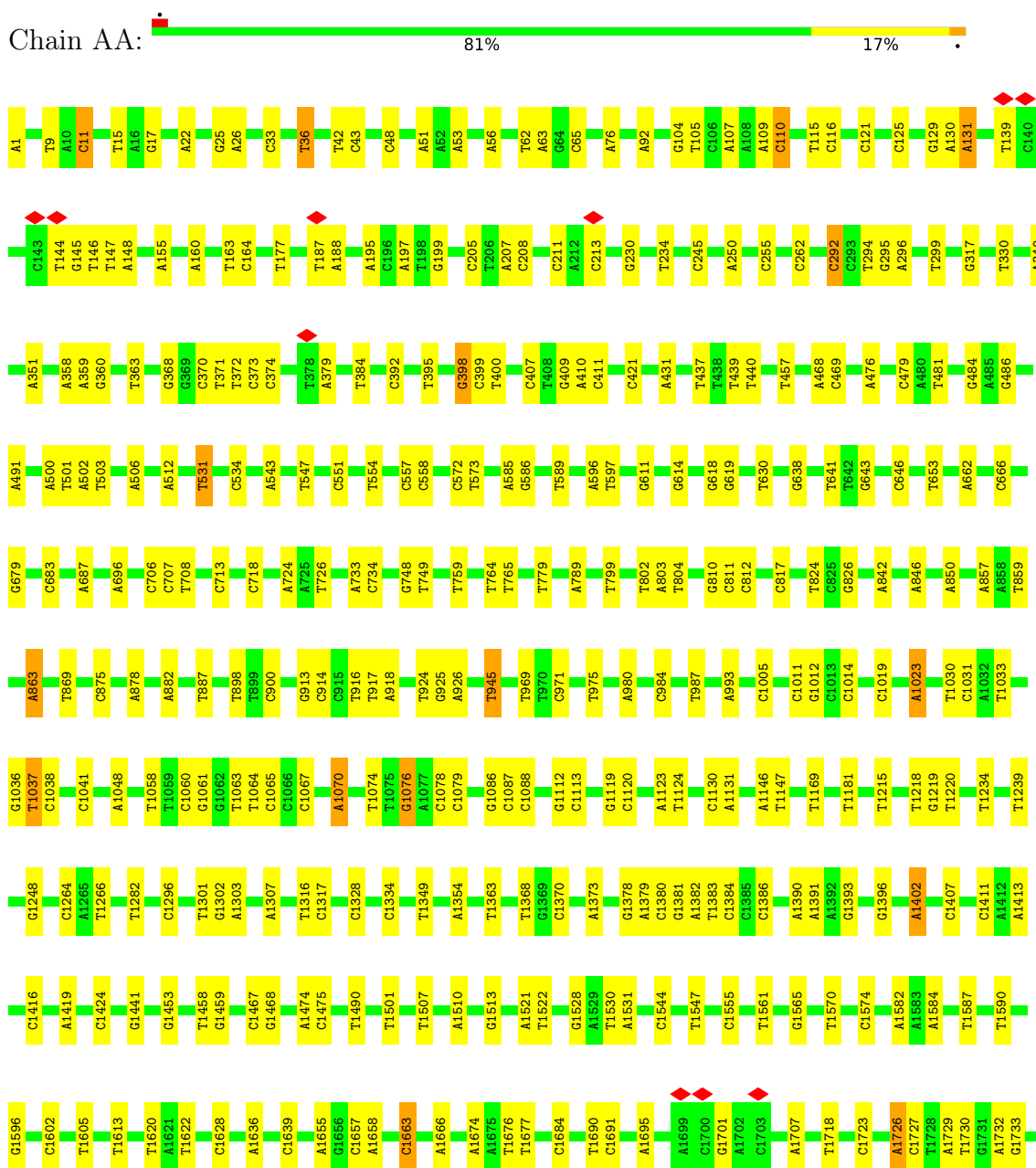
- Molecule 203 is a DNA chain called STAPLE STRAND.

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

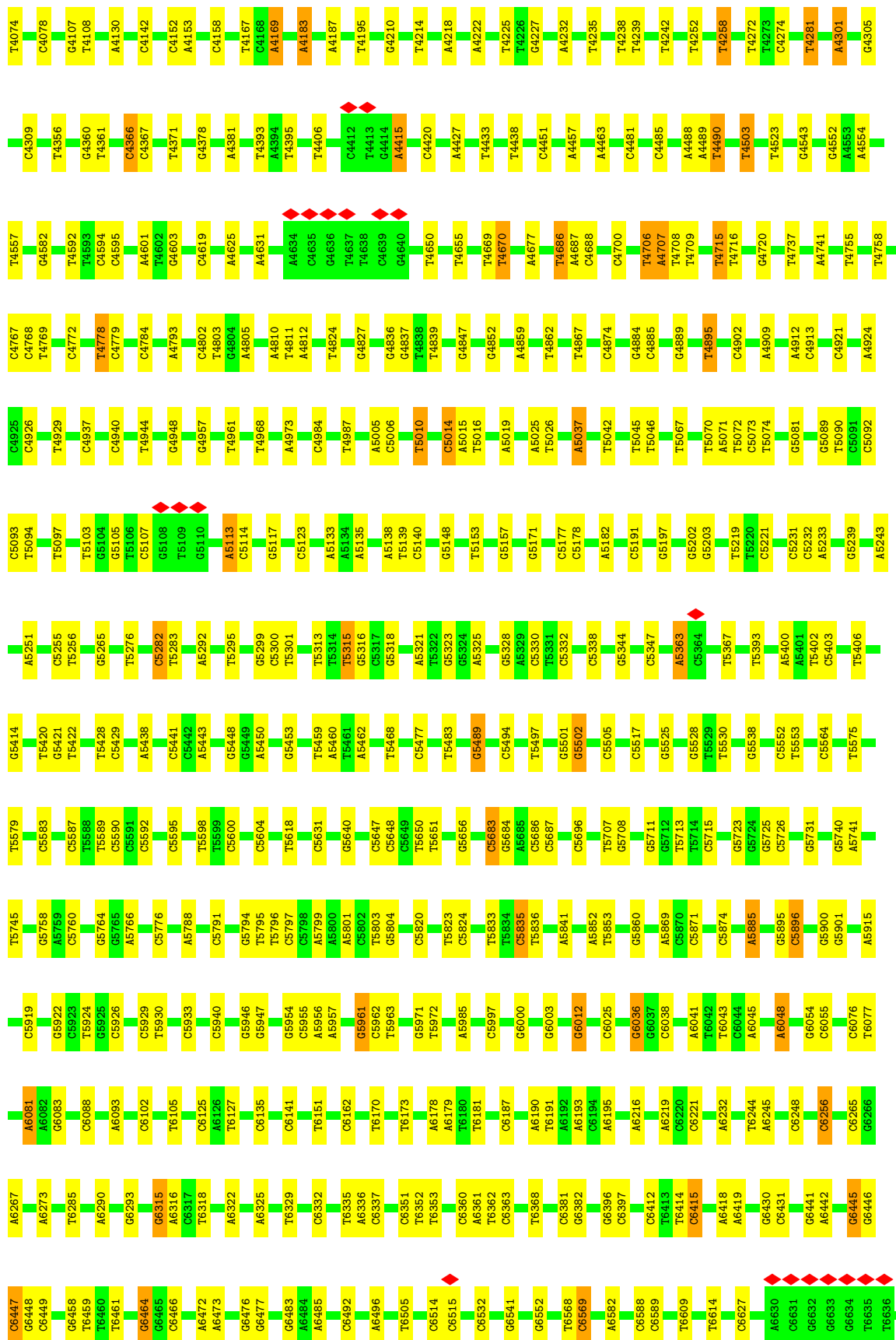
3 Residue-property plots

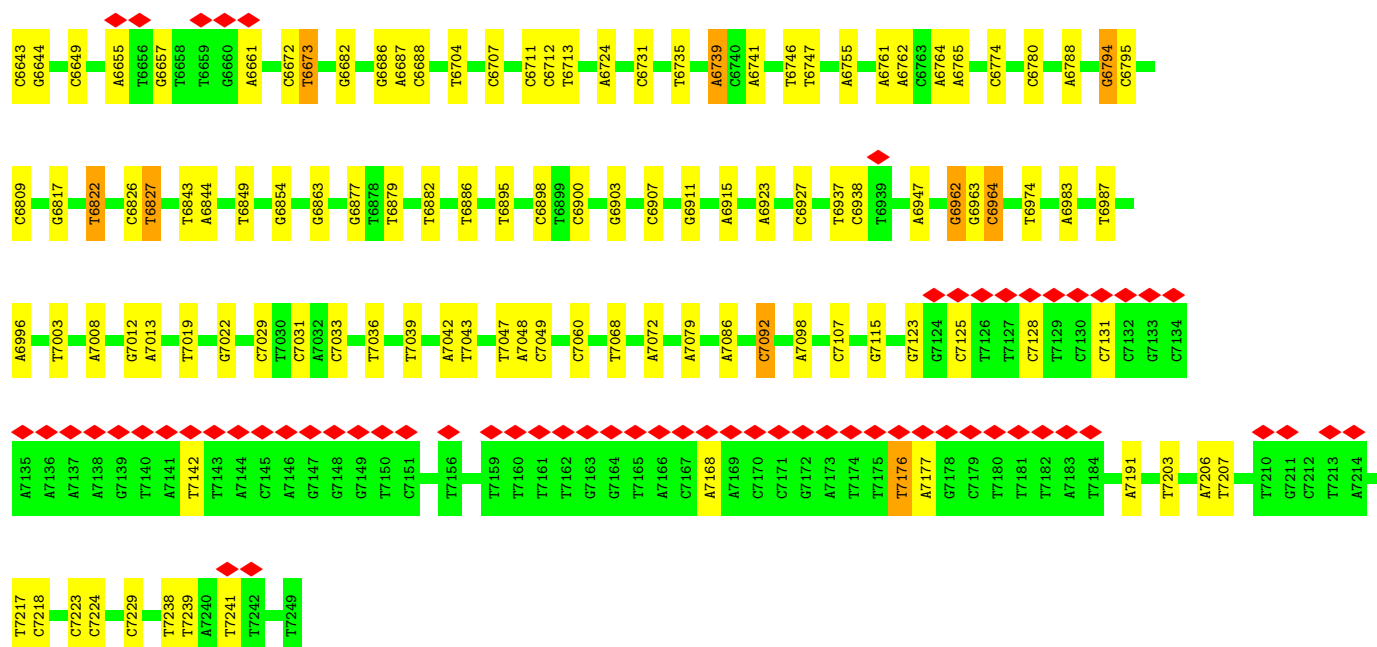
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: SCAFFOLD STRAND

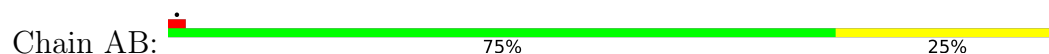


A3920	A3926	A3927	A3928	A3929	A3930	A3931	A3934	A3935	A3936	A3937	A3938	A3939	A3946	C3953	T3958	T3965	A3974	T3981	T3982	T3983	T3984	T3985	T3986	T4001	T4002	T4003	T4004	T4005	T4006	T4007	T4011	T4016	T4017	T4018	T4019	T4020	T4021	T4028	T4044	T4045	T4046	T4051	T4057	T4072	T4073
T3750	T3751	A3752	A3753	G3754	G3755	G3756	C3760	G3767	C3768	T3782	G3783	A3808	A3809	A3810	T3825	C3826	T3827	A3832	T3833	T3834	A3835	T3836	C3841	G3844	T3848	C3853	C3862	G3863	C3864	A3868	T3869	T3870	A3875	T3881	A3893	C3894	C3895	A3896	T3897	A3905	A3912				
T3579	T3583	A3592	A3593	G3599	T3609	A3617	T3632	C3633	G3634	A3651	C3652	T3654	C3658	G3667	T3668	A3669	C3670	T3671	T3672	T3673	A3674	T3675	A3676	T3677	T3678	C3679	T3680	C3681	T3682	T3683	C3688	T3706	C3709	C3717	T3728	G3729	G3738	T3746	C3747	A3748	A3749				
A3386	T3387	C3388	T3389	C3396	T3397	G3406	G3407	C3408	A3415	T3422	T3423	A3430	C3447	T3448	T3451	A3457	G3461	A3480	C3483	T3497	G3505	A3506	G3524	T3527	C3528	T3529	A3530	C3531	A3532	C3535	G3538	A3548	A3553	T3565	T3566	G3567	T3568	C3575							
A3233	G3239	C3240	T3241	A3258	T3259	T3260	A3285	A3288	T3274	A3275	G3276	C3277	T3278	T3301	A3304	G3311	C3312	C3315	A3318	T3322	C3323	G3337	G3342	C3349	G3350	C3351	C3352	T3353	C3354	T3358	T3359	C3360	A3366	A3373	C3378	C3379	T3382	T3383	A3384	T3385					
G3032	A3033	G3041	C3042	T3055	G3056	A3057	C3074	T3077	C3085	T3275	G3088	T3089	A3093	C3098	C3102	G3103	T3104	T3117	G3131	C3135	T3136	A3137	T3138	A3143	T3146	T3147	T3148	T3165	C3171	T3172	T3181	A3186	A3193	A3213	A3221	T3230	G3231	G3232							
T2874	T2879	T2880	T2881	T2882	C2902	T2905	A2911	A2912	C2913	T2914	T2915	T2916	G2917	C2923	A2933	C2934	T2937	T2938	C2939	G2947	A2960	T2967	T2968	G2969	C2984	A2993	A2996	T2997	G3000	G3001	A3005	C3009	T3012	T3013	C3014	T3015	T3027	C3028	T3029						
A2719	A2720	C2721	C2722	A2725	A2728	C2734	A2740	A2746	C2747	A2751	C2756	T2757	T2758	A2759	G2766	G2767	C2771	T2783	T2784	T2785	A2786	T2787	T2792	T2800	T2801	A2802	C2817	T2818	G2819	T2820	C2824	C2828	T2833	T2837	T2853	T2858	C2861								
C2537	G2541	G2542	C2552	G2553	G2554	C2555	C2556	G2574	C2578	G2581	A2584	T2591	C2603	A2607	G2610	C2611	G2622	A2693	C2624	T2633	T2634	A2643	A2647	C2658	T2663	T2664	T2665	C2667	C2668	T2669	C2675	G2688	G2692	T2693	C2694	G2695	G2710								
C2389	T2390	G2391	T2392	C2396	A2401	A2410	G2420	G2421	A2422	A2423	A2425	C2426	G2427	G2436	T2441	A2442	A2452	C2456	G2457	A2458	T2459	A2464	C2465	G2466	C2467	G2468	C2469	C2480	G2481	C2482	T2483	G2488	C2493	T2494	T2495	C2504	C2509	A2515	T2527	C2528					
C2254	T2255	C2268	C2269	T2279	G2280	C2281	C2291	G2295	G2296	T2297	C2305	T2306	G2311	C2312	G2313	C2314	C2315	T2318	G2319	A2320	G2325	C2326	T2327	G2328	T2331	A2335	G2336	G2337	T2348	G2349	A2350	G2359	C2362	A2365	G2366	C2367	C2372	T2375	C2383	C2387	T2388				
T2045	C2055	G2067	T2073	T2074	A2075	A2076	T2078	T2082	G2089	C2090	A2091	C2107	A2120	A2121	A2125	T2126	T2127	A2128	C2129	C2130	T2141	C2156	A2157	C2167	A2170	G2178	G2194	C2197	C2206	T2232	A2237	T2240	G2245	T2250	C2251	G2252	T2253								
T1905	A1914	C1915	T1921	T1922	G1926	C1927	C1928	T1931	A1932	C1933	T1934	G1976	C1943	C1947	T1958	T1968	T1973	C1982	C1983	C1984	C1985	G1986	C1987	T1988	A1989	A1990	T1991	G1992	C1993	G1998	C1999	T2000	G2007	T2013	T2024	A2028	C2033	G2036	T2037	C2040	A2041	G2042	A2043	A2044	
G1744	G1745	G1749	C1757	G1758	T1759	T1760	G1764	T1765	T1766	C1771	G1776	C1783	A1799	T1810	T1810	C1815	A1821	T1822	C1823	A1830	G1833	G1840	T1841	G1842	G1843	T1859	G1863	G1870	G1881	G1882	T1883	G1888	T1889	A1890	C1891	A1895	C1896	G1897	C1900						

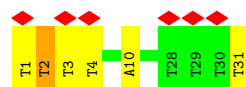
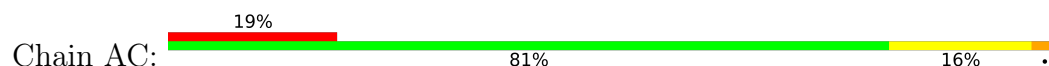




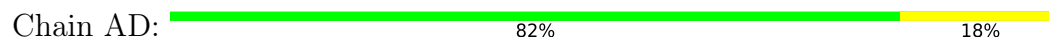
- Molecule 2: STAPLE STRAND



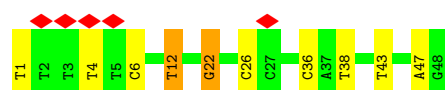
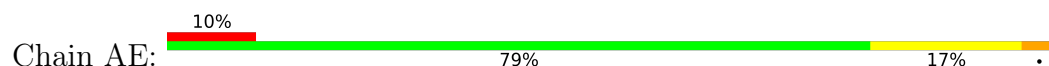
- Molecule 3: STAPLE STRAND



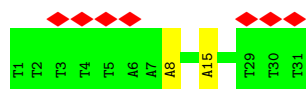
- Molecule 4: STAPLE STRAND



- Molecule 5: STAPLE STRAND



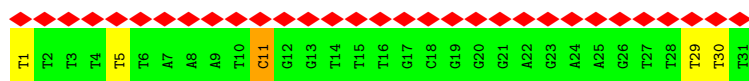
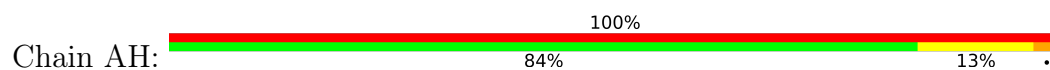
- Molecule 6: STAPLE STRAND



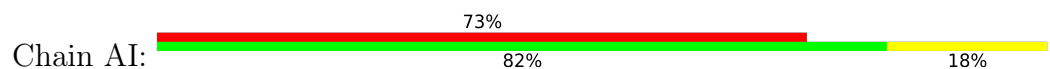
- Molecule 7: STAPLE STRAND



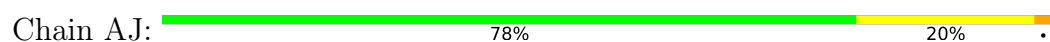
- Molecule 8: STAPLE STRAND



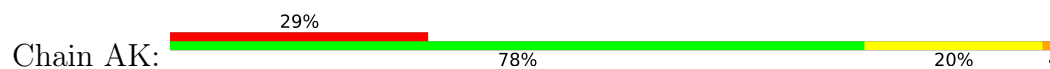
- Molecule 9: STAPLE STRAND



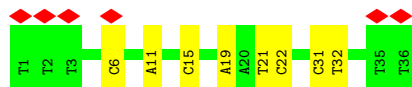
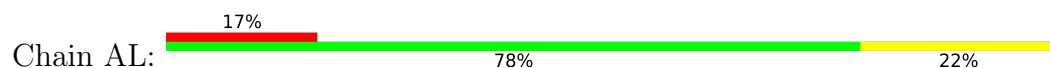
- Molecule 10: STAPLE STRAND



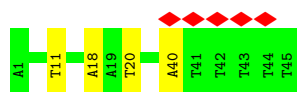
- Molecule 11: STAPLE STRAND



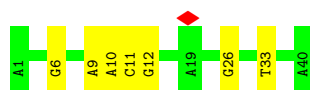
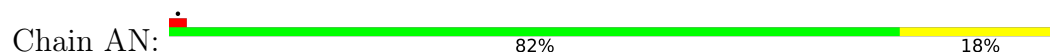
- Molecule 12: STAPLE STRAND



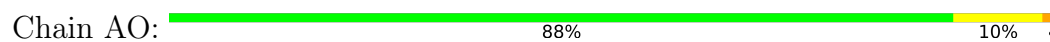
- Molecule 13: STAPLE STRAND



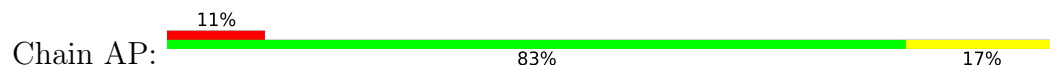
- Molecule 14: STAPLE STRAND



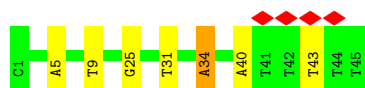
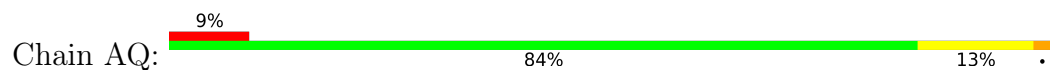
- Molecule 15: STAPLE STRAND



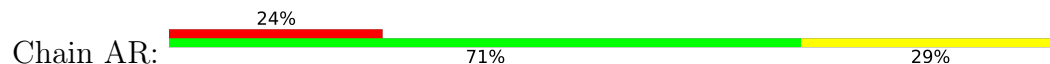
- Molecule 16: STAPLE STRAND



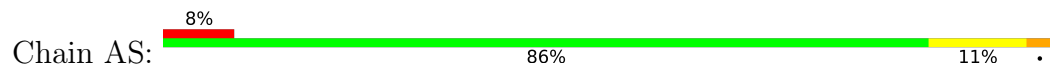
- Molecule 17: STAPLE STRAND



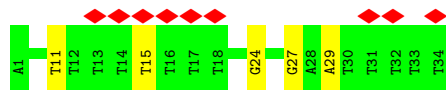
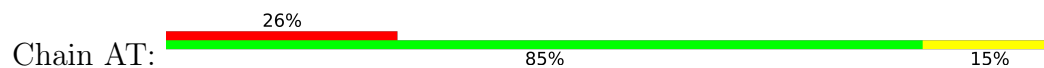
- Molecule 18: STAPLE STRAND



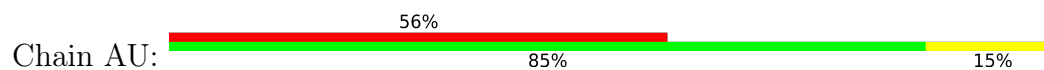
- Molecule 19: STAPLE STRAND



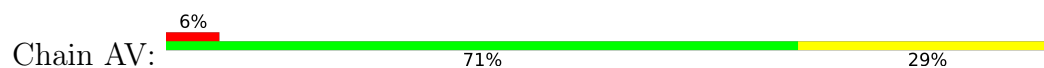
• Molecule 20: STAPLE STRAND



• Molecule 21: STAPLE STRAND



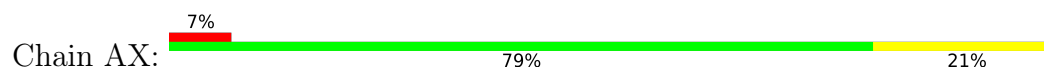
• Molecule 22: STAPLE STRAND



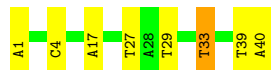
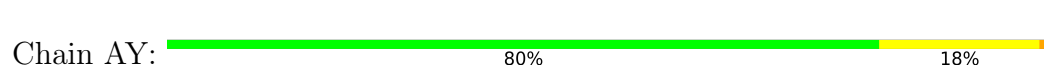
• Molecule 23: STAPLE STRAND



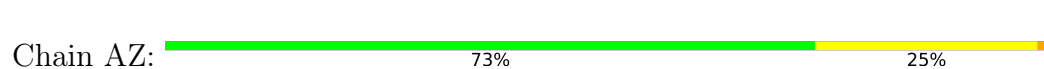
• Molecule 24: STAPLE STRAND



• Molecule 25: STAPLE STRAND



• Molecule 26: STAPLE STRAND



- Molecule 27: STAPLE STRAND

Chain Aa:  75% 22% .



- Molecule 28: STAPLE STRAND

Chain Ab:  35% 84% 16%



- Molecule 29: STAPLE STRAND

Chain Ac:  86% 12% .



- Molecule 30: STAPLE STRAND

Chain Ad:  82% 18%



- Molecule 31: STAPLE STRAND

Chain Ae:  24% 84% 16%



- Molecule 32: STAPLE STRAND

Chain Af:  85% 15%

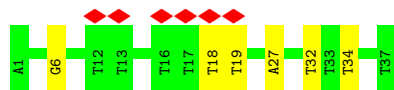
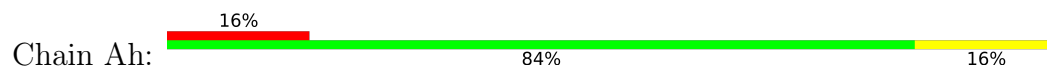


- Molecule 33: STAPLE STRAND

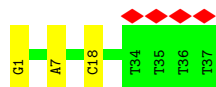
Chain Ag:  12% 83% 17%



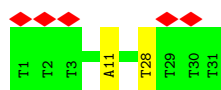
- Molecule 34: STAPLE STRAND



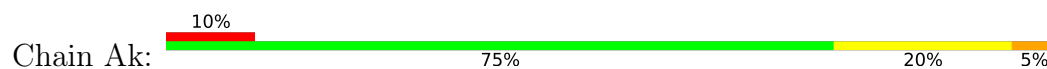
- Molecule 35: STAPLE STRAND



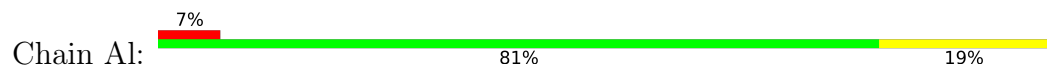
- Molecule 36: STAPLE STRAND



- Molecule 37: STAPLE STRAND



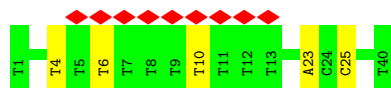
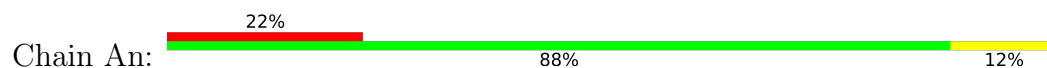
- Molecule 38: STAPLE STRAND



- Molecule 39: STAPLE STRAND



- Molecule 40: STAPLE STRAND



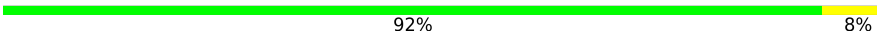
• Molecule 41: STAPLE STRAND

Chain Ao:  84% 12%

• Molecule 42: STAPLE STRAND

Chain Ap:  86% 14%

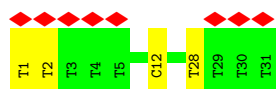
• Molecule 43: STAPLE STRAND

Chain Aq:  92% 8%

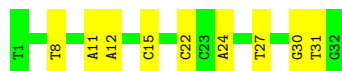
• Molecule 44: STAPLE STRAND

Chain Ar:  75% 20% 5%

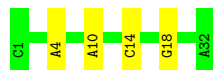
• Molecule 45: STAPLE STRAND

Chain As:  26% 87% 13%

• Molecule 46: STAPLE STRAND

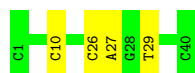
Chain At:  72% 28%

• Molecule 47: STAPLE STRAND

Chain Au:  88% 12%

• Molecule 48: STAPLE STRAND

Chain Av:  90% 10%



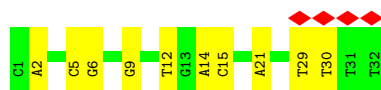
- Molecule 49: STAPLE STRAND

Chain Aw:  90% 10%



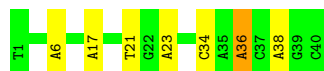
- Molecule 50: STAPLE STRAND

Chain Ax:  12% 69% 31%



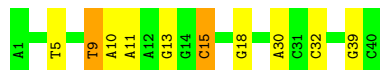
- Molecule 51: STAPLE STRAND

Chain Ay:  82% 15% .



- Molecule 52: STAPLE STRAND

Chain Az:  75% 20% 5%



- Molecule 53: STAPLE STRAND

Chain A0:  85% 12% .

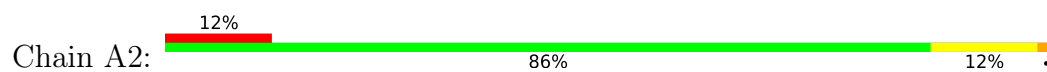


- Molecule 54: STAPLE STRAND

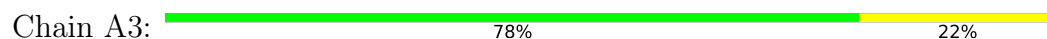
Chain A1:  29% 74% 26%



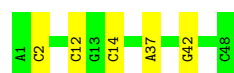
- Molecule 55: STAPLE STRAND



- Molecule 56: STAPLE STRAND



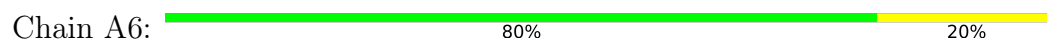
- Molecule 57: STAPLE STRAND



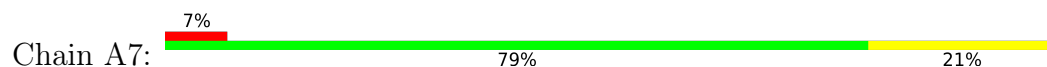
- Molecule 58: STAPLE STRAND



- Molecule 59: STAPLE STRAND



- Molecule 60: STAPLE STRAND



- Molecule 61: STAPLE STRAND

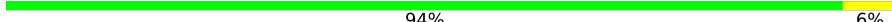


- Molecule 62: STAPLE STRAND

Chain A9:  88% 12%



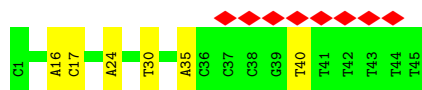
- Molecule 63: STAPLE STRAND

Chain BA:  94% 6%



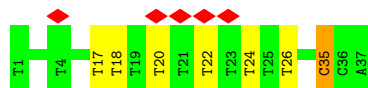
- Molecule 64: STAPLE STRAND

Chain BB:  18% 87% 13%



- Molecule 65: STAPLE STRAND

Chain BC:  14% 81% 16%



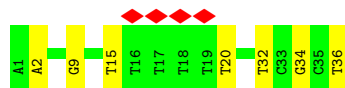
- Molecule 66: STAPLE STRAND

Chain BD:  78% 16% 6%



- Molecule 67: STAPLE STRAND

Chain BE:  11% 81% 19%

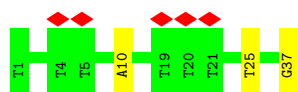
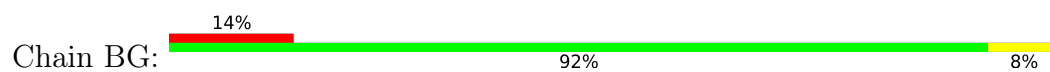


- Molecule 68: STAPLE STRAND

Chain BF:  7% 83% 17%



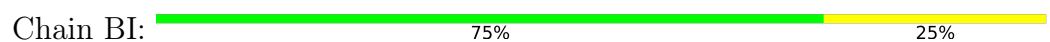
- Molecule 69: STAPLE STRAND



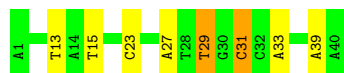
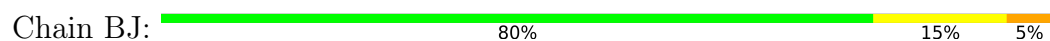
- Molecule 70: STAPLE STRAND



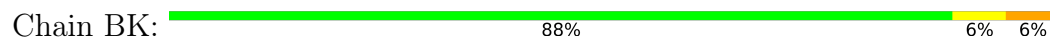
- Molecule 71: STAPLE STRAND



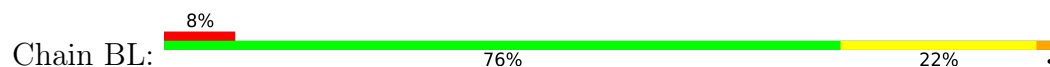
- Molecule 72: STAPLE STRAND



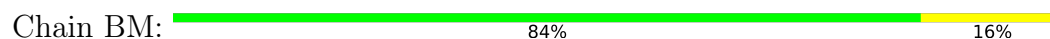
- Molecule 73: STAPLE STRAND



- Molecule 74: STAPLE STRAND

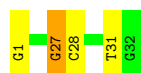


- Molecule 75: STAPLE STRAND



- Molecule 76: STAPLE STRAND

Chain BN:  88% 9%



- Molecule 77: STAPLE STRAND

Chain BO:  92% 8%



- Molecule 78: STAPLE STRAND

Chain BP:  94% 6%



- Molecule 79: STAPLE STRAND

Chain BQ:  88% 12%



- Molecule 80: STAPLE STRAND

Chain BR:  82% 15%



- Molecule 81: STAPLE STRAND

Chain BS:  88% 12%



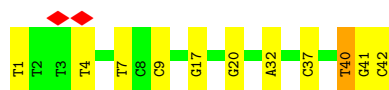
- Molecule 82: STAPLE STRAND

Chain BT:  78% 22%



- Molecule 83: STAPLE STRAND

Chain BU:  5% 74% 24%



• Molecule 84: STAPLE STRAND

Chain BV: 83% 17%



• Molecule 85: STAPLE STRAND

Chain BW: 56% 75% 25%



• Molecule 86: STAPLE STRAND

Chain BX: 18% 95% ..



• Molecule 87: STAPLE STRAND

Chain BY: 80% 18% .



• Molecule 88: STAPLE STRAND

Chain BZ: 85% 15%



• Molecule 89: STAPLE STRAND

Chain Ba: 75% 25%

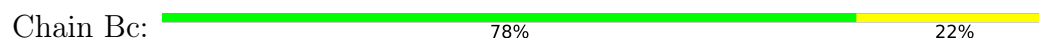


• Molecule 90: STAPLE STRAND

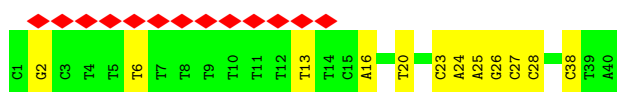
Chain Bb: 80% 18% .



- Molecule 91: STAPLE STRAND



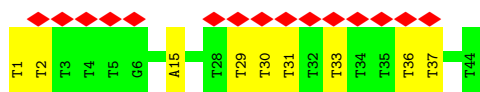
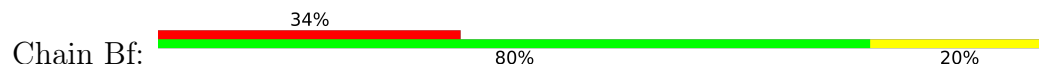
- Molecule 92: STAPLE STRAND



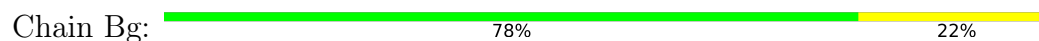
- Molecule 93: STAPLE STRAND



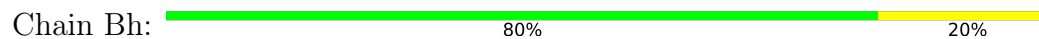
- Molecule 94: STAPLE STRAND



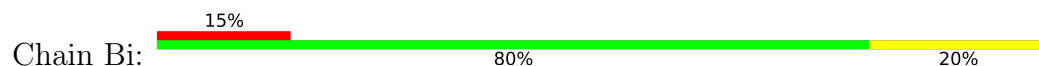
- Molecule 95: STAPLE STRAND



- Molecule 96: STAPLE STRAND

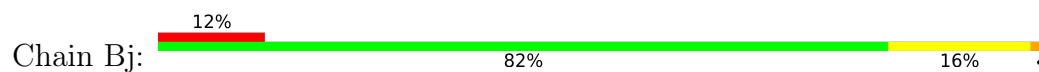


- Molecule 97: STAPLE STRAND

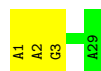




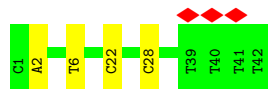
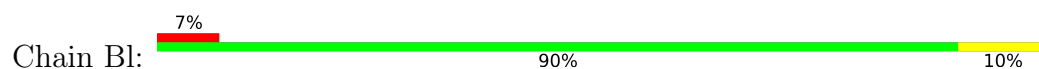
- Molecule 98: STAPLE STRAND



- Molecule 99: STAPLE STRAND



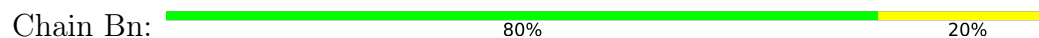
- Molecule 100: STAPLE STRAND



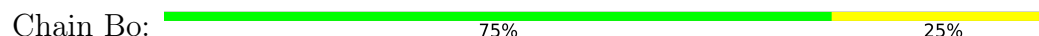
- Molecule 101: STAPLE STRAND



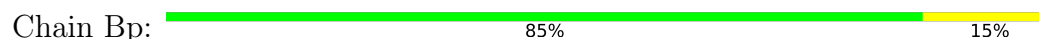
- Molecule 102: STAPLE STRAND

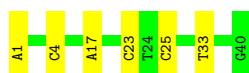


- Molecule 103: STAPLE STRAND

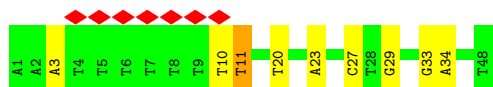
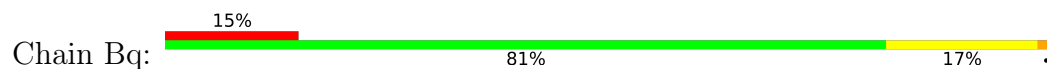


- Molecule 104: STAPLE STRAND





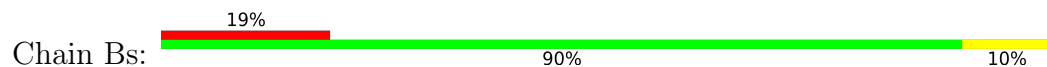
- Molecule 105: STAPLE STRAND



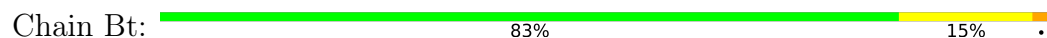
- Molecule 106: STAPLE STRAND



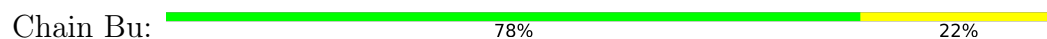
- Molecule 107: STAPLE STRAND



- Molecule 108: STAPLE STRAND



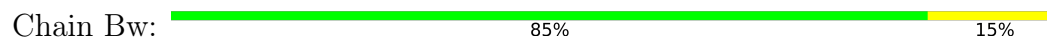
- Molecule 109: STAPLE STRAND



- Molecule 110: STAPLE STRAND



- Molecule 111: STAPLE STRAND

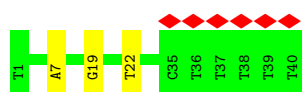
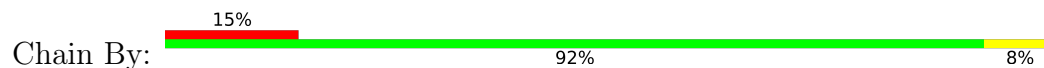




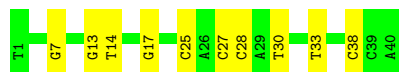
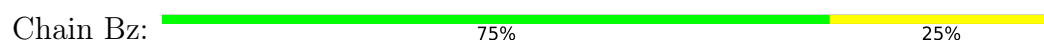
- Molecule 112: STAPLE STRAND



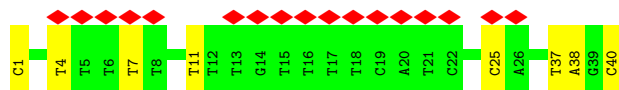
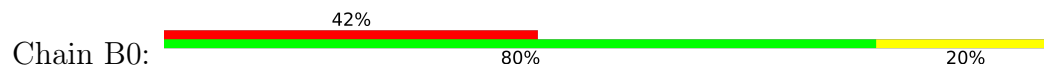
- Molecule 113: STAPLE STRAND



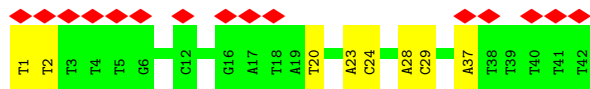
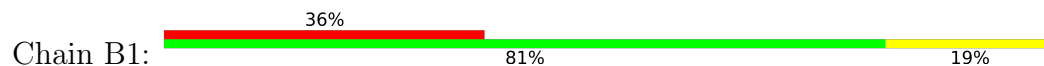
- Molecule 114: STAPLE STRAND



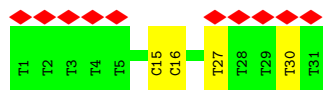
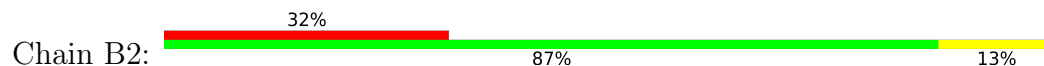
- Molecule 115: STAPLE STRAND



- Molecule 116: STAPLE STRAND



- Molecule 117: STAPLE STRAND

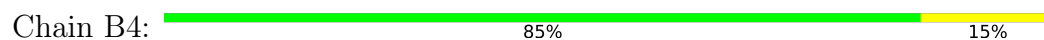


- Molecule 118: STAPLE STRAND





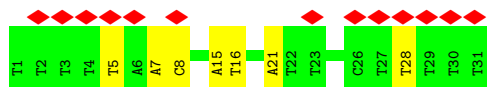
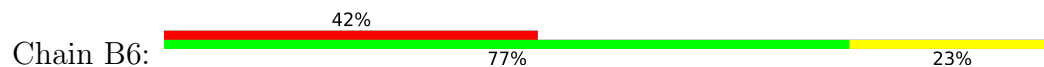
- Molecule 119: STAPLE STRAND



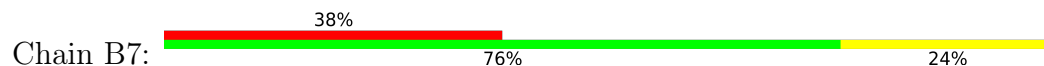
- Molecule 120: STAPLE STRAND



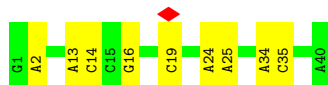
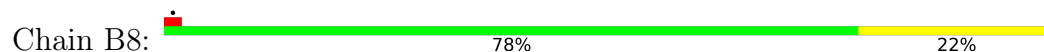
- Molecule 121: STAPLE STRAND



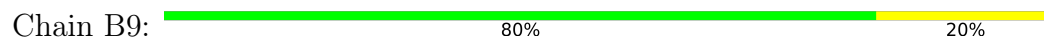
- Molecule 122: STAPLE STRAND



- Molecule 123: STAPLE STRAND



- Molecule 124: STAPLE STRAND

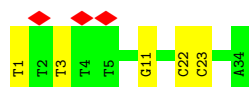
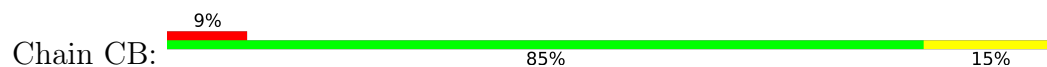


- Molecule 125: STAPLE STRAND





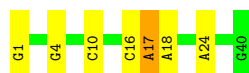
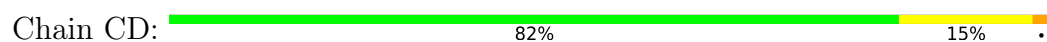
- Molecule 126: STAPLE STRAND



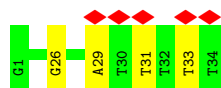
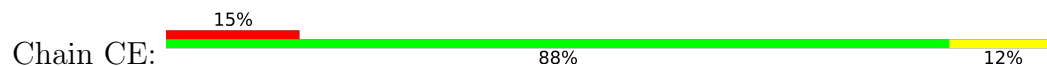
- Molecule 127: STAPLE STRAND



- Molecule 128: STAPLE STRAND



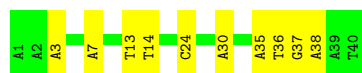
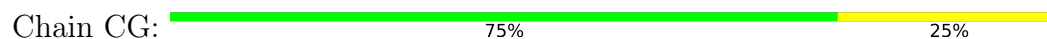
- Molecule 129: STAPLE STRAND



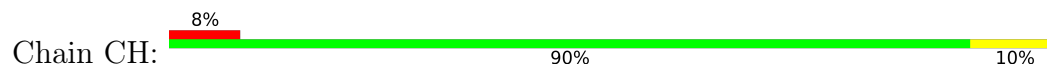
- Molecule 130: STAPLE STRAND

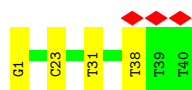


- Molecule 131: STAPLE STRAND



- Molecule 132: STAPLE STRAND





- Molecule 133: STAPLE STRAND

Chain CI: 90% 10%



- Molecule 134: STAPLE STRAND

Chain CJ: 78% 22%



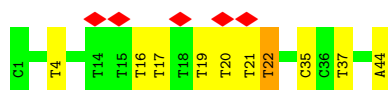
- Molecule 135: STAPLE STRAND

Chain CK: 78% 22%



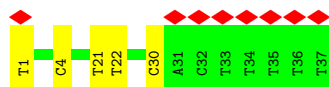
- Molecule 136: STAPLE STRAND

Chain CL: 11% 77% 20%



- Molecule 137: STAPLE STRAND

Chain CM: 22% 86% 14%



- Molecule 138: STAPLE STRAND

Chain CN: 88% 12%



- Molecule 139: STAPLE STRAND

Chain CO: 80% 18%



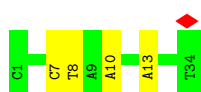
- Molecule 140: STAPLE STRAND

Chain CP: 83% 17%



- Molecule 141: STAPLE STRAND

Chain CQ: 88% 12%



- Molecule 142: STAPLE STRAND

Chain CR: 80% 20%



- Molecule 143: STAPLE STRAND

Chain CS: 85% 15%



- Molecule 144: STAPLE STRAND

Chain CT: 79% 21%



- Molecule 145: STAPLE STRAND

Chain CU: 85% 12%



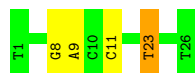
- Molecule 146: STAPLE STRAND

Chain CV: 29% 79% 21%



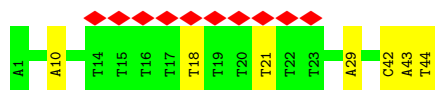
• Molecule 147: STAPLE STRAND

Chain CW: 85% 12% .



• Molecule 148: STAPLE STRAND

Chain CX: 23% 84% 16%



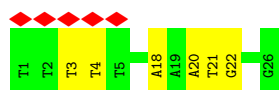
• Molecule 149: STAPLE STRAND

Chain CY: 81% 19%



• Molecule 150: STAPLE STRAND

Chain CZ: 19% 77% 23%



• Molecule 151: STAPLE STRAND

Chain Ca: 80% 15% 5%



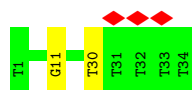
• Molecule 152: STAPLE STRAND

Chain Cb: 6% 85% 9% 6%



• Molecule 153: STAPLE STRAND

Chain Cc: 9% 94% 6%



- Molecule 154: STAPLE STRAND

Chain Cd: 75% 25%



- Molecule 155: STAPLE STRAND

Chain Ce: 80% 15% 5%



- Molecule 156: STAPLE STRAND

Chain Cf: 80% 20%



- Molecule 157: STAPLE STRAND

Chain Cg: 79% 17% .



- Molecule 158: STAPLE STRAND

Chain Ch: 73% 27%



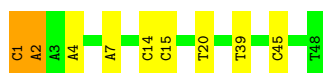
- Molecule 159: STAPLE STRAND

Chain Ci: 85% 13% .

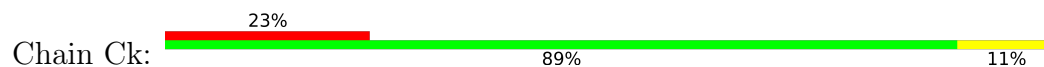


- Molecule 160: STAPLE STRAND

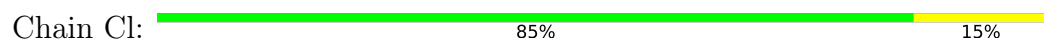
Chain Cj: 81% 15% .



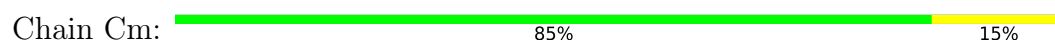
- Molecule 161: STAPLE STRAND



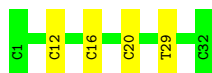
- Molecule 162: STAPLE STRAND



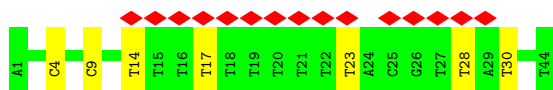
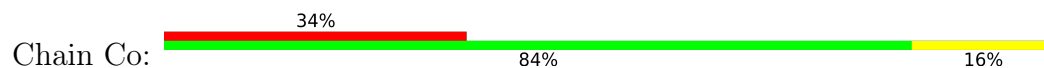
- Molecule 163: STAPLE STRAND



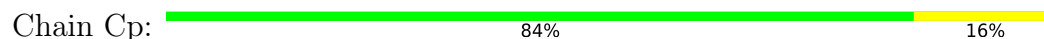
- Molecule 164: STAPLE STRAND



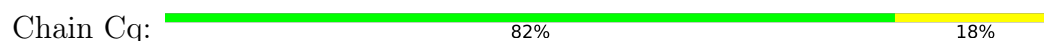
- Molecule 165: STAPLE STRAND



- Molecule 166: STAPLE STRAND

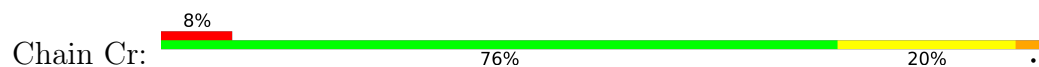


- Molecule 167: STAPLE STRAND

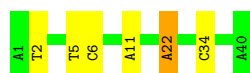
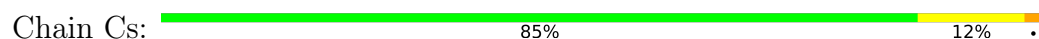




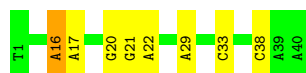
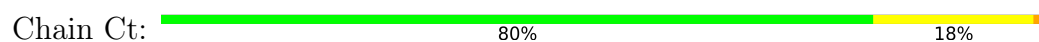
- Molecule 168: STAPLE STRAND



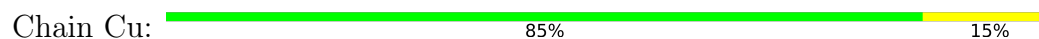
- Molecule 169: STAPLE STRAND



- Molecule 170: STAPLE STRAND



- Molecule 171: STAPLE STRAND



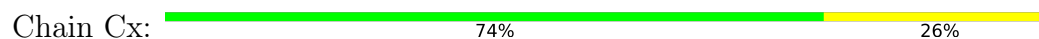
- Molecule 172: STAPLE STRAND



- Molecule 173: STAPLE STRAND

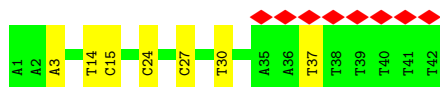
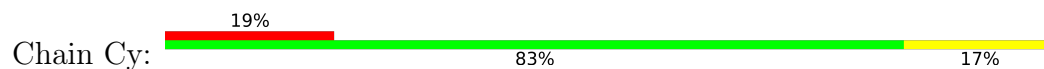


- Molecule 174: STAPLE STRAND





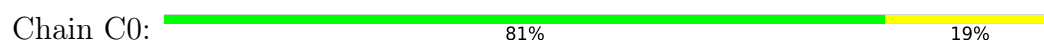
- Molecule 175: STAPLE STRAND



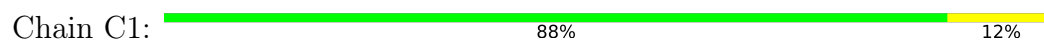
- Molecule 176: STAPLE STRAND



- Molecule 177: STAPLE STRAND



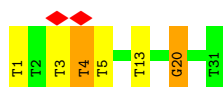
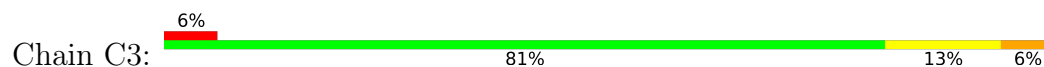
- Molecule 178: STAPLE STRAND



- Molecule 179: STAPLE STRAND



- Molecule 180: STAPLE STRAND



- Molecule 181: STAPLE STRAND





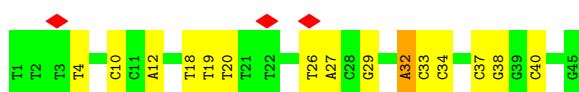
- Molecule 182: STAPLE STRAND

Chain C5: 78% 20% .



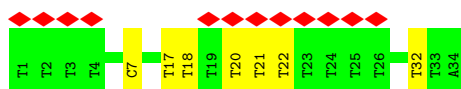
- Molecule 183: STAPLE STRAND

Chain C6: 7% 67% 31% .



- Molecule 184: STAPLE STRAND

Chain C7: 35% 79% 21% .



- Molecule 185: STAPLE STRAND

Chain C8: 85% 12% .



- Molecule 186: STAPLE STRAND

Chain C9: 79% 19% .



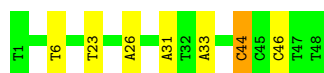
- Molecule 187: STAPLE STRAND

Chain DA: 82% 12% 5% .

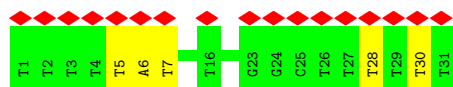
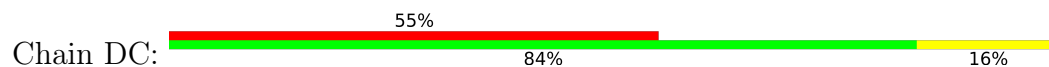


- Molecule 188: STAPLE STRAND

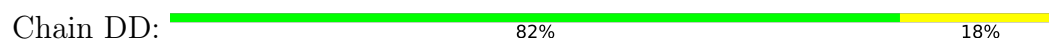
Chain DB: 85% 12% .



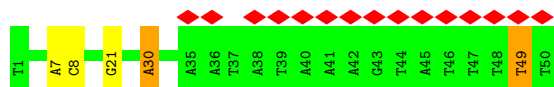
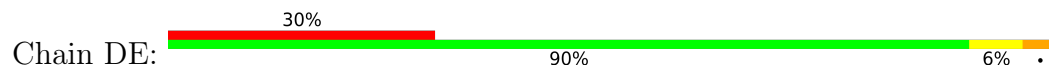
- Molecule 189: STAPLE STRAND



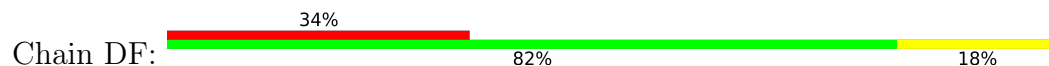
- Molecule 190: STAPLE STRAND



- Molecule 191: STAPLE STRAND



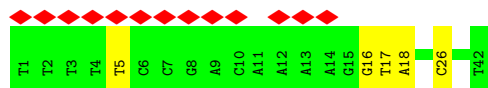
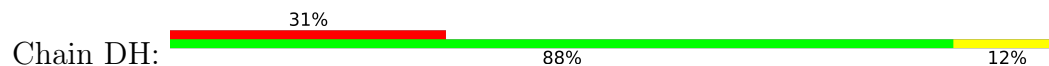
- Molecule 192: STAPLE STRAND



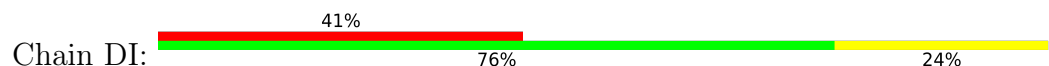
- Molecule 193: STAPLE STRAND

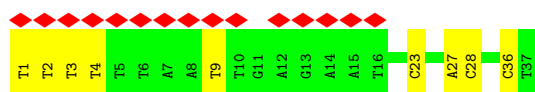


- Molecule 194: STAPLE STRAND



- Molecule 195: STAPLE STRAND





- Molecule 196: STAPLE STRAND

Chain DJ: 88% 8%



- Molecule 197: STAPLE STRAND

Chain DK: 85% 15%



- Molecule 198: STAPLE STRAND

Chain DL: 72% 28%



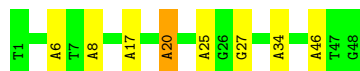
- Molecule 199: STAPLE STRAND

Chain DM: 88% 12%



- Molecule 200: STAPLE STRAND

Chain DN: 83% 15%



- Molecule 201: STAPLE STRAND

Chain DO: 12% 75% 25%



- Molecule 202: STAPLE STRAND

Chain DP: 91% 9%



- Molecule 203: STAPLE STRAND

Chain DQ:  90% 10%



4 Experimental information

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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

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

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

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

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

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if

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

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

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

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

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

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

There are no bond length outliers.

All (887) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
186	C9	34	DG	P-O3'-C3'	12.67	139.21	120.20
1	AA	3505	DG	P-O3'-C3'	12.33	138.69	120.20
198	DL	30	DC	P-O3'-C3'	12.31	138.67	120.20
97	Bi	12	DT	P-O3'-C3'	11.89	138.03	120.20
1	AA	3322	DT	P-O3'-C3'	11.85	137.98	120.20
164	Cn	20	DC	P-O3'-C3'	11.83	137.94	120.20
1	AA	5650	DT	P-O3'-C3'	11.81	137.91	120.20
123	B8	34	DA	P-O3'-C3'	11.81	137.91	120.20
1	AA	5133	DA	P-O3'-C3'	11.73	137.80	120.20
1	AA	1986	DG	P-O3'-C3'	11.71	137.77	120.20
1	AA	398	DG	P-O3'-C3'	11.71	137.77	120.20
9	AI	27	DT	P-O3'-C3'	11.66	137.70	120.20
25	AY	33	DT	P-O3'-C3'	11.53	137.50	120.20
5	AE	26	DC	P-O3'-C3'	11.49	137.43	120.20
1	AA	1730	DT	P-O3'-C3'	11.43	137.34	120.20
1	AA	5233	DA	P-O3'-C3'	11.36	137.24	120.20
155	Ce	10	DC	P-O3'-C3'	11.14	136.91	120.20
1	AA	6568	DT	P-O3'-C3'	11.13	136.89	120.20
1	AA	1086	DG	P-O3'-C3'	11.12	136.88	120.20
1	AA	502	DA	P-O3'-C3'	11.04	136.77	120.20
1	AA	4371	DT	P-O3'-C3'	11.00	136.70	120.20
1	AA	3632	DT	P-O3'-C3'	10.98	136.67	120.20
1	AA	3864	DC	P-O3'-C3'	10.93	136.60	120.20
27	Aa	11	DA	P-O3'-C3'	10.90	136.56	120.20
1	AA	2194	DG	P-O3'-C3'	10.86	136.49	120.20
1	AA	4415	DA	P-O3'-C3'	10.75	136.33	120.20
60	A7	28	DC	P-O3'-C3'	10.75	136.33	120.20
1	AA	3350	DG	P-O3'-C3'	10.75	136.32	120.20
105	Bq	11	DT	P-O3'-C3'	10.70	136.24	120.20
7	AG	26	DC	P-O3'-C3'	10.68	136.22	120.20
174	Cx	15	DC	P-O3'-C3'	10.49	135.93	120.20
22	AV	4	DT	P-O3'-C3'	10.43	135.84	120.20
1	AA	586	DG	P-O3'-C3'	10.41	135.82	120.20
1	AA	1303	DA	P-O3'-C3'	10.41	135.81	120.20
3	AC	2	DT	P-O3'-C3'	10.38	135.77	120.20
123	B8	16	DG	P-O3'-C3'	10.37	135.75	120.20
1	AA	2178	DG	P-O3'-C3'	10.35	135.73	120.20
1	AA	1113	DC	P-O3'-C3'	10.35	135.72	120.20
47	Au	10	DA	P-O3'-C3'	10.33	135.70	120.20
1	AA	6672	DC	P-O3'-C3'	10.33	135.69	120.20
1	AA	3895	DC	P-O3'-C3'	10.26	135.59	120.20
1	AA	4812	DA	P-O3'-C3'	10.26	135.59	120.20
81	BS	10	DT	P-O3'-C3'	10.24	135.56	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
126	CB	3	DT	P-O3'-C3'	10.18	135.47	120.20
1	AA	5037	DA	P-O3'-C3'	10.14	135.41	120.20
62	A9	7	DT	P-O3'-C3'	10.14	135.41	120.20
1	AA	6514	DC	P-O3'-C3'	10.13	135.40	120.20
13	AM	18	DA	P-O3'-C3'	10.11	135.36	120.20
145	CU	19	DT	P-O3'-C3'	10.10	135.35	120.20
2	AB	30	DG	P-O3'-C3'	10.09	135.34	120.20
136	CL	22	DT	P-O3'-C3'	9.99	135.19	120.20
147	CW	23	DT	P-O3'-C3'	9.97	135.15	120.20
1	AA	2969	DG	P-O3'-C3'	9.95	135.12	120.20
1	AA	5318	DG	P-O3'-C3'	9.94	135.10	120.20
44	Ar	4	DA	P-O3'-C3'	9.92	135.08	120.20
32	Af	27	DG	P-O3'-C3'	9.91	135.07	120.20
37	Ak	4	DT	P-O3'-C3'	9.88	135.02	120.20
55	A2	10	DA	P-O3'-C3'	9.88	135.02	120.20
93	Be	16	DA	P-O3'-C3'	9.87	135.00	120.20
83	BU	40	DT	P-O3'-C3'	9.83	134.95	120.20
9	AI	3	DG	P-O3'-C3'	9.73	134.80	120.20
1	AA	5093	DC	P-O3'-C3'	9.71	134.76	120.20
183	C6	38	DG	P-O3'-C3'	9.68	134.72	120.20
174	Cx	36	DC	P-O3'-C3'	9.62	134.62	120.20
197	DK	23	DA	P-O3'-C3'	9.55	134.53	120.20
1	AA	2297	DT	P-O3'-C3'	9.54	134.51	120.20
1	AA	379	DA	P-O3'-C3'	9.52	134.49	120.20
128	CD	10	DC	P-O3'-C3'	9.51	134.46	120.20
1	AA	2156	DC	P-O3'-C3'	9.45	134.38	120.20
1	AA	2819	DG	P-O3'-C3'	9.44	134.36	120.20
37	Ak	26	DG	P-O3'-C3'	9.43	134.35	120.20
1	AA	2306	DT	P-O3'-C3'	9.43	134.34	120.20
1	AA	6492	DC	P-O3'-C3'	9.42	134.32	120.20
1	AA	1881	DG	P-O3'-C3'	9.41	134.32	120.20
1	AA	1248	DG	P-O3'-C3'	9.40	134.30	120.20
1	AA	3782	DT	P-O3'-C3'	9.37	134.25	120.20
1	AA	6673	DT	P-O3'-C3'	9.36	134.23	120.20
1	AA	3056	DG	P-O3'-C3'	9.35	134.22	120.20
1	AA	255	DC	P-O3'-C3'	9.35	134.22	120.20
1	AA	4803	DT	P-O3'-C3'	9.34	134.21	120.20
1	AA	6764	DA	P-O3'-C3'	9.34	134.21	120.20
1	AA	6248	DC	P-O3'-C3'	9.33	134.20	120.20
68	BF	41	DC	P-O3'-C3'	9.32	134.19	120.20
200	DN	34	DA	P-O3'-C3'	9.32	134.19	120.20
1	AA	5708	DG	P-O3'-C3'	9.31	134.17	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	5764	DG	P-O3'-C3'	9.31	134.17	120.20
1	AA	6688	DC	P-O3'-C3'	9.29	134.13	120.20
1	AA	145	DG	P-O3'-C3'	9.28	134.12	120.20
1	AA	213	DC	P-O3'-C3'	9.28	134.12	120.20
44	Ar	26	DG	P-O3'-C3'	9.27	134.11	120.20
48	Av	27	DA	P-O3'-C3'	9.27	134.10	120.20
56	A3	22	DC	P-O3'-C3'	9.21	134.02	120.20
1	AA	1655	DA	P-O3'-C3'	9.20	134.01	120.20
1	AA	2041	DA	P-O3'-C3'	9.21	134.01	120.20
170	Ct	17	DA	P-O3'-C3'	9.21	134.01	120.20
30	Ad	9	DC	P-O3'-C3'	9.19	133.99	120.20
26	AZ	43	DG	P-O3'-C3'	9.19	133.98	120.20
110	Bv	26	DA	P-O3'-C3'	9.18	133.97	120.20
22	AV	33	DA	P-O3'-C3'	9.14	133.91	120.20
150	CZ	22	DG	P-O3'-C3'	9.14	133.91	120.20
191	DE	49	DT	P-O3'-C3'	9.10	133.85	120.20
119	B4	33	DA	P-O3'-C3'	9.10	133.84	120.20
73	BK	18	DA	P-O3'-C3'	9.09	133.84	120.20
106	Br	25	DG	P-O3'-C3'	9.07	133.81	120.20
1	AA	2467	DC	P-O3'-C3'	9.07	133.81	120.20
84	BV	34	DG	P-O3'-C3'	9.07	133.80	120.20
1	AA	1833	DG	P-O3'-C3'	9.05	133.78	120.20
1	AA	6515	DC	P-O3'-C3'	9.03	133.74	120.20
58	A5	10	DA	P-O3'-C3'	9.03	133.74	120.20
142	CR	20	DC	P-O3'-C3'	8.99	133.69	120.20
1	AA	36	DT	P-O3'-C3'	8.98	133.67	120.20
37	Ak	6	DC	P-O3'-C3'	8.98	133.67	120.20
1	AA	4153	DA	P-O3'-C3'	8.97	133.66	120.20
29	Ac	19	DG	P-O3'-C3'	8.93	133.59	120.20
83	BU	20	DG	P-O3'-C3'	8.87	133.50	120.20
1	AA	5046	DT	P-O3'-C3'	8.86	133.49	120.20
1	AA	6418	DA	P-O3'-C3'	8.86	133.49	120.20
110	Bv	11	DG	P-O3'-C3'	8.83	133.45	120.20
155	Ce	9	DG	P-O3'-C3'	8.83	133.45	120.20
1	AA	4677	DA	P-O3'-C3'	8.81	133.42	120.20
52	Az	10	DA	P-O3'-C3'	8.79	133.39	120.20
33	Ag	28	DA	P-O3'-C3'	8.78	133.37	120.20
1	AA	51	DA	P-O3'-C3'	8.77	133.36	120.20
1	AA	3312	DC	P-O3'-C3'	8.77	133.35	120.20
1	AA	1413	DA	P-O3'-C3'	8.75	133.33	120.20
50	Ax	30	DT	P-O3'-C3'	8.74	133.31	120.20
1	AA	5589	DT	P-O3'-C3'	8.73	133.30	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	AG	15	DC	P-O3'-C3'	8.72	133.28	120.20
114	Bz	7	DG	P-O3'-C3'	8.71	133.26	120.20
1	AA	2422	DC	P-O3'-C3'	8.66	133.19	120.20
1	AA	2313	DG	P-O3'-C3'	8.65	133.18	120.20
1	AA	3275	DA	P-O3'-C3'	8.63	133.15	120.20
138	CN	12	DT	P-O3'-C3'	8.63	133.15	120.20
1	AA	2947	DG	P-O3'-C3'	8.63	133.14	120.20
1	AA	6964	DC	P-O3'-C3'	8.61	133.12	120.20
1	AA	2916	DT	P-O3'-C3'	8.60	133.10	120.20
32	Af	34	DT	P-O3'-C3'	8.59	133.09	120.20
68	BF	22	DG	P-O3'-C3'	8.59	133.08	120.20
1	AA	5014	DC	P-O3'-C3'	8.58	133.08	120.20
52	Az	9	DT	P-O3'-C3'	8.57	133.06	120.20
1	AA	5640	DG	P-O3'-C3'	8.56	133.05	120.20
48	Av	10	DC	P-O3'-C3'	8.54	133.02	120.20
1	AA	3337	DG	P-O3'-C3'	8.53	132.99	120.20
134	CJ	27	DA	P-O3'-C3'	8.52	132.98	120.20
46	At	8	DT	P-O3'-C3'	8.52	132.97	120.20
11	AK	22	DT	P-O3'-C3'	8.50	132.96	120.20
55	A2	18	DG	P-O3'-C3'	8.47	132.91	120.20
160	Cj	2	DA	P-O3'-C3'	8.46	132.89	120.20
11	AK	36	DC	P-O3'-C3'	8.44	132.85	120.20
1	AA	1565	DG	P-O3'-C3'	8.43	132.85	120.20
1	AA	1012	DG	P-O3'-C3'	8.42	132.83	120.20
1	AA	4183	DA	P-O3'-C3'	8.42	132.82	120.20
37	Ak	2	DT	P-O3'-C3'	8.42	132.83	120.20
1	AA	5525	DG	P-O3'-C3'	8.41	132.81	120.20
1	AA	5231	DC	P-O3'-C3'	8.40	132.80	120.20
1	AA	6447	DC	P-O3'-C3'	8.40	132.80	120.20
17	AQ	40	DA	P-O3'-C3'	8.38	132.78	120.20
109	Bu	3	DC	P-O3'-C3'	8.38	132.78	120.20
1	AA	6822	DT	P-O3'-C3'	8.37	132.75	120.20
1	AA	6552	DG	P-O3'-C3'	8.36	132.74	120.20
1	AA	4582	DG	P-O3'-C3'	8.33	132.70	120.20
1	AA	5502	DG	P-O3'-C3'	8.32	132.68	120.20
158	Ch	39	DA	P-O3'-C3'	8.31	132.67	120.20
72	BJ	29	DT	P-O3'-C3'	8.30	132.64	120.20
90	Bb	2	DA	P-O3'-C3'	8.29	132.63	120.20
1	AA	3055	DT	P-O3'-C3'	8.27	132.61	120.20
1	AA	2611	DC	P-O3'-C3'	8.27	132.60	120.20
57	A4	42	DG	P-O3'-C3'	8.26	132.59	120.20
45	As	2	DT	P-O3'-C3'	8.25	132.57	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	4490	DT	P-O3'-C3'	8.24	132.56	120.20
1	AA	2607	DA	P-O3'-C3'	8.22	132.53	120.20
1	AA	4488	DA	P-O3'-C3'	8.21	132.51	120.20
1	AA	1620	DT	P-O3'-C3'	8.18	132.47	120.20
159	Ci	44	DT	P-O3'-C3'	8.18	132.46	120.20
103	Bo	7	DC	P-O3'-C3'	8.16	132.44	120.20
183	C6	32	DA	P-O3'-C3'	8.14	132.41	120.20
1	AA	3386	DA	P-O3'-C3'	8.12	132.39	120.20
73	BK	22	DA	P-O3'-C3'	8.12	132.38	120.20
84	BV	20	DG	P-O3'-C3'	8.12	132.38	120.20
159	Ci	16	DA	P-O3'-C3'	8.12	132.38	120.20
1	AA	4378	DG	P-O3'-C3'	8.10	132.35	120.20
56	A3	23	DT	P-O3'-C3'	8.10	132.35	120.20
1	AA	1776	DG	P-O3'-C3'	8.10	132.34	120.20
115	B0	38	DA	P-O3'-C3'	8.06	132.29	120.20
1	AA	5443	DA	P-O3'-C3'	8.05	132.28	120.20
1	AA	6473	DA	P-O3'-C3'	8.06	132.28	120.20
159	Ci	16	DA	C4-N9-C1'	8.05	139.13	127.05
1	AA	5363	DA	P-O3'-C3'	8.05	132.28	120.20
174	Cx	40	DT	P-O3'-C3'	8.05	132.28	120.20
159	Ci	16	DA	C8-N9-C1'	-8.05	114.98	127.05
145	CU	23	DT	P-O3'-C3'	8.04	132.25	120.20
1	AA	925	DG	P-O3'-C3'	8.03	132.24	120.20
1	AA	3483	DC	P-O3'-C3'	8.03	132.24	120.20
183	C6	18	DT	P-O3'-C3'	8.03	132.24	120.20
1	AA	3783	DG	P-O3'-C3'	8.02	132.24	120.20
1	AA	6081	DA	P-O3'-C3'	8.00	132.20	120.20
131	CG	30	DA	P-O3'-C3'	7.97	132.15	120.20
1	AA	4019	DG	P-O3'-C3'	7.94	132.10	120.20
117	B2	16	DC	P-O3'-C3'	7.87	132.00	120.20
183	C6	12	DA	P-O3'-C3'	7.86	131.99	120.20
73	BK	5	DA	P-O3'-C3'	7.85	131.97	120.20
98	Bj	20	DT	P-O3'-C3'	7.83	131.94	120.20
1	AA	292	DC	P-O3'-C3'	7.83	131.94	120.20
1	AA	4552	DG	P-O3'-C3'	7.83	131.94	120.20
50	Ax	2	DA	P-O3'-C3'	7.83	131.94	120.20
152	Cb	2	DA	P-O3'-C3'	7.81	131.92	120.20
25	AY	27	DT	P-O3'-C3'	7.81	131.92	120.20
1	AA	5963	DT	P-O3'-C3'	7.79	131.89	120.20
76	BN	27	DG	P-O3'-C3'	7.79	131.89	120.20
65	BC	20	DT	P-O3'-C3'	7.79	131.88	120.20
167	Cq	33	DC	P-O3'-C3'	7.78	131.87	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	437	DT	P-O3'-C3'	7.75	131.83	120.20
1	AA	5517	DC	P-O3'-C3'	7.74	131.81	120.20
156	Cf	2	DG	P-O3'-C3'	7.74	131.81	120.20
1	AA	596	DA	P-O3'-C3'	7.72	131.79	120.20
108	Bt	26	DC	P-O3'-C3'	7.72	131.79	120.20
1	AA	6739	DA	P-O3'-C3'	7.72	131.78	120.20
39	Am	18	DC	P-O3'-C3'	7.72	131.78	120.20
170	Ct	33	DC	P-O3'-C3'	7.71	131.77	120.20
176	Cz	15	DC	P-O3'-C3'	7.71	131.77	120.20
1	AA	1889	DT	P-O3'-C3'	7.70	131.75	120.20
134	CJ	19	DC	P-O3'-C3'	7.68	131.72	120.20
1	AA	3383	DT	P-O3'-C3'	7.67	131.70	120.20
40	An	6	DT	P-O3'-C3'	7.62	131.64	120.20
1	AA	3009	DC	P-O3'-C3'	7.62	131.62	120.20
93	Be	16	DA	C8-N9-C1'	-7.62	115.62	127.05
61	A8	18	DT	P-O3'-C3'	7.60	131.60	120.20
98	Bj	13	DG	P-O3'-C3'	7.60	131.60	120.20
1	AA	148	DA	P-O3'-C3'	7.59	131.58	120.20
1	AA	107	DA	P-O3'-C3'	7.58	131.56	120.20
183	C6	4	DT	P-O3'-C3'	7.57	131.55	120.20
188	DB	44	DC	P-O3'-C3'	7.57	131.55	120.20
112	Bx	1	DA	P-O3'-C3'	7.57	131.55	120.20
1	AA	7203	DT	P-O3'-C3'	7.56	131.54	120.20
61	A8	9	DC	P-O3'-C3'	7.55	131.53	120.20
1	AA	359	DA	P-O3'-C3'	7.54	131.52	120.20
144	CT	9	DT	P-O3'-C3'	7.54	131.51	120.20
1	AA	160	DA	P-O3'-C3'	7.53	131.49	120.20
1	AA	1065	DC	P-O3'-C3'	7.52	131.49	120.20
1	AA	5265	DG	P-O3'-C3'	7.51	131.46	120.20
1	AA	1060	DC	P-O3'-C3'	7.50	131.45	120.20
17	AQ	34	DA	P-O3'-C3'	7.49	131.44	120.20
1	AA	1823	DC	C2-N1-C1'	7.49	130.94	119.70
105	Bq	3	DA	P-O3'-C3'	7.48	131.42	120.20
1	AA	3012	DT	P-O3'-C3'	7.48	131.42	120.20
175	Cy	15	DC	P-O3'-C3'	7.48	131.42	120.20
1	AA	2495	DT	P-O3'-C3'	7.47	131.40	120.20
76	BN	31	DT	P-O3'-C3'	7.46	131.39	120.20
1	AA	812	DC	P-O3'-C3'	7.46	131.39	120.20
1	AA	2089	DG	P-O3'-C3'	7.46	131.38	120.20
1	AA	1391	DA	P-O3'-C3'	7.45	131.38	120.20
106	Br	17	DG	P-O3'-C3'	7.45	131.38	120.20
1	AA	2824	DC	P-O3'-C3'	7.45	131.38	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	759	DT	P-O3'-C3'	7.45	131.37	120.20
1	AA	1726	DA	P-O3'-C3'	7.44	131.36	120.20
152	Cb	14	DC	P-O3'-C3'	7.43	131.35	120.20
1	AA	6794	DG	P-O3'-C3'	7.42	131.32	120.20
168	Cr	41	DA	P-O3'-C3'	7.42	131.32	120.20
1	AA	1602	DC	P-O3'-C3'	7.41	131.31	120.20
44	Ar	30	DG	P-O3'-C3'	7.40	131.30	120.20
1	AA	1841	DT	P-O3'-C3'	7.39	131.29	120.20
1	AA	6589	DC	P-O3'-C3'	7.38	131.27	120.20
18	AR	21	DC	P-O5'-C5'	7.38	131.06	120.00
96	Bh	10	DG	P-O3'-C3'	7.37	131.25	120.20
3	AC	3	DT	P-O3'-C3'	7.36	131.24	120.20
1	AA	6265	DC	P-O3'-C3'	7.36	131.24	120.20
1	AA	4011	DC	P-O3'-C3'	7.35	131.23	120.20
168	Cr	49	DA	P-O3'-C3'	7.35	131.22	120.20
1	AA	3575	DC	P-O3'-C3'	7.33	131.20	120.20
1	AA	4235	DT	P-O3'-C3'	7.33	131.20	120.20
201	DO	18	DT	P-O3'-C3'	7.33	131.19	120.20
1	AA	4406	DT	P-O3'-C3'	7.33	131.19	120.20
1	AA	5139	DT	P-O3'-C3'	7.32	131.19	120.20
1	AA	4895	DT	P-O3'-C3'	7.32	131.18	120.20
80	BR	36	DC	P-O3'-C3'	7.32	131.18	120.20
176	Cz	7	DT	P-O3'-C3'	7.32	131.18	120.20
106	Br	29	DT	P-O3'-C3'	7.31	131.17	120.20
1	AA	1613	DT	P-O3'-C3'	7.31	131.16	120.20
106	Br	27	DG	C8-N9-C1'	-7.31	116.04	127.00
106	Br	27	DG	C4-N9-C1'	7.30	137.95	127.00
1	AA	6827	DT	P-O3'-C3'	7.29	131.13	120.20
1	AA	1932	DA	P-O3'-C3'	7.26	131.09	120.20
1	AA	5221	DC	P-O5'-C5'	7.26	130.88	120.00
1	AA	5592	DC	P-O3'-C3'	7.25	131.08	120.20
1	AA	4709	DT	P-O3'-C3'	7.25	131.07	120.20
131	CG	3	DA	P-O3'-C3'	7.25	131.07	120.20
1	AA	799	DT	P-O3'-C3'	7.24	131.06	120.20
198	DL	4	DC	P-O3'-C3'	7.23	131.05	120.20
1	AA	2326	DG	P-O3'-C3'	7.23	131.05	120.20
1	AA	4889	DG	P-O3'-C3'	7.23	131.05	120.20
1	AA	2383	DG	P-O3'-C3'	7.23	131.04	120.20
93	Be	16	DA	C4-N9-C1'	7.23	137.89	127.05
87	BY	6	DT	P-O3'-C3'	7.22	131.03	120.20
1	AA	5528	DG	P-O3'-C3'	7.22	131.02	120.20
91	Bc	18	DA	P-O3'-C3'	7.21	131.02	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	1215	DT	P-O3'-C3'	7.21	131.02	120.20
170	Ct	21	DG	P-O3'-C3'	7.21	131.02	120.20
81	BS	22	DT	P-O3'-C3'	7.21	131.01	120.20
1	AA	2759	DA	P-O3'-C3'	7.20	131.01	120.20
1	AA	5301	DT	P-O3'-C3'	7.20	131.00	120.20
119	B4	19	DT	P-O3'-C3'	7.20	131.00	120.20
1	AA	5489	DG	P-O3'-C3'	7.19	130.98	120.20
154	Cd	4	DG	P-O3'-C3'	7.19	130.98	120.20
10	AJ	27	DC	P-O3'-C3'	7.18	130.97	120.20
1	AA	5010	DT	P-O3'-C3'	7.17	130.95	120.20
1	AA	5595	DC	P-O3'-C3'	7.16	130.94	120.20
28	Ab	21	DT	P-O3'-C3'	7.14	130.92	120.20
184	C7	22	DT	P-O3'-C3'	7.14	130.91	120.20
171	Cu	9	DA	P-O3'-C3'	7.13	130.90	120.20
53	A0	5	DA	P-O3'-C3'	7.12	130.89	120.20
1	AA	4670	DT	P-O3'-C3'	7.12	130.88	120.20
23	AW	5	DA	P-O3'-C3'	7.12	130.88	120.20
1	AA	3323	DC	P-O5'-C5'	7.11	130.67	120.00
1	AA	3033	DA	P-O3'-C3'	7.11	130.86	120.20
173	Cw	4	DT	P-O3'-C3'	7.11	130.86	120.20
1	AA	3089	DT	P-O3'-C3'	7.09	130.83	120.20
1	AA	3388	DC	P-O3'-C3'	7.09	130.83	120.20
1	AA	706	DC	P-O5'-C5'	7.08	130.62	120.00
1	AA	3810	DA	P-O3'-C3'	7.08	130.82	120.20
1	AA	3826	DC	P-O5'-C5'	7.08	130.62	120.00
74	BL	20	DC	P-O3'-C3'	7.08	130.81	120.20
51	Ay	36	DA	P-O3'-C3'	7.07	130.80	120.20
58	A5	7	DA	P-O3'-C3'	7.07	130.80	120.20
191	DE	30	DA	P-O3'-C3'	7.06	130.79	120.20
44	Ar	12	DC	P-O3'-C3'	7.06	130.79	120.20
77	BO	19	DA	P-O3'-C3'	7.05	130.77	120.20
136	CL	17	DT	P-O3'-C3'	7.04	130.76	120.20
1	AA	6221	DC	P-O3'-C3'	7.03	130.75	120.20
1	AA	5315	DT	P-O3'-C3'	7.03	130.74	120.20
1	AA	4594	DC	P-O5'-C5'	7.02	130.53	120.00
157	Cg	7	DG	P-O3'-C3'	7.02	130.73	120.20
9	AI	15	DC	P-O3'-C3'	7.02	130.73	120.20
155	Ce	21	DT	P-O3'-C3'	7.01	130.72	120.20
1	AA	4281	DT	P-O3'-C3'	7.01	130.71	120.20
1	AA	2314	DG	P-O3'-C3'	7.00	130.71	120.20
181	C4	24	DT	P-O3'-C3'	7.00	130.71	120.20
5	AE	12	DT	P-O3'-C3'	7.00	130.70	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
58	A5	37	DG	P-O3'-C3'	7.00	130.70	120.20
1	AA	3868	DA	P-O3'-C3'	7.00	130.69	120.20
1	AA	5113	DA	P-O3'-C3'	7.00	130.69	120.20
1	AA	2125	DA	P-O3'-C3'	6.99	130.68	120.20
1	AA	4902	DC	P-O3'-C3'	6.98	130.67	120.20
136	CL	35	DC	P-O3'-C3'	6.98	130.66	120.20
187	DA	15	DT	P-O3'-C3'	6.97	130.66	120.20
169	Cs	22	DA	P-O3'-C3'	6.96	130.64	120.20
1	AA	802	DT	P-O3'-C3'	6.93	130.60	120.20
1	AA	1823	DC	C6-N1-C1'	-6.93	109.30	119.70
73	BK	21	DT	P-O3'-C3'	6.93	130.60	120.20
8	AH	29	DT	P-O3'-C3'	6.93	130.59	120.20
1	AA	5191	DC	P-O5'-C5'	6.93	130.39	120.00
1	AA	4301	DA	P-O3'-C3'	6.92	130.58	120.20
1	AA	5647	DC	P-O5'-C5'	6.91	130.36	120.00
1	AA	6012	DG	P-O3'-C3'	6.90	130.55	120.20
1	AA	5429	DC	P-O3'-C3'	6.90	130.54	120.20
1	AA	294	DT	P-O3'-C3'	6.89	130.54	120.20
1	AA	945	DT	P-O3'-C3'	6.89	130.54	120.20
156	Cf	20	DC	P-O3'-C3'	6.88	130.52	120.20
35	Ai	1	DG	P-O3'-C3'	6.88	130.51	120.20
1	AA	4074	DT	P-O3'-C3'	6.87	130.50	120.20
1	AA	6025	DC	P-O3'-C3'	6.87	130.50	120.20
60	A7	38	DA	P-O3'-C3'	6.87	130.50	120.20
1	AA	3579	DT	P-O3'-C3'	6.86	130.49	120.20
180	C3	3	DT	P-O3'-C3'	6.85	130.48	120.20
1	AA	2268	DC	P-O5'-C5'	6.84	130.26	120.00
1	AA	2858	DC	P-O3'-C3'	6.84	130.46	120.20
180	C3	13	DT	P-O3'-C3'	6.84	130.46	120.20
154	Cd	9	DA	P-O3'-C3'	6.83	130.45	120.20
1	AA	1041	DC	P-O5'-C5'	6.83	130.24	120.00
185	C8	1	DA	P-O3'-C3'	6.83	130.44	120.20
1	AA	6655	DA	P-O3'-C3'	6.83	130.44	120.20
20	AT	11	DT	P-O3'-C3'	6.82	130.42	120.20
1	AA	105	DT	P-O3'-C3'	6.81	130.42	120.20
1	AA	3387	DT	C2-N1-C1'	6.81	129.56	119.35
1	AA	1900	DC	P-O5'-C5'	6.81	130.21	120.00
1	AA	7125	DC	P-O3'-C3'	6.81	130.41	120.20
70	BH	3	DC	P-O3'-C3'	6.81	130.41	120.20
1	AA	1943	DC	P-O3'-C3'	6.80	130.41	120.20
56	A3	7	DC	P-O5'-C5'	6.80	130.21	120.00
15	AO	35	DC	P-O3'-C3'	6.80	130.40	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
29	Ac	40	DG	P-O3'-C3'	6.80	130.40	120.20
1	AA	4309	DC	P-O5'-C5'	6.79	130.18	120.00
185	C8	22	DA	P-O3'-C3'	6.79	130.38	120.20
1	AA	4784	DC	P-O5'-C5'	6.78	130.18	120.00
1	AA	3001	DG	P-O3'-C3'	6.78	130.37	120.20
1	AA	6974	DT	P-O3'-C3'	6.78	130.37	120.20
1	AA	3382	DC	P-O5'-C5'	6.77	130.16	120.00
85	BW	23	DT	P-O3'-C3'	6.76	130.34	120.20
160	Cj	1	DC	P-O3'-C3'	6.76	130.34	120.20
1	AA	4078	DC	P-O5'-C5'	6.76	130.14	120.00
170	Ct	16	DA	O3'-P-O5'	6.75	114.13	104.00
1	AA	7092	DC	P-O5'-C5'	6.75	130.13	120.00
1	AA	110	DC	P-O5'-C5'	6.74	130.11	120.00
1	AA	6151	DT	P-O3'-C3'	6.74	130.31	120.20
200	DN	20	DA	P-O3'-C3'	6.74	130.31	120.20
1	AA	817	DC	P-O3'-C3'	6.73	130.30	120.20
1	AA	1467	DC	P-O3'-C3'	6.73	130.30	120.20
11	AK	28	DT	P-O3'-C3'	6.73	130.30	120.20
116	B1	24	DC	P-O3'-C3'	6.73	130.30	120.20
1	AA	4420	DC	P-O5'-C5'	6.73	130.09	120.00
1	AA	1070	DA	P-O3'-C3'	6.72	130.28	120.20
5	AE	4	DT	P-O3'-C3'	6.72	130.28	120.20
1	AA	1328	DC	P-O5'-C5'	6.72	130.08	120.00
196	DJ	22	DC	P-O3'-C3'	6.71	130.26	120.20
82	BT	35	DA	P-O3'-C3'	6.71	130.26	120.20
180	C3	20	DG	P-O3'-C3'	6.71	130.26	120.20
1	AA	3532	DA	P-O3'-C3'	6.70	130.26	120.20
52	Az	15	DC	P-O3'-C3'	6.69	130.24	120.20
151	Ca	18	DT	P-O3'-C3'	6.69	130.24	120.20
151	Ca	27	DA	P-O3'-C3'	6.69	130.24	120.20
114	Bz	33	DT	P-O3'-C3'	6.68	130.22	120.20
151	Ca	16	DT	P-O3'-C3'	6.68	130.21	120.20
5	AE	22	DG	P-O3'-C3'	6.67	130.20	120.20
1	AA	1067	DC	P-O5'-C5'	6.66	130.00	120.00
1	AA	817	DC	P-O5'-C5'	6.66	129.99	120.00
44	Ar	3	DT	P-O3'-C3'	6.66	130.19	120.20
50	Ax	29	DT	P-O3'-C3'	6.66	130.19	120.20
1	AA	3311	DG	P-O3'-C3'	6.65	130.18	120.20
1	AA	5776	DC	P-O5'-C5'	6.65	129.98	120.00
1	AA	3406	DG	P-O3'-C3'	6.65	130.17	120.20
202	DP	17	DC	P-O3'-C3'	6.65	130.17	120.20
81	BS	14	DT	P-O3'-C3'	6.63	130.15	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	4238	DT	P-O3'-C3'	6.63	130.14	120.20
1	AA	3193	DA	P-O3'-C3'	6.62	130.13	120.20
1	AA	5123	DC	P-O5'-C5'	6.62	129.93	120.00
28	Ab	17	DT	P-O3'-C3'	6.62	130.12	120.20
175	Cy	3	DA	P-O3'-C3'	6.60	130.10	120.20
1	AA	5367	DT	P-O3'-C3'	6.60	130.10	120.20
1	AA	5604	DC	P-O3'-C3'	6.59	130.08	120.20
85	BW	30	DT	P-O3'-C3'	6.59	130.08	120.20
1	AA	4361	DT	P-O3'-C3'	6.58	130.07	120.20
1	AA	6895	DT	P-O3'-C3'	6.58	130.06	120.20
1	AA	5683	DC	P-O3'-C3'	6.58	130.06	120.20
1	AA	1023	DA	P-O3'-C3'	6.57	130.06	120.20
1	AA	1079	DC	P-O3'-C3'	6.57	130.06	120.20
1	AA	3360	DC	P-O5'-C5'	6.57	129.85	120.00
161	Ck	19	DT	P-O3'-C3'	6.57	130.05	120.20
1	AA	3982	DC	P-O3'-C3'	6.56	130.04	120.20
1	AA	734	DC	P-O3'-C3'	6.56	130.04	120.20
184	C7	7	DC	P-O5'-C5'	6.55	129.83	120.00
1	AA	5961	DG	P-O3'-C3'	6.54	130.01	120.20
1	AA	6054	DG	P-O3'-C3'	6.54	130.01	120.20
26	AZ	31	DC	P-O5'-C5'	6.54	129.81	120.00
109	Bu	24	DA	C4-N9-C1'	6.53	136.85	127.05
148	CX	18	DT	P-O3'-C3'	6.53	129.99	120.20
1	AA	1984	DC	P-O5'-C5'	6.52	129.78	120.00
1	AA	5860	DG	P-O3'-C3'	6.52	129.98	120.20
100	Bl	2	DA	P-O3'-C3'	6.52	129.97	120.20
1	AA	1036	DG	P-O3'-C3'	6.51	129.97	120.20
55	A2	31	DC	P-O3'-C3'	6.51	129.97	120.20
1	AA	370	DC	P-O3'-C3'	6.51	129.96	120.20
1	AA	2007	DG	P-O3'-C3'	6.50	129.96	120.20
1	AA	4772	DC	P-O5'-C5'	6.50	129.74	120.00
1	AA	4258	DT	P-O3'-C3'	6.49	129.94	120.20
1	AA	2335	DA	P-O3'-C3'	6.49	129.94	120.20
171	Cu	31	DG	P-O3'-C3'	6.49	129.94	120.20
27	Aa	5	DC	P-O3'-C3'	6.49	129.93	120.20
1	AA	4366	DC	P-O5'-C5'	6.47	129.71	120.00
182	C5	7	DC	P-O5'-C5'	6.47	129.71	120.00
1	AA	2574	DG	P-O3'-C3'	6.47	129.90	120.20
1	AA	4481	DC	P-O5'-C5'	6.47	129.70	120.00
1	AA	5153	DT	P-O3'-C3'	6.47	129.91	120.20
74	BL	21	DA	C4-N9-C1'	6.47	136.75	127.05
155	Ce	14	DT	P-O3'-C3'	6.47	129.91	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	4926	DC	P-O5'-C5'	6.46	129.70	120.00
1	AA	5441	DC	P-O5'-C5'	6.46	129.69	120.00
164	Cn	16	DC	P-O3'-C3'	6.45	129.87	120.20
98	Bj	39	DT	P-O3'-C3'	6.44	129.86	120.20
1	AA	5922	DG	P-O3'-C3'	6.44	129.86	120.20
1	AA	614	DG	P-O3'-C3'	6.42	129.84	120.20
169	Cs	6	DC	P-O3'-C3'	6.42	129.82	120.20
1	AA	900	DC	P-O5'-C5'	6.40	129.60	120.00
1	AA	2493	DC	P-O5'-C5'	6.39	129.59	120.00
186	C9	35	DC	P-O5'-C5'	6.39	129.59	120.00
1	AA	1922	DT	P-O5'-C5'	6.39	129.58	120.00
182	C5	20	DT	P-O3'-C3'	6.39	129.79	120.20
1	AA	3422	DC	P-O5'-C5'	6.39	129.58	120.00
1	AA	5758	DG	P-O3'-C3'	6.38	129.78	120.20
24	AX	13	DG	P-O3'-C3'	6.38	129.78	120.20
1	AA	666	DC	P-O5'-C5'	6.38	129.57	120.00
1	AA	1078	DC	P-O3'-C3'	6.36	129.74	120.20
1	AA	6361	DA	P-O3'-C3'	6.34	129.71	120.20
1	AA	6256	DC	P-O5'-C5'	6.33	129.50	120.00
140	CP	2	DT	P-O3'-C3'	6.33	129.70	120.20
1	AA	810	DG	P-O3'-C3'	6.33	129.70	120.20
74	BL	21	DA	C8-N9-C1'	-6.33	117.55	127.05
1	AA	2837	DT	P-O3'-C3'	6.33	129.69	120.20
1	AA	5420	DT	P-O3'-C3'	6.33	129.69	120.20
87	BY	30	DC	P-O5'-C5'	6.31	129.46	120.00
1	AA	6541	DG	P-O3'-C3'	6.30	129.65	120.20
1	AA	1381	DG	P-O3'-C3'	6.30	129.65	120.20
41	Ao	2	DA	P-O3'-C3'	6.30	129.65	120.20
1	AA	4169	DA	P-O3'-C3'	6.29	129.64	120.20
1	AA	4007	DC	P-O5'-C5'	6.29	129.43	120.00
1	AA	1947	DC	P-O5'-C5'	6.28	129.43	120.00
1	AA	2771	DC	P-O5'-C5'	6.28	129.42	120.00
1	AA	5896	DC	P-O3'-C3'	6.28	129.62	120.20
162	Cl	18	DA	P-O3'-C3'	6.28	129.62	120.20
1	AA	11	DC	P-O5'-C5'	6.27	129.41	120.00
14	AN	9	DA	P-O3'-C3'	6.27	129.61	120.20
151	Ca	31	DT	P-O3'-C3'	6.27	129.60	120.20
66	BD	1	DC	P-O3'-C3'	6.26	129.59	120.20
1	AA	6025	DC	P-O5'-C5'	6.26	129.39	120.00
1	AA	1982	DC	P-O3'-C3'	6.26	129.59	120.20
1	AA	2305	DC	P-O5'-C5'	6.25	129.38	120.00
157	Cg	44	DG	P-O3'-C3'	6.25	129.57	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
65	BC	22	DT	P-O3'-C3'	6.25	129.57	120.20
1	AA	262	DC	P-O5'-C5'	6.24	129.36	120.00
108	Bt	28	DG	P-O3'-C3'	6.22	129.53	120.20
1	AA	2833	DT	P-O3'-C3'	6.21	129.52	120.20
9	AI	27	DT	O4'-C1'-C2'	-6.21	97.08	106.40
65	BC	35	DC	P-O3'-C3'	6.20	129.50	120.20
1	AA	7029	DC	P-O5'-C5'	6.20	129.30	120.00
1	AA	512	DA	P-O3'-C3'	6.19	129.48	120.20
1	AA	971	DC	P-O5'-C5'	6.18	129.27	120.00
88	BZ	20	DG	O4'-C4'-C3'	-6.18	96.13	105.40
19	AS	11	DA	P-O3'-C3'	6.17	129.46	120.20
1	AA	6290	DA	P-O3'-C3'	6.17	129.45	120.20
1	AA	6907	DC	P-O5'-C5'	6.17	129.25	120.00
1	AA	421	DC	P-O3'-C3'	6.16	129.44	120.20
1	AA	2913	DC	P-O3'-C3'	6.14	129.41	120.20
109	Bu	24	DA	C8-N9-C1'	-6.13	117.86	127.05
1	AA	646	DC	P-O5'-C5'	6.12	129.19	120.00
1	AA	5835	DC	P-O5'-C5'	6.12	129.19	120.00
1	AA	5600	DC	P-O5'-C5'	6.12	129.19	120.00
52	Az	39	DG	P-O3'-C3'	6.12	129.38	120.20
177	C0	19	DT	P-O3'-C3'	6.12	129.38	120.20
1	AA	5929	DC	P-O5'-C5'	6.12	129.17	120.00
166	Cp	2	DC	P-O5'-C5'	6.12	129.17	120.00
1	AA	5282	DC	P-O5'-C5'	6.10	129.15	120.00
80	BR	2	DC	P-O5'-C5'	6.10	129.15	120.00
1	AA	3352	DC	P-O3'-C3'	6.09	129.34	120.20
168	Cr	30	DG	P-O3'-C3'	6.09	129.34	120.20
1	AA	2720	DA	O4'-C4'-C3'	-6.09	96.27	105.40
1	AA	5595	DC	P-O5'-C5'	6.09	129.13	120.00
74	BL	28	DA	P-O3'-C3'	6.08	129.32	120.20
89	Ba	3	DC	P-O3'-C3'	6.08	129.32	120.20
1	AA	2911	DA	P-O3'-C3'	6.07	129.30	120.20
1	AA	5081	DG	P-O3'-C3'	6.06	129.29	120.20
1	AA	7031	DC	P-O5'-C5'	6.05	129.08	120.00
1	AA	3387	DT	C6-N1-C1'	-6.05	110.28	119.35
65	BC	35	DC	P-O5'-C5'	6.05	129.07	120.00
12	AL	15	DC	P-O5'-C5'	6.04	129.07	120.00
1	AA	4655	DT	P-O5'-C5'	6.03	129.05	120.00
1	AA	6382	DG	P-O3'-C3'	6.03	129.25	120.20
41	Ao	3	DT	O4'-C4'-C3'	-6.03	96.36	105.40
1	AA	4686	DT	P-O5'-C5'	6.02	129.03	120.00
1	AA	3461	DG	P-O3'-C3'	6.01	129.22	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
74	BL	27	DC	P-O3'-C3'	6.00	129.20	120.20
1	AA	1677	DT	P-O5'-C5'	5.99	128.98	120.00
1	AA	4707	DA	P-O3'-C3'	5.98	129.18	120.20
1	AA	713	DC	P-O5'-C5'	5.98	128.97	120.00
170	Ct	17	DA	O4'-C1'-C2'	-5.98	97.44	106.40
1	AA	1076	DG	P-O3'-C3'	5.98	129.16	120.20
139	CO	10	DG	P-O3'-C3'	5.97	129.16	120.20
1	AA	407	DC	P-O5'-C5'	5.96	128.94	120.00
170	Ct	17	DA	O5'-C5'-C4'	5.95	119.72	110.80
1	AA	1897	DC	P-O5'-C5'	5.94	128.92	120.00
1	AA	1657	DC	P-O3'-C3'	5.94	129.12	120.20
1	AA	2984	DC	P-O5'-C5'	5.94	128.91	120.00
1	AA	557	DC	P-O5'-C5'	5.93	128.90	120.00
1	AA	3965	DT	P-O3'-C3'	5.92	129.08	120.20
1	AA	1895	DA	O4'-C4'-C3'	-5.92	96.52	105.40
57	A4	2	DC	P-O5'-C5'	5.91	128.87	120.00
1	AA	4937	DC	P-O5'-C5'	5.89	128.83	120.00
1	AA	3354	DC	P-O5'-C5'	5.88	128.82	120.00
1	AA	2758	DT	P-O3'-C3'	5.85	128.97	120.20
1	AA	6464	DG	P-O3'-C3'	5.84	128.97	120.20
1	AA	4715	DT	P-O3'-C3'	5.83	128.95	120.20
66	BD	31	DC	P-O5'-C5'	5.83	128.75	120.00
187	DA	14	DG	P-O3'-C3'	5.83	128.94	120.20
1	AA	1926	DG	P-O3'-C3'	5.80	128.90	120.20
1	AA	3005	DA	P-O5'-C5'	5.80	128.70	120.00
131	CG	37	DG	P-O3'-C3'	5.80	128.90	120.20
92	Bd	24	DA	P-O3'-C3'	5.78	128.87	120.20
1	AA	4909	DA	P-O5'-C5'	5.78	128.66	120.00
1	AA	572	DC	P-O3'-C3'	5.77	128.86	120.20
1	AA	1005	DC	P-O3'-C3'	5.77	128.85	120.20
99	Bk	2	DA	P-O3'-C3'	5.77	128.85	120.20
1	AA	4485	DC	P-O5'-C5'	5.76	128.65	120.00
1	AA	6962	DG	P-O3'-C3'	5.76	128.85	120.20
144	CT	34	DT	P-O3'-C3'	5.76	128.83	120.20
1	AA	1119	DG	O4'-C4'-C3'	-5.74	96.79	105.40
195	DI	23	DC	P-O3'-C3'	5.73	128.79	120.20
136	CL	20	DT	P-O3'-C3'	5.72	128.78	120.20
1	AA	869	DT	P-O5'-C5'	5.70	128.56	120.00
154	Cd	25	DC	P-O3'-C3'	5.70	128.75	120.20
89	Ba	5	DC	P-O5'-C5'	5.70	128.55	120.00
1	AA	1863	DG	P-O3'-C3'	5.70	128.75	120.20
1	AA	3853	DC	P-O5'-C5'	5.70	128.54	120.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	7229	DC	P-O5'-C5'	5.69	128.53	120.00
1	AA	15	DT	O4'-C1'-C2'	-5.68	97.88	106.40
1	AA	5477	DC	P-O5'-C5'	5.67	128.51	120.00
43	Aq	24	DT	P-O3'-C3'	5.67	128.71	120.20
1	AA	5715	DC	P-O5'-C5'	5.67	128.50	120.00
168	Cr	21	DA	P-O3'-C3'	5.67	128.70	120.20
1	AA	3131	DG	P-O5'-C5'	5.66	128.49	120.00
120	B5	26	DC	P-O5'-C5'	5.66	128.49	120.00
25	AY	1	DA	P-O3'-C3'	5.65	128.67	120.20
1	AA	5648	DC	P-O5'-C5'	5.64	128.46	120.00
1	AA	6614	DT	C2-N1-C1'	5.64	127.81	119.35
52	Az	32	DC	P-O5'-C5'	5.64	128.46	120.00
159	Ci	24	DC	P-O5'-C5'	5.64	128.46	120.00
1	AA	1999	DC	P-O5'-C5'	5.64	128.45	120.00
1	AA	3387	DT	O4'-C4'-C3'	-5.63	96.95	105.40
41	Ao	3	DT	C2-N1-C1'	5.63	127.80	119.35
1	AA	5650	DT	O4'-C1'-C2'	-5.63	97.96	106.40
1	AA	164	DC	P-O5'-C5'	5.62	128.44	120.00
1	AA	4451	DC	P-O5'-C5'	5.62	128.43	120.00
123	B8	14	DC	P-O5'-C5'	5.61	128.42	120.00
196	DJ	42	DT	P-O3'-C3'	5.61	128.62	120.20
1	AA	4778	DT	P-O5'-C5'	5.61	128.42	120.00
1	AA	3137	DA	P-O3'-C3'	5.61	128.62	120.20
1	AA	3171	DC	P-O5'-C5'	5.61	128.41	120.00
1	AA	6036	DG	P-O5'-C5'	5.60	128.40	120.00
1	AA	7176	DT	P-O3'-C3'	5.60	128.60	120.20
80	BR	26	DA	P-O3'-C3'	5.60	128.60	120.20
1	AA	6038	DC	P-O5'-C5'	5.60	128.40	120.00
1	AA	6649	DC	P-O3'-C3'	5.60	128.60	120.20
58	A5	24	DC	P-O5'-C5'	5.59	128.39	120.00
1	AA	6445	DG	P-O5'-C5'	5.59	128.38	120.00
1	AA	2766	DG	P-O3'-C3'	5.58	128.58	120.20
1	AA	5954	DG	P-O3'-C3'	5.58	128.58	120.20
92	Bd	38	DC	P-O5'-C5'	5.58	128.37	120.00
1	AA	1087	DC	P-O5'-C5'	5.58	128.37	120.00
1	AA	5590	DC	P-O5'-C5'	5.58	128.37	120.00
1	AA	3809	DT	P-O3'-C3'	5.58	128.56	120.20
1	AA	399	DC	P-O5'-C5'	5.57	128.36	120.00
1	AA	295	DG	P-O3'-C3'	5.56	128.54	120.20
1	AA	863	DA	P-O5'-C5'	5.56	128.34	120.00
129	CE	26	DG	P-O3'-C3'	5.56	128.54	120.20
1	AA	5494	DC	P-O5'-C5'	5.55	128.33	120.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	2077	DC	P-O3'-C3'	5.55	128.53	120.20
89	Ba	21	DC	P-O5'-C5'	5.55	128.32	120.00
1	AA	1130	DC	P-O5'-C5'	5.54	128.31	120.00
1	AA	4503	DT	P-O3'-C3'	5.54	128.51	120.20
1	AA	3027	DT	P-O5'-C5'	5.54	128.31	120.00
1	AA	3423	DT	P-O5'-C5'	5.52	128.28	120.00
1	AA	1037	DT	P-O3'-C3'	5.52	128.48	120.20
1	AA	2041	DA	O4'-C1'-C2'	-5.52	98.12	106.40
118	B3	30	DC	P-O5'-C5'	5.52	128.28	120.00
83	BU	17	DG	P-O3'-C3'	5.51	128.46	120.20
26	AZ	43	DG	O4'-C1'-C2'	-5.51	98.14	106.40
181	C4	16	DC	P-O5'-C5'	5.50	128.26	120.00
202	DP	13	DA	P-O3'-C3'	5.50	128.46	120.20
1	AA	6588	DC	P-O3'-C3'	5.50	128.45	120.20
1	AA	6315	DG	P-O3'-C3'	5.50	128.45	120.20
1	AA	107	DA	C1'-O4'-C4'	-5.50	101.46	109.70
1	AA	4706	DT	P-O3'-C3'	5.48	128.42	120.20
1	AA	4543	DG	P-O3'-C3'	5.48	128.42	120.20
50	Ax	15	DC	P-O5'-C5'	5.48	128.22	120.00
158	Ch	6	DC	P-O5'-C5'	5.48	128.21	120.00
1	AA	2828	DC	P-O5'-C5'	5.47	128.21	120.00
21	AU	15	DC	P-O5'-C5'	5.47	128.21	120.00
10	AJ	10	DA	P-O3'-C3'	5.47	128.40	120.20
1	AA	116	DC	P-O3'-C3'	5.46	128.40	120.20
1	AA	6569	DC	P-O5'-C5'	5.46	128.20	120.00
1	AA	1915	DC	P-O3'-C3'	5.46	128.39	120.20
1	AA	5797	DC	P-O5'-C5'	5.46	128.19	120.00
1	AA	2719	DA	P-O3'-C3'	5.46	128.39	120.20
1	AA	5015	DA	P-O3'-C3'	5.45	128.38	120.20
61	A8	14	DT	P-O5'-C5'	5.45	128.17	120.00
71	BI	26	DA	P-O3'-C3'	5.45	128.38	120.20
75	BM	22	DC	P-O5'-C5'	5.44	128.17	120.00
1	AA	4019	DG	C1'-O4'-C4'	-5.44	101.54	109.70
43	Aq	1	DA	O4'-C4'-C3'	-5.44	97.24	105.40
1	AA	6938	DC	P-O5'-C5'	5.43	128.15	120.00
1	AA	3738	DG	P-O3'-C3'	5.43	128.35	120.20
137	CM	30	DC	P-O5'-C5'	5.43	128.15	120.00
120	B5	41	DC	P-O3'-C3'	5.43	128.34	120.20
1	AA	2603	DC	P-O5'-C5'	5.42	128.14	120.00
1	AA	7128	DC	P-O5'-C5'	5.42	128.14	120.00
1	AA	3322	DT	C6-N1-C1'	-5.41	111.23	119.35
1	AA	3567	DG	P-O3'-C3'	5.41	128.31	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
123	B8	35	DC	P-O5'-C5'	5.40	128.11	120.00
1	AA	3322	DT	C2-N1-C1'	5.40	127.45	119.35
189	DC	30	DT	P-O3'-C3'	5.40	128.30	120.20
181	C4	9	DC	P-O3'-C3'	5.39	128.29	120.20
16	AP	23	DC	P-O5'-C5'	5.39	128.09	120.00
117	B2	16	DC	P-O5'-C5'	5.39	128.08	120.00
72	BJ	15	DT	P-O3'-C3'	5.39	128.28	120.20
106	Br	27	DG	C1'-O4'-C4'	-5.39	101.62	109.70
123	B8	19	DC	P-O5'-C5'	5.38	128.07	120.00
1	AA	6661	DA	P-O3'-C3'	5.38	128.27	120.20
60	A7	15	DC	P-O5'-C5'	5.38	128.07	120.00
1	AA	5197	DG	P-O3'-C3'	5.37	128.26	120.20
1	AA	4768	DC	P-O5'-C5'	5.37	128.05	120.00
78	BP	39	DC	P-O5'-C5'	5.36	128.04	120.00
128	CD	16	DC	P-O3'-C3'	5.36	128.24	120.20
1	AA	7033	DC	P-O3'-C3'	5.36	128.24	120.20
1	AA	1402	DA	C1'-O4'-C4'	-5.35	101.68	109.70
11	AK	14	DA	P-O3'-C3'	5.34	128.21	120.20
62	A9	7	DT	O4'-C1'-C2'	-5.34	98.39	106.40
1	AA	1407	DC	P-O5'-C5'	5.33	128.00	120.00
41	Ao	8	DG	P-O3'-C3'	5.33	128.19	120.20
1	AA	5402	DT	P-O3'-C3'	5.32	128.19	120.20
1	AA	5947	DG	P-O3'-C3'	5.32	128.18	120.20
1	AA	6337	DC	P-O5'-C5'	5.32	127.98	120.00
49	Aw	7	DC	P-O5'-C5'	5.32	127.99	120.00
74	BL	21	DA	C1'-O4'-C4'	-5.32	101.72	109.70
158	Ch	39	DA	O4'-C1'-C2'	-5.32	98.41	106.40
5	AE	47	DA	P-O3'-C3'	5.32	128.18	120.20
83	BU	9	DC	P-O5'-C5'	5.32	127.98	120.00
1	AA	6515	DC	O4'-C1'-C2'	-5.32	98.42	106.40
176	Cz	30	DC	P-O5'-C5'	5.31	127.97	120.00
90	Bb	26	DC	P-O3'-C3'	5.31	128.16	120.20
1	AA	3632	DT	O4'-C1'-C2'	-5.30	98.45	106.40
81	BS	6	DC	P-O5'-C5'	5.30	127.95	120.00
1	AA	2396	DC	P-O5'-C5'	5.30	127.94	120.00
177	C0	30	DT	P-O5'-C5'	5.30	127.94	120.00
18	AR	22	DC	P-O5'-C5'	5.29	127.94	120.00
1	AA	7131	DC	P-O5'-C5'	5.29	127.93	120.00
67	BE	34	DG	P-O3'-C3'	5.28	128.12	120.20
125	CA	21	DG	O4'-C4'-C3'	-5.28	97.48	105.40
1	AA	2537	DC	P-O5'-C5'	5.27	127.91	120.00
1	AA	1993	DC	P-O5'-C5'	5.27	127.90	120.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	131	DA	P-O3'-C3'	5.27	128.10	120.20
1	AA	1317	DC	P-O5'-C5'	5.27	127.90	120.00
93	Be	37	DC	P-O5'-C5'	5.26	127.89	120.00
58	A5	33	DA	P-O3'-C3'	5.26	128.09	120.20
1	AA	6093	DA	P-O5'-C5'	5.26	127.88	120.00
1	AA	2934	DC	P-O5'-C5'	5.25	127.88	120.00
1	AA	125	DC	P-O5'-C5'	5.25	127.88	120.00
91	Bc	4	DG	P-O3'-C3'	5.25	128.08	120.20
118	B3	16	DG	P-O5'-C5'	5.25	127.88	120.00
122	B7	13	DC	P-O5'-C5'	5.25	127.87	120.00
1	AA	2938	DT	P-O5'-C5'	5.24	127.86	120.00
37	Ak	4	DT	O4'-C1'-C2'	-5.24	98.54	106.40
128	CD	17	DA	O4'-C1'-C2'	-5.24	98.54	106.40
1	AA	1031	DC	P-O5'-C5'	5.24	127.86	120.00
1	AA	6826	DC	P-O5'-C5'	5.23	127.85	120.00
1	AA	5587	DC	P-O5'-C5'	5.23	127.85	120.00
71	BI	20	DC	P-O5'-C5'	5.23	127.84	120.00
1	AA	4153	DA	O4'-C1'-C2'	-5.23	98.56	106.40
117	B2	27	DT	P-O3'-C3'	5.23	128.04	120.20
183	C6	38	DG	O4'-C1'-C2'	-5.23	98.56	106.40
1	AA	1663	DC	P-O3'-C3'	5.22	128.04	120.20
1	AA	2622	DG	P-O3'-C3'	5.22	128.04	120.20
1	AA	3085	DC	P-O5'-C5'	5.22	127.83	120.00
1	AA	4700	DC	P-O5'-C5'	5.22	127.83	120.00
1	AA	4913	DC	P-O5'-C5'	5.22	127.83	120.00
196	DJ	38	DC	P-O5'-C5'	5.21	127.82	120.00
41	Ao	3	DT	C6-N1-C1'	-5.21	111.53	119.35
131	CG	14	DT	P-O5'-C5'	5.21	127.82	120.00
143	CS	33	DA	P-O5'-C5'	5.21	127.82	120.00
1	AA	373	DC	P-O5'-C5'	5.21	127.81	120.00
93	Be	24	DC	P-O5'-C5'	5.21	127.81	120.00
58	A5	33	DA	O4'-C1'-C2'	-5.20	98.59	106.40
180	C3	4	DT	C4'-C3'-O3'	5.20	117.80	110.00
1	AA	5178	DC	P-O5'-C5'	5.20	127.80	120.00
1	AA	5148	DG	P-O3'-C3'	5.20	127.99	120.20
126	CB	1	DT	O4'-C1'-C2'	-5.19	98.61	106.40
115	B0	1	DC	O4'-C4'-C3'	-5.19	97.61	105.40
145	CU	19	DT	O4'-C1'-C2'	-5.19	98.61	106.40
102	Bn	39	DC	P-O5'-C5'	5.19	127.78	120.00
165	Co	4	DC	P-O5'-C5'	5.19	127.78	120.00
195	DI	36	DC	P-O5'-C5'	5.19	127.78	120.00
1	AA	207	DA	P-O3'-C3'	5.18	127.97	120.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	2996	DA	P-O5'-C5'	5.18	127.78	120.00
1	AA	2917	DG	O4'-C4'-C3'	-5.18	97.63	105.40
88	BZ	12	DG	P-O3'-C3'	5.18	127.97	120.20
174	Cx	1	DT	C1'-O4'-C4'	-5.18	101.93	109.70
1	AA	3315	DC	P-O5'-C5'	5.18	127.77	120.00
1	AA	4707	DA	O4'-C1'-C2'	-5.18	98.64	106.40
190	DD	9	DA	O4'-C1'-C2'	-5.18	98.64	106.40
12	AL	31	DC	P-O5'-C5'	5.17	127.76	120.00
198	DL	17	DA	P-O3'-C3'	5.17	127.96	120.20
1	AA	230	DG	P-O5'-C5'	5.17	127.76	120.00
1	AA	4107	DG	P-O3'-C3'	5.17	127.96	120.20
107	Bs	15	DC	P-O5'-C5'	5.17	127.75	120.00
164	Cn	12	DC	P-O5'-C5'	5.17	127.75	120.00
194	DH	26	DC	P-O5'-C5'	5.17	127.75	120.00
116	B1	29	DC	P-O5'-C5'	5.17	127.75	120.00
11	AK	34	DC	P-O5'-C5'	5.16	127.74	120.00
1	AA	802	DT	O4'-C1'-C2'	-5.16	98.66	106.40
50	Ax	5	DC	P-O5'-C5'	5.16	127.74	120.00
159	Ci	44	DT	O4'-C1'-C2'	-5.16	98.66	106.40
1	AA	5092	DC	P-O3'-C3'	5.16	127.94	120.20
59	A6	32	DC	P-O5'-C5'	5.16	127.74	120.00
1	AA	6476	DG	P-O3'-C3'	5.15	127.93	120.20
53	A0	46	DA	P-O5'-C5'	5.15	127.73	120.00
1	AA	4488	DA	C4'-C3'-O3'	5.15	117.73	110.00
123	B8	16	DG	O4'-C1'-C2'	-5.15	98.68	106.40
27	Aa	9	DA	O4'-C1'-C2'	-5.15	98.68	106.40
1	AA	2675	DC	P-O5'-C5'	5.14	127.72	120.00
1	AA	2747	DC	P-O5'-C5'	5.14	127.72	120.00
1	AA	3014	DC	P-O5'-C5'	5.14	127.71	120.00
1	AA	409	DG	P-O3'-C3'	5.14	127.91	120.20
1	AA	6125	DC	P-O5'-C5'	5.14	127.70	120.00
55	A2	23	DC	P-O5'-C5'	5.14	127.70	120.00
126	CB	23	DC	P-O5'-C5'	5.14	127.70	120.00
1	AA	6048	DA	P-O3'-C3'	5.13	127.90	120.20
1	AA	3028	DC	P-O3'-C3'	5.13	127.89	120.20
77	BO	1	DA	O4'-C4'-C3'	-5.12	97.72	105.40
1	AA	2055	DC	P-O5'-C5'	5.12	127.68	120.00
25	AY	4	DC	P-O5'-C5'	5.12	127.68	120.00
121	B6	8	DC	P-O5'-C5'	5.12	127.68	120.00
159	Ci	19	DA	P-O3'-C3'	5.12	127.87	120.20
143	CS	12	DC	P-O3'-C3'	5.11	127.87	120.20
174	Cx	1	DT	O4'-C1'-C2'	-5.11	98.73	106.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	3012	DT	C4'-C3'-O3'	5.11	117.66	110.00
70	BH	6	DC	P-O5'-C5'	5.11	127.66	120.00
1	AA	3538	DG	P-O3'-C3'	5.11	127.86	120.20
1	AA	5006	DC	P-O5'-C5'	5.11	127.66	120.00
1	AA	7048	DA	P-O5'-C5'	5.11	127.66	120.00
72	BJ	31	DC	P-O3'-C3'	5.11	127.86	120.20
136	CL	19	DT	O4'-C1'-C2'	-5.11	98.74	106.40
1	AA	1296	DC	P-O5'-C5'	5.10	127.66	120.00
50	Ax	12	DT	P-O3'-C3'	5.10	127.86	120.20
1	AA	4802	DC	P-O5'-C5'	5.10	127.65	120.00
38	Al	31	DC	P-O5'-C5'	5.10	127.65	120.00
86	BX	9	DA	P-O3'-C3'	5.10	127.85	120.20
139	CO	35	DC	P-O3'-C3'	5.10	127.85	120.20
193	DG	37	DG	P-O3'-C3'	5.10	127.84	120.20
1	AA	2033	DC	P-O5'-C5'	5.09	127.64	120.00
1	AA	618	DG	P-O3'-C3'	5.09	127.84	120.20
1	AA	5997	DC	P-O5'-C5'	5.09	127.63	120.00
1	AA	6415	DC	P-O5'-C5'	5.09	127.63	120.00
53	A0	48	DC	P-O5'-C5'	5.09	127.63	120.00
1	AA	683	DC	P-O5'-C5'	5.09	127.63	120.00
108	Bt	17	DG	P-O3'-C3'	5.09	127.83	120.20
186	C9	32	DC	P-O5'-C5'	5.08	127.63	120.00
1	AA	6412	DC	P-O5'-C5'	5.08	127.62	120.00
21	AU	1	DT	O4'-C4'-C3'	-5.08	97.78	105.40
154	Cd	17	DA	O4'-C1'-C2'	-5.08	98.78	106.40
1	AA	1733	DG	P-O3'-C3'	5.08	127.82	120.20
195	DI	28	DC	P-O5'-C5'	5.08	127.62	120.00
106	Br	23	DC	P-O3'-C3'	5.08	127.82	120.20
1	AA	3652	DC	P-O5'-C5'	5.08	127.62	120.00
1	AA	2969	DG	O4'-C1'-C2'	-5.08	98.79	106.40
1	AA	4827	DG	P-O3'-C3'	5.08	127.81	120.20
124	B9	3	DG	P-O3'-C3'	5.07	127.81	120.20
186	C9	15	DC	P-O5'-C5'	5.07	127.61	120.00
188	DB	26	DA	P-O3'-C3'	5.07	127.81	120.20
189	DC	30	DT	C4'-C3'-O3'	5.07	117.61	110.00
1	AA	4371	DT	C2-N1-C1'	5.07	126.96	119.35
18	AR	6	DG	P-O3'-C3'	5.07	127.81	120.20
1	AA	2269	DC	P-O5'-C5'	5.07	127.60	120.00
1	AA	4595	DC	P-O5'-C5'	5.07	127.60	120.00
1	AA	43	DC	P-O5'-C5'	5.07	127.60	120.00
1	AA	531	DT	P-O3'-C3'	5.07	127.80	120.20
1	AA	707	DC	P-O5'-C5'	5.06	127.60	120.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AA	4274	DC	P-O5'-C5'	5.06	127.60	120.00
1	AA	2902	DC	P-O5'-C5'	5.06	127.59	120.00
106	Br	9	DC	P-O5'-C5'	5.06	127.59	120.00
1	AA	6809	DC	P-O5'-C5'	5.06	127.59	120.00
66	BD	25	DC	P-O3'-C3'	5.06	127.79	120.20
109	Bu	8	DC	P-O5'-C5'	5.06	127.59	120.00
146	CV	11	DC	P-O5'-C5'	5.06	127.59	120.00
144	CT	46	DC	P-O5'-C5'	5.06	127.59	120.00
142	CR	16	DC	P-O5'-C5'	5.06	127.58	120.00
89	Ba	15	DC	P-O5'-C5'	5.05	127.58	120.00
53	A0	2	DC	P-O3'-C3'	5.05	127.77	120.20
68	BF	1	DT	O4'-C4'-C3'	-5.05	97.83	105.40
109	Bu	31	DC	P-O5'-C5'	5.05	127.57	120.00
125	CA	38	DC	P-O5'-C5'	5.04	127.56	120.00
187	DA	23	DC	P-O5'-C5'	5.04	127.56	120.00
1	AA	6442	DA	P-O3'-C3'	5.04	127.76	120.20
1	AA	6614	DT	C6-N1-C1'	-5.04	111.79	119.35
1	AA	3135	DC	P-O3'-C3'	5.04	127.75	120.20
203	DQ	36	DC	P-O5'-C5'	5.04	127.55	120.00
1	AA	5687	DC	P-O5'-C5'	5.03	127.55	120.00
79	BQ	28	DC	P-O5'-C5'	5.03	127.55	120.00
1	AA	5502	DG	C4'-C3'-O3'	5.03	117.55	110.00
135	CK	12	DC	P-O5'-C5'	5.03	127.55	120.00
1	AA	65	DC	P-O3'-C3'	5.03	127.75	120.20
1	AA	2666	DA	P-O3'-C3'	5.03	127.75	120.20
8	AH	11	DC	P-O5'-C5'	5.03	127.54	120.00
140	CP	37	DC	P-O5'-C5'	5.03	127.54	120.00
1	AA	5930	DT	P-O5'-C5'	5.02	127.54	120.00
1	AA	6900	DC	P-O5'-C5'	5.02	127.54	120.00
88	BZ	4	DC	P-O5'-C5'	5.02	127.54	120.00
1	AA	5318	DG	O4'-C1'-C2'	-5.02	98.87	106.40
125	CA	30	DC	P-O5'-C5'	5.02	127.53	120.00
1	AA	3102	DC	P-O5'-C5'	5.02	127.53	120.00
1	AA	5885	DA	P-O3'-C3'	-5.02	112.67	120.20
1	AA	6083	DG	P-O3'-C3'	5.02	127.73	120.20
1	AA	3379	DC	P-O5'-C5'	5.02	127.52	120.00
1	AA	2075	DA	P-O3'-C3'	5.01	127.72	120.20
1	AA	5871	DC	P-O5'-C5'	5.01	127.52	120.00
191	DE	8	DC	P-O5'-C5'	5.01	127.52	120.00
1	AA	2157	DA	O4'-C4'-C3'	-5.01	97.89	105.40
1	AA	3717	DC	P-O5'-C5'	5.01	127.51	120.00
55	A2	10	DA	O4'-C1'-C2'	-5.01	98.89	106.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
183	C6	37	DC	P-O5'-C5'	5.01	127.51	120.00
1	AA	5255	DC	P-O5'-C5'	5.00	127.51	120.00
114	Bz	28	DC	P-O5'-C5'	5.00	127.51	120.00
1	AA	245	DC	P-O3'-C3'	5.00	127.70	120.20

All (11) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	AA	627	DG	C3'
1	AA	767	DT	C3'
1	AA	885	DA	C3'
1	AA	1025	DA	C3'
1	AA	1143	DG	C3'
1	AA	1763	DA	C3'
1	AA	4125	DG	C3'
1	AA	4213	DA	C3'
1	AA	4821	DG	C3'
1	AA	5109	DT	C3'
1	AA	5365	DA	C3'

All (2081) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
53	A0	13	DT	Sidechain
53	A0	29	DC	Sidechain
53	A0	47	DC	Sidechain
53	A0	5	DA	Sidechain
54	A1	1	DT	Sidechain
54	A1	10	DT	Sidechain
54	A1	16	DA	Sidechain
54	A1	28	DT	Sidechain
54	A1	31	DT	Sidechain
54	A1	6	DC	Sidechain
54	A1	7	DG	Sidechain
54	A1	9	DA	Sidechain
55	A2	12	DA	Sidechain
55	A2	31	DC	Sidechain
55	A2	9	DC	Sidechain
56	A3	12	DG	Sidechain
56	A3	13	DT	Sidechain
56	A3	17	DG	Sidechain
56	A3	21	DC	Sidechain

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Mol	Chain	Res	Type	Group
57	A4	12	DC	Sidechain
57	A4	14	DC	Sidechain
57	A4	37	DA	Sidechain
58	A5	14	DA	Sidechain
58	A5	15	DC	Sidechain
58	A5	19	DA	Sidechain
58	A5	21	DT	Sidechain
58	A5	23	DA	Sidechain
58	A5	33	DA	Sidechain
58	A5	34	DA	Sidechain
58	A5	35	DA	Sidechain
58	A5	36	DT	Sidechain
58	A5	37	DG	Sidechain
59	A6	1	DA	Sidechain
59	A6	10	DC	Sidechain
59	A6	21	DG	Sidechain
59	A6	22	DT	Sidechain
59	A6	27	DA	Sidechain
59	A6	30	DT	Sidechain
59	A6	35	DG	Sidechain
60	A7	1	DT	Sidechain
60	A7	11	DA	Sidechain
60	A7	16	DA	Sidechain
60	A7	27	DG	Sidechain
60	A7	31	DT	Sidechain
60	A7	5	DT	Sidechain
61	A8	16	DG	Sidechain
61	A8	18	DT	Sidechain
61	A8	19	DT	Sidechain
61	A8	21	DT	Sidechain
61	A8	23	DT	Sidechain
61	A8	25	DT	Sidechain
61	A8	27	DC	Sidechain
61	A8	31	DA	Sidechain
61	A8	35	DA	Sidechain
61	A8	37	DT	Sidechain
62	A9	14	DA	Sidechain
62	A9	31	DC	Sidechain
62	A9	39	DC	Sidechain
62	A9	6	DA	Sidechain
1	AA	1	DA	Sidechain
1	AA	1011	DC	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	1014	DC	Sidechain
1	AA	1019	DC	Sidechain
1	AA	1023	DA	Sidechain
1	AA	1030	DT	Sidechain
1	AA	1033	DT	Sidechain
1	AA	1037	DT	Sidechain
1	AA	1038	DC	Sidechain
1	AA	104	DG	Sidechain
1	AA	1048	DA	Sidechain
1	AA	1058	DT	Sidechain
1	AA	1061	DG	Sidechain
1	AA	1063	DT	Sidechain
1	AA	1064	DT	Sidechain
1	AA	1070	DA	Sidechain
1	AA	1074	DT	Sidechain
1	AA	1076	DG	Sidechain
1	AA	1088	DC	Sidechain
1	AA	109	DA	Sidechain
1	AA	11	DC	Sidechain
1	AA	110	DC	Sidechain
1	AA	1112	DG	Sidechain
1	AA	1120	DC	Sidechain
1	AA	1123	DA	Sidechain
1	AA	1124	DT	Sidechain
1	AA	1131	DA	Sidechain
1	AA	1146	DA	Sidechain
1	AA	1147	DT	Sidechain
1	AA	115	DT	Sidechain
1	AA	1169	DT	Sidechain
1	AA	1181	DT	Sidechain
1	AA	121	DC	Sidechain
1	AA	1218	DT	Sidechain
1	AA	1219	DG	Sidechain
1	AA	1220	DT	Sidechain
1	AA	1234	DT	Sidechain
1	AA	1239	DT	Sidechain
1	AA	1264	DC	Sidechain
1	AA	1266	DT	Sidechain
1	AA	1282	DT	Sidechain
1	AA	129	DG	Sidechain
1	AA	130	DA	Sidechain
1	AA	1301	DT	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	1302	DG	Sidechain
1	AA	1307	DA	Sidechain
1	AA	131	DA	Sidechain
1	AA	1316	DT	Sidechain
1	AA	1334	DC	Sidechain
1	AA	1349	DT	Sidechain
1	AA	1354	DA	Sidechain
1	AA	1363	DT	Sidechain
1	AA	1368	DT	Sidechain
1	AA	1370	DC	Sidechain
1	AA	1373	DA	Sidechain
1	AA	1378	DG	Sidechain
1	AA	1379	DA	Sidechain
1	AA	1380	DC	Sidechain
1	AA	1382	DA	Sidechain
1	AA	1383	DT	Sidechain
1	AA	1384	DC	Sidechain
1	AA	1386	DC	Sidechain
1	AA	139	DT	Sidechain
1	AA	1390	DA	Sidechain
1	AA	1393	DG	Sidechain
1	AA	1396	DG	Sidechain
1	AA	1402	DA	Sidechain
1	AA	1411	DC	Sidechain
1	AA	1416	DC	Sidechain
1	AA	1419	DA	Sidechain
1	AA	1424	DC	Sidechain
1	AA	144	DT	Sidechain
1	AA	1441	DG	Sidechain
1	AA	1453	DG	Sidechain
1	AA	1458	DT	Sidechain
1	AA	1459	DG	Sidechain
1	AA	146	DT	Sidechain
1	AA	1468	DG	Sidechain
1	AA	147	DT	Sidechain
1	AA	1474	DA	Sidechain
1	AA	1475	DC	Sidechain
1	AA	1490	DT	Sidechain
1	AA	1501	DT	Sidechain
1	AA	1507	DT	Sidechain
1	AA	1510	DA	Sidechain
1	AA	1513	DG	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	1521	DA	Sidechain
1	AA	1522	DT	Sidechain
1	AA	1528	DG	Sidechain
1	AA	1530	DT	Sidechain
1	AA	1531	DA	Sidechain
1	AA	1544	DC	Sidechain
1	AA	1547	DT	Sidechain
1	AA	155	DA	Sidechain
1	AA	1555	DC	Sidechain
1	AA	1561	DT	Sidechain
1	AA	1570	DT	Sidechain
1	AA	1574	DC	Sidechain
1	AA	1582	DA	Sidechain
1	AA	1584	DA	Sidechain
1	AA	1587	DT	Sidechain
1	AA	1590	DT	Sidechain
1	AA	1596	DG	Sidechain
1	AA	1605	DT	Sidechain
1	AA	1622	DT	Sidechain
1	AA	1628	DC	Sidechain
1	AA	163	DT	Sidechain
1	AA	1636	DA	Sidechain
1	AA	1639	DC	Sidechain
1	AA	1658	DA	Sidechain
1	AA	1663	DC	Sidechain
1	AA	1666	DA	Sidechain
1	AA	1674	DA	Sidechain
1	AA	1676	DT	Sidechain
1	AA	1684	DC	Sidechain
1	AA	1690	DT	Sidechain
1	AA	1691	DC	Sidechain
1	AA	1695	DA	Sidechain
1	AA	17	DG	Sidechain
1	AA	1701	DG	Sidechain
1	AA	1707	DA	Sidechain
1	AA	1718	DT	Sidechain
1	AA	1723	DC	Sidechain
1	AA	1726	DA	Sidechain
1	AA	1727	DC	Sidechain
1	AA	1729	DA	Sidechain
1	AA	1732	DA	Sidechain
1	AA	1744	DG	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	1745	DG	Sidechain
1	AA	1749	DG	Sidechain
1	AA	1757	DC	Sidechain
1	AA	1759	DT	Sidechain
1	AA	1760	DT	Sidechain
1	AA	1764	DG	Sidechain
1	AA	1766	DT	Sidechain
1	AA	177	DT	Sidechain
1	AA	1771	DC	Sidechain
1	AA	1783	DC	Sidechain
1	AA	1799	DA	Sidechain
1	AA	1810	DT	Sidechain
1	AA	1815	DC	Sidechain
1	AA	1821	DA	Sidechain
1	AA	1830	DA	Sidechain
1	AA	1840	DG	Sidechain
1	AA	1843	DG	Sidechain
1	AA	1859	DT	Sidechain
1	AA	187	DT	Sidechain
1	AA	1870	DG	Sidechain
1	AA	188	DA	Sidechain
1	AA	1883	DT	Sidechain
1	AA	1888	DG	Sidechain
1	AA	1889	DT	Sidechain
1	AA	1891	DC	Sidechain
1	AA	1895	DA	Sidechain
1	AA	1900	DC	Sidechain
1	AA	1905	DT	Sidechain
1	AA	1914	DA	Sidechain
1	AA	1921	DT	Sidechain
1	AA	1922	DT	Sidechain
1	AA	1926	DG	Sidechain
1	AA	1927	DG	Sidechain
1	AA	1928	DC	Sidechain
1	AA	1931	DT	Sidechain
1	AA	1933	DC	Sidechain
1	AA	1934	DT	Sidechain
1	AA	195	DA	Sidechain
1	AA	1958	DT	Sidechain
1	AA	197	DA	Sidechain
1	AA	1973	DT	Sidechain
1	AA	1983	DC	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	199	DG	Sidechain
1	AA	1998	DC	Sidechain
1	AA	2000	DT	Sidechain
1	AA	2013	DT	Sidechain
1	AA	2024	DT	Sidechain
1	AA	2028	DA	Sidechain
1	AA	2036	DG	Sidechain
1	AA	2037	DT	Sidechain
1	AA	2040	DC	Sidechain
1	AA	2041	DA	Sidechain
1	AA	205	DC	Sidechain
1	AA	2067	DG	Sidechain
1	AA	2075	DA	Sidechain
1	AA	2078	DT	Sidechain
1	AA	208	DC	Sidechain
1	AA	2082	DT	Sidechain
1	AA	2091	DA	Sidechain
1	AA	2107	DC	Sidechain
1	AA	211	DC	Sidechain
1	AA	2141	DT	Sidechain
1	AA	2167	DC	Sidechain
1	AA	2170	DA	Sidechain
1	AA	2197	DC	Sidechain
1	AA	22	DA	Sidechain
1	AA	2206	DC	Sidechain
1	AA	2232	DT	Sidechain
1	AA	2237	DA	Sidechain
1	AA	2240	DT	Sidechain
1	AA	2245	DG	Sidechain
1	AA	2279	DT	Sidechain
1	AA	2281	DC	Sidechain
1	AA	2291	DC	Sidechain
1	AA	2295	DG	Sidechain
1	AA	2297	DT	Sidechain
1	AA	2311	DG	Sidechain
1	AA	2313	DG	Sidechain
1	AA	2314	DG	Sidechain
1	AA	2315	DC	Sidechain
1	AA	2318	DT	Sidechain
1	AA	2320	DA	Sidechain
1	AA	2325	DG	Sidechain
1	AA	2328	DG	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	2331	DT	Sidechain
1	AA	2335	DA	Sidechain
1	AA	2337	DG	Sidechain
1	AA	234	DT	Sidechain
1	AA	2348	DT	Sidechain
1	AA	2350	DA	Sidechain
1	AA	2359	DG	Sidechain
1	AA	2362	DC	Sidechain
1	AA	2365	DA	Sidechain
1	AA	2367	DG	Sidechain
1	AA	2372	DC	Sidechain
1	AA	2375	DT	Sidechain
1	AA	2387	DC	Sidechain
1	AA	2389	DC	Sidechain
1	AA	2391	DG	Sidechain
1	AA	2392	DG	Sidechain
1	AA	2393	DT	Sidechain
1	AA	2401	DA	Sidechain
1	AA	2410	DA	Sidechain
1	AA	2420	DG	Sidechain
1	AA	2422	DC	Sidechain
1	AA	2423	DA	Sidechain
1	AA	2425	DA	Sidechain
1	AA	2427	DG	Sidechain
1	AA	2436	DG	Sidechain
1	AA	2440	DC	Sidechain
1	AA	2442	DA	Sidechain
1	AA	2452	DA	Sidechain
1	AA	2464	DA	Sidechain
1	AA	2469	DC	Sidechain
1	AA	2480	DC	Sidechain
1	AA	2481	DG	Sidechain
1	AA	2483	DT	Sidechain
1	AA	2488	DG	Sidechain
1	AA	2495	DT	Sidechain
1	AA	25	DG	Sidechain
1	AA	250	DA	Sidechain
1	AA	2504	DC	Sidechain
1	AA	2509	DC	Sidechain
1	AA	2515	DA	Sidechain
1	AA	2527	DT	Sidechain
1	AA	2528	DC	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	2541	DG	Sidechain
1	AA	2542	DG	Sidechain
1	AA	2552	DC	Sidechain
1	AA	2554	DG	Sidechain
1	AA	2556	DC	Sidechain
1	AA	2574	DG	Sidechain
1	AA	2578	DC	Sidechain
1	AA	2581	DG	Sidechain
1	AA	2584	DA	Sidechain
1	AA	2591	DT	Sidechain
1	AA	26	DA	Sidechain
1	AA	2610	DG	Sidechain
1	AA	2611	DC	Sidechain
1	AA	2622	DG	Sidechain
1	AA	2624	DC	Sidechain
1	AA	2633	DT	Sidechain
1	AA	2634	DT	Sidechain
1	AA	2643	DA	Sidechain
1	AA	2647	DA	Sidechain
1	AA	2658	DC	Sidechain
1	AA	2663	DT	Sidechain
1	AA	2664	DT	Sidechain
1	AA	2667	DC	Sidechain
1	AA	2669	DT	Sidechain
1	AA	2688	DG	Sidechain
1	AA	2692	DG	Sidechain
1	AA	2693	DT	Sidechain
1	AA	2695	DG	Sidechain
1	AA	2710	DG	Sidechain
1	AA	2719	DA	Sidechain
1	AA	2721	DC	Sidechain
1	AA	2722	DC	Sidechain
1	AA	2725	DA	Sidechain
1	AA	2728	DA	Sidechain
1	AA	2734	DC	Sidechain
1	AA	2740	DA	Sidechain
1	AA	2746	DA	Sidechain
1	AA	2751	DA	Sidechain
1	AA	2756	DC	Sidechain
1	AA	2758	DT	Sidechain
1	AA	2759	DA	Sidechain
1	AA	2766	DG	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	2767	DG	Sidechain
1	AA	2783	DT	Sidechain
1	AA	2785	DT	Sidechain
1	AA	2787	DT	Sidechain
1	AA	2792	DT	Sidechain
1	AA	2800	DT	Sidechain
1	AA	2802	DA	Sidechain
1	AA	2817	DA	Sidechain
1	AA	2820	DT	Sidechain
1	AA	2824	DC	Sidechain
1	AA	2853	DT	Sidechain
1	AA	2861	DG	Sidechain
1	AA	2874	DT	Sidechain
1	AA	2879	DT	Sidechain
1	AA	2890	DT	Sidechain
1	AA	2892	DT	Sidechain
1	AA	2905	DT	Sidechain
1	AA	2911	DA	Sidechain
1	AA	2914	DT	Sidechain
1	AA	292	DC	Sidechain
1	AA	2923	DC	Sidechain
1	AA	2933	DA	Sidechain
1	AA	2937	DT	Sidechain
1	AA	2939	DC	Sidechain
1	AA	296	DA	Sidechain
1	AA	2960	DA	Sidechain
1	AA	2967	DT	Sidechain
1	AA	2984	DC	Sidechain
1	AA	299	DT	Sidechain
1	AA	2993	DA	Sidechain
1	AA	2997	DT	Sidechain
1	AA	3000	DG	Sidechain
1	AA	3009	DC	Sidechain
1	AA	3012	DT	Sidechain
1	AA	3015	DT	Sidechain
1	AA	3028	DC	Sidechain
1	AA	3029	DT	Sidechain
1	AA	3032	DG	Sidechain
1	AA	3033	DA	Sidechain
1	AA	3041	DG	Sidechain
1	AA	3042	DC	Sidechain
1	AA	3057	DA	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	3074	DC	Sidechain
1	AA	3077	DT	Sidechain
1	AA	3088	DG	Sidechain
1	AA	3089	DT	Sidechain
1	AA	3093	DA	Sidechain
1	AA	3098	DC	Sidechain
1	AA	3104	DT	Sidechain
1	AA	3117	DT	Sidechain
1	AA	3138	DT	Sidechain
1	AA	3143	DA	Sidechain
1	AA	3146	DT	Sidechain
1	AA	3148	DT	Sidechain
1	AA	3165	DT	Sidechain
1	AA	317	DG	Sidechain
1	AA	3172	DT	Sidechain
1	AA	3181	DT	Sidechain
1	AA	3186	DA	Sidechain
1	AA	3193	DA	Sidechain
1	AA	3213	DA	Sidechain
1	AA	3221	DA	Sidechain
1	AA	3230	DT	Sidechain
1	AA	3231	DG	Sidechain
1	AA	3233	DA	Sidechain
1	AA	3239	DG	Sidechain
1	AA	3241	DT	Sidechain
1	AA	3258	DA	Sidechain
1	AA	3260	DT	Sidechain
1	AA	3265	DA	Sidechain
1	AA	3268	DA	Sidechain
1	AA	3274	DT	Sidechain
1	AA	3275	DA	Sidechain
1	AA	3276	DG	Sidechain
1	AA	3278	DT	Sidechain
1	AA	33	DC	Sidechain
1	AA	330	DT	Sidechain
1	AA	3301	DT	Sidechain
1	AA	3304	DA	Sidechain
1	AA	3318	DA	Sidechain
1	AA	3322	DT	Sidechain
1	AA	3342	DG	Sidechain
1	AA	3349	DC	Sidechain
1	AA	3351	DC	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	3358	DT	Sidechain
1	AA	3366	DA	Sidechain
1	AA	3373	DA	Sidechain
1	AA	3378	DC	Sidechain
1	AA	3384	DA	Sidechain
1	AA	3385	DT	Sidechain
1	AA	3387	DT	Sidechain
1	AA	3388	DC	Sidechain
1	AA	3389	DT	Sidechain
1	AA	3396	DC	Sidechain
1	AA	3397	DT	Sidechain
1	AA	340	DA	Sidechain
1	AA	3406	DG	Sidechain
1	AA	3408	DC	Sidechain
1	AA	3415	DA	Sidechain
1	AA	3423	DT	Sidechain
1	AA	3430	DA	Sidechain
1	AA	3451	DT	Sidechain
1	AA	3457	DA	Sidechain
1	AA	3480	DA	Sidechain
1	AA	3497	DT	Sidechain
1	AA	3506	DA	Sidechain
1	AA	351	DA	Sidechain
1	AA	3524	DG	Sidechain
1	AA	3527	DT	Sidechain
1	AA	3529	DT	Sidechain
1	AA	3530	DA	Sidechain
1	AA	3532	DA	Sidechain
1	AA	3535	DC	Sidechain
1	AA	3538	DG	Sidechain
1	AA	3548	DA	Sidechain
1	AA	3553	DA	Sidechain
1	AA	3565	DT	Sidechain
1	AA	3568	DT	Sidechain
1	AA	3575	DC	Sidechain
1	AA	3579	DT	Sidechain
1	AA	358	DA	Sidechain
1	AA	3583	DT	Sidechain
1	AA	3592	DA	Sidechain
1	AA	3593	DA	Sidechain
1	AA	3599	DG	Sidechain
1	AA	36	DT	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	360	DG	Sidechain
1	AA	3609	DT	Sidechain
1	AA	3617	DA	Sidechain
1	AA	363	DT	Sidechain
1	AA	3632	DT	Sidechain
1	AA	3634	DG	Sidechain
1	AA	3651	DA	Sidechain
1	AA	3654	DT	Sidechain
1	AA	3658	DC	Sidechain
1	AA	3668	DT	Sidechain
1	AA	3677	DT	Sidechain
1	AA	368	DG	Sidechain
1	AA	3680	DT	Sidechain
1	AA	3682	DT	Sidechain
1	AA	3688	DC	Sidechain
1	AA	3706	DT	Sidechain
1	AA	3709	DC	Sidechain
1	AA	371	DT	Sidechain
1	AA	372	DT	Sidechain
1	AA	3728	DT	Sidechain
1	AA	3729	DG	Sidechain
1	AA	374	DC	Sidechain
1	AA	3751	DT	Sidechain
1	AA	3760	DC	Sidechain
1	AA	3767	DG	Sidechain
1	AA	3768	DC	Sidechain
1	AA	3808	DA	Sidechain
1	AA	3810	DA	Sidechain
1	AA	3825	DT	Sidechain
1	AA	3826	DC	Sidechain
1	AA	3827	DT	Sidechain
1	AA	384	DT	Sidechain
1	AA	3841	DC	Sidechain
1	AA	3844	DG	Sidechain
1	AA	3848	DT	Sidechain
1	AA	3862	DC	Sidechain
1	AA	3868	DA	Sidechain
1	AA	3870	DT	Sidechain
1	AA	3875	DA	Sidechain
1	AA	3881	DT	Sidechain
1	AA	3893	DA	Sidechain
1	AA	3894	DC	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	3895	DC	Sidechain
1	AA	3897	DT	Sidechain
1	AA	3905	DA	Sidechain
1	AA	3912	DA	Sidechain
1	AA	392	DC	Sidechain
1	AA	3920	DA	Sidechain
1	AA	3926	DT	Sidechain
1	AA	3934	DA	Sidechain
1	AA	3946	DT	Sidechain
1	AA	395	DT	Sidechain
1	AA	3953	DC	Sidechain
1	AA	3958	DT	Sidechain
1	AA	3965	DT	Sidechain
1	AA	3974	DA	Sidechain
1	AA	398	DG	Sidechain
1	AA	3981	DT	Sidechain
1	AA	3983	DA	Sidechain
1	AA	3984	DG	Sidechain
1	AA	400	DT	Sidechain
1	AA	4001	DT	Sidechain
1	AA	4003	DT	Sidechain
1	AA	4004	DA	Sidechain
1	AA	4005	DA	Sidechain
1	AA	4011	DC	Sidechain
1	AA	4016	DG	Sidechain
1	AA	4018	DC	Sidechain
1	AA	4020	DG	Sidechain
1	AA	4021	DA	Sidechain
1	AA	4028	DA	Sidechain
1	AA	4044	DA	Sidechain
1	AA	4046	DC	Sidechain
1	AA	4051	DA	Sidechain
1	AA	4057	DA	Sidechain
1	AA	4072	DA	Sidechain
1	AA	410	DA	Sidechain
1	AA	4108	DT	Sidechain
1	AA	411	DC	Sidechain
1	AA	4130	DA	Sidechain
1	AA	4142	DC	Sidechain
1	AA	4152	DC	Sidechain
1	AA	4158	DC	Sidechain
1	AA	4167	DT	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	4169	DA	Sidechain
1	AA	4183	DA	Sidechain
1	AA	4187	DA	Sidechain
1	AA	4195	DT	Sidechain
1	AA	42	DT	Sidechain
1	AA	4210	DG	Sidechain
1	AA	4214	DT	Sidechain
1	AA	4218	DA	Sidechain
1	AA	4222	DA	Sidechain
1	AA	4225	DT	Sidechain
1	AA	4227	DG	Sidechain
1	AA	4232	DA	Sidechain
1	AA	4239	DT	Sidechain
1	AA	4242	DT	Sidechain
1	AA	4252	DT	Sidechain
1	AA	4258	DT	Sidechain
1	AA	4272	DT	Sidechain
1	AA	4281	DT	Sidechain
1	AA	4301	DA	Sidechain
1	AA	4305	DG	Sidechain
1	AA	431	DA	Sidechain
1	AA	4356	DT	Sidechain
1	AA	4360	DG	Sidechain
1	AA	4366	DC	Sidechain
1	AA	4367	DC	Sidechain
1	AA	4381	DA	Sidechain
1	AA	439	DT	Sidechain
1	AA	4393	DT	Sidechain
1	AA	4395	DT	Sidechain
1	AA	440	DT	Sidechain
1	AA	4415	DA	Sidechain
1	AA	4427	DA	Sidechain
1	AA	4433	DT	Sidechain
1	AA	4438	DT	Sidechain
1	AA	4457	DA	Sidechain
1	AA	4463	DA	Sidechain
1	AA	4489	DA	Sidechain
1	AA	4490	DT	Sidechain
1	AA	4503	DT	Sidechain
1	AA	4523	DT	Sidechain
1	AA	4554	DA	Sidechain
1	AA	4557	DT	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	457	DT	Sidechain
1	AA	4592	DT	Sidechain
1	AA	4601	DA	Sidechain
1	AA	4603	DG	Sidechain
1	AA	4619	DC	Sidechain
1	AA	4625	DA	Sidechain
1	AA	4631	DA	Sidechain
1	AA	4650	DT	Sidechain
1	AA	4669	DT	Sidechain
1	AA	4670	DT	Sidechain
1	AA	468	DA	Sidechain
1	AA	4686	DT	Sidechain
1	AA	4687	DA	Sidechain
1	AA	4688	DC	Sidechain
1	AA	469	DC	Sidechain
1	AA	4706	DT	Sidechain
1	AA	4707	DA	Sidechain
1	AA	4708	DT	Sidechain
1	AA	4715	DT	Sidechain
1	AA	4716	DT	Sidechain
1	AA	4720	DG	Sidechain
1	AA	4737	DT	Sidechain
1	AA	4741	DA	Sidechain
1	AA	4755	DT	Sidechain
1	AA	4758	DT	Sidechain
1	AA	476	DA	Sidechain
1	AA	4767	DC	Sidechain
1	AA	4769	DT	Sidechain
1	AA	4778	DT	Sidechain
1	AA	4779	DC	Sidechain
1	AA	479	DC	Sidechain
1	AA	4793	DA	Sidechain
1	AA	48	DC	Sidechain
1	AA	4805	DA	Sidechain
1	AA	481	DT	Sidechain
1	AA	4810	DA	Sidechain
1	AA	4811	DT	Sidechain
1	AA	4824	DT	Sidechain
1	AA	4836	DG	Sidechain
1	AA	4837	DG	Sidechain
1	AA	4839	DT	Sidechain
1	AA	484	DG	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	4847	DG	Sidechain
1	AA	4852	DG	Sidechain
1	AA	4859	DA	Sidechain
1	AA	486	DG	Sidechain
1	AA	4862	DT	Sidechain
1	AA	4867	DT	Sidechain
1	AA	4874	DC	Sidechain
1	AA	4884	DG	Sidechain
1	AA	4885	DC	Sidechain
1	AA	4895	DT	Sidechain
1	AA	491	DA	Sidechain
1	AA	4912	DA	Sidechain
1	AA	4921	DC	Sidechain
1	AA	4924	DA	Sidechain
1	AA	4929	DT	Sidechain
1	AA	4940	DC	Sidechain
1	AA	4944	DT	Sidechain
1	AA	4948	DG	Sidechain
1	AA	4957	DG	Sidechain
1	AA	4961	DT	Sidechain
1	AA	4968	DT	Sidechain
1	AA	4973	DA	Sidechain
1	AA	4984	DC	Sidechain
1	AA	4987	DT	Sidechain
1	AA	500	DA	Sidechain
1	AA	5005	DA	Sidechain
1	AA	501	DT	Sidechain
1	AA	5010	DT	Sidechain
1	AA	5014	DC	Sidechain
1	AA	5016	DT	Sidechain
1	AA	5019	DA	Sidechain
1	AA	5025	DA	Sidechain
1	AA	5026	DT	Sidechain
1	AA	503	DT	Sidechain
1	AA	5037	DA	Sidechain
1	AA	5042	DT	Sidechain
1	AA	5045	DT	Sidechain
1	AA	506	DA	Sidechain
1	AA	5067	DT	Sidechain
1	AA	5070	DT	Sidechain
1	AA	5071	DA	Sidechain
1	AA	5072	DT	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	5073	DC	Sidechain
1	AA	5074	DT	Sidechain
1	AA	5089	DG	Sidechain
1	AA	5090	DT	Sidechain
1	AA	5094	DT	Sidechain
1	AA	5097	DT	Sidechain
1	AA	5103	DT	Sidechain
1	AA	5105	DG	Sidechain
1	AA	5107	DC	Sidechain
1	AA	5113	DA	Sidechain
1	AA	5114	DC	Sidechain
1	AA	5117	DG	Sidechain
1	AA	5135	DA	Sidechain
1	AA	5138	DA	Sidechain
1	AA	5140	DC	Sidechain
1	AA	5157	DG	Sidechain
1	AA	5171	DG	Sidechain
1	AA	5177	DC	Sidechain
1	AA	5182	DA	Sidechain
1	AA	5202	DG	Sidechain
1	AA	5203	DG	Sidechain
1	AA	5219	DT	Sidechain
1	AA	5232	DC	Sidechain
1	AA	5239	DG	Sidechain
1	AA	5243	DA	Sidechain
1	AA	5251	DA	Sidechain
1	AA	5256	DT	Sidechain
1	AA	5276	DT	Sidechain
1	AA	5282	DC	Sidechain
1	AA	5283	DT	Sidechain
1	AA	5292	DA	Sidechain
1	AA	5295	DT	Sidechain
1	AA	5299	DG	Sidechain
1	AA	53	DA	Sidechain
1	AA	5300	DC	Sidechain
1	AA	531	DT	Sidechain
1	AA	5313	DT	Sidechain
1	AA	5315	DT	Sidechain
1	AA	5316	DG	Sidechain
1	AA	5321	DA	Sidechain
1	AA	5323	DG	Sidechain
1	AA	5325	DA	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	5328	DG	Sidechain
1	AA	5330	DC	Sidechain
1	AA	5332	DC	Sidechain
1	AA	5338	DC	Sidechain
1	AA	534	DC	Sidechain
1	AA	5344	DG	Sidechain
1	AA	5347	DC	Sidechain
1	AA	5363	DA	Sidechain
1	AA	5393	DT	Sidechain
1	AA	5400	DA	Sidechain
1	AA	5403	DC	Sidechain
1	AA	5406	DT	Sidechain
1	AA	5414	DG	Sidechain
1	AA	5421	DG	Sidechain
1	AA	5422	DT	Sidechain
1	AA	5428	DT	Sidechain
1	AA	543	DA	Sidechain
1	AA	5438	DA	Sidechain
1	AA	5448	DG	Sidechain
1	AA	5450	DA	Sidechain
1	AA	5453	DG	Sidechain
1	AA	5459	DT	Sidechain
1	AA	5460	DA	Sidechain
1	AA	5462	DA	Sidechain
1	AA	5468	DT	Sidechain
1	AA	547	DT	Sidechain
1	AA	5483	DT	Sidechain
1	AA	5489	DG	Sidechain
1	AA	5497	DT	Sidechain
1	AA	5501	DG	Sidechain
1	AA	5502	DG	Sidechain
1	AA	5505	DC	Sidechain
1	AA	551	DC	Sidechain
1	AA	5530	DT	Sidechain
1	AA	5538	DG	Sidechain
1	AA	554	DT	Sidechain
1	AA	5552	DC	Sidechain
1	AA	5553	DT	Sidechain
1	AA	5564	DC	Sidechain
1	AA	5575	DT	Sidechain
1	AA	5579	DT	Sidechain
1	AA	558	DC	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	5583	DC	Sidechain
1	AA	5598	DT	Sidechain
1	AA	56	DA	Sidechain
1	AA	5618	DT	Sidechain
1	AA	5631	DC	Sidechain
1	AA	5651	DT	Sidechain
1	AA	5656	DG	Sidechain
1	AA	5683	DC	Sidechain
1	AA	5684	DG	Sidechain
1	AA	5686	DC	Sidechain
1	AA	5696	DC	Sidechain
1	AA	5707	DT	Sidechain
1	AA	5711	DG	Sidechain
1	AA	5713	DT	Sidechain
1	AA	5723	DG	Sidechain
1	AA	5725	DG	Sidechain
1	AA	5726	DC	Sidechain
1	AA	573	DT	Sidechain
1	AA	5731	DG	Sidechain
1	AA	5740	DG	Sidechain
1	AA	5741	DA	Sidechain
1	AA	5745	DT	Sidechain
1	AA	5760	DC	Sidechain
1	AA	5766	DA	Sidechain
1	AA	5788	DA	Sidechain
1	AA	5791	DC	Sidechain
1	AA	5794	DG	Sidechain
1	AA	5795	DT	Sidechain
1	AA	5796	DT	Sidechain
1	AA	5799	DA	Sidechain
1	AA	5801	DA	Sidechain
1	AA	5803	DT	Sidechain
1	AA	5804	DG	Sidechain
1	AA	5820	DC	Sidechain
1	AA	5823	DT	Sidechain
1	AA	5824	DC	Sidechain
1	AA	5833	DT	Sidechain
1	AA	5835	DC	Sidechain
1	AA	5836	DT	Sidechain
1	AA	5841	DA	Sidechain
1	AA	585	DA	Sidechain
1	AA	5852	DA	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	5853	DT	Sidechain
1	AA	5869	DA	Sidechain
1	AA	5874	DC	Sidechain
1	AA	5885	DA	Sidechain
1	AA	589	DT	Sidechain
1	AA	5895	DG	Sidechain
1	AA	5896	DC	Sidechain
1	AA	5900	DG	Sidechain
1	AA	5901	DG	Sidechain
1	AA	5915	DA	Sidechain
1	AA	5919	DC	Sidechain
1	AA	5924	DT	Sidechain
1	AA	5926	DC	Sidechain
1	AA	5933	DC	Sidechain
1	AA	5940	DC	Sidechain
1	AA	5946	DG	Sidechain
1	AA	5955	DC	Sidechain
1	AA	5956	DA	Sidechain
1	AA	5957	DA	Sidechain
1	AA	5961	DG	Sidechain
1	AA	5962	DC	Sidechain
1	AA	597	DT	Sidechain
1	AA	5971	DG	Sidechain
1	AA	5972	DT	Sidechain
1	AA	5985	DA	Sidechain
1	AA	6000	DG	Sidechain
1	AA	6003	DG	Sidechain
1	AA	6012	DG	Sidechain
1	AA	6036	DG	Sidechain
1	AA	6041	DA	Sidechain
1	AA	6043	DT	Sidechain
1	AA	6045	DA	Sidechain
1	AA	6048	DA	Sidechain
1	AA	6055	DC	Sidechain
1	AA	6076	DC	Sidechain
1	AA	6077	DT	Sidechain
1	AA	6081	DA	Sidechain
1	AA	6088	DC	Sidechain
1	AA	6102	DC	Sidechain
1	AA	6105	DT	Sidechain
1	AA	611	DG	Sidechain
1	AA	6127	DT	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	6135	DC	Sidechain
1	AA	6141	DC	Sidechain
1	AA	6162	DC	Sidechain
1	AA	6170	DT	Sidechain
1	AA	6173	DT	Sidechain
1	AA	6178	DA	Sidechain
1	AA	6179	DA	Sidechain
1	AA	6181	DT	Sidechain
1	AA	6187	DC	Sidechain
1	AA	619	DG	Sidechain
1	AA	6190	DA	Sidechain
1	AA	6191	DT	Sidechain
1	AA	6193	DA	Sidechain
1	AA	6195	DA	Sidechain
1	AA	62	DT	Sidechain
1	AA	6216	DA	Sidechain
1	AA	6219	DA	Sidechain
1	AA	6232	DA	Sidechain
1	AA	6244	DT	Sidechain
1	AA	6245	DA	Sidechain
1	AA	6256	DC	Sidechain
1	AA	6267	DA	Sidechain
1	AA	6273	DA	Sidechain
1	AA	6285	DT	Sidechain
1	AA	6293	DG	Sidechain
1	AA	63	DA	Sidechain
1	AA	630	DT	Sidechain
1	AA	6315	DG	Sidechain
1	AA	6316	DA	Sidechain
1	AA	6318	DT	Sidechain
1	AA	6322	DA	Sidechain
1	AA	6325	DA	Sidechain
1	AA	6329	DT	Sidechain
1	AA	6332	DC	Sidechain
1	AA	6335	DT	Sidechain
1	AA	6336	DA	Sidechain
1	AA	6351	DC	Sidechain
1	AA	6352	DT	Sidechain
1	AA	6353	DT	Sidechain
1	AA	6360	DC	Sidechain
1	AA	6362	DT	Sidechain
1	AA	6363	DC	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	6368	DT	Sidechain
1	AA	638	DG	Sidechain
1	AA	6381	DC	Sidechain
1	AA	6396	DG	Sidechain
1	AA	6397	DC	Sidechain
1	AA	641	DT	Sidechain
1	AA	6414	DT	Sidechain
1	AA	6415	DC	Sidechain
1	AA	6419	DA	Sidechain
1	AA	643	DG	Sidechain
1	AA	6430	DG	Sidechain
1	AA	6431	DC	Sidechain
1	AA	6441	DG	Sidechain
1	AA	6445	DG	Sidechain
1	AA	6446	DG	Sidechain
1	AA	6447	DC	Sidechain
1	AA	6448	DG	Sidechain
1	AA	6449	DC	Sidechain
1	AA	6458	DG	Sidechain
1	AA	6459	DT	Sidechain
1	AA	6461	DT	Sidechain
1	AA	6464	DG	Sidechain
1	AA	6466	DC	Sidechain
1	AA	6472	DA	Sidechain
1	AA	6477	DG	Sidechain
1	AA	6483	DG	Sidechain
1	AA	6485	DA	Sidechain
1	AA	6496	DA	Sidechain
1	AA	6505	DT	Sidechain
1	AA	653	DT	Sidechain
1	AA	6532	DC	Sidechain
1	AA	6569	DC	Sidechain
1	AA	6582	DA	Sidechain
1	AA	6609	DT	Sidechain
1	AA	662	DA	Sidechain
1	AA	6627	DC	Sidechain
1	AA	6643	DC	Sidechain
1	AA	6644	DG	Sidechain
1	AA	6657	DG	Sidechain
1	AA	6673	DT	Sidechain
1	AA	6682	DG	Sidechain
1	AA	6686	DG	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	6687	DA	Sidechain
1	AA	6704	DT	Sidechain
1	AA	6707	DC	Sidechain
1	AA	6711	DC	Sidechain
1	AA	6712	DC	Sidechain
1	AA	6713	DT	Sidechain
1	AA	6724	DA	Sidechain
1	AA	6731	DC	Sidechain
1	AA	6735	DT	Sidechain
1	AA	6739	DA	Sidechain
1	AA	6741	DA	Sidechain
1	AA	6746	DT	Sidechain
1	AA	6747	DT	Sidechain
1	AA	6755	DA	Sidechain
1	AA	6761	DA	Sidechain
1	AA	6762	DA	Sidechain
1	AA	6765	DA	Sidechain
1	AA	6774	DC	Sidechain
1	AA	6780	DC	Sidechain
1	AA	6788	DA	Sidechain
1	AA	679	DG	Sidechain
1	AA	6794	DG	Sidechain
1	AA	6795	DC	Sidechain
1	AA	6817	DG	Sidechain
1	AA	6822	DT	Sidechain
1	AA	6827	DT	Sidechain
1	AA	6843	DT	Sidechain
1	AA	6844	DA	Sidechain
1	AA	6849	DT	Sidechain
1	AA	6854	DG	Sidechain
1	AA	6863	DG	Sidechain
1	AA	687	DA	Sidechain
1	AA	6877	DG	Sidechain
1	AA	6879	DT	Sidechain
1	AA	6882	DT	Sidechain
1	AA	6886	DT	Sidechain
1	AA	6898	DC	Sidechain
1	AA	6903	DG	Sidechain
1	AA	6911	DG	Sidechain
1	AA	6915	DA	Sidechain
1	AA	6923	DA	Sidechain
1	AA	6927	DC	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	6937	DT	Sidechain
1	AA	6947	DA	Sidechain
1	AA	696	DA	Sidechain
1	AA	6962	DG	Sidechain
1	AA	6963	DG	Sidechain
1	AA	6964	DC	Sidechain
1	AA	6983	DA	Sidechain
1	AA	6987	DT	Sidechain
1	AA	6996	DA	Sidechain
1	AA	7003	DT	Sidechain
1	AA	7008	DA	Sidechain
1	AA	7012	DG	Sidechain
1	AA	7013	DA	Sidechain
1	AA	7019	DT	Sidechain
1	AA	7022	DG	Sidechain
1	AA	7036	DT	Sidechain
1	AA	7039	DT	Sidechain
1	AA	7042	DA	Sidechain
1	AA	7043	DT	Sidechain
1	AA	7047	DT	Sidechain
1	AA	7049	DC	Sidechain
1	AA	7060	DC	Sidechain
1	AA	7068	DT	Sidechain
1	AA	7072	DA	Sidechain
1	AA	7079	DA	Sidechain
1	AA	708	DT	Sidechain
1	AA	7086	DA	Sidechain
1	AA	7092	DC	Sidechain
1	AA	7098	DA	Sidechain
1	AA	7107	DC	Sidechain
1	AA	7115	DG	Sidechain
1	AA	7123	DG	Sidechain
1	AA	7142	DT	Sidechain
1	AA	7168	DA	Sidechain
1	AA	7176	DT	Sidechain
1	AA	7177	DA	Sidechain
1	AA	718	DC	Sidechain
1	AA	7191	DA	Sidechain
1	AA	7206	DA	Sidechain
1	AA	7207	DT	Sidechain
1	AA	7217	DT	Sidechain
1	AA	7218	DC	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	7223	DC	Sidechain
1	AA	7224	DC	Sidechain
1	AA	7238	DT	Sidechain
1	AA	7239	DT	Sidechain
1	AA	724	DA	Sidechain
1	AA	7241	DT	Sidechain
1	AA	726	DT	Sidechain
1	AA	733	DA	Sidechain
1	AA	748	DG	Sidechain
1	AA	749	DT	Sidechain
1	AA	76	DA	Sidechain
1	AA	764	DT	Sidechain
1	AA	765	DT	Sidechain
1	AA	779	DT	Sidechain
1	AA	789	DA	Sidechain
1	AA	803	DA	Sidechain
1	AA	804	DT	Sidechain
1	AA	811	DC	Sidechain
1	AA	824	DT	Sidechain
1	AA	826	DG	Sidechain
1	AA	842	DA	Sidechain
1	AA	846	DA	Sidechain
1	AA	850	DA	Sidechain
1	AA	857	DA	Sidechain
1	AA	859	DT	Sidechain
1	AA	863	DA	Sidechain
1	AA	875	DC	Sidechain
1	AA	878	DA	Sidechain
1	AA	882	DA	Sidechain
1	AA	887	DT	Sidechain
1	AA	898	DT	Sidechain
1	AA	9	DT	Sidechain
1	AA	913	DG	Sidechain
1	AA	914	DC	Sidechain
1	AA	916	DT	Sidechain
1	AA	917	DT	Sidechain
1	AA	918	DA	Sidechain
1	AA	92	DA	Sidechain
1	AA	924	DT	Sidechain
1	AA	926	DA	Sidechain
1	AA	945	DT	Sidechain
1	AA	969	DT	Sidechain

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Mol	Chain	Res	Type	Group
1	AA	975	DT	Sidechain
1	AA	980	DA	Sidechain
1	AA	984	DC	Sidechain
1	AA	987	DT	Sidechain
1	AA	993	DA	Sidechain
2	AB	1	DT	Sidechain
2	AB	10	DT	Sidechain
2	AB	2	DT	Sidechain
2	AB	22	DT	Sidechain
2	AB	23	DA	Sidechain
2	AB	29	DC	Sidechain
2	AB	35	DC	Sidechain
2	AB	5	DT	Sidechain
2	AB	6	DA	Sidechain
3	AC	1	DT	Sidechain
3	AC	10	DA	Sidechain
3	AC	2	DT	Sidechain
3	AC	31	DT	Sidechain
3	AC	4	DT	Sidechain
4	AD	1	DA	Sidechain
4	AD	11	DT	Sidechain
4	AD	16	DG	Sidechain
4	AD	21	DA	Sidechain
4	AD	38	DA	Sidechain
4	AD	5	DT	Sidechain
4	AD	7	DT	Sidechain
5	AE	1	DT	Sidechain
5	AE	12	DT	Sidechain
5	AE	22	DG	Sidechain
5	AE	36	DC	Sidechain
5	AE	38	DT	Sidechain
5	AE	43	DT	Sidechain
5	AE	6	DC	Sidechain
6	AF	15	DA	Sidechain
6	AF	8	DA	Sidechain
7	AG	15	DC	Sidechain
7	AG	3	DT	Sidechain
7	AG	8	DG	Sidechain
7	AG	9	DC	Sidechain
8	AH	1	DT	Sidechain
8	AH	11	DC	Sidechain
8	AH	30	DT	Sidechain

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Mol	Chain	Res	Type	Group
8	AH	5	DT	Sidechain
9	AI	1	DA	Sidechain
9	AI	10	DT	Sidechain
9	AI	16	DT	Sidechain
9	AI	42	DT	Sidechain
9	AI	6	DC	Sidechain
10	AJ	11	DA	Sidechain
10	AJ	15	DG	Sidechain
10	AJ	18	DT	Sidechain
10	AJ	21	DT	Sidechain
10	AJ	27	DC	Sidechain
10	AJ	3	DG	Sidechain
10	AJ	31	DA	Sidechain
10	AJ	37	DC	Sidechain
11	AK	15	DC	Sidechain
11	AK	24	DT	Sidechain
11	AK	26	DT	Sidechain
11	AK	32	DT	Sidechain
11	AK	36	DC	Sidechain
11	AK	43	DA	Sidechain
12	AL	11	DA	Sidechain
12	AL	19	DA	Sidechain
12	AL	21	DT	Sidechain
12	AL	22	DC	Sidechain
12	AL	32	DT	Sidechain
12	AL	6	DC	Sidechain
13	AM	11	DT	Sidechain
13	AM	20	DT	Sidechain
13	AM	40	DA	Sidechain
14	AN	10	DA	Sidechain
14	AN	11	DC	Sidechain
14	AN	12	DG	Sidechain
14	AN	26	DG	Sidechain
14	AN	33	DT	Sidechain
14	AN	6	DG	Sidechain
15	AO	16	DA	Sidechain
15	AO	27	DA	Sidechain
15	AO	31	DT	Sidechain
15	AO	35	DC	Sidechain
15	AO	38	DC	Sidechain
16	AP	14	DG	Sidechain
16	AP	22	DA	Sidechain

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Mol	Chain	Res	Type	Group
16	AP	25	DG	Sidechain
16	AP	4	DT	Sidechain
16	AP	6	DA	Sidechain
17	AQ	25	DG	Sidechain
17	AQ	31	DT	Sidechain
17	AQ	34	DA	Sidechain
17	AQ	43	DT	Sidechain
17	AQ	5	DA	Sidechain
17	AQ	9	DT	Sidechain
18	AR	10	DT	Sidechain
18	AR	16	DT	Sidechain
18	AR	18	DT	Sidechain
18	AR	24	DT	Sidechain
18	AR	31	DT	Sidechain
18	AR	4	DG	Sidechain
18	AR	5	DA	Sidechain
19	AS	1	DT	Sidechain
19	AS	11	DA	Sidechain
19	AS	2	DT	Sidechain
19	AS	21	DA	Sidechain
19	AS	23	DG	Sidechain
20	AT	15	DT	Sidechain
20	AT	24	DG	Sidechain
20	AT	27	DG	Sidechain
20	AT	29	DA	Sidechain
21	AU	11	DT	Sidechain
21	AU	12	DT	Sidechain
21	AU	26	DT	Sidechain
22	AV	11	DT	Sidechain
22	AV	15	DA	Sidechain
22	AV	25	DG	Sidechain
22	AV	26	DA	Sidechain
22	AV	27	DG	Sidechain
22	AV	30	DT	Sidechain
22	AV	34	DA	Sidechain
22	AV	7	DT	Sidechain
23	AW	12	DT	Sidechain
23	AW	2	DA	Sidechain
24	AX	14	DT	Sidechain
24	AX	16	DA	Sidechain
24	AX	18	DG	Sidechain
24	AX	2	DT	Sidechain

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Mol	Chain	Res	Type	Group
24	AX	22	DA	Sidechain
24	AX	33	DT	Sidechain
24	AX	38	DG	Sidechain
24	AX	42	DA	Sidechain
25	AY	17	DA	Sidechain
25	AY	29	DT	Sidechain
25	AY	33	DT	Sidechain
25	AY	39	DT	Sidechain
25	AY	40	DA	Sidechain
26	AZ	11	DA	Sidechain
26	AZ	12	DT	Sidechain
26	AZ	17	DG	Sidechain
26	AZ	22	DA	Sidechain
26	AZ	27	DT	Sidechain
26	AZ	31	DC	Sidechain
26	AZ	32	DT	Sidechain
26	AZ	33	DG	Sidechain
26	AZ	34	DA	Sidechain
26	AZ	35	DT	Sidechain
26	AZ	45	DC	Sidechain
26	AZ	7	DG	Sidechain
27	Aa	11	DA	Sidechain
27	Aa	13	DG	Sidechain
27	Aa	23	DA	Sidechain
27	Aa	25	DC	Sidechain
27	Aa	29	DT	Sidechain
27	Aa	37	DC	Sidechain
27	Aa	39	DC	Sidechain
27	Aa	4	DG	Sidechain
28	Ab	18	DT	Sidechain
28	Ab	19	DT	Sidechain
28	Ab	32	DG	Sidechain
28	Ab	37	DT	Sidechain
29	Ac	11	DC	Sidechain
29	Ac	13	DA	Sidechain
29	Ac	18	DA	Sidechain
29	Ac	32	DA	Sidechain
29	Ac	35	DG	Sidechain
29	Ac	40	DG	Sidechain
30	Ad	18	DG	Sidechain
30	Ad	20	DA	Sidechain
30	Ad	23	DA	Sidechain

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Mol	Chain	Res	Type	Group
30	Ad	3	DA	Sidechain
30	Ad	30	DG	Sidechain
30	Ad	36	DT	Sidechain
31	Ae	17	DT	Sidechain
31	Ae	22	DG	Sidechain
31	Ae	23	DA	Sidechain
31	Ae	3	DT	Sidechain
31	Ae	34	DT	Sidechain
31	Ae	36	DT	Sidechain
32	Af	13	DG	Sidechain
32	Af	24	DC	Sidechain
32	Af	29	DA	Sidechain
32	Af	39	DC	Sidechain
32	Af	8	DA	Sidechain
33	Ag	10	DA	Sidechain
33	Ag	12	DA	Sidechain
33	Ag	15	DG	Sidechain
33	Ag	19	DG	Sidechain
33	Ag	21	DG	Sidechain
33	Ag	24	DA	Sidechain
34	Ah	18	DT	Sidechain
34	Ah	19	DT	Sidechain
34	Ah	27	DA	Sidechain
34	Ah	32	DT	Sidechain
34	Ah	34	DT	Sidechain
34	Ah	6	DG	Sidechain
35	Ai	18	DC	Sidechain
35	Ai	7	DA	Sidechain
36	Aj	11	DA	Sidechain
36	Aj	28	DT	Sidechain
37	Ak	11	DT	Sidechain
37	Ak	12	DT	Sidechain
37	Ak	2	DT	Sidechain
37	Ak	23	DG	Sidechain
37	Ak	24	DA	Sidechain
37	Ak	25	DC	Sidechain
37	Ak	3	DT	Sidechain
37	Ak	4	DT	Sidechain
38	Al	11	DA	Sidechain
38	Al	19	DC	Sidechain
38	Al	2	DA	Sidechain
38	Al	21	DT	Sidechain

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Mol	Chain	Res	Type	Group
38	Al	37	DT	Sidechain
38	Al	38	DT	Sidechain
38	Al	5	DA	Sidechain
39	Am	15	DT	Sidechain
39	Am	29	DT	Sidechain
39	Am	4	DT	Sidechain
40	An	10	DT	Sidechain
40	An	23	DA	Sidechain
40	An	25	DC	Sidechain
40	An	4	DT	Sidechain
41	Ao	28	DA	Sidechain
41	Ao	3	DT	Sidechain
41	Ao	4	DC	Sidechain
42	Ap	1	DT	Sidechain
42	Ap	12	DA	Sidechain
42	Ap	19	DA	Sidechain
42	Ap	26	DG	Sidechain
42	Ap	37	DG	Sidechain
43	Aq	23	DT	Sidechain
44	Ar	13	DA	Sidechain
44	Ar	14	DA	Sidechain
44	Ar	20	DC	Sidechain
44	Ar	3	DT	Sidechain
44	Ar	35	DA	Sidechain
44	Ar	4	DA	Sidechain
44	Ar	7	DG	Sidechain
45	As	1	DT	Sidechain
45	As	12	DC	Sidechain
45	As	28	DT	Sidechain
46	At	11	DA	Sidechain
46	At	12	DA	Sidechain
46	At	15	DC	Sidechain
46	At	22	DC	Sidechain
46	At	24	DA	Sidechain
46	At	27	DT	Sidechain
46	At	30	DG	Sidechain
46	At	31	DT	Sidechain
47	Au	14	DC	Sidechain
47	Au	18	DG	Sidechain
47	Au	4	DA	Sidechain
48	Av	26	DC	Sidechain
48	Av	29	DT	Sidechain

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Mol	Chain	Res	Type	Group
49	Aw	14	DA	Sidechain
49	Aw	18	DC	Sidechain
49	Aw	24	DC	Sidechain
50	Ax	14	DA	Sidechain
50	Ax	21	DA	Sidechain
50	Ax	6	DG	Sidechain
50	Ax	9	DG	Sidechain
51	Ay	17	DA	Sidechain
51	Ay	21	DT	Sidechain
51	Ay	23	DA	Sidechain
51	Ay	34	DC	Sidechain
51	Ay	36	DA	Sidechain
51	Ay	38	DA	Sidechain
51	Ay	6	DA	Sidechain
52	Az	11	DA	Sidechain
52	Az	13	DG	Sidechain
52	Az	15	DC	Sidechain
52	Az	18	DG	Sidechain
52	Az	30	DA	Sidechain
52	Az	5	DT	Sidechain
52	Az	9	DT	Sidechain
115	B0	11	DT	Sidechain
115	B0	25	DC	Sidechain
115	B0	37	DT	Sidechain
115	B0	4	DT	Sidechain
115	B0	40	DC	Sidechain
115	B0	7	DT	Sidechain
116	B1	1	DT	Sidechain
116	B1	2	DT	Sidechain
116	B1	20	DT	Sidechain
116	B1	23	DA	Sidechain
116	B1	28	DA	Sidechain
116	B1	37	DA	Sidechain
117	B2	15	DC	Sidechain
117	B2	30	DT	Sidechain
118	B3	16	DG	Sidechain
118	B3	29	DC	Sidechain
118	B3	3	DA	Sidechain
119	B4	15	DC	Sidechain
119	B4	3	DG	Sidechain
119	B4	30	DG	Sidechain
119	B4	31	DA	Sidechain

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Mol	Chain	Res	Type	Group
119	B4	35	DA	Sidechain
120	B5	11	DT	Sidechain
120	B5	25	DC	Sidechain
120	B5	42	DA	Sidechain
120	B5	46	DT	Sidechain
121	B6	15	DA	Sidechain
121	B6	16	DT	Sidechain
121	B6	21	DA	Sidechain
121	B6	28	DT	Sidechain
121	B6	5	DT	Sidechain
121	B6	7	DA	Sidechain
122	B7	12	DC	Sidechain
122	B7	15	DA	Sidechain
122	B7	16	DT	Sidechain
122	B7	19	DT	Sidechain
122	B7	25	DT	Sidechain
122	B7	28	DT	Sidechain
123	B8	13	DA	Sidechain
123	B8	2	DA	Sidechain
123	B8	24	DA	Sidechain
123	B8	25	DA	Sidechain
124	B9	15	DC	Sidechain
124	B9	25	DC	Sidechain
124	B9	27	DA	Sidechain
124	B9	34	DC	Sidechain
124	B9	37	DT	Sidechain
124	B9	5	DG	Sidechain
124	B9	6	DA	Sidechain
63	BA	1	DG	Sidechain
63	BA	6	DT	Sidechain
64	BB	16	DA	Sidechain
64	BB	17	DC	Sidechain
64	BB	24	DA	Sidechain
64	BB	30	DT	Sidechain
64	BB	35	DA	Sidechain
64	BB	40	DT	Sidechain
65	BC	17	DT	Sidechain
65	BC	18	DT	Sidechain
65	BC	24	DT	Sidechain
65	BC	26	DT	Sidechain
65	BC	35	DC	Sidechain
66	BD	1	DC	Sidechain

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Mol	Chain	Res	Type	Group
66	BD	15	DG	Sidechain
66	BD	25	DC	Sidechain
66	BD	28	DT	Sidechain
66	BD	4	DA	Sidechain
66	BD	7	DC	Sidechain
67	BE	15	DT	Sidechain
67	BE	2	DA	Sidechain
67	BE	20	DT	Sidechain
67	BE	32	DT	Sidechain
67	BE	36	DT	Sidechain
67	BE	9	DG	Sidechain
68	BF	21	DA	Sidechain
68	BF	27	DG	Sidechain
68	BF	33	DT	Sidechain
68	BF	37	DT	Sidechain
69	BG	10	DA	Sidechain
69	BG	25	DT	Sidechain
69	BG	37	DG	Sidechain
70	BH	14	DT	Sidechain
70	BH	22	DT	Sidechain
70	BH	31	DC	Sidechain
71	BI	1	DT	Sidechain
71	BI	13	DT	Sidechain
71	BI	16	DT	Sidechain
71	BI	19	DA	Sidechain
71	BI	22	DC	Sidechain
71	BI	5	DT	Sidechain
72	BJ	13	DT	Sidechain
72	BJ	23	DC	Sidechain
72	BJ	27	DA	Sidechain
72	BJ	29	DT	Sidechain
72	BJ	31	DC	Sidechain
72	BJ	33	DA	Sidechain
72	BJ	39	DA	Sidechain
73	BK	21	DT	Sidechain
73	BK	22	DA	Sidechain
74	BL	17	DC	Sidechain
74	BL	27	DC	Sidechain
74	BL	29	DA	Sidechain
74	BL	31	DG	Sidechain
74	BL	32	DC	Sidechain
74	BL	4	DT	Sidechain

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Mol	Chain	Res	Type	Group
75	BM	20	DT	Sidechain
75	BM	23	DT	Sidechain
75	BM	29	DA	Sidechain
75	BM	5	DT	Sidechain
76	BN	1	DG	Sidechain
76	BN	27	DG	Sidechain
76	BN	28	DC	Sidechain
77	BO	27	DG	Sidechain
78	BP	20	DT	Sidechain
78	BP	33	DA	Sidechain
79	BQ	27	DA	Sidechain
79	BQ	6	DA	Sidechain
79	BQ	9	DA	Sidechain
80	BR	14	DC	Sidechain
80	BR	21	DA	Sidechain
80	BR	36	DC	Sidechain
80	BR	7	DG	Sidechain
80	BR	9	DA	Sidechain
81	BS	13	DT	Sidechain
81	BS	5	DC	Sidechain
82	BT	1	DA	Sidechain
82	BT	13	DA	Sidechain
82	BT	23	DA	Sidechain
82	BT	29	DA	Sidechain
82	BT	3	DG	Sidechain
82	BT	31	DC	Sidechain
82	BT	39	DC	Sidechain
82	BT	5	DT	Sidechain
83	BU	1	DT	Sidechain
83	BU	32	DA	Sidechain
83	BU	37	DC	Sidechain
83	BU	4	DT	Sidechain
83	BU	40	DT	Sidechain
83	BU	41	DG	Sidechain
83	BU	42	DC	Sidechain
83	BU	7	DT	Sidechain
84	BV	10	DA	Sidechain
84	BV	12	DT	Sidechain
84	BV	22	DT	Sidechain
84	BV	23	DT	Sidechain
84	BV	45	DC	Sidechain
84	BV	9	DG	Sidechain

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Mol	Chain	Res	Type	Group
85	BW	11	DT	Sidechain
85	BW	13	DA	Sidechain
85	BW	14	DC	Sidechain
85	BW	26	DT	Sidechain
85	BW	27	DT	Sidechain
85	BW	32	DT	Sidechain
85	BW	34	DT	Sidechain
85	BW	40	DG	Sidechain
85	BW	44	DT	Sidechain
85	BW	47	DT	Sidechain
86	BX	18	DC	Sidechain
86	BX	9	DA	Sidechain
87	BY	11	DT	Sidechain
87	BY	13	DT	Sidechain
87	BY	17	DC	Sidechain
87	BY	22	DC	Sidechain
87	BY	27	DA	Sidechain
87	BY	39	DA	Sidechain
87	BY	6	DT	Sidechain
88	BZ	1	DA	Sidechain
88	BZ	21	DC	Sidechain
88	BZ	3	DC	Sidechain
89	Ba	1	DC	Sidechain
89	Ba	11	DG	Sidechain
89	Ba	14	DA	Sidechain
89	Ba	23	DT	Sidechain
89	Ba	25	DA	Sidechain
89	Ba	27	DG	Sidechain
90	Bb	1	DC	Sidechain
90	Bb	11	DA	Sidechain
90	Bb	2	DA	Sidechain
90	Bb	29	DG	Sidechain
90	Bb	40	DA	Sidechain
90	Bb	6	DC	Sidechain
90	Bb	7	DA	Sidechain
91	Bc	1	DA	Sidechain
91	Bc	14	DT	Sidechain
91	Bc	17	DA	Sidechain
91	Bc	27	DA	Sidechain
91	Bc	7	DC	Sidechain
92	Bd	13	DT	Sidechain
92	Bd	16	DA	Sidechain

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Mol	Chain	Res	Type	Group
92	Bd	2	DG	Sidechain
92	Bd	20	DT	Sidechain
92	Bd	23	DC	Sidechain
92	Bd	25	DA	Sidechain
92	Bd	26	DG	Sidechain
92	Bd	27	DC	Sidechain
92	Bd	28	DC	Sidechain
92	Bd	6	DT	Sidechain
93	Be	23	DA	Sidechain
93	Be	33	DA	Sidechain
94	Bf	1	DT	Sidechain
94	Bf	15	DA	Sidechain
94	Bf	2	DT	Sidechain
94	Bf	29	DT	Sidechain
94	Bf	30	DT	Sidechain
94	Bf	31	DT	Sidechain
94	Bf	33	DT	Sidechain
94	Bf	36	DT	Sidechain
94	Bf	37	DT	Sidechain
95	Bg	11	DT	Sidechain
95	Bg	14	DA	Sidechain
95	Bg	23	DT	Sidechain
95	Bg	29	DG	Sidechain
95	Bg	30	DA	Sidechain
95	Bg	6	DA	Sidechain
95	Bg	7	DT	Sidechain
96	Bh	13	DA	Sidechain
96	Bh	16	DC	Sidechain
96	Bh	17	DG	Sidechain
96	Bh	20	DC	Sidechain
96	Bh	33	DA	Sidechain
96	Bh	38	DG	Sidechain
96	Bh	39	DG	Sidechain
97	Bi	14	DC	Sidechain
97	Bi	21	DA	Sidechain
97	Bi	22	DG	Sidechain
97	Bi	26	DC	Sidechain
97	Bi	33	DT	Sidechain
97	Bi	5	DT	Sidechain
97	Bi	9	DT	Sidechain
98	Bj	16	DT	Sidechain
98	Bj	21	DT	Sidechain

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Mol	Chain	Res	Type	Group
98	Bj	28	DA	Sidechain
98	Bj	39	DT	Sidechain
98	Bj	4	DC	Sidechain
98	Bj	45	DT	Sidechain
98	Bj	49	DT	Sidechain
99	Bk	1	DA	Sidechain
99	Bk	3	DG	Sidechain
100	Bl	22	DC	Sidechain
100	Bl	28	DC	Sidechain
100	Bl	6	DT	Sidechain
101	Bm	31	DC	Sidechain
101	Bm	5	DC	Sidechain
101	Bm	6	DC	Sidechain
102	Bn	1	DC	Sidechain
102	Bn	11	DG	Sidechain
102	Bn	12	DA	Sidechain
102	Bn	3	DT	Sidechain
102	Bn	31	DG	Sidechain
102	Bn	38	DA	Sidechain
102	Bn	5	DA	Sidechain
103	Bo	1	DT	Sidechain
103	Bo	15	DC	Sidechain
103	Bo	23	DA	Sidechain
103	Bo	26	DT	Sidechain
103	Bo	29	DT	Sidechain
103	Bo	6	DG	Sidechain
103	Bo	8	DA	Sidechain
104	Bp	1	DA	Sidechain
104	Bp	17	DA	Sidechain
104	Bp	23	DC	Sidechain
104	Bp	25	DC	Sidechain
104	Bp	33	DT	Sidechain
104	Bp	4	DC	Sidechain
105	Bq	10	DT	Sidechain
105	Bq	11	DT	Sidechain
105	Bq	20	DT	Sidechain
105	Bq	23	DA	Sidechain
105	Bq	27	DC	Sidechain
105	Bq	29	DG	Sidechain
105	Bq	33	DG	Sidechain
105	Bq	34	DA	Sidechain
106	Br	16	DA	Sidechain

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Mol	Chain	Res	Type	Group
106	Br	17	DG	Sidechain
106	Br	21	DG	Sidechain
106	Br	25	DG	Sidechain
106	Br	26	DG	Sidechain
106	Br	27	DG	Sidechain
106	Br	3	DA	Sidechain
106	Br	31	DG	Sidechain
106	Br	35	DG	Sidechain
106	Br	8	DC	Sidechain
107	Bs	1	DT	Sidechain
107	Bs	26	DG	Sidechain
108	Bt	1	DA	Sidechain
108	Bt	18	DA	Sidechain
108	Bt	20	DA	Sidechain
108	Bt	23	DG	Sidechain
108	Bt	28	DG	Sidechain
108	Bt	38	DA	Sidechain
109	Bu	21	DT	Sidechain
109	Bu	23	DA	Sidechain
109	Bu	30	DC	Sidechain
109	Bu	39	DC	Sidechain
109	Bu	4	DA	Sidechain
110	Bv	38	DC	Sidechain
110	Bv	47	DT	Sidechain
111	Bw	20	DG	Sidechain
111	Bw	22	DT	Sidechain
111	Bw	27	DA	Sidechain
111	Bw	29	DC	Sidechain
111	Bw	32	DT	Sidechain
111	Bw	37	DT	Sidechain
112	Bx	21	DC	Sidechain
112	Bx	22	DT	Sidechain
113	By	19	DG	Sidechain
113	By	22	DT	Sidechain
113	By	7	DA	Sidechain
114	Bz	13	DG	Sidechain
114	Bz	14	DT	Sidechain
114	Bz	17	DG	Sidechain
114	Bz	25	DC	Sidechain
114	Bz	27	DC	Sidechain
114	Bz	30	DT	Sidechain
114	Bz	38	DC	Sidechain

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Mol	Chain	Res	Type	Group
177	C0	11	DG	Sidechain
177	C0	12	DA	Sidechain
177	C0	23	DG	Sidechain
177	C0	31	DA	Sidechain
177	C0	45	DT	Sidechain
177	C0	46	DA	Sidechain
177	C0	7	DT	Sidechain
178	C1	23	DC	Sidechain
178	C1	25	DG	Sidechain
178	C1	29	DT	Sidechain
178	C1	5	DT	Sidechain
178	C1	6	DA	Sidechain
179	C2	2	DG	Sidechain
179	C2	3	DA	Sidechain
179	C2	9	DG	Sidechain
180	C3	1	DT	Sidechain
180	C3	20	DG	Sidechain
180	C3	4	DT	Sidechain
180	C3	5	DT	Sidechain
181	C4	15	DG	Sidechain
181	C4	3	DA	Sidechain
182	C5	12	DT	Sidechain
182	C5	17	DT	Sidechain
182	C5	20	DT	Sidechain
182	C5	24	DA	Sidechain
182	C5	25	DC	Sidechain
182	C5	29	DA	Sidechain
182	C5	30	DG	Sidechain
182	C5	5	DT	Sidechain
183	C6	10	DC	Sidechain
183	C6	19	DT	Sidechain
183	C6	20	DT	Sidechain
183	C6	26	DT	Sidechain
183	C6	27	DA	Sidechain
183	C6	29	DG	Sidechain
183	C6	32	DA	Sidechain
183	C6	33	DC	Sidechain
183	C6	34	DC	Sidechain
183	C6	40	DC	Sidechain
184	C7	17	DT	Sidechain
184	C7	18	DT	Sidechain
184	C7	20	DT	Sidechain

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Mol	Chain	Res	Type	Group
184	C7	21	DT	Sidechain
184	C7	32	DT	Sidechain
185	C8	1	DA	Sidechain
185	C8	29	DA	Sidechain
185	C8	37	DG	Sidechain
185	C8	43	DA	Sidechain
185	C8	46	DA	Sidechain
185	C8	7	DA	Sidechain
186	C9	1	DA	Sidechain
186	C9	25	DA	Sidechain
186	C9	31	DA	Sidechain
186	C9	33	DC	Sidechain
186	C9	34	DG	Sidechain
186	C9	40	DA	Sidechain
186	C9	6	DA	Sidechain
125	CA	1	DA	Sidechain
125	CA	15	DT	Sidechain
125	CA	17	DA	Sidechain
125	CA	21	DG	Sidechain
125	CA	22	DC	Sidechain
125	CA	26	DC	Sidechain
125	CA	33	DC	Sidechain
125	CA	35	DC	Sidechain
125	CA	8	DA	Sidechain
126	CB	11	DG	Sidechain
126	CB	22	DC	Sidechain
127	CC	14	DT	Sidechain
127	CC	16	DA	Sidechain
127	CC	31	DT	Sidechain
127	CC	36	DT	Sidechain
127	CC	40	DA	Sidechain
128	CD	1	DG	Sidechain
128	CD	17	DA	Sidechain
128	CD	18	DA	Sidechain
128	CD	24	DA	Sidechain
128	CD	4	DG	Sidechain
129	CE	29	DA	Sidechain
129	CE	31	DT	Sidechain
129	CE	33	DT	Sidechain
130	CF	15	DT	Sidechain
130	CF	16	DT	Sidechain
130	CF	19	DT	Sidechain

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Mol	Chain	Res	Type	Group
131	CG	13	DT	Sidechain
131	CG	24	DC	Sidechain
131	CG	35	DA	Sidechain
131	CG	36	DT	Sidechain
131	CG	38	DA	Sidechain
131	CG	7	DA	Sidechain
132	CH	1	DG	Sidechain
132	CH	23	DC	Sidechain
132	CH	31	DT	Sidechain
132	CH	38	DT	Sidechain
133	CI	1	DG	Sidechain
133	CI	13	DC	Sidechain
133	CI	3	DA	Sidechain
133	CI	39	DA	Sidechain
134	CJ	11	DA	Sidechain
134	CJ	13	DA	Sidechain
134	CJ	2	DT	Sidechain
134	CJ	21	DA	Sidechain
134	CJ	22	DT	Sidechain
134	CJ	28	DA	Sidechain
134	CJ	32	DC	Sidechain
135	CK	15	DG	Sidechain
135	CK	19	DT	Sidechain
135	CK	3	DT	Sidechain
135	CK	31	DA	Sidechain
135	CK	34	DA	Sidechain
135	CK	5	DA	Sidechain
135	CK	7	DC	Sidechain
135	CK	9	DA	Sidechain
136	CL	16	DT	Sidechain
136	CL	21	DT	Sidechain
136	CL	22	DT	Sidechain
136	CL	37	DT	Sidechain
136	CL	4	DT	Sidechain
136	CL	44	DA	Sidechain
137	CM	1	DT	Sidechain
137	CM	21	DT	Sidechain
137	CM	22	DT	Sidechain
137	CM	4	DC	Sidechain
138	CN	19	DA	Sidechain
138	CN	27	DG	Sidechain
138	CN	35	DT	Sidechain

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Mol	Chain	Res	Type	Group
138	CN	9	DC	Sidechain
139	CO	10	DG	Sidechain
139	CO	19	DC	Sidechain
139	CO	22	DC	Sidechain
139	CO	23	DT	Sidechain
139	CO	30	DT	Sidechain
139	CO	32	DG	Sidechain
139	CO	38	DC	Sidechain
140	CP	14	DA	Sidechain
140	CP	22	DA	Sidechain
140	CP	3	DC	Sidechain
140	CP	41	DA	Sidechain
140	CP	48	DA	Sidechain
140	CP	8	DT	Sidechain
141	CQ	10	DA	Sidechain
141	CQ	13	DA	Sidechain
141	CQ	7	DC	Sidechain
141	CQ	8	DT	Sidechain
142	CR	15	DA	Sidechain
142	CR	21	DA	Sidechain
142	CR	25	DA	Sidechain
142	CR	27	DA	Sidechain
142	CR	31	DC	Sidechain
142	CR	6	DT	Sidechain
143	CS	10	DT	Sidechain
143	CS	13	DA	Sidechain
143	CS	37	DC	Sidechain
143	CS	4	DC	Sidechain
144	CT	1	DT	Sidechain
144	CT	12	DT	Sidechain
144	CT	16	DA	Sidechain
144	CT	2	DT	Sidechain
144	CT	27	DT	Sidechain
144	CT	31	DA	Sidechain
144	CT	37	DC	Sidechain
145	CU	10	DC	Sidechain
145	CU	14	DC	Sidechain
145	CU	23	DT	Sidechain
145	CU	24	DA	Sidechain
145	CU	43	DT	Sidechain
145	CU	7	DA	Sidechain
146	CV	10	DC	Sidechain

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Mol	Chain	Res	Type	Group
146	CV	13	DG	Sidechain
146	CV	19	DT	Sidechain
146	CV	21	DC	Sidechain
146	CV	25	DT	Sidechain
146	CV	9	DA	Sidechain
147	CW	11	DC	Sidechain
147	CW	23	DT	Sidechain
147	CW	8	DG	Sidechain
147	CW	9	DA	Sidechain
148	CX	10	DA	Sidechain
148	CX	21	DT	Sidechain
148	CX	29	DA	Sidechain
148	CX	42	DC	Sidechain
148	CX	43	DA	Sidechain
148	CX	44	DT	Sidechain
149	CY	12	DA	Sidechain
149	CY	15	DT	Sidechain
149	CY	25	DA	Sidechain
149	CY	4	DT	Sidechain
149	CY	7	DC	Sidechain
149	CY	9	DA	Sidechain
150	CZ	18	DA	Sidechain
150	CZ	20	DA	Sidechain
150	CZ	21	DT	Sidechain
150	CZ	3	DT	Sidechain
150	CZ	4	DT	Sidechain
151	Ca	15	DA	Sidechain
151	Ca	16	DT	Sidechain
151	Ca	3	DG	Sidechain
151	Ca	31	DT	Sidechain
151	Ca	4	DA	Sidechain
151	Ca	6	DG	Sidechain
152	Cb	14	DC	Sidechain
152	Cb	15	DC	Sidechain
152	Cb	2	DA	Sidechain
152	Cb	26	DT	Sidechain
152	Cb	34	DT	Sidechain
153	Cc	11	DG	Sidechain
153	Cc	30	DT	Sidechain
154	Cd	1	DA	Sidechain
154	Cd	15	DC	Sidechain
154	Cd	22	DG	Sidechain

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Mol	Chain	Res	Type	Group
154	Cd	36	DC	Sidechain
154	Cd	39	DA	Sidechain
154	Cd	5	DC	Sidechain
155	Ce	10	DC	Sidechain
155	Ce	16	DT	Sidechain
155	Ce	17	DG	Sidechain
155	Ce	37	DT	Sidechain
155	Ce	8	DA	Sidechain
155	Ce	9	DG	Sidechain
156	Cf	23	DG	Sidechain
156	Cf	26	DT	Sidechain
156	Cf	33	DG	Sidechain
156	Cf	35	DA	Sidechain
156	Cf	39	DC	Sidechain
156	Cf	6	DG	Sidechain
157	Cg	17	DG	Sidechain
157	Cg	21	DC	Sidechain
157	Cg	30	DA	Sidechain
157	Cg	31	DT	Sidechain
157	Cg	4	DT	Sidechain
157	Cg	40	DT	Sidechain
157	Cg	41	DA	Sidechain
157	Cg	44	DG	Sidechain
157	Cg	7	DG	Sidechain
157	Cg	8	DA	Sidechain
158	Ch	1	DG	Sidechain
158	Ch	13	DA	Sidechain
158	Ch	15	DA	Sidechain
158	Ch	16	DC	Sidechain
158	Ch	19	DT	Sidechain
158	Ch	25	DA	Sidechain
158	Ch	34	DG	Sidechain
158	Ch	35	DC	Sidechain
158	Ch	36	DT	Sidechain
158	Ch	38	DC	Sidechain
158	Ch	9	DA	Sidechain
159	Ci	2	DA	Sidechain
159	Ci	30	DT	Sidechain
159	Ci	42	DT	Sidechain
159	Ci	44	DT	Sidechain
160	Cj	1	DC	Sidechain
160	Cj	14	DC	Sidechain

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Mol	Chain	Res	Type	Group
160	Cj	15	DC	Sidechain
160	Cj	2	DA	Sidechain
160	Cj	20	DT	Sidechain
160	Cj	39	DT	Sidechain
160	Cj	4	DA	Sidechain
160	Cj	45	DC	Sidechain
160	Cj	7	DA	Sidechain
161	Ck	22	DT	Sidechain
161	Ck	29	DA	Sidechain
161	Ck	40	DA	Sidechain
161	Ck	43	DG	Sidechain
162	Cl	1	DA	Sidechain
162	Cl	22	DA	Sidechain
162	Cl	23	DC	Sidechain
162	Cl	27	DA	Sidechain
162	Cl	29	DT	Sidechain
163	Cm	13	DA	Sidechain
163	Cm	2	DA	Sidechain
163	Cm	20	DA	Sidechain
163	Cm	22	DA	Sidechain
163	Cm	31	DA	Sidechain
163	Cm	37	DC	Sidechain
163	Cm	40	DA	Sidechain
164	Cn	29	DT	Sidechain
165	Co	14	DT	Sidechain
165	Co	17	DT	Sidechain
165	Co	23	DT	Sidechain
165	Co	28	DT	Sidechain
165	Co	30	DT	Sidechain
165	Co	9	DC	Sidechain
166	Cp	22	DT	Sidechain
166	Cp	25	DA	Sidechain
166	Cp	32	DG	Sidechain
166	Cp	8	DA	Sidechain
167	Cq	15	DT	Sidechain
167	Cq	18	DT	Sidechain
167	Cq	23	DT	Sidechain
167	Cq	28	DT	Sidechain
167	Cq	39	DA	Sidechain
167	Cq	9	DG	Sidechain
168	Cr	1	DT	Sidechain
168	Cr	12	DC	Sidechain

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Mol	Chain	Res	Type	Group
168	Cr	17	DT	Sidechain
168	Cr	35	DT	Sidechain
168	Cr	4	DT	Sidechain
168	Cr	40	DT	Sidechain
168	Cr	41	DA	Sidechain
168	Cr	44	DG	Sidechain
168	Cr	49	DA	Sidechain
168	Cr	9	DA	Sidechain
169	Cs	11	DA	Sidechain
169	Cs	2	DT	Sidechain
169	Cs	22	DA	Sidechain
169	Cs	34	DC	Sidechain
169	Cs	5	DT	Sidechain
170	Ct	16	DA	Sidechain
170	Ct	20	DG	Sidechain
170	Ct	22	DA	Sidechain
170	Ct	29	DA	Sidechain
170	Ct	38	DC	Sidechain
171	Cu	1	DC	Sidechain
171	Cu	15	DA	Sidechain
171	Cu	32	DT	Sidechain
171	Cu	6	DC	Sidechain
172	Cv	14	DA	Sidechain
172	Cv	29	DT	Sidechain
172	Cv	35	DG	Sidechain
172	Cv	6	DA	Sidechain
173	Cw	10	DT	Sidechain
173	Cw	32	DT	Sidechain
174	Cx	10	DG	Sidechain
174	Cx	17	DT	Sidechain
174	Cx	23	DC	Sidechain
174	Cx	24	DT	Sidechain
174	Cx	27	DA	Sidechain
174	Cx	3	DT	Sidechain
174	Cx	39	DC	Sidechain
174	Cx	4	DT	Sidechain
174	Cx	41	DG	Sidechain
175	Cy	14	DT	Sidechain
175	Cy	24	DC	Sidechain
175	Cy	27	DC	Sidechain
175	Cy	30	DT	Sidechain
175	Cy	37	DT	Sidechain

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Mol	Chain	Res	Type	Group
176	Cz	24	DG	Sidechain
176	Cz	28	DA	Sidechain
187	DA	14	DG	Sidechain
187	DA	15	DT	Sidechain
187	DA	3	DA	Sidechain
187	DA	35	DT	Sidechain
187	DA	7	DA	Sidechain
187	DA	8	DC	Sidechain
188	DB	23	DT	Sidechain
188	DB	31	DA	Sidechain
188	DB	33	DA	Sidechain
188	DB	44	DC	Sidechain
188	DB	46	DC	Sidechain
188	DB	6	DT	Sidechain
189	DC	28	DT	Sidechain
189	DC	5	DT	Sidechain
189	DC	6	DA	Sidechain
189	DC	7	DT	Sidechain
190	DD	11	DT	Sidechain
190	DD	14	DT	Sidechain
190	DD	27	DG	Sidechain
190	DD	36	DC	Sidechain
190	DD	38	DA	Sidechain
190	DD	4	DA	Sidechain
191	DE	21	DG	Sidechain
191	DE	30	DA	Sidechain
191	DE	49	DT	Sidechain
191	DE	7	DA	Sidechain
192	DF	16	DT	Sidechain
192	DF	20	DA	Sidechain
192	DF	25	DT	Sidechain
192	DF	33	DT	Sidechain
192	DF	39	DA	Sidechain
192	DF	42	DA	Sidechain
192	DF	46	DC	Sidechain
192	DF	50	DA	Sidechain
192	DF	8	DA	Sidechain
193	DG	13	DG	Sidechain
193	DG	16	DA	Sidechain
193	DG	20	DA	Sidechain
194	DH	16	DG	Sidechain
194	DH	17	DT	Sidechain

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Mol	Chain	Res	Type	Group
194	DH	18	DA	Sidechain
194	DH	5	DT	Sidechain
195	DI	1	DT	Sidechain
195	DI	2	DT	Sidechain
195	DI	27	DA	Sidechain
195	DI	3	DT	Sidechain
195	DI	4	DT	Sidechain
195	DI	9	DT	Sidechain
196	DJ	22	DC	Sidechain
196	DJ	24	DG	Sidechain
196	DJ	26	DA	Sidechain
196	DJ	4	DG	Sidechain
196	DJ	42	DT	Sidechain
197	DK	16	DA	Sidechain
197	DK	20	DT	Sidechain
197	DK	24	DT	Sidechain
197	DK	25	DT	Sidechain
197	DK	4	DG	Sidechain
198	DL	1	DA	Sidechain
198	DL	16	DA	Sidechain
198	DL	19	DT	Sidechain
198	DL	26	DC	Sidechain
198	DL	29	DA	Sidechain
198	DL	3	DG	Sidechain
199	DM	1	DA	Sidechain
199	DM	11	DC	Sidechain
199	DM	17	DA	Sidechain
199	DM	26	DA	Sidechain
199	DM	40	DA	Sidechain
199	DM	48	DA	Sidechain
200	DN	17	DA	Sidechain
200	DN	20	DA	Sidechain
200	DN	25	DA	Sidechain
200	DN	27	DG	Sidechain
200	DN	46	DA	Sidechain
200	DN	6	DA	Sidechain
200	DN	8	DA	Sidechain
201	DO	11	DT	Sidechain
201	DO	14	DA	Sidechain
201	DO	20	DT	Sidechain
201	DO	23	DT	Sidechain
201	DO	9	DA	Sidechain

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Mol	Chain	Res	Type	Group
202	DP	29	DC	Sidechain
203	DQ	10	DC	Sidechain
203	DQ	15	DG	Sidechain
203	DQ	35	DT	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	148273	0	82149	0	0
2	AB	819	0	454	0	0
3	AC	630	0	357	0	0
4	AD	812	0	458	0	0
5	AE	978	0	545	0	0
6	AF	630	0	361	0	0
7	AG	814	0	458	0	0
8	AH	637	0	358	0	0
9	AI	911	0	512	0	0
10	AJ	826	0	450	0	0
11	AK	909	0	520	0	0
12	AL	733	0	415	0	0
13	AM	925	0	513	0	0
14	AN	819	0	455	0	0
15	AO	818	0	452	0	0
16	AP	736	0	411	0	0
17	AQ	912	0	513	0	0
18	AR	686	0	400	0	0
19	AS	734	0	420	0	0
20	AT	699	0	393	0	0
21	AU	679	0	400	0	0
22	AV	698	0	388	0	0
23	AW	660	0	357	0	0
24	AX	867	0	472	0	0
25	AY	813	0	456	0	0
26	AZ	993	0	544	0	0
27	Aa	815	0	456	0	0
28	Ab	747	0	433	0	0
29	Ac	1033	0	567	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	Ad	832	0	450	0	0
31	Ae	746	0	431	0	0
32	Af	981	0	540	0	0
33	Ag	871	0	471	0	0
34	Ah	746	0	427	0	0
35	Ai	756	0	424	0	0
36	Aj	641	0	358	0	0
37	Ak	816	0	454	0	0
38	Al	858	0	479	0	0
39	Am	809	0	456	0	0
40	An	811	0	461	0	0
41	Ao	651	0	365	0	0
42	Ap	766	0	417	0	0
43	Aq	824	0	449	0	0
44	Ar	834	0	449	0	0
45	As	619	0	358	0	0
46	At	660	0	361	0	0
47	Au	665	0	356	0	0
48	Av	809	0	453	0	0
49	Aw	813	0	457	0	0
50	Ax	655	0	363	0	0
51	Ay	823	0	448	0	0
52	Az	822	0	448	0	0
53	A0	984	0	536	0	0
54	A1	625	0	358	0	0
55	A2	840	0	475	0	0
56	A3	652	0	360	0	0
57	A4	984	0	540	0	0
58	A5	820	0	449	0	0
59	A6	829	0	452	0	0
60	A7	851	0	481	0	0
61	A8	746	0	430	0	0
62	A9	819	0	454	0	0
63	BA	656	0	361	0	0
64	BB	928	0	508	0	0
65	BC	754	0	427	0	0
66	BD	642	0	361	0	0
67	BE	733	0	413	0	0
68	BF	855	0	477	0	0
69	BG	760	0	431	0	0
70	BH	811	0	454	0	0
71	BI	642	0	364	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
72	BJ	814	0	454	0	0
73	BK	654	0	364	0	0
74	BL	751	0	422	0	0
75	BM	660	0	364	0	0
76	BN	656	0	363	0	0
77	BO	819	0	451	0	0
78	BP	969	0	538	0	0
79	BQ	660	0	359	0	0
80	BR	812	0	452	0	0
81	BS	984	0	545	0	0
82	BT	817	0	450	0	0
83	BU	852	0	478	0	0
84	BV	988	0	546	0	0
85	BW	960	0	562	0	0
86	BX	805	0	458	0	0
87	BY	806	0	458	0	0
88	BZ	818	0	452	0	0
89	Ba	804	0	449	0	0
90	Bb	815	0	453	0	0
91	Bc	656	0	359	0	0
92	Bd	809	0	458	0	0
93	Be	818	0	447	0	0
94	Bf	900	0	508	0	0
95	Bg	664	0	365	0	0
96	Bh	835	0	445	0	0
97	Bi	824	0	459	0	0
98	Bj	997	0	562	0	0
99	Bk	599	0	326	0	0
100	Bl	859	0	476	0	0
101	Bm	811	0	449	0	0
102	Bn	817	0	447	0	0
103	Bo	655	0	363	0	0
104	Bp	806	0	453	0	0
105	Bq	977	0	554	0	0
106	Br	820	0	447	0	0
107	Bs	629	0	357	0	0
108	Bt	983	0	536	0	0
109	Bu	807	0	448	0	0
110	Bv	976	0	544	0	0
111	Bw	824	0	455	0	0
112	Bx	820	0	454	0	0
113	By	810	0	456	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
114	Bz	819	0	452	0	0
115	B0	807	0	463	0	0
116	B1	854	0	486	0	0
117	B2	627	0	357	0	0
118	B3	813	0	451	0	0
119	B4	989	0	541	0	0
120	B5	1023	0	569	0	0
121	B6	634	0	358	0	0
122	B7	589	0	335	0	0
123	B8	819	0	449	0	0
124	B9	828	0	450	0	0
125	CA	808	0	449	0	0
126	CB	699	0	384	0	0
127	CC	814	0	457	0	0
128	CD	817	0	445	0	0
129	CE	699	0	384	0	0
130	CF	651	0	374	0	0
131	CG	823	0	449	0	0
132	CH	814	0	456	0	0
133	CI	823	0	447	0	0
134	CJ	815	0	452	0	0
135	CK	823	0	449	0	0
136	CL	893	0	500	0	0
137	CM	746	0	424	0	0
138	CN	808	0	460	0	0
139	CO	805	0	453	0	0
140	CP	987	0	539	0	0
141	CQ	686	0	383	0	0
142	CR	820	0	449	0	0
143	CS	808	0	453	0	0
144	CT	965	0	549	0	0
145	CU	980	0	542	0	0
146	CV	691	0	393	0	0
147	CW	535	0	296	0	0
148	CX	902	0	501	0	0
149	CY	670	0	357	0	0
150	CZ	534	0	296	0	0
151	Ca	824	0	450	0	0
152	Cb	690	0	388	0	0
153	Cc	693	0	388	0	0
154	Cd	818	0	448	0	0
155	Ce	822	0	455	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
156	Cf	826	0	448	0	0
157	Cg	991	0	538	0	0
158	Ch	983	0	545	0	0
159	Ci	942	0	526	0	0
160	Cj	981	0	544	0	0
161	Ck	899	0	507	0	0
162	Cl	809	0	452	0	0
163	Cm	990	0	539	0	0
164	Cn	640	0	361	0	0
165	Co	889	0	510	0	0
166	Cp	664	0	365	0	0
167	Cq	813	0	457	0	0
168	Cr	1022	0	567	0	0
169	Cs	812	0	455	0	0
170	Ct	819	0	455	0	0
171	Cu	819	0	450	0	0
172	Cv	832	0	454	0	0
173	Cw	856	0	480	0	0
174	Cx	1019	0	567	0	0
175	Cy	854	0	481	0	0
176	Cz	818	0	452	0	0
177	C0	990	0	544	0	0
178	C1	830	0	449	0	0
179	C2	824	0	452	0	0
180	C3	626	0	363	0	0
181	C4	824	0	451	0	0
182	C5	826	0	453	0	0
183	C6	910	0	519	0	0
184	C7	684	0	400	0	0
185	C8	980	0	539	0	0
186	C9	984	0	535	0	0
187	DA	814	0	450	0	0
188	DB	975	0	545	0	0
189	DC	632	0	362	0	0
190	DD	821	0	459	0	0
191	DE	1024	0	568	0	0
192	DF	1024	0	570	0	0
193	DG	821	0	452	0	0
194	DH	850	0	478	0	0
195	DI	747	0	424	0	0
196	DJ	985	0	541	0	0
197	DK	816	0	454	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
198	DL	649	0	365	0	0
199	DM	988	0	540	0	0
200	DN	987	0	543	0	0
201	DO	481	0	284	0	0
202	DP	654	0	358	0	0
203	DQ	826	0	449	0	0
All	All	311400	0	172940	0	0

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

There are no clashes within the asymmetric unit.

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein molecules in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein molecules in this entry.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Map visualisation [i](#)

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

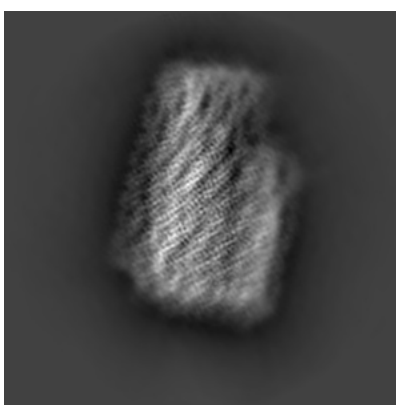
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

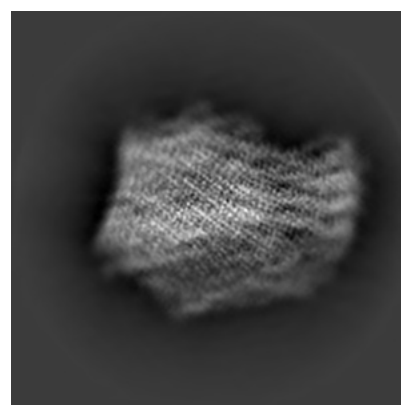
6.1.1 Primary map



X



Y

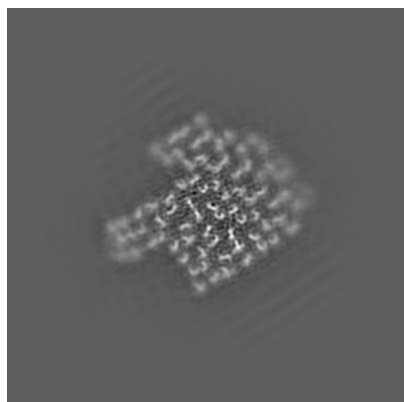


Z

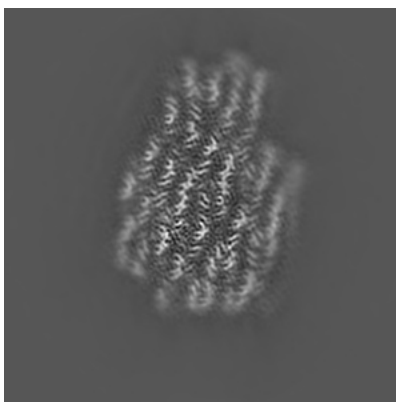
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

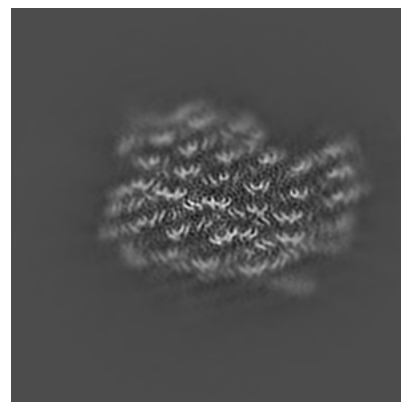
6.2.1 Primary map



X Index: 180



Y Index: 180

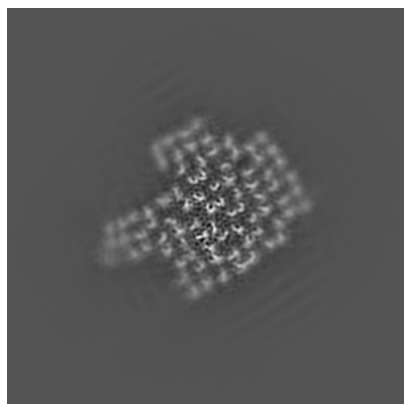


Z Index: 180

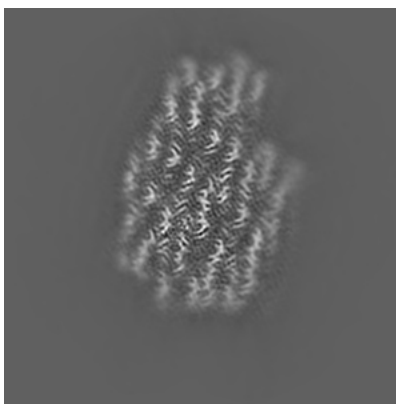
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

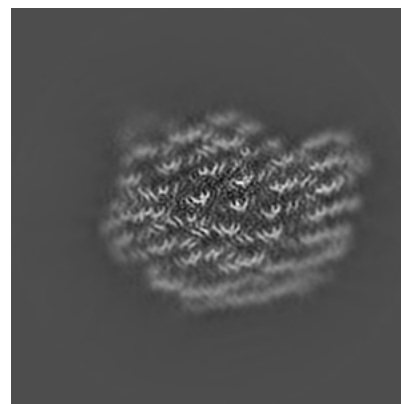
6.3.1 Primary map



X Index: 159



Y Index: 183

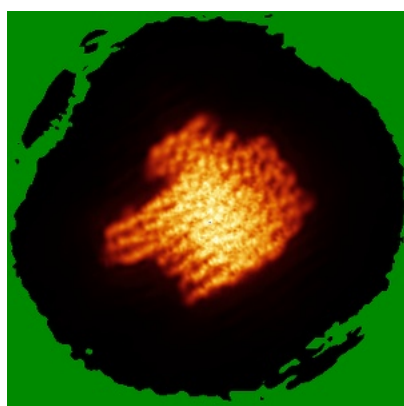


Z Index: 166

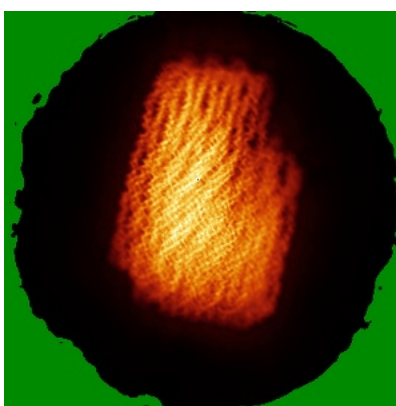
The images above show the largest variance slices of the map in three orthogonal directions.

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

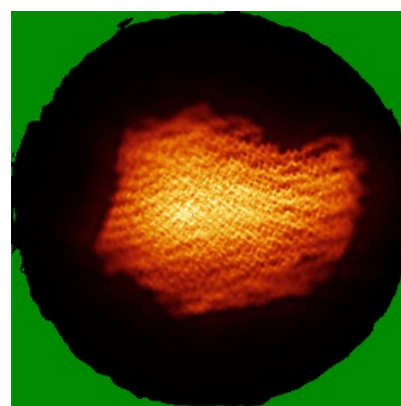
6.4.1 Primary map



X



Y

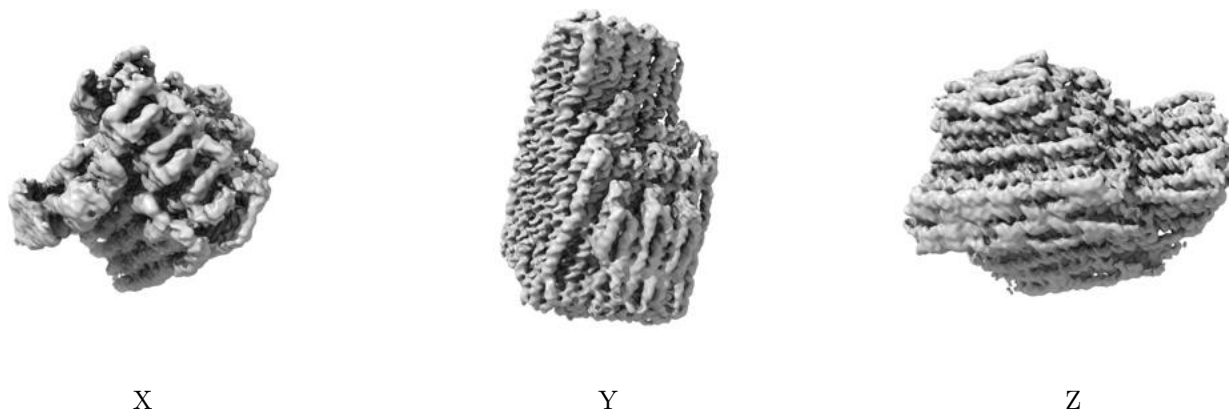


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



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

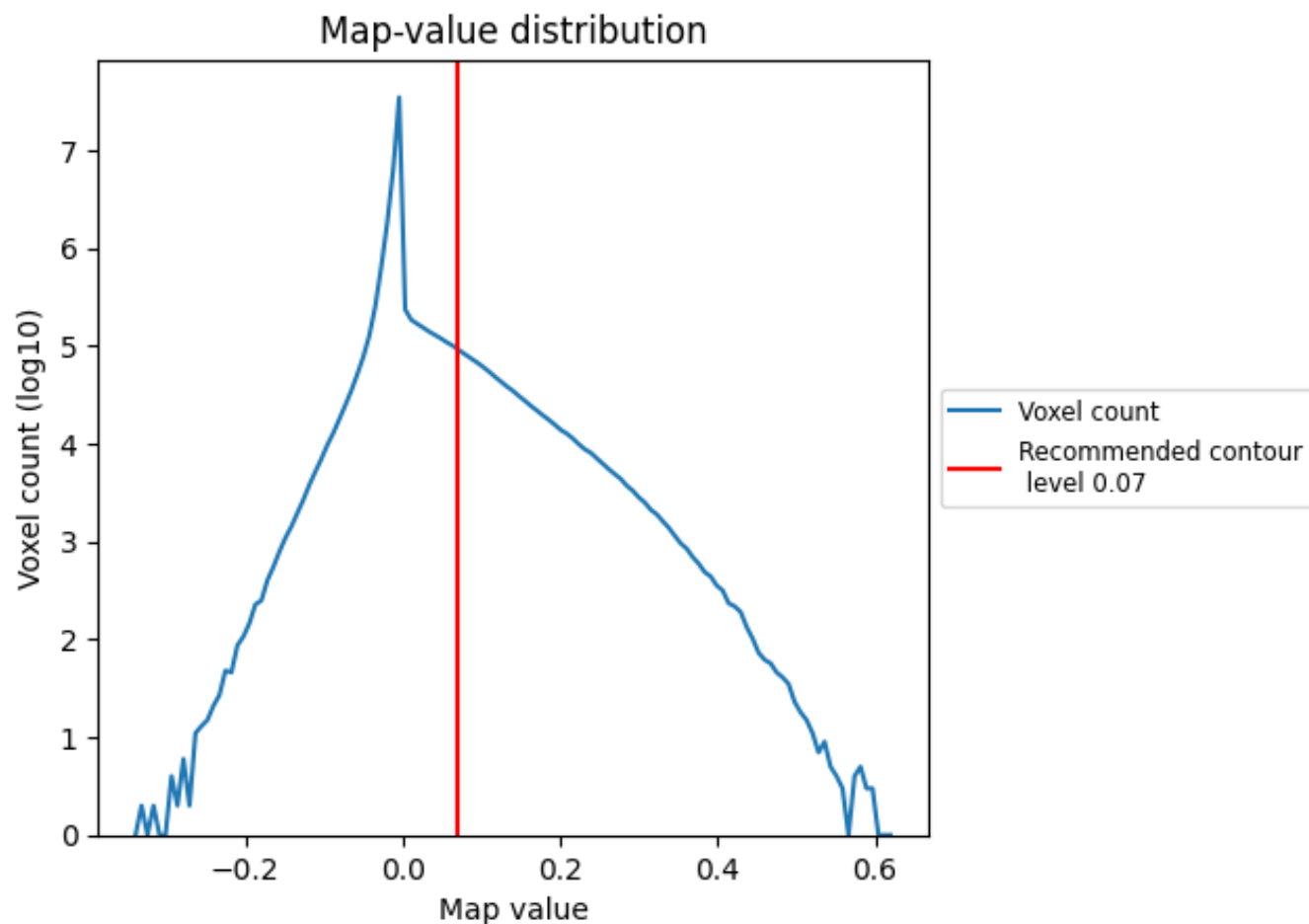
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

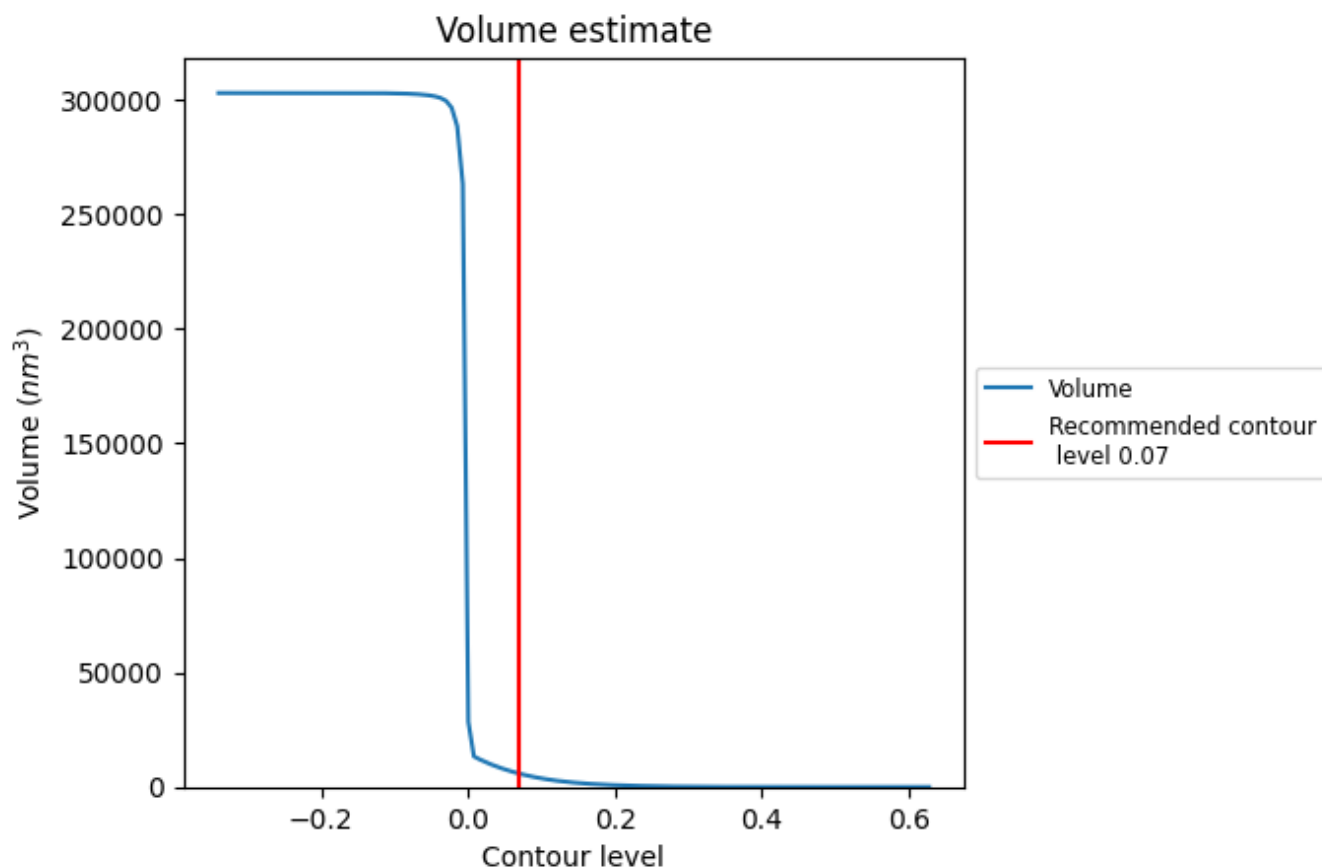
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

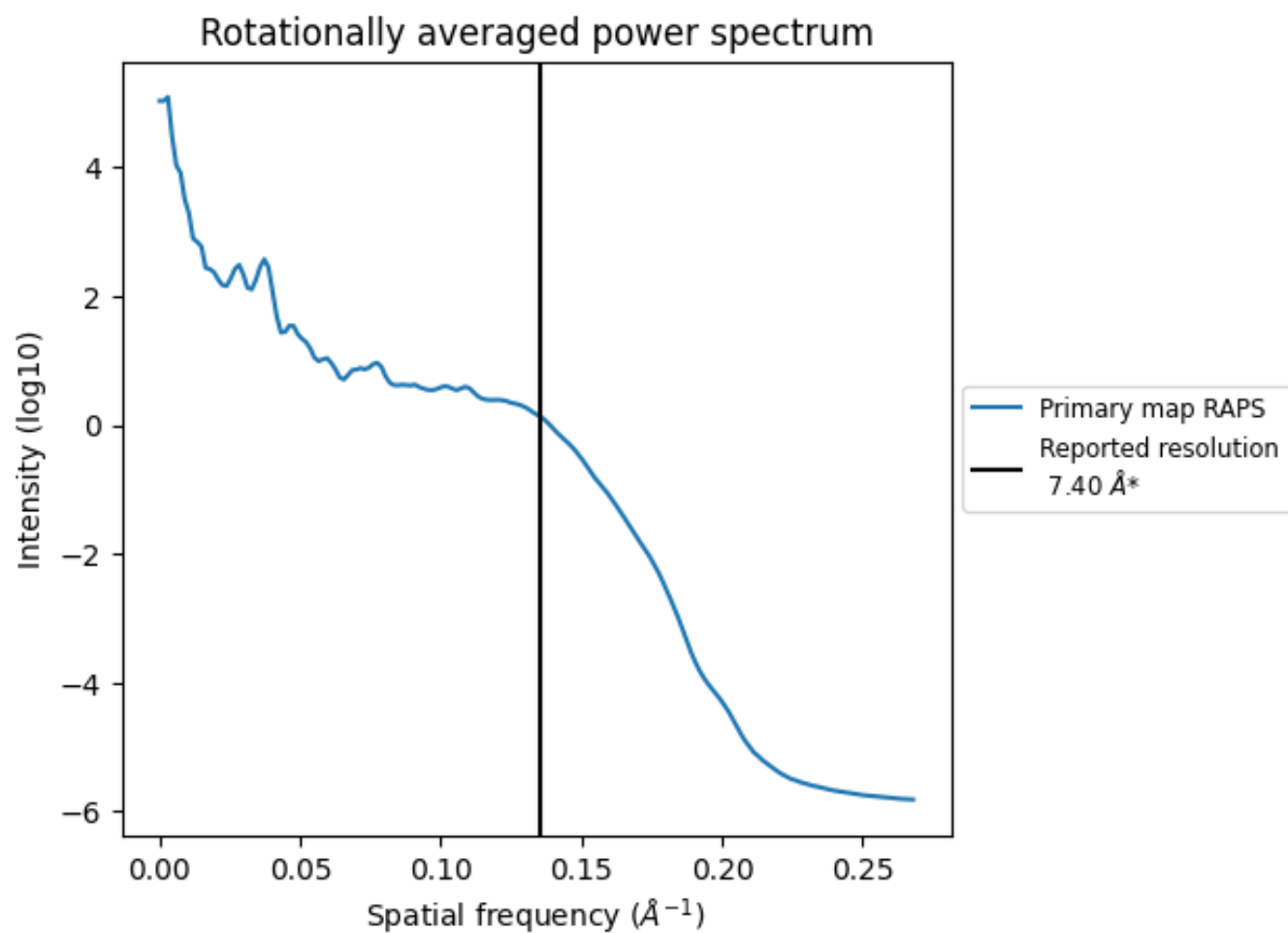
7.2 Volume estimate [i](#)



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

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

7.3 Rotationally averaged power spectrum ⓘ

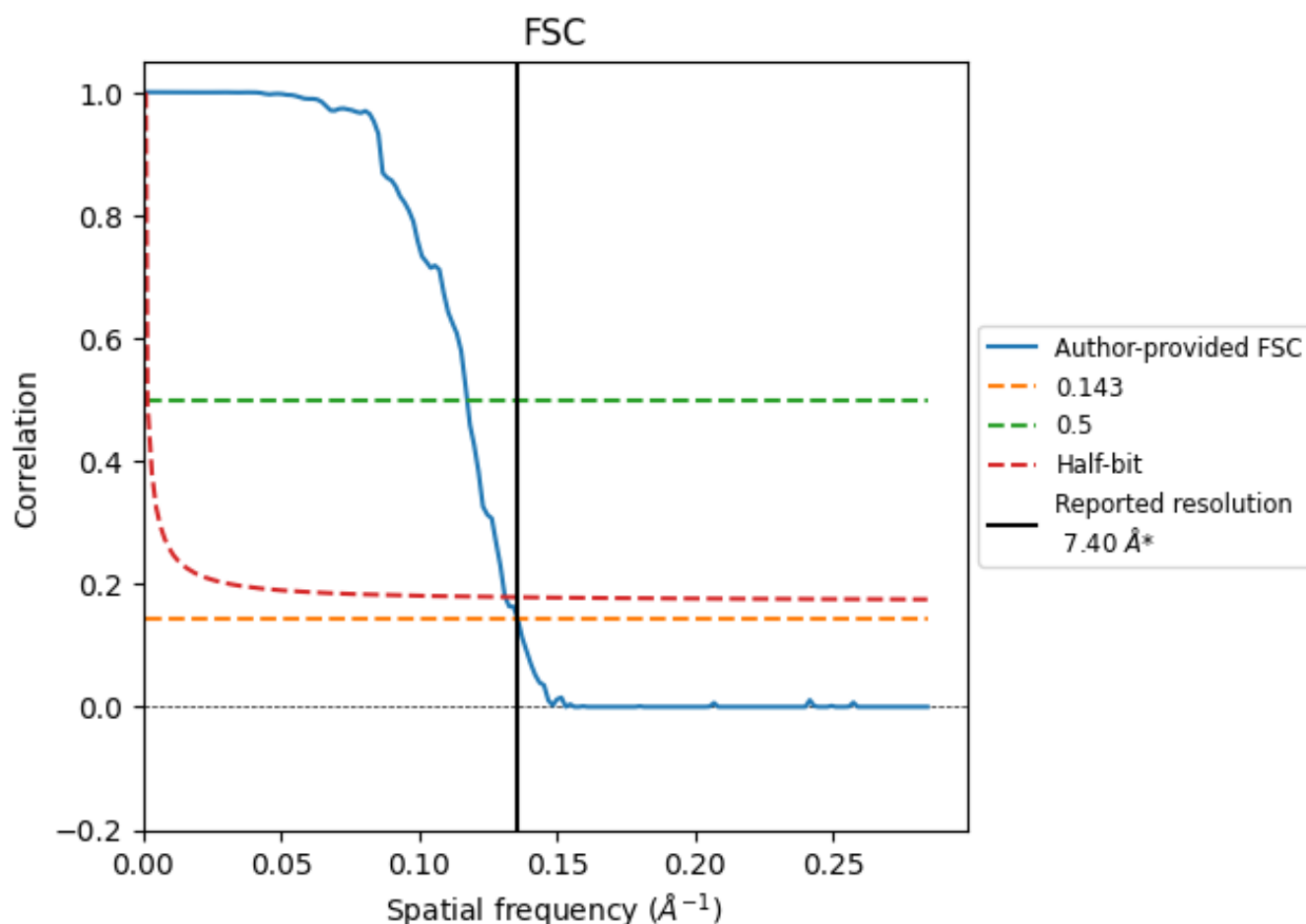


*Reported resolution corresponds to spatial frequency of 0.135 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



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

8.2 Resolution estimates [i](#)

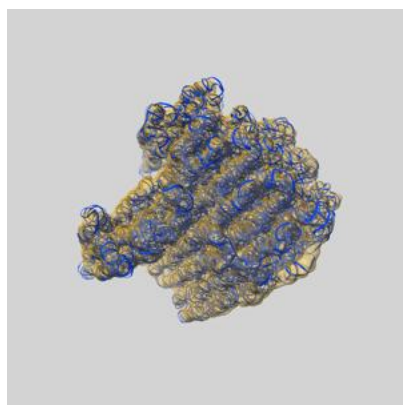
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	7.40	-	-
Author-provided FSC curve	7.37	8.53	7.62
Unmasked-calculated*	-	-	-

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

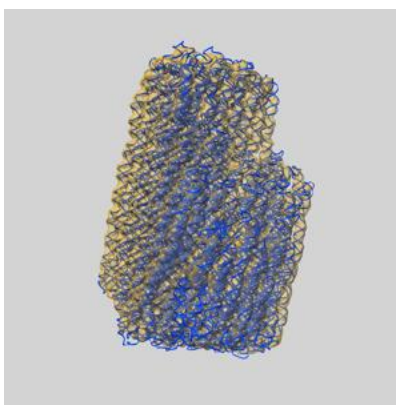
9 Map-model fit [i](#)

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

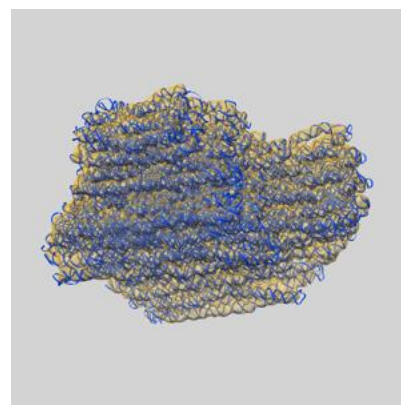
9.1 Map-model overlay [i](#)



X



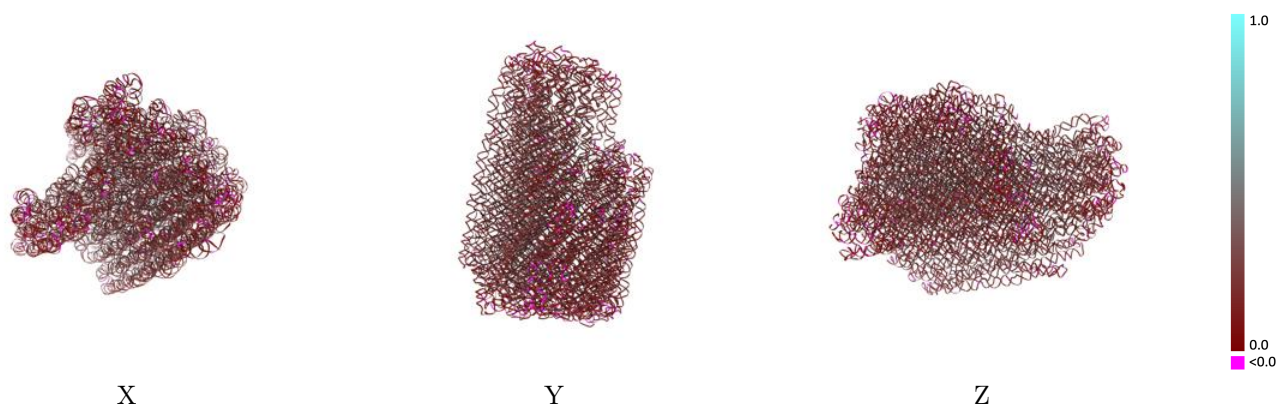
Y



Z

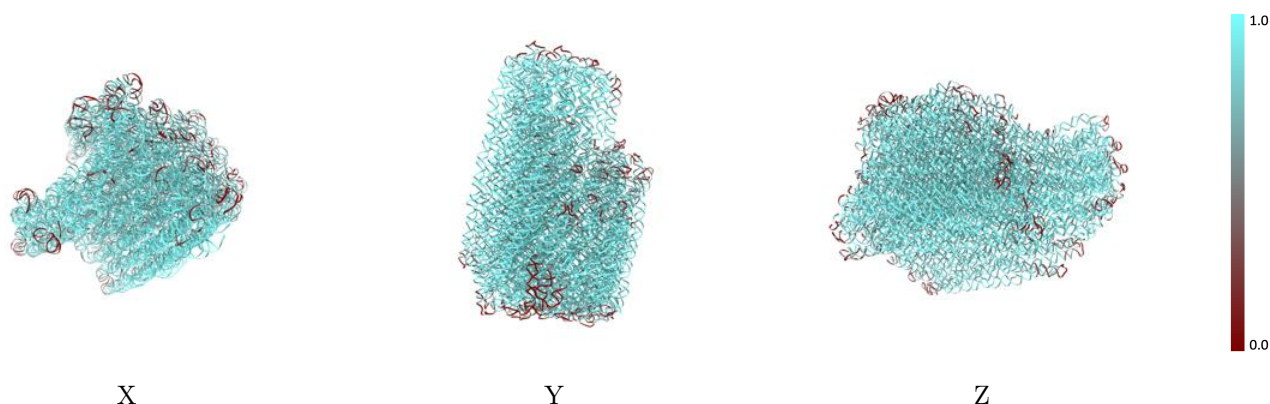
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



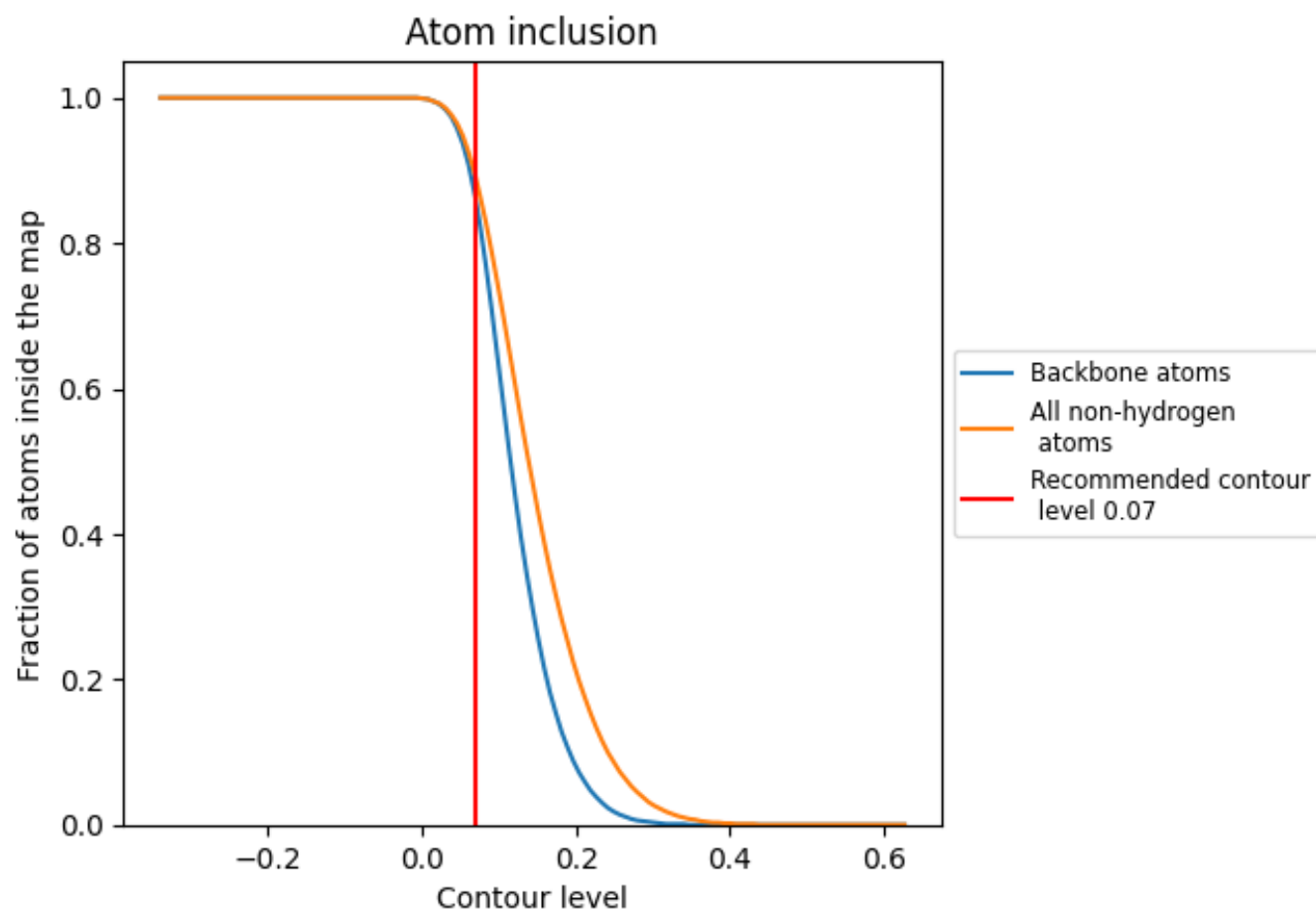
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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

9.4 Atom inclusion [i](#)



At the recommended contour level, 86% of all backbone atoms, 89% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.07) and Q-score for the entire model and for each chain.

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



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

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

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

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

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Chain	Atom inclusion	Q-score
DQ	 0.9750	 0.2560