

Structure of d(GCGAAAGC) (hexagonal form): a base-intercalated duplex as a stable structure. Erratum

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In the paper by Sunami *et al.* [(2004), *Acta Cryst. D* **60**, 90–96] an incorrect version of Table 2 was published. The correct version is given here.

References

- Lu, X.-J. & Olson, W. K. (2003). *Nucleic Acids. Res.* **31**, 5108–5121.
Shepard, W., Cruse, W. B., Fourme, R., de La Fortelle, E. & Prangé, T. (1998). *Structure*, **6**, 849–861.
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Table 2

Some helical parameters and sugar puckers of the base-intercalated duplexes.

Inclin, Prop, Buckl and Open represent inclination, propeller twist, buckle and opening angles (see Lu & Olson, 2003). The C₂ residue is iodinated in 9hmt-I and brominated in 9hmt-Br. For each base pair, the upper line is for 9hmt-I, the middle line for 8hmt-h and the lower line for 9hmt-Br (Shepard *et al.*, 1998). The corresponding values for the remaining half of the duplex are omitted owing to crystallographic symmetry.

(a) Helical parameters.

Base pair	Inclin	Tip	Twist	dz	Prop	Buckl	Open	Cl'...Cl'
G ₁ :C ₈ *	1	−6	26	3.1	6	−2	−3	10.7
	−2	−8	28	3.0	9	0	3	10.5
	2	3	31	3.2	6	−1	1	10.5
C ₂ :G ₇ *	6	0	55	3.3	10	13	0	10.5
	10	3	52	3.2	4	16	1	10.5
	10	0	52	3.4	8	9	−1	10.6
G ₃ :A ₆ *	†	†	†	†	−12	29	9	8.3
	†	†	†	†	−4	31	8	8.4
	†	†	†	†	−15	25	10	8.5
A form	20	0	33	2.3	12	0	−2	10.7
B form	−5	0	36	3.4	−1	0	−2	10.7

(b) Sugar puckers.

Nucleotide	Pucker, 9hmt-I	Pucker, 8hmt-h	Pucker, 9hmt-Br
G ₁	C3'-exo	C3'-exo	C3'-exo
C ₂	C1'-exo	C1'-exo	C1'-exo
G ₃	C2'-endo	C2'-endo	C2'-endo
A ₄	C3'-endo	C3'-endo	C4'-exo
A ₅	C1'-exo	C1'-exo	C1'-exo
A ₆	C2'-endo	C2'-endo	C2'-endo
G ₇	C1'-exo	C1'-exo	C2'-endo
C ₈	C2'-endo	C4'-exo	C3'-exo
T ₉	‡	‡	‡
A form	C3'-endo	C3'-endo	C3'-endo
B form	C2'-endo	C2'-endo	C2'-endo

† A₄ and A₅ are not paired with any bases. ‡ T₉ is disordered.