

Corrections

Crystal Structures of Eosinophil-Derived Neurotoxin (EDN) in Complex with the Inhibitors 5'-ATP, Ap₃A, Ap₄A, and Ap₅A, by Matthew D. Baker, Daniel E. Holloway, G. Jawahar Swaminathan, and K. Ravi Acharya*, Volume 45, Number 2, January 17, 2006, pages 416–426.

Page 421. The correct backbone torsion angles are listed below.

Table 5: Conformation of Ap₅A When Bound to EDN

torsion angles (deg) ^a	
N-glycosidic bond	
AO4'–AC1'–AN9–AC4 (χ_A)	–77 (<i>anti</i>)
backbone ^b	
AC5'–AC4'–AC3'–AO3' (δ_A)	90 (+sc)
AO5'–AC5'–AC4'–AC3' (γ_A)	40 (+sc)
PA–AO5'–AC5'–AC4' (β_A)	–141 (–ac)
O3A–PA–AO5'–AC5' (α_A)	78 (+sc)
PB–O3A–PA–AO5' (ζ_{p1})	–142
O3B–PB–O3A–PA (ζ_{p2})	–164
PG–O3B–PB–O3A (ζ_{p3})	–58
O3G–PG–O3B–PB (ζ_{p4})	–157
PD–O3G–PG–O3B (ζ_{p5})	44
O3D–PD–O3G–PG (ζ_{p6})	–124
PE–O3D–PD–O3G (ζ_{p7})	31
BO5'–PE–O3D–PD (ζ_{p8})	23
O3D–PE–BO5'–BC5' (α_B)	66 (+sc)
PE–BO5'–BC5'–BC4' (β_B)	–176 (<i>ap</i>)
BO5'–BC5'–BC4'–BC3' (γ_B)	46 (+sc)
BC5'–BC4'–BC3'–BO3' (δ_B)	155 (+ac)
N-glycosidic bond	
BO4'–BC1'–BN9–BC4 (χ_B)	–107 (<i>anti</i>)
ribose A pucker	
pseudorotation phase angle (deg) ^c	38
conformation	C4'- <i>exo</i>
ribose B pucker	
pseudorotation phase angle (deg) ^c	144
conformation	C2'- <i>endo</i>

^a Torsion angle definitions follow IUPAC–IUB recommendations (66) where possible. ^b Backbone torsion angles are listed in sequence from adenine A to adenine B as illustrated in Figure 1. ^c As described by Altona and Sundaralingam (67).

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