Structural Plasticity of Eph-Receptor A4 Facilitates Cross-Class Ephrin Signaling

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Due to an author error, an affinity plot in Figure 2 was inadvertently mislabeled. The stated K_D for panel (C) should be "360 nM"; the corrected Figure 2C is printed below. As a result of this correction, the second paragraph of page 1388 should read as follows:

Our results show that the EphA4 receptor has a broad affinity range for different types of ephrin ligands with cross-class Eph receptor binding weaker (5–30 times) than EphA-ephrinA interactions. We find that EphA4 has greatest affinity for ephrinA4 (K_D = 360 nM ± 20 nM) and ephrinA5 (K_D = 360 nM ± 10 nM), intermediate affinities to ephrinA1 and ephrinA2 (K_D = 1.2 μM ± 0.1 μM and K_D = 2.3 μM ± 0.1 μM, respectively), binds most weakly to ephrinB2 (K_D = 10.8 μM ± 2.1 μM), and shows no detectable binding to ephrinB1.

We apologize for this error, which, however, has no impact on any of the conclusions drawn in this article.
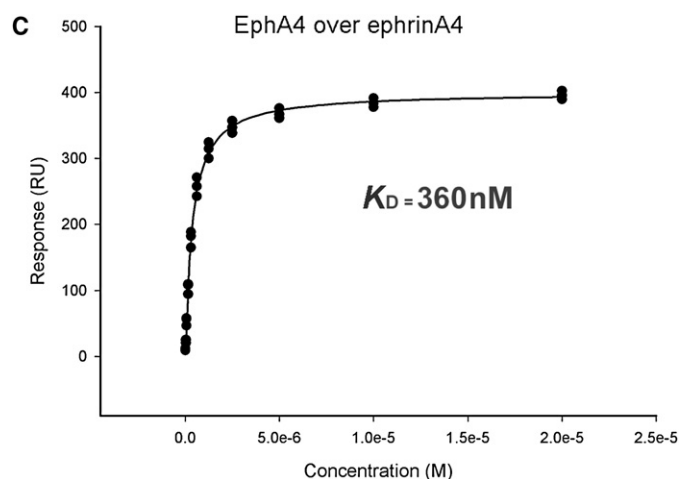
Preparation of Multimilligram Quantities of Large, Linear DNA Molecules for Structural Studies

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There is an error in the sequence of one of the DNA primer sequences reported in Muecke et al., in the June 2008 issue of *Structure*. The sequence as published is partially inverted relative to the correct sequence.

The published sequence for the "right" primer in our procedure is 5′ **CCCGCCGCTGGA**GATATC 3′. The correct sequence should read as follows: 5′ **AGGTCGCCGCCC**GATATC 3′. The two sequences differ in the bolded region, which have been partially inverted from 3′ to 5′. The authors regret this error.