

# Correction to Inhibition of Hypoxia Inducible Factor 1–Transcription Coactivator Interaction by a Hydrogen Bond Surrogate $\alpha$ -Helix

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*J. Am. Chem. Soc.* **2010**, 132, 941–943. DOI: 10.1021/ja9082864

Page 942. Table 1 shows incorrect placement of cross-links in sequences 1–3. The pentenoic acid residue (X) was cross-

**Table 1. Summary of Key Biophysical and in Vitro Data for Peptides Designed to Target HIF 1 $\alpha$ –p300 Interactions**

compound	sequence <sup>a</sup>	% helicity <sup>b</sup>	K <sub>d</sub> (nM) <sup>c</sup>	transcription inhibition <sup>d</sup>
1	XTAADCEYNA	40	950 $\pm$ 90	0 $\pm$ 3
2	XTAADCEYNAR	53	420 $\pm$ 35	45 $\pm$ 8
3	XTAADREYNAR	51	$\gg$ 2200	2 $\pm$ 7
4	AcTAADCEYNAR	15	825 $\pm$ 50	8 $\pm$ 3
chetomin	—	—	120 $\pm$ 25	50 $\pm$ 5

<sup>a</sup>X denotes pentenoic acid residue in the HBS macrocycle. <sup>b</sup>Values obtained from circular dichroism spectroscopy studies. <sup>c</sup>From isothermal titration microcalorimetry analysis. <sup>d</sup>% Inhibition of VEGF gene evaluated by real-time qRT-PCR assays in HeLa cells with 1  $\mu$ M of peptide or 200 nM of chetomin.

linked to the fourth residue (alanine) rather than glutamic acid, which is the fifth residue in the sequence. The corrected table is shown above.