

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

Laura K. Henchey, Swati Kushal, Ramin Dubey, Ross N. Chapman, Bogdan Z. Olenyuk,\* and Paramjit S. Arora\*

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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>	$K_{\rm d} ({\rm nM})^c$	transcription inhibition <sup>d</sup>
1	XTAADCEYNA	40	$950 \pm 90$	$0 \pm 3$
2	XTAADCEYNAR	53	$420\pm35$	$45 \pm 8$
3	XTAADREYNAR	51	≫2200	$2 \pm 7$
4	AcTAADCEYNAR	15	$825\pm50$	$8 \pm 3$
chetomin	_	_	$120\pm25$	$50 \pm 5$

 $<sup>^</sup>a$ X denotes pentenoic acid residue in the HBS macrocycle.  $^b$ Values obtained from circular dichroism spectroscopy studies.  $^c$ From isothermal titration microcalorimetry analysis.  $^d$ % 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.