TABLE 1 Binding constants for TBP and each probe

	k_{on} ($M^{-1}s^{-1}$)	k_{off} (s^{-1})	K_d (M)
Circular TATA-37	$6.2 \pm 3.3 \times 10^{5}$	$1.7 \pm 0.1 \times 10^{-5}$	2.7×10^{-11}
Circular TATA-31	$8.1 \pm 4.7 \times 10^{4}$	$7.6 \pm 2.0 \times 10^{-4}$	9.4×10^{-9}
Linear TATA-37	$1.3 \pm 0.4 \times 10^{5}$	$3.1 \pm 0.8 \times 10^{-4}$	2.4×10^{-9}
Linear TATA-31	$1.2 \pm 0.2 \times 10^{5}$	$3.8 \pm 0.6 \times 10^{-4}$	3.2×10^{-9}

The association, k_{on}, and dissociation, k_{off}, rate constants were determined in three or four separate experiments with TBP concentrations ranging from 1 to 6 nM. (Linear TATA-31 k_{off} is from two experiments.) The standard error of the mean is indicated. The dissociation equilibrium constant, K_d, was determined by dividing k_{off} by k_{on}.

electrophoresis[13], TFIID binding to circular TATA-37 probe was most efficient (Fig. 3*d*, lane 4) whereas circular TATA-31/TFIID was undetectable (lane 2), and complexes containing the linear counterparts were reproducibly present, but weaker (lanes 6 and 8).

For probes with identical binding sequences, TBP affinity varied up to 300-fold depending upon only slight pre-bending of the TATA box. This method[5] produces a phased DNA bend due to A-tracts and circularization of short DNA fragments. If the DNA is uniformly bent in the circular conformation, the magnitude of the pre-bend is small (16–20° for 7 bp) as compared to the 80° DNA bend in TBP–DNA co-crystals[1,3]. If DNA were bent to a greater extent, then the observed 300-fold preference for pre-bent DNA may substantially underestimate the total effect. Importantly, this suggests that even modest constraints imposed by a system may significantly impact affinity and affect transcription regulation. Altering the architecture of promoter DNA may be achieved by, for example, activators and HMG-box proteins which bend the DNA[14–16], superhelical turns created by topoisomerases, or through wrapping DNA around nucleosomes. When histones are properly phased on promoter sequences, TBP in the presence of the SWI protein complex can bind in a phase-dependent fashion[17]. Sequence-independent alteration in TBP affinity may thus provide a link between chromatin structure and regulated gene expression. □

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