

CTCF: making the right connections

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Abstract

CCCTC-binding factor (CTCF), an eleven zinc finger protein initially described as a negative regulator of *myc* expression, and cohesin are known to tether distal regions of chromatin, thus forming chromatin loops. This looping mechanism requires a convergent orientation of the two CTCF motifs. Sanborn et al. proposed a “extrusion model” to explain a wide range of experimental observations and demonstrated that the extrusion model accurately predicted in silico the 3D maps using only the location of CTCF-binding sites. The authors discussed the studies about a chromatin loop forming protein, CTCF, published during the last 2 years.

References:

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