Binding of TFIIIA To type 1 Promoter

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Introduction

Reactome is open-source, open access, manually curated and peer-reviewed pathway database. Pathway annotations are authored by expert biologists, in collaboration with Reactome editorial staff and cross-referenced to many bioinformatics databases. A system of evidence tracking ensures that all assertions are backed up by the primary literature. Reactome is used by clinicians, geneticists, genomics researchers, and molecular biologists to interpret the results of high-throughput experimental studies, by bioinformaticians seeking to develop novel algorithms for mining knowledge from genomic studies, and by systems biologists building predictive models of normal and disease variant pathways.

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Literature references

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Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics, 33*, 3461-3467. ↗

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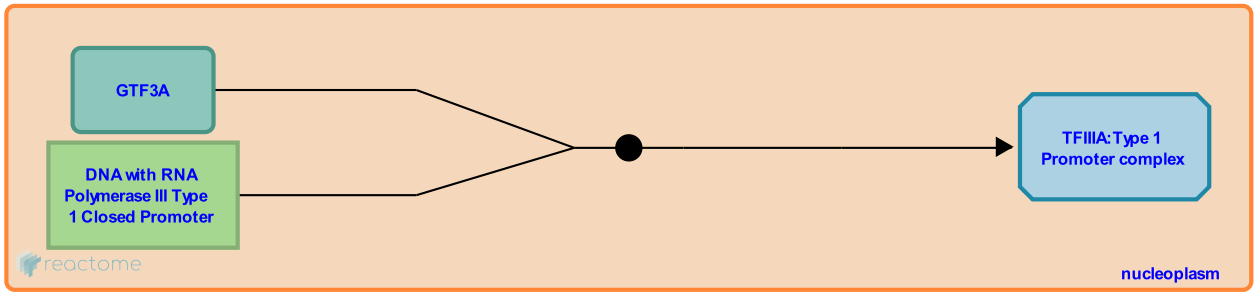
Stable identifier: R-HSA-76052

Type: binding

Compartments: nucleoplasm



TFIIIA contains nine C2H2 zinc fingers (Arakawa et al., 1995). It binds to both the ICR region of the 5S RNA genes and to 5S RNA to form the 7S storage ribonucleoprotein particle (Pelham and Brown, 1980). Upon TFIIIA binding to the 5S gene, the TFIIIA zinc fingers are aligned over the length of the ICR with the C-terminal zinc fingers in proximity to the 5 end, and the N-terminal zinc fingers in proximity to the 3 end, of the ICR. Zinc fingers 1-3 contact the C block within the ICR and have been reported to contribute most of the binding energy of the full-length protein (Clemens et al., 1992). However, TFIIIA fragments containing zinc fingers 4-9 bind to the A block and intermediate element within the ICR with affinities close to those of the full-length protein. This and other observations suggest that simultaneous binding by all nine TFIIIA zinc fingers requires energetically unfavorable distortions within the DNA, the protein, or both (Kehres et al., 1997).

Editions

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