

DEK binds TFAP2A homodimers

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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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Reactome database release: 88

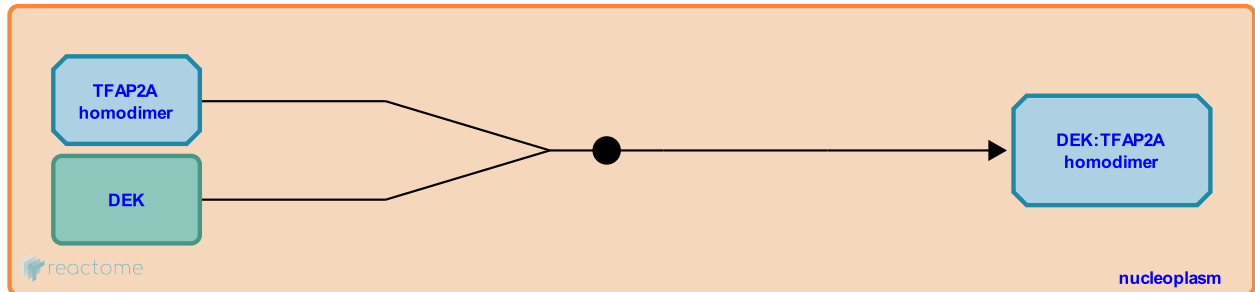
This document contains 1 reaction ([see Table of Contents](#))

DEK binds TFAP2A homodimers [↗](#)

Stable identifier: R-HSA-8869580

Type: binding

Compartments: nucleoplasm



DEK forms a complex with TFAP2A homodimers (Campillos et al. 2003).

Literature references

Campillos, M., Valdivieso, F., Vázquez, J., García, MA. (2003). Transcriptional activation by AP-2alpha is modulated by the oncogene DEK. *Nucleic Acids Res.*, 31, 1571-5. [↗](#)

Editions

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