

# TFAP2A in complex with DEK binds the APOE gene 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

- Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics*, 18, 142. [↗](#)
- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. [↗](#)
- Fabregat, A., Jupe, S., Matthews, L., Sidiropoulos, K., Gillespie, M., Garapati, P. et al. (2018). The Reactome Pathway Knowledgebase. *Nucleic Acids Res*, 46, D649-D655. [↗](#)
- Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology*, 14, e1005968. [↗](#)

Reactome database release: 88

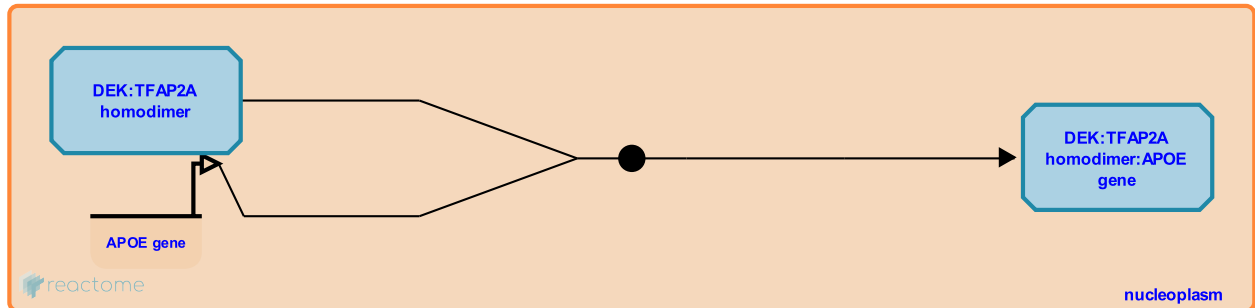
This document contains 1 reaction ([see Table of Contents](#))

## TFAP2A in complex with DEK binds the APOE gene promoter ↗

**Stable identifier:** R-HSA-8869575

**Type:** binding

**Compartments:** nucleoplasm



DEK is recruited to the APOE gene promoter via its interaction with the TFAP2A (AP-2 alpha) homodimer. In the presence of DEK, TFAP2A associates with the APOE promoter more tightly (Campillos et al. 2003). Binding of TFAP2A to the APOE gene promoter may be stimulated by PKA-mediated phosphorylation of TFAP2A (Garcia et al. 1999).

### 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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