

# AP-2 (TFAP2) transcription factors form homo- and heterodimers

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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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Reactome database release: 88

This document contains 1 reaction (see Table of Contents)

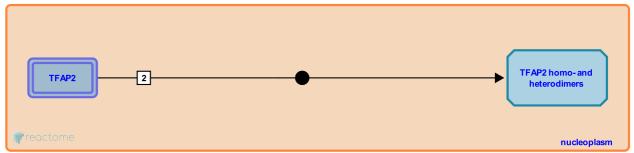
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Stable identifier: R-HSA-8864278

Type: binding

**Compartments:** nucleoplasm



AP-2 family transcription factors (TFAP2) bind palindromic DNA response elements as dimers. AP-2 family members are able to form homo- and heterodimers through the interaction of their C-terminal helix-span-helix (HSH) motifs. Both HSH motifs and centrally located basic regions are needed for DNA binding (Williams and Tjian 1991a, Williams and Tjian 1991b).

# Literature references

Tjian, R., Williams, T. (1991). Characterization of a dimerization motif in AP-2 and its function in heterologous DNA-binding proteins. *Science*, 251, 1067-71. *¬* 

Tjian, R., Williams, T. (1991). Analysis of the DNA-binding and activation properties of the human transcription factor AP-2. *Genes Dev.*, 5, 670-82.

### **Editions**

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