

Recruitment Tbk1 to dsDNA:Dai followed by its activation

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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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- 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

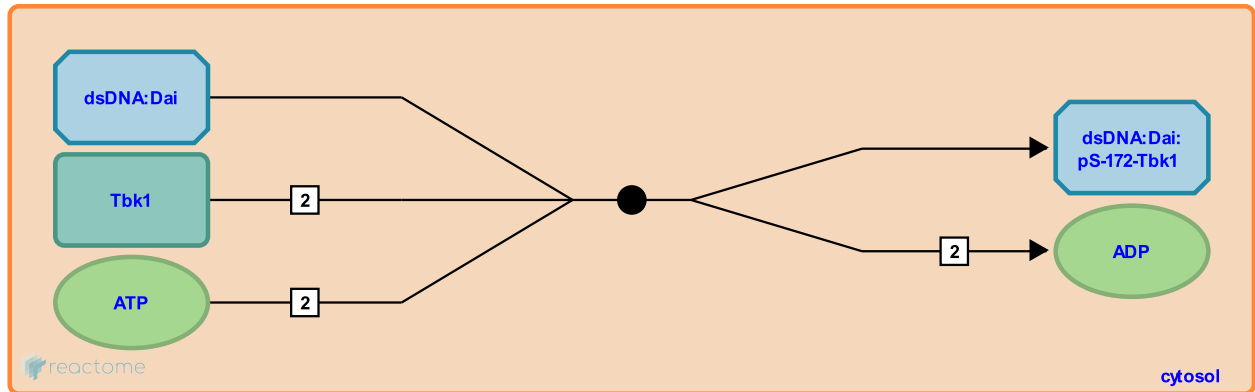
This document contains 1 reaction ([see Table of Contents](#))

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Stable identifier: R-MMU-1810473

Type: binding

Compartments: cytosol



In murine L929 cells Dai dimer formation enables recruitment of Tbk1 and Irf3 to the C-terminal region of Dai in response to cytosolic DNA. This interaction is DNA-dependent as Dai mutants that lack DNA binding domains neither recruited Tbk1 nor activated Irf3 (Takaoka A et al 2007).

Literature references

Lu, Y., Choi, MK., Ohba, Y., Ban, T., Miyagishi, M., Yanai, H. et al. (2007). DAI (DLM-1/ZBP1) is a cytosolic DNA sensor and an activator of innate immune response. *Nature*, 448, 501-5. [↗](#)

Editions

2011-09-21	Authored	Shamovsky, V.
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