

TPX2 binds AURKA at centrosomes

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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

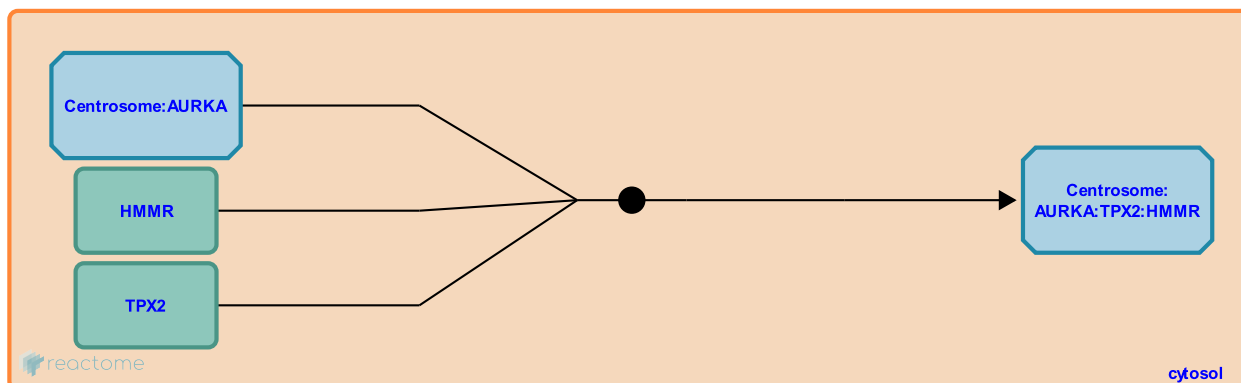
This document contains 1 reaction ([see Table of Contents](#))

TPX2 binds AURKA at centrosomes ↗

Stable identifier: R-HSA-8853405

Type: binding

Compartments: cytosol



TPX2 binds to aurora kinase A (AURKA) at centrosomes. The first 43 amino acids at the N-terminus of TPX2 are needed for binding to AURKA (Bayliss et al. 2003). HMMR (RHAMM) binds to TPX2 (Groen et al. 2004, Maxwell et al. 2005) and is involved in the proper localization of TPX2 to centrosomes and TPX2-mediated AURKA activation (Chen et al. 2014, Scrofani et al. 2015).

TPX2 binding to Aurora A protects premature AURKA degradation by APC/C-mediated proteolysis during early mitosis. TPX2 differentially regulates AURKA stability, activity and localization. While amino acids 1-43 in TPX2 facilitate complex formation between AURKA and TPX2 and promote kinase activation, they are insufficient for AURKA targeting to the mitotic spindle (Giubettini et al. 2011).

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Editions

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|------------|------------------|------------------------|
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