CEBPA binds CDK4

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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. ↗

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. ↗

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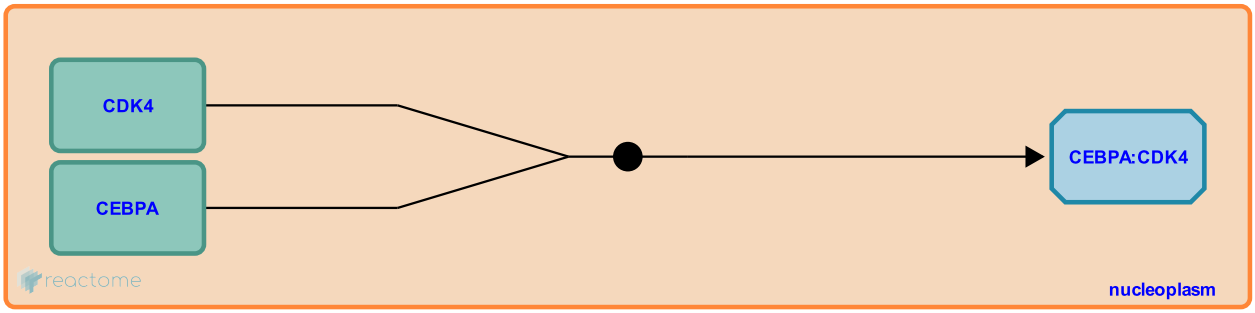
Stable identifier: R-HSA-9624112

Type: binding

Compartments: nucleoplasm



CEBPA binds CDK4, inhibits the kinase activity of CDK4, and enhances the proteasomal degradation of CDK4 (Wang et al. 2001, Wang et al. 2002). These mechanisms may contribute to the inhibition of cell proliferation observed in response to CEBPA. CEBPA interacts with the T loop region of CDK4. In mouse liver cells, 5%-10% of Cdk4 is associated with Cebpa (Wang et al. 2001).

Literature references

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Editions

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