CEBPA binds CDK2

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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. ↗

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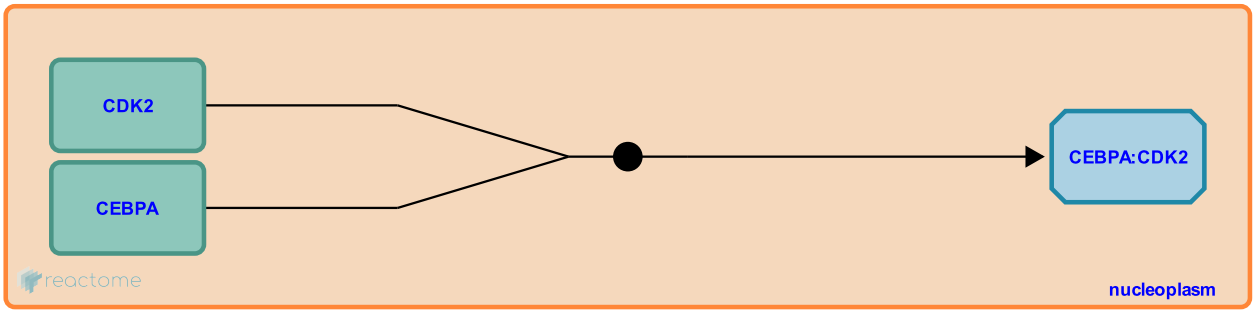
Stable identifier: R-HSA-9624120

Type: binding

Compartments: nucleoplasm



CEBPA binds CDK2 and disrupts CDK2:cyclin complexes thereby inhibiting kinase activity of CDK2, which may contribute to the inhibition of cellular proliferation observed in response to CEBPA (Wang et al. 2001). CEBPA interacts with the T loop region of CDK2. In mouse liver cells, 35%-50% of Cdk2 is associated with Cebpa (Wang et al. 2001).

Literature references

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Editions

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