CEBPB homodimerization

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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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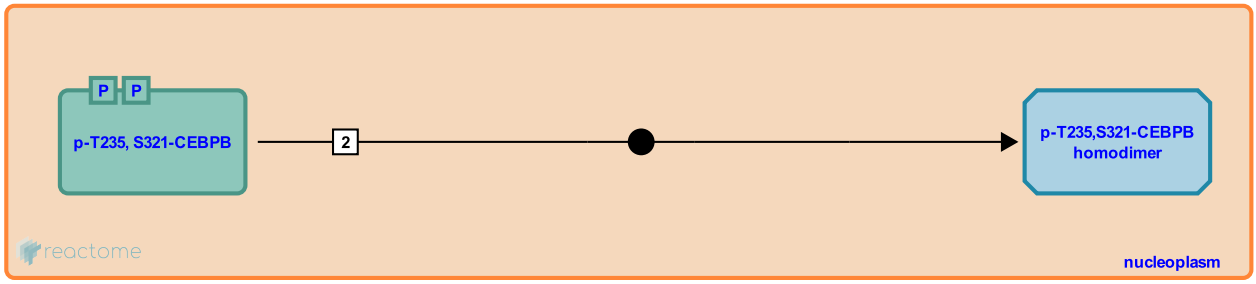
Stable identifier: R-HSA-3857336

Type: binding

Compartments: nucleoplasm



RSK1/2/3-mediated phosphorylation of CEBPB promotes the formation of CEBPB homodimers which are active as transcription factors (Lee, Miller et al. 2010; Lee, Shuman et al. 2010).

Literature references

Lee, S., Shuman, JD., Guszczynski, T., Sakchaisri, K., Sebastian, T., Copeland, TD. et al. (2010). RSK-mediated phosphorylation in the C/EBP{beta} leucine zipper regulates DNA binding, dimerization, and growth arrest activity. *Mol. Cell. Biol., 30*, 2621-35. ↗

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Editions

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