XPO1 (CRM1) binds to BACH1:Hemes

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05/05/2024

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.

The development of Reactome is supported by grants from the US National Institutes of Health (P41 HG003751), University of Toronto (CFREF Medicine by Design), European Union (EU STRP, EMI-CD), and the European Molecular Biology Laboratory (EBI Industry program).

Literature references

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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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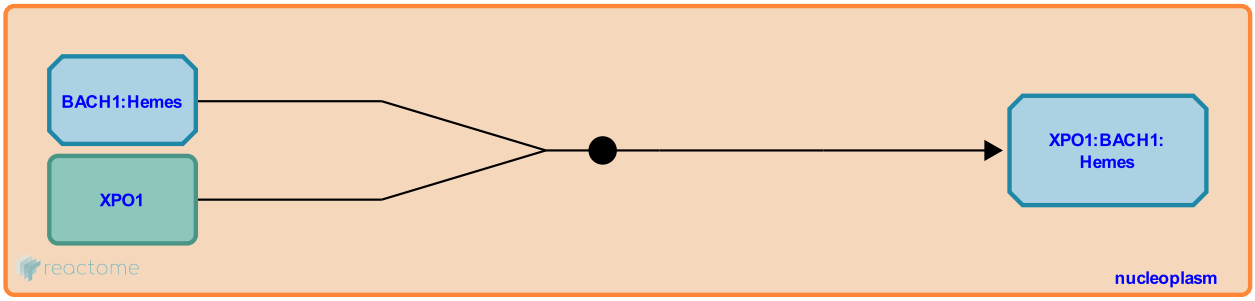
Stable identifier: R-HSA-9708430

Type: binding

Compartments: nucleoplasm



A small but significant fraction of XPO1 (CRM1) binds to BACH1. Several cysteine–proline (CP) dipeptide sequence in BACH1 are involved in heme binding, they also contain a nuclear export signal. The simplest model is that this region is involved in a heme-regulated interaction with XPO1 that mediates nuclear export. While XPO1 bound to BACH1 in GST pull-down assays, the nature of this interaction has yet to be extensively characterized (Suzuki et al, 2004).

Literature references

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Editions

2020-11-23	Authored, Edited	Stephan, R.
2021-01-23	Reviewed	Somers, J.