

# Phosphorylated BSK kinase is dephos-

# phorylated and deactivated by PUC phos-

# phatase

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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

- Fabregat, A., Sidiropoulos, K., Viteri, G., Forner, O., Marin-Garcia, P., Arnau, V. et al. (2017). Reactome pathway analysis: a high-performance in-memory approach. *BMC bioinformatics, 18,* 142. 7
- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. A
- 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. ↗
- Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology*, *14*, e1005968. *オ*

This document contains 1 reaction (see Table of Contents)

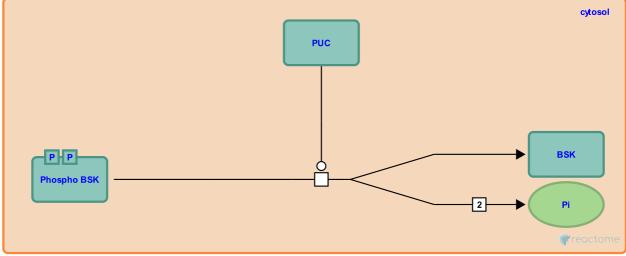
## Phosphorylated BSK kinase is dephosphorylated and deactivated by PUC phosphata-

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#### Stable identifier: R-DME-209157

#### Type: transition

#### Compartments: cytosol



The JUN kinase phosphatase Puckered (PUC) dephosphorylates and consequently deactivates the phosphorylated Basket (BSK) kinase. The gene that encodes PUC is a target of the AP-1 transcription factor making this interaction part of a regulatory negative feedback loop.

### Literature references

Martinez-Arias, A., Tolkovsky, AM., Gampel, A., Ring, J., Virdee, K., Kirov, N. et al. (1998). puckered encodes a phosphatase that mediates a feedback loop regulating JNK activity during dorsal closure in Drosophila. *Genes Dev, 12*, 557-70. 7

### **Editions**

2007-07-11	Authored	Williams, MG.
2008-06-20	Reviewed	Lemaitre, B., Silverman, N.
2014-05-20	Edited	Williams, MG.