AKT phosphorylates BAD

Annibali, D., Greene, LA., Nasi, S., Orlic-Milacic, M.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

22/10/2019

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

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. ↗

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. ↗

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. ↗

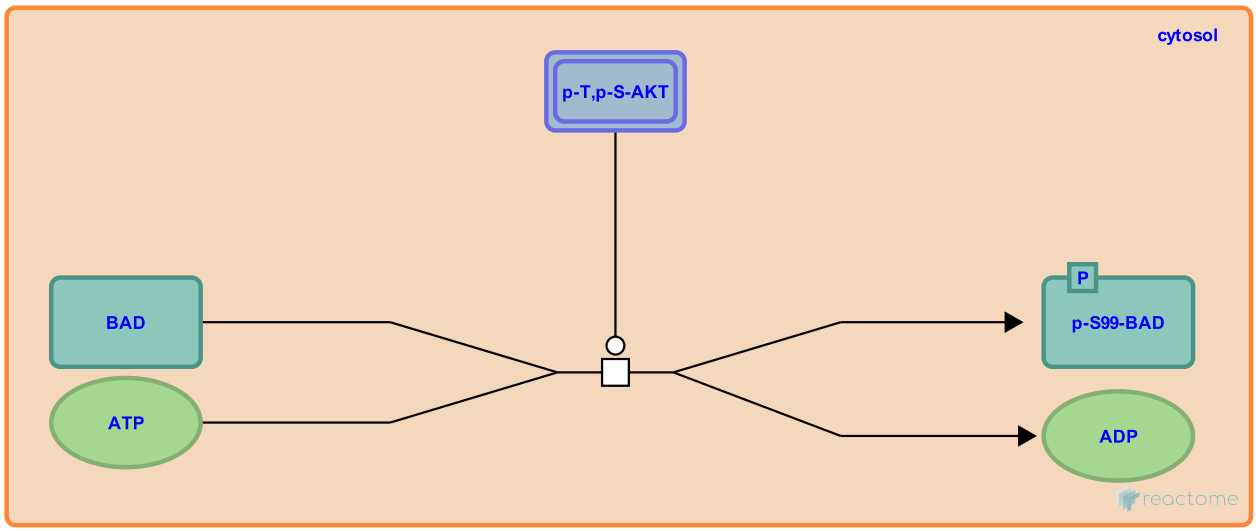
AKT phosphorylates BAD ↗

Stable identifier: R-HSA-198347

Type: transition

Compartments: cytosol

Inferred from: AKT phosphorylates Bad (Homo sapiens)



Activated AKT phosphorylates the BCL-2 family member BAD at serine 99 (corresponds to serine residue S136 of mouse Bad), blocking the BAD-induced cell death (Datta et al. 1997, del Peso et al. 1997, Khor et al. 2004).

Literature references

Datta, SR., Dudek, H., Tao, X., Masters, S., Fu, H., Gotoh, Y. et al. (1997). Akt phosphorylation of BAD couples survival signals to the cell-intrinsic death machinery. *Cell, 91*, 231-41. ↗

del Peso, L., Gonzalez-Garcia, M., Page, CP., Herrera, R., Nunez, G. (1997). Interleukin-3-induced phosphorylation of BAD through the protein kinase Akt. *Science, 278*, 687-9. ↗

Khor, TO., Gul, YA., Ithnin, H., Seow, HF. (2004). Positive correlation between overexpression of phospho-BAD with phosphorylated Akt at serine 15183529. *Cancer Lett, 210*, 139-50. ↗

Editions

2006-10-10	Authored	Annibali, D., Nasi, S.
2007-11-08	Reviewed	Greene, LA.
2013-02-13	Revised	Orlic-Milacic, M.