

AKT1 phosphorylates eNOS

Enikolopov, G., Hemish, J.

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

The contents of this document may be freely copied and distributed in any media, provided the authors, plus the institutions, are credited, as stated under the terms of [Creative Commons Attribution 4.0 International \(CC BY 4.0\) License](#). For more information see our [license](#).

04/05/2024

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

- 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. [↗](#)

Reactome database release: 88

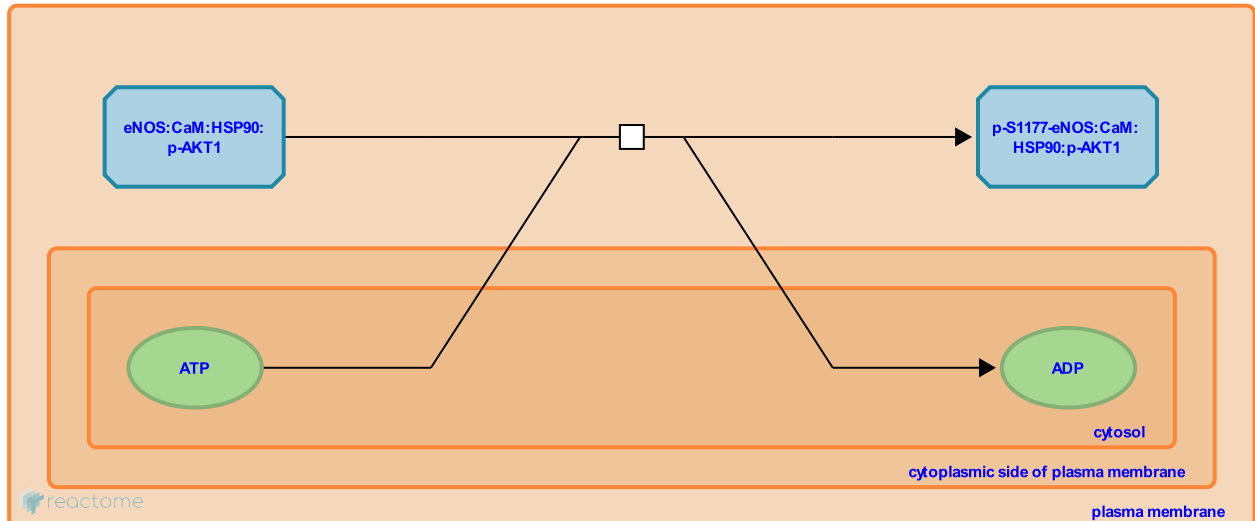
This document contains 1 reaction ([see Table of Contents](#))

AKT1 phosphorylates eNOS [↗](#)

Stable identifier: R-HSA-202111

Type: transition

Compartments: cytosol, plasma membrane



HSP90 serves as a scaffold to promote productive interaction between AKT1 and eNOS. Due to the proximity of these proteins once complexed with HSP90, AKT1 phosphorylates eNOS at Ser1177. When Ser1177 is phosphorylated, the level of NO production is elevated two- to three-fold above basal level.

Literature references

- Fontana, J., Sessa, WC., Franke, TF., Walsh, K., Fulton, D., Gratton, JP. et al. (1999). Regulation of endothelium-derived nitric oxide production by the protein kinase Akt. *Nature*, 399, 597-601. [↗](#)
- Pearson, RB., Bozinovski, S., Rodriguez-Crespo, I., Griffiths, JE., de Montellano, PR., Kemp, BE. et al. (1999). The Akt kinase signals directly to endothelial nitric oxide synthase. *Curr Biol*, 9, 845-8. [↗](#)
- Hermann, C., Zeiher, AM., Fleming, I., Fisslthaler, B., Busse, R., Dimmeler, S. (1999). Activation of nitric oxide synthase in endothelial cells by Akt-dependent phosphorylation. *Nature*, 399, 601-5. [↗](#)

Editions

2007-10-19	Authored	Hemish, J.
2008-02-28	Reviewed	Enikolopov, G.