

BTK autophosphorylates

May, B., Wienands, J.

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

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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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Reactome database release: 88

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

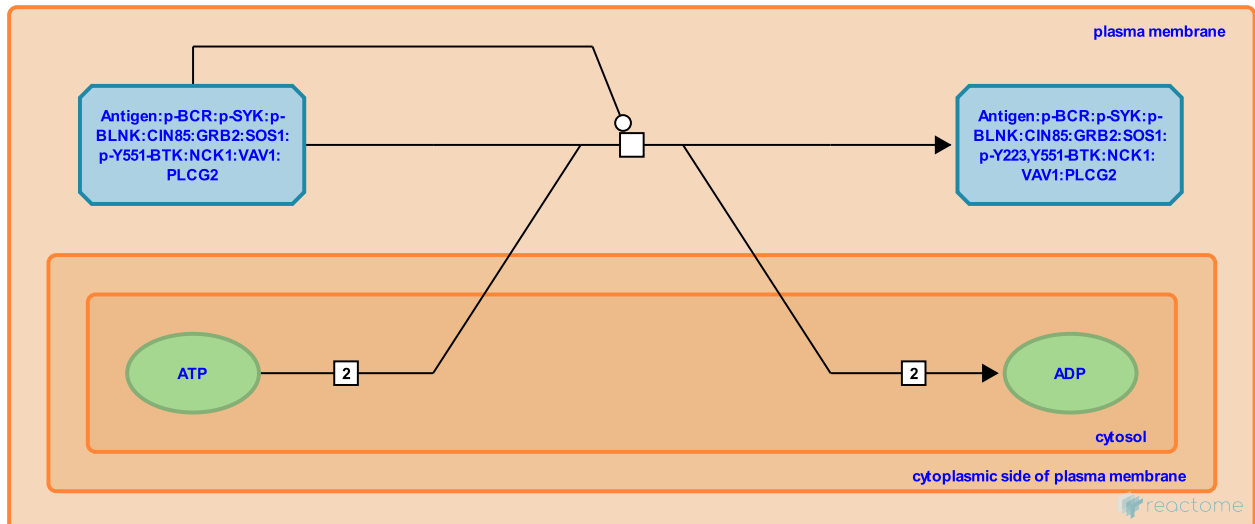
BTK autophosphorylates [↗](#)

Stable identifier: R-HSA-9606159

Type: transition

Compartments: plasma membrane

Inferred from: [Btk autophosphorylates \(Mus musculus\)](#)



After phosphorylation on tyrosine-551 by LYN or SYK, BTK autophosphorylates tyrosine-223 (Wahl et al. 1997, Nore et al. 2003, and inferred from mouse homologs). Maximum autophosphorylation occurs 5 minutes after activation of the B cell receptor and returns to low phosphorylation after 30 minutes (Nisitani et al. 1999).

Literature references

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Bäckesjö, CM., Nore, BF., Smith, CI., Mattsson, PT., Hansson, H., Westlund, A. et al. (2003). Identification of phosphorylation sites within the SH3 domains of Tec family tyrosine kinases. *Biochim. Biophys. Acta*, 1645, 123-32. [↗](#)

Park, H., Witte, ON., Kato, RM., Fluckiger, AC., Wahl, MI., Rawlings, DJ. (1997). Phosphorylation of two regulatory tyrosine residues in the activation of Bruton's tyrosine kinase via alternative receptors. *Proc. Natl. Acad. Sci. U.S.A.*, 94, 11526-33. [↗](#)

Editions

2018-04-14	Authored, Edited	May, B.
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