

# **SBH1:GET3:ATP:GET4:MDY2:SGT2 dissociates and GET3 hydrolyzes ATP yielding**

## **SBH1:GET3:ADP**

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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

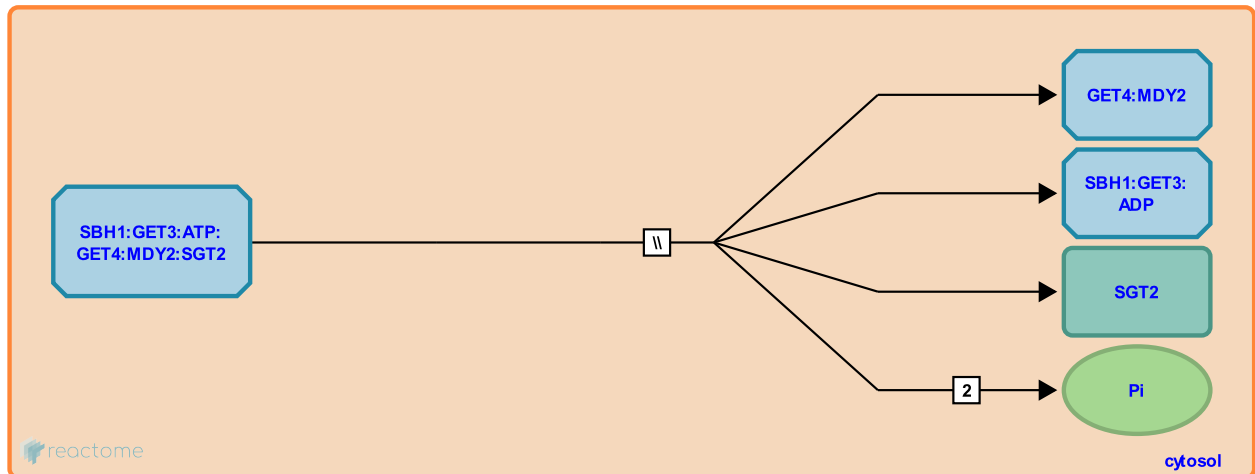
This document contains 1 reaction ([see Table of Contents](#))

## SBH1:GET3:ATP:GET4:MDY2:SGT2 dissociates and GET3 hydrolyzes ATP yielding SBH1:GET3:ADP ↗

**Stable identifier:** R-SCE-9629050

**Type:** omitted

**Compartments:** cytosol



A tail-anchored protein such as SBH1 (Sec61beta) is transferred from SGT2 to a GET3:ATP dimer via the GET4:MDY2 (GET4:GET5) complex (Chartron et al. 2010, Gristick et al. 2014, Gristick et al. 2015, Mateja et al. 2015). After transfer the SBH1:GET3:ATP complex dissociates from GET4:MDY2 and ATP is hydrolyzed by the GET3 dimer (Gristick et al. 2014, Chio et al. 2017), resulting in a change in conformation and a change in affinity for other molecules in the insertion pathway (Rome et al. 2014, Chio et al. 2017). The timing of the hydrolysis of ATP is uncertain. GET4:MDY2 inhibits ATP hydrolysis by GET3 so ATP hydrolysis may occur after GET3:ATP has dissociated from GET4:MDY2 (Rome et al. 2013, Gristick et al. 2014).

### Literature references

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### Editions

2018-11-17	Authored, Edited	May, B.
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