

UBA6 adenylates ubiquitin in the cytosol

Azevedo, J.E., May, B.

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](#).

25/08/2021

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: 77

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

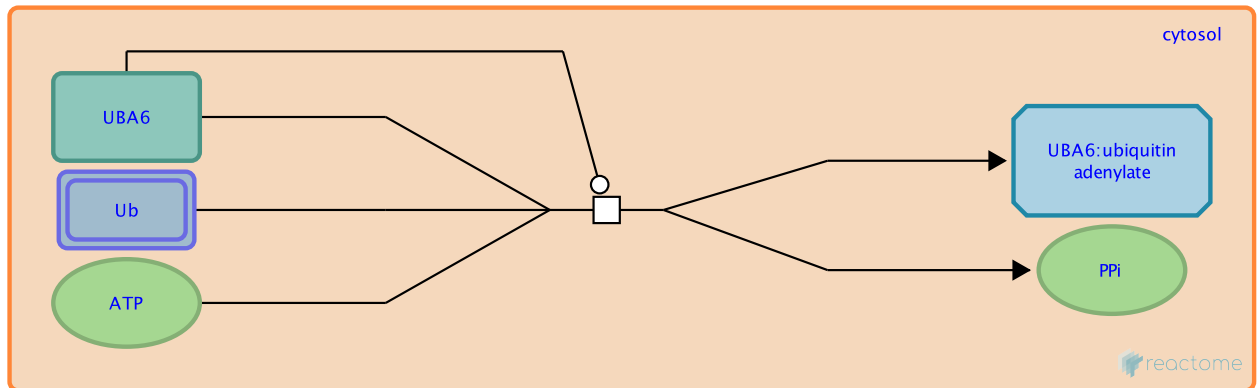
UBA6 adenylates ubiquitin in the cytosol [↗](#)

Stable identifier: R-HSA-8865090

Type: transition

Compartments: cytosol

Inferred from: [UBA1 adenylates ubiquitin in the cytosol \(Homo sapiens\)](#)



As inferred from the homologous UBA1, activation of ubiquitin by UBA6 (UBE1L1) proceeds through 3 steps: adenylation of ubiquitin, conjugation of ubiquitin from adenylyl-ubiquitin to an internal cysteine residue of UBA6, and adenylation of a second molecule of ubiquitin. In the first step, the adenylation module of UBA6 catalyzes the acyl-adenylation of the C-terminal glycine of ubiquitin (Jin et al. 2007, Pelzer et al. 2007, Groettrup et al. 2008).

Literature references

- Groettrup, M., Pelzer, C., Schmidtke, G., Hofmann, K. (2008). Activating the ubiquitin family: UBA6 challenges the field. *Trends Biochem. Sci.*, 33, 230-7. [↗](#)
- Pelzer, C., Kassner, I., Matentzoglou, K., Singh, RK., Wollscheid, HP., Scheffner, M. et al. (2007). UBE1L2, a novel E1 enzyme specific for ubiquitin. *J. Biol. Chem.*, 282, 23010-4. [↗](#)
- Jin, J., Li, X., Gygi, SP., Harper, JW. (2007). Dual E1 activation systems for ubiquitin differentially regulate E2 enzyme charging. *Nature*, 447, 1135-8. [↗](#)

Editions

2016-01-12	Authored, Edited	May, B.
2016-08-11	Reviewed	Azevedo, JE.