

RAB43:GTP binds USP8NL

Gillespie, ME., Rothfels, K.

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](#).

10/05/2024

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

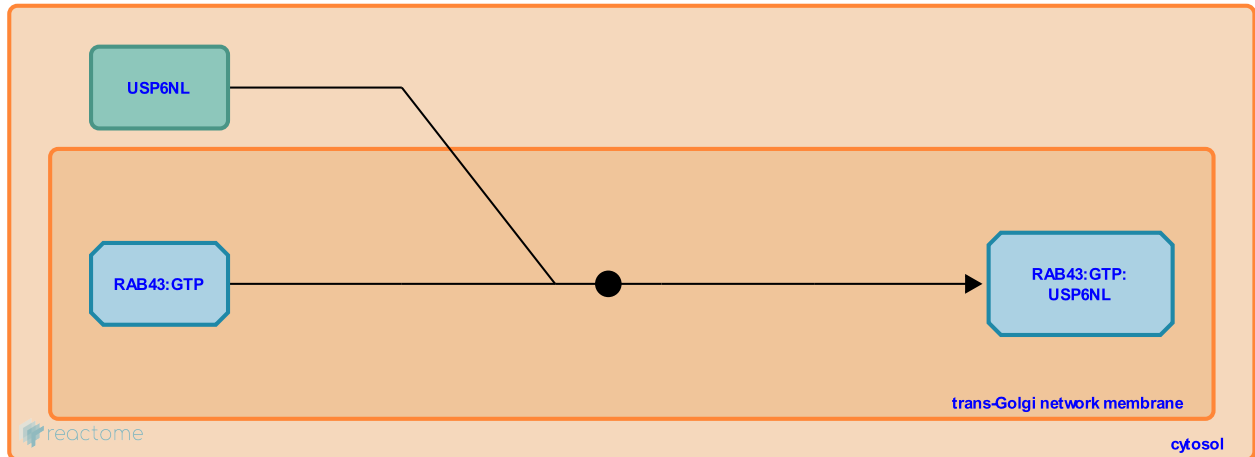
This document contains 1 reaction ([see Table of Contents](#))

RAB43:GTP binds USP6NL [↗](#)

Stable identifier: R-HSA-8847537

Type: binding

Compartments: trans-Golgi network membrane



RAB43 contributes to the maintenance of Golgi structure and is required for the RAB6-dependent retrograde trafficking of Shiga toxin (Fuchs et al, 2007; Haas et al, 2007). RAB43 appears to be localized to the cis side of the Golgi, so the details of how and when it affects Shiga transport remain to be clarified (Dejgaard et al, 2007). Screens of human cells identified USP6NL as a RAB43-specific GTPase activating (GAP) protein that is also implicated in Shiga trafficking (Fuchs et al, 2007; Haas et al, 2007; reviewed in Pfeffer, 2011).

Literature references

- Spooner, RA., Barr, FA., Lord, JM., Haas, AK., Yoshimura, S., Fuchs, E. (2007). Specific Rab GTPase-activating proteins define the Shiga toxin and epidermal growth factor uptake pathways. *J. Cell Biol.*, 177, 1133-43. [↗](#)
- Presley, JF., Verbich, D., Lodge, R., Murshid, A., Dejgaard, K., Kizilay, O. et al. (2008). Rab18 and Rab43 have key roles in ER-Golgi trafficking. *J. Cell. Sci.*, 121, 2768-81. [↗](#)
- Pfeffer, SR. (2011). Entry at the trans-face of the Golgi. *Cold Spring Harb Perspect Biol*, 3. [↗](#)
- Barr, FA., Haas, AK., Stephens, DJ., Yoshimura, S., Fuchs, E., Preisinger, C. (2007). Analysis of GTPase-activating proteins: Rab1 and Rab43 are key Rabs required to maintain a functional Golgi complex in human cells. *J. Cell. Sci.*, 120, 2997-3010. [↗](#)

Editions

2015-11-09	Authored, Edited	Rothfels, K.
2016-02-02	Reviewed	Gillespie, ME.