

Tail-anchored protein:SGTA dimer binds BAG6:GET4:UBL4A and ASNA1:ATP

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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

- 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](#))

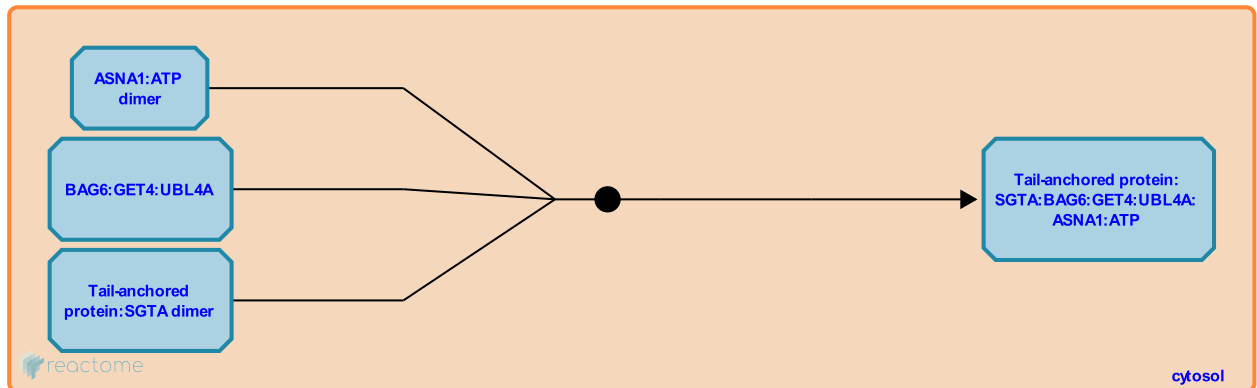
Tail-anchored protein:SGTA dimer binds BAG6:GET4:UBL4A and ASNA1:ATP ↗

Stable identifier: R-HSA-9610442

Type: binding

Compartments: cytosol

Inferred from: BAG6:GET4:UBL4A binds SEC61B (Homo sapiens)



A SGTA dimer bound to a tail-anchored (TA) protein binds the BAG6 complex (BAG6:GET4:UBL4A) via UBL4A (Winnefeld et al. 2006, Chartron et al. 2012, Xu et al. 2012, Leznicki et al. 2013, Darby et al. 2014, Kuwabara et al. 2015, Mock et al. 2015, Shao et al. 2017, also inferred from rabbit homologs in Mariappan et al. 2010). At some point, ASNA1 (TRC40) also binds the complex (Shao et al. 2017). SGTA interacts with the ubiquitin-like domain (UBL) of BAG6 and the UBL of UBL4A competes with BAG6 for binding to SGTA (Chartron et al. 2012, Xu et al. 2012, Leznicki et al. 2013, Darby et al. 2014, Shao et al. 2017).

Literature references

- VanderVelde, DG., Clemons, WM., Chartron, JW. (2012). Structures of the Sgt2/SGTA dimerization domain with the Get5/UBL4A UBL domain reveal an interaction that forms a conserved dynamic interface. *Cell Rep*, 2, 1620-32. ↗
- Yang, Y., Ye, Y., Huang, L., Cai, M., Xu, Y. (2012). SGTA recognizes a noncanonical ubiquitin-like domain in the Bag6-Ubl4A-Trc35 complex to promote endoplasmic reticulum-associated degradation. *Cell Rep*, 2, 1633-44. ↗
- Senda, T., Kawahara, H., Kuwabara, N., Matsumoto, H., Minami, R., Yokota, N. et al. (2015). Structure of a BAG6 (Bcl-2-associated athanogene 6)-Ubl4a (ubiquitin-like protein 4a) complex reveals a novel binding interface that functions in tail-anchored protein biogenesis. *J. Biol. Chem.*, 290, 9387-98. ↗
- High, S., Warwicker, J., Schwappach, B., Isaacson, RL., Krysztofinska, EM., Leznicki, P. et al. (2013). The association of BAG6 with SGTA and tail-anchored proteins. *PLoS ONE*, 8, e59590. ↗
- Zaslaver, M., Chartron, JW., Mock, JY., Clemons, WM., Ye, Y., Xu, Y. (2015). Bag6 complex contains a minimal tail-anchor-targeting module and a mock BAG domain. *Proc. Natl. Acad. Sci. U.S.A.*, 112, 106-11. ↗

Editions

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