

MEMO1 binds RHOA:GTP:DIAPH1

Badache, A., Orlic-Milacic, M.

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 <u>Creative Commons Attribution 4.0 International (CC BY 4.0)</u>
<u>License</u>. For more information see our <u>license</u>.

30/04/2024

https://reactome.org

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 data-base: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968.

Reactome database release: 88

This document contains 1 reaction (see Table of Contents)

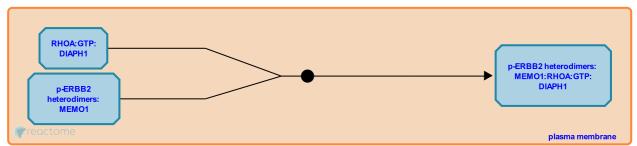
https://reactome.org Page 2

MEMO1 binds RHOA:GTP:DIAPH1

Stable identifier: R-HSA-6785648

Type: binding

Compartments: cytosol, plasma membrane



MEMO1, in complex with phosphorylated ERBB2 heterodimers, associates with the complex of activated RHOA and formin family member DIAPH1. MEMO1 maintains the plasma membrane association of the RHOA:GTP:DIAPH1 complex (Zaoui et al. 2008) and modulates RHOA:GTP:DIAPH1-regulated actin and microtubule dynamics and the consequent cell motility/migration downstream of ERBB2 (Marone et al. 2004, Zaoui et al. 2010).

Literature references

Zaoui, K., Benseddik, K., Salaün, D., Daou, P., Badache, A. (2010). ErbB2 receptor controls microtubule capture by recruiting ACF7 to the plasma membrane of migrating cells. *Proc. Natl. Acad. Sci. U.S.A.*, 107, 18517-22.

Zaoui, K., Isnardon, D., Honoré, S., Braguer, D., Badache, A. (2008). Memo-RhoA-mDia1 signaling controls microtubules, the actin network, and adhesion site formation in migrating cells. *J. Cell Biol.*, 183, 401-8.

Dankort, D., Hess, D., Muller, WJ., Marone, R., Hynes, NE., Badache, A. (2004). Memo mediates ErbB2-driven cell motility. *Nat. Cell Biol.*, 6, 515-22.

Editions

2016-01-28	Authored, Edited	Orlic-Milacic, M.
2016-02-03	Reviewed	Badache, A.