Mitofusins trans-interact linking mitochondria prior to fusion

Akkerman, JW., Jupe, S., Ouwehand, WH.

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.

18/05/2024

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

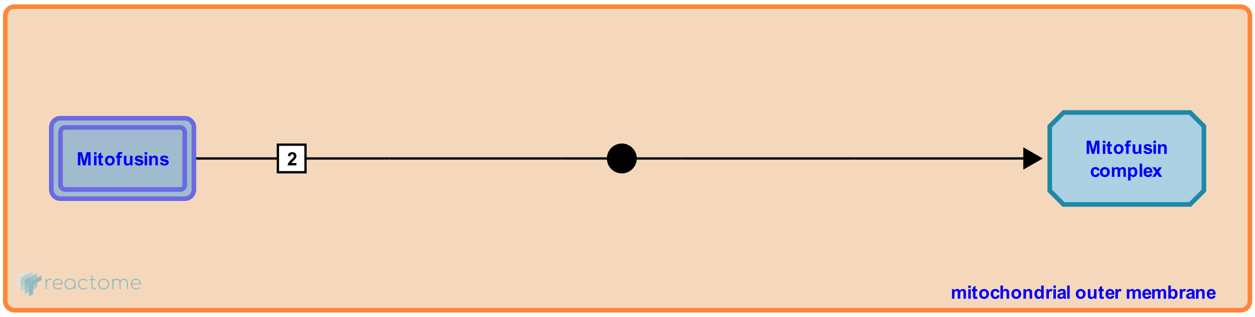
This document contains 1 reaction (see Table of Contents)

Mitofusins trans-interact linking mitochondria prior to fusion ↗

Stable identifier: R-HSA-992703

Type: binding

Compartments: mitochondrial outer membrane



Mitochondria frequently fuse and divide (Bereiter-Hahn & Voth 1994); these processes affect morphology and are important for normal mitochondrial functions such as respiration, development and apoptosis. Mitofusins (MFNs) are mitochondrial GTPases that mediate mitochondrial outer membrane fusion. Mammals have two mitofusins; Mfn1-null or Mfn2-null mouse embryonic fibroblast cells show predominantly fragmented mitochondria and have greatly reduced mitochondrial fusion in vivo (Chen et al. 2003, 2005). MFNs acts in trans to bring mitochondria into close proximity prior to fusion (Koshiba et al. 2004). They also tether the endoplasmic reticulum (ER) to mitochondria, cross-linking MFNs expressed on the mitochondrial outer membrane and ER membrane (de Brito & Scorrano 2008).

Literature references

Lombès, A., Legros, F., Château, D., Rojo, M. (2002). Membrane topology and mitochondrial targeting of mitofusins, ubiquitous mammalian homologs of the transmembrane GTPase Fzo. *J Cell Sci, 115*, 1663-74. ↗

Editions

2010-10-29	Authored	Akkerman, JW.
2010-11-12	Edited	Jupe, S.
2010-11-12	Reviewed	Ouwehand, WH.