

DCC interacts with DIP13alpha

Cooper, HM., Garapati, PV.

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>.

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. 7
- Sidiropoulos, K., Viteri, G., Sevilla, C., Jupe, S., Webber, M., Orlic-Milacic, M. et al. (2017). Reactome enhanced pathway visualization. *Bioinformatics*, 33, 3461-3467. A
- 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. *オ*

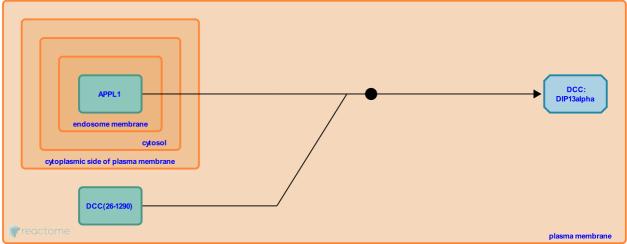
This document contains 1 reaction (see Table of Contents)

DCC interacts with DIP13alpha 7

Stable identifier: R-HSA-373717

Type: binding

Compartments: plasma membrane



The ADD domain of DCC binds DCC-interacting 13alpha (DIP13alpha), which serves as an adaptor mediating the DCC apoptotic signal. The DIP13alpha protein has a pleckstrin homology domain and a phosphotyrosine binding domain. It interacts with the ADD region on the DCC cytoplasmic domain that is available after the caspase cleavage. This interaction is required for the induction of apoptosis.

Literature references

- Wu, R., Yao, F., Liu, J., Finley RL, Jr., Morgan, M., Chen, YQ. et al. (2002). Mediation of the DCC apoptotic signal by DIP13 alpha. J Biol Chem, 277, 26281-5.
- Mehlen, P., Bredesen, DE., Ye, X., Shin, H., Corset, V., Granger, L. et al. (2001). The dependence receptor DCC (deleted in colorectal cancer) defines an alternative mechanism for caspase activation. *Proc Natl Acad Sci U S A*, *98*, 3416-21. 7

Editions

2008-07-16	Authored	Garapati, P V.
2008-07-30	Edited	Garapati, P V.
2010-02-16	Reviewed	Cooper, HM.