

PI(3,4,5)P3 binds VAV1,2,3

Harper, MT., Jones, ML., Jupe, S., Poole, AW.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

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14/05/2024

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)

PI(3,4,5)P3 binds VAV1,2,3 7

Stable identifier: R-HSA-434637

Type: binding

Compartments: cytosol, plasma membrane

Inferred from: PIP3 stimulates Vav1 (Mus musculus)



Vav interacts directly with PIP2 and PIP3, with a fivefold selectivity for PIP3 over PIP2. PIP3 gives a twofold stimulation of Vav1 GEF activity while PIP2 leads to 90% inhibition. Binding probably occurs through the PH domain, known to bind phosphoinositides.

Literature references

White, MA., Falck, JR., Mosteller, RD., Xia, Y., Han, J., Shu, X. et al. (1998). Role of substrates and products of PI 3kinase in regulating activation of Rac-related guanosine triphosphatases by Vav. *Science*, *279*, 558-60. *¬*

Editions

2009-09-02	Authored	Jupe, S.
2009-11-02	Reviewed	Poole, AW., Jones, ML., Harper, MT.
2009-11-03	Edited	Jupe, S.