

FZ and VANG bind to STAN homodimer

Axelrod, JD., Williams, MG.

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](#).

07/05/2024

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

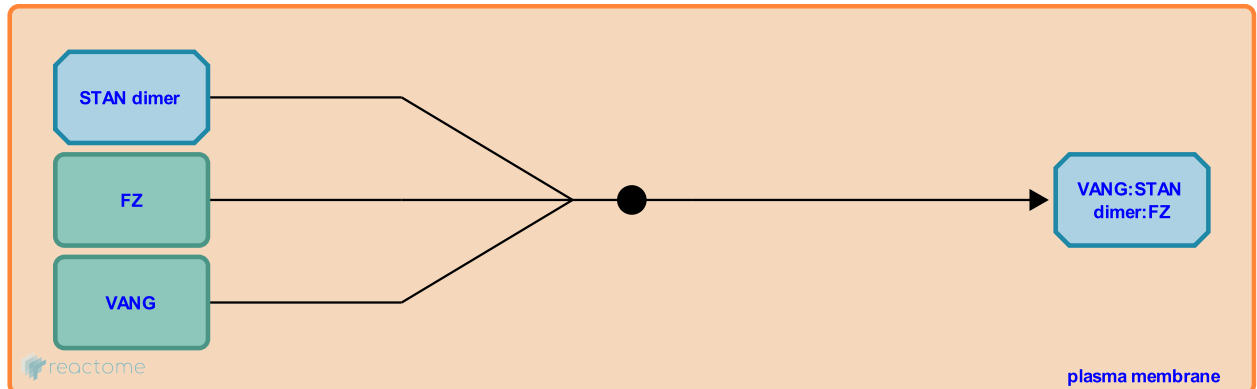
This document contains 1 reaction ([see Table of Contents](#))

FZ and VANG bind to STAN homodimer [↗](#)

Stable identifier: R-DME-450802

Type: binding

Compartments: plasma membrane



The seven-pass transmembrane protein Frizzled (FZ) and the four-pass transmembrane protein Van Gogh (VANG) aka Strabismus (Stbm) bind to opposite ends of the seven-pass transmembrane atypical cadherin Starry Night (STAN) aka Flamingo homodimer. In the case of VANG, this interaction is to the C-terminal domain of STAN. Additionally, there's a possibility of a direct interaction between FZ and VANG.

Literature references

Axelrod, JD., Povelones, M., Matis, M., Logan, CY., Nusse, R., Antic, D. et al. (2008). Asymmetric homotypic interactions of the atypical cadherin flamingo mediate intercellular polarity signaling. *Cell*, 133, 1093-105. [↗](#)

Strutt, H., Strutt, D. (2008). Differential stability of flamingo protein complexes underlies the establishment of planar polarity. *Curr Biol*, 18, 1555-64. [↗](#)

Fuchs, E., Devenport, D. (2008). Planar polarization in embryonic epidermis orchestrates global asymmetric morphogenesis of hair follicles. *Nat Cell Biol*, 10, 1257-68. [↗](#)

Editions

2009-11-19	Reviewed	Axelrod, JD.
2009-12-11	Authored	Williams, MG.
2014-05-20	Edited	Williams, MG.