

GSDMD oligomerizes into arc-, slit-shaped structures

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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.

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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

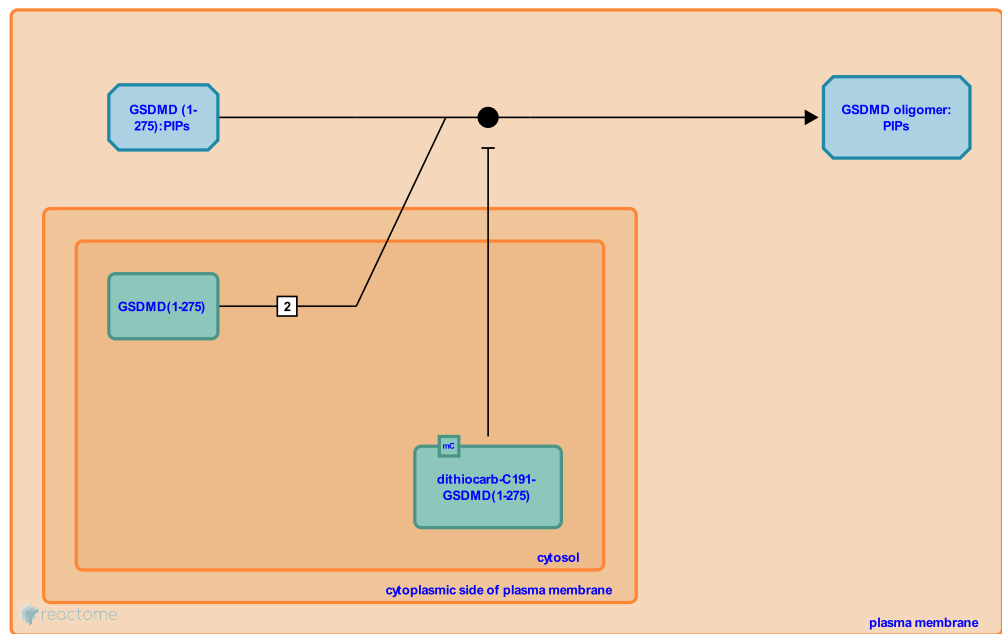
This document contains 1 reaction ([see Table of Contents](#))

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Stable identifier: R-HSA-9647645

Type: binding

Compartments: cytosol, plasma membrane



Gasdermin D (GSDMD) is a member of the gasdermin (GSDM) protein family, which is processed by inflammatory caspases and cleaved into an N-terminal (GSDMD(1-275)) and a C-terminal (GSDMD (276-484)) fragments (Shi J et al, 2015). Once GSDMD is cleaved, the N-terminal fragment of GSDMD (1-275) targets and permeabilizes cellular membranes by assembling transmembrane pores (Ding J et al, 2016; Liu X et al, 2016; Sborgi L et al, 2016). High-resolution (≤ 2 nm) atomic force microscopy (AFM) showed that GSDMD N-terminus inserts into various lipid membranes (Mulvihill E et al. 2018). Once inserted, the N-terminal fragment of GSDMD assembles arc-, slit-, and ring-shaped oligomers, which eventually incorporate additional oligomers and transform into larger thermodynamically stable ring-shaped oligomers (Mulvihill E et al. 2018).

Literature references

Pfreundschuh, M., Mari, SA., Sborgi, L., Hiller, S., Müller, DJ., Mulvihill, E. (2018). Mechanism of membrane pore formation by human gasdermin-D. *EMBO J.*, 37. ↗

Editions

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