

SMAC (DIABLO) forms dimer

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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

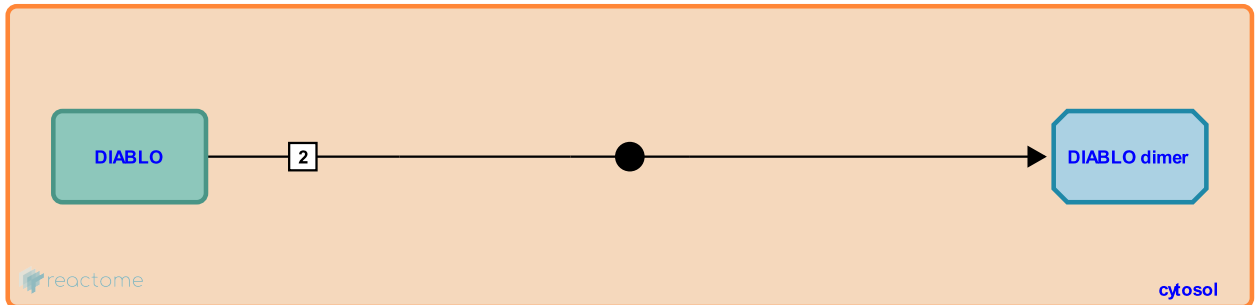
This document contains 1 reaction ([see Table of Contents](#))

SMAC (DIABLO) forms dimer [↗](#)

Stable identifier: R-HSA-9627106

Type: binding

Compartments: cytosol



The crystal structure of SMAC(DIABLO) at 2.2Å resolution revealed that it homodimerized through an extensive hydrophobic interface and formed an elongated arch shaped quaternary structure (Chai J et al. 2000). Missense mutations that disrupt SMAC (DIABLO) dimeric interface, abrogated the XIAP-neutralizing function of SMAC (DIABLO), suggesting that SMAC dimerization is essential for its pro-apoptotic activity (Chai et al. 2000). SMAC (DIABLO) was also found to adopt a tetrameric assembly in solution (Mastrangelo E et al. 2015).

Literature references

Yin, Q., Gao, Z., Li, YM., Wang, J., Wu, H., Jiang, X. et al. (2007). A dimeric Smac/diablo peptide directly relieves caspase-3 inhibition by XIAP. Dynamic and cooperative regulation of XIAP by Smac/Diablo. *J. Biol. Chem.*, 282, 30718-27. [↗](#)

Chai, J., Wang, X., Shi, Y., Wu, JW., Du, C., Kyin, S. (2000). Structural and biochemical basis of apoptotic activation by Smac/DIABLO. *Nature*, 406, 855-62. [↗](#)

Editions

2017-07-26	Authored	Shamovsky, V.
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