

# Cohesin binds PDS5 and WAPAL

Gillespie, ME., Matthews, L., Orlic-Milacic, M., Tanno, Y., Watanabe, Y., Zhang, N.

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](#).

28/01/2023

## 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: 83

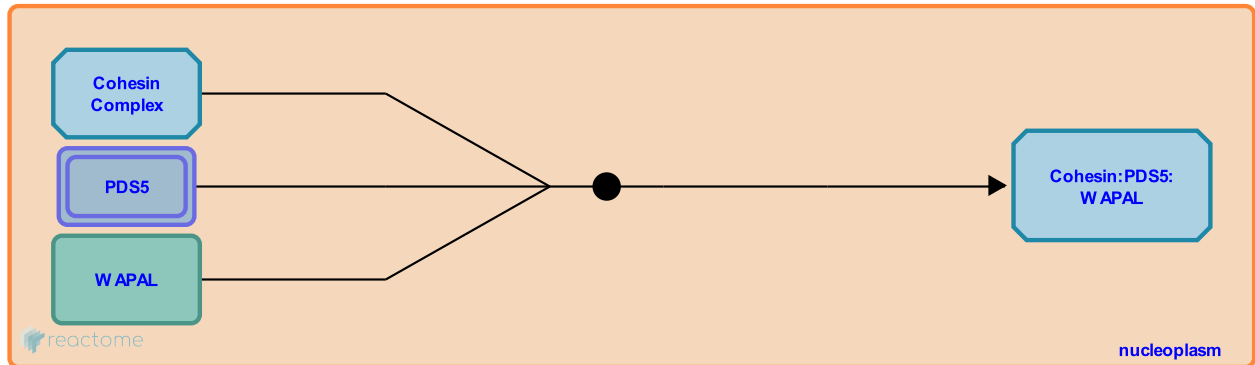
This document contains 1 reaction ([see Table of Contents](#))

## Cohesin binds PDS5 and WAPAL [↗](#)

**Stable identifier:** R-HSA-2468040

**Type:** binding

**Compartments:** nucleoplasm



WAPAL (WAPL) and PDS5 proteins (PDS5A and/or PDS5B) are associated with cohesin throughout most of the cell cycle (Kueng et al. 2006, Gandhi et al. 2006). FGF motifs present in the N-terminal region of WAPAL participate in WAPAL binding to PDS5 and cohesin subunits RAD21, STAG1 (SA1) and STAG2 (SA2) (Shintomi and Hirano 2009).

### Literature references

- Peters, BH., Hegemann, B., Peters, JM., Mechtler, K., Schleiffer, A., Kueng, S. et al. (2006). Wapl controls the dynamic association of cohesin with chromatin. *Cell*, 127, 955-67. [↗](#)
- Shintomi, K., Hirano, T. (2009). Releasing cohesin from chromosome arms in early mitosis: opposing actions of Wapl-Pds5 and Sgo1. *Genes Dev.*, 23, 2224-36. [↗](#)
- Gandhi, R., Hirano, T., Gillespie, PJ. (2006). Human Wapl is a cohesin-binding protein that promotes sister-chromatid resolution in mitotic prophase. *Curr. Biol.*, 16, 2406-17. [↗](#)

### Editions

2012-10-02	Authored	Orlic-Milacic, M.
2012-10-05	Edited	Gillespie, ME., Matthews, L.
2012-10-22	Reviewed	Zhang, N.
2012-11-20	Reviewed	Watanabe, Y., Tanno, Y.