Phosphorylation of cohesin by PLK1 at chromosomal arms

Gillespie, ME., Lee, KS., 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.

29/04/2024

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. ↗

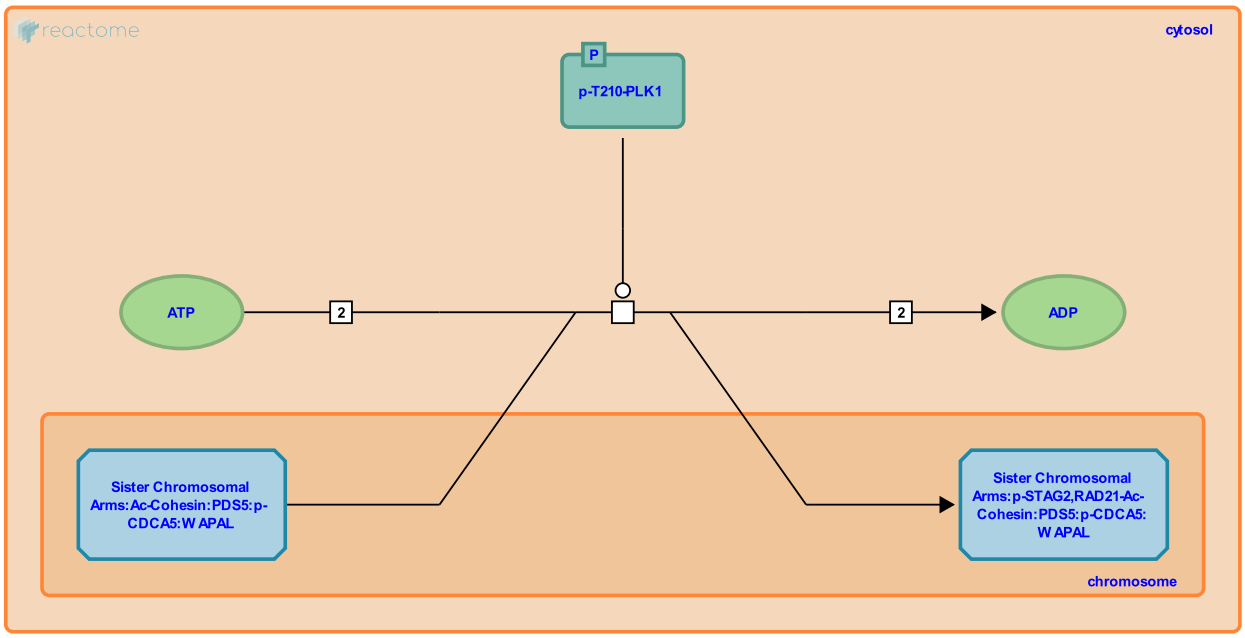
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

Phosphorylation of cohesin by PLK1 at chromosomal arms ↗

Stable identifier: R-HSA-2466068

Type: transition

Compartments: chromosome, cytosol



Prior to anaphase onset, sister-chromatids are held together by cohesin complexes. PLK1-dependent phosphorylation of the cohesin subunit STAG2 (SA2) (Hauf et al. 2005) promotes dissociation of cohesins from chromosomal arms in prometaphase (Hauf et al. 2001). Besides phosphorylating STAG2, PLK1 also phosphorylates RAD21 cohesin subunit, but the phosphorylation of RAD21 is not required for the dissociation of cohesin from chromosomal arms in early mitosis (Hauf et al. 2005). There are several potential PLK1 phosphorylation sites in STAG2 and RAD21, but the exact positions of in vivo phosphorylation of STAG2 and RAD21 by PLK1 have not been explicitly established (Hauf et al. 2005). It is likely that the phosphorylation of cohesin-bound CDCA5 (Sororin) by CDK1 creates a docking site for PLK1 at threonine T159 of CDCA5, thus enabling PLK1 to phosphorylate cohesin subunits (Zhang et al. 2011).

Literature references

Peters, JM., Hauf, S., Waizenegger, IC. (2001). Cohesin cleavage by separase required for anaphase and cytokinesis in human cells. *Science, 293*, 1320-3. ↗

Pati, D., Mao, Q., Panigrahi, AK., Zhang, N. (2011). Interaction of Sororin protein with polo-like kinase 1 mediates resolution of chromosomal arm cohesion. *J. Biol. Chem., 286*, 41826-37. ↗

Roitinger, E., Mechtler, K., Dittrich, CM., Peters, JM., Hauf, S., Koch, B. (2005). Dissociation of cohesin from chromosome arms and loss of arm cohesion during early mitosis depends on phosphorylation of SA2. *PLoS Biol, 3*, e69. ↗

Editions

2004-12-09	Authored	Lee, KS.
2005-04-12	Edited	Gillespie, ME.
2012-10-02	Revised	Orlic-Milacic, M.
2012-10-22	Reviewed	Zhang, N.
2012-11-20	Reviewed	Watanabe, Y., Tanno, Y.