

REV1 recruits POLZ to (AP:Cyt)-DNA Template

Borowiec, JA., Orlic-Milacic, M.

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](#).

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: 75

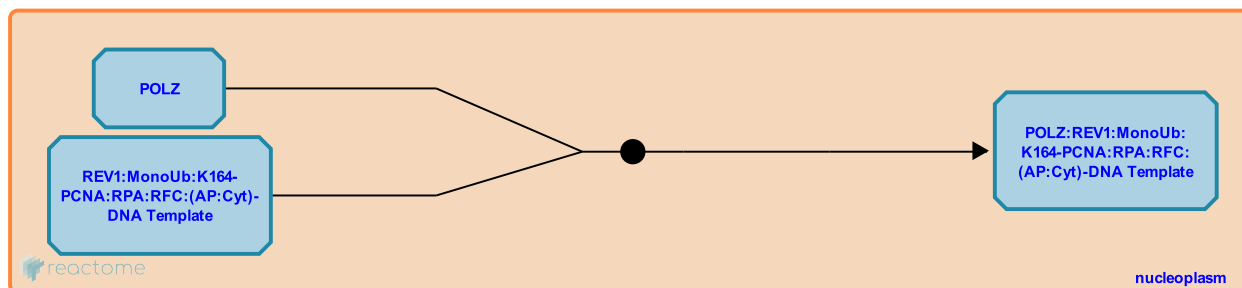
This document contains 1 reaction ([see Table of Contents](#))

REV1 recruits POLZ to (AP:Cyt)-DNA Template ↗

Stable identifier: R-HSA-5652151

Type: binding

Compartments: nucleoplasm



REV1, bound to the replication complex, recruits DNA polymerase zeta (POLZ, REV3L:MAD2L2) to the damaged DNA template. REV3L does not bind REV1 directly. Instead, REV3L binding to MAD2L2 (REV7) during the formation of POLZ complex causes a conformational change in MAD2L2 that allows the C-terminal domain of MAD2L2 to bind the C-terminus of REV1 (Nelson et al. 1996, Hara et al. 2010, Kikuchi et al. 2012, Xie et al. 2012)

Literature references

- Kikuchi, S., Hara, K., Shimizu, T., Sato, M., Hashimoto, H. (2012). Structural basis of recruitment of DNA polymerase ? by interaction between REV1 and REV7 proteins. *J. Biol. Chem.*, 287, 33847-52. ↗
- Hara, K., Hashimoto, H., Murakumo, Y., Kobayashi, S., Kogame, T., Unzai, S. et al. (2010). Crystal structure of human REV7 in complex with a human REV3 fragment and structural implication of the interaction between DNA polymerase zeta and REV1. *J. Biol. Chem.*, 285, 12299-307. ↗
- Nelson, JR., Lawrence, CW., Hinkle, DC. (1996). Deoxycytidyl transferase activity of yeast REV1 protein. *Nature*, 382, 729-31. ↗
- Xie, W., Yang, X., Xu, M., Jiang, T. (2012). Structural insights into the assembly of human translesion polymerase complexes. *Protein Cell*, 3, 864-74. ↗

Editions

2014-12-11	Authored, Edited	Orlic-Milacic, M.
2015-01-07	Reviewed	Borowiec, JA.