Displacement of MBD4 glycosylase by APEX1 at the AP site

Borowiec, JA., Matthews, L., Orlic-Milacic, M.

European Bioinformatics Institute, New York University Langone Medical Center, Ontario Institute for Cancer Research, Oregon Health and Science University.

17/09/2019

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. ↗

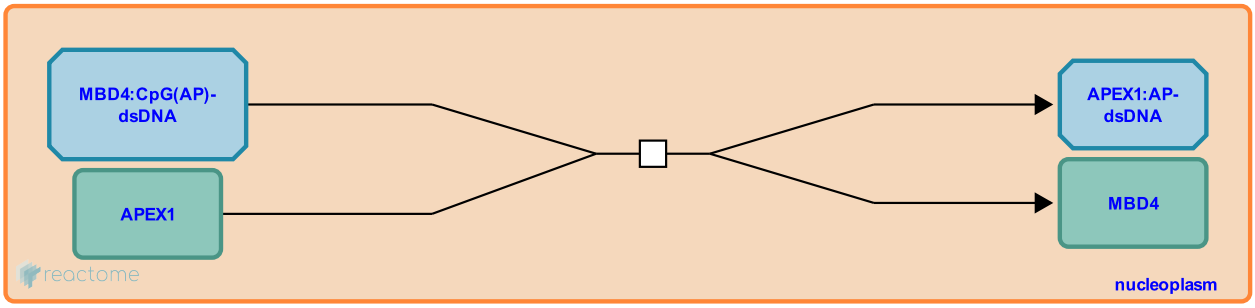
Fabregat, A., Korninger, F., Viteri, G., Sidiropoulos, K., Marin-Garcia, P., Ping, P. et al. (2018). Reactome graph database: Efficient access to complex pathway data. *PLoS computational biology, 14*, e1005968. ↗

Displacement of MBD4 glycosylase by APEX1 at the AP site ↗

Stable identifier: R-HSA-110353

Type: transition

Compartments: nucleoplasm



APEX1 (APE1, HAP1), a DNA apurinic/apyrimidinic (AP) site lyase, displaces MBD4 (MED1) from the AP site generated by the MBD4 DNA glycosylase activity (Kuznetsova et al. 2014).

Literature references

Kuznetsova, AA., Kuznetsov, NA., Ishchenko, AA., Saparbaev, MK., Fedorova, OS. (2014). Pre-steady-state fluorescence analysis of damaged DNA transfer from human DNA glycosylases to AP endonuclease APE1. *Biochim. Biophys. Acta, 1840*, 3042-51. ↗

Editions

2004-02-03	Authored, Edited	Matthews, L.
2014-12-03	Edited, Revised	Orlic-Milacic, M.
2014-12-22	Reviewed	Borowiec, JA.