

MLH1:PMS2 makes single strand incision near 1-2 base mismatch

Edelbrock, MA., May, B.

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](#).

03/05/2024

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. [↗](#)

Reactome database release: 88

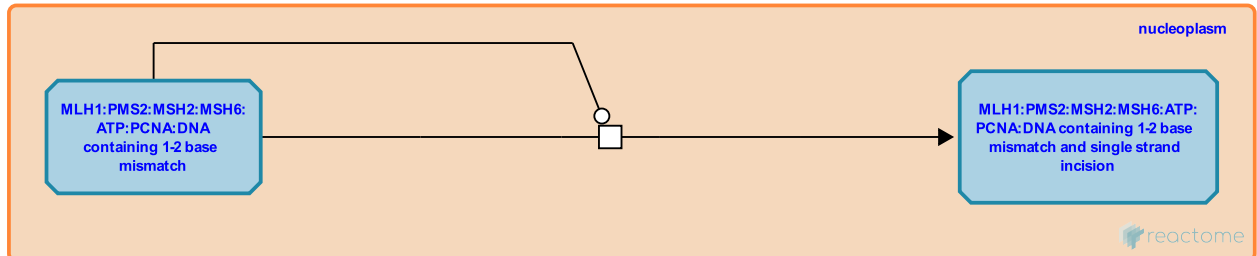
This document contains 1 reaction ([see Table of Contents](#))

MLH1:PMS2 makes single strand incision near 1-2 base mismatch ↗

Stable identifier: R-HSA-5358518

Type: transition

Compartments: nucleoplasm



The latent endonuclease activity of MLH1:PMS2 (MutLalpha) is activated by interaction with MSH2:MSH6 and PCNA (Kadyrov et al 2006). MLH1:PMS2 makes a nick in the replicated strand of DNA. As inferred from yeast, more than one MLH1:PMS2 may bind per MSH2:MSH6 (Hombauer et al. 2011). Strand selection of the nick is determined by interaction with PCNA, though the exact mechanism is unknown (Pluciennik et al 2010).

Literature references

- Gao, Y., Zhang, Y., Li, GM., Yuan, F., Tian, K., Presnell, SR. et al. (2005). Reconstitution of 5'-directed human mismatch repair in a purified system. *Cell*, 122, 693-705. ↗
- Dzantiev, L., Modrich, P., Iyer, RR., Kadyrov, FA., Pluciennik, A., Constantin, N. (2010). PCNA function in the activation and strand direction of MutL α endonuclease in mismatch repair. *Proc. Natl. Acad. Sci. U.S.A.*, 107, 16066-71. ↗
- Dzantiev, L., Modrich, P., Kadyrov, FA., Constantin, N. (2005). Human mismatch repair: reconstitution of a nick-directed bidirectional reaction. *J. Biol. Chem.*, 280, 39752-61. ↗
- Desai, A., Hombauer, H., Kolodner, RD., Smith, CE., Campbell, CS. (2011). Visualization of eukaryotic DNA mismatch repair reveals distinct recognition and repair intermediates. *Cell*, 147, 1040-53. ↗
- Dzantiev, L., Modrich, P., Kadyrov, FA., Constantin, N. (2006). Endonucleolytic function of MutLalpha in human mismatch repair. *Cell*, 126, 297-308. ↗

Editions

2014-03-28	Authored, Edited	May, B.
2014-05-23	Reviewed	Edelbrock, MA.