Formation of meiotic holliday junction

Bolcun-Filas, E., Cohen, PE., Holloway, JK., Lyndaker, A., May, B., Schimenti, JC., Strong, E.

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

26/02/2021

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. ↗

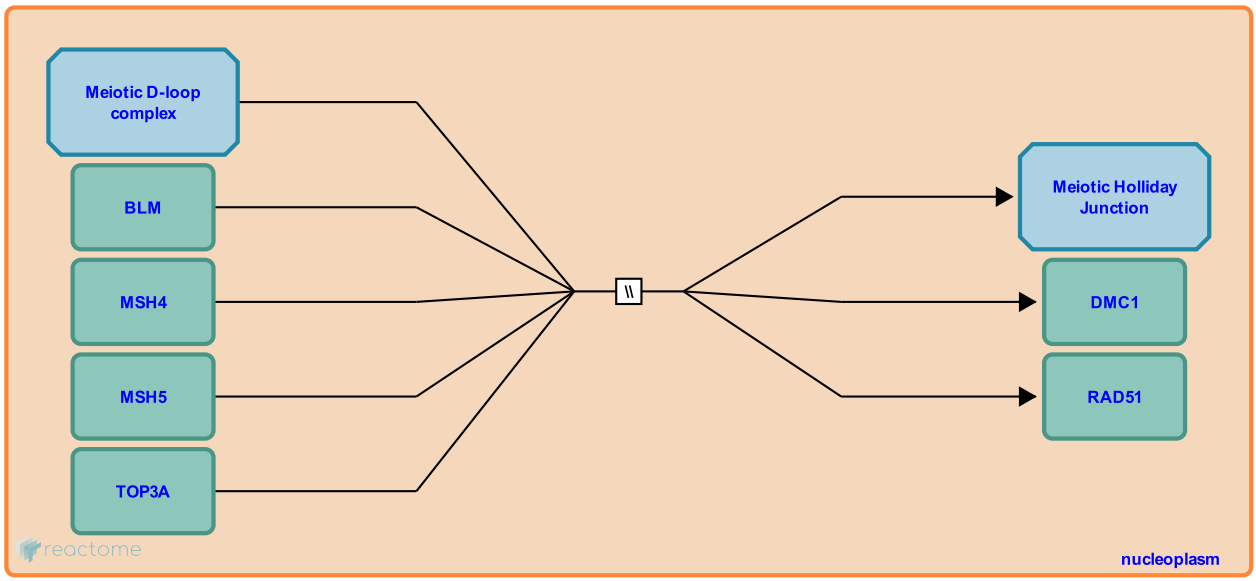
Formation of meiotic holliday junction ↗

Stable identifier: R-HSA-912496

Type: omitted

Compartments: nucleoplasm

Inferred from: Formation of Meiotic Holliday Junction (Mus musculus)



The 3' end of the invading strand is extended by an unknown DNA polymerase and the extended strand is then ligated back to the original homolog, generating a double Holliday junction. MSH4 and MSH5 form heterodimers which bind Holliday junctions and, in the presence of ATP, slide along the parental duplexes (Bocker et al. 1999, Snowden et al. 2004, Snowden et al. 2008). MSH4 is present at hundreds of meiotic nodules during late zygotene but only about 10% of these nodules become crossovers (Oliver-Bonet et al. 2005). Bloom Syndrome protein (BLM) and Topoisomerase IIIa (TOP3A) are also present and may promote homologous recombination repair without crossing over (Johnson et al. 2000, Wu et al. 2000).

Literature references

Oliver-Bonet, M., Turek, PJ., Sun, F., Ko, E., Martin, RH. (2005). Temporal progression of recombination in human males. *Mol Hum Reprod, 11*, 517-22. ↗

Johnson, FB., Lombard, DB., Neff, NF., Mastrangelo, MA., Dewolf, W., Ellis, NA. et al. (2000). Association of the Bloom syndrome protein with topoisomerase IIIalpha in somatic and meiotic cells. *Cancer Res, 60*, 1162-7. ↗

Wu, L., Davies, SL., North, PS., Goulaouic, H., Riou, JF., Turley, H. et al. (2000). The Bloom's syndrome gene product interacts with topoisomerase III. *J Biol Chem, 275*, 9636-44. ↗

Bocker, T., Barusevicius, A., Snowden, T., Rasio, D., Guerrette, S., Robbins, D. et al. (1999). hMSH5: a human MutS homologue that forms a novel heterodimer with hMSH4 and is expressed during spermatogenesis. *Cancer Res, 59*, 816-22. ↗

Snowden, T., Shim, KS., Schmutte, C., Acharya, S., Fishel, R. (2008). hMSH4-hMSH5 adenosine nucleotide processing and interactions with homologous recombination machinery. *J Biol Chem, 283*, 145-54. ↗

Editions

2010-07-03	Authored, Edited	May, B.
2011-02-05	Reviewed	Schimenti, JC., Cohen, PE., Holloway, JK.
2011-02-25	Reviewed	Bolcun-Filas, E., Lyndaker, A., Strong, E.