MSH2:MSH6 binds 1 base mismatch or 1-2 base insertion/deletion loop

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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.

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Literature references

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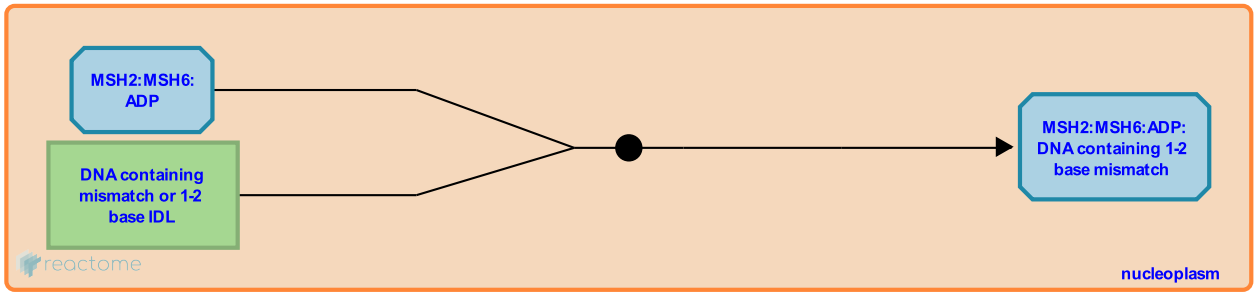
Stable identifier: R-HSA-5358525

Type: binding

Compartments: nucleoplasm



The MSH2:MSH6 (MutSalpha) heterodimer binds single base mismatches and insertion or deletion loops (IDLs) of 1-2 bases (Drummond et al. 1997, Genschel et al. 1998, Gradia et al. 2000, Zhang et al. 2005, Constantin et al. 2005, Tian et al. 2009, reviewed in Edelbrock et al. 2013). The MSH6 subunit contains a Phe-X-Glu motif that binds the mismatched base (Dufner et al 2000, Warren et al. 2007). During replication most nuclear MSH2:MSH6 is observed to colocalize with PCNA via an interaction between PCNA and MSH6 at replication forks during S phase (Kleczkowska et al. 2001), presumably coupling mismatch repair to DNA replication. The MSH6 subunit of MSH2:MSH6 also binds histone H3 methylated at lysine-36, which is enriched in chromatin during G1 and early S phase (Li et al. 2013).

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Editions

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