AGO1,2:small RNA complexes interact with chromatin

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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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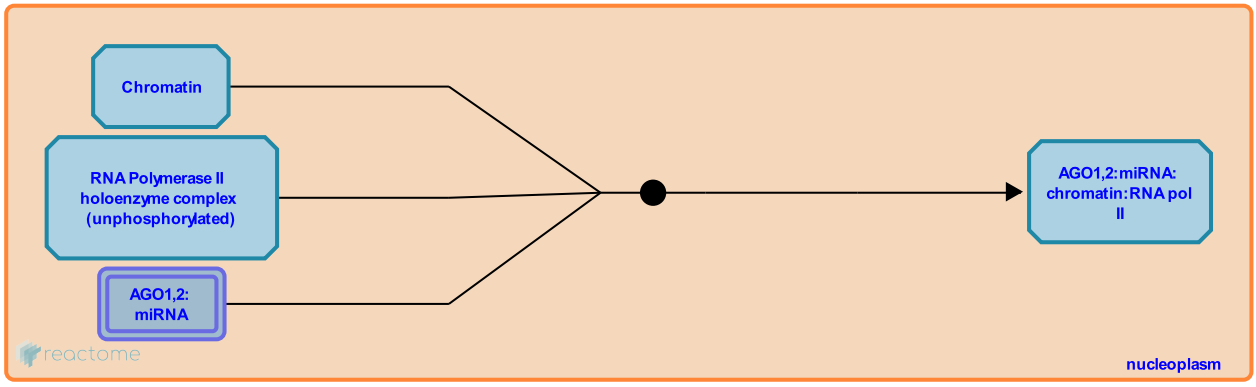
Stable identifier: R-HSA-5578742

Type: binding

Compartments: nucleoplasm



Complexes containing small RNAs and AGO1 or AGO2 are observed within the nucleus and at the inner nuclear envelope, respectively, associated with the actin cytoskeleton (Ahlenstiel et al. 2012, Huang et al. 2013). Argonaute:miRNA complexes associate with genomic regions possessing sequences that match the miRNA, possibly via RNA transcripts tethered to chromatin (Li et al. 2006, Weinber et al. 2006, Kim et al. 2008, Younger and Corey 2011). AGO2:miRNA appears to be in complexes containing DICER and TNRC6A (Gagnon et al. 2014) and AGO1 has been shown to associate with RNA polymerase II, TARBP2, and EZH2 at transcriptionally silenced promoters (Kim et al. 2006, Huang et al. 2013). AGO1 also associates with RNA polymerase II at active promoters (Huang et al. 2013). Other AGO:miRNA complexes may form similar complexes.
Association of AGO:miRNA complexes with genes may cause transcriptional activation (Li et al. 2006), transcriptional repression (Kim et al. 2008, Younger and Corey 2011), alternative splicing (Ameyar-Zazoua et al. 2012), or DNA repair (Francia et al. 2012, Wei et al. 2012). The determinants for transcriptional activation and repression are not known. Transcriptional effects are mediated through changes in histone methylation, especially methylation of histone H3 at lysine-4, lysine-9, and lysine-27 (Li et al. 2006, Kim et al. 2006, Kim et al. 2008, Younger and Corey 2011).

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Editions

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