# SnapShot: Chromatin Remodeling: ISWI

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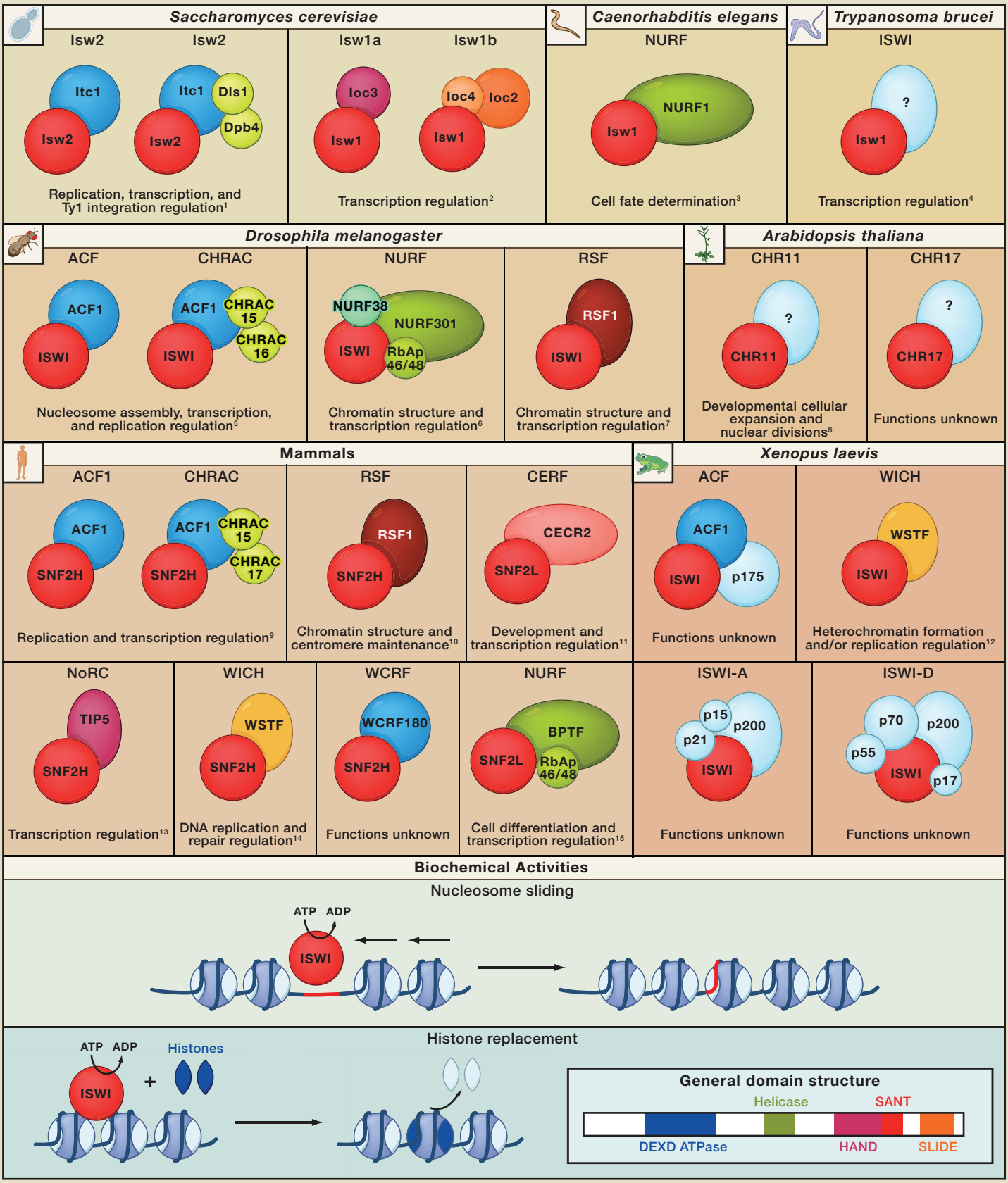




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Cell

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The imitation *s*witch (ISWI) family of ATP-dependent chromatin-remodeling enzymes comprises highly conserved protein complexes that utilize the energy of ATP hydrolysis to slide nucleosomes along DNA and/or replace histones within nucleosomes. All ATP-dependent chromatin-remodeling complexes, including the ISWI family, contain a conserved catalytic DEXD ATPase domain and a helicase domain. However, the combination of three C-terminally located domains, known as HAND, SANT, and SLIDE, is unique to ISWI family members. The SANT domain (structurally related to the c-Myb DNA-binding domains) binds unmodified histone tails, the SLIDE (SANT-like ISWI domain) domain binds nucleosomal DNA near the dyad axis, and the HAND domain is implicated in both histone and DNA binding/recognition. Representative ISWI-containing protein complexes from multiple species are depicted in this SnapShot, with specific in vivo biological functions for each listed below.

## Biological Functions of ISWI-Containing Complexes

***1. Replication, Transcription, and Ty Integration Regulation***
Facilitates replication fork progression through late-replicating regions; represses mRNA and cryptic noncoding RNA transcription by negatively regulating NFR size; required for the periodic integration pattern of the Ty1 retrotransposon.

***2. Transcription Regulation***
Represses and activates transcription at a small number of loci and is implicated in transcription elongation and termination regulation.

***3. Cell Fate Determination***
Promotes the expression of vulval cell fates by antagonizing the transcriptional and chromatin-remodeling activities of complexes similar to Myb-MuvB/dREAM, NuRD, and Tip60/NuA4.

***4. Transcription Regulation***
Downregulates VSV expression sites.

***5. Nucleosome Assembly, Transcription, and Replication Regulation***
Required for the establishment and/or maintenance of periodic nucleosome arrays that contributes to pericentric position-effect variegation (PEV) and heterochromatic *Polycomb*-mediated transcriptional gene silencing; implicated in the regulation of S phase length/progression.

***6. Chromatin Structure and Transcription Regulation***
Maintains higher-order chromatin structure by mediating chromatin compaction; disrupts the enhancer-blocking function of Fab7 and SF1 while augmenting the function of Fab8; activates transcription of GAGA target genes and ecdysone-responsive genes and is a coactivator of Armadillo; regulates innate immunity by repressing transcription of JAK/STAT target genes.

***7. Chromatin Structure and Transcription Regulation***
Involved in formation of silent heterochromatin by incorporating the histone variant H2Av, thus suppressing position-effect variegation (PEV).

***8. Developmental Cellular Expansion and Nuclear Divisions***
Necessary for cell expansion during late-diploid (sporophytic) embryogenesis and mitotic nuclear divisions during haploid (gametophytic) phase.

***9. Replication and Transcription Regulation***
Required for S phase progression and facilitates pericentromeric heterochromatin DNA replication; represses transcription of the vitamin D3 receptor-regulated genes in humans.

***10. Chromatin Structure and Centromere Maintenance***
Implicated in chromatin assembly and actively supports the assembly of CENP-A chromatin in humans.

***11. Development and Transcription Regulation***
Functions in neural tube formation and terminal differentiation of ovarian granulose cells through regulation of *StAR* gene expression in mice.

***12. Heterochromatin Formation and/or Replication Regulation***
Targeted to pericentromeric heterochromatin during early stages of chromosome condensation and DNA replication.

***13. Transcription Regulation***
Involved in the transcriptional repression of ribosomal RNA genes.

***14. DNA Replication and Repair Regulation***
Implicated in heterochromatin DNA replication by binding PCNA in mice; necessary for cell survival following DNA damage by methyl methanesulfate (MMS); and facilitates a DNA damage response pathway by controlling histone H2A.Z function in mice.

***15. Cell Differentiation and Transcription Regulation***
Promotes neurite outgrowth and transcription of *engrailed 1* and *2* in humans.

## ACKNOWLEDGMENTS

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